	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
2	a1	anthocyaninless1	GRMZM2G026930	B73 RefGen_v3	Gene	Chr3	216386031	216387865	a1	a1, anthocyaninless1, bnl(a1), gsy38(A1), npi467, npi51, umc199(a1)	colorless aleurone, green or brown plant; brown pericarp with P1-rr
3	a2	anthocyaninless2	GRMZM2G345717	B73 RefGen_v3	Gene	Chr5	66136522	66139360	a2	a2, anthocyaninless2	like a1, but red pericarp with P1-rr
4	a4	anthocyaninless4	GRMZM2G013726	B73 RefGen_v3	Gene	Chr8	145645771	145647394	a4	A1*, a1(6), a4, anthocyaninless4, bnl17.01, umc189a, umc189(a1), umc189a(a1)	in tissues analyzed-cob, husks, kernel; function of gene product not known (Bernhardt et al. 1998)
5	aaa1	adenosylmethionine aminotransferase1	GRMZM5G817886	B73 RefGen_v3	Gene	Chr2	10216755	10222011	aaa1	aaa1, adenosylmethionine aminotransferase1, PCO069643, pco069643(115), uaz113, uaz113(gfu)	endosperm cDNA 5C01E09 (uaz113) similar to bacterial biotin synthesis enzyme
6	aap1	acylaminoacyl-peptidase1	GRMZM2G120302	B73 RefGen_v3	Gene	Chr9	7579688	7587102	aap1	aap1, acylaminoacyl-peptidase1, PCO061185, uaz5c09a06(gfu)	endosperm cDNA 5C09A06, similar to acylaminoacyl-peptidase
7	aasr1	abscisic acid stress ripening1	GRMZM2G136910	B73 RefGen_v3	Gene	Chr10	8852553	8853933	aasr1	csu103(hupm), csu250a, csu250a(aba), csuh103, gnp_L346, gpm930, hhp1, IDP9044, phi059, umc1582, umc364(gfu), ZmAsr1	protects the major ARS protein in maize; protects kernel yield under water deficit; SSR pio059, IDP9044
8	aasr2	abscisic acid stress ripening2	GRMZM5G854138	B73 RefGen_v3	Gene	Chr2	139700113	139701207	aasr2	aasr2, abscisic acid stress ripening2, csu850, csu851a, csuh00850, csuh850, ZmASR2	
9	aasr3	abscisic acid stress ripening3	GRMZM2G044132	B73 RefGen_v3	Gene	Chr2	54473360	54474872	aasr3	aasr3, abscisic acid stress ripening3, pco156020, umc2088, ZmASR3	
10	aasr5	abscisic acid stress ripening5	GRMZM2G052100	B73 RefGen_v3	Gene	Chr10	116077391	116078438	aasr5	aasr5, aba5, abscisic acid stress ripening5, AY109698, CL4149_1, IDP2437, ZmASR5	
11	aasr6	abscisic acid stress ripening6	GRMZM2G057841	B73 RefGen_v3	Gene	Chr5	171162247	171162872	aasr6	aasr6, aba6, abscisic acid stress ripening6, abscisic stress-ripening protein 3-like, TIDP9149, ZmASR6	
12	aasr7	abscisic acid stress ripening7	GRMZM2G014797	B73 RefGen_v3	Gene	Chr3	65662114	65662673	aasr7	aasr7, aba7, abscicic acid stress ripening7, ZmASR7-1	
13	aasr8	abscisic acid stress ripening8	GRMZM2G314075	B73 RefGen_v3	Gene	Chr3	65665421	65666059	aasr8	aasr8, aba8, abscisic acid stress ripening8, ZmASR7-2	
14	aasr9	abscisic acid stress ripening9	GRMZM2G383699	B73 RefGen_v3	Gene	Chr3	65739867	65740452	aasr9	aasr9, aba9, abscisic acid stress ripening9, IDP6829, ZmASR7-3	
15	abc1	ABC(yeast) homolog1	GRMZM2G157369	B73 RefGen_v3	Gene	Chr4	171570493	171575379	abc1	abc1, ABC(yeast) homolog1, CL26230_1, CL26230_1(329), activator of cytochrom bc1 complex (ABC1) kinases, uaz263, uaz263(gfu), uaz5c06a01	endosperm cDNA 5C05H02(uaz263) similar to yeast ABC1 protein
16	abcf1	ABC family1	GRMZM2G105570	B73 RefGen_v3	Gene	Chr2	229565962	229569990	abcf1	abcf1, ATP-binding cassette transporterF1, PCO135043	transmembrane transport
17	abcg11	ABC transporter G family member 11	GRMZM2G177812	B73 RefGen_v3	Gene	Chr2	24498593	24503843	abcg11	abcg11, ATP-binding cassette transporterG11, gnp_QCF18c07a, gnp_QCF5a04, gpm627a, gpm636, PCO068684	cassette transporter; cutin transport to extracellular matrix. Ortholog of Arabidopsis ABCG11/COF1/WBC11. Plasma membrane-localized ATP-binding cassette transporter; cutin
18	abh1	abscisic acid 8'-hydroxylase1	GRMZM2G179147	B73 RefGen_v3	Gene	Chr5	200705194	200707991	abh1	ABA8ox1a, abh1, CYP707A3, PCO110502(446), PCO110502b	
19	abh2	abscisic acid 8'-hydroxylase2	GRMZM2G126505	B73 RefGen_v3	Gene	Chr4	159692123	159694949	abh2	ABA8ox1b, abh2, bnl29(pds2), PCO110502a, umc1299	
20	abh3	abscisic acid 8'-hydroxylase3	GRMZM2G105954	B73 RefGen_v3	Gene	Chr4	57970815	57976241	abh3	ABA8ox2, abh3, abscisic acid 8'-hydroxylase3	
21	abh4	abscisic acid 8'-hydroxylase4	GRMZM2G065928	B73 RefGen_v3	Gene	Chr7	126008605	126011545	abh4	ABA8Ox3a, abh4, abscisic acid 8'-hydroxylase4	
22	abh5	abscisic acid 8'-hydroxylase5	GRMZM2G002142	B73 RefGen_v3	Gene	Chr2	186842961	186845670	abh5	ABA8Ox3b, abh5, abscisic acid 8'-hydroxylase5	
23	abi10	ABI3-VP1-transcription factor 10	AC193767.3_FG003	B73 RefGen_v3	Gene	Chr10	148761047	148762234	abi10		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
24	abi11	ABI3-VP1-transcription factor 11	GRMZM2G065478	B73 RefGen_v3	Gene	Chr1	165089891	165092452	abi11		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
25	abi12	ABI3-VP1-transcription factor 12	GRMZM2G102059	B73 RefGen_v3	Gene	Chr2	15033794	15035837	abi12		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
26	abi13	ABI3-VP1-transcription factor 13	GRMZM2G018336	B73 RefGen_v3	Gene	Chr5	28659785	28661138	abi13		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
27	abi14	ABI3-VP1-transcription factor 14	GRMZM2G106673	B73 RefGen_v3	Gene	Chr4	26518896	26526586	abi14		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
28	abi15	ABI3-VP1-transcription factor 15	GRMZM2G361376	B73 RefGen_v3	Gene	Chr3	232108213	232112166	abi15		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
29	abi16	ABI3-VP1-transcription factor 16	GRMZM2G024948	B73 RefGen_v3	Gene	Chr5	196729019	196731042	abi16		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
30	abi17	ABI3-VP1-transcription factor 17	GRMZM2G017187	B73 RefGen_v3	Gene	Chr2	48136356	48141220	abi17		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
31	abi18	ABI3-VP1-transcription factor 18	GRMZM2G019956	B73 RefGen_v3	Gene	Chr5	18152128	18154870	abi18		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
32	abi19	ABI3-VP1-transcription factor 19	GRMZM2G035701	B73 RefGen_v3	Gene	Chr8	154216668	154220485	abi19	ZmAFL2	and assigned to a transcription factor family by the GRASSIUS project (Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
33	abi2	ABI3-VP1-transcription factor 2	GRMZM2G018485	B73 RefGen_v3	Gene	Chr10	134624802	134626574	abi2		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
34	abi20	ABI3-VP1-transcription factor 20	GRMZM2G313737	B73 RefGen_v3	Gene	Chr8	155378968	155387313	abi20		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
35	abi21	ABI3-VP1-transcription factor 21	GRMZM2G126194	B73 RefGen_v3	Gene	Chr10	109396005	109397093	abi21		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
36	abi22	ABI3-VP1-transcription factor 22	GRMZM2G008356	B73 RefGen_v3	Gene	Chr7	157708697	157716763	abi22	abi22, ABI3-VP1-transcription factor 22, hca1, PCO071471, pco071471(576), uaz199, uaz5c04c07, ZmAFL1	assigned to a transcription factor family by the GRASSIUS project (Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
37	abi23	ABI3-VP1-transcription factor 23	GRMZM2G180168	B73 RefGen_v3	Gene	Chr10	78160467	78161649	abi23		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
38	abi24	ABI3-VP1-transcription factor 24	GRMZM2G088413	B73 RefGen_v3	Gene	Chr1	254478910	254482162	abi24		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
39	abi25	ABI3-VP1-transcription factor 25	GRMZM2G344521	B73 RefGen_v3	Gene	Chr1	254590445	254594484	abi25		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
40	abi26	ABI3-VP1-transcription factor 26	GRMZM2G423393	B73 RefGen_v3	Gene	Chr10	67375028	67375918	abi26		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
41	abi27	ABI3-VP1-transcription factor 27	GRMZM2G123461	B73 RefGen_v3	Gene	Chr1	180722884	180724089	abi27		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
42	abi28	ABI3-VP1-transcription factor 28	GRMZM2G109879	B73 RefGen_v3	Gene	Chr2	103802791	103809253	abi28		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
43	abi29	ABI3-VP1-transcription factor 29	GRMZM2G084173	B73 RefGen_v3	Gene	Chr6	68219540	68224677	abi29		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
44	abi3	ABI3-VP1-transcription factor 3	GRMZM2G149940	B73 RefGen_v3	Gene	Chr2	1684944	1691150	abi3	abi3, ABI3-VP1-transcription factor 3, ZmAFL4	and assigned to a transcription factor family by the GRASSIUS project (Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
45	abi30	ABI3-VP1-transcription factor 30	GRMZM2G088427	B73 RefGen_v3	Gene	Chr1	254487577	254489679	abi30		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
46	abi31	ABI3-VP1-transcription factor 31	GRMZM2G177244	B73 RefGen_v3	Gene	Chr3	165897795	165900405	abi31		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
47	abi32	ABI3-VP1-transcription factor 32	GRMZM2G158162	B73 RefGen_v3	Gene	Chr7	173216702	173223537	abi32		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
48	abi33	ABI3-VP1-transcription factor 33	GRMZM2G065538	B73 RefGen_v3	Gene	Chr8	152001159	152002001	abi33		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
49	abi34	ABI3-VP1-transcription factor 34	GRMZM2G125095	B73 RefGen_v3	Gene	Chr1	83653655	83654919	abi34		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
50	abi35	ABI3-VP1-transcription factor 35	GRMZM5G834874	B73 RefGen_v3	Gene	Chr5	181252639	181256424	abi35		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
51	abi36	ABI3-VP1-transcription factor 36	GRMZM2G001048	B73 RefGen_v3	Gene	Chr4	14748387	14751790	abi36		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
52	abi37	ABI3-VP1-transcription factor 37	GRMZM2G027253	B73 RefGen_v3	Gene	Chr6	56611496	56612170	abi37		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
53	abi38	ABI3-VP1-transcription factor 38	GRMZM2G142999	B73 RefGen_v3	Gene	Chr9	125822461	125823598	abi38		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
54	abi39	ABI3-VP1-transcription factor 39	GRMZM2G172621	B73 RefGen_v3	Gene	Chr2	217651494	217673563	abi39		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
55	abi4	ABI3-VP1-transcription factor 4	GRMZM2G098063	B73 RefGen_v3	Gene	Chr1	254460346	254462461	abi4		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
56	abi40	ABI3-VP1-transcription factor 40	GRMZM2G328742	B73 RefGen_v3	Gene	Chr4	189990840	189992872	abi40		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
57	abi41	ABI3-VP1-transcription factor 41	GRMZM5G805685	B73 RefGen_v3	Gene	Chr10	6074814	6076964	abi41		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
58	abi42	ABI3-VP1-transcription factor 42	GRMZM2G098443	B73 RefGen_v3	Gene	Chr8	96201480	96202346	abi42		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
59	abi43	ABI3-VP1-transcription factor 43	GRMZM2G028794	B73 RefGen_v3	Gene	Chr9	150250653	150252625	abi43		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
60	abi44	ABI3-VP1-transcription factor 44	GRMZM2G405170	B73 RefGen_v3	Gene	Chr10	44129684	44130359	abi44		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
61	abi45	ABI3-VP1-transcription factor 45	GRMZM2G174610	B73 RefGen_v3	Gene	Chr6	154832684	154837678	abi45		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
62	abi46	ABI3-VP1-transcription factor 46	GRMZM2G065496	B73 RefGen_v3	Gene	Chr1	165085207	165088108	abi46		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
63	abi47	ABI3-VP1-transcription factor 47	GRMZM2G125596	B73 RefGen_v3	Gene	Chr4	195559254	195562953	abi47	ZmAFL6	assigned to a transcription factor family by the GRASSIUS project (Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
64	abi48	ABI3-VP1-transcription factor 48	GRMZM2G111123	B73 RefGen_v3	Gene	Chr3	221999802	222002668	abi48		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
65	abi49	ABI3-VP1-transcription factor 49	GRMZM2G405699	B73 RefGen_v3	Gene	Chr6	267970	270851	abi49	ABI3-VP1-transcription factor 49, abi49, ZmAFL5	and assigned to a transcription factor family by the GRASSIUS project (Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
66	abi5	ABI3-VP1-transcription factor 5	GRMZM2G320754	B73 RefGen_v3	Gene	Chr5	18103497	18105325	abi5		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
67	abi50	ABI3-VP1-transcription factor 50	GRMZM2G102938	B73 RefGen_v3	Gene	Chr6	57753651	57755275	abi50		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
68	abi51	ABI3-VP1-transcription factor 51	GRMZM2G173321	B73 RefGen_v3	Gene	Chr10	65200137	65213038	abi51		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
69	abi6	ABI3-VP1-transcription factor 6	GRMZM2G160224	B73 RefGen_v3	Gene	Chr1	25616688	25619269	abi6		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
70	abi7	ABI3-VP1-transcription factor 7	GRMZM2G109480	B73 RefGen_v3	Gene	Chr1	17698816	17700801	abi7		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
71	abi8	ABI3-VP1-transcription factor 8	GRMZM2G082227	B73 RefGen_v3	Gene	Chr1	4541352	4542978	abi8		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
72	abi9	ABI3-VP1-transcription factor 9	GRMZM2G522066	B73 RefGen_v3	Gene	Chr1	165099882	165101147	abi9		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
73	abil1	abelson interactor1-like protein1	GRMZM5G832362	B73 RefGen_v3	Gene	Chr3	226961580	226962818	abil1	ABI-1-like protein, abil1	
74	abk1	aurora b kinase1	GRMZM2G132116	B73 RefGen_v3	Gene	Chr3	6793085	6797402	abk1	abk1	
75	abp1	auxin binding protein1	GRMZM2G116204	B73 RefGen_v3	Gene	Chr3	133916691	133921441	abp1	abp1, aux311, auxin binding protein1, axr1	putative auxin receptor; single band in Southerns, endoplasmic reticulum and plasma membrane locales (aka axr1, aux311)
76	abp4	auxin binding protein homolog4	GRMZM2G064371	B73 RefGen_v3	Gene	Chr10	26670823	26673897	abp4	abp4, auxin binding protein homolog4, CL1150_1, cl1150_1(726), Zm-ERabp4	putative auxin receptor; genomic clone, promoter-reporter gene fusion functional in maize leaf protoplasts. cDNA ZmERabp4 probes one band on Southerns
77	abph1	aberrant phyllotaxy1	GRMZM2G035688	B73 RefGen_v3	Gene	Chr2	28104302	28109281	abph1	aberrant phyllotaxy1, abph1, abphyl, response regulator3, rs129036669, rs131175414, rs131175415, rs131175416, rs131175417, ss196415049, ss196415051, ZmOrphan266, ZmRR3	decussate leaves and ear shoots (opposite at nodes) frequent; variable, recessive
78	AC199769		GRMZM2G333861	B73 RefGen_v3	BAC	Chr8	163203515	163205870	AC199769	c0274C20	
79	AC210173.4_FG005		AC210173.4_FG005	B73 RefGen_v3	Gene	Chr1	224102016	224105678	AC210173.4_F	cytochrome P450 84A1-like, ZmF5H	
80	acb1	Acyl-CoA-binding protein1	GRMZM2G079908	B73 RefGen_v3	Gene	Chr10	76415905	76418574	acb1	acb1, csu613(acb), PCO107996af, rgpr1908b(acb)	
81	acc1	acetyl-coenzyme A carboxylase1	AC197672.3_FG002	B73 RefGen_v3	Gene	Chr10	98149608	98168566	acc1	acc1, acc2, acc*-pA4, acc*-U90128, acetyl CoA carboxylase*-pA4, acetyl-CoA carboxylase A candidate, acetyl-CoA carboxylase II, CL2223_1a, gnp_QCG7e03, gpm656, MR3, pA4	tissue-culture selected resistance to cyclohexanedione (e.g., sethoxydim) and aryloxy phenoxypropionate (e.g., haloxyfop) herbicides; encodes acetyl-CoA carboxylase
82	acc2	acetyl-CoA carboxylase2	GRMZM5G858094	B73 RefGen_v3	Gene	Chr2	83024018	83036516	acc2	acc2, ACCase II, accB, acc*-pA3, Acc-S2, acc*-U19183, acetyl CoA carboxylase*-pA3, acetyl-coenzyme A carboxylase I, CL2223_1b, MR1, MR2, pA3, umn1, umn1(acc), umng1, umng2	graminicide (e.g., sethoxydim, haloxyfop) resistance; encodes acetyl-CoA carboxylase
83	acco1	1-aminocyclopropane-1-carboxylate oxid	GRMZM2G164883	B73 RefGen_v3	Gene	Chr6	104114291	104115533	acco1	acco1, ZmACOA	
84	acco15	1-aminocyclopropane-1-carboxylate oxid	GRMZM2G166639	B73 RefGen_v3	Gene	Chr10	90488171	90489769	acco15	acco15, ZmACO15	
85	acco2	1-aminocyclopropane-1-carboxylate oxid	GRMZM2G007249	B73 RefGen_v3	Gene	Chr7	124313854	124315851	acco2	acco2, cl955_1, cl955_1(563), ZmACOB	
86	acco20	1-aminocyclopropane-1-carboxylate oxid	GRMZM2G126732	B73 RefGen_v3	Gene	Chr4	177657802	177660210	acco20	acco20, ACC oxidase20, ACO20, ZmACO20	
87	acco3	1-aminocyclopropane-1-carboxylate oxid	GRMZM2G166616	B73 RefGen_v3	Gene	Chr10	90480467	90481799	acco3	acco3, ZmACOC	
88	acco31	1-aminocyclopropane-1-carboxylate oxid	GRMZM2G072529	B73 RefGen_v3	Gene	Chr10	90301775	90303069	acco31	acco31, ZmACO31	
89	acco35	1-aminocyclopropane-1-carboxylate oxid	GRMZM2G052422	B73 RefGen_v3	Gene	Chr5	210825846	210828416	acco35	1-aminocyclopropane-1-carboxylate oxidase 1, acco35, ACC oxidase35, PCO145638(452), PCO145638b, ZmACO35	
90	acco4	1-aminocyclopropane-1-carboxylate oxid	GRMZM2G332423	B73 RefGen_v3	Gene	Chr10	90448978	90450072	acco4	acco4, ZmACOD	
91	ache1	acetylcholinesterase1	GRMZM6G953609	B73 RefGen_v3	Gene	scaffold_:9		854	ache1	acetylcholinesterase1, AChE, ache1, alpha-L-fucosidase 2 precursor, PCO131316	
92	aco1	aconitase1	GRMZM2G020801	B73 RefGen_v3	Gene	Chr4	28147612	28154163	aco1	aco1, aconitase1	electrophoretic mobility; monomeric
93	aco2	aconitase2	GRMZM5G858454	B73 RefGen_v3	Gene	Chr10	96344573	96353240	aco2	aco2, IDP1618, PCO139346	electrophoretic mobility
94	aco3	aconitase3	GRMZM2G009808	B73 RefGen_v3	Gene	Chr9	152030140	152038415	aco3	aco3, aconitase3, pco068697(524)	electrophoretic mobility
95	aco5	aconitase5	GRMZM2G171707	B73 RefGen_v3	Gene	Chr2	203572465	203578306	aco5	aco4, aco5	
96	acp1	acid phosphatase1	AC211394.4_FG004	B73 RefGen_v3	Gene	Chr9	95254430	95260811	acp1	acid phosphatase1, acp1, Acph1, Ap1, Phos, purple acid phosphatase	electrophoretic mobility; cytosolic; dimeric
97	acpt1	acyl carrier protein1	GRMZM2G175818	B73 RefGen_v3	Gene	Chr1	206784775	206787442	acpt1	Acl1, acpt1, acyl carrier protein1, gnp_QAE18b02a, gpm276a, IDP812, IDP862, pco060888, pco060888(64)	acyl carrier protein (acp) cDNA, encodes 121 aa polypeptide, contains transit peptide sequence
98	acs1	1-aminocyclopropane-1-carboxylate synt	GRMZM2G163015	B73 RefGen_v3	Gene	Chr3	6433703	6435769	acs1	accs1, acs1, ZmACSA	
99	acs2	1-aminocyclopropane-1-carboxylate synt	GRMZM2G164405	B73 RefGen_v3	Gene	Chr2	15900748	15904400	acs2	1-aminocyclopropane-1-carboxylate synthase2, accs2, ACC synthase2, acs2, ACS47, ZmACS2, ZmACS7	

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
100	acs3	1-aminocyclopropane-1-carboxylate synt	GRMZM2G018006	B73 RefGen_v3	Gene	Chr9	23963178	23966958	acs3	accs3, acs3, ZmACSB	
101	acs6	1-aminocyclopropane-1-carboxylate synt	GRMZM2G054361	B73 RefGen_v3	Gene	Chr1	271834818	271837308	acs6	1-aminocyclopropane-1-carboxylate synthase6, accs6, ACC synthase6, acs6, ACS65, ZmAcs6, ZmACS6	
102	acs7	1-aminocyclopropane-1-carboxylate synt	GRMZM5G894619	B73 RefGen_v3	Gene	Chr10	136107954	136110772	acs7	1-aminocyclopropane-1-carboxylate synthase7, accs7, ACC synthase7, ACS50, acs7, PCO143423, PCO143423(757), ZmACS2, ZmAcs7	
103	act1	actin1	GRMZM2G126010	B73 RefGen_v3	Gene	Chr8	99906105	99909909	act1	act1, actin 1, bnl(act1), npi368-act1, npi368(act1), PCO080070, phi115	actin, one of six potential genes; genomic DNA clone; 3 introns); SSR phi115
104	act2	actin2	Zm00001d012277	Zm-B73-REFERENCE-G	Gene	Chr8	171775071	171778423	act2	act2, actin2, actin-7, CL1968_3k, Maz89	
105	adf1	actin depolymerizing factor1	GRMZM2G117603	B73 RefGen_v3	Gene	Chr7	148916447	148917753	adf1	actin depolymerizing factor1, adf1, PCO095832, pco095832(571), ZmABP1	pollen-specific cDNA similar to vertebrate actin polymerization/depolymerization factors
106	adf2	actin depolymerizing factor2	GRMZM2G097122	B73 RefGen_v3	Gene	Chr2	200140261	200141322	adf2	actin depolymerizing factor2, adf2, pco095832, pco095832(571), ZmABP2	pollen-specific cDNA similar to vertebrate actin polymerization/depolymerization factors
107	adf3	actin depolymerizing factor3	GRMZM2G060702	B73 RefGen_v3	Gene	Chr1	293239343	293243048	adf3	ABP3, actin depolymerizing factor3, adf3, ADF3, pco115125(102), pco115125a, ZmABP3, ZmADF3	pollen; expressed in E. coli; two copies detected in Southerns and by one overgo (PCO115125a in ctg64, 1L; PCO115125b in ctg204, 5S), which are syntenous regions.
108	adf5	actin depolymerizing factor5	GRMZM2G077942	B73 RefGen_v3	Gene	Chr1	32872877	32876200	adf5	actin depolymerizing factor5, adf5, pco091760, pco091760(14), rs128410876 , rs131232694 , umc1044, umc1073	
109	adh1	alcohol dehydrogenase1	GRMZM2G442658	B73 RefGen_v3	Gene	Chr1	274050254	274054148	adh1	IDP35, magi75238, npi21-adh1, npi21(adh1), PCO141653, rgpc496a(adh), umc1726, umc(adh1)	electrophoretic mobility; null alleles are known; dimeric; intra/interlocus hybrid bands occur); SSR umc1726
110	adh2	alcohol dehydrogenase2	GRMZM2G098346	B73 RefGen_v3	Gene	Chr4	13409584	13412986	adh2	adh2, alcohol dehydrogenase2, nc004, npi228-adh2, phi021, rgpc496b(adh), umc200a, umc200a(adh2)	electrophoretic mobility, null alleles are known; dimeric, intra/interlocus hybrid bands occur; SSRs nc004, phi021
111	adk1	adenylate kinase1	GRMZM2G178192	B73 RefGen_v3	Gene	Chr6	2450158	2455264	adk1	adenylate kinase1, adk1, pco088037(462), pco088037a	electrophoretic mobility; plastidial
112	adss1	adenylosuccinate synthetase	GRMZM2G119852	B73 RefGen_v3	Gene	Chr1	15773077	15777890	adss1	adenylosuccinate synthetase, ads1, adss1, CL2010_1, pza02094	
113	adt6	arogenate dehydratase6	GRMZM2G437912	B73 RefGen_v3	Gene	Chr2	59667646	59669581	adt6	adt6	
114	adxr1	adrenodoxin reductase1	Zm00001d053301	Zm-B73-REFERENCE-G	Gene	Chr4	225026663	225038512	adxr1	pco114328(55)	
115	ae1	amylose extender1	GRMZM2G032628	B73 RefGen_v3	Gene	Chr5	168492139	168509225	ae1	ae1, amylose extender1, AY109532, CL1742_1, ha1, high amylose1, rs131175699, rs131175700, Sbe, sbe2, ss196416186, ss196416189, starch branching enzyme2	glassy, tarnished endosperm; high amylose content; application: highly linear starch is used for food films, fibers, and other industrial purposes
116	afd1	absence of first division1	GRMZM2G059037	B73 RefGen_v3	Gene	Chr6	166795461	166827341	afd1	absence of first division1, afd1, REC8, si618011B05, si618011b05(525)	male and female sterility; early meiosis
117	agal1	alpha-galactosidase1	GRMZM2G095126	B73 RefGen_v3	Gene	Chr1	228378444	228381659	agal1	agal1, CL6071_1, CL6071_1(71), phi037, phi038, phi039, rs131860003, umc1013, umc128a, umc128(aga), umc128b	Entrez Gene relates to alpha-galactosidase 1 (AGAL) of Arabidopsis
118	ago1	argonaute1	GRMZM2G162525	B73 RefGen_v3	Gene	Chr8	134439555	134444960	ago1	ago1, ago113, argonaute1, cl857_3(631), cl857_3b, gpm630	Proposed to interact with small RNAs in dorsiventral leaf patterning
119	ago101	argonaute101	AC189879.3_FG003	B73 RefGen_v3	Gene	Chr9	87408375	87414276	ago101	AGO10a, gpm721	
120	ago104	argonaute104	GRMZM2G141818	B73 RefGen_v3	Gene	Chr6	168642369	168650358	ago104	ago104, AGO4b, argonaute104, dnr4	
121	ago105	argonaute105	GRMZM2G089743	B73 RefGen_v3	Gene	Chr3	43646012	43657336	ago105	CL881_1	
122	ago108	argonaute108	GRMZM2G461936	B73 RefGen_v3	Gene	Chr5	13611800	13618698	ago108	ago108, ago5a	
123	ago10b	argonaute10b	GRMZM2G079080	B73 RefGen_v3	Gene	Chr6	103286236	103293200	ago10b	ago10b, argonaute PNH1-like	
124	ago18a	argonaute18a	GRMZM2G105250	B73 RefGen_v3	Gene	Chr2	199510528	199516085	ago18a	ago18a, argonaute 18-like, phm7953, PZA02533, rs131980012, ss196415237	
125	ago18b	argonaute18b	GRMZM2G457370	B73 RefGen_v3	Gene	Chr1	250132189	250137737	ago18b	ago18b, cl909_1, cl909_1(82), rs128929565 , rs131877871	
126	ago1a	argonaute1a	GRMZM2G441583	B73 RefGen_v3	Gene	Chr6	43253105	43261555	ago1a	ago1a, argonaute 1B-like, ZmAGO1a	Ortholog of Arabidopsis ago1
127	ago1b	argonaute1b	AC209206.3_FG011	B73 RefGen_v3	Gene	Chr10	137506877	137513415	ago1b	ago1b, argonaute 1B-like, ZmAGO1b	Ortholog of Arabidopsis ago1
128	ago1c	argonaute1c	GRMZM2G039455	B73 RefGen_v3	Gene	Chr2	17563301	17573156	ago1c	ago1c, ZmAGO1c	Ortholog of Arabidopsis ago1
129	ago1d	argonaute1d	GRMZM2G361518	B73 RefGen_v3	Gene	Chr5	64791077	64796881	ago1d	ago1d, argonaute 1D-like, ZmAGO1d, ZmAGO1f	Ortholog of Arabidopsis ago1
130	ago2a	argonaute2a	GRMZM2G007791	B73 RefGen_v3	Gene	Chr2	9973816	9981340	ago2a	ago2a	
131	ago2b	argonaute2b	GRMZM2G354867	B73 RefGen_v3	Gene	Chr10	141823070	141828449	ago2b	ago2b, argonaute 2-like	
132	ago4a	argonaute4a	GRMZM2G589579	B73 RefGen_v3	Gene	Chr8	2511463	2518808	ago4a	ago4a	
133	ago5b	argonaute5b	GRMZM2G059033	B73 RefGen_v3	Gene	Chr2	233385077	233392000	ago5b	ago5b	
134	ago5c	argonaute5c	GRMZM2G123063	B73 RefGen_v3	Gene	Chr5	4001278	4009529	ago5c	ago5c, argonaute MEL1-like, MEIOSIS ARRESTED AT LEPTOTENE 1 (mel1) ortholog	
135	ago6	argonaute6	GRMZM2G347402	B73 RefGen_v3	Gene	Chr7	72044775	72053779	ago6	ago6	
136	agp1	ADP glucose pyrophosphorylase small su	GRMZM2G106213	B73 RefGen_v3	Gene	Chr2	174023583	174034507	agp1	ADP glucose pyrophosphorylase small subunit embryo 1, agp1, agp2, agpsemzm, AY105915, PCO131593, sc237, ufg2, ufg2(agp2), ufg(agp2)	embryo cDNA that hybridizes to endosperm transcripts, distinct from sh2 and bt2 but most similar to the bt2 gene product
137	agp2	ADP glucose pyrophosphorylase2	GRMZM2G027955	B73 RefGen_v3	Gene	Chr6	166787452	166793059	agp2	gpm779, L2, pco103001, PHM5361, PZA00910, rs131175777, rs131175778, sc236, ss196416505, ss196416507, ufg(agp1)	embryo specific counterpart to sh2
138	agpll1	ADP glucose pyrophosphorylase large su	GRMZM2G391936	B73 RefGen_v3	Gene	Chr1	273514151	273518985	agpll1	AGPL4, agpll1, agpllzm, ZmagpL1	
139	agpll2	ADP glucose pyrophosphorylase large su	GRMZM2G144002	B73 RefGen_v3	Gene	Chr7	23769242	23780203	agpll2	AGPL, AGPL3, agpll2	
140	agpsl1	ADP glucose pyrophosphorylase small su	GRMZM2G163437	B73 RefGen_v3	Gene	Chr1	221701404	221705997	agpsl1	bnl17.15b, bnl17.15b(agp), bnl17.15b(bt2), btl1, btl2, gnp_QAN9g11, gpm377, gsy60b(bt2), gsy61(btl2), L2, sc61, SC61B13, siS72425, sis72425(71)	leaf-specific
141	agrr21		GRMZM2G302639	B73 RefGen_v3	Gene	Chr8	172961620	172964067	agrr21	agrr21, AY110127, CL4812_1, PZA02281, rs131175916, ss196417076	NCBI: protein CURVATURE THYLAKOID 1C, chloroplastic
142	ahh1	adenosyl homocysteine hydrolase1	GRMZM2G015295	B73 RefGen_v3	Gene	Chr4	21158461	21161610	ahh1	gpm544a, IDP38, PCO113569, pco113569a, rz900a(ahh), rz900(ahh), TIDP3741, uaz145, UAZ145(AhCH), uaz145(ahh), uaz145(gfu)	endosperm cDNA 5C01H11 (uaz145) similar to plant activated methyl cycle enzyme
143	AI714808		GRMZM2G005346	B73 RefGen_v3	Gene	Chr2	47788105	47793199	AI714808		similar to Arabidopsis protein phosphatase methylesterase 1
144	AI861369		GRMZM6G177089	B73 RefGen_v3	Gene	Chr2	187273065	187274870	AI861369		similar to B. distachyon PREDICTED: receptor-like protein 2-like
145	aic1	auxin import carrier1	GRMZM2G129413	B73 RefGen_v3	Gene	Chr1	119659886	119663853	aic1	aic1, aux1, auxin import carrier1, CL468_2, cl468_2(41), Like Auxin-Resistant 2 (ZmLAX2), umc1689, ZmAUX1	cDNA encoding a protein with a deduced amino acid showing 73% identity to AtAUX1.
146	ak1	Adenylyl-sulfate kinase1	GRMZM2G061234	B73 RefGen_v3	Gene	Chr7	159799011	159812272	ak1	adenosine-5'-phosphosulfate kinase, Adenylyl-sulfate kinase1, ak1, CL95_-2b	
147	ak2	ankyrin repeat protein2	GRMZM2G019838	B73 RefGen_v3	Gene	Chr4	239494965	239497297	ak2	ak2, Ankyrin repeat domain-containing protein EMB506 chloroplastic, pco138649, pco138649(366), PZA01243	
148	akh2	aspartate kinase homoserine dehydroger	GRMZM2G104546	B73 RefGen_v3	Gene	Chr2	173486913	173506976	akh2	akh2, AK-HSDH2, aspartate kinase homoserine dehydrogenase2, CL2352_-1a	cDNA sequence 75% homologous to carrot threonine sensitive AK-HSDH bifunctional enzyme

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
149	akin1	AKINbetagamma-1 protein kinase	GRMZM2G047774	B73 RefGen_v3	Gene	Chr1	299540824	299549015	akin1	akin1, AKINbetagamma-1 protein kinase, CL367_1, csu1114, gnp_QBB7c06a, gpm434a	
150	akr1	aldo/keto reductase AKR1	GRMZM2G052812	B73 RefGen_v3	Gene	Chr6	64079621	64110792	akr1	akr1, auxin induced protein homolog1, csu190, csu190(gfu), In2-2, pco148860, saf2, safener induced2, TIDP3456	leaf cDNA csu190, similar to auxin-induced protein
151	al9	aleurone9	GRMZM2G091054	B73 RefGen_v3	Gene	Chr8	171118734	171119464	al9	al9, al-9, aleurone9	aleurone specific cDNA, unknown function
152	ald1	aldolase1	GRMZM2G057823	B73 RefGen_v3	Gene	Chr3	165765568	165768179	ald1	ald1, aldolase, aldolase1, fructose-bisphosphate aldolase cytoplasmic isozyme	cytosolic aldolase; cDNA and genomic clones; Southern blots give single or double band; promoter functional in transient expression assay
153	ald2	aldolase2	GRMZM2G066024	B73 RefGen_v3	Gene	Chr8	162856704	162859417	ald2	ald2, aldolase2, gnp_QAM23g02, gpm362, umc216(ald1)	second aldolase locus initially found by RFLP mapping using an ald1 probe
154	aldh2	aldehyde dehydrogenase2	GRMZM2G125268	B73 RefGen_v3	Gene	Chr4	165996358	165999622	aldh2	aldehyde dehydrogenase2, aldh2, ALDH2B6, rf2b	complement the ALDH deficient E. coli mutant; mitochondrial location inferred from presence of leader sequence
155	aldh3	aldehyde dehydrogenase3	GRMZM2G071021	B73 RefGen_v3	Gene	Chr3	221771183	221775333	aldh3	aldehyde dehydrogenase 3, ALDH2C2, aldh3, IDP10, IDP9, rf2c	cDNA sequence similar to rf2; complements E. coli JA111 with defective ALDH
156	aldh5	aldehyde dehydrogenase5	GRMZM2G097706	B73 RefGen_v3	Gene	Chr3	221783373	221791498	aldh5	aldehyde dehydrogenase5, ALDH2C3, aldh5, PCO073335, rf2d, rf2d1	cDNA similar to rf2 (prf2d-exprA7); complements E. coli
157	alf1	Alfin-like-transcription factor 1	GRMZM2G148810	B73 RefGen_v3	Gene	Chr6	124888239	124892792	alf1	ZmAL9	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
158	alf10	Alfin-like-transcription factor 10	GRMZM2G050495	B73 RefGen_v3	Gene	Chr10	119722635	119728067	alf10	ZmAL18	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
159	alf11	Alfin-like-transcription factor 11	GRMZM2G158918	B73 RefGen_v3	Gene	Chr8	102976534	102982864	alf11	ZmAL13	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
160	alf12	Alfin-like-transcription factor 12	GRMZM5G893976	B73 RefGen_v3	Gene	Chr8	15276414	15280931	alf12	ZmAL12	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
161	alf13	Alfin-like-transcription factor 13	GRMZM2G080917	B73 RefGen_v3	Gene	Chr3	170149613	170154226	alf13	pco073257a, ZmAL4	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
162	alf14	Alfin-like-transcription factor 14	GRMZM2G156088	B73 RefGen_v3	Gene	Chr10	119489514	119496893	alf14	ZmAL17	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
163	alf15	Alfin-like-transcription factor 15	AC225147.4_FG003	B73 RefGen_v3	Gene	Chr1	292952249	292956375	alf15	ZmAL1	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
164	alf16	Alfin-like-transcription factor 16	GRMZM2G016564	B73 RefGen_v3	Gene	Chr10	119517572	119518319	alf16		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
165	alf17	Alfin-like-transcription factor 17	GRMZM2G110952	B73 RefGen_v3	Gene	Chr5	2576260	2595158	alf17	ZmAL7	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
166	alf18	Alfin-like-transcription factor 18	GRMZM2G008259	B73 RefGen_v3	Gene	Chr4	11403566	11428284	alf18	alf18, AY110398, CL736_1, PZA02358, umc31a, ZmAL5	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
167	alf19	Alfin-like-transcription factor 19	GRMZM2G047316	B73 RefGen_v3	Gene	Chr2	158912747	158917610	alf19	ZmAL2	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
168	alf2	Alfin-like-transcription factor 2	GRMZM2G063864	B73 RefGen_v3	Gene	Chr5	174455049	174458989	alf2	chr111 chromatin complex subunit A, ZmAL8	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
169	alf3	Alfin-like-transcription factor 3	GRMZM2G038066	B73 RefGen_v3	Gene	Chr7	165038048	165044961	alf3	ZmAL11	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
170	alf4	Alfin-like-transcription factor 4	GRMZM2G153087	B73 RefGen_v3	Gene	Chr3	135934895	135940205	alf4	alf4, TIDP3057, ZmAL3	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
171	alf5	Alfin-like-transcription factor 5	GRMZM2G016817	B73 RefGen_v3	Gene	Chr6	147835864	147843229	alf5	ZmAL10	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
172	alf6	Alfin-like-transcription factor 6	GRMZM2G115424	B73 RefGen_v3	Gene	Chr10	31315303	31320114	alf6	ZmAL16	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
173	alf7	Alfin-like-transcription factor 7	GRMZM2G107807	B73 RefGen_v3	Gene	Chr4	120648398	120651921	alf7	ZmAL6	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
174	alf8	Alfin-like-transcription factor 8	GRMZM2G172001	B73 RefGen_v3	Gene	Chr8	164293635	164297965	alf8	ZmAL15	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
175	alf9	Alfin-like-transcription factor 9	GRMZM2G017142	B73 RefGen_v3	Gene	Chr8	125066160	125069152	alf9	ZmAL14	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
176	algt1	alanine--glyoxylate aminotransferase1	GRMZM2G030571	B73 RefGen_v3	Gene	Chr1	56676074	56678959	algt1	alanine--glyoxylate aminotransferase1, algt1, alt6, rs128445321	
177	alp1	aluminum-induced protein homolog1	GRMZM2G003762	B73 RefGen_v3	Gene	Chr10	4676400	4679041	alp1	ALP, alp1, csu359(alp), csu359(gfu), csu577, pco130572(712), PCO130572c	leaf cDNA csu359 similar to wheat aluminum-induced protein, GenBank accession L28008
178	als1	acetolactate synthase1	GRMZM2G143357	B73 RefGen_v3	Gene	Chr4	96832612	96834891	als1	acetolactate synthase1, AHAS109, als1, Als*-109, bnl#(als), dup, dup(als1), MALSb, PZA03231, rs129762878, rs55622883 , ss196415776	sensitive to imidazolinone herbicides; acetohydroxyacid synthase has altered herbicide inhibition kinetics
179	als2	acetolactate synthase2	GRMZM2G143008	B73 RefGen_v3	Gene	Chr5	164024379	164026683	als2	acetolactate synthase2, als1, Als*-108, als2, bnl#(als), dup, dup(als2), MALSa, XA-17	dup(als2) probe. sensitive to imidazolinone herbicides; acetohydroxyacid synthase has altered herbicide inhibition kinetics
180	alt10	alanine aminotransferase10	GRMZM2G124963	B73 RefGen_v3	Gene	Chr2	212180526	212185824	alt10	alt10, idp136, rs131180249, rs131993455	putative alanine aminotransferase weakly expressed in seedling leaf (Tausta et al 2014)
181	alt4	L-alanine:2-oxoglutarate aminotransferas	GRMZM2G088064	B73 RefGen_v3	Gene	Chr5	37251082	37256273	alt4	AlaAT, alt4, L-alanine:2-oxoglutarate aminotransferase4, rz892b(alt), uaz158, uaz158(alt)	the relationship between alt4 and previously reported genes alt1, alt2 or alt3 is not clear as sequences for the latter were not published;
182	alt5	alanine aminotransferase5	GRMZM2G088028	B73 RefGen_v3	Gene	Chr5	37248072	37250198	alt5	AlaAT, alanine aminotransferase5, alt5, CL2764_1, CL2764_1(562), gnp_AW066742, gpm149, PCO123780, PCO123780(562)	putative alanine aminotransferase; found in embryo (Davidson 2011), not reported in seedling leaf (Tausta et al 2014)
183	alt7	alanine aminotransferase7	GRMZM2G120563	B73 RefGen_v3	Gene	Chr7	1309331	1321760	alt7	AlaAT, alanine aminotransferase7, alt7, CL1839_2(547), CL1839_2b, PCO087866(528), PCO087866b, rs131591583	bundle sheath alanine transasminase; see also alt8, alt9
184	alt8	alanine amino transferase8	GRMZM5G840582	B73 RefGen_v3	Gene	Chr2	236204010	236208701	alt8	AlaAT, alanine amino transferase8, alt8, rs129259495, rs129259505, rs129259506	bundle sheath alanine transaminase; see also alt7 and alt9
185	alt9	alanine aminotransferase9	GRMZM2G053999	B73 RefGen_v3	Gene	Chr7	165787766	165790666	alt9	AlaAT, alanine aminotransferase9, alt9, pco113489, pco113489(579), rs130683341	putative leaf alanine transminase
186	am1	ameiotic1	GRMZM5G883855	B73 RefGen_v3	Gene	Chr5	16109038	16115968	am1	am1, am2, am*-485, ameiotic1, pra1	affects switch to meiotic cell cycle. male and female sterility - anaphase I equatorial; alleles am1-pra1(was pra1), am1-2 (was am2)
187	ami1	amidase1	GRMZM2G060400	B73 RefGen_v3	Gene	Chr2	183985910	183988519	ami1	ami1	
188	ami2	amidase2	GRMZM2G137676	B73 RefGen_v3	Gene	Chr7	120006864	120009317	ami2	ami2, amidase2, ZmAMI1	
189	amo1	amine oxidase1	GRMZM2G359298	B73 RefGen_v3	Gene	Chr10	103645937	103651506	amo1	amine oxidase1, amo1, primary amine oxidase-like, rz69	single copy rice cDNA rz69
190	amt1	ammonium transporter1	GRMZM2G175140	B73 RefGen_v3	Gene	Chr10	130101668	130103747	amt1	amt1, ZmAMT1;1a	
191	amt2	ammonium transporter2	GRMZM2G028736	B73 RefGen_v3	Gene	Chr5	185705977	185707950	amt2	amt2, ZmAMT1;3	
192	amt3	ammonium transporter3	GRMZM2G118950	B73 RefGen_v3	Gene	Chr2	28938473	28940284	amt3	amt3, ZmAMT1;1b	
193	amya3	alpha amylase3	GRMZM2G138468	B73 RefGen_v3	Gene	Chr2	186911744	186913606	amya3	alpha amylase3, alpha amylase L25805, amy3, amya3, amy*-L25805, ast, ast(amy4), ast(amyBS2)b, umc223(amy)	aleurone cDNA pMAs5, 94% similarity to rice alpha amylase; possibly identical to amy1
194	amyb2	beta amylase2	GRMZM2G450125	B73 RefGen_v3	Gene	Chr1	9051958	9054939	amyb2	amy2, amyb2, beta amylase2, pco104637, PCO133818a	electrophoretic mobility; monomeric
195	amyb4	beta amylase4	GRMZM2G175218	B73 RefGen_v3	Gene	Chr3	1535920	1540195	amyb4	amy4, amyb4, beta amylase4, PCO082879(199), PCO082879a	sequence similar to rice BAD81275.1| putative beta-amylase PCT-BMYI per D. Lisch
196	amyb5	beta amylase5	GRMZM2G058310	B73 RefGen_v3	Gene	Chr7	155396510	155399710	amyb5	Amy2, amy5, amyb5, amy*-Z25871, ast, ast(amy3), ast(amyBS2)a, CL1598_1, cl1598_1(575), gnp_QAH4e11, gpm343, gsy250(amy), pZMB2	enzyme and cDNA isolated; aleurone layer of germinating seed
197	an1	anther ear1	GRMZM2G081554	B73 RefGen_v3	Gene	Chr1	241277428	241285679	an1	an1, an1.5, an2.6, anther ear1, copalyl diphosphate synthase1, cpps1, cps1, rs131175334, ss196414714, ZmCPS2	andromonoecious dwarf, intermediate stature; few tassel branches; responds to gibberellins; an1-6923 includes deletion of Bz2+

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
198	ane1	androgenic embryo1	GRMZM2G039942	B73 RefGen_v3	Gene	Chr4	222614892	222615724	ane1	AE1, androgenic embryo1, ane1, ensl002b, ZmAE1	multigene family; sequence suggests extracellular location; expressed in embryo surrounding region of developing endosperm and in basal endosperm transfer layer
199	ane3	androgenic embryo3	GRMZM2G372553	B73 RefGen_v3	Gene	Chr10	80752876	80753536	ane3	ae3, AE3, androgenic embryo3, ane3, ensl003, IDP1, ZmAE3	single copy; specifically expressed in embryo surrounding region during early stages of endosperm development
200	ans1	anthranilate synthase homolog1	GRMZM2G325131	B73 RefGen_v3	Gene	Chr2	41652488	41657690	ans1	ans1, anthranilate synthase component II, anthranilate synthase homolog1, csu65, csuM95067(ans), PCO123247a	leaf cDNA csu65 sequence similar to yeast TRP3 gene
201	ans2	anthranilate synthase component II homc	GRMZM2G171383	B73 RefGen_v3	Gene	Chr10	123312541	123317141	ans2	ans2, anthranilate synthase component II	
202	ant1	adenine nucleotide translocator1	GRMZM5G837108	B73 RefGen_v3	Gene	Chr5	203603047	203604860	ant1	cdo507b(ant), CL2269_1, cl2269_1(446), csu26, csu26a, csu26a(ant), csu26c(ant), gnp_QAE6c03b, gnp_QBN12a02, gpm303b, gpm546, rz273(ant), rz273b, rz273b(ant),	leaf cDNA, open reading frame encodes 40,519 Da polypeptide; single site (5L, MNL 67) contradicted by two sites probed in Tropical Maize F2's by p-csuh26
203	ant2	adenine nucleotide translocator2	GRMZM2G135186	B73 RefGen_v3	Gene	Chr4	163798958	163802105	ant2	adenine nucleotide translocator2, ant2, ANT-G2, ATP*, cdo507c(ant), csu26b, csu26b(ant), rz273a, rz273a(ant), umc318b	cDNA sequence corresponds to genomic sequence; actively transcribed in basal meristem, not in green leaves
204	anx1	annexin1	GRMZM2G064993	B73 RefGen_v3	Gene	Chr6	112316067	112319639	anx1	annexin-like protein RJ4, anx1, p33, PCO072293	
205	anx2	annexin2	GRMZM2G061950	B73 RefGen_v3	Gene	Chr5	208242490	208245487	anx2	anx2, gnp_QBI11g10, gpm478, p35, PCO122403	
206	ao1	aldehyde oxidase1	GRMZM2G141535	B73 RefGen_v3	Gene	Chr1	286519501	286527285	ao1	aldehyde oxidase1, ao1, cl1856_2b	functionally cloned (Sekimoto et al 1997)
207	ao2	aldehyde oxidase2	GRMZM5G899851	B73 RefGen_v3	Gene	Chr5	4589117	4593360	ao2	ao2	
208	ao3	aldehyde oxidase3	GRMZM2G019799	B73 RefGen_v3	Gene	Chr1	286429198	286437131	ao3	AAO3, abscisic aldehyde oxidase3, aldehyde oxidase3, ao3, GRMZM2G124260, IDP2436, pzb01403, rs131175362, ss196414838, TMR51	associated with ABA levels in silks of water-stressed plants (Setter et al 2011)
209	ao4	aldehyde oxidase4	GRMZM2G141473	B73 RefGen_v3	Gene	Chr1	286577038	286584000	ao4	ao4	
210	ao5	aldehyde oxidase5	GRMZM2G406830	B73 RefGen_v3	Gene	Chr7	7451202	7456538	ao5	ao5	
211	aoc1	allene oxide cyclase1	GRMZM2G077316	B73 RefGen_v3	Gene	Chr1	76740125	76741716	aoc1	allene oxide cyclase1, aoc1, AY103942, rs128475648	jasmonate pathway gene induced by herbivory
212	aos1	allene oxide synthase1	GRMZM2G067225	B73 RefGen_v3	Gene	Chr9	145603968	145606347	aos1	aos1, IDP493, PCO060855, PCO060855(700), ZmAOS2b	expression induction by herbivory and methyl jasmonate
213	aos2	allene oxide synthesis2	GRMZM2G002178	B73 RefGen_v3	Gene	Chr1	28926395	28928612	aos2	aos2, ZmAOS2a	
214	aos3	allene oxide synthesis3	GRMZM2G376661	B73 RefGen_v3	Gene	Chr1	280918468	280920450	aos3	aos3	
215	aos4	allene oxide synthesis4	GRMZM2G072653	B73 RefGen_v3	Gene	Chr1	280908391	280910737	aos4	aos4	
216	aox1	alternative oxidase1	AC233960.1_FG002	B73 RefGen_v3	Gene	Chr5	200032552	200035241	aox1	alternative oxidase1, aox1, IM1, IMMUTANS1	primers give PCR product closely similar to alternative oxidase in other species
217	aox2	alternative oxidase2	GRMZM2G125669	B73 RefGen_v3	Gene	Chr2	12345073	12348033	aox2	alternate oxidase2, aox2, IM2, IMMUTANS2, PCO108471	primers give PCR product closely similar to alternative oxidase in other species
218	aox3	alternative oxidase3	GRMZM2G074743	B73 RefGen_v3	Gene	Chr2	12274611	12276371	aox3	alternate oxidase3, aox3	
219	ap17	clathrin coat assembly protein AP17	AC195874.2_FG002	B73 RefGen_v3	Gene	Chr2	220221529	220227569	ap17	ap17, clathrin coat assembly protein AP17, pco070889, sigma 2	single copy; cDNA and genomic clones; expressed in all organs; constitutively expressed in developing embryo
220	apg1	albino or pale green mutant1	GRMZM2G082998	B73 RefGen_v3	Gene	Chr1	174010202	174012244	apg1	apg1, pco114350	ortholog of Arabidopsis At3g63410, which encodes MPBQ/MSBQ methyltransferase involved in plastoquinone synthesis (Belcher et al 2015)
221	apo1	accumulation of photosystem one1	GRMZM2G007453	B73 RefGen_v3	Gene	Chr2	9988448	9994999	apo1	apo1	plastid splicing in Arabidopsis ortholog, apo1
222	aprl1	adenosine 5'-phosphosulfate reductase-li	AC189750.4_FG004	B73 RefGen_v3	Gene	Chr7	152388543	152391232	aprl1	aprl1, APRL1, PCO125975, PCO125975(574), ZmAPRL1	
223	aprl2	adenosine 5'-phosphosulfate reductase-li	GRMZM2G087254	B73 RefGen_v3	Gene	Chr2	203181028	203184356	aprl2	aprl2, APRL2, ZmAPRL2	
224	aprl3	adenosine 5'-phosphosulfate reductase-li	GRMZM2G042582	B73 RefGen_v3	Gene	Chr4	180575468	180577838	aprl3	aprl3, APRL3, ZmAPRL3	
225	aprl4	adenosine 5'-phosphosulfate reductase-li	GRMZM2G159535	B73 RefGen_v3	Gene	Chr5	208428136	208430824	aprl4	aprl4, APRL4, ZmAPRL4	
226	aprl5	adenosine 5'-phosphosulfate reductase-li	GRMZM2G085249	B73 RefGen_v3	Gene	Chr1	218147403	218155498	aprl5	aprl5, APRL5, CL36137_1, CL36137_1(71), ZmAPRL5	
227	aprl6	adenosine 5'-phosphosulfate reductase6	GRMZM2G141848	B73 RefGen_v3	Gene	Chr10	24452184	24457178	aprl6	aprl6, IDP807, ZmAPRL6	member of protein disulfide isomerase family involved in protein folding, but having putative nonisomerase-like activity
228	aprl7	adenosine 5'-phosphosulfate reductase-li	GRMZM2G155073	B73 RefGen_v3	Gene	Chr3	132867816	132870557	aprl7	aprl7, APRL7, ZmAPRL7	
229	aprl8	adenosine 5'-phosphosulfate reductase-li	GRMZM2G046231	B73 RefGen_v3	Gene	Chr1	290214394	290215834	aprl8	aprl8, APRL8, ZmAPRL8	
230	aprl9	adenosine 5'-phosphosulfate reductase-li	GRMZM2G025248	B73 RefGen_v3	Gene	Chr5	3553168	3555891	aprl9	aprl9, APRL9, ZmAPRL9	
231	aprt1	adenine phosphoribosyltransferase1	GRMZM2G170101	B73 RefGen_v3	Gene	Chr2	31501795	31510516	aprt1	adenine phosphoribosyltransferase1, aprt1, apt1, PCO120693, pco120693(127), umi13	
232	aps1	ATP sulfurylase1	GRMZM2G149952	B73 RefGen_v3	Gene	Chr1	275157705	275161519	aps1	aps1, ATP-sulfurylase 3, chloroplastic-like, bifunctional 3-phosphoadenosine 5-phosphosulfate synthetase, cl30_1d, sed1, senescence-diminished1, ZmAS1	mRNA differentially diminished in early- vs. late-senescing lines; similarity to ATP sulfurylase mRNA of Arabidopsis
233	apt1	aberrant pollen transmission1	GRMZM2G448687	B73 RefGen_v3	Gene	Chr9	129022644	129046413	apt1	apt1	Ac-tagged mutation, pollen-grain specific pollen tube shortening and twisting
234	apx1	ascorbate peroxidase homolog	GRMZM2G054300	B73 RefGen_v3	Gene	Chr9	138678093	138682438	apx1	apx1, APx1, csu710e(apx), ZmAPx05	
235	apx2	ascorbate peroxidase2	GRMZM2G140667	B73 RefGen_v3	Gene	Chr2	219258176	219261097	apx2	apx2, APx2 - Cytosolic Ascorbate Peroxidase, ascorbate peroxidase2, IDP162, IDP3857, IDP3884, magi72449, PCO104002a, ZmAPx02	leaf cDNA, similar to plant cytosolic ascorbate peroxidase; sequence distinct from apx1
236	apx3	ascorbate peroxidase homolog3	GRMZM2G137839	B73 RefGen_v3	Gene	Chr1	43682818	43686019	apx3	APx1, apx3, csu238a(apx), csu710a(apx), pod1, ZmAPx01	
237	ara3	ras-related protein ARA-3	GRMZM2G061900	B73 RefGen_v3	Gene	Chr1	293212122	293215703	ara3	ara3, ARA-3, CL2811_2c, ZmRab8A3	
238	arf1	ADP-ribosylation factor homolog1	GRMZM2G395844	B73 RefGen_v3	Gene	Chr5	3055229	3058761	arf1	ADP-ribosylation factor homolog1, arf1, gnp_QCF21f04, gpm632	cDNA similar to ARF family of GTP binding proteins
239	arftf1	ARF-transcription factor 1	GRMZM2G169820	B73 RefGen_v3	Gene	Chr1	190580078	190595543	arftf1	arf1	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
240	arftf10	ARF-transcription factor 10	GRMZM2G338259	B73 RefGen_v3	Gene	Chr3	156523681	156529660	arftf10	arf10	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
241	arftf11	ARF-transcription factor 11	GRMZM2G056120	B73 RefGen_v3	Gene	Chr3	196638145	196644110	arftf11	arf11, arf3c, auxin response factor	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
242	arftf12	ARF-transcription factor 12	GRMZM2G437460	B73 RefGen_v3	Gene	Chr3	210346707	210354569	arftf12	arf12, arf3d, auxin response factor	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
243	arftf13	ARF-transcription factor 13	GRMZM2G378580	B73 RefGen_v3	Gene	Chr4	23548742	23554591	arftf13	arf13	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
244	arftf14	ARF-transcription factor 14	GRMZM2G137413	B73 RefGen_v3	Gene	Chr4	118717709	118723692	arftf14	arf14	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
245	arftf15	ARF-transcription factor 15	GRMZM2G081406	B73 RefGen_v3	Gene	Chr4	143829841	143832631	arftf15	arf15	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
246	arftf16	ARF-transcription factor 16	GRMZM2G028980	B73 RefGen_v3	Gene	Chr4	237016081	237022029	arftf16	arf16	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
247	arftf17	ARF-transcription factor 17	GRMZM2G159399	B73 RefGen_v3	Gene	Chr5	27964682	27969438	arftf17	arf17	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
248	arftf18	ARF-transcription factor 18	GRMZM2G035405	B73 RefGen_v3	Gene	Chr5	42328068	42332365	arftf18	arf18	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
249	arftf19	ARF-transcription factor 19	AC207656.3_FG002	B73 RefGen_v3	Gene	Chr5	49282509	49284911	arftf19	arf19	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
250	arftf2	ARF-transcription factor 2	GRMZM2G153233	B73 RefGen_v3	Gene	Chr1	230778452	230782861	arftf2	arf2	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
251	arftf20	ARF-transcription factor 20	GRMZM2G102845	B73 RefGen_v3	Gene	Chr5	78415886	78423936	arftf20	arf20	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
252	arftf21	ARF-transcription factor 21	GRMZM2G390641	B73 RefGen_v3	Gene	Chr6	89284779	89287980	arftf21	arf21	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
253	arftf22	ARF-transcription factor 22	GRMZM2G089640	B73 RefGen_v3	Gene	Chr6	91485004	91487958	arftf22	arf22	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
254	arftf23	ARF-transcription factor 23	GRMZM2G441325	B73 RefGen_v3	Gene	Chr6	158843020	158849314	arftf23	arf23, arf3b, auxin response factor	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
255	arftf24	ARF-transcription factor 24	GRMZM2G030710	B73 RefGen_v3	Gene	Chr6	164719893	164725158	arftf24	arf24, arf3a, auxin response factor	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
256	arftf25	ARF-transcription factor 25	GRMZM2G116557	B73 RefGen_v3	Gene	Chr8	159641546	159646951	arftf25	arf25	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
257	arftf26	ARF-transcription factor 26	GRMZM5G874163	B73 RefGen_v3	Gene	Chr8	173768820	173775129	arftf26	arf26, arf3e, auxin response factor	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
258	arftf27	ARF-transcription factor 27	GRMZM2G160005	B73 RefGen_v3	Gene	Chr9	11128329	11140405	arftf27	arf27	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
259	arftf28	ARF-transcription factor 28	GRMZM2G006042	B73 RefGen_v3	Gene	Chr10	13788443	13794457	arftf28	arf28	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
260	arftf29	ARF-transcription factor 29	GRMZM2G086949	B73 RefGen_v3	Gene	Chr10	146553165	146558259	arftf29	arf29	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
261	arftf3	ARF-transcription factor 3	GRMZM2G078274	B73 RefGen_v3	Gene	Chr2	2271404	2279360	arftf3	arf3	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
262	arftf30	ARF-transcription factor 30	GRMZM2G475882	B73 RefGen_v3	Gene	Chr10	147154383	147163265	arftf30	arf30	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
263	arftf31	ARF-transcription factor 31	GRMZM2G023813	B73 RefGen_v3	Gene	Chr10	148635880	148637733	arftf31	arf31, auxin response factor 31, B3 DNA binding domain containing protein, ZmARF31	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.. plays a key role in low P responses and root architecture regulation
264	arftf32	ARF-transcription factor 32	GRMZM2G181254	B73 RefGen_v3	Gene	Chr1	159192608	159194386	arftf32	arf32	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
265	arftf33	ARF-transcription factor 33	GRMZM2G179121	B73 RefGen_v3	Gene	Chr1	158940439	158942519	arftf33	arf33	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
266	arftf34	ARF-transcription factor 34	GRMZM2G081158	B73 RefGen_v3	Gene	Chr1	173434033	173442028	arftf34	arf34	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
267	arftf35	ARF-transcription factor 35	GRMZM2G317900	B73 RefGen_v3	Gene	Chr5	57456264	57463575	arftf35	arf35	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
268	arftf36	ARF-transcription factor 36	GRMZM2G702026	B73 RefGen_v3	Gene	Chr5	173850054	173855670	arftf36	arf36	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
269	arftf37	ARF-transcription factor 37	GRMZM2G075715	B73 RefGen_v3	Gene	Chr7	39745937	39752588	arftf37	arf37	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
270	arftf38	ARF-transcription factor 38	GRMZM2G005284	B73 RefGen_v3	Gene	Chr10	130985138	130987563	arftf38	arf38	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
271	arftf4	ARF-transcription factor 4	GRMZM2G034840	B73 RefGen_v3	Gene	Chr2	3342917	3349175	arftf4	arf4	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
272	arftf5	ARF-transcription factor 5	GRMZM5G808366	B73 RefGen_v3	Gene	Chr2	26048274	26053073	arftf5	arf5	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
273	arftf6	ARF-transcription factor 6	GRMZM2G122614	B73 RefGen_v3	Gene	Chr2	28604618	28606017	arftf6	arf6	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
274	arftf7	ARF-transcription factor 7	GRMZM2G475263	B73 RefGen_v3	Gene	Chr3	1552179	1556524	arftf7	arf7	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
275	arftf8	ARF-transcription factor 8	GRMZM2G352159	B73 RefGen_v3	Gene	Chr3	107585492	107591866	arftf8	arf8	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
276	arftf9	ARF-transcription factor 9	GRMZM2G073750	B73 RefGen_v3	Gene	Chr3	123881899	123888098	arftf9	arf9	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
277	arid1	ARID-transcription factor 1	GRMZM2G365731	B73 RefGen_v3	Gene	Chr1	236206412	236245981	arid1	AT-rich interactive domain-containing protein 1-like, IDP5983, rs131865894 , umc1085	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
278	arid10	ARID-transcription factor 10	GRMZM5G883993	B73 RefGen_v3	Gene	Chr9	100869848	100876008	arid10		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
279	arid2	ARID-transcription factor 2	GRMZM2G140156	B73 RefGen_v3	Gene	Chr2	184041779	184053401	arid2		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
280	arid3	ARID-transcription factor 3	GRMZM2G110109	B73 RefGen_v3	Gene	Chr4	162151216	162155711	arid3		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
281	arid4	ARID-transcription factor 4	GRMZM2G138976	B73 RefGen_v3	Gene	Chr7	120237787	120284629	arid4		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
282	arid5	ARID-transcription factor 5	GRMZM2G421899	B73 RefGen_v3	Gene	Chr5	202662495	202668619	arid5		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
283	arid6	ARID-transcription factor 6	GRMZM2G024976	B73 RefGen_v3	Gene	Chr5	159240339	159247522	arid6		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
284	arid7	ARID-transcription factor 7	GRMZM2G466292	B73 RefGen_v3	Gene	Chr5	65453074	65462393	arid7		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
285	arid8	ARID-transcription factor 8	GRMZM2G180654	B73 RefGen_v3	Gene	Chr6	98248764	98255015	arid8		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
286	arid9	ARID-transcription factor 9	GRMZM5G866423	B73 RefGen_v3	Gene	Chr1	209583050	209585556	arid9		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
287	arp4	actin related protein like4	GRMZM2G015384	B73 RefGen_v3	Gene	Chr1	2874117	2894252	arp4	arp4, pco093035, pco093035(3), rs131177022 , rs131192334	Ortholog of Arabidopsis ARP4 (AT1G18450)
288	arp7	Actin-related protein Like 7	GRMZM2G015861	B73 RefGen_v3	Acronym	Chr5	31838656	31847972	arp7	Actin-related protein Like 7, arp7	
289	arpp0	60S acidic ribosomal protein P0	GRMZM2G066460	B73 RefGen_v3	Gene	Chr6	9206517	9209074	arpp0	arpp0, RP-P0, ZmrpP0	
290	arpp1a	acidic ribosomal protein P1a	GRMZM2G032315	B73 RefGen_v3	Gene	Chr6	4596812	4609378	arpp1a	60S acidic ribosomal protein P1, arpp1a, L12, rpa1, rpl12*-T1996, rpl12*-U40147, rpp1, rpp1a	pollen cDNA similar to acidic L7/L12 ribosomal protein
291	arpp2a	acidic ribosomal protein P2a	GRMZM2G119809	B73 RefGen_v3	Gene	Chr8	72904843	72907132	arpp2a	arpp2a, arpp2a*-uaz5c06c03, arpp2a*-X86553, PCO075293b, rp2, rpa2-1, rpa*-uaz5c06c03, rpl12, rpp*-uaz5c06c03, uaz294, uaz5c06c03(gfu), uaz5c06c03(rpl12)	cDNA sequence similar to P2-type acidic ribosomal protein
292	arpp2a-2	acidic ribosomal protein P2a-2	GRMZM2G102891	B73 RefGen_v3	Gene	Chr8	72750165	72752947	arpp2a-2	arpp2a-2, rpp2a-2	
293	arpp2a-3	acidic ribosomal protein P2a-3	GRMZM2G010257	B73 RefGen_v3	Gene	Chr2	2550585	2552593	arpp2a-3	arpp2a-3	
294	arpp2b	acidic ribosomal protein P2b (rpp2b)	GRMZM2G114954	B73 RefGen_v3	Gene	Chr8	98106249	98110627	arpp2b	arpp2b, PCO102315, rpp2b	
295	arpp3	acidic ribosomal protein P3	GRMZM2G077208	B73 RefGen_v3	Gene	Chr5	56870925	56872383	arpp3	acidic ribosomal protein P3, arpp3, PCO073423, PCO073423(400), rpp3, rpp3a	novel acidic phosphoprotein

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
296	arpp40	acidic ribosomal protein P40	GRMZM2G126821	B73 RefGen_v3	Gene	Chr9	151935786	151938224	arpp40	acidic ribosomal protein P40, arpp40, PCO143386, PCO143386(707), rpa40, rpp40, uaz7C02D05(gfu)	vegetative meristem cDNA 7C02D05 similar to cytoplasmic ribosomal protein
297	arr1	ARR-B-transcription factor 1	GRMZM2G126834	B73 RefGen_v3	Gene	Chr9	146136871	146143251	arr1	response regulator10, ZmRR10	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
298	arr2	ARR-B-transcription factor 2	GRMZM2G409974	B73 RefGen_v3	Gene	Chr9	13465293	13469635	arr2		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
299	arr3	ARR-B-transcription factor 3	GRMZM2G099797	B73 RefGen_v3	Gene	Chr1	28417831	28422778	arr3		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
300	arr4	ARR-B-transcription factor 4	GRMZM2G360523	B73 RefGen_v3	Gene	Chr9	101990935	101999695	arr4		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
301	arr5	ARR-B-transcription factor 5	GRMZM2G133262	B73 RefGen_v3	Gene	Chr5	58834080	58845813	arr5		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
302	arr6	ARR-B-transcription factor 6	GRMZM2G177220	B73 RefGen_v3	Gene	Chr3	165939858	165943821	arr6		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
303	arr7	ARR-B-transcription factor 7	GRMZM2G100318	B73 RefGen_v3	Gene	Chr8	163129203	163133084	arr7		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
304	arr8	ARR-B-transcription factor 8	GRMZM2G479110	B73 RefGen_v3	Gene	Chr5	213780789	213785593	arr8		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
305	asc1	asceapen1	GRMZM2G140633	B73 RefGen_v3	Gene	Chr7	127925177	127927750	asc1	asceapen1, CL2906_1, cyclin, IDP1668, IDP1670, IDP71, leaf cyclinD42	Recessive plants shortened, infertile with narrowed leaves; stomatal patterns altered
306	asg12a		GRMZM2G048375	B73 RefGen_v3	Gene	Chr9	148237745	148240963	asg12a	asg012, asg12, asg12a, rs131180036	genomic clone, single copy. NCBI: putative glycosyl hydrolase family 10 protein
307	asg3		GRMZM2G418289	B73 RefGen_v3	Gene	Chr1	82397413	82401819	asg3	asg3	NCBI identifies as "putative protein kinase superfamily protein"
308	asg34a(msd)		GRMZM2G054267	B73 RefGen_v3	Gene	Chr7	13967993	13969287	asg34a(msd)	asg034, asg34a, asg34a(msd), rs131605071, umc1068	
309	asg48a		GRMZM2G158342	B73 RefGen_v3	Gene	Chr3	13109108	13110869	asg48a	asg48, asg48a, flavonoid 3',5'-hydroxylase-like, rs131178361	NCBI: flavonoid 3',5'-hydroxylase-like
310	asg49		GRMZM2G003869	B73 RefGen_v3	Gene	Chr7	128171458	128175453	asg49	asg49, rs132393719, si486067f01, si486067f01(564)	NCBI: Pentatricopeptide repeat-containing protein
311	asg73		GRMZM2G122863	B73 RefGen_v3	Gene	Chr5	9339454	9342646	asg73	asg73, pco076369b, rs129988042 , rs129988055 , rs129988060 , rs131180783 , rs131180783 , rs131180784	
312	ask2	aspartate kinase2	GRMZM2G052935	B73 RefGen_v3	Gene	Chr2	157355447	157361044	ask2	ask2, aspartate kinase2, LT20, Monofunctional aspartate kinase 2	lysine-threonine resistance
313	asn1	asparagine synthetase1	GRMZM2G074589	B73 RefGen_v3	Gene	Chr9	32468024	32477360	asn1	AS, asn1, AsnS1, asparagine synthetase1, zas1	cDNA sequence 70% identical to asparagine synthetase from Pisum sativum
314	asn2	asparagine synthetase2	GRMZM2G093175	B73 RefGen_v3	Gene	Chr3	229507263	229511632	asn2	asn2, AsnS2	
315	asn3	asparagine synthetase3	GRMZM2G053669	B73 RefGen_v3	Gene	Chr1	45118780	45122813	asn3	asn3, AsnS3, umc1701	
316	asn4	asparagine synthetase4	GRMZM2G078472	B73 RefGen_v3	Gene	Chr9	138041002	138044999	asn4	asn4, AsnS4	
317	ast91	anti-sigma factor antagonist domain of su	GRMZM2G395114	B73 RefGen_v3	Gene	Chr2	4895674	4900685	ast91	anti-sigma factor antagonist domain of SulP-like sulfate transportors91, ast91, pco089998, sulfate transporter 91	
318	atl1	auxin transporter-like1	GRMZM2G127949	B73 RefGen_v3	Gene	Chr3	178053577	178060075	atl1	atl1, AUXIN1, auxin transporter-like protein 1, CL468_1, plt1, sparse panicle1, spp1, ZmAUX1	mutant tassels have reduced branch numbers; bald tip on ears with fewer spikelets per row, and agravitropic root growth
319	atp1	ATPase1	GRMZM2G101020	B73 RefGen_v3	Gene	Chr3	141387560	141390705	atp1	atp1, ATPase1, csu30, csu30a, csua(vatp), csuh30, sog0862a, umc308c, umc322	leaf cDNA csu30 is identical to Avena sativa vacuolar ATPase subunit
320	atp2	ATP synthase2	GRMZM2G113408	B73 RefGen_v3	Gene	Chr6	163133778	163137313	atp2	atp2, ATPase2, atpB (cp), ATP synthase2, uaz243b(atp), uaz243b(atpb)	cDNA clone
321	atp3	ATP synthase3	GRMZM2G171628	B73 RefGen_v3	Gene	Chr2	202325435	202328872	atp3	atp3, ATP synthase3, ATP synthase delta chain, csu657(atpd), pco138774, uaz7c02a03(gfu)	
322	atp4	ATP synthase4	GRMZM2G128665	B73 RefGen_v3	Gene	Chr1	26825757	26828101	atp4	atp4, ZmPPR017	Chloroplast PPR-SMR protein. Activates atpB translation. Binds atpB 5'UTR. (A. Barkan, 2015). required for normal accumulation of the chloroplast ATP synthase
323	atpc1	ATP synthase chloroplast subunit1	GRMZM5G862663	B73 RefGen_v3	Gene	Chr5	208034934	208036864	atpc1	atpc1, ATP synthase chloroplast subunit1, ATP synthase delta chain	Gamma subunit of chloroplast ATP synthase (ATPC1). (A. Barkan, 2015). N-terminal amino acid sequence, cDNA sequence from clone selected using anti-delta-CF1 serum
324	atpc2	ATP synthase chloroplast subunit2	GRMZM2G048907	B73 RefGen_v3	Gene	Chr7	152868671	152870546	atpc2	atpc1, atpc2, ATP synthase chloroplast subunit2	chloroplast ATP synthase (ATPC); gamma subunit based on similarity to Arabidopsis atpc1 (Belcher et al 2015)
325	AW036917		GRMZM2G106218	B73 RefGen_v3	Gene	Chr6	149672083	149678650	AW036917		
326	AW231791		GRMZM2G140590	B73 RefGen_v3	Gene	Chr8	114541249	114555400	AW231791		NCBI: Protein kinase superfamily protein
327	AY103622		GRMZM2G014240	B73 RefGen_v3	Gene	Chr9	14328479	14333699	AY103622		NCBI: vacuolar proton pump-like protein
328	AY103944		GRMZM2G352129	B73 RefGen_v3	Gene	Chr2	31534332	31539953	AY103944	PZA01336	similar to Arabidopsis poly(A) binding protein 8
329	AY105479		GRMZM2G063754	B73 RefGen_v3	Gene	Chr6	123931291	123934591	AY105479	PZA01729, rs128284500, rs55626592 , ss196416415	
330	AY106040		GRMZM2G303118	B73 RefGen_v3	Gene	Chr2	14837139	14848360	AY106040	AY106040, PCO125510, PZA01753, rs131175401, ss196414999	
331	AY106170		GRMZM2G069676	B73 RefGen_v3	Gene	Chr7	41746480	41810114	AY106170	PZA00084, rs130520204, rs55622270 , ss196416582	
332	AY106313		GRMZM2G153138	B73 RefGen_v3	Gene	Chr3	2070509	2079118	AY106313		
333	AY106825		GRMZM2G068117	B73 RefGen_v3	Gene	Chr1	293700005	293704720	AY106825	PZA00991, rs131175378, ss196414889	
334	AY107034		GRMZM2G404973	B73 RefGen_v3	Gene	Chr2	22692870	22695229	AY107034	PHM6111, PZA00590, rs131175411, ss196415029	
335	AY107053		GRMZM2G383404	B73 RefGen_v3	Gene	Chr6	120201718	120203603	AY107053	PZA01055, rs131175755, rs55626278 , ss196416403	
336	AY107200		GRMZM2G085718	B73 RefGen_v3	Gene	Chr4	229715408	229720104	AY107200	PZA00521, rs128282702, rs55625294 , ss196415937	
337	AY107329		GRMZM2G007466	B73 RefGen_v3	Gene	Chr5	183171312	183177271	AY107329	PZA01575, rs131175712, rs55623286 , ss196416231	
338	AY107489		GRMZM2G394212	B73 RefGen_v3	Gene	Chr1	50093597	50096783	AY107489	PHM4913, PZA00468, rs131175281, ss196414500	
339	AY107496		GRMZM2G467169	B73 RefGen_v3	Gene	Chr9	12108547	12115783	AY107496	PZA00466, rs128282928, rs130966566, rs55626361 , ss196417099, ss196417101	
340	AY109128		GRMZM2G459811	B73 RefGen_v3	Gene	Chr1	293870055	293875566	AY109128	PZA00235, rs131918087, rs131918088, rs55622861 , ss196414891, ss196414893	
341	AY109534		GRMZM2G021605	B73 RefGen_v3	Gene	Chr4	181259476	181262496	AY109534	AY109534, CL50733_1, PHM14618, PZA02289, rs128284122, rs55624314 , ss196415883	
342	AY109543		GRMZM2G028039	B73 RefGen_v3	Gene	Chr9	149430555	149437059	AY109543	AY109543, CL854_1, PZA02381, rs131175971, rs55623831 , ss196417285	
343	AY109644		GRMZM2G111309	B73 RefGen_v3	Gene	Chr7	148490575	148493173	AY109644	AY109644, CL12102_-1, PHM16437, PZA02004, rs128281419, ss196416687	
344	AY109678		GRMZM2G110198	B73 RefGen_v3	Gene	Chr1	115412522	115416244	AY109678	AY109678, PZA02070, rs131175301, rs55624850 , ss196414592	

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
345	AY109917		GRMZM2G004619	B73 RefGen_v3	Gene	Chr2	199378455	199380799	AY109917	AY109917, CL13558_2, PZA02017, rs131175463, ss196415235	
346	AY109929		GRMZM2G012566	B73 RefGen_v3	Gene	Chr1	38552479	38555256	AY109929	AY109929, PHM4597, PZA02271, rs131175270, ss196414456	
347	AY110019		GRMZM2G019267	B73 RefGen_v3	Gene	Chr1	271027530	271032041	AY110019	AY110019, gnp_QAM14g05a, gpm359a, PZA02278, rs131175349, ss196414795	
348	AY110160		GRMZM2G139041	B73 RefGen_v3	Gene	Chr1	295097497	295100438	AY110160	AY110160, PZA02359, rs131918961, rs55626524 , ss196414899	
349	AY110191		GRMZM2G703928	B73 RefGen_v3	Gene	Chr1	227428695	227431105	AY110191	AY110191	
350	AY110253		GRMZM2G070011	B73 RefGen_v3	Gene	Chr4	15320600	15322087	AY110253	AY110253, CL871_1, PZA02385, rs129644038, rs131175575, rs55623327 , ss196415690, ss196415692	
351	AY110297		GRMZM2G031568	B73 RefGen_v3	Gene	Chr3	67694182	67699591	AY110297	AY110297, PZA02134, rs131413662, rs55622131 , ss196415389	
352	AY110356		GRMZM2G703918	B73 RefGen_v3	Gene	Chr1	224142943	224149783	AY110356	AY110356, PZA02117, rs128882638, rs55626868 , ss196414688	
353	AY110393		GRMZM2G084783	B73 RefGen_v3	Gene	Chr1	51288714	51290044	AY110393	AY110393, CL5132_1, gnp_AI737875, gpm70, PZA02292	
354	AY110426		GRMZM2G006047	B73 RefGen_v3	Gene	Chr1	287181576	287182811	AY110426	AY110426	similar to Arabidopsis bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein
355	AY110435		GRMZM2G032047	B73 RefGen_v3	Gene	Chr1	46129394	46130844	AY110435	AY110435, CL57831_1, PZA02328, rs131175275, ss196414479	
356	AY110542		GRMZM2G462635	B73 RefGen_v3	Gene	Chr6	135110368	135111326	AY110542	AY110542, CL4202_1, PZA02262, rs132331263, rs55624016 , ss196416439	
357	AY110562		GRMZM2G374302	B73 RefGen_v3	Gene	Chr4	144862958	144868207	AY110562	AY110562, CL26590_1, PZA02147, rs129808587, rs55625090 , ss196415824	
358	AY110569		GRMZM2G149265	B73 RefGen_v3	Gene	Chr8	167827882	167831438	AY110569	AY110569, CL10335_2, gnp_AI783381, gpm88, PHM765, PZA01964, rs130927373, rs55624960 , ss196417066	
359	AY110625		GRMZM2G313678	B73 RefGen_v3	Gene	Chr5	1033436	1038047	AY110625	AY110625, CL1125_2, PZA01983, rs128281924, ss196416311	
360	AY111089		GRMZM2G179308	B73 RefGen_v3	Gene	Chr5	180787355	180790720	AY111089	PZA02633, rs132252479, rs55622858 , ss196416223	
361	AY111333		GRMZM2G018793	B73 RefGen_v3	Gene	Chr3	93198079	93199928	AY111333	PHM7417, PZA02645, rs131175496, ss196415401	
362	AY111962		GRMZM2G125239	B73 RefGen_v3	Gene	Chr4	221138448	221144193	AY111962	PZA00878, rs128282183, rs55622480 , ss196415935	
363	AY112175		GRMZM2G120440	B73 RefGen_v3	Gene	Chr1	294807181	294809796	AY112175	PZA00623, rs128281693, rs131175379, rs55624180 , ss196414895, ss196414897	
364	az19D1	alpha zein 19kDa D1	AF546187.1_FG001	B73 RefGen_v3	Gene	Chr1	161790710	161791432	az19D1	az19D1, azD1, z1D1	member of a two-gene family, z1D, closely linked
365	az19D2	alpha zein 19kDa D2	AF546187.1_FG007	B73 RefGen_v3	Gene	Chr1	162006911	162007636	az19D2	az19D2, azd2, z1D, z1D2	member of a two-gene family, z1D, closely linked
366	az22z3	22kD alpha zein3	GRMZM2G044625	B73 RefGen_v3	Gene	Chr4	5122439	5123472	az22z3	az22z3, azs22.4, uat3b(fl2), umc2409a, umc2409b, Z1C, z1C/SF4	mRNA for 22kD zein; in z1c(zp22) cluster
367	az22z4	22kD alpha zein4	GRMZM2G346897	B73 RefGen_v3	Gene	Chr4	5145291	5146364	az22z4	az22z4, azs22.7, z1C, z1C/SF4	mRNA for 22kD zein; in z1c(zp22) cluster
368	az22z5	22kD alpha zein5	GRMZM2G088365	B73 RefGen_v3	Gene	Chr4	5083079	5084155	az22z5	az22z5, z1C/SF4	mRNA for 22kD zein; in z1c(zp22) cluster
369	b1	colored plant1	GRMZM2G172795	B73 RefGen_v3	Gene	Chr2	19041697	19046154	b1	b1, booster, colored plant1, gsy1(b1), npi248-b1, R2, R-2, sc1, SC1, umc1776, ZmbHLH2	dominant B1 plants have anthocyanin in major plant tissues; some alleles affect aleurone and embryo color; regulates flavonoid enzymes; SSR umc1776
370	ba1	barren stalk1	GRMZM2G397518	B73 RefGen_v3	Gene	Chr3	183139911	183140880	ba1	ba1, barren stalk1, rs131175536, rs131175537, rs131175538, ss196415558, ss196415561, ss196415563, ZmbHLH67	ear shoots and most tassel branches and spikelets absent
371	baf1	barren stalk fastigiate1	GRMZM2G072274	B73 RefGen_v3	Gene	Chr9	21976903	21978472	baf1	baf1, barren stalk fastigiate1, ba^s, ba-s, ba*-s	ear shoots often absent, or distorted and fused to culm at base; tassel branches erect, bundled, fused to culm at base
372	bak1	brassinosteroid insensitive1-associated r	GRMZM2G145720	B73 RefGen_v3	Gene	Chr9	35179613	35185362	bak1	bak1	
373	bap1a	basal layer antifungal protein1a	GRMZM2G008271	B73 RefGen_v3	Gene	Chr10	80861842	80863106	bap1a	bap1, bap1a, bap1b, basal layer antifungal protein1a, gnp_QAN3g09, gpm376, PCO132095j	cDNA, similar to bap2
374	bap1b	basal layer antifungal protein1b	GRMZM2G008403	B73 RefGen_v3	Gene	Chr10	80878304	80878997	bap1b	bap1, bap1b	
375	bap2	basal layer antifungal protein2	GRMZM2G152655	B73 RefGen_v3	Gene	Chr4	34294927	34295919	bap2	bap2, basal endosperm transfer layer2 , basal layer antifungal protein2, bet2, betl2, BETL2, gnp_QBQ11e10, gpm558	cDNA, multiple copies; antifungal activity; basal endosperm cell specific
376	bas1	beta alanine synthase1	GRMZM2G077673	B73 RefGen_v3	Gene	Chr7	149169258	149171046	bas1	bas1, beta alanine synthase1, beta-ureidopropionase, cdo385, CL36182_1, CL36182_1(571)	single copy, oat cDNA cdo385
377	bbi1	bowman-birk inhibitor1	GRMZM2G007928	B73 RefGen_v3	Gene	Chr3	179685800	179686954	bbi1	bbi1, bioactive bowman-birk inhibitor1, bowman-birk type trypsin inhibitor1	encodes a bioactive Bowman-Birk Inhibitor that apparently confers insect resistance
378	bbr1	BBR/BPC-transcription factor 1	GRMZM2G179366	B73 RefGen_v3	Gene	Chr1	192523101	192525654	bbr1		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
379	bbr2	BBR/BPC-transcription factor 2	GRMZM2G166230	B73 RefGen_v3	Gene	Chr2	157868458	157869994	bbr2		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
380	bbr3	BBR/BPC-transcription factor 3	GRMZM2G164735	B73 RefGen_v3	Gene	Chr4	43266139	43268012	bbr3		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
381	bbr4	BBR/BPC-transcription factor 4	GRMZM2G118690	B73 RefGen_v3	Gene	Chr9	23765880	23771224	bbr4		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
382	bd1	branched silkless1	GRMZM2G307119	B73 RefGen_v3	Gene	Chr7	172248843	172250339	bd1	bd1, branched silkless1, ereb151, rs131187034	ear silkless with indeterminate branches at base; tassel proliferated, bushy
383	bde1	bearded-ear1	GRMZM2G160565	B73 RefGen_v3	Gene	Chr5	196601246	196608839	bde1	bde1, bearded-ear1, Bearded-ear*-McClintock, polytypic ear2, pt2, pt*-McClintock, pzd00017, tufted silky*-5267, tus*-5257, ucsd72e, zag3, zag5, zea agamous3, ZmMADS12	floral development MADS box transcription factor; recessive mutant has silky-polytypic-like ear
384	BE639338		GRMZM2G104226	B73 RefGen_v3	Gene	Chr3	214143658	214147325	BE639338	BE639338, si946021A07	NCBI: GDSL esterase/lipase At1g28600-like
385	ben1	bentazon resistance1	GRMZM2G090432	B73 RefGen_v3	Gene	Chr5	6548812	6551287	ben1	ben1, bentazon resistance1, CL377_1, CL377_1(376), CYP, isoflavone 2'-hydroxylase-like, mesotrione resistance, nicosulfuron susceptible, nsf1	Dominant Ben1 resistant, with Ben2. recessive susceptibility to nicosulfuron (Accent) and mesotrione herbicides
386	bes1	brassinosteroid insensitive EMS-suppres	GRMZM2G102514	B73 RefGen_v3	Gene	Chr7	160551419	160553078	bes1	bes1, brassinosteroid insensitive EMS-suppressor homolog1, bzr10, BZR-transcription factor 10, rs132427387	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
387	betl1	basal endosperm transfer layer1	GRMZM2G082785	B73 RefGen_v3	Chromosomal Se	Chr2	225662083	225662933	betl1	basal endosperm transfer layer1, bet1, betl1	(aka bet1) tissue specific cDNA; variable copies in tandem, 17 amino acid extensin-like signal peptide, ser-(pro)4 motif
388	betl10	basal endosperm transfer layer10	GRMZM2G091445	B73 RefGen_v3	Gene	Chr3	155423558	155424150	betl10	basal endosperm transfer layer10, betl10, betl-10, IDP277, PCO082094	endosperm transfer cell specific protein, regulated by mrp1 myp related protein 1; probe IDP277
389	betl3	basal endosperm transfer layer3	GRMZM2G175976	B73 RefGen_v3	Gene	Chr3	132282587	132283333	betl3	basal endosperm transfer layer3, BETL-1D, betl3, PCO072069	cDNA sequence, specific to basal endosperm transfer layer
390	betl4	basal endosperm transfer layer4	GRMZM2G073290	B73 RefGen_v3	Gene	Chr4	209022805	209023472	betl4	basal endosperm transfer layer4, BELT4, betl4	cDNA sequence, basal endosperm specific
391	betl9	basal endosperm transfer layer9	GRMZM2G087413	B73 RefGen_v3	Gene	Chr3	138651695	138652380	betl9	5a2 protein, basal endosperm transfer layer9, betl9, betl-9, gnp_AI812206, gpm92, PCO092107, ZmLTPd6	endosperm transfer cell specific protein regulated by mrp1 myb related protein1; RFLP gpm92
392	bf1	blue fluorescent1	GRMZM2G051219	B73 RefGen_v3	Gene	Chr9	153861473	153877358	bf1	bf1, blue fluorescent1, PCO127845, PCO127845(707)	ultraviolet light; anthranilic acid accumulates, anthranilate synthase has altered inhibition kinetics
393	bgaf1	beta glucosidase aggregating factor1	GRMZM2G172204	B73 RefGen_v3	Gene	Chr7	26167430	26169874	bgaf1	beta glucosidase aggregating factor1, bgaf1, IDP46, PCO130729	

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
394	bhlh10	bHLH-transcription factor 10	GRMZM2G067654	B73 RefGen_v3	Gene	Chr9	12986561	12988736	bhlh10		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
395	bhlh100	bHLH-transcription factor 100	GRMZM2G313756	B73 RefGen_v3	Gene	Chr10	108376074	108377174	bhlh100	transcription factor FER-LIKE IRON DEFICIENCY-INDUCED TRANSCRIPTION FACTOR-like, ZmFIT (FER like)	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
396	bhlh101	bHLH-transcription factor 101	GRMZM2G173521	B73 RefGen_v3	Gene	Chr2	73730378	73731762	bhlh101		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
397	bhlh102	bHLH-transcription factor 102	GRMZM2G355469	B73 RefGen_v3	Gene	Chr10	118390725	118392197	bhlh102		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
398	bhlh103	bHLH-transcription factor 103	GRMZM2G301089	B73 RefGen_v3	Gene	Chr1	274801584	274803327	bhlh103		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
399	bhlh104	bHLH-transcription factor 104	GRMZM2G088443	B73 RefGen_v3	Gene	Chr3	14937168	14939315	bhlh104		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
400	bhlh105	bHLH-transcription factor 105	GRMZM2G082586	B73 RefGen_v3	Gene	Chr7	128740346	128742573	bhlh105		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
401	bhlh106	bHLH-transcription factor 106	GRMZM2G089501	B73 RefGen_v3	Gene	Chr7	130270033	130277723	bhlh106		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
402	bhlh107	bHLH-transcription factor 107	GRMZM2G145146	B73 RefGen_v3	Gene	Chr7	127620549	127621728	bhlh107		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
403	bhlh108	bHLH-transcription factor 108	GRMZM2G119823	B73 RefGen_v3	Gene	Chr10	105635764	105638288	bhlh108		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
404	bhlh109	bHLH-transcription factor 109	GRMZM2G013688	B73 RefGen_v3	Gene	Chr7	139760958	139761887	bhlh109		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
405	bhlh11	bHLH-transcription factor 11	GRMZM2G176289	B73 RefGen_v3	Gene	Chr4	160021000	160023829	bhlh11		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
406	bhlh110	bHLH-transcription factor 110	GRMZM2G452996	B73 RefGen_v3	Gene	Chr1	12462798	12465171	bhlh110		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
407	bhlh111	bHLH-transcription factor 111	GRMZM2G150327	B73 RefGen_v3	Gene	Chr1	112414537	112416571	bhlh111		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
408	bhlh112	bHLH-transcription factor 112	GRMZM5G879527	B73 RefGen_v3	Gene	Chr1	188065123	188068113	bhlh112		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
409	bhlh113	bHLH-transcription factor 113	GRMZM2G471635	B73 RefGen_v3	Gene	Chr4	57373825	57374550	bhlh113		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
410	bhlh114	bHLH-transcription factor 114	GRMZM2G095899	B73 RefGen_v3	Gene	Chr1	257635033	257637914	bhlh114		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
411	bhlh115	bHLH-transcription factor 115	GRMZM2G068604	B73 RefGen_v3	Gene	Chr1	178455867	178460697	bhlh115		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
412	bhlh116	bHLH-transcription factor 116	GRMZM2G042895	B73 RefGen_v3	Gene	Chr10	76600002	76602213	bhlh116		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
413	bhlh117	bHLH-transcription factor 117	GRMZM2G062541	B73 RefGen_v3	Gene	Chr10	87704026	87706060	bhlh117		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
414	bhlh118	bHLH-transcription factor 118	GRMZM2G061906	B73 RefGen_v3	Gene	Chr6	151319278	151321414	bhlh118		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
415	bhlh119	bHLH-transcription factor 119	GRMZM5G863198	B73 RefGen_v3	Gene	Chr5	150359143	150360185	bhlh119		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
416	bhlh12	bHLH-transcription factor 12	GRMZM2G316758	B73 RefGen_v3	Gene	Chr4	174031590	174034049	bhlh12		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
417	bhlh120	bHLH-transcription factor 120	GRMZM2G109605	B73 RefGen_v3	Gene	Chr6	49157774	49159839	bhlh120		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
418	bhlh121	bHLH-transcription factor 121	GRMZM2G083504	B73 RefGen_v3	Gene	Chr2	192028339	192031016	bhlh121		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
419	bhlh122	bHLH-transcription factor 122	AC233960.1_FG005	B73 RefGen_v3	Gene	Chr5	200017893	200019898	bhlh122		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
420	bhlh123	bHLH-transcription factor 123	GRMZM2G369629	B73 RefGen_v3	Gene	Chr6	124380275	124381777	bhlh123		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
421	bhlh124	bHLH-transcription factor 124	GRMZM2G132550	B73 RefGen_v3	Gene	Chr6	132371821	132374168	bhlh124		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
422	bhlh125	bHLH-transcription factor 125	GRMZM2G017349	B73 RefGen_v3	Gene	Chr9	16492659	16496592	bhlh125		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
423	bhlh126	bHLH-transcription factor 126	GRMZM2G057413	B73 RefGen_v3	Gene	Chr3	148071103	148072213	bhlh126		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
424	bhlh127	bHLH-transcription factor 127	GRMZM2G128807	B73 RefGen_v3	Gene	Chr5	62292037	62293983	bhlh127		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
425	bhlh128	bHLH-transcription factor 128	GRMZM2G314882	B73 RefGen_v3	Gene	Chr4	240582530	240585487	bhlh128		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
426	bhlh129	bHLH-transcription factor 129	GRMZM5G856837	B73 RefGen_v3	Gene	Chr5	69476595	69479221	bhlh129		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
427	bhlh13	bHLH-transcription factor 13	GRMZM2G091003	B73 RefGen_v3	Gene	Chr4	157508570	157511308	bhlh13		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
428	bhlh130	bHLH-transcription factor 130	GRMZM2G033356	B73 RefGen_v3	Gene	Chr4	23448577	23452318	bhlh130	bhlh130, scream, transcription factor SCREAM2-like, ZmICEb	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
429	bhlh131	bHLH-transcription factor 131	GRMZM2G171464	B73 RefGen_v3	Gene	Chr9	154113331	154114780	bhlh131		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
430	bhlh132	bHLH-transcription factor 132	GRMZM2G114873	B73 RefGen_v3	Gene	Chr3	166491755	166495032	bhlh132	AY111296, bhlh132, ZmKS, ZmOST1 (Open Stomata1) Kinase Substrate	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
431	bhlh133	bHLH-transcription factor 133	GRMZM2G437481	B73 RefGen_v3	Gene	Chr10	126674304	126678092	bhlh133		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
432	bhlh134	bHLH-transcription factor 134	GRMZM2G086474	B73 RefGen_v3	Gene	Chr10	135701832	135705430	bhlh134		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
433	bhlh135	bHLH-transcription factor 135	GRMZM2G134735	B73 RefGen_v3	Gene	Chr1	199103560	199104328	bhlh135		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
434	bhlh136	bHLH-transcription factor 136	GRMZM2G144275	B73 RefGen_v3	Gene	Chr7	137522634	137525144	bhlh136		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
435	bhlh137	bHLH-transcription factor 137	GRMZM2G019806	B73 RefGen_v3	Gene	Chr1	271047086	271049436	bhlh137		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
436	bhlh138	bHLH-transcription factor 138	GRMZM2G176141	B73 RefGen_v3	Gene	Chr2	180804696	180807605	bhlh138		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
437	bhlh139	bHLH-transcription factor 139	GRMZM2G064638	B73 RefGen_v3	Gene	Chr5	140971813	140976844	bhlh139		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
438	bhlh14	bHLH-transcription factor 14	GRMZM5G817854	B73 RefGen_v3	Gene	Chr3	159527964	159528647	bhlh14		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
439	bhlh140	bHLH-transcription factor 140	GRMZM2G475289	B73 RefGen_v3	Gene	Chr1	4742268	4744173	bhlh140	bhlh140, rs131186261, ss196527489, transcription factor bHLH57-like, umc164c	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
440	bhlh141	bHLH-transcription factor 141	GRMZM2G080168	B73 RefGen_v3	Gene	Chr4	17257180	17259695	bhlh141		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
441	bhlh142	bHLH-transcription factor 142	GRMZM2G074438	B73 RefGen_v3	Gene	Chr6	98786270	98791819	bhlh142		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
442	bhlh143	bHLH-transcription factor 143	GRMZM2G043854	B73 RefGen_v3	Gene	Chr9	141691622	141695021	bhlh143		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
443	bhlh144	bHLH-transcription factor 144	GRMZM2G042893	B73 RefGen_v3	Gene	Chr2	81074165	81077414	bhlh144		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
444	bhlh145	bHLH-transcription factor 145	GRMZM2G472671	B73 RefGen_v3	Gene	Chr1	196839526	196840758	bhlh145		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
445	bhlh146	bHLH-transcription factor 146	GRMZM2G085467	B73 RefGen_v3	Gene	Chr7	132922697	132925252	bhlh146		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
446	bhlh147	bHLH-transcription factor 147	GRMZM2G383841	B73 RefGen_v3	Gene	Chr2	209280712	209282012	bhlh147		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
447	bhlh148	bHLH-transcription factor 148	GRMZM2G080054	B73 RefGen_v3	Gene	Chr2	9449250	9451125	bhlh148		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
448	bhlh15	bHLH-transcription factor 15	GRMZM2G057260	B73 RefGen_v3	Gene	Chr7	162119125	162124837	bhlh15		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
449	bhlh150	bHLH-transcription factor 150	GRMZM2G045431	B73 RefGen_v3	Gene	Chr7	125355436	125357466	bhlh150		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
450	bhlh151	bHLH-transcription factor 151	GRMZM2G137541	B73 RefGen_v3	Gene	Chr2	189054253	189057549	bhlh151		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
451	bhlh152	bHLH-transcription factor 152	GRMZM5G839518	B73 RefGen_v3	Gene	Chr5	174979821	174983548	bhlh152		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
452	bhlh153	bHLH-transcription factor 153	GRMZM2G036554	B73 RefGen_v3	Gene	Chr10	87433402	87434930	bhlh153		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
453	bhlh154	bHLH-transcription factor 154	GRMZM2G385543	B73 RefGen_v3	Gene	Chr5	9129443	9131483	bhlh154		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
454	bhlh155	bHLH-transcription factor 155	GRMZM2G042101	B73 RefGen_v3	Gene	Chr4	181930597	181931947	bhlh155		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
455	bhlh156	bHLH-transcription factor 156	GRMZM2G317450	B73 RefGen_v3	Gene	Chr5	204572094	204577083	bhlh156		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
456	bhlh157	bHLH-transcription factor 157	GRMZM2G009478	B73 RefGen_v3	Gene	Chr2	189179955	189185728	bhlh157		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
457	bhlh158	bHLH-transcription factor 158	GRMZM2G165090	B73 RefGen_v3	Gene	Chr1	168447178	168451942	bhlh158		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
458	bhlh159	bHLH-transcription factor 159	GRMZM2G004356	B73 RefGen_v3	Gene	Chr5	4217936	4222849	bhlh159		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
459	bhlh160	bHLH-transcription factor 160	GRMZM2G006631	B73 RefGen_v3	Gene	Chr1	19099172	19101186	bhlh160		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
460	bhlh161	bHLH-transcription factor 161	GRMZM2G045883	B73 RefGen_v3	Gene	Chr5	208944482	208949818	bhlh161		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
461	bhlh162	bHLH-transcription factor 162	GRMZM2G093744	B73 RefGen_v3	Gene	Chr10	83606148	83609440	bhlh162		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
462	bhlh163	bHLH-transcription factor 163	GRMZM5G865967	B73 RefGen_v3	Gene	Chr1	172897122	172899655	bhlh163		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
463	bhlh164	bHLH-transcription factor 164	GRMZM2G058451	B73 RefGen_v3	Gene	Chr7	155380896	155384951	bhlh164		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
464	bhlh165	bHLH-transcription factor 165	GRMZM2G145579	B73 RefGen_v3	Gene	Chr4	47618440	47620839	bhlh165		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
465	bhlh166	bHLH-transcription factor 166	GRMZM2G114444	B73 RefGen_v3	Gene	Chr3	218561885	218567450	bhlh166		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
466	bhlh167	bHLH-transcription factor 167	GRMZM2G147685	B73 RefGen_v3	Gene	Chr2	52437508	52442955	bhlh167	bhlh167, zhoupi (Chinese for 'shrivelled'), ZmZHOUPI, ZmZOU, zou1	transcription factor family by the GRASSIUS project (Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
467	bhlh168	bHLH-transcription factor 168	GRMZM2G030744	B73 RefGen_v3	Gene	Chr5	214476567	214480784	bhlh168		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
468	bhlh169	bHLH-transcription factor 169	GRMZM2G113257	B73 RefGen_v3	Gene	Chr2	187772580	187773665	bhlh169		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
469	bhlh17	bHLH-transcription factor 17	GRMZM2G137358	B73 RefGen_v3	Gene	Chr1	289415533	289418791	bhlh17		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
470	bhlh170	bHLH-transcription factor 170	GRMZM2G082630	B73 RefGen_v3	Gene	Chr1	200448170	200449019	bhlh170		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
471	bhlh171	bHLH-transcription factor 171	GRMZM2G024530	B73 RefGen_v3	Gene	Chr9	11565132	11570108	bhlh171		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
472	bhlh172	bHLH-transcription factor 172	GRMZM2G017586	B73 RefGen_v3	Gene	Chr4	35609001	35611562	bhlh172		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
473	bhlh173	bHLH-transcription factor 173	GRMZM5G882527	B73 RefGen_v3	Gene	Chr1	195753205	195755657	bhlh173		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
474	bhlh174	bHLH-transcription factor 174	GRMZM2G016039	B73 RefGen_v3	Gene	Chr4	63778666	63781023	bhlh174		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
475	bhlh175	bHLH-transcription factor 175	GRMZM2G173534	B73 RefGen_v3	Gene	Chr3	156404566	156407511	bhlh175	bhlh175, cl27985_1a, scream, transcription factor SCREAM2-like, ZmICEa, ZmmICE1	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
476	bhlh18	bHLH-transcription factor 18	GRMZM2G082343	B73 RefGen_v3	Gene	Chr5	9626997	9629496	bhlh18		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
477	bhlh19	bHLH-transcription factor 19	GRMZM2G066057	B73 RefGen_v3	Gene	Chr8	8416520	8418397	bhlh19		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
478	bhlh20	bHLH-transcription factor 20	GRMZM2G414252	B73 RefGen_v3	Gene	Chr2	185616246	185617611	bhlh20		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
479	bhlh21	bHLH-transcription factor 21	AC233899.1_FG002	B73 RefGen_v3	Gene	Chr9	149930657	149932165	bhlh21		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
480	bhlh22	bHLH-transcription factor 22	GRMZM2G162450	B73 RefGen_v3	Gene	Chr8	75508770	75510438	bhlh22		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
481	bhlh23	bHLH-transcription factor 23	GRMZM2G178182	B73 RefGen_v3	Gene	Chr2	193433358	193435869	bhlh23		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
482	bhlh24	bHLH-transcription factor 24	GRMZM2G085751	B73 RefGen_v3	Gene	Chr4	225161834	225165399	bhlh24		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
483	bhlh25	bHLH-transcription factor 25	GRMZM2G081816	B73 RefGen_v3	Gene	Chr3	219263852	219266149	bhlh25		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
484	bhlh26	bHLH-transcription factor 26	GRMZM2G018472	B73 RefGen_v3	Gene	Chr1	168430589	168435266	bhlh26		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
485	bhlh27	bHLH-transcription factor 27	GRMZM2G092091	B73 RefGen_v3	Gene	Chr1	272109897	272113700	bhlh27		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
486	bhlh28	bHLH-transcription factor 28	GRMZM2G155043	B73 RefGen_v3	Gene	Chr1	257844735	257852201	bhlh28		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
487	bhlh29	bHLH-transcription factor 29	GRMZM2G101350	B73 RefGen_v3	Gene	Chr5	200993308	200996110	bhlh29		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
488	bhlh3	bHLH-transcription factor 3	GRMZM2G180452	B73 RefGen_v3	Gene	Chr1	29260545	29264281	bhlh3	bhlh3, putative HLH DNA-binding domain superfamily protein, umc76, umc76a, umc76(gne)	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
489	bhlh30	bHLH-transcription factor 30	GRMZM2G036092	B73 RefGen_v3	Gene	Chr5	207554896	207556510	bhlh30		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
490	bhlh31	bHLH-transcription factor 31	GRMZM2G435015	B73 RefGen_v3	Gene	Chr7	140262343	140265347	bhlh31		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
491	bhlh32	bHLH-transcription factor 32	GRMZM2G180406	B73 RefGen_v3	Gene	Chr3	162105905	162109184	bhlh32		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
492	bhlh33	bHLH-transcription factor 33	GRMZM2G015666	B73 RefGen_v3	Gene	Chr2	188465323	188467491	bhlh33		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
493	bhlh34	bHLH-transcription factor 34	GRMZM2G045109	B73 RefGen_v3	Gene	Chr9	68081459	68085268	bhlh34		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
494	bhlh35	bHLH-transcription factor 35	GRMZM2G173372	B73 RefGen_v3	Gene	Chr1	7991271	7993431	bhlh35	DNA binding protein , umc1269, umc1305	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
495	bhlh36	bHLH-transcription factor 36	GRMZM2G008691	B73 RefGen_v3	Gene	Chr4	179831785	179834012	bhlh36		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
496	bhlh37	bHLH-transcription factor 37	GRMZM2G107672	B73 RefGen_v3	Gene	Chr2	160532119	160533504	bhlh37		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
497	bhlh38	bHLH-transcription factor 38	GRMZM2G165188	B73 RefGen_v3	Gene	Chr4	4752932	4754547	bhlh38		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
498	bhlh39	bHLH-transcription factor 39	GRMZM2G162382	B73 RefGen_v3	Gene	Chr7	10699275	10703311	bhlh39		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
499	bhlh4	bHLH-transcription factor 4	AC177924.2_FG001	B73 RefGen_v3	Gene	Chr2	71347459	71352265	bhlh4		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
500	bhlh40	bHLH-transcription factor 40	GRMZM2G526668	B73 RefGen_v3	Gene	Chr4	82667624	82670258	bhlh40		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
501	bhlh41	bHLH-transcription factor 41	GRMZM2G171818	B73 RefGen_v3	Gene	Chr2	221338746	221341097	bhlh41		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
502	bhlh42	bHLH-transcription factor 42	GRMZM2G107276	B73 RefGen_v3	Gene	Chr1	214199438	214201742	bhlh42		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
503	bhlh43	bHLH-transcription factor 43	GRMZM2G165042	B73 RefGen_v3	Gene	Chr1	252434109	252437685	bhlh43		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
504	bhlh44	bHLH-transcription factor 44	GRMZM2G175480	B73 RefGen_v3	Gene	Chr8	91709652	91711010	bhlh44		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
505	bhlh45	bHLH-transcription factor 45	GRMZM2G481280	B73 RefGen_v3	Gene	Chr6	6917077	6917523	bhlh45		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
506	bhlh46	bHLH-transcription factor 46	GRMZM2G148723	B73 RefGen_v3	Gene	Chr3	1600639	1613076	bhlh46		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
507	bhlh47	bHLH-transcription factor 47	GRMZM2G065374	B73 RefGen_v3	Gene	Chr1	283670986	283676031	bhlh47	transcription factor PIF5	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
508	bhlh48	bHLH-transcription factor 48	GRMZM2G027068	B73 RefGen_v3	Gene	Chr1	291976341	291978412	bhlh48	rs131185500 , ss196524020	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
509	bhlh49	bHLH-transcription factor 49	GRMZM2G137374	B73 RefGen_v3	Gene	Chr1	6562587	6564261	bhlh49		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
510	bhlh5	bHLH-transcription factor 5	GRMZM2G116785	B73 RefGen_v3	Gene	Chr6	107553355	107556923	bhlh5		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
511	bhlh50	bHLH-transcription factor 50	GRMZM2G137380	B73 RefGen_v3	Gene	Chr1	6567359	6573560	bhlh50		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
512	bhlh51	bHLH-transcription factor 51	GRMZM2G139372	B73 RefGen_v3	Gene	Chr4	238494709	238498244	bhlh51		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
513	bhlh52	bHLH-transcription factor 52	GRMZM5G812883	B73 RefGen_v3	Gene	Chr4	39775178	39776044	bhlh52		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
514	bhlh53	bHLH-transcription factor 53	GRMZM2G111146	B73 RefGen_v3	Gene	Chr5	198825972	198829612	bhlh53		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
515	bhlh54	bHLH-transcription factor 54	AC193786.3_FG005	B73 RefGen_v3	Gene	Chr8	157462749	157463805	bhlh54		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
516	bhlh55	bHLH-transcription factor 55	GRMZM2G030762	B73 RefGen_v3	Gene	Chr8	162106868	162110024	bhlh55		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
517	bhlh56	bHLH-transcription factor 56	GRMZM2G072376	B73 RefGen_v3	Gene	Chr1	36921186	36922008	bhlh56		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
518	bhlh57	bHLH-transcription factor 57	GRMZM2G159937	B73 RefGen_v3	Gene	Chr3	204715844	204717904	bhlh57		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
519	bhlh58	bHLH-transcription factor 58	AC198518.3_FG005	B73 RefGen_v3	Gene	Chr3	107386150	107387495	bhlh58		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
520	bhlh59	bHLH-transcription factor 59	GRMZM2G303463	B73 RefGen_v3	Gene	Chr2	227935074	227939134	bhlh59	homologue to AtMYC2, transcription factor bHLH13-like, ZmMYC2a	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
521	bhlh6	bHLH-transcription factor 6	GRMZM2G417597	B73 RefGen_v3	Gene	Chr2	190350810	190353409	bhlh6		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
522	bhlh60	bHLH-transcription factor 60	GRMZM2G016756	B73 RefGen_v3	Gene	Chr5	5102185	5106027	bhlh60		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
523	bhlh61	bHLH-transcription factor 61	GRMZM5G818776	B73 RefGen_v3	Gene	Chr4	39756428	39757291	bhlh61		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
524	bhlh62	bHLH-transcription factor 62	GRMZM2G333582	B73 RefGen_v3	Gene	Chr8	21912581	21916036	bhlh62		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
525	bhlh63	bHLH-transcription factor 63	GRMZM2G166642	B73 RefGen_v3	Gene	Chr3	3342194	3344518	bhlh63		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
526	bhlh64	bHLH-transcription factor 64	GRMZM2G175955	B73 RefGen_v3	Gene	Chr1	182200079	182224660	bhlh64		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
527	bhlh66	bHLH-transcription factor 66	GRMZM2G163233	B73 RefGen_v3	Lapsed Locus	Chr2	205125283	205135718	bhlh66	ms32	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
528	bhlh68	bHLH-transcription factor 68	GRMZM2G115960	B73 RefGen_v3	Gene	Chr3	48806991	48810673	bhlh68	phytochrome interacting factor3.1, ZmPif3.1	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
529	bhlh69	bHLH-transcription factor 69	GRMZM2G378653	B73 RefGen_v3	Gene	Chr9	102204171	102210509	bhlh69		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
530	bhlh7	bHLH-transcription factor 7	GRMZM2G042920	B73 RefGen_v3	Gene	Chr10	142141640	142143666	bhlh7		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
531	bhlh70	bHLH-transcription factor 70	GRMZM2G397755	B73 RefGen_v3	Gene	Chr3	5777497	5779734	bhlh70		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
532	bhlh71	bHLH-transcription factor 71	GRMZM2G120021	B73 RefGen_v3	Gene	Chr1	257791786	257797338	bhlh71		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
533	bhlh72	bHLH-transcription factor 72	GRMZM2G170559	B73 RefGen_v3	Gene	Chr5	155134147	155137380	bhlh72		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
534	bhlh73	bHLH-transcription factor 73	GRMZM2G008898	B73 RefGen_v3	Gene	Chr2	233050785	233053965	bhlh73		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
535	bhlh74	bHLH-transcription factor 74	GRMZM2G035156	B73 RefGen_v3	Gene	Chr1	15133264	15135363	bhlh74		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
536	bhlh75	bHLH-transcription factor 75	GRMZM2G395549	B73 RefGen_v3	Gene	Chr3	113451859	113489330	bhlh75		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
537	bhlh76	bHLH-transcription factor 76	GRMZM2G112629	B73 RefGen_v3	Gene	Chr3	29613767	29617374	bhlh76		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
538	bhlh77	bHLH-transcription factor 77	GRMZM2G463133	B73 RefGen_v3	Gene	Chr8	138472851	138478264	bhlh77		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
539	bhlh78	bHLH-transcription factor 78	GRMZM2G049686	B73 RefGen_v3	Gene	Chr1	178465632	178471112	bhlh78		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
540	bhlh79	bHLH-transcription factor 79	GRMZM2G173862	B73 RefGen_v3	Gene	Chr8	171949309	171951373	bhlh79		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
541	bhlh8	bHLH-transcription factor 8	GRMZM2G038479	B73 RefGen_v3	Gene	Chr4	195089318	195090145	bhlh8		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
542	bhlh80	bHLH-transcription factor 80	GRMZM2G142932	B73 RefGen_v3	Gene	Chr2	205425915	205430161	bhlh80		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
543	bhlh81	bHLH-transcription factor 81	GRMZM5G828396	B73 RefGen_v3	Gene	Chr1	192065332	192068032	bhlh81		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
544	bhlh82	bHLH-transcription factor 82	GRMZM2G417164	B73 RefGen_v3	Gene	Chr8	78660104	78661278	bhlh82		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
545	bhlh83	bHLH-transcription factor 83	GRMZM2G169947	B73 RefGen_v3	Gene	Chr3	29652992	29653739	bhlh83		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
546	bhlh84	bHLH-transcription factor 84	GRMZM2G159456	B73 RefGen_v3	Gene	Chr1	15267736	15269173	bhlh84		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
547	bhlh85	bHLH-transcription factor 85	GRMZM2G354618	B73 RefGen_v3	Gene	Chr4	39739891	39740988	bhlh85		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
548	bhlh86	bHLH-transcription factor 86	GRMZM5G818643	B73 RefGen_v3	Gene	Chr7	129994890	129998161	bhlh86		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
549	bhlh87	bHLH-transcription factor 87	GRMZM2G027563	B73 RefGen_v3	Gene	Chr7	115302848	115305396	bhlh87		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
550	bhlh88	bHLH-transcription factor 88	GRMZM2G350165	B73 RefGen_v3	Gene	Chr2	181310638	181313797	bhlh88		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
551	bhlh89	bHLH-transcription factor 89	AC216731.3_FG001	B73 RefGen_v3	Gene	Chr5	201922854	201924055	bhlh89		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
552	bhlh9	bHLH-transcription factor 9	GRMZM2G407119	B73 RefGen_v3	Gene	Chr9	145064265	145067533	bhlh9		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
553	bhlh90	bHLH-transcription factor 90	GRMZM2G153454	B73 RefGen_v3	Gene	Chr7	156776841	156779616	bhlh90		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
554	bhlh91	bHLH-transcription factor 91	GRMZM2G049229	B73 RefGen_v3	Gene	Chr9	112025169	112028072	bhlh91		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
555	bhlh92	bHLH-transcription factor 92	GRMZM2G164341	B73 RefGen_v3	Gene	Chr8	137796648	137798798	bhlh92		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
556	bhlh93	bHLH-transcription factor 93	GRMZM5G899865	B73 RefGen_v3	Gene	Chr1	267629500	267631521	bhlh93		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
557	bhlh94	bHLH-transcription factor 94	GRMZM5G849600	B73 RefGen_v3	Gene	Chr3	219912558	219917830	bhlh94		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
558	bhlh95	bHLH-transcription factor 95	GRMZM2G107560	B73 RefGen_v3	Gene	Chr2	194532042	194532930	bhlh95		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
559	bhlh96	bHLH-transcription factor 96	GRMZM2G172297	B73 RefGen_v3	Gene	Chr2	223952471	223954890	bhlh96	bhlh96, scream, transcription factor SCREAM2-like, ZmICEc	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
560	bhlh97	bHLH-transcription factor 97	AC149829.2_FG004	B73 RefGen_v3	Gene	Chr9	151395822	151396321	bhlh97		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
561	bhlh98	bHLH-transcription factor 98	GRMZM2G340177	B73 RefGen_v3	Gene	Chr9	80126699	80131343	bhlh98		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
562	bhlh99	bHLH-transcription factor 99	GRMZM2G076636	B73 RefGen_v3	Gene	Chr8	29235609	29238897	bhlh99		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
563	bif1	barren inflorescence1	GRMZM2G130953	B73 RefGen_v3	Gene	Chr8	18321199	18323290	bif1	AUX22 AUX/IAA transcription factor, Aux/IAA-transcription factor 35, barren inflorescence1, bif1, Bif*-1440, iaa35, Tht*-1440	dominant Bif1 plants have ear and tassel with many fewer spikelets, bare rachis appendages
564	bif2	barren inflorescence2	GRMZM2G171822	B73 RefGen_v3	Gene	Chr1	173865554	173867297	bif2	ba*-1447, ba*-74-369-2, barren inflorescence2, bif2, bif*-47330, bif*-N2354	recessive few-branched tassel, normally no pollen shed; variable expression on ear with 0-2 spikelets produced at each floral node
565	bif4	barren inflorescence4	GRMZM5G864847	B73 RefGen_v3	Gene	Chr6	130188997	130190406	bif4	Aux/IAA-transcription factor 27, bif4, GRMZM5G864847/IAA20 , IAA16 - auxin-responsive Aux/IAA family member , iaa27, ZmIAA20	like Bif1; dominant plants have ear and tassel with many fewer spikelets, bare rachis appendage
566	bige1	big embryo1	GRMZM2G148937	B73 RefGen_v3	Gene	Chr5	1543960	1547006	bige1	be1, bige1, umc1423	mutant causes accelerated leaf and root initiation as well as enlargement of the embryo scutellum
567	bip1	Binding protein homolog1	GRMZM2G114793	B73 RefGen_v3	Gene	Chr5	69354043	69357915	bip1	b-70, Binding protein homolog1, bip1, BiP homolog1, gsy249b(b70), ncr200b, ncr200b(rip), Stress70er	cDNA clone, protein body, putative molecular chaperone of hsp70 family
568	bip2	Binding protein homolog2	GRMZM2G415007	B73 RefGen_v3	Gene	Chr4	240596989	240600763	bip2	Binding protein homolog2, bip2, cBiPe3, lumenal binding protein cBiPe3, umc1058	cDNA, SSR umc1058; regulation similar to bip1; 2 loci, one on 5L, the other 4L
569	bk2	brittle stalk2	GRMZM2G109326	B73 RefGen_v3	Gene	Chr9	123497640	123499951	bk2	bk2, brittle stalk2	brittle plant parts after 4-leaf stage
570	bm1	brown midrib1	GRMZM5G844562	B73 RefGen_v3	Gene	Chr5	99030278	99034633	bm1	bm1, brown midrib1, cad2, cdh2, cinnamyl alcohol dehydrogenase2, CL1675_1, CL1675_1(412), ZmCAD	the midribs of healthy leaves at flowering; lignin content at maturity 86% of normal; encodes cinnamyl alcohol dehydrogenase
571	bm2	brown midrib2	GRMZM2G347056	B73 RefGen_v3	Gene	Chr1	292165519	292171793	bm2	AY109096, bm2, brown midrib2, csu134a, csu134a(thf), methylenetetrahydrofolate reductase1, mtf1, PCO119715(100), ZmMTHFR-1	brown pigmentation in the leaf midrib and tissues accumulate reduced levels of lignin; like bm1
572	bm3	brown midrib3	AC196475.3_FG004	B73 RefGen_v3	Gene	Chr4	32278881	32280752	bm3	bm3, brown midrib3, comt, IDP1403, mc1, omt1, ZmCOMT1	has improved digestibility in ruminants; silage corn with bm3 is in production. However, bm3 results in weaker stalks, reduced stover and grain yield, and in some cases reduced maturity;
573	bm4	brown midrib4	GRMZM2G393334	B73 RefGen_v3	Gene	Chr9	154723992	154730009	bm4	bm4, brown midrib4, fgp1, PCO067114, PCO067114(707), ZmFPGS	mutant looks like bm1; encodes folylpolyglutamate synthetase
574	bnl(pho80)	phosphate regulatory homolog1	GRMZM2G063162	B73 RefGen_v3	Gene	Chr5	139395266	139403105	bnl(pho80)	05c04b08, BAG family molecular chaperone regulator 6, bnl(pho80), phosphate regulatory homolog1	endosperm cDNA 5C04B08, similar to yeast pho80 gene
575	bnl10.13a		GRMZM2G142832	B73 RefGen_v3	Gene	Chr10	137853898	137858727	bnl10.13a	bnl10.13, bnl10.13a	NCBI: probable serine/threonine-protein kinase PIX13
576	bnl8.15		GRMZM2G153127	B73 RefGen_v3	Gene	Chr3	2060989	2068244	bnl8.15	bnl8.15	NCBI: putative E3 ubiquitin-protein ligase LIN
577	bpd1	BTB/POZ domain1	GRMZM5G805008	B73 RefGen_v3	Gene	Chr7	37739239	37740147	bpd1	bpd1, ZmTRAF46	encodes BTB/POZ domain protein orthologous to AT3G06190.1, LOC_Os06g45730.1, Sb02g010170
578	br2	brachytic2	GRMZM2G315375	B73 RefGen_v3	Gene	Chr1	202334824	202342008	br2	abcb1, br2, brachytic2, Hahn 6 dwarf, mi1, Oakes dwarf, pgp1, R4 dwarf, rs131839167 , umc2238, umc2239, ZmPGP1	like Arabidopsis ABC transporter B family member 1. like br1; mi1 is allelic and preceded (1935), but br2 name is retained due to long usage
579	brd1	brassinosteroid-deficient dwarf1	GRMZM2G103773	B73 RefGen_v3	Gene	Chr1	249371977	249376239	brd1	brassinosteroid-deficient dwarf1, brd1, cytochrome P450 CYP85A1, tiny plant*-8446, ty*-8446	Mutant plants have essentially no internode elongation and exhibit no etiolation response when germinated in the dark.
580	bri1a	brassinosteroid insensitive1a	GRMZM2G048294	B73 RefGen_v3	Gene	Chr8	154615633	154619705	bri1a	bri1a	Encodes a brassinosteroid receptor
581	bri1b	brassinosteroid insensitive1b	GRMZM2G449830	B73 RefGen_v3	Gene	Chr5	60684674	60686106	bri1b	bri1b	Encodes a brassinosteroid receptor
582	brk1	brick1	GRMZM5G842058	B73 RefGen_v3	Gene	Chr5	216747837	216749400	brk1	brick1, brk1	Involved in formation of epidermal cell lobes as well as for properly polarized divisions of stomatal subsidiary mother cells.
583	brk3	brick3	GRMZM2G180150	B73 RefGen_v3	Gene	Chr10	2033382	2034248	brk3	brick3, brk3, nap1 homolog	Involved in formation of epidermal cell lobes as well as for properly polarized divisions of stomatal subsidiary mother cells.
584	brk3	brick3	GRMZM5G886363	B73 RefGen_v3	Gene	Chr10	2011814	2017183	brk3	brick3, brk3, nap1 homolog	Involved in formation of epidermal cell lobes as well as for properly polarized divisions of stomatal subsidiary mother cells.
585	brl1	bri1-like receptor kinase1	GRMZM2G092604	B73 RefGen_v3	Gene	Chr7	79119386	79123848	brl1	brassinosteroid insensitive1-like receptor kinase, brl1	Encodes a brassinosteroid insensitive1-like receptor kinase.
586	brl2	bri1-like receptor kinase2	GRMZM2G002515	B73 RefGen_v3	Gene	Chr1	113534938	113538490	brl2	brassinosteroid insensitive1-like receptor kinase, brl2	Encodes a brassinosteroid insensitive1-like receptor kinase.
587	brl3	bri1-like receptor kinase3	GRMZM2G438007	B73 RefGen_v3	Gene	Chr4	65769675	65773352	brl3	brassinosteroid insensitive1-like receptor kinase, brl3	Encodes a brassinosteroid insensitive1-like receptor kinase.
588	brm1	brahma1	GRMZM2G163849	B73 RefGen_v3	Gene	Chr5	68902393	68913355	brm1	brahma, BRAHMA, brm1, pco141670, pco141670(283)	protein, then copurified from maize with complexes that regulate cellular growth and division.. transcription regulatory protein SNF2 putative
589	brs1	brassinosteroid synthesis1	GRMZM2G065635	B73 RefGen_v3	Gene	Chr1	30536285	30542652	brs1	brassinosteroid synthesis1, brs1, CYP90B14v1, cytochrome P450 CYP90B14v1, cytochrome P450 CYP90B14v2, Dwf4, DWF4, steroid 22-alpha-hydroxylase protein (Dwf4), ZmDWF4	

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
590	bsd2	bundle sheath defective2	GRMZM2G062788	B73 RefGen_v3	Gene	Chr1	158329236	158340592	bsd2	bsd2, bundle sheath defective2, CL1540_1	bundle sheath chloroplasts disrupted; high chlorophyll fluorescence, seedling lethal
591	bsdtf1	BSD-transcription factor 1	GRMZM2G170161	B73 RefGen_v3	Gene	Chr2	226346872	226351462	bsdtf1	bsd1	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
592	bsdtf10	BSD-transcription factor 10	GRMZM2G368898	B73 RefGen_v3	Gene	Chr10	146122401	146124707	bsdtf10	bsd10	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
593	bsdtf2	BSD-transcription factor 2	GRMZM2G013378	B73 RefGen_v3	Gene	Chr3	41600483	41602814	bsdtf2	bsd2	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
594	bsdtf3	BSD-transcription factor 3	GRMZM5G870572	B73 RefGen_v3	Gene	Chr4	33727744	33735419	bsdtf3	bsd3	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
595	bsdtf4	BSD-transcription factor 4	GRMZM2G127548	B73 RefGen_v3	Gene	Chr4	164281187	164285309	bsdtf4	bsd4	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
596	bsdtf5	BSD-transcription factor 5	GRMZM2G451806	B73 RefGen_v3	Gene	Chr5	121089794	121095789	bsdtf5	bsd5	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
597	bsdtf6	BSD-transcription factor 6	GRMZM2G145594	B73 RefGen_v3	Gene	Chr5	204479884	204482990	bsdtf6	bsd6	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
598	bsdtf7	BSD-transcription factor 7	GRMZM2G111672	B73 RefGen_v3	Gene	Chr7	170460497	170462364	bsdtf7	bsd7	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
599	bsdtf8	BSD-transcription factor 8	GRMZM2G027535	B73 RefGen_v3	Gene	Chr8	172530034	172533971	bsdtf8	bsd8	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
600	bsdtf9	BSD-transcription factor 9	GRMZM2G167207	B73 RefGen_v3	Gene	Chr9	14848000	14852986	bsdtf9	bsd9	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
601	bss1	bundle sheath strands specific1	GRMZM2G168552	B73 RefGen_v3	Gene	Chr8	156640234	156641211	bss1	aba2, abscisic acid stress and ripening-induced4, B70, BSP1, bss1, bundle sheath strands specific, csu725, umc1287, ZmASR4	encodes a photosynthesis-related protein with a deduced amino acid sequence with high homology to tomato Asr1 in the C-terminal region; stress-inducilible;
602	bt1	brittle endosperm1	GRMZM2G144081	B73 RefGen_v3	Gene	Chr5	112964229	112966353	bt1	brittle endosperm1, bt1, cv, gsy60c(bt2), sh3, sh*-459, sh5, sh*-N1992, sh*-op1992	mature kernel collapsed, angular, often translucent and brittle (alleles sh3, sh5)
603	bt2	brittle endosperm2	GRMZM2G068506	B73 RefGen_v3	Gene	Chr4	58979526	58985686	bt2	rs131175589, rs131175590, rs131175591, ss196415731, ss196415734, ss196415736, ss196415738	like bt1; endosperm ADPG pyrophosphorylase subunit; with sh2 complements E. coli glgC
604	Bt2		GRMZM2G068506	B73 RefGen_v3	Probed Site	Chr4	58979526	58985686	Bt2	Bt2	
605	btf3	BTF3 homolog	GRMZM2G041881	B73 RefGen_v3	Gene	Chr1	2798951	2801848	btf3	btf3, BTF3b, BTF3 homolog, IDP1700, IDP2009, IDP286, PCO108140(3), PCO108140a, putative transcription factor	putative transcription factor, homology of mRNA to rice AY224525, identified by yeast two-hybrid assays as a gene for proteins interacting with cell cycling components (TIGR TC338706)
606	bub1	budding unhibited by benzimidazoles hor	GRMZM2G105750	B73 RefGen_v3	Gene	Chr7	151985560	152001155	bub1	bub1, Mitotic checkpoint serine/threonine-protein kinase, rs130662382 , rs130662533 , rs132415122	
607	bub3	budding unhibited by benzimidazoles hor	GRMZM5G899300	B73 RefGen_v3	Gene	Chr9	20608590	20614721	bub3	bub3, pco107270a, pco107270b	encodes WD40 repeat-like superfamily protein that is a mitotic checkpoint
608	bv1	brevis plant1	GRMZM2G366698	B73 RefGen_v3	Gene	Chr5	160747586	160759982	bv1	AY110906, br3, brachytic3, brevis plant1, bv1	short internodes, short plant
609	bx1	benzoxazinless1	GRMZM2G085381	B73 RefGen_v3	Gene	Chr4	3260762	3263006	bx1	benzoxazinless1, bx1, PCO064449, pco064449(287), trp1, TRPA, umc1022, umi7	plastid localized, committed step in cyclic hydroxamates/DIMBOA synthesis; insect resistance in young seedlings; SSR umc1022
610	bx10	benzoxazinone synthesis10	GRMZM2G311036	B73 RefGen_v3	Gene	Chr1	66310637	66312743	bx10	5-pentadecatrienyl resorcinol O-methyltransferase-like, bx10, bx10a	
611	bx11	benzoxazinone synthesis11	GRMZM2G336824	B73 RefGen_v3	Gene	Chr1	66393409	66395849	bx11	bx10b, bx11, pco138435	
612	bx12	benzoxazinone synthesis12	GRMZM2G023325	B73 RefGen_v3	Gene	Chr1	66506457	66507471	bx12	bx10c, bx12	
613	bx13	benzoxazinone synthesis13	AC148152.3_FG005	B73 RefGen_v3	Gene	Chr2	231952642	231954277	bx13	bx13	Glc into a new benzoxazinoid intermediate (TRIMBOA-Glc) by an uncommon reaction involving a hydroxylation and a likely ortho-rearrangement of a methoxy group.
614	bx14	benzoxazinone synthesis14	GRMZM2G127418	B73 RefGen_v3	Gene	Chr2	144827059	144828816	bx14	bx14, TIDP3344	encodes an O-methyltransferase that converts DIM2BOA-Glc to HDM2BOA-Glc.
615	bx2	benzoxazinone synthesis2	GRMZM2G085661	B73 RefGen_v3	Gene	Chr4	3265213	3267368	bx2	benzoxazin2, benzoxazinone synthesis2, bx2, cyp5, CYP71C3v2, cyp71c4, CYP71C4, cyp*-Y11368, CYPzm4, cytochrome P450 5, mpik8, umc1164, umc1682	endoplasmic reticulum P450 monoxygenase; synthesis cyclic hyroxamates/DIMBOA; insect resistance in young seedlings; SSR umc1164, umc1682
616	bx3	benzoxazinone synthesis3	GRMZM2G167549	B73 RefGen_v3	Gene	Chr4	3003162	3005932	bx3	benzoxazin3, benzoxazinone synthesis3, bx3, CL1574_1, cyp3, CYP71, CYP71C2, CYPZm2, cytochrome P450, cytochrome P450 CYP71C2v2, gnp_QAE32a05, gpm290, mpik6, umc1017	endoplasmic reticulum P450 monoxygenase; synthesis of cyclic hydroxamates/DIMBOA; insect resistance in young seedlings; SSR umc1017
617	bx4	benzoxazinone synthesis4	GRMZM2G172491	B73 RefGen_v3	Gene	Chr4	3051215	3054036	bx4	cytochrome P450 homolog, mpik5a, mpik5A, mpik5b, mpik5B, pco117584(287), PCO117584b, PHM1184, PZA00136, TIDP9229	endoplasmic reticulum P450 monoxygenase; synthesis of cyclic hydroxamates/DIMBOA; insect resistance in young seedlings; NAM SNP PHM1184
618	bx5	benzoxazinone synthesis5	GRMZM2G063756	B73 RefGen_v3	Gene	Chr4	3112925	3115501	bx5	benzoxazin5, benzoxazinone synthesis5, bx5, csu618(P450), cyp4, cyp71c3, CYP71C3, CYP71C3v2, CYPzm3, mpik7, PCO142958b, umc1276	endoplasmic reticulum monoxygenase; synthesis of cyclic hydroxamates/DIMBOA; insect resistance in young seedlings; SSR umc1276.
619	bx6	benzoxazinone synthesis6	GRMZM6G617209	B73 RefGen_v3	Gene	Chr4	1252638	1254044	bx6	1-aminocyclopropane-1-carboxylate oxidase, 2-oxoglutarate-dependent oxygenase, benzoxazin6, benzoxazinone synthesis6, bx6, umc1232	cytosolic 2-oxoglutarate-dependent dioxygenase; synthesis of cyclohydroxamates/DIMBOA; insect resistance in young seedlings; SSR umc1232
620	bx7	benzoxazinone synthesis7	GRMZM2G441753	B73 RefGen_v3	Gene	Chr4	18244663	18245553	bx7	AY106107, benzoxazinone synthesis7, bx7, IDP478, O-methyltransferase, PCO065952, PCO088803(361), PCO088803a, PZA00115, umc2039	cytosolic O-methyl transferase; synthesis of cyclohydroxamates/DIMBOA; insect resistance in young seedlings; SSR umc2039, INDEL IDP478.
621	bx8	benzoxazinone synthesis8	GRMZM2G085054	B73 RefGen_v3	Gene	Chr4	3214647	3216558	bx8	benzoxazinone synthesis8, bx8, gnp_QBS13f04, gpm562, PCO085820, PCO085820(287)	cytosolic glucosyltransferase; synthesis of cyclic hydroxamates/DIMBOA; insect resistance in young seedlings
622	bx9	benzoxazinone synthesis9	GRMZM2G161335	B73 RefGen_v3	Gene	Chr1	180333582	180335486	bx9	benzoxazinone synthesis9, bx9, gnp_QBL10f08, gpm524, PCO129924, pco129924(50), pza00484, rs131186109	cytosolic glucosyl transferase; redundant with bx8; synthesis of cyclic hydroxamates/DIMBOA; insect resistance in young seedlings
623	bz1	bronze1	GRMZM2G165390	B73 RefGen_v3	Gene	Chr9	11779648	11781406	bz1	agr(bz1), bnl(bz1), bronze1, bz1, npi8-bz1, phi017, umc192(bz1)	modifies purple aleurone and plant color to pale or reddish brown; anthers yellow-fluorescent; allele bz1-m4 = sh1-bz1-m4; SSR phi017. NCBI: UDPG-flavonoid 3-oxy glucosyl transferase
624	bz2	bronze2	GRMZM2G016241	B73 RefGen_v3	Gene	Chr1	241430768	241432121	bz2	bronze2, bz2, GSTU4, pa, umc181(bz2)	like bz1; anthers not fluorescent; an1-6923 mutation includes deletion for Bz2; encodes a glutathione S-transferase conjugating anthocyanins into the vacuole
625	bzip1	bZIP transcription factor1	GRMZM2G117851	B73 RefGen_v3	Gene	Chr3	212260636	212276109	bzip1	BZ-1, bzip1, gnp_QAI2g07, gpm792, ZmbZIP99	
626	bzip10	bZIP-transcription factor 10	GRMZM2G136266	B73 RefGen_v3	Gene	Chr10	7921801	7925637	bzip10		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
627	bzip100	bZIP-transcription factor 100	GRMZM2G033413	B73 RefGen_v3	Gene	Chr9	8230021	8240287	bzip100		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
628	bzip101	bZIP-transcription factor 101	GRMZM2G129247	B73 RefGen_v3	Gene	Chr6	150274418	150276924	bzip101		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
629	bzip102	bZIP-transcription factor 102	GRMZM2G159134	B73 RefGen_v3	Gene	Chr3	186805980	186810898	bzip102		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
630	bzip103	bZIP-transcription factor 103	GRMZM2G092609	B73 RefGen_v3	Gene	Chr5	170106632	170111141	bzip103		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
631	bzip104	bZIP-transcription factor 104	GRMZM2G098904	B73 RefGen_v3	Gene	Chr5	87150348	87153356	bzip104		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
632	bzip105	bZIP-transcription factor 105	GRMZM2G056099	B73 RefGen_v3	Gene	Chr9	134188555	134195791	bzip105		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
633	bzip106	bZIP-transcription factor 106	GRMZM2G055413	B73 RefGen_v3	Gene	Chr6	83866787	83869911	bzip106		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
634	bzip107	bZIP-transcription factor 107	GRMZM2G094352	B73 RefGen_v3	Gene	Chr10	49989443	49992484	bzip107		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
635	bzip108	bZIP-transcription factor 108	GRMZM2G033230	B73 RefGen_v3	Gene	Chr8	120135941	120137704	bzip108		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
636	bzip109	bZIP-transcription factor 109	GRMZM2G366264	B73 RefGen_v3	Gene	Chr10	5534459	5537102	bzip109		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
637	bzip110	bZIP-transcription factor 110	GRMZM2G079365	B73 RefGen_v3	Gene	Chr4	213863947	213880121	bzip110		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
638	bzip111	bZIP-transcription factor 111	GRMZM2G073427	B73 RefGen_v3	Gene	Chr1	170592733	170597621	bzip111		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
639	bzip113	bZIP-transcription factor 113	GRMZM2G445575	B73 RefGen_v3	Gene	Chr10	143949572	143957213	bzip113		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
640	bzip114	bZIP-transcription factor 114	GRMZM2G428184	B73 RefGen_v3	Gene	Chr1	5738361	5741644	bzip114		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
641	bzip115	bZIP-transcription factor 115	GRMZM2G157177	B73 RefGen_v3	Gene	Chr1	32163794	32172639	bzip115		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
642	bzip116	bZIP-transcription factor 116	GRMZM2G132868	B73 RefGen_v3	Gene	Chr8	100221799	100225360	bzip116		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
643	bzip117	bZIP-transcription factor 117	AC233853.1_FG002	B73 RefGen_v3	Gene	Chr3	3820878	3822105	bzip117		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
644	bzip118	bZIP-transcription factor 118	GRMZM2G164848	B73 RefGen_v3	Gene	Chr6	168467346	168469169	bzip118		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
645	bzip119	bZIP-transcription factor 119	GRMZM2G120167	B73 RefGen_v3	Gene	Chr4	16152931	16158076	bzip119		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
646	bzip120	bZIP-transcription factor 120	GRMZM2G052102	B73 RefGen_v3	Gene	Chr4	227156011	227158307	bzip120		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
647	bzip121	bZIP-transcription factor 121	GRMZM2G112483	B73 RefGen_v3	Gene	Chr2	33969678	33974472	bzip121		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
648	bzip122	bZIP-transcription factor 122	GRMZM2G171912	B73 RefGen_v3	Gene	Chr8	17665206	17666030	bzip122		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
649	bzip123	bZIP-transcription factor 123	GRMZM2G002075	B73 RefGen_v3	Gene	Chr2	186805631	186808459	bzip123		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
650	bzip124	bZIP-transcription factor 124	GRMZM2G151295	B73 RefGen_v3	Gene	Chr9	131353502	131359160	bzip124		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
651	bzip125	bZIP-transcription factor 125	GRMZM2G008166	B73 RefGen_v3	Gene	Chr6	111882466	111885951	bzip125		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
652	bzip126	bZIP-transcription factor 126	AC186606.4_FG003	B73 RefGen_v3	Gene	Chr1	182653546	182654452	bzip126		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
653	bzip127	bZIP-transcription factor 127	GRMZM2G175280	B73 RefGen_v3	Gene	Chr1	197089134	197092935	bzip127		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
654	bzip13	bZIP-transcription factor 13	GRMZM2G020799	B73 RefGen_v3	Gene	Chr5	204603643	204604321	bzip13		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
655	bzip14	bZIP-transcription factor 14	GRMZM2G153144	B73 RefGen_v3	Gene	Chr5	74180653	74185259	bzip14		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
656	bzip15	bZIP-transcription factor 15	GRMZM2G402862	B73 RefGen_v3	Gene	Chr6	83701174	83703062	bzip15		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
657	bzip16	bZIP-transcription factor 16	GRMZM2G144480	B73 RefGen_v3	Gene	Chr4	197332482	197333254	bzip16		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
658	bzip160	bZIP-transcription factor 60	GRMZM2G444748	B73 RefGen_v3	Gene	Chr5	74948230	74950097	bzip160	bzip160, bzip60, bZIP-transcription factor 60	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
659	bzip17	bZIP-transcription factor 17	GRMZM2G103647	B73 RefGen_v3	Gene	Chr9	109162612	109164995	bzip17		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
660	bzip19	bZIP-transcription factor 19	GRMZM5G848942	B73 RefGen_v3	Gene	Chr3	210000778	210007937	bzip19		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
661	bzip20	bZIP-transcription factor 20	GRMZM2G170079	B73 RefGen_v3	Gene	Chr8	173480420	173483149	bzip20		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
662	bzip21	bZIP-transcription factor 21	GRMZM2G368491	B73 RefGen_v3	Gene	Chr3	227566001	227567569	bzip21		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
663	bzip22	bZIP-transcription factor 22	GRMZM2G043600	B73 RefGen_v3	Gene	Chr7	140743498	140746868	bzip22	transcription factor RF2a-like, vip1 (VirE2-interacting protein1) homolog, VirulenceE2-interacting protein1 homolog, ZmbZIP91	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
664	bzip23	bZIP-transcription factor 23	GRMZM5G821024	B73 RefGen_v3	Gene	Chr2	140955847	140960153	bzip23		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
665	bzip24	bZIP-transcription factor 24	GRMZM2G038015	B73 RefGen_v3	Gene	Chr1	49087360	49088276	bzip24		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
666	bzip25	bZIP-transcription factor 25	GRMZM2G080731	B73 RefGen_v3	Gene	Chr8	119662868	119665630	bzip25		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
667	bzip26	bZIP-transcription factor 26	GRMZM2G177046	B73 RefGen_v3	Gene	Chr1	281401644	281402596	bzip26		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
668	bzip27	bZIP-transcription factor 27	GRMZM2G131961	B73 RefGen_v3	Gene	Chr2	6719168	6724854	bzip27		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
669	bzip28	bZIP-transcription factor 28	GRMZM2G029979	B73 RefGen_v3	Gene	Chr5	122676355	122688947	bzip28		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
670	bzip29	bZIP-transcription factor 29	GRMZM2G138340	B73 RefGen_v3	Gene	Chr1	291173937	291177741	bzip29		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
671	bzip3	bZIP-transcription factor 3	GRMZM2G074373	B73 RefGen_v3	Gene	Chr3	98816200	98821699	bzip3		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
672	bzip31	bZIP-transcription factor 31	GRMZM2G370026	B73 RefGen_v3	Gene	Chr1	179860588	179861190	bzip31		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
673	bzip32	bZIP-transcription factor 32	GRMZM5G884349	B73 RefGen_v3	Gene	Chr10	62486203	62490700	bzip32		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
674	bzip34	bZIP-transcription factor 34	GRMZM2G045236	B73 RefGen_v3	Gene	Chr6	147087480	147092015	bzip34		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
675	bzip35	bZIP-transcription factor 35	GRMZM2G407631	B73 RefGen_v3	Gene	Chr9	98758805	98759314	bzip35		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
676	bzip36	bZIP-transcription factor 36	GRMZM2G080111	B73 RefGen_v3	Gene	Chr5	101670496	101671080	bzip36		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
677	bzip37	bZIP-transcription factor 37	GRMZM2G088140	B73 RefGen_v3	Gene	Chr10	37914656	37954097	bzip37		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
678	bzip38	bZIP-transcription factor 38	GRMZM2G073892	B73 RefGen_v3	Gene	Chr5	217591763	217592969	bzip38		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
679	bzip4	bZIP-transcription factor 4	GRMZM2G479760	B73 RefGen_v3	Gene	Chr5	210099032	210100747	bzip4		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
680	bzip40	bZIP-transcription factor 40	AC203957.3_FG004	B73 RefGen_v3	Gene	Chr2	175112514	175113156	bzip40		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
681	bzip41	bZIP-transcription factor 41	GRMZM2G019446	B73 RefGen_v3	Gene	Chr1	288150005	288174446	bzip41		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
682	bzip42	bZIP-transcription factor 42	GRMZM2G160136	B73 RefGen_v3	Gene	Chr3	47233315	47236145	bzip42		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
683	bzip43	bZIP-transcription factor 43	GRMZM2G149150	B73 RefGen_v3	Gene	Chr4	194939730	194943802	bzip43		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
684	bzip44	bZIP-transcription factor 44	GRMZM2G438293	B73 RefGen_v3	Gene	Chr8	165990148	165991775	bzip44		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
685	bzip45	bZIP-transcription factor 45	GRMZM2G093020	B73 RefGen_v3	Gene	Chr1	143352528	143354301	bzip45		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
686	bzip46	bZIP-transcription factor 46	GRMZM2G037910	B73 RefGen_v3	Gene	Chr2	194763066	194765126	bzip46		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
687	bzip47	bZIP-transcription factor 47	AC200057.4_FG007	B73 RefGen_v3	Gene	Chr7	140723278	140728024	bzip47		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
688	bzip48	bZIP-transcription factor 48	GRMZM2G160902	B73 RefGen_v3	Gene	Chr3	128957708	128959418	bzip48		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
689	bzip49	bZIP-transcription factor 49	GRMZM2G478417	B73 RefGen_v3	Gene	Chr1	199519465	199525696	bzip49		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
690	bzip5	bZIP-transcription factor 5	GRMZM2G358701	B73 RefGen_v3	Gene	Chr10	123688845	123694048	bzip5		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
691	bzip50	bZIP-transcription factor 50	GRMZM2G336766	B73 RefGen_v3	Gene	Chr4	234937825	234938696	bzip50		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
692	bzip51	bZIP-transcription factor 51	GRMZM2G438652	B73 RefGen_v3	Gene	Chr7	3077372	3078435	bzip51		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
693	bzip52	bZIP-transcription factor 52	GRMZM2G174284	B73 RefGen_v3	Gene	Chr1	51753616	51759590	bzip52		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
694	bzip53	bZIP-transcription factor 53	GRMZM2G027976	B73 RefGen_v3	Gene	Chr3	196217599	196220887	bzip53		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
695	bzip54	bZIP-transcription factor 54	GRMZM2G361847	B73 RefGen_v3	Gene	Chr7	174267403	174273062	bzip54		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
696	bzip55	bZIP-transcription factor 55	GRMZM2G386273	B73 RefGen_v3	Gene	Chr5	5632236	5633262	bzip55		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
697	bzip56	bZIP-transcription factor 56	GRMZM2G019907	B73 RefGen_v3	Gene	Chr3	187349410	187394170	bzip56		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
698	bzip58	bZIP-transcription factor 58	GRMZM2G149040	B73 RefGen_v3	Gene	Chr7	173190014	173195685	bzip58		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
699	bzip59	bZIP-transcription factor 59	GRMZM2G396632	B73 RefGen_v3	Gene	Chr6	119010423	119011019	bzip59		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
700	bzip6	bZIP-transcription factor 6	GRMZM2G039828	B73 RefGen_v3	Gene	Chr3	11637318	11638804	bzip6		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
701	bzip60	bZIP transcription factor60	GRMZM2G025812	B73 RefGen_v3	Gene	Chr9	100855159	100857284	bzip60	bzip60, bZIP60, bZIP60(673), bZIP transcription factor60, ZmbZIP112	endoplasmic reticulum [ER] stress response
702	bzip61	bZIP-transcription factor 61	GRMZM2G137046	B73 RefGen_v3	Gene	Chr5	112670143	112675317	bzip61		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
703	bzip62	bZIP-transcription factor 62	GRMZM2G332294	B73 RefGen_v3	Gene	Chr1	196404600	196407477	bzip62		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
704	bzip63	bZIP-transcription factor 63	GRMZM2G011119	B73 RefGen_v3	Gene	Chr4	189210328	189213307	bzip63		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
705	bzip64	bZIP-transcription factor 64	GRMZM2G473274	B73 RefGen_v3	Gene	Chr9	153788422	153790144	bzip64		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
706	bzip65	bZIP-transcription factor 65	GRMZM2G180847	B73 RefGen_v3	Gene	Chr2	194071950	194077869	bzip65		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
707	bzip66	bZIP-transcription factor 66	GRMZM2G342424	B73 RefGen_v3	Gene	Chr5	58361634	58369149	bzip66		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
708	bzip67	bZIP-transcription factor 67	GRMZM2G365754	B73 RefGen_v3	Gene	Chr10	5921816	5922855	bzip67		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
709	bzip68	bZIP-transcription factor 68	GRMZM2G157722	B73 RefGen_v3	Gene	Chr4	57698284	57703555	bzip68		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
710	bzip69	bZIP-transcription factor 69	GRMZM2G111504	B73 RefGen_v3	Gene	Chr5	186117899	186119612	bzip69		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
711	bzip7	bZIP-transcription factor 7	GRMZM2G006578	B73 RefGen_v3	Gene	Chr7	133162136	133172180	bzip7		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
712	bzip70	bZIP-transcription factor 70	GRMZM2G060290	B73 RefGen_v3	Gene	Chr9	101925918	101931804	bzip70		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
713	bzip71	bZIP-transcription factor 71	GRMZM2G019106	B73 RefGen_v3	Gene	Chr4	239534487	239538429	bzip71		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
714	bzip72	bZIP-transcription factor 72	GRMZM2G030280	B73 RefGen_v3	Gene	Chr8	1640229	1650451	bzip72		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
715	bzip73	bZIP-transcription factor 73	GRMZM2G175870	B73 RefGen_v3	Gene	Chr6	156230705	156237177	bzip73		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
716	bzip74	bZIP-transcription factor 74	GRMZM2G358796	B73 RefGen_v3	Gene	Chr7	129930503	129931378	bzip74		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
717	bzip75	bZIP-transcription factor 75	GRMZM2G168079	B73 RefGen_v3	Gene	Chr8	166357554	166362143	bzip75		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
718	bzip76	bZIP-transcription factor 76	GRMZM2G134863	B73 RefGen_v3	Gene	Chr6	96717113	96724364	bzip76		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
719	bzip77	bZIP-transcription factor 77	GRMZM2G066734	B73 RefGen_v3	Gene	Chr9	135645489	135646430	bzip77		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
720	bzip78	bZIP-transcription factor 78	GRMZM2G353553	B73 RefGen_v3	Gene	Chr1	81928301	81930832	bzip78		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
721	bzip79	bZIP-transcription factor 79	GRMZM2G030877	B73 RefGen_v3	Gene	Chr4	188665527	188672962	bzip79		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
722	bzip8	bZIP-transcription factor 8	GRMZM2G146020	B73 RefGen_v3	Gene	Chr3	142765244	142769768	bzip8		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
723	bzip80	bZIP-transcription factor 80	GRMZM2G140355	B73 RefGen_v3	Gene	Chr9	85130086	85132905	bzip80		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
724	bzip81	bZIP-transcription factor 81	AC190609.3_FG001	B73 RefGen_v3	Gene	Chr4	194461406	194464593	bzip81		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
725	bzip82	bZIP-transcription factor 82	GRMZM2G137532	B73 RefGen_v3	Gene	Chr2	189016699	189017193	bzip82		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
726	bzip83	bZIP-transcription factor 83	GRMZM2G000171	B73 RefGen_v3	Gene	Chr5	61724734	61728541	bzip83		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
727	bzip84	bZIP-transcription factor 84	GRMZM2G361611	B73 RefGen_v3	Gene	Chr4	239887667	239890292	bzip84		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
728	bzip85	bZIP-transcription factor 85	GRMZM2G125934	B73 RefGen_v3	Gene	Chr2	190471098	190480166	bzip85		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
729	bzip86	bZIP-transcription factor 86	GRMZM2G171370	B73 RefGen_v3	Gene	Chr2	161590575	161596682	bzip86		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
730	bzip87	bZIP-transcription factor 87	GRMZM2G000842	B73 RefGen_v3	Gene	Chr6	149721944	149728050	bzip87		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
731	bzip88	bZIP-transcription factor 88	GRMZM2G425920	B73 RefGen_v3	Gene	Chr10	122253987	122259270	bzip88		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
732	bzip89	bZIP-transcription factor 89	GRMZM2G158313	B73 RefGen_v3	Gene	Chr5	144011521	144013252	bzip89		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
733	bzip9	bZIP-transcription factor 9	GRMZM2G092137	B73 RefGen_v3	Gene	Chr7	83788712	83791125	bzip9		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
734	bzip90	bZIP-transcription factor 90	AC232238.2_FG004	B73 RefGen_v3	Gene	Chr8	166341735	166349613	bzip90	lrs1	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
735	bzip91	bZIP-transcription factor 91	GRMZM2G060109	B73 RefGen_v3	Gene	Chr2	214613200	214616521	bzip91		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
736	bzip92	bZIP-transcription factor 92	GRMZM2G077124	B73 RefGen_v3	Gene	Chr7	174321118	174323831	bzip92		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
737	bzip93	bZIP-transcription factor 93	GRMZM2G050912	B73 RefGen_v3	Gene	Chr9	93665910	93671589	bzip93		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
738	bzip95	bZIP-transcription factor 95	GRMZM5G858197	B73 RefGen_v3	Gene	Chr3	175672623	175675787	bzip95		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
739	bzip96	bZIP-transcription factor 96	GRMZM2G161009	B73 RefGen_v3	Gene	Chr8	119246143	119249647	bzip96		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
740	bzip97	bZIP-transcription factor 97	GRMZM2G122846	B73 RefGen_v3	Gene	Chr4	165667701	165668420	bzip97		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
741	bzip98	bZIP-transcription factor 98	GRMZM2G062391	B73 RefGen_v3	Gene	Chr1	56217970	56223418	bzip98		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
742	bzr1	BZR-transcription factor 1	GRMZM5G812774	B73 RefGen_v3	Gene	Chr9	77471270	77474631	bzr1		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
743	bzr2	BZR-transcription factor 2	GRMZM5G852801	B73 RefGen_v3	Gene	Chr3	5297544	5298608	bzr2		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
744	bzr3	BZR-transcription factor 3	GRMZM2G307241	B73 RefGen_v3	Gene	Chr4	229089140	229092844	bzr3		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
745	bzr4	BZR-transcription factor 4	GRMZM2G446515	B73 RefGen_v3	Gene	Chr7	62317634	62323803	bzr4		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
746	bzr5	BZR-transcription factor 5	GRMZM2G069486	B73 RefGen_v3	Gene	Chr4	239624836	239636828	bzr5		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
747	bzr6	BZR-transcription factor 6	GRMZM5G868061	B73 RefGen_v3	Gene	Chr3	10517485	10518461	bzr6		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
748	bzr7	BZR-transcription factor 7	AC194970.5_FG002	B73 RefGen_v3	Gene	Chr2	207890126	207891291	bzr7		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
749	bzr8	BZR-transcription factor 8	GRMZM2G369018	B73 RefGen_v3	Gene	Chr5	147915664	147917490	bzr8		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
750	bzr9	BZR-transcription factor 9	GRMZM2G152172	B73 RefGen_v3	Gene	Chr1	8453673	8455727	bzr9		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
751	c1	colored aleurone1	GRMZM2G005066	B73 RefGen_v3	Gene	Chr9	9746518	9747591	c1	c1, colored aleurone1, gsy39(c1), I, IDP2530, IDP2531, IDP2568, myb1, SC39, umc1809, umc1809a, umc205b, ZmMYB1	C1 colored; C1-I dominant colorless; c1 colorless, includes c1-p (pigment inducible by light at germination), c1-n (not inducible)
752	c2	colorless2	GRMZM2G422750	B73 RefGen_v3	Gene	Chr4	192758391	192761788	c2	c2, colorless2, diffuse, ldf, IDP2144, IDP863, mpik(chs1a), umc198, umc198(c2)	colorless aleurone, reduced plant and cob color; C2-ldf dominant inhibitor; duplicate factor with whp1 for pollen color and for anthocyanins
753	c2h1	C2H2-transcription factor 21	GRMZM2G380515	B73 RefGen_v3	Gene	Chr8	125606805	125613287	c2h1		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
754	c2h133	C2H2-transcription factor 2133	GRMZM5G885700	B73 RefGen_v3	Gene	Chr5	172058302	172062571	c2h133		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
755	c2h2	C2H2-transcription factor 22	GRMZM2G074032	B73 RefGen_v3	Gene	Chr9	144292832	144296553	c2h2		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
756	c2h25	C2H2-transcription factor 225	GRMZM2G465595	B73 RefGen_v3	Gene	Chr1	31769080	31772988	c2h25		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
757	c2h26	C2H2-transcription factor 226	GRMZM2G050939	B73 RefGen_v3	Gene	Chr6	29281533	29285348	c2h26		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
758	c2h3	C2H2-transcription factor 23	GRMZM2G023988	B73 RefGen_v3	Gene	Chr5	175731230	175738132	c2h3		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
759	c2h35	C2H2-transcription factor 235	GRMZM2G068710	B73 RefGen_v3	Gene	Chr10	10140592	10148973	c2h35		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
760	c2h4	C2H2-transcription factor 24	GRMZM2G175000	B73 RefGen_v3	Gene	Chr6	40052653	40057169	c2h4		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
761	c2h46	C2H2-transcription factor 246	GRMZM2G136494	B73 RefGen_v3	Gene	Chr10	148529899	148531915	c2h46		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
762	c2h5	C2H2-transcription factor 25	GRMZM2G470422	B73 RefGen_v3	Gene	Chr1	296848076	296849261	c2h5		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
763	c3h1	C3H-transcription factor 31	GRMZM2G119640	B73 RefGen_v3	Gene	Chr4	237433598	237440210	c3h1		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
764	c3h10	C3H-transcription factor 310	GRMZM2G147623	B73 RefGen_v3	Gene	Chr2	114431775	114441385	c3h10		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
765	c3h11	C3H-transcription factor 311	GRMZM2G146514	B73 RefGen_v3	Gene	Chr4	20203138	20224156	c3h11		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
766	c3h12	C3H-transcription factor 312	GRMZM2G069009	B73 RefGen_v3	Gene	Chr3	36833446	36838605	c3h12		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
767	c3h13	C3H-transcription factor 313	GRMZM2G087032	B73 RefGen_v3	Gene	Chr3	161685821	161692051	c3h13		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
768	c3h14	C3H-transcription factor 314	GRMZM2G150262	B73 RefGen_v3	Gene	Chr10	147037098	147041632	c3h14		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
769	c3h15	C3H-transcription factor 315	GRMZM2G099622	B73 RefGen_v3	Gene	Chr2	206567610	206570522	c3h15		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
770	c3h16	C3H-transcription factor 316	GRMZM2G071034	B73 RefGen_v3	Gene	Chr2	3094658	3099169	c3h16		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
771	c3h17	C3H-transcription factor 317	GRMZM2G180979	B73 RefGen_v3	Gene	Chr1	263796852	263800378	c3h17		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
772	c3h18	C3H-transcription factor 318	GRMZM2G151689	B73 RefGen_v3	Gene	Chr9	101513894	101516776	c3h18		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
773	c3h19	C3H-transcription factor 319	GRMZM2G100794	B73 RefGen_v3	Gene	Chr2	122860183	122884420	c3h19		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
774	c3h2	C3H-transcription factor 32	GRMZM2G306357	B73 RefGen_v3	Gene	Chr3	219556286	219569553	c3h2		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
775	c3h20	C3H-transcription factor 320	GRMZM2G311665	B73 RefGen_v3	Gene	Chr7	173486547	173490629	c3h20		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
776	c3h21	C3H-transcription factor 321	GRMZM2G157927	B73 RefGen_v3	Gene	Chr3	214832691	214834785	c3h21		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
777	c3h22	C3H-transcription factor 322	GRMZM2G422205	B73 RefGen_v3	Gene	Chr3	225673226	225688992	c3h22		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
778	c3h23	C3H-transcription factor 323	GRMZM2G475017	B73 RefGen_v3	Gene	Chr8	4955650	4961914	c3h23		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
779	c3h24	C3H-transcription factor 324	GRMZM2G005126	B73 RefGen_v3	Gene	Chr10	84252239	84259713	c3h24		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
780	c3h25	C3H-transcription factor 325	GRMZM5G849788	B73 RefGen_v3	Gene	Chr5	173803063	173806170	c3h25		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
781	c3h26	C3H-transcription factor 326	GRMZM2G110402	B73 RefGen_v3	Gene	Chr6	98477144	98480310	c3h26		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
782	c3h27	C3H-transcription factor 327	GRMZM5G845366	B73 RefGen_v3	Gene	Chr5	12394277	12396390	c3h27		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
783	c3h28	C3H-transcription factor 328	GRMZM2G036837	B73 RefGen_v3	Gene	Chr8	4916708	4925557	c3h28		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
784	c3h29	C3H-transcription factor 329	GRMZM2G089050	B73 RefGen_v3	Gene	Chr5	58232976	58237550	c3h29		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
785	c3h3	C3H-transcription factor 33	GRMZM2G149347	B73 RefGen_v3	Gene	Chr6	166060984	166063087	c3h3		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
786	c3h30	C3H-transcription factor 330	GRMZM2G123876	B73 RefGen_v3	Gene	Chr1	294963341	294966931	c3h30		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
787	c3h31	C3H-transcription factor 331	GRMZM2G305582	B73 RefGen_v3	Gene	Chr10	77459194	77463222	c3h31		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
788	c3h32	C3H-transcription factor 332	GRMZM5G842019	B73 RefGen_v3	Gene	Chr7	158715746	158718906	c3h32		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
789	c3h33	C3H-transcription factor 333	AC233871.1_FG008	B73 RefGen_v3	Gene	Chr6	1823275	1825348	c3h33		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
790	c3h34	C3H-transcription factor 334	GRMZM2G037200	B73 RefGen_v3	Gene	Chr5	196068947	196075524	c3h34		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
791	c3h35	C3H-transcription factor 335	GRMZM2G086994	B73 RefGen_v3	Gene	Chr3	36943805	36949840	c3h35		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
792	c3h36	C3H-transcription factor 336	GRMZM2G031827	B73 RefGen_v3	Gene	Chr8	69651989	69660585	c3h36		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
793	c3h37	C3H-transcription factor 337	GRMZM2G171942	B73 RefGen_v3	Gene	Chr8	17672604	17674106	c3h37		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
794	c3h38	C3H-transcription factor 338	GRMZM2G056920	B73 RefGen_v3	Gene	Chr4	234301708	234304462	c3h38		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
795	c3h39	C3H-transcription factor 339	GRMZM5G801627	B73 RefGen_v3	Gene	Chr6	132847404	132849278	c3h39		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
796	c3h4	C3H-transcription factor 34	GRMZM2G025014	B73 RefGen_v3	Gene	Chr2	233311308	233314199	c3h4		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
797	c3h40	C3H-transcription factor 340	GRMZM2G177229	B73 RefGen_v3	Gene	Chr7	133562993	133564875	c3h40		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
798	c3h41	C3H-transcription factor 341	GRMZM2G427438	B73 RefGen_v3	Gene	Chr1	47597558	47599537	c3h41		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
799	c3h42	C3H-transcription factor 342	GRMZM2G024655	B73 RefGen_v3	Gene	Chr8	5908910	5912846	c3h42		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
800	c3h43	C3H-transcription factor 343	GRMZM2G164359	B73 RefGen_v3	Gene	Chr4	225552715	225560422	c3h43		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
801	c3h44	C3H-transcription factor 344	GRMZM2G162119	B73 RefGen_v3	Gene	Chr3	130398102	130399300	c3h44		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
802	c3h45	C3H-transcription factor 345	GRMZM2G003424	B73 RefGen_v3	Gene	Chr1	54122528	54126795	c3h45		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
803	c3h46	C3H-transcription factor 346	GRMZM2G039889	B73 RefGen_v3	Gene	Chr8	143230970	143239777	c3h46		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
804	c3h47	C3H-transcription factor 347	GRMZM2G173124	B73 RefGen_v3	Gene	Chr8	20674613	20676836	c3h47		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
805	c3h48	C3H-transcription factor 348	GRMZM2G044004	B73 RefGen_v3	Gene	Chr3	230611403	230615986	c3h48		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
806	c3h49	C3H-transcription factor 349	GRMZM2G107491	B73 RefGen_v3	Gene	Chr8	161770572	161775615	c3h49		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
807	c3h5	C3H-transcription factor 35	GRMZM2G395842	B73 RefGen_v3	Gene	Chr9	44938811	44971017	c3h5		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
808	c3h50	C3H-transcription factor 350	GRMZM2G346113	B73 RefGen_v3	Gene	Chr4	185559571	185563721	c3h50		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
809	c3h51	C3H-transcription factor 351	GRMZM2G068476	B73 RefGen_v3	Gene	Chr1	262230777	262236243	c3h51		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
810	c3h52	C3H-transcription factor 352	GRMZM2G124476	B73 RefGen_v3	Gene	Chr10	146582797	146586445	c3h52		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
811	c3h53	C3H-transcription factor 353	GRMZM2G020928	B73 RefGen_v3	Gene	Chr6	164773159	164775979	c3h53		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
812	c3h54	C3H-transcription factor 354	GRMZM2G006493	B73 RefGen_v3	Gene	Chr10	13006885	13025813	c3h54		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
813	c3h6	C3H-transcription factor 36	GRMZM2G086614	B73 RefGen_v3	Gene	Chr9	132165988	132170589	c3h6		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
814	c3h7	C3H-transcription factor 37	GRMZM2G117007	B73 RefGen_v3	Gene	Chr8	130574595	130576060	c3h7		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
815	c3h8	C3H-transcription factor 38	GRMZM2G315515	B73 RefGen_v3	Gene	Chr4	31410265	31411096	c3h8		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
816	c3h9	C3H-transcription factor 39	GRMZM5G830949	B73 RefGen_v3	Gene	Chr8	146510296	146512179	c3h9		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
817	ca2p1	CCAAT-HAP2-transcription factor 21	GRMZM2G026157	B73 RefGen_v3	Gene	Chr5	12557664	12558570	ca2p1		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
818	ca2p10	CCAAT-HAP2-transcription factor 210	GRMZM2G165488	B73 RefGen_v3	Gene	Chr5	16480475	16484858	ca2p10	ZmNF-YA10	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
819	ca2p12	CCAAT-HAP2-transcription factor 212	GRMZM2G104396	B73 RefGen_v3	Gene	Chr3	123431302	123438343	ca2p12	CA2P12 CCAAT-HAP2 transcription factor, ZmNF-YA9	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
820	ca2p13	CCAAT-HAP2-transcription factor 213	GRMZM5G857944	B73 RefGen_v3	Gene	Chr5	211715089	211720032	ca2p13	nuclear transcription factor Y subunit A-3, ZmNF-YA12	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
821	ca2p14	CCAAT-HAP2-transcription factor 214	GRMZM2G096016	B73 RefGen_v3	Gene	Chr2	235103649	235106245	ca2p14	nuclear transcription factor Y subunit A-10, ZmNF-YA8	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
822	ca2p15	CCAAT-HAP2-transcription factor 215	GRMZM2G038303	B73 RefGen_v3	Gene	Chr7	165030959	165035270	ca2p15	nuclear transcription factor Y subunit A-3, ZmNF-YA13	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
823	ca2p16	CCAAT-HAP2-transcription factor 216	GRMZM2G091964	B73 RefGen_v3	Gene	Chr1	263505895	263513358	ca2p16	uaz7c01g06 NF-YA6 , ZmNF-YA6	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
824	ca2p2	CCAAT-HAP2-transcription factor 22	GRMZM2G582893	B73 RefGen_v3	Gene	Chr5	22308191	22311425	ca2p2	ZmNF-YA11	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
825	ca2p3	CCAAT-HAP2-transcription factor 23	GRMZM2G037630	B73 RefGen_v3	Gene	Chr1	71589264	71595809	ca2p3		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
826	ca2p4	CCAAT-HAP2-transcription factor 24	GRMZM2G040349	B73 RefGen_v3	Gene	Chr2	211453451	211457855	ca2p4	nuclear transcription factor Y subunit A-3, ZmNF-YA7	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
827	ca2p5	CCAAT-HAP2-transcription factor 25	GRMZM5G853836	B73 RefGen_v3	Gene	Chr1	174875434	174876987	ca2p5	ZmNF-YA3	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
828	ca2p6	CCAAT-HAP2-transcription factor 26	GRMZM5G829103	B73 RefGen_v3	Gene	Chr1	250377935	250382233	ca2p6	ca2p6, nuclear transcription factor Y subunit A-10, rs128928950, umc1914, ZmNF-YA4	
829	ca2p7	CCAAT-HAP2-transcription factor 27	GRMZM2G126957	B73 RefGen_v3	Gene	Chr10	141891517	141897548	ca2p7	CA2P7 nuclear transcription factor Y subunit A-3, ZmNF-YA14	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
830	ca2p8	CCAAT-HAP2-transcription factor 28	GRMZM2G361842	B73 RefGen_v3	Gene	Chr1	173335601	173340617	ca2p8	cl982_-1b, ZmNF-YA2	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
831	ca2p9	CCAAT-HAP2-transcription factor 29	GRMZM5G865626	B73 RefGen_v3	Gene	Chr1	268504277	268506002	ca2p9	ZmNF-YA5	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
832	ca3p1	CCAAT-HAP3-transcription factor 31	GRMZM2G303465	B73 RefGen_v3	Gene	Chr3	182472591	182474866	ca3p1	CA3P1 nuclear transcription factor Y subunit B-3, ZmNF-YB8	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
833	ca3p2	CCAAT-HAP3-transcription factor 32	GRMZM2G480621	B73 RefGen_v3	Gene	Chr2	567968	568904	ca3p2	nuclear transcription factor Y subunit B-4-like, ZmNF-YB3	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
834	ca3p3	CCAAT-HAP3-transcription factor 33	GRMZM2G169884	B73 RefGen_v3	Gene	Chr3	154457527	154458030	ca3p3	CA3P3 HAP3-like protein, ZmNF-YB7	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
835	ca3p4	CCAAT-HAP3-transcription factor 34	GRMZM2G384528	B73 RefGen_v3	Gene	Chr7	164733507	164734923	ca3p4	nuclear transcription factor Y subunit B-3, ZmNF-YB16	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
836	ca5p1	CCAAT-HAP5-transcription factor 51	GRMZM2G074773	B73 RefGen_v3	Gene	Chr10	148048984	148050065	ca5p1	ZmNF-YC15, ZmNF-YC18	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
837	ca5p10	CCAAT-HAP5-transcription factor 510	GRMZM2G440949	B73 RefGen_v3	Gene	Chr6	155856085	155862224	ca5p10	dr1-associated corepressor, ZmNF-YA11, ZmNF-YC11, ZmNF-YC9	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
838	ca5p11	CCAAT-HAP5-transcription factor 511	GRMZM2G089812	B73 RefGen_v3	Gene	Chr1	34599368	34601378	ca5p11	nuclear transcription factor Y subunit C-1, ZmNF-YC1	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
839	ca5p12	CCAAT-HAP5-transcription factor 512	GRMZM2G022162	B73 RefGen_v3	Gene	Chr2	189855073	189858562	ca5p12	nuclear transcription factor Y subunit C-2-like, ZmNF-YC3, ZmNF-YC5	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
840	ca5p13	CCAAT-HAP5-transcription factor 513	GRMZM2G113127	B73 RefGen_v3	Gene	Chr1	183805913	183807419	ca5p13	pco147903a, ZmNF-YC2, ZmNF-YC3	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
841	ca5p14	CCAAT-HAP5-transcription factor 514	GRMZM2G174776	B73 RefGen_v3	Gene	Chr4	198165814	198167061	ca5p14	ZmNF-YC7, ZmNF-YC9	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
842	ca5p15	CCAAT-HAP5-transcription factor 515	GRMZM2G099461	B73 RefGen_v3	Gene	Chr3	9072834	9073771	ca5p15	histone-like transcription factor and archaeal histone family protein, ZmNF-YC5, ZmNF-YC7	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
843	ca5p16	CCAAT-HAP5-transcription factor 516	GRMZM2G078691	B73 RefGen_v3	Gene	Chr7	131218518	131219657	ca5p16	magi42672, TIDP3758, ZmNF-YC10, ZmNF-YC12	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
844	ca5p17	CCAAT-HAP5-transcription factor 517	GRMZM2G052499	B73 RefGen_v3	Gene	Chr10	6682348	6683697	ca5p17	ZmNF-YC16	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
845	ca5p18	CCAAT-HAP5-transcription factor 518	AC201832.3_FG006	B73 RefGen_v3	Gene	Chr8	119573868	119575960	ca5p18		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
846	ca5p2	CCAAT-HAP5-transcription factor 52	GRMZM2G479610	B73 RefGen_v3	Gene	Chr8	163223636	163224280	ca5p2	ZmNF-YC12, ZmNF-YC13	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
847	ca5p3	CCAAT-HAP5-transcription factor 53	GRMZM2G161680	B73 RefGen_v3	Gene	Chr6	93659875	93665056	ca5p3	nuclear transcription factor Y subunit C-2, ZmNF-YC10, ZmNF-YC8	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
848	ca5p4	CCAAT-HAP5-transcription factor 54	GRMZM2G083964	B73 RefGen_v3	Gene	Chr1	298942487	298959287	ca5p4	neurofilament heavy polypeptide-like, ZmNF-YC4	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
849	ca5p5	CCAAT-HAP5-transcription factor 55	GRMZM2G311316	B73 RefGen_v3	Gene	Chr10	57549401	57552804	ca5p5	nuclear transcription factor Y subunit C-2, ZmNF-YC14, ZmNF-YC17	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
850	ca5p6	CCAAT-HAP5-transcription factor 56	GRMZM2G375448	B73 RefGen_v3	Gene	Chr8	163213351	163214685	ca5p6	CA5P6 nuclear transcription factor Y subunit C-9, ZmNF-YC11, ZmNF-YC14	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
851	ca5p7	CCAAT-HAP5-transcription factor 57	GRMZM2G124421	B73 RefGen_v3	Gene	Chr9	110476000	110480388	ca5p7	si605027f07(712), ZmNF-YC13, ZmNF-YC15	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
852	ca5p8	CCAAT-HAP5-transcription factor 58	GRMZM2G105317	B73 RefGen_v3	Gene	Chr2	225260746	225264684	ca5p8	repressor protein, ZmNF-YC4, ZmNF-YC6	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
853	ca5p9	CCAAT-HAP5-transcription factor 59	GRMZM2G091433	B73 RefGen_v3	Gene	Chr4	191046626	191052377	ca5p9	cl181_1(359), cl181_1c, ZmNF-YC6, ZmNF-YC8	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
854	cad1	cinnamyl alcohol dehydrogenase1	GRMZM2G046070	B73 RefGen_v3	Gene	Chr2	10537220	10541464	cad1	cad1, cdh1, gnp_QAE37c01, gnp_QBB21c04, gpm294, gpm431, PCO143419b	identification based on two EST/RFLP sequences that match in one TIGR contig and in the Cornsensus sequence for the overgo (EH Coe Dec 2006)
855	cadtfr10	CCAAT-DR1-transcription factor 10	GRMZM2G121897	B73 RefGen_v3	Gene	Chr9	68729341	68730919	cadtfr10	cadr10	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
856	cadtfr11	CCAAT-DR1-transcription factor 11	GRMZM2G146286	B73 RefGen_v3	Gene	Chr1	219431537	219437566	cadtfr11	cadr11, pco107514, ZmNF-YB2	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
857	cadtfr12	CCAAT-DR1-transcription factor 12	GRMZM2G167576	B73 RefGen_v3	Gene	Chr9	37856306	37857363	cadtfr12	cadr12, pco127516, pco127516(676), ZmNF-YB18	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
858	cadtfr13	CCAAT-DR1-transcription factor 13	GRMZM2G020305	B73 RefGen_v3	Gene	Chr5	204568019	204571253	cadtfr13	cadr13	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
859	cadtfr14	CCAAT-DR1-transcription factor 14	GRMZM2G152822	B73 RefGen_v3	Gene	Chr7	16202771	16203691	cadtfr14	cadr14, nuclear transcription factor Y subunit B-4-like, ZmNF-YB14	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
860	cadtfr15	CCAAT-DR1-transcription factor 15	GRMZM2G064426	B73 RefGen_v3	Gene	Chr8	117330071	117333930	cadtfr15	caat1 CAAT box binding protein 1, cadr15, ZmNF-YB17	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
861	cadtfr16	CCAAT-DR1-transcription factor 16	GRMZM2G012654	B73 RefGen_v3	Gene	Chr7	68994825	68997112	cadtfr16	cadr16, CADR16 DNA polymerase epsilon subunit 3, ZmNF-YB15	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
862	cadtfr2	CCAAT-DR1-transcription factor 2	GRMZM2G473152	B73 RefGen_v3	Gene	Chr3	154450608	154451831	cadtfr2	cadr2, nuclear transcription factor Y subunit B-1-like, ZmNF-YB6	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
863	cadtfr3	CCAAT-DR1-transcription factor 3	GRMZM2G147712	B73 RefGen_v3	Gene	Chr4	72873166	72879736	cadtfr3	cadr3, CADR3 repressor protein, ZmNF-YB10	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
864	cadtfr4	CCAAT-DR1-transcription factor 4	GRMZM2G478501	B73 RefGen_v3	Gene	Chr3	21156624	21175149	cadtfr4	cadr4, ZmNF-YB5	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
865	cadtfr5	CCAAT-DR1-transcription factor 5	GRMZM2G444073	B73 RefGen_v3	Gene	Chr4	30460409	30461221	cadtfr5	cadr5, nuclear transcription factor Y subunit B-3-like, ZmNF-YB9	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
866	cadtfr6	CCAAT-DR1-transcription factor 6	GRMZM2G180947	B73 RefGen_v3	Gene	Chr2	211052666	211054021	cadtfr6	cadr6, nuclear transcription factor Y subunit B-3-like, ZmNF-YB4	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
867	cadtfr7	CCAAT-DR1-transcription factor 7	GRMZM2G124663	B73 RefGen_v3	Gene	Chr4	164127479	164128599	cadtfr7	cadr7, nuclear transcription factor Y subunit B-2-like, ZmNF-YB11	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
868	cadtfr8	CCAAT-DR1-transcription factor 8	GRMZM5G866699	B73 RefGen_v3	Gene	Chr8	168982663	168990876	cadtfr8	cadr8	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
869	cadtfr9	CCAAT-DR1-transcription factor 9	GRMZM5G809663	B73 RefGen_v3	Gene	Chr1	106425069	106426667	cadtfr9	cadr9, CADR9 nuclear transcription factor Y subunit B-4-like, ZmNF-YB1	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
870	caf1	crs2 associated factor1	GRMZM2G089222	B73 RefGen_v3	Gene	Chr7	42230925	42231874	caf1	caf1, chloroplast splicing factor, crs2 associated factor1	promotes splicing of several chloroplast group II introns and binds to those introns in vivo. (A. Barkan, 2015). ivory to very pale yellow leaf, seedling lethal, chloroplast intron II splicing
871	caf1	crs2 associated factor1	GRMZM2G173923	B73 RefGen_v3	Gene	Chr7	42211043	42244189	caf1	caf1, chloroplast splicing factor, crs2 associated factor1	promotes splicing of several chloroplast group II introns and binds to those introns in vivo. (A. Barkan, 2015). ivory to very pale yellow leaf, seedling lethal, chloroplast intron II splicing
872	caf2	crs2 associated factor2	AC199526.5_FG003	B73 RefGen_v3	Gene	Chr3	58874517	58886337	caf2	caf2, chloroplast associated splicing factor, crs2 associated factor2	promotes splicing of several chloroplast group II introns and binds to those introns in vivo. (A. Barkan, 2015). ivory colored leaf, seedling lethal; RNA splicing
873	cah1	carbonic anhydrase1	GRMZM2G121878	B73 RefGen_v3	Gene	Chr3	215547876	215555228	cah1	ca1, cah1, rs129586143	C4 carbonic anhydrase; higher transcripts in mesophyll cells (Tausta 2014); double mutants with cah2 virutally remove this activity from leaf (Studer et al 2014).
874	cah123	carbonic anhydrase123	GRMZM2G121878	B73 RefGen_v3	Chromosomal Se	Chr3	215547876	215555228	cah123	ca1, CA1, ca2, CA2, cah123, cah2, cah3, carbonic anhydrase1, CL2331_1a, csu125a, csu125a(cah), csu397(cah), csu869(cah), csuM95073(gfu)	tandem repeated genes encoding C4-photosynthesis carbonic anhydrase; see also cah1, cah2, cah3; RFLP csu125.
875	cah123	carbonic anhydrase123	GRMZM2G348512	B73 RefGen_v3	Chromosomal Se	Chr3	215506034	215518935	cah123	ca1, CA1, ca2, CA2, cah123, cah2, cah3, carbonic anhydrase1, CL2331_1a, csu125a, csu125a(cah), csu397(cah), csu869(cah), csuM95073(gfu)	tandem repeated genes encoding C4-photosynthesis carbonic anhydrase; see also cah1, cah2, cah3; RFLP csu125.
876	cah2	carbonic anhydrase2	GRMZM2G348512	B73 RefGen_v3	Gene	Chr3	215506034	215518935	cah2	cah2, carbonic anhydrase2, csu869(cah)	with cah1 promotes leaf CO2 availability for photosynthesis (Studer et al 2014)
877	cah3	carbonic anhydrase3	GRMZM2G348512	B73 RefGen_v3	Gene	Chr3	215506034	215518935	cah3	CA3, cah3, carbonic anhydrase3	
878	cah4	carbonic anhydrase4	GRMZM2G414528	B73 RefGen_v3	Gene	Chr2	187772976	187777268	cah4	cah4	putative mitochondrial carbonic anhydrase (Studer et al 2014)
879	cah5	carbonic anhydrase5	GRMZM2G145101	B73 RefGen_v3	Gene	Chr7	127621256	127626940	cah5	cah5	predicted mitochondrial carbonic anhydrase
880	cah6	carbonic anhydrase6	GRMZM2G094165	B73 RefGen_v3	Gene	Chr8	146085244	146092203	cah6	cah6, csu125b, csu125b(cah), rs132482512, umc2175	predicted beta carbonic anhydrase
881	cal1	calmodulin1	GRMZM2G117582	B73 RefGen_v3	Gene	Chr6	155708190	155712626	cal1	cal1, calmodulin1, CL1769_2, cl1769_2(519), ZMCALM1	cDNA sequence identical to plant calmodulin consensus sequence
882	cal2	calmodulin2	GRMZM2G067511	B73 RefGen_v3	Gene	Chr3	38428315	38432905	cal2	cal2, calmodulin2, calmodulin X77397, cal*-X77397, CaM2, PCO074292, pco074292(270)	
883	cal3	calmodulin3	GRMZM2G152891	B73 RefGen_v3	Gene	Chr1	52092838	52096639	cal3	cal3, calmodulin X77396, cam1, CaM1	

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
884	camta1	CAMTA-transcription factor 1	GRMZM2G143205	B73 RefGen_v3	Gene	Chr2	70964747	70973190	camta1		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
885	camta2	CAMTA-transcription factor 2	GRMZM2G032336	B73 RefGen_v3	Gene	Chr7	149639376	149658357	camta2		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
886	camta3	CAMTA-transcription factor 3	GRMZM2G171600	B73 RefGen_v3	Gene	Chr3	158938555	158944768	camta3		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
887	camta4	CAMTA-transcription factor 4	GRMZM2G447551	B73 RefGen_v3	Gene	Chr1	19788672	19813731	camta4		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
888	camta5	CAMTA-transcription factor 5	GRMZM2G152661	B73 RefGen_v3	Gene	Chr10	109591875	109599342	camta5		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
889	cap1	calcium pump1	GRMZM2G056014	B73 RefGen_v3	Gene	Chr8	132408451	132413070	cap1	calcium pump1, cap1, eca1, endoplasmic reticulum calcium ATPase1	anoxic root cDNA, low or single copy, complements yeast mutants defective in Ca++-pumps
890	cap2	calcium pump2	GRMZM2G428096	B73 RefGen_v3	Gene	Chr1	42855656	42857040	cap2	cap2, eca2, endoplasmic reticulum calcium ATPase2	paralog of cap1; calcium-transporting ATPase
891	cap3	calcium pump3	GRMZM2G162426	B73 RefGen_v3	Gene	Chr9	139025595	139031089	cap3	cap3, eca3, endoplasmic reticulum calcium ATPase3	paralog of cap1; calcium-transporting ATPase
892	cap4	calcium pump4	AC233878.1_FG004	B73 RefGen_v3	Gene	Chr1	272711753	272730612	cap4	cap4, eca4, endoplasmic reticulum calcium ATPase2	paralog of cap1; calcium-transporting ATPase
893	cas1	cycloartenol synthase1	GRMZM2G065494	B73 RefGen_v3	Gene	Chr4	238310811	238319374	cas1	cas1, csu265, csu265(gfu), cycloartenol synthase1, lss1, PCO144257, pco144257(362)	leaf cDNA csu265
894	cat1	catalase1	GRMZM2G088212	B73 RefGen_v3	Gene	Chr5	63593142	63597617	cat1	Cat0, cat1, catalase1, Ct1, ncr, ncr(cat1), uaz226, uaz226(cat1)	electrophoretic mobility; cytosolic/glyoxysomal; tetrameric; intra/interlocus hybrid bands occur
895	cat2	catalase2	GRMZM2G090568	B73 RefGen_v3	Gene	Chr1	7153870	7156146	cat2	Cat0, cat2, catalase2, Ct2, IDP3825, ncr(cat2), pco104975, pco104975(5)	electrophoretic mobility; null allele is known; cytosolic/glyoxysomal; tetrameric; intra/interlocus hybrid bands occur
896	cat3	catalase3	GRMZM2G079348	B73 RefGen_v3	Gene	Chr4	240651914	240655881	cat3	cat3, catalase3, Ct3, IDP3, IDP590, ncr(cat3), PCO080157, phi006, phi019, phi076, umc1050, umc1197, umc2290	electrophoretic mobility, null allele is known; mitochondrial; tetrameric, intralocus hybrid bands occur; SSRs phi006, phi019, phi076, umc1197
897	cax1	calcium exchanger1	GRMZM5G809587	B73 RefGen_v3	Gene	Chr8	78171551	78175986	cax1	calcium exchanger1, cax1, hcx1	cDNA with extensive sequence homology to characterized plant CAX (calcium exchanger) genes but not capable of suppressing defects in vacuolar calcium ion transport in yeast.
898	cax2	calcium exchanger2	GRMZM2G040017	B73 RefGen_v3	Gene	Chr2	4585422	4590928	cax2	AtCAX homolog2, cax2, pco139871(140), pco139871a	homolog of Arabiodopsis protein involved in auxin transduction pathway; expression not affected by Ca or auxin (Jurisic-Knezev et al 2014)
899	cax3	calcium exchanger3	GRMZM2G011592	B73 RefGen_v3	Gene	Chr3	227277700	227282452	cax3	AtCAX homolog3, cax3, cax3(279), pco087284, rs129589401	Expression affected by ABP4, auxin, and Ca++. Homolog of Arabidopsis CAX1 involved in auxin transduction pathway.
900	cbl1	calcineurin B-like1	GRMZM2G107575	B73 RefGen_v3	Gene	Chr1	94993988	94998653	cbl1	cbl1	
901	cbl10	calcineurin B-like10	GRMZM2G116584	B73 RefGen_v3	Gene	Chr3	220604800	220608677	cbl10	cbl10, CBL10	
902	cbl11	calcineurin B-like11	GRMZM2G007555	B73 RefGen_v3	Gene	Chr1	167215863	167225574	cbl11	cbl11, CBL2-1 calcineurin B-like protein 3	
903	cbl12	calcineurin B-like12	GRMZM2G137751	B73 RefGen_v3	Gene	Chr2	30021407	30023024	cbl12	calcineurin B-like protein 7, cbl12, CBL8-2	
904	cbl2	calcineurin B-like2	GRMZM2G173424	B73 RefGen_v3	Gene	Chr3	115377120	115403275	cbl2	cbl2, CBL2-2 calcineurin B-like protein	
905	cbl3	calcineurin B-like3	GRMZM2G112672	B73 RefGen_v3	Gene	Chr1	253698726	253716291	cbl3	cbl3, TIDP3120	
906	cbl4	calcineurin B-like2	GRMZM2G001221	B73 RefGen_v3	Gene	Chr6	159455359	159458229	cbl4	cbl4, si496006g11, si496006g11(520)	
907	cbl5	calcineurin B-like5	GRMZM2G041729	B73 RefGen_v3	Gene	Chr3	223169117	223172637	cbl5	cbl5, CBL5 calcineurin B-like protein	
908	cbl6	calcineurin B-like6	GRMZM2G010093	B73 RefGen_v3	Gene	Chr10	7732074	7735779	cbl6	cbl6, CBL6-1, IDP1992, PCO131392b	
909	cbl7	calcineurin B-like7	GRMZM2G033680	B73 RefGen_v3	Gene	Chr10	7869640	7874007	cbl7	calcineurin B-like protein 6 , CBL6-2, cbl7	
910	cbl8	calcineurin B-like8	GRMZM2G110080	B73 RefGen_v3	Gene	Chr4	220865888	220867679	cbl8	calcineurin B-like protein 4, cbl8, CBL8-1	
911	cbl9	calcineurin B-like9	GRMZM2G015324	B73 RefGen_v3	Gene	Chr9	114480823	114485894	cbl9	calcineurin B-like protein 9, cbl9, CBL9	
912	cbp1	calmodulin binding protein1	GRMZM2G113453	B73 RefGen_v3	Gene	Chr5	174362481	174368947	cbp1	AY109682, calmodulin binding protein1, cbp1, CBP-1, CL2492_-1	partial cDNA clone from a root tip expression library; fusion protein binds calmodulin; 1-2 copies estimated
913	cbp2	calmodulin binding protein2	GRMZM2G018837	B73 RefGen_v3	Gene	Chr4	235806854	235815316	cbp2	calmodulin binding protein2, cbp2, CBP-5, CL2491_1, CL2491_1(360), gnp_QCD15e04, gpm607, uaz279(cbp)	partial root tip cDNA; fusion protein binds calmodulin; wind-induced; 1-2 copies
914	cbs1	cystathionine beta synthase domain prot	GRMZM2G416388	B73 RefGen_v3	Gene	Chr1	273932226	273937442	cbs1	334B7.8, cbs1, CBS domain protein, cystathionine beta synthase, gene 11, PCO141653, PCO141653(89), u22	single-copy sequence in Adh1-F region, homoeologous to exons of rice cDNA
915	cca1	circadian clock associated1	GRMZM2G014902	B73 RefGen_v3	Gene	Chr4	32527798	32560791	cca1	cca1, LHY protein, mybr79, MYB-related-transcription factor 79, PCO118792a, ZmCCA1b	myb transcription factor - clock gene
916	ccamk1	calcium/calmodulin dependent protein kii	GRMZM2G062772	B73 RefGen_v3	Gene	Chr4	201540262	201543535	ccamk1	calcium/calmodulin dependent protein kinase1, CCaMK, ccamk1	involved in ABA signaling (Ma et al 2012)
917	ccd7	carotenoid cleavage dioxygenase7	GRMZM2G158657	B73 RefGen_v3	Gene	Chr2	20083041	20085698	ccd7	ccd7, max3, more axillary growth3	
918	ccd8	carotenoid cleavage dioxygenase8	GRMZM2G446858	B73 RefGen_v3	Gene	Chr3	197085779	197089273	ccd8	ccd8, ccd8a, Zmccd8	Mutants have mild branching, short stature, small ear size, and narrow-stalk
919	ccp1	cysteine protease1	GRMZM2G098298	B73 RefGen_v3	Gene	Chr5	158904820	158908319	ccp1	ccp1, CCP1, cysteine protease1, pZSS5, thiol protease -D45402, thiol protease X82185, thp*-D45402, thp*-X82185	seed cDNA sequence
920	ccp2	cysteine protease2	GRMZM2G038636	B73 RefGen_v3	Gene	Chr7	122016558	122021703	ccp2	ige1b(thp), iger1b(thp), npi348-alr2, npi349(alr), PCO114759, rs131176291, rs131176292, rs131180896, rs131180897, rs131180898, rs131180899, see1, see1b, see2, senescence-	mRNA differentially enhanced in late- vs. early-senescing lines; similarity to rice oryzain gamma (cysteine protease) and castor bean vacuolar processing enzyme
921	ccp3	cysteine protease3	GRMZM2G073465	B73 RefGen_v3	Gene	Chr10	144912181	144916261	ccp3	ccp3, CP1-likeB, mir3c, mir3c(thp)	apoplastic; cysteine protease
922	ccp4	cysteine protease4	GRMZM2G108849	B73 RefGen_v3	Probed Site	Chr7	152808839	152813057	ccp4	cathepsin B-like cysteine proteinase, ccp4, ccp4(574), cl31697_1	apoplastic; pest defense response
923	ccp5	cysteine protease5	GRMZM2G066326	B73 RefGen_v3	Gene	Chr6	39529235	39530882	ccp5	ccp5, IDP105, PCO132946, PCO132946(479), PZA01509, XCP2-like	apoplastic; response to U. maydis infection
924	ccr1	cytochrome c reductase1	GRMZM2G170457	B73 RefGen_v3	Gene	Chr1	290295024	290298191	ccr1	ccr1, csu381, csu576, cytochrome c reductase1	single copy leaf cDNA csu576
925	ccr2	ubiquinol-cytochrome c reductase2	GRMZM2G064896	B73 RefGen_v3	Gene	Chr2	149136004	149139243	ccr2	ccr2	
926	ccs1	C-type cytochrome synthesis protein1	GRMZM2G038301	B73 RefGen_v3	Gene	Chr1	281272122	281275134	ccs1	ccs1, rs128964469	ortholog of Arabidopsis CCS1. Required for cytb6f assembly. Ortholog of CCS1. Required for cytb6f assembly. (A. Barkan, 2015)
927	cct1	CO CO-LIKE TIMING OF CAB1 protein dc	GRMZM2G381691	B73 RefGen_v3	Gene	Chr10	94262291	94264845	cct1	cct1, CCT protein domain1, CO, CO-LIKE, TIMING OF CAB1 protein domain1, CONSTANS (CO), CO-LIKE and TIMING OF chlorophyll a/b binding protein1 (CAB1), Zmcct, ZmOrphan30	maize inbred lines, including some adapted to tropical regions, have cct1 alleles insensitive to photoperiod (Hung et al 2012)
928	cda1	cytidine deaminase1	GRMZM2G082924	B73 RefGen_v3	Gene	Chr7	24237831	24240669	cda1	cda1, cytidine deaminase1	
929	cda2	cytidine deaminase2	GRMZM2G008216	B73 RefGen_v3	Gene	Chr2	170859967	170862507	cda2	cda2, cytidine deaminase2, PCO083489, PCO083489(159)	
930	cdc2	cell division control protein2 homolog	GRMZM2G008327	B73 RefGen_v3	Gene	Chr1	3872113	3877700	cdc2	cdc2, CDKA;1, cell division control protein2 homolog, p34cdc2	cDNA sequence homologous to cdc2/cdc28 subfamily of serine/threonine protein kinases, complements yeast cdc28
931	cdc201	cell division cycle201	GRMZM2G063192	B73 RefGen_v3	Gene	Chr4	159201602	159204082	cdc201	cdc201, cdc20-1, CL11432_1b, IDP308	
932	cdc202	cell division cycle202	GRMZM2G130425	B73 RefGen_v3	Gene	Chr5	137431853	137435424	cdc202	cdc202, cdc20-2	

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
933	cdj1	chaperone DNA J homolog1	GRMZM2G134917	B73 RefGen_v3	Gene	Chr1	285992073	285995271	cdj1	cdj1, chaperone DNA J homolog1, csu63, csu63a, csu63a(cdj), csu63(dnaj), gnp_QAP4e06a, gpm394a, PCO082317, pco082317(95), umc343	leaf cDNA csu63, deduced amino acid sequence nearly identical to chaperone DNA J, multiple copies
934	cdj2	chaperone DNA J2	GRMZM2G364069	B73 RefGen_v3	Gene	Chr1	250153164	250156813	cdj2	cdj2, chaperone DNA J2, csu164, csu164a, csuh164, gnp_QAU1c10b, gpm404b, mdJ1, p-umc1968, umc1512, umc1968(82), umc388	ubiquitous tissue expression; cDNA and genomic clones, SSR umc 1512
935	cdk8	cyclin dependent kinase8	GRMZM2G166771	B73 RefGen_v3	Gene	Chr5	45567569	45573392	cdk8	cdk8, cl17437_1, cl17437_1(395)	encodes part of the "CDK8" module that mediates transcription initiation with RNA Polymerase II
936	cdo1081a		GRMZM2G119494	B73 RefGen_v3	Gene	Chr1	5338770	5342488	cdo1081a	cdo1081a, glycoside hydrolase, family 28	probed with an oat leaf cDNA.
937	cdpk1	calcium dependent protein kinase1	GRMZM2G115518	B73 RefGen_v3	Gene	Chr5	60830003	60836777	cdpk1	D84507, CDPK related kinase1, cdpk*-S82324, CL1173_1, CL1173_1(485), mck1, uaz197, uaz197(gfu), ZmCRK1	sequence and motifs similar to calcium-dependent protein kinases, but CDPK1 has high activity in absence of calcium, and is not activated by calcium (Furumoto 1996).
938	cdpk10	calcium-dependent protein kinase 10	GRMZM2G320506	B73 RefGen_v3	Gene	Chr5	4670693	4674066	cdpk10	calcium-dependent protein kinase 10, cdpk10, cl146_1	
939	cdpk11	calcium dependent protein kinase11	GRMZM2G047486	B73 RefGen_v3	Gene	Chr2	136808741	136813600	cdpk11	calcium dependent protein kinase11, calcium dependent protein kinase12, cdpk11, cdpk12, CL53944_1(150), CL53944_1a, CPK11, rs131184318, rs131184323, rs131184325, ZmCPK11	encodes a protein that functions in abscisic acid signaling upstream of the MAP kinase encoded by mpk2, aka MPK5 (Ding et al 2012)
940	cdpk13	calcium dependent protein kinase13	GRMZM2G173928	B73 RefGen_v3	Gene	Chr6	84540654	84547361	cdpk13	cdpk13, cdpk*-D84508, ZmCRK3	E. coli expressed fusion protein does not appear to require calcium
941	cdpk14	calcium dependent protein kinase14	GRMZM2G178756	B73 RefGen_v3	Gene	Chr6	62895992	62899068	cdpk14	cdpk14, cdpk*-D87045, ZMZK19	
942	cdpk2	calcium dependent protein kinase2	GRMZM2G365815	B73 RefGen_v3	Gene	Chr2	149142039	149144480	cdpk2	calcium dependent protein kinase2, cdpk2	genomic and cDNA clones; genomic sequence similar to plant CDPK; pollen-specific expression; possibly two copies (Southern blot); antisense oligonucleotides disrupt pollen tubes
943	cdpk3	calcium dependent protein kinase3	GRMZM2G168706	B73 RefGen_v3	Gene	Chr2	203612491	203616678	cdpk3	calcium dependent protein kinase3, cdpk3, CDPK9, cdpk*-D87043, CL1577_1b, rs129210365, ZMZK6	full-length cDNA, kinase function confirmed by direct assay of enzyme raised in E. coli (Saijo 1997)
944	cdpk4	calcium dependent protein kinase4	GRMZM2G321239	B73 RefGen_v3	Gene	Chr10	134942355	134946973	cdpk4	calcium dependent protein kinase4, cdpk4, CDPK7, cdpk*-D87046, CL1905_1(728), CL1905_1c, ZMZK24	cDNA sequence, functional gene product in E. coli
945	cdpk5	calcium dependent protein kinase5	GRMZM2G314396	B73 RefGen_v3	Gene	Chr2	14545463	14553791	cdpk5	calcium dependent protein kinase5, CDPK1, cdpk5, CL1905_1(119), CL1905_1b, ZmCDPK1	single copy;
946	cdpk7	calcium dependent protein kinase7	GRMZM2G081310	B73 RefGen_v3	Gene	Chr4	157020786	157026774	cdpk7	calcium dependent protein kinase homolog-L15390, cdpk7, cdpk*-L15390, siL15390(324), siL15390a	unpublished root cDNA sequence
947	cdpk8	calcium dependent protein kinase8	GRMZM2G154489	B73 RefGen_v3	Gene	Chr7	152988408	152989553	cdpk8	cdpk8, cdpk*-U28376, CL1577_1(574), CL1577_1c, CPK2, MZECDPK2	
948	cef1	Zea CEFD homolog1	GRMZM2G322186	B73 RefGen_v3	Gene	Chr3	49620840	49626586	cef1	cef1, csu188, csu188(gfu), PCO061342, PCO061342(219), zcef1, Zea CEFD homolog1	leaf cDNA csu188, similar to Streptomyces clavuligerus protein
949	cenH3	centromeric histone H3	GRMZM2G158526	B73 RefGen_v3	Gene	Chr6	155443675	155448220	cenH3	cenH3, centromeric histone H3, CL12047_1, CL12047_1(519), IDP262	
950	cenpc1	centromere protein C 1	GRMZM2G114315	B73 RefGen_v3	Gene	Chr3	218621155	218631182	cenpc1	cenpc1, CenpcA, CENPCA, CenpcC, centromere protein C 1, cl1157_1(276), cl1157_1c	cDNA sequence
951	cesa1	cellulose synthase1	GRMZM2G112336	B73 RefGen_v3	Gene	Chr8	79738607	79744724	cesa1	cellulose synthase1, cesa1, CesA-1, CL1166_1c, ZmCesA-1	
952	cesa10	cellulose synthase10	GRMZM2G445905	B73 RefGen_v3	Gene	Chr1	234316246	234326747	cesa10	cellulose synthase10, cesa10, CesA10	gene exhibits coexpression with the genes cesa11 and cesa12.
953	cesa11	cellulose synthase 11	GRMZM2G055795	B73 RefGen_v3	Gene	Chr3	198438731	198444359	cesa11	cellulose synthase 11, cesa11, CesA11, csu567(ces), PCO143801, PCO143801(266), SOG0169a	coordinately expressed with loci cesa10 and cesa12
954	cesa12	cellulose synthase 12	GRMZM2G142898	B73 RefGen_v3	Gene	Chr7	117546197	117550877	cesa12	cellulose synthase 12, cesa12, CesA12	coordinately expressed with cesa10 and cesa11
955	cesa13	cellulose synthase13	GRMZM2G037413	B73 RefGen_v3	Gene	Chr2	29981034	29986917	cesa13	cellulose synthase A catalytic subunit 4 [UDP-forming]-like, cesa13, ZmCESA4	NCBI: cellulose synthase A catalytic subunit 4 [UDP-forming]-like
956	cesa2	cellulose synthase2	GRMZM2G027723	B73 RefGen_v3	Gene	Chr6	128743576	128750030	cesa2	cellulose synthase2, cesa2, cesA2, CesA-2, CL1166_1a, gnp_AI622068a, gnp_QAG5a02, gnp_QAG5f02a, gpm337, gpm339a, gpm33a, ZmCes-A2	cDNA
957	cesa3	cellulose synthase3	GRMZM2G039454	B73 RefGen_v3	Gene	Chr3	11648913	11655958	cesa3	cellulose synthase3, cesa3, CesA-3, PCO121439, ZmCesA-3	cDNA
958	cesa4	cellulose synthase4	GRMZM2G424832	B73 RefGen_v3	Gene	Chr7	18620330	18626341	cesa4	cellulose synthase4, cesa4, CesA-4, cesa4b, cesa9, pco126465, pco126465(541), ZmCesA-4	cDNA
959	cesa5	cellulose synthase5	GRMZM2G111642	B73 RefGen_v3	Gene	Chr1	290666783	290672751	cesa5	cellulose synthase5, cesa5, CesA-5, CL1164_1a, gnp_QAF3c07d, gpm329d, ZmCesA-5	
960	cesa6	cellulose synthase6	GRMZM2G113137	B73 RefGen_v3	Gene	Chr1	296334073	296339855	cesa6	cellulose synthase6, cesa6, CesA-6, gnp_QCF17c07, gnp_QCI2h07a, gpm625, gpm671a, IDP208, IDP542, PCO100501, pco100501(106), ZmCesA-6	
961	cesa7	cellulose synthase7	GRMZM2G025231	B73 RefGen_v3	Gene	Chr7	37037007	37042784	cesa7	gnp_QBL11h08b, gnp_QCJ29e03a, gpm213b, gpm322a, gpm477a, gpm526b, gpm675a, PCO096398(546), PCO096398b, ZmCesA-7	
962	cesa8	cellulose synthase8	GRMZM2G177631	B73 RefGen_v3	Gene	Chr7	26503597	26509680	cesa8	cellulose synthase8, cesa8, CesA-8, IDP2486, ZmCesA-8	cDNA
963	cesa9	cellulose synthase9	GRMZM2G018241	B73 RefGen_v3	Gene	Chr2	161757546	161763704	cesa9	CL1160_1a, gnp_AW330905a, gnp_QBL8d07a, gpm194a, gpm536a, IDP384, ZmCesA-4, ZmCesA-9	cDNA
964	cf1	camouflage1	GRMZM2G026117	B73 RefGen_v3	Gene	Chr5	84284464	84288424	cf1	cf1, pza01693, PZA01693, Zm-HEMC	porphyrin synthesis; zebra bands, yellow progressing to necrotic, suppressed by continuous light
965	cfm1	cp RNA splicing factor, CRM domain cont	GRMZM5G813259	B73 RefGen_v3	Gene	Chr6	162967857	162970961	cfm1	cfm1	
966	cfm2	CRM family member2	GRMZM2G094072	B73 RefGen_v3	Gene	Chr10	123593979	123609810	cfm2	cfm2, chloroplast RNA splicing and ribosome maturation (CRM) family member2, CRM family member2	RNA binding; part of a chloroplast stroma ribonucleoprotein complex with CAF1, CAF2 (Asakura and Barkan 2007)
967	cfm3	CRM family member3	GRMZM2G436001	B73 RefGen_v3	Gene	Chr2	228710700	228721042	cfm3	cfm3, chloroplast RNA splicing and ribosome maturation (CRM) family member3	
968	cfm4	cp RNA splicing factor, CRM domain cont	GRMZM2G142740	B73 RefGen_v3	Gene	Chr7	98272614	98278027	cfm4	cfm4, CRM-domain containing factor CFM3, chloroplastic/mitochondrial	
969	cfm6	CRM family member6	AC214507.3_FG001	B73 RefGen_v3	Gene	Chr10	125952699	125954050	cfm6	cfm6, chloroplast RNA splicing and ribosome maturation (CRM) family member6, si687066e03	
970	cg1	corngrass1	GRMZM2G022489	B73 RefGen_v3	Gene	Chr3	7774552	7776125	cg1	cg1, corngrass1, miR156, miR156b, miR156c	Cg1 encodes two tandem miR156 genes that are overexpressed in the meristem and lateral organs. George Chuck, 2007. semidominant Cg1 plants have narrow leaves, extreme tillering
971	cgs1	cystathionine gamma-synthase1	GRMZM2G113873	B73 RefGen_v3	Gene	Chr9	118703401	118709158	cgs1	cgs1, cgs1b, cystathionine gamma-synthase1, PZA03235, rs131175956, rz672b(cgs), ss196417235	
972	chi1	chalcone flavanone isomerase1	GRMZM2G155329	B73 RefGen_v3	Gene	Chr1	293118119	293119647	chi1	chalcone flavanone isomerase1, chi1, chi*-Z22760, csh, csh1a(chi), csh1(chi), csh(chi1), PZA00307	genomic sequence, gene-specific probe, transcript defined by S1-nuclease protection analysis
973	chi3	chalcone flavanone isomerase3	GRMZM2G119186	B73 RefGen_v3	Gene	Chr5	2496042	2497691	chi3	chalcone flavanone isomerase3, chi3, csh1c, csh1c(chi), csh1(chi3), csh(chi3)	Similar to chi1; expressed in various tissues, but not root, embryo, or internode (Sekhon et al 2011)
974	chld1	Mg chelataseD1	GRMZM2G043453	B73 RefGen_v3	Gene	Chr5	3095928	3103654	chld1	cl561_1, cl561_1(458), Mg chelataseD1, PZA02316, rs128283133, rs55623905 , ss196415969	One of 3 subunits predicted to form the Mg chelatase; see also oy1, l13.
975	chlh1	Mg chelatase subunit H 1	GRMZM2G323024	B73 RefGen_v3	Gene	Chr10	147389924	147396098	chlh1	chlh1, chlHa, Mg chelatase subunit H, Mg chelatase subunit H 1	
976	chn1	chitinase chem5	GRMZM2G453805	B73 RefGen_v3	Gene	Chr3	212090496	212091850	chn1	CHEM 5, chemically induced5, chitinase chem5, chn1, chn*-chem5, PCO125117, PCO125117(273), PRm3	cDNA derived from a library originating from a mercuric chloride treated line, INRA258; pathogenesis-related protein (Nasser 1988) induced by fungal infection and other stresses
977	chn2	chitinase2	GRMZM2G145461	B73 RefGen_v3	Gene	Chr6	83025839	83027065	chn2	chitinase candidateL00973, chn2, chn*-L00973, pCh2, uiu5(chn)	acidic chitinase I, based on cDNA sequence similarity; Southern blots suggest multiple copies
978	chn3	chitinase3	GRMZM2G389582	B73 RefGen_v3	Gene	Chr5	63306100	63308250	chn3	chi*-L16798, chitinase candidateL16798, chn3, chn*-L16798, class I acidic chitinase, pCH11, uiu6, uiu6(chn)	acidic chitinase I by cDNA sequence similarity; Southern blots suggest single or low copy number
979	chph1	chlorophyllase1	GRMZM2G170734	B73 RefGen_v3	Gene	Chr7	62149059	62150389	chph1	chph1	encodes a chlorophyllase
980	chph2	chlorophyllase2	GRMZM2G127421	B73 RefGen_v3	Gene	Chr1	239887471	239889132	chph2	chl2, chlorophyllase-2, chph2	encodes a chlorophyllase
981	chr101	chromatin complex subunit A 101	GRMZM2G177165	B73 RefGen_v3	Gene	Chr2	237177008	237182832	chr101	chr101, chr101b, PZA03576, PZA03577, rs131175478, rs132016615, ss196415299, ss196415301	

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
982	chr106	chromatin complex subunit A 106	GRMZM2G071025	B73 RefGen_v3	Gene	Chr1	270318386	270325104	chr106	cha101, chr101, chr101a, chr106, chromatin complex subunit A 101, PCO087393	
983	chr122	chromatin complex subunit A	GRMZM2G097289	B73 RefGen_v3	Gene	Chr10	89218737	89223927	chr122	cha122, chr122, chromatin complex subunit A	
984	chr124	chromatin complex subunit A	GRMZM2G130739	B73 RefGen_v3	Gene	Chr1	235255302	235258327	chr124	cha124, chr124, chromatin complex subunit A	
985	chr124	chromatin complex subunit A	GRMZM2G435541	B73 RefGen_v3	Gene	Chr1	235254537	235254864	chr124	cha124, chr124, chromatin complex subunit A	
986	chs1	chitin synthase homolog1	GRMZM6G007923	B73 RefGen_v3	Gene	Chr10	18758297	18761647	chs1	05c04c09, chitin synthase homolog1, chs1, CL40167_1, CL40167_1(721), MinE, uaz289	endosperm cDNA 5C04C09, similar to chitin synthase of Candida albicans
987	cip1	cytokinin inducible protease1	GRMZM2G009443	B73 RefGen_v3	Gene	Chr10	35591531	35598325	cip1	cip1, cytokinin inducible protease1, uaz242, uaz242(clp), uaz98	endosperm cDNA 5C02D08 similar to chloroplast Clp ATP-dependent protease
988	cipk3	calcineurin B-like-interacting protein kina	GRMZM2G174896	B73 RefGen_v3	Gene	Chr1	52148170	52153288	cipk3	cipk31, CIPK-like protein 1, CIPK-like protein 1 , PCO079320(20), PCO079320a, protein kinase homolog, rs131251484 , rs131251531 , tdsgR30A04 , ZmCIPK3	single copy genomic clone similar to plant protein kinase
989	cipk8	calcineurin B-like-interacting protein kina	GRMZM2G383240	B73 RefGen_v3	Gene	Chr3	372718	380906	cipk8	calcineurin B-like-interacting protein kinase3, CBL-interacting protein kinase8, CBL-interacting serine/threonine-protein kinase 8, cipk8, zmCIPK8	
990	cipk8	calcineurin B-like-interacting protein kina	Zm00001d000080	Zm-B73-REFERENCE-G	Gene	B73V4_cl421411		431957	cipk8	calcineurin B-like-interacting protein kinase3, CBL-interacting protein kinase8, CBL-interacting serine/threonine-protein kinase 8, cipk8, zmCIPK8	
991	citt1	citrate transporter1	GRMZM2G028521	B73 RefGen_v3	Gene	Chr1	10540341	10544903	citt1	citt1, PCO091082, PCO091082(7), umc1685	
992	cka1	CK2 protein kinase alpha 1	GRMZM2G143602	B73 RefGen_v3	Gene	Chr2	236711216	236716685	cka1	ck2, CK2, CK2-1 alpha, CK2 protein kinase alpha 1, cka1	(Superseded Nov 2012; ck2 merged with cka1 - EHC Nov 2012) small gene family. see also CK2.
993	cka2	CK2 protein kinase alpha 2	GRMZM2G047855	B73 RefGen_v3	Gene	Chr1	279484878	279490883	cka2	casein kinase2 subunit alpha, casein protein kinase subunit alpha, ck2a2, CK2 alpha subunit, CK2 protein kinase alpha 2, cka2, PCO082342	cDNA clone; small gene family; see also ck2.
994	cka4	CK2 protein kinase alpha 4	GRMZM5G845755	B73 RefGen_v3	Gene	Chr7	2138862	2144213	cka4	4, cka3, cka4, cka5, cl1074_1b, gnp_QCU21a03a, gnp_QCU21a03b, gpm755a, gpm755b, protein kinase2 alpha, umc1241	
995	ckb1	CK2 regulatory subunit B1	GRMZM5G857992	B73 RefGen_v3	Gene	Chr2	21659964	21665567	ckb1	CK2B1, CK2beta1, ckb1, protein kinase CK2 regulatory subunit CK2B1, siaf239816, siaf239816(122)	
996	cki1	cyclin-dependent kinase inhibitor1	GRMZM2G116885	B73 RefGen_v3	Gene	Chr1	232980076	232983251	cki1	cki1, rs128895594 , rs131863741 , ss196430913 , ss196430915 , umc166b, Zeama;KRP;1, ZmICK1	
997	cki2	cyclin-dependent kinase inhibitor2	GRMZM2G037926	B73 RefGen_v3	Gene	Chr5	29641580	29644988	cki2	cki2, Cyclin-dependent kinase inhibitor 5, rs131507988 , rs131507995, rs131508000, ZmICK2	
998	cki3	cyclin-dependent kinase inhibitor3	GRMZM2G157510	B73 RefGen_v3	Gene	Chr1	8442682	8446230	cki3	cki3, Cyclin-dependent kinase inhibitor, rs131203669, ZmICK3	
999	cki4	cyclin-dependent kinase inhibitor4	GRMZM2G358931	B73 RefGen_v3	Gene	Chr9	152252293	152255778	cki4	cki4, Cyclin-dependent kinase inhibitor, ZmICK4	
1000	cki5	cyclin-dependent kinase inhibitor5	GRMZM2G101613	B73 RefGen_v3	Gene	Chr5	209770434	209772179	cki5	cki2, cki5, cl528_-1, cl528_-1(451), Cyclin-dependent kinase inhibitor 2, ZmICK5	
1001	cki6	cyclin-dependent kinase inhibitor6	GRMZM2G084570	B73 RefGen_v3	Gene	Chr4	178774992	178776727	cki6	cki6, cki9, cyclin-dependent kinase inhibitor 1-like, pco119368, pco119368(330), ZmICK6.1, ZmICK6.2	
1002	cki6	cyclin-dependent kinase inhibitor6	Zm00001d052174	Zm-B73-REFERENCE-G	Gene	Chr4	181715802	181717531	cki6	cki6, cki9, cyclin-dependent kinase inhibitor 1-like, pco119368, pco119368(330), ZmICK6.1, ZmICK6.2	
1003	cki7	cyclin-dependent kinase inhibitor7	GRMZM2G343769	B73 RefGen_v3	Gene	Chr9	7870479	7871904	cki7	cki7, cyclin-dependent kinase inhibitor 1-like, rs131695170, ZmICK7	
1004	cki8	cyclin-dependent kinase inhibitor8	GRMZM2G154414	B73 RefGen_v3	Gene	Chr4	5410267	5411691	cki8	cki8, cyclin-dependent kinase inhibitor 3-like, ZmICK8	
1005	cko1	cytokinin oxidase1	GRMZM2G146644	B73 RefGen_v3	Gene	Chr3	7601132	7605870	cko1	cko1, ckx1, cytokinin oxidase1, umc1057, umc1059	peptide, cDNA, and genomic sequence, transgenic expression; aka ckx1; SSR umc1057
1006	cko2	cytokinin oxidase 2	GRMZM2G050997	B73 RefGen_v3	Gene	Chr3	152240440	152243093	cko2	cko2, ckx5, cytokinin oxidase 2, gnp_CK2-1_PCR, gpm128	
1007	cko3	cytokinin oxidase 3	GRMZM2G167220	B73 RefGen_v3	Gene	Chr8	158737677	158740474	cko3	ck03, cko3, ckx4, cytokinin oxidase 3	
1008	cko4	cytokinin oxidase 4	GRMZM5G817173	B73 RefGen_v3	Gene	Chr3	191899705	191903570	cko4	cko4, ckx3, ckx4, cytokinin oxidase 4	
1009	cko4b	cytokinin oxidase4b	GRMZM2G024476	B73 RefGen_v3	Gene	Chr8	171917567	171921620	cko4b	cko4b, ckx4b	
1010	cko5	cytokinin oxidase 5	GRMZM2G325612	B73 RefGen_v3	Gene	Chr8	22250244	22254270	cko5	cko5, ckx2, ckx5, cytokinin oxidase 5	
1011	ckx10	cytokinin oxidase10	GRMZM2G348452	B73 RefGen_v3	Gene	Chr1	207753174	207757725	ckx10	cko10, ckx10	
1012	ckx11	cytokinin oxidase11	GRMZM2G122340	B73 RefGen_v3	Gene	Chr10	131816214	131824636	ckx11	cko11, ckx11	
1013	ckx12	cytokinin oxidase12	GRMZM2G008792	B73 RefGen_v3	Gene	Chr2	28171679	28176605	ckx12	cko12, ckx12	
1014	ckx6	cytokinin oxidase6	GRMZM2G404443	B73 RefGen_v3	Gene	Chr1	230073700	230077262	ckx6	cko6, ckx6, umc37a	
1015	ckx7	cytokinin oxidase7	GRMZM2G114427	B73 RefGen_v3	Gene	Chr4	230558257	230560081	ckx7	ckx7	
1016	ckx8	cytokinin oxidase8	GRMZM2G134634	B73 RefGen_v3	Gene	Chr4	230648266	230650090	ckx8	cko8, ckx8	
1017	ckx8b	cytokinin oxidase8b	GRMZM2G162048	B73 RefGen_v3	Gene	Chr4	230722879	230724687	ckx8b	cko8b, ckx8b	
1018	ckx9	cytokinin oxidase9	GRMZM2G303707	B73 RefGen_v3	Gene	Chr9	81495589	81497784	ckx9	cko9, ckx9	
1019	cl10130_1		GRMZM2G325762	B73 RefGen_v3	Probed Site	Chr2	107818821	107820874	cl10130_1	cl10130_1, phm4880, PZA02549	
1020	cl10169_-1		GRMZM2G159291	B73 RefGen_v3	Probed Site	Chr5	5025863	5032416	cl10169_-1	cl10169_-1(374)	
1021	cl10732_1		GRMZM2G081652	B73 RefGen_v3	Probed Site	Chr3	173515706	173518871	cl10732_1	PZA00783	
1022	cl11011_1		GRMZM2G024231	B73 RefGen_v3	Probed Site	Chr1	277659611	277669564	cl11011_1	cl11011_1(92), PZA01978, rs128282288, rs55623208 , ss196414822	
1023	cl11096_1		GRMZM2G009994	B73 RefGen_v3	Probed Site	Chr2	2544057	2550523	cl11096_1	cl11096_1(197), PHM13440, PZA00525, rs128283300, rs55624919 , ss196414937	
1024	cl11614_1		GRMZM2G030529	B73 RefGen_v3	Probed Site	Chr1	82020741	82030263	cl11614_1	PZA00752	
1025	cl1288_1a		GRMZM2G005990	B73 RefGen_v3	Probed Site	Chr2	221982609	221995090	cl1288_1a	cl1288_1(193), PZA02012, rs129235802, ss196415303	
1026	cl13018_1		GRMZM2G435274	B73 RefGen_v3	Probed Site	Chr1	148467319	148467778	cl13018_1	cl13018_1(44), PZA02577, rs131804329, rs55625984 , ss196414605	
1027	cl23597_2		GRMZM2G060919	B73 RefGen_v3	Probed Site	Chr5	199272243	199280188	cl23597_2	cl23597_2(445), PZA00652, rs131175724, ss196416267	
1028	cl24029_1		GRMZM2G129804	B73 RefGen_v3	Probed Site	Chr10	4074286	4076892	cl24029_1	cl24029_1(712), PZA01313, rs131175976, ss196417307	
1029	cl25041_1a		GRMZM2G104538	B73 RefGen_v3	Probed Site	Chr2	2500510	2502357	cl25041_1a	cl25041_1(197), PHM1511, PZA02133, rs128285038, rs128285039, rs55624567 , ss196414929, ss196414935	
1030	cl2592_1		GRMZM2G102779	B73 RefGen_v3	Probed Site	Chr6	165090982	165093128	cl2592_1	cl2592_1(524), PHM2658, PZA02141, rs130450282, rs55623442 , ss196416503	

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
1031	cl26491_-1		GRMZM2G094698	B73 RefGen_v3	Probed Site	Chr1	262785068	262791083	cl26491_-1	cl26491_-1(98), PHM5526, PZA00709, rs128281475, rs55622688 , ss196414740	
1032	cl26752_1		GRMZM2G444808	B73 RefGen_v3	Probed Site	Chr2	152841914	152871443	cl26752_1	cl26752_1(155), PZA01280, rs128284167, rs55624369 , ss196415148	
1033	cl3166_1a		GRMZM2G110143	B73 RefGen_v3	Probed Site	Chr1	182564660	182568332	cl3166_1a	cl3166_1(51), PZA02191, rs128284264, ss196414626	
1034	cl32627_1e		GRMZM2G021912	B73 RefGen_v3	Probed Site	Chr4	181251421	181255561	cl32627_1e	cl32627_1(332), PZA02194, rs128282854, rs55626179 , ss196415880	
1035	cl32758_1		GRMZM2G010797	B73 RefGen_v3	Probed Site	Chr10	118011019	118013627	cl32758_1	cl32758_1(747), PHM13687, PZA00712, rs128282561, rs128611864, ss196417419, ss196417421	
1036	cl35669_1		GRMZM2G114634	B73 RefGen_v3	Probed Site	Chr5	5933678	5937461	cl35669_1	cl35669_1(376), PHM3762, PZA02653, rs128282999, rs55622947 , ss196415981	
1037	cl37086_1		GRMZM2G006341	B73 RefGen_v3	Probed Site	Chr9	136765593	136770088	cl37086_1	cl37086_1(695), PZA02235, rs128282661, rs55625245 , ss196417259	
1038	cl37280_1		GRMZM2G084491	B73 RefGen_v3	Probed Site	Chr10	137987861	138021103	cl37280_1	cl37280_1(758), PZA02663, rs128632345, rs55624594 , ss196417456	
1039	cl3927_1a		GRMZM2G018579	B73 RefGen_v3	Probed Site	Chr1	8347283	8348889	cl3927_1a	cl3927_1(5), PHM13094, PZA00528, rs131175253, rs55623316 , ss196414361	
1040	cl39957_1		GRMZM2G062657	B73 RefGen_v3	Probed Site	Chr6	142637425	142646491	cl39957_1	cl39957_1(511), PZA02673, rs128283568, rs55626440 , ss196416447	
1041	cl40463_1a		GRMZM2G031043	B73 RefGen_v3	Probed Site	Chr3	33556709	33563069	cl40463_1a	cl40463_1(215), PZA02255, rs128285026, rs55624549 , ss196415351	
1042	cl40794_1		GRMZM2G133314	B73 RefGen_v3	Probed Site	Chr3	5438548	5449063	cl40794_1	cl40794_1(200), PZA02678, rs128283880, ss196415317	
1043	cl42326_1		GRMZM2G142344	B73 RefGen_v3	Probed Site	Chr4	191944776	191948747	cl42326_1	cl42326_1(341), PHM4348, PZA02685, rs131175648, ss196415959	
1044	cl42453_1		GRMZM2G150383	B73 RefGen_v3	Probed Site	Chr2	229529084	229531382	cl42453_1	PZA02266	
1045	cl439_1b		GRMZM2G116243	B73 RefGen_v3	Probed Site	Chr5	60026465	60031511	cl439_1b	cl439_1(399), PHM1870, rs131175676, ss196416076	
1046	cl44168_1		GRMZM2G308957	B73 RefGen_v3	Probed Site	Chr2	9966256	9966760	cl44168_1	cl44168_1(115), PZA02272, rs129012510, rs129012511, rs55624469 , ss196414983, ss196414985	
1047	cl48276_1		GRMZM2G010342	B73 RefGen_v3	Probed Site	Chr7	171273581	171292567	cl48276_1	cl48276_1(579), PZA00695, rs130691626, rs130691627, rs131175835, rs55624999 , ss196416753, ss196416755, ss196416757	
1048	cl5367_1b		GRMZM2G107116	B73 RefGen_v3	Probed Site	Chr6	120823156	120846260	cl5367_1b	cl5367_1(498), PZA00571, rs128283086, rs55623456 , ss196416407	
1049	cl5882_1		GRMZM2G050845	B73 RefGen_v3	Probed Site	Chr3	5674392	5677199	cl5882_1	cl5882_1(200), PHM12859, PZA00100, rs128282785, rs128282791, rs55626102 , ss196415319, ss196415321	
1050	cl61573_1		GRMZM2G125494	B73 RefGen_v3	Probed Site	Chr2	15582030	15592514	cl61573_1	cl61573_1(120), PZA02337	
1051	cl7866_1		GRMZM2G072894	B73 RefGen_v3	Probed Site	Chr5	859812	865105	cl7866_1	cl7866_1(458), PZA02367, rs131175649, ss196415963	
1052	cl7929_1		GRMZM2G090500	B73 RefGen_v3	Probed Site	Chr1	102589780	102593584	cl7929_1	cl7929_1(36), PHM10621, PHM6795, PZA02763, rs128687143, rs131175672, ss196414581, ss196416066	
1053	cl7929_1		GRMZM2G128737	B73 RefGen_v3	Probed Site	Chr5	44432947	44436968	cl7929_1	cl7929_1(36), PHM10621, PHM6795, PZA02763, rs128687143, rs131175672, ss196414581, ss196416066	
1054	cl8508_1		GRMZM2G119696	B73 RefGen_v3	Probed Site	Chr4	72079159	72083571	cl8508_1	cl8508_1(317), PZA02767, rs131175599, ss196415768	
1055	cld1	cold regulated protein homolog1	GRMZM2G064868	B73 RefGen_v3	Gene	Chr4	29145785	29159221	cld1	CL45463_1, CL45463_1(299), cld1, cold regulated protein homolog1, csu19, umc315	leaf cDNA csu19, similar to barley cold-regulated protein
1056	cle14	clavata3/esr-related14	AC191109.3_FG001	B73 RefGen_v3	Gene	Chr2	228749730	228750254	cle14	clavata (CLV), cle14, embryo-surrounding region (ESR), FLORAL ORGAN NUMBER2-like	candidate for clavata3 (CLV3) ortholog; peptides encoded by this gene shown to have a negative effect on SAM size when applied exogenously
1057	cle16	clavata3/esr-related16	GRMZM5G818232	B73 RefGen_v3	Gene	Chr9	141708812	141709096	cle16	clavata (CLV), cle16, embryo-surrounding region (ESR)	candidate for clavata3 (CLV3) ortholog
1058	cle20	clavata3/esr-related20	GRMZM2G008651	B73 RefGen_v3	Gene	Chr7	162750384	162751038	cle20	clavata (CLV), cle20, embryo-surrounding region (ESR)	candidate for clavata3 (CLV3) ortholog
1059	cle21	clavata3/esr-related21	GRMZM5G826174	B73 RefGen_v3	Gene	Chr1	226281053	226281753	cle21	clavata (CLV), cle21, embryo-surrounding region (ESR)	candidate for clavata3 (CLV3) ortholog
1060	cle22	clavata3/esr-related22	GRMZM2G070192	B73 RefGen_v3	Gene	Chr6	158463657	158465175	cle22	clavata (CLV), cle22, embryo-surrounding region (ESR)	candidate for clavata3 (CLV3) ortholog
1061	cle23	clavata3/esr-related23	GRMZM2G098918	B73 RefGen_v3	Gene	Chr5	54443972	54445002	cle23	clavata (CLV), cle23, embryo-surrounding region (ESR)	candidate for clavata3 (CLV3) ortholog
1062	cle24	clavata3/esr-related24	GRMZM2G123818	B73 RefGen_v3	Gene	Chr4	169575895	169576594	cle24	clavata (CLV), cle24, embryo-surrounding region (ESR)	candidate for clavata3 (CLV3) ortholog
1063	cle25	clavata3/esr-related25	GRMZM2G525788	B73 RefGen_v3	Gene	Chr1	63215440	63215543	cle25	CLAVATA3/ESR (CLE)-related protein 22, clavata (CLV), cle25, embryo-surrounding region (ESR)	candidate for clavata3 (CLV3) ortholog
1064	cle26	clavata3/esr-related26	GRMZM2G473147	B73 RefGen_v3	Gene	Chr8	17245262	17246579	cle26	clavata (CLV), cle26, embryo-surrounding region (ESR)	candidate for clavata3 (CLV3) ortholog
1065	cle27	clavata3/esr-related27	GRMZM2G468688	B73 RefGen_v3	Gene	Chr10	132555330	132555915	cle27	clavata (CLV), cle27, embryo-surrounding region (ESR)	candidate for clavata3 (CLV3) ortholog
1066	cle5	clavata3/esr-related5	GRMZM5G875999	B73 RefGen_v3	Gene	Chr5	13148983	13151122	cle5	clavata (CLV), cle5, embryo-surrounding region (ESR), IDP222, IDP559	candidate for clavata3 (CLV3) ortholog
1067	cle6	clavata3/esr-related6	GRMZM2G052776	B73 RefGen_v3	Gene	Chr3	196510926	196511186	cle6	clavata (CLV), cle6, embryo-surrounding region (ESR), pzb01109, rs129520212, rs131175549, rs55623274 , ss196415593, ss196415595	
1068	cle7	clavata3/esr-related7	GRMZM2G372364	B73 RefGen_v3	Gene	Chr4	7570324	7571104	cle7	clavata (CLV), cle7, embryo-surrounding region (ESR), FLORAL ORGAN NUMBER2-like	candidate for clavata3 (CLV3) ortholog; peptides encoded by this gene shown to have a negative effect on SAM size when applied exogenously
1069	clpp2	chloroplast protease complex P2	GRMZM2G056373	B73 RefGen_v3	Gene	Chr1	49617140	49619406	clpp2	ATP-dependent Clp protease proteolytic subunit 5, chloroplastic-like, Chr.1_chloroplast protease complex P5, Chr.1_ClpP5, clpp2, pco093974(84), pco093974a, rs128282907	encodes subunit of chloroplast protease complex; paralog of v30 (a.k.a. clpp1).
1070	clx1	calnexin homolog1	GRMZM2G134668	B73 RefGen_v3	Gene	Chr2	62121211	62125114	clx1	calnexin homolog1, clx1, csu148, csu148b, csu148(clx), csuh148, umc381	low copy number, leaf cDNA csu148, similar to Arabidopsis calnexin
1071	clx2	calnexin homolog2	GRMZM2G022180	B73 RefGen_v3	Gene	Chr10	112603406	112606897	clx2	CL2224_1c, cln, clx2, clx*-X77569, CNX, csu148a, csu148a(clx), csu255	
1072	cmk1	cytidine methyl kinase1	GRMZM5G859195	B73 RefGen_v3	Gene	Chr3	187980568	187985888	cmk1	4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol kinase1, 4-diphosphocytidyl-2-C-methyl-D-erythritol kinase1, cdpmek1, cdp-me kinase1, cmk1, ispE, umc2169	encodes 4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol kinase [a.k.a. 4-diphosphocytidyl-2-C-methyl-D-erythritol kinase]
1073	cml1	coumarate ligase1	GRMZM2G075333	B73 RefGen_v3	Gene	Chr5	89189678	89194264	cml1	4-coumarate--CoA ligase 1, cml1, pco063262, pco063262(411), Zm4CL, Zm4CL2	
1074	cmu1	chorismate mutase1	GRMZM2G116087	B73 RefGen_v3	Gene	Chr8	172665323	172669357	cmu1	AY103806, cmu1, PCO111734, PHM5019, PZA01290, rs131175915, ss196417074, Zmcm1	function largely predicted; protein heterodimerizes with fungal chorismate mutase
1075	cmu2	chorismate mutase2	GRMZM2G179454	B73 RefGen_v3	Gene	Chr5	92220297	92223624	cmu2	cmu2, pco120903(415), pco120903b	enzyme activity from protein raised in E coli
1076	cncr1	cinnamoyl CoA reductase1	GRMZM2G131205	B73 RefGen_v3	Gene	Chr1	211567137	211573211	cncr1	ccr2, CCR2, CCR3, cinnamoyl CoA reductase1, cncr1, IDP241, PCO114642, TIDP3284, umc1706, ZmCCR1	Mutant results in plants with improved cell wall digestibility
1077	cncr2	cinnamoyl CoA reductase2	GRMZM2G131836	B73 RefGen_v3	Gene	Chr7	47738518	47740886	cncr2	ccr2, CCR4, cinnamoyl CoA reductase2, cncr2, dihydroflavonol-4-reductase, IDP2415, siy15069(547), umc1095, ZmCCR2	cDNA similar to Eucalyptus gunnii sequence; weaker homology to hm1 and a1; SSR umc1095
1078	cngt1	cytokinin N-glucosyl transferase1	GRMZM2G097030	B73 RefGen_v3	Gene	Chr7	23728517	23730596	cngt1	cl26839_1, cl26839_1(545)	function based on similarity to Arabidopsis protein and expression
1079	cnh1	carbon-nitrogen hydrolase homolog1	GRMZM2G169365	B73 RefGen_v3	Gene	Chr9	151083033	151087840	cnh1	carbon-nitrogen hydrolase homolog1, cnh1, IDP579, IDP634, Omega-amidase chloroplastic, omega amidase homolog, PCO141375(707), PCO141375c	

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
1080	col10	C2C2-CO-like-transcription factor 10	GRMZM2G012717	B73 RefGen_v3	Gene	Chr6	117553493	117555386	col10		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1081	col11	C2C2-CO-like-transcription factor 11	GRMZM2G095598	B73 RefGen_v3	Gene	Chr2	33216134	33217640	col11	zinc finger protein CONSTANS-LIKE 3-like	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1082	col12	2C2-CO-like-transcription factor 12	GRMZM2G041991	B73 RefGen_v3	Gene	Chr5	204659225	204661268	col12	col12, phi048, phi058, umc108	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.. NCBI: zinc finger protein CONSTANS-LIKE 16
1083	col13	C2C2-CO-like-transcription factor 13	GRMZM2G038783	B73 RefGen_v3	Gene	Chr9	108447974	108449794	col13	CONSTANS-like protein CO6	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1084	col14	C2C2-CO-like-transcription factor 14	GRMZM2G042198	B73 RefGen_v3	Gene	Chr4	162885359	162891594	col14		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1085	col2	C2C2-CO-like-transcription factor 2	GRMZM2G144346	B73 RefGen_v3	Gene	Chr1	267460450	267462897	col2		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1086	col3	C2C2-CO-like-transcription factor 3	GRMZM2G021777	B73 RefGen_v3	Gene	Chr5	183418226	183419769	col3		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1087	col4	C2C2-CO-like-transcription factor 4	GRMZM2G107886	B73 RefGen_v3	Gene	Chr9	31881581	31883549	col4		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1088	col5	C2C2-CO-like-transcription factor 5	GRMZM2G075562	B73 RefGen_v3	Gene	Chr5	204223654	204228519	col5		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1089	col6	C2C2-CO-like-transcription factor 6	GRMZM2G013398	B73 RefGen_v3	Gene	Chr9	39579626	39585243	col6		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1090	col7	C2C2-CO-like-transcription factor 7	AC233888.1_FG002	B73 RefGen_v3	Gene	Chr10	127941747	127942849	col7		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1091	col8	C2C2-CO-like-transcription factor 8	GRMZM2G114137	B73 RefGen_v3	Gene	Chr5	11383616	11385590	col8		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1092	col9	C2C2-CO-like-transcription factor 9	GRMZM2G167560	B73 RefGen_v3	Gene	Chr4	165343973	165348286	col9		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1093	conz1	constans1	GRMZM2G405368	B73 RefGen_v3	Gene	Chr9	35635308	35639846	conz1	constans1, conz1, Hd1, ZmCOL1	homologous to photoperiod genes constans (co) from Arabiodopsis and heading date 1 (hd1) in rice. (Miller 2008)
1094	cop1	coatomer protein1	GRMZM2G143354	B73 RefGen_v3	Gene	Chr3	137371268	137378912	cop1	CL1247_1(237), CL1247_1a, coatomer protein1, cop1, delta COP	
1095	cop2	coatomer protein2	GRMZM2G028929	B73 RefGen_v3	Gene	Chr10	141389160	141394314	cop2	coatomer protein2, cop2, epsilon COP, PCO148993, PCO148993(759)	cDNA
1096	cpn1	chaperonin 1	GRMZM2G111477	B73 RefGen_v3	Gene	Chr5	31014041	31015732	cpn1	chaperonin 1, cpn1, cpn60-1, cpn60I, CPNA, csu396, heat shock protein60, hsp60, hsp60"-L21007, hsp60"-Z11546, hsp60"-Z12114, mitochondrial chaperonin-60, PZA02113	cDNA sequence homologous to hsp60 family; 2 copies
1097	cpn1	chaperonin 1	GRMZM2G458208	B73 RefGen_v3	Gene	Chr5	31022591	31026410	cpn1	chaperonin 1, cpn1, cpn60-1, cpn60I, CPNA, csu396, heat shock protein60, hsp60, hsp60"-L21007, hsp60"-Z11546, hsp60"-Z12114, mitochondrial chaperonin-60, PZA02113	cDNA sequence homologous to hsp60 family; 2 copies
1098	cpn10	chaperonin10	GRMZM2G091189	B73 RefGen_v3	Gene	Chr4	176529663	176531725	cpn10	chaperonin10, cpn10, pco132358a, uaz222, umc1610	cDNA sequences; SSR umc1610
1099	cpn2	chaperonin2	GRMZM2G416120	B73 RefGen_v3	Gene	Chr1	234834523	234840412	cpn2	chaperonin2, CL2221_1a, cpn2, cpn60II, CPN60II, CPN60-II, CPNB, heat shock protein60, hsp60"-L21006, hsp60"-L21008, hsp60"-Z12115, mtcpn60II	cDNA and genomic clones similar to mitochondrial cpn60 (hsp60); 2 copies
1100	cpp1	CPP-transcription factor 1	GRMZM2G153754	B73 RefGen_v3	Gene	Chr7	9332269	9337505	cpp1	cysteine-rich polycomb-like protein (CPP), protein tesmin/TSO1-like CXC 3, ZmCPP10	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1101	cpp10	CPP-transcription factor 10	GRMZM2G701689	B73 RefGen_v3	Gene	Chr3	119999294	120014210	cpp10	cysteine-rich polycomb-like protein (CPP), ZmCPP5	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1102	cpp11	CPP-transcription factor 11	GRMZM2G059678	B73 RefGen_v3	Gene	Chr3	195307506	195312044	cpp11	cysteine-rich polycomb-like protein (CPP), ZmCPP6	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1103	cpp12	CPP-transcription factor 12	GRMZM2G342588	B73 RefGen_v3	Gene	Chr6	122278172	122285658	cpp12	cysteine-rich polycomb-like protein (CPP), ZmCPP8	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1104	cpp13	CPP-transcription factor 13	AC203865.3_FG001	B73 RefGen_v3	Gene	Chr3	119995077	119998350	cpp13	cysteine-rich polycomb-like protein (CPP), ZmCPP4	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1105	cpp2	CPP-transcription factor 2	GRMZM2G015097	B73 RefGen_v3	Gene	Chr1	171249195	171254764	cpp2	cysteine-rich polycomb-like protein (CPP), tesmin/TSO1-like CXC domain containing protein, ZmCPP3	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1106	cpp3	CPP-transcription factor 3	GRMZM2G173198	B73 RefGen_v3	Gene	Chr8	121766217	121767657	cpp3	cysteine-rich polycomb-like protein (CPP), protein tesmin/TSO1-like CXC 2, ZmCPP12	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1107	cpp4	CPP-transcription factor 4	GRMZM2G060170	B73 RefGen_v3	Gene	Chr6	158012795	158016012	cpp4	CXC domain containing TSO1-like protein 1, cysteine-rich polycomb-like protein (CPP), ZmCPP9	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1108	cpp5	CPP-transcription factor 5	GRMZM2G322090	B73 RefGen_v3	Gene	Chr1	171296402	171301898	cpp5	cysteine-rich polycomb-like protein (CPP), ZmCPP1.1, ZmCPP1.2	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1109	cpp6	CPP-transcription factor 6	GRMZM2G366584	B73 RefGen_v3	Gene	Chr1	252868475	252877327	cpp6	cysteine-rich polycomb-like protein (CPP), ZmCPP2	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1110	cpp7	CPP-transcription factor 7	GRMZM2G104246	B73 RefGen_v3	Gene	Chr8	172942841	172947390	cpp7	cysteine-rich polycomb-like protein (CPP), protein tesmin/TSO1-like CXC 5, ZmCPP13.1, ZmCPP13.2	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1111	cpp8	CPP-transcription factor 8	GRMZM2G096600	B73 RefGen_v3	Gene	Chr8	121748701	121752582	cpp8	CXC domain containing TSO1-like protein 1, cysteine-rich polycomb-like protein (CPP), ZmCPP11.1, ZmCPP11.2	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1112	cpp9	CPP-transcription factor 9	GRMZM2G388148	B73 RefGen_v3	Gene	Chr5	134229441	134245208	cpp9	cysteine-rich polycomb-like protein (CPP), ZmCPP7.1, ZmCPP7.2	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1113	cpps2	copalyl diphosphate synthase2	GRMZM2G044481	B73 RefGen_v3	Gene	Chr1	79711199	79714961	cpps2	an2, anther ear2, cpps2, gnp_QCB6b03, gpm843, kaurene synthase2, ZmAffx.12.1, ZmCPS1	with An1 gene product; likely duplicate function explains why an1 plants are not fully dwarfed (Harris et al. 2005)
1114	cpps3	copalyl diphosphate synthase3	GRMZM2G068808	B73 RefGen_v3	Gene	Chr10	75822918	75828439	cpps3	cpps3, syn-copalyl diphosphate synthase-like, ZmCPS3	
1115	cps1	chloroplast protein synthesis1	GRMZM2G156565	B73 RefGen_v3	Gene	Chr1	295555161	295563804	cps1	chloroplast protein synthesis1, cps1, cysteine--tRNA ligase, cytoplasmic-like	reduced levels of RUBISCO and all thylakoid membrane complexes; unaltered chloroplast mRNA; decreased chloroplast polysomes
1116	cps2	chloroplast protein synthesis2	AC215201.3_FG005	B73 RefGen_v3	Gene	Chr6	142273603	142277674	cps2	chloroplast protein synthesis2, CPN60, cps2, hcf133, PCO123570c, ruBisCO large subunit-binding protein subunit alpha, chloroplastic	of ribosomes on chloroplast mRNAs. (A. Barkan, 2015). CPN60 ortholog; 20-fold reduced RUBISCO, 2-fold reduced thylakoid polypeptides, decreased chloroplast polysomes (aka
1117	cps5	chloroplast protein synthesis5	GRMZM2G566786	B73 RefGen_v3	Gene	Chr8	10072049	10076873	cps5	putative leucine--tRNA ligase, mitochondrial, rs130711403 , rs130711407 , rs130711409 , rs130711411 , rs130711419 , rs130711420 , rs130711437 , rs130711438 , rs130711441 ,	Chloroplast protein synthesis 5: chloroplast leucyl-tRNA synthetase (A. Barkan, 2015). NCBI: putative leucine--tRNA ligase, mitochondrial
1118	cps5	chloroplast protein synthesis5	GRMZM5G858471	B73 RefGen_v3	Gene	Chr8	10078647	10080295	cps5	putative leucine--tRNA ligase, mitochondrial, rs130711403 , rs130711407 , rs130711409 , rs130711411 , rs130711419 , rs130711420 , rs130711437 , rs130711438 , rs130711441 ,	Chloroplast protein synthesis 5: chloroplast leucyl-tRNA synthetase (A. Barkan, 2015). NCBI: putative leucine--tRNA ligase, mitochondrial
1119	cps5	chloroplast protein synthesis5	Zm00001d008497	Zm-B73-REFERENCE-G	Gene	Chr8	10439104	10447983	cps5	putative leucine--tRNA ligase, mitochondrial, rs130711403 , rs130711407 , rs130711409 , rs130711411 , rs130711419 , rs130711420 , rs130711437 , rs130711438 , rs130711441 ,	Chloroplast protein synthesis 5: chloroplast leucyl-tRNA synthetase (A. Barkan, 2015). NCBI: putative leucine--tRNA ligase, mitochondrial
1120	cptk1	chloroplast thymidine kinase1	GRMZM2G048821	B73 RefGen_v3	Gene	Chr1	79243435	79249210	cptk1	chloroplast thymidine kinase, cptk1, tk1	Mutants have aberrant chloroplast DNA metabolism. Alice Barkan, 2011
1121	cpx2	coproporphyrinogen III oxidase2	GRMZM2G032282	B73 RefGen_v3	Gene	Chr10	141340391	141349914	cpx2	coproporphyrinogen III oxidase2, cpx, cpx2, dks8B, umc400b(cpx)	duplicate to cpx1 (nec4)
1122	cr4	crinkly4	GRMZM2G051637	B73 RefGen_v3	Gene	Chr10	5591911	5595821	cr4	adherentN590, adherentN647, ad*-N411, ad*-N590C, ad*-N647, AY110360, CL2011_1, cr4, crinkly4, crinkly leaf, dap*-6143, PZA02095, rs128284103, ss196417309	crinkly seedling leaves; plants short with rough, sometimes knot-bearing, extremely crinkly leaves and club tassel; aleurone mosaic
1123	crp1	chloroplast RNA processing1	GRMZM2G083950	B73 RefGen_v3	Gene	Chr7	155872362	155876338	crp1	chloroplast RNA processing1, CL1533_1, cl1533_1(576), crp1, hcf111, hcf136, uor2, uor2(crp), uor2(crp1), ZmPPR404	intergenic RNA termini. Binds petA, psaC, petD 5'UTRs. (A. Barkan, 2015). pale green seedling lethal, high chlorophyll leaf fluorescence;cytochromeb6/f and PSI deficient; protein translation
1124	crp11	cp 3'-tRNA processing endoribonuclease	GRMZM5G802566	B73 RefGen_v3	Gene	Chr7	131855975	131859128	crp11	crp11, nuclear ribonuclease Z, ortholog of CPZ	
1125	crp4	chloroplast RNA processing4	GRMZM2G377761	B73 RefGen_v3	Gene	Chr7	8183160	8199889	crp4	crp4, probable polyribonucleotide nucleotidyltransferase 1, chloroplastic, TIDP3337	and decay. (A. Barkan, 2015). chloroplast RNA processing and turnover; INDEL probe TIDP3337.
1126	crr1	cytokinin response regulator1	GRMZM2G040736	B73 RefGen_v3	Gene	Chr2	2084221	2085003	crr1	cip1, crr1, cytokinin response regulator1, uaz242, umc1622, ZmCip1, ZmOrphan186, ZmRR1	single copy,cDNA and genomic sequences; induced in leaf by cytokinin, and inorganic nitrogen; SSR umc1622
1127	crr2	cytokinin response regulator2	GRMZM2G392101	B73 RefGen_v3	Gene	Chr10	147279947	147281251	crr2	crr2, cytokinin response regulator2, umc1344, umc1569, ZmOrphan259, ZmRR2	single copy, cDNA and genomic sequences; SSRs umc1569, umc1344; induced by cytokinin, and inorganic nitrogen
1128	crr4	cytokinin response regulator4	GRMZM2G319187	B73 RefGen_v3	Gene	Chr8	157499048	157505111	crr4	crr4, gnp_AI770684, gpm84, ZmOrphan151, ZmRR4	

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
1129	crr5	cytokinin response regulator5	GRMZM6G980248	B73 RefGen_v3	Gene	Chr3	148064771	148065302	crr5	crr5, IDP769, magi17165, PCO113156, PCO113156(218), probable dolichyl pyrophosphate Man9GlcNAc2 alpha-1,3-glucosyltransferase, PZB02044, rs129271489, ss196415459, ZmRR5	
1130	crr7	cytokinin response regulator7	GRMZM2G096171	B73 RefGen_v3	Gene	Chr4	118088455	118091073	crr7	crr7, ZmOrphan235, ZmRR7	
1131	crr8	cytokinin response regulator8	GRMZM2G099797	B73 RefGen_v3	Gene	Chr1	28417831	28422778	crr8	CL34529_1a, PZB02058, rs128283614, rs128406169, rs131175266, rs55626497 , ss196414431, ss196414433, ss196414435, ZmRR8	
1132	crs1	chloroplast RNA splicing1	GRMZM2G078412	B73 RefGen_v3	Gene	Chr1	221032166	221044222	crs1	CL1179_1, rs131186689	Binds atpF intron, promotes atpF splicing. (A. Barkan, 2015). pale green seedling lethal; chloroplast ATP synthase null; promotes atpF intron splicing
1133	crs2	chloroplast RNA splicing2	GRMZM2G132021	B73 RefGen_v3	Gene	Chr8	12557722	12566051	crs2	chloroplast RNA splicing2, crs2, pza01951, siAF225708	splicing 2; required for splicing of chloroplast subgroup IIB introns. peptidyl tRNA hydrolase homolog. (A. Barkan, 2015)
1134	crs3	chloroplast RNA splicing3	GRMZM2G053196	B73 RefGen_v3	Gene	Chr9	10846021	10852948	crs3	chloroplast RNA splicing4, crs3, crs4 paralog, pentatricopeptide repeat7, pentatricopeptide repeat-containing protein At3g18110, chloroplastic-like, ppr7, ZmPPR462	pale yellow green seedling lethal; splicing of ndhA and ndhB transcprits
1135	crs4	chloroplast RNA splicing4	GRMZM2G481231	B73 RefGen_v3	Gene	Chr2	160534929	160541718	crs4	chloroplast RNA splicing4, crs4, pentatricopeptide repeat7, pentatricopeptide repeat-containing protein At3g18110, chloroplastic-like, ppr7, ZmPPR117	pale yellow green seedling lethal; splicing of ndhA and ndhB transcprits
1136	crt2	calreticulin2	GRMZM2G358059	B73 RefGen_v3	Gene	Chr7	24423090	24427016	crt2	csu1140, csuh1140, gnp_QCN15h11, gnp_QCT9h04a, gpm698, gpm754a, pco074428(545), PCO074428(545), PCO074428b	calcium-binding activity; endoplasmic reticulum; N-terminal sequence of purified protein and cDNA sequence 96% identical to barley homolog; single copy leaf cDNA csu1140
1137	crti1	carotene isomerase1	GRMZM2G108457	B73 RefGen_v3	Gene	Chr4	201046911	201051551	crti1	carotenoid isomerase1, crti1, CRTISO1	enclodes carotene isomerase1
1138	crti2	carotene isomerase2	GRMZM2G106531	B73 RefGen_v3	Gene	Chr2	227035811	227040800	crti2	carotenoid isomerase2, crti2, CRTISO2	encodes carotene isomerase2
1139	crti3	carotene isomerase3	GRMZM2G144273	B73 RefGen_v3	Gene	Chr5	1333687	1341860	crti3	carotenoid isomerase 1, crti3, CRTISO3	enclodes carotene isomerase
1140	crup1	CruP paralog1	GRMZM2G017805	B73 RefGen_v3	Gene	Chr5	35290697	35295045	crup1	CruP paralog1	
1141	cry2	cryptochrome2	GRMZM2G049549	B73 RefGen_v3	Gene	Chr2	44186481	44190062	cry2	cry2, cryptochrome2, PZB00017, PZB00183, rs131175426, ss196415073	
1142	csd1	CSD-transcription factor 1	GRMZM2G356459	B73 RefGen_v3	Gene	Chr1	39400907	39403446	csd1		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1143	csd2	CSD-transcription factor 2	GRMZM2G389768	B73 RefGen_v3	Gene	Chr4	238665158	238666872	csd2		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1144	csd3	CSD-transcription factor 3	GRMZM2G141150	B73 RefGen_v3	Gene	Chr10	72594595	72596618	csd3		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1145	csd4	CSD-transcription factor 4	GRMZM5G895313	B73 RefGen_v3	Gene	Chr10	143487131	143488239	csd4		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1146	csr1	chloroplast srp54 receptor1	Zm00001d042044	Zm-B73-REFERENCE-G	Gene	Chr3	148445216	148448764	csr1	chloroplast srp54 receptor1, CL3959_3(579), CL3959_3b, csr1	Chloroplast srp receptor 1. CpFtsY, chloroplast FtsY homolog involved in thylakoid protein targeting. (A. Barkan, 2015). pale yellow green seedling lethal; thylakoid protein targeting
1147	csu1138		GRMZM2G009465	B73 RefGen_v3	Gene	Chr1	120200389	120202682	csu1138	csu1138, rs131175303, rs131175304, ss196414596, ss196414598	
1148	csu1171		GRMZM2G026807	B73 RefGen_v3	Gene	Chr1	14623612	14638761	csu1171	csu1171, rs128381186, ss196414393	
1149	csu134b(thf)		GRMZM2G034182	B73 RefGen_v3	Probed Site	Chr5	2883764	2885159	csu134b(thf)	csu134b, csu134b(thf), csu134c, csuh134b, methylenetetrahydrofolate reductase2, mtf2, umc372b, umc372c, ZmMTHFR-2	
1150	csu134b(thf)		GRMZM2G034278	B73 RefGen_v3	Probed Site	Chr5	2861668	2866402	csu134b(thf)	csu134b, csu134b(thf), csu134c, csuh134b, methylenetetrahydrofolate reductase2, mtf2, umc372b, umc372c, ZmMTHFR-2	
1151	csu147		GRMZM2G037485	B73 RefGen_v3	Gene	Chr9	101747048	101748531	csu147	csu147, rs131740387, sc183, TIDP2768, umc380	
1152	csu173		GRMZM2G030606	B73 RefGen_v3	Gene	Chr5	181437480	181439392	csu173	cl7280_1, csu173, csuh173, PHM5296, PZA02356, rs128282276, rs55622794 , ss196416225, umc392	single copy, novel leaf cDNA sequence
1153	csu3		GRMZM2G162292	B73 RefGen_v3	Gene	Chr1	82584684	82587334	csu3	CL34571_1, cl34571_1(32), CL34571_2, csu3, csuh3, IDP3851, IDP3940, umc302	cDNA partially sequenced, weak homology to yeast heat shock protein 26, SwissProt P15992 and to leghemoglobin, GenBank accession M91075
1154	csu31a		GRMZM2G154508	B73 RefGen_v3	Gene	Chr8	146425699	146426962	csu31a	csu31, csu31a, csuh31, PCO104134, rs131176469, rs132482751 , umc323	NCBI: Tat pathway signal sequence. partially sequenced cDNA to leaf mRNA
1155	csu32a		GRMZM2G093405	B73 RefGen_v3	Gene	Chr3	3885932	3888723	csu32a	cl7341_1(199), cl7341_1a, csu32, csu32a, csuh32, tdsgR40G04 , umc324	NCBI: heme-binding protein 2 alex heme-binding protein 2 precursor
1156	csu337		GRMZM2G164440	B73 RefGen_v3	Gene	Chr2	156962054	156963314	csu337	csu337, csu624, PVR3-like protein, umc1235	
1157	csu454(gst)		GRMZM2G096247	B73 RefGen_v3	Gene	Chr1	7858766	7859978	csu454(gst)	CL1117_-2, csu454(gst), glutathione S-transferase 6	
1158	csu634		GRMZM2G006429	B73 RefGen_v3	Gene	Chr9	136805443	136808919	csu634	csu634, ZmOrphan83	protein phosphatase 2C-like (Alexandrov et al.)
1159	csu849(atpb)		GRMZM2G021331	B73 RefGen_v3	Gene	Chr8	65484575	65488309	csu849(atpb)	csu849(atpb)	zEST00849 Maize Leaf, Stratagene #937005 Zea mays cDNA clone csuh00849 5- end similar to mitochondrial ATP synthase beta subunit, mRNA sequence
1160	csu923(sec61)		GRMZM2G089491	B73 RefGen_v3	Gene	Chr6	95634080	95636134	csu923(sec61)	csu923, csu923(sec61), rs130346804	NCBI: Protein transport protein SEC61 gamma subunit
1161	csu948		GRMZM2G147390	B73 RefGen_v3	Gene	Chr10	113729637	113731267	csu948	csu948, csuh00948, csuh948	
1162	csy1	chloroplast SecY-1	GRMZM5G809546	B73 RefGen_v3	Gene	Chr10	52428891	52457207	csy1	chloroplast SecY-1, csy1, scy1	Chloroplast secY 1. Required for thylakoid protein targeting via the cpSec pathway. SecY homolog. (A. Barkan, 2015). pale yellow seedling lethal; membrane protein translocon
1163	ct2	compact plant2	GRMZM2G064732	B73 RefGen_v3	Gene	Chr1	16348267	16356203	ct2	codw, compact plant2, ct2, IDP407, pco117747, rd3	semi-dwarf plant, 1/3 height; shortened internodes; club tassel, fasciated ear
1164	cta1	chitinase A1	GRMZM2G051943	B73 RefGen_v3	Gene	Chr2	34162588	34163936	cta1	chiA, chita, chitinase A1, cta1, gnp_QBG19a05a, gpm460a, umc1783	cDNA sequence corresponds to peptide sequence of maize 28kDa chitinase A
1165	ctb1	chitinase B1	GRMZM2G005633	B73 RefGen_v3	Gene	Chr10	127392328	127393918	ctb1	chiB, chitb, chitinase B1, ctb1	cDNA sequence corresponds to protein sequence of maize chitinase B
1166	ctn1	caltractin1	GRMZM2G048846	B73 RefGen_v3	Gene	Chr7	165886707	165889308	ctn1	cal, caltractin1, centrin, ctn1, uaz322, uaz322(gfu)	endosperm cDNA 5C06B08, similar to algal caltractin
1167	cts1	citrate synthase1	GRMZM2G063851	B73 RefGen_v3	Gene	Chr5	123666786	123673425	cts1	cdo534b(cts), citrate synthase1, csu324, cts1, PCO125766b	leaf cDNA csu324
1168	cyb6	cytochrome b6	GRMZM2G463640	B73 RefGen_v3	Gene	Chr5	21522922	21524744	cyb6	cyb6, petB, photosynthetic electron transport B	
1169	cyc1	cyclin1	GRMZM2G034647	B73 RefGen_v3	Gene	Chr8	119587820	119590668	cyc1	CL2527_1, csh9, csh9(cyc1), cyc1, CYClb, CyclbZm, cyclin1, PHM3993, PZA02136, Zeama;CycB1;2	classI; sense RNA functions in Xenopus oocytes
1170	cyc10	cyclin10	GRMZM2G107377	B73 RefGen_v3	Gene	Chr7	49750260	49752394	cyc10	cyc10, CycD3;1a	Associates to cyclin dependent kinase proteins during germination and the complexes formed develop kinase activity.
1171	cyc11	cyclin11	GRMZM2G161382	B73 RefGen_v3	Gene	Chr2	163951423	163953820	cyc11	cyc11, CycD3;1b, cyclin delta-3	Associates to cyclin dependent kinase proteins during germination and the complexes formed develop kinase activity.
1172	cyc12	cyclin12	GRMZM2G408242	B73 RefGen_v3	Gene	Chr7	137132640	137137679	cyc12	cyc12, cycC, cyclin-C, gnp_QCG20h06, gpm643	encodes part of the "CDK8" module that mediates transcription initiation with RNA Polymerase II
1173	cyc13	cyclin13	GRMZM2G075117	B73 RefGen_v3	Gene	Chr4	179655519	179658130	cyc13	cyc13, cycD2, D-type cyclin, umc1775	
1174	cyc3	cyclin3	GRMZM2G073671	B73 RefGen_v3	Gene	Chr6	82783470	82787296	cyc3	cyc3, CycIIIZm, cyclin3, umc1186, Zeama;CycB2;1	classIII; sense RNA functions in Xenopus oocytes; SSR umc1186
1175	cyc4	cyclin4	GRMZM2G310115	B73 RefGen_v3	Gene	Chr8	170942614	170961820	cyc4	csh8a, csh8a(cyc4), cyc4, cyc4a, CYCI-A, cyclin IaZm, gnp_AI714405b, gnp_AI739771, gpm61b, gpm72, Ia, PCO130346(644), PCO130346b	
1176	cyc5	cyclin5	GRMZM2G005619	B73 RefGen_v3	Gene	Chr8	1514389	1517712	cyc5	CL1316_1(648), CL1316_1b, cyc5, cyclin5, cyclin type B-like, cyclin type B-like transcript, cyc*-U80248 , cycZme1, CycZmG1	
1177	cyc6	cyclin6	Zm00001d009011	Zm-B73-REFERENCE-G	Gene	Chr8	30110204	30114064	cyc6	cyc2, cyc6, cyclin2, cyc*-U50064 , CYCZM2W, type A-like cyclin	

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
1178	cyc7	cyclin7	GRMZM2G310115	B73 RefGen_v3	Gene	Chr8	170942614	170961820	cyc7	cyc4, cyc4b, cyc7, CyclaZm, cyclin4, cyclin IaZm, gnp_AI714405a, gpm61a, PCO136403, PCO136403(259), Zeama;CycB1;1	Class I; sense RNA functions in Xenopus oocytes
1179	cyc8	cyclin8	GRMZM2G138886	B73 RefGen_v3	Gene	Chr2	18100584	18104322	cyc8	cyc8, CYCB2;2, cyclin B2;2	functions primarily during the mitotic cell cycle during maize endosperm development
1180	cyc9	cyclin9	GRMZM2G017081	B73 RefGen_v3	Gene	Chr5	59835715	59840942	cyc9	cyc9, cyclin-A2	
1181	cyp1	cytochrome P450 homolog1	GRMZM5G899349	B73 RefGen_v3	Gene	Chr3	232159860	232163704	cyp1	csu25, csu25a, csu25a(P450), csu25(P450), csuh25, cyp1, cytochrome P450 homolog1, umc317	leaf cDNA csu25, similar to P450 lanosterol 14-alpha-demethylase
1182	cyp10	cytochrome P450 10	GRMZM2G370745	B73 RefGen_v3	Gene	Chr3	217067316	217070532	cyp10	cyp10, CYP72A28, CYP72A28v2, CYP72A28v3, cytochrome P450 10, PCO073684b	Unpublished DNA sequence submitted to GenBank
1183	cyp11	cytochrome P450 11	GRMZM2G129860	B73 RefGen_v3	Gene	Chr3	217218199	217221692	cyp11	cyp11, CYP72A5, cytochrome P450, PCO091556, PCO091557(275), PCO091557a	Transcript induced by naphthalic anhydride or triasulfuron herbicide
1184	cyp12	cytochrome P450 12	GRMZM2G091588	B73 RefGen_v3	Gene	Chr2	184817709	184821832	cyp12	cyp12, CYP92A1, cytochrome P450 12, flavonoid 3-monooxygenase	
1185	cyp13	cytochrome P450 13	GRMZM5G837869	B73 RefGen_v3	Gene	Chr5	215877677	215882183	cyp13	cyp13, CYP97A, Cytochrome P450 CYP97A16, lut5, lutein5	encodes CYP97A
1186	cyp14	cytochrome P450 14	GRMZM2G143202	B73 RefGen_v3	Gene	Chr1	86848122	86858514	cyp14	carotenoid epsilon hydroxylase, cyp14, CYP97C, CYP97C19, cytochrome P450-type monooxygenase CYP97C1, lut1, lutein1	encodes CYP97C
1187	cyp15	cytochrome P450 15	GRMZM2G010221	B73 RefGen_v3	Gene	Chr4	236268174	236272709	cyp15	cyp15, CYP97B, cytochrome P450-type monooxygenase CYP97B3	encodes CYP97B
1188	cyp16	cytochrome P450 16	Zm00001d002937	Zm-B73-REFERENCE-G	Gene	Chr2	27420578	27426388	cyp16	cyp16, CYP72A27, cytochrome P450 16	
1189	cyp17	cytochrome P-450 17	GRMZM2G138008	B73 RefGen_v3	Gene	Chr7	164026278	164028417	cyp17	cyp17, CYP78A, ge1, giant embryo ortholog	A CYP78A ortholog of rice giant embryo1; regulated by bige1.
1190	cyp18	cytochrome P-450 18	GRMZM2G470442	B73 RefGen_v3	Gene	Chr1	73382596	73385374	cyp18	cyp18, CYP78A, cytochrome P450 78A5-like, ge2, giant embryo ortholog	A CYP78A ortholog of rice giant embryo2
1191	cyp19	cytochrome P-450 19	GRMZM2G102079	B73 RefGen_v3	Gene	Chr7	6540482	6542475	cyp19	cyp19, cyp92C5, flavonoid 3'-monooxygenase-like	
1192	cyp20	cytochrome P-450 20	GRMZM2G139467	B73 RefGen_v3	Gene	Chr2	234927959	234929946	cyp20	cyp20, cyp92C6	
1193	cyp21	cytochrome P-450 21	GRMZM2G054603	B73 RefGen_v3	Gene	Chr9	156449824	156452070	cyp21	cyp21, cytochrome P450 78A1-like, cytochrome P450 family 78 subfamily A	
1194	cyp6	cytochrome P450	Zm00001d019415	Zm-B73-REFERENCE-G	Gene	Chr7	32852022	32852396	cyp6	cyp6, cytochrome P450, phi034, uaz338, uaz338(gfu)	leaf cDNA 6C06B11 (uaz338) similar to eggplant protein, SSR phi034
1195	cyp8	cytochrome P-450 8	GRMZM2G167986	B73 RefGen_v3	Gene	Chr1	243707108	243709449	cyp8	450 8, cytochrome P-450 candidate, Cytochrome P450 CYP78A1, PLA1, pla1a, PLASTOCHRON1, plastochron1A ortholog	developing inflorescence, cDNA clone, assayed in transgenic yeast microsomes
1196	cyp9	cytochrome P450 9	GRMZM2G138248	B73 RefGen_v3	Gene	Chr9	79214248	79216270	cyp9	cyp79A61, cyp9, tyrosine N-monooxygenase-like	
1197	cys1	cysteine synthase1	GRMZM2G082185	B73 RefGen_v3	Gene	Chr8	6465005	6468479	cys1	CL5251_1(582), CL5251_1b, cys1, cysteine synthase1, uaz7c02b02(gfu)	vegetative meristem cDNA 7C02B02
1198	cys2	cysteine synthase2	GRMZM2G005887	B73 RefGen_v3	Gene	Chr1	177054678	177059679	cys2	cys2, cys*-X85803, gnp_QAP2a09b, gpm385b, maize cysteine synthase homologue1, Mcysp	cDNA sequence similar to wheat cysteine synthase
1199	czog1	cis-zeatin O-glucosyltransferase1	GRMZM2G168474	B73 RefGen_v3	Gene	Chr2	19085185	19087692	czog1	cis-zeatin O-glucosyltransferase1, cisZOG1, czog1, gnp_AW065903b, gpm143b	gene intronless, genomic and cDNA sequences identical (Martin et al., 2001 PNAS 98:5922); expression high in roots and kernels (compare czog2).
1200	czog2	cis-zeatin O-glucosyltransferase2	GRMZM2G110511	B73 RefGen_v3	Gene	Chr8	166957556	166959303	czog2	cis-zeatin O-glucosyltransferase2, cisZOG2, czog2	enzymatic activity like that of czog1 but high in roots and low in kernels; 97.8% identity at amino acid level
1201	d1	dwarf plant1	GRMZM2G036340	B73 RefGen_v3	Gene	Chr3	10455337	10457618	d1	d1, dwarf plant1, ga3ox1, ga3ox2, gibberellin 3-oxidase2, qPH3.1, Zea mays GA 3-oxidase 1 (D1), ZmGA3ox1, ZmGA3ox2	andromonoecious, short, compact plants; responds to gibberellins; d1-t intermediate in height
1202	d3	dwarf plant3	GRMZM2G093195	B73 RefGen_v3	Gene	Chr9	26725936	26729883	d3	d2, d3, dwarf plant3, ZmKAO, ZmKAO1	like d1, plant short and compact; "d2" mutation(s) are allelic (d2 is lapsed)
1203	d8	dwarf plant8	GRMZM2G144744	B73 RefGen_v3	Gene	Chr1	266160101	266163168	d8	d8, dwarf plant8, gnp_AI770444b, gpm82b, miniplant1, mpl1, PCO148437, rs128285143, rs55625097 , ss196414776, ZmGRAS8	Dominant D8 plants resemble d1; extreme alleles not responsive to gibberellins.
1204	d9	dwarf plant9	GRMZM2G024973	B73 RefGen_v3	Gene	Chr5	11793473	11795945	d9	D*-2319, d9, D*-N2319, dwarf plant9, gnp_AI770444a, gpm82a, PZB00079, PZD00066, rs128285141, rs55625095 , ss196414774, ZmGRAS44	dominant D9 plants semidwarf with broad, dark green leaves; andromonoecious, not responsive to gibberellins; possible duplicate locus of d8
1205	dar1	monodehydroascorbate reductase homol	GRMZM2G084881	B73 RefGen_v3	Gene	Chr2	166248729	166253814	dar1	csu196, csu196(gfu), dar1, gnp_QAE25c08, gpm286, monodehydroascorbate reductase homolog1, PCO066827(182), PCO066827b	leaf cDNA csu196 sequence similar to cucumber monodehydroascorbate reductase (NADH)
1206	dba2	DNA binding activity2	GRMZM2G070360	B73 RefGen_v3	Gene	Chr3	212237694	212247053	dba2	dba2, DNA binding activity2, PCO079851b, std8, V-type proton ATPase subunit E-like	cDNA pAS12 has binding activity; gene specific
1207	dba3	DNA binding activity3	GRMZM2G011513	B73 RefGen_v3	Gene	Chr10	147971633	147973013	dba3	dba3, DNA binding activity3, IDP167, IDP9081, PCO079133, std5	cDNA pAS13 has binding activity; gene specific
1208	dbb1	double B-box zinc finger protein1	GRMZM2G018876	B73 RefGen_v3	Gene	Chr2	34309164	34353587	dbb1	AY107218, dbb1, PCO140184, ZmOrphan198	
1209	dbb10	double B-box zinc finger protein10	GRMZM2G143718	B73 RefGen_v3	Gene	Chr7	142719045	142722858	dbb10	dbb10, salt tolerance-like protein, ZmOrphan191	
1210	dbb11	double B-box zinc finger protein11	GRMZM2G028594	B73 RefGen_v3	Gene	Chr9	19034863	19041148	dbb11	dbb11, Profilin homolog5, ZmOrphan243	
1211	dbb12	double B-box zinc finger protein12	GRMZM2G098442	B73 RefGen_v3	Gene	Chr10	133526489	133528033	dbb12	dbb10, salt tolerance-like protein, ZmOrphan175	
1212	dbb2	double B-box zinc finger protein2	GRMZM2G131982	B73 RefGen_v3	Gene	Chr2	22527448	22530936	dbb2	B-box zinc finger protein 20, dbb2, rs131183118	
1213	dbb3	double B-box zinc finger protein3	GRMZM5G834596	B73 RefGen_v3	Gene	Chr3	5041526	5161029	dbb3	b-box zinc finger family protein, dbb3, ORPHAN transcription factor, ZmOrphan153	similar to Arabidopsis light-regulated zinc finger protein 1
1214	dbb4	double B-box zinc finger protein4	GRMZM2G019335	B73 RefGen_v3	Gene	Chr4	134046087	134047565	dbb4	B-box zinc finger protein 24, cl359_1, cl359_1(434), dbb4, ZmOrphan179	
1215	dbb5	double B-box zinc finger protein5	GRMZM2G118884	B73 RefGen_v3	Gene	Chr5	60454730	60456814	dbb5	B-box zinc finger protein 20, dbb5, ZmOrphan31	
1216	dbb6	double B-box zinc finger protein6	GRMZM2G095299	B73 RefGen_v3	Gene	Chr5	182486593	182488058	dbb6	dbb6, gnp_QBF3h10, gpm454, ZmOrphan117	
1217	dbb7	double B-box zinc finger protein7	GRMZM2G110541	B73 RefGen_v3	Gene	Chr5	190103401	190104973	dbb7	B-box zinc finger protein 21-like, dbb7, ZmOrphan134	
1218	dbb8	double B-box zinc finger protein8	GRMZM2G070446	B73 RefGen_v3	Gene	Chr6	74621148	74626420	dbb8	dbb8, probable salt tolerance protein, ZmOrphan348	
1219	dbb9	double B-box zinc finger protein9	GRMZM2G116475	B73 RefGen_v3	Gene	Chr6	84690279	84691702	dbb9	dbb9, salt tolerance protein, ZmOrphan149	
1220	dbf1	DRE-binding protein 1	GRMZM2G061487	B73 RefGen_v3	Gene	Chr1	217638400	217639968	dbf1	dbf1, DRE-binding protein 1, pza03740, pza03741, si707074g06	
1221	dbf3	DRE-binding protein3	GRMZM2G124037	B73 RefGen_v3	Gene	Chr2	195129909	195130993	dbf3	cbf3, dbf3, DREB1A, stress-responsive transcription factor, ZmEREB3	
1222	dbp4	DRE-binding protein4	GRMZM2G380377	B73 RefGen_v3	Gene	Chr6	62712930	62714535	dbp4	dbp4, dehyrdration responsive element binding protein4, ZmEREB56	AP2/ERF transcription factor; confers resistance to drought and cold when transferred to Arabidopsis
1223	dbptf1	DBP-transcription factor 1	GRMZM2G108147	B73 RefGen_v3	Gene	Chr4	173593079	173596604	dbptf1	dbp1	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1224	dbptf2	DBP-transcription factor 2	GRMZM2G180430	B73 RefGen_v3	Gene	Chr5	214138462	214147660	dbptf2	dbp2	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1225	dbptf3	DBP-transcription factor 3	GRMZM2G149132	B73 RefGen_v3	Gene	Chr9	14021102	14026143	dbptf3	dbp3	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1226	dbptf4	DBP-transcription factor 4	GRMZM2G158734	B73 RefGen_v3	Gene	Chr9	88137603	88141355	dbptf4	dbp4	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
1227	dcd1	discordia1	GRMZM2G083459	B73 RefGen_v3	Gene	Chr10	90776034	90781199	dcd1	dcd1, discordia1, pco119117b	leaf epidermis cell divisions are misoriented, resulting in abnormal stomata, cork cells, and silica cells
1228	dcl101	dicer-like 101	GRMZM2G040762	B73 RefGen_v3	Gene	Chr1	4600841	4608248	dcl101	dcl1, fuzzy tassel, fzt, gnp_AW067486, gpm153, PCO092088, PCO092088(4)	mutant plants have 'fuzzy tassel' and reduced stature.
1229	dcl102	dicer-like 102	GRMZM2G413853	B73 RefGen_v3	Gene	Chr1	229801762	229819069	dcl102	endoribonuclease Dicer homolog 3b-like	
1230	dcl103	dicer-like 103	GRMZM2G160473	B73 RefGen_v3	Gene	Chr10	129990456	129992917	dcl103	CL34281_1	
1231	dcl104	dicer-like 104	GRMZM5G814985	B73 RefGen_v3	Gene	Chr3	164408916	164418189	dcl104	dcl104	
1232	dcl105	dicer-like 105	GRMZM2G301405	B73 RefGen_v3	Gene	Chr5	19916753	19927967	dcl105	dcl105	
1233	dcl4	dicer-like4	GRMZM2G024466	B73 RefGen_v3	Gene	Chr10	130059161	130061644	dcl4	dcl4, ragged3, rgd3, rgd*-766B, rgd*-N766B, shoot meristemless1, sml1	(was rgd*-N766B) like rgd1
1234	dcl4	dicer-like4	GRMZM2G050869	B73 RefGen_v3	Gene	Chr10	130072344	130073641	dcl4	dcl4, ragged3, rgd3, rgd*-766B, rgd*-N766B, shoot meristemless1, sml1	(was rgd*-N766B) like rgd1
1235	dcl4	dicer-like4	GRMZM2G050882	B73 RefGen_v3	Gene	Chr10	130081664	130095543	dcl4	dcl4, ragged3, rgd3, rgd*-766B, rgd*-N766B, shoot meristemless1, sml1	(was rgd*-N766B) like rgd1
1236	dcl4	dicer-like4	GRMZM2G160473	B73 RefGen_v3	Gene	Chr10	129990456	129992917	dcl4	dcl4, ragged3, rgd3, rgd*-766B, rgd*-N766B, shoot meristemless1, sml1	(was rgd*-N766B) like rgd1
1237	dct1	dicarboxylic acid transporter1	GRMZM2G040933	B73 RefGen_v3	Gene	Chr2	188701434	188706443	dct1	dct1, dicarboxylic acid transporter1	plastid transporter, specific to mesophyll cells (Taniguchi et al 2004)
1238	dct2	dicarboxylic acid transporter2	GRMZM2G086258	B73 RefGen_v3	Gene	Chr1	181895436	181907817	dct2	dct2, ZmpDCT2	plastid transporter, specific to bundle sheath cells (Taniguchi et al 2004)
1239	ddt1	DDT-transcription factor 1	GRMZM2G403562	B73 RefGen_v3	Gene	Chr2	145263420	145271766	ddt1		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1240	ddt2	DDT-transcription factor 2	GRMZM2G064145	B73 RefGen_v3	Gene	Chr4	117286975	117292108	ddt2		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1241	ddt3	DDT-transcription factor 3	GRMZM2G337749	B73 RefGen_v3	Gene	Chr5	173435057	173440344	ddt3		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1242	ddt4	DDT-transcription factor 4	GRMZM2G128176	B73 RefGen_v3	Gene	Chr7	171605886	171616500	ddt4		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1243	ddt5	DDT-transcription factor 5	AC196465.3_FG006	B73 RefGen_v3	Gene	Chr8	149438422	149444943	ddt5		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1244	ddt6	DDT-transcription factor 6	GRMZM2G314661	B73 RefGen_v3	Gene	Chr10	4874772	4883107	ddt6		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1245	de18	defective18	GRMZM2G091819	B73 RefGen_v3	Gene	Chr10	16522572	16525775	de18	de18, de*-B18, defective endosperm-B18, flavin monoxygenase, fmo, IDP6953, yuc1, YUCCA1	Defective kernel: seed weight less than half of normal (B37) (Torti et al. 1984)
1246	de30	defective endosperm B30	AF546188.1_FG007	B73 RefGen_v3	Gene	Chr7	18877460	18878182	de30	de30, deB30, de-B30, de*B30, de*-B30, defective endosperm B30, defective endosperm B-30	dominant De*-B30 has opaque, high lysine endosperm
1247	def1	defensin-like protein1	GRMZM2G368890	B73 RefGen_v3	Gene	Chr10	63633347	63634218	def1	def1, pco122672, pco122672(730)	
1248	def2	defensin-like protein2	GRMZM2G368861	B73 RefGen_v3	Gene	Chr10	63631377	63634230	def2	def2, flower-specific gamma-thionin	
1249	dek1	defective kernel1	GRMZM2G321753	B73 RefGen_v3	Gene	Chr1	47296057	47325628	dek1	clf, clf*-792, clf*-E792, defective kernel1, dek1, gay	germless; colorless (mosaic) aleurone; floury white endosperm; anthocyanins and carotenoids absent; cultured embryos not obtained (aka clf1, gay1)
1250	dek10	defective kernel10	GRMZM2G087226	B73 RefGen_v3	Gene	Chr4	236755443	236770419	dek10	cp*-1176A, defective kernel10, dek10	collapsed endosperm; lethal; cultured embryos green, curled, stubby; encodes a E-subgroup PPR protein
1251	dek2	defective kernel2	GRMZM2G110851	B73 RefGen_v3	Gene	Chr1	299174521	299176527	dek2	defective kernel2, dek2, dsc*-1315A, dsc*-N1315A, pentatricopeptide repeat-containing protein At4g20090-like, ZmPPR080	discolored, scarred endosperm; lethal; cultured embryos green
1252	dek35	defective kernel35	GRMZM2G066749	B73 RefGen_v3	Gene	Chr1	267973485	267976040	dek35	de*-2424, dek35, pentatricopeptide repeat-containing protein, ZmPPR068	mutants have defective kernels
1253	dek36	defective kernel36	GRMZM5G892151	B73 RefGen_v3	Gene	Chr5	5205807	5208368	dek36	dek36, o*-N1434, pentatricopeptide repeat-containing protein At4g21300-like, rs129982276, rs131480842	mutant kernels have a small and collapsed appearance at maturity, with a drastic size reduction in both embryo and endosperm; encodes an E+ subgroup PPR protein
1254	dek38	defective kernel38	GRMZM2G048851	B73 RefGen_v3	Gene	Chr5	53023389	53032516	dek38	ARM repeat superfamily protein, defective kernel38, dek38, tel2-interacting protein2, tti2	mutants are embryonic lethal, has a defective basal endosperm transfer (BETL) layer, and results in a smaller seed with highly underdeveloped endosperm.
1255	der1	derlin1	GRMZM2G117388	B73 RefGen_v3	Gene	Chr8	108530756	108538547	der1	CL1200_1, der1, derlin1, derlin1-1, derlin-3, gnp_QCT4c09a, gpm750a, sor gene	endoplasmic reticulum-associated degradation protein
1256	der2	derlin2	GRMZM2G082976	B73 RefGen_v3	Gene	Chr5	924282	928929	der2	der2, der2-1, derlin2, derlin-2, derlin2-1	
1257	der3	derlin3	GRMZM2G143817	B73 RefGen_v3	Gene	Chr6	130081997	130086777	der3	der3, derlin1-2, derlin-3, IDP2409	
1258	der4	derlin4	GRMZM2G112609	B73 RefGen_v3	Gene	Chr1	298904989	298911945	der4	der4, derlin-2, derlin2-2	
1259	dfr1	dihydroflavonoid reductase1	GRMZM2G004683	B73 RefGen_v3	Gene	Chr7	134116825	134118763	dfr1	cl56120_1(566), CL56120_1a, dfr1, dihydroflavanoid reductase, ms*-bs7	male sterile; identification to potential function based on GenBank and TIGR annotations
1260	dhar1	dehydroascorbate reductase like1	GRMZM5G855672	B73 RefGen_v3	Gene	Chr8	132704679	132707776	dhar1	dhar1, idp4400	
1261	dhar3	dehydroascorbate reductase like3	GRMZM2G035502	B73 RefGen_v3	Gene	Chr6	34430158	34433252	dhar3	dhar3, magi56098	
1262	dhn1	dehydrin1	GRMZM2G079440	B73 RefGen_v3	Gene	Chr6	137332062	137333893	dhn1	dehydrin1, dhn1, dhn3, lea2, PCO142314, pco142314(508), rab17, rab25, responsive to abscisic acid17, rny1, RNY1, rs132332327, umc170(dhn), umc170(rab17)	protein induced by abscisic acid; cDNA sequence agrees with amino acid sequence (aka dhn3, rab17, rny1)
1263	dhn13	dehydrin13	GRMZM2G169372	B73 RefGen_v3	Gene	Chr1	259363954	259365311	dhn13	csu222a, csu222a(hsp90), csu222a(wsi1), dhn13, umc1298	
1264	dhn3	dehydrin3	GRMZM2G373522	B73 RefGen_v3	Gene	Chr4	154337342	154339063	dhn3	cl2452_1(323), CL2452_1a, dhn-2, dhn2 dehydrin, dhn3, umc2391	
1265	dhn6	dehydrin6	GRMZM2G031308	B73 RefGen_v3	Gene	Chr3	200237243	200241761	dhn6	CL9078_1(266), CL9078_1a, dhn6, dhy-l, seed maturation protein, uaz7c01g04	
1266	dhn7	dehydrin7	GRMZM2G002786	B73 RefGen_v3	Gene	Chr8	174954713	174956656	dhn7	dehydrin7, dhn7, PCO138180(647), PCO138180b, seed maturation protein	
1267	dhr2	dhurrinase2	GRMZM2G076946	B73 RefGen_v3	Gene	Chr3	136590830	136594609	dhr2	dhr2, dhurrinase2, dhurrinase-like B-glucosidase	
1268	dla1	dihydrolipoamide S-acetyltransferase1	GRMZM2G015132	B73 RefGen_v3	Gene	Chr5	155570391	155577785	dla1	CL1480_2b, dihydrolipoamide S-acetyltransferase1, dla1	cDNA sequence
1269	dlc1	dynein light chain homolog1	GRMZM2G080116	B73 RefGen_v3	Gene	Chr8	61613853	61615071	dlc1	dlc1, dynein light chain homolog1, rs130773415	
1270	dlf1	delayed flowering1	GRMZM2G067921	B73 RefGen_v3	Gene	Chr7	175583965	175585451	dlf1	delayed flowering1, dlf1, dlf*-2389A, dlf*-N2461, ZmbZIP2	tall late plant with additional nodes and leaves at flowering; no apparent response to day length
1271	dlo1	drooping leaf ortholog1	GRMZM2G088309	B73 RefGen_v3	Gene	Chr1	26576546	26581707	dlo1	C2C2-YABBY transcription factor, C2C2-YABBY-transcription factor 2, dlo1, PCO142391, PCO142391(11), yab2, ZmDL1	
1272	dlo2	drooping leaf ortholog2	GRMZM2G102218	B73 RefGen_v3	Gene	Chr9	146951299	146956590	dlo2	C2C2-YABBY-transcription factor 7, dlo2, yab7, ZmDL2	
1273	dmag1	DNA-3-methyladenine glycosylase1	GRMZM2G171317	B73 RefGen_v3	Gene	Chr6	96096133	96100449	dmag1	dmag1	
1274	dmag2a	DNA-2-methyladenine glycosylase II A	GRMZM2G113228	B73 RefGen_v3	Gene	Chr10	5735648	5739240	dmag2a	dmag2a	
1275	dmag2b	DNA-2-methyladenine glycosylase II B	GRMZM2G114592	B73 RefGen_v3	Gene	Chr6	166365839	166367252	dmag2b	dmag2b	

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
1276	dmc1	disrupted meiotic cDNA homolog1	GRMZM2G109618	B73 RefGen_v3	Gene	Chr3	229761643	229766558	dmc1	dmc1, meiotic recombination protein DMC1	
1277	dmes1	diphosphocytidyl methyl erythritol synth	GRMZM5G856881	B73 RefGen_v3	Gene	Chr3	170159124	170162114	dmes1	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase1, 4-diphosphocytidyl-2C-methyl-D-erythritol synthase1, dmes1, si618008b02(470), si618008b02f	encodes 4-Diphosphocytidyl-2C-methyl-D-erythritol synthase
1278	dmes2	diphosphocytidyl methyl erythritol synth	GRMZM2G172032	B73 RefGen_v3	Gene	Chr8	164298387	164301819	dmes2	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase2, 4-diphosphocytidyl-2C-methyl-D-erythritol synthase2, dmes2	
1279	dnp1	diphosphonucleotide phosphatase1	GRMZM2G152757	B73 RefGen_v3	Gene	Chr10	15721331	15725740	dnp1	CL10219_1, CL10219_1(721), diphosphonucleotide phosphatase1, dnp1, ZmDP1	single copy
1280	dnp2	diphosphonucleotide phosphatase2	GRMZM2G111510	B73 RefGen_v3	Gene	Chr3	200107689	200115853	dnp2	diphosphonucleotide phosphatase2, dnp2, ZmDP2	single copy;
1281	dof1	DNA-binding with one finger1	Zm00001d031278	Zm-B73-REFERENCE-G	Gene	Chr1	184859499	184860221	dof1	DNA-binding protein MNB1, DNA-binding with one finger1, dof1, mnb1, MNB1a, umc1508	cDNA sequence, Southern blots indicate a multigene family whose members have highly homologous N-terminal basic domain; sequence very distinct from mnb2
1282	dof10	C2C2-Dof-transcription factor 10	GRMZM2G435475	B73 RefGen_v3	Gene	Chr6	158675548	158676679	dof10	ZmDof36	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1283	dof11	C2C2-Dof-transcription factor 11	GRMZM2G123900	B73 RefGen_v3	Gene	Chr1	154329458	154331722	dof11	ZmDof04	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1284	dof12	C2C2-Dof-transcription factor 12	GRMZM2G178767	B73 RefGen_v3	Gene	Chr5	19549995	19551017	dof12	dof zinc finger protein DOF5.8, ZmDof30	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1285	dof13	C2C2-Dof-transcription factor 13	GRMZM2G456452	B73 RefGen_v3	Gene	Chr1	227596191	227597088	dof13	ZmDof06	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1286	dof14	C2C2-Dof-transcription factor 14	GRMZM2G134545	B73 RefGen_v3	Gene	Chr7	152100148	152102643	dof14	ZmDof38	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1287	dof15	C2C2-Dof-transcription factor 15	GRMZM2G451771	B73 RefGen_v3	Gene	Chr10	88301230	88302056	dof15	ZmDof44	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1288	dof16	C2C2-Dof-transcription factor 16	GRMZM2G089850	B73 RefGen_v3	Gene	Chr7	130393751	130395017	dof16	ZmDof37	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1289	dof17	C2C2-Dof-transcription factor 17	GRMZM2G114998	B73 RefGen_v3	Gene	Chr4	155035798	155038140	dof17	ZmDof23	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1290	dof18	C2C2-Dof-transcription factor 18	GRMZM2G131897	B73 RefGen_v3	Gene	Chr1	164644881	164645955	dof18	ZmDof05	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1291	dof19	C2C2-Dof-transcription factor 19	GRMZM2G135703	B73 RefGen_v3	Gene	Chr3	176010296	176011726	dof19	ZmDof20	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1292	dof2	DNA binding with one finger2	GRMZM2G009406	B73 RefGen_v3	Gene	Chr2	189176444	189178274	dof2	DNA binding protein MNB2, DNA binding with one finger2, dof2, MNB1b, mnb2, nfd103, nfd111, nucleosome/chromatin assembly factor D 103, ZmDof14, ZmDOF2	cDNA sequence, Southern blots indicate small gene family; transcriptional repressor
1293	dof20	C2C2-Dof-transcription factor 20	GRMZM2G371058	B73 RefGen_v3	Gene	Chr6	149318311	149319745	dof20	ZmDof35	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1294	dof21	C2C2-Dof-transcription factor 21	GRMZM2G162749	B73 RefGen_v3	Gene	Chr1	14850152	14853035	dof21	dof21, rs128382116 , rs128382120 , rs131212524 , tdsgR34F09, umc2225, ZmDof01	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1295	dof22	C2C2-Dof-transcription factor 22	GRMZM2G171852	B73 RefGen_v3	Gene	Chr5	194884355	194887188	dof22	ZmDof31	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1296	dof23	C2C2-Dof-transcription factor 23	GRMZM2G010290	B73 RefGen_v3	Gene	Chr10	137229762	137232013	dof23	ZmDof45	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1297	dof24	C2C2-Dof-transcription factor 24	GRMZM2G084130	B73 RefGen_v3	Gene	Chr5	6118778	6119924	dof24	ZmDof28	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1298	dof25	C2C2-Dof-transcription factor 25	GRMZM2G108865	B73 RefGen_v3	Gene	Chr1	280409564	280411218	dof25	ZmDof10	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1299	dof26	C2C2-Dof-transcription factor 26	GRMZM2G061292	B73 RefGen_v3	Gene	Chr5	18177711	18179160	dof26	ZmDof29	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1300	dof27	C2C2-Dof-transcription factor 27	GRMZM2G017470	B73 RefGen_v3	Gene	Chr1	293405280	293407607	dof27	ZmDof11	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1301	dof28	C2C2-Dof-transcription factor 28	GRMZM2G093725	B73 RefGen_v3	Gene	Chr1	293486116	293487783	dof28	ZmDof12	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1302	dof29	C2C2-Dof-transcription factor 29	GRMZM2G140694	B73 RefGen_v3	Gene	Chr5	201437666	201441763	dof29	ZmDof32	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1303	dof3	DNA binding with one finger3	GRMZM2G179069	B73 RefGen_v3	Gene	Chr6	36946638	36948605	dof3	DNA binding with one finger3, dof3, dof35, gnp_QAO3e04, gpm382, ZmDof34	cDNA sequence distinct from dof1, dof2
1304	dof30	C2C2-Dof-transcription factor 30	AC233935.1_FG005	B73 RefGen_v3	Gene	Chr1	40917520	40918920	dof30	ZmDof02	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1305	dof31	C2C2-Dof-transcription factor 31	GRMZM2G144188	B73 RefGen_v3	Gene	Chr5	2344044	2345532	dof31	DOF31 dof zinc finger protein DOF3.6-like, Dof-type zinc finger DNA-binding family protein, ZmDof27	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1306	dof32	C2C2-Dof-transcription factor 32	GRMZM2G011832	B73 RefGen_v3	Gene	Chr1	246538639	246539936	dof32	ZmDof08	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1307	dof33	C2C2-Dof-transcription factor 33	GRMZM2G144172	B73 RefGen_v3	Gene	Chr5	2336487	2338861	dof33	ZmDof26	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1308	dof34	C2C2-Dof-transcription factor 34	GRMZM2G064655	B73 RefGen_v3	Gene	Chr2	203073326	203075231	dof34	ZmDof15	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1309	dof36	C2C2-Dof-transcription factor 36	GRMZM2G137502	B73 RefGen_v3	Gene	Chr1	72625013	72627421	dof36	cl830_1(337), cl830_1b, ZmDof03, ZmDof3	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1310	dof37	C2C2-Dof-transcription factor 37	GRMZM2G394973	B73 RefGen_v3	Gene	Chr3	195990512	195991615	dof37	ZmDof21	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1311	dof38	C2C2-Dof-transcription factor 38	GRMZM2G042218	B73 RefGen_v3	Gene	Chr8	166129975	166131371	dof38	ZmDof42	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1312	dof39	C2C2-Dof-transcription factor 39	GRMZM2G045678	B73 RefGen_v3	Gene	Chr1	254619872	254621178	dof39	ZmDof09	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1313	dof4	C2C2-Dof-transcription factor 4	GRMZM2G327189	B73 RefGen_v3	Gene	Chr3	209919655	209921032	dof4	IDP472, ZmDof22	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1314	dof40	C2C2-Dof-transcription factor 40	GRMZM2G138455	B73 RefGen_v3	Gene	Chr1	242766583	242768989	dof40	ZmDof07	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1315	dof41	C2C2-Dof-transcription factor 41	GRMZM2G142718	B73 RefGen_v3	Gene	Chr10	147844469	147845926	dof41	ZmDof46	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1316	dof42	C2C2-Dof-transcription factor 42	GRMZM2G394941	B73 RefGen_v3	Gene	Chr5	204282491	204284190	dof42	ZmDof33	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1317	dof43	C2C2-Dof-transcription factor 43	GRMZM2G589696	B73 RefGen_v3	Gene	Chr4	160304743	160307885	dof43	ZmDof24	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1318	dof44	C2C2-Dof-transcription factor 44	AC209819.3_FG009	B73 RefGen_v3	Gene	Chr8	122590335	122590955	dof44	ZmDof40	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1319	dof45	C2C2-Dof-transcription factor 45	GRMZM2G082490	B73 RefGen_v3	Gene	Chr8	173272809	173273930	dof45	ZmDof43	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1320	dof46	C2C2-Dof-transcription factor 46	GRMZM2G176063	B73 RefGen_v3	Gene	Chr3	126327930	126330315	dof46	ZmDof19	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1321	dof47	C2C2-Dof-transcription factor 1	AC155434.2_FG006	B73 RefGen_v3	Gene	Chr7	173848308	173849744	dof47	C2C2-Dof-transcription factor 1, dof1, dof101, dof47, ZmDof39	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1322	dof5	C2C2-Dof-transcription factor 5	GRMZM5G880268	B73 RefGen_v3	Gene	Chr8	133370483	133372747	dof5	ZmDof41	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1323	dof6	C2C2-Dof-transcription factor 6	GRMZM2G089949	B73 RefGen_v3	Gene	Chr3	40521477	40522945	dof6	ZmDof17	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1324	dof7	C2C2-Dof-transcription factor 7	GRMZM2G378490	B73 RefGen_v3	Gene	Chr3	6300724	6302028	dof7	ZmDof16	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
1325	dof8	C2C2-Dof-transcription factor 8	GRMZM2G463525	B73 RefGen_v3	Gene	Chr3	44598043	44601358	dof8	ZmDof18	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1326	dof9	C2C2-Dof-transcription factor 9	GRMZM2G449950	B73 RefGen_v3	Gene	Chr4	164205529	164206744	dof9	ZmDof25	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1327	dpold3a	DNA polymerase delta subunit 3a	GRMZM2G435338	B73 RefGen_v3	Gene	Chr3	5429348	5438197	dpold3a	dpold3a	
1328	dpold3b	DNA polymerase delta subunit 3b	GRMZM2G005536	B73 RefGen_v3	Gene	Chr8	23383967	23389363	dpold3b	dpold3b	
1329	dpr1	dihydrodipicolinate reductase1	GRMZM2G044247	B73 RefGen_v3	Gene	Chr1	3642611	3645502	dpr1	bnl5.62, bnl5.62a, dpr1, IDP1447, NBL5.62	
1330	dps1	dihydrodipicolinate synthase1	GRMZM2G027835	B73 RefGen_v3	Gene	Chr9	107331165	107334148	dps1	dhp1, DHPS gene, dihydrodipicolinate synthase1, dps1, rs132525905	cDNA complements E. coli mutant (AT997dapA-) blocked in DHPS (aka dhp1)
1331	drh1	DEAD box RNA helicase1	GRMZM2G362850	B73 RefGen_v3	Gene	Chr3	163786353	163791421	drh1	DEAD box RNA helicase1, drh1, gpm283a, PCO117725, ZmDRH1	protein is part of a ribonucleoprotein complex in rRNA metabolism - mRNA yeast two-hybrid screening showed interaction of protein with MA16 nucleolar protein
1332	drm1	dormancy associated1	GRMZM2G123896	B73 RefGen_v3	Gene	Chr1	222643514	222645307	drm1	ARDA, Auxin Repressed Dormancy Associated, drm1, PCO099562, ZmDRM1	lower expression overcomes tiller repression of tb1 in certain maize lines; e.g., P39 (Kebrom & Brutnell, 2015)
1333	dsc1	discolored kernel1	GRMZM2G117329	B73 RefGen_v3	Gene	Chr4	47714348	47736769	dsc1	ADP-ribosylation factor GTPase-activating protein AGD3-like, dek*-2058, dek*-3252, dek-Mu*2058, discolored kernel1, dsc1	crumpled, discolored, germless lethal
1334	dsc2	Discolored-paralog2	GRMZM5G872204	B73 RefGen_v3	Gene	Chr1	195791317	195802900	dsc2	dsc2, putative ARF GTPase activating domain protein with ankyrin repeat-containing protein	
1335	dsc3	Discolored-paralog3	GRMZM2G059225	B73 RefGen_v3	Gene	Chr7	135541997	135550832	dsc3	ADP-ribosylation factor GTPase-activating protein AGD3, dsc3, van3-like, vascular network defective3-like	
1336	dsul1	diSUMO-like1	GRMZM2G006324	B73 RefGen_v3	Gene	Chr7	159979076	159979972	dsul1	dicot-small ubiquitin-related modifier-like1, dsul1	
1337	dsy2	desynaptic2	AC210848.3_FG004	B73 RefGen_v3	Gene	Chr5	89755508	89760884	dsy2	desynaptic2, dsy2	synapsis and recombination reduced; RAD51 complexes abnormal
1338	dts1	aspartyl-tRNA synthetase1	GRMZM2G019121	B73 RefGen_v3	Gene	Chr5	75965462	75969666	dts1	aspartyl-tRNA synthetase1, dts1, dts1a, PCO070562, PZA00261, rs128282243, rs55622756 , ss196416132, uaz132, uaz132a(dts), uaz132(gfu), uaz31	endosperm cDNA 5C01B12 (uaz131), similar to rat aspartyl-tRNA synthetase subunit
1339	du1	dull endosperm1	GRMZM2G141399	B73 RefGen_v3	Gene	Chr10	59516234	59527812	du1	CL1800_1b, du1, dull endosperm1, ha2, ham, high amylose2, sslII, starch synthase III, ZmSSIIIa	glassy, tarnished endosperm; encodes a starch synthase III, that with an isoamylase-type debranching enzyme represses accumulation of phytoglycogen
1340	duf177	domain of unknown function177	GRMZM2G433025	B73 RefGen_v3	Gene	Chr5	216820554	216821708	duf177	duf177, duf177a	mutants block development at an early transition stage of embryogenesis
1341	dv1	divergent spindle1	GRMZM2G114861	B73 RefGen_v3	Gene	Chr2	7626633	7631527	dv1	divergent spindle1, dv1, kin6, KIN6, kinesin-1, kinesin-related protein6, krp6, ZmaKIN6, ZmKin6	chromosomes unoriented at metaphase I; partial male and female sterility; encodes a kinesin-14A motor protein
1342	dvr1	divinyl reductase1	GRMZM2G063048	B73 RefGen_v3	Gene	Chr1	59865304	59866740	dvr1	divinyl chlorophyllide reductase1, divinyl reductase1, dvr1, rs128449014	single copy, activity of encoded enzyme confirmed in heterologous host Wang et al 2013)
1343	dwil1	dwarf & irregular leaf1	GRMZM2G013657	B73 RefGen_v3	Gene	Chr6	143487859	143494583	dwil1	dil1, dwil1, EREB171 putative AP2/EREBP transcription factor superfamily protein isoform 1	mutant plants have shorter internodes, shorter, wider and wrinkled leaves, as well as smaller leaf angle
1344	dxr1	deoxy xylulose reductoisomerase1	GRMZM2G056975	B73 RefGen_v3	Gene	Chr3	30227477	30234031	dxr1	1-deoxy-D-xylulose 5-phosphate reductoisomerase1, CL389_1(210), CL389_1b, deoxy xylulose reductoisomerase1, dxr1, IDP154	enzyme catalyzes the first committed step of the plastidial pathway to apocarotenoids during mycorrhizal establishment
1345	dxr2	deoxy xylulose reductoisomerase2	GRMZM2G036290	B73 RefGen_v3	Gene	Chr8	8094882	8101495	dxr2	1-deoxy-D-xylulose 5-phosphate reductoisomerase, chloroplastic-like, dxr2	
1346	dxs1	deoxy xylulose synthase 1	GRMZM2G137151	B73 RefGen_v3	Gene	Chr6	146570742	146575010	dxs1	AY110050, CL392_1, deoxy xylulose synthase 1, dxs1, PZA02247	leaf specific; function inferred from Medicago trunculata gene sequence and expression pattern (Walter 2002)
1347	dxs2	deoxy xylulose synthase 2	GRMZM2G493395	B73 RefGen_v3	Gene	Chr7	14086686	14089909	dxs2	CL732_-1, deoxy xylulose synthase 2, dxs2	root specific; function inferred from sequence and expression pattern comparison with Medicago trunculata genes
1348	dxs3	deoxy xylulose synthase3	GRMZM2G173641	B73 RefGen_v3	Gene	Chr9	20471360	20476373	dxs3	dxs3, pco071268	
1349	dzs10	delta zein structural10	Zm00001d045937	Zm-B73-REFERENCE-G	Gene	Chr9	47916398	47916850	dzs10	delta zein structural10, dz-10, dzs10, gnp_QCH27f12, gpm659, PCO139211, zein, zps10/(22)	[was Zps10/(22)]; high (22.5%) methionine 10kDa delta zein; RFLP (probe 10kZ-1)
1350	dzs18	delta zein structural18	GRMZM2G100018	B73 RefGen_v3	Gene	Chr6	121573176	121574010	dzs18	delta zein structural18, delta zein structural23, dz18, dz-18, dz23, dzs18, high sulfur zein1, hsz1, PCO142924	high (26%) methionine 18 kDa delta zein, similar to dzs10
1351	e2f1	E2F-DP-transcription factor 21	GRMZM2G001699	B73 RefGen_v3	Gene	Chr1	233461624	233465523	e2f1		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1352	e2f10	E2F-DP-transcription factor 210	GRMZM2G169709	B73 RefGen_v3	Gene	Chr9	9941701	9945712	e2f10		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1353	e2f11	E2F-DP-transcription factor 211	GRMZM2G052515	B73 RefGen_v3	Gene	Chr10	6663939	6668632	e2f11		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1354	e2f12	E2F-DP-transcription factor 212	GRMZM2G060000	B73 RefGen_v3	Gene	Chr6	115306684	115309679	e2f12		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1355	e2f13	E2F-DP-transcription factor 213	GRMZM2G361659	B73 RefGen_v3	Gene	Chr4	182904238	182907831	e2f13		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1356	e2f14	E2F-DP-transcription factor 214	GRMZM5G829408	B73 RefGen_v3	Gene	Chr6	158198224	158202485	e2f14		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1357	e2f15	E2F-DP-transcription factor 215	GRMZM2G148506	B73 RefGen_v3	Gene	Chr10	142876623	142885325	e2f15		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1358	e2f16	E2F-DP-transcription factor 216	GRMZM2G041701	B73 RefGen_v3	Gene	Chr4	109547016	109551841	e2f16		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1359	e2f17	E2F-DP-transcription factor 217	AC214168.3_FG001	B73 RefGen_v3	Gene	Chr2	56303461	56307449	e2f17		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1360	e2f18	E2F-DP-transcription factor 218	GRMZM2G139024	B73 RefGen_v3	Gene	Chr5	32444644	32482308	e2f18		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1361	e2f19	E2F-DP-transcription factor 219	GRMZM2G086072	B73 RefGen_v3	Gene	Chr1	11479832	11487112	e2f19		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1362	e2f2	E2F-DP-transcription factor 22	GRMZM2G333591	B73 RefGen_v3	Gene	Chr2	223993795	223997480	e2f2		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1363	e2f3	E2F-DP-transcription factor 23	GRMZM2G351232	B73 RefGen_v3	Gene	Chr1	262525868	262531447	e2f3		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1364	e2f4	E2F-DP-transcription factor 24	AC233850.1_FG005	B73 RefGen_v3	Gene	Chr5	169877246	169881176	e2f4		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1365	e2f5	E2F-DP-transcription factor 25	GRMZM2G050590	B73 RefGen_v3	Gene	Chr2	113226437	113231629	e2f5		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1366	e2f6	E2F-DP-transcription factor 26	GRMZM2G063387	B73 RefGen_v3	Gene	Chr9	152941252	152946177	e2f6		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1367	e2f7	E2F-DP-transcription factor 27	GRMZM2G378665	B73 RefGen_v3	Gene	Chr5	205840277	205843667	e2f7		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1368	e2f8	E2F-DP-transcription factor 28	GRMZM2G404769	B73 RefGen_v3	Gene	Chr5	175687853	175693606	e2f8		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1369	e2f9	E2F-DP-transcription factor 29	GRMZM2G462623	B73 RefGen_v3	Gene	Chr8	150408103	150413617	e2f9		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1370	ea1	egg apparatus1	GRMZM2G456746	B73 RefGen_v3	Gene	Chr7	164503140	164503655	ea1	ea1, egg apparatus1, ZmEA1	
1371	ebe1	embryo-sac basal-endosperm layer embr	GRMZM2G129157	B73 RefGen_v3	Gene	Chr8	158567300	158572192	ebe1	ebe1, embryo-sac basal-endosperm layer embryo-surrounding-region, embryo-sac basal-endosperrm layer embryo-surrounding-region, ensl009	low copy number; cDNA expressed in central cell of female gametophyte, and in developing endosperm regions surrounding the embryo sac and in the basal endosperm transfer layer
1372	ebe2	embryo-sac basal-endosperm-layer embr	GRMZM2G167733	B73 RefGen_v3	Gene	Chr6	109030239	109033033	ebe2	ebe2, embryo-sac basal-endosperm-layer embryo-surrounding-region2, ensl010, ENSL010	like ebe1
1373	ebf1	EIN3-binding F-box protein1	GRMZM2G137582	B73 RefGen_v3	Gene	Chr6	102392990	102395999	ebf1	ebf1, si687013d08, si687013d08(489)	

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
1374	ech1	enoyl-CoA hydratase1	GRMZM2G132903	B73 RefGen_v3	Gene	Chr8	40263840	40270804	ech1	ech1, enoyl-CoA hydratase1, uaz348, uaz348(gfu)	leaf cDNA 6C06C04 (uaz348) similar to animal fatty acid beta-oxidation enzyme
1375	eif2	elongation initiation factor2	GRMZM2G107654	B73 RefGen_v3	Gene	Chr7	158175062	158191500	eif2	eif2, elongation initiation factor2, PCO146692(576), PCO146692d, uaz224, uaz224(eif2), uaz224(gfu), UAZ224(TIF2), uaz229	etiolated leaf cDNA 6C02E11(uaz224) similar to eIF-2 gamma chain
1376	eif3	eukaryotic initiation factor3	GRMZM2G093050	B73 RefGen_v3	Gene	Chr3	7406093	7414401	eif3	AY109549, CL1501_1a, eif3, eIF3A, eucaryotic initiation factor 3A, eukaryotic initiation factor3, IDP306, IDP797, magi64472, ZmeIF3A	cDNA encodes a protein homologous to the large subunit (eIF3) of the eukaryotic initiation factor essential to protein initiation
1377	eif4	eucaryotic initiation factor4	GRMZM2G116034	B73 RefGen_v3	Gene	Chr5	56805146	56809251	eif4	eif4, eIF4A, eucaryotic initiation factor4, gnp_QAE12h04a, gpm272a, PCO149753, tif-4A, tif4A2, ucr1b, ucr1b(eif)	cDNA; one of two with map sites on chr 5 and chr 6
1378	eif4a	eukaryotic initiation factor4a	GRMZM2G027995	B73 RefGen_v3	Gene	Chr6	87282559	87286379	eif4a	eif4a, gpm272b, IDP1635, TIDP3537, tif4A, tif-4A3, ucr1a, ucr1a(eif)	
1379	eif5	eucaryotic translation initiation factor5	GRMZM2G165917	B73 RefGen_v3	Gene	Chr4	238064651	238068549	eif5	csu981, eif5, eif5*-X99517, eucaryotic translation initiation factor5, IDP568, IDP627, magi16779, PCO112790	
1380	eif5a	elongation initiation factor5A	GRMZM2G113696	B73 RefGen_v3	Gene	Chr2	209954275	209957586	eif5a	csu154a(eif5A), csu175a(eif5A), csu203b(eif5A), csu702(eif5A), csuh154a, eif5a, eif5*-uaz7c01b10, PCO150862, PCO150862(182), umc384a	
1381	eif6	eucaryotic initiation factor6	GRMZM2G002616	B73 RefGen_v3	Gene	Chr3	132487154	132491827	eif6	eif4e, eIF4E, eif6, eucaryotic initiation factor6, PCO081734	member of a small multi-gene family; shares high sequence identity with eif7.
1382	eif7	eucaryotic initiation factor7	GRMZM2G022019	B73 RefGen_v3	Gene	Chr5	30318321	30323991	eif7	translation initiation factor 4E-2, eukaryotic translation initiation factor p28 subunit, IDP298, IDP555, magi61881	belongs to a small gene family, and shares significant sequence homology with eif6.
1383	eil1	ethylene insensitive-like1	GRMZM2G317584	B73 RefGen_v3	Gene	Chr9	133469222	133473010	eil1	eil1, EIL1, eil9, ethylene insensitive-like1, PCO092604, PCO092604(691), ZmEIL1-1	
1384	eil13	EIL-transcription factor 3	AC234203.1_FG011	B73 RefGen_v3	Gene	Chr1	188105263	188107161	eil13	eil13, eil3, EIL-transcription factor 3	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1385	eil2	EIL-transcription factor 2	GRMZM2G003558	B73 RefGen_v3	Gene	Chr2	218017798	218019723	eil2		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1386	eil3	ethylene insensitive-like3	GRMZM2G033570	B73 RefGen_v3	Gene	Chr1	52561894	52565938	eil3	eil1, EIL1, eil3, ethylene insensitive-like3, ZmEIL1-3	
1387	eil4	EIL-transcription factor 4	GRMZM2G006752	B73 RefGen_v3	Gene	Chr7	133190586	133195177	eil4		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1388	eil5	EIL-transcription factor 5	AC210616.4_FG005	B73 RefGen_v3	Gene	Chr4	124304670	124305995	eil5		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1389	eil6	EIL-transcription factor 6	GRMZM2G151811	B73 RefGen_v3	Gene	Chr7	173994325	173996353	eil6		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1390	eil7	EIL-transcription factor 7	GRMZM2G044322	B73 RefGen_v3	Gene	Chr2	43586438	43588329	eil7		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1391	eil8	EIL-transcription factor 8	GRMZM2G040481	B73 RefGen_v3	Gene	Chr5	176155464	176156801	eil8		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1392	ein2	ethylene insensitive 2	GRMZM2G068217	B73 RefGen_v3	Gene	Chr3	2874629	2881174	ein2	CL2979_1, CL2979_1(199), ein2, Ein2-25, IDP297	
1393	elfa1	elongation factor alpha1	AC233866.1_FG006	B73 RefGen_v3	Gene	Chr6	137601820	137603647	elfa1	csu116, csu116b(efia), csu116c(elf1), EFI, Efib, elf1, elfa1, elongation factor alpha1, sc172b	(was csu116) multiple copies; leaf cDNA csu116, partial sequence identical to a tomato elongation factor
1394	elfa10	elongation factor 1-alpha10	GRMZM2G343543	B73 RefGen_v3	Gene	Chr6	102923481	102926877	elfa10	elf*-uaz7c01f12	
1395	elfa2	elongation factor alpha2	GRMZM2G149768	B73 RefGen_v3	Gene	Chr6	136755765	136759415	elfa2	eEF1Aa, elf1a, elfa2, elongation factor alpha2	belongs to a gene family that includes genes elf1a-g (aka clones eEF1Aa-g) with highly conserved coding sequences.
1396	elfa3	elongation factor alpha3	GRMZM2G154218	B73 RefGen_v3	Gene	Chr6	136703065	136706224	elfa3	CL1256_1, eEF1Ab, elf1b, elfa3, elongation factor alpha3	shares high (89-99%) nucleotide sequence identity with genes elf1a to elf1g, with a 99% sequence identity with elf1a.
1397	elfa7	elongation factor alpha7	GRMZM2G110509	B73 RefGen_v3	Gene Family	Chr8	84127927	84131151	elfa7	eEF1Af, elf1f, elfa7, elongation factor 1-alpha-like, elongation factor alpha7	shares 89-99% nucleotide sequence identity with genes elf1a to elf1g (aka eEF1Aa to eEF1Ag).
1398	elfa9	elongation factor 1-alpha9	GRMZM2G153541	B73 RefGen_v3	Gene	Chr9	88067950	88071249	elfa9	elfa9, elf*-D45407, elf*-D45408, elf*-U76259, elongation factor 1A D45407, elongation factor 1A D45408, IDP709, IDP742, ttu2(elf1)	shares 89-99% nucleotide sequence identity with genes elf1a to alf1g (aka clones eEF1Aa to eEF1Ag).
1399	elfg1	elongation factor gamma1	GRMZM2G122871	B73 RefGen_v3	Gene	Chr6	104230611	104235309	elfg1	elfg1, elongation factor alpha5, elongation factor gamma1, uaz161, uaz161a, uaz161a(elf), umc369a, umc369b	endosperm cDNA 5C04C04 (uaz161), similar to Trypanosoma translation factor
1400	elip1	early light inducible protein1	GRMZM2G355752	B73 RefGen_v3	Gene	Chr2	234220402	234221935	elip1	elip1	Encodes a protein that binds chlorophyll to avoid cross-reactions that could lead to the generation of harmful reactive oxygen species
1401	elip2	early light inducible protein2	GRMZM2G425728	B73 RefGen_v3	Gene	Chr7	9706644	9708137	elip2	elip2	Encodes a protein that binds chlorophyll to avoid cross-reactions that could lead to the generation of harmful reactive oxygen species
1402	elm1	elongated mesocotyl1	GRMZM5G861678	B73 RefGen_v3	Gene	Chr8	158299004	158303170	elm1	elm1, elongated mesocotyl1, Hy2, phycoerythrobilin ferredoxin oxidoreductase, PZB00160, ZmHy2	elongated mesocotyl, pale green seedling leaves; pale green plant internodes; increased plant height; early flowering; phytochrome deficient.
1403	elm2	elongated mesocotyl2	GRMZM2G101004	B73 RefGen_v3	Gene	Chr9	89924624	89933813	elm2	elm2, elm2-chr9, heme oxygenase, ho1	mutant like elm1; encodes heme oxygenase
1404	emb14	embryo defective 14	GRMZM2G384293	B73 RefGen_v3	Gene	Chr4	241018915	241022802	emb14	emb14	mutant has defective embryo; unlinked suppressor(s) give an albino seedling phenotype
1405	emb17	embryo defective17	GRMZM2G119691	B73 RefGen_v3	Gene	Chr5	213411819	213415006	emb17	emb12, emb*-12BCT, emb17	in mutants, embryogenesis is arrested at or before transition stage; encodes plastid initiation factor 3
1406	emb18	embryo specific18	GRMZM2G136559	B73 RefGen_v3	Gene	Chr9	93426568	93429048	emb18	emb18, emb8516, emb*-8516, embryo specific*-8516, prpl35, ZmPRPL35-1	embryo development arrested at the transition stage from proembryo; embryo usually necrotic
1407	emb2	embryo specific2	GRMZM5G884466	B73 RefGen_v3	Gene	Chr1	301344228	301363304	emb2	emb2, emb8522, emb*-8522, embryo specific2, PPR8522, ZmPPR084	(was emb*-8522) embryo development blocked at the transition stage, tubular
1408	embp1	EM binding protein1 homologue	GRMZM2G095078	B73 RefGen_v3	Gene	Chr7	19265565	19270520	embp1	CL1309_1, cl1309_1(541), EM binding protein1 homologue, embp1, EmBP-1a, ZmbZIP30	bZIP protein binds to O2 box; wheat EM orthologue
1409	emp10	empty pericarp10	GRMZM2G078416	B73 RefGen_v3	Gene	Chr1	275735516	275741414	emp10	emp10, Pentatricopeptide repeat-containing protein mitochondrial, rs128955966 , rs128955968 , rs128955986 , rs128955993 , rs128956000 , rs128956001 , rs131896869	mutant effects the cis-splicing of nad2 intron 1 and seed development
1410	emp16	empty pericarp16	GRMZM2G060516	B73 RefGen_v3	Gene	Chr8	149423147	149426931	emp16	emp16, ZmPPR445	mutant homozyous kernels have empty pericarp and are non-viable.
1411	emp17	empty pericarp17	AC212684.3_FG012	B73 RefGen_v3	Gene	Chr7	172405097	172407361	emp17	emp17, emp9, pentatricopeptide repeat-containing protein At4g32430, mitochondrial, rs132446893	mutants abolish the C-to-U editing of ccmB-43 and rps4-335 sites in mitochondria
1412	emp2	empty pericarp 2	GRMZM2G039155	B73 RefGen_v3	Gene	Chr2	178295993	178300823	emp2	AY108804, dek1047, dek*-1047, dek*-Mu1047, emp2, empty pericarp2, empty pericarp 2, heat shock binding factor protein, hsbp1, isu9, PCO063114, ZmHSBP1	germless, unfilled kernel
1413	emp4	empty pericarp4	GRMZM2G092198	B73 RefGen_v3	Gene	Chr1	272101204	272103668	emp4	aborted seed*-7065, abs*-7065, emp4, empty pericarp4, pentatricopeptide repeat protein-like, ZmPPR069	mitochondrion pentatricopeptide repeat (PPR) protein involved in specific expression of mitochondrial transcripts; impaired differentiation of basal endosperm transfer cells
1414	emp5	empty pericarp5	GRMZM2G060536	B73 RefGen_v3	Gene	Chr3	147043139	147046048	emp5	emp5	encodes a mitochondrion-targeted DYW subgroup pentatricopeptide repeat (PPR) protein; mutant has empty pericarp phenotype
1415	emp6	empty pericarp6	GRMZM2G048392	B73 RefGen_v3	Gene	Chr2	188808679	188813282	emp6	Basal endosperm transfer layer, emp6, empty pericarp6, plant organelle RNA recognition, rs129192749, umc2129	mutant causes early arrest in grain development leading to an empty pericarp phenotype.. similar to Arabidopsis ubiquitin thiolesterase
1416	emp7	empty pericarp7	GRMZM2G041231	B73 RefGen_v3	Gene	Chr8	4335406	4337599	emp7	emp7, ZmPPR421	mutant confers an embryo-lethal phenotype
1417	endo1	endosperm specific protein1	GRMZM2G144610	B73 RefGen_v3	Gene	Chr9	37552323	37553942	endo1	cl1711_1, cl1711_1(676), endo1, endosperm specific protein1	
1418	endo3	endonuclease3	GRMZM2G113228	B73 RefGen_v3	Gene	Chr10	5735648	5739240	endo3	endo3	
1419	eng1	endo-1,3-1,4-beta-D-glucanase1	GRMZM2G073079	B73 RefGen_v3	Gene	Chr4	70091436	70093852	eng1	endo-1,3-1,4-beta-D-glucanase1, eng1, IDP686, PCO136367, PCO136367(317)	coleoptile enzyme, orthologous to rice enzyme; located in cell wall, IAA- stimulated coleoptile growth inhibited by antibody
1420	eno1	enolase1	GRMZM2G064302	B73 RefGen_v3	Gene	Chr9	22112240	22116928	eno1	gnp_QAF23c04c, gpm320c, PCO080341, pco080341(663), Pgh1, PZB01042, rs128282601, rs131175934, sc189, ss196417130, ss196417132, umc215(eno1), umc386	cDNA clone pZm245 complements enolase mutant in E. coli; leaf cDNA csu158 probes same site
1421	eno2	enolase2	GRMZM2G048371	B73 RefGen_v3	Gene	Chr1	125081143	125088083	eno2	eno2, enolase2, PCO068679, Pgh-	constitutive cDNA pENO2
1422	epl101	enhancer of polycomb-like protein101	GRMZM2G110548	B73 RefGen_v3	Probed Site	Chr7	78366133	78396394	epl101	enhancer of polycomb-like protein101, epc101, epl101, Zmepl101	

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
1423	epr4	endochitinase precursor4	GRMZM2G129189	B73 RefGen_v3	Gene	Chr5	182569001	182570164	epr4	Endochitinase PR4 precursor, Endochitinase precursor4, epr4, pathogenesis related4, pr4	involved in inducing pathogen defenses and suppressing herbivore defenses
1424	eps1	enolpyruvylshikimate phosphate synthas	GRMZM5G877500	B73 RefGen_v3	Gene	Chr9	22689315	22692638	eps1	enolpyruvylshikimate phosphate synthase1, eps1, EPSP synthase, PCO094563	unpubl sequence
1425	era1	E. coli Ras-like protein1	GRMZM2G158024	B73 RefGen_v3	Gene	Chr8	70795031	70799216	era1	era1, umc1360	name. Required for cp ribosome accumulation. Putative chloroplast ribosome assembly factor. ERA domain (IPR005662). (A. Barkan, 2015). Ortholog of Arabidopsis ERA1. Required for cp
1426	ereb1	AP2-EREBP-transcription factor 1	GRMZM5G889719	B73 RefGen_v3	Gene	Chr9	115615847	115616692	ereb1	dbf2, dreb1, DREB1A, DRE-binding protein 2, DREB-like protein (dreb1), ereb1	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1427	ereb10	AP2-EREBP-transcription factor 10	GRMZM2G434203	B73 RefGen_v3	Gene	Chr5	195729657	195730672	ereb10		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1428	ereb100	AP2-EREBP-transcription factor 100	AC209257.4_FG006	B73 RefGen_v3	Gene	Chr6	153427827	153429877	ereb100		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1429	ereb101	AP2-EREBP-transcription factor 101	GRMZM2G003466	B73 RefGen_v3	Gene	Chr1	20094144	20095477	ereb101		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1430	ereb102	AP2-EREBP-transcription factor 102	GRMZM2G052667	B73 RefGen_v3	Gene	Chr7	120384696	120387770	ereb102		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1431	ereb103	AP2-EREBP-transcription factor 103	GRMZM2G133168	B73 RefGen_v3	Gene	Chr3	4660995	4665940	ereb103		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1432	ereb104	AP2-EREBP-transcription factor 104	GRMZM5G816314	B73 RefGen_v3	Gene	Chr5	191933955	191934641	ereb104		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1433	ereb105	AP2-EREBP-transcription factor 105	GRMZM2G042756	B73 RefGen_v3	Gene	Chr2	16543815	16545074	ereb105		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1434	ereb106	AP2-EREBP-transcription factor 106	AC198403.3_FG001	B73 RefGen_v3	Gene	Chr4	10908008	10908646	ereb106		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1435	ereb107	AP2-EREBP-transcription factor 107	GRMZM2G057386	B73 RefGen_v3	Gene	Chr5	191428547	191430072	ereb107		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1436	ereb108	AP2-EREBP-transcription factor 108	GRMZM2G480434	B73 RefGen_v3	Gene	Chr1	189829804	189830412	ereb108		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1437	ereb109	AP2-EREBP-transcription factor 109	GRMZM2G141679	B73 RefGen_v3	Gene	Chr7	100267099	100269276	ereb109		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1438	ereb111	AP2-EREBP-transcription factor 111	GRMZM2G076896	B73 RefGen_v3	Gene	Chr4	215636055	215638692	ereb111		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1439	ereb112	AP2-EREBP-transcription factor 112	GRMZM2G039870	B73 RefGen_v3	Gene	Chr1	138460613	138461461	ereb112		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1440	ereb113	AP2-EREBP-transcription factor 113	GRMZM2G457562	B73 RefGen_v3	Gene	Chr8	100502242	100503899	ereb113		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1441	ereb114	AP2-EREBP-transcription factor 114	GRMZM2G008234	B73 RefGen_v3	Gene	Chr7	3186862	3189788	ereb114		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1442	ereb115	AP2-EREBP-transcription factor 115	GRMZM2G069146	B73 RefGen_v3	Gene	Chr7	141174421	141175245	ereb115		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1443	ereb116	AP2-EREBP-transcription factor 116	GRMZM2G131281	B73 RefGen_v3	Gene	Chr7	135625864	135626905	ereb116		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1444	ereb117	AP2-EREBP-transcription factor 117	GRMZM2G113078	B73 RefGen_v3	Gene	Chr8	135582288	135584343	ereb117		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1445	ereb118	AP2-EREBP-transcription factor 118	GRMZM2G081892	B73 RefGen_v3	Gene	Chr8	12197384	12199394	ereb118		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1446	ereb119	AP2-EREBP-transcription factor 119	GRMZM2G309731	B73 RefGen_v3	Gene	Chr1	195911073	195911583	ereb119		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1447	ereb12	AP2-EREBP-transcription factor 12	GRMZM2G100982	B73 RefGen_v3	Gene	Chr8	71940571	71941451	ereb12		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1448	ereb120	AP2-EREBP-transcription factor 120	AC200038.4_FG011	B73 RefGen_v3	Gene	Chr1	21602442	21603594	ereb120		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1449	ereb121	AP2-EREBP-transcription factor 121	GRMZM2G176175	B73 RefGen_v3	Gene	Chr7	22015365	22026546	ereb121		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1450	ereb122	AP2-EREBP-transcription factor 122	GRMZM2G301860	B73 RefGen_v3	Gene	Chr9	16258284	16259458	ereb122		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1451	ereb123	AP2-EREBP-transcription factor 123	GRMZM2G461907	B73 RefGen_v3	Gene	Chr1	21635058	21635844	ereb123		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1452	ereb124	AP2-EREBP-transcription factor 124	GRMZM2G399098	B73 RefGen_v3	Gene	Chr9	151187691	151189042	ereb124		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1453	ereb125	AP2-EREBP-transcription factor 125	GRMZM2G023708	B73 RefGen_v3	Gene	Chr10	112324342	112325371	ereb125		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1454	ereb126	AP2-EREBP-transcription factor 126	GRMZM2G169654	B73 RefGen_v3	Gene	Chr3	206678255	206680041	ereb126		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1455	ereb127	AP2-EREBP-transcription factor 127	GRMZM2G000520	B73 RefGen_v3	Gene	Chr4	155637630	155639087	ereb127		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1456	ereb128	AP2-EREBP-transcription factor 128	AC233933.1_FG001	B73 RefGen_v3	Gene	Chr7	34482445	34483233	ereb128		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1457	ereb129	AP2-EREBP-transcription factor 129	GRMZM2G016434	B73 RefGen_v3	Gene	Chr5	166359251	166361971	ereb129		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1458	ereb13	AP2-EREBP-transcription factor 13	GRMZM2G011110	B73 RefGen_v3	Gene	Chr4	178417315	178418683	ereb13		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1459	ereb130	AP2-EREBP-transcription factor 130	GRMZM2G399072	B73 RefGen_v3	Gene	Chr1	16118043	16122450	ereb130		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1460	ereb131	AP2-EREBP-transcription factor 131	GRMZM2G087059	B73 RefGen_v3	Gene	Chr2	64001713	64004098	ereb131		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1461	ereb132	AP2-EREBP-transcription factor 132	GRMZM2G165257	B73 RefGen_v3	Gene	Chr4	130100068	130101363	ereb132		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1462	ereb133	AP2-EREBP-transcription factor 133	GRMZM2G100727	B73 RefGen_v3	Gene	Chr6	150487664	150489012	ereb133		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1463	ereb134	AP2-EREBP-transcription factor 134	GRMZM2G474326	B73 RefGen_v3	Gene	Chr3	198667814	198668962	ereb134		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1464	ereb135	AP2-EREBP-transcription factor 135	GRMZM2G328197	B73 RefGen_v3	Gene	Chr6	77131623	77132592	ereb135		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1465	ereb136	AP2-EREBP-transcription factor 136	GRMZM2G021369	B73 RefGen_v3	Gene	Chr5	210323041	210324358	ereb136		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1466	ereb137	AP2-EREBP-transcription factor 137	GRMZM2G028386	B73 RefGen_v3	Gene	Chr1	201993810	201995393	ereb137		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1467	ereb138	AP2-EREBP-transcription factor 138	GRMZM2G079653	B73 RefGen_v3	Gene	Chr5	100107595	100108704	ereb138		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1468	ereb139	AP2-EREBP-transcription factor 139	GRMZM2G103085	B73 RefGen_v3	Gene	Chr5	209945135	209946354	ereb139		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1469	ereb14	AP2-EREBP-transcription factor 14	GRMZM2G018398	B73 RefGen_v3	Gene	Chr4	176066660	176069349	ereb14		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1470	ereb140	AP2-EREBP-transcription factor 140	GRMZM2G348307	B73 RefGen_v3	Gene	Chr4	65968744	65972918	ereb140		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1471	ereb141	AP2-EREBP-transcription factor 141	GRMZM2G097182	B73 RefGen_v3	Gene	Chr3	145467972	145468863	ereb141		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
1472	ereb142	AP2-EREBP-transcription factor 142	GRMZM2G010100	B73 RefGen_v3	Gene	Chr1	255604709	255605965	ereb142		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1473	ereb143	AP2-EREBP-transcription factor 143	GRMZM2G141219	B73 RefGen_v3	Gene	Chr7	117877954	117881926	ereb143		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1474	ereb144	AP2-EREBP-transcription factor 144	GRMZM2G005301	B73 RefGen_v3	Gene	Chr5	150664312	150665813	ereb144		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1475	ereb145	AP2-EREBP-transcription factor 145	GRMZM2G106591	B73 RefGen_v3	Gene	Chr6	102578638	102580044	ereb145		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1476	ereb146	AP2-EREBP-transcription factor 146	GRMZM2G021790	B73 RefGen_v3	Gene	Chr8	69893597	69894451	ereb146		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1477	ereb147	AP2-EREBP-transcription factor 147	GRMZM2G310368	B73 RefGen_v3	Gene	Chr3	188728319	188729366	ereb147		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1478	ereb148	AP2-EREBP-transcription factor 148	GRMZM2G053503	B73 RefGen_v3	Gene	Chr8	35566541	35567721	ereb148	ERF1 ethylene-responsive factor-like protein 1, ZmERF1	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1479	ereb149	AP2-EREBP-transcription factor 149	GRMZM2G425798	B73 RefGen_v3	Gene	Chr10	111635997	111638209	ereb149		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1480	ereb15	AP2-EREBP-transcription factor 15	GRMZM2G111415	B73 RefGen_v3	Gene	Chr4	173829508	173830759	ereb15		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1481	ereb150	AP2-EREBP-transcription factor 150	GRMZM2G033656	B73 RefGen_v3	Gene	Chr1	189870771	189871628	ereb150		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1482	ereb151	AP2-EREBP-transcription factor 151	GRMZM2G307119	B73 RefGen_v3	Lapsed Locus	Chr7	172248843	172250339	ereb151	bd1	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1483	ereb153	AP2-EREBP-transcription factor 153	GRMZM2G379652	B73 RefGen_v3	Gene	Chr7	15671318	15672307	ereb153		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1484	ereb154	AP2-EREBP-transcription factor 154	GRMZM2G026926	B73 RefGen_v3	Gene	Chr2	24360914	24363125	ereb154		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1485	ereb155	AP2-EREBP-transcription factor 155	GRMZM2G060465	B73 RefGen_v3	Gene	Chr4	185036196	185037019	ereb155		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1486	ereb156	AP2-EREBP-transcription factor 156	GRMZM2G421033	B73 RefGen_v3	Gene	Chr10	144707377	144708793	ereb156	dehydration responsive element binding protein	designated and assigned to a transcription factor family by the GRASSIUS project (Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene
1487	ereb157	AP2-EREBP-transcription factor 157	GRMZM2G087040	B73 RefGen_v3	Gene	Chr5	174205686	174206245	ereb157		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1488	ereb158	AP2-EREBP-transcription factor 158	GRMZM2G002119	B73 RefGen_v3	Gene	Chr3	188630301	188631150	ereb158		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1489	ereb159	AP2-EREBP-transcription factor 159	GRMZM2G009598	B73 RefGen_v3	Gene	Chr1	292178941	292180261	ereb159		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1490	ereb16	AP2-EREBP-transcription factor 16	GRMZM2G137341	B73 RefGen_v3	Gene	Chr5	195885970	195887098	ereb16		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1491	ereb160	AP2-EREBP-transcription factor 160	GRMZM2G171179	B73 RefGen_v3	Gene	Chr9	11535025	11537985	ereb160	ereb160, Tsh, umc1588	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1492	ereb161	AP2-EREBP-transcription factor 161	GRMZM2G021573	B73 RefGen_v3	Gene	Chr9	145136034	145140341	ereb161		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1493	ereb162	AP2-EREBP-transcription factor 162	GRMZM2G059939	B73 RefGen_v3	Gene	Chr6	162767827	162769490	ereb162		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1494	ereb163	AP2-EREBP-transcription factor 163	GRMZM2G022359	B73 RefGen_v3	Gene	Chr10	73140439	73143884	ereb163		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1495	ereb164	AP2-EREBP-transcription factor 164	GRMZM2G093595	B73 RefGen_v3	Gene	Chr6	140882370	140883690	ereb164		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1496	ereb165	AP2-EREBP-transcription factor 165	GRMZM2G317596	B73 RefGen_v3	Gene	Chr6	164875430	164876438	ereb165		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1497	ereb166	AP2-EREBP-transcription factor 166	GRMZM2G478965	B73 RefGen_v3	Gene	Chr7	15838022	15839110	ereb166		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1498	ereb167	AP2-EREBP-transcription factor 167	GRMZM2G050851	B73 RefGen_v3	Gene	Chr1	209401525	209403939	ereb167		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1499	ereb168	AP2-EREBP-transcription factor 168	GRMZM2G039112	B73 RefGen_v3	Gene	Chr1	162442365	162444201	ereb168		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1500	ereb169	AP2-EREBP-transcription factor 169	GRMZM2G016079	B73 RefGen_v3	Gene	Chr1	189807563	189808400	ereb169		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1501	ereb17	AP2-EREBP-transcription factor 17	GRMZM2G029323	B73 RefGen_v3	Gene	Chr4	181088255	181090094	ereb17		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1502	ereb170	AP2-EREBP-transcription factor 170	GRMZM2G300924	B73 RefGen_v3	Gene	Chr4	146313370	146315508	ereb170		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1503	ereb171	AP2-EREBP-transcription factor 171	GRMZM2G013657	B73 RefGen_v3	Gene	Chr6	143487859	143494583	ereb171		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1504	ereb172	AP2-EREBP-transcription factor 172	GRMZM2G369472	B73 RefGen_v3	Gene	Chr1	199674463	199675600	ereb172		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1505	ereb173	AP2-EREBP-transcription factor 173	GRMZM2G007406	B73 RefGen_v3	Gene	Chr9	141206088	141207032	ereb173		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1506	ereb174	AP2-EREBP-transcription factor 174	GRMZM2G149756	B73 RefGen_v3	Gene	Chr3	175592023	175595225	ereb174		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1507	ereb175	AP2-EREBP-transcription factor 175	GRMZM2G429378	B73 RefGen_v3	Gene	Chr9	17655509	17656456	ereb175		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1508	ereb176	AP2-EREBP-transcription factor 176	GRMZM2G072926	B73 RefGen_v3	Gene	Chr4	152189367	152190424	ereb176		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1509	ereb177	AP2-EREBP-transcription factor 177	GRMZM2G123119	B73 RefGen_v3	Gene	Chr7	52773401	52774399	ereb177		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1510	ereb178	AP2-EREBP-transcription factor 178	GRMZM2G047999	B73 RefGen_v3	Gene	Chr5	166555654	166556595	ereb178		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1511	ereb179	AP2-EREBP-transcription factor 179	GRMZM2G129674	B73 RefGen_v3	Gene	Chr1	17461265	17462932	ereb179		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1512	ereb18	AP2-EREBP-transcription factor 18	GRMZM2G055204	B73 RefGen_v3	Gene	Chr5	208210507	208213447	ereb18		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1513	ereb180	AP2-EREBP-transcription factor 180	GRMZM2G018984	B73 RefGen_v3	Gene	Chr1	17492641	17494645	ereb180		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1514	ereb181	AP2-EREBP-transcription factor 181	AC206951.3_FG016	B73 RefGen_v3	Gene	Chr1	17518824	17519639	ereb181		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1515	ereb182	AP2-EREBP-transcription factor 182	AC206951.3_FG017	B73 RefGen_v3	Gene	Chr1	17525572	17526492	ereb182		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1516	ereb183	AP2-EREBP-transcription factor 183	GRMZM2G458437	B73 RefGen_v3	Gene	Chr2	216615448	216616387	ereb183		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1517	ereb184	AP2-EREBP-transcription factor 184	GRMZM2G028151	B73 RefGen_v3	Gene	Chr1	281700006	281703981	ereb184		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1518	ereb185	AP2-EREBP-transcription factor 185	GRMZM2G028969	B73 RefGen_v3	Gene	Chr2	20720151	20721075	ereb185		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1519	ereb186	AP2-EREBP-transcription factor 186	AC187157.4_FG001	B73 RefGen_v3	Gene	Chr8	22690444	22691545	ereb186		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1520	ereb187	AP2-EREBP-transcription factor 187	GRMZM2G130459	B73 RefGen_v3	Gene	Chr5	207437058	207441313	ereb187		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
1521	ereb188	AP2-EREBP-transcription factor 188	GRMZM2G477287	B73 RefGen_v3	Gene	Chr1	80875824	80876762	ereb188		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1522	ereb189	AP2-EREBP-transcription factor 189	GRMZM2G060517	B73 RefGen_v3	Gene	Chr7	53484637	53485245	ereb189		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1523	ereb19	AP2-EREBP-transcription factor 19	GRMZM2G175543	B73 RefGen_v3	Gene	Chr6	88910388	88912086	ereb19		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1524	ereb190	AP2-EREBP-transcription factor 190	GRMZM2G104260	B73 RefGen_v3	Gene	Chr10	145554185	145555089	ereb190		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1525	ereb191	AP2-EREBP-transcription factor 191	GRMZM2G047918	B73 RefGen_v3	Gene	Chr5	150972392	150973390	ereb191		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1526	ereb192	AP2-EREBP-transcription factor 192	GRMZM2G129777	B73 RefGen_v3	Gene	Chr3	22395049	22397063	ereb192		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1527	ereb193	AP2-EREBP-transcription factor 193	GRMZM2G169382	B73 RefGen_v3	Gene	Chr3	56326099	56327373	ereb193		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1528	ereb194	AP2-EREBP-transcription factor 194	GRMZM2G120401	B73 RefGen_v3	Gene	Chr8	80500107	80501402	ereb194		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1529	ereb195	AP2-EREBP-transcription factor 195	GRMZM2G466044	B73 RefGen_v3	Gene	Chr5	191270861	191272390	ereb195		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1530	ereb196	AP2-EREBP-transcription factor 196	GRMZM2G020150	B73 RefGen_v3	Gene	Chr6	156591969	156593826	ereb196		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1531	ereb197	AP2-EREBP-transcription factor 197	GRMZM2G174784	B73 RefGen_v3	Gene	Chr2	5520018	5524385	ereb197		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1532	ereb198	AP2-EREBP-transcription factor 198	GRMZM2G055180	B73 RefGen_v3	Gene	Chr2	21347526	21348862	ereb198	AP2-EREBP transcription factor (EREB198), ethylene-responsive transcription factor 2, homologue to AtERF1 and 2, ZmERF2	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1533	ereb199	AP2-EREBP-transcription factor 199	GRMZM2G163745	B73 RefGen_v3	Gene	Chr1	208809359	208810072	ereb199		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1534	ereb2	AP2-EREBP-transcription factor 2	GRMZM2G080516	B73 RefGen_v3	Gene	Chr10	139299146	139301101	ereb2		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1535	ereb200	AP2-EREBP-transcription factor 200	GRMZM2G025062	B73 RefGen_v3	Gene	Chr7	172771420	172772631	ereb200		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1536	ereb201	AP2-EREBP-transcription factor 201	GRMZM2G384386	B73 RefGen_v3	Gene	Chr7	160094706	160096131	ereb201		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1537	ereb202	AP2-EREBP-transcription factor 202	GRMZM2G148333	B73 RefGen_v3	Gene	Chr2	184209896	184212209	ereb202		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1538	ereb203	AP2-EREBP-transcription factor 203	GRMZM2G104866	B73 RefGen_v3	Gene	Chr9	98042537	98044099	ereb203		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1539	ereb204	AP2-EREBP-transcription factor 204	GRMZM2G061487	B73 RefGen_v3	Gene	Chr1	217638400	217639968	ereb204		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1540	ereb205	AP2-EREBP-transcription factor 205	GRMZM2G438202	B73 RefGen_v3	Gene	Chr10	141249356	141251027	ereb205		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1541	ereb206	AP2-EREBP-transcription factor 206	GRMZM2G366434	B73 RefGen_v3	Gene	Chr5	184337648	184342194	ereb206		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1542	ereb207	AP2-EREBP-transcription factor 207	GRMZM2G156006	B73 RefGen_v3	Gene	Chr9	13761895	13762657	ereb207		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1543	ereb208	AP2-EREBP-transcription factor 208	GRMZM2G160971	B73 RefGen_v3	Gene	Chr3	212582559	212584989	ereb208		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1544	ereb209	AP2-EREBP-transcription factor 209	GRMZM2G089995	B73 RefGen_v3	Gene	Chr4	26450939	26451894	ereb209		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1545	ereb21	AP2-EREBP-transcription factor 21	GRMZM2G175525	B73 RefGen_v3	Gene	Chr10	116699951	116700712	ereb21		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1546	ereb210	AP2-EREBP-transcription factor 210	GRMZM2G125460	B73 RefGen_v3	Gene	Chr2	214344857	214345995	ereb210		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1547	ereb211	AP2-EREBP-transcription factor 211	GRMZM2G138396	B73 RefGen_v3	Gene	Chr2	186957472	186958546	ereb211		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1548	ereb212	AP2-EREBP-transcription factor 212	GRMZM2G076602	B73 RefGen_v3	Gene	Chr10	144777835	144780346	ereb212		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1549	ereb22	AP2-EREBP-transcription factor 22	GRMZM2G006745	B73 RefGen_v3	Gene	Chr8	94530861	94534207	ereb22		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1550	ereb23	AP2-EREBP-transcription factor 23	GRMZM2G069126	B73 RefGen_v3	Gene	Chr7	141170323	141171382	ereb23		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1551	ereb24	AP2-EREBP-transcription factor 24	GRMZM2G086573	B73 RefGen_v3	Gene	Chr2	4666315	4671738	ereb24		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1552	ereb25	AP2-EREBP-transcription factor 25	GRMZM2G119865	B73 RefGen_v3	Gene	Chr6	79717475	79718928	ereb25		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1553	ereb26	AP2-EREBP-transcription factor 26	GRMZM2G317160	B73 RefGen_v3	Gene	Chr1	51014131	51020257	ereb26		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1554	ereb27	AP2-EREBP-transcription factor 27	GRMZM2G084264	B73 RefGen_v3	Gene	Chr6	110073119	110074320	ereb27		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1555	ereb28	AP2-EREBP-transcription factor 28	GRMZM2G544539	B73 RefGen_v3	Gene	Chr10	9217173	9219426	ereb28		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1556	ereb29	AP2-EREBP-transcription factor 29	GRMZM2G132223	B73 RefGen_v3	Gene	Chr8	171190647	171191502	ereb29		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1557	ereb30	AP2-EREBP-transcription factor 30	GRMZM5G842961	B73 RefGen_v3	Gene	Chr5	191829610	191830443	ereb30		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1558	ereb31	AP2-EREBP-transcription factor 31	GRMZM5G852704	B73 RefGen_v3	Gene	Chr9	5877307	5878356	ereb31		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1559	ereb32	AP2-EREBP-transcription factor 32	GRMZM2G139740	B73 RefGen_v3	Gene	Chr4	119105133	119105723	ereb32		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1560	ereb33	AP2-EREBP-transcription factor 33	GRMZM2G073982	B73 RefGen_v3	Gene	Chr9	20121733	20123748	ereb33		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1561	ereb34	AP2-EREBP-transcription factor 34	GRMZM5G846057	B73 RefGen_v3	Gene	Chr6	165687986	165689517	ereb34		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1562	ereb35	AP2-EREBP-transcription factor 35	GRMZM2G415251	B73 RefGen_v3	Gene	Chr1	21678126	21679947	ereb35		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1563	ereb36	AP2-EREBP-transcription factor 36	GRMZM2G069082	B73 RefGen_v3	Gene	Chr7	141162777	141163747	ereb36		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1564	ereb37	AP2-EREBP-transcription factor 37	GRMZM2G322672	B73 RefGen_v3	Gene	Chr5	81797663	81800162	ereb37		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1565	ereb38	AP2-EREBP-transcription factor 38	GRMZM2G419901	B73 RefGen_v3	Gene	Chr1	15773208	15774173	ereb38		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1566	ereb39	AP2-EREBP-transcription factor 39	GRMZM2G073047	B73 RefGen_v3	Gene	Chr9	76481085	76482299	ereb39		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1567	ereb4	AP2-EREBP-transcription factor 4	GRMZM2G015281	B73 RefGen_v3	Gene	Chr1	37721439	37722170	ereb4		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1568	ereb40	AP2-EREBP-transcription factor 40	GRMZM2G164591	B73 RefGen_v3	Gene	Chr10	146788916	146790031	ereb40		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1569	ereb41	AP2-EREBP-transcription factor 41	GRMZM2G146688	B73 RefGen_v3	Gene	Chr2	237250179	237253121	ereb41		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
1570	ereb42	AP2-EREBP-transcription factor 42	GRMZM2G020016	B73 RefGen_v3	Gene	Chr6	156579550	156581365	ereb42		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1571	ereb43	AP2-EREBP-transcription factor 43	GRMZM2G399598	B73 RefGen_v3	Gene	Chr2	219318493	219323840	ereb43		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1572	ereb44	AP2-EREBP-transcription factor 44	GRMZM5G806839	B73 RefGen_v3	Gene	Chr1	90116618	90117418	ereb44		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1573	ereb45	AP2-EREBP-transcription factor 45	GRMZM2G067463	B73 RefGen_v3	Gene	Chr2	4352876	4353499	ereb45		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1574	ereb46	AP2-EREBP-transcription factor 46	GRMZM2G085678	B73 RefGen_v3	Gene	Chr5	114131334	114133006	ereb46		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1575	ereb47	AP2-EREBP-transcription factor 47	GRMZM2G174917	B73 RefGen_v3	Gene	Chr2	5568515	5570186	ereb47		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1576	ereb48	AP2-EREBP-transcription factor 48	GRMZM2G376255	B73 RefGen_v3	Gene	Chr9	151134794	151135999	ereb48		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1577	ereb49	AP2-EREBP-transcription factor 49	GRMZM2G159592	B73 RefGen_v3	Gene	Chr8	64222278	64223655	ereb49		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1578	ereb5	AP2-EREBP-transcription factor 5	GRMZM2G048621	B73 RefGen_v3	Gene	Chr4	152103666	152104731	ereb5		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1579	ereb50	AP2-EREBP-transcription factor 50	GRMZM2G142179	B73 RefGen_v3	Gene	Chr3	2629088	2630607	ereb50		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1580	ereb51	AP2-EREBP-transcription factor 51	GRMZM2G055070	B73 RefGen_v3	Gene	Chr10	71678821	71679414	ereb51		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1581	ereb52	AP2-EREBP-transcription factor 52	GRMZM2G105266	B73 RefGen_v3	Gene	Chr3	170265321	170267160	ereb52		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1582	ereb53	AP2-EREBP-transcription factor 53	GRMZM2G141638	B73 RefGen_v3	Gene	Chr3	166836222	166840043	ereb53	AP2-like ethylene-responsive transcription factor BBM2, baby boom1, bbm1, ereb53, odp2, ovule development protein 2, Zm-Bbm	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1583	ereb54	AP2-EREBP-transcription factor 54	GRMZM2G020054	B73 RefGen_v3	Gene	Chr10	65437299	65438594	ereb54		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1584	ereb57	AP2-EREBP-transcription factor 57	GRMZM2G097081	B73 RefGen_v3	Gene	Chr4	176557756	176558869	ereb57		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1585	ereb58	AP2-EREBP-transcription factor 58	GRMZM2G381441	B73 RefGen_v3	Gene	Chr1	300119372	300120555	ereb58	EREB58 putative AP2/EREBP transcription factor superfamily protein, homologue to AtERF1 and 2, ZmERF6	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1586	ereb59	AP2-EREBP-transcription factor 59	GRMZM5G837876	B73 RefGen_v3	Gene	Chr4	13240123	13240995	ereb59		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1587	ereb6	AP2-EREBP-transcription factor 6	GRMZM2G172936	B73 RefGen_v3	Gene	Chr2	20632553	20633410	ereb6		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1588	ereb60	AP2-EREBP-transcription factor 60	GRMZM2G131266	B73 RefGen_v3	Gene	Chr1	211370663	211373082	ereb60		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1589	ereb61	AP2-EREBP-transcription factor 61	GRMZM2G475678	B73 RefGen_v3	Gene	Chr2	21187724	21188794	ereb61		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1590	ereb62	AP2-EREBP-transcription factor 62	GRMZM2G011236	B73 RefGen_v3	Gene	Chr2	207364254	207365473	ereb62		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1591	ereb63	AP2-EREBP-transcription factor 63	GRMZM2G307152	B73 RefGen_v3	Gene	Chr3	170466981	170467714	ereb63		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1592	ereb64	AP2-EREBP-transcription factor 64	GRMZM2G171569	B73 RefGen_v3	Gene	Chr7	21160811	21162260	ereb64		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1593	ereb65	AP2-EREBP-transcription factor 65	GRMZM2G124011	B73 RefGen_v3	Gene	Chr2	195135264	195136246	ereb65		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1594	ereb66	AP2-EREBP-transcription factor 66	GRMZM2G041839	B73 RefGen_v3	Gene	Chr5	191904539	191906156	ereb66		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1595	ereb67	AP2-EREBP-transcription factor 67	GRMZM2G114820	B73 RefGen_v3	Gene	Chr9	125166271	125168025	ereb67		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1596	ereb68	AP2-EREBP-transcription factor 68	GRMZM2G368838	B73 RefGen_v3	Gene	Chr2	16555808	16557224	ereb68		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1597	ereb69	AP2-EREBP-transcription factor 69	GRMZM2G085964	B73 RefGen_v3	Gene	Chr6	138751831	138753113	ereb69		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1598	ereb7	AP2-EREBP-transcription factor 7	GRMZM2G173771	B73 RefGen_v3	Gene	Chr4	178620836	178621888	ereb7		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1599	ereb70	AP2-EREBP-transcription factor 70	AC213666.3_FG003	B73 RefGen_v3	Gene	Chr4	24212770	24213261	ereb70		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1600	ereb71	AP2-EREBP-transcription factor 71	GRMZM2G113060	B73 RefGen_v3	Gene	Chr9	149648095	149649451	ereb71		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1601	ereb72	AP2-EREBP-transcription factor 72	GRMZM2G135452	B73 RefGen_v3	Gene	Chr6	51805587	51806576	ereb72		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1602	ereb73	AP2-EREBP-transcription factor 73	GRMZM2G060876	B73 RefGen_v3	Gene	Chr7	165849278	165850111	ereb73		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1603	ereb74	AP2-EREBP-transcription factor 74	GRMZM2G024871	B73 RefGen_v3	Gene	Chr5	31877779	31878301	ereb74		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1604	ereb75	AP2-EREBP-transcription factor 75	GRMZM2G060249	B73 RefGen_v3	Gene	Chr7	165822785	165823252	ereb75		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1605	ereb76	AP2-EREBP-transcription factor 76	GRMZM2G139765	B73 RefGen_v3	Gene	Chr5	188716605	188718676	ereb76		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1606	ereb77	AP2-EREBP-transcription factor 77	GRMZM2G451031	B73 RefGen_v3	Gene	Chr3	186781331	186784258	ereb77		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1607	ereb78	AP2-EREBP-transcription factor 78	GRMZM2G060206	B73 RefGen_v3	Gene	Chr4	49346413	49347038	ereb78		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1608	ereb79	AP2-EREBP-transcription factor 79	GRMZM2G175856	B73 RefGen_v3	Gene	Chr1	197306494	197307177	ereb79		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1609	ereb8	AP2-EREBP-transcription factor 8	GRMZM2G146028	B73 RefGen_v3	Gene	Chr4	234986414	234987698	ereb8		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1610	ereb80	AP2-EREBP-transcription factor 80	GRMZM2G151542	B73 RefGen_v3	Gene	Chr8	147672456	147674477	ereb80		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1611	ereb81	AP2-EREBP-transcription factor 81	GRMZM2G416701	B73 RefGen_v3	Gene	Chr6	29008639	29012194	ereb81		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1612	ereb82	AP2-EREBP-transcription factor 82	GRMZM2G019443	B73 RefGen_v3	Gene	Chr7	17154984	17156006	ereb82		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1613	ereb83	AP2-EREBP-transcription factor 83	GRMZM2G132185	B73 RefGen_v3	Gene	Chr8	171200009	171201130	ereb83		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1614	ereb84	AP2-EREBP-transcription factor 84	GRMZM2G481668	B73 RefGen_v3	Gene	Chr6	147998722	147999285	ereb84		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1615	ereb86	AP2-EREBP-transcription factor 86	GRMZM2G040664	B73 RefGen_v3	Gene	Chr10	132343963	132345739	ereb86		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1616	ereb87	AP2-EREBP-transcription factor 87	GRMZM5G805505	B73 RefGen_v3	Gene	Chr2	21231379	21232602	ereb87		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1617	ereb88	AP2-EREBP-transcription factor 88	GRMZM2G018138	B73 RefGen_v3	Gene	Chr7	141464460	141465197	ereb88		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1618	ereb89	AP2-EREBP-transcription factor 89	GRMZM2G156737	B73 RefGen_v3	Gene	Chr4	48661492	48662964	ereb89		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
1619	ereb9	AP2-EREBP-transcription factor 9	GRMZM2G323172	B73 RefGen_v3	Gene	Chr6	124705032	124709397	ereb9		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1620	ereb90	AP2-EREBP-transcription factor 90	GRMZM2G110333	B73 RefGen_v3	Gene	Chr5	212398699	212401458	ereb90		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1621	ereb91	AP2-EREBP-transcription factor 91	GRMZM2G079825	B73 RefGen_v3	Gene	Chr2	63265056	63266421	ereb91		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1622	ereb92	AP2-EREBP-transcription factor 92	GRMZM2G174347	B73 RefGen_v3	Gene	Chr8	120487038	120488230	ereb92		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1623	ereb93	AP2-EREBP-transcription factor 93	GRMZM2G066158	B73 RefGen_v3	Gene	Chr8	120401709	120402944	ereb93		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1624	ereb94	AP2-EREBP-transcription factor 94	GRMZM2G363052	B73 RefGen_v3	Gene	Chr7	85662465	85665508	ereb94		strongly expressed in the maize endosperm; might act as a key regulator of starch synthesis in maize (Li et al., 2017)
1625	ereb95	AP2-EREBP-transcription factor 95	AC198979.4_FG009	B73 RefGen_v3	Gene	Chr1	10988032	10988424	ereb95		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1626	ereb96	AP2-EREBP-transcription factor 96	GRMZM2G044077	B73 RefGen_v3	Gene	Chr8	26886791	26888388	ereb96		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1627	ereb97	AP2-EREBP-transcription factor 97	GRMZM2G068967	B73 RefGen_v3	Gene	Chr2	10793567	10794323	ereb97		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1628	ereb98	AP2-EREBP-transcription factor 98	GRMZM2G052720	B73 RefGen_v3	Gene	Chr4	237684792	237686205	ereb98		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1629	ereb99	AP2-EREBP-transcription factor 99	GRMZM2G073258	B73 RefGen_v3	Gene	Chr5	134961620	134962623	ereb99		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1630	ers14	ethylene receptor1-14	GRMZM2G102601	B73 RefGen_v3	Gene	Chr5	12230588	12235844	ers14	ers1-14, ers14, ers25, ethylene receptor1-25 , gnp_QAE7c12a, gnp_QAO3d04b, gnp_QAO3d04c, gpm381b, gpm381c, gpm774a, PCO067639b	
1631	ers25	ethylene receptor1-25	GRMZM2G073668	B73 RefGen_v3	Gene	Chr1	264657422	264662580	ers25	ERS1-25, ers25, ethylene receptor isoform 1, gnp_QAE7c12c, gnp_QAO3d04a, gpm774c, pco067639(84), PCO067639a	
1632	es1	embryo sac1	GRMZM2G012012	B73 RefGen_v3	Gene	Chr9	126975034	126975819	es1	defensin-like cysteine-rich proteins, embryo sac1, es1, ZmES1	one of 4-5 copy gene family; pre-zygotic embryo sac specific; required for pollen tube growth arrest and burst
1633	es2	embryo sac2	GRMZM2G009359	B73 RefGen_v3	Gene	Chr9	126170000	126170583	es2	defensin-like cysteine-rich proteins, embryo sac2, es2, ZmES2	one of 4-5 copy gene family; pre-zygotic embryo sac specific; required for pollen tube growth arrest and burst
1634	es2	embryo sac2	GRMZM2G128301	B73 RefGen_v3	Gene	Chr9	126256594	126257200	es2	defensin-like cysteine-rich proteins, embryo sac2, es2, ZmES2	one of 4-5 copy gene family; pre-zygotic embryo sac specific; required for pollen tube growth arrest and burst
1635	es3	embryo sac3	GRMZM2G009359	B73 RefGen_v3	Gene	Chr9	126170000	126170583	es3	defensin-like cysteine-rich proteins, embryo sac3, es3, ZmES3	one of 4-5 copy gene family; pre-zygotic embyro sac specific; required for pollen tube growth arrest and burst
1636	es3	embryo sac3	GRMZM2G128301	B73 RefGen_v3	Gene	Chr9	126256594	126257200	es3	defensin-like cysteine-rich proteins, embryo sac3, es3, ZmES3	one of 4-5 copy gene family; pre-zygotic embyro sac specific; required for pollen tube growth arrest and burst
1637	es4	embryo sac4	GRMZM2G009359	B73 RefGen_v3	Gene	Chr9	126170000	126170583	es4	defensin-like cysteine-rich protein, embryo sac4, es4, ZmES4	one of 4-5 copy gene family; pre-zygotic, embryo sac specific; required for pollen tube growth arrest and burst
1638	es4	embryo sac4	GRMZM2G128301	B73 RefGen_v3	Gene	Chr9	126256594	126257200	es4	defensin-like cysteine-rich protein, embryo sac4, es4, ZmES4	one of 4-5 copy gene family; pre-zygotic, embryo sac specific; required for pollen tube growth arrest and burst
1639	esp1	embryo specific protein1	AC233879.1_FG002	B73 RefGen_v3	Gene	Chr6	140536934	140537348	esp1	em1, EMB564, embryonic abundant protein 1, embryo specific protein1, esp1, PCO083850, wheat Em ortholog1	late embryonic protein, induced by abscisic acid and osmotic stress; cDNA similar to other LEA proteins. ortholog of wheat Em; protein and mRNA in embryo from 16 days after pollination
1640	esp5	embryo specific protein5	GRMZM2G162659	B73 RefGen_v3	Gene	Chr6	140501700	140502699	esp5	emb5, embryo specific protein5, esp5, M90554, PCO100617	(was Emb5); cDNA clone, embryo specific, ABA responsive, deduced amino acid sequence very hydrophilic and gly/glu-rich (aka emb5)
1641	esr1	embryo surrounding region1	GRMZM2G046086	B73 RefGen_v3	Gene	Chr1	14286859	14287441	esr1	embryo surrounding region1, esr1, pco129241(9)	cDNA expressed 4 to 28 DAP in endosperm locally surrounding the embryo
1642	esr2	embryo surrounding region2	GRMZM2G315601	B73 RefGen_v3	Gene	Chr1	14256833	14257545	esr2	embryo surrounding region2, esr2, pco067764(9)	cDNA expressed 4 to 28 DAP in endosperm locally surrounding the embryo
1643	esr3	embryo surrounding region3	GRMZM2G140302	B73 RefGen_v3	Gene	Chr1	14300150	14300705	esr3	embryo surrounding region3, esr3, ESR3g2	cDNA expressed 4 to 28 DAP in endosperm locally surrounding the embryo
1644	esr6	embryo surrounding region6	GRMZM2G048353	B73 RefGen_v3	Gene	Chr4	210979213	210979886	esr6	defensin, embryo surrounding region6, esr6, esr6a	transcript specific to embryo surrounding region near basal endosperm transfer layer
1645	et1	etched1	GRMZM2G157574	B73 RefGen_v3	Gene	Chr3	223825954	223827718	et1	et1, etched1	pitted, scarred endosperm, virescent seedling; plastid membranes altered
1646	etr2	ethylene receptor homolog2	GRMZM2G420801	B73 RefGen_v3	Gene	Chr10	101173508	101177424	etr2	etr2, ETR2, etr2-9, ETR6, ETR9, orphans transcription factor (Orphan84), PCO124492, PCO124492(742), ZmETR2-9, ZmOrphan84	
1647	etr40	ethylene receptor homolog40	GRMZM2G089010	B73 RefGen_v3	Gene	Chr2	104591127	104595720	etr40	ETR2, etr40, ETR61, ZmETR2-40, ZmOrphan221	
1648	exg1	exoglucanase1	GRMZM2G147687	B73 RefGen_v3	Gene	Chr1	276371915	276377603	exg1	exg1, exoglucanase1, PCO090119	genomic and cDNA clones; role in cell wall expansion
1649	expa1	alpha expansin1	GRMZM2G339122	B73 RefGen_v3	Gene	Chr3	184419336	184421693	expa1	alpha expansin1, alpha-expansin 10, Exp1, expa1, PCO064861(257), PCO064861a	belongs to a multigene family and probably exists as a single copy.
1650	expa2	alpha expansin2	GRMZM2G105844	B73 RefGen_v3	Gene	Chr5	206888609	206890560	expa2	alpha expansin2, Exp2, expa2, PCO099009, PCO099009(430)	belongs to a multigene family and probably exists as a single copy.
1651	expa3	alpha expansin3	GRMZM2G074585	B73 RefGen_v3	Gene	Chr10	99487994	99489313	expa3	expa3, umc2632	
1652	expa4	alpha-expansin4	GRMZM2G368886	B73 RefGen_v3	Gene	Chr1	293705165	293708788	expa4	, rs131185432 , rs131917822 , ss196433067 , ss196433069 , ss196523758 , ss196523760 , umc1630	
1653	expa5	alpha expansin5	GRMZM2G361064	B73 RefGen_v3	Gene	Chr6	154325086	154327260	expa5	alpha expansin5, expa5	alpha expansins function as wall loosening agents for control of plant cell growth.
1654	expa6	expansin-like6	GRMZM2G095968	B73 RefGen_v3	Gene	Chr1	7353116	7355434	expa6	expa6, expansin-like 3, expansin-like A1 , umc1363, umc1363a	
1655	expb1	beta expansin1	GRMZM2G146551	B73 RefGen_v3	Gene	Chr9	118273115	118274521	expb1	beta expansin1, expb1, expb1a, ExpB1a, PCO124530	belongs to a multigene family; most likely exists as two or more copies.
1656	expb10a	beta expansin10a	GRMZM2G089699	B73 RefGen_v3	Gene	Chr9	152409062	152410472	expb10a	AY104999, beta expansin10a, expb10a, expb10b, PCO110981	
1657	expb10c	beta expansin10c	GRMZM2G007685	B73 RefGen_v3	Gene	Chr3	53557663	53558609	expb10c	beta expansin10c, expb10c, pco110981a	
1658	expb10d	beta expansin10d	GRMZM2G164785	B73 RefGen_v3	Gene	Chr3	53392404	53393425	expb10d	AY104999, beta expansin10d, expb10d, PCO110981	
1659	expb11	beta expansin11	GRMZM2G127106	B73 RefGen_v3	Gene	Chr5	200274645	200279681	expb11	expb11, pco068046, Zea m 1 allergen	
1660	expb2	beta expansin2	GRMZM2G021621	B73 RefGen_v3	Gene	Chr1	91256138	91259053	expb2	beta-expansin 1a, csu658( ), expansin-B4, expb2, expB2, expB8, magi104824, PCO140045b, rs131277820, umc2025	expressed specifically in the elongating region of maize primary root
1661	expb3	beta expansin3	GRMZM2G474194	B73 RefGen_v3	Gene	Chr1	1662969	1664360	expb3	beta-expansin 1a precursor, beta-expansin 3, expansin-B7, expb3, rs128357385	
1662	expb4	beta expansin4	GRMZM2G154178	B73 RefGen_v3	Gene	Chr7	41067901	41069524	expb4	expb4	
1663	expb5	beta expansin5	GRMZM2G013671	B73 RefGen_v3	Gene	Chr9	116292644	116294506	expb5	expb5	
1664	expb6	beta expansin6	GRMZM2G176595	B73 RefGen_v3	Gene	Chr1	91884842	91886219	expb6	beta-expansin 1a precursor, expb6, PCO112411a	
1665	expb7	beta expansin7	GRMZM2G342246	B73 RefGen_v3	Gene	Chr1	91511981	91513768	expb7	expb7, rs128674220 , rs128674225, rs131278031 , rs131278040	
1666	expb8	beta expansin8	GRMZM2G013002	B73 RefGen_v3	Gene	Chr9	116265519	116268415	expb8	beta expansin8, csu658(mam), expb8	Expb2 specifically expressed in the elongationg region of maize primary roots
1667	fab1	fatty acid biosynthesis1	GRMZM2G099696	B73 RefGen_v3	Gene	Chr10	108139878	108147684	fab1	fab1, fabg, fatty acid biosynthesis1, PCO074795(744), PCO074795b, uaz099, uaz99, uaz99(gfu)	endosperm cDNA 2C01H08 (uaz99) similar to fatty acid biosynthesis enzyme

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
1668	fad7	fatty acid desaturase7	GRMZM2G128971	B73 RefGen_v3	Gene	Chr9	138099701	138102875	fad7	IDP218, IDP4, IDP550, PCO145451, PCO145451(695), PHM1599, PZA01096, rs13117596 8, ss196417263	leaf cDNA and genomic clones similar to Arabidopsis FAD7, cold-induced
1669	fad8	fatty acid desaturase8	GRMZM2G074401	B73 RefGen_v3	Gene	Chr1	44805347	44808260	fad8	fad8, fatty acid desaturase8, umc1021, umc1021(fad8)	leaf cDNA and genomic clones with sequence similarity to Arabidopsis FAD7; unlike maize fad7, not expressed at cold; SSR umc1021
1670	fae2	fatty acid elongase2	GRMZM2G022558	B73 RefGen_v3	Gene	Chr9	87869349	87871737	fae2	CL1191_1, fae1 fatty acid elongase 1, fae2	
1671	farl1	FAR1-like-transcription factor 1	GRMZM2G001663	B73 RefGen_v3	Gene	Chr1	35738669	35743639	farl1		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1672	farl10	FAR1-like-transcription factor 10	GRMZM2G406651	B73 RefGen_v3	Gene	Chr7	150316196	150320346	farl10		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1673	farl11	FAR1-like-transcription factor 11	GRMZM2G048987	B73 RefGen_v3	Gene	Chr7	152856122	152861721	farl11		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1674	farl12	FAR1-like-transcription factor 12	GRMZM2G129311	B73 RefGen_v3	Gene	Chr7	157771968	157777346	farl12		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1675	farl13	FAR1-like-transcription factor 13	GRMZM2G114461	B73 RefGen_v3	Gene	Chr7	165506191	165510340	farl13		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1676	farl14	FAR1-like-transcription factor 14	GRMZM2G148940	B73 RefGen_v3	Gene	Chr9	87667166	87669926	farl14		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1677	farl15	FAR1-like-transcription factor 15	GRMZM2G104268	B73 RefGen_v3	Gene	Chr10	145543618	145550014	farl15		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1678	farl2	FAR1-like-transcription factor 2	GRMZM2G463730	B73 RefGen_v3	Gene	Chr1	283389452	283396343	farl2		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1679	farl3	FAR1-like-transcription factor 3	GRMZM2G155980	B73 RefGen_v3	Gene	Chr1	297376151	297380168	farl3		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1680	farl4	FAR1-like-transcription factor 4	GRMZM2G083374	B73 RefGen_v3	Gene	Chr3	9771491	9806346	farl4		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1681	farl5	FAR1-like-transcription factor 5	GRMZM2G034868	B73 RefGen_v3	Gene	Chr3	142975242	142986336	farl5		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1682	farl6	FAR1-like-transcription factor 6	GRMZM2G302323	B73 RefGen_v3	Gene	Chr4	30795954	30799228	farl6		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1683	farl7	FAR1-like-transcription factor 7	GRMZM2G043250	B73 RefGen_v3	Gene	Chr5	171564949	171567349	farl7		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1684	farl8	FAR1-like-transcription factor 8	GRMZM2G117108	B73 RefGen_v3	Gene	Chr5	182810298	182816922	farl8		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1685	farl9	FAR1-like-transcription factor 9	GRMZM2G106653	B73 RefGen_v3	Gene	Chr5	182948968	182952939	farl9		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1686	fat1	fatty acyl thioesterase1	GRMZM2G406603	B73 RefGen_v3	Gene	Chr9	88263061	88268115	fat1	CL2720_2, csu817, csuh00817, csuh817, fat1, Fat[AB], fatty acyl thioesterase1, myristoyl-acyl carrier protein thioesterase	leaf cDNA csu817 similar to plant fatty acid metabolism protein
1687	fat2	fatty acyl-ACP thioesterase2	GRMZM5G829544	B73 RefGen_v3	Gene	Chr9	20595102	20599326	fat2	fat2, fatb, fatty acyl-ACP thioesterase2, pco086030b	
1688	fbn1	fibrillin1	GRMZM2G003318	B73 RefGen_v3	Gene	Chr1	101275701	101279519	fbn1	csu653, csu653(fbn), fbn1, fibrillin1, plastid-lipid associated protein PAP	leaf cDNA csu653, moderate copy number, similar to plastid protein
1689	fcp1	fon2-like cle protein1	GRMZM2G165836	B73 RefGen_v3	Gene	Chr2	39188755	39190131	fcp1	CLAVATA3/EMBRYO-SURROUNDING REGION (CLE), fcp1, FLORAL ORGAN NUMBER 2 (FON2), FON2-LIKE CLE PROTEIN 1 (FCP1), ZmFCP1	mutants have a fasciated ear phenotype
1690	fcr1	ferric-chelate reductase (NADH)1	GRMZM2G133213	B73 RefGen_v3	Gene	Chr3	186291885	186295766	fcr1	fcr1, ferric-chelate reductase (NADH)1, NFR, pco074166(259), PCO074166a	member of a multi-gene family
1691	fcr2	ferric-chelate reductase (NADH)2	GRMZM2G157263	B73 RefGen_v3	Gene	Chr6	155408534	155412926	fcr2	CL1597_2, CL1597_2(519), fcr2, ferric-chelate reductase (NADH)2, NADH-cytochrome b5 reductase, NFR II	
1692	fdad1	false DAD1	GRMZM5G847530	B73 RefGen_v3	Gene	Chr9	26606314	26608509	fdad1	AY109816, CL0_-2, dad1, defender against cell death 1, fdad1, gnp_QCJ15g11, gpm673	similar to Oryza and Hordeum Defender against apoptotic cell death protein (DAD-1, DAD-2 respectively)
1693	fdh1	formaldehyde dehydrogenase homolog1	GRMZM5G824600	B73 RefGen_v3	Gene	Chr5	215541812	215545867	fdh1	CL1875_1b, fadh1, fdh1, formaldehyde dehydrogenase homolog1, IDP332	cDNA sequence; single copy
1694	fdh2	formate dehydrogenase2	GRMZM2G423972	B73 RefGen_v3	Gene	Chr1	264221357	264225484	fdh2	CL15209_1(674), CL15209_1f, fdh2, fdh2b, formate dehydrogenase 1	
1695	fdl1	fused leaves1	GRMZM2G056407	B73 RefGen_v3	Gene	Chr7	167647343	167649332	fdl1	fdl1, fused leaves1, myb94, MYB-transcription factor 94, ZmMYB94	coleoptile-first or first-second leaves fused at epidermis, curly
1696	fdx1	ferredoxin1	GRMZM2G122337	B73 RefGen_v3	Gene	Chr6	1340417	1341388	fdx1	chloroplast ferredoxin 1, fdx1, ferredoxin1, pFD1	chloroplast, light induced, N-terminal amino acid sequence of mature protein, cDNA sequence, SSR phi075
1697	fdx2	ferredoxin2	GRMZM2G048313	B73 RefGen_v3	Gene	Chr6	1373405	1374333	fdx2	fdx2, ferredoxin-1, ferredoxin2, pFD2, umc1002, umc1023	encoded protein sequence distinct from fdx1; leaf cDNA, SSRs umc1002, umc1023
1698	fdx3	ferredoxin3	GRMZM2G053458	B73 RefGen_v3	Gene	Chr1	296097227	296102118	fdx3	fd3, fdx3, ferredoxin3, pFD3, PHM1275, PHM174, PZA03018, umc1064, umc1064(fdx3)	ubiquitous, cDNA clone, gene specific probe, amino acid sequence; SSR umc1064, pFD3
1699	fdx5	ferredoxin5	GRMZM2G122327	B73 RefGen_v3	Gene	Chr6	1343906	1345155	fdx5	fdx5, ferredoxin5, PCO142214, PCO142214(187), pfd5	leaf protein, cDNA clone, distinct amino acid sequence compared to other ferredoxins, gene specific probe (aka pfd5)
1700	fea2	fasciated ear2	GRMZM2G104925	B73 RefGen_v3	Gene	Chr4	133689783	133692271	fea2	CL21626_1a, fae2, fasciated ear2, fea2, rs129795307, rs13175610, rs131175611, rs132136021, ss196415811, ss196415814, ss196415816	ear fasciated, broadened and flattened at the tip; rows irregular; similar to CLAVATA 2 of Arabidopsis thaliana
1701	fea3	fasciated ear3	GRMZM2G166524	B73 RefGen_v3	Gene	Chr3	29095292	29098726	fea3	fae3, fasciated ear3, fea3	ear tip broad and branched, typically splitting and showing ring fasciation to form a hollow ear.
1702	fea4	fasciated ear4	GRMZM2G133331	B73 RefGen_v3	Gene	Chr6	116934690	116937455	fea4	bzip57, bZIP-transcription factor 57, fea4	Mutants are semidwarfed with fasciated ears and tassels as well as greatly enlarged vegetative and inflorescence meristems.
1703	fer1	ferritin1	GRMZM2G325575	B73 RefGen_v3	Gene	Chr4	183760831	183763850	fer1	csu313a(fer), csu584a(fer), csu626a(fer), fer1, Ferr, ferritin1, FM1A, gsy82(fer1), PCO065378	iron induced, cDNA sequences and expression pattern indicate two genes, fer1, fer2 (Lobreaux et al 1992)
1704	fer2	ferritin homolog2	GRMZM2G147266	B73 RefGen_v3	Gene	Chr10	1279030	1283646	fer2	csu306a(fer), csu306(fer), csu313b(fer), csu584b(fer), csu626b(fer), fer2, ferritin homolog2, FM2, PCO065377	iron induced, cDNA sequences, differential expression indicate 2 genes(Lobreaux et al. 1992)
1705	fgp2	folylpolyglutamate synthetase2	GRMZM5G869779	B73 RefGen_v3	Gene	Chr1	226063076	226070426	fgp2	fgp2	Paralog of bm4 also encoding FPGS
1706	fgs1	ferredoxin-dependent glutamate synthas	GRMZM2G036609	B73 RefGen_v3	Gene	Chr7	171002271	171021085	fgs1	CL2484_1b, FD-GOGAT, ferredoxin-dependent glutamate synthase1, fgs1, PCO065377	deduced amino acid sequence homologous with E. coli NADPH-glutamate synthase, single copy by Southern blot analysis
1707	fha1	FHA-transcription factor 1	GRMZM2G129243	B73 RefGen_v3	Gene	Chr1	5741207	5746550	fha1	asg31, fha1, FHA9, myosin-9-like, p-umc1104, p-umc1104(4), rs131177709, rs131198815 , ss196422318 , ss196422320	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1708	fha10	FHA-transcription factor 10	AC211652.4_FG002	B73 RefGen_v3	Gene	Chr4	20429258	20434163	fha10		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1709	fha11	FHA-transcription factor 11	GRMZM2G701297	B73 RefGen_v3	Gene	Chr5	3944081	3952303	fha11		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1710	fha12	FHA-transcription factor 12	GRMZM2G105822	B73 RefGen_v3	Gene	Chr5	8623516	8626712	fha12		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1711	fha13	FHA-transcription factor 13	GRMZM2G081221	B73 RefGen_v3	Gene	Chr5	19207810	19212507	fha13		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1712	fha14	FHA-transcription factor 14	GRMZM2G006246	B73 RefGen_v3	Gene	Chr5	26333085	26337585	fha14		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1713	fha15	FHA-transcription factor 15	GRMZM2G113156	B73 RefGen_v3	Gene	Chr6	140068111	140076698	fha15		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1714	fha17	FHA-transcription factor 17	GRMZM2G172021	B73 RefGen_v3	Gene	Chr9	153782357	153788188	fha17		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1715	fha18	FHA-transcription factor 18	GRMZM2G136344	B73 RefGen_v3	Gene	Chr10	120802689	120805284	fha18		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1716	fha2	FHA-transcription factor 2	GRMZM2G424241	B73 RefGen_v3	Gene	Chr1	193349658	193355990	fha2		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
1717	fha3	FHA-transcription factor 3	GRMZM2G086138	B73 RefGen_v3	Gene	Chr1	248377825	248386493	fha3		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1718	fha4	FHA-transcription factor 4	GRMZM2G359217	B73 RefGen_v3	Gene	Chr1	272641851	272643707	fha4		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1719	fha5	FHA-transcription factor 5	GRMZM2G127139	B73 RefGen_v3	Gene	Chr2	45068944	45077882	fha5		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1720	fha6	FHA-transcription factor 6	GRMZM2G133716	B73 RefGen_v3	Gene	Chr2	136740049	136745997	fha6		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1721	fha7	FHA-transcription factor 7	GRMZM2G150608	B73 RefGen_v3	Gene	Chr2	161415278	161423070	fha7		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1722	fha8	FHA-transcription factor 8	GRMZM2G391164	B73 RefGen_v3	Gene	Chr2	230519202	230523747	fha8		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1723	fha9	FHA-transcription factor 9	GRMZM2G177895	B73 RefGen_v3	Gene	Chr3	230599139	230600906	fha9		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1724	fht1	flavanone 3-hydroxylase1	GRMZM2G062396	B73 RefGen_v3	Gene	Chr2	3561475	3563418	fht1	f3βh, f3h, fht1, fl3h, flavanone 3-hydroxylase1, flavanone hydroxyl transferase1	(aka f3h) single copy cDNA similar to Antirrhinum homolog
1725	fie1	fertilization independent endosperm1	GRMZM2G118205	B73 RefGen_v3	Gene	Chr4	35790694	35796700	fie1	CL600_7b, fertilization independent endosperm1, fie1, PZA00541, ZMfie1	
1726	fie2	fertilization independent endosperm2	GRMZM2G148924	B73 RefGen_v3	Gene	Chr10	84106322	84110776	fie2	fertilization independent endosperm2, fie102, fie2, IDP1405, PZB00409, Zmfie2	
1727	fim1	fimbrin homolog1	GRMZM2G010937	B73 RefGen_v3	Gene	Chr4	163873554	163879688	fim1	fim1	sequence similar to Arabidopsis fim1, flourescently labelled by Cell Genomics Proejct
1728	fl1	floury endosperm1	GRMZM2G094532	B73 RefGen_v3	Gene	Chr2	41853494	41855092	fl1	fl1, fl-a, floury endosperm1, o4, o*-4915, o8, opaque 4915	(was o4) endosperm opaque, soft; dosage effect with fl1-ref allele, but o4 allele is recessive
1729	fl2	floury2	GRMZM2G397687	B73 RefGen_v3	Gene	Chr4	21334901	21335970	fl2	uat3a(fl2), uaz185, UAZ185(22AZ), uaz185(zp22), umc2409.A, umc2409b, z1C, z1C/SF4, zp19/22*-L34340	removal of its signal peptide, preventing transfer to lumen of the endoplasmic reticulum. mRNA for 22kD zein; in z1c(zp22) cluster
1730	fl4	floury4	GRMZM2G353272	B73 RefGen_v3	Gene	Chr4	5539880	5541152	fl4	fl4, zein-alpha A30-like	semi-dominant opaque mutant that produces small, misshapen, and aggregated protein bodies; encodes member of 19kD α-zein z1A-1 subfamily
1731	fls1	flavonol synthase1	GRMZM2G152801	B73 RefGen_v3	Gene	Chr5	210204906	210206387	fls1	fls1, ZmFLS1	partially complements the flavonol deficiency of the Arabidopsis fls1 mutant
1732	fls2	flavonol synthase2	GRMZM2G069298	B73 RefGen_v3	Gene	Chr5	210154373	210155706	fls2	flavonol synthase/flavanone 3-hydroxylase-like, fls2, ZmFLS2	Tightly linked tandem duplication of fls1
1733	fnr1	ferredoxin NADP reductase1	GRMZM2G058760	B73 RefGen_v3	Gene	Chr1	285208091	285211692	fnr1	AY109758, CL1976_1, CL1976_1(95), ferredoxin NADP reductase1, fnr1, PHM9241, PZA02087, rs131175360, ss196414831, usu1, usu1a(fnr), usu1a(fnr1)	single or low copy; root, nitrate induced cDNA; deduced amino acid sequence >90% similar to rice FNR; produces an active FNR product in E. coli
1734	fnr2	ferredoxin NADP reductase2	GRMZM2G058760	B73 RefGen_v3	Gene	Chr1	285208091	285211692	fnr2	fnr2, IDP808, phm9241, PZA02087, rs131175360, ss196414831, usu1b(fnr), usu1b(fnr1)	
1735	fns1	flavone synthase1	GRMZM2G167336	B73 RefGen_v3	Gene	Chr9	128676962	128678835	fns1	cytochrome P450 93A3-like, fns1	
1736	fnsi1	flavone synthase typeI1	GRMZM2G099467	B73 RefGen_v3	Gene	Chr1	83410152	83414307	fnsi1	dmr6, fnsi1, gibberellin 20 oxidase	Encodes a flavone synthase that is of the soluble Fe2+/2- oxoglutarate-dependent dioxygenase class
1737	fnsi2	flavone synthase typeI2	GRMZM2G475380	B73 RefGen_v3	Gene	Chr1	4760983	4765716	fnsi2	dmr6, flavonol synthase/flavanone 3-hydroxylase-like, fnsi2	Encodes a flavone synthase that is of the soluble Fe2+/2- oxoglutarate-dependent dioxygenase class
1738	fnsii1	flavone synthase typeII1	GRMZM2G148441	B73 RefGen_v3	Gene	Chr10	96108546	96110569	fnsii1	cytochrome P450 93A2-like, fnsii1, ZmCYP93G7	Encodes a flavone synthase that is of the oxygen- and NADPH-dependent cytochrome P450 membrane-bound monooxygenase class
1739	fpox1	fowlpox viral protein homolog1	GRMZM2G108767	B73 RefGen_v3	Gene	Chr7	165719833	165723658	fpox1	csu906, csuh00906, csuh906, fowlpox viral protein homolog1, fpox1, pox1, senescence-associated-like protein, uaz278, uazT14744(gfu)	endosperm cDNA 5C04H07, similar to virus major core protein
1740	fps1	farnesyl pyrophosphate synthase1	GRMZM2G168681	B73 RefGen_v3	Gene	Chr8	62786955	62791232	fps1	farnesyl diphosphate synthase1, farnesyl pyrophosphate synthase1, fdps1, FPPS, fps1, gnp_QBB18h08b, gpm430b, PCO074380(592), PCO074380b	endosperm cDNA sequence; two copies detected; up-regulated in endosperm mutants, o2 and fl2 (Li et al. 1996).
1741	fps2	farnesyl diphosphate synthase2	GRMZM2G147721	B73 RefGen_v3	Gene	Chr8	153104841	153108971	fps2	fpps2, fps2	weakly expressed in wounded leaves (Richter et al 2015)
1742	fps3	farnesyl diphosphate synthase3	GRMZM2G098569	B73 RefGen_v3	Gene	Chr3	205218174	205222694	fps3	cl242_1(269), cl242_1b, fpps3, rs129403832	terpene based defense (Richter et al 2015)
1743	frk1	fructokinase1	GRMZM2G086845	B73 RefGen_v3	Gene	Chr3	168566367	168569728	frk1	frk1	
1744	frk2	fructokinase2	GRMZM2G051677	B73 RefGen_v3	Probed Site	Chr6	3573121	3576235	frk2	CL966_1, csu926(frk), frk2, umc1143	
1745	fro2	ferric-chelate reductase2	GRMZM2G068557	B73 RefGen_v3	Gene	Chr2	46785444	46790374	fro2	ferric reductase-like transmembrane component, fro2, ZmFRO2	
1746	fsu1b(smh)		GRMZM2G087817	B73 RefGen_v3	Probed Site	Chr3	221663066	221667898	fsu1b(smh)	fsu1b(smh), hon107, smh2	
1747	ftcl1	5-formyltetrahydrofolate cyclo-ligase1	GRMZM2G001904	B73 RefGen_v3	Gene	Chr10	9142799	9147733	ftcl1	ftcl1	
1748	ftr1	ferredoxin-thioredoxin1	GRMZM2G122793	B73 RefGen_v3	Gene	Chr9	9969973	9974729	ftr1	ferredoxin-thioredoxin1, ferredoxin-thioredoxin reductase catalytic chain , ftr1, PCO088330, PCO088330(652), PZA01799	cDNA sequence
1749	fus6	fusca homolog	GRMZM2G062210	B73 RefGen_v3	Gene	Chr1	3548036	3558270	fus6	cl32446_1, cl32446_1(4), COP9 signalosome complex subunit 1, csu896, csuh00896, csuh896, fus6, fusca homolog	leaf cDNA csu896, single copy, similar to Arabidopsis fusca protein
1750	g2	golden plant2	GRMZM2G087804	B73 RefGen_v3	Gene	Chr3	1464299	1469099	g2	bsd1, bundle sheath defective1, g2, g5, glk13, golden plant2, pg14, pg-m, umc2101, umc2102, umc2103, umc2104, umc2105, umc2106, umc2107, umc2108, umc2109, v19	pg-m (now g2-pg14::I) of Peterson is a mutable allele that responds to En; small bundle sheath plastids; SSR umc2101, umc2102, umc2103, umc2104, umc2105, umc2106, umc2107,
1751	ga16,17ox1	gibberellin 16,17-oxidase1	GRMZM2G167673	B73 RefGen_v3	Gene	Chr6	155034889	155036270	ga16,17ox1	ga16,17ox1, ZmGA16,17ox	
1752	ga20ox1	gibberellin 20-oxidase1	AC203966.5_FG005	B73 RefGen_v3	Gene	Chr1	299607382	299608497	ga20ox1	ga20ox1, pco130567, pco130567(111), rs131924714, ZmGA20ox1	
1753	ga20ox2	gibberellin 20-oxidase2	GRMZM2G021051	B73 RefGen_v3	Gene	Chr2	234425722	234427421	ga20ox2	ga20ox2, ZmGA3ox2, ZmGA3ox3	
1754	ga20ox3	gibberellin 20-oxidase3	GRMZM2G368411	B73 RefGen_v3	Gene	Chr3	170942901	170945698	ga20ox3	ga20ox3, ZmGA20ox2.1, ZmGA3ox3	
1755	ga20ox4	gibberellin 20-oxidase4	GRMZM2G060940	B73 RefGen_v3	Gene	Chr5	18192142	18193721	ga20ox4	ga20ox4, umc2388, ZmGA3ox4	
1756	ga20ox5	gibberellin 20-oxidase5	GRMZM2G049418	B73 RefGen_v3	Gene	Chr8	164487836	164490694	ga20ox5	ga20ox5, ZmGA20ox2.2, ZmGA3ox5	
1757	ga2ox1	gibberellin 2-oxidase1	GRMZM2G078798	B73 RefGen_v3	Gene	Chr6	126063717	126069395	ga2ox1	ga2ox1, gibberellin 2-oxidase1, ZmGA2ox2.1, ZmGA2ox5	See Supplemental Figure 6. Comparison of syntenic regions containing ga2ox1 in different
1758	ga2ox10	gibberellin 2-oxidase10	GRMZM2G031724	B73 RefGen_v3	Gene	Chr8	173402117	173404386	ga2ox10	ga2ox10, ZmGA2ox10, ZmGA2ox3.2	
1759	ga2ox11	gibberellin 2-oxidase11	GRMZM2G127757	B73 RefGen_v3	Gene	Chr6	158703759	158705083	ga2ox11	ga2ox11, ZmGA2ox	
1760	ga2ox12	gibberellin 2-oxidase12	GRMZM2G177104	B73 RefGen_v3	Gene	Chr7	725316	726416	ga2ox12	ga2ox12, ZmGA2ox5	
1761	ga2ox13	gibberellin 2-oxidase13	GRMZM2G031432	B73 RefGen_v3	Gene	Chr3	3994138	3996082	ga2ox13	ga2ox13, ZmGA2ox7.3	
1762	ga2ox2	gibberellin 2-oxidase2	GRMZM2G006964	B73 RefGen_v3	Gene	Chr2	28389255	28392075	ga2ox2	ga2ox2, gibberellin 2-oxidase2, ZmGA2ox1, ZmGA2ox6.1	
1763	ga2ox3	gibberellin 2-oxidase3	GRMZM2G022679	B73 RefGen_v3	Gene	Chr3	196126846	196128900	ga2ox3	ga2ox3, gibberellin 2-oxidase2, ZmGA2ox3, ZmGA2ox3.1	
1764	ga2ox4	gibberellin 2-oxidase4	GRMZM2G153359	B73 RefGen_v3	Gene	Chr5	187018204	187022091	ga2ox4	ga2ox4, ZmGA2ox4, ZmGA2ox6.2	
1765	ga2ox5	gibberellin 2-oxidase5	GRMZM2G176963	B73 RefGen_v3	Gene	Chr3	60943471	60951573	ga2ox5	ga2ox5, ZmGA2ox2, ZmGA2ox2.2	

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
1766	ga2ox6	gibberellin 2-oxidase6	GRMZM2G051619	B73 RefGen_v3	Gene	Chr6	131338805	131342645	ga2ox6	ga2ox6, pzb00414, PZB00416, rs131175761, ss196416429, ZmGA2ox6, ZmGA2ox7.1	
1767	ga2ox7	gibberellin 2-oxidase7	GRMZM2G427618	B73 RefGen_v3	Gene	Chr6	158703023	158704867	ga2ox7	ga2ox7, ZmGA2ox4, ZmGA2ox7	
1768	ga2ox8	gibberellin 2-oxidase8	GRMZM2G155686	B73 RefGen_v3	Gene	Chr6	164507675	164509560	ga2ox8	ga2ox8, ZmGA2ox8	
1769	ga2ox9	gibberellin 2-oxidase9	GRMZM2G152354	B73 RefGen_v3	Gene	Chr8	23992337	23994920	ga2ox9	ga2ox9, ZmGA2ox7.2, ZmGA2ox9	
1770	ga3ox1	gibberellin 3-oxidase1	GRMZM2G044358	B73 RefGen_v3	Gene	Chr6	128498080	128499807	ga3ox1	ga3ox1, Zea mays GA 3-oxidase 2 gene, Zmga3ox1, Zmga3ox2, ZmGA3ox2	homologue of d1
1771	gap1	Golgi associated protein homolog	GRMZM2G073725	B73 RefGen_v3	Gene	Chr1	248922560	248925400	gap1	CL1948_1a, gap1, Golgi associated protein homolog, sewap41, se-wap41	
1772	gar1	gibberellin responsive1	GRMZM2G061695	B73 RefGen_v3	Gene	Chr3	219494801	219498659	gar1	gar1, gibberellin responsive1, umc1203, ZmGR2c	
1773	gar2	gibberellin responsive2	GRMZM2G429000	B73 RefGen_v3	Gene	Chr10	138833997	138835213	gar2	cortical cell-delineating protein, gar2, ZmGR1a, ZmGR1b	
1774	gar3	gibberellin responsive3	GRMZM2G142705	B73 RefGen_v3	Gene	Chr8	138985268	138986891	gar3	GR2b, umc1777, ZmGR2a, ZmGR2b	
1775	gata1	C2C2-GATA-transcription factor 1	GRMZM2G025002	B73 RefGen_v3	Gene	Chr2	149357261	149359087	gata1		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1776	gata10	C2C2-GATA-transcription factor 10	GRMZM2G532534	B73 RefGen_v3	Gene	Chr9	152533064	152538147	gata10		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1777	gata11	C2C2-GATA-transcription factor 11	GRMZM2G404973	B73 RefGen_v3	Gene	Chr2	22692870	22695229	gata11		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1778	gata12	C2C2-GATA-transcription factor 12	AC194965.4_FG004	B73 RefGen_v3	Gene	Chr6	127629032	127630234	gata12	GATA transcription factor 23-like	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1779	gata13	C2C2-GATA-transcription factor 13	GRMZM2G044576	B73 RefGen_v3	Gene	Chr8	174313923	174315776	gata13		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1780	gata14	C2C2-GATA-transcription factor 14	GRMZM5G879778	B73 RefGen_v3	Gene	Chr4	239234358	239235044	gata14		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1781	gata15	C2C2-GATA-transcription factor 15	GRMZM2G031983	B73 RefGen_v3	Gene	Chr5	155457609	155459172	gata15		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1782	gata16	C2C2-GATA-transcription factor 16	GRMZM2G113098	B73 RefGen_v3	Gene	Chr1	90962372	90964067	gata16		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1783	gata17	C2C2-GATA-transcription factor 17	GRMZM2G138967	B73 RefGen_v3	Gene	Chr8	155999788	156001252	gata17		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1784	gata18	C2C2-GATA-transcription factor 18	GRMZM2G114775	B73 RefGen_v3	Gene	Chr1	295848928	295850422	gata18	gata18, umc2045	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1785	gata19	C2C2-GATA-transcription factor 19	GRMZM2G421212	B73 RefGen_v3	Gene	Chr10	134118624	134123159	gata19		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1786	gata2	C2C2-GATA-transcription factor 2	GRMZM2G104390	B73 RefGen_v3	Gene	Chr8	40841370	40843380	gata2		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1787	gata21	C2C2-GATA-transcription factor 21	GRMZM5G887975	B73 RefGen_v3	Gene	Chr8	71168700	71169448	gata21		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1788	gata22	C2C2-GATA-transcription factor 22	AC184831.3_FG005	B73 RefGen_v3	Gene	Chr4	239028639	239029484	gata22		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1789	gata23	C2C2-GATA-transcription factor 23	GRMZM2G110295	B73 RefGen_v3	Gene	Chr1	286470199	286472456	gata23		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1790	gata24	C2C2-GATA-transcription factor 24	GRMZM2G163200	B73 RefGen_v3	Gene	Chr5	214574879	214580853	gata24		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1791	gata25	C2C2-GATA-transcription factor 25	AC202864.3_FG002	B73 RefGen_v3	Gene	Chr6	160741348	160742841	gata25		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1792	gata26	C2C2-GATA-transcription factor 26	GRMZM2G397616	B73 RefGen_v3	Gene	Chr8	73412731	73413812	gata26		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1793	gata27	C2C2-GATA-transcription factor 27	GRMZM2G052616	B73 RefGen_v3	Gene	Chr3	64821137	64823713	gata27		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1794	gata28	C2C2-GATA-transcription factor 28	GRMZM2G101058	B73 RefGen_v3	Gene	Chr9	115980192	115982001	gata28		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1795	gata29	C2C2-GATA-transcription factor 29	GRMZM2G039586	B73 RefGen_v3	Gene	Chr9	81178852	81181039	gata29		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1796	gata3	C2C2-GATA-transcription factor 3	GRMZM2G140669	B73 RefGen_v3	Gene	Chr5	190024321	190026323	gata3		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1797	gata30	C2C2-GATA-transcription factor 30	GRMZM2G464037	B73 RefGen_v3	Gene	Chr4	186548299	186549717	gata30		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1798	gata31	C2C2-GATA-transcription factor 31	GRMZM2G067171	B73 RefGen_v3	Gene	Chr3	141471190	141473058	gata31		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1799	gata32	C2C2-GATA-transcription factor 32	GRMZM2G135381	B73 RefGen_v3	Gene	Chr8	123887193	123889333	gata32		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1800	gata33	C2C2-GATA-transcription factor 33	GRMZM2G048850	B73 RefGen_v3	Gene	Chr10	9477435	9478816	gata33		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1801	gata34	C2C2-GATA-transcription factor 34	GRMZM2G396451	B73 RefGen_v3	Gene	Chr1	274561455	274577750	gata34		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1802	gata35	C2C2-GATA-transcription factor 35	GRMZM2G123909	B73 RefGen_v3	Gene	Chr3	211762877	211763862	gata35		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1803	gata36	C2C2-GATA-transcription factor 36	AC184831.3_FG008	B73 RefGen_v3	Gene	Chr4	239100691	239101536	gata36		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1804	gata4	C2C2-GATA-transcription factor 4	GRMZM2G379005	B73 RefGen_v3	Gene	Chr4	172789633	172794795	gata4		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1805	gata5	C2C2-GATA-transcription factor 5	GRMZM2G077002	B73 RefGen_v3	Gene	Chr2	22022637	22026411	gata5		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1806	gata6	C2C2-GATA-transcription factor 6	GRMZM2G054615	B73 RefGen_v3	Gene	Chr10	133391911	133394043	gata6		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1807	gata7	C2C2-GATA-transcription factor 7	GRMZM2G118214	B73 RefGen_v3	Gene	Chr10	9409405	9411344	gata7		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1808	gata8	C2C2-GATA-transcription factor 8	GRMZM2G324131	B73 RefGen_v3	Gene	Chr10	9535048	9537066	gata8		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1809	gata9	C2C2-GATA-transcription factor 9	GRMZM2G009530	B73 RefGen_v3	Gene	Chr1	177060036	177061909	gata9		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1810	gbf1	G-box binding factor	GRMZM2G011932	B73 RefGen_v3	Gene	Chr6	165543429	165548373	gbf1	AY109996, bzip18, bZIP-transcription factor 18, gbf1, G-box binding factor, putative bZIP transcription factor superfamily protein isoform 1	anoxia induced, nuclear, basic-region leucine zipper protein; low copy number; cDNA clone
1811	gbp1	GTP-binding protein homolog1	GRMZM2G131939	B73 RefGen_v3	Gene	Chr1	300951400	300963846	gbp1	AY104686, csu108, csu108b(gbp), csuh00532, csuh108, gbp1, GTP-binding protein homolog1, PCO088233(108), ras-related protein RHN1, umc365, ZmRab5B2	leaf cDNA csu108, partial sequence similar to Arabidopsis GTP binding protein, RHA1
1812	gbp2	GTP binding protein2	GRMZM2G045314	B73 RefGen_v3	Gene	Chr1	258058680	258065662	gbp2	CL2390_1, gbp2, gbp*-zgb1, GTP binding protein2, ZGB1	cDNA sequence similar animal G protein beta-subunits; single copy
1813	gbptf1	GeBP-transcription factor 1	GRMZM2G392516	B73 RefGen_v3	Gene	Chr6	19962225	19966288	gbptf1	gbp1	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1814	gbptf10	GeBP-transcription factor 10	GRMZM2G008558	B73 RefGen_v3	Gene	Chr6	109773723	109788339	gbptf10	gbp10	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
1815	gbptf11	GeBP-transcription factor 11	GRMZM2G006871	B73 RefGen_v3	Gene	Chr10	94066876	94068249	gbptf11	gbp11	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1816	gbptf12	GeBP-transcription factor 12	GRMZM2G082318	B73 RefGen_v3	Gene	Chr7	168446968	168448568	gbptf12	gbp12	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1817	gbptf13	GeBP-transcription factor 13	GRMZM2G155252	B73 RefGen_v3	Gene	Chr6	21463521	21465358	gbptf13	gbp13	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1818	gbptf14	GeBP-transcription factor 14	GRMZM2G125239	B73 RefGen_v3	Gene	Chr4	221138448	221144193	gbptf14	gbp14	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1819	gbptf15	GeBP-transcription factor 15	GRMZM2G036966	B73 RefGen_v3	Gene	Chr6	18918022	18924439	gbptf15	gbp15	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1820	gbptf16	GeBP-transcription factor 16	GRMZM2G174240	B73 RefGen_v3	Gene	Chr5	210638738	210640244	gbptf16	gbp16	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1821	gbptf17	GeBP-transcription factor 17	GRMZM2G083886	B73 RefGen_v3	Gene	Chr5	210800522	210802083	gbptf17	gbp17	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1822	gbptf18	GeBP-transcription factor 18	GRMZM2G026417	B73 RefGen_v3	Gene	Chr1	64021150	64022771	gbptf18	gbp18	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1823	gbptf19	GeBP-transcription factor 19	GRMZM5G868875	B73 RefGen_v3	Gene	Chr5	5211419	5213711	gbptf19	gbp19	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1824	gbptf2	GeBP-transcription factor 2	GRMZM2G065506	B73 RefGen_v3	Gene	Chr5	131400636	131401747	gbptf2	gbp2	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1825	gbptf20	GeBP-transcription factor 20	GRMZM2G423292	B73 RefGen_v3	Gene	Chr4	55782767	55784875	gbptf20	gbp20	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1826	gbptf21	GeBP-transcription factor 21	EF517601.1_FG010	B73 RefGen_v3	Gene	Chr3	34497929	34499128	gbptf21	gbp21	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1827	gbptf3	GeBP-transcription factor 3	GRMZM2G041818	B73 RefGen_v3	Gene	Chr1	267056816	267058352	gbptf3	gbp3	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1828	gbptf4	GeBP-transcription factor 4	GRMZM2G066373	B73 RefGen_v3	Gene	Chr9	8465318	8474373	gbptf4	gbp4	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1829	gbptf5	GeBP-transcription factor 5	GRMZM2G162405	B73 RefGen_v3	Gene	Chr5	11602126	11603804	gbptf5	gbp5	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1830	gbptf6	GeBP-transcription factor 6	GRMZM2G075122	B73 RefGen_v3	Gene	Chr2	213839868	213841452	gbptf6	gbp6	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1831	gbptf7	GeBP-transcription factor 7	GRMZM2G092409	B73 RefGen_v3	Gene	Chr7	124438515	124440381	gbptf7	gbp7	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1832	gbptf8	GeBP-transcription factor 8	GRMZM2G134866	B73 RefGen_v3	Gene	Chr2	186232100	186234162	gbptf8	gbp8	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1833	gbptf9	GeBP-transcription factor 9	GRMZM2G030458	B73 RefGen_v3	Gene	Chr9	127611740	127613300	gbptf9	gbp9	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1834	gbss1b	granule-bound starch synthase1b	GRMZM2G008263	B73 RefGen_v3	Gene	Chr7	34885173	34892432	gbss1b	gbss1b, gnp_QCG14d01a, gpm864a, granule-bound starch synthase1b, Granule bound starch synthase IIa	
1835	gcs1	generative cell specific1	GRMZM2G412911	B73 RefGen_v3	Gene	Chr2	221734091	221744424	gcs1	gcs1, hap2, Protein HAPLESS 2, rs129235413	
1836	gcsh1	glycine cleavage system protein H1	GRMZM2G399183	B73 RefGen_v3	Gene	Chr10	15804790	15806176	gcsh1	csu681, gcsh1, glycine cleavage system protein H1	single copy leaf cDNA, csu681
1837	gdcp1	glycine decarboxylase1	GRMZM2G104310	B73 RefGen_v3	Gene	Chr10	5874253	5880613	gdcp1	csu825, gdcp1, glycine cleavage complex P-protein, glycine decarboxylase1, pic7C, umc1576, umc1576(gdcp1)	cDNA sequences, SSR umc1526
1838	gdh1	glutamic dehydrogenase1	GRMZM2G178415	B73 RefGen_v3	Gene	Chr1	287360596	287367735	gdh1	gdh1, gdh*-D49475, gdh*-U93560, gdh*-U93561, glutamic dehydrogenase1, PCO074386	electrophoretic mobility; null allele is known (cold sensitivity); intra/interlocus hybrid bands occur - merge with GenBank sequences inferred by overgo map location matches
1839	gdh2	glutamic dehydrogenase2	GRMZM2G427097	B73 RefGen_v3	Gene	Chr10	134077909	134082362	gdh2	gdh2, glutamate dehydrogenase2, glutamic dehydrogenase2	electrophoretic mobility; intralocus hybrid bands occur
1840	geb1	glucan endo-1,3-beta-glucosidase homol	GRMZM2G065585	B73 RefGen_v3	Gene	Chr3	152010337	152011716	geb1	CL1243_1a, E13_, geb1, geb*-CHEM9, glu*, glucan endo-1,3-beta-glucosidase homolog1, PRm 6b, PRM6b, uiu8, uiu8(geb), uiu8(geb1)	cDNA sequence homologous to 1,3-beta glucanase, possibly single copy
1841	geb7	glucan endo-1,3-beta-glucosidase7	GRMZM2G046101	B73 RefGen_v3	Gene	Chr1	258105155	258107917	geb7	geb7, glucan endo-1,3-beta-glucosidase 7 , rs131881860 , umc129, umc129(geb)	
1842	gfa1	glucosamine fructose-6-phosphate amino	GRMZM2G005849	B73 RefGen_v3	Gene	Chr3	230088470	230094105	gfa1	gfa1, glucosamine fructose-6-phosphate aminotransferase1, uaz309, uaz309(gfu)	endosperm cDNA 5C01G05 (uaz309) similar to rate limiting enzyme of hexosamine synthesis
1843	ggh1	geranylgeranyl hydrogenase1	GRMZM2G105644	B73 RefGen_v3	Gene	Chr5	206940311	206942851	ggh1	ggh1	
1844	ggh2	geranylgeranyl hydrogenase2	GRMZM2G419111	B73 RefGen_v3	Gene	Chr3	40062815	40065077	ggh2	ggh2	
1845	ggps1	geranylgeranyl pyrophosphate synthase1	AC194970.5_FG001	B73 RefGen_v3	Gene	Chr2	207900564	207901904	ggps1	ggdps1, GGPPS1, ggps1	part of multigene family encoding geranylgeranyl diphosphate synthase
1846	ggps2	geranylgeranyl pyrophosphate synthase2	GRMZM2G102550	B73 RefGen_v3	Gene	Chr7	160571102	160573151	ggps2	ggdps2, GGPPS2, ggps2	part of multigene family encoding geranylgeranyl diphosphate synthase
1847	ggps3	geranylgeranyl pyrophosphate synthase3	GRMZM2G058404	B73 RefGen_v3	Gene	Chr8	6359238	6360557	ggps3	ggdps3, GGPPS3, ggps3	part of multigene family encoding geranylgeranyl diphosphate synthase
1848	ggps4	geranylgeranyl pyrophosphate synthase4	GRMZM2G005909	B73 RefGen_v3	Gene	Chr5	193709210	193710641	ggps4	ggdps4, GGPPS4, ggps4	part of multigene family encoding geranylgeranyl diphosphate synthase
1849	gi1	gigantea1	GRMZM2G107101	B73 RefGen_v3	Gene	Chr8	21104080	21112365	gi1	gi1, gigantea like1A, gigz1A	homologous to Arabidopsis photoperiod gene gigantea
1850	gi2	gigantea2	GRMZM5G844173	B73 RefGen_v3	Gene	Chr3	9306265	9317285	gi2	gi2, gigantea like1B, gigz1B	homologous to Arabidopsis photoperiod gene gigantea.
1851	gif1	growth-regulating-factor-interacting facto	GRMZM2G180246	B73 RefGen_v3	Gene	Chr1	273393236	273396891	gif1	agustifolia3/GRF-interactingfactor1, agustifolia3/growth-regulating-factor-interactingfactor1, an3, an3/gif1, AY104234, gif1, gif2, PCO127974	
1852	gif2	growth-regulating-factor-intecting factor	GRMZM2G154169	B73 RefGen_v3	Gene	Chr4	5380348	5385430	gif2	gif2	
1853	gif3	growth-regulating-factor-intecting factor	Zm00001d023767	Zm-B73-REFERENCE-G	Gene	Chr10	19457326	19463711	gif3	gif3, pco074690, TIDP3215	
1854	gl1	glossy1	GRMZM2G114642	B73 RefGen_v3	Gene	Chr7	118550916	118556690	gl1	gl1, glossy1	cuticle wax altered; leaf surface bright, water adheres
1855	gl13	glossy13	GRMZM2G118243	B73 RefGen_v3	Gene	Chr3	10276457	10286585	gl13	gl13, gl19, glossy13	necrotic glossy leaf; plants that survive to maturity are sterile (both male and female) and smaller than nonmutant sibs.
1856	gl15	glossy15	GRMZM2G160730	B73 RefGen_v3	Gene	Chr9	96744684	96748035	gl15	gl15, gl4, Glossy10, glossy15, nc134, third leaf glossy, umc1688, umc1691, ZmEREB55	glossy leaf surface expressed after 3rd leaf (aka gl4)
1857	gl2	glossy2	GRMZM2G098239	B73 RefGen_v3	Gene	Chr2	10630672	10633711	gl2	CL2305_1, cl2305_1(115), gl2, gl*-N239, gl*-N718, glossy2	like gl1, but surface wax is all rice-grain-type particles
1858	gl3	glossy3	GRMZM2G162434	B73 RefGen_v3	Gene	Chr4	185828677	185830259	gl3	gl3, gl56:312-27, glossy3, myb-related protein 306, ZmMYB97	like gl1, but surface wax has all rice-grain-type particles
1859	gl8	glossy8	AC205703.4_FG006	B73 RefGen_v3	Gene	Chr5	181248005	181251026	gl8	gl10, gl*-166A, gl8, gl8a, gl*-N166A, glossy8, gnp_QAG5e04_PCR, gpm338	(was gl10) like gl1; cuticle wax in rice-grain-type particles; cDNA probe
1860	gl8b	3-ketoacyl reductase GL8B	GRMZM2G087323	B73 RefGen_v3	Gene	Chr4	132787074	132790535	gl8b	3-ketoacyl reductase GL8B, gl8b, IDP12, siu89509, very-long-chain 3-oxoacyl-CoA reductase 1-like	encodes fatty acid elongase, paralogous to gl8, maps in syntenous region, expression distinct but similar, double mutant embryos are non-viable
1861	gla3	beta-glucanase3	GRMZM2G473711	B73 RefGen_v3	Gene	Chr5	7263570	7266166	gla3	CL6987_1, gla3	
1862	glb1	globulin1	GRMZM2G067919	B73 RefGen_v3	Gene	Chr1	258423143	258426448	glb1	glb1, globulin1, mzeglb10, phi011, phi011(glb1), phi055, phi094, Pro, prot1, Prot1, umc184a(glb1)	was prot1; electrophoretic mobility, null allele is known; embryo protein; SSRs phi011, 055, 094
1863	glb2	globulin2	GRMZM2G026703	B73 RefGen_v3	Gene	Chr1	287133859	287135934	glb2	glb2, globulin-1 S allele, globulin2, PCO081708, PCO081708(96), PHM2306, rs131175366, rs131175367, ss196414853, ss196414856	presence-absence

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
1864	glb3	globulin3	GRMZM2G410134	B73 RefGen_v3	Gene	Chr6	156729182	156730333	glb3	18-kD alpha globulin, ag, glb3, PCO101751	18-kD alpha globulin
1865	glct1	glucose translocator1	GRMZM2G153704	B73 RefGen_v3	Gene	Chr8	12789263	12803873	glct1	CL1214_1b, glct1, glct1 (cp), glucose translocator1, IDP2416, pGlcT	
1866	gldh1	galactono lactone dehydrogenase1	GRMZM2G469969	B73 RefGen_v3	Gene	Chr2	146649171	146653569	gldh1	cl277_1, gldh1, gldh1(152)	ascorbate biosynthesis, based on orthology to the Arabidopsis gene vtc2.
1867	glk1	G2-like1	GRMZM2G026833	B73 RefGen_v3	Gene	Chr9	2711604	2714038	glk1	G2-like1, glk1, ZmGLK57	g2 golden2 paralog; specifically affects mesophyll chloroplast assembly, but not bundle sheath chloroplast assembly (Wang et al 2013)
1868	glk10	G2-like-transcription factor 10	GRMZM2G083472	B73 RefGen_v3	Gene	Chr5	58165088	58167724	glk10		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1869	glk101	G2-like-transcription factor 1	GRMZM2G064197	B73 RefGen_v3	Gene	Chr7	83167441	83173051	glk101	G2-like-transcription factor 1, glk1, glk101	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1870	glk11	G2-like-transcription factor 11	AC233960.1_FG003	B73 RefGen_v3	Gene	Chr5	200029375	200031847	glk11		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1871	glk12	G2-like-transcription factor 12	GRMZM2G401835	B73 RefGen_v3	Gene	Chr6	98583806	98586467	glk12		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1872	glk14	G2-like-transcription factor 14	GRMZM2G348238	B73 RefGen_v3	Gene	Chr3	10524574	10526809	glk14		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1873	glk15	G2-like-transcription factor 15	GRMZM2G162409	B73 RefGen_v3	Gene	Chr7	39518700	39524889	glk15		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1874	glk16	G2-like-transcription factor 16	GRMZM2G035370	B73 RefGen_v3	Gene	Chr2	3109831	3112898	glk16		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1875	glk17	G2-like-transcription factor 17	GRMZM2G006477	B73 RefGen_v3	Gene	Chr1	54344216	54350977	glk17		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1876	glk18	G2-like-transcription factor 18	GRMZM2G010920	B73 RefGen_v3	Gene	Chr5	77781452	77784526	glk18		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1877	glk19	G2-like-transcription factor 19	GRMZM2G396825	B73 RefGen_v3	Gene	Chr3	55169832	55172779	glk19		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1878	glk2	G2-like-transcription factor 2	GRMZM2G333083	B73 RefGen_v3	Gene	Chr9	61962138	61964866	glk2		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1879	glk20	G2-like-transcription factor 20	GRMZM2G106185	B73 RefGen_v3	Gene	Chr5	194303751	194306883	glk20		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1880	glk22	G2-like-transcription factor 22	GRMZM2G315506	B73 RefGen_v3	Gene	Chr4	31335510	31339291	glk22	bngl490, bnlg490, glk22, rs131444279	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.. NCBI: Putative MYB DNA-binding domain superfamily protein
1881	glk23	G2-like-transcription factor 23	GRMZM2G039074	B73 RefGen_v3	Gene	Chr1	254304178	254313183	glk23		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1882	glk24	G2-like-transcription factor 24	GRMZM2G060485	B73 RefGen_v3	Gene	Chr5	93274325	93277370	glk24	response regulator9, ZmRR9	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1883	glk25	G2-like-transcription factor 25	AC234155.1_FG002	B73 RefGen_v3	Gene	Chr8	119108477	119111419	glk25		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1884	glk26	G2-like-transcription factor 26	GRMZM2G009060	B73 RefGen_v3	Gene	Chr1	52392455	52394837	glk26		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1885	glk27	G2-like-transcription factor 27	GRMZM2G173882	B73 RefGen_v3	Gene	Chr2	237012379	237014288	glk27		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1886	glk28	G2-like-transcription factor 28	GRMZM2G100176	B73 RefGen_v3	Gene	Chr7	2630972	2634436	glk28		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1887	glk29	G2-like-transcription factor 29	GRMZM2G070865	B73 RefGen_v3	Gene	Chr4	158095257	158100338	glk29		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1888	glk3	G2-like-transcription factor 3	GRMZM2G471600	B73 RefGen_v3	Gene	Chr8	104345279	104346616	glk3		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1889	glk30	G2-like-transcription factor 30	GRMZM2G374986	B73 RefGen_v3	Gene	Chr9	153719210	153723103	glk30		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1890	glk31	G2-like-transcription factor 31	GRMZM2G100709	B73 RefGen_v3	Gene	Chr6	93393018	93401220	glk31		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1891	glk32	G2-like-transcription factor 32	GRMZM2G454449	B73 RefGen_v3	Gene	Chr9	111271909	111274197	glk32		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1892	glk33	G2-like-transcription factor 33	AC219020.4_FG002	B73 RefGen_v3	Gene	Chr6	105920220	105922516	glk33		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1893	glk34	G2-like-transcription factor 34	GRMZM2G081671	B73 RefGen_v3	Gene	Chr9	109631596	109634230	glk34		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1894	glk35	G2-like-transcription factor 35	GRMZM5G846506	B73 RefGen_v3	Gene	Chr2	153730130	153732080	glk35		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1895	glk36	G2-like-transcription factor 36	GRMZM2G125704	B73 RefGen_v3	Gene	Chr2	12354844	12357846	glk36		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1896	glk37	G2-like-transcription factor 37	GRMZM2G069525	B73 RefGen_v3	Gene	Chr2	17494663	17498413	glk37		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1897	glk38	G2-like-transcription factor 38	GRMZM2G113742	B73 RefGen_v3	Gene	Chr1	221627183	221637379	glk38		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1898	glk39	G2-like-transcription factor 39	GRMZM2G477238	B73 RefGen_v3	Gene	Chr5	145144168	145146397	glk39		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1899	glk4	G2-like-transcription factor 4	GRMZM2G159119	B73 RefGen_v3	Gene	Chr10	5125137	5127242	glk4		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1900	glk41	G2-like-transcription factor 41	GRMZM2G090230	B73 RefGen_v3	Gene	Chr10	137379294	137383113	glk41		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1901	glk42	G2-like-transcription factor 42	GRMZM2G370425	B73 RefGen_v3	Gene	Chr3	114449322	114452475	glk42		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1902	glk43	G2-like-transcription factor 43	GRMZM2G701218	B73 RefGen_v3	Gene	Chr6	155372479	155375684	glk43		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1903	glk44	G2-like-transcription factor 44	GRMZM2G124540	B73 RefGen_v3	Gene	Chr1	280284828	280286869	glk44		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1904	glk45	G2-like-transcription factor 45	GRMZM2G379656	B73 RefGen_v3	Gene	Chr1	234479845	234481852	glk45		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1905	glk47	G2-like-transcription factor 47	GRMZM2G060834	B73 RefGen_v3	Gene	Chr5	199338568	199343584	glk47		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1906	glk48	G2-like-transcription factor 48	GRMZM5G887276	B73 RefGen_v3	Gene	Chr1	6525346	6530541	glk48		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1907	glk49	G2-like-transcription factor 49	GRMZM2G168002	B73 RefGen_v3	Gene	Chr4	83222890	83225112	glk49		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1908	glk5	G2-like-transcription factor 5	GRMZM2G016370	B73 RefGen_v3	Gene	Chr10	5388541	5390606	glk5		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1909	glk50	G2-like-transcription factor50	GRMZM2G034563	B73 RefGen_v3	Gene	Chr1	165151519	165153474	glk50	glk50, rs131812041, umc1321	
1910	glk50	G2-like-transcription factor 50	GRMZM2G034563	B73 RefGen_v3	Gene	Chr1	165151519	165153474	glk50		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1911	glk51	G2-like-transcription factor 51	GRMZM2G398055	B73 RefGen_v3	Gene	Chr6	147216522	147218561	glk51		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1912	glk52	G2-like-transcription factor 52	GRMZM2G124495	B73 RefGen_v3	Gene	Chr10	146575608	146578425	glk52		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
1913	glk53	G2-like-transcription factor 53	GRMZM2G052544	B73 RefGen_v3	Gene	Chr5	86297888	86301099	glk53		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1914	glk54	G2-like-transcription factor 54	GRMZM2G074908	B73 RefGen_v3	Gene	Chr3	180310733	180312482	glk54		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1915	glk55	G2-like-transcription factor 55	GRMZM2G123308	B73 RefGen_v3	Gene	Chr10	77348006	77352823	glk55		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1916	glk56	G2-like-transcription factor 56	GRMZM2G067702	B73 RefGen_v3	Gene	Chr8	156260024	156261399	glk56		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1917	glk58	G2-like-transcription factor 58	GRMZM2G117854	B73 RefGen_v3	Gene	Chr6	155715032	155718706	glk58		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1918	glk59	G2-like-transcription factor 59	AC155434.2_FG005	B73 RefGen_v3	Gene	Chr7	173860841	173863018	glk59		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1919	glk6	G2-like-transcription factor 6	GRMZM2G117193	B73 RefGen_v3	Gene	Chr1	213277645	213280082	glk6	glk6, IDP8564, rs131185245, rs131847840 , umc23a	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1920	glk7	G2-like-transcription factor 7	GRMZM2G173943	B73 RefGen_v3	Gene	Chr7	83291537	83295947	glk7		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1921	glk8	G2-like-transcription factor 8	GRMZM2G171468	B73 RefGen_v3	Gene	Chr5	6146192	6148391	glk8		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1922	glk9	G2-like-transcription factor 9	AC234520.1_FG003	B73 RefGen_v3	Gene	Chr1	164385468	164386298	glk9		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1923	gln1	glutamine synthetase1	GRMZM2G098290	B73 RefGen_v3	Gene	Chr10	145900776	145906241	gln1	bnlGS6.15(gln1), Gln-, gln1, gln7, gln8, glutamine synthetase1, gnp_QCC13a07a, gpm846a, GS2, GS202, MS5	chloroplast, gene specific cDNA probe, GS2 isoform; 6-member nuclear gene family
1924	gln2	glutamine synthetase2	GRMZM2G024104	B73 RefGen_v3	Gene	Chr1	267960169	267963551	gln2	Gln-, gln2, glutamine synthetase2, GS1-2, GS1931	family; contary to preceding notes, Rastogi et. al., 1998 Plant Cell Phyol. 39:443-446, observed gln2 trancripts primarily in the pedicels but at undetectable levels in roots (TM).
1925	gln3	glutamine synthetase3	GRMZM2G046601	B73 RefGen_v3	Gene	Chr9	146319631	146327940	gln3	CL1911_3b, Gln-, gln3, gln6, glutamine synthetase3, glutamine synthetase root isozyme 5, GS117, GS1-5, GS1752	cytosolic GS1-5 isoform, a major species in root; gene specific cDNA probe, 6-member nuclear gene family
1926	gln3	glutamine synthetase3	GRMZM2G050514	B73 RefGen_v3	Gene	Chr1	27978351	27982007	gln3	CL1911_3b, Gln-, gln3, gln6, glutamine synthetase3, glutamine synthetase root isozyme 5, GS117, GS1-5, GS1752	cytosolic GS1-5 isoform, a major species in root; gene specific cDNA probe, 6-member nuclear gene family
1927	gln4	glutamine synthetase4	GRMZM5G872068	B73 RefGen_v3	Gene	Chr5	205293914	205297428	gln4	Gln-, gln4, glutamine synthetase4, GS112, GS1-3, GS15-35, phi085	cytosolic GS1-3 isoform, major species in both root and leaf, gene specific cDNA probes, 6-member nuclear gene family; SSR phi085
1928	gln5	glutamine synthetase5	GRMZM2G036464	B73 RefGen_v3	Gene	Chr4	167111248	167114579	gln5	Gln-, gln5, glutamine synthetase5, GS107, GS1-4, GS691	cytosolic GS1-4 isoform, major species in both leaf and root, gene specific cDNA probe, 6-member nuclear gene family
1929	gln6	glutamine synthetase6	GRMZM2G050514	B73 RefGen_v3	Gene	Chr1	27978351	27982007	gln6	CL1911_3a, DP1, gln6, glutamine synthetase6, gnp_gsy289a, GS1-1, GS122, gsy289a, gsy290	cytosolic GS1-1 isoform, gene specific cDNA probe, 6-member nuclear gene family
1930	glp1	germin-like protein1	GRMZM2G064096	B73 RefGen_v3	Gene	Chr6	123959994	123961169	glp1	csu835, csuh00835, csuh835, germin-like protein1, glp1, Zmglp1	
1931	glu1	beta glucosidase1	GRMZM2G016890	B73 RefGen_v3	Gene	Chr10	34240659	34246077	glu1	beta glucosidase1, CL539_1c, glu1, gnp_QAE18h05, gpm278, gsy316(glu), non-cyanogenic beta-glucosidase, uaz178	electrophoretic mobility; plastidic; dimeric; intralocus hybrid bands occur
1932	glu2	beta-glucosidase2	GRMZM2G008247	B73 RefGen_v3	Gene	Chr10	37762909	37767713	glu2	beta-glucosidase2, CL539_1b, glu2, p60, umr1, Zm-p60.1	cDNA produces higher activity in transgenic tobacco; shares 20 amino acids with an N-terminal sequence reported for membrane-bound beta-glucosidase
1933	glu3	beta-glucosidase3	GRMZM2G014844	B73 RefGen_v3	Gene	Chr10	34733949	34737952	glu3	beta-glucosidase3, glu3, non-cyanogenic beta-glucosidase	
1934	glx1	glyoxylase1	GRMZM2G181192	B73 RefGen_v3	Gene	Chr10	60090336	60096837	glx1	glx1, GLX-I, glyoxylase1, pco099929	
1935	gly1	glycine1	GRMZM2G078143	B73 RefGen_v3	Gene	Chr4	20795669	20799891	gly1	gly1, glycine1, serine hydroxymethyltransferase , uaz7c04a02(gfu)	leaf cDNA 7C04A02 similar to a fungal and E. coli enzyme used in glycine metabolism
1936	gn1	gnarley1	GRMZM2G452178	B73 RefGen_v3	Gene	Chr2	237298075	237304344	gn1	gn1, gnarley1, homeobox protein rough sheath 1, knox4, pge16a(knox4), ZmHB61	dominant Gn1 characterized by reduced internodal length, sinuously curving culm, lack of distinct boundary between blade and sheath, extra silks
1937	go1	glycolate oxidase1	GRMZM2G129246	B73 RefGen_v3	Gene	Chr7	5528435	5532236	go1	PCO065133	seedling lethal necrotic unless supplied high CO2; photorespiration.
1938	gol1	goliath1	GRMZM2G080079	B73 RefGen_v3	Gene	Chr4	182134219	182136764	gol1	csu216, csu216(gfu), gol1, goliath1, goliath homolog1, PCO086747(334), PCO086747b	leaf cDNA csu216 single copy, similar to Drosophila Goliath protein
1939	gols1	galactinol synthase1	GRMZM2G165919	B73 RefGen_v3	Gene	Chr1	51531588	51533796	gols1	csu924(wsi), csu935, galactinol synthase1, galactinol synthase 3	Similar to water stress-induced protein of rice (per Baysdorfer, C.)
1940	gols3	galactinol synthase3	GRMZM5G872256	B73 RefGen_v3	Gene	Chr9	134152466	134154240	gols3	galactinol synthase3, gols2, gols3, PCO107484, PCO107484(694)	Expessed late in seed development
1941	gos1	GOS2 homolog	GRMZM2G113414	B73 RefGen_v3	Gene	Chr3	189403504	189406550	gos1	gos1, GOS2 homolog, PCO112988, PCO112988(260), protein translation factor SUI1, uaz5c09h04(gfu)	endosperm cDNA 5C09H04, similar to rice GOS2 protein
1942	got1	glutamate-oxaloacetate transaminase1	GRMZM2G094712	B73 RefGen_v3	Gene	Chr3	195377312	195383470	got1	transaminase1, got1, pco118382(264), pza03255, rs128283716, rs131175547, ss196415585, ss196415587	electrophoretic mobility; null allele is known; glyoxysomal; dimeric; intralocus hybrid bands occur
1943	got2	glutamate-oxaloacetate transaminase2	GRMZM5G836910	B73 RefGen_v3	Gene	Chr5	213953336	213958271	got2	aspartate aminotransferase, glutamate-oxaloacetate transaminase2, gnp_QCO25e08, got2, gpm724, PCO107699	C4-photosynthesis enzyme; electrophoretic mobility; null allele is known; plastidial; dimeric; intralocus hybrid bands occur
1944	got3	glutamate-oxaloacetic transaminase3	GRMZM2G146677	B73 RefGen_v3	Gene	Chr5	146880878	146886034	got3	149012758-768, PUT-163a-149012758-769, PZE-105099104 1, PZE-105099105, rs131176378 , rs132229835, rs132229836, rs132229839, ss196418470, ss196466214	electrophoretic mobility; null allele is known; mitochondrial; dimeric; intralocus hybrid bands occur
1945	got4	glutamate-oxaloacetate transaminase4	GRMZM2G400604	B73 RefGen_v3	Gene	Chr3	174411027	174414395	got4	AspT, glutamate-oxaloacetate transaminase4, got4, PZE-103114700 1, PZE-103114703, rs129366904, rs132060983, ss196448890, TIDP5760	putative aspartate aminotransferase; cytosolic (PPDB prediction; Sun et al 2009)
1946	got5	glutamate-oxaloacetate transaminase5	GRMZM2G033799	B73 RefGen_v3	Gene	Chr8	100920138	100924873	got5	aspartate transaminase5, got5, IDP6942, PCO075539, PCO075539(610), PZE-108056460 1, rs130826224, ss196485451	putative aspartate transaminase; plastidial (Huang et al 2013);
1947	gpa1	glyceraldehyde-3-phosphate dehydrogen	GRMZM2G337113	B73 RefGen_v3	Gene	Chr2	42886006	42888042	gpa1	csu140, csu610, G3PD, GapA1, glyceraldehyde-3-phosphate dehydrogenase1, gpa1, gpa*-csu140, umc188(gpa1), umc375	(correction from previous maps); two pseudogenes have been identified, and leaf cDNA csu140 hybridizes to 2 other bands
1948	gpat1	glycerol-3-phosphate acyltransferas	GRMZM2G083195	B73 RefGen_v3	Gene	Chr3	178232720	178236298	gpat1	AY105347, gpat1, IDP226, IDP569, PCO089398, umc2266	
1949	gpb1	glyceraldehyde phosphate dehydrogenas	GRMZM5G845611	B73 RefGen_v3	Gene	Chr1	6404117	6406779	gpb1	csu152, csuM95076(gfu), GapB1, glyceraldehyde-3-phosphate dehydrogenase B , glyceraldehyde phosphate dehydrogenase B1, gpb1, PCO123560, umc1282, umc1282a	leaf cDNA csu152 similar to Arabidopsis GapB
1950	gpc1	glyceraldehyde-3-phosphate dehydrogen	GRMZM2G046804	B73 RefGen_v3	Gene	Chr4	36912994	36917779	gpc1	phi026, phi026(gpc1), phi079, phi079(gpc1), rz143b, rz143b(gpc), umc1088, umc1191, umc191(gpc1)	cytosolic, C subunit, type 3 gene; coding region has sequence homology to gpc2, unique 3' untranslated region, constitutive expression; SSRs phi026, 079
1951	gpc2	glyceraldehyde-3-phosphate dehydrogen	GRMZM2G180625	B73 RefGen_v3	Gene	Chr6	6901483	6906034	gpc2	CL2022_2, GapC2, GAPC2, glyceraldehyde-3-phosphate dehydrogenase2, gpc2, IDP2526, rz143a, rz143a(gpc), rz143(gpc), umc1018, umc203(gpc2)	cytosolic, C subunit; coding region has homology to gpc1, unique 3' untranslated region; constitutive expression; genomic and cDNA clones, SSR umc1018
1952	gpc3	glyceraldehyde-3-phosphate dehydrogen	GRMZM2G071630	B73 RefGen_v3	Gene	Chr4	133130993	133134382	gpc3	CL2022_1b, GapC3, glyceraldehyde-3-phosphate dehydrogenase3, gpc3, mzaGPA1, umc211a	cytosolic, C subunit 3; coding sequence homology to gpc4, unique 3' untranslated region
1953	gpc4	glyceraldehyde-3-phosphate dehydrogen	GRMZM2G176307	B73 RefGen_v3	Gene	Chr5	181570933	181575725	gpc4	cl2022_1(433), CL2022_1d, GAPC2, GapC4, GAPC4, glyceraldehyde-3-phosphate dehydrogenase4, gnp_QAF9e03, gpc4, gpc*-X73151, gpm333, TIDP3317, umc211b	C subunit, electrophoretic mobility, coding sequence homology to gpc3, unique 3' untranslated region
1954	gpdh1	glucose-6-phosphate dehydrogenase1	GRMZM2G130230	B73 RefGen_v3	Gene	Chr2	37085168	37093582	gpdh1	csu350(gfu), csu350(gpdh), glucose-6-phosphate 1-dehydrogenase, cytoplasmic isoform, glucose-6-phosphate dehydrogenase1, gpdh1, PCO098806	leaf cDNA csu350, 5' sequence similar to plant glucose-6-phosphate dehydrogenase
1955	gpm125		GRMZM2G430998	B73 RefGen_v3	Probed Site	Chr2	229229497	229231927	gpm125	cl38236_1(6), CL38236_1a, gnp_AI979732, PZA00566, rs128285204, ss196417508	
1956	gpm367a		GRMZM2G146514	B73 RefGen_v3	Probed Site	Chr4	20203138	20224156	gpm367a	gnp_QAN15h04a, PCO089407, PCO089407(294), PZA00139, rs131175576, ss196415698	
1957	gpm4		GRMZM2G094742	B73 RefGen_v3	Gene	Chr1	177072656	177077812	gpm4	CL6272_1, gnp_AW455663, gpm4, IDP26, IDP814	cDNA std707087E05 mapped by RFLP and by overgo to the same anchored BAC contig
1958	gpm405		GRMZM2G320325	B73 RefGen_v3	Probed Site	Chr1	55071447	55076253	gpm405	CL1013_1, CL1013_1(23), gnp_QAU3h02, PZA02550, rs131175283, ss196414511	
1959	gpm46		GRMZM2G174738	B73 RefGen_v3	Gene	Chr9	85075052	85078713	gpm46	BT1-2, gnp_AI665712, gpm46, PCO149530, PCO149530(669)	ubiquitous expression; putative adenylate translocase
1960	gpm465		GRMZM2G089982	B73 RefGen_v3	Probed Site	Chr3	40528986	40531530	gpm465	gnp_QBH11c09, PCO084450, PZA01114, rs128282844, rs128282845, rs55626169 , ss196415362, ss196415364	
1961	gpm6		GRMZM2G119411	B73 RefGen_v3	Gene	Chr9	25726920	25741443	gpm6	gnp_AI612204, gpm6, PZA02648, rs130983607, rs55626296 , ss196417146	

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
1962	gpm693		GRMZM2G385543	B73 RefGen_v3	Probed Site	Chr5	9129443	9131483	gpm693	CL13916_1, CL13916_1(378), gnp_QCL6d12, gpm693	
1963	gpm7		GRMZM2G031981	B73 RefGen_v3	Gene	Chr2	13838928	13861148	gpm7	gnp_AW330742, gpm7, PZA00108, rs128281577, rs55623523 , ss196414997	
1964	gpm707		GRMZM2G024657	B73 RefGen_v3	Probed Site	Chr5	3535893	3539529	gpm707	gnp_QCN27e10, PCO122572, PCO122572(458), PHM3096, PZA01570, rs129978429, rs55624065 , ss196415973	
1965	gpm734		GRMZM2G067080	B73 RefGen_v3	Probed Site	Chr8	83586988	83591490	gpm734	gnp_QCO3h10, PCO086041, PCO086041(600), PHM1534, PZA01297, rs128281630, rs55623587 , ss196416866	
1966	gpm803b		GRMZM2G166035	B73 RefGen_v3	Probed Site	Chr4	238052005	238055564	gpm803b	gnp_QAU2f03b, PCO116866, ZmOrphan136	
1967	gpm863		GRMZM2G017351	B73 RefGen_v3	Probed Site	Chr2	210584713	210592622	gpm863	gnp_QCG11e02, PCO139236, PCO139236(183), PZA00390, rs128282331, rs55623257 , ss196415263	
1968	gpm874b		GRMZM2G070045	B73 RefGen_v3	Probed Site	Chr5	207758143	207780399	gpm874b	CL20409_1, CL20409_1(449), gnp_QCH31c03b, PZA00545, rs131175729, ss196416283	
1969	gpn1	glyceraldehyde-3-phosphate deHaseN1	GRMZM2G035268	B73 RefGen_v3	Gene	Chr4	84132782	84137970	gpn1	gapn1, GapN1, glyceraldehyde-3-phosphate deHaseN1, gpn1	cDNA sequence
1970	gpt1	glucose 6-phosphate/phosphate transloc	GRMZM2G180720	B73 RefGen_v3	Gene	Chr10	58309702	58313911	gpt1	glucose 6-phosphate/phosphate translocator1, gpt1, pco073572(727), PCO073572b	
1971	gras1	GRAS-transcription factor 1	GRMZM2G098784	B73 RefGen_v3	Gene	Chr9	140092351	140096097	gras1		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1972	gras10	GRAS-transcription factor 10	GRMZM2G110579	B73 RefGen_v3	Gene	Chr5	192899281	192902025	gras10		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1973	gras11	GRAS-transcription factor 11	GRMZM2G097456	B73 RefGen_v3	Gene	Chr7	162247332	162249303	gras11		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1974	gras12	GRAS-transcription factor 12	GRMZM5G826526	B73 RefGen_v3	Gene	Chr3	214641511	214642665	gras12		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1975	gras13	GRAS-transcription factor 13	GRMZM2G140094	B73 RefGen_v3	Gene	Chr4	187219736	187222248	gras13		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1976	gras14	GRAS-transcription factor 14	GRMZM2G070371	B73 RefGen_v3	Gene	Chr2	231610740	231612552	gras14		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1977	gras15	GRAS-transcription factor 15	GRMZM5G874545	B73 RefGen_v3	Gene	Chr3	232137122	232158937	gras15		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1978	gras16	GRAS-transcription factor 16	GRMZM2G335814	B73 RefGen_v3	Gene	Chr1	248734599	248737101	gras16		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1979	gras17	GRAS-transcription factor 17	GRMZM2G143433	B73 RefGen_v3	Gene	Chr5	120520869	120522119	gras17		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1980	gras18	GRAS-transcription factor 18	GRMZM2G011947	B73 RefGen_v3	Gene	Chr6	55555919	55556867	gras18		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1981	gras19	GRAS-transcription factor 19	GRMZM2G172657	B73 RefGen_v3	Gene	Chr7	161941687	161944142	gras19		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1982	gras2	GRAS-transcription factor 2	GRMZM2G129154	B73 RefGen_v3	Gene	Chr8	158560400	158562023	gras2		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1983	gras21	GRAS-transcription factor 21	GRMZM2G116638	B73 RefGen_v3	Gene	Chr1	137434183	137440188	gras21		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1984	gras22	GRAS-transcription factor 22	GRMZM2G173429	B73 RefGen_v3	Gene	Chr10	135825173	135827459	gras22		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1985	gras23	GRAS-transcription factor 23	GRMZM2G157679	B73 RefGen_v3	Gene	Chr3	180798590	180801759	gras23		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1986	gras24	GRAS-transcription factor 24	GRMZM2G140085	B73 RefGen_v3	Gene	Chr4	187217605	187218942	gras24		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1987	gras25	GRAS-transcription factor 25	GRMZM2G420280	B73 RefGen_v3	Gene	Chr2	51272702	51274207	gras25		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1988	gras26	GRAS-transcription factor 26	GRMZM5G868355	B73 RefGen_v3	Gene	Chr4	839965	841260	gras26		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1989	gras27	GRAS-transcription factor 27	GRMZM2G110067	B73 RefGen_v3	Gene	Chr1	71030279	71032027	gras27		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1990	gras28	GRAS-transcription factor 28	GRMZM2G342217	B73 RefGen_v3	Gene	Chr4	21604764	21607924	gras28	gras28, npi386, npi386a(eks), npi386(eks), npi386(eks2), umc1067	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.. NCBI: DELLA protein GAI-like
1991	gras29	GRAS-transcription factor 29	AC198366.3_FG004	B73 RefGen_v3	Gene	Chr10	1890881	1892401	gras29		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1992	gras3	GRAS-transcription factor 3	GRMZM2G179325	B73 RefGen_v3	Gene	Chr1	155690714	155694188	gras3		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1993	gras30	GRAS-transcription factor 30	GRMZM2G176537	B73 RefGen_v3	Gene	Chr10	117338432	117340217	gras30		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1994	gras31	GRAS-transcription factor 31	GRMZM5G825321	B73 RefGen_v3	Gene	Chr2	19769962	19772850	gras31		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1995	gras32	GRAS-transcription factor 32	GRMZM2G051785	B73 RefGen_v3	Gene	Chr9	27346189	27348215	gras32		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1996	gras33	GRAS-transcription factor 33	GRMZM2G079470	B73 RefGen_v3	Gene	Chr1	88488422	88491040	gras33		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1997	gras34	GRAS-transcription factor 34	GRMZM2G163427	B73 RefGen_v3	Gene	Chr4	842617	845669	gras34		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1998	gras35	GRAS-transcription factor 35	GRMZM2G386362	B73 RefGen_v3	Gene	Chr2	4624290	4626096	gras35		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
1999	gras36	GRAS-transcription factor 36	GRMZM2G348780	B73 RefGen_v3	Gene	Chr1	161047325	161049647	gras36		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2000	gras37	GRAS-transcription factor 37	GRMZM2G015080	B73 RefGen_v3	Gene	Chr2	150778730	150782551	gras37		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2001	gras38	GRAS-transcription factor 38	GRMZM2G098517	B73 RefGen_v3	Gene	Chr7	161325637	161329188	gras38		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2002	gras39	GRAS-transcription factor 39	GRMZM2G408012	B73 RefGen_v3	Gene	Chr5	181911451	181912595	gras39		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2003	gras4	GRAS-transcription factor 4	GRMZM2G082387	B73 RefGen_v3	Gene	Chr3	150869807	150871966	gras4		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2004	gras40	GRAS-transcription factor 40	GRMZM2G368909	B73 RefGen_v3	Gene	Chr1	293715271	293717691	gras40		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2005	gras41	GRAS-transcription factor 41	GRMZM5G885274	B73 RefGen_v3	Gene	Chr5	205139992	205141687	gras41		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2006	gras42	GRAS-transcription factor 42	AC234164.1_FG004	B73 RefGen_v3	Gene	Chr9	24984785	24987244	gras42		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2007	gras43	GRAS-transcription factor 43	GRMZM5G895672	B73 RefGen_v3	Gene	Chr4	827079	829016	gras43		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2008	gras45	GRAS-transcription factor 45	GRMZM2G028039	B73 RefGen_v3	Gene	Chr9	149430555	149437059	gras45		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2009	gras46	GRAS-transcription factor 46	GRMZM2G001426	B73 RefGen_v3	Gene	Chr3	69955114	69957195	gras46		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2010	gras47	GRAS-transcription factor 47	GRMZM2G089782	B73 RefGen_v3	Gene	Chr3	124035075	124037072	gras47		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
2011	gras48	GRAS-transcription factor 48	GRMZM2G018254	B73 RefGen_v3	Gene	Chr4	513060	515231	gras48		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2012	gras49	GRAS-transcription factor 49	GRMZM5G821439	B73 RefGen_v3	Gene	Chr2	204949825	204954417	gras49		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2013	gras5	GRAS-transcription factor 5	GRMZM2G146018	B73 RefGen_v3	Gene	Chr3	142759880	142761574	gras5		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2014	gras50	GRAS domain family50	GRMZM2G159475	B73 RefGen_v3	Gene	Chr3	125733039	125735799	gras50	CL5760_4, gnp_QBM25b03a, gras50, GRAS domain family50, GRAS-family transcription factor50, ZmGRAS50	
2015	gras51	GRAS-transcription factor 51	GRMZM2G028608	B73 RefGen_v3	Gene	Chr2	46590168	46592051	gras51		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2016	gras52	GRAS-transcription factor 52	GRMZM2G109869	B73 RefGen_v3	Gene	Chr2	15351727	15354059	gras52		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2017	gras53	GRAS-transcription factor 53	GRMZM2G060265	B73 RefGen_v3	Gene	Chr1	1953455	1955531	gras53	rs128358215 , scarecrow-like protein 6, ss196500938	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2018	gras54	GRAS-transcription factor 54	GRMZM2G106548	B73 RefGen_v3	Gene	Chr7	158406894	158408665	gras54		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2019	gras55	GRAS-transcription factor 55	GRMZM2G104342	B73 RefGen_v3	Gene	Chr5	9827131	9829504	gras55		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2020	gras56	GRAS-transcription factor 56	GRMZM2G037286	B73 RefGen_v3	Gene	Chr6	155175171	155176649	gras56		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2021	gras57	GRAS-transcription factor 57	GRMZM2G089662	B73 RefGen_v3	Gene	Chr6	38410832	38413066	gras57		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2022	gras58	GRAS-transcription factor 58	GRMZM2G132794	B73 RefGen_v3	Gene	Chr1	77494290	77496510	gras58	rs128477164 , rs131267169 , short-root1, shr1, shrt1, ZmShr1	family by the GRASSIUS project (Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2023	gras59	GRAS-transcription factor 59	AC204621.4_FG006	B73 RefGen_v3	Gene	Chr4	1274853	1275830	gras59		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2024	gras6	GRAS-transcription factor 6	GRMZM2G346706	B73 RefGen_v3	Gene	Chr8	133612993	133614885	gras6		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2025	gras60	GRAS-transcription factor 60	GRMZM2G089636	B73 RefGen_v3	Gene	Chr6	38422200	38424095	gras60		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2026	gras61	GRAS-transcription factor 61	GRMZM2G055263	B73 RefGen_v3	Gene	Chr1	37809278	37810975	gras61		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2027	gras62	GRAS-transcription factor 62	GRMZM2G313078	B73 RefGen_v3	Gene	Chr6	156946311	156947989	gras62		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2028	gras63	GRAS-transcription factor 63	GRMZM2G418899	B73 RefGen_v3	Gene	Chr7	162852139	162862787	gras63		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2029	gras64	GRAS-transcription factor 64	GRMZM2G425366	B73 RefGen_v3	Gene	Chr2	219524850	219526665	gras64		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2030	gras65	GRAS-transcription factor 65	GRMZM2G133169	B73 RefGen_v3	Gene	Chr1	270571160	270573052	gras65		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2031	gras66	GRAS-transcription factor 66	AC200124.3_FG005	B73 RefGen_v3	Gene	Chr6	62906676	62907011	gras66		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2032	gras67	GRAS-transcription factor 67	GRMZM2G049159	B73 RefGen_v3	Gene	Chr1	40143545	40147542	gras67		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2033	gras68	GRAS-transcription factor 68	GRMZM2G073823	B73 RefGen_v3	Gene	Chr4	829955	831938	gras68		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2034	gras69	GRAS-transcription factor 69	GRMZM2G153333	B73 RefGen_v3	Gene	Chr6	148102723	148106458	gras69		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2035	gras7	GRAS-transcription factor 7	GRMZM2G013016	B73 RefGen_v3	Gene	Chr3	166194240	166195917	gras7		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2036	gras70	GRAS-transcription factor 70	GRMZM2G114680	B73 RefGen_v3	Gene	Chr9	103353117	103362197	gras70		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2037	gras71	GRAS-transcription factor 71	GRMZM2G117949	B73 RefGen_v3	Gene	Chr9	117530782	117531764	gras71		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2038	gras72	GRAS-transcription factor 72	GRMZM2G073805	B73 RefGen_v3	Gene	Chr4	832522	834779	gras72		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2039	gras73	GRAS-transcription factor 73	GRMZM2G125501	B73 RefGen_v3	Gene	Chr2	209545748	209547741	gras73		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2040	gras74	GRAS-transcription factor 74	GRMZM2G359304	B73 RefGen_v3	Gene	Chr9	123178843	123180450	gras74		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2041	gras75	GRAS-transcription factor 75	GRMZM2G431309	B73 RefGen_v3	Gene	Chr2	208500828	208504903	gras75		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2042	gras76	GRAS-transcription factor 76	GRMZM2G028438	B73 RefGen_v3	Gene	Chr4	156049665	156051935	gras76		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2043	gras77	GRAS-transcription factor 77	GRMZM5G889326	B73 RefGen_v3	Gene	Chr6	137480065	137481525	gras77		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2044	gras79	GRAS-transcription factor 79	GRMZM2G037792	B73 RefGen_v3	Gene	Chr10	138720419	138723128	gras79		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2045	gras80	GRAS-transcription factor 80	GRMZM2G098800	B73 RefGen_v3	Gene	Chr4	153223584	153226721	gras80		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2046	gras81	GRAS-transcription factor 81	GRMZM2G169636	B73 RefGen_v3	Gene	Chr7	165196140	165197777	gras81		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2047	gras82	GRAS-transcription factor 82	GRMZM2G106356	B73 RefGen_v3	Gene	Chr4	2656855	2659044	gras82		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2048	gras83	GRAS-transcription factor 83	GRMZM2G073779	B73 RefGen_v3	Gene	Chr4	836061	838338	gras83		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2049	gras84	GRAS-transcription factor 84	GRMZM2G106336	B73 RefGen_v3	Gene	Chr4	2654200	2655918	gras84		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2050	gras85	GRAS-transcription factor 85	GRMZM2G019060	B73 RefGen_v3	Gene	Chr2	209040871	209042963	gras85		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2051	gras86	GRAS-transcription factor 86	GRMZM2G317287	B73 RefGen_v3	Gene	Chr10	1886674	1888997	gras86		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2052	gras9	GRAS-transcription factor 9	GRMZM2G091656	B73 RefGen_v3	Gene	Chr4	213905717	213907179	gras9		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2053	grf1	general regulatory factor1	GRMZM2G102499	B73 RefGen_v3	Gene	Chr2	41931698	41935612	grf1	14-3-3-like protein GF14-6, AY110485, cl1980_1(131), CL1980_1a, CL1980_2b, gbf14, general regulatory factor1, gf14, GF14, grf1	cDNA sequence; protein co-immunoprecipitates with G-box binding complex but does not bind to DNA;low copy number
2054	grf2	general regulatory factor2	GRMZM2G078641	B73 RefGen_v3	Gene	Chr10	123126089	123136710	grf2	general regulatory factor2, GF14(14-3-3), grf2, ufg8(grf), ufg8(grf1)	genomic sequence similar to grf1
2055	grf9	growth-regulating factor9	GRMZM5G893117	B73 RefGen_v3	Gene	Chr5	211773221	211774543	grf9	bnl5.24, bnl5.24a, bnlg118, grf9, Growth-regulating factor 1, Growth-regulating factor 6 , growth-regulating factor 9, ZmOrphan340	NCBI: growth-regulating factor 9-like
2056	grftf1	GRF-transcription factor 1	GRMZM2G178261	B73 RefGen_v3	Gene	Chr1	272415607	272419742	grftf1	grf1	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2057	grftf10	GRF-transcription factor 10	GRMZM2G105335	B73 RefGen_v3	Gene	Chr4	177152123	177154056	grftf10	grf10	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2058	grftf11	GRF-transcription factor 11	GRMZM5G850129	B73 RefGen_v3	Gene	Chr6	108478031	108479906	grftf11	grf11	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2059	grftf12	GRF-transcription factor 12	GRMZM2G067743	B73 RefGen_v3	Gene	Chr9	9818084	9819919	grftf12	grf12	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
2060	grftf13	GRF-transcription factor 13	GRMZM2G045977	B73 RefGen_v3	Gene	Chr5	196193200	196194593	grftf13	grf13	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2061	grftf14	GRF-transcription factor 14	GRMZM5G853392	B73 RefGen_v3	Gene	Chr5	8709195	8720923	grftf14	grf14	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2062	grftf15	GRF-transcription factor 15	GRMZM2G099862	B73 RefGen_v3	Gene	Chr2	225828392	225831803	grftf15	grf15	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2063	grftf2	GRF-transcription factor 2	GRMZM2G004619	B73 RefGen_v3	Gene	Chr2	199378455	199380799	grftf2	grf2	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2064	grftf3	GRF-transcription factor 3	GRMZM2G096709	B73 RefGen_v3	Gene	Chr7	145016797	145019476	grftf3	grf3	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2065	grftf4	GRF-transcription factor 4	GRMZM2G018414	B73 RefGen_v3	Gene	Chr1	257246035	257248752	grftf4	grf4	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2066	grftf5	GRF-transcription factor 5	GRMZM2G129147	B73 RefGen_v3	Gene	Chr10	140394154	140397947	grftf5	grf5	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2067	grftf6	GRF-transcription factor 6	GRMZM2G034876	B73 RefGen_v3	Gene	Chr5	200344613	200348143	grftf6	grf6	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2068	grftf7	GRF-transcription factor 7	GRMZM2G098594	B73 RefGen_v3	Gene	Chr6	60352538	60355691	grftf7	grf7	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2069	grftf8	GRF-transcription factor 8	GRMZM2G041223	B73 RefGen_v3	Gene	Chr2	12202775	12208055	grftf8	grf8	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2070	grftf9	GRF-transcription factor 9	GRMZM2G124566	B73 RefGen_v3	Gene	Chr4	155831893	155833246	grftf9	grf9	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2071	GRMZM2G021694		GRMZM2G021694	B73 RefGen_v3	Gene	Chr2	27625614	27627505	GRMZM2G021	duf177b, GRMZM2G021694	encodes a DUF177
2072	GRMZM2G023347		GRMZM2G023347	B73 RefGen_v3	Gene	Chr5	17340297	17343212	GRMZM2G023	ABI3-interacting protein 3/prefoldin subunit, GRMZM2G023347, probable prefoldin subunit 4	
2073	GRMZM2G033962		GRMZM2G033962	B73 RefGen_v3	Gene	Chr2	219435832	219441286	GRMZM2G033	GRMZM2G033962, two-component response regulator-like PRR37, ZmOrphan352	Targeted region of interest associated with flowering time (Jamann et al., 2017)
2074	GRMZM2G043191		GRMZM2G043191	B73 RefGen_v3	Gene	Chr1	253852796	253855290	GRMZM2G043	GRMZM2G043191, Inositol polyphosphate 5-phosphatase 11	
2075	GRMZM2G048522		GRMZM2G048522	B73 RefGen_v3	Gene	Chr1	210142896	210145204	GRMZM2G048	putative AMP-dependent synthetase and ligase superfamily protein, Zm4CL1	
2076	GRMZM2G055238		GRMZM2G055238	B73 RefGen_v3	Gene	Chr6	9651143	9652873	GRMZM2G055	GRMZM2G055238, ureide permease 1-like, Ureide permease 5	
2077	GRMZM2G077227		GRMZM2G077227	B73 RefGen_v3	Gene	Chr3	5995366	5998366	GRMZM2G077	calmodulin binding protein, GRMZM2G077227, IQ calmodulin-binding motif domain 6 containing protein	
2078	GRMZM2G085218		GRMZM2G085218	B73 RefGen_v3	Gene	Chr9	106530026	106531123	GRMZM2G085	B-box zinc finger family protein, GRMZM2G085218	Targeted region of interest associated with flowering time (Jamann et al., 2017)
2079	GRMZM2G097297		GRMZM2G097297	B73 RefGen_v3	Gene	Chr4	193094389	193096319	GRMZM2G097	GRMZM2G097297, O-methyltransferase family protein, O-methyltransferase ZRP4-like	
2080	GRMZM2G102770		GRMZM2G102770	B73 RefGen_v3	Gene	Chr3	3428861	3429262	GRMZM2G102	clavata3/esr-related10B, clavata (CLV), embryo-surrounding region (ESR), GRMZM2G102770, inactive protein FON2 SPARE1-like, ZmCLE10B	candidate for clavata3 (CLV3) ortholog
2081	GRMZM2G119067		GRMZM2G119067	B73 RefGen_v3	Gene	Chr9	127725764	127727228	GRMZM2G119	Cytochrome P450 (CYP75B1,D501,TT7), flavonoid 3',5'-hydroxylase-like, GRMZM2G119067	
2082	GRMZM2G128995		GRMZM2G128995	B73 RefGen_v3	Gene	Chr8	77266793	77270611	GRMZM2G12	GRMZM2G128995, vacuolar ATP synthase subunit C, Vacuolar ATP synthase subunit C (VATC) / V-ATPase C subunit / vacuolar proton pump C subunit (DET3)	
2083	GRMZM2G132169		GRMZM2G132169	B73 RefGen_v3	Gene	Chr3	183701021	183703536	GRMZM2G132	GRMZM2G132169, Laccase 12, L-ascorbate oxidase	
2084	GRMZM2G138074		GRMZM2G138074	B73 RefGen_v3	Gene	Chr3	187768902	187771862	GRMZM2G138	putative cytochrome P450 superfamily protein, ZmC3H	
2085	GRMZM2G145152		GRMZM2G145152	B73 RefGen_v3	Gene	Chr7	127613281	127615125	GRMZM2G145	GRMZM2G145152, Tsi1-interacting protein TSIP1(DnaJ/Hsp40)	
2086	GRMZM2G153722		GRMZM2G153722	B73 RefGen_v3	Gene	Chr4	62590194	62601980	GRMZM2G153	1-phosphatidylinositol-3-phosphate 5-kinase FAB1B-like, GRMZM2G153722	Candidate gene for QTL involved in root development at the seedling stage.
2087	GRMZM2G154580		GRMZM2G154580	B73 RefGen_v3	Gene	Chr1	90223947	90224841	GRMZM2G154	GRMZM2G154580, two-component response regulator-like PRR37	Targeted region of interest associated with flowering time (Jamann et al., 2017)
2088	GRMZM2G158062		GRMZM2G158062	B73 RefGen_v3	Gene	Chr7	155653647	155658404	GRMZM2G158	Eukaryotic translation initiation factor-related, GRMZM2G158062	
2089	GRMZM2G161004		GRMZM2G161004	B73 RefGen_v3	Gene	Chr1	188202887	188206003	GRMZM2G161	GRMZM2G161004, nucleic acid binding protein, Splicing factor suppressor of abi3-5	
2090	GRMZM2G179768		GRMZM2G179768	B73 RefGen_v3	Gene	Chr5	205986569	205987795	GRMZM2G17	GRMZM2G179768, metalloendoproteinase 1, Zinc-dependent matrix metalloproteinase/predicted GPI-anchored protein	
2091	GRMZM2G315431		GRMZM2G315431	B73 RefGen_v3	Gene	Chr7	103904514	103907063	GRMZM2G31	GRMZM2G315431, ubiquitin-protein ligase	identified to be highly inducible by Rhizoctonia solani infection
2092	GRMZM2G329181		GRMZM2G329181	B73 RefGen_v3	Gene	Chr1	286049789	286052959	GRMZM2G32	FASCICLIN-like arabinogalactan protein 17, GRMZM2G329181	
2093	GRMZM2G350428		GRMZM2G350428	B73 RefGen_v3	Gene	Chr5	3782236	3785900	GRMZM2G35	clavata3/esr-related4B, clavata (CLV), embryo-surrounding region (ESR), GRMZM2G350428, ZmCLE4B	candidate for clavata3 (CLV3) ortholog
2094	GRMZM2G359322		GRMZM2G359322	B73 RefGen_v3	Gene	Chr9	123215070	123216079	GRMZM2G35	EARLY flowering 4 protein, GRMZM2G359322	Targeted region of interest associated with flowering time (Jamann et al., 2017)
2095	GRMZM2G380227		GRMZM2G380227	B73 RefGen_v3	Gene	Chr1	197608242	197610896	GRMZM2G38	GRMZM2G380227, probable receptor-like protein kinase At5g15080-like, Serine/threonine-protein kinase (SIK: salt-inducible kinase)	
2096	GRMZM2G391746		GRMZM2G391746	B73 RefGen_v3	Gene	Chr2	4045899	4046558	GRMZM2G391	clavata3/esr-related19A, clavata (CLV), embryo-surrounding region (ESR), GRMZM2G391746, ZmCLE19A	candidate for clavata3 (CLV3) ortholog
2097	GRMZM2G418415		GRMZM2G418415	B73 RefGen_v3	Gene	Chr2	206376607	206378103	GRMZM2G41	ZmCSE	
2098	GRMZM2G423617		GRMZM2G423617	B73 RefGen_v3	Gene	Chr8	24647332	24648491	GRMZM2G42	clavata3/esr-related10A, clavata (CLV), embryo-surrounding region (ESR), GRMZM2G423617, ZmCLE10A	candidate for clavata3 (CLV3) ortholog
2099	GRMZM2G427603		GRMZM2G427603	B73 RefGen_v3	Gene	Chr10	145857098	145858255	GRMZM2G42	clavata3/esr-related19B, clavata (CLV), embryo-surrounding region (ESR), GRMZM2G427603, ZmCLE19B	candidate for clavata3 (CLV3) ortholog
2100	GRMZM2G443509		GRMZM2G443509	B73 RefGen_v3	Gene	Chr10	113181083	113188620	GRMZM2G44	GRMZM2G443509, Protein phosphatase 2C, ZmOrphan170	
2101	GRMZM2G480050		GRMZM2G480050	B73 RefGen_v3	Gene	Chr7	15467965	15468908	GRMZM2G48	clavata3/esr-related4C, clavata (CLV), embryo-surrounding region (ESR), GRMZM2G480050, ZmCLE4C	candidate for clavata3 (CLV3) ortholog
2102	grp1	glycine-rich protein1	GRMZM2G080603	B73 RefGen_v3	Gene	Chr1	178503667	178505233	grp1	1055, CHEM2, glycine-rich protein1, glycine-rich RNA-binding protein 2, grp1, NcNi55	protein with high glycine content and repetitive glycine stretches; putative cell wall components
2103	grp2	glycine-rich protein2	GRMZM2G009448	B73 RefGen_v3	Gene	Chr10	17611993	17615725	grp2	CHEM 11, grp2, grp*-chem11, PCO151485, umc1312	
2104	grp3	glycine-rich protein3	GRMZM2G154954	B73 RefGen_v3	Gene	Chr5	31464367	31465552	grp3	glycine-rich protein3, grp3, grp*-Y07781, siy07781, siy07781(389)	single or low copy number cDNA;
2105	grp4	glycine rich protein4	GRMZM2G025205	B73 RefGen_v3	Gene	Chr2	130608944	130609749	grp4	al1, aluminum-induced protein, c109, glycine rich protein 4, grp4, rc109, root cap109, root cap-specific glycine-rich protein, Zmal1	
2106	grx1	glutaredoxin homolog1	GRMZM2G150295	B73 RefGen_v3	Gene	Chr2	30571551	30574948	grx1	csu40, csu40(glr), csu40(grx), csuh40, glutaredoxin homolog1, grx1, umc331	leaf cDNA csu40, similar to E. coli glutaredoxin
2107	gsh1	gamma-glutamylcysteine synthetase1	GRMZM2G111579	B73 RefGen_v3	Gene	Chr6	24549311	24554370	gsh1	gnp_QBL4e12, gpm533, gsh1, PCO145292, PCO145292(467)	
2108	gsht1	glutathione transporter1	GRMZM2G421491	B73 RefGen_v3	Gene	Chr1	276882449	276887250	gsht1	glutathione transporter1, gsht1, ZmGT1	

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
2109	gsr1	glutathione reductase1	GRMZM2G172322	B73 RefGen_v3	Gene	Chr1	12985602	12991971	gsr1	csu111, csuh111, glutathione reductase1, gor1, gsr1, gsy308(gsr), siaj006055(8), siaj006055a , umc368	single copy leaf cDNA csu111, similar to pea glutathione reductase
2110	gss1	starch synthase homolog1	Zm00001d052263	Zm-B73-REFERENCE-G	Gene	Chr4	185228834	185234452	gss1	gss1, starch synthase homolog1, uaz218, uaz218(strs)	endosperm cDNA 5C04B10 (uaz218), similar to pea starch synthase isoform II
2111	gst1	glutathione-S-transferase1	GRMZM2G116273	B73 RefGen_v3	Gene	Chr8	172671226	172674089	gst1	csu970, glutathione-S-transferase1, gst1, GSTF1, GSTF2, gstI, GSTI, GST-I, gst*-X06754, pco151099(646), PCO151099b, phi015, phi080, umc1069	bands; transcripts correlate with dimer isoforms; single copy in Southerns; SSRs phi080, phi015, umc1069
2112	gst10	glutathione transferase10	GRMZM2G096153	B73 RefGen_v3	Gene	Chr1	7861824	7863470	gst10	glutathione transferase10, gst10, IDP131, IDP2490	
2113	gst11	glutathione transferase11	GRMZM2G119499	B73 RefGen_v3	Gene	Chr1	7819661	7821095	gst11	glutathione transferase11, gst11, PCO064413, PCO064413(5)	
2114	gst12	glutathione S-transferase12	GRMZM2G096269	B73 RefGen_v3	Gene	Chr1	7854954	7856758	gst12	glutathione transferase12, gst12, PCO132785, PCO132785(5), umc1071	One of 12 Type I GSTs typed by sequence similarity
2115	gst13	glutathione transferase13	GRMZM2G126781	B73 RefGen_v3	Gene	Chr9	151975181	151977920	gst13	glutathione transferase13, gst13, umc2099	cDNA; SSR umc2099
2116	gst14	glutathione transferase14	GRMZM2G175134	B73 RefGen_v3	Gene	Chr1	85725085	85726426	gst14	glutathione transferase14, gst14	
2117	gst15	glutathione transferase15	GRMZM2G150474	B73 RefGen_v3	Gene	Chr8	127252872	127255231	gst15	glutathione transferase15, gst15	
2118	gst16	glutathione transferase16	GRMZM5G895383	B73 RefGen_v3	Gene	Chr7	147866596	147870180	gst16	CL1110_1, CL1110_1(571), glutathione transferase16, gst16	
2119	gst17	glutathione transferase17	GRMZM2G064255	B73 RefGen_v3	Gene	Chr5	174453111	174454058	gst17	CL1109_1b, glutathione transferase17, gst17, umc2026	
2120	gst18	glutathione transferase18	GRMZM2G019090	B73 RefGen_v3	Gene	Chr3	136292387	136351651	gst18	glutathione transferase18, gst18	
2121	gst19	glutathione transferase19	GRMZM2G335618	B73 RefGen_v3	Gene	Chr6	104021616	104022697	gst19	glutathione transferase19, gst19, IDP2497, pco100643, pco100643(490)	
2122	gst2	glutathione S-transferase2	GRMZM2G132093	B73 RefGen_v3	Gene	Chr10	90214397	90215794	gst2	glutathione S-transferase2, gst2, GST-27, PCO060686	safener-induced; heterodimer; 2 map sites have been reported on chr 8 and 10
2123	gst20	glutathione transferase20	GRMZM2G447632	B73 RefGen_v3	Gene	Chr3	206949798	206950761	gst20	glutathione transferase20, gnp_AI861129, gpm107, gst20	
2124	gst21	glutathione transferase21	GRMZM2G428168	B73 RefGen_v3	Gene	Chr3	149352435	149353721	gst21	glutathione transferase21, gst21, PCO117787(240), PCO117787a	
2125	gst22	glutathione transferase22	GRMZM2G330635	B73 RefGen_v3	Gene	Chr10	96774298	96775703	gst22	glutathione transferase22, gst22, PCO099552(740), PCO099552b	
2126	gst23	glutathione transferase23	GRMZM2G416632	B73 RefGen_v3	Gene	Chr7	128406348	128407955	gst23	glutathione transferase23, gst23, gst36, PCO072967, PZA00616, umc2098	cDNA, SSR umc2098
2127	gst24	glutathione transferase24	GRMZM2G032856	B73 RefGen_v3	Gene	Chr5	211087584	211088858	gst24	glutathione transferase24, gst24	
2128	gst25	glutathione transferase25	GRMZM2G161905	B73 RefGen_v3	Gene	Chr9	155866676	155867611	gst25	glutathione transferase25, gst25	
2129	gst26	glutathione transferase26	GRMZM2G363540	B73 RefGen_v3	Gene	Chr4	37262740	37264743	gst26	glutathione transferase26, gst26, siaf244691b, siaf244691b(303)	
2130	gst27	glutathione transferase27	GRMZM2G077206	B73 RefGen_v3	Gene	Chr8	136446031	136447290	gst27	glutathione transferase27, gst27, PCO061770d	
2131	gst28	glutathione transferase28	GRMZM2G146475	B73 RefGen_v3	Gene	Chr3	149448034	149449090	gst28	glutathione transferase28, gst28, PCO110359, PCO110359(240)	
2132	gst29	glutathione transferase29	GRMZM2G127789	B73 RefGen_v3	Gene	Chr3	149351129	149351997	gst29	glutathione transferase29, gst29, siaf244694(240), siaf244694b	
2133	gst30	glutathione transferase30	GRMZM2G044383	B73 RefGen_v3	Gene	Chr1	81787076	81788381	gst30	glutathione transferase30, gst30	
2134	gst31	glutathione transferase31	GRMZM2G475059	B73 RefGen_v3	Gene	Chr1	8107800	8109879	gst31	AY103844, glutathione transferase31, gst31, IDP108, PCO132874	glutathione S-transferase subunit 31; matches PCO132874 (in silico from AF244696) placed by overgo on chromosome 1
2135	gst32	glutathione transferase32	GRMZM2G041685	B73 RefGen_v3	Gene	Chr1	81512105	81512883	gst32	glutathione transferase32, gst32	
2136	gst34	glutathione transferase34	GRMZM2G145069	B73 RefGen_v3	Gene	Chr1	81325327	81326926	gst34	glutathione S-transferase U17-like, glutathione transferase34, gst34	
2137	gst34	glutathione transferase34	Zm00001d029696	Zm-B73-REFERENCE-G	Gene	Chr1	82924832	82926012	gst34	glutathione S-transferase U17-like, glutathione transferase34, gst34	
2138	gst35	glutathione transferase35	GRMZM2G161891	B73 RefGen_v3	Gene	Chr9	155857221	155858230	gst35	glutathione transferase35, gst35, siaf244700, siaf244700(707)	
2139	gst37	glutathione transferase37	GRMZM2G178079	B73 RefGen_v3	Gene	Chr1	81588783	81594131	gst37	glutathione transferase37, gst37, siaf244702, siaf244702(579)	
2140	gst38	glutathione transferase38	GRMZM2G066369	B73 RefGen_v3	Gene	Chr1	81649181	81650653	gst38	glutathione transferase38, gst38, siAF244703	
2141	gst39	glutathione transferase39	GRMZM2G028821	B73 RefGen_v3	Gene	Chr1	81612701	81613806	gst39	glutathione transferase39, gnp_AW330983, gpm198, gst39	
2142	gst4	glutathione S-transferase4	GRMZM2G146246	B73 RefGen_v3	Gene	Chr3	155015581	155017338	gst4	csu44(gst), glutathione-S-transferase4, gst4, Gst-III, GSTIII, PCO132886, phi073	constitutive and major subunit;amino acid sequence, cDNA sequence, transgenic expression, single or low copy gene, SSR phi073.
2143	gst40	glutathione transferase40	GRMZM2G054653	B73 RefGen_v3	Gene	Chr1	81526010	81527198	gst40	glutathione transferase40, gnp_AW424838, gpm224, gst40, probable glutathione S-transferase GSTU6	
2144	gst41	glutathione transferase41	GRMZM2G097989	B73 RefGen_v3	Gene	Chr6	147253085	147254465	gst41	CL1085_1, glutathione transferase41, gnp_AI770339, gpm80, gst41	
2145	gst42	glutathione transferase42	GRMZM2G025190	B73 RefGen_v3	Gene	Chr1	81450790	81452151	gst42	glutathione transferase42, gst42, PCO100973, PCO100973(31)	
2146	gst5	glutathione transferase5	GRMZM2G308687	B73 RefGen_v3	Gene	Chr1	285410265	285411865	gst5	glutathione transferase5, gst5, GSTV, PCO118532, PCO118532(95)	cDNA, safener-induced; high activity with fluorodifen herbicide
2147	gst6	glutathione transferase6	GRMZM2G129357	B73 RefGen_v3	Gene	Chr7	5520895	5524522	gst6	glutathione transferase6, gst6, GST VI, PCO143084, PCO143084(287)	cDNA, functionally expressed in E. coli
2148	gst7	glutathione transferase7	GRMZM2G028556	B73 RefGen_v3	Gene	Chr3	149477875	149478958	gst7	glutathione transferase7, gst7, GST VII, PCO133241, PCO133241(240)	cDNA, functionally expressed in E. coli
2149	gst8	glutathione transferase8	GRMZM2G156877	B73 RefGen_v3	Gene	Chr3	194233310	194235176	gst8	glutathione S-transferase IV , glutathione transferase8, gst8	
2150	gst9	glutathione transferase9	GRMZM2G126763	B73 RefGen_v3	Gene	Chr9	151986613	151988051	gst9	CL1117_-1, CL1117_-1(707), glutathione S-transferase 6, glutathione transferase9, gst9, PHM1699, PZA00708, rs131175252, ss196414359	
2151	gt1	grassy tillers1	GRMZM2G005624	B73 RefGen_v3	Gene	Chr1	23240104	23243489	gt1	grassy tillers1, gt1, HD-Zip, PCO139174, umc2204, ZmHB68	numerous basal branches; vegetatively totipotent in combination with id1 and factors for perennialism. putative transcription factor that reduces branching, and is induced by shade
2152	gtr1	glutamyl-tRNA reductase1	GRMZM2G177412	B73 RefGen_v3	Gene	Chr10	144041132	144046169	gtr1	plant elicitor peptide2, precursor elicitor peptide2, propep2, PZA00007, rs131176021, ss196417481, ZmPep2	leaf cDNA csu839, plastid porphyrin biosynthesis
2153	gts1	Glutamine--tRNA ligase cytoplasmic1	GRMZM2G048012	B73 RefGen_v3	Gene	Chr3	8594070	8599931	gts1	1574, asg24, asg24a(gts), asg24(gts), gts1, rs131186892, rs131186893 , rs131377812 , TIDP3331	
2154	gun1	genomes uncoupled1	GRMZM2G432850	B73 RefGen_v3	Gene	Chr1	147903774	147907639	gun1	gun1, pentatricopeptide repeat-containing protein At2g31400, chloroplastic-like, ZmPPR042	ortholog of Arabidopsis GUN1 (At2g31400) pentatricopeptide repeat-containing protein, chloroplastic-like
2155	gun4	genomes uncoupled4 homolog	GRMZM2G464328	B73 RefGen_v3	Gene	Chr10	5645820	5646965	gun4	gun4	ortholog of Arabidopsis GUN4, a Mg-chelatase cofactor and porphyrin binding protein. Ortholog of Arabidopsis GUN4; Mg-chelatase cofactor and porphyrin binding protein. (A. Barkan, 2015)
2156	gz50	50kD gamma zein	GRMZM2G138689	B73 RefGen_v3	Gene	Chr7	120206897	120208211	gz50	gz50, PCO155483, PCO155483(562)	endosperm-specific protein cDNA
2157	haf101b		GRMZM2G042231	B73 RefGen_v3	Gene	Chr9	94384689	94388247	haf101b	PZA03595, PZA03596, rs128282682, rs131085246, rs131085250, rs131085254, rs131175947, rs55625269 , ss196417197, ss196417199, ss196417201, ss196417203, ss196417205	

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
2158	hag101	histone acetyl transferase GNAT/MYST 1(	GRMZM2G046021	B73 RefGen_v3	Gene	Chr5	33838765	33844703	hag101	gcn5, GNAT-transcription factor 23, hac104, hag101, hag23, hagtf23, histone acetyl transferase GNAT/MYST 101, pco145010(391), PCO145010a	single copy; enzyme activity confirmed by assay of recombinant protein
2159	hagtf1	GNAT-transcription factor 1	AC209858.4_FG004	B73 RefGen_v3	Gene	Chr1	11299653	11300336	hagtf1	hag1	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2160	hagtf11	GNAT-transcription factor 11	GRMZM2G100872	B73 RefGen_v3	Gene	Chr2	37226550	37231577	hagtf11	hag11	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2161	hagtf12	GNAT-transcription factor 12	GRMZM2G126856	B73 RefGen_v3	Gene	Chr2	77310976	77311742	hagtf12	hag12	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2162	hagtf13	GNAT-transcription factor 13	GRMZM2G162056	B73 RefGen_v3	Gene	Chr2	118365107	118365860	hagtf13	hag13	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2163	hagtf14	GNAT-transcription factor 14	GRMZM5G875676	B73 RefGen_v3	Gene	Chr2	224059127	224063731	hagtf14	hag14	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2164	hagtf15	GNAT-transcription factor 15	GRMZM2G371912	B73 RefGen_v3	Gene	Chr3	145855491	145858353	hagtf15	hag15	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2165	hagtf16	GNAT-transcription factor 16	GRMZM2G333775	B73 RefGen_v3	Gene	Chr3	222666939	222668487	hagtf16	hag16	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2166	hagtf17	GNAT-transcription factor 17	GRMZM2G137961	B73 RefGen_v3	Gene	Chr3	224625939	224628844	hagtf17	hag17	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2167	hagtf18	GNAT-transcription factor 18	GRMZM2G055141	B73 RefGen_v3	Gene	Chr4	31089308	31092725	hagtf18	hag18	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2168	hagtf19	GNAT-transcription factor 19	GRMZM2G011624	B73 RefGen_v3	Gene	Chr4	163657377	163666263	hagtf19	hag19	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2169	hagtf2	GNAT-transcription factor 2	GRMZM2G114184	B73 RefGen_v3	Gene	Chr1	21720037	21721470	hagtf2	hag2	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2170	hagtf20	GNAT-transcription factor 20	GRMZM2G059302	B73 RefGen_v3	Gene	Chr4	192962918	192974114	hagtf20	hag20	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2171	hagtf21	GNAT-transcription factor 21	GRMZM2G431445	B73 RefGen_v3	Gene	Chr5	4426539	4427138	hagtf21	hag21	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2172	hagtf22	GNAT-transcription factor 22	GRMZM2G176723	B73 RefGen_v3	Gene	Chr5	14609875	14610673	hagtf22	hag22	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2173	hagtf24	GNAT-transcription factor 24	GRMZM2G479325	B73 RefGen_v3	Gene	Chr5	92208775	92210342	hagtf24	hag24	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2174	hagtf25	GNAT-transcription factor 25	GRMZM2G169326	B73 RefGen_v3	Gene	Chr5	199021128	199022386	hagtf25	hag25	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2175	hagtf26	GNAT-transcription factor 26	GRMZM2G046288	B73 RefGen_v3	Gene	Chr5	210937687	210940587	hagtf26	hag26	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2176	hagtf27	GNAT-transcription factor 27	GRMZM2G049730	B73 RefGen_v3	Gene	Chr6	95875402	95877132	hagtf27	hag27	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2177	hagtf28	GNAT-transcription factor 28	GRMZM2G402538	B73 RefGen_v3	Gene	Chr6	124479190	124483759	hagtf28	hag28	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2178	hagtf29	GNAT-transcription factor 29	GRMZM2G062657	B73 RefGen_v3	Gene	Chr6	142637425	142646491	hagtf29	hag29	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2179	hagtf3	GNAT-transcription factor 3	GRMZM2G131618	B73 RefGen_v3	Gene	Chr1	226679443	226680502	hagtf3	hag3	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2180	hagtf30	GNAT-transcription factor 30	GRMZM2G701207	B73 RefGen_v3	Gene	Chr6	154534441	154541243	hagtf30	hag30	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2181	hagtf31	GNAT-transcription factor 31	GRMZM2G458082	B73 RefGen_v3	Gene	Chr7	2295884	2296892	hagtf31	hag31	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2182	hagtf32	GNAT-transcription factor 32	GRMZM2G302778	B73 RefGen_v3	Gene	Chr7	27695451	27697345	hagtf32	hag32	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2183	hagtf33	GNAT-transcription factor 33	GRMZM5G813007	B73 RefGen_v3	Gene	Chr7	161697850	161703669	hagtf33	hag33	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2184	hagtf34	GNAT-transcription factor 34	GRMZM2G034495	B73 RefGen_v3	Gene	Chr8	100928654	100930976	hagtf34	hag34	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2185	hagtf35	GNAT-transcription factor 35	GRMZM2G050137	B73 RefGen_v3	Gene	Chr9	104883790	104886205	hagtf35	hag35	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2186	hagtf36	GNAT-transcription factor 36	GRMZM2G096352	B73 RefGen_v3	Gene	Chr9	149311288	149315650	hagtf36	hag36	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2187	hagtf37	GNAT-transcription factor 37	GRMZM2G136389	B73 RefGen_v3	Gene	Chr9	150989308	151005342	hagtf37	hag37	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2188	hagtf38	GNAT-transcription factor 38	AC149475.2_FG007	B73 RefGen_v3	Gene	Chr9	152822528	152823205	hagtf38	hag38	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2189	hagtf39	GNAT-transcription factor 39	GRMZM2G134426	B73 RefGen_v3	Gene	Chr9	156523971	156546958	hagtf39	hag39	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2190	hagtf4	GNAT-transcription factor 4	GRMZM2G135849	B73 RefGen_v3	Gene	Chr1	226894220	226895735	hagtf4	hag4	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2191	hagtf40	GNAT-transcription factor 40	GRMZM2G137715	B73 RefGen_v3	Gene	Chr10	51010484	51019069	hagtf40	hag40	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2192	hagtf41	GNAT-transcription factor 41	GRMZM2G057554	B73 RefGen_v3	Gene	Chr10	123707093	123710625	hagtf41	hag41	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2193	hagtf42	GNAT-transcription factor 42	GRMZM2G359735	B73 RefGen_v3	Gene	Chr10	126160152	126165437	hagtf42	hag42	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2194	hagtf43	GNAT-transcription factor 43	GRMZM5G818977	B73 RefGen_v3	Gene	Chr10	143741016	143743695	hagtf43	hag43	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2195	hagtf6	GNAT-transcription factor 6	GRMZM2G099305	B73 RefGen_v3	Gene	Chr1	279963848	279966746	hagtf6	hag6	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2196	hagtf7	GNAT-transcription factor 7	GRMZM2G031062	B73 RefGen_v3	Gene	Chr1	287272867	287273796	hagtf7	hag7	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2197	hagtf8	GNAT-transcription factor 8	GRMZM2G342856	B73 RefGen_v3	Gene	Chr1	287341950	287342703	hagtf8	hag8	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2198	hagtf9	GNAT-transcription factor 9	GRMZM2G478798	B73 RefGen_v3	Gene	Chr1	287360790	287362436	hagtf9	hag9	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2199	ham101	histone acetyl transferase MYST family 1(	GRMZM2G044126	B73 RefGen_v3	Gene	Chr2	213200911	213205830	ham101	hac105, hac108, hag104, hag105, ham101, histone acetyl transferase108, histone acetyl transferase GNAT/MYST 104, histone acetyl transferase MYST family 101, pco097531a	
2200	hat1	histone acetyltransferase1	GRMZM5G851405	B73 RefGen_v3	Gene	Chr7	95111087	95115489	hat1	hac106, hac109, hag102, hat1, hatb, HAT B, hatB1, histone acetyltransferase1	cDNA, genomic and peptide sequence; antibody cross-reactivity
2201	hb1	hemoglobin1	GRMZM2G067402	B73 RefGen_v3	Gene	Chr9	145596856	145598153	hb1	AY104188, hb1, hbt1, hemoglobin1, PHM1931, phytoglobin1.1, PZA01369, teosinte haemoglobin, umc1733, umc2345, ZmPgb1.1	cDNA sequence; SSR umc1733;cloned hb gene codes for a predicted protein of 164 amino acids. suppression of expression associated with programmed cell death (Huang et al 2014)
2202	hb10	Homeobox-transcription factor 10	GRMZM2G004334	B73 RefGen_v3	Gene	Chr6	109244071	109247202	hb10		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2203	hb100	Homeobox-transcription factor 100	GRMZM2G064466	B73 RefGen_v3	Gene	Chr1	82921613	82926989	hb100		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2204	hb101	Homeobox-transcription factor 101	GRMZM2G111964	B73 RefGen_v3	Gene	Chr8	25478199	25487470	hb101		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2205	hb102	Homeobox-transcription factor 102	GRMZM2G139963	B73 RefGen_v3	Gene	Chr1	14957965	14960921	hb102	hat7, hb102, homeobox-leucine zipper protein HAT7, Homeobox-transcription factor 102, umc1166	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2206	hb103	Homeobox-transcription factor 103	GRMZM2G136369	B73 RefGen_v3	Lapsed Locus	Chr8	123435516	123441977	hb103		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
2207	hb106	Homeobox-transcription factor 106	GRMZM2G162481	B73 RefGen_v3	Gene	Chr9	133354525	133358466	hb106	homeobox domain containing protein, wox12B, ZmWOX11/12B	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2208	hb107	Homeobox-transcription factor 107	GRMZM2G062244	B73 RefGen_v3	Gene	Chr2	208276499	208277537	hb107		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2209	hb108	Homeobox-transcription factor 108	GRMZM2G060050	B73 RefGen_v3	Gene	Chr10	6753231	6754253	hb108		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2210	hb109	Homeobox-transcription factor 109	GRMZM5G805026	B73 RefGen_v3	Gene	Chr8	170258101	170261292	hb109	WUSCHEL-related homeobox 8-like, ZmWOX13B	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2211	hb11	Homeobox-transcription factor 11	GRMZM2G127537	B73 RefGen_v3	Gene	Chr7	123539134	123541042	hb11		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2212	hb110	Homeobox-transcription factor 110	GRMZM2G061101	B73 RefGen_v3	Gene	Chr1	257512113	257518809	hb110		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2213	hb112	Homeobox-transcription factor 112	GRMZM2G003304	B73 RefGen_v3	Gene	Chr1	218768608	218773418	hb112		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2214	hb113	Homeobox-transcription factor 113	GRMZM2G060541	B73 RefGen_v3	Gene	Chr8	149427195	149428878	hb113		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2215	hb114	Homeobox-transcription factor 114	GRMZM2G381748	B73 RefGen_v3	Gene	Chr6	137335415	137341548	hb114		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2216	hb115	Homeobox-transcription factor 115	GRMZM2G021339	B73 RefGen_v3	Gene	Chr4	165861785	165863994	hb115		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2217	hb116	Homeobox-transcription factor 116	GRMZM2G069274	B73 RefGen_v3	Gene	Chr3	185489797	185493650	hb116	WUSCHEL-related homeobox 8-like, ZmWOX13A	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2218	hb118	Homeobox-transcription factor 118	GRMZM2G386276	B73 RefGen_v3	Gene	Chr3	189749774	189754836	hb118		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2219	hb119	Homeobox-transcription factor 119	GRMZM2G003509	B73 RefGen_v3	Gene	Chr1	173247423	173257862	hb119		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2220	hb12	Homeobox-transcription factor 12	AC233899.1_FG004	B73 RefGen_v3	Gene	Chr9	149912584	149914098	hb12		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2221	hb120	Homeobox-transcription factor 120	GRMZM2G056600	B73 RefGen_v3	Gene	Chr7	129296234	129298384	hb120		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2222	hb121	Homeobox-transcription factor 121	GRMZM2G131476	B73 RefGen_v3	Gene	Chr1	109642904	109644735	hb121		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2223	hb122	Homeobox-transcription factor 122	GRMZM2G028622	B73 RefGen_v3	Gene	Chr10	146494874	146496217	hb122	hb122, Homeobox-transcription factor 122, wus2, wus2 WUS2 protein, wuschel2 ortholog, ZmWus2	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2224	hb123	Homeobox-transcription factor 123	GRMZM2G074645	B73 RefGen_v3	Gene	Chr8	95285620	95290526	hb123	BELL1-like Homeobox13, putative POX domain/homeobox DNA-binding domain family protein, ZmBLH13	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2225	hb124	Homeobox-transcription factor 124	GRMZM2G023291	B73 RefGen_v3	Gene	Chr1	251772748	251774599	hb124		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2226	hb126	Homeobox-transcription factor 126	GRMZM2G034113	B73 RefGen_v3	Gene	Chr2	195705583	195707271	hb126		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2227	hb127	Homeobox-transcription factor 127	GRMZM2G119999	B73 RefGen_v3	Gene	Chr1	139960481	139962631	hb127		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2228	hb128	Homeobox-transcription factor 128	GRMZM2G041462	B73 RefGen_v3	Gene	Chr7	142432248	142434060	hb128		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2229	hb129	Homeobox-transcription factor 129	GRMZM2G142962	B73 RefGen_v3	Gene	Chr1	198225939	198227907	hb129		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2230	hb13	Homeobox-transcription factor 13	GRMZM2G104204	B73 RefGen_v3	Gene	Chr7	160792661	160793924	hb13		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2231	hb130	Homeobox-transcription factor 130	GRMZM2G314064	B73 RefGen_v3	Gene	Chr1	52343963	52347384	hb130		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2232	hb131	Homeobox-transcription factor 131	GRMZM2G111204	B73 RefGen_v3	Gene	Chr2	175320204	175326578	hb131		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2233	hb16	Homeobox-transcription factor 16	GRMZM2G140083	B73 RefGen_v3	Gene	Chr8	131860635	131861792	hb16		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2234	hb17	Homeobox-transcription factor 17	GRMZM2G118063	B73 RefGen_v3	Gene	Chr10	58000726	58009266	hb17		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2235	hb18	Homeobox-transcription factor 18	GRMZM2G004957	B73 RefGen_v3	Gene	Chr10	84242542	84246083	hb18		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2236	hb19	Homeobox-transcription factor 19	GRMZM2G478396	B73 RefGen_v3	Gene	Chr8	166836265	166837239	hb19	WUSCHEL-related homeobox 9, ZmWOX5A	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2237	hb2	hemoglobin2	GRMZM2G168898	B73 RefGen_v3	Gene	Chr6	159342531	159343955	hb2	hb2, hemoglobin2, IDP9056, phytoglobin1.2, ZmPgb1.2	suppression of expression is associated with programmed cell death (Huang et al 2014)
2238	hb20	Homeobox-transcription factor 20	GRMZM2G060507	B73 RefGen_v3	Gene	Chr9	154007940	154011643	hb20		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2239	hb21	Homeobox-transcription factor 21	GRMZM2G076272	B73 RefGen_v3	Gene	Chr9	58196208	58199144	hb21		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2240	hb22	Homeobox-transcription factor 22	GRMZM2G178741	B73 RefGen_v3	Gene	Chr9	151525953	151528343	hb22		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2241	hb24	Homeobox-transcription factor 24	GRMZM2G166041	B73 RefGen_v3	Gene	Chr4	238046062	238047920	hb24		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2242	hb25	Homeobox-transcription factor 25	GRMZM2G178102	B73 RefGen_v3	Gene	Chr3	123281942	123288759	hb25	hb25, Homeobox-leucine zipper family protein / lipid-binding START domain-containing protein, TIDP3177	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2243	hb26	Homeobox-transcription factor 26	GRMZM2G010929	B73 RefGen_v3	Gene	Chr8	14086644	14092137	hb26		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2244	hb27	Homeobox-transcription factor 27	GRMZM2G426140	B73 RefGen_v3	Gene	Chr5	102549951	102556475	hb27		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2245	hb28	Homeobox-transcription factor 28	GRMZM2G033138	B73 RefGen_v3	Gene	Chr5	79734099	79747217	hb28		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2246	hb29	Homeobox-transcription factor 29	GRMZM2G125294	B73 RefGen_v3	Gene	Chr8	68635067	68646943	hb29		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2247	hb3	Homeobox-transcription factor 3	GRMZM2G122750	B73 RefGen_v3	Gene	Chr6	164671161	164681928	hb3		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2248	hb30	Homeobox-transcription factor 30	GRMZM2G327059	B73 RefGen_v3	Gene	Chr1	5080780	5086704	hb30	bel1, BEL1-related homeotic protein 14, hb30, mmp49, rs131180467 , rs131180471 , ss196501594 , ss196501604	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2249	hb33	Homeobox-transcription factor 33	GRMZM2G011588	B73 RefGen_v3	Gene	Chr1	256543119	256549354	hb33		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2250	hb34	Homeobox-transcription factor 34	GRMZM2G002915	B73 RefGen_v3	Gene	Chr2	178781917	178784182	hb34		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2251	hb35	Homeobox-transcription factor 35	GRMZM2G333565	B73 RefGen_v3	Gene	Chr5	212127074	212129332	hb35		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2252	hb36	Homeobox-transcription factor 36	GRMZM2G396114	B73 RefGen_v3	Gene	Chr1	273157848	273168093	hb36	rs131182170 , rs131182172 , rs131182173 , rs131893889 , rs131893992 , rs131894001 , umc2149	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.. NCBI: homeodomain protein JUBEL1
2253	hb37	Homeobox-transcription factor 37	GRMZM2G148098	B73 RefGen_v3	Gene	Chr5	13673081	13677600	hb37		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2254	hb38	Homeobox-transcription factor 38	GRMZM2G013617	B73 RefGen_v3	Gene	Chr6	56969090	56972316	hb38		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2255	hb4	Homeobox-transcription factor 4	GRMZM2G106276	B73 RefGen_v3	Gene	Chr9	20880508	20881839	hb4		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
2256	hb40	Homeobox-transcription factor 40	GRMZM2G158403	B73 RefGen_v3	Gene	Chr3	155487601	155494622	hb40		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2257	hb41	Homeobox-transcription factor 41	GRMZM2G117164	B73 RefGen_v3	Gene	Chr5	190526953	190528628	hb41		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2258	hb42	Homeobox-transcription factor 42	GRMZM2G477415	B73 RefGen_v3	Gene	Chr5	54874440	54875451	hb42		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2259	hb43	Homeobox-transcription factor 43	GRMZM2G307397	B73 RefGen_v3	Gene	Chr5	54944892	54945953	hb43		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2260	hb44	Homeobox-transcription factor 44	GRMZM2G307400	B73 RefGen_v3	Gene	Chr5	54947382	54948335	hb44		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2261	hb45	Homeobox-transcription factor 45	GRMZM2G126808	B73 RefGen_v3	Gene	Chr1	29542179	29544587	hb45		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2262	hb46	Homeobox-transcription factor 46	GRMZM2G126239	B73 RefGen_v3	Gene	Chr3	214938624	214943016	hb46		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2263	hb47	Homeobox-transcription factor 47	GRMZM2G474656	B73 RefGen_v3	Gene	Chr6	160917510	160922715	hb47		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2264	hb48	Homeobox-transcription factor 48	GRMZM2G154641	B73 RefGen_v3	Gene	Chr3	179564866	179569662	hb48	BEL1-like homeodomain protein 9, BELL1-like Homeobox12, ZmBLH12	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2265	hb49	Homeobox-transcription factor 49	GRMZM2G097349	B73 RefGen_v3	Gene	Chr1	243185151	243187447	hb49		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2266	hb5	Homeobox-transcription factor 5	GRMZM2G132367	B73 RefGen_v3	Gene	Chr1	19250088	19252388	hb5		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2267	hb52	Homeobox-transcription factor 52	AC187157.4_FG005	B73 RefGen_v3	Gene	Chr8	22645969	22650386	hb52		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2268	hb53	Homeobox-transcription factor 53	GRMZM2G044752	B73 RefGen_v3	Gene	Chr2	21024779	21026404	hb53		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2269	hb54	Homeobox-transcription factor 54	GRMZM2G041127	B73 RefGen_v3	Gene	Chr2	188712314	188714917	hb54		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2270	hb55	Homeobox-transcription factor 55	GRMZM2G126170	B73 RefGen_v3	Gene	Chr7	85732538	85749435	hb55		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2271	hb56	Homeobox-transcription factor 56	GRMZM2G047715	B73 RefGen_v3	Gene	Chr4	121587332	121589718	hb56		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2272	hb57	Homeobox-transcription factor 57	GRMZM2G060444	B73 RefGen_v3	Gene	Chr2	92273726	92276759	hb57		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2273	hb59	Homeobox-transcription factor 59	GRMZM2G366130	B73 RefGen_v3	Gene	Chr2	186502150	186503354	hb59		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2274	hb6	Homeobox-transcription factor 6	GRMZM2G458728	B73 RefGen_v3	Gene	Chr4	212853641	212859163	hb6		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2275	hb60	Homeobox-transcription factor 60	GRMZM2G068672	B73 RefGen_v3	Gene	Chr6	70173601	70175049	hb60		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2276	hb62	Homeobox-transcription factor 62	GRMZM2G105834	B73 RefGen_v3	Gene	Chr9	145045937	145048121	hb62		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2277	hb63	Homeobox-transcription factor 63	GRMZM2G116063	B73 RefGen_v3	Gene	Chr3	178369720	178371133	hb63	WUSCHEL-related homeobox 9-like, ZmWOX5B	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2278	hb64	Homeobox-transcription factor 64	GRMZM2G004641	B73 RefGen_v3	Gene	Chr1	13640026	13643872	hb64		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2279	hb65	Homeobox-transcription factor 65	GRMZM2G151266	B73 RefGen_v3	Gene	Chr1	289933104	289944419	hb65		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2280	hb66	Homeobox-transcription factor 66	GRMZM2G351330	B73 RefGen_v3	Gene	Chr2	22220873	22222180	hb66		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2281	hb67	Homeobox-transcription factor 67	GRMZM2G047448	B73 RefGen_v3	Gene	Chr2	3392385	3393860	hb67	wus1 WUS1 protein, wuschel1 ortholog, ZmWUS1	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2282	hb69	Homeobox-transcription factor 69	GRMZM2G469551	B73 RefGen_v3	Gene	Chr1	230596368	230608346	hb69		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2283	hb7	Homeobox-transcription factor 7	GRMZM2G122076	B73 RefGen_v3	Gene	Chr4	77636576	77641035	hb7		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2284	hb70	Homeobox-transcription factor 70	GRMZM2G396527	B73 RefGen_v3	Gene	Chr10	133750205	133750699	hb70		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2285	hb71	Homeobox-transcription factor 71	GRMZM2G145690	B73 RefGen_v3	Gene	Chr5	211123234	211127092	hb71		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2286	hb73	Homeobox-transcription factor 73	GRMZM2G170958	B73 RefGen_v3	Gene	Chr10	70352497	70354031	hb73		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2287	hb74	Homeobox-transcription factor 74	GRMZM2G087741	B73 RefGen_v3	Gene	Chr3	53883227	53893066	hb74		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2288	hb75	Homeobox-transcription factor 75	GRMZM2G001289	B73 RefGen_v3	Gene	Chr2	8289450	8295761	hb75		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2289	hb76	Homeobox-transcription factor 76	GRMZM2G125976	B73 RefGen_v3	Gene	Chr6	151227594	151231779	hb76	BEL1-like homeodomain protein 9, BELL1-like Homeobox14, ZmBLH14	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2290	hb77	Homeobox-transcription factor 77	GRMZM2G134260	B73 RefGen_v3	Gene	Chr9	20839231	20841005	hb77		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2291	hb78	Homeobox-transcription factor 78	GRMZM2G148074	B73 RefGen_v3	Gene	Chr1	93082039	93083670	hb78		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2292	hb79	Homeobox-transcription factor 79	GRMZM2G370332	B73 RefGen_v3	Gene	Chr5	94481164	94484870	hb79	knox6	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2293	hb8	Homeobox-transcription factor 8	GRMZM2G135447	B73 RefGen_v3	Gene	Chr1	281887974	281894959	hb8	cR18, hb8, Homeobox-transcription factor 8, knotted related homeobox8a, knox8, knox8a, pge16c(knox8), pge(F8)	cDNA, shoot meristem and developing stem specific, similar in sequence and expression pattern to kn1
2294	hb81	Homeobox-transcription factor 81	GRMZM5G830671	B73 RefGen_v3	Gene	Chr6	88279708	88280617	hb81		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2295	hb82	Homeobox-transcription factor 82	GRMZM2G122537	B73 RefGen_v3	Gene	Chr6	30106417	30108536	hb82		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2296	hb83	Homeobox-transcription factor 83	GRMZM2G126646	B73 RefGen_v3	Gene	Chr4	177612036	177616331	hb83		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2297	hb84	Homeobox-transcription factor 84	GRMZM2G099319	B73 RefGen_v3	Gene	Chr1	179614336	179618197	hb84	hb84, IDP8401, umc1988, umc2083	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.. NCBI:putative POX domain/homeobox DNA-binding domain family
2298	hb86	Homeobox-transcription factor 86	GRMZM2G008286	B73 RefGen_v3	Gene	Chr8	80197949	80198613	hb86		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2299	hb87	Homeobox-transcription factor 87	GRMZM2G163641	B73 RefGen_v3	Gene	Chr9	85249981	85252420	hb87		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2300	hb88	Homeobox-transcription factor 88	GRMZM2G038252	B73 RefGen_v3	Gene	Chr1	26128999	26132973	hb88		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2301	hb89	Homeobox-transcription factor 89	GRMZM2G339751	B73 RefGen_v3	Gene	Chr8	168495729	168496249	hb89	WUSCHEL-related homeobox 5-like, ZmWOX2B	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2302	hb9	Homeobox-transcription factor 9	GRMZM2G351018	B73 RefGen_v3	Gene	Chr8	174048466	174058838	hb9		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2303	hb90	Homeobox-transcription factor 90	GRMZM2G419252	B73 RefGen_v3	Gene	Chr4	89175622	89178462	hb90		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2304	hb91	Homeobox-transcription factor 91	GRMZM2G122897	B73 RefGen_v3	Gene	Chr10	142812773	142817535	hb91	bnl7.49, bnl7.49a, bnl7.49a(hmd), hb91, HDZIV8_OCL8, rs128351664 , rs128351665 , rs128351668 , rs131185945 , rs132617720 , rs132617743 , rs132617775	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.. NCBI: Homeodomain leucine zipper family IV protein. Tests with B-

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
2305	hb92	Homeobox-transcription factor 92	GRMZM2G094935	B73 RefGen_v3	Gene	Chr6	161060698	161065860	hb92		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2306	hb93	Homeobox-transcription factor 93	GRMZM2G318412	B73 RefGen_v3	Gene	Chr2	227700670	227702965	hb93		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2307	hb94	Homeobox-transcription factor 94	GRMZM2G108933	B73 RefGen_v3	Gene	Chr3	181120106	181123399	hb94	WUSCHEL-related homeobox 5, ZmWOX2A	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2308	hb96	Homeobox-transcription factor 96	GRMZM2G438260	B73 RefGen_v3	Gene	Chr2	92119412	92123393	hb96		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2309	hb98	Homeobox-transcription factor 98	GRMZM5G803812	B73 RefGen_v3	Gene	Chr5	35029700	35031902	hb98		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2310	hb99	Homeobox-transcription factor 99	GRMZM2G159357	B73 RefGen_v3	Gene	Chr3	210208545	210222742	hb99		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2311	hbtf2	Homeobox-transcription factor 2	GRMZM2G161435	B73 RefGen_v3	Gene	Chr5	152442185	152445449	hbtf2	hb2, ZmHB2	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2312	hcf106	high chlorophyll fluorescence106	GRMZM5G898735	B73 RefGen_v3	Gene	Chr2	65813104	65819647	hcf106	cl1262_1(138), CL1262_1a, hcf106, high chlorophyll fluorescence106	affects PSI, PSII, cytochrome bf. Required for thylakoid protein targeting via the TAT pathway. Ortholog of bacterial TatB. (A. Barkan, 2015)
2313	hcf106c	high chlorophyll fluorescence106c	GRMZM2G151529	B73 RefGen_v3	Gene	Chr10	110944324	110948048	hcf106c	CL1262_1b, hcf106c, hcf106 cognate, high chlorophyll fluorescence106c	encodes a homolog of hcf106 with which it is 90% identical in nucleotide sequence and 87% identical in amino acid sequence.
2314	hcf148	high chlorophyll fluorescence148	GRMZM2G002165	B73 RefGen_v3	Gene	Chr3	188589432	188595258	hcf148	hcf148, pco091280, pco091280(260), y3IP1, ycf3 intracting protein homolog1	PSI assembly factor and cooperates with Ycf3. Ortholog of Arabidopsis Y3IP1. PSI assembly factor, cooperates with Ycf3. (A. Barkan, 2015)
2315	hcf3	high chlorophyll fluorescence3	GRMZM2G121960	B73 RefGen_v3	Gene	Chr1	49770451	49792278	hcf3	hcf107, hcf3, hcf*-846B, hcf9, hcf*-N846B, high chlorophyll fluorescence3, umc(hcf3)	(aka hcf9, hcf107) missing PSII thylakoid membrane core complex; green seedling; RNA metabolism
2316	hcf60	high chlorophyll fluorescence60	GRMZM2G038013	B73 RefGen_v3	Gene	Chr10	148969561	148970286	hcf60	hcf60, high chlorophyll fluorescence60, RPS17	green to pale green seedling leaves, deficiency in photosystem I
2317	hcp101a		GRMZM2G030628	B73 RefGen_v3	Gene	Chr4	66925030	66935727	hcp101a	PZA03597, rs131175597, ss196415764	
2318	hcp101b		GRMZM2G060669	B73 RefGen_v3	Gene	Chr4	238860480	238864568	hcp101b	PZA03598, rs129966070, rs55624447 , ss196415955	
2319	hct1	hydroxycinnamoyltransferase1	GRMZM2G061806	B73 RefGen_v3	Gene	Chr1	17782100	17783717	hct1	agmatine coumaroyltransferase-1-like, hct1, HCT1806	up-regulated in the Rp1-D21 mutant lines; colocalized with the SNP associated with Rp1-D21-induced HR
2320	hct10	hydroxycinnamoyltransferase10	GRMZM2G034360	B73 RefGen_v3	Gene	Chr8	166031514	166034207	hct10	hct10	
2321	hct11	hydroxycinnamoyltransferase11	GRMZM2G156296	B73 RefGen_v3	Gene	Chr7	117397049	117407481	hct11	hct11, IDP2411, IDP2494	
2322	hct12	hydroxycinnamoyltransferase12	GRMZM2G179703	B73 RefGen_v3	Gene	Chr1	202955872	202958418	hct12	hct12	
2323	hct13	hydroxycinnamoyltransferase13	GRMZM2G129266	B73 RefGen_v3	Gene	Chr1	225937241	225939365	hct13	hct13	
2324	hct2	hydroxycinnamoyltransferase2	GRMZM2G114918	B73 RefGen_v3	Gene	Chr1	17842579	17844302	hct2	hct2, HCT4918	up-regulated in the Rp1-D21 mutant lines; colocalized with the SNP associated with Rp1-D21-induced HR
2325	hct3	hydroxycinnamoyltransferase3	GRMZM2G127251	B73 RefGen_v3	Gene	Chr6	107006046	107007725	hct3	hct3, HCT7251	up-regulated in the Rp1-D21 mutant lines
2326	hct4	hydroxycinnamoyltransferase4	GRMZM2G030436	B73 RefGen_v3	Gene	Chr1	140328950	140330902	hct4	HCT0436, hct4	up-regulated in the Rp1-D21 mutant lines
2327	hct5	hydroxycinnamoyltransferase5	GRMZM2G158083	B73 RefGen_v3	Gene	Chr2	32452526	32458616	hct5	hct5, HCT8083, TIDP2701, ZmHCT2	up-regulated in the Rp1-D21 mutant lines
2328	hct6	hydroxycinnamoyltransferase6	GRMZM2G035584	B73 RefGen_v3	Gene	Chr5	183658122	183663110	hct6	CL531_1, CL531_1(436), gnp_AI857226, gpm105, HCT5584, hct6, PZA03435, PZA03452, rs128283141, ss196416233, ZmHCT1	up-regulated in the Rp1-D21 mutant lines
2329	hct7	hydroxycinnamoyltransferase7	AC215260.3_FG003	B73 RefGen_v3	Gene	Chr3	17028296	17029723	hct7	hct7	down-regulated in Rp1-D21 mutant lines
2330	hct8	hydroxycinnamoyltransferase8	GRMZM2G178769	B73 RefGen_v3	Gene	Chr3	21151937	21153907	hct8	hct8	down-regulated in Rp1-D21 mutant lines
2331	hct9	hydroxycinnamoyltransferase9	GRMZM2G131165	B73 RefGen_v3	Gene	Chr1	211484865	211490236	hct9	hct9	down-regulated in Rp1-D21 mutant lines
2332	hda102	histone deacetylase	GRMZM2G119703	B73 RefGen_v3	Gene	Chr2	59091885	59102871	hda102	hda102, hda112, histone deacetylase, IDP1401, PCO127561, ZmRpd3/102	
2333	hda108	histone deacetylase	GRMZM2G136067	B73 RefGen_v3	Gene	Chr4	65983218	65988818	hda108	PZA03587, PZA03751, PZA03752, PZA03753, rs129719420, rs129719435, rs131175593, rs131175594, rs131175595, rs131175596, rs55622927 , ss196415752, ss196415754,	
2334	hda109	histone deacetylase	GRMZM2G457889	B73 RefGen_v3	Gene	Chr2	210299363	210310868	hda109	hda1, hda109, histone deacetylase, histone deacetylase 6, rpd3	
2335	hda110	histone deacetylase	GRMZM2G107309	B73 RefGen_v3	Gene	Chr7	7273053	7285361	hda110	hda110, histone deacetylase	
2336	hds1	hydroxymethylbutenyl diphosphate synth	GRMZM2G137409	B73 RefGen_v3	Gene	Chr5	182174564	182181190	hds1	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase1, hds1, Hydroxymethylbutenyl diphosphate synthase1	
2337	hdt102	histone deacetylase102	GRMZM2G100146	B73 RefGen_v3	Gene	Chr8	135663882	135666488	hdt102	gnp_QCI25g10, gpm669, hd2b, HD2b, hda103, hdt102, PCO120143	
2338	hdt103	histone deacetylase103	GRMZM2G159032	B73 RefGen_v3	Probed Site	Chr6	161426908	161429635	hdt103	HD2a, hd2c, HD2c, HD2-p39, hda104, hda105, hdt103, PCO151917	
2339	hen1	hua enhancer1	GRMZM2G107457	B73 RefGen_v3	Gene	Chr7	7266068	7271089	hen1	enhancer of agamous-4 1, hen1, HUA means "flower" in Chinese, small RNA 2'-O-methyltransferase	mutant has a shoot-meristemless phenotype
2340	hex1	hexokinase1	GRMZM2G104081	B73 RefGen_v3	Gene	Chr3	7079526	7083312	hex1	hex1, hexokinase1, ZmHXK1, ZmHXK8	electrophoretic mobility; null allele is known; cytosolic; monomeric
2341	hex2	hexokinase2	GRMZM2G432801	B73 RefGen_v3	Gene	Chr6	160433339	160440597	hex2	hex2, hexokinase2, ZmHXK5, ZmHXK7	electrophoretic mobility; null allele is known; cytosolic; monomeric
2342	hex3	hexokinase3	GRMZM2G058745	B73 RefGen_v3	Gene	Chr8	124182497	124187982	hex3	hex3, HXK, PCO074668, PCO074668(625), ZmHXK4, ZmHXK8	
2343	hex4	hexokinase4	GRMZM2G068913	B73 RefGen_v3	Gene	Chr3	152214617	152221102	hex4	hex4, ZmHXK2, ZmHXK3a	
2344	hex5	hexokinase5	GRMZM5G856653	B73 RefGen_v3	Gene	Chr3	199340491	199346889	hex5	hex5, ZmHXK3, ZmHXK6	
2345	hex6	hexokinase6	GRMZM2G171373	B73 RefGen_v3	Gene	Chr3	201861549	201871591	hex6	hex6, ZmHXK4, ZmHXK9	
2346	hex7	hexokinase7	GRMZM2G051806	B73 RefGen_v3	Gene	Chr6	130163346	130166258	hex7	hex7, ZmHXK5, ZmHXK7	
2347	hex8	hexokinase8	GRMZM2G046686	B73 RefGen_v3	Gene	Chr6	136146698	136151875	hex8	hex8, ZmHXK10, ZmHXK6	
2348	hex9	hexokinase9	GRMZM2G467069	B73 RefGen_v3	Gene	Chr8	158729478	158739079	hex9	hex9, ZmHXK3b, ZmHXK9	
2349	hfi1	corn-activated Hageman factor inhibitor1	GRMZM2G304548	B73 RefGen_v3	Gene	Chr2	160784375	160785866	hfi1	chfi, corn-activated Hageman factor inhibitor1, gnp_QDA2E10a, gpm942a, hfi1, PCO139754	cDNA clone corresponds to partial amino acid sequence; expression in yeast confirms product inhibits trypsin
2350	hggt1	homogentisate geranylgeranyl transferas	GRMZM2G173358	B73 RefGen_v3	Gene	Chr9	93489726	93493445	hggt1	hggt1, homogentisate geranylgeranyl transferase1	vitamin E synthesis; contributes to variation in levels of tocotrienol (Lipka et al 2013)
2351	hir1	hypersensitive induced reaction1	GRMZM2G117755	B73 RefGen_v3	Gene	Chr4	74484144	74488082	hir1	gnp_QBF11d12, gpm448, hdr10, highly disease-resistant10, hir1, hypersensitive induced reaction1, PCO110854, PCO110854(317), Zm-hir1	
2352	hir2	hypersensitive induced response2	GRMZM2G150762	B73 RefGen_v3	Gene	Chr2	177284136	177287072	hir2	hir2, hypersensitive induced response2, Zm-hir2	cDNA sequence
2353	hir3	hypersensitive induced reaction3	GRMZM2G070659	B73 RefGen_v3	Gene	Chr6	167774457	167777264	hir3	hir3, hypersensitive induced reaction3, PCO125989, umc2324, Zm-hir3	cDNA, up-regulated in Les9

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
2354	his1a	histone1a	GRMZM2G401308	B73 RefGen_v3	Gene	Chr7	11446087	11450539	his1a	csu13, csuh13, his1a, histone1a, hon102, umc1577, umc312, umc312(gfu)	cDNA sequences, SSR umc1577
2355	his2a1	histone2A1	GRMZM2G305046	B73 RefGen_v3	Gene	Chr9	139441605	139442697	his2a1	CL2029_4(696), CL2029_4b, H2A, his2a1, histone2A1, Zm.ov5	cDNA from unfertilized ovule, similar to histone2A
2356	his2b1	histone2b1	GRMZM2G071959	B73 RefGen_v3	Gene	Chr7	119943268	119944091	his2b1	h2b(1), h2b(2), his2b1, histone2b1	cDNA to mRNA from 8 day seedlings, protein reacts with antibodies for histone H2B
2357	his2b2	histone2b2	GRMZM2G119071	B73 RefGen_v3	Gene	Chr4	63118802	63120057	his2b2	cH2B221, h2b, H2B.2, his2b2, histone2b2	cDNA to mRNA from seedlings, protein reacts with histone2B antibodies
2358	his2b3	histone 2B3	GRMZM2G057852	B73 RefGen_v3	Gene	Chr2	183846599	183847686	his2b3	his2b3, histone 2B3, uaz228a(his2b), uaz28(h2b)	genomic sequence selected with his2B cDNA probe
2359	his2b4	histone 2B4	GRMZM2G306258	B73 RefGen_v3	Gene	Chr3	181560116	181560956	his2b4	his2b4, histone 2B4	genomic sequence selected with his2B cDNA probe
2360	his2b5	histone 2B5	GRMZM2G342515	B73 RefGen_v3	Gene	Chr4	160982217	160983377	his2b5	H2B, his2b5, his2b*-U08226, histone 2B*-U08226, Zm.ov1	cDNA from unfertilized maize ovule, similar to histone 2B, distinct from previous sequences reported
2361	hk1	histidine kinase1	GRMZM2G151223	B73 RefGen_v3	Gene	Chr5	205601061	205610801	hk1	CL29589_1(447), CL29589_1b, hk1, ZmOrphan238	cytokinin receptor; cytokinin responsive histidine protein kinase
2362	hk2	histidine kinase2	GRMZM2G471529	B73 RefGen_v3	Gene	Chr3	158932008	158938325	hk2	rs129449829, rs131175517, rs132046727, rs132046746, rs132046749, rs132046750, ss196415481, ss196415483, ss196415485, TIDP5840, ZmOrphan59	cytokinin responsive histidine protein kinase
2363	hk3	histidine kinase3	GRMZM2G158252	B73 RefGen_v3	Gene	Chr5	38775552	38832527	hk3	gnp_AW433448a, gpm227a, hk3, hk3a, hk3b, TIDP5368, ZmOrphan248	cytokinin responsive histidine protein kinase
2364	hk4	histidine kinase4	GRMZM2G155767	B73 RefGen_v3	Gene	Chr1	269016266	269022761	hk4	gnp_QAI15h08, gpm791, HK1b1; ZmHK1b1, hk4, ZmOrphan157	
2365	hk5	histidine kinase5	GRMZM2G025579	B73 RefGen_v3	Gene	Chr9	108537120	108544101	hk5	hk5, Signal-TF, ZmOrphan79	
2366	hk6	histidine kinase6	GRMZM2G125943	B73 RefGen_v3	Gene	Chr4	167410132	167416477	hk6	HK1a2, hk6, ZmOrphan61	
2367	hm1	Helminthosporium carbonum susceptibili	GRMZM5G881887	B73 RefGen_v3	Gene	Chr1	199788957	199790819	hm1	Helminthosporium carbonum susceptibility1, hm1, umc276a	disease lesions vs. yellowish flecks (Hm1, resistant) on leaves with Cochliobolus carbonum race 1
2368	hm2	Helminthosporium carbonum susceptibili	GRMZM2G086773	B73 RefGen_v3	Gene	Chr9	104241216	104242847	hm2	anthocyanidin reductase-like, Helminthosporium carbonum susceptibility2, hm2, umc276b	dominant Hm2 plants resistant to Cochliobolus carbonum; like Hm1, masked by Hm1
2369	hma1	heavy metal associated1	GRMZM2G136859	B73 RefGen_v3	Gene	Chr1	4439061	4441061	hma1	cl15090_1(4), hma1, metal ion binding protein, PZA02032	
2370	hmg1	high mobility group protein1	GRMZM5G834758	B73 RefGen_v3	Gene	Chr5	63828350	63830554	hmg1	high mobility group protein1, hmg1, MNB1b for DNA-binding protein, PCO080122, ZmHMG8	cDNA sequence isolated by immunoscreening, homologous to vertebrate HMG1 family, single or low copy gene
2371	hmg10	HMG-transcription factor 10	GRMZM2G013821	B73 RefGen_v3	Lapsed Locus	Chr5	194096097	194097995	hmg10	hmg2	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2372	hmg101	HMG-transcription factor 101	AC186524.3_FG005	B73 RefGen_v3	Gene	Chr1	180986274	180988780	hmg101	hmg1, hmg101, HMG-transcription factor 101	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2373	hmg103	HMG-transcription factor 3	GRMZM2G162284	B73 RefGen_v3	Gene	Chr2	198277094	198279041	hmg103	hmg103, hmg3, HMG-transcription factor 3	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2374	hmg11	HMG-transcription factor 11	GRMZM2G150348	B73 RefGen_v3	Gene	Chr6	82492934	82493876	hmg11		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2375	hmg12	HMG-transcription factor 12	GRMZM5G842484	B73 RefGen_v3	Gene	Chr6	128066887	128073852	hmg12		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2376	hmg13	HMG-transcription factor 13	GRMZM2G066528	B73 RefGen_v3	Gene	Chr7	146931998	146933950	hmg13		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2377	hmg14	HMG-transcription factor 14	GRMZM2G032252	B73 RefGen_v3	Gene	Chr8	21829304	21836106	hmg14	nfd110	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2378	hmg2	high mobility group box protein2	GRMZM2G013821	B73 RefGen_v3	Gene	Chr5	194096097	194097995	hmg2	gnp_QCl21c11b, gpm936b, high mobility group box protein2, hmg10, hmg2, HMGc1, nfd104, nfd104a, nucleosome/chromatin assembly factor D	cDNA and protein sequences correspond; protein expressed in E. coli has anticipated specificity of binding to DNA structures
2379	hmg3	high mobility group protein3	GRMZM2G156785	B73 RefGen_v3	Gene	Chr4	154652176	154654247	hmg3	gnp_QCl21c11a, gpm936a, high mobility group protein3, hmg3, hmg6, HMGc2, ZmHMG6	
2380	hmg4	HMG-transcription factor 4	GRMZM2G024247	B73 RefGen_v3	Gene	Chr3	210840744	210844797	hmg4		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2381	hmg5	HMG-transcription factor 5	GRMZM2G144398	B73 RefGen_v3	Gene	Chr4	142353620	142359570	hmg5		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2382	hmg9	HMG-transcription factor 9	GRMZM2G060253	B73 RefGen_v3	Gene	Chr5	140132841	140135501	hmg9		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2383	hmga102	high mobility group family A 102	GRMZM2G106133	B73 RefGen_v3	Gene	Chr1	215379973	215381486	hmga102	cl1069_1, cl1069_1(62), high mobility group family A 102, hmg2, hmga102, hmgi/y, hmgi/y2, hon105	confers nickel resistance when expressed in yeast
2384	hmt1	homocysteine S-methyltransferase 1	GRMZM6G310687	B73 RefGen_v3	Gene	Chr9	146516121	146519277	hmt1	hmt1, homocysteine S-methyltransferase 1	
2385	hmt4	homocysteine S-methyltransferase4	GRMZM2G039166	B73 RefGen_v3	Gene	Chr3	192284006	192285910	hmt4	cl1142_1, cl1142_1(262), hmt4, homocysteine S-methyltransferase4, PHM824, PZA01986	
2386	ho2	heme oxygenase2	GRMZM2G043277	B73 RefGen_v3	Gene	Chr6	102756604	102759557	ho2	elm2-chr6, heme oxygenase, ho2	encodes a heme oxygenase
2387	ho3	heme oxygenase3	GRMZM2G157936	B73 RefGen_v3	Gene	Chr9	89991673	89992909	ho3	heme oxygenase, heme oxygenase-like, ho3	encodes a heme oxygenase
2388	hon101	histone one (H1) 101	GRMZM2G080274	B73 RefGen_v3	Gene	Chr2	16047725	16049837	hon101	histone one (H1) 101, hon101	
2389	hon110	histone one (H1)	GRMZM2G164020	B73 RefGen_v3	Gene	Chr1	288803887	288805620	hon110	alh1, alpha subfraction lysine-rich histones1, H1a, histone la, histone one (H1), hon110, rs128975628, rs128975633 i	(was H1a); mapped by electrophoretic mobility polymorphism as alh1
2390	hox1	homeobox1	GRMZM2G136369	B73 RefGen_v3	Gene	Chr8	123435516	123441977	hox1	CL1479_1, gsy242a(hox1), hb103, homeobox1, Homeobox-transcription factor 103, hox1, hox1a, koln1a, koln1A, umc1309, umc1343, Zmhox1.1, Zmhox1a	cDNA Zmhox1a, meristem specific, nuclear, protein product binds to feedback control element of sh1 promoter; SSR's umc1309, umc1343
2391	hox2	homeobox2	GRMZM2G094935	B73 RefGen_v3	Gene	Chr6	161060698	161065860	hox2	CL1479_1a, homeobox2, hox1b, hox2, koln1b, Zmhox1b	cDNA ZmHox1b, meristem specific, duplicate of hox1 based on sequence and expression
2392	hox3	homeobox3	GRMZM2G314546	B73 RefGen_v3	Gene	Chr3	197462441	197475910	hox3	cl2032_1(265), CL2032_1a, hb32, homeobox3, Homeobox-transcription factor 32, hox2a, hox3, ZmHox2a	cDNA ZmHox2a, meristem specific, duplicate of hox4, based on sequence and expression; sequence distinct from knotted related homeobox genes
2393	hp1	histidine-containing phosphotransfer pro	GRMZM2G016439	B73 RefGen_v3	Gene	Chr1	205263817	205266907	hp1	hp1, ZmHP1	
2394	hp2	histidine-containing phosphotransfer pro	GRMZM2G014154	B73 RefGen_v3	Gene	Chr2	166064149	166067375	hp2	histidine-containing phosphotransfer protein2, hp2, ZmHP2	single copy, cDNA sequence, ubiquitous
2395	hp3	histidine-containing phosphotransfer pro	GRMZM2G451604	B73 RefGen_v3	Gene	Chr4	52969280	52972871	hp3	histidine-containing phosphotransfer protein 5, hp3, ZmHP3	
2396	hpl1	hydroperoxide lyase1	GRMZM6G986387	B73 RefGen_v3	Gene	Chr4	240875600	240876493	hpl1	hpl1	
2397	hppd1	4-hydroxyphenylpyruvate dioxygenase 1	GRMZM2G088396	B73 RefGen_v3	Gene	Chr5	83895923	83898077	hppd1	4-hydroxyphenylpyruvate dioxygenase 1, hppd1	
2398	hrbp1	harpin binding protein1	GRMZM2G015285	B73 RefGen_v3	Gene	Chr2	228792133	228793917	hrbp1	csu393(fbn), hrbp1	
2399	hrg1	hydroxyproline rich glycoprotein1	GRMZM2G168651	B73 RefGen_v3	Gene	Chr2	55391917	55393690	hrg1	Ext0, hrg1, HRGP, hydroxyproline rich glycoprotein1, IDP20, IDP21, IDP2491, IDP2509, PCO091178, umc145-hrg, umc1485	cDNA, genomic clones, peptide sequence, single site (Southern analysis), accumulates in dividing cells, preferentially in provascular cells
2400	hsbp1	herbicide safener binding protein1	GRMZM2G085924	B73 RefGen_v3	Gene	Chr2	127723813	127725400	hsbp1	herbicide safener binding protein1, hsbp1, O-methyltransferase ZRP4, SafBP, safener binding protein, SBP1, umc1535, ZRP4	coleoptile; cDNA sequences, SSR umc1535; antisera; transgenic expression
2401	hsbp2	heat shock factor binding protein2	GRMZM2G065355	B73 RefGen_v3	Gene	Chr9	34805920	34808236	hsbp2	heat shock factor-binding protein 1, heat shock factor binding protein2, hsbp2, PCO089094b	
2402	hscf1	heat shock complementing factor1	GRMZM2G139082	B73 RefGen_v3	Gene	Chr9	107641598	107645415	hscf1	aintegumenta-like protein, heat shock complementing factor1, hscf1, MHCF1, PCO137288, PCO137288(679), PZA00225, ZmEREB152	cDNA with 2 APETALA2-like binding domains

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
2403	hsftf1	HSF-transcription factor 1	GRMZM2G002131	B73 RefGen_v3	Gene	Chr2	186829423	186833487	hsftf1	hsf1	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2404	hsftf10	HSF-transcription factor 10	GRMZM2G165272	B73 RefGen_v3	Gene	Chr7	142270318	142272208	hsftf10	hsf10	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2405	hsftf11	HSF-transcription factor 11	GRMZM2G132971	B73 RefGen_v3	Gene	Chr1	287786016	287790222	hsftf11	hsf11	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2406	hsftf12	HSF-transcription factor 12	GRMZM2G173090	B73 RefGen_v3	Gene	Chr9	59460534	59462007	hsftf12	hsf12	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2407	hsftf13	HSF-transcription factor 13	GRMZM2G165972	B73 RefGen_v3	Gene	Chr1	12518410	12520734	hsftf13	hsf13	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2408	hsftf14	HSF-transcription factor 14	GRMZM2G118485	B73 RefGen_v3	Gene	Chr1	28522823	28530238	hsftf14	hsf14	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2409	hsftf15	HSF-transcription factor 15	AC206165.3_FG007	B73 RefGen_v3	Gene	Chr6	159812447	159814105	hsftf15	hsf15	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2410	hsftf16	HSF-transcription factor 16	AC205471.4_FG003	B73 RefGen_v3	Gene	Chr8	124710390	124712153	hsftf16	hsf16	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2411	hsftf17	HSF-transcription factor 17	GRMZM2G003489	B73 RefGen_v3	Gene	Chr1	275536823	275539066	hsftf17	hsf17	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2412	hsftf18	HSF-transcription factor 18	GRMZM2G105348	B73 RefGen_v3	Gene	Chr5	150228697	150230232	hsftf18	hsf18	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2413	hsftf19	HSF-transcription factor 19	AC216247.3_FG001	B73 RefGen_v3	Gene	Chr1	63539447	63541926	hsftf19	hsf19	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2414	hsftf2	HSF-transcription factor 2	GRMZM2G088242	B73 RefGen_v3	Gene	Chr2	185666362	185668432	hsftf2	hsf2	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2415	hsftf20	HSF-transcription factor 20	GRMZM2G301485	B73 RefGen_v3	Gene	Chr10	137124859	137126235	hsftf20	hsf20	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2416	hsftf21	HSF-transcription factor 21	GRMZM2G139535	B73 RefGen_v3	Gene	Chr7	125896425	125900126	hsftf21	hsf21	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2417	hsftf22	HSF-transcription factor 22	GRMZM2G384339	B73 RefGen_v3	Gene	Chr5	889476	893867	hsftf22	hsf22	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2418	hsftf23	HSF-transcription factor 23	GRMZM2G089525	B73 RefGen_v3	Gene	Chr3	217438918	217440728	hsftf23	hsf23	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2419	hsftf24	HSF-transcription factor 24	GRMZM2G010871	B73 RefGen_v3	Gene	Chr1	239674470	239678097	hsftf24	hsf24	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2420	hsftf25	HSF-transcription factor 25	GRMZM2G086880	B73 RefGen_v3	Gene	Chr8	144887947	144889311	hsftf25	hsf25	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2421	hsftf27	HSF-transcription factor 27	GRMZM2G025685	B73 RefGen_v3	Gene	Chr7	169214787	169218220	hsftf27	hsf27	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2422	hsftf28	HSF-transcription factor 28	GRMZM2G118047	B73 RefGen_v3	Gene	Chr9	77070952	77072996	hsftf28	hsf28	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2423	hsftf29	HSF-transcription factor 29	GRMZM2G179802	B73 RefGen_v3	Gene	Chr5	162047215	162053475	hsftf29	hsf29	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2424	hsftf3	HSF-transcription factor 3	GRMZM2G005815	B73 RefGen_v3	Gene	Chr3	219545854	219552097	hsftf3	hsf3	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2425	hsftf4	HSF-transcription factor 4	GRMZM2G125969	B73 RefGen_v3	Gene	Chr7	9712577	9716596	hsftf4	hsf4	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2426	hsftf5	HSF-transcription factor 5	GRMZM2G115456	B73 RefGen_v3	Gene	Chr1	299272434	299277717	hsftf5	hsf5	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2427	hsftf6	HSF-transcription factor 6	GRMZM2G059851	B73 RefGen_v3	Gene	Chr5	168263116	168266561	hsftf6	hsf6	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2428	hsftf7	HSF-transcription factor 7	GRMZM2G098696	B73 RefGen_v3	Gene	Chr4	195298840	195300584	hsftf7	hsf7	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2429	hsftf8	HSF-transcription factor 8	GRMZM2G164909	B73 RefGen_v3	Gene	Chr1	197781323	197783002	hsftf8	hsf8	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2430	hsftf9	HSF-transcription factor 9	GRMZM2G026742	B73 RefGen_v3	Gene	Chr9	146028201	146032662	hsftf9	hsf9	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2431	hsk1	high-sulfur keratin homolog1	GRMZM5G844723	B73 RefGen_v3	Gene	Chr9	129484814	129489588	hsk1	high-sulfur keratin homolog1, hsk1, uaz144	endosperm cDNA 5C04B04 (uaz144), similar to high-sulfur keratin; relation to uaz144a (bin 4.06) and uaz144b (bin 5.06) unclear
2432	hsp1	heat shock protein1	GRMZM2G310431	B73 RefGen_v3	Gene	Chr8	168506539	168509902	hsp1	CL45_1, CL45_1(648), heat shock protein1, hsp1, hsp70, npi119-hsp1	genomic clones, single copy (Southern blots), transcribed (Northern blots), transgenic (petunia) expression
2433	hsp101	heat-shock protein 101	GRMZM2G360681	B73 RefGen_v3	Gene	Chr6	160816570	160820239	hsp101	CL1518_1, heat-shock protein 101, hsp101, PZB01569, rs130443277, ss196416492	normal primary roots contain protein HSP101 conferring acclimation at 40C; to 50C shock; null mutants fail to acclimate and shock is lethal
2434	hsp17.2	heat shock protein17.2	GRMZM2G422240	B73 RefGen_v3	Gene	Chr3	20468262	20468719	hsp17.2	16.9 kDa class I heat shock protein 1, CL13719_1, CL13719_1(207), CL2172_1(207), CL2172_1a, heat shock protein 18, hsp17.2, hsp18-X65725, Zmhsp17.2	seedling expressed heat shock protein; cDNA sequence similar to other plant 18 kDa heat shock proteins but distinct in maize
2435	hsp18a	18 kda heat shock protein18a	GRMZM2G404249	B73 RefGen_v3	Gene	Chr9	132803660	132804501	hsp18a	17.5 kDa class II heat shock protein, 18 kda heat shock protein18a, hsp18a, IDP1957, Mhsp18-1, MHSP18-1, uwo9	induced by heat shock specifically in anthers or spikelets containing meitotic microsporocytes
2436	hsp18c	heat shock protein18c	GRMZM2G034157	B73 RefGen_v3	Gene	Chr8	21620266	21621116	hsp18c	17.5 kDa class II heat shock protein, heat shock protein18c, hsp18c, IDP2369, IDP6930, MHSP18-3, Mhsp18-9, uwo11	induced by heat shock specifically in anthers or spikelets containing meiotic microsporocytes
2437	hsp18f	heat shock protein18f	GRMZM2G083810	B73 RefGen_v3	Gene	Chr3	8887555	8888747	hsp18f	cMHSP18-9, heat shock protein18f, hsp18f, Mhsp18-3, pZmhsp 17.2, ttu1(hsp18), uaz210, uaz210(heat), uaz210(hsp18), uwo10	induction by heat shock is developmentally constitutive
2438	hsp22	heat shock protein22	GRMZM2G007729	B73 RefGen_v3	Gene	Chr4	179852643	179853912	hsp22	hsp22, pco116068, pco116068(332)	mitochondrial protein
2439	hsp26	heat shock protein26	GRMZM2G149647	B73 RefGen_v3	Gene	Chr1	33464178	33465385	hsp26	heat shock protein26, hsp26, sil28712, sil28712(14), umc195(hsp26)	was umc195; cDNA, single mRNA species induced by heat shock, in vitro HSP26 imported by isolated chloroplasts, cross-reacts with anti-pea-chloroplast-HSP21 antibodies
2440	hsp3	heat shock protein3	GRMZM6G199466	B73 RefGen_v3	Gene	scaffold_:81		586	hsp3	heat shock protein3, hsp3, umc1545, umc1546	cDNA sequences, SSRs umc1546, umc1545
2441	hsp70-4	heat shock protein70-4	GRMZM2G340251	B73 RefGen_v3	Gene	Chr3	126479381	126484522	hsp70-4	early responsive to dehydration2, heat shock protein70*-X78414, hsp70-4, hsp70*-X78414, ZmERD2	
2442	hsp90	heat shock protein, 90 kDa	GRMZM5G833699	B73 RefGen_v3	Gene	Chr10	93697766	93700740	hsp90	heat shock protein, 90 kDa, hsp82, hsp90, hsp90*, phi071	heat-induced; encoded protein interacts with HSP101
2443	hstf2	heat shock transcription factor2	GRMZM2G118453	B73 RefGen_v3	Gene	Chr8	173979796	173982203	hstf2	CL2307_1, CL2307_1(646), heat shock transcription factor2, hsfb, hsftf26, HSF-transcription factor 26, hstf2	pollen cDNA similar to eucaryotic heat shock factor
2444	htn1	Helminthosporium turcicum resistanceN1	GRMZM2G164612	B73 RefGen_v3	Gene	Chr8	151637927	151643014	htn1	Helminthosporium turcicum resistanceN1, HtN, htn1, wall-associated receptor-like kinase1, ZmWAK-RLK1	formerly HtN; dominant Htn1 plants resistant to Exserohilum turcicum
2445	hvp1	human viral protein homolog1	GRMZM5G852396	B73 RefGen_v3	Gene	Chr9	18325419	18326021	hvp1	human viral protein homolog1, hvp1, uazT14771(gfu), UPF0369 protein C6orf57 homolog	endosperm cDNA 5C02B04, similar to a virus transcription activator
2446	hyd3	hydroxylase3	GRMZM2G152135	B73 RefGen_v3	Gene	Chr10	136081567	136084686	hyd3	bch2, beta-carotene hydroxylase 1, BOHase1, crtRB1, CrtR-B1, hyd3	beta-carotene hydroxylase
2447	hyd4	hydroxylase4	GRMZM2G164318	B73 RefGen_v3	Gene	Chr2	15877183	15879464	hyd4	bch1, BCH1, beta-carotene hydroxylase homolog, BOHase2, crtRB3, HYD1, hyd4	beta-carotene hydroxylase
2448	hyd5	hydroxylase5	GRMZM2G382534	B73 RefGen_v3	Gene	Chr9	153962138	153964502	hyd5	crtRB5, hyd5	beta-carotene hydroxylase
2449	hyd6	hydroxylase6	GRMZM2G090051	B73 RefGen_v3	Gene	Chr1	5373808	5376230	hyd6	beta-carotene hydroxylase homolog, crtRB2, hyd6	beta-carotene hydroxylase
2450	hyd7	hydroxylase7	GRMZM2G163683	B73 RefGen_v3	Gene	Chr4	236566951	236568885	hyd7	crtRB4, hyd3, hyd7, hydroxylase7	beta-carotene hydroxylase
2451	hyd8	hydroxylase8	GRMZM5G826824	B73 RefGen_v3	Gene	Chr1	6347072	6348308	hyd8	hyd8	

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
2452	hyp1	hybrid proline-rich protein1	GRMZM2G304378	B73 RefGen_v3	Gene	Chr9	15981191	15983094	hyp1	gnp_QCI38g03, gpm672, hybrid proline-rich protein1, hyp1, Hyprp, PCO123892, PCO123892(660)	domains: proline-rich with PPVV and PPTPRPS elements and hydrophobic, cysteine-rich domain
2453	iaa1	Aux/IAA-transcription factor 1	GRMZM2G137367	B73 RefGen_v3	Gene	Chr1	6550506	6561486	iaa1		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2454	iaa10	Aux/IAA-transcription factor 10	GRMZM2G138268	B73 RefGen_v3	Gene	Chr3	117785060	117789665	iaa10		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2455	iaa11	Aux/IAA-transcription factor 11	GRMZM2G167794	B73 RefGen_v3	Gene	Chr3	118083629	118085345	iaa11		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2456	iaa12	Aux/IAA-transcription factor 12	GRMZM2G057067	B73 RefGen_v3	Gene	Chr3	199377733	199380221	iaa12		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2457	iaa13	Aux/IAA-transcription factor 13	GRMZM2G037368	B73 RefGen_v3	Lapsed Locus	Chr3	209176237	209179599	iaa13		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2458	iaa14	Aux/IAA-transcription factor 14	GRMZM2G031615	B73 RefGen_v3	Gene	Chr4	16440811	16449027	iaa14		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2459	iaa15	Aux/IAA-transcription factor 15	GRMZM2G148188	B73 RefGen_v3	Gene	Chr4	16521450	16523297	iaa15		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2460	iaa16	Aux/IAA-transcription factor 16	GRMZM2G059544	B73 RefGen_v3	Gene	Chr4	39589807	39591031	iaa16	ZmIAA11	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2461	iaa17	Aux/IAA-transcription factor 17	GRMZM2G390691	B73 RefGen_v3	Gene	Chr4	131399345	131410844	iaa17		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2462	iaa18	Aux/IAA-transcription factor 18	GRMZM2G142768	B73 RefGen_v3	Gene	Chr4	171402585	171405007	iaa18		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2463	iaa19	Aux/IAA-transcription factor 19	GRMZM2G152796	B73 RefGen_v3	Gene	Chr5	4201092	4202519	iaa19		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2464	iaa2	Aux/IAA-transcription factor 2	GRMZM2G079957	B73 RefGen_v3	Gene	Chr1	170553927	170555938	iaa2		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2465	iaa20	Aux/IAA-transcription factor 20	AC195340.3_FG004	B73 RefGen_v3	Gene	Chr5	5379304	5384290	iaa20		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2466	iaa21	Aux/IAA-transcription factor 21	GRMZM2G077356	B73 RefGen_v3	Gene	Chr5	7780495	7783441	iaa21		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2467	iaa22	Aux/IAA-transcription factor 22	GRMZM2G128421	B73 RefGen_v3	Gene	Chr5	17364530	17365963	iaa22	ZmIAA15	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2468	iaa23	Aux/IAA-transcription factor 23	GRMZM2G121309	B73 RefGen_v3	Gene	Chr5	151751416	151755323	iaa23		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2469	iaa24	Aux/IAA-transcription factor 24	GRMZM2G030465	B73 RefGen_v3	Gene	Chr5	214460676	214461910	iaa24		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2470	iaa25	Aux/IAA-transcription factor 25	GRMZM2G000158	B73 RefGen_v3	Gene	Chr6	80078086	80079839	iaa25		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2471	iaa26	Aux/IAA-transcription factor 26	GRMZM2G079200	B73 RefGen_v3	Gene	Chr6	103303641	103305338	iaa26		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2472	iaa28	Aux/IAA-transcription factor 28	GRMZM2G147243	B73 RefGen_v3	Gene	Chr6	133380995	133384727	iaa28	iaa17, iaa28	a transcription factor family by the GRASSIUS project (Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2473	iaa29	Aux/IAA-transcription factor 29	GRMZM2G141205	B73 RefGen_v3	Gene	Chr6	146698068	146698763	iaa29		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2474	iaa3	Aux/IAA-transcription factor 3	GRMZM2G366373	B73 RefGen_v3	Gene	Chr1	253362067	253363413	iaa3		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2475	iaa30	Aux/IAA-transcription factor 30	GRMZM2G074427	B73 RefGen_v3	Gene	Chr6	160362230	160365730	iaa30		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2476	iaa31	Aux/IAA-transcription factor 31	GRMZM2G149449	B73 RefGen_v3	Gene	Chr7	9398079	9398800	iaa31		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2477	iaa32	Aux/IAA-transcription factor 32	GRMZM2G115357	B73 RefGen_v3	Gene	Chr7	10975561	10976899	iaa32		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2478	iaa33	Aux/IAA-transcription factor 33	GRMZM2G048131	B73 RefGen_v3	Gene	Chr7	142810056	142811513	iaa33		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2479	iaa34	Aux/IAA-transcription factor 34	GRMZM5G853479	B73 RefGen_v3	Gene	Chr8	814321	815001	iaa34		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2480	iaa36	Aux/IAA-transcription factor 36	GRMZM2G573324	B73 RefGen_v3	Gene	Chr8	67598583	67602666	iaa36		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2481	iaa37	Aux/IAA-transcription factor 37	GRMZM2G359924	B73 RefGen_v3	Gene	Chr8	108094649	108096892	iaa37	ZmIAA33	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2482	iaa38	Aux/IAA-transcription factor 38	GRMZM2G035465	B73 RefGen_v3	Gene	Chr8	110338289	110342132	iaa38		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2483	iaa4	Aux/IAA-transcription factor4	GRMZM2G159285	B73 RefGen_v3	Gene	Chr1	275098311	275101078	iaa4	iaa4, umc1534, ZmIAA2	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2484	iaa40	Aux/IAA-transcription factor 40	GRMZM2G435290	B73 RefGen_v3	Gene	Chr9	4283462	4287324	iaa40		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2485	iaa41	Aux/IAA-transcription factor 41	GRMZM2G001799	B73 RefGen_v3	Gene	Chr9	16255609	16257497	iaa41		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2486	iaa42	Aux/IAA-transcription factor 42	GRMZM2G479834	B73 RefGen_v3	Gene	Chr10	35447564	35453445	iaa42		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2487	iaa43	Aux/IAA-transcription factor 43	GRMZM2G134517	B73 RefGen_v3	Gene	Chr10	134279626	134280393	iaa43		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2488	iaa44	Aux/IAA-transcription factor 44	GRMZM2G143352	B73 RefGen_v3	Gene	Chr10	145384711	145385639	iaa44		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2489	iaa5	Aux/IAA-transcription factor5	GRMZM5G809195	B73 RefGen_v3	Gene	Chr1	288465742	288467255	iaa5	auxin-responsive Aux/IAA NM_001154876.1, IAA14, iaa5, IDP691, rs131178044, umc1129	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2490	iaa6	Aux/IAA-transcription factor 6	GRMZM5G825707	B73 RefGen_v3	Gene	Chr2	128381501	128388580	iaa6		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2491	iaa7	Aux/IAA-transcription factor 7	GRMZM2G104176	B73 RefGen_v3	Gene	Chr3	7118667	7121305	iaa7		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2492	iaa8	Aux/IAA-transcription factor 8	GRMZM2G004696	B73 RefGen_v3	Gene	Chr3	10076687	10080041	iaa8		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2493	iaa9	Aux/IAA-transcription factor 9	GRMZM2G074742	B73 RefGen_v3	Gene	Chr3	48983289	48985069	iaa9		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2494	iaglu1	indol-3-ylacetyl glucosyl transferase1	GRMZM2G024131	B73 RefGen_v3	Gene	Chr1	262955292	262957901	iaglu1	iaglu1, indol-3-ylacetyl glucosyl transferase1, msu2(iaglu)	indol-3-ylacetyl glucosyl transferase and, in transformed E. coli, produces a catalytically active protein
2495	ial1	ig1-as2 like1	GRMZM2G133806	B73 RefGen_v3	Gene	Chr8	164174038	164177190	ial1	ial1, ig1-as2 like1, lbd40, LBD-transcription factor 40	Sequence highly similar to ig1 and to ASYMMETRIC LEAVES2 of Arabidopsis
2496	ibp1	initiator binding protein1	GRMZM2G063151	B73 RefGen_v3	Gene	Chr9	140000852	140005166	ibp1	CL2161_2b, ibp1, initiator binding protein1, koln9b	cDNA sequence encodes protein binding to the shrunken promoter; duplicate loci distinguished by gene-specific sequences, both transcribed
2497	ibp2	initiator-binding protein2	GRMZM2G110309	B73 RefGen_v3	Gene	Chr1	40356719	40362217	ibp2	ibp2, initiator-binding protein2, koln9A	cDNA sequence selected as encoding protein binding to the shrunken promoter; duplicate lo ci distinguished by gene-specific sequences, both transcribed
2498	icl1	isocitrate lyase1	GRMZM2G056369	B73 RefGen_v3	Gene	Chr7	154227775	154230208	icl1	icl1, isocitrate lyase1, rs130666374 , rs132417884	
2499	id1	indeterminate growth1	GRMZM2G011357	B73 RefGen_v3	Gene	Chr1	239667869	239671192	id1	csh4, csh4(id1), csh850(p1), id1, idd*-2286A, idd*-N2286A, indeterminate growth1, p850	requires extended growth for flowering; vegetatively totipotent with gt1 and factors for perennialism
2500	idc1	iron deficiency candidate1	Zm00001d035308	Zm-B73-REFERENCE-G	Gene	Chr6	20483349	20484802	idc1	hyoscyamine 6-dioxygenase, idc1, iron deficiency candidate1, PCO076122, PCO076122(468), uaz80	endosperm cDNA 2C02A04 (uaz80) similar to barley sequences D10058, D37796

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
2501	idd7	indeterminate1 domain7	GRMZM2G042666	B73 RefGen_v3	Gene	Chr7	146276397	146281153	idd7	AI987507, csh14, ID1 domain7, ID7, idd7, iddveg7, indeterminate1 domain7, si614054G01, veg7	
2502	iddp1	indeterminate domain p1	GRMZM2G179677	B73 RefGen_v3	Gene	Chr1	206161656	206168807	iddp1	gnp_Id1b, gpm243b, iddp1	
2503	iddp10	indeterminate domain p10	GRMZM2G090595	B73 RefGen_v3	Gene	Chr5	194215974	194223601	iddp10	iddp10	
2504	idh1	isocitrate dehydrogenase1	GRMZM2G432128	B73 RefGen_v3	Gene	Chr8	147224301	147229189	idh1	cl62576_1d, gnp_QBM22d04, gpm541, idh1, isocitrate dehydrogenase1	electrophoretic mobility; null allele is known; cytosolic; dimeric; intra/interlocus hybrid bands occur
2505	idh2	isocitrate dehydrogenase2	GRMZM5G829778	B73 RefGen_v3	Gene	Chr6	165734052	165737680	idh2	CL62576_1c, gnp_QAV1b02, gpm407, idh2, isocitrate dehydrogenase2, PCO115488, PCO115488(524)	electrophoretic mobility; null allele is known; cytosolic; dimeric; intra/interlocus hybrid bands occur
2506	IDP1465		GRMZM2G321725	B73 RefGen_v3	Gene	Chr9	147172658	147176871	IDP1465	PCO083558, PCO083558(703), PZA00323, rs131160417, rs131160418, rs55625721 , ss196417277, ss196417280	
2507	IDP1489		GRMZM2G043493	B73 RefGen_v3	Gene	Chr1	56577187	56579012	IDP1489	bHLH, IDP3984	
2508	IDP1639		GRMZM2G139797	B73 RefGen_v3	Gene	Chr10	130166275	130168203	IDP1639	caleosin family member, IDP1626, IDP1639, IDP1666, PCO069403b, ZmCLO2b	
2509	IDP1657		GRMZM2G154574	B73 RefGen_v3	Gene	Chr7	152997411	153005288	IDP1657	CL9402_1, CL9402_1(185), PHM14412, rs129210351, ss196415257	
2510	IDP2375		GRMZM2G121514	B73 RefGen_v3	Gene	Chr6	147413665	147418505	IDP2375	CL2631_1, PCO124093, PHM11985, PZA01712, rs131175765, ss196416467	
2511	IDP2440		GRMZM2G061662	B73 RefGen_v3	Gene	Chr1	293217775	293228618	IDP2440	PCO116288, pco116288(102), PZA00276, rs128281479, rs55622693 , ss196414887	
2512	IDP2454		GRMZM2G353822	B73 RefGen_v3	Gene	Chr8	124537076	124538244	IDP2454	PCO105981, PCO105981(625), PZA01038, rs131175878, ss196416920	
2513	IDP257		GRMZM2G061043	B73 RefGen_v3	Gene	Chr8	166638225	166643039	IDP257	PCO110653, PCO110653(641), PHM13493, PZA00904, rs131175912, ss196417060	
2514	IDP263		GRMZM2G128057	B73 RefGen_v3	Gene	Chr10	139399452	139402605	IDP263	CL11825_1b, PZA01995, rs131176014, ss196417468	
2515	IDP441		GRMZM2G103266	B73 RefGen_v3	Gene	Chr6	81850247	81856948	IDP441	CL448_1, PZA00543, rs128285150, rs55625305 , ss196416354	
2516	IDP472		GRMZM2G327189	B73 RefGen_v3	Gene	Chr3	209919655	209921032	IDP472	ZmDOF4	
2517	IDP51		GRMZM2G093716	B73 RefGen_v3	Gene	Chr5	172973456	172980736	IDP51	PCO140690(429), PCO140690a, PZA00987, rs131175705, rs55623557 , ss196416205	
2518	IDP844		GRMZM2G110832	B73 RefGen_v3	Gene	Chr9	4009489	4011176	IDP844	PCO148074, PCO148074(649), PHM3925, PZA00596, rs131175919, ss196417084, TIDP6261	
2519	ig1	indeterminate gametophyte1	GRMZM2G118250	B73 RefGen_v3	Gene	Chr3	169260970	169264296	ig1	ig1, indeterminate gametophyte1, ZmLBD19	low male fertility, polyembryony, heterofertilization, polyploidy, androgenesis (male and female affected)
2520	igl1	indole-3-glycerol phosphate lyase1	GRMZM2G046191	B73 RefGen_v3	Gene	Chr1	288331936	288337173	igl1	IDP3781, IDP7872, igl1, indole-3-glycerol phosphate lyase1, pco082497, umc1681	mRNA production induced by volicitin, forms free indole
2521	ij1	iojap striping1	GRMZM2G004583	B73 RefGen_v3	Gene	Chr7	134118864	134129700	ij1	ij1, iojap striping1, str2-7C44, umc221(ij)	many variable white stripes and margin patterns on leaves (compare cm1); conditions chloroplast defects that are cytoplasmically inherited;binds to large plastid ribosomal protein L14
2522	im30p1	IM30 protein homolog1	GRMZM2G017077	B73 RefGen_v3	Gene	Chr3	168411704	168416865	im30p1	homolog1, magi16124, PCO095419, pco095419(246), rs131176379 , rs131176380, TIDP2926, zim1	leaf cDNA csu159 similar to pea IM30 protein
2523	imd1	isopropylmalate dehydrogenase1	GRMZM2G173251	B73 RefGen_v3	Gene	Chr1	44533349	44534414	imd1	3-isopropylmalate dehydrogenase , CL1046_1, cl1046_1(18), imd1, isopropylmalate dehydrogenase1, PZB00033, uaz7c03e11(gfu)	vegetative meristem cDNA 7C03E11 similar to potato sequence X67310, with less similarity to various mammalian isocitrate dehydrogenases
2524	imd2	isopropylmalate dehydrogenase2	GRMZM5G803490	B73 RefGen_v3	Gene	Chr2	24987243	24990796	imd2	3-isopropylmalate dehydrogenase 2, cl362_2(123), cl362_2b, imd2	
2525	imd3	isopropylmalate dehydrogenase3	GRMZM2G104613	B73 RefGen_v3	Gene	Chr10	148406957	148410672	imd3	3-isopropylmalate dehydrogenase 2 , imd3	
2526	imp1	importin1	GRMZM2G088088	B73 RefGen_v3	Gene	Chr8	82956568	82961691	imp1	AY103821, csu244, csu244a(imp), csu244(gfu), imp1, importin1, PCO084551b, PZA01301, rs131175862, rs55626841 , ss196416864	leaf cDNA csu244 similar to importin
2527	in1	intensifier1	GRMZM2G042733	B73 RefGen_v3	Gene	Chr7	19360149	19366043	in1	basic helix-loop-helix protein A, in1, intensifier1, pa*-brawn, umc1213	intensifies aleurone anthocyanin pigments; In1-D dominant dilute; sequence similar to r1/b1
2528	incw1	cell wall invertase1	GRMZM2G139300	B73 RefGen_v3	Gene	Chr5	169497597	169502089	incw1	cell wall invertase1, incw1, sc343b, ufg5(incw), ufg5(incw1), ufg5(inv), umc1171	suspension and developing endosperm 28-32 DAP; expressed protein cross-reacts with antibodies to carrot cell-wall invertase; low copy number
2529	incw3	invertase cell wall3	GRMZM2G123633	B73 RefGen_v3	Gene	Chr10	114308530	114310922	incw3	incw3, invertase cell wall3, umc1053, umc1053(incw), umc1054	genomic sequence (GenBank); SSR umc1053
2530	incw4	invertase cell wall4	GRMZM2G119941	B73 RefGen_v3	Gene	Chr2	3190291	3193646	incw4	CL1272_1, CL1272_1(230), gpm837, incw4, incw4 invertase cell wall4, invertase cell wall4	genomic sequence (Genbank)
2531	ipe1	irregular pollen exine1	GRMZM2G434500	B73 RefGen_v3	Gene	Chr1	80973413	80975997	ipe1	Group 8, ipe1, male sterile6034, ms*-6034, ms*-6044	mutants are male sterile and exhibit a glossy outer anther surface, abnormal Ubish bodies, and defective pollen exine
2532	ippi1	isopentenyl pyrophosphate isomerase1	GRMZM2G108285	B73 RefGen_v3	Gene	Chr7	155598887	155602061	ippi1	ippi1, isopentenyl diphosphate isomerase1, isopentenyl pyrophosphate isomerase1	part of multigene family encoding isopentenyl pyrophosphate isomerase
2533	ippi2	isopentenyl pyrophosphate isomerase2	GRMZM2G145029	B73 RefGen_v3	Gene	Chr8	104182030	104186085	ippi2	ippi2, isopentenyl diphosphate isomerase2, isopentenyl pyrophosphate isomerase2	part of multigene family encoding isopentenyl pyrophosphate isomerase
2534	ippi3	isopentenyl pyrophosphate isomerase3	GRMZM2G133082	B73 RefGen_v3	Gene	Chr6	147323465	147329028	ippi3	ippi3, isopentenyl diphosphate isomerase3, isopentenyl pyrophosphate isomerase3	part of multigene family encoding isopentenyl pyrophosphate isomerase
2535	ipt1	isopentenyl transferase1	GRMZM2G097258	B73 RefGen_v3	Gene	Chr3	145470464	145473438	ipt1	ipt1, ZmIPT1, ZmIPT3	encodes an isopentenyl transferase
2536	ipt10	isopentenyl transferase10	GRMZM2G102915	B73 RefGen_v3	Gene	Chr6	81887637	81889903	ipt10	IPT, ipt10	encodes an isopentenyl transferase
2537	ipt2	isopentenyl transferase2	GRMZM2G084462	B73 RefGen_v3	Gene	Chr2	63147052	63148227	ipt2	ipt2, ZmIPT2	encodes an isopentenyl transferase
2538	ipt3	isopentenyl transferase3	GRMZM2G393014	B73 RefGen_v3	Gene	Chr8	151130587	151131675	ipt3	ipt3	encodes an isopentenyl transferase
2539	ipt3B	isopentenyl transferase3B	GRMZM2G415751	B73 RefGen_v3	Gene	Chr3	207330115	207331215	ipt3B	ipt3B	encodes an isopentenyl transferase
2540	ipt4	isopentenyl transferase4	GRMZM2G104559	B73 RefGen_v3	Gene	Chr7	19429668	19430971	ipt4	ipt4, ZmIPT4	encodes an isopentenyl transferase
2541	ipt5	isopentenyl transferase5	AC210013.4_FG005	B73 RefGen_v3	Gene	Chr5	3324796	3325809	ipt5	ipt5, npi409, npi409a, php09409, ZmIPT5	encodes an isopentenyl transferase
2542	ipt6	isopentenyl transferase6	GRMZM2G116878	B73 RefGen_v3	Gene	Chr1	291634128	291635190	ipt6	ipt6, ZmIPT6	encodes an isopentenyl transferase
2543	ipt7	isopentenyl transferase7	GRMZM2G436770	B73 RefGen_v3	Gene	Chr3	67172553	67173644	ipt7	ipt7, ZmIPT7	encodes an isopentenyl transferase
2544	ipt8	isopentenyl transferase8	GRMZM2G025429	B73 RefGen_v3	Gene	Chr6	162939562	162941480	ipt8	ipt8, ZmIPT8	encodes an isopentenyl transferase
2545	ipt9	isopentenyl transferase9	GRMZM2G018046	B73 RefGen_v3	Gene	Chr2	161360574	161361649	ipt9	ipt9	encodes an isopentenyl transferase
2546	irl1	isoflavone reductase-like1	AC226235.2_FG001	B73 RefGen_v3	Gene	Chr3	30997053	30998201	irl1	CL1726_-1, CL1726_-1(210), irl1, isoflavone reductase-like1	low or single copy, cDNA induced by sulfur starvation; recombinant IRL protein binds NADPH and reacts with anti-pea isoflavone reducatase serum
2547	iso3	isoamylase-type starch debranching enzy	GRMZM2G150796	B73 RefGen_v3	Gene	Chr7	129134063	129145654	iso3	gnp_QAG4h11a, gpm788a, isa3, iso3	
2548	isp1	iron-sulfur protein1	GRMZM2G023194	B73 RefGen_v3	Gene	Chr10	111795775	111798782	isp1	AY109584, CL2436_1, csu893(isp), iron-sulfur protein1, isp1, risp	cDNA, nuclear-encoded mitochondrial Rieske iron-sulfur protein, functional analysis in yeast
2549	isr1	inhibitor of striate1	GRMZM5G803874	B73 RefGen_v3	Gene	Chr10	138512812	138515509	isr1	Ej1, extension of japonica, inhibitor of striate1, isr1	(a.k.a. Ej1), dominant Isr1 plants have reduced expression of sr2 and other leaf-striping factors

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
2550	ivr1	invertase1	GRMZM2G394450	B73 RefGen_v3	Gene	Chr2	23504839	23509410	ivr1	cl1418_1, cl1418_1(126), gsy348c_ivr1, invertase1, ivr1, ufg3a, ufg3a(ivr), ufg3a(ivr1), ufg(ivr1B)	cDNA, genomic clones similar to soluble plant invertase; induced by sugar depletion
2551	ivr2	invertase2	GRMZM2G089836	B73 RefGen_v3	Gene	Chr5	67537393	67540691	ivr2	gnp_AW282399b, gpm127a, gpm183b, invertase2, ivr2, PCO109921, ufg5a(inv), ufg5(inv), ufg(ivr2B)	genomic and cDNA for soluble invertase, single band on Southerns, upregulated by increased carbohydrate levels
2552	iws1	IWS1/SPN1-transcription factor 1	GRMZM2G465553	B73 RefGen_v3	Gene	Chr1	292209665	292211668	iws1		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2553	iws2	IWS1/SPN1-transcription factor 2	GRMZM2G108716	B73 RefGen_v3	Gene	Chr5	2792516	2796308	iws2		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2554	jac1	jacalin1	GRMZM2G050412	B73 RefGen_v3	Gene	Chr6	31707695	31709328	jac1	jacalin-like lectin domain, mannose-binding lectin domain, pco083451, rs128384727	
2555	jmj1	JUMONJI-transcription factor 1	GRMZM2G142964	B73 RefGen_v3	Gene	Chr8	60821906	60898916	jmj1		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2556	jmj10	JUMONJI-transcription factor 10	GRMZM2G044301	B73 RefGen_v3	Gene	Chr6	134321285	134327453	jmj10		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2557	jmj11	JUMONJI-transcription factor 11	GRMZM2G339379	B73 RefGen_v3	Gene	Chr8	162996669	163001414	jmj11		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2558	jmj12	JUMONJI-transcription factor 12	GRMZM2G054162	B73 RefGen_v3	Gene	Chr4	240883468	240895570	jmj12		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2559	jmj13	JUMONJI-transcription factor 13	GRMZM2G078198	B73 RefGen_v3	Gene	Chr4	201051876	201056117	jmj13		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2560	jmj14	JUMONJI-transcription factor 14	GRMZM2G057466	B73 RefGen_v3	Gene	Chr1	103624693	103630846	jmj14		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2561	jmj15	JUMONJI-transcription factor 15	GRMZM2G060919	B73 RefGen_v3	Gene	Chr5	199272243	199280188	jmj15		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2562	jmj16	JUMONJI-transcription factor 16	GRMZM2G180086	B73 RefGen_v3	Gene	Chr5	44657285	44663403	jmj16		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2563	jmj17	JUMONJI-transcription factor 17	GRMZM2G152877	B73 RefGen_v3	Gene	Chr1	66961410	66967126	jmj17		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2564	jmj18	JUMONJI-transcription factor 18	GRMZM2G321810	B73 RefGen_v3	Gene	Chr3	165491789	165497935	jmj18		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2565	jmj19	JUMONJI-transcription factor 19	GRMZM2G108589	B73 RefGen_v3	Gene	Chr7	1519824	1523155	jmj19		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2566	jmj2	JUMONJI-transcription factor 2	GRMZM2G171163	B73 RefGen_v3	Gene	Chr4	172386710	172389864	jmj2		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2567	jmj20	JUMONJI-transcription factor 20	AC149475.2_FG005	B73 RefGen_v3	Gene	Chr9	152791245	152801912	jmj20		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2568	jmj21	JUMONJI-transcription factor 21	GRMZM2G383210	B73 RefGen_v3	Gene	Chr4	169239655	169259508	jmj21		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2569	jmj22	JUMONJI-transcription factor 22	GRMZM2G417089	B73 RefGen_v3	Gene	Chr1	248568098	248575059	jmj22		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2570	jmj3	JUMONJI-transcription factor 3	GRMZM2G428933	B73 RefGen_v3	Gene	Chr9	130273915	130282483	jmj3		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2571	jmj4	JUMONJI-transcription factor 4	GRMZM2G027075	B73 RefGen_v3	Gene	Chr4	172459736	172468782	jmj4		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2572	jmj5	JUMONJI-transcription factor 5	GRMZM2G070885	B73 RefGen_v3	Gene	Chr7	106518289	106522429	jmj5		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2573	jmj6	JUMONJI-transcription factor 6	GRMZM2G107109	B73 RefGen_v3	Gene	Chr4	172286685	172295419	jmj6		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2574	jmj7	JUMONJI-transcription factor 7	GRMZM2G156910	B73 RefGen_v3	Gene	Chr6	116655146	116661337	jmj7		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2575	jmj8	JUMONJI-transcription factor 8	GRMZM2G431157	B73 RefGen_v3	Gene	Chr10	19854631	19862449	jmj8		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2576	jmj9	JUMONJI-transcription factor 9	GRMZM2G140524	B73 RefGen_v3	Gene	Chr4	172338861	172347926	jmj9		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2577	kan1	KANADI1	GRMZM2G056400	B73 RefGen_v3	Gene	Chr1	215657189	215662587	kan1	G2-like transcription factor, kan1, kan1a, KANADI1, ZmGLK40	
2578	kan3	kanadi3	GRMZM2G175827	B73 RefGen_v3	Gene	Chr4	80099618	80112468	kan3	G2-like transcription factor, kan3, kanadi3, ZmGLK46	
2579	kao2	kaurenoic acid oxidase2	GRMZM2G089803	B73 RefGen_v3	Gene	Chr9	140279526	140282696	kao2	kao2, ZmKAO2	
2580	kcbp1	kinesin-like calmodulin binding protein1	GRMZM2G070273	B73 RefGen_v3	Gene	Chr2	3067260	3076483	kcbp1		
2581	kch1	potassium channel 1	GRMZM2G022915	B73 RefGen_v3	Gene	Chr3	214355254	214361335	kch1	kch1, potassium channel 1, siy07632b, zmk1, Zmk1	
2582	kch2	potassium channel2	GRMZM2G020859	B73 RefGen_v3	Gene	Chr6	148554980	148565653	kch2	cl1397_1b, kch2, potassium channel2, zmk2	
2583	kch3	potassium channel3	GRMZM2G081666	B73 RefGen_v3	Gene	Chr4	227476359	227480644	kch3	kch3, kzm1, potassium channel3, ZmK2.1	single copy (Southern blot), function confirmed by expression in Xenopus oocytes (Philippar 2003; Su 2005)
2584	kch4	potassium channel4	GRMZM2G093313	B73 RefGen_v3	Gene	Chr3	3843599	3847168	kch4	kch4, kch5, KZM2, potassium channel4	
2585	kch5	potassium channel5	GRMZM2G171279	B73 RefGen_v3	Gene	Chr8	146628450	146633412	kch5	kch5, K+ channel 1, potassium channel5, siy07632c, zmk1	
2586	kch6	potassium channel6	AC234152.1_FG002	B73 RefGen_v3	Gene	Chr8	101614919	101619583	kch6	AY109626, CL1397_1, K2 potassium channel protein ZMK2, kch2, kch6, PZA02019, rs131175864, ss196416872, ZMK2	
2587	kds1	CMP-KDO synthetase1	GRMZM2G119256	B73 RefGen_v3	Gene	Chr8	68450787	68453575	kds1	3-deoxy-manno-octulosonate cytidylyltransferase, cks1, CL1184_1, CL1184_1(595), CMP-KDO synthetase1, kds1	author match, gene identification in TIGR contig
2588	kelp1	p15 (PC4 Sub1)-transcription factor 1	GRMZM2G159948	B73 RefGen_v3	Gene	Chr3	204699354	204701927	kelp1		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2589	kelp2	p15 (PC4 Sub1)-transcription factor 2	GRMZM2G090213	B73 RefGen_v3	Gene	Chr5	172514217	172520347	kelp2		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2590	kelp3	p15 (PC4 Sub1)-transcription factor 3	GRMZM2G112535	B73 RefGen_v3	Gene	Chr8	153332086	153334819	kelp3		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2591	kik1	kinase interacting kinase1	GRMZM5G889999	B73 RefGen_v3	Gene	Chr7	156219814	156225643	kik1	CL1831_1, CL1831_1(576), gnp_AW042267, gpm131, kik1, kinase interacting kinase1	
2592	kin1	knotted1 induced1	GRMZM2G158394	B73 RefGen_v3	Gene	Chr7	176260711	176262411	kin1	kin1, knotted1 induced1, PCO098786, pco098786(579)	
2593	kip1	knotted interacting protein1	GRMZM2G163761	B73 RefGen_v3	Gene	Chr1	256573454	256575135	kip1	kip1, knotted interacting protein1, PCO071715, PCO071715(29), ZmHB105	
2594	kn1	knotted1	GRMZM2G017087	B73 RefGen_v3	Gene	Chr1	271407490	271415210	kn1	AY107752, gsy19(kn1), homeobox protein OSH1, kn1, knotted1, OSH1, PCO065671, sc19, SC19, ZmHB1	dominant Kn1 plants have localized proliferation of tissue at vascular bundles on leaf
2595	knox1	knotted related homeobox1	GRMZM2G159431	B73 RefGen_v3	Gene	Chr1	5003070	5007708	knox1	knotted related homeobox1, knox1, pco127444, pge132, pge22(knox1), ZmHB51	class 2 root homeobox; cDNA and genomic clones; gene-specific probe
2596	knox10	knotted related homeobox10	GRMZM2G002225	B73 RefGen_v3	Gene	Chr5	13957726	13980235	knox10	FCL1 fused compound leaf 1, knotted related homeobox10, knox10, pge(B5), pgeB5(knox10), ZmHB111	class I homeobox, gene-specific probe; cDNA and genomic clones
2597	knox2	knotted related homeobox2	GRMZM2G055243	B73 RefGen_v3	Gene	Chr9	93868786	93877183	knox2	homeobox protein knotted-1-like 11, knotted related homeobox2, knox2, pge4, pge4(knox2), ZmHB72	sequence similar to knox6 and knox7; gene specific probe; cDNA and genomic clones
2598	knox3	knotted related homeobox3	GRMZM2G000743	B73 RefGen_v3	Gene	Chr1	271693702	271695058	knox3	ECA, knotted related homeobox3, knox3, PCO112760(88), pge5a(knox3), pge(C2), ZmHB95	shoot meristem and developing stem specific, very similar in sequence and expression pattern to rs1, kn1, knox4 and knox8

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
2599	knox5	knotted related homeobox5	GRMZM5G832409	B73 RefGen_v3	Gene	Chr6	24181173	24192653	knox5	knotted related homeobox5, knox5, lg4b, pge(A4), pgeA4(knox5), ZmHB39	class I homeobox; cDNA and genomic clones; gene-specific probe; sequence and expression similar to lg3 and knox11
2600	knox6	knotted related homeobox6	GRMZM2G370332	B73 RefGen_v3	Gene	Chr5	94481164	94484870	knox6	hb79, Homeobox-transcription factor 79, knotted related homeobox6, knox6, ORPHAN transcription factor, pge(R6), pgeR6(knox6)	similar to knox2 in sequence and expression; cDNA and genomic clones; gene specific probe
2601	knox7	knotted related homeobox7	GRMZM2G433591	B73 RefGen_v3	Gene	Chr4	235745133	235750283	knox7	knotted related homeobox7, knox7, PCO075632c, pge15(knox7), pge(R7), ZmHB80	sequence and expression similar to knox6; gene specific probes
2602	ko1	kaurene oxidase1	GRMZM2G059308	B73 RefGen_v3	Gene	Chr9	79864518	79871342	ko1	ko1, ZmKO1	
2603	ko2	kaurene oxidase2	GRMZM2G161472	B73 RefGen_v3	Gene	Chr9	79629933	79634006	ko2	ent-kaurene oxidase, chloroplastic-like, ko2, ZmKO2	
2604	kpp1	kinase associated protein phosphatase1	GRMZM2G042627	B73 RefGen_v3	Gene	Chr7	19331382	19358462	kpp1	fha16, FHA-transcription factor 16, KAPP, kinase associated protein phosphatase1, kpp1, umc1016, umc267	cDNA similar to Arabidopsis KAPP sequence; SSR umc1016
2605	kri1	ketol-acid reductoisomerase1	GRMZM2G161868	B73 RefGen_v3	Gene	Chr3	202434872	202437694	kri1	cdo1160c, cdo1160c(kri), ketol-acid reductoisomerase1, kri1, rs131186669, uaz269, uaz269(gfu)	cdo Probe is an oat leaf cDNA. Minor band maps to this site.. endosperm cDNA 5C05H04 similar to plant branched chain amino acid synthesis enzyme (aka uaz269)
2606	kri2	ketol-acid reductoisomerase2	Zm00001d009638	Zm-B73-REFERENCE-G	Gene	Chr8	73989684	73993106	kri2	kri2, uaz269, uaz269a, uaz269a(kari), uaz269a(kri)	
2607	krp1	kinesin-related protein1	GRMZM2G129569	B73 RefGen_v3	Gene	Chr4	149310956	149317153	krp1	KIN1, kinesin-like protein1, kinesin-related protein1, krp1, PCO082735, ZmaKIN1	
2608	krp11	kinesin-related protein11	GRMZM2G436981	B73 RefGen_v3	Gene	Chr7	1144796	1151528	krp11	kin11, KIN11, kinesin-related protein11, krp11, ZmaKIN11	
2609	krp13	kinesin-related protein13	GRMZM2G034828	B73 RefGen_v3	Gene	Chr1	246878397	246883986	krp13	kin13, KIN13, kinesin-like protein13, krp13, ZmaKIN13	
2610	krp15	kinesin-related protein15	GRMZM2G054418	B73 RefGen_v3	Gene	Chr10	133348999	133354774	krp15	kin15, KIN15, kinesin-related protein15, krp15, PCO127685, ZmaKIN15	
2611	krp16	kinesin-related protein16	GRMZM2G124883	B73 RefGen_v3	Gene	Chr8	174510782	174515041	krp16	kin16, KIN16, kinesin-like protein16, krp16, PCO068534, PCO068534(646), ZmaKIN16	
2612	krp2	kinesin-related protein2	GRMZM2G136838	B73 RefGen_v3	Gene	Chr9	26591337	26597907	krp2	kin2, KIN2, kinesin-related protein2, krp2, ZmaKIN2	
2613	krp3	kinesin-related protein3	GRMZM2G173700	B73 RefGen_v3	Gene	Chr8	123987283	123994126	krp3	kin3, KIN3, kinesin-like protein3, krp3, PCO116522(625), PCO116522b, ZmaKIN3	
2614	krp4	kinesin-related protein4	GRMZM2G320689	B73 RefGen_v3	Gene	Chr1	204903790	204910966	krp4	IDP687, kin4, KIN4, kinesin-related protein4, krp4, PCO120417b, ZmaKIN4	
2615	krp5	kinesin-related protein5	GRMZM2G093391	B73 RefGen_v3	Gene	Chr6	105208479	105214743	krp5	kin5, KIN5, kinesin-related protein5, krp5, ZmaKIN5	
2616	krp8	kinesin-related protein8	GRMZM2G132371	B73 RefGen_v3	Gene	Chr4	51919903	51926112	krp8	kin8, KIN8, kinesin-related protein8, krp8, pco120417c, ZmaKIN8	
2617	krp9	kinesin-related protein9	GRMZM5G881464	B73 RefGen_v3	Gene	Chr6	127292905	127310354	krp9	kin9, KIN9, kinesin-related protein9, krp9, PCO064769, PCO064769(502), ZmaKIN9	Is a member of MCAK family and may depolymerize microtubules per C. Lawrence.
2618	ks1	kaurene synthase1	GRMZM2G016922	B73 RefGen_v3	Gene	Chr1	237109339	237115584	ks1	ks1, ZmKS1, ZmKS3	
2619	ks2	kaurene synthase2	GRMZM2G093526	B73 RefGen_v3	Gene	Chr2	10574515	10578571	ks2	ks2, ZmKS2, ZmKS2.2, ZmKSL5	
2620	ks3	kaurene synthase3	GRMZM2G093603	B73 RefGen_v3	Gene	Chr2	10562532	10567539	ks3	ks3, ks389, ZmKS1, ZmKS3, ZmKSL3	functionality inferred from expression data and sequence similarity (Song et al 2011; Nelissen et al 2012)
2621	ks4	kaurene synthase4	AC214360.3_FG001	B73 RefGen_v3	Gene	Chr3	110200299	110204076	ks4	ks4, ZmKS3, ZmKSL4	
2622	ks5	kaurene synthase5	Zm00001d024514	Zm-B73-REFERENCE-G	Gene	Chr10	75446562	75449964	ks5	ent-kaur-16-ene synthase, chloroplastic-like, ks5, ZmKS4	
2623	ks6	kaurene synthase6	GRMZM2G391312	B73 RefGen_v3	Gene	Chr4	53284808	53288327	ks6	ent-kaurene synthases-like2, ks6, ZmKSL2	
2624	l15	luteus15	GRMZM2G177169	B73 RefGen_v3	Gene	Chr6	95481573	95484475	l15	l15, l*-Blandy3, l*-Brawn, luteus15, pentatricopeptide10, ppr10, ZmPPR341	Binds atpI-atpH and psaJ-rpl33 intergenic regions. (A. Barkan, 2015). like l4; lethal yellow seedling; chloroplast mRNA processing.
2625	la1	lazy plant1	GRMZM2G135019	B73 RefGen_v3	Gene	Chr4	18000248	18006785	la1	contolling leaf angle qtl4, la1, lazy plant1, prostrate stem1, qLA4-1 QTL, ZmCLA4	prostrate growth habit
2626	lac10	laccase10	GRMZM2G140527	B73 RefGen_v3	Gene	Chr4	4216683	4219243	lac10	lac10, putative laccase family protein	
2627	lbd1	LBD-transcription factor 1	GRMZM2G092483	B73 RefGen_v3	Gene	Chr1	10818799	10819994	lbd1		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2628	lbd10	LBD-transcription factor 10	GRMZM2G154320	B73 RefGen_v3	Gene	Chr1	254949670	254950944	lbd10		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2629	lbd11	LBD-transcription factor 11	GRMZM2G017319	B73 RefGen_v3	Gene	Chr1	255383520	255385569	lbd11		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2630	lbd12	LBD-transcription factor 12	GRMZM2G447176	B73 RefGen_v3	Gene	Chr1	258866950	258868413	lbd12		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2631	lbd13	LBD-transcription factor 13	GRMZM2G011385	B73 RefGen_v3	Gene	Chr1	286409470	286410127	lbd13		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2632	lbd14	LBD-transcription factor 14	GRMZM2G177110	B73 RefGen_v3	Gene	Chr2	209518630	209519766	lbd14		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2633	lbd15	LBD-transcription factor 15	AC207888.3_FG009	B73 RefGen_v3	Gene	Chr2	234934167	234936218	lbd15		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2634	lbd17	LBD-transcription factor 17	GRMZM2G132693	B73 RefGen_v3	Gene	Chr3	23103082	23104417	lbd17		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2635	lbd18	LBD-transcription factor 18	AC218973.3_FG003	B73 RefGen_v3	Gene	Chr3	93840474	93841301	lbd18		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2636	lbd20	LBD-transcription factor 20	GRMZM2G092517	B73 RefGen_v3	Gene	Chr3	184175771	184177879	lbd20		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2637	lbd21	LBD-transcription factor 21	GRMZM2G025758	B73 RefGen_v3	Gene	Chr3	192970241	192971643	lbd21		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2638	lbd22	LBD-transcription factor 22	GRMZM2G095982	B73 RefGen_v3	Gene	Chr4	6391031	6392616	lbd22		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2639	lbd23	LBD-transcription factor 23	GRMZM2G079768	B73 RefGen_v3	Gene	Chr4	74723078	74724495	lbd23		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2640	lbd24	LBD-transcription factor 24	GRMZM2G075499	B73 RefGen_v3	Gene	Chr4	170838318	170839405	lbd24		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2641	lbd25	LBD-transcription factor 25	GRMZM2G025989	B73 RefGen_v3	Gene	Chr4	183769526	183770541	lbd25		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2642	lbd26	LBD-transcription factor 26	GRMZM2G079185	B73 RefGen_v3	Gene	Chr5	15203964	15206688	lbd26		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2643	lbd27	LBD-transcription factor 27	GRMZM2G362627	B73 RefGen_v3	Gene	Chr5	18398844	18400101	lbd27		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2644	lbd28	LBD-transcription factor 28	GRMZM2G165805	B73 RefGen_v3	Gene	Chr6	28091948	28093028	lbd28		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2645	lbd29	LBD-transcription factor 29	GRMZM2G386095	B73 RefGen_v3	Gene	Chr6	64768557	64769285	lbd29		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2646	lbd3	LBD-transcription factor 3	GRMZM2G110913	B73 RefGen_v3	Gene	Chr1	33801737	33804005	lbd3		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2647	lbd30	LBD-transcription factor 30	GRMZM2G180319	B73 RefGen_v3	Gene	Chr6	85751370	85752655	lbd30		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
2648	lbd31	LBD-transcription factor 31	GRMZM2G044150	B73 RefGen_v3	Gene	Chr6	141232270	141233226	lbd31		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2649	lbd32	LBD-transcription factor 32	GRMZM2G121487	B73 RefGen_v3	Gene	Chr6	147424552	147430624	lbd32		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2650	lbd33	LBD-transcription factor 33	GRMZM2G386674	B73 RefGen_v3	Gene	Chr6	159313186	159314511	lbd33		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2651	lbd34	LBD-transcription factor 34	GRMZM2G704330	B73 RefGen_v3	Gene	Chr7	6439450	6441294	lbd34		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2652	lbd35	LBD-transcription factor 35	GRMZM5G868471	B73 RefGen_v3	Gene	Chr8	81896223	81898153	lbd35		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2653	lbd36	LBD-transcription factor 36	GRMZM2G096064	B73 RefGen_v3	Gene	Chr8	103789363	103790421	lbd36		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2654	lbd37	LBD-transcription factor 37	AC234149.1_FG002	B73 RefGen_v3	Gene	Chr8	122851972	122852823	lbd37		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2655	lbd38	LBD-transcription factor 38	GRMZM2G073044	B73 RefGen_v3	Gene	Chr8	122998640	123000039	lbd38		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2656	lbd39	LBD-transcription factor 39	AC214648.3_FG005	B73 RefGen_v3	Gene	Chr8	131315533	131316325	lbd39		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2657	lbd4	LBD-transcription factor 4	GRMZM2G021095	B73 RefGen_v3	Gene	Chr1	44165940	44167054	lbd4		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2658	lbd41	LBD-transcription factor 41	GRMZM2G145568	B73 RefGen_v3	Gene	Chr9	138557713	138558785	lbd41		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2659	lbd42	LBD-transcription factor 42	GRMZM2G150594	B73 RefGen_v3	Gene	Chr9	143011637	143013786	lbd42		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2660	lbd44	LBD-transcription factor 44	GRMZM5G873586	B73 RefGen_v3	Gene	Chr10	3275775	3281566	lbd44		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2661	lbd5	LBD-transcription factor 5	GRMZM2G060544	B73 RefGen_v3	Gene	Chr1	72360144	72361438	lbd5		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2662	lbd6	LBD-transcription factor 6	GRMZM2G044902	B73 RefGen_v3	Gene	Chr1	77152675	77154117	lbd6		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2663	lbd7	LBD-transcription factor 7	GRMZM2G076327	B73 RefGen_v3	Gene	Chr1	124634056	124634920	lbd7		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2664	lbd8	LBD-transcription factor 8	GRMZM2G132667	B73 RefGen_v3	Gene	Chr1	191562085	191562888	lbd8		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2665	lbd9	LBD-transcription factor 9	AC217910.3_FG006	B73 RefGen_v3	Gene	Chr1	217326067	217327326	lbd9		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2666	lbp1	lipid binding protein1	GRMZM6G851663	B73 RefGen_v3	Gene	Chr2	58076051	58076601	lbp1	lbp1	over-expressed after stress application
2667	ldh1	lactate dehydrogenase1	GRMZM2G128929	B73 RefGen_v3	Gene	Chr5	67432367	67434244	ldh1	cl2158_1, lactate dehydrogenase1 (candidate)1, ldh1	first report; genomic clone showing homology to ldh from barley; contains anaerobic regulatory element sequence; no expression data
2668	ldp1	luminidependens protein1	GRMZM2G106613	B73 RefGen_v3	Gene	Chr3	154702548	154712172	ldp1	csu838, flowering-time protein isoforms alpha and beta, ldp1, ldp2, luminidependens protein1, ZmLD	single copy leaf cDNA, csu838, similar to Arabidopsis luminidependens protein which regulates floral induction
2669	lec1	LEC1 transcription factor1	GRMZM2G011789	B73 RefGen_v3	Gene	Chr5	204386830	204388007	lec1	CADR9, CL691_1(446), CL691_1b, leafy cotyledon, lec1, LEC1 leafy cotyledon transcription factor1, ZmCADR1, Zmlec1, ZmNF-YB12	
2670	leg1	legumin1	GRMZM2G174883	B73 RefGen_v3	Gene	Chr6	40050689	40052652	leg1	CL29033_1b, gnp_QDA2G1, gpm944, leg1, legumin1, umc1498	50kD legumin, mRNA
2671	lem1	lethal embryo mutant1	AC234157.1_FG002	B73 RefGen_v3	Gene	Chr1	281175269	281177006	lem1	chloroplast ribosomal protein 9, cprps9, lem1, lethal embryo mutant1, prps9, tac902.33	lethal embryo, quasi-normal endosperm; single copy genomic sequence; green fluorescent protein fusion constructs localize to plastid
2672	les22	lesion22	GRMZM2G044074	B73 RefGen_v3	Gene	Chr1	56560198	56564777	les22	les22, les*-2552, Les2552, les29, lesion22, lesion29, lesion*-J2552, les*-J2552	(was Les*-J2552, les29) dominant leaf lesions,early-medium timing, small size, white color; porphyria
2673	lg1	liguleless1	GRMZM2G036297	B73 RefGen_v3	Gene	Chr2	4265163	4268840	lg1	lg1, liguleless1, ZmSBP15	In the liguleless1 mutant, ligule and auricle are missing; leaves are upright
2674	lg2	liguleless2	GRMZM2G060216	B73 RefGen_v3	Gene	Chr3	176845304	176853978	lg2	lg2, liguleless2, rs131175528, ss196415536, ZmbZIP11	like lg1, less extreme
2675	lg3	liguleless3	GRMZM2G087741	B73 RefGen_v3	Gene	Chr3	53883227	53893066	lg3	gnp_QBS9g05a, gpm568a, lg3, liguleless3, PCO074163, pge(D1), pge(R4), PHM15474, PZA01447, rs128281406, rs55622604 , ss196415373	dominant Lg3 plants lack ligule; leaves upright, broad, often concave and pleated; homeobox similar to knox5 and knox11
2676	lg4	liguleless4	GRMZM2G094241	B73 RefGen_v3	Gene	Chr8	130383323	130388890	lg4	knotted related homeobox11, knox11, lg4, Lg*-403, lg4a, liguleless4, pge11(knox11), ZmHB23	class I homeobox; cDNA and genomic clones; sequence and expression similar to lg3 and knox5. dominant Lg4 plants lack ligule and auricle but show vestiges sporadically in blade
2677	lgn1	liguleless narrow1	GRMZM2G134382	B73 RefGen_v3	Gene	Chr9	47658297	47660713	lgn1	Lgn, lgn1, LgN*-N2529, liguleless narrow, liguleless narrow1, tac905.29	Mutant leaves are narrow and branching in the inflorescence is reduced.
2678	lhca1	light harvesting complex A1	GRMZM2G038519	B73 RefGen_v3	Gene	Chr2	207611861	207618663	lhca1	chlorophyll a-b binding protein , csu800, csu800(lhca), csu818a(lhca), csu847a(lhcb), csuh00800, csuh800, lhca1, Lhca2, light harvesting complex A1	leaf cDNA csu800 similar to photosystem I antenna protein
2679	lhcb1	light harvesting chlorophyll a/b binding p	GRMZM2G351977	B73 RefGen_v3	Gene	Chr8	141176051	141177936	lhcb1	lhcb1, Lhcb1, lhcb48, light harvesting chlorophyll a/b binding protein1, npi477(cab), umc24a(cab), umc24a(lhcb), umc24(cab)	sequence; promoter is light regulated in tobacco and maize leaf mesophyll protoplasts (Knight et al. 1992)
2680	lhcb2	light harvesting chlorophyll a/b binding p	AC207722.2_FG009	B73 RefGen_v3	Gene	Chr7	147094052	147095217	lhcb2	cab1, cab-1, cab2, cab3, cab-m5, gnp_QAP1f07, gpm384, Lhcb1, lhcb2, light harvesting chlorophyll a/b binding protein2, npi478(cab)	gene specific cDNA probe; expressed in dark (aka cab1, cab2)
2681	lhcb3	light harvesting chlorophyll a/b binding p	GRMZM2G155216	B73 RefGen_v3	Gene	Chr8	70312571	70314733	lhcb3	cab4, cab m-2, cab-m9, csu224, csu66, csu66b(lhcb), csuh00224, lhcb3, lhcb*-X55892, light harvesting chlorophyll a/b binding protein3, npi479(cab), umc174(cab)	probed by clone provided by L. Bogorad (aka cab4)
2682	lhcb4	light harvesting complex a/b protein4	GRMZM2G103101	B73 RefGen_v3	Gene	Chr5	209922350	209924302	lhcb4	csu1028(lhcb), csu227, csu227(gfu), lhcb4, lhcb*-csu227, light harvesting complex a/b protein4, PCO079073, pco079073(451)	leaf cDNA csu227, single site
2683	lhcb5	light harvesting chlorophyll a/b binding p	GRMZM2G149428	B73 RefGen_v3	Gene	Chr2	220058172	220060652	lhcb5	CP26, gnp_QCA20d07b, gpm574b, lhcb5, LHcb5-1, Lhcb5-2, light harvesting chlorophyll a/b binding protein5, PCO135935, PCO135935(191)	
2684	lhcb6	light harvesting chlorophyll a/b binding p	GRMZM2G092427	B73 RefGen_v3	Gene	Chr10	147325724	147327040	lhcb6	CP24, lhcb6, lhcb6-1, Lhcb6-1, lhcb*-U23190	
2685	lhcb7	light harvesting complex mesophyll7	GRMZM2G402936	B73 RefGen_v3	Gene	Chr6	165101052	165102377	lhcb7	CAB homolog8, cab-m7, CL187_1, CL187_1(524), csu889, Lhcb1, lhcb7, lhcb8, lhcbm7, light harvesting complex mesophyll7	cDNA sequence distinct from other light harvesting chlorophyll polypeptides; two copies by Southern blot analysis (aka cab-m7)
2686	lhcb9	light harvesting chlorophyll binding prote	GRMZM2G018627	B73 RefGen_v3	Gene	Chr1	247817664	247819376	lhcb9	csu645, csu66a, csu66a(lhcb), csu71, csu889b(lhcb), csuh102, csuh20, csuh66, csuh71, Lhcb2*Zm1, lhcb9, lhcb*-X68682, light harvesting chlorophyll binding protein9, Type II light	cDNA sequence is a classII lhcb, unlike previously characterized lhcb genes which are classI (Viret et al 1993)
2687	lhcb9	light harvesting chlorophyll binding prote	GRMZM2G414192	B73 RefGen_v3	Gene	Chr1	247786586	247788296	lhcb9	csu645, csu66a, csu66a(lhcb), csu71, csu889b(lhcb), csuh102, csuh20, csuh66, csuh71, Lhcb2*Zm1, lhcb9, lhcb*-X68682, light harvesting chlorophyll binding protein9, Type II light	cDNA sequence is a classII lhcb, unlike previously characterized lhcb genes which are classI (Viret et al 1993)
2688	lhy1	late hypocotyl elongation protein ortholo	GRMZM2G474769	B73 RefGen_v3	Gene	Chr10	78333991	78337257	lhy1	cca2, circadian clock associated2, late hypocotyl elongation protein ortholog, late hypocotyl elongation protein ortholog1, LHY, lhy1, ZmCCA1a	myb transcription factor - core clock gene (Hayes et al. 2010)
2689	limtf1	LIM-transcription factor 1	GRMZM2G128206	B73 RefGen_v3	Gene	Chr1	38621379	38628799	limtf1	lim1	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2690	limtf10	LIM-transcription factor 10	GRMZM2G004959	B73 RefGen_v3	Gene	Chr6	21973369	21975498	limtf10	lim10	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2691	limtf11	LIM-transcription factor 11	GRMZM2G017845	B73 RefGen_v3	Gene	Chr6	52901117	52909594	limtf11	lim11	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2692	limtf12	LIM-transcription factor 12	GRMZM2G010960	B73 RefGen_v3	Gene	Chr6	114357794	114367987	limtf12	lim12	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2693	limtf13	LIM-transcription factor 13	GRMZM2G151934	B73 RefGen_v3	Gene	Chr9	140469500	140474431	limtf13	lim13	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2694	limtf14	LIM-transcription factor 14	GRMZM2G024887	B73 RefGen_v3	Gene	Chr10	132724522	132726075	limtf14	lim14	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2695	limtf2	LIM-transcription factor 2	GRMZM2G160198	B73 RefGen_v3	Gene	Chr1	39040586	39044425	limtf2	lim2	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2696	limtf3	LIM-transcription factor 3	GRMZM2G385236	B73 RefGen_v3	Gene	Chr1	123983180	123985570	limtf3	lim3	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
2697	limtf4	LIM-transcription factor 4	GRMZM2G099328	B73 RefGen_v3	Gene	Chr1	167019236	167024935	limtf4	DA1-related 1, DA = "Large" in Chinese, LIM5, limtf4, pco156068, pco156068(373), Zinc ion binding protein, ZmDAR1	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2698	limtf5	LIM-transcription factor 5	GRMZM2G342105	B73 RefGen_v3	Gene	Chr1	253827545	253837409	limtf5	lim5	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2699	limtf6	LIM-transcription factor 6	GRMZM2G153268	B73 RefGen_v3	Gene	Chr2	23758072	23759626	limtf6	lim6	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2700	limtf7	LIM-transcription factor 7	GRMZM2G175761	B73 RefGen_v3	Gene	Chr3	134641615	134643267	limtf7	lim7	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2701	limtf8	LIM-transcription factor 8	GRMZM2G134752	B73 RefGen_v3	Gene	Chr4	147679277	147680759	limtf8	lim8	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2702	limtf9	LIM-transcription factor 9	GRMZM2G170034	B73 RefGen_v3	Gene	Chr5	188946269	188947853	limtf9	lim9	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2703	lip15	low temperature-induced protein15	GRMZM2G448607	B73 RefGen_v3	Gene	Chr6	24280540	24281904	lip15	CL1909_-1, CL1909_-1(467), gmlip15, IDP402, lip15, maize low temperature-induced protein15, mlip15, ZmbZIP12	cDNA cross hybridizing to rice lip19, bZIP protein from rabbit reticulocytes or E. coli binds wheat histone H3 gene promoter; single band in Southerns
2704	lkrsdh1	lysine-ketoglutarate reductase/saccharop	GRMZM2G181362	B73 RefGen_v3	Gene	Chr4	175769672	175780762	lkrsdh1	CL1148_1, CL1148_1(330), lkrsdh1, lysine-ketoglutarate reductase/saccharopine dehydrogenase1, umi9, ZLKRSDH	
2705	lls1	lethal leaf spot1	GRMZM2G339563	B73 RefGen_v3	Gene	Chr1	10090835	10095173	lls1	PZA03521, rs128284648, rs128372273, rs131175254, rs131175255, rs131206378, rs55622265 , ss196414377, ss196414379, ss196414381, ss196414383, ss196414387	chlorotic-necrotic lesions resembling Helminthosporium carbonum infection
2706	ln1	linoleic acid1	GRMZM2G169089	B73 RefGen_v3	Gene	Chr6	105027581	105034465	ln1	CL739_1, CL739_1(490), dgat1, DGAT1-2, diacyglycerol acyltransferase1, linoleic acid1, ln1, opd1, qHO6	embryo oil content and composition,cloned by chromosome walk to high oil QTL; maybe allele of ln1 (Zheng 2008). lower ratio of oleate to linoleate in kernel
2707	lon1	LON peptidase1	GRMZM2G109560	B73 RefGen_v3	Gene	Chr7	143360732	143369569	lon1	CL1713_1, CL1713_1(569), lon1, LON peptidase1	cDNA similar to lon of E. coli and partially substitutes for pim1 in yeast
2708	lon2	LON protease2	GRMZM2G113056	B73 RefGen_v3	Gene	Chr7	174539360	174548995	lon2	CL1712_1(579), CL1712_1b, lon2, LON protease2, umsl1(lon2)	cDNA similar to lon of E. coil
2709	lop1	lo1 pl allergen homolog1	GRMZM2G072886	B73 RefGen_v3	Gene	Chr9	117765965	117767293	lop1	beta-expansin 1 protein (EXPB1), beta-expansin 9, expb9, expb9a, lo1 pl allergen homolog1, lop1, ml, PCO124530	cDNA sequence homologous to allergen Lo1 pl
2710	lox1	lipoxygenase1	GRMZM2G156861	B73 RefGen_v3	Gene	Chr3	168738873	168882335	lox1	9-LOX, lipoxygenase1, Lox-, lox1, LOX1-Zm1	Full length cDNA is expressed in E. coli (Kim et al. 2003)
2711	lox10	lipoxygenase10	GRMZM2G015419	B73 RefGen_v3	Gene	Chr4	234164919	234168681	lox10	csu719(lox), lox1, lox10, PCO093659, PCO093659(360), rs131181024, rs132204115, umc2360	green leaf volatiles, circadian, herbivore defense; sequence predicts plastidic location; images show location in non-chlorophyll containing organelles
2712	lox11	lipoxygenase11	GRMZM2G009479	B73 RefGen_v3	Gene	Chr5	123239668	123243697	lox11	lox11	
2713	lox12	lipoxygenase12	GRMZM2G106748	B73 RefGen_v3	Gene	Chr3	93841905	93845764	lox12	lox12	single copy, required for resistance to Fusarium stalk and ear rot
2714	lox2	lipoxygenase2	GRMZM2G156861	B73 RefGen_v3	Gene	Chr3	168738873	168882335	lox2	lox2	
2715	lox3	lipoxygenase3	GRMZM2G109130	B73 RefGen_v3	Gene	Chr1	264266381	264271190	lox3	cho1c.pk002.j23, cssap92, Lipoxygenase L2, lox3, ZmLOX3	
2716	lox4	lipoxygenase4	GRMZM2G109056	B73 RefGen_v3	Gene	Chr1	264275083	264291510	lox4	6C02F07, lox4, uat1(lox)	
2717	lox5	lipoxygenase5	GRMZM2G102760	B73 RefGen_v3	Gene	Chr5	12285656	12290564	lox5	lox5	
2718	lox6	lipoxygenase6	GRMZM2G040095	B73 RefGen_v3	Gene	Chr2	4192152	4196263	lox6	CL907_1, CL907_1(113), lox6, lox6(gag), PHM5628, PZA00172, rs129002748, rs131288107 , umc53a	
2719	lox7	lipoxygenase7	GRMZM2G070092	B73 RefGen_v3	Gene	Chr10	120237308	120241527	lox7	lox7, ts1b	
2720	lox9	lipoxygenase9	GRMZM2G017616	B73 RefGen_v3	Gene	Chr1	16573827	16580722	lox9	cl902_1, lox9, PZA02393, rs128384929	
2721	lpa1	low phytic acid1	GRMZM2G155242	B73 RefGen_v3	Gene	Chr1	25282951	25287161	lpa1	inositol-3-phosphate synthase, low phytic acid1, lpa1, myo-inositol 1-phosphate synthase	decreased phytic acid in grain with corresponding increases in inorganic phosphate
2722	lpa2	low phytic acid2	GRMZM2G456626	B73 RefGen_v3	Gene	Chr1	101838959	101841220	lpa2	inositol phosphate kinase, inositol-tetrakisphosphate 1-kinase 1, ipk, low phytic acid2, lpa2, Zmlpk	low phytic acid
2723	lpa3	low phytic acid3	GRMZM2G361593	B73 RefGen_v3	Gene	Chr1	273963482	273967146	lpa3	334B7.5, Gene 6, lpa3	mutants have low phytic acid
2724	lpe1	leaf permease1	GRMZM5G858417	B73 RefGen_v3	Gene	Chr1	263063356	263068441	lpe1	leaf permease1, lpe1, umc1693b, ynh20	pale green (lpe1-m1 mutable) under high light, green in low light; defective chloroplasts
2725	lrk1	Ser/Thr receptor-like kinase1	GRMZM2G064750	B73 RefGen_v3	Gene	Chr8	9630289	9634061	lrk1	lrk1, ZmLrk-1	induced by fungal infection
2726	lrp1	lateral root primordia1	GRMZM2G077752	B73 RefGen_v3	Gene	Chr8	157286610	157288482	lrp1	lrp1, SHI/STY (SRS)-transcription factor 9, srs9, ZmLrp1	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2727	lrs1	liguleless related sequence1	AC232238.2_FG004	B73 RefGen_v3	Gene	Chr8	166341735	166349613	lrs1	bzip90, lg2-like, liguleless2-like, lrs1	
2728	ltk1	leucine-rich transmembrane protein kinas	GRMZM2G153393	B73 RefGen_v3	Gene	Chr1	17640006	17655596	ltk1	leucine-rich transmembrane protein kinase1, ltk1	endosperm cDNA, multiple copy; one copy is near pds1
2729	ltk2	leucine-rich transmembrane protein kinas	GRMZM2G330907	B73 RefGen_v3	Gene	Chr9	150263840	150275563	ltk2	cl1762_1(707), CL1762_1b, leucine-rich transmembrane protein kinase2, ltk2, ltk3	belongs to a small gene family; ltk2 shares 98.6% nucleotide sequence homology with ltk3, and these genes could be products of a recent gene duplication located on chromosome 9L.
2730	ltp1	lipid transfer protein1	GRMZM2G320373	B73 RefGen_v3	Gene	Chr6	162859289	162860116	ltp1	ltp1, nonspecific lipid-transfer protein AKCS9	
2731	lug1	leunig-related1	GRMZM2G361398	B73 RefGen_v3	Gene	Chr3	224206634	224220693	lug1	lug1	
2732	lug2	leunig-related2	GRMZM2G079013	B73 RefGen_v3	Gene	Chr5	215387951	215401364	lug2	lug2, pco149257, pco149257(455)	
2733	lug3	leunig-related3	GRMZM2G036169	B73 RefGen_v3	Gene	Chr1	300351265	300364771	lug3	lug3, pco116270, pco116270(108)	
2734	lug4	leunig-related4	GRMZM2G097640	B73 RefGen_v3	Gene	Chr1	233885155	233892825	lug4	lug4, WD repeat-containing protein 26-like	
2735	lug5	leunig-related5	GRMZM2G037683	B73 RefGen_v3	Gene	Chr3	58295849	58307713	lug5	lug5, pco091329, pco091329(220), PHM2324, PZA00509, rs128282657, rs55625236 , ss196415382	
2736	lug6	leunig-related6	GRMZM2G149708	B73 RefGen_v3	Gene	Chr2	105360159	105380776	lug6	F-box-like/WD repeat-containing protein TBL1XR1, lug6	
2737	lug7	leunig-related7	GRMZM2G111247	B73 RefGen_v3	Gene	Chr4	36237183	36244148	lug7	lug7	
2738	lug8	leunig-related8	GRMZM2G061186	B73 RefGen_v3	Gene	Chr6	8382834	8403391	lug8	lug8	
2739	lw1	lemon white1	GRMZM2G027059	B73 RefGen_v3	Gene	Chr1	273003521	273007187	lw1	hydroxymethylbutenyl diphosphate reductase1, ispH, l17, l*-544, lemon white1, luteus17, lw1, pco067553, zb*-101, zb7, zb*-N101, zebra crossbands7	white seedling, pale yellow endosperm; some alleles have zebra or luteus phenotypes
2740	lyce1	lycopene epsilon cyclase1	GRMZM2G012966	B73 RefGen_v3	Gene	Chr8	138416903	138424121	lyce1	lcyE, LCY-E, lcye1, lycE, lyce1, lycopene epsilon cyclase1	determines qualitative composition of endosperm carotenoids
2741	mab1	math-btb1	AC195147.3_FG001	B73 RefGen_v3	Gene	Chr7	168147615	168148658	mab1	BTB/POZ and MATH domain-containing protein 1-like, mab1, rs132440882, ZmTRAF1	
2742	mab10	math-btb10	GRMZM2G154437	B73 RefGen_v3	Gene	Chr2	273517	274882	mab10	mab10, rs131280597, ZmTRAF35	
2743	mab11	math-btb11	GRMZM2G077428	B73 RefGen_v3	Gene	Chr1	246318002	246319761	mab11	mab11, speckle-type POZ protein, ZmTRAF22	
2744	mab12	math-btb12	GRMZM2G181276	B73 RefGen_v3	Gene	Chr1	262061380	262063351	mab12	BTB/POZ and MATH domain-containing protein 1-like, mab12, ZmOrphan222	
2745	mab13	math-btb13	GRMZM2G027688	B73 RefGen_v3	Gene	Chr1	239162396	239163906	mab13	BTB/POZ and MATH domain-containing protein 1-like, mab13, rs128905179 , rs131867855, ZmOrphan129	

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
2746	mab14	math-btb14	GRMZM2G052985	B73 RefGen_v3	Gene	Chr2	235827342	235833741	mab14	mab14, rs129259159 , rs129259160, ZmTRAF17	
2747	mab15	math-btb15	GRMZM2G148213	B73 RefGen_v3	Gene	Chr7	170591410	170601470	mab15	mab15, Orphan18 speckle-type POZ protein, PCO106936, PCO106936(579), rs130689924, rs131182979, ZmOrphan18	
2748	mab16	math-btb16	GRMZM2G172210	B73 RefGen_v3	Gene	Chr2	215193244	215198622	mab16	mab16, Orphan47, rs129226497, rs131184299 , rs131184301 , ZmOrphan47	
2749	mab17	math-btb17	GRMZM2G166049	B73 RefGen_v3	Gene	Chr5	4571239	4574942	mab17	mab17, Orphan133 speckle-type POZ protein, rs131479110, ZmOrphan133	
2750	mab18	math-btb18	GRMZM2G060765	B73 RefGen_v3	Gene	Chr1	286737004	286741315	mab18	BTB/POZ and MATH domain-containing protein 4, cl49535_1, mab18, rs128972551, rs131909710, ZmTRAF19	
2751	mab19	math-btb19	GRMZM2G074323	B73 RefGen_v3	Gene	Chr7	8066461	8071872	mab19	mab19, pco096759, pco096759(535), ZmOrphan267	
2752	mab2	math-btb2	GRMZM2G404188	B73 RefGen_v3	Gene	Chr1	191709343	191710638	mab2	BTB/POZ and MATH domain-containing protein 1-like, mab2, ZmTRAF44	
2753	mab20	math-btb20	GRMZM2G009724	B73 RefGen_v3	Gene	Chr9	110588223	110590058	mab20	mab20, speckle-type POZ protein, ZmTRAF5	
2754	mab21	math-btb21	GRMZM2G109738	B73 RefGen_v3	Gene	Chr7	32747039	32748599	mab21	BTB/POZ and MATH domain-containing protein 2-like, mab21, rs130507533, ZmTRAF30	
2755	mab22	math-btb22	GRMZM2G046238	B73 RefGen_v3	Gene	Chr10	17890884	17892278	mab22	BTB/POZ and MATH domain-containing protein 1-like, mab22, ZmTRAF14	
2756	mab23	math-btb23	GRMZM2G143782	B73 RefGen_v3	Gene	Chr6	93484977	93486919	mab23	mab23, TIDP3181, ZmTRAF34	
2757	mab24	math-btb24	GRMZM2G103251	B73 RefGen_v3	Gene	Chr6	93500453	93502316	mab24	mab24, TRAF29 TRAF transcription factor, ZmTRAF29	
2758	mab25	math-btb25	GRMZM2G088086	B73 RefGen_v3	Gene	Chr6	93605547	93607608	mab25	mab25, rs131187234, TRAF25 speckle-type POZ protein, ZmTRAF25	
2759	mab26	math-btb26	GRMZM2G161610	B73 RefGen_v3	Gene	Chr6	93653946	93656228	mab26	mab26, ZmTRAF37	
2760	mab27	math-btb27	GRMZM2G161569	B73 RefGen_v3	Gene	Chr10	66779201	66780619	mab27	BTB/POZ and MATH domain-containing protein 1-like, mab27, ZmTRAF36	
2761	mab28	math-btb28	GRMZM2G041963	B73 RefGen_v3	Gene	Chr10	66889695	66890958	mab28	BTB/POZ and MATH domain-containing protein 1-like, mab28, rs128560386, ZmTRAF13	
2762	mab29	math-btb29	GRMZM2G077951	B73 RefGen_v3	Gene	Chr10	94602802	94605162	mab29	mab29, rs131785930, ZmTRAF23	
2763	mab3	math-btb3	GRMZM2G337139	B73 RefGen_v3	Gene	Chr1	191652759	191653770	mab3	BTB/POZ and MATH domain-containing protein 1-like, mab3, ZmOrphan171	
2764	mab30	math-btb30	GRMZM2G319215	B73 RefGen_v3	Gene	Chr1	252199381	252201244	mab30	mab30, Orphan113, rs131875840, Speckle-type POZ protein, ZmOrphan113	
2765	mab31	math-btb31	Zm00008a006240	Zm-PH207-REFERENCE	Gene	chr2	7994778	7995320	mab31	mab31, speckle-type POZ protein	
2766	mab4	math-btb4	GRMZM2G081441	B73 RefGen_v3	Gene	Chr4	42393046	42394177	mab4	BTB/POZ and MATH domain-containing protein 1-like, mab4, rs129682954 , rs131451025, TRAF transcription factor (TRAF24) , ZmTRAF24	
2767	mab5	math-btb5	GRMZM2G372171	B73 RefGen_v3	Gene	Chr4	42424938	42426486	mab5	mab5, rs131451058, ZmTRAF43	
2768	mab6	math-btb6	GRMZM2G125162	B73 RefGen_v3	Gene	Chr4	42454238	42456109	mab6	BTB/POZ and MATH domain-containing protein 1-like, mab6, ZmOrphan144	
2769	mab7	math-btb7	GRMZM2G110531	B73 RefGen_v3	Gene	Chr1	240647475	240649230	mab7	mab7, Orphan138 speckle-type POZ protein, ZmOrphan138	
2770	mab8	math-btb8	GRMZM2G418031	B73 RefGen_v3	Gene	Chr5	33629741	33631155	mab8	BTB/POZ and MATH domain-containing protein 1-like, mab8, rs131510772, ZmOrphan5	
2771	mab9	math-btb9	GRMZM2G574887	B73 RefGen_v3	Gene	Chr4	5470074	5471217	mab9	BTB/POZ and MATH domain-containing protein 1-like, mab9, rs131428360, TRAF transcription factor (TRAF45), ZmTRAF45	
2772	mac1	multiple archesporial cells1	GRMZM2G027522	B73 RefGen_v3	Gene	Chr10	14913865	14916717	mac1	lar*-487, leptotene arrest*-487, mac1, multiple archesporial cells1	called MAc1 in past publications!. (was lar*-487) several archesporial cells undergo normal meiosis; plants partially female sterile but completely male sterile
2773	mads1	MADS1	GRMZM2G171365	B73 RefGen_v3	Gene	Chr9	154082657	154102449	mads1	mads1, MADS1, zmm5, ZmMADS1	antipodal cells. during flower development expressed in all ear spikelet organ primordia at intermediate stages
2774	mads13	MADS-transcription factor 13	GRMZM2G472100	B73 RefGen_v3	Gene	Chr7	21134716	21135537	mads13		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2775	mads14	MADS-transcription factor 14	GRMZM2G099522	B73 RefGen_v3	Gene	Chr1	26671505	26681206	mads14		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2776	mads15	MADS-transcription factor 15	GRMZM2G553379	B73 RefGen_v3	Gene	Chr5	6993294	7011505	mads15	zmm15	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2777	mads17	MADS-transcription factor 17	GRMZM2G337892	B73 RefGen_v3	Gene	Chr2	207704174	207705556	mads17		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2778	mads18	MADS-transcription factor 18	GRMZM5G805387	B73 RefGen_v3	Gene	Chr8	102542053	102545720	mads18	zmm18	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2779	mads19	MADS-transcription factor 19	GRMZM2G316366	B73 RefGen_v3	Gene	Chr5	177268178	177269968	mads19		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2780	mads20	MADS-transcription factor 20	GRMZM2G137387	B73 RefGen_v3	Gene	Chr5	217863477	217870145	mads20		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2781	mads21	MADS-transcription factor 21	AC233912.1_FG001	B73 RefGen_v3	Gene	Chr7	19993628	19995763	mads21		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2782	mads22	MADS-transcription factor 22	GRMZM2G052045	B73 RefGen_v3	Gene	Chr1	214460902	214461626	mads22		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2783	mads25	MADS-transcription factor 25	GRMZM2G099408	B73 RefGen_v3	Gene	Chr4	6442913	6443786	mads25		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2784	mads26	MADS-transcription factor 26	GRMZM2G044408	B73 RefGen_v3	Gene	Chr5	204799296	204799985	mads26		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2785	mads27	MADS-transcription factor 27	GRMZM2G135018	B73 RefGen_v3	Gene	Chr2	33471001	33472629	mads27		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2786	mads28	MADS-transcription factor 28	GRMZM2G128953	B73 RefGen_v3	Gene	Chr9	138090540	138096148	mads28		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2787	mads3	MADS3	GRMZM2G072582	B73 RefGen_v3	Gene	Chr7	2065444	2076981	mads3	mads3, MADS3, MADS-transcription factor 3, ucsd106b, umc2090, zap1b	
2788	mads30	MADS-transcription factor 30	GRMZM2G069370	B73 RefGen_v3	Gene	Chr10	119044582	119046541	mads30		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2789	mads32	MADS-transcription factor 32	GRMZM2G105387	B73 RefGen_v3	Gene	Chr4	38790111	38793001	mads32		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2790	mads33	MADS-transcription factor 33	GRMZM2G459864	B73 RefGen_v3	Gene	Chr10	69143279	69144043	mads33		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2791	mads34	MADS-transcription factor 34	GRMZM2G137510	B73 RefGen_v3	Gene	Chr10	17785901	17791457	mads34		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2792	mads36	MADS-transcription factor 36	GRMZM2G079727	B73 RefGen_v3	Gene	Chr3	201371185	201375806	mads36		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2793	mads38	MADS-transcription factor 38	GRMZM2G334225	B73 RefGen_v3	Gene	Chr6	112393075	112399500	mads38		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2794	mads39	MADS-transcription factor 39	GRMZM2G055782	B73 RefGen_v3	Gene	Chr4	126011254	126012505	mads39		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
2795	mads4	MADS-transcription factor 4	GRMZM2G032339	B73 RefGen_v3	Gene	Chr1	277218151	277298925	mads4		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2796	mads40	MADS-transcription factor 40	GRMZM2G441115	B73 RefGen_v3	Gene	Chr4	2892328	2894627	mads40		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2797	mads41	MADS-transcription factor 41	GRMZM2G018589	B73 RefGen_v3	Gene	Chr3	170408317	170413958	mads41		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2798	mads42	MADS-transcription factor 42	GRMZM2G375707	B73 RefGen_v3	Gene	Chr8	142010577	142012164	mads42		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2799	mads43	MADS-transcription factor 43	GRMZM2G001139	B73 RefGen_v3	Gene	Chr8	155471127	155475291	mads43		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2800	mads44	MADS-transcription factor 44	GRMZM2G130382	B73 RefGen_v3	Gene	Chr5	85114743	85115386	mads44	zmm17	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2801	mads45	MADS-transcription factor 45	GRMZM2G117961	B73 RefGen_v3	Gene	Chr6	3237228	3240201	mads45		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2802	mads46	MADS-transcription factor 46	GRMZM2G306610	B73 RefGen_v3	Gene	Chr8	40959292	40960647	mads46		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2803	mads47	MADS-transcription factor 47	GRMZM2G099577	B73 RefGen_v3	Gene	Chr9	70600799	70601941	mads47		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2804	mads48	MADS-transcription factor 48	GRMZM2G148220	B73 RefGen_v3	Gene	Chr1	193288684	193293762	mads48		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2805	mads49	MADS-transcription factor 49	GRMZM2G129034	B73 RefGen_v3	Gene	Chr2	192877045	192885419	mads49	zmm27	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2806	mads50	MADS-transcription factor 50	GRMZM2G038878	B73 RefGen_v3	Gene	Chr6	108882764	108883558	mads50		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2807	mads51	MADS-transcription factor 51	GRMZM2G161666	B73 RefGen_v3	Gene	Chr6	93656696	93658911	mads51		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2808	mads52	MADS-transcription factor 52	GRMZM2G446426	B73 RefGen_v3	Gene	Chr4	191720338	191722587	mads52		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2809	mads53	MADS-transcription factor 53	GRMZM2G035092	B73 RefGen_v3	Gene	Chr3	168968579	168969501	mads53		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2810	mads54	MADS-transcription factor 54	GRMZM2G320549	B73 RefGen_v3	Gene	Chr3	19792210	19807087	mads54		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2811	mads55	MADS-transcription factor 55	GRMZM2G137289	B73 RefGen_v3	Gene	Chr3	127959457	127959975	mads55		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2812	mads56	MADS-transcription factor 56	GRMZM2G026223	B73 RefGen_v3	Gene	Chr1	4855703	4871281	mads56	zag6	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2813	mads57	MADS-transcription factor 57	GRMZM2G470857	B73 RefGen_v3	Gene	Chr8	19431756	19432706	mads57		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2814	mads58	MADS-transcription factor 58	GRMZM2G073357	B73 RefGen_v3	Gene	Chr6	141270744	141271664	mads58		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2815	mads59	MADS-transcription factor 59	AC234185.1_FG006	B73 RefGen_v3	Gene	Chr8	72172257	72173003	mads59		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2816	mads60	MADS-transcription factor 60	GRMZM2G152415	B73 RefGen_v3	Gene	Chr9	5512084	5517672	mads60		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2817	mads62	MADS-transcription factor 62	GRMZM5G878490	B73 RefGen_v3	Gene	Chr2	234414387	234415043	mads62		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2818	mads63	MADS-transcription factor 63	GRMZM2G032905	B73 RefGen_v3	Gene	Chr2	42386298	42388815	mads63		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2819	mads64	MADS-transcription factor 64	GRMZM5G853066	B73 RefGen_v3	Gene	Chr5	19800106	19800942	mads64		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2820	mads65	MADS-transcription factor 65	AC212823.4_FG003	B73 RefGen_v3	Gene	Chr5	167376720	167382187	mads65		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2821	mads66	MADS-transcription factor 66	GRMZM5G839969	B73 RefGen_v3	Gene	Chr5	172002654	172003517	mads66		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2822	mads67	MADS-transcription factor 67	GRMZM2G147716	B73 RefGen_v3	Gene	Chr7	164451097	164456819	mads67		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2823	mads68	MADS-transcription factor 68	GRMZM2G059102	B73 RefGen_v3	Gene	Chr1	17964695	17986258	mads68	m20, mads68, MADS-box transcription factor 47 [Zea mays], TIDP3516, ZMM20, ZmMADS47	Ortholog of rice MADS47; regulates zein gene transcription by interacting with o2 (Qiao et al., 2016)
2824	mads69	MADS-transcription factor 69	GRMZM2G171650	B73 RefGen_v3	Gene	Chr3	159022119	159050063	mads69		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2825	mads7	MADS-transcription factor 7	GRMZM2G097059	B73 RefGen_v3	Gene	Chr7	136296029	136307251	mads7	zmm7	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2826	mads70	MADS-transcription factor 70	GRMZM5G891280	B73 RefGen_v3	Gene	Chr6	165738341	165739291	mads70		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2827	mads71	MADS-transcription factor 71	GRMZM2G110582	B73 RefGen_v3	Gene	Chr9	78317642	78332274	mads71		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2828	mads73	MADS-transcription factor 73	GRMZM2G046885	B73 RefGen_v3	Gene	Chr5	209573312	209581383	mads73	MADS-TF (M26), ZMM26	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2829	mads74	MADS-transcription factor 74	GRMZM5G814279	B73 RefGen_v3	Gene	Chr9	7111132	7121722	mads74	ZMM21	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2830	mads75	MADS-transcription factor 75	GRMZM2G472096	B73 RefGen_v3	Gene	Chr7	21145677	21146564	mads75		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2831	mads76	MADS-transcription factor 76	GRMZM2G070034	B73 RefGen_v3	Gene	Chr9	125606160	125639409	mads76		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2832	mads77	MADS-transcription factor 77	GRMZM2G098986	B73 RefGen_v3	Gene	Chr1	194482102	194488891	mads77		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2833	mads78	MADS-transcription factor 78	GRMZM2G492156	B73 RefGen_v3	Gene	Chr5	177275445	177279005	mads78	mads78, zmm2 MADS2	mads-like gene orthologous to Si019862m.g, LOC_Os02g36924, Bradi3g46920
2834	mads9	MADS-transcription factor 9	GRMZM2G005155	B73 RefGen_v3	Gene	Chr2	10371800	10374751	mads9		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2835	maf1	MFP1 attachment factor1	GRMZM2G479245	B73 RefGen_v3	Gene	Chr9	147736551	147737374	maf1	maf1, MFP1 attachment factor1	cDNA
2836	mas1	malate synthase1	GRMZM2G102183	B73 RefGen_v3	Gene	Chr2	36945679	36948155	mas1	malate synthase1, Mas-, mas1, PCO110469	cDNA isolated by antibody screen
2837	mate1	multidrug and toxic compound extrusion	GRMZM5G870170	B73 RefGen_v3	Gene	Chr6	5869544	5874565	mate1	mate1, multidrug and toxic compound extrusion1, qALT6	confers aluminum tolerance in lines that carry 3 adjacent identical copies of the mate1 gene (Maron et al 2013)
2838	mate2	multidrug and toxic compound extrusion	GRMZM2G170128	B73 RefGen_v3	Gene	Chr5	20622821	20626799	mate2	mate2, multidrug and toxic compound extrusion2, transparent testa 12 protein	Is or is very tightly linked to a QTL that confers aluminum tolerance in lines (Maron et al 2010)
2839	mate3	multidrug and toxic compound extrusion	GRMZM2G163154	B73 RefGen_v3	Gene	Chr1	27099590	27103458	mate3	als1, aluminum sensitive ortholog1, mate3	Sorghum ortholog: Sb01g042740
2840	mate4	multidrug and toxic compound extrusion	GRMZM2G080450	B73 RefGen_v3	Gene	Chr3	57084587	57091384	mate4	cl19958_1, cl19958_1(220), mate4	Sorghum ortholog: Sb03g012960
2841	mate5	multidrug and toxic compound extrusion	GRMZM5G890665	B73 RefGen_v3	Gene	Chr2	153549513	153553629	mate5	mate5	Sorghum ortholog: Sb05g000630
2842	mate6	multidrug and toxic compound extrusion	GRMZM2G065154	B73 RefGen_v3	Gene	Chr5	71724077	71731917	mate6	mate6	Sorghum ortholog: Sb04g001840
2843	matl1	matrilineal1	GRMZM2G471240	B73 RefGen_v3	Gene	Chr1	68248585	68250379	matl1	haploid inducer, high haploidy, matl1, MTL, NLD, NOT LIKE DAD, patatin-like protein 1, rs128460736, ZmPLA1	encodes a pollen-specific phospholipase; novel edits lead to a 6.7% haploid induction rate

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
2844	mbd101a	methyl binding domain101a	GRMZM2G040131	B73 RefGen_v3	Gene	Chr8	106608894	106621408	mbd101a	mbd101a, methyl binding domain, PHM4134, PZA00739, PZA03579	
2845	mbd101b	methyl binding domain	GRMZM2G069254	B73 RefGen_v3	Gene	Chr6	146224513	146226056	mbd101b	mbd101b, methyl binding domain	
2846	mbd105	methyl binding domain105	GRMZM2G476933	B73 RefGen_v3	Gene	Chr3	88540265	88546003	mbd105	mbd105, methyl binding domain, Zmmbd1	
2847	mbd106	methyl binding domain106	GRMZM2G022365	B73 RefGen_v3	Gene	Chr1	175322304	175330120	mbd106	mbd106, methyl binding domain, Zmmbd2	
2848	mbd108	methyl binding domain108	GRMZM2G168269	B73 RefGen_v3	Gene	Chr7	134171280	134175278	mbd108	mbd108, PZA03582, PZA03583	
2849	mbd109	methyl binding domain109	GRMZM2G112679	B73 RefGen_v3	Gene	Chr5	16320354	16321171	mbd109	mbd109, methyl binding domain, PCO146112, PCO146112(383), PZA03578, rs131176058, ss196417608	
2850	mbd111	methyl binding domain111	GRMZM2G025095	B73 RefGen_v3	Gene	Chr2	191314651	191336825	mbd111	mbd111, methyl binding domain111, PCO097059(175), PCO097059a	
2851	mbd113	methyl binding domain113	GRMZM2G126545	B73 RefGen_v3	Gene	Chr10	105058169	105069085	mbd113	CL26423_1, CL26423_1(742), mbd113, methyl binding domain 113	
2852	mbd115	methyl binding domain115	GRMZM2G157470	B73 RefGen_v3	Gene	Chr1	250122582	250128271	mbd115	mbd115, PCO146110, PCO146110(82)	
2853	mbd117	methyl binding domain117	GRMZM2G048411	B73 RefGen_v3	Gene	Chr2	188802765	188808500	mbd117	cl34363_1, mbd117, methylcytosine binding domain protein	
2854	mbd123	methyl binding domain123	GRMZM2G119802	B73 RefGen_v3	Gene	Chr10	141516809	141520645	mbd123	CL5028_1, mbd123	
2855	mbf1	multi-protein bridging factor homolog1	GRMZM2G101480	B73 RefGen_v3	Gene	Chr4	24639257	24642130	mbf1	gnp_QAY2d02b, gpm415b, mbf1, multi-protein bridging factor homolog1, PCO106666, PZA01422, uaz246, uaz246a(mbf), UAZ246A(VSP), uaz246(vsp)	endosperm cDNA 5C01C06 (uaz246), similar to MBF1 of Bombyx mori
2856	mc1	mucronate1	GRMZM2G518638	B73 RefGen_v3	Gene	Chr2	183992102	183992798	mc1	15-kDa zein protein candidate, 16kD gamma zein, gz16, mc1, mucronate1, prolamin PPROL 17 precursor, Zc1, zp15*, zp16	dominant Mc1 kernels have opaque endosperm. endosperm-specific protein cDNA
2857	mcf1	mitochondrial carrier family protein1	GRMZM2G161299	B73 RefGen_v3	Gene	Chr5	152470618	152479871	mcf1	cl6429_1, cl6429_1(261), mcf1, rs130128692, rs131183458, rs131183459 , rs132232007 , rs132232013 , rs132232020	mitochondrion CoA transporter confirmed by yeast mutant complementation, and localization of encoded protein to mitochondrion (Zallot et al 2013
2858	mcf2	mitochrondrial carrier family protein2	GRMZM2G420119	B73 RefGen_v3	Gene	Chr8	139126558	139129894	mcf2	mcf2, pco110559, pco110559(632), rs130883616	complements yeast mutant deficienct in mitochondrial Coenzyme A transport; mitochondrial (Zallot et al 2013)
2859	mch2	maize CRY1 homolog2	GRMZM2G069762	B73 RefGen_v3	Gene	Chr4	108571396	108574204	mch2	CL25046_1(316), CL25046_1a, maize CRY1 homolog2, mch2	Homolog to yeast 40S ribosomal protein S14 gene family (cDNA probe)
2860	mde1	mouse DNA EBV homolog1	GRMZM2G155281	B73 RefGen_v3	Gene	Chr2	69807566	69810549	mde1	mde1, mouse DNA EBV homolog1, PCO123189	endosperm cDNA 5C02D07, similar to mouse homolog to Epstein-Barr virus IR3 repeat
2861	mdh2	malate dehydrogenase2	GRMZM2G154595	B73 RefGen_v3	Gene	Chr6	165831537	165836297	mdh2	malate dehydrogenase2, mdh2, mMdh1, mMdh2, PCO062153, PCO062153(524)	electrophoretic mobility; null allele is known; mitochondrial; dimeric; intra/interlocus hybrid bands occur
2862	mdh3	malate dehydrogenase3	GRMZM2G466833	B73 RefGen_v3	Gene	Chr3	213978038	213986724	mdh3	malate dehydrogenase3, mdh3	electrophoretic mobility; null allele is known; mitochondrial; dimeric; intra/interlocus hybrid bands occur
2863	mdh4	malate dehydrogenase4	GRMZM2G415359	B73 RefGen_v3	Gene	Chr1	231398148	231403913	mdh4	csu198, csu580a(mdh), csu77, csu77a, csuh77, malate dehydrogenase4, Mdh-, mdh4, sMdh1, umc351	electrophoretic mobility; null allele is known; cytosolic; dimeric; intra/interlocus hybrid bands occur; probed by csu77
2864	mdh6	malate dehydrogenase6	GRMZM2G129513	B73 RefGen_v3	Gene	Chr1	203209824	203213983	mdh6	csu374b, gnp_QCK20f01, gpm886, mdh6, PCO072788, rs128846139, rs128846153 , rs131175317, rs131175318 i, rs131175319, umc1661	mesophyll cells, C4 photosynthesis; a second copy may not function in photosynthesis
2865	me2	NADP-dependent malic enzyme2	GRMZM2G122479	B73 RefGen_v3	Gene	Chr6	139464390	139470075	me2	ChlMe2B, ChlMe2A, me2, NADP-dependent malic enzyme, non-photosynthetic NADP-malic enzyme , pRC14, pRC94, ynh, ynh(me2), ZmChlMe2A, ZmChlMe2B, ZmnonC4	cDNA in roots, preprotein contains chloroplast transit peptide sequences and is imported and processed; C3-like enzyme
2866	me3	NADP malic enzyme3	GRMZM2G085019	B73 RefGen_v3	Gene	Chr3	7276387	7281737	me3	csu16, csu16a, csuh16, Me1, me3, Mod1, NADP malic enzyme3, npi231(me), npi231-me1, umc13a, umc313(csuh16), ZmC4, ZmChlMe1	chloroplast C4-photosynthesis, delivers CO2 to ribulose bisphosphate carboylase
2867	me4	malic enzyme4	GRMZM2G118770	B73 RefGen_v3	Gene	Chr8	174612565	174617106	me4	IDP5, me4, me5, NADP malic enzyme4, nadpme-l, Zmcyt3, ZmCytNADP-ME	Embryo and root specific; cytosolic
2868	me5	malic enzyme5	GRMZM2G122479	B73 RefGen_v3	Gene	Chr6	139464390	139470075	me5	csu481, me5	
2869	me6	NADP-dependent malic enzyme6	GRMZM2G159724	B73 RefGen_v3	Gene	Chr3	201756751	201761835	me6	AY104511, me6, PHM2919, PZA00892	
2870	mecs1	methyl erythritol cyclodiphosphate synth	GRMZM5G835542	B73 RefGen_v3	Gene	Chr4	155857959	155859966	mecs1	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase1, MDS1, mecs1	
2871	mecs2	methyl erythritol cyclodiphosphate synth	AC209374.4_FG002	B73 RefGen_v3	Gene	Chr5	196331063	196332805	mecs2	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase2, MDS2, mecs2	
2872	meg1	maternally expressed gene1	GRMZM2G354335	B73 RefGen_v3	Gene	Chr7	13073446	13074744	meg1	maternally expressed gene1, meg1, meg3	Maternally transmitted alleles preferentially expressed in endosperm
2873	meg10	maternally expressed gene10	GRMZM2G086827	B73 RefGen_v3	Gene	Chr7	12673702	12674015	meg10	meg10	
2874	meg11	maternally expressed gene11	GRMZM2G181051	B73 RefGen_v3	Gene	Chr7	12626477	12627199	meg11	meg11	
2875	meg12	maternally expressed gene12	GRMZM2G175896	B73 RefGen_v3	Gene	Chr7	12531786	12532621	meg12	meg12	
2876	meg13	maternally expressed gene13	GRMZM2G175912	B73 RefGen_v3	Gene	Chr7	12484473	12485342	meg13	meg13	
2877	meg14	maternally expressed gene14	GRMZM2G145466	B73 RefGen_v3	Gene	Chr7	13178054	13178841	meg14	meg14	
2878	meg15	maternally expressed gene15	GRMZM2G137959	B73 RefGen_v3	Gene	Chr7	12591109	12591978	meg15	meg15, meg4	
2879	meg2	maternally expressed gene2	GRMZM2G088896	B73 RefGen_v3	Gene	Chr7	12676389	12677577	meg2	meg2, meg9	Maternally transmitted alleles preferentially expressed in endosperm
2880	meg3	maternally expressed gene3	GRMZM2G344323	B73 RefGen_v3	Gene	Chr7	12776201	12779156	meg3	meg3	Maternally transmitted alleles preferentially expressed in endosperm
2881	meg4	maternally expressed gene4	GRMZM5G896560	B73 RefGen_v3	Gene	Chr7	39888296	39889211	meg4	meg4	Maternally transmitted alleles preferentially expressed in endosperm
2882	meg6	maternally expressed gene6	GRMZM2G094054	B73 RefGen_v3	Gene	Chr7	12709254	12710092	meg6	meg6	
2883	meg7	maternally expressed gene7	GRMZM2G116212	B73 RefGen_v3	Gene	Chr7	13003435	13004149	meg7	meg7	
2884	meg8	maternally expressed gene8	GRMZM2G123153	B73 RefGen_v3	Gene	Chr7	12859255	12859461	meg8	meg8	
2885	meg9	maternally expressed gene9	GRMZM2G502035	B73 RefGen_v3	Gene	Chr7	12752035	12752664	meg9	meg2, meg9	
2886	mek1	MEK homolog1	GRMZM2G167856	B73 RefGen_v3	Gene	Chr3	201966295	201973589	mek1	gnp_QBG9b07, gpm463, MAPKK1, mek1, MEK homolog1, mitogen-activated; ERK-activating protein kinase (MEK) homolog, PCO073471, PCO073471(268), rs131181540 , ZmMEK1	abundant in primary roots and coleoptiles of maize seedlings and exist in lower levels in mature stems and leaves.. function inferred from sequence similarity, gene expression and confirmed
2887	met1	DNA methyl transferase1	GRMZM2G333916	B73 RefGen_v3	Gene	Chr7	11133095	11139492	met1	CL147_1, cytosine-5 DNA methyltransferase, dmt1, dmt101, DNA methyl transferase1, met1, MET1-like, zmet1, ZMET1, ZmMET1, ZmMET1b-1, ZmMET2	cDNA clones
2888	met2	DNA methyl transferase2	GRMZM2G025592	B73 RefGen_v3	Gene	Chr10	141612636	141620390	met2	PZA03603, PZA03604, PZA03605, PZA03606, PZA03607, rs131176015, rs131176059, ss196417470, ss196417610, Zea methyltransferase2, ZmCMT1, zmet2	
2889	met3	DNA methyl transferase3	GRMZM2G092497	B73 RefGen_v3	Gene	Chr9	154729337	154755677	met3	PZA03572, PZA03573, rs131175972, rs131175973, rs131175974, rs131175975, siaf242320d, ss196417291, ss196417293, ss196417295, ss196417297, ZmDRM1, Zmet3, ZMET3	
2890	met4	DNA methyl transferase4	GRMZM2G157589	B73 RefGen_v3	Gene	Chr8	142201711	142206667	met4	met4, si687064e06, si687064e06(646), ZmDNMT2, zmet4	
2891	met5	DNA methyl transferase5	GRMZM2G005310	B73 RefGen_v3	Gene	Chr2	10343925	10353440	met5	CL611_1, CL611_1(115), dmt102b, dmt105, DNA methyl transferase, met5, PCO092475, ZmCMT2, zmet5	
2892	met6	DNA methyl transferase6	GRMZM2G065599	B73 RefGen_v3	Gene	Chr8	129490869	129493053	met6	dmt106, DNA methyl transferase 106, met6, PCO143520, PCO143520(628), ZmDRML	

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
2893	met7	DNA methyl transferase7	GRMZM2G137366	B73 RefGen_v3	Gene	Chr1	2930055	2935014	met7	cytosine methyltransferase Zmet3, dmt103b, DMT107, DNA methyl transferase, met7, PZA03613, PZA03614, ZmDRM2	
2894	met8	DNA methyl transferase8	GRMZM2G334041	B73 RefGen_v3	Gene	Chr7	11151804	11157815	met8	dmt101, MET1-like, met8, ZmMET1, ZmMET1b-2	
2895	mez1	enhancer of zeste1	GRMZM2G157820	B73 RefGen_v3	Gene	Chr6	79622840	79633054	mez1	enhancer of zeste1, ez1, mez1, sdg124, set124, SET domain group	
2896	mez2	enhancer of zeste2	GRMZM5G875502	B73 RefGen_v3	Gene	Chr9	135509551	135524285	mez2	enhancer of zeste2, ez2, mez2, sdg125, set125, SET domain group125	
2897	mez3	enhancer of zeste3	GRMZM2G043484	B73 RefGen_v3	Gene	Chr1	49403087	49413070	mez3	enhancer of zeste3, ez3, me4z3, mez3, Mez3	
2898	mfs18	male flower specific18	EF517601.1_FG016	B73 RefGen_v3	Gene	Chr3	34681198	34681584	mfs18	male flower specific18, mfs18, MFS18, umc1810, umc1810a, umi6	cDNA sequence, associated with tassel glume vascular bundles
2899	mfsd1	major facilitator superfamily defense1	GRMZM2G161310	B73 RefGen_v3	Gene	Chr3	45563077	45577326	mfsd1	mfs1, mfsd1	Defense-inducible protein related to integral membrane permeases and bacterial antiporters
2900	mfsd2	major facilitator superfamily defense2	GRMZM5G877788	B73 RefGen_v3	Gene	Chr4	186656010	186660015	mfsd2	mfs2, mfsd2, pco117107, transporter of mugineic acid, ZmTOM2	Protein related to integral membrane permeases and bacterial antiporters
2901	mgs1	male-gametophyte specific1	GRMZM2G317406	B73 RefGen_v3	Gene	Chr10	111861870	111862808	mgs1	AY109538, CL1988_1, gsy15(pol), male-gametophyte specific1, mgs1, phi062, Pol, PZA00215, sc15, SC15, Zm13, Zmc13	mRNA in cytoplasm of both vegetative cell (pollen grain) and pollen tube; not expressed in shoot, root, kernel, ovule, silk; SSR phi062
2902	mgs2	male gametophyte-specific2	GRMZM2G080056	B73 RefGen_v3	Gene	Chr4	231421874	231423870	mgs2	bnl-mgs2, male gametophyte-specific2, mgs2, Mgs2A, pectate lyase homolog, pel*-L20139, Zm58.1	pollen-specific cDNA with pectate lyase homology
2903	mgs3	male gametophyte specific3	GRMZM2G323418	B73 RefGen_v3	Gene	Chr9	20163896	20165966	mgs3	gnp_QBJ2e08, gpm508, male gametophyte specific3, mgs2B, mgs3, pectate lyase homolog, pel*-L20140_, Zm58.2	genomic sequence with homology to mgs2 cDNA
2904	mgt1	magnesium transporter1	GRMZM2G108477	B73 RefGen_v3	Gene	Chr9	104353895	104357808	mgt1	mgt1, MRS2-10	encodes CorA/MRS2/MGT-type magnesium transporter
2905	mgt10	magnesium transporter10	GRMZM2G018706	B73 RefGen_v3	Gene	Chr1	8348905	8351557	mgt10	mgt10, putative magnesium transporter MRS2-H	encodes CorA/MRS2/MGT-type magnesium transporter
2906	mgt11	magnesium transporter11	GRMZM2G054632	B73 RefGen_v3	Gene	Chr10	116913274	116917658	mgt11	mgt11, putative magnesium transporter MRS2-D	encodes CorA/MRS2/MGT-type magnesium transporter
2907	mgt12	magnesium transporter12	GRMZM2G420436	B73 RefGen_v3	Gene	Chr1	260979921	260988130	mgt12	GMN10, mgt12	encodes CorA/MRS2/MGT-type magnesium transporter
2908	mgt2	magnesium transporter2	GRMZM2G170326	B73 RefGen_v3	Gene	Chr6	95771854	95778367	mgt2	cl34393_1, cl34393_1(673), mgt2	encodes CorA/MRS2/MGT-type magnesium transporter
2909	mgt3	magnesium transporter3	GRMZM2G064467	B73 RefGen_v3	Gene	Chr2	32222808	32227738	mgt3	mgt3	encodes CorA/MRS2/MGT-type magnesium transporter
2910	mgt4	magnesium transporter4	GRMZM2G145794	B73 RefGen_v3	Gene	Chr9	126705574	126709100	mgt4	mgt4	encodes CorA/MRS2/MGT-type magnesium transporter
2911	mgt5	magnesium transporter5	GRMZM2G159295	B73 RefGen_v3	Gene	Chr1	275052382	275058949	mgt5	mgt5, pco092863, pco092863(90)	encodes CorA/MRS2/MGT-type magnesium transporter
2912	mgt6	magnesium transporter6	GRMZM2G453832	B73 RefGen_v3	Gene	Chr1	85998310	86001537	mgt6	mgt6, putative magnesium transporter MRS2-G	encodes CorA/MRS2/MGT-type magnesium transporter
2913	mgt7	magnesium transporter7	GRMZM2G458879	B73 RefGen_v3	Gene	Chr2	51802797	51804523	mgt7	mgt7, putative magnesium transporter MRS2-D	encodes CorA/MRS2/MGT-type magnesium transporter
2914	mgt8	magnesium transporter8	GRMZM2G065971	B73 RefGen_v3	Gene	Chr8	162836382	162842987	mgt8	mgt8	encodes CorA/MRS2/MGT-type magnesium transporter
2915	mgt9	magnesium transporter9	GRMZM2G139822	B73 RefGen_v3	Gene	Chr3	164927197	164941379	mgt9	magnesium transporter MRS2-F, mgt9	encodes CorA/MRS2/MGT-type magnesium transporter
2916	mha1	membrane H(+)-ATPase1	GRMZM2G144821	B73 RefGen_v3	Gene	Chr2	233155669	233160713	mha1	IDP2508, IDP2512, membrane H(+)-ATPase1, mha1, pma1, umc1207, Zmpma1	cDNA and genomic sequences similar to plant plasma membrane proton-translocating ATPase, major band in Southerns; partly contained in Bs-1 retroelement; SSR umc1207
2917	mha2	plasma-membrane H+ATPase2	GRMZM2G019404	B73 RefGen_v3	Gene	Chr2	4305357	4312971	mha2	CL1965_1, H+ATPase 2, mha2, MHA-2, mha3, plasma-membrane H+ATPase2	cDNA sequence similar to plant plasma-membrane [H+]-ATPase and distinct from mha1
2918	mha3	membrane H(+)-ATPase3	GRMZM2G104325	B73 RefGen_v3	Gene	Chr7	14468797	14474919	mha3	mha3, pco106203, pco106203(255)	
2919	mha4	proton-exporting ATPase4	GRMZM2G006894	B73 RefGen_v3	Gene	Chr10	145614824	145621943	mha4	mha4	
2920	mir1	maize insect resistance1	GRMZM2G150276	B73 RefGen_v3	Gene	Chr6	89072247	89074183	mir1	CL872_-2, maize insect resistance1, mir1, mir1(thp)	single copy cDNA
2921	mir2	maize insect resistance2	GRMZM2G150256	B73 RefGen_v3	Gene	Chr6	89066267	89071191	mir2	CL872_-2, gnp_AW438150, gpm228, maize insect resistance2, mir2, mir2(thp), thp*-Mp708, umc1178	cDNA; SSR umc1178
2922	mir3	maize insect resistance3	GRMZM2G166281	B73 RefGen_v3	Gene	Chr2	5275102	5279397	mir3	gnp_QBI2g05a, gnp_QCB2c09b, gpm493a, gpm588b, maize insect resistance3, mir3, mir3b, mir3b(thp), pco102242(113), PCO102242a	apoplastic; pest defense protease
2923	mis1	putative aldehyde dehydrogenase MIS1	GRMZM2G090087	B73 RefGen_v3	Gene	Chr6	161650053	161657588	mis1	mis1, PCO077463, PCO077463(520), PZA00266.7, ZmRab7A1	
2924	mis12a	minichromosome instability12a	GRMZM2G173660	B73 RefGen_v3	Gene	Chr10	147960260	147963853	mis12a	minichromosome instability12, minichromosome instability12a, mis12-1, mis12a, si618030e11, si618030e11(761)	encodes a core kinetochore protein required in meiosis I
2925	mis12b	minichromosome instability12b	GRMZM2G049495	B73 RefGen_v3	Gene	Chr2	1049355	1141492	mis12b	CL37982_1, CL37982_1(197), minichromosome instability12b, mis12-2, mis12b, PZA00680, rs131175383, ss196414921	encodes a kinetochore protein required for meiosis I
2926	mkk3	MAP kinase kinase3	GRMZM5G867568	B73 RefGen_v3	Gene	Chr3	111094841	111094990	mkk3	MAPKK3, mkk3, pco130948	stress response; induced by abscisic acid
2927	mkk4	MAP kinase kinase4	GRMZM5G878379	B73 RefGen_v3	Gene	Chr5	212702420	212703869	mkk4	MAPKK4, mitogen-activated protein kinase kinase4, mkk4	function inferred from sequence similarity, and gene expression analyses.
2928	mkkk10	MAP kinase kinase kinase10	GRMZM2G180555	B73 RefGen_v3	Gene	Chr9	141628047	141638073	mkkk10	MAPKKK10, mitogen-activated protein kinase kinase kinase10, mkkk10	Function inferred from sequence similarilty
2929	mkkk11	MAP kinase kinase kinase11	GRMZM2G066120	B73 RefGen_v3	Gene	Chr1	37470728	37476121	mkkk11	MAPKKK11, mitogen-activated protein kinase kinase kinase11, mkkk11, TIDP6724	function inferred from sequence similarity
2930	mkkk16	MAP kinase kinase kinase16	GRMZM2G098828	B73 RefGen_v3	Probed Site	Chr2	178911234	178919677	mkkk16	cl10379_1, cl10379_1(164), MAPKKK16, mitogen-activated protein kinase kinase kinase16	Function inferred from sequence similarity (Kong 2013)
2931	mkkk18	MAP kinase kinase kinase18	GRMZM2G305066	B73 RefGen_v3	Gene	Chr8	152510200	152511639	mkkk18	MAPKKK18, mitogen-activated protein kinase kinase kinase18, mkkk18	function inferred from sequence similarity (Kong et al 2013)
2932	mkkk27	MAP kinase kinase kinase27	GRMZM2G089159	B73 RefGen_v3	Gene	Chr2	207080135	207083546	mkkk27	MAPKKK27, mitogen-activated protein kinase kinase kinase27, pco137357, pco137357(180)	function inferred from sequence similarity (Kong et al 2013)
2933	mkkk47	MAP kinase kinase kinase47	GRMZM2G045366	B73 RefGen_v3	Gene	Chr3	197586815	197591360	mkkk47	MAPKKK47, mitogen-activated protein kinase kinase kinase47, mkkk47, rs131181661	function inferrred from sequence similarity (Kong et al 2013)
2934	mkkk51	MAP kinase kinase kinase51	GRMZM2G019434	B73 RefGen_v3	Gene	Chr1	171553382	171558256	mkkk51	MAPKKK51, mitogen-activated protein kinase kinase kinase51, mkkk51, rs128803682	function inferred from sequence similarity (Kong et al 2013)
2935	mkkk55	MAP kinase kinase kinase55	GRMZM2G088299	B73 RefGen_v3	Gene	Chr3	215295086	215300436	mkkk55	MAPKKK55, mitogen-activated protein kinase kinase kinase55, mkkk55	function inferred from sequence similarity (Kong et al 2013)
2936	mkkk63	MAP kinase kinase kinase63	GRMZM2G152889	B73 RefGen_v3	Gene	Chr3	142725252	142734848	mkkk63	MAPKKK63, mitogen-activated protein kinase kinase kinase63, mkkk63, rs131176465, rs131176466, rs131176467, rs131176468	function inferred from sequence similarity (Kong et al 2013)
2937	mlg3	lea protein group3	GRMZM2G096475	B73 RefGen_v3	Gene	Chr6	162162303	162163681	mlg3	lea protein group3, mlg3, PCO084365, pco084365(520), phi070, pMEc, umc1063	cDNA similar to wheat Ec; SSR phi070
2938	mlo1	barley mlo defense gene homolog1	GRMZM2G032219	B73 RefGen_v3	Gene	Chr1	6227483	6231125	mlo1	AY110401, barley mildew resistance locus o (Mlo) homolog, barley mlo defense gene homolog1, mlo1, PHM7935, PZA02372	one of 9 seven-transmembrane homologues to barley powdery mildew defense response gene
2939	mlo2	barley mlo defense gene homolog2	GRMZM2G040441	B73 RefGen_v3	Gene	Chr1	84547891	84553701	mlo2	barley mlo defense gene homolog2, mlo2, pco148749, PCO148749(33)	one of 9 seven-transmembrane homologues to barley powdery mildew defense response gene
2940	mlo3	barley mlo defense gene homolog3	GRMZM2G031331	B73 RefGen_v3	Gene	Chr2	47067541	47072637	mlo3	barley mlo defense gene homolog3, mlo3, pco123899, PCO123899(132)	one of 9 seven-transmembrane homologues to barley powdery mildew defense response gene
2941	mlo4	barley mlo defense gene homolog4	GRMZM2G089259	B73 RefGen_v3	Gene	Chr4	207435849	207441283	mlo4	barley mlo defense gene homolog4, mlo4, pco095788, PZA01332, rs129901352, rs131175638, rs55625194 , ss196415913, ss196415915	one of 9 seven-transmembrane homologues to barley powdery mildew defense response gene

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
2942	mlo5	barley mlo defense gene homolog5	GRMZM2G471142	B73 RefGen_v3	Gene	Chr3	169916619	169920590	mlo5	barley mlo defense gene homolog5, mlo5, tdsgR11F05	one of 9 seven-transmembrane homologues to barley powdery mildew defense response gene
2943	mlo6	barley mlo defense gene homolog6	GRMZM2G325653	B73 RefGen_v3	Gene	Chr5	64702557	64709182	mlo6	barley mlo defense gene homolog6, mlo6	one of 9 seven-transmembrane homologues to barley powdery mildew defense response gene
2944	mlo7	barley mlo defense gene homolog7	GRMZM2G416887	B73 RefGen_v3	Gene	Chr9	103186013	103204159	mlo7	barley mlo defense gene homolog7, mlo7	one of 9 seven-transmembrane homologues to barley powdery mildew defense response gene
2945	mlo8	barley mlo defense gene homolog8	GRMZM5G881803	B73 RefGen_v3	Gene	Chr6	147620043	147639499	mlo8	barley mlo defense gene homolog8, mlo8, PCO070411	one of 9 seven-transmembrane homologues to barley powdery mildew defense response gene
2946	mlo9	barley mlo defense gene homolog9	GRMZM2G051974	B73 RefGen_v3	Gene	Chr2	1273216	1278753	mlo9	barley mlo defense gene homolog9, IDP3784, mlo9	one of 9 seven-transmembrane homologues to barley powdery mildew defense response gene
2947	mmp93		GRMZM2G087918	B73 RefGen_v3	Gene	Chr1	10220690	10229909	mmp93	mmp93	
2948	mn1	miniature seed1	GRMZM2G119689	B73 RefGen_v3	Gene	Chr2	57435843	57439124	mn1	beta-fructofuranosidase, insoluble isoenzyme 2 , CL1139_1, cl1139_1(136), incw2, miniature seed1, mn1, ufg6, ufg6(incw2)	small, somewhat defective kernel, fully viable; invertase reduced
2949	mop1	mediator of paramutation1	GRMZM2G042443	B73 RefGen_v3	Gene	Chr2	41131324	41136928	mop1	CL3242_1, CL3242_1(29), mediator of paramutation1, modifier of pigmentation1, mop1, PHM10404, rdr101, RNA-dependent RNA polymerase 101, sde102	recessive changes B' phenotype to dark, similar to B1-I
2950	mpk1	MAP kinase1	GRMZM2G053987	B73 RefGen_v3	Gene	Chr9	138684018	138689891	mpk1	MAP kinase1, MAP kinase 4, mitogen-activated protein kinase, mpk1, siab016801(695), siab016801b, ZmMPK4	cDNA sequence; single copy
2951	mpk14	MAP kinase14	GRMZM2G062914	B73 RefGen_v3	Gene	Chr5	79898949	79904417	mpk14	MAPK14, mitogen-activated protein kinase14, pco126466(421), pco126466e, ZmMPK7	
2952	mpk2	MAP kinase2	GRMZM2G020216	B73 RefGen_v3	Gene	Chr9	18879527	18885415	mpk2	MAP kinase2, MAP kinase 5, mitogen-activated protein kinase, mpk2, MPK6, PCO143674(662), PCO143674b, ZmMPK5	functions in brassinosteroid signaling in antioxidant defense (Zhang et al 2010) cDNA sequence; single copy (Berberich et al 1999)
2953	mpk3	MAP kinase3	GRMZM2G017792	B73 RefGen_v3	Gene	Chr1	43690126	43693022	mpk3	gnp_QBE2b06, gpm443, mitogen-activated protein kinase, ZmMPK3	transcript and protein activity upregulated by ABA and H2O2
2954	mpk6	MAP kinase6	GRMZM2G089484	B73 RefGen_v3	Gene	Chr10	88695003	88700854	mpk6	CL3584_1, CL3584_1(736), mitogen-activated protein kinase, mpk6	
2955	mpk7	MAP kinase7	GRMZM2G002100	B73 RefGen_v3	Gene	Chr6	74762186	74767526	mpk7	ABA stimulation MAP kinase, mitogen-activated protein kinase, mpk7, PCO143674, umc2074	
2956	mpt1	mitochondrial phosphate transporter1	GRMZM2G152827	B73 RefGen_v3	Gene	Chr5	210195424	210200092	mpt1	mitochondrial phosphate transporter1, mpt1, PCO060710b	cDNA sequence
2957	mre11a	meiotic recombination protein 11 homolo	GRMZM2G106056	B73 RefGen_v3	Gene	Chr2	6993096	7000975	mre11a	double-strand break repair protein MRE11, mre11a, rs131295069	
2958	mre11b	meiotic recombination protein 11 homolo	GRMZM2G309109	B73 RefGen_v3	Gene	Chr4	29935686	29941454	mre11b	mre11b	
2959	mrp1	Myb related protein1	GRMZM2G111306	B73 RefGen_v3	Gene	Chr8	127960823	127962081	mrp1	mrp1, Myb related protein1, mzMRP-1, ZmMYBR1	transforms aleurone cells into endosperm transfer cells and required to maintain transfer cell phenotype
2960	mrpa1	multidrug resistance protein associated1	GRMZM2G113203	B73 RefGen_v3	Gene	Chr9	58021949	58028182	mrpa1	ATP-binding cassette (ABC) transporter, MRP1, mrpa1, MRP associated1, multidrug resistance protein associated, PCO120900b	ATP-binding cassette (ABC) transporter
2961	mrpa2	multidrug resistance associated protein2	GRMZM5G832772	B73 RefGen_v3	Gene	Chr7	123394542	123423972	mrpa2	ATP-binding cassette (ABC) transporter, MRP1, MRP10, mrp2, MRP2, mrpa2, multidrug resistance protein associated	ATP-binding cassette (ABC) transporter
2962	mrpa3	multidrug resistance-associated protein3	GRMZM2G111903	B73 RefGen_v3	Gene	Chr9	17746515	17758407	mrpa3	cmt1, mrp3, MRP3, MRP4, mrpa3, PCO078370, PCO078370(661), PZA02844	Transport of anthocyanin into vacuole
2963	mrpa4	multidrug resistance-associated protein 4	GRMZM5G820122	B73 RefGen_v3	Gene	Chr1	9298049	9301828	mrpa4	cl10432_1, gnp_QAH5b09, gpm790, lpa1, MRP4, mrpa4, mrpa4(6), PZA00731, rs128285109, rs128285110, rs55625054 , ss196414373, ss196414375	
2964	mrpa6	multidrug resistance associated protein6	GRMZM2G142870	B73 RefGen_v3	Gene	Chr8	45267687	45282726	mrpa6	ABC transporter C family member 14-like, mrpa6	
2965	mrpa7	multidrug resistance associated protein7	GRMZM5G830695	B73 RefGen_v3	Gene	Chr3	11403408	11407172	mrpa7	mrpa7	
2966	mrpi1	MRP interacting1	GRMZM2G139160	B73 RefGen_v3	Gene	Chr8	171358270	171363973	mrpi1	CL2697_1, mrpi1, mrpi-1, MRP interacting1, myb-related protein-interacting	C2H2 zinc finger protein
2967	mrpi2	MRP interacting2	GRMZM2G105224	B73 RefGen_v3	Gene	Chr3	190121699	190124115	mrpi2	C2H2 zinc finger protein, cl2697_1(260), cl2697_1a, mrpi2, mrpi-2, MRP interacting2, myb-related protein-interacting, nucleic acid binding protein	nucleic acid binding protein
2968	ms10	male sterile10	GRMZM5G830329	B73 RefGen_v3	Gene	Chr10	84622439	84624344	ms10	abnormal pollen vacuolation1, apv1, male sterile10, ms10, pco115177, pco115177(735)	like ms5; affected at microspore vacuolation
2969	ms22	male sterile22	GRMZM2G442791	B73 RefGen_v3	Gene	Chr7	5333364	5334245	ms22	glutaredoxin, glutaredoxin-C9-like, grx, male sterile22, male sterile converted anther1, ms22, ms*-6036, ms*-6064, msca1	pollen mother cells degenerate
2970	ms23	male sterile23	GRMZM2G021276	B73 RefGen_v3	Gene	Chr8	95823	98367	ms23	bhlh16, bHLH-transcription factor 16, male sterile23, ms23, ms35, ms*-6011, ms*-6018, ms*-6027, ms*-6031, ms*-6059, ms*-Bear7, TIDP2747	pollen mother cells degenerate
2971	ms26	male sterile26	GRMZM2G091822	B73 RefGen_v3	Gene	Chr1	14505716	14508042	ms26	male sterile26, ms26, ms*-sb200	tapetal cells abnormal, die early; microspores vacuolate early and abort after the tetrad stage
2972	ms32	male sterile32	GRMZM2G163233	B73 RefGen_v3	Gene	Chr2	205125283	205135718	ms32	bhlh66, bHLH-transcription factor 66, male sterile32, ms32, ms*-6066	like ms1
2973	ms44	male sterile44	AC225127.3_FG003	B73 RefGen_v3	Gene	Chr4	195238767	195239581	ms44	anther-specific protein1, Anther specific protein (Ltp-like protein)LIM1 protein Precursor, LIM1, male flower specific14, male sterile44, MFS14, ms44, Ms*-7255, nthr1, ZmLTPc1	dominant Ms44 plants male sterile
2974	ms45	male sterile45	GRMZM2G307906	B73 RefGen_v3	Gene	Chr9	141198898	141203399	ms45	Group 6, male sterile45, ms45, ms45'-9301, ms*-6006, ms*-6040, ms*-BS1, ms*-BS2, ms*-BS3, strictosidine synthase 1	abnormal microspore wall formation, tassel specific, cDNA clone
2975	ms8	male sterile8	GRMZM2G119265	B73 RefGen_v3	Gene	Chr8	164959333	164961811	ms8	male sterile8, ms8, umc1724	pollen mother cells degenerate
2976	ms9	male sterile9	GRMZM2G308034	B73 RefGen_v3	Gene	Chr1	45942719	45945140	ms9	DNA binding protein, Group 5, male sterile9, ms9, myb46, MYB-transcription factor 46, pza03183, rs131175273, ss196414474, umc13	family by the GRASSIUS project (Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2977	msf1	mRNA splicing factor1	GRMZM2G057450	B73 RefGen_v3	Gene	Chr4	2116635	2122723	msf1	CL3975_1, cl3975_1(287), csu363(gfu), mRNA splicing factor1, mRNA splicing factor homolog1, msf1, PCO122195, pco122195(287), splicing factor U2AF 65 kDa	leaf cDNA csu363 similar to animal mRNA splicing factor
2978	msh1	male sterile protein homolog1	GRMZM2G036217	B73 RefGen_v3	Gene	Chr4	52923800	52927833	msh1	male sterile protein 2, male sterile protein homolog1, msh1, uaz195, uaz195(gfu), uaz6c06c01(gfu), zms1	leaf cDNA 6C06C01, similar to Arabidopsis MS2
2979	msrb2	methionine sulfoxide reductase b2	GRMZM2G089308	B73 RefGen_v3	Gene	Chr8	107317423	107322839	msrb2	cl827_1, cl827_1(623), msrb2	
2980	mss1	MSS1 homolog	GRMZM2G110185	B73 RefGen_v3	Gene	Chr5	212423808	212427681	mss1	csu834, csu834(mss), csuh00834, csuh834, mammalian suppressor of sgv-1 (Suppressor of GPA1-Val50 mutation protein 1) of yeast homolog, mss1, MSS1 homolog	leaf cDNA csu834 similar to human protease
2981	mstr1	monosaccharide transporter1	GRMZM2G135739	B73 RefGen_v3	Gene	Chr7	1232553	1236835	mstr1	monosaccharide transporter1, mst1, mstr1	
2982	mstr2	monosaccharide transporter2	GRMZM2G141034	B73 RefGen_v3	Gene	Chr4	29873533	29875971	mstr2	mst2, mst3, mstr2, mstr3	
2983	mstr4	monosaccharide transporter4	GRMZM2G034061	B73 RefGen_v3	Gene	Chr9	115519260	115524432	mstr4	hexose carrier protein HEX6-like, mst4, mstr4	
2984	mta1	ribosomal protein L13A homolog	GRMZM2G090422	B73 RefGen_v3	Gene	Chr1	277805915	277807951	mta1	CL4861_1a, mouse transplantation antigen homolog1, mta1, ribosomal protein, rpl13, uaz126, uaz126(gfu), uaz208, uaz208(mta), uaz208(tsta)	endosperm cDNA 5C03G09, similar to rodent ribosomal protein. endosperm cDNA 5C04D09 (uaz208) single copy, similar to Arabidopsis homolog of a mouse transplantation antigen
2985	mterf1	mTERF-domain protein1	GRMZM2G168665	B73 RefGen_v3	Gene	Chr1	62678623	62679874	mterf1	Atmterf3, mterf1, ZmTERF1	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2986	mterf10	mTERF domain protein10	GRMZM2G177019	B73 RefGen_v3	Gene	Chr3	125764251	125766015	mterf10	Atmterf15, mterf10, ZmTERF10	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2987	mterf11	mTERF domain protein11	GRMZM2G023257	B73 RefGen_v3	Gene	Chr3	164545324	164547139	mterf11	Atmterf7, mterf11, ZmTERF11	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2988	mterf12	mTERF protein domain12	GRMZM2G113181	B73 RefGen_v3	Gene	Chr4	40732037	40733517	mterf12	Atmterf6, mterf12, ZmTERF12	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2989	mterf13	mTERF-domain protein13	GRMZM2G312806	B73 RefGen_v3	Gene	Chr4	125520897	125522276	mterf13	Atmterf1, mterf13, rs131183034 , rs131183035, ZmTERF13	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2990	mterf14	mTERF protein domain21	GRMZM2G000610	B73 RefGen_v3	Gene	Chr4	175942990	175945922	mterf14	Atmterf21, mterf14, ZmTERF14	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
2991	mterf15	mTERF domain protein27c	GRMZM2G119921	B73 RefGen_v3	Gene	Chr5	97211503	97213224	mterf15	Atmterf27, mterf15, ZmTERF15	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2992	mterf16	mTERF domain protein16	GRMZM2G395850	B73 RefGen_v3	Gene	Chr5	160553137	160554858	mterf16	Atmterf27, mterf16, ZmTERF16	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2993	mterf17	mTERF domain protein17	GRMZM2G024550	B73 RefGen_v3	Gene	Chr5	181938089	181940862	mterf17	Atmterf5, mterf17, ZmMTERF17	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2994	mterf18	mTERF domain protein7b	GRMZM2G017355	B73 RefGen_v3	Gene	Chr5	207946920	207948448	mterf18	Atmterf7, mterf18, ZmTERF18	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2995	mterf19	mTERF-domain protein19	GRMZM2G017429	B73 RefGen_v3	Gene	Chr5	207948915	207950416	mterf19	mterf19, mterf7, ZmTERF19	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2996	mterf2	mTERF protein domain2	GRMZM2G061542	B73 RefGen_v3	Gene	Chr1	191096212	191098816	mterf2	Atmterf26, mterf2, ZmMTERF2	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2997	mterf20	mTERF domain protein28e	GRMZM2G158854	B73 RefGen_v3	Gene	Chr5	208026456	208027062	mterf20	Atmterf27, mterf20, ZmTERF20	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2998	mterf21	mTERF domain protein21	GRMZM2G161146	B73 RefGen_v3	Gene	Chr5	208983535	208985153	mterf21	Atmterf7, mterf21, ZmTERF21	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
2999	mterf22	mTERF-domain protein22	GRMZM2G012999	B73 RefGen_v3	Gene	Chr6	145978354	145980232	mterf22	Atmterf7, mterf22, ZmTERF22	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3000	mterf23	mTERF-domain protein23	GRMZM2G426154	B73 RefGen_v3	Gene	Chr7	4125505	4128341	mterf23	Atmterf2, mterf23, ZmTERF23	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3001	mterf24	mTERF-domain protein24	GRMZM2G175930	B73 RefGen_v3	Gene	Chr7	4166250	4167474	mterf24	Atmterf2, mterf24, ZmTERF23	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3002	mterf25	mTERF-domain protein16	GRMZM2G142150	B73 RefGen_v3	Gene	Chr7	145340020	145344782	mterf25	Atmterf16, mterf25, ZmTERF24	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3003	mterf26	mTERF-domain protein26	GRMZM2G062910	B73 RefGen_v3	Gene	Chr7	149471798	149473953	mterf26	AtMterf18, mterf26, ZmTERF25	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3004	mterf27	mTERF-domain protein27	GRMZM2G325350	B73 RefGen_v3	Gene	Chr8	107021009	107022559	mterf27	Atmterf7, mterf27, ZmTERF26	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3005	mterf29	mTERF-domain protein29	GRMZM2G068462	B73 RefGen_v3	Gene	Chr8	149784489	149785027	mterf29	Atmterf10, mterf29, ZmTERF28	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3006	mterf3	mTERF domain protein3	GRMZM2G034217	B73 RefGen_v3	Gene	Chr1	247924596	247928127	mterf3	Atmterf27, mterf3, ZmTERF3	
3007	mterf30	mTERF-domain protein30	GRMZM2G157716	B73 RefGen_v3	Gene	Chr9	128351184	128353531	mterf30	Atmterf3, mterf30, ZmTERF29	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3008	mterf32	mTERF domain protein32	GRMZM2G054517	B73 RefGen_v3	Gene	Chr1	293596590	293597275	mterf32	Atmterf27, mterf32, mterf4, ZmmTERF4	
3009	mterf33	mTERF domain protein33	GRMZM2G044832	B73 RefGen_v3	Gene	Chr4	72413770	72415391	mterf33	mterf33, mterf33(317), si618037g07	mTERF domain from NCBI protein NP_001152154.1 (Zhao et al 2014)
3010	mterf4	mTERF-domain protein4	GRMZM2G029933	B73 RefGen_v3	Gene	Chr8	107478416	107481820	mterf4	Atmterf4, BSM, mterf28, mterf4, RUG2, RUGOSA2, Zm-mTERF4, ZmTERF27	splicing. (A. Barkan, 2015). cp mTERF domain protein. Binds in vivo to multiple group II introns and promotes their splicing
3011	mterf5	mTERF-domain protein5	GRMZM2G159766	B73 RefGen_v3	Gene	Chr1	293884036	293885697	mterf5	Atmterf7, mterf5, ZmMTERF5	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3012	mterf6	mTERF-domain protein6	GRMZM2G170137	B73 RefGen_v3	Gene	Chr1	296849440	296855068	mterf6	Atmterf12, mterf6, ZmMTERF6	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3013	mterf7	mTERF-domain protein7	GRMZM2G087679	B73 RefGen_v3	Gene	Chr2	200677205	200677752	mterf7	Atmterf18, mterf7, ZmMTERF7	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3014	mterf8	mTERF-domain protein8	GRMZM2G060114	B73 RefGen_v3	Gene	Chr2	206785654	206788258	mterf8	Atmterf7, mterf8, ZmTERF8	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3015	mterf9	mTERF-domain protein9	GRMZM2G130773	B73 RefGen_v3	Gene	Chr2	208493066	208496996	mterf9	Atmterf9, mterf9, ZmTERF9	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3016	mtf1	methylenetetrahydrofolate reductase1	GRMZM2G347056	B73 RefGen_v3	Probed Site	Chr1	292165519	292171793	mtf1	AY109096, bm2, csu134a, csu134a(thf), csuh134a, methylenetetrahydrofolate reductase1, mtf1, umc372a, ZmMTHFR-1	cDNA complements yeast met12 met13 mutant; one of two or more loci, second locus may be on chromosome 5 near gln4
3017	mtl1	metallothionein1	GRMZM2G164229	B73 RefGen_v3	Gene	Chr4	1078840	1080800	mtl1	csu206, csu606, gnp_QAP2b01, gpm386, metallothionein1, metallothionein homolog1, Mt, MT-L, mtl1, phi072, phi072a, S57628, umc1008, umc1011	genomic clone, transcriptional and translation start sites mapped, Northern blots, similar to other class-I metallothioneins, root specific; SSR phi072, umc1008
3018	mtl2	metallothionein2	GRMZM2G402564	B73 RefGen_v3	Gene	Chr1	84824229	84824959	mtl2	AY106088_IDP, metallothionein2, mtl2, PCO099462	seed cDNA sequence similar to wheat sequence (SwissProt P30569) and distinct from mtl1
3019	mtl3	metallothionein3	GRMZM2G099340	B73 RefGen_v3	Gene	Chr3	17614009	17614990	mtl3	metallothionein3, mtl3, MZm3-4	cDNA highly expressed during microsporogenesis, one (or two) copies, high sequence homology with type 2 metallothionein.
3020	murE1	MureinE1	GRMZM2G009070	B73 RefGen_v3	Gene	Chr9	117602450	117606164	murE1	murE1, ZmmurE	Maize ortholog of Arabidopsis MurE. Associates with Plastid Encoded RNA polymerase (PEP). Required for PEP-mediated transcription. (A. Barkan, 2015). orthologous to At1g63680
3021	mus1	MutS homolog1	GRMZM2G056075	B73 RefGen_v3	Gene	Chr7	162805707	162815421	mus1	DNA mismatch repair protein1, gnp_QCL26f06, gnp_QCN25c06, gpm689, gpm704, mus1, MutS homolog1	cDNA similar to E. coli mutS
3022	mus2	MutS homolog2	GRMZM2G110212	B73 RefGen_v3	Gene	Chr3	9425062	9436121	mus2	CL1521_1, cl1521_1(201), DNA mismatch repair ATPase2, mus2, MutS homolog2, rs129388633 , rs131378632	NCBI: DNA mismatch repair protein MSH7
3023	mus3	mismatch binding protein Mus3	GRMZM2G421541	B73 RefGen_v3	Gene	Chr7	110073686	110083762	mus3	mismatch binding protein Mus3, MSH6, mus3, MutS homolog3, siaf227632(560), siaf227632a	
3024	mwp1	milkweed pod1	GRMZM2G082264	B73 RefGen_v3	Gene	Chr7	107261176	107267803	mwp1	milkweed pod1, mwp1, sog1743, ZmGLK21	leaf development transcription factor controlling abaxial cell fate, delineation of leaf margins, initiation of vascular and photosynthetic tissues.
3025	myb1	myb1	GRMZM2G102790	B73 RefGen_v3	Gene	Chr6	57696052	57697795	myb1	myb1, MYB39-like, myb(475), r2r3_pcr	
3026	myb10	MYB-transcription factor 10	GRMZM2G395672	B73 RefGen_v3	Gene	Chr8	152307135	152308035	myb10		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3027	myb100	MYB-transcription factor 100	GRMZM2G143046	B73 RefGen_v3	Gene	Chr1	148636099	148638077	myb100	myb100, rs131804525, umc1676	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3028	myb101	MYB-transcription factor 101	GRMZM2G425427	B73 RefGen_v3	Gene	Chr10	85332939	85334512	myb101		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3029	myb102	MYB-transcription factor 102	GRMZM2G392823	B73 RefGen_v3	Gene	Chr5	24562822	24564246	myb102		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3030	myb103	MYB-transcription factor 103	GRMZM2G111045	B73 RefGen_v3	Gene	Chr4	147942670	147945039	myb103		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3031	myb104	MYB-transcription factor 104	GRMZM2G105137	B73 RefGen_v3	Gene	Chr2	20746096	20747513	myb104		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3032	myb105	MYB-transcription factor 105	GRMZM2G031323	B73 RefGen_v3	Gene	Chr7	157205480	157207019	myb105		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3033	myb106	MYB-transcription factor 106	GRMZM2G048910	B73 RefGen_v3	Gene	Chr6	118137380	118139235	myb106		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3034	myb107	MYB-transcription factor 107	GRMZM2G172575	B73 RefGen_v3	Gene	Chr10	2635968	2636971	myb107		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3035	myb108	MYB-transcription factor 108	GRMZM2G011422	B73 RefGen_v3	Gene	Chr4	68821398	68822736	myb108		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3036	myb109	MYB-transcription factor 109	GRMZM2G052606	B73 RefGen_v3	Gene	Chr10	28608735	28611473	myb109		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3037	myb11	MYB-transcription factor 11	GRMZM2G000818	B73 RefGen_v3	Gene	Chr7	176175338	176183379	myb11		
3038	myb110	MYB-transcription factor 110	GRMZM2G176327	B73 RefGen_v3	Gene	Chr2	218127126	218128844	myb110		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3039	myb111	MYB-transcription factor 111	GRMZM2G115859	B73 RefGen_v3	Gene	Chr2	183375901	183377379	myb111		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
3040	myb112	MYB-transcription factor 112	GRMZM5G803308	B73 RefGen_v3	Gene	Chr9	97396868	97398308	myb112		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3041	myb113	MYB-transcription factor 113	GRMZM2G090837	B73 RefGen_v3	Gene	Chr2	164905509	164906823	myb113		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3042	myb114	MYB-transcription factor 114	GRMZM2G151205	B73 RefGen_v3	Gene	Chr8	155174836	155176075	myb114		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3043	myb115	MYB-transcription factor 115	GRMZM2G423833	B73 RefGen_v3	Gene	Chr6	89300616	89303600	myb115		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3044	myb116	MYB-transcription factor 116	GRMZM2G343068	B73 RefGen_v3	Gene	Chr6	91094278	91096039	myb116		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3045	myb117	MYB-transcription factor 117	GRMZM2G470307	B73 RefGen_v3	Gene	Chr3	2100964	2106267	myb117		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3046	myb118	MYB-transcription factor 118	GRMZM2G160840	B73 RefGen_v3	Gene	Chr3	127632800	127634389	myb118		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3047	myb119	MYB-transcription factor 119	AC213884.3_FG002	B73 RefGen_v3	Gene	Chr6	140735955	140737064	myb119		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3048	myb12	MYB-transcription factor 12	GRMZM2G104789	B73 RefGen_v3	Gene	Chr5	5492315	5496291	myb12		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3049	myb120	MYB-transcription factor 120	GRMZM2G054111	B73 RefGen_v3	Gene	Chr1	9210655	9212108	myb120		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3050	myb121	MYB-transcription factor 121	GRMZM2G147346	B73 RefGen_v3	Gene	Chr1	231339380	231341787	myb121		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3051	myb122	MYB-transcription factor 122	GRMZM2G416652	B73 RefGen_v3	Gene	Chr9	91044353	91053527	myb122		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3052	myb123	MYB-transcription factor 123	GRMZM2G172487	B73 RefGen_v3	Gene	Chr10	2629931	2630888	myb123		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3053	myb124	MYB-transcription factor 124	GRMZM2G003406	B73 RefGen_v3	Gene	Chr8	153001174	153002887	myb124		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3054	myb125	MYB-transcription factor 125	GRMZM2G079123	B73 RefGen_v3	Gene	Chr1	213964635	213966254	myb125		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3055	myb126	MYB-transcription factor 126	GRMZM2G001223	B73 RefGen_v3	Gene	Chr5	177037863	177039897	myb126		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3056	myb127	MYB-transcription factor 127	GRMZM2G369799	B73 RefGen_v3	Gene	Chr3	143516968	143518615	myb127		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3057	myb128	MYB-transcription factor 128	GRMZM2G017520	B73 RefGen_v3	Gene	Chr3	48494886	48497275	myb128	myb128, TIDP3391	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3058	myb129	MYB-transcription factor 129	GRMZM2G070523	B73 RefGen_v3	Gene	Chr5	20219035	20221972	myb129		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3059	myb13	MYB-transcription factor 13	GRMZM2G038722	B73 RefGen_v3	Gene	Chr2	13306159	13307935	myb13	myb-related protein Zm1	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3060	myb130	MYB-transcription factor 130	GRMZM2G069325	B73 RefGen_v3	Gene	Chr6	163187174	163188702	myb130		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3061	myb131	MYB-transcription factor 131	GRMZM2G001875	B73 RefGen_v3	Gene	Chr3	6740166	6741503	myb131		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3062	myb132	MYB-transcription factor 132	AC206901.3_FG005	B73 RefGen_v3	Gene	Chr10	130744061	130745625	myb132		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3063	myb133	MYB-transcription factor 133	GRMZM2G149958	B73 RefGen_v3	Gene	Chr2	1678831	1682752	myb133		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3064	myb134	MYB-transcription factor 134	GRMZM2G001824	B73 RefGen_v3	Gene	Chr10	85407063	85408480	myb134		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3065	myb136	MYB-transcription factor 136	GRMZM2G460869	B73 RefGen_v3	Gene	Chr3	43581101	43582165	myb136		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3066	myb137	MYB-transcription factor 137	GRMZM2G162709	B73 RefGen_v3	Gene	Chr3	23685016	23686756	myb137		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3067	myb138	MYB-transcription factor 138	GRMZM2G139688	B73 RefGen_v3	Gene	Chr3	187060539	187064561	myb138	MYBGA transcription factor	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.. verified to promote embryonic callus formation in the maize embryo
3068	myb139	MYB-transcription factor 139	GRMZM2G087955	B73 RefGen_v3	Gene	Chr2	164459324	164461196	myb139		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3069	myb14	MYB-transcription factor 14	GRMZM2G172327	B73 RefGen_v3	Gene	Chr7	150123692	150125127	myb14		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3070	myb140	MYB-transcription factor 140	GRMZM2G117244	B73 RefGen_v3	Gene	Chr7	118942837	118944366	myb140		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3071	myb141	MYB-transcription factor 141	GRMZM2G166337	B73 RefGen_v3	Gene	Chr2	205695705	205697501	myb141		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3072	myb142	MYB-transcription factor 142	GRMZM2G055158	B73 RefGen_v3	Gene	Chr4	166940293	166941682	myb142		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3073	myb144	MYB-transcription factor 144	GRMZM2G043792	B73 RefGen_v3	Gene	Chr4	140905500	140906629	myb144		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3074	myb145	MYB-transcription factor 145	GRMZM2G158700	B73 RefGen_v3	Gene	Chr3	52310607	52311832	myb145		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3075	myb146	MYB-transcription factor 146	GRMZM2G106558	B73 RefGen_v3	Gene	Chr1	215390233	215391851	myb146		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3076	myb147	MYB-transcription factor 147	GRMZM2G330475	B73 RefGen_v3	Gene	Chr8	129632727	129634070	myb147		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3077	myb148	MYB-transcription factor 148	GRMZM2G044824	B73 RefGen_v3	Gene	Chr9	26643904	26645305	myb148		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3078	myb149	MYB-transcription factor 149	GRMZM2G127490	B73 RefGen_v3	Gene	Chr10	87801492	87804648	myb149		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3079	myb15	MYB-transcription factor 15	GRMZM2G081919	B73 RefGen_v3	Gene	Chr3	180868369	180880014	myb15		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3080	myb150	MYB-transcription factor 150	GRMZM2G161512	B73 RefGen_v3	Gene	Chr5	41714515	41716637	myb150		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3081	myb151	MYB-transcription factor 151	GRMZM2G167829	B73 RefGen_v3	Gene	Chr3	202003124	202004769	myb151		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3082	myb152	MYB-transcription factor 152	GRMZM2G104551	B73 RefGen_v3	Gene	Chr7	143239537	143250321	myb152	cl51309_1, cl51309_1(569), myb152, ZmMYB111	
3083	myb153	MYB-transcription factor 153	GRMZM2G050550	B73 RefGen_v3	Gene	Chr7	51486945	51489455	myb153		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3084	myb154	MYB-transcription factor 154	GRMZM2G022686	B73 RefGen_v3	Gene	Chr9	136428923	136433765	myb154		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3085	myb155	MYB-transcription factor 155	GRMZM2G150680	B73 RefGen_v3	Gene	Chr10	74619373	74623124	myb155		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3086	myb156	MYB-transcription factor 156	GRMZM2G147698	B73 RefGen_v3	Gene	Chr1	64243765	64245594	myb156	myb156, MYB-transcription factor 156, umc1144	
3087	myb157	MYB-transcription factor 157	GRMZM2G073836	B73 RefGen_v3	Gene	Chr5	135315692	135321511	myb157		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3088	myb158	MYB-transcription factor 158	GRMZM2G078820	B73 RefGen_v3	Gene	Chr6	97484061	97485484	myb158		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
3089	myb159	MYB-transcription factor 159	GRMZM2G126566	B73 RefGen_v3	Gene	Chr7	108815110	108818213	myb159		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3090	myb16	MYB-transcription factor 16	GRMZM2G015021	B73 RefGen_v3	Gene	Chr4	175365997	175368482	myb16		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3091	myb160	MYB-transcription factor 160	GRMZM2G302549	B73 RefGen_v3	Gene	Chr5	4156159	4161139	myb160		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3092	myb161	MYB-transcription factor 161	GRMZM2G088189	B73 RefGen_v3	Gene	Chr5	69331089	69332668	myb161		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3093	myb162	MYB-transcription factor 162	GRMZM2G045748	B73 RefGen_v3	Gene	Chr7	112497750	112499904	myb162		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3094	myb163	MYB-transcription factor 163	GRMZM2G405094	B73 RefGen_v3	Gene	Chr8	165425516	165426742	myb163		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3095	myb164	MYB-transcription factor 164	GRMZM2G110135	B73 RefGen_v3	Gene	Chr1	182569440	182570779	myb164		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3096	myb165	MYB-transcription factor 165	GRMZM2G089686	B73 RefGen_v3	Gene	Chr9	152402913	152404601	myb165		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3097	myb166	MYB-transcription factor 166	GRMZM2G496770	B73 RefGen_v3	Gene	Chr4	147813432	147816122	myb166		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3098	myb167	MYB-transcription factor 167	GRMZM2G037650	B73 RefGen_v3	Gene	Chr1	207220915	207226619	myb167		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3099	myb17	MYB-transcription factor 17	GRMZM2G138427	B73 RefGen_v3	Gene	Chr4	216738472	216740213	myb17		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3100	myb18	MYB-transcription factor 18	GRMZM2G356718	B73 RefGen_v3	Gene	Chr1	281831441	281837582	myb18		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3101	myb19	MYB-transcription factor 19	GRMZM5G833253	B73 RefGen_v3	Gene	Chr4	157794216	157795479	myb19	myb-related protein Zm1	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3102	myb2	myb transcription factor2	AC203535.4_FG001	B73 RefGen_v3	Gene	Chr3	157551793	157560623	myb2	CDC5, csu184, csu184(csa), csu184(myb), myb1, myb2, myb homolog zm1, myb transcription factor2, myb*-zm1, ZM1, ZmMYB135	single copy leaf cDNA similar to Arabidopsis cdc5 myb protein
3103	myb20	MYB-transcription factor 20	GRMZM2G052377	B73 RefGen_v3	Gene	Chr3	13212794	13213981	myb20		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3104	myb21	MYB-transcription factor 21	GRMZM2G305856	B73 RefGen_v3	Gene	Chr6	34889113	34891065	myb21		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3105	myb22	MYB-transcription factor 22	GRMZM2G096358	B73 RefGen_v3	Gene	Chr8	11486302	11488135	myb22		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3106	myb23	MYB-transcription factor 23	GRMZM2G150841	B73 RefGen_v3	Gene	Chr7	168329433	168331529	myb23		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3107	myb24	MYB-transcription factor 24	GRMZM2G006352	B73 RefGen_v3	Gene	Chr8	150874045	150875425	myb24		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3108	myb25	MYB-transcription factor 25	GRMZM2G431156	B73 RefGen_v3	Gene	Chr8	101285814	101286751	myb25		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3109	myb26	MYB-transcription factor 26	GRMZM2G170049	B73 RefGen_v3	Gene	Chr5	188966583	188971226	myb26		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3110	myb27	MYB-transcription factor 27	GRMZM2G064744	B73 RefGen_v3	Gene	Chr3	227482800	227485105	myb27		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3111	myb28	MYB-transcription factor 28	GRMZM2G111117	B73 RefGen_v3	Gene	Chr4	82918804	82920269	myb28		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3112	myb29	MYB-transcription factor 29	GRMZM2G134279	B73 RefGen_v3	Gene	Chr9	134045064	134047281	myb29		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3113	myb3		GRMZM2G099334	B73 RefGen_v3	Gene	Chr5	167471479	167473890	myb3	csh15(myb), GP47, Mp1, myb3, WD40 repeat protein	single copy; encodes WD-repeat protein
3114	myb30	MYB-transcription factor 30	GRMZM2G171781	B73 RefGen_v3	Gene	Chr8	128605416	128608501	myb30		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3115	myb31	MYB31 transcription factor31	GRMZM2G050305	B73 RefGen_v3	Gene	Chr2	196943580	196945201	myb31	myb31, R2R3-MYB transcription factor, Zea mays MYB 31	R2R3-MYB factor, regulates lignin genes
3116	myb32	MYB-transcription factor 32	GRMZM2G160838	B73 RefGen_v3	Gene	Chr3	173563412	173564760	myb32		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3117	myb33	MYB-transcription factor 33	GRMZM2G131937	B73 RefGen_v3	Gene	Chr1	212948280	212949607	myb33		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3118	myb34	MYB-transcription factor 34	GRMZM2G125522	B73 RefGen_v3	Gene	Chr3	178602360	178604208	myb34		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3119	myb35	MYB-transcription factor 35	AC165178.2_FG004	B73 RefGen_v3	Gene	Chr2	182073111	182074488	myb35		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3120	myb36	MYB-transcription factor 36	GRMZM2G169316	B73 RefGen_v3	Gene	Chr8	167538578	167540715	myb36		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3121	myb37	MYB-transcription factor 37	GRMZM2G455869	B73 RefGen_v3	Gene	Chr5	10183391	10185240	myb37		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3122	myb38	myb transcription factor38	GRMZM2G084583	B73 RefGen_v3	Gene	Chr1	206902673	206903955	myb38	myb38 , myb homolog zm38, myb-related protein Zm38, myb*-zm38, rs128852892, rs128852893, rs131842218 , umc1358, ZM38	cDNA isolated by homology to C1, sequence distinct from C1
3123	myb39	myb transcription factor39	GRMZM2G127857	B73 RefGen_v3	Gene	Chr4	142662999	142664773	myb39	myb39, myb transcription factor39, MYB-transcription factor 39, R2R3-MYB transcription factor, Zea mays MYB 39, ZmMYB39	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3124	myb4	MYB-transcription factor 4	GRMZM2G131442	B73 RefGen_v3	Gene	Chr4	2048276	2051646	myb4		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3125	myb40	myb transcription factor40	GRMZM2G051256	B73 RefGen_v3	Gene	Chr3	54471016	54474812	myb40	myb40, myb transcription factor40, PZA03119, R2R3 myb, ZmMYB-IF35, ZmMYBIM44	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3126	myb41	MYB-transcription factor 41	GRMZM2G095904	B73 RefGen_v3	Gene	Chr5	186464058	186465312	myb41		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3127	myb42	myb transcription factor 42	GRMZM2G419239	B73 RefGen_v3	Gene	Chr4	217140381	217141824	myb42	myb42, myb transcription factor 42, MYB-transcription factor 42, PCO117007an, pza03155, R2R3-MYB transcription factor, Zea mays MYB 42, ZmMYB42	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3128	myb43	MYB-transcription factor 43	GRMZM2G083239	B73 RefGen_v3	Gene	Chr3	43407839	43409117	myb43		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3129	myb44	MYB-transcription factor 44	GRMZM2G111731	B73 RefGen_v3	Gene	Chr3	43359914	43361633	myb44		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3130	myb45	MYB-transcription factor 45	GRMZM2G051793	B73 RefGen_v3	Gene	Chr7	4708398	4726962	myb45	asg8, asg8(myb), myb45, MYB-transcription factor 45, rs130463343 , rs130463344	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.. NCBI: myb domain protein 4r1. single copy genomic clone asg8
3131	myb47	MYB-transcription factor 47	GRMZM2G088783	B73 RefGen_v3	Gene	Chr3	204223730	204225741	myb47		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3132	myb48	MYB-transcription factor 48	GRMZM2G159547	B73 RefGen_v3	Gene	Chr5	208398128	208399748	myb48		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3133	myb49	MYB-transcription factor 49	GRMZM2G032655	B73 RefGen_v3	Gene	Chr2	42399734	42402189	myb49		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3134	myb5	MYB-transcription factor 5	GRMZM2G097636	B73 RefGen_v3	Gene	Chr10	139613167	139614620	myb5	ZmMYB148	
3135	myb50	MYB-transcription factor 50	GRMZM2G145444	B73 RefGen_v3	Gene	Chr5	98692287	98694146	myb50		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3136	myb51	MYB-transcription factor 51	GRMZM5G803355	B73 RefGen_v3	Gene	Chr3	138430393	138432531	myb51		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3137	myb52	MYB-transcription factor 52	GRMZM2G098179	B73 RefGen_v3	Gene	Chr9	119563181	119564683	myb52		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
3138	myb53	MYB-transcription factor 53	GRMZM2G143328	B73 RefGen_v3	Gene	Chr3	215930994	215932039	myb53		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3139	myb54	MYB-transcription factor 54	GRMZM2G123202	B73 RefGen_v3	Gene	Chr2	23621911	23623663	myb54		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3140	myb56	MYB-transcription factor 56	GRMZM2G130149	B73 RefGen_v3	Gene	Chr1	150717400	150722235	myb56		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3141	myb57	MYB-transcription factor 57	GRMZM2G102790	B73 RefGen_v3	Gene	Chr6	57696052	57697795	myb57		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3142	myb58	MYB-transcription factor 58	AC217264.3_FG005	B73 RefGen_v3	Gene	Chr1	246090026	246092492	myb58		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3143	myb59	MYB-transcription factor 59	GRMZM2G093789	B73 RefGen_v3	Gene	Chr6	89403121	89416241	myb59		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3144	myb6	MYB-transcription factor 6	GRMZM2G047626	B73 RefGen_v3	Gene	Chr3	127316146	127317795	myb6		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3145	myb60	MYB-transcription factor 60	GRMZM2G312419	B73 RefGen_v3	Gene	Chr8	2761493	2763284	myb60		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3146	myb61	MYB-transcription factor 61	GRMZM2G108959	B73 RefGen_v3	Gene	Chr4	211371663	211373398	myb61		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3147	myb62	MYB-transcription factor 62	GRMZM2G013581	B73 RefGen_v3	Gene	Chr6	34825413	34826773	myb62		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3148	myb63	MYB-transcription factor 63	GRMZM2G017268	B73 RefGen_v3	Gene	Chr4	197249760	197251014	myb63	Band 2, myb63, myb6 candidate, myb-related protein Zm38-like, Prep410	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3149	myb64	MYB-transcription factor 64	GRMZM2G124715	B73 RefGen_v3	Gene	Chr2	131979387	131980997	myb64		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3150	myb65	MYB-transcription factor 65	GRMZM2G097638	B73 RefGen_v3	Gene	Chr10	139616209	139617701	myb65		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3151	myb66	MYB-transcription factor 66	GRMZM2G169356	B73 RefGen_v3	Gene	Chr7	108726504	108727871	myb66		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3152	myb67	MYB-transcription factor 67	GRMZM2G089244	B73 RefGen_v3	Gene	Chr4	207043753	207046336	myb67		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3153	myb68	MYB-transcription factor 68	GRMZM2G311059	B73 RefGen_v3	Gene	Chr10	139262188	139263199	myb68		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3154	myb69	MYB-transcription factor 69	AC197146.3_FG002	B73 RefGen_v3	Gene	Chr10	2469595	2470558	myb69		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3155	myb7	MYB-transcription factor 7	GRMZM2G064630	B73 RefGen_v3	Gene	Chr2	213301143	213305674	myb7		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3156	myb70	MYB-transcription factor 70	GRMZM2G139284	B73 RefGen_v3	Gene	Chr2	213409017	213410688	myb70		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3157	myb71	MYB-transcription factor 71	GRMZM2G093647	B73 RefGen_v3	Gene	Chr6	140863600	140864545	myb71		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3158	myb72	MYB-transcription factor 72	GRMZM2G048295	B73 RefGen_v3	Gene	Chr2	30170679	30172939	myb72		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3159	myb73	MYB-transcription factor 73	GRMZM2G121570	B73 RefGen_v3	Gene	Chr1	252379991	252382041	myb73		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3160	myb74	MYB-transcription factor 74	GRMZM2G028054	B73 RefGen_v3	Gene	Chr8	170725034	170728865	myb74		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3161	myb75	MYB-transcription factor 75	GRMZM2G070849	B73 RefGen_v3	Gene	Chr1	51395397	51397668	myb75		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3162	myb76	MYB-transcription factor 76	GRMZM2G143274	B73 RefGen_v3	Gene	Chr8	16772384	16773583	myb76		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3163	myb77	MYB-transcription factor 77	GRMZM2G077147	B73 RefGen_v3	Gene	Chr1	269707858	269709728	myb77		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3164	myb78	MYB-transcription factor 78	GRMZM2G428555	B73 RefGen_v3	Gene	Chr1	213582734	213586180	myb78		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3165	myb79	MYB-transcription factor 79	GRMZM2G056986	B73 RefGen_v3	Gene	Chr8	167004561	167005794	myb79		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3166	myb8	myb transcription factor8	GRMZM2G041415	B73 RefGen_v3	Gene	Chr3	140151898	140153093	myb8	myb8, myb transcription factor8, R2R3-MYB transcription factor, ZmMYB8	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3167	myb80	MYB-transcription factor 80	GRMZM5G870592	B73 RefGen_v3	Gene	Chr1	288542157	288545680	myb80		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3168	myb81	MYB-transcription factor 81	GRMZM2G020772	B73 RefGen_v3	Gene	Chr3	19005064	19007583	myb81		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3169	myb82	MYB-transcription factor 82	GRMZM2G167088	B73 RefGen_v3	Gene	Chr9	91085847	91092849	myb82		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3170	myb83	MYB-transcription factor 83	GRMZM2G024468	B73 RefGen_v3	Gene	Chr1	212890592	212892164	myb83	myb83, myb83rs131175320, pza03194, rs128863216, rs55624814, ss196414667	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3171	myb84	MYB-transcription factor 84	GRMZM2G173633	B73 RefGen_v3	Gene	Chr10	124346736	124348421	myb84		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3172	myb85	MYB-transcription factor 85	GRMZM2G077789	B73 RefGen_v3	Gene	Chr6	150884611	150885947	myb85		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3173	myb86	MYB-transcription factor 86	GRMZM2G027697	B73 RefGen_v3	Gene	Chr5	185547753	185549361	myb86		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3174	myb87	MYB-transcription factor 87	GRMZM2G004090	B73 RefGen_v3	Gene	Chr9	91131737	91138554	myb87		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3175	myb88	MYB-transcription factor 88	GRMZM2G048136	B73 RefGen_v3	Gene	Chr4	1269236	1270429	myb88		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3176	myb89	MYB-transcription factor 89	GRMZM2G040924	B73 RefGen_v3	Gene	Chr5	189017104	189019282	myb89	Band 21, csh, myb4 candidate, myb89, prep53, P-type R2R3 Myb protein	homology to R2R3 Myb genes
3177	myb9	MYB transcription factor9	GRMZM2G081557	B73 RefGen_v3	Gene	Chr10	139471900	139473418	myb9	myb9, MYB transcription factor9, R2R3-MYB transcription factor, ZmMYB2	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3178	myb90	MYB-transcription factor 90	GRMZM2G047600	B73 RefGen_v3	Gene	Chr8	33141828	33143103	myb90		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3179	myb91	MYB-transcription factor 91	GRMZM2G119693	B73 RefGen_v3	Gene	Chr8	63068162	63069647	myb91		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3180	myb92	MYB-transcription factor 92	GRMZM2G325907	B73 RefGen_v3	Gene	Chr10	81840592	81843874	myb92		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3181	myb93	MYB-transcription factor 93	GRMZM2G093660	B73 RefGen_v3	Gene	Chr6	140832154	140833178	myb93		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3182	myb95	myb transcription factor95	GRMZM2G051528	B73 RefGen_v3	Gene	Chr8	34675104	34689130	myb95	myb95, ZmMYB-IF25	
3183	myb96	MYB-transcription factor 96	GRMZM2G322490	B73 RefGen_v3	Gene	Chr8	40556783	40558240	myb96		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3184	myb98	MYB-transcription factor 98	GRMZM2G046443	B73 RefGen_v3	Gene	Chr1	190346919	190348170	myb98		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3185	myb99	MYB-transcription factor 99	GRMZM2G175232	B73 RefGen_v3	Gene	Chr6	162305213	162306663	myb99		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3186	mybr10	MYB-related-transcription factor 10	GRMZM2G477533	B73 RefGen_v3	Gene	Chr4	20943684	20945224	mybr10		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
3187	mybr100	MYB-related-transcription factor 100	GRMZM5G833032	B73 RefGen_v3	Gene	Chr5	196333385	196347387	mybr100		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3188	mybr101	MYB-related-transcription factor 101	GRMZM2G136887	B73 RefGen_v3	Gene	Chr8	139912821	139920531	mybr101		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3189	mybr102	MYB-related-transcription factor 102	GRMZM2G129872	B73 RefGen_v3	Gene	Chr1	48011049	48012183	mybr102		(Goettel and Messing 2009). Locus designated and assigned to a transcription factor family by the GRASSIUS project (Yilmaz et al 2009) , which also provided the mappings to the
3190	mybr103	MYB-related-transcription factor 103	GRMZM2G022499	B73 RefGen_v3	Gene	Chr1	188491207	188494857	mybr103		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3191	mybr104	MYB-related-transcription factor 104	GRMZM2G023557	B73 RefGen_v3	Gene	Chr1	299468335	299469321	mybr104		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3192	mybr105	MYB-related-transcription factor 105	GRMZM2G471039	B73 RefGen_v3	Gene	Chr2	44822275	44823668	mybr105		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3193	mybr106	MYB-related-transcription factor 106	GRMZM2G129817	B73 RefGen_v3	Gene	Chr5	7149223	7161457	mybr106		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3194	mybr107	MYB-related-transcription factor 107	GRMZM2G456960	B73 RefGen_v3	Gene	Chr8	1837921	1839249	mybr107		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3195	mybr108	MYB-related-transcription factor 108	GRMZM2G304840	B73 RefGen_v3	Gene	Chr8	149181160	149185462	mybr108		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3196	mybr109	MYB-related-transcription factor 109	GRMZM2G433450	B73 RefGen_v3	Gene	Chr8	62424724	62426967	mybr109		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3197	mybr11	MYB-related-transcription factor 11	GRMZM2G071468	B73 RefGen_v3	Gene	Chr5	192547214	192555085	mybr11		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3198	mybr110	MYB-related-transcription factor 110	GRMZM2G443202	B73 RefGen_v3	Gene	Chr3	221293909	221300124	mybr110		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3199	mybr111	MYB-related-transcription factor 111	GRMZM2G181030	B73 RefGen_v3	Gene	Chr10	134854638	134857160	mybr111		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3200	mybr112	MYB-related-transcription factor 112	GRMZM2G370896	B73 RefGen_v3	Gene	Chr8	96553982	96582581	mybr112		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3201	mybr113	MYB-related-transcription factor 113	GRMZM2G001106	B73 RefGen_v3	Gene	Chr10	132817600	132819290	mybr113		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3202	mybr114	MYB-related-transcription factor 114	GRMZM2G119261	B73 RefGen_v3	Gene	Chr2	113806626	113816795	mybr114	mybr114, MYB-related-transcription factor 114, ZmCHB107	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3203	mybr115	MYB-related-transcription factor 115	GRMZM2G049378	B73 RefGen_v3	Gene	Chr8	148179996	148182680	mybr115		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3204	mybr116	MYB-related-transcription factor 116	GRMZM5G847287	B73 RefGen_v3	Gene	Chr2	194297473	194298570	mybr116		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3205	mybr12	MYB-related-transcription factor 12	GRMZM2G112263	B73 RefGen_v3	Gene	Chr1	48154654	48155041	mybr12		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3206	mybr13	MYB-related-transcription factor 13	GRMZM2G091201	B73 RefGen_v3	Gene	Chr6	149547176	149548435	mybr13		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3207	mybr14	MYB-related-transcription factor 14	GRMZM2G340756	B73 RefGen_v3	Gene	Chr3	139757841	139764438	mybr14	mybr14, MYB-related-transcription factor 14, SWI3C1, SWI3C (SWIRM), SWITCH/SUCROSE NONFERMENTING (SWI/SNF) 3C, ZmCHB106, ZmSWI3C1_GQ429003	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3208	mybr15	MYB-related-transcription factor 15	GRMZM2G048403	B73 RefGen_v3	Gene	Chr1	210149799	210173485	mybr15		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3209	mybr16	MYB-related-transcription factor 16	GRMZM2G382029	B73 RefGen_v3	Gene	Chr8	8495835	8497325	mybr16		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3210	mybr17	MYB-related-transcription factor 17	GRMZM2G071977	B73 RefGen_v3	Gene	Chr3	223767189	223769272	mybr17		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3211	mybr18	MYB-related-transcription factor 18	GRMZM2G176568	B73 RefGen_v3	Gene	Chr8	13792506	13793319	mybr18		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3212	mybr19	MYB-related-transcription factor 19	GRMZM2G402156	B73 RefGen_v3	Gene	Chr9	15055667	15056797	mybr19		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3213	mybr2	MYB-related-transcription factor 2	GRMZM2G400489	B73 RefGen_v3	Gene	Chr8	824954	835548	mybr2		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3214	mybr20	MYB-related-transcription factor 20	GRMZM2G421256	B73 RefGen_v3	Gene	Chr2	14726120	14728827	mybr20		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3215	mybr21	MYB-related-transcription factor 21	GRMZM2G079458	B73 RefGen_v3	Gene	Chr8	13801696	13804475	mybr21		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3216	mybr22	MYB-related-transcription factor 22	GRMZM2G468479	B73 RefGen_v3	Gene	Chr3	6089921	6097881	mybr22		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3217	mybr23	MYB-related-transcription factor 23	GRMZM2G075064	B73 RefGen_v3	Gene	Chr6	102481776	102484118	mybr23		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3218	mybr24	MYB-related-transcription factor 24	GRMZM2G049695	B73 RefGen_v3	Gene	Chr8	20520277	20522116	mybr24		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3219	mybr25	MYB-related-transcription factor 25	GRMZM5G848185	B73 RefGen_v3	Gene	Chr5	212643601	212645908	mybr25		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3220	mybr26	MYB-related-transcription factor 26	GRMZM2G112764	B73 RefGen_v3	Gene	Chr6	85321554	85325088	mybr26		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3221	mybr28	MYB-related-transcription factor 28	GRMZM2G119133	B73 RefGen_v3	Gene	Chr5	171749221	171756808	mybr28		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3222	mybr29	MYB-related-transcription factor 29	AC199820.4_FG006	B73 RefGen_v3	Gene	Chr2	210594735	210595406	mybr29		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3223	mybr3	MYB-related-transcription factor 3	GRMZM2G002128	B73 RefGen_v3	Gene	Chr6	149021224	149023568	mybr3		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3224	mybr30	MYB-related-transcription factor 30	GRMZM2G169991	B73 RefGen_v3	Gene	Chr7	32103896	32105382	mybr30		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3225	mybr31	MYB-related-transcription factor 31	GRMZM2G034110	B73 RefGen_v3	Gene	Chr9	115514419	115517835	mybr31		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3226	mybr32	MYB-related-transcription factor 32	GRMZM2G088524	B73 RefGen_v3	Gene	Chr1	94375921	94377959	mybr32		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3227	mybr33	MYB-related-transcription factor 33	GRMZM2G422083	B73 RefGen_v3	Gene	Chr10	88729270	88730919	mybr33		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3228	mybr34	MYB-related-transcription factor 34	GRMZM2G101806	B73 RefGen_v3	Gene	Chr4	24642311	24643851	mybr34		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3229	mybr35	MYB-related-transcription factor 35	GRMZM2G065829	B73 RefGen_v3	Gene	Chr8	141446174	141448103	mybr35	putative MYB DNA-binding domain superfamily protein	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3230	mybr36	MYB-related-transcription factor 36	GRMZM2G014534	B73 RefGen_v3	Gene	Chr2	13349180	13350397	mybr36	Band 31, myb5 - candidate, mybr36, prepGU18, transcription factor MYB39-like	single copy genomic; similar to R2R3 Myb genes
3231	mybr37	MYB-related-transcription factor 37	GRMZM2G027914	B73 RefGen_v3	Gene	Chr3	176478861	176480372	mybr37		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3232	mybr38	MYB-related-transcription factor 38	GRMZM2G059167	B73 RefGen_v3	Gene	Chr4	115304028	115319510	mybr38		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3233	mybr39	MYB-related-transcription factor 39	GRMZM2G451116	B73 RefGen_v3	Gene	Chr3	216327065	216328448	mybr39		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3234	mybr4	MYB-related-transcription factor 4	GRMZM2G032180	B73 RefGen_v3	Gene	Chr2	152273149	152273832	mybr4		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3235	mybr40	MYB-related-transcription factor 40	GRMZM2G088005	B73 RefGen_v3	Gene	Chr5	19456504	19458038	mybr40		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
3236	mybr41	MYB-related-transcription factor 41	GRMZM2G150260	B73 RefGen_v3	Gene	Chr3	216312171	216314107	mybr41		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3237	mybr42	MYB-related-transcription factor 42	GRMZM2G369993	B73 RefGen_v3	Gene	Chr1	155061845	155063380	mybr42		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3238	mybr43	MYB-related-transcription factor 43	GRMZM5G813892	B73 RefGen_v3	Gene	Chr1	89448263	89451835	mybr43		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3239	mybr44	MYB-related-transcription factor 44	GRMZM2G016020	B73 RefGen_v3	Gene	Chr1	48014364	48015108	mybr44		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3240	mybr45	MYB-related-transcription factor 45	GRMZM2G415077	B73 RefGen_v3	Gene	Chr1	300823403	300824061	mybr45		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3241	mybr46	MYB-related-transcription factor 46	GRMZM2G005112	B73 RefGen_v3	Gene	Chr3	179262685	179263682	mybr46		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3242	mybr47	MYB-related-transcription factor 47	GRMZM2G117497	B73 RefGen_v3	Gene	Chr6	165301952	165303494	mybr47		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3243	mybr48	MYB-related-transcription factor 48	GRMZM2G175265	B73 RefGen_v3	Gene	Chr10	78356797	78358456	mybr48		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3244	mybr49	MYB-related-transcription factor 49	GRMZM2G416708	B73 RefGen_v3	Gene	Chr3	41295336	41296872	mybr49		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3245	mybr5	MYB-related-transcription factor 5	GRMZM2G401809	B73 RefGen_v3	Gene	Chr2	211646121	211647607	mybr5		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3246	mybr50	MYB-related-transcription factor 50	GRMZM2G337011	B73 RefGen_v3	Gene	Chr2	9316108	9317023	mybr50		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3247	mybr51	MYB-related-transcription factor 51	GRMZM2G379167	B73 RefGen_v3	Gene	Chr5	215521132	215523527	mybr51	RESPONSE 1 , php10017, pio100017, rs130206020 , rs130206022 , rs130206037 , rs132302817	
3248	mybr52	MYB-related-transcription factor 52	GRMZM2G029850	B73 RefGen_v3	Gene	Chr5	197657418	197660109	mybr52		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3249	mybr53	MYB-related-transcription factor 53	GRMZM2G047038	B73 RefGen_v3	Gene	Chr1	270191276	270202265	mybr53	mybr53, MYB-related-transcription factor 53, SWI3D (CHB3)	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3250	mybr54	MYB-related-transcription factor 54	GRMZM2G152319	B73 RefGen_v3	Gene	Chr9	143795886	143800919	mybr54		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3251	mybr55	MYB-related-transcription factor 55	GRMZM2G143640	B73 RefGen_v3	Gene	Chr8	166202168	166203590	mybr55		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3252	mybr56	MYB-related-transcription factor 56	GRMZM2G398758	B73 RefGen_v3	Gene	Chr2	235101440	235102975	mybr56		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3253	mybr57	MYB-related-transcription factor 57	GRMZM2G139174	B73 RefGen_v3	Gene	Chr6	166438508	166439034	mybr57		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3254	mybr58	MYB-related-transcription factor 58	GRMZM2G170322	B73 RefGen_v3	Gene	Chr4	156546886	156549720	mybr58		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3255	mybr59	MYB-related-transcription factor 59	GRMZM2G085427	B73 RefGen_v3	Gene	Chr1	32374231	32382033	mybr59		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3256	mybr6	MYB-related-transcription factor 6	GRMZM2G087817	B73 RefGen_v3	Gene	Chr3	221663066	221667898	mybr6		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3257	mybr60	MYB-related-transcription factor 60	GRMZM5G845296	B73 RefGen_v3	Gene	Chr8	113866855	113869756	mybr60		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3258	mybr61	MYB-related-transcription factor 61	GRMZM2G139760	B73 RefGen_v3	Gene	Chr4	208030163	208035544	mybr61	mybr61, MYB-related-transcription factor 61, SWI3C2, SWI3C (SWIRM), SWITCH/SUCROSE NONFERMENTING (SWI/SNF) 3C2, ZmCHB105, ZmSWI3C2_ACL53385	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3259	mybr62	MYB-related-transcription factor 62	GRMZM2G531738	B73 RefGen_v3	Gene	Chr6	135326257	135335990	mybr62		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3260	mybr63	MYB-related-transcription factor 63	GRMZM2G447745	B73 RefGen_v3	Gene	Chr6	26908013	26915169	mybr63		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3261	mybr64	MYB-related-transcription factor 64	GRMZM2G118693	B73 RefGen_v3	Gene	Chr4	155860243	155865096	mybr64		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3262	mybr65	MYB-related-transcription factor 65	GRMZM2G546369	B73 RefGen_v3	Gene	Chr10	144803533	144808264	mybr65		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3263	mybr67	MYB-related-transcription factor 67	GRMZM2G049194	B73 RefGen_v3	Gene	Chr5	211753884	211765564	mybr67		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3264	mybr68	MYB-related-transcription factor 68	GRMZM2G410083	B73 RefGen_v3	Gene	Chr10	129607133	129610574	mybr68		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3265	mybr69	MYB-related-transcription factor 69	GRMZM2G135052	B73 RefGen_v3	Gene	Chr9	27185077	27191507	mybr69		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3266	mybr70	MYB-related-transcription factor 70	GRMZM2G071648	B73 RefGen_v3	Gene	Chr6	100111985	100113471	mybr70		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3267	mybr71	MYB-related-transcription factor 71	GRMZM2G448104	B73 RefGen_v3	Gene	Chr10	142938806	142965743	mybr71		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3268	mybr72	MYB-related-transcription factor 72	GRMZM2G700011	B73 RefGen_v3	Gene	Chr9	137511121	137512076	mybr72		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3269	mybr73	MYB-related-transcription factor 73	GRMZM2G147152	B73 RefGen_v3	Gene	Chr2	126546425	126548480	mybr73		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3270	mybr74	MYB-related-transcription factor 74	GRMZM2G073826	B73 RefGen_v3	Gene	Chr5	135342824	135344111	mybr74		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3271	mybr75	MYB-related-transcription factor 75	GRMZM2G023667	B73 RefGen_v3	Gene	Chr8	153685211	153695652	mybr75		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3272	mybr76	MYB-related-transcription factor 76	GRMZM2G301642	B73 RefGen_v3	Gene	Chr3	45267830	45269717	mybr76		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3273	mybr77	MYB-related-transcription factor 77	GRMZM2G057408	B73 RefGen_v3	Gene	Chr6	93259854	93265695	mybr77		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3274	mybr78	MYB-related-transcription factor 78	AC204212.4_FG001	B73 RefGen_v3	Gene	Chr5	201176614	201176904	mybr78		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3275	mybr8	MYB-related-transcription factor 8	GRMZM2G177760	B73 RefGen_v3	Gene	Chr8	62405348	62407503	mybr8		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3276	mybr80	MYB-related-transcription factor 80	GRMZM2G163291	B73 RefGen_v3	Gene	Chr3	14476929	14481586	mybr80		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3277	mybr81	MYB-related-transcription factor 81	GRMZM2G121111	B73 RefGen_v3	Gene	Chr10	88764345	88765689	mybr81		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3278	mybr82	MYB-related-transcription factor 82	GRMZM2G103783	B73 RefGen_v3	Gene	Chr7	133402091	133405607	mybr82		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3279	mybr83	MYB-related-transcription factor 83	GRMZM2G098884	B73 RefGen_v3	Gene	Chr4	30961505	30976774	mybr83		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3280	mybr84	MYB-related-transcription factor 84	GRMZM2G108892	B73 RefGen_v3	Gene	Chr10	81701345	81729386	mybr84		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3281	mybr85	MYB-related-transcription factor 85	GRMZM2G089406	B73 RefGen_v3	Gene	Chr8	130868798	130875685	mybr85		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3282	mybr86	MYB-related-transcription factor 86	GRMZM2G170148	B73 RefGen_v3	Gene	Chr9	110859050	110870308	mybr86		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3283	mybr87	MYB-related-transcription factor 87	GRMZM2G158117	B73 RefGen_v3	Gene	Chr8	70808377	70809767	mybr87		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3284	mybr88	MYB-related-transcription factor 88	GRMZM2G064328	B73 RefGen_v3	Gene	Chr4	234391361	234395800	mybr88	chb102, chromatin remodeling complex102, mybr88	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
3285	mybr89	MYB-related-transcription factor 89	GRMZM2G121753	B73 RefGen_v3	Gene	Chr3	211692320	211693746	mybr89		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3286	mybr9	MYB-related-transcription factor 9	GRMZM2G030403	B73 RefGen_v3	Gene	Chr10	89125351	89126605	mybr9		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3287	mybr90	MYB-related-transcription factor 90	GRMZM2G046438	B73 RefGen_v3	Gene	Chr5	31921424	31926755	mybr90		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3288	mybr91	MYB-related-transcription factor 91	GRMZM2G111990	B73 RefGen_v3	Gene	Chr1	48136700	48137829	mybr91		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3289	mybr92	MYB-related-transcription factor 92	GRMZM2G157306	B73 RefGen_v3	Gene	Chr4	34498413	34504954	mybr92		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3290	mybr93	MYB-related-transcription factor 93	GRMZM2G135410	B73 RefGen_v3	Gene	Chr2	37825696	37830335	mybr93		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3291	mybr94	MYB-related-transcription factor 94	GRMZM2G328814	B73 RefGen_v3	Gene	Chr5	175758339	175759719	mybr94		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3292	mybr95	MYB-related-transcription factor 95	GRMZM2G115070	B73 RefGen_v3	Gene	Chr1	300879227	300880127	mybr95		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3293	mybr96	MYB-related-transcription factor 96	GRMZM2G145041	B73 RefGen_v3	Gene	Chr5	64145458	64148638	mybr96		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3294	mybr97	MYB-related-transcription factor 97	GRMZM2G057955	B73 RefGen_v3	Gene	Chr3	218099741	218101238	mybr97		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3295	mybr98	MYB-related-transcription factor 98	GRMZM2G111906	B73 RefGen_v3	Gene	Chr6	82660395	82663470	mybr98		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3296	mybr99	MYB-related-transcription factor 99	GRMZM2G024054	B73 RefGen_v3	Gene	Chr5	21005810	21011591	mybr99		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3297	mybst1	single-repeat Myb protein1	GRMZM2G034110	B73 RefGen_v3	Gene	Chr9	115514419	115517835	mybst1	mybst1, single-repeat Myb protein, TIDP3321	
3298	myc7	myc transcription factor7	GRMZM2G001930	B73 RefGen_v3	Gene	Chr1	98363081	98365897	myc7	7e, AY109646, bhlh149, bHLH-transcription factor 149, CL1599_-1a, gnp_QBI19e09, gpm818, myc7, myc7(35), myc7e	transcription factor induced by iron starvation; restores yeast fet3 fet4
3299	myo1	myosin1	AC155377.1_FG001	B73 RefGen_v3	Gene	Chr3	220967145	220986200	myo1	cl1535_1, myo1, myosin1, ZmOrphan82	
3300	myo2	myosin2	GRMZM2G034362	B73 RefGen_v3	Gene	Chr5	215754092	215764902	myo2	CL1510_1(455), CL1510_1a, M2, myo2, myosin2, myosin-6-like, myosin XI, ZmOrphan20	
3301	myo2	myosin2	GRMZM2G332687	B73 RefGen_v3	Gene	Chr5	215751740	215753860	myo2	CL1510_1(455), CL1510_1a, M2, myo2, myosin2, myosin-6-like, myosin XI, ZmOrphan20	
3302	myo3	myosin1	GRMZM2G113202	B73 RefGen_v3	Gene	Chr1	229251332	229267181	myo3	cl1520_1(73), cl1520_1a, myo3, myosin1, myosin VIII ZMM3, ZmOrphan115	
3303	na1	nana plant1	GRMZM2G449033	B73 RefGen_v3	Gene	Chr3	179041147	179042863	na1	d*-282, det2, d*-N282, dwarfN282, na1, nana plant1, Zmdet2	short, erect dwarf; no response to gibberellins
3304	na2	nana plant2	GRMZM2G057000	B73 RefGen_v3	Gene	Chr5	65138723	65143833	na2	brassinosteroid biosynthesis-like, dwf1, DWF1 like1, dwfl1, na2, nana plant2, pco076650, umc1389, Zmdwf1	like na1
3305	naat1	nicotianamine aminotransferase1	GRMZM2G096958	B73 RefGen_v3	Gene	Chr4	220114792	220118307	naat1	naat1, nicotianamine aminotransferase1	similar to rice NAAT1 gene likely involved in iron uptake.
3306	nac1	NaCl stress protein1	GRMZM2G015605	B73 RefGen_v3	Gene	Chr10	87283919	87284844	nac1	cl37957_1, cl37957_1(737), nac1, NaCl stress protein1, phi084, PMP3-1, proteolipid membrane potential modulator1, PZA00814, uaz250, uaz250(nacl), UAZ250(NaCl)	encodes small plama membrane proteolipid involved in ion homeostasis, and response to salinity
3307	nactf1	NAC-transcription factor 1	GRMZM2G134717	B73 RefGen_v3	Gene	Chr8	149342434	149343235	nactf1	nac1	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3308	nactf10	NAC-transcription factor 10	GRMZM2G315140	B73 RefGen_v3	Gene	Chr5	189452831	189457211	nactf10	nac10	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3309	nactf100	NAC-transcription factor 100	AC211478.3_FG004	B73 RefGen_v3	Gene	Chr3	141524464	141524928	nactf100	nac100	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3310	nactf101	NAC-transcription factor 101	GRMZM2G104078	B73 RefGen_v3	Gene	Chr4	130546212	130550063	nactf101	nac101	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3311	nactf102	NAC-transcription factor 102	GRMZM5G894234	B73 RefGen_v3	Gene	Chr9	146509128	146512839	nactf102	nac102	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3312	nactf103	NAC-transcription factor 103	AC212859.3_FG008	B73 RefGen_v3	Gene	Chr2	26370683	26372492	nactf103	nac103	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3313	nactf104	NAC-transcription factor 104	GRMZM5G857701	B73 RefGen_v3	Gene	Chr5	214998412	215000055	nactf104	nac104	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3314	nactf105	NAC-transcription factor 105	GRMZM2G123246	B73 RefGen_v3	Gene	Chr4	38574124	38577183	nactf105	nac105	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3315	nactf106	NAC-transcription factor 106	GRMZM2G031120	B73 RefGen_v3	Gene	Chr1	254134957	254136440	nactf106	nac106	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3316	nactf107	NAC-transcription factor 107	GRMZM2G172264	B73 RefGen_v3	Gene	Chr8	98794488	98795642	nactf107	nac107	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3317	nactf108	NAC-transcription factor 108	GRMZM2G114850	B73 RefGen_v3	Gene	Chr3	122090412	122094741	nactf108	nac108	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3318	nactf109	NAC-transcription factor 109	GRMZM2G014653	B73 RefGen_v3	Gene	Chr3	170863580	170866035	nactf109	nac109	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3319	nactf11	NAC-transcription factor 11	GRMZM2G031001	B73 RefGen_v3	Gene	Chr1	53419144	53421347	nactf11	nac11	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3320	nactf110	NAC-transcription factor 110	GRMZM2G167018	B73 RefGen_v3	Gene	Chr10	61009621	61012269	nactf110	nac110	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3321	nactf111	NAC-transcription factor 111	GRMZM2G450445	B73 RefGen_v3	Gene	Chr2	38182053	38187930	nactf111	nac111	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3322	nactf112	NAC-transcription factor 112	GRMZM2G456568	B73 RefGen_v3	Gene	Chr6	148114978	148119765	nactf112	nac112	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3323	nactf113	NAC-transcription factor 113	GRMZM2G063522	B73 RefGen_v3	Gene	Chr5	43445603	43449974	nactf113	nac113	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3324	nactf114	NAC-transcription factor 114	GRMZM2G430522	B73 RefGen_v3	Gene	Chr1	188939619	188942480	nactf114	nac114	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3325	nactf115	NAC-transcription factor 115	GRMZM2G069047	B73 RefGen_v3	Gene	Chr4	38060800	38063263	nactf115	nac115	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3326	nactf116	NAC-transcription factor 116	GRMZM2G041746	B73 RefGen_v3	Gene	Chr6	106419729	106421601	nactf116	nac116	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3327	nactf117	NAC-transcription factor 117	GRMZM2G163914	B73 RefGen_v3	Gene	Chr9	28857463	28862279	nactf117	nac117, ZmNTL6	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3328	nactf118	NAC-transcription factor 118	GRMZM2G109627	B73 RefGen_v3	Gene	Chr8	7036425	7039141	nactf118	nac118	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3329	nactf119	NAC-transcription factor 119	GRMZM2G393433	B73 RefGen_v3	Gene	Chr6	16291317	16293647	nactf119	nac119	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3330	nactf12	NAC-transcription factor 12	GRMZM2G125777	B73 RefGen_v3	Gene	Chr4	50123857	50128792	nactf12	nactf12, TIDP2954, ZmNTL2	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3331	nactf120	NAC-transcription factor 120	GRMZM2G176677	B73 RefGen_v3	Gene	Chr2	27056209	27064181	nactf120	nac120, ras18A1	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3332	nactf121	NAC-transcription factor 121	AC233865.1_FG003	B73 RefGen_v3	Gene	Chr7	146634161	146635852	nactf121	nac121	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3333	nactf122	NAC-transcription factor 122	GRMZM2G430849	B73 RefGen_v3	Gene	Chr7	173556184	173558723	nactf122	nac122	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
3334	nactf123	NAC-transcription factor 123	GRMZM2G092465	B73 RefGen_v3	Gene	Chr6	4308720	4311321	nactf123	nac123	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3335	nactf124	NAC-transcription factor 124	GRMZM2G104074	B73 RefGen_v3	Gene	Chr9	65939491	65941420	nactf124	nac124	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3336	nactf125	NAC-transcription factor 125	GRMZM2G123667	B73 RefGen_v3	Gene	Chr4	208153304	208156017	nactf125	nac125	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3337	nactf126	NAC-transcription factor 126	GRMZM2G018436	B73 RefGen_v3	Gene	Chr2	150664743	150666249	nactf126	nac126	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3338	nactf127	NAC-transcription factor 127	GRMZM2G389557	B73 RefGen_v3	Gene	Chr5	63305824	63308265	nactf127	nac127	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3339	nactf129	NAC-transcription factor 129	GRMZM2G078954	B73 RefGen_v3	Gene	Chr6	116856576	116860095	nactf129	nac129	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3340	nactf13	NAC-transcription factor 13	GRMZM2G038073	B73 RefGen_v3	Gene	Chr5	180419619	180423120	nactf13	nac13	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3341	nactf130	NAC-transcription factor 130	GRMZM2G154182	B73 RefGen_v3	Gene	Chr8	7300179	7302179	nactf130	nac130	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3342	nactf131	NAC-transcription factor 131	GRMZM2G178998	B73 RefGen_v3	Gene	Chr2	23327304	23330538	nactf131	nac131	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3343	nactf132	NAC-transcription factor 132	GRMZM2G179885	B73 RefGen_v3	Gene	Chr7	158275103	158277300	nactf132	nac132, NAC-B1	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3344	nactf133	NAC-transcription factor 133	GRMZM2G094067	B73 RefGen_v3	Gene	Chr5	172963066	172964225	nactf133	nac133	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3345	nactf134	NAC-transcription factor 134	GRMZM2G163843	B73 RefGen_v3	Gene	Chr8	150104921	150106384	nactf134	nac134	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3346	nactf14	NAC-transcription factor 14	GRMZM2G159094	B73 RefGen_v3	Gene	Chr7	111693679	111695863	nactf14	nac14	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3347	nactf15	NAC-transcription factor 15	GRMZM2G111770	B73 RefGen_v3	Gene	Chr10	125215781	125218953	nactf15	nac15	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3348	nactf16	NAC-transcription factor 16	GRMZM2G166721	B73 RefGen_v3	Gene	Chr3	6939608	6945972	nactf16	nac16	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3349	nactf17	NAC-transcription factor 17	GRMZM2G062009	B73 RefGen_v3	Gene	Chr4	142276736	142279162	nactf17	nac17	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3350	nactf18	NAC-transcription factor 18	GRMZM5G885329	B73 RefGen_v3	Gene	Chr7	146638618	146642822	nactf18	nac18	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3351	nactf19	NAC-transcription factor 19	GRMZM2G155816	B73 RefGen_v3	Gene	Chr5	142222049	142223803	nactf19	nac19	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3352	nactf2	NAC-transcription factor 2	GRMZM2G181605	B73 RefGen_v3	Gene	Chr7	173780290	173782115	nactf2	nac2	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3353	nactf20	NAC-transcription factor 20	GRMZM2G180328	B73 RefGen_v3	Gene	Chr6	148062214	148064233	nactf20	nac20	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3354	nactf21	NAC-transcription factor 21	GRMZM2G091490	B73 RefGen_v3	Gene	Chr6	66186789	66189233	nactf21	nac21, NAC domain-containing protein 43, NAC transcriptional factor3, ZmNST3	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3355	nactf22	NAC-transcription factor 22	GRMZM2G156977	B73 RefGen_v3	Gene	Chr2	9417298	9419858	nactf22	nac22	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3356	nactf23	NAC-transcription factor 23	GRMZM2G068973	B73 RefGen_v3	Gene	Chr8	170415625	170417408	nactf23	nac23	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3357	nactf24	NAC-transcription factor 24	GRMZM2G008374	B73 RefGen_v3	Gene	Chr2	191504046	191505927	nactf24	nac24	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3358	nactf25	NAC-transcription factor 25	GRMZM2G127379	B73 RefGen_v3	Gene	Chr10	2682268	2684357	nactf25	nac25, ZmNAC111	Lines with a MITE insert in the promotor region are more sensitive to drought than those lacking this MITE insert.
3359	nactf26	NAC-transcription factor 26	GRMZM2G113950	B73 RefGen_v3	Gene	Chr4	170273726	170278146	nactf26	nac26, NAC domain-containing protein 78, ZmNTL3	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3360	nactf27	NAC-transcription factor 27	GRMZM2G354151	B73 RefGen_v3	Gene	Chr4	148843760	148847667	nactf27	nac27	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3361	nactf28	NAC-transcription factor 28	GRMZM2G033014	B73 RefGen_v3	Gene	Chr7	2720485	2721893	nactf28	nac28	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3362	nactf29	NAC-transcription factor 29	GRMZM2G159500	B73 RefGen_v3	Gene	Chr9	133066105	133068297	nactf29	nac29	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3363	nactf3	NAC-transcription factor 3	GRMZM2G147867	B73 RefGen_v3	Gene	Chr6	147704754	147707417	nactf3	nac3	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3364	nactf30	NAC-transcription factor 30	GRMZM2G146380	B73 RefGen_v3	Gene	Chr5	176985518	176986621	nactf30	nac30	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3365	nactf31	NAC-transcription factor 31	GRMZM2G465835	B73 RefGen_v3	Gene	Chr6	149591626	149592760	nactf31	nac31	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3366	nactf32	NAC-transcription factor 32	GRMZM2G009892	B73 RefGen_v3	Gene	Chr2	42514433	42516336	nactf32	nac32	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3367	nactf33	NAC-transcription factor 33	GRMZM2G025642	B73 RefGen_v3	Gene	Chr1	5629470	5636419	nactf33	nac33	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3368	nactf34	NAC-transcription factor 34	AC208663.3_FG002	B73 RefGen_v3	Gene	Chr2	30554102	30555190	nactf34	nac34	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3369	nactf35	NAC-transcription factor 35	GRMZM2G179049	B73 RefGen_v3	Gene	Chr2	193103406	193105706	nactf35	nac35	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3370	nactf36	NAC-transcription factor 36	GRMZM2G081930	B73 RefGen_v3	Gene	Chr2	29749591	29752453	nactf36	nac36	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3371	nactf37	NAC-transcription factor 37	AC198937.4_FG005	B73 RefGen_v3	Gene	Chr4	83598016	83599406	nactf37	nac37	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3372	nactf38	NAC-transcription factor 38	GRMZM2G104400	B73 RefGen_v3	Gene	Chr8	102056994	102060989	nactf38	nac38	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3373	nactf39	NAC-transcription factor 39	GRMZM2G126817	B73 RefGen_v3	Gene	Chr9	151938782	151940287	nactf39	nac39	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3374	nactf4	NAC-transcription factor 4	GRMZM2G079632	B73 RefGen_v3	Gene	Chr7	20903390	20905225	nactf4	nac4	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3375	nactf40	NAC-transcription factor 40	GRMZM5G898290	B73 RefGen_v3	Gene	Chr4	125797543	125799275	nactf40	nac40	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3376	nactf41	NAC-transcription factor 41	GRMZM2G439903	B73 RefGen_v3	Gene	Chr4	189283188	189284375	nactf41	nac41	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3377	nactf42	NAC-transcription factor 42	GRMZM2G074358	B73 RefGen_v3	Gene	Chr6	82927597	82929052	nactf42	nac42	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3378	nactf43	NAC-transcription factor43	GRMZM2G082709	B73 RefGen_v3	Gene	Chr1	98104945	98106412	nactf43	nac43, nactf43, rs128678993 , rs128678997 , rs128679011 , rs131279378 , ss196425806 , ss196425808, ss196425810 , ss196425812 , umc1515	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.. NCBI: NAC domain-containing protein 67-like
3379	nactf44	NAC-transcription factor 44	GRMZM2G011598	B73 RefGen_v3	Gene	Chr1	53631300	53633544	nactf44	nac44	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3380	nactf45	NAC-transcription factor 45	GRMZM2G126936	B73 RefGen_v3	Gene	Chr9	146100422	146101729	nactf45	nac45	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3381	nactf46	NAC-transcription factor 46	GRMZM2G440219	B73 RefGen_v3	Gene	Chr9	28147827	28149574	nactf46	nac46	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3382	nactf47	NAC-transcription factor 47	GRMZM2G112681	B73 RefGen_v3	Gene	Chr8	20832776	20839314	nactf47	nac47	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
3383	nactf48	NAC-transcription factor 48	GRMZM2G054252	B73 RefGen_v3	Gene	Chr1	195218120	195221530	nactf48	NAC domain-containing protein 68, nactf48, NAC-transcription factor 48, pco113991, pco113991(59), umc58	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3384	nactf49	NAC-transcription factor 49	GRMZM2G347043	B73 RefGen_v3	Gene	Chr1	292162441	292164227	nactf49	NAC1 transcription factor, nac49, ZmSNAC1	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3385	nactf5	NAC-transcription factor 5	GRMZM2G162739	B73 RefGen_v3	Gene	Chr2	159575160	159577058	nactf5	nac5	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3386	nactf50	NAC-transcription factor 50	GRMZM2G475014	B73 RefGen_v3	Gene	Chr1	178427919	178429404	nactf50	nac50	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3387	nactf51	NAC-transcription factor 51	GRMZM2G140901	B73 RefGen_v3	Gene	Chr4	172222465	172224718	nactf51	nac51	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3388	nactf52	NAC-transcription factor 52	GRMZM2G342647	B73 RefGen_v3	Gene	Chr8	20171779	20179415	nactf52	nac52	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3389	nactf53	NAC-transcription factor 53	GRMZM2G059428	B73 RefGen_v3	Gene	Chr1	7483453	7485519	nactf53	nac53, nactf53, umc2012	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3390	nactf54	NAC-transcription factor 54	GRMZM2G030325	B73 RefGen_v3	Gene	Chr6	3872449	3875734	nactf54	nac54	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3391	nactf55	NAC-transcription factor 55	GRMZM2G152543	B73 RefGen_v3	Gene	Chr1	212998702	213000426	nactf55	nac55	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3392	nactf56	NAC-transcription factor 56	GRMZM2G386163	B73 RefGen_v3	Gene	Chr7	134727893	134737413	nactf56	nac56	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3393	nactf57	NAC-transcription factor 57	GRMZM2G174070	B73 RefGen_v3	Gene	Chr9	154227661	154232106	nactf57	nac57	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3394	nactf58	NAC-transcription factor 58	AC205484.3_FG005	B73 RefGen_v3	Gene	Chr4	124806079	124815002	nactf58	nac58	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3395	nactf59	NAC-transcription factor 59	GRMZM2G100593	B73 RefGen_v3	Gene	Chr5	207025280	207028850	nactf59	nac59	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3396	nactf6	NAC-transcription factor 6	GRMZM2G018553	B73 RefGen_v3	Gene	Chr5	2917818	2919494	nactf6	nac6	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3397	nactf60	NAC-transcription factor 60	GRMZM2G336533	B73 RefGen_v3	Gene	Chr5	2887335	2889124	nactf60	nac60	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3398	nactf61	NAC-transcription factor 61	GRMZM2G003715	B73 RefGen_v3	Gene	Chr10	78142498	78146839	nactf61	nac61, NAC61 putative NAC domain transcription factor superfamily protein, ZmNTL7	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3399	nactf62	NAC-transcription factor 62	GRMZM2G052239	B73 RefGen_v3	Gene	Chr6	779681	780894	nactf62	nac62	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3400	nactf63	NAC-transcription factor 63	GRMZM2G054277	B73 RefGen_v3	Gene	Chr7	135925560	135927070	nactf63	nac63	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3401	nactf64	NAC-transcription factor 64	GRMZM2G077045	B73 RefGen_v3	Gene	Chr1	25170856	25179088	nactf64	nac64	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3402	nactf65	NAC-transcription factor 65	GRMZM2G043813	B73 RefGen_v3	Gene	Chr10	130642692	130645462	nactf65	nac65	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3403	nactf66	NAC-transcription factor 66	GRMZM2G064541	B73 RefGen_v3	Gene	Chr3	38053466	38062764	nactf66	nac66, NAC66 NAC domain-containing protein 74-like, NAC membrane-bound TF1, ZmNTL1	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3404	nactf67	NAC-transcription factor 67	GRMZM2G083347	B73 RefGen_v3	Gene	Chr10	14449665	14451543	nactf67	nac67	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3405	nactf68	NAC-transcription factor 68	GRMZM2G459156	B73 RefGen_v3	Gene	Chr9	28855314	28857245	nactf68	nac68	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3406	nactf69	NAC-transcription factor 69	GRMZM2G379608	B73 RefGen_v3	Gene	Chr6	116852378	116855345	nactf69	nac69	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3407	nactf7	NAC-transcription factor 7	GRMZM2G163251	B73 RefGen_v3	Gene	Chr1	283321395	283323293	nactf7	nac7	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3408	nactf70	NAC-transcription factor 70	GRMZM2G312201	B73 RefGen_v3	Gene	Chr3	186256882	186265853	nactf70	nac70	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3409	nactf71	NAC-transcription factor 71	GRMZM2G099144	B73 RefGen_v3	Gene	Chr2	47676667	47678102	nactf71	nac71	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3410	nactf72	NAC-transcription factor 72	GRMZM2G163841	B73 RefGen_v3	Gene	Chr8	150109224	150110189	nactf72	nac72	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3411	nactf73	NAC-transcription factor 73	GRMZM2G479980	B73 RefGen_v3	Gene	Chr7	4587851	4589019	nactf73	nac73	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3412	nactf74	NAC-transcription factor 74	GRMZM2G112548	B73 RefGen_v3	Gene	Chr5	5328429	5329897	nactf74	nac74	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3413	nactf75	NAC-transcription factor 75	GRMZM2G100583	B73 RefGen_v3	Gene	Chr4	46961569	46964308	nactf75	nac75	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3414	nactf76	NAC-transcription factor 76	GRMZM2G316840	B73 RefGen_v3	Gene	Chr2	49451938	49453443	nactf76	nac76	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3415	nactf77	NAC-transcription factor 77	AC196475.3_FG005	B73 RefGen_v3	Gene	Chr4	32272270	32275424	nactf77	nac77	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3416	nactf78	NAC-transcription factor 78	GRMZM2G406204	B73 RefGen_v3	Gene	Chr1	4241971	4245996	nactf78	nac78	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3417	nactf79	NAC-transcription factor 79	GRMZM2G004531	B73 RefGen_v3	Gene	Chr7	134132129	134135181	nactf79	nac79, NAC79 putative NAC domain transcription factor superfamily protein, ZmNTL4	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3418	nactf8	NAC-transcription factor 8	GRMZM2G086768	B73 RefGen_v3	Gene	Chr6	116840085	116849846	nactf8	nac8	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3419	nactf80	NAC-transcription factor 80	GRMZM2G060116	B73 RefGen_v3	Gene	Chr3	155888047	155889189	nactf80	nac80	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3420	nactf81	NAC-transcription factor 81	GRMZM2G042494	B73 RefGen_v3	Gene	Chr9	132501909	132504247	nactf81	nac81	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3421	nactf82	NAC-transcription factor 82	GRMZM2G058518	B73 RefGen_v3	Gene	Chr3	210312706	210317109	nactf82	nac82	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3422	nactf83	NAC-transcription factor 83	GRMZM2G158204	B73 RefGen_v3	Gene	Chr8	45532530	45535404	nactf83	nac83	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3423	nactf84	NAC-transcription factor 84	GRMZM2G139700	B73 RefGen_v3	Gene	Chr3	137606842	137608651	nactf84	nac84	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3424	nactf85	NAC-transcription factor 85	GRMZM2G435824	B73 RefGen_v3	Gene	Chr10	119146473	119148431	nactf85	nac85	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3425	nactf86	NAC-transcription factor 86	GRMZM2G171395	B73 RefGen_v3	Gene	Chr9	23290000	23294805	nactf86	nac86, putative NAC domain transcription factor superfamily protein, ZmNST4	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3426	nactf87	NAC-transcription factor 87	GRMZM2G031200	B73 RefGen_v3	Gene	Chr6	164697457	164699173	nactf87	nac87	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3427	nactf88	NAC-transcription factor 88	GRMZM2G134687	B73 RefGen_v3	Gene	Chr8	102889073	102892003	nactf88	nac88	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3428	nactf89	NAC-transcription factor 89	GRMZM2G340305	B73 RefGen_v3	Gene	Chr1	203127019	203131923	nactf89	nac89	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3429	nactf9	NAC-transcription factor 9	GRMZM2G134073	B73 RefGen_v3	Gene	Chr8	159967636	159969818	nactf9	nac9	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3430	nactf90	NAC-transcription factor 90	AC203535.4_FG002	B73 RefGen_v3	Gene	Chr3	157618651	157620063	nactf90	nac90	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3431	nactf91	NAC-transcription factor 91	GRMZM2G041668	B73 RefGen_v3	Gene	Chr9	28053152	28057136	nactf91	nac91	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
3432	nactf92	NAC-transcription factor 92	GRMZM2G048826	B73 RefGen_v3	Gene	Chr4	59362407	59363516	nactf92	nac92	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3433	nactf93	NAC-transcription factor 93	GRMZM5G832473	B73 RefGen_v3	Gene	Chr3	176555601	176557109	nactf93	nac93	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3434	nactf94	NAC-transcription factor 94	GRMZM2G122615	B73 RefGen_v3	Gene	Chr3	209169170	209170481	nactf94	nac94	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3435	nactf95	NAC-transcription factor 95	GRMZM5G813651	B73 RefGen_v3	Gene	Chr3	170066207	170069008	nactf95	nac95	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3436	nactf96	NAC-transcription factor 96	GRMZM5G803888	B73 RefGen_v3	Gene	Chr2	237492353	237493667	nactf96	nac96	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3437	nactf97	NAC-transcription factor 97	GRMZM2G167492	B73 RefGen_v3	Gene	Chr8	4542485	4559631	nactf97	nac97, TIP putative NAC domain transcription factor superfamily protein, ZmNTL5	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3438	nactf98	NAC-transcription factor 98	GRMZM2G115721	B73 RefGen_v3	Gene	Chr9	56518998	56523929	nactf98	nac98	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3439	nactf99	NAC-transcription factor 99	GRMZM2G027309	B73 RefGen_v3	Gene	Chr6	116761395	116766110	nactf99	nac99	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3440	nad1	NADH ubiquinone oxidoreductase1	GRMZM2G018941	B73 RefGen_v3	Gene	Chr1	51011368	51013407	nad1	CL3751_1, CL3751_1(20), nad1, NADH ubiquinone oxidoreductase1, uaz266, uaz266a(nad), uaz266(gfu)	endosperm cDNA 5C05D10 (uaz266), similar to a NADH-ubiquinone oxidoreductase subunit
3441	nad2	NADH dehydrogenase2	GRMZM5G878308	B73 RefGen_v3	Gene	Chr8	154962386	154965330	nad2	nad2, NADH dehydrogenase2, PCO094981, uaz7c02a11(gfu)	vegetative meristem cDNA 7C02A11
3442	nad3	NADH-ubiquinone oxidorectase3	GRMZM2G008464	B73 RefGen_v3	Gene	Chr8	80199540	80203096	nad3	nad3	
3443	nad4	NADH-ubiquinone oxidoreductase B18 su	GRMZM2G137312	B73 RefGen_v3	Gene	Chr1	6540564	6544389	nad4	nad4, NADH-ubiquinone oxidoreductase B18 subunit , pco110646(5), PCO110646a, rs131176360 , rs131200366 , umc1106	
3444	nad5	NADH ubiquinone oxidoreductase B14 su	GRMZM2G014382	B73 RefGen_v3	Gene	Chr1	4055334	4063464	nad5	nad5, NADH ubiquinone oxidoreductase B14 subunit, umc1619	
3445	nas1	nicotianamine synthase1	GRMZM2G385200	B73 RefGen_v3	Gene	Chr9	135804104	135805335	nas1	nas1;1	expressed in iron deficient roots; function confirmed by enzymatic assay of fusion proteins raised in E. coli.
3446	nas10	nicotianamine synthase10	GRMZM2G034956	B73 RefGen_v3	Gene	Chr9	136049697	136050938	nas10	nas1, nas10	
3447	nas2	nicotianamine synthase2	GRMZM2G030036	B73 RefGen_v3	Gene	Chr1	49283725	49286176	nas2	nas2;1	fusion proteins raised in E. coli.
3448	nas3	nicotianamine synthase 3	GRMZM2G478568	B73 RefGen_v3	Gene	Chr1	259836588	259838272	nas3	nas3, nicotianamine synthase 3	unlike nas1, nas2, expressed in roots under iron sufficient conditions; function confirmed by enzymatic assay of fusion proteins raised in E. coli.
3449	nas4	nicotianamine synthase 4	GRMZM2G439195	B73 RefGen_v3	Gene	Chr5	15816565	15818557	nas4	nas4, ZmNAS4	
3450	nas5	nicotianamine synthase5	GRMZM2G050108	B73 RefGen_v3	Gene	Chr7	174448119	174450107	nas5	nas5	function inferred from sequence similarity
3451	nas6	nicotianamine synthase6	GRMZM2G704488	B73 RefGen_v3	Gene	Chr9	135552425	135553600	nas6	nas6, nas6;1	
3452	nas7	nicotianamine synthase7	AC233955.1_FG003	B73 RefGen_v3	Gene	Chr9	135559726	135560709	nas7	nas6;2, nas7	function inferred from sequence and gene expression pattern
3453	nas8	nicotianamine synthase8	GRMZM2G312481	B73 RefGen_v3	Gene	Chr9	135973757	135974988	nas8	nas1;2, nas8	function inferred from expression pattern and sequence similarity
3454	nas9	nicotianamine synthase9	GRMZM2G124785	B73 RefGen_v3	Gene	Chr1	49317235	49319685	nas9	nas2;2, nas9	function inferred from sequence and gene expression pattern
3455	natl1	nana2-like1	GRMZM2G455658	B73 RefGen_v3	Gene	Chr4	169187814	169189693	natl1	DWF1-like, dwfl1, na2-like, na2-paralog, nana-two-like1, natl1	ortholog of Arabidopsis brassinosteriod biosynthesis gene DWF1; paralog of na2
3456	nbp1	nucleic acid binding protein1	GRMZM2G011129	B73 RefGen_v3	Gene	Chr7	46493910	46497427	nbp1	CL2457_1, IDP33, nabp1, nbp1, nucleic acid binding protein1, PZA02612, rs128281913, rs55625452 , ss196416595, umc(nabp1)	genomic and cDNA clones; product is imported in vitro into chloroplasts; expressed only in leaf
3457	nbp35	nuclear binding protein35	GRMZM2G031496	B73 RefGen_v3	Gene	Chr5	181446831	181450049	nbp35	csu598, nbp35, nuclear binding protein35, PCO112083b	single copy leaf cDNA, csu598, similar to NBP35 protein
3458	nced2	nine-cis-epoxycarotenoid dioxygenase2	GRMZM2G407181	B73 RefGen_v3	Gene	Chr1	174550907	174553815	nced2	9-cis-epoxycarotenoid dioxygenase5a, nced2, NCED2, NCED5a,, vp14 homolog	
3459	nced3	nine-cis-epoxycarotenoid dioxygenase3	GRMZM5G858784	B73 RefGen_v3	Gene	Chr3	87358369	87360132	nced3	9-cis-epoxycarotenoid dioxygenase5b, nced3, NCED3, NCED5b, vp14 homolog	
3460	nced4	nine-cis-epoxycarotenoid dioxygenase4	GRMZM2G408158	B73 RefGen_v3	Gene	Chr2	235244890	235246909	nced4	9-cis-epoxycarotenoid dioxygenase9a, nced4, NCED9a, vp14 homolog	
3461	nced5	nine-cis-epoxycarotenoid dioxygenase5	GRMZM2G417954	B73 RefGen_v3	Gene	Chr7	5981141	5983425	nced5	9-cis-epoxycarotenoid dioxygenase9b, nced5, NCED9b, vp14 homolog	
3462	nced6	nine-cis-epoxycarotenoid dioxygenase6	GRMZM2G110192	B73 RefGen_v3	Gene	Chr4	159750700	159753143	nced6	Carotenoid cleavage dioxygenase4a, CCD4a, nced6, NCED6	
3463	nced7	nine-cis-epoxycarotenoid dioxygenase7	GRMZM2G330848	B73 RefGen_v3	Gene	Chr7	175907236	175908949	nced7	9-cis-epoxycarotenoid dioxygenase9c, nced7, NCED9c, vp14 homolog	
3464	nced8	nine-cis-epoxycarotenoid dioxygenase8	GRMZM2G150363	B73 RefGen_v3	Gene	Chr5	200743141	200745544	nced8	Carotenoid cleavage dioxygenase4b, CCD4b, NCED5, nced8	
3465	nced9	nine-cis-epoxycarotenoid dioxygenase9	GRMZM5G838285	B73 RefGen_v3	Gene	Chr5	16869343	16871148	nced9	9-cis-epoxycarotenoid dioxygenase9d, nced9, NCED9d	
3466	ncsu4(cca1)	circadian clock associated1 ortholog	GRMZM2G145041	B73 RefGen_v3	Gene candidate	Chr5	64145458	64148638	ncsu4(cca1)	cca1, circadian clock associated1 ortholog, ncsu4(cca1), ncsu(cca1), pzb02023, rs131175684, rs131528053, ss196416110, ss196416112	
3467	ndk1	nucleotide diphosphate kinase1	GRMZM2G134797	B73 RefGen_v3	Gene	Chr7	149952414	149954818	ndk1	csu269, csu269(gfu), IDP1613, ndk1, nucleotide diphosphate kinase1, UAZ091(NDpK), uaz91(ndk)	leaf cDNA csu269, single copy
3468	ndpk1	nucleoside diphosphate kinase1	GRMZM2G178576	B73 RefGen_v3	Gene	Chr1	94688138	94693847	ndpk1	ndpk1, ZmNDPK1	encodes a G4-binding protein
3469	nec4	necrotic4	GRMZM5G870342	B73 RefGen_v3	Gene	Chr2	10671618	10672229	nec4	cpx1, dks8, dks8A, nec4, nec*-516B, necrotic4, oxygen-dependent coproporphyrinogen-III oxidase, chloroplastic-like, PCO087466(115), PCO087466a	seedling yellow, leaf tips necrotic; lethal
3470	nfa104	nucleosome/chromatin assembly factor A	GRMZM2G075637	B73 RefGen_v3	Gene	Chr5	176433165	176437607	nfa104	NAP1, nfa104, nucleosome/chromatin assembly factor A104	similar to Homo sapiens SET domain protein; participates in silencing of MuDR (Woodhouse et al 2006)
3471	nfc103a	nucleosome/chromatin assembly factor C	GRMZM2G090217	B73 RefGen_v3	Gene	Chr1	251873300	251887770	nfc103a	nfc103a, nucleosome/chromatin assembly factor C	
3472	nfc103b	nucleosome/chromatin assembly factor C	GRMZM2G320606	B73 RefGen_v3	Gene	Chr5	17928839	17933771	nfc103b	nfc103b, nucleosome/chromatin assembly factor C	
3473	nfc104a	nucleosome/chromatin assembly factor 1	GRMZM2G032711	B73 RefGen_v3	Gene	Chr7	175605746	175613533	nfc104a	gnp_QBI8g02, gpm500, nfc104a	First identified by the Maize Chromatin Project, who supplied map scores to the Maize Mapping Project towards placement on the CIMDE IBM maps.
3474	nfd102	nucleosome/chromatin assembly factor D	GRMZM2G145968	B73 RefGen_v3	Gene	Chr2	17972424	17980326	nfd102	high mobility group protein5, HMG1/2-like protein, hmg5, hmge, nfd102, nucleosome/chromatin assembly factor D, PCO097256, ZmHMG2	novel HMG, cDNA and peptide sequences
3475	nfd106	nucleosome/chromatin assembly factor D	GRMZM2G125648	B73 RefGen_v3	Gene	Chr4	195556757	195558537	nfd106	HMG1/2-like protein, hmg7, HMG-transcription factor 7, HMG type nucleosome/chromatin assembly factor D, nfd106, nucleosome/chromatin assembly factor D, PCO136722	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3476	nfd110	nucleosome/chromatin assembly factor D	GRMZM2G032252	B73 RefGen_v3	Gene	Chr8	21829304	21836106	nfd110	hmg14, nfd110, nucleosome/chromatin assembly factor D110, PHM1978, ssrp1, structure-specific recognition protein 1	
3477	nfy2	NF-YB homolog	GRMZM5G804893	B73 RefGen_v3	Gene	Chr6	152381850	152387535	nfy2	cadtfr17, CBFB, CCAAT-DR1-transcription factor 17, nfy2, NF-YB, nfyb2, NF-YB homolog, PCO065518(517), PCO065518b, siX59714(517), siX59714d, ZmNF-YB13, ZmNF-YB2	single PCR-isolated sequence with strong homology to CCAAT-box binding protein subunit
3478	nfya1	nuclear transcription factor y subunit a1	GRMZM2G000686	B73 RefGen_v3	Gene	Chr1	15805373	15808637	nfya1	ca2p11, ca2p11 - CCAAT-HAP2-transcription factor 211, nfya1, NF-YA1 nuclear transcription factor Y subunit A-3 , umc1568, ZmNF-YA1	
3479	nfyc2	nuclear transcription factor y subunit c2	GRMZM2G110210	B73 RefGen_v3	Gene	Chr1	73920871	73922877	nfyc2	nfyc2, protein FAR-RED IMPAIRED RESPONSE 1-like, ZmNF-YC2	
3480	nii2	nitrite reductase2	GRMZM2G079381	B73 RefGen_v3	Gene	Chr4	178613063	178616618	nii2	ferredoxin--nitrite reductase, gnp_AI861177a, gpm108a, gpm108b, nii2, NIR, nitrite reductase2, pCIB808	cDNA homologous to spinach gene, induced by nitrate, putative chloroplast transit peptide, two copies

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
3481	nip1a	NOD26-like membrane intrinsic protein1	GRMZM2G041980	B73 RefGen_v3	Gene	Chr5	148343674	148346041	nip1a	csu177, csu177(gfu), major intrinsic membrane protein1, mip1, nip1a, NOD26-like membrane intrinsic protein1, pco067174b, ZmNIP1-1	leaf cDNA csu177 similar to rice nodulin
3482	nip2a	NOD26-like membrane intrinsic protein2	GRMZM2G028325	B73 RefGen_v3	Gene	Chr5	206972501	206976357	nip2a	nip2a, NOD26-like membrane intrinsic protein2, umc1537, ZmNIP2-1	
3483	nip2b	NOD26-like membrane intrinsic protein2	GRMZM2G137108	B73 RefGen_v3	Gene	Chr6	113136258	113140405	nip2b	CL26323_2, CL26323_2(495), nip2b, NOD26-like membrane intrinsic protein2, ZmNIP2-2	
3484	nip2c	NOD26-like membrane intrinsic protein2	GRMZM2G081239	B73 RefGen_v3	Gene	Chr9	4504176	4507865	nip2c	aquaporin NIP2-3, CL6730_1d, NIP2-3, nip2c, NOD26-like membrane intrinsic protein2, ZmNIP2-3	
3485	nit1	nitrilase1	GRMZM2G178517	B73 RefGen_v3	Gene	Chr5	188512723	188518155	nit1	mmp104, nit1	
3486	nit2	nitrilase2	GRMZM2G111225	B73 RefGen_v3	Gene	Chr4	145590144	145596670	nit2	nit2	
3487	nkd1	naked endosperm1	GRMZM2G129261	B73 RefGen_v3	Gene	Chr2	17718739	17726319	nkd1	idd9, INDETERMINATE-related protein 9, nkd1, pco148979b, ZmIDDveg9	double mutants have multiple (2-5) layers of peripheral endosperm cells that lack starch granules or other features of starchy endosperm
3488	nkd2	naked endosperm2	GRMZM5G884137	B73 RefGen_v3	Gene	Chr10	137525111	137530608	nkd2	idd9, nkd2, ZmIDD9	double mutants have multiple (2-5) layers of peripheral endosperm cells that lack starch granules or other features of starchy endosperm
3489	nlp1	NLP-transcription factor 1	AC233880.1_FG006	B73 RefGen_v3	Gene	Chr3	1290534	1292045	nlp1		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3490	nlp10	NLP-transcription factor 10	GRMZM2G071322	B73 RefGen_v3	Gene	Chr3	226910212	226911995	nlp10		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3491	nlp11	NLP-transcription factor 11	GRMZM2G472589	B73 RefGen_v3	Gene	Chr4	226922510	226928416	nlp11		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3492	nlp12	NLP-transcription factor 12	GRMZM2G105641	B73 RefGen_v3	Gene	Chr5	206943203	206944195	nlp12		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3493	nlp13	NLP-transcription factor 13	GRMZM2G053298	B73 RefGen_v3	Gene	Chr7	147146774	147152347	nlp13		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3494	nlp14	NLP-transcription factor 14	GRMZM2G392306	B73 RefGen_v3	Gene	Chr9	4398480	4399600	nlp14		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3495	nlp15	NLP-transcription factor 15	GRMZM2G042278	B73 RefGen_v3	Gene	Chr5	76715126	76718411	nlp15		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3496	nlp16	NLP-transcription factor 16	GRMZM2G004663	B73 RefGen_v3	Gene	Chr3	98208303	98218330	nlp16		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3497	nlp17	NLP-transcription factor 17	GRMZM2G048582	B73 RefGen_v3	Gene	Chr2	198102096	198107328	nlp17		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3498	nlp2	NLP-transcription factor 2	GRMZM2G057131	B73 RefGen_v3	Gene	Chr2	18055134	18060421	nlp2		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3499	nlp3	NLP-transcription factor 3	GRMZM2G031398	B73 RefGen_v3	Gene	Chr2	33701563	33710286	nlp3		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3500	nlp4	NLP-transcription factor 4	GRMZM2G375675	B73 RefGen_v3	Gene	Chr8	29209906	29216097	nlp4		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3501	nlp5	NLP-transcription factor 5	AC207342.3_FG001	B73 RefGen_v3	Gene	Chr8	135914954	135916479	nlp5		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3502	nlp6	NLP-transcription factor 6	GRMZM2G475305	B73 RefGen_v3	Gene	Chr3	1540716	1545106	nlp6		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3503	nlp7	NLP-transcription factor 7	GRMZM2G109509	B73 RefGen_v3	Gene	Chr1	7079807	7085736	nlp7		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3504	nlp8	NLP-transcription factor 8	GRMZM2G176655	B73 RefGen_v3	Gene	Chr6	133982025	133991228	nlp8		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3505	nlp9	NLP-transcription factor 9	GRMZM2G105004	B73 RefGen_v3	Gene	Chr10	127592222	127597271	nlp9		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3506	nnr1	nitrate reductase(NADH)1	GRMZM2G568636	B73 RefGen_v3	Gene	Chr4	56335735	56340792	nnr1	cl1506_1c, csu509, NAR1S, ncr(nrB), nia1, Nia1, nitrate reductase B, nitrate reductase(NADH)1, nnr1, nnr3, NR1, PHM1307, PZA02031, umc201, umc201(nr), ZmnrS	leaf, scutellum cDNA's; flavin and cyt b domains functional in E. coli, may be allelic to nnr3
3507	nod1	narrow odd dwarf1	GRMZM2G027821	B73 RefGen_v3	Gene	Chr1	11979866	11984789	nod1	CNR13 cell number regulator 13, nod1, rs131176789, rs131184656	mutants are small plants with narrow leaves
3508	not1	neighbor of tga1	AC233751.1_FG002	B73 RefGen_v3	Gene	Chr4	44806723	44811049	not1	AC233751.1_FG002, neighbor of tga1, not1, squamosa promoter-binding-like protein 16, ZmSBP32	compared to tga1, expressed much higher in maize than teosinte; INDEL probe (Preston et al 2011)
3509	npi285a(cac)		GRMZM2G350841	B73 RefGen_v3	Gene	Chr10	5006086	5010500	npi285a(cac)	npi285, npi285a, npi285a(cac), npi285(cac), phi052, php90285, rs131748267	
3510	npi393		GRMZM2G158668	B73 RefGen_v3	Gene	Chr6	96837112	96840842	npi393	npi393, rs131587943	
3511	npi414a		GRMZM2G069260	B73 RefGen_v3	Gene	Chr8	169336134	169340170	npi414a	cl58541_1, cl58541_1(642), npi414, npi414a, rs130930360	similar to Arabidopsis NADH dehydrogenase
3512	nrat1	nramp aluminum transporter1	GRMZM2G069198	B73 RefGen_v3	Gene	Chr5	43175325	43180945	nrat1	Nramp (natural resistance-associated macrophage protein), nrat1, qALT5	encodes an aluminum transporter localized on the plasma membrane, which is required in the initial steps of internal Al detoxification
3513	nrp1	no-apical-meristem-related protein1	GRMZM2G062650	B73 RefGen_v3	Gene	Chr3	31805298	31807331	nrp1	nactf128, NAC-transcription factor 128, NAM-related protein1, no-apical-meristem (NAM) related protein1, no-apical-meristem-related protein1, nrp1	project (Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3514	nrpd2/e2	nuclear RNA polymerase D2/E2	GRMZM2G054225	B73 RefGen_v3	Gene	Chr2	6336518	6347954	nrpd2/e2	RNA polymerase D2, nuclear RNA polymerase D2/E2, required to maintain repression7, required to maintain repression 7, rmr7, RNA polymerase D2a, rpd2a, nrdp2	This gene was found by both the Chandler Lab (as mop2) and the Hollick lab (as rmr7).
3515	nrt1	nitrate transport1	GRMZM2G010251	B73 RefGen_v3	Gene	Chr4	240790398	240792301	nrt1	nrt1, nrt2-2, nrt2.2	
3516	nrt2	nitrate transport2	GRMZM2G010280	B73 RefGen_v3	Gene	Chr4	240779448	240781473	nrt2	nitrate transport2, nrt2, nrt2-1, nrt2.1	
3517	nrt3	nitrate transport3	GRMZM2G163866	B73 RefGen_v3	Gene	Chr5	68900266	68902129	nrt3	nrt2-3, nrt2.3, nrt3	
3518	nrt4	nitrate transport4	GRMZM2G163494	B73 RefGen_v3	Gene	Chr2	37958393	37960212	nrt4	nar2-2, nar2.2, nrt4	
3519	nrx1	nucleoredoxin1	GRMZM2G048324	B73 RefGen_v3	Gene	Chr1	70432377	70436980	nrx1	CL1652_1, CL1652_1(29), nrx1, nucleoredoxin1	single copy cDNA sequence; thioredoxin-like
3520	ns1	narrow sheath1	GRMZM2G069028	B73 RefGen_v3	Gene	Chr2	143166134	143168172	ns1	HB-type transcription factor, narrow sheath1, ns1, prs, WUSCHEL-related homeobox 3B, ZmHB125	plant brachytic, duplicate factor with ns2; leaf sheath and blade taper, blade widens toward tip; husks narrowed, ears exposed
3521	ns2	narrow sheath2	Zm00001d052598	Zm-B73-REFERENCE-G	Gene	Chr4	194314663	194315585	ns2	narrow sheath2, ns2	duplicate factor with ns1
3522	nta1	N-terminal amidase1	GRMZM2G110258	B73 RefGen_v3	Gene	Chr9	154869141	154872005	nta1	CemA-like proton extrusion protein-related , csu365, csu54b, csuh54, nta1, rs131182706, umc337	NCBI: CemA-like proton extrusion protein-related
3523	ntf1	nuclear transport factor1	GRMZM2G006953	B73 RefGen_v3	Gene	Chr4	44885697	44888397	ntf1	csu608, ntf1, nuclear transport factor1, TIDP3001	single copy leaf cDNA csu608, similar to yeast nuclear tranport factor
3524	ntf1	nuclear transport factor1	GRMZM2G407249	B73 RefGen_v3	Gene	Chr1	194524205	194526962	ntf1	csu608, ntf1, nuclear transport factor1, TIDP3001	single copy leaf cDNA csu608, similar to yeast nuclear tranport factor
3525	nthr3	anther-specific protein 3	GRMZM2G073377	B73 RefGen_v3	Gene	Chr7	141680355	141682024	nthr3	anther-specific protein 3, MZm3-3, nthr3, ZmLTPc2	
3526	nudix1	NUDIX domain hydrolase1	GRMZM2G031461	B73 RefGen_v3	Gene	Chr7	88132355	88151112	nudix1	Nucleoside Diphosphate linked to X, nudix1, NUDIX domain hydrolase1	metabolite proof-reading; encodes a NUDIX domain protein that hydrolyzes thiamin diphosphate and related metabolites
3527	nyc1	non-yellow coloring1	GRMZM2G170013	B73 RefGen_v3	Gene	Chr3	2138069	2142526	nyc1	gnp_QCB20b03_PCR, gpm587, nyc1, PCO113306a	plays an important role in chlorophyll content and other related traits, and different sites act on chlorophyll metabolism under different light intensities in maize seedlings
3528	o1	opaque endosperm1	GRMZM2G449909	B73 RefGen_v3	Gene	Chr4	176899980	176926797	o1	myosin-15, o1, opaque endosperm1, ZmOrphan279	endosperm starch soft, opaque
3529	o10	opaque endosperm10	GRMZM2G346263	B73 RefGen_v3	Gene	Chr1	265018615	265025388	o10	dentin sialophosphoprotein-like, o10, o*-1356, o*-E1356, opaque endosperm10, ox*-7747	like o1

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
3530	o2	opaque endosperm2	GRMZM2G015534	B73 RefGen_v3	Gene	Chr7	10798507	10801399	o2	gnp_QDA2D8, gpm941, gsy02(o2), IDP2521, IDP2523, o2, opaque2, opaque endosperm2, phi057, phi112, umc1066, ZmbZIP1	like o1; high lysine content; regulates b-32 protein (see rip1); reduced lysine degradation (lysine-ketoglutaric reductase); SSRs phi057, 112
3531	o5	opaque endosperm5	GRMZM2G142873	B73 RefGen_v3	Gene	Chr7	117734381	117741648	o5	MGDG synthase type A, o5, opaque endosperm5	like o1; virescent to yellow or white seedlings
3532	o7	opaque endosperm7	GRMZM2G074759	B73 RefGen_v3	Gene	Chr10	148065471	148067620	o7	cl7206_1, o7, opaque endosperm7, peroxisomal-coenzyme A synthetase	like o1; high lysine content
3533	obf1	octopine synthase binding factor1	GRMZM2G479885	B73 RefGen_v3	Gene	Chr1	147170752	147172309	obf1	bzip39, bZIP-transcription factor 39, gsy217(obf1), obf1, ocsbf-1, octopine synthase binding factor1, PCO086174a	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.. encodes protein with bZIP motif that binds to transcriptional
3534	obf3	octopine synthase binding factor3	GRMZM2G019907	B73 RefGen_v3	Gene	Chr3	187349410	187394170	obf3	CL2140_1a, obf3, OBF3.1, obf*-X69153, octopine synthase binding factor3, ucla(obf3A)	cDNA clones, candidates for ocs-element transcription factor; a small gene family containing a minimum of two OBF3 loci.
3535	obf4	octopine synthase binding factor4	GRMZM2G125243	B73 RefGen_v3	Gene	Chr8	170849743	170855748	obf4	X69152, octopine synthase binding factor4, PZA00189, rs131175914, ss196417072, ucla(obf3B), ZmbZIP33	cDNA clone, candidate for ocs-element transcription factor, small gene family
3536	ocl1	outer cell layer1	GRMZM2G026643	B73 RefGen_v3	Gene	Chr3	27552061	27559751	ocl1	HDGL2 family, Homeo domain leucin zipper IV 1_outer cell layer1, ocl1, outer cell layer1, siy17898(210), ZmHB31, ZmHDZIV1_OCL1, ZmOCL1	homeobox protein expressed in outer layers of embryo axis and in developing endosperm; maps near glossy6 on chromosome 3 (Ingram et al 1999)
3537	ocl2	outer cell layer2	AC235534.1_FG007	B73 RefGen_v3	Gene	Chr10	136957427	136964001	ocl2	HD-ZipIV family, ocl2, outer cell layer2, ZmHB104, ZmOCL2	
3538	ocl3	outer cell layer3	GRMZM2G116658	B73 RefGen_v3	Gene	Chr7	141712281	141718468	ocl3	CL1209_1, cl1209_1(569), HD-ZipIV family, ocl3, outer cell layer3, ZmHB14, ZmOCL3	
3539	ocl4	outer cell layer4	GRMZM2G123140	B73 RefGen_v3	Gene	Chr1	100912576	100918541	ocl4	gnp_OCL4_PCR, HD-ZipIV family, ocl4, outer cell layer4, ZmHB15, ZmOCL4	
3540	ocl5a	outer cell layer5a	GRMZM2G130442	B73 RefGen_v3	Gene	Chr4	29008617	29014800	ocl5a	CL1207_1, cl1207_1(299), HD-ZipIV family, ocl5, ocl5a, outer cell layer5a, PZA02002, ZmHB97, ZmOCL5	
3541	odo1	alpha keto dehydrogenase candidate1	GRMZM2G151041	B73 RefGen_v3	Gene	Chr10	109817358	109823752	odo1	alpha keto dehydrogenase candidate1, odo1, PCO096873, PZA01292, rs132581681, rs55624419 , ss196417411, TIDP3354, uaz215, uaz215(gfu)	etiolated leaf cDNA 6C02A09 (uaz215) similar to microbial TCA cycle enzyme
3542	oec2	oxygen evolving complex2	GRMZM2G021617	B73 RefGen_v3	Gene	Chr9	57921763	57923880	oec2	OEC 16 kDa subunit, oec2, oxygen-evolving enhancer protein 3-1, chloroplast, oxygen evolving enhancer protein 3 domain containing protein	
3543	oec23	oxygen evolving complex23	GRMZM2G156857	B73 RefGen_v3	Gene	Chr8	78520915	78522102	oec23	npi472e(oec23), npi476, npi476(oec), npi476(oec23), oec23, oec5, oxygen evolving complex23, umc1627, umc171	cDNA sequences; SSR umc1627; see also loci probed by umc171 and npi472
3544	oec33	oxygen evolving complex, 33kDa subunit	GRMZM2G175562	B73 RefGen_v3	Gene	Chr6	88908079	88909780	oec33	CL4601_3(486), CL4601_3c, OE33, oec33, oxygen evolving complex, 33kDa subunit, PsbO, umc172(oec33)	(was umc172) cDNA identified by hybrid-selection, in vitro translation and immunoprecipitation with antisera against spinach OEC33
3545	oec33b	oxygen-evolving complex 33 kda protein	GRMZM2G113349	B73 RefGen_v3	Gene	Chr5	51897880	51899471	oec33b	cl4601_3(397), cl4601_3b, PsbO	mesophyll cell specific, expressed at about 50% of the oec33 gene on chromosome 6; function inferred by sequence similarity to oec33
3546	oec6	oxygen evolving complex6	GRMZM2G058070	B73 RefGen_v3	Gene	Chr7	155404548	155405848	oec6	chi*-Z26824, Ferredoxin-NADP reductase binding protein, oec17*-Z26824, oec23, oec6, oxygen evolving complex17 candidate, phi114	genomic sequence similar to maize oec17 sequence; minus strand similar to maize chi1
3547	ofp1	OVATE-transcription factor 1	GRMZM2G055737	B73 RefGen_v3	Gene	Chr1	5511015	5512341	ofp1		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3548	ofp10	OVATE-transcription factor 10	GRMZM2G032478	B73 RefGen_v3	Gene	Chr2	142057406	142058499	ofp10		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3549	ofp11	OVATE-transcription factor 11	GRMZM2G130131	B73 RefGen_v3	Gene	Chr2	142230107	142231460	ofp11		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3550	ofp12	OVATE-transcription factor 12	GRMZM2G359116	B73 RefGen_v3	Gene	Chr2	217596031	217596732	ofp12		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3551	ofp13	OVATE-transcription factor 13	GRMZM2G169973	B73 RefGen_v3	Gene	Chr3	2145565	2147044	ofp13		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3552	ofp14	OVATE-transcription factor 14	GRMZM2G434098	B73 RefGen_v3	Gene	Chr3	176376917	176378611	ofp14		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3553	ofp15	OVATE-transcription factor 15	GRMZM2G133311	B73 RefGen_v3	Gene	Chr3	176399487	176401158	ofp15		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3554	ofp16	OVATE-transcription factor 16	GRMZM2G330159	B73 RefGen_v3	Gene	Chr3	184369059	184370437	ofp16		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3555	ofp17	OVATE-transcription factor 17	GRMZM2G127431	B73 RefGen_v3	Gene	Chr3	198109815	198111352	ofp17		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3556	ofp18	OVATE-transcription factor 18	GRMZM2G023285	B73 RefGen_v3	Gene	Chr3	200770762	200772307	ofp18		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3557	ofp19	OVATE-transcription factor 19	AC198725.4_FG004	B73 RefGen_v3	Gene	Chr3	217373974	217375254	ofp19		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3558	ofp2	OVATE-transcription factor 2	GRMZM2G096252	B73 RefGen_v3	Gene	Chr1	12208463	12209068	ofp2		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3559	ofp20	OVATE-transcription factor 20	GRMZM2G150823	B73 RefGen_v3	Gene	Chr3	222037098	222037820	ofp20		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3560	ofp21	OVATE-transcription factor 21	GRMZM2G013302	B73 RefGen_v3	Gene	Chr4	190514387	190515895	ofp21		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3561	ofp22	OVATE-transcription factor 22	GRMZM2G013271	B73 RefGen_v3	Gene	Chr4	190553240	190554695	ofp22		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3562	ofp23	OVATE-transcription factor 23	GRMZM2G041761	B73 RefGen_v3	Gene	Chr5	196301608	196303357	ofp23		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3563	ofp24	OVATE-transcription factor 24	GRMZM2G436659	B73 RefGen_v3	Gene	Chr6	475010	478353	ofp24		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3564	ofp25	OVATE-transcription factor 25	GRMZM2G100133	B73 RefGen_v3	Gene	Chr6	134751875	134753206	ofp25		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3565	ofp26	OVATE-transcription factor 26	GRMZM2G122709	B73 RefGen_v3	Gene	Chr6	149397746	149398805	ofp26		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3566	ofp27	OVATE-transcription factor 27	GRMZM2G430871	B73 RefGen_v3	Gene	Chr6	149479675	149480789	ofp27		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3567	ofp28	OVATE-transcription factor 28	GRMZM2G026927	B73 RefGen_v3	Gene	Chr6	154037242	154038876	ofp28	ofp28, OFP8 OFP transcription factor, Ovate family protein 4 (OFP4)	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3568	ofp29	OVATE-transcription factor 29	GRMZM2G127680	B73 RefGen_v3	Gene	Chr6	159209864	159210811	ofp29		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3569	ofp3	OVATE-transcription factor 3	GRMZM2G121706	B73 RefGen_v3	Gene	Chr1	23422957	23424234	ofp3		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3570	ofp30	OVATE-transcription factor 30	GRMZM2G037043	B73 RefGen_v3	Gene	Chr7	95805103	95806257	ofp30		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3571	ofp31	OVATE-transcription factor 31	GRMZM5G845472	B73 RefGen_v3	Gene	Chr7	173016115	173017181	ofp31		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3572	ofp32	OVATE-transcription factor 32	GRMZM2G001721	B73 RefGen_v3	Gene	Chr8	19242262	19242864	ofp32		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3573	ofp33	OVATE-transcription factor 33	GRMZM2G067376	B73 RefGen_v3	Gene	Chr8	91371796	91372796	ofp33		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3574	ofp34	OVATE-transcription factor 34	GRMZM2G028982	B73 RefGen_v3	Gene	Chr8	144996205	144997637	ofp34		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3575	ofp35	OVATE-transcription factor 35	GRMZM2G085035	B73 RefGen_v3	Gene	Chr8	166174085	166175881	ofp35		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3576	ofp36	OVATE-transcription factor 36	AC204502.4_FG006	B73 RefGen_v3	Gene	Chr8	169827040	169828125	ofp36		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3577	ofp37	OVATE-transcription factor 37	GRMZM2G137869	B73 RefGen_v3	Gene	Chr9	125223241	125224349	ofp37		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3578	ofp38	OVATE-transcription factor 38	GRMZM2G057753	B73 RefGen_v3	Gene	Chr10	6401895	6403520	ofp38		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
3579	ofp39	OVATE-transcription factor 39	AC187891.3_FG006	B73 RefGen_v3	Gene	Chr10	6406678	6407469	ofp39		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3580	ofp4	OVATE-transcription factor 4	GRMZM2G075988	B73 RefGen_v3	Gene	Chr1	56308513	56309790	ofp4		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3581	ofp40	OVATE-transcription factor 40	GRMZM2G432846	B73 RefGen_v3	Gene	Chr10	120555416	120556201	ofp40		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3582	ofp41	OVATE-transcription factor 41	GRMZM2G040673	B73 RefGen_v3	Gene	Chr10	136127929	136129652	ofp41		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3583	ofp42	OVATE-transcription factor 42	GRMZM2G106836	B73 RefGen_v3	Gene	Chr10	148249961	148250692	ofp42		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3584	ofp43	OVATE-transcription factor 43	GRMZM2G106781	B73 RefGen_v3	Gene	Chr10	148265774	148266844	ofp43		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3585	ofp5	OVATE-transcription factor 5	GRMZM2G039312	B73 RefGen_v3	Gene	Chr1	82197775	82199916	ofp5		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3586	ofp6	OVATE-transcription factor 6	GRMZM2G095452	B73 RefGen_v3	Gene	Chr1	238871804	238872878	ofp6		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3587	ofp7	OVATE-transcription factor 7	GRMZM2G164428	B73 RefGen_v3	Gene	Chr2	15919760	15921239	ofp7		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3588	ofp8	OVATE-transcription factor 8	GRMZM2G053985	B73 RefGen_v3	Gene	Chr2	45347688	45348600	ofp8		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3589	ofp9	OVATE-transcription factor 9	GRMZM2G055257	B73 RefGen_v3	Gene	Chr2	56421131	56422484	ofp9		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3590	ogg1	8-oxoguanine DNA glycolyase1	GRMZM2G139031	B73 RefGen_v3	Gene	Chr5	172334155	172337856	ogg1	ogg1	
3591	ohp1	opaque2 heterodimerizing protein1	GRMZM2G016150	B73 RefGen_v3	Gene	Chr1	288278441	288283216	ohp1	bZIP-type transcription factor, ohp1, ohp1*-, ohp1b, opaque2 heterodimerizing protein1, ucsd44a, ZmbZIP128	o2 heterodimerizing protein; one of two loci
3592	ohp2	opaque2 heterodimerizing protein2	GRMZM2G007063	B73 RefGen_v3	Gene	Chr5	4253958	4257719	ohp2	gnp_QAF9h03a, gpm787a, nc007, ohp2, opaque2 heterodimerizing protein2, phi024, ucsd44b, ZmbZIP94	cDNA sequence, SSRs nc007, phi024
3593	ole1	oleosin1	GRMZM2G337229	B73 RefGen_v3	Gene	Chr2	21389641	21391610	ole1	KD16, L3, ole1, ole16, oleosin1, PCO090509(122), PCO090509a, umc1185, umc1185(ole1)	major protein from lipid bodies, cDNA and genomic clones; SSR umc1185
3594	ole3	oleosin3	AC206941.2_FG002	B73 RefGen_v3	Gene	Chr5	12302727	12303287	ole3	L2, ole18, ole3, oleosin3, phi113	embryo lipid body protein, peptide, cDNA and genomic sequences; SSR phi113
3595	ole4	oleosin4	GRMZM2G480954	B73 RefGen_v3	Gene	Chr1	263817609	263818594	ole4	ole17, ole4, oleosin 18 kDa, oleosin4, umc1184	genomic clone; SSR umc1184
3596	ommp1	outer mitochondrial membrane porin1	GRMZM2G018417	B73 RefGen_v3	Gene	Chr1	8306859	8347066	ommp1	ommp1, outer mitochondrial membrane protein porin1, PZA00181, umc1977	
3597	omt1	Caffeoyl-CoA O-methyltransferase1	GRMZM2G127948	B73 RefGen_v3	Gene	Chr6	79357043	79359228	omt1	ccmt1, ccoAOMT, ccoAOMT1, CCoAOMT1, csu414, gnp_AI637136a, gnp_AI855245a, gpm40a, gpm99a, omt1, PCO108855, PCO108855(484)	
3598	omt2	Caffeoyl CoA O-methyltransferase2	GRMZM2G099363	B73 RefGen_v3	Gene	Chr9	16325170	16327546	omt2	ccoAOMT, CCoAOMT2, omt2, umc1636	
3599	omt3	Caffeoyl CoA O-methyltransferase3	GRMZM2G077486	B73 RefGen_v3	Gene	Chr10	80419760	80423498	omt3	ccoaomt3, omt3	
3600	omt4	Caffeoyl CoA O-methyltransferase4	GRMZM2G332522	B73 RefGen_v3	Gene	Chr4	198256537	198258374	omt4	ccoaomt4, omt4, pza01810, PZA01810, rs129886478, ss196415905	
3601	opr1	12-oxo-phytodienoic acid reductase1	GRMZM2G106303	B73 RefGen_v3	Gene	Chr9	7393651	7395331	opr1	opr1, PCO079165, rs131177145, Zmcoi6.12	Cytoplasmic
3602	opr2	12-oxo-phytodienoic acid reductase2	GRMZM2G000236	B73 RefGen_v3	Gene	Chr9	7308584	7310337	opr2	opr2, rs131694665	Cytoplasmic
3603	opr3	12-oxo-phytodienoic acid reductase3	GRMZM2G156712	B73 RefGen_v3	Gene	Chr6	111640645	111642331	opr3	opr3, rs130365658, rs132311887	
3604	opr4	12-oxo-phytodienoic acid reductase4	Zm00001d011097	Zm-B73-REFERENCE-G	Gene	Chr8	138824703	138825854	opr4	12-oxo-phytodienoic acid reductase4, opr4, rs132472908, rs132472917	Cytoplasmic
3605	opr5	12-oxo-phytodienoic acid reductase5	GRMZM2G087192	B73 RefGen_v3	Gene	Chr2	47717535	47720768	opr5	IDP1994, opr5, rs129061636, rs131341826	Predicted to have cytoplasmic localization (Zhang et al. 2005)
3606	opr6	12-oxo-phytodienoic acid reductase6	GRMZM2G068947	B73 RefGen_v3	Gene	Chr3	69859514	69861831	opr6	opr6, PCO134627(238), PCO134627b, rs128284147	Cytoplasmic
3607	opr7	12-oxo-phytodienoic acid reductase7	GRMZM2G148281	B73 RefGen_v3	Gene	Chr1	207946160	207950205	opr7	opr7, PCO088243(64)	peroxisomal; jasmonic acid synthesis; opr7 opr8 double mutants are feminized, and have increased susceptibiliy to insect and fungal pests
3608	opr8	12-oxo-phytodienoic acid reductase8	GRMZM2G082087	B73 RefGen_v3	Gene	Chr4	63562327	63567747	opr8	opr8, PCO088244(311), PCO088244a	peroxisomal; synthesis of jasmonic acid
3609	orc1	origin recognition complex1	GRMZM2G455243	B73 RefGen_v3	Gene	Chr9	12350567	12372569	orc1	AY104252, orc1, origin recognition complex1, PCO110637, PZA01386, ZmORC1, ZmPHD37	member of a complex having a role in recognition and binding to origins of DNA replication; evidence from yeast two-hybrid assays and expression profiles
3610	orc2	origin recognition complex2	GRMZM2G117238	B73 RefGen_v3	Gene	Chr5	190532565	190536335	orc2	orc2, origin recognition complex2, ZmORC2	member of a complex having a role in recognition and binding to origins of DNA replication; evidence from yeast two-hybrid assays and expression profiles
3611	orc3	origin recognition complex3	GRMZM2G381822	B73 RefGen_v3	Gene	Chr1	174021190	174024616	orc3	orc3, origin recognition complex3, ZmORC3	member of a complex having a role in recognition and binding to origins of DNA replication; evidence from yeast two-hybrid assays and expression profiles
3612	orc4	origin recognition complex4	GRMZM5G876520	B73 RefGen_v3	Gene	Chr3	207987759	207990967	orc4	orc4, origin recognition complex4, ZmORC4	member of a complex having a role in recognition and binding to origins of DNA replication; evidence from yeast two-hybrid assays and expression profiles
3613	orc5	origin recognition complex5	GRMZM2G089556	B73 RefGen_v3	Gene	Chr5	6552930	6555038	orc5	orc5, origin recognition complex5, ZmORC5	member of a complex having a role in recognition and binding to origins of DNA replication; evidence from yeast two-hybrid assays and expression profile
3614	orf140-b (mt)		GRMZM5G834666	B73 RefGen_v3	Gene	ChrMt	265988	266410	orf140-b (mt)	orf140-b (mt)	
3615	ork1	outward rectifying potassium channel1	GRMZM2G156255	B73 RefGen_v3	Gene	Chr6	115732874	115738363	ork1	ork1, outward rectifying potassium channel1, potassium outward rectifying channel, ZORK	
3616	orp1	orange pericarp1	GRMZM2G169593	B73 RefGen_v3	Gene	Chr4	35950109	35954045	orp1	BNL-ORP(trpB), orange pericarp1, orp1, orp*-1186A, ORP(trpB), PCO122526, PZA03247, rs131175582, ss196415710, tbs1, umc193a(orp1), umcorp1, umc(orp1)	duplicate factor with orp2; pericarp orange over orp1 orp2 kernels, manifesting metaxenia; lethal, tryptophan auxotroph
3617	orp2	orange pericarp2	GRMZM2G005024	B73 RefGen_v3	Gene	Chr10	84247242	84250053	orp2	BNL#-ORP(trpB), orange pericarp2, orp*-1186B, orp2, ORP(trpB), umc193b(orp2), umc(orp2)	duplicate factor with orp2; pericarp orange over orp1 orp2 kernels, manifesting metaxenia; lethal, tryptophan auxotroph
3618	orrm1	organelle RRM protein1	GRMZM5G899787	B73 RefGen_v3	Gene	Chr5	204811304	204817342	orrm1	chloroplast protein synthesis 4, cps4, organelle RNA recognition motif protein1, organelle RRM protein1, orrm1, pco143014, pco143014(448)	encodes an essential plastid editing factor. ORRM-domain protein, involved in chloroplast RNA editing. (A. Barkan, 2015)
3619	ost1	oligosaccharide transferase1	GRMZM2G462325	B73 RefGen_v3	Gene	Chr7	19083049	19101243	ost1	dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDasubunit, oligosaccharide transferase1, ost1, PCO149739, PCO149739(541), uaz7c02f04(gfu)	vegetative meristem cDNA 7C02F04 similar to an integral endoplasmic reticulum protein
3620	otp51	organelle transcript processing51	GRMZM2G325019	B73 RefGen_v3	Gene	Chr5	200487577	200491114	otp51	otp51, pentatricopeptide repeat-containing protein At2g15820-like	Chloroplast PPR protein with LAGLIDADG domain. Required for splicing chloroplast ycf3-int2 intron (A. Barkan, 2015). . Enclodes PR-LAGLIDADG protein; required for splicing cp ycf3-int2
3621	oxmt1	oxo-glutarate/malate transporter1	GRMZM2G383088	B73 RefGen_v3	Gene	Chr10	28396447	28402412	oxmt1	OMT1, oxmt1, oxo-glutarate/malate transporter1, pco103506(726), rs128511102, ZmpOMT1	single copy, plastid tranporter specific to mesophyll cells (Taniguchi et al 2004)
3622	oy1	oil yellow1	GRMZM2G419806	B73 RefGen_v3	Gene	Chr10	9225307	9229786	oy1	chll, CHL I, CL865_1, CL865_1(717), csu998, csuh00998, magnesium chelatase subunit I, oil yellow1, oy1	oy1-t tinged green; oy1-1039, oy1-1040 lethal; Oy1-700 dominant yellow-green; gene product confirmed by transgenic expression and genetic mapping.
3623	P	plant color component at R1	GRMZM5G822829	B73 RefGen_v3	Gene	Chr10	138489998	138498818	P	P, plant color component at R1	anthocyanin pigmentation in seedling leaf tip, coleoptile, anthers
3624	p1	pericarp color1	GRMZM2G084799	B73 RefGen_v3	Gene	Chr1	48118788	48129338	p1	fv, gsy271(P), npi281(P1), npi370, npi370-p1, npi370(p1), p1, pericarp color1, phi095, php90281, sc271, umc185(p1), ZmMYB3	rr red pericarp and cob) and in tassel glumes and husks; tissue-specific allele variations; SSR phi095
3625	p2	pericarp color2	GRMZM2G057027	B73 RefGen_v3	Gene	Chr1	48096443	48101954	p2	myb-related protein P-like, p2, pericarp color2, umc2096, umc2097, ZmMYB55	nearly identical to p1, active in anther and silk but does not determine pericarp color; SSR's umc2096, umc2097.
3626	paac1	putative ADP-ATP carrier1	GRMZM2G178460	B73 RefGen_v3	Gene	Chr3	39820091	39823461	paac1	paac1, paac1(219), pco142634, PHM2985, putative envelope ADP/ATP carrier protein chloroplastic	
3627	pac1	pale aleurone color1	GRMZM2G058292	B73 RefGen_v3	Gene	Chr5	196661199	196666224	pac1	mitochondrial import inner membrane translocase subunit Tim13, pac1, pale aleurone color1, pco108935, pco108935(444)	recessive, non-lethal, regulates reduced pigment in kernels

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
3628	pal1	phenylalanine ammonia lyase homolog1	GRMZM2G074604	B73 RefGen_v3	Gene	Chr5	186727239	186730980	pal1	bnl17.23a, bnl17.23(pal1), csu156, Pal-, pal1, pal3, pal3 phenylalanine ammonia lyase 3, phenylalanine ammonia lyase1, sc403, sc405	leaf cDNA csu156 similar to rice phenylalanine ammonia lyase, single copy
3629	pal2	phenylalanine ammonia lyase2	GRMZM2G441347	B73 RefGen_v3	Gene	Chr2	28745742	28748887	pal2	bnl17.23b, bnl17.23b(pal), bnl17.23(pal2), mu1079393, pal2, PCO142079, PCO142079(124), phenylalanine ammonia lyase homolog, phi109642, rs131325406	
3630	pal3	phenylalanine ammonia lyase3	GRMZM2G160541	B73 RefGen_v3	Gene	Chr4	143404315	143408521	pal3	bnl17.23c, bnl17.23c(pal), bnl17.23(pal3), csu358b(pal), pal3, phenylalanine ammonia lyase homolog, phenylalanine/tyrosine ammonia-lyase-like	used primers on cDNA from glume bars to PCR out RFLP probe. 190 bp ss-mRNA with homology to phenylalanine ammonia lyase. Mapped minor band to this site.
3631	pal4	phenylalanine ammonia lyase4	GRMZM2G063917	B73 RefGen_v3	Gene	Chr4	143539451	143542437	pal4	pal4	
3632	pal5	phenylalanine ammonia lyase5	GRMZM2G081582	B73 RefGen_v3	Gene	Chr4	143491905	143496980	pal5	pal5, ZmPAL	
3633	pal6	phenylalanine ammonia lyase6	GRMZM2G118345	B73 RefGen_v3	Gene	Chr2	28677255	28680358	pal6	pal6	
3634	pal7	phenylalanine ammonia lyase7	GRMZM2G170692	B73 RefGen_v3	Gene	Chr5	186845785	186848361	pal7	PAL3, pal7	
3635	pal8	phenylalanine ammonia lyase8	GRMZM2G334660	B73 RefGen_v3	Gene	Chr5	186783199	186785900	pal8	pal8	
3636	pal9	phenylalanine ammonia lyase9	GRMZM2G029048	B73 RefGen_v3	Gene	Chr5	186776435	186780444	pal9	pal9	
3637	pan1	pangloss1	GRMZM5G836190	B73 RefGen_v3	Gene	Chr1	188011520	188014028	pan1	pan1, pangloss1	Defines polarization in divisions of subsidiary mother cells at guard cells
3638	pan2	pangloss2	GRMZM2G034572	B73 RefGen_v3	Gene	Chr2	237789995	237798040	pan2	pan2	Defines polarization in divisions of subsidiary mother cells at guard cells
3639	pao1	polyamine oxidase1	GRMZM2G034152	B73 RefGen_v3	Gene	Chr10	62260920	62265303	pao1	IDP2513, MPAO1, pao1, PCO061908, PHM1155, polyamine oxidase1, umc2016	cDNA and genomic clones, low copy number
3640	parp1	poly(ADP-ribose) polymerase1	GRMZM2G124718	B73 RefGen_v3	Gene	Chr8	44048003	44054105	parp1	parp1, poly(ADP-ribose) polymerase1, siaj222588, ZAP1	
3641	parp2	poly(ADP-ribose) polymerase2	GRMZM5G831712	B73 RefGen_v3	Gene	Chr2	158095514	158128380	parp2	CL1689_1, CL1689_1(156), PARP1, parp2, parp3, poly(ADP-ribose) polymerase2, ZAP2	
3642	pba1	PBA1 homolog1	GRMZM2G177508	B73 RefGen_v3	Gene	Chr1	5582721	5584189	pba1	pba1, phm2244, PHM2244.142, protesome subunit PBA1 like	AY107335; contains a CAAD domain, found in aminoacyl-tRHN syntheases; a PFAM functionally uncharacterized domain
3643	pbf1	prolamin-box binding factor1	GRMZM2G146283	B73 RefGen_v3	Gene	Chr2	154144472	154148029	pbf1	binding factor1, rs131175439, rs131175440, rs131175441, rs131175442, ss196415153, ss196415156, ss196415158, ss196415160, umc1065, umc1065(pbf1), ZmDof13, ZmDOF3	endosperm cDNA, SSR umc1065
3644	pc326	plasmacytoma 326 homolog	GRMZM2G123709	B73 RefGen_v3	Gene	Chr9	126453735	126456483	pc326	pc326, PCO149370(689), PCO149370f, plasmacytoma 326 homolog, uaz123, uaz123(gfu), zpc326	endosperm cDNA 5C03G07, similar to human H326 and to murine plasmacytoma protein, PC326
3645	pck1	phosphoenolpyruvate carboxykinase1	GRMZM2G001696	B73 RefGen_v3	Gene	Chr1	35744406	35748813	pck1	cl1267_2(15), cl1267_2a, csu145c, csu145c(pck), csuh145c, IDP461, pck1, phosphoenolpyruvate carboxykinase homolog1, umc378	C4 photosynthesis, decarboxylation of aspartate in bundle sheath cytosol, accounts for transfer of about 1/4 C02 fixed in mesophyll cells
3646	pck2	phosphoenolpyruvate carboxykinase hon	GRMZM5G870932	B73 RefGen_v3	Gene	Chr9	142082081	142086925	pck2	CL1267_2(697), CL1267_2b, csu145a, csu145a(pck), csuh145a(pck), IDP63, pck2, PEPCK, phosphoenolpyruvate carboxykinase homolog2, umc378a	syntenic with pck1; leaf cDNA csu145, low copy, similar to yeast phosphoenolpyruvate carboxykinase
3647	pcna1	proliferating cell nuclear antigen1	GRMZM2G030523	B73 RefGen_v3	Gene	Chr5	214473508	214475861	pcna1	CL1137_1, CL1137_1(454), pcna1, proliferating cell nuclear antigen1	full-length cDNA; predicted protein shows high similarity to rice, human, others
3648	pcna2	proliferating cell nuclear antigen2	GRMZM2G108712	B73 RefGen_v3	Gene	Chr4	173062872	173064850	pcna2	IDP281, magi81248 , pcna2, proliferating cell nuclear antigen2, (ZmPCNA2)	
3649	pco060326		GRMZM2G458549	B73 RefGen_v3	Probed Site	Chr1	295530301	295537431	pco060326	pco060326(104), PZA01238, rs128985103, rs55626202 , ss196414901	
3650	pco061578		GRMZM2G168337	B73 RefGen_v3	Probed Site	Chr4	167219964	167225717	pco061578	pco061578(328), PZA00453, rs131175623, ss196415862	
3651	pco061803		GRMZM2G168375	B73 RefGen_v3	Gene	Chr8	156176245	156178529	pco061803	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein, not pyg18, pco061803(636)	
3652	pco061840b		GRMZM2G123660	B73 RefGen_v3	Probed Site	Chr2	147944955	147959273	pco061840b	pco061840(159), PZA00029, rs128282105, rs128282106, rs128282110, rs55626283 , ss196415137, ss196415140, ss196415142	
3653	pco065449		GRMZM2G072911	B73 RefGen_v3	Gene	Chr5	196155729	196159058	pco065449	pco065449(444), RHM2	
3654	pco066126		GRMZM2G086801	B73 RefGen_v3	Probed Site	Chr2	4693195	4697981	pco066126	PZA00396, rs131175389, ss196414950	
3655	pco066521		GRMZM2G410812	B73 RefGen_v3	Gene	Chr6	153662746	153665882	pco066521	brk3 paralog, nap1 homolog, pco066521(477)	
3656	pco066724		GRMZM2G112782	B73 RefGen_v3	Probed Site	Chr10	71063036	71066861	pco066724	PZA01677	
3657	pco067132		GRMZM2G000615	B73 RefGen_v3	Probed Site	Chr3	191672177	191679011	pco067132	pco067132(262), PHM3075, PZA01228, rs131175546, ss196415583	
3658	pco071369		GRMZM2G097249	B73 RefGen_v3	Probed Site	Chr1	83790524	83797094	pco071369	pco071369(32), PHM4185, PZA01135, rs131175294, ss196414555	
3659	pco077760		GRMZM2G167548	B73 RefGen_v3	Probed Site	Chr1	204799202	204802905	pco077760	pco077760(64), PHM5480, PZA01391, rs128284917, rs55624017 , ss196414663	
3660	pco078062b		GRMZM2G547542	B73 RefGen_v3	Probed Site	Chr10	106969915	107000846	pco078062b	pco078062(744), PHM18195, PZA00444, rs131175999, ss196417407	
3661	pco079267		GRMZM2G011213	B73 RefGen_v3	Probed Site	Chr8	14070896	14073613	pco079267	pco079267(586), PZA01079, rs131175845, ss196416804	
3662	pco080224b		GRMZM2G364068	B73 RefGen_v3	Probed Site	Chr4	172551715	172560136	pco080224b	PZA00271	
3663	pco081168		GRMZM2G129444	B73 RefGen_v3	Probed Site	Chr3	172489869	172523664	pco081168	pco081168(641), PZA00020, rs128281545, rs55623180 , ss196417053	
3664	pco082032		GRMZM2G061745	B73 RefGen_v3	Probed Site	Chr2	3610614	3614343	pco082032	pco082032(197), PZA01211, rs131175388, rs55626346 , ss196414947	
3665	pco082944		GRMZM2G440280	B73 RefGen_v3	Probed Site	Chr1	14957965	14958681	pco082944	pco082944(9), PHM1653, PZA01652, rs128382426, rs55623586 , ss196414398	
3666	pco083348		GRMZM2G102548	B73 RefGen_v3	Probed Site	Chr1	61145033	61150184	pco083348	pco083348(25), PZA01476, rs128284378, rs55626044 , ss196414522	
3667	pco093291		GRMZM2G324540	B73 RefGen_v3	Probed Site	Chr5	30760520	30770795	pco093291	pco093291(388), PZA00934, rs131175668, ss196416050	
3668	pco093974(367)		GRMZM2G111756	B73 RefGen_v3	Probed Site	Chr4	145268260	145269812	pco093974(36	pco093974(clpp)	
3669	pco093974b		GRMZM2G053236	B73 RefGen_v3	Probed Site	Chr5	188151059	188152501	pco093974b	pco093974b(clpp)	
3670	pco095480		GRMZM2G115750	B73 RefGen_v3	Probed Site	Chr1	201522268	201525873	pco095480	pco095480(61), PZA03074, rs131175314, ss196414643	
3671	pco098048		GRMZM2G118316	B73 RefGen_v3	Probed Site	Chr10	9366054	9382922	pco098048	pco098048(717), PZA01451, rs131175977, ss196417311	
3672	pco098394		GRMZM2G149257	B73 RefGen_v3	Probed Site	Chr1	9045050	9047916	pco098394	pco098394(6), PZA00447, rs128284630, rs128284631, rs128284632, rs55622247 , ss196414363, ss196414365, ss196414367	
3673	pco099975		GRMZM2G084812	B73 RefGen_v3	Probed Site	Chr6	124987113	124988429	pco099975	pza01591	
3674	pco101325		GRMZM2G103721	B73 RefGen_v3	Probed Site	Chr4	71658540	71668712	pco101325	pco101325(317), PZA00218, rs131175598, ss196415766	
3675	pco101682(581)		GRMZM2G178958	B73 RefGen_v3	Gene	Chr5	213590124	213594002	pco101682(58	pco101682(5), putative neutral leucine aminopeptidase	
3676	pco101682(8)		GRMZM2G388453	B73 RefGen_v3	Probed Site	Chr8	71583929	71644926	pco101682(8)	leucine aminopeptidase 2, chloroplastic-like, pco101682(581), pco101682(8)	

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
3677	pco102265b		GRMZM2G417843	B73 RefGen_v3	Probed Site	Chr1	299277345	299281841	pco102265b	pco102265(112), PZA00477, rs131924356, rs55625653 , ss196414917	
3678	pco105903		GRMZM2G152853	B73 RefGen_v3	Probed Site	Chr5	37727150	37742667	pco105903	pco105903(394), PZA00981, rs128283261, rs55624478 , ss196416062	
3679	pco110957		GRMZM2G033199	B73 RefGen_v3	Probed Site	Chr7	139637508	139639636	pco110957	pco110957(568), PZA00740, rs130645340, rs55622976 , ss196416670	
3680	pco111589		GRMZM2G084729	B73 RefGen_v3	Probed Site	Chr10	99014059	99017672	pco111589	pco111589(743), PZA00400, rs128284371, rs55626035 , ss196417397	
3681	pco112439		GRMZM2G143625	B73 RefGen_v3	Probed Site	Chr1	107371746	107373355	pco112439	PZA01254	
3682	pco115388		GRMZM2G125617	B73 RefGen_v3	Probed Site	Chr1	225187496	225196802	pco115388	pco115388(72), PZA00658, rs131175328, rs131175329, rs55623499 , ss196414694, ss196414696	
3683	pco117644		GRMZM2G026807	B73 RefGen_v3	Probed Site	Chr1	14623612	14638761	pco117644	pco117644(9), PZA01497, rs131175258, ss196414396	
3684	pco118092		GRMZM2G070389	B73 RefGen_v3	Probed Site	Chr2	3082367	3086726	pco118092	pco118092(197), PZA00902, rs128284817, rs55623087 , ss196414941	
3685	pco120183		GRMZM2G083418	B73 RefGen_v3	Probed Site	Chr3	9808777	9811667	pco120183	pco120183(201), PZA01765, rs129367180, rs55623283 , ss196415327	
3686	pco123247b		GRMZM2G148508	B73 RefGen_v3	Probed Site	Chr10	105444953	105446192	pco123247b	pco123247(742)	
3687	pco124824		GRMZM2G043291	B73 RefGen_v3	Gene	Chr1	43114366	43116827	pco124824	pco124824(18), putative glutathione S-transferase	
3688	pco125096		GRMZM2G374574	B73 RefGen_v3	Probed Site	Chr5	66460326	66470597	pco125096	pco125096(402), PZA03095, rs128281880, rs131175685, rs131175686, rs55625408 , ss196416114, ss196416116, ss196416118	
3689	pco125437		GRMZM2G092129	B73 RefGen_v3	Probed Site	Chr7	34183685	34198384	pco125437	PZA00260, rs131615517, rs55623609 , ss196416576	
3690	pco129491		GRMZM2G075956	B73 RefGen_v3	Probed Site	Chr8	165628436	165631708	pco129491	pco129491(641), PZA00001, rs130923004, rs55625229 , ss196417057	
3691	pco131924a		GRMZM2G006791	B73 RefGen_v3	Gene	Chr5	172434779	172439962	pco131924a	pco111578, pco111578(428), pco131924(428), PZA00300, rs128281788, rs131175703, rs55624691 , ss196416199, ss196416201	NCBI: similar to Arabdopsis L-ascorbate peroxidase
3692	PCO134814		GRMZM2G055678	B73 RefGen_v3	Gene	Chr6	134643812	134656424	PCO134814	PCO134814, PZA00357, rs128283078, rs55623446 , ss196416437	
3693	PCO135705		GRMZM2G026892	B73 RefGen_v3	Gene	Chr5	23284770	23288690	PCO135705	PCO135705, PZA01427, rs131175667, ss196416043	
3694	pco135758		GRMZM2G045275	B73 RefGen_v3	Gene	Chr3	218979525	218985381	pco135758	pco135758(276), rs131175561	Targeted region of interest associated with flowering time (Jamann et al., 2017)
3695	pco136000		GRMZM2G104258	B73 RefGen_v3	Probed Site	Chr7	31785259	31790644	pco136000	PZA00132	
3696	pco136292		GRMZM2G047720	B73 RefGen_v3	Probed Site	Chr6	117286818	117288287	pco136292	pco136292(496), pza01589, rs128284646, rs55622263 , ss196416397	
3697	pco136491		GRMZM2G118917	B73 RefGen_v3	Probed Site	Chr1	238384036	238403459	pco136491	PZA00381	
3698	pco136495a		GRMZM2G451314	B73 RefGen_v3	Probed Site	Chr5	170458851	170463366	pco136495a	pco136495(428), PHM3568, PZA00255, rs131175702, ss196416195	
3699	pco137163		GRMZM2G049021	B73 RefGen_v3	Gene	Chr5	133656772	133665057	pco137163	Isochorismatase family protein, pco137163, pco137163(463)	
3700	pco137413a		GRMZM2G051917	B73 RefGen_v3	Probed Site	Chr2	1267102	1272359	pco137413a	pco137413(197), PHM5817, PZA00365, rs128281593, rs55623541 , ss196414925	
3701	pco138736		GRMZM2G061681	B73 RefGen_v3	Probed Site	Chr3	225532457	225540553	pco138736	PZA01360	
3702	pco139265		GRMZM2G180471	B73 RefGen_v3	Probed Site	Chr10	143089757	143102281	pco139265	pco139265(759), PZA00130, rs131176019, rs131176020, ss196417477, ss196417479	
3703	pco139551		GRMZM2G174315	B73 RefGen_v3	Probed Site	Chr6	118783891	118788430	pco139551	pco139551(497), PZA00382, rs131175753, ss196416399	
3704	pco140565		GRMZM2G701180	B73 RefGen_v3	Probed Site	Chr6	148827215	148832434	pco140565	pco140565(513), PZA01342, rs128282821, ss196416469	
3705	pco141133		GRMZM2G073535	B73 RefGen_v3	Probed Site	Chr6	156713541	156715788	pco141133	pco141133(519), PZA03027, rs131175770, ss196416479, TIDP3683	
3706	pco143498		GRMZM2G166082	B73 RefGen_v3	Probed Site	Chr5	14070028	14076354	pco143498	pco143498(382), PZA00985, rs129995806, rs55624977 , ss196416023	
3707	pco144235		GRMZM2G110381	B73 RefGen_v3	Probed Site	Chr10	13497213	13499095	pco144235	pco144235(719), PZA00463, rs128492024, rs55623299 , ss196417321	
3708	pco148373a		GRMZM2G004397	B73 RefGen_v3	Probed Site	Chr1	21464564	21467986	pco148373a	pco148373(10), PZA00425, rs128393174, rs55622808 , ss196414409	
3709	pco154872		GRMZM2G113720	B73 RefGen_v3	Probed Site	Chr8	70026829	70029429	pco154872	pco154872(595), PZA01257, rs130783454, rs55625276 , ss196416854	
3710	pcr1	protochlorophyllide reductase1	GRMZM2G084958	B73 RefGen_v3	Gene	Chr2	1463875	1465462	pcr1	Chl-, csu349(gfu), PCO151862, PCO151862(197), pcr1, protochlorophyllide reductase1, protochlorophyllide reductase A, rnypcr3, rny(pcr3), rny(pcr)c	leaf cDNA csu349 similar to plant protochlorophyllide reductase
3711	pdc1	pyruvate decarboxylase1	AC197705.4_FG001	B73 RefGen_v3	Gene	Chr8	117692828	117694964	pdc1	pdc1, pyruvate decarboxylase1, umc1172, umc212(pdc1)	cDNA and genomic clone, SSR UMC1163
3712	pdc2	pyruvate decarboxylase2	GRMZM2G038821	B73 RefGen_v3	Gene	Chr8	15550758	15554318	pdc2	CL1917_1, IDP18, Pdc-, pdc2, pyruvate decarboxylase2, umc213, umc213(pdc), wusl1042	cDNA available; gene-specific probe
3713	pdc3	pyruvate decarboxylase3	GRMZM2G087186	B73 RefGen_v3	Gene	Chr1	45517324	45520500	pdc3	Pdc-, pdc3, pyruvate decarboxylase3, PZA00081, umc214, umc214(pdc), umc214(pdc3), wusl1120	cDNA sequence, gene-specific probe
3714	pdh1	pyruvate dehydrogenase1	GRMZM2G361693	B73 RefGen_v3	Gene	Chr4	182908776	182913540	pdh1	E1 alpha, pdh1, PDH E1 alpha, pyruvate dehydrogenase1, umc1466	cDNA, SSR umc1466;
3715	pdh2	pyruvate dehydrogenase2	GRMZM2G043198	B73 RefGen_v3	Gene	Chr1	195433120	195449499	pdh2	E1 beta isoform, IDP438, PCO074087, pco074087(59), pdh2, PDH E1 beta, pyruvate dehydrogenase E1 component subunit beta	multi-copy, cDNA sequence
3716	pdh3	pyruvate dehydrogenase3	GRMZM2G097226	B73 RefGen_v3	Gene	Chr2	193226331	193233048	pdh3	CL1583_1d, pdh3, pdhE1b, pyruvate dehydrogenase3, pyruvate dehydrogenase E1 beta subunit isoform2	multi-copy family
3717	pdh4	pyruvate dehydrogenase4	GRMZM2G128121	B73 RefGen_v3	Gene	Chr7	135870838	135874027	pdh4	CL1583_1(566), CL1583_1e, pdh4, pyruvate dehydrogenase4, pyruvate dehydrogenase E1 beta subunit isoform 3	multi-copy,beta subunit
3718	pdi1	protein disulfide isomerase1	GRMZM2G091481	B73 RefGen_v3	Gene	Chr4	14877067	14881858	pdi1	pdi1, PDIL1-1, protein disulfide isomerase1, protein disulfide isomerase homolog, rs131434715, rs131434718, TIDP5666, uaz298, uaz298(gfu), umc1550, ZmPDIL1-1	single copy cDNA, SSR umc1550
3719	pdi10	protein disulfide isomerase10	GRMZM2G113629	B73 RefGen_v3	Gene	Chr2	50618990	50621060	pdi10	PCO103226, PCO103226(134), pdi10, PDIL5-2, ZmPDIL5-2	
3720	pdi11	protein disulfide isomerase11	GRMZM2G176443	B73 RefGen_v3	Gene	Chr10	117344580	117348113	pdi11	cl284_2(747), cl284_2b, pdi11, PDIL5-3, ZmPDIL5-3	
3721	pdi12	protein disulfide isomerase12	GRMZM2G067063	B73 RefGen_v3	Gene	Chr2	204369552	204379182	pdi12	csu78, PCO115735, PCO115735(178), pdi12, PDIL5-4, ZmPDIL5-4	
3722	pdi2	protein disulfide isomerase2	GRMZM2G163421	B73 RefGen_v3	Gene	Chr2	221208466	221212560	pdi2	pdi2, PDIL1-2, ZmPDIL1-2	
3723	pdi3	protein disulfide isomerase3	GRMZM2G134889	B73 RefGen_v3	Gene	Chr4	241788226	241794277	pdi3	PCO103373, PCO103373(369), pdi3, PDIL1-3, PDIL1-4, ZmPDIL1-3	
3724	pdi4	protein disulfide isomerase4	GRMZM2G033829	B73 RefGen_v3	Gene	Chr5	66062056	66073374	pdi4	pdi4, PDIL1-4, ZmPDIL1-4	
3725	pdi5	protein disulfide isomerase5	GRMZM2G014076	B73 RefGen_v3	Gene	Chr9	16724287	16729342	pdi5	CL33641_1, CL33641_1(660), pdi5, PDIL1-5, ZmPDIL1-5	

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
3726	pdi6	protein disulfide isomerase6	GRMZM2G128171	B73 RefGen_v3	Gene	Chr3	64460450	64464396	pdi6	pdi6, PDIL2-1, PDIL2-2, ZmPDIL2-1	
3727	pdi7	protein disulfide isomerase7	GRMZM2G159369	B73 RefGen_v3	Gene	Chr6	126962678	126967338	pdi7	pdi7, PDIL2-2, ZmPDIL2-2	
3728	pdi8	protein disulfide isomerase8	GRMZM2G389173	B73 RefGen_v3	Gene	Chr7	124417173	124422099	pdi8	CL286_2(563), CL286_2b, pdi8, ZmPDIL2-3	
3729	pdi9	protein disulfide isomerase9	GRMZM2G073628	B73 RefGen_v3	Gene	Chr1	44196096	44197753	pdi9	IDP349, IDP853, PCO130768, PCO130768(18), pdi9, PDIL5-1, ZmPDIL5-1	
3730	pdk1	pyruvate, orthophosphate dikinase1	GRMZM2G306345	B73 RefGen_v3	Gene	Chr6	146179404	146189965	pdk1	csu764a(pdk), csu979, CyPPDK1, cyppdkZm1, gnp_CYPPDK_011_PCR, gnp_QAW1b05, gnp_QCA5h09b, gpm410, gpm578b, IDP1630, mgh1b(pdk), mzePDKA, nc012, npi(pdk1),	cDNA, genomic and peptide sequences; microsatellite mapped (SSRs phi025, phi078, phi081; nc012); cytosolic or plastidic, dependent on transcript processing
3731	pdk2	pyruvate, orthophosphate dikinase2	GRMZM2G097457	B73 RefGen_v3	Gene	Chr8	106530187	106541083	pdk2	mgh1a(pdk), npi230, npi230-pdk2, npi300ppdkB, npi(pdk2), NPI(PPDKA), pAS11, pco068469(623), PCO068469(623), PCO068469b, pdk2, pyruvate, orthophosphate dikinase2,	cytosolic
3732	pdk3	phosphoinositide dependent protein kina	GRMZM2G097821	B73 RefGen_v3	Gene	Chr3	174102966	174108133	pdk3	3-phosphoinositide-dependent protein kinase 2-like, pdk3, pyruvate, orthophosphate dikinase3	
3733	pdk4	pyruvate, orthophosphate dikinase4	AC217975.3_FG001	B73 RefGen_v3	Gene	Chr7	168632072	168635401	pdk4	PDK2, pdk4, pdlk2, pyruvate dehydrogenase (lipoamide) kinase2	
3734	pdlk1	pyruvate dehydrogenase (lipoamide) kina	GRMZM2G107196	B73 RefGen_v3	Gene	Chr1	64007986	64013684	pdlk1	cl1702_1(27), cl1702_1a, pdlk1, pyruvate dehydrogenase kinase, pyruvate dehydrogenase (lipoamide) kinase1	
3735	pdlp1	plasmodesmatal located protein1	GRMZM2G066860	B73 RefGen_v3	Gene	Chr1	8877557	8880470	pdlp1	pdlp1	cDNA, plasmodesmata protein
3736	pdrp1	PDK regulatory protein1	GRMZM2G131286	B73 RefGen_v3	Gene	Chr2	204498422	204501387	pdrp1	pco142971, pdrp1, pdrp1(178), pyruvate Pi dikinase regulatory protein1	
3737	pebp1	phosphatidylethanolamine-binding protei	GRMZM2G092008	B73 RefGen_v3	Gene	Chr3	231199114	231200263	pebp1	CENTRORADIALIS-like, gpm255, pebp1, phosphatidylethanolamine-binding protein1, terminal flower 1, TFL1-like, zcn1	
3738	pebp10	phosphatidylethanolamine-binding protei	GRMZM2G152689	B73 RefGen_v3	Gene	Chr3	28400356	28402122	pebp10	CENTRORADIALIS-like, MFT-like, pebp10, phosphatidylethanolamine-binding protein10, zcn10	
3739	pebp11	phosphatidylethanolamine-binding protei	GRMZM2G117057	B73 RefGen_v3	Gene	Chr6	121720043	121721582	pebp11	CENTRORADIALIS-like, MFT-like, pebp11, phosphatidylethanolamine-binding protein11, zcn11	
3740	pebp12	phosphatidylethanolamine-binding protei	GRMZM2G103666	B73 RefGen_v3	Gene	Chr3	197706353	197708239	pebp12	CENTRORADIALIS-like, FT-like II, gnp_QBF6f06, gpm811, pebp12, phosphatidylethanolamine-binding protein12, zcn12	
3741	pebp13	phosphatidylethanolamine-binding protei	GRMZM2G108016	B73 RefGen_v3	Gene	Chr5	150036613	150037929	pebp13	CENTRORADIALIS-like, FT-like II, pebp13, phosphatidylethanolamine-binding protein13, zcn13	
3742	pebp14	phosphatidylethanolamine-binding protei	GRMZM2G373928	B73 RefGen_v3	Gene	Chr8	25338663	25347919	pebp14	CENTRORADIALIS-like, FT-like I, pebp14, phosphatidylethanolamine-binding protein, zcn14	
3743	pebp15	phosphatidylethanolamine-binding protei	GRMZM2G051338	B73 RefGen_v3	Gene	Chr6	76400211	76402023	pebp15	CENTRORADIALIS-like, CL846_1, CL846_1(512), FT-like I, pebp15, phosphatidylethanolamine-binding protein15, zcn15	
3744	pebp16	phosphatidylethanolamine-binding protei	GRMZM2G127121	B73 RefGen_v3	Gene	Chr5	181990493	181993244	pebp16	CENTRORADIALIS-like, FT-like I, pebp16, phosphatidylethanolamine-binding protein16, zcn16	
3745	pebp17	phosphatidylethanolamine-binding protei	GRMZM2G075215	B73 RefGen_v3	Gene	Chr2	120292154	120293853	pebp17	CENTRORADIALIS-like, FT-like I, pebp17, phosphatidylethanolamine-binding protein17, zcn17	
3746	pebp18	phosphatidylethanolamine-binding protei	GRMZM2G158809	B73 RefGen_v3	Gene	Chr2	193839589	193845094	pebp18	CENTRORADIALIS-like, FT-like I, pebp18, phosphatidylethanolamine-binding protein18, zcn18	
3747	pebp19	phosphatidylethanolamine-binding protei	GRMZM2G062052	B73 RefGen_v3	Gene	Chr10	126937360	126941217	pebp19	CENTRORADIALIS-like, FT-like I, pebp19, phosphatidylethanolamine-binding protein, zcn19	
3748	pebp2	phosphatidylethanolamine-binding protei	GRMZM2G156079	B73 RefGen_v3	Gene	Chr4	106696523	106697982	pebp2	CENTRORADIALIS-like, pebp2, phosphatidylethanolamine-binding protein2, TFL1-like, zcn2	
3749	pebp20	phosphatidylethanolamine-binding protei	AC214791.2_FG002	B73 RefGen_v3	Gene	Chr10	36388693	36389588	pebp20	pebp20, phosphatidylethanolamine-binding protein20, protein TWIN SISTER of FT, zcn20	
3750	pebp21	phosphatidylethanolamine-binding protei	GRMZM2G019993	B73 RefGen_v3	Gene	Chr2	74102888	74107552	pebp21	CENTRORADIALIS-like, FLOWERING LOCUS T-like, FT-like II, MADS-TF (ZCN21), pebp21, phosphatidylethanolamine-binding protein21, zcn21	
3751	pebp24	phosphatidylethanolamine-binding protei	GRMZM2G440005	B73 RefGen_v3	Gene	Chr7	138923902	138933246	pebp24	CENTRORADIALIS-like, FT-like I, pebp24, phosphatidylethanolamine-binding protein24, protein FLOWERING LOCUS T-like, zcn24	
3752	pebp25	phosphatidylethanolamine-binding protei	GRMZM2G021560	B73 RefGen_v3	Gene	Chr2	35895307	35898831	pebp25	CENTRORADIALIS-like, FT-like I, pebp25, phosphatidylethanolamine-binding protein25, zcn25	
3753	pebp26	phosphatidylethanolamine-binding protei	GRMZM2G400167	B73 RefGen_v3	Gene	Chr9	77335866	77339429	pebp26	CENTRORADIALIS-like, FT-like II, gnp_QCC6e03, gpm849, pebp26, phosphatidylethanolamine-binding protein26, zcn26	
3754	pebp3	phosphatidylethanolamine-binding protei	GRMZM2G338454	B73 RefGen_v3	Gene	Chr10	5465315	5465881	pebp3	CENTRORADIALIS-like, pebp3, phosphatidylethanolamine-binding protein3, TFL1-like, zcn3	
3755	pebp4	phosphatidylethanolamine-binding protei	GRMZM2G075081	B73 RefGen_v3	Gene	Chr2	58373992	58376007	pebp4	CENTRORADIALIS-like, pebp4, phosphatidylethanolamine-binding protein4, RCN4-like, TFL1-like, zcn4	
3756	pebp5	phosphatidylethanolamine-binding protei	AC217051.3_FG006	B73 RefGen_v3	Gene	Chr10	114050161	114051244	pebp5	CENTRORADIALIS-like, pebp5, phosphatidylethanolamine-binding protein, TFL1-like, zcn5, zea centroradialis1, zen1	
3757	pebp6	phosphatidylethanolamine-binding protei	GRMZM2G132880	B73 RefGen_v3	Gene	Chr4	188561914	188563106	pebp6	CENTRORADIALIS-like, pebp6, phosphatidylethanolamine-binding protein6, TFL1-like, zcn6	
3758	pebp7	phosphatidylethanolamine-binding protei	GRMZM2G141756	B73 RefGen_v3	Gene	Chr6	159399177	159400713	pebp7	CENTRORADIALIS-like, FT-like II, pebp7, phosphatidylethanolamine-binding protein7, zcn7	
3759	pebp8	phosphatidylethanolamine-binding protei	GRMZM2G179264	B73 RefGen_v3	Gene	Chr8	123030387	123032175	pebp8	CENTRORADIALIS-like, FT-like II, pebp8, phosphatidylethanolamine-binding protein8, vegetative to generative transition2, vgt2, zcn8, zea centroradialis8	florigen activity: complements Arabidopsis FT mutants, promoting flowering at short days. Requires functional id1 gene.(Lazakis et al 2011)
3760	pebp9	phosphatidylethanolamine-binding protei	GRMZM2G021614	B73 RefGen_v3	Gene	Chr8	8472799	8475229	pebp9	CENTRORADIALIS-like, MFT-like, pebp9, phosphatidylethanolamine-binding protein9, zcn9	
3761	pep1	phosphoenolpyruvate carboxylase1	GRMZM2G083841	B73 RefGen_v3	Gene	Chr9	62306266	62311673	pep1	csu905, csu975, csuh00905, csuh00975, IDP2529, npi332(pep), pep1, PEPC1, phi065, phosphoenolpyruvate carboxylase1, Ppc1	cytosolic C4 isozyme; single copy, similar to C3-PEPCase genes; cDNA complements E. coli mutant; genomic and partial amino acid sequences compare; SSR phi065
3762	pep2	phosphoenolpyruvate carboxylase2	GRMZM2G069542	B73 RefGen_v3	Gene	Chr5	144847481	144855080	pep2	CL1793_1, gsy34b(pep), npi(pmr15), pep2, pep6*-, pep7, pep8, Pepb, PEPC, pepcZm2A, pep*-pepcZm2A, phosphoenolpyruvate carboxylase2, pMR15, Ppc1, Ppc1C	cDNA sequence, encodes C3 enzyme in roots (Northern blot analysis)
3763	pep3	phosphoenolpyruvate carboxylase3	GRMZM2G074122	B73 RefGen_v3	Gene	Chr4	227807369	227818655	pep3	gsy34a(pep) , IDP1621, pep3, Pepa, phosphoenolpyruvate carboxylase3, pMR15	possibly duplicate gene; both pep2 and pep3 hybridize to a C3 PEPCase isozyme genomic probe, p-H1(lambda)22 and to root PEPCase cDNA.
3764	pep4	phosphoenolpyruvate carboxylase4	GRMZM2G473001	B73 RefGen_v3	Gene	Chr7	86459173	86464913	pep4	gnp_QAN24f10, gnp_QCH5g04, gpm372, gpm879, pep4, PepC2, phosphoenolpyruvate carboxylase4, Ppc-, six61489, six61489(466)	cDNA for anaplerotic C3 isozyme; gene specific cDNA probe;
3765	pet2	photosynthetic electron transport2	GRMZM2G087063	B73 RefGen_v3	Gene	Chr1	80629933	80632693	pet2	LOC100194324, MAGI_114073, pet2, photosynthetic electron transport2, TIDP5737, ZmHcf208	lacks cytochrome bf polypeptides. Ortholog of Arabidopsis HCF208 and Chlamydomonas CCB2. Cyt b6 heme attachment factor. (A. Barkan, 2015)
3766	pet3	photosynthetic electron transport3	GRMZM2G177145	B73 RefGen_v3	Gene	Chr2	5103401	5103769	pet3	hcf6, pet3, photosynthetic electron transport3, protein COFACTOR ASSEMBLY OF COMPLEX C SUBUNIT B CCB4, chloroplastic	assembly. (A. Barkan, 2015). This gene creates a product required for cytochrome b6f accumulation. Mu tagging and cloning finds this loci to be gene model GRMZM2G177145,
3767	pex1	pollen extensin-like1	GRMZM5G841015	B73 RefGen_v3	Gene	Chr2	231055349	231059232	pex1	CL844_2, fco1a(pex), fco1b(pex), mPex1, pex1, pollen extensin-like1	clone specifies repeat motif ser-pro4
3768	pex2	pollen extensin-like2	GRMZM2G478929	B73 RefGen_v3	Gene	Chr4	3413177	3413824	pex2	CL844_1, CL844_1(287), pex2, pollen extensin-like2, pollen-specific leucine-rich repeat extensin-like protein 3	clone like pex1
3769	pfk1	phosphofructose kinase1	GRMZM2G059151	B73 RefGen_v3	Gene	Chr6	115372536	115378936	pfk1	CL46_1, pfk1, phosphofructose kinase1, uaz7c02a06(gfu)	vegetative meristem cDNA 7C02A06
3770	pfk2	phosphofructose kinase2	GRMZM2G450163	B73 RefGen_v3	Gene	Chr1	221791929	221796752	pfk2	pfk2	
3771	pgd1	6-phosphogluconate dehydrogenase1	GRMZM2G127798	B73 RefGen_v3	Gene	Chr6	57903596	57906292	pgd1	6-phosphogluconate dehydrogenase1, csu262, csu262(gfu), PCO144547, pco144547(475), pdh2, pgd1, pgd2 6-phosphogluconate dehydrogenase 2, pgd*-csu262	electrophoretic mobility, null alleles occur; cytosolic; dimeric, intra/interlocus hybrid bands occur; cDNA csu262 single copy
3772	pgd2	6-phosphogluconate dehydrogenase2	GRMZM2G145715	B73 RefGen_v3	Gene	Chr3	153964271	153968156	pgd2	6-phosphogluconate dehydrogenase2, csu262, pdh1, pdh1 NADPH producing dehydrogenase of the oxidative pentose phosphate pathway, pgd2	electrophoretic mobility, null allele is known; cytosolic; dimeric; intra/interlocus hybrid bands occur; cDNA probe
3773	pgd3	phosphogluconate dehydrogenase3	GRMZM2G440208	B73 RefGen_v3	Gene	Chr4	18596164	18598086	pgd3	gnp_AI745985, gpm76, pco126621(294), PCO126621a, pgd3, phosphogluconate dehydrogenase3, rgh5	single copy cDNA, csu843, similar to alfalfa enzyme; pentose phosphate pathway
3774	pgl1	exopolygalacturonase1	GRMZM2G094811	B73 RefGen_v3	Gene	Chr6	99520235	99522243	pgl1	exopolygalacturonase1, exopolygalacturonase-like, PG1, Pga2, pgl1	cDNA clone nearly identical but distinct from other pgl reading frames of inbred Mo17, sequence match to N-terminal sequence of maize exopolygalacturonase

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
3775	pgl2	polygalacturonase2	GRMZM2G320175	B73 RefGen_v3	Gene	Chr6	99582016	99584295	pgl2	PG2, Pga2, pgl2, pgl*X62385, polygalacturonase2	cDNA and genomic clones, sequence nearly identical to pgl1; one of 10-12 member gene family
3776	pgl7	exopolygalacturonase7	GRMZM2G160526	B73 RefGen_v3	Gene	Chr6	99103865	99105564	pgl7	exopolygalacturonase7, Pga2, PGg2C, PGg6, pgl7, pgl*X66422, Zea m 13 allergen	genomic clone, open reading frames nearly identical to pgl1 but distinct 3' non-coding sequence
3777	pgl8	exopolygalacturonase8	GRMZM2G394259	B73 RefGen_v3	Gene	Chr6	99529941	99532218	pgl8	exopolygalacturonase8, Pga2, PGg9, pgl8	genomic clone, open reading frame nearly identical to pgl1 but distinct 3' non-coding sequence; mRNA product confirmed by PCR
3778	pgm1	phosphoglucomutase1	GRMZM2G023289	B73 RefGen_v3	Gene	Chr1	267953427	267960205	pgm1	cl1708_1(88), CL1708_1a, pgm1, phosphoglucomutase1	electrophoretic mobility; null allele is known; cytosolic; monomeric
3779	pgm2	phosphoglucomutase2	GRMZM2G109383	B73 RefGen_v3	Gene	Chr5	10865997	10872126	pgm2	cl1708_1(380), cl1708_1b, pgm2, phosphoglucomutase2	electrophoretic mobility; null allele is known; cytosolic; monomeric
3780	pgr3	proton gradient regulation3 homolog	GRMZM2G372632	B73 RefGen_v3	Gene	Chr9	124424696	124428135	pgr3	crp17, pentatricopeptide repeat-containing protein At4g31850, chloroplastic-like, pgr3, proton gradient regulation3 homolog	required for NDH accumulation. Additional functions in maize, with more global effect on accumulation of cp complexes.. Ortholog of Arabidopsis PGR3. Chloroplast PPR protein that
3781	phb1	prohibitin1	GRMZM2G134955	B73 RefGen_v3	Gene	Chr2	171554524	171555173	phb1	CL123_1, CL123_1(159), mitochondrial prohibitin complex protein 2 , phb1, prohibitin1, Zm-phb1	cDNA sequence
3782	phb2	prohibitin2	GRMZM2G107114	B73 RefGen_v3	Gene	Chr10	123209142	123210706	phb2	PCO132416, PCO132416(750), phb2, prohibitin2, Zm-phb2	cDNA
3783	phb3	prohibitin3	GRMZM2G410710	B73 RefGen_v3	Gene	Chr5	177870707	177873657	phb3	mitochondrial prohibitin complex protein 1, PCO060271, phb3, prohibitin3, Zm-phb3	cDNA sequence
3784	phb4	prohibitin4	AC217358.3_FG005	B73 RefGen_v3	Gene	Chr1	296971341	296973619	phb4	mitochondrial prohibitin complex protein 2, PCO099135, PCO099135(106), phb4, prohibitin4, PZA00243, rs128283600, rs55626482 , ss196414905, Zm-phb4	cDNA
3785	phd1	PHD-transcription factor 1	GRMZM2G039895	B73 RefGen_v3	Gene	Chr6	1537642	1541643	phd1		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3786	phd10	PHD-transcription factor 10	GRMZM2G335720	B73 RefGen_v3	Gene	Chr8	136676466	136698927	phd10		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3787	phd11	PHD-transcription factor 11	GRMZM2G408897	B73 RefGen_v3	Gene	Chr5	10447338	10450616	phd11		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3788	phd12	PHD-transcription factor 12	GRMZM2G455664	B73 RefGen_v3	Gene	Chr6	27533651	27548861	phd12		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3789	phd13	PHD-transcription factor 13	GRMZM2G059266	B73 RefGen_v3	Gene	Chr4	40387081	40391160	phd13		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3790	phd14	PHD-transcription factor 14	GRMZM2G178072	B73 RefGen_v3	Gene	Chr9	152453261	152461059	phd14		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3791	phd15	PHD-transcription factor 15	GRMZM2G173852	B73 RefGen_v3	Gene	Chr1	276041856	276051331	phd15		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3792	phd16	PHD-transcription factor 16	GRMZM2G168249	B73 RefGen_v3	Gene	Chr6	107265910	107274437	phd16		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3793	phd17	PHD-transcription factor 17	GRMZM2G155123	B73 RefGen_v3	Gene	Chr8	131105649	131117697	phd17		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3794	phd18	PHD-transcription factor 18	GRMZM2G443565	B73 RefGen_v3	Gene	Chr10	4449604	4458482	phd18		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3795	phd19	PHD-transcription factor 19	GRMZM2G412492	B73 RefGen_v3	Gene	Chr7	8831484	8837242	phd19		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3796	phd2	PHD-transcription factor 2	GRMZM2G119357	B73 RefGen_v3	Gene	Chr1	216523958	216531563	phd2		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3797	phd20	PHD-transcription factor 20	GRMZM5G843893	B73 RefGen_v3	Gene	Chr8	1903989	1908431	phd20		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3798	phd21	PHD-transcription factor 21	GRMZM2G156129	B73 RefGen_v3	Gene	Chr9	29170751	29171909	phd21		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3799	phd22	PHD-transcription factor 22	GRMZM2G045544	B73 RefGen_v3	Gene	Chr5	203702356	203707024	phd22		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3800	phd23	PHD-transcription factor 23	GRMZM2G103230	B73 RefGen_v3	Gene	Chr6	58423170	58430307	phd23		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3801	phd24	PHD-transcription factor 24	GRMZM2G434715	B73 RefGen_v3	Gene	Chr7	174811135	174819968	phd24		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3802	phd25	PHD-transcription factor 25	GRMZM2G087482	B73 RefGen_v3	Gene	Chr5	7451874	7467413	phd25		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3803	phd26	PHD-transcription factor 26	GRMZM2G316191	B73 RefGen_v3	Gene	Chr7	150195961	150215431	phd26		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3804	phd27	PHD-transcription factor 27	GRMZM2G071613	B73 RefGen_v3	Gene	Chr9	36768420	36771264	phd27		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3805	phd28	PHD-transcription factor 28	GRMZM2G068331	B73 RefGen_v3	Gene	Chr4	10235511	10240157	phd28		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3806	phd29	PHD-transcription factor 29	GRMZM2G466270	B73 RefGen_v3	Gene	Chr5	65470804	65484230	phd29		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3807	phd3	PHD-transcription factor 3	GRMZM2G097726	B73 RefGen_v3	Gene	Chr7	13356454	13364295	phd3		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3808	phd30	PHD-transcription factor 30	GRMZM2G091265	B73 RefGen_v3	Gene	Chr7	105935513	105940065	phd30		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3809	phd31	PHD-transcription factor 31	GRMZM2G181158	B73 RefGen_v3	Gene	Chr2	201783834	201787692	phd31		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3810	phd32	PHD-transcription factor 32	GRMZM2G134214	B73 RefGen_v3	Gene	Chr6	54934854	54944793	phd32		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3811	phd33	PHD-transcription factor 33	GRMZM5G871463	B73 RefGen_v3	Gene	Chr4	79026612	79032492	phd33		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3812	phd34	PHD-transcription factor 34	GRMZM2G158194	B73 RefGen_v3	Gene	Chr3	9045175	9047443	phd34		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3813	phd35	PHD-transcription factor 35	GRMZM5G813111	B73 RefGen_v3	Gene	Chr1	276177130	276182727	phd35		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3814	phd36	PHD-transcription factor 36	GRMZM5G889372	B73 RefGen_v3	Gene	Chr9	136728879	136733895	phd36		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3815	phd38	PHD-transcription factor 38	GRMZM2G473258	B73 RefGen_v3	Gene	Chr6	94679099	94681569	phd38		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3816	phd39	PHD-transcription factor 39	GRMZM2G385338	B73 RefGen_v3	Gene	Chr4	234727096	234739242	phd39		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3817	phd4	PHD-transcription factor 4	GRMZM2G365888	B73 RefGen_v3	Gene	Chr10	27274598	27281804	phd4		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3818	phd40	PHD-transcription factor 40	GRMZM2G081350	B73 RefGen_v3	Gene	Chr3	133770585	133777342	phd40		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3819	phd41	PHD-transcription factor 41	GRMZM2G013794	B73 RefGen_v3	Gene	Chr7	72261177	72305728	phd41		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3820	phd42	PHD-transcription factor 42	GRMZM2G149587	B73 RefGen_v3	Gene	Chr8	156446973	156452761	phd42		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3821	phd43	PHD-transcription factor 43	GRMZM2G025703	B73 RefGen_v3	Gene	Chr3	171075200	171078825	phd43		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3822	phd5	PHD-transcription factor 5	GRMZM2G391413	B73 RefGen_v3	Gene	Chr4	239865653	239878509	phd5		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3823	phd6	PHD-transcription factor 6	GRMZM2G022945	B73 RefGen_v3	Gene	Chr1	48527429	48531044	phd6		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
3824	phd7	PHD-transcription factor 7	GRMZM2G305124	B73 RefGen_v3	Gene	Chr5	71873816	71875082	phd7		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3825	phd8	PHD-transcription factor 8	GRMZM2G038050	B73 RefGen_v3	Gene	Chr10	148985897	148996435	phd8		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3826	phd9	PHD-transcription factor 9	GRMZM2G073581	B73 RefGen_v3	Gene	Chr10	141102389	141111678	phd9		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3827	phi002		GRMZM2G346455	B73 RefGen_v3	Gene	Chr1	228306620	228318304	phi002	phi002	
3828	phi1	phosphohexose isomerase1	GRMZM2G065083	B73 RefGen_v3	Gene	Chr1	283156653	283159112	phi1	glucose-6-phosphate isomerase, cytosolic B , phi1, phosphohexose isomerase1, pza03020, uiu1a(phi)	electrophoretic mobility; null allele is known; cytosolic; dimeric; intralocus hybrid bands occur; cDNA clone pGPI1a (Lal & Sachs, 1995)
3829	phm10525		GRMZM2G380515	B73 RefGen_v3	Gene	Chr8	125606805	125613287	phm10525	rs131175879, ss196416928	
3830	phm13360		GRMZM2G069773	B73 RefGen_v3	Gene	Chr2	111452832	111456698	phm13360	PZA00291, rs128284468, rs55626558 , ss196415112	
3831	phm13823		GRMZM2G022088	B73 RefGen_v3	Gene	Chr3	40318889	40324047	phm13823	PZA00297, rs131175491, ss196415360	
3832	phm15278		GRMZM2G067601	B73 RefGen_v3	Gene	Chr8	156263468	156265092	phm15278	PHM1668, rs131175895, ss196417008	
3833	phm1558		GRMZM2G098800	B73 RefGen_v3	Gene	Chr4	153223584	153226721	phm1558	PZA02411	
3834	phm15899		GRMZM2G003883	B73 RefGen_v3	Gene	Chr3	44224072	44229612	phm15899	PZA03070, rs128284912, ss196415370	
3835	phm1675		GRMZM2G096470	B73 RefGen_v3	Gene	Chr3	182131706	182144018	phm1675	PZA00107, rs131175532, ss196415548	
3836	phm1959		GRMZM2G080917	B73 RefGen_v3	Gene	Chr3	170149613	170154226	phm1959	PZA03073	
3837	phm229		GRMZM2G472428	B73 RefGen_v3	Gene	Chr9	30063256	30088418	phm229	rs131175938, ss196417156	
3838	phm2343		GRMZM2G076104	B73 RefGen_v3	Gene	Chr3	28334298	28336773	phm2343	PZA01880, rs129362782, ss196415347	
3839	phm3226		GRMZM2G119104	B73 RefGen_v3	Gene	Chr1	22583820	22595788	phm3226	PZA02487, rs131175261, ss196414413	
3840	phm3342		GRMZM2G041015	B73 RefGen_v3	Gene	Chr3	217773782	217777054	phm3342	PZA01154, rs131175560, ss196415637	
3841	phm3457		GRMZM2G023020	B73 RefGen_v3	Gene	Chr2	63554418	63558011	phm3457	PZA02881, rs129081422, rs55626669 , ss196415090	
3842	phm4341		GRMZM2G072337	B73 RefGen_v3	Gene	Chr10	117586271	117590284	phm4341	PZA01089	
3843	phm4353		GRMZM2G092129	B73 RefGen_v3	Gene	Chr7	34183685	34198384	phm4353	PZA00260, rs131615517, ss196416576	
3844	phm4880		GRMZM2G325762	B73 RefGen_v3	Gene	Chr2	107818821	107820874	phm4880	PZA02549	
3845	phm532		GRMZM2G112247	B73 RefGen_v3	Gene	Chr5	193782893	193784506	phm532	PZA03050, rs131175717, rs131175718, ss196416253, ss196416255	
3846	phm5822		GRMZM2G345667	B73 RefGen_v3	Gene	Chr2	10522351	10526336	phm5822	EMB2217, pentatricopeptide repeat-containing protein At1g79490, mitochondrial-like, PZA00620, rs128284983, rs55624097 , ss196414990, ZmPPR090	
3847	phm662		GRMZM2G313481	B73 RefGen_v3	Gene	Chr5	1045283	1050017	phm662	rs131175734, ss196416309	
3848	phm8909		GRMZM2G110408	B73 RefGen_v3	Gene	Chr9	110677553	110681978	phm8909	PZA00152	
3849	phm9695		GRMZM2G156713	B73 RefGen_v3	Gene	Chr8	12285354	12288966	phm9695	PZA02249, rs131175843, rs131175844, ss196416799, ss196416802	
3850	phm9914		GRMZM2G140107	B73 RefGen_v3	Gene	Chr3	161295516	161301138	phm9914	PZA02126, rs129419287, ss196415489	
3851	pho1	starch phosphorylase1	GRMZM2G074158	B73 RefGen_v3	Gene	Chr1	278250612	278259617	pho1	gnp_QCO10e08, gpm718, PCO070449, pho1, umc1774	amyloplast starch phosphorylase
3852	pho2	starch phoshorylase2	GRMZM2G085577	B73 RefGen_v3	Gene	Chr3	179031418	179040320	pho2	gnp_QAE15d08, gpm274, PCO093963, PCO093963(250)	cytosolic starch phosphorylase inferred from data in Yu et al 2001 (MS 2015)
3853	phos1	phosphate transporter1	GRMZM5G891944	B73 RefGen_v3	Gene	Chr3	28919073	28923612	phos1	phos1, ZmPHO1, ZmPho1;1	
3854	phos2	phosphate transporter2	GRMZM2G466545	B73 RefGen_v3	Gene	Chr4	171946555	171952268	phos2	phos2, phosphate transporter PHO1-2-like, ZmPHO1, ZmPho1;2a	
3855	phos3	phosphate transporter3	GRMZM5G851655	B73 RefGen_v3	Gene	Chr5	215112901	215114452	phos3	GRMZM2G058444, phos3, phosphate transporter PHO1-2-like, ZmPHO1, ZmPho1;2b	
3856	phos4	phosphate transporter4	GRMZM2G064657	B73 RefGen_v3	Gene	Chr6	122577593	122582074	phos4	phos4, phosphate transporter PHO1-3-like, ZmPHO1, ZmPho1;3	
3857	phot1	blue-light receptor phototropin 1	GRMZM2G001457	B73 RefGen_v3	Gene	Chr3	229220592	229241592	phot1	blue-light receptor phototropin 1, CL1834_1, nonphototropic hypocotyl 1 (nph1) , NPH, nph1, phot1, umc1062, ZmPHOT1	cDNA sequence similar to Arabidopsis NPH1, (GenBank AF039864, AF053941) protein involved in phototropism; SSR umc1062
3858	phot2	blue-light receptor phototropin 2	GRMZM2G032351	B73 RefGen_v3	Gene	Chr1	220359597	220392126	phot2	phot2, phototropin-1, ZmPHOT2	
3859	php20075a(gast)		GRMZM2G172596	B73 RefGen_v3	Gene	Chr10	2649738	2651194	php20075a(ga	GAST1 protein, phi20075a, php20075a, php20075a(gast), pio200075a, pio20075a	NCBI: GAST1 protein
3860	php20537b		GRMZM2G089056	B73 RefGen_v3	Gene	Chr1	6914659	6919235	php20537b	ss196503179 , ss196503184 , ss196503186 , ss196503193 , ss196503197 , ufg31, ufg32, ufg33, ufg34	
3861	php20603		GRMZM2G172751	B73 RefGen_v3	Gene	Chr1	8533004	8536769	php20603	php20603, pio200603	
3862	php20608a		GRMZM2G101818	B73 RefGen_v3	Gene	Chr4	237244514	237245531	php20608a	pco106324, pco106324(362), php20608, php20608a, pio200608	
3863	php20725a		GRMZM2G076435	B73 RefGen_v3	Gene	Chr4	5044212	5046753	php20725a	php20725a, php20725a(ext), pio200725	NCBI: plant viral-response family protein
3864	phs1	poor homologous synapsis1	GRMZM2G100103	B73 RefGen_v3	Gene	Chr9	52042688	52059619	phs1	asy498, desynaptic 498, dsy498, phs1, poor homologous synapsis1	affects homology search
3865	pht1	phosphate transporter protein1	GRMZM2G326707	B73 RefGen_v3	Gene	Chr5	31900810	31903008	pht1	phosphate transporter 4, pht1, Pht1;2, Pht1;4, pt1, ZmPHT1;1	
3866	pht10	phosphate transporter protein10	GRMZM2G075870	B73 RefGen_v3	Gene	Chr1	8032558	8034556	pht10	pht10, ZmPHT1;7, Zmpt7	
3867	pht11	phosphate transporter protein11	GRMZM2G139639	B73 RefGen_v3	Gene	Chr7	34937541	34939375	pht11	pht11, ZmPHT1;2, Zmpt2	
3868	pht12	phosphate transporter protein12	GRMZM2G009800	B73 RefGen_v3	Gene	Chr2	99926376	99930029	pht12	pht12, Pht1;2, ZmPHT1;12, Zmpt12	
3869	pht13	phosphate transporter protein13	GRMZM2G170208	B73 RefGen_v3	Gene	Chr2	99805638	99807544	pht13	pht13, ZmPHT1;4, Zmpt4	
3870	pht2	phosphate transporter protein2	GRMZM2G154090	B73 RefGen_v3	Gene	Chr1	236840157	236842176	pht2	Pht1;1, pht2, pt2, PT2, ZmPHT1;9, Zmpt9	
3871	pht3	phosphate transporter protein3	GRMZM2G045473	B73 RefGen_v3	Gene	Chr2	99381968	99383837	pht3	pht3, PT3, ZmPHT1;8, Zmpt8	
3872	pht4	phosphate transporter protein4	GRMZM2G159075	B73 RefGen_v3	Gene	Chr10	100011935	100014106	pht4	pht4, pt4, ZmPHT1;10, Zmpt10	

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
3873	pht5	phosphate transporter protein5	GRMZM2G041595	B73 RefGen_v3	Gene	Chr7	172022758	172024519	pht5	Pht1;5, pht5, ZmPHT1;5, Zmpt5	
3874	pht6	phosphate transporter protein6	GRMZM5G881088	B73 RefGen_v3	Gene	Chr8	147629397	147631460	pht6	pht1-6, Pht1;6, pht6, ZmPHT1;6, Zmpt6	
3875	pht7	phosphate transporter protein7	GRMZM2G112377	B73 RefGen_v3	Gene	Chr1	202585823	202587997	pht7	Pht1;3, pht7, ZmPHT1;3, Zmpt3	
3876	pht8	phosphate transporter protein8	GRMZM2G009779	B73 RefGen_v3	Gene	Chr2	99885266	99886925	pht8	pht8, ZmPHT1;11, Zmpt11	
3877	pht9	phosphate transporter protein9	GRMZM2G070087	B73 RefGen_v3	Gene	Chr1	11209543	11211528	pht9	pht9, ZmPHT1;13, Zmpt13	
3878	phyA1	phytochromeA1	GRMZM2G157727	B73 RefGen_v3	Gene	Chr1	269388274	269395277	phyA1	npi251(phy), npi251-Phy1, pco126085, pco126085(88), phy1, phyA1, phytochromeA1, PZB00895, rs128284664, rz912a(phy), ss196414783	and mesocotyl under dark light conditions; is greatly reduced in white or red light. See also phyA2, phyB1, phyB2, phyC1, phyC2.
3879	phyA2	phytochromeA2	GRMZM2G181028	B73 RefGen_v3	Gene	Chr5	10111505	10117216	phyA2	npi369(phy), phy2, phyA1, phyA2, rz912b(phy)	red/far red light signal receptor; minor phytochrome A trancript in dark grown seedling leaf blade, sheath, mesocotyl. See also phyA1, phyB1, phyB2, phyC1, phyC2
3880	phyB1	phytochromeB1	GRMZM2G124532	B73 RefGen_v3	Gene	Chr1	50023180	50034523	phyB1	pge, pge(phyB1), phyB1	narrow with elongated leaf blades, elongated internodes, less anthocyanin in sheath tissues, and earlier flowering time.
3881	phyB2	phytochromeB2	GRMZM2G092174	B73 RefGen_v3	Gene	Chr9	135245567	135251882	phyB2	pge, pge(phyB2), phyB2	phyB2 mutant is early flowering. Double mutant with phyB1 is pale, narrow with elongated leaf blades and elongated internodes, and contains less anthocyanin in sheath tissues.
3882	phyC1	phytochromeC1	GRMZM2G057935	B73 RefGen_v3	Gene	Chr1	277059620	277064623	phyC1	phyC1, phytochrome C, phytochrome C1	red/far red light signal receptor; major phytochrome C trancript in light and dark grown seedling leaf blade, sheath, mesocotyl. See also phyC2, phyA1, phyA2 phyB1, phyB2.
3883	phyC2	phytochromeC2	GRMZM2G129889	B73 RefGen_v3	Gene	Chr5	7129937	7134953	phyC2	phyC2, phytochrome C, phytochrome C2	red/far red light signal receptor; minor phytochrome C transcript in seedling leaf blade, sheath, mesocotyl. See also phyC1, phyA1, phyA2 phyB1, phyB2.
3884	phys1	phytase1	GRMZM2G140101	B73 RefGen_v3	Gene	Chr3	131730020	131731520	phys1	CL1547_1, phy I, phys1, phyS11, phy S11, phys1a, PHYT1, phytase1	cDNA sequence, correspondence with N-terminal amino acid sequence, expressed in E. coli; adjacent duplicate phys2 (Maugenest, 1997)
3885	phys2	phytase2	GRMZM2G043336	B73 RefGen_v3	Gene	Chr3	132181945	132183468	phys2	Phy II, phys2, phytase2, PHYT II, umc1158	cDNA sequence, correspondence with N-terminal amino acid sequence, expressed in E. coli; adjacent duplicate phys1
3886	pif3	phytochrome interacting factor3	GRMZM2G387528	B73 RefGen_v3	Gene	Chr8	935667	938714	pif3	bhlh65, bHLH-transcription factor 65, helix-loop-helix DNA-binding domain, phytochrome interacting factor3, pif3, ZmPi3f.2	ortholog of Arabidopsis PIF3; nuclear localized protein; transgenic expression in rice suggest role in stress response (Gao Y et al 2015)
3887	piip1	physical impedance induced protein1	AC234161.1_FG001	B73 RefGen_v3	Gene	Chr9	117425596	117425985	piip1	IIG1, PCO121733, physical impedance induced protein1, piip1, Zea root protein3, zrp3	piip1 mRNA transcript levels increase several fold in root cortical cells and protocambium 10 minutes after impedance stress; cDNA shows 97% similarity at the nucleotide level with zrp3;
3888	piip2	physical impedance induced protein2	GRMZM2G300135	B73 RefGen_v3	Gene	Chr5	61702710	61706176	piip2	CL1744_1, IIG2, physical impedance induced protein2, piip2	
3889	pin1	PIN-formed protein1	GRMZM2G098643	B73 RefGen_v3	Gene	Chr9	3650989	3654397	pin1	cl464_3(649), cl464_3c, pin1, PIN-formed protein1, rs130951864, rs131691606, ZmPIN, ZmPIN1a	gene product cross-reacts with anti-AtPIN1 antibody and in tassel and ear, the PIN proteins are localized to a group of cells in subepidermal meristematic layers.
3890	pin10	PIN-formed protein10	GRMZM2G126260	B73 RefGen_v3	Gene	Chr3	214980803	214985892	pin10	pin10, ZmPIN10a	similar to Arabidopsis PIN10 (Forestan et al 2012)
3891	pin11	PIN-formed protein11	GRMZM2G040911	B73 RefGen_v3	Gene	Chr2	192510578	192514240	pin11	pin11, ZmPIN5c	similar to Arabiodopsis PIN5 (Forestan et al 2012)
3892	pin12	PIN-formed protein12	GRMZM2G160496	B73 RefGen_v3	Gene	Chr9	16732113	16734511	pin12	PIN10b putative auxin efflux carrier component 3b, TIDP4653, ZmPIN10b	similar to Arabidopsis PIN10 (Forestan et al 2012)
3893	pin14	PIN-formed protein14	GRMZM2G050089	B73 RefGen_v3	Gene	Chr3	185812392	185817191	pin14	PINY putative auxin efflux carrier-like protein PINY, TIDP8880, ZmPINY	similar to PIN-formed proteins (Forestan et al 2012)
3894	pin15	PIN-formed protein15	GRMZM2G403601	B73 RefGen_v3	Gene	Chr3	20120984	20121889	pin15	pin15	similar to rice OsPIN1b and OsPIN1d
3895	pin2	PIN-formed protein2	GRMZM2G074267	B73 RefGen_v3	Gene	Chr5	206777162	206780578	pin2	auxin efflux carrier component, PCO072074(449), PCO072074c, pco136059, pco136059(449), PIN1b, pin2, PIN-formed protein 2, ZmPIN1b	see pin1
3896	pin3	PIN-formed protein3	GRMZM2G149184	B73 RefGen_v3	Gene	Chr4	182180280	182183396	pin3	auxin efflux carrier component 1-like, pco072074(334), pin3, ZmPIN1c	
3897	pin4	PIN-formed protein4	GRMZM2G171702	B73 RefGen_v3	Gene	Chr4	186818289	186821067	pin4	pin4 , pin4 cl464_-1, pin4 cl464_-1(336), sister of pin1, ZmPIN1d, ZmSoPIN1	auxin efflux carriter similar to Arabidopsis PIN1 (Forestan et al 2012), but from PIN clade not found in all flowering plants save for the Brassicacease (O'Connor 2014 et al
3898	pin5	PIN-formed protein5	GRMZM2G025742	B73 RefGen_v3	Gene	Chr3	160795816	160799946	pin5	pin5, ZmPIN5a	similar to Arabiodopsis PIN5 (Forestan et al 2012)
3899	pin7	PIN-formed protein7	GRMZM2G148648	B73 RefGen_v3	Gene	Chr1	193487892	193489699	pin7	pin7, probable auxin efflux carrier component 4, ZmPIN5b	simlar to Arabiodopsis PIN5 (Forestan et al 2012)
3900	pin8	PIN-formed protein8	GRMZM5G839411	B73 RefGen_v3	Gene	Chr3	203002580	203005107	pin8	gnp_QCN1e04, gpm700, pin8, ZmPIN8	similar to Arabidopsis PIN8 (Forestan et al 2012)
3901	pin9	PIN-formed protein9	GRMZM5G859099	B73 RefGen_v3	Gene	Chr3	187868057	187871142	pin9	pin9, TIDP5769, ZmPIN9	similar to Arabidopsis PIN9 (Forestan et al 2012)
3902	pip1a	plasma membrane intrinsic protein1	GRMZM2G174807	B73 RefGen_v3	Gene	Chr2	18757671	18759694	pip1a	inra1, inra1(tmp), PIP1-1, pip1a, plasma membrane intrinsic protein1, tmp, ZmPIP1;1, ZmPIP1a	
3903	pip1b	plasma membrane intrinsic protein1	AC209208.3_FG002	B73 RefGen_v3	Gene	Chr5	193359341	193362190	pip1b	aquaporin PIP1.1, pip1-2, PIP1;2, pip1b, plasma membrane intrinsic protein1, ZmPIP1;2, ZmPIP1b	
3904	pip1c	plasma membrane intrinsic protein1	GRMZM2G392975	B73 RefGen_v3	Gene	Chr4	153654423	153658268	pip1c	pip1c, plasma membrane intrinsic protein1, ZmPIP1-3, ZmPIP1;3	Differs in nucleotide sequence from pip1d but encodes the same protein.
3905	pip1d	plasma membrane intrinsic protein1	GRMZM2G392975	B73 RefGen_v3	Gene	Chr4	153654423	153658268	pip1d	IDP251, IDP410, pip1c, pip1d, plasma membrane intrinsic protein1, ZmPIP1-3, ZmPIP1;3, ZmPIP1-4, ZmPIP1;4	differs in nucleotide sequence from pip1c but encodes the same protein.
3906	pip1e	plasma membrane intrinsic protein1	GRMZM2G081843	B73 RefGen_v3	Gene	Chr4	170004633	170006133	pip1e	PCO112712, pco112712(328), PCO112712(328), pip1e, pip4, plasma membrane intrinsic protein1, ZmPIP1-5, ZmPIP1;5	
3907	pip1f	plasma membrane intrinsic protein1	GRMZM2G136032	B73 RefGen_v3	Gene	Chr9	6467685	6469385	pip1f	aquaporin PIP1-6, pip1f, plasma membrane intrinsic protein1, ZmPIP1-6, ZmPIP1;6	
3908	pip2a	plasma membrane intrinsic protein2	GRMZM2G178693	B73 RefGen_v3	Gene	Chr2	28493204	28495467	pip2a	aquaporin (PIP2-5), gnp_AI947770f, gpm117f, pip2-5, PIP2;5, pip2a, plasma membrane intrinsic protein2, ZmPIP2-5, ZmPIP2;5, ZmPIP2a	
3909	pip2b	plasma membrane intrinsic protein2	GRMZM2G092125	B73 RefGen_v3	Gene	Chr2	169186912	169190423	pip2b	aquaporin PIP2.1, gnp_AI947770e, gpm117e, pip2-2, pip2b, plasma membrane integral protein ZmPIP2-2, plasma membrane intrinsic protein2, ZmPIP2-2, ZmPIP2;2	
3910	pip2c	plasma membrane intrinsic protein2	GRMZM2G081192	B73 RefGen_v3	Gene	Chr4	143891075	143894123	pip2c	gnp_AI947770b, gpm117b, pip2-3, pip2c, plasma membrane intrinsic protein2, ZmPIP2-3, ZmPIP2;3	
3911	pip2d	plasma membrane intrinsic protein2	GRMZM2G154628	B73 RefGen_v3	Gene	Chr5	195239679	195242694	pip2d	aquaporin PIP2.2 , IDP287, pip2d, plasma membrane integral protein ZmPIP2-4, plasma membrane intrinsic protein2, ZmPIP2-4, ZmPIP2;4	member of the aquaporin family
3912	pip2e	plasma membrane intrinsic protein2	GRMZM2G014914	B73 RefGen_v3	Gene	Chr7	41435006	41438812	pip2e	aquaporin (PIP2-1), gnp_AI947770d, gpm117d, pip2-1, pip2e, plasma membrane integral protein ZmPIP2-1, plasma membrane intrinsic protein2, ZmPIP2-1, ZmPIP2;1	
3913	pip2f	plasma membrane intrinsic protein2	GRMZM2G047368	B73 RefGen_v3	Gene	Chr7	41553959	41555454	pip2f	aquaporin PIP2.4, CL502_5, gnp_AI947770d, gpm117d, pip2f, plasma membrane integral protein ZmPIP2-6, plasma membrane intrinsic protein2, ZmPIP2-6, ZmPIP2;6	
3914	pk3	S-domain class receptor-like kinase3	GRMZM2G309025	B73 RefGen_v3	Gene	Chr7	156513100	156515973	pk3	pk3, S-domain class receptor-like, S-domain class receptor-like kinase, siAJ010166, siaj010166(576)	
3915	pk4	protein kinase4	GRMZM2G014833	B73 RefGen_v3	Gene	Chr3	195572570	195576335	pk4	CBL-interacting serine/threonine-protein kinase 11, CL1242_1(264), CL1242_1a, pk4, protein kinase4, ZmPK4	cDNA sequence
3916	pki1	protein kinase inhibitor1	GRMZM2G018728	B73 RefGen_v3	Gene	Chr1	52805139	52807763	pki1	fmi1, fmi1(pki), fmi1(pki1), Mz2-12, PKCI, pki1, protein kinase inhibitor1, ZBP14	endosperm cDNA sequence, contains conserved Zn++ binding motif of yeast protein kinase C inhibitor
3917	pks1	polyketide synthesis homolog1	GRMZM2G091302	B73 RefGen_v3	Gene	Chr2	8724139	8731931	pks1	pks1, polyketide synthesis homolog1, uaz7c02f01(gfu)	vegetative meristem cDNA 7C02F01 similar to an acyl CoA condensing enzyme
3918	pl1	purple plant1	GRMZM2G701063	B73 RefGen_v3	Gene	Chr6	108491299	108492380	pl1	bh1, bnlg1136b, gsy244(pl1), nc009, nc010, nc10, nc9, phi031, phi31, pl1, purple plant1, umc1014, umc205(pl), ZmMYB2	patches in c1 aleurone and in plant; transcriptional activator for flavonoid genes; SSR phi031, nc009, nc010. umc1014
3919	platz1	PLATZ-transcription factor 1	GRMZM2G408887	B73 RefGen_v3	Gene	Chr1	39877358	39878626	platz1		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3920	platz10	PLATZ-transcription factor 10	GRMZM2G323553	B73 RefGen_v3	Gene	Chr5	124275861	124276933	platz10		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3921	platz11	PLATZ-transcription factor 11	GRMZM2G004548	B73 RefGen_v3	Gene	Chr5	198868436	198870185	platz11		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
3922	platz12	PLATZ-transcription factor 12	GRMZM2G006585	B73 RefGen_v3	Gene	Chr8	51608197	51609614	platz12		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3923	platz13	PLATZ-transcription factor 13	GRMZM2G093270	B73 RefGen_v3	Gene	Chr9	112352112	112354428	platz13		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3924	platz14	PLATZ-transcription factor 14	GRMZM2G077495	B73 RefGen_v3	Gene	Chr9	122343878	122349453	platz14		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3925	platz15	PLATZ-transcription factor 15	GRMZM2G086403	B73 RefGen_v3	Gene	Chr10	135709748	135712426	platz15		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3926	platz2	PLATZ-transcription factor 2	GRMZM2G311656	B73 RefGen_v3	Gene	Chr1	69256093	69257978	platz2		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3927	platz3	PLATZ-transcription factor 3	GRMZM2G094168	B73 RefGen_v3	Gene	Chr1	98770498	98772402	platz3		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3928	platz4	PLATZ-transcription factor 4	GRMZM2G171934	B73 RefGen_v3	Gene	Chr1	204103938	204106057	platz4		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3929	platz5	PLATZ-transcription factor 5	GRMZM2G131280	B73 RefGen_v3	Gene	Chr2	13553048	13555243	platz5		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3930	platz6	PLATZ-transcription factor 6	GRMZM2G342691	B73 RefGen_v3	Gene	Chr4	152864604	152869253	platz6		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3931	platz7	PLATZ-transcription factor 7	GRMZM2G091044	B73 RefGen_v3	Gene	Chr4	157531940	157533735	platz7		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3932	platz8	PLATZ-transcription factor 8	GRMZM2G017882	B73 RefGen_v3	Gene	Chr5	85901285	85902702	platz8		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3933	platz9	PLATZ-transcription factor 9	GRMZM2G070295	B73 RefGen_v3	Gene	Chr5	95257993	95259419	platz9		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
3934	plc1	phospholipase C1	GRMZM5G889467	B73 RefGen_v3	Gene	Chr5	65559888	65563651	plc1	plc1, ZmPLC	
3935	pld1	phospholipase D1	GRMZM2G054559	B73 RefGen_v3	Gene	Chr3	12195404	12200349	pld1	CL1830_1a, phospholipase D1, pld1, ZmPLDα1	cDNA clone, amino acid sequence 90% similar to rice PLD
3936	pld10	phospholipase D10	GRMZM2G108912	B73 RefGen_v3	Gene	Chr2	197187325	197194172	pld10	phospholipase D delta-like, pld10, ZmPLDδ1	
3937	pld11	phospholipase D11	GRMZM2G140811	B73 RefGen_v3	Gene	Chr7	175225393	175232833	pld11	pld11, ZmPLDδ2	
3938	pld12	phospholipase D12	GRMZM2G145944	B73 RefGen_v3	Gene	Chr2	171514014	171519145	pld12	phospholipase D delta-like, pld12, ZmPLDδ3	
3939	pld13	phospholipase D13	GRMZM2G066485	B73 RefGen_v3	Gene	Chr6	138879310	138901971	pld13	phospholipase D p1, pld13, ZmPLDζ, ZmPLDZeta	
3940	pld14	phospholipase D14	GRMZM2G158008	B73 RefGen_v3	Gene	Chr8	33876556	33895080	pld14	pld14	
3941	pld15	phospholipase D15	GRMZM2G312438	B73 RefGen_v3	Gene	Chr1	4034105	4039749	pld15	phospholipase D beta 1, pld15	
3942	pld16	phospholipase D16	GRMZM2G343588	B73 RefGen_v3	Gene	Chr8	33850982	33854872	pld16	pld16	
3943	pld17	phospholipase D17	GRMZM5G865943	B73 RefGen_v3	Gene	Chr5	70898275	70901412	pld17	phospholipase D delta-like, pld17	
3944	pld2	phospholipase D2	GRMZM2G061969	B73 RefGen_v3	Gene	Chr8	17391163	17395926	pld2	pld2, ZmPLDα2	
3945	pld3	phospholipase D3	GRMZM2G438378	B73 RefGen_v3	Gene	Chr6	128905006	128908832	pld3	phospholipase D alpha 1-like, pld3, ZmPLDα3	
3946	pld4	phospholipase D4	GRMZM2G043340	B73 RefGen_v3	Gene	Chr6	94011753	94013434	pld4	phospholipase D alpha 1-like, pld4, ZmPLDα4	
3947	pld5	phospholipase D5	GRMZM2G442551	B73 RefGen_v3	Gene	Chr9	90709327	90713727	pld5	pld5, ZmPLDα5	
3948	pld6	phospholipase D6	GRMZM2G019029	B73 RefGen_v3	Gene	Chr9	121042044	121044689	pld6	phospholipase D alpha 1-like, pld6, ZmPLDα6	
3949	pld7	phospholipase D7	GRMZM2G179792	B73 RefGen_v3	Gene	Chr1	67777685	67781676	pld7	pld7, ZmPLDα7	
3950	pld8	phospholipase D8	GRMZM2G159125	B73 RefGen_v3	Gene	Chr2	182836551	182840311	pld8	phospholipase D alpha 1-like, pld8, ZmPLDα8	
3951	pld9	phospholipase D9	GRMZM2G133943	B73 RefGen_v3	Gene	Chr1	80976254	80982317	pld9	pld9, ZmPLDβ	
3952	ploc1	plastocyanin homolog1	GRMZM2G071450	B73 RefGen_v3	Gene	Chr6	54372730	54374538	ploc1	csu257, csu257(gfu), PCO133617, plastocyanin homolog1, ploc1	leaf cDNA csu257, similar to plastocyanin
3953	ploc2	plastocyanin2	GRMZM2G078409	B73 RefGen_v3	Gene	Chr2	24166809	24167435	ploc2	PC, plastocyanin2, ploc2, umc1769	
3954	pls1	phospholipid synthesis1	GRMZM2G037104	B73 RefGen_v3	Gene	Chr2	230276620	230282304	pls1	1-acyl-sn-glycerol-3-phosphate acyltransferase PLS1, pls1, pls1 phospholipid synthesis1	endosperm cDNA complements E. coli temperature sensitive mutant in plsC
3955	pls2	phospholipid synthesis2	GRMZM5G878139	B73 RefGen_v3	Gene	Chr4	4398962	4410023	pls2	gnp_QCT9c09k, gnp_QCT9c09l, gpm753k, gpm753l, IDP1659, IDP429, phospholipid synthesis1, phospholipid synthesis2, pls1, pls2, pMAT1	endosperm cDNA complements E. coli temperature sensitive mutant in plsC
3956	plt1	phospholipid transfer protein homolog1	GRMZM2G101958	B73 RefGen_v3	Gene	Chr10	4168397	4169548	plt1	csu136, csu136(plt), csuh136, nonspecific lipid-transfer protein 2, phospholipid transfer protein homolog1, plt1, PLTP, umc373	amino acid sequence, deduced from coleoptile cDNA, homologous to phospholipid transfer proteins
3957	plt2	phospholipid transfer protein homolog2	GRMZM2G010868	B73 RefGen_v3	Gene	Chr3	230694240	230696031	plt2	csu136, nonspecific lipid-transfer protein 1, phospholipid transfer protein homolog2, plt2, plt*-U66105, umc1010, ZmLTP1.2	amino acid sequence, deduced from coleoptile cDNA; SSR locus umc1010
3958	plt3	phospholipid transfer protein homolog3	GRMZM2G126397	B73 RefGen_v3	Gene	Chr3	184490364	184491451	plt3	IDP1501, LTP3, PCO086864(257), PCO086864a, plt3, ZmLTP1.1	
3959	plt4	phospholipid transfer protein homolog4	GRMZM2G174680	B73 RefGen_v3	Gene	Chr1	52623482	52624713	plt4	lipid binding protein, plt4, rs131252109 , rs131252116	
3960	plt5	phospholipid transfer protein homolog5	GRMZM2G005991	B73 RefGen_v3	Gene	Chr1	287217033	287218320	plt5	non-specific lipid-transfer protein-like protein At2g13820-like, plt5, rs131910334	
3961	plt6	phospholipid transfer protein homolog6	GRMZM2G116167	B73 RefGen_v3	Gene	Chr5	60007150	60008477	plt6	lipid transfer-like protein VAS, pco075087(399), pco075087a, plt6, rs131525220	
3962	pme1	pectin methylesterase1	GRMZM2G125356	B73 RefGen_v3	Gene	Chr10	122250862	122253051	pme1	CL1790_1, CL1790_1(750), pectin methylesterase1, pme1	pollen; cDNA and genomic sequences
3963	pme2	pectin methylesterase2	GRMZM2G046618	B73 RefGen_v3	Gene	Chr9	11632550	11635276	pme2	pme2	
3964	pmg1	phosphoglycerate mutase1	GRMZM5G833389	B73 RefGen_v3	Gene	Chr8	170315932	170320657	pmg1	2,3-bisphosphoglycerate-independent phosphoglycerate mutase , gsy298e(pmg), pgam1, pgam2, Pgm1, phosphoglycerate mutase1, pmg1, umc1020	cDNA, genomic and protein sequences; protein sequence similar to alkaline phosphatases (yeast, E. coli, human); SSR umc1020
3965	pmk1	Phosphomevalonate kinase1	GRMZM2G019260	B73 RefGen_v3	Gene	Chr1	34940742	34950638	pmk1	CL135_4, cl135__4(15), php246, pmk1, rs128414267 , rs128414272 , rs128414280 , rs131235021 , umc11a, umc230	
3966	pmp1	peroxisomal membrane protein homolog	GRMZM2G029824	B73 RefGen_v3	Gene	Chr1	3701760	3704275	pmp1	rs128361019, rs128361021, rs128361028, rs131180498, rs131180501, rs131194025, rs131194026, TIDP3590	
3967	pmpm2	proteolipid membrane potential regulator	GRMZM2G153369	B73 RefGen_v3	Gene	Chr2	199044953	199046279	pmpm2	pco116945(174), pco116945a, PMP3-2, pmpm2, proteolipid membrane potential regulator2	encodes plasma membrane proteolipid involved in ion homeostasis and response to salinity
3968	pmpm3	proteolipid membrane potential regulator	GRMZM2G079306	B73 RefGen_v3	Gene	Chr9	12875822	12883410	pmpm3	PMP3-3, pmpm3	encodes plasma membrane proteolipid involved in ion homeostasis and response to salinity
3969	pmpm4	proteolipid membrane potential regulator	GRMZM2G179462	B73 RefGen_v3	Gene	Chr1	43986382	43987175	pmpm4	PMP3-4, pmpm4	encodes plasma membrane proteolipid involved in ion homeostasis and response to salinity
3970	pmpm5	proteolipid membrane potential regulator	GRMZM2G477325	B73 RefGen_v3	Gene	Chr7	168441642	168442771	pmpm5	AY10384, IDP1610, IDP657, IDP849, PCO061754, PMP3-5, pmpm5	encodes plasma membrane proteolipid involved in ion homeostasis and response to salinity

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
3971	pmpm7	proteolipid membrane potential regulator	GRMZM2G099984	B73 RefGen_v3	Gene	Chr8	853213	853915	pmpm7	IDP8989, PMP3-7, pmpm7	encodes plasma membrane proteolipid involved in ion homeostasis and response to salinity
3972	pmpm8	proteolipid membrane potential regulator	GRMZM2G066870	B73 RefGen_v3	Gene	Chr3	49118179	49119770	pmpm8	PMP3-8, pmpm8	encodes plasma membrane proteolipid involved in ion homeostasis and response to salinity
3973	pol1	DNA polymerase like1	GRMZM2G023422	B73 RefGen_v3	Gene	Chr10	71277936	71288557	pol1	DNA polymerase A like, GRMZM2G023422, paralog of w2, pol1	W2 also contributes to mitochondrial DNA replication, and that another DNA polymerase (likely the paralog GRMZM2G023422) makes an equal contribution.
3974	polm1	polymerase II transcription-mediator1	GRMZM2G114459	B73 RefGen_v3	Gene	Chr1	2088572	2102312	polm1	med12a, mediator of RNA polymerase II transcription subunit 12-like, polm1	encodes part of the "CDK8" module that mediates transcription initiation with RNA Polymerase II
3975	polm2	polymerase II transcription-mediator2	GRMZM5G828278	B73 RefGen_v3	Gene	Chr9	155361528	155366191	polm2	med12b.1, med12b.2, mediator of RNA polymerase II transcription subunit 12-like, polm2, umc1505	encodes part of the "CDK8" module that mediates transcription initiation with RNA Polymerase II
3976	polm2	polymerase II transcription-mediator2	GRMZM5G844080	B73 RefGen_v3	Gene	Chr9	155371097	155373747	polm2	med12b.1, med12b.2, mediator of RNA polymerase II transcription subunit 12-like, polm2, umc1505	encodes part of the "CDK8" module that mediates transcription initiation with RNA Polymerase II
3977	polm2	polymerase II transcription-mediator2	Zm00001d048541	Zm-B73-REFERENCE-G	Gene	Chr9	158173924	158186211	polm2	med12b.1, med12b.2, mediator of RNA polymerase II transcription subunit 12-like, polm2, umc1505	encodes part of the "CDK8" module that mediates transcription initiation with RNA Polymerase II
3978	polm3	polymerase II transcription-mediator3	GRMZM2G053588	B73 RefGen_v3	Gene	Chr9	28392287	28396846	polm3	med13.1, med13.2, mediator of RNA polymerase II transcription subunit 13-like, PHM1871, polm3, PZA00693, rs131175937, ss196417152, umc2338	encodes part of the "CDK8" module that mediates transcription initiation with RNA Polymerase II
3979	polm3	polymerase II transcription-mediator3	GRMZM2G153792	B73 RefGen_v3	Gene	Chr9	28406066	28413513	polm3	med13.1, med13.2, mediator of RNA polymerase II transcription subunit 13-like, PHM1871, polm3, PZA00693, rs131175937, ss196417152, umc2338	encodes part of the "CDK8" module that mediates transcription initiation with RNA Polymerase II
3980	polm3	polymerase II transcription-mediator3	Zm00001d045603	Zm-B73-REFERENCE-G	Gene	Chr9	28436212	28457275	polm3	med13.1, med13.2, mediator of RNA polymerase II transcription subunit 13-like, PHM1871, polm3, PZA00693, rs131175937, ss196417152, umc2338	encodes part of the "CDK8" module that mediates transcription initiation with RNA Polymerase II
3981	pop1	organelle permease1	GRMZM2G024823	B73 RefGen_v3	Gene	Chr1	99180327	99184416	pop1	organelle permease1, pop1, putative organelle permease1, uaz282	endosperm cDNA 5C02F05 (uaz 282)single copy, similar to yeast putative mitochondrial carrier protein
3982	por1	porin1	GRMZM2G155021	B73 RefGen_v3	Gene	Chr8	139629328	139632254	por1	CL2099_1b, outer plastidial membrane protein porin, PCO123686, por1, porin1, VDAC, voltage-dependent anion-selective channel protein	cDNA sequence
3983	por2	porin2	GRMZM2G125023	B73 RefGen_v3	Gene	Chr10	139149943	139152962	por2	porin2, tip2c, tip5, tonoplast aquaporin, tonoplast intrinsic protein2, tonoplast intrinsic protein 2-3, tonoplast membrane integral protein ZmTIP2-3, tonoplast water channel, umc1061, ZmTIP2-	cDNA similar to plant tonoplast aquaporins; SSR umc1061
3984	pox1	guaiacol peroxidase1	GRMZM2G104394	B73 RefGen_v3	Gene	Chr3	59039454	59047011	pox1	pox1, rs131410680 , ZmPrx01	
3985	pox2	guaiacol peroxidase2	GRMZM2G040638	B73 RefGen_v3	Gene	Chr1	63648608	63650100	pox2	pox2, pox2(27), rs131260586, ZmPrx02	
3986	pox3	guaiacol peroxidase3	GRMZM2G135108	B73 RefGen_v3	Gene	Chr6	125194486	125196087	pox3	gnp_QBF2g08, gpm452, guaiacol peroxidase3, pox3, Zmpox3, ZmPrx03	
3987	ppck1	phosphoenolpyruvate carboxylase kinas	GRMZM2G178074	B73 RefGen_v3	Gene	Chr5	214764762	214766299	ppck1	ppck1	C4 photosynthesis; gene function assigned based on sequence similarity and regulation by light
3988	ppck2	phosphoenolpyruvate carboxylase kinas	GRMZM2G135091	B73 RefGen_v3	Gene	Chr4	143105617	143107036	ppck2	ppck2	
3989	ppck3	phosphoenolpyruvate carboxylase kinas	GRMZM2G096753	B73 RefGen_v3	Gene	Chr5	186556056	186557725	ppck3	ppck3	
3990	ppck4	phosphoenolpyruvate carboxylase kinas	GRMZM2G049541	B73 RefGen_v3	Gene	Chr2	30268597	30270037	ppck4	ppck4	
3991	ppd1	photo-system b P domain-containing pro	GRMZM6G924006	B73 RefGen_v3	Gene	Chr1	151734051	151736151	ppd1	ppd1, PsbP domain-containing protein 1 chloroplastic	
3992	ppi1	peptidyl-prolyl isomerase1	GRMZM2G326111	B73 RefGen_v3	Gene	Chr5	167791848	167793057	ppi1	CHEM 7, cyclophilin, cyp, peptidyl-prolyl cis-trans isomerase, peptidyl-prolyl isomerase1, peptidylprolyl isomerase1, ppi1, rot1, UAZ238(PpCl, uaz238(ppi)	cDNA homologous to tomato peptidyl-prolyl cis-trans isomerase
3993	ppo1	polyphenol oxidase1	GRMZM5G851266	B73 RefGen_v3	Gene	Chr10	59669631	59671907	ppo1	polyphenol oxidase1, polyphenol oxidase I, chloroplastic-like , ppo1, uaz7C02D02(gfu)	vegetative meristem cDNA 7C02D02
3994	ppp1	pyrophosphate-energized proton pump1	GRMZM2G090718	B73 RefGen_v3	Gene	Chr5	210643769	210647890	ppp1	csu220, inorganic pyrophosphatase, ppp1, ppp*-csu220, pyrophosphate-energized proton pump1, uaz280, vpp*-uaz280	endosperm and leaf cDNA's 5C02E08 (uaz280),csu220; single copy; similar to plant vacuolar pyrophosphate-energized ATPase
3995	ppr*-59040	pentatricopeptide repeat*-59040	GRMZM2G005938	B73 RefGen_v3	Gene	Chr10	60236510	60241598	ppr*-59040	At3g59040 ortholog, pentatricopeptide repeat*-59040, ppr*-59040, ZmPPR496	pentatricopeptide repeat-containing protein orthologous to At3g59040
3996	ppr*-GRMZM2G47	pentatricopeptide repeat*-GRMZM2G4758	GRMZM2G475897	B73 RefGen_v3	Gene	Chr1	180544078	180547525	ppr*-GRMZM2	ppr*-GRMZM2G475897, ZmPPR046	
3997	ppr100	pentatricopeptide repeat100	GRMZM2G428579	B73 RefGen_v3	Gene	Chr9	118298087	118300177	ppr100	pentatricopeptide repeat protein PPR566-6, ppr100	
3998	ppr102	pentatricopeptide repeat102	GRMZM2G012174	B73 RefGen_v3	Gene	Chr3	200829117	200833808	ppr102	pentatricopeptide repeat-containing protein At5g50280, chloroplastic, ppr102	
3999	ppr103	pentatricopeptide repeat-containing prot	GRMZM2G170896	B73 RefGen_v3	Gene	Chr2	234360122	234362918	ppr103	EMB175 - Arabidopsis, pentatricopeptide repeat-containing protein At5g03800-like, ppr103, ZmPPR155	required for the accumulation of plastid ribosomes
4000	ppr13	pentatricopeptide repeat13	GRMZM2G099604	B73 RefGen_v3	Gene	Chr5	4335522	4337752	ppr13	ppr13	
4001	ppr152	pentatricopeptide repeat protein152	GRMZM2G050697	B73 RefGen_v3	Gene	Chr3	206557927	206560435	ppr152	pentatricopeptide repeat-containing protein At3g09650, chloroplastic-like, pentatricopeptide repeat protein152, ppr152, ZmHCF152, ZmPPR202	PPR protein involved in chloroplast mRNA processing
4002	ppr2	pentatricopeptide repeat 2	GRMZM2G341621	B73 RefGen_v3	Gene	Chr7	2584810	2587604	ppr2	CL15341_1, CL15341_1(529), IDP1402, pentatricopeptide2, ppr2, PZA02035, ZmPPR372	albino seedling lethal; chloroplast translation. Chloroplast PPR protein. Required for plastid ribosome accumulation. (A. Barkan, 2015)
4003	ppr2263	pentatricopeptide repeat protein2263	AC215198.3_FG002	B73 RefGen_v3	Gene	Chr9	12723540	12725903	ppr2263	ppr2263, ZmPPR463	encodes a protein required for RNA editing in mitochondrial nad5 and cob transcript (Sosso et al 2012)
4004	ppr36	pentatricopeptide repeat36	GRMZM2G333678	B73 RefGen_v3	Gene	Chr4	15638404	15640330	ppr36	ppr36, Tetratricopeptide-like helical	
4005	ppr4	pentatricopeptide repeat 4	Zm00001d026654	Zm-B73-REFERENCE-G	Gene	Chr10	149493959	149499804	ppr4	pentatricopeptide4, ppr4	Chloroplast PPR protein required for rps12 trans-splicing. Binds rps12 intron 1. (A. Barkan, 2015). PPR protein required for rps12 trans-splicing; binds rps12 intron 1
4006	ppr5	pentatricopeptide repeat 5	GRMZM2G025409	B73 RefGen_v3	Gene	Chr4	181456446	181458981	ppr5	pentatricopeptide5, ppr5, ZmPPR245	unspliced trnG precursor and stimulates its splicing. Binds the trnG intron. Required for plastid translation. (A. Barkan, 2015)
4007	ppr521	pentatricopeptide repeat521	GRMZM2G337701	B73 RefGen_v3	Gene	scaffold_4	111300	114195	ppr521	pentatricopeptide repeat-containing protein At5g14770, mitochondrial-like, ppr521	
4008	ppr53	pentatricopeptide repeat53	GRMZM2G438524	B73 RefGen_v3	Gene	Chr1	299484354	299486920	ppr53	ppr53, salt-inducible protein, ZmPPR081	mutants exhibit a range of chlorotic phenotypes; specifically reduce transcript levels of ndhA (cp) and rrn23 (cp)
4009	ppr6	pentatricopeptide repeat6	GRMZM2G093291	B73 RefGen_v3	Gene	Chr9	26487832	26491734	ppr6	ppr6	
4010	ppr61	pentatricopeptide repeat61	GRMZM2G341479	B73 RefGen_v3	Gene	Chr5	204809810	204811353	ppr61	pentatricopeptide repeat-containing protein At3g22690, ppr61	
4011	pprsmr4	pentatricopeptide repeat smr4	GRMZM2G164202	B73 RefGen_v3	Gene	Chr5	70802337	70804170	pprsmr4	pentatricopeptide repeat-Small MutS Related4, pprsmr4, ppr-smr4, ZmPPR290	
4012	ppt1	plastid phosphate/phosphoenolpyruvate	GRMZM2G047404	B73 RefGen_v3	Gene	Chr2	173925593	173929511	ppt1	MZPPT1, ppt1, PPT1, triose phosphate/phosphate translocator, non-green plastid, chloroplast	
4013	ppt2	plastid phosphate/phosphoenolpyruvate	GRMZM2G103047	B73 RefGen_v3	Gene	Chr7	82105784	82109932	ppt2	MZPPT4, ppt2, PPT4, ppt*-U66404, triose phosphate/phosphate translocator, non-green plastid,chloroplast	
4014	pr1	red aleurone1	GRMZM2G025832	B73 RefGen_v3	Gene	Chr5	180084037	180086107	pr1	flavonoid 3' hydroxylase, pr1, purple aleurone1, red aleurone1, Zmf3'h1	changes purple aleurone to red; encodes flavonoid 3'-hydroxylase
4015	prc1	proteasome component1	GRMZM2G120047	B73 RefGen_v3	Gene	Chr6	81137995	81139170	prc1	prc1, prc1 proteasome C9 1, uaz237, uaz237b, uaz237b(prc), UAZ237B(Pros)	
4016	prc2	proteasome component2	GRMZM2G111566	B73 RefGen_v3	Gene	Chr5	12576565	12579887	prc2	prc2, proteasome component2	vegetative meristem cDNA 7C02B10
4017	prc3	proteasome component3	GRMZM2G472167	B73 RefGen_v3	Gene	Chr1	8552957	8556040	prc3	peptide transporter PTR2, PHM5438, prc3, proteasome component3, PTR2, PZA00175.2, umc1727	cDNA sequence; SSR umc1727
4018	prc4	proteasome component4	GRMZM2G171604	B73 RefGen_v3	Gene	Chr5	116903623	116911871	prc4	26S protease regulatory subunit S10B, HIV1 TAT-binding protein homolog, prc4, proteasome component4, uaz118, uaz118(gfu), Zea TAT binding protein1, Zta1	endosperm cDNA 5C01A07, similar to TAT binding protein
4019	prcw1	proline rich cell wall protein1	GRMZM2G049915	B73 RefGen_v3	Gene	Chr10	36785988	36787819	prcw1	prcw1, proline rich cell wall protein, proline rich cell wall protein1, proline rich protein, prp	

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
4020	prda1	pep-related development arrested1 homo	GRMZM2G079452	B73 RefGen_v3	Gene	Chr4	16807094	16815389	prda1	crp19, pep-related development arrested1 homolog, prda1	cpRNA defects in maize similar to other PEP-deficient mutants. Ortholog of Arabidopsis PRDA1. Chloroplast nucleoid protein. Required for transcription by the plastid-encoded polymerase
4021	prep2	presequence protease2	GRMZM2G072861	B73 RefGen_v3	Gene	Chr5	209718873	209720882	prep2	prep2, presequence protease 1, chloroplastic/mitochondrial	
4022	prf1	profilin homolog1	GRMZM2G074361	B73 RefGen_v3	Gene	Chr6	160357192	160358354	prf1	CL2097_1, CL2097_1(520), prf1, profilin homolog1, ZmPRO1	deduced amino acid sequence from cDNA shares 76-85% identity with two other plant profiiins; 3-6 member multigene family; gene specific probe
4023	prf2	profilin homolog2	GRMZM2G109842	B73 RefGen_v3	Gene	Chr8	124237915	124239012	prf2	CL2096_2a, pollen profilin variant 3, prf2, profilin A , profilin homolog2, ZmPRO2	amino acid sequence, deduced from cDNA, shares 76-85% identity with two other plant profiiins; 3-6 member gene family; gene specific probe
4024	prf3	Profilin homolog3	GRMZM5G876285	B73 RefGen_v3	Gene	Chr8	174848342	174876645	prf3	prf3, Profilin homolog3, ZmPRO3	amino acid sequence deduced from cDNA shares 76-85% identity with two other plant profiiins; 3-6 member gene family; gene specific probe
4025	prf5	Profilin homolog5	GRMZM5G877388	B73 RefGen_v3	Gene	Chr9	19041804	19045538	prf5	prf5, Profilin homolog5, ZmPRO5	Deduced amino acid sequence shares 95% identity with PRF4 (aka ZmPRO4) and 79-80% identity with other maize profiiins PRF1, PRF2 and PRF3.
4026	prh1	ser/thr protein phosphatase1	GRMZM2G112240	B73 RefGen_v3	Gene	Chr4	170944444	170947965	prh1	CL2394_1, cl2394_1(329), gnp_AI948384b, gpm118b, prh1, ser/thr protein phosphatase1, umc202(prh), umc202(prp)	PCR clone from root mRNA; expressed in E. coli as active kinase; 4-8 copies by Southern analyses; gene specific probe
4027	prh10	protein phosphatase homolog10	GRMZM2G019819	B73 RefGen_v3	Gene	Chr2	103675901	103679774	prh10	PP2C8, prh10, probable protein phosphatase 2C 37, ZmOrphan262, ZmPP2C-A8	
4028	prh11	protein phosphatase homolog11	GRMZM2G159811	B73 RefGen_v3	Gene	Chr10	101377174	101382475	prh11	Orphan337 probable protein phosphatase 2C 37, PP2C13, prh11, ZmOrphan337, ZmPP2C-A9	
4029	prh12	protein phosphatase homolog12	GRMZM2G177386	B73 RefGen_v3	Gene	Chr6	161744096	161747484	prh12	pco092707, pco092707(520), PHM2108, PP2C4 2C-type protein phosphatase protein, prh12, PZA01468, rs130444556, rs55625585 , ss196416494, ZmOrphan249, ZmPP2C-A10	
4030	prh13	protein phosphatase homolog13	GRMZM2G134628	B73 RefGen_v3	Gene	Chr3	220928320	220934085	prh13	magi100654, prh13, ZmOrphan56, ZmPP2C-A11	
4031	prh14	protein phosphatase homolog14	GRMZM2G102255	B73 RefGen_v3	Gene	Chr6	167604993	167607983	prh14	Orphan169 probable protein phosphatase 2C 53, prh14, ZmOrphan169, ZmPP2C-A12	
4032	prh15	protein phosphatase homolog15	GRMZM2G383807	B73 RefGen_v3	Gene	Chr8	77501631	77504702	prh15	prh15, protein phosphatase 2C ABI2, ZmOrphan39, ZmPP2C-A13	
4033	prh16	putative protein phosphatase 2C 16	GRMZM2G056572	B73 RefGen_v3	Gene	Chr2	3973404	3978693	prh16	Orphan130 , putative protein phosphatase 2C, rs129002266, umc1165, ZmOrphan130	
4034	prh17	protein phosphatase homolog17	GRMZM2G164352	B73 RefGen_v3	Gene	Chr6	64676766	64683561	prh17	rs131175750 , rs131584967 , Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform, ZmPP2AA1	responds to Pi starvation
4035	prh2	protein phosphatase homolog2	GRMZM2G140288	B73 RefGen_v3	Gene	Chr7	167183707	167192292	prh2	PCO097531(579), prh2, protein phosphatase homolog2, uaz241, uaz241(gfu)	endosperm cDNA 5C04B06 (uaz244), similar to human cell transforming protein
4036	prh3	protein phosphatase homolog3	GRMZM2G059453	B73 RefGen_v3	Gene	Chr3	180096139	180098099	prh3	prh3, protein phosphatase 2C, ZmOrphan355, ZmPP2C-A1	
4037	prh4	protein phosphatase homolog4	GRMZM2G166297	B73 RefGen_v3	Gene	Chr8	168030486	168032471	prh4	PP2C20 probable protein phosphatase 2C 9, prh4, ZmOrphan11, ZmPP2C-A2	
4038	prh5	protein phosphatase homolog5	GRMZM2G010855	B73 RefGen_v3	Gene	Chr1	39144013	39146119	prh5	PP2C14 2C-type protein phosphatase protein, prh5, ZmOrphan122, ZmPP2C-A3	
4039	prh6	protein phosphatase homolog6	GRMZM2G308615	B73 RefGen_v3	Gene	Chr7	89059718	89061311	prh6	prh6, ZmOrphan320, ZmPP2C-A4	
4040	prh7	protein phosphatase homolog7	GRMZM2G082487	B73 RefGen_v3	Gene	Chr2	176186305	176187719	prh7	PP2C16, prh7, probable protein phosphatase 2C 68, ZmOrphan328, ZmPP2C-A5	
4041	prh8	protein phosphatase homolog8	GRMZM2G122228	B73 RefGen_v3	Gene	Chr3	212913668	212919667	prh8	PP2C9, prh8, probable protein phosphatase 2C 8, ZmOrphan304, ZmPP2C-A6	
4042	prh9	protein phosphatase homolog9	GRMZM5G818101	B73 RefGen_v3	Gene	Chr8	72141439	72143820	prh9	PP2C12 putative protein phosphatase 2C family protein, prh9, ZmOrphan142, ZmPP2C-A7	
4043	prin2	plastid redox insensitive2	GRMZM2G119906	B73 RefGen_v3	Gene	Chr2	178872908	178874445	prin2	prin2, Zmprin2	Maize ortholog of Arabidopsis PRIN2. Required for transcription by the plastid-encoded polymerase (PEP). (A. Barkan, 2015). orthologous to At1g10522
4044	prk1	phosphoribulokinase1	GRMZM2G162529	B73 RefGen_v3	Gene	Chr5	199643154	199645484	prk1	pco092382, pco092382(445)	
4045	prl1	protease PrlC candidate1	GRMZM2G133919	B73 RefGen_v3	Gene	Chr5	216749557	216756161	prl1	PCO118287, PCO118287(457), prl1, protease PrlC candidate1, uaz100, uaz100(gfu)	endosperm cDNA 2C01C07, similar to bacterial oligopeptidase A
4046	prm5	powdery mildew resistant protein5	GRMZM2G409309	B73 RefGen_v3	Gene	Chr3	56470193	56479063	prm5	prm5, protein trichome birefringence-like 3	
4047	pro1	proline responding1	GRMZM2G375504	B73 RefGen_v3	Gene	Chr8	95226658	95237335	pro1	AY109740, o6, pro1, proline responding1	(allele o6) crumpled opaque kernel; green-striped lethal seedling; responds to proline in culture
4048	propep1	precursor elicitor peptide1	GRMZM5G899080	B73 RefGen_v3	Gene	Chr2	6583856	6584704	propep1	precursor elicitor peptide1, propep1, ZmPep1	
4049	propep3	precursor elicitor peptide3	GRMZM2G339117	B73 RefGen_v3	Gene	Chr2	6597929	6598629	propep3	ZmPep3	herbivore defense signal
4050	propep4	precursor elicitor peptide4	GRMZM2G141133	B73 RefGen_v3	Gene	Chr10	72626088	72626699	propep4	propep4	
4051	propep5	precursor elicitor peptide5	GRMZM2G141071	B73 RefGen_v3	Gene	Chr10	72636057	72636866	propep5	propep5, ZmPep5	
4052	prp1	pathogenesis-related protein1	AC205274.3_FG001	B73 RefGen_v3	Gene	Chr8	51816721	51817224	prp1	pathogenesis-related protein1, pco115804b, PHM191, PRms, prp1, pza00498, TIDP2793	cDNA clone, single copy, deduced protein product is basic (vs. acidic), normally accumulates during germination,induced by fungal elicitors but not wounding
4053	prp2	pathogenesis-related protein2	GRMZM2G102356	B73 RefGen_v3	Gene	Chr2	41216939	41217919	prp2	CL10221_1, csu133, csu133(prp), csuh133, idp42, pathogenesis-related protein2, pathogenesis-related protein homolog2, phi083, prp2, prp3, uaz5C04F07, uazT14732(gfu), umc371	leaf cDNA csu133, single copy; SSR phi083 from endosperm cDNA's 5C04F07
4054	prp3	pathogenesis-related protein3	GRMZM2G117989	B73 RefGen_v3	Gene	Chr4	9662595	9664016	prp3	barwin-like, inra2, inra2(prp), PCO105158, PCO105158(343), pr4, prp3	
4055	prp4	pathogenesis related protein4	GRMZM2G465226	B73 RefGen_v3	Gene	Chr7	3487009	3488071	prp4	PR1, PR-1, PR1-F/R , prp4	
4056	prp5	pathogenesis related protein5	GRMZM2G402631	B73 RefGen_v3	Gene	Chr1	178035095	178036072	prp5	PR5, prp5, umc1972	
4057	prpo1	protoporphyrinogen IX oxidase1	GRMZM2G039396	B73 RefGen_v3	Gene	Chr8	876212	882478	prpo1	PCO076390, PCO076390(648), PPO, protoporphyrinogen IX oxidase1, prpo1, Zm-ppox	(DeMarco et al 2000). Ortholog of Arabidopsis PPOX/ PPO1. protoporphyrinogen oxidase. (A. Barkan, 2015)
4058	prpo2	protoporphyrinogen IX oxidase2	GRMZM2G364901	B73 RefGen_v3	Gene	Chr2	35316673	35329767	prpo2	CL1174_1b, protoporphyrinogen IX oxidase2, prpo2	
4059	prr1	putidaredoxin reductase homolog1	GRMZM2G320307	B73 RefGen_v3	Gene	Chr5	201317849	201326036	prr1	prr1, putidaredoxin reductase homolog1, uaz204	endosperm cDNA 5C04E05 (uaz204), similar to NADH-putidaredoxin reductase
4060	prx35	peroxidase35	GRMZM2G177792	B73 RefGen_v3	Gene	Chr10	86298080	86299400	prx35	B6T173, peroxidase 1, prx35, ZmPrx35	responsible for the majority of the peroxidase activity of the kernel
4061	ps1	pink scutellum1	GRMZM5G849107	B73 RefGen_v3	Gene	Chr5	100737438	100739288	ps1	lcyb, lcyb1, lyc1, lycB, lycb1, pink scutellum1, ps1, ps*-8205, ps*-85-3288-28, ps*-Mu85-3061-21, vp7	(aka vp7, lyc1, lycB) some alleles viviparous; endosperm and scutellum pink, seedling white with pink flush
4062	psa1	photosystemI1	GRMZM2G100976	B73 RefGen_v3	Gene	Chr6	88729231	88730546	psa1	NFU3, photosystemI1, psa1, rs131180589 , rs131581027 , rs131581044, umc1006	assembly. NCBI: NFU3 NifU-like protein 3. Required for PSI accumulation. Harbors NifU domain implicated in Fe-S cluster assembly. Ortholog of Arabidopsis Nfu-IVa. (A. Barkan, 2015)
4063	psa2	photosystemI2	GRMZM2G021687	B73 RefGen_v3	Gene	Chr1	197879675	197881628	psa2	photosystemI2, psa2	assembly. (A. Barkan, 2015). thylakoid lumen protein with protein disulfied isomerase activity; mutants lack photosystem I core complex polypeptides
4064	psa3	photosystemI3	GRMZM2G051403	B73 RefGen_v3	Gene	Chr5	7706026	7707915	psa3	calcium homeostasis regulator CHoR1, photosystemI3, psa3	Mutants have a pale green seedling phenotype; lacks photosystem I core complex polypeptides
4065	psa6	photosystem I reaction center6	GRMZM2G012397	B73 RefGen_v3	Gene	Chr7	5134217	5135120	psa6	csu67, csu67(psaK), PCO061381(532), PCO061381b, photosystem I reaction center6, photosystem I reaction center subunit psaK , psa6	leaf cDNA csu67, similar to barley photosystem I subunit
4066	psad1	photosystem I subunit d1	GRMZM2G024150	B73 RefGen_v3	Gene	Chr5	3530018	3531150	psad1	ferredoxin-binding subunit, IDP2410, photosystem I reaction center subunit II, photosystem I subunit d1, PsaD, psad1, psi-d1	Designated from Zhao,Y.Y. and Bogorad,L. unpublished submission to GenBank
4067	psah1	photosystem I H subunit1	GRMZM2G451224	B73 RefGen_v3	Gene	Chr6	164173766	164175105	psah1	csu519, csu686, gnp_QCA18d09a, gpm572a, IDP740, PCO099414(523), PCO099414a, photosystem I H subunit1, psaH, psah1	cDNA sequence from csu686, csu704 similar to plant psaH sequences
4068	psan1	photosystem I N subunit1	GRMZM2G080107	B73 RefGen_v3	Gene	Chr3	138460913	138462021	psan1	csu18, csu237b, csu237b(psaN), photosystem I N subunit1, PsaN, psan1, PSI-N, umc18a, umc18a(psaN)	cDNA sequence derived from csu517,csu539,csu937 similar to barley psaN

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
4069	psb1	photosystem II1	GRMZM2G102838	B73 RefGen_v3	Gene	Chr6	81891034	81893207	psb1	hcf134, photosystem II1, photosystem II stability/assembly factor HCF136, chloroplastic, psb1, Zm-hcf136	Ortholog of Arabidopsis HCF136. Photosystem II assembly factor. (A. Barkan, 2015). (was hcf134) lacks PSII core complex; pale seedling; mutable (Mu-induced)
4070	psb29	photosystem II subunit29	GRMZM2G033885	B73 RefGen_v3	Gene	Chr7	157314547	157315990	psb29	cp29, CP29, csu847b(lhcb), IDP1651, PCO102677, PCO102677(576), psb29	
4071	psb3	photosystem II3	GRMZM2G174984	B73 RefGen_v3	Gene	Chr4	27121588	27123964	psb3	csu754, photosystem II 10 kDa polypeptide, psb3, zinc finger protein 3	
4072	psbJ (cp)		GRMZM5G834496	B73 RefGen_v3	Gene	ChrPt	63347	63469	psbJ (cp)	photosystem II reaction center subunit X, psbJ (cp)	
4073	psbs1	photosystem II subunit PsbS1	GRMZM2G077333	B73 RefGen_v3	Gene	Chr3	174868242	174870828	psbs1	IDP1983, PCO078649, photosystem II subunit PsbS, psbs1, TIDP5528, umc1266	subunit elicits defense against destructive effects of excess absorbed light energy
4074	psei1	cystatin1	GRMZM2G438551	B73 RefGen_v3	Gene	Chr3	187772204	187778415	psei1	cc1, CCI, csu223b(psei) , csu96a(psei) , csu96(proi), csuh96, cystatin1, cystatin I, psei1, ramdaZC7, umc361	cDNA, isolated protein inhibits papain, developing endosperm
4075	psei10	cystatin10	GRMZM2G030717	B73 RefGen_v3	Gene	Chr8	162128796	162129551	psei10	cc10, CC10, cystatin10, cysteine proteinase inhibitor B , psei10	
4076	psei2	cystatin2	GRMZM2G012160	B73 RefGen_v3	Gene	Chr8	170965314	170968006	psei2	cc2, CCII, CC-II, csu223a(psei) , csu96, csu96b(psei) , cystatin2, cystatin II, gCC42, gnp_QAY2e12a, gpm416a, IDP119, psei2, psei*-D63342	cDNA expressed in E. coli inhibits cysteine proteinases; sequence and gene product activity distinct from psei1
4077	psei3	cystatin3	GRMZM2G440968	B73 RefGen_v3	Gene	Chr6	155861031	155863018	psei3	cc3, CC3, cystatin3, cysteine proteinase inhibitor 2, psei3	
4078	psei4	cystatin4	GRMZM2G013461	B73 RefGen_v3	Gene	Chr8	3347946	3350818	psei4	cc4, CC4, cystatin3, cystatin4, multidomain cystatin, psei4	
4079	psei5	cystatin5	GRMZM2G024264	B73 RefGen_v3	Gene	Chr6	146669647	146672066	psei5	cc5, CC5, cystatin5, multicystatin, psei5	
4080	psei6	cystatin6	GRMZM2G401328	B73 RefGen_v3	Gene	Chr1	79139823	79140627	psei6	cc6, CC6, cystatin6, psei6	
4081	psei7	cystatin7	GRMZM2G148925	B73 RefGen_v3	Gene	Chr1	79075655	79077147	psei7	cc7, CC7, cystatin7, psei7	
4082	psei8	cystatin8	GRMZM2G401374	B73 RefGen_v3	Gene	Chr1	79147344	79148016	psei8	cc8, CC8, cystatin8, psei8	
4083	psei9	cystatin9	AC196110.4_FG004	B73 RefGen_v3	Gene	Chr4	15343574	15344100	psei9	CC9, cystatin9, psei9	apoplastic; necessary for Ustilago maydis infection;induced by U. maydis to bypass host immunity provided by apoplostic proteases(van der Linde 2012)
4084	psk1	phytosulfokine peptide precursor1	GRMZM2G044194	B73 RefGen_v3	Gene	Chr7	3025543	3026306	psk1	gnp_AI712273, gpm60, PCO079082, psk1, umc1694, umc1695	cDNA from inbred LC, very similar to rice PSK4; similarity to maize psk3 less but closer than to psk2 or psk4
4085	psk2	phytosulfokine2	GRMZM2G079290	B73 RefGen_v3	Gene	Chr3	143262466	143263677	psk2	psk2, umc1167	
4086	psk3	phytosulfokine peptide precursor3	GRMZM2G084859	B73 RefGen_v3	Gene	Chr9	145248876	145249788	psk3	csu93a, csuh93, gnp_QBE4e09, gpm444, psk3, umc358	BK000135 cDNA from B73, very similar to rice PSK6; similarity to maize psk1 less but closer than to psk2 or psk4
4087	psk4	phytosulfokine4	GRMZM2G031261	B73 RefGen_v3	Gene	Chr10	4752399	4753182	psk4	phytosulfokines 5 precursor, psk4	
4088	psy2	phytoene synthase2	GRMZM2G149317	B73 RefGen_v3	Gene	Chr8	167823550	167826600	psy2	csu572, pco1310147(641), PCO131047b, phytoene synthase2, psy2	single copy cDNA, csu572, similar to tomato phytoene synthase; carotenoid biosynthesis
4089	psy3	phytoene synthase3	Zm00001d021410	Zm-B73-REFERENCE-G	Gene	Chr7	151481395	151484398	psy3	IDP8700, psy3, umc111b, umc111b(psy)	induced by salt and drought but not ABA; complements bacterial PSY deficiency (Li et al 2008)
4090	ptac10	plastid transcriptionally active chromoso	GRMZM2G091419	B73 RefGen_v3	Gene	Chr8	163288195	163292627	ptac10	ptac10, Zmptac10	orthologous to At3g48500
4091	ptac12	plastid transcriptionally active chromoso	GRMZM5G897926	B73 RefGen_v3	Gene	Chr3	193671883	193678209	ptac12	CL60164_1b, crp5, plastid transcriptionally active chromosome 12 homolog, ptac12, ZM_BFb0227G12, ZmPTAC12	PTAC12. Associates with Plastid Encoded RNA polymerase (PEP). Required for PEP-mediated transcription. (A. Barkan, 2015)
4092	ptac14	plastid transcriptionally active14	GRMZM5G807767	B73 RefGen_v3	Gene	Chr8	76011360	76016337	ptac14	ptac14	transcription; cpRNA defects in maize similar to other PEP-deficient mutants. Ortholog of Arabidopsis PTAC14. Associates with Plastid Encoded RNA polymerase (PEP). Required for
4093	ptac17	plastid transcriptionally active17	GRMZM2G180418	B73 RefGen_v3	Gene	Chr5	214171178	214181309	ptac17	ptac17	
4094	ptac18	plastid transcriptionally active18	GRMZM2G306104	B73 RefGen_v3	Gene	Chr1	106505916	106506716	ptac18	ptac18	
4095	ptac2	plastid transcriptionally active chromoso	GRMZM2G122116	B73 RefGen_v3	Gene	Chr7	175323051	175332481	ptac2	ptac2, Zmptac2	Encoded RNA polymerase (PEP). Required for PEP-mediated transcription. (A. Barkan, 2015). orthologous to At1g74850
4096	ptf1	Pi starvation-induced transcription factor	GRMZM2G024530	B73 RefGen_v3	Gene	Chr9	11565132	11570108	ptf1	Pi starvation-induced transcription factor1, ptf1, umc2362, ZmbHLH194	single copy, may be involved in regulating carbohydrate metabolism
4097	pth1	peptidyl-tRNA hydrolase1	GRMZM2G050596	B73 RefGen_v3	Gene	Chr3	206596608	206608212	pth1	cl41614_1, pth1	
4098	ptk1	protein kinase1	GRMZM2G328785	B73 RefGen_v3	Gene	Chr6	133823627	133826469	ptk1	CL1194_1, CL1194_1(506), protein kinase1, ptk1, umc265(ptk1), X52384, ZmPK1	cDNA, genomic clones homologous to serine/threonine protein kinases (one domain) and to Brassica self-incompatibility locus glycoprotein (a second domain)
4099	ptk2	protein kinase homolog2	GRMZM2G099754	B73 RefGen_v3	Gene	Chr4	185250108	185255064	ptk2	CL12097_1(336), CL12097_1e, PCO107590, protein kinase homolog2, ptk2, uaz252, UAZ252A(PKin), uaz252a(ptk), uaz252(gfu)	endosperm cDNA 5C02A07, similar to Arabidopsis tyr-ser-thr protein kinase
4100	ptk3	receptor-like protein kinase3	GRMZM2G151216	B73 RefGen_v3	Gene	Chr1	190127790	190130328	ptk3	probable LRR receptor-like serine/threonine-protein kinase At4g31250-like, ptk3, receptor-like protein kinase3, ZmPRK1-11	mature pollen-specific cDNA, single copy, like tomato and Arabidopsis genes
4101	ptk4	protein kinase homolog4	AC217842.3_FG001	B73 RefGen_v3	Gene	Chr2	156421058	156425687	ptk4	CL968_1(156), CL968_1a, gsy199(ptk), Pkin, protein kinase homolog M62985, ptk4, ptk*-M62985	cDNA sequence similar to fungal and mammalian protein kinases that function in signal transduction
4102	ptk5	receptor-like kinase4	GRMZM2G473511	B73 RefGen_v3	Gene	Chr8	9436053	9438289	ptk5	ptk5, ptk*-AF100769, receptor-like kinase4, siaf100769(584), tak1, Triticum aestivum kinase, ZM2ARK, Zm2Tak	
4103	ptr1	peptide transporter1	GRMZM5G867390	B73 RefGen_v3	Gene	Chr1	269419683	269424715	ptr1	peptide transporter1, ptr1	putative transporter of small peptides into the embryo during germination; also expressed in roots and shoots
4104	pve1	puncate vascular expression1	AC211276.4_FG008	B73 RefGen_v3	Gene	Chr5	16435871	16436953	pve1	AC211276.4_FG008, cl12053_1, cl12053_1(383), puncate vascular expression1, punctate, pve1	PVE1 may function downstream of RGD2 in a pathway that intersects and interacts with the ta-siARF pathway (Zhang et al 2012)
4105	px13	peroxidase 13	GRMZM2G134947	B73 RefGen_v3	Gene	Chr5	32055951	32057280	px13	anionic peroxidase H, peroxidase 13, peroxidase N-like , px13, umc1056	
4106	px14	peroxidase14	GRMZM2G108219	B73 RefGen_v3	Gene	Chr2	25437820	25439417	px14	anionic peroxidase H, ap1, CL1874_1, CL1874_1(123), peroxidase14, PHM1962, Px11, px14, PZA02080, ZmAP1	
4107	px3	peroxidase3	GRMZM2G427815	B73 RefGen_v3	Gene	Chr7	172809274	172811080	px3	gnp_AW331843, gpm206, PCO104850, PCO104850(579), peroxidase3, peroxidase J, prx3, px3	electrophoretic mobility, anodal; monomeric; widely distributed in tissues
4108	px5	peroxidase 5	GRMZM2G450233	B73 RefGen_v3	Gene	Chr6	125337844	125340176	px5	gnp_AW461049, gpm233, PCO080642	cathodal, presence-absence; expressed in all tissues except pollen; insect resistance
4109	pyg7	pale yellowgreen7	GRMZM5G809292	B73 RefGen_v3	Gene	Chr7	145184348	145188920	pyg7	pyg7, Tetratricopeptide repeat (TPR)-like superfamily protein	mutants are pale yellow green; encodes an assembly factor that interacts with PSA3
4110	pyk1	pyruvate kinase1	GRMZM2G033526	B73 RefGen_v3	Gene	Chr1	97682229	97687870	pyk1	pco129562, phm9418, pyk1, rs128678251, ss196414579	
4111	pyk2	pyruvate kinase2	GRMZM2G004534	B73 RefGen_v3	Gene	Chr10	4697235	4702142	pyk2	IDP178, PCO073639, pyk2, pyruvate kinase2, umc2053	
4112	pyk3	pyruvate kinase3	GRMZM2G144730	B73 RefGen_v3	Gene	Chr9	113493606	113499029	pyk3	pco129562, pyk3	
4113	pyrd1	pyrimidine deaminase1	GRMZM2G320099	B73 RefGen_v3	Gene	Chr1	3704159	3706769	pyrd1	PyrD, pyrd1, riboflavin biosynthesis protein ribD, rs131194045, ss196501744	
4114	pyrr1	pyrimidine reductase riboflavin1	GRMZM2G090068	B73 RefGen_v3	Gene	Chr5	160118507	160129431	pyrr1	pyrimidine reductase riboflavin1, PyrR, pyrr1	
4115	pza00048		GRMZM2G007721	B73 RefGen_v3	Gene	Chr10	98714259	98732307	pza00048	rs131175996, rs131175997, ss196417393, ss196417395	
4116	pza00067		GRMZM2G121790	B73 RefGen_v3	Gene	Chr4	229199657	229204882	pza00067	PZA00067, rs130121150, rs130121151, rs55625365 , ss196416170, ss196416172	
4117	pza00111		GRMZM2G040634	B73 RefGen_v3	Gene	Chr7	139402429	139406268	pza00111	rs132404609, rs55626825 , ss196416668	

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
4118	pza00131		GRMZM2G314292	B73 RefGen_v3	Gene	Chr1	203986419	203987178	pza00131	PHM15268, PZA00131, rs131840215, rs55626031 , ss196414661	
4119	pza00132		GRMZM2G104258	B73 RefGen_v3	Gene	Chr7	31785259	31790644	pza00132	rs128283401, rs131175794, ss196416572, ss196416574	
4120	pza00152		GRMZM2G110408	B73 RefGen_v3	Gene	Chr9	110677553	110681978	pza00152	PHM8909, rs128283337, ss196417223	
4121	pza00270		GRMZM2G012923	B73 RefGen_v3	Gene	Chr5	151484639	151489634	pza00270	PZA00270, rs128281427, rs131176028, ss196417501, ss196417503	
4122	pza00271		GRMZM2G364068	B73 RefGen_v3	Gene	Chr4	172551715	172560136	pza00271	rs128282447, rs55624204 , ss196415868	
4123	pza00285		GRMZM2G142072	B73 RefGen_v3	Gene	Chr9	8949490	8962539	pza00285	rs131175920, rs55625252 , ss196417086	
4124	pza00297		GRMZM2G022088	B73 RefGen_v3	Gene	Chr3	40318889	40324047	pza00297	PHM13823	
4125	pza00316		GRMZM2G002578	B73 RefGen_v3	Gene	Chr3	225185182	225186943	pza00316	rs129305859, rs55622635 , ss196415652	
4126	pza00332		GRMZM2G011173	B73 RefGen_v3	Gene	Chr4	189215297	189219182	pza00332	rs128283479, rs131175633, rs131175634, ss196415891, ss196415893, ss196415895	
4127	pza00363		GRMZM2G153087	B73 RefGen_v3	Gene	Chr3	135934895	135940205	pza00363	rs128282491, rs129281698, rs55624252 , ss196415435, ss196415437	
4128	pza00381		GRMZM2G118917	B73 RefGen_v3	Gene	Chr1	238384036	238403459	pza00381	rs131175332, ss196414708	
4129	pza00413		GRMZM2G122443	B73 RefGen_v3	Gene	Chr3	128928165	128931335	pza00413	rs131175505, ss196415429	
4130	pza00424		GRMZM2G434696	B73 RefGen_v3	Gene	Chr7	174820350	174831406	pza00424	rs128283189, rs55623982 , ss196416768	
4131	pza00473		GRMZM2G002959	B73 RefGen_v3	Gene	Chr6	124328526	124334707	pza00473	rs128283897, rs131175758, rs55622846 , ss196416417, ss196416419	
4132	pza00495		GRMZM2G047095	B73 RefGen_v3	Gene	Chr2	173887377	173894291	pza00495	rs129169770, rs129169772, rs55624863 , ss196415195, ss196415197	
4133	pza00497		GRMZM2G101181	B73 RefGen_v3	Gene	Chr2	20541703	20545865	pza00497	PHM4425, rs128282579, rs128282580, rs55624746 , ss196415009, ss196415011	
4134	pza00538		GRMZM2G152127	B73 RefGen_v3	Gene	Chr3	208546055	208552820	pza00538	rs128281505, rs131175554, rs131175555, rs55623126 , ss196415616, ss196415618, ss196415620	
4135	pza00667		GRMZM2G164475	B73 RefGen_v3	Gene	Chr3	162783765	162786921	pza00667	rs128285178, ss196415491	
4136	pza00726		GRMZM2G049525	B73 RefGen_v3	Gene	Chr4	53468183	53474421	pza00726	phm14055, pza00726, rs129703932, ss196415724	
4137	pza00752		GRMZM2G030529	B73 RefGen_v3	Gene	Chr1	82020741	82030263	pza00752	rs131269951, rs55623101 , ss196414553	
4138	pza00783		GRMZM2G081652	B73 RefGen_v3	Gene	Chr3	173515706	173518871	pza00783	rs131175526, ss196415530	
4139	pza00793		GRMZM2G101042	B73 RefGen_v3	Gene	Chr8	65656733	65662011	pza00793	rs131175858, ss196416846	
4140	pza00818		GRMZM2G313481	B73 RefGen_v3	Gene	Chr5	1045283	1050017	pza00818	PHM662, PZA00818	
4141	pza00827		GRMZM2G031584	B73 RefGen_v3	Gene	Chr3	156830533	156833606	pza00827	rs129350590, rs55622457 , ss196415474	
4142	pza00838		GRMZM2G054380	B73 RefGen_v3	Gene	Chr8	159782943	159797629	pza00838	rs130911462, rs55625071 , ss196417028	
4143	pza00944		GRMZM2G089121	B73 RefGen_v3	Gene	Chr1	89006779	89009728	pza00944	rs128283224, rs55624434 , ss196414575	
4144	pza00978		GRMZM2G038964	B73 RefGen_v3	Gene	Chr1	284081140	284083876	pza00978	PHM720, rs131175359, ss196414829	
4145	pza01089		GRMZM2G072337	B73 RefGen_v3	Gene	Chr10	117586271	117590284	pza01089	PHM4341, rs131176001, ss196417417	
4146	pza01154		GRMZM2G041015	B73 RefGen_v3	Gene	Chr3	217773782	217777054	pza01154	PHM3342, rs128284760, ss196415635	
4147	pza01272		GRMZM2G102596	B73 RefGen_v3	Gene	Chr9	18903400	18906316	pza01272	PZA01272, rs128282672, rs55625257 , ss196417119	
4148	pza01304		GRMZM2G089517	B73 RefGen_v3	Gene	Chr5	179240778	179243919	pza01304	PZA01304, rs128283490, rs55625952 , ss196416221	
4149	pza01360		GRMZM2G061681	B73 RefGen_v3	Gene	Chr3	225532457	225540553	pza01360	rs128281668, rs55624148 , ss196415654	
4150	pza01396		GRMZM2G059108	B73 RefGen_v3	Gene	Chr3	166420293	166422669	pza01396	rs128281417, rs55622615 , ss196415508	
4151	pza01527		GRMZM2G103230	B73 RefGen_v3	Gene	Chr6	58423170	58430307	pza01527	PZA01527, rs130286525, rs55626024 , ss196416340	
4152	pza01552		GRMZM2G403007	B73 RefGen_v3	Gene	Chr6	129885873	129886948	pza01552	rs128285121, rs55625068 , ss196416427	
4153	pza01623		GRMZM2G044128	B73 RefGen_v3	Gene	Chr8	5160708	5162795	pza01623	PHM4512, rs130703918, rs55624140 , ss196416791	
4154	pza01677		GRMZM2G112782	B73 RefGen_v3	Gene	Chr10	71063036	71066861	pza01677	rs128284850, rs55623636 , ss196417365	
4155	pza01714		GRMZM2G168364	B73 RefGen_v3	Gene	Chr7	134168464	134170246	pza01714	Endochitinase A2, rs128283153, rs55623929 , ss196416658	
4156	pza01735		GRMZM2G061885	B73 RefGen_v3	Gene	Chr2	185341447	185347936	pza01735	rs129187917, rs55624128 , ss196415211	
4157	pza01791		GRMZM2G305822	B73 RefGen_v3	Gene	Chr9	82022416	82025519	pza01791	rs131059345, rs55626139 , ss196417184	
4158	pza01877		GRMZM2G001530	B73 RefGen_v3	Gene	Chr10	77686954	77691931	pza01877	rs128329334, rs55625587 , ss196417375	
4159	pza01883		GRMZM2G118286	B73 RefGen_v3	Gene	Chr10	9383491	9407372	pza01883	rs131175978, ss196417313	
4160	pza01921		GRMZM2G068259	B73 RefGen_v3	Gene	Chr1	262219645	262230412	pza01921	rs128283557, ss196414737	
4161	pza01936		GRMZM2G054803	B73 RefGen_v3	Gene	Chr7	45400081	45402022	pza01936	PZA01936, rs131175801, rs55622154 , ss196416593	
4162	pza01946		GRMZM2G115304	B73 RefGen_v3	Gene	Chr7	129376221	129383767	pza01946	PZA01946, rs130633016, ss196416656	
4163	pza02040		GRMZM2G165631	B73 RefGen_v3	Gene	Chr5	172133346	172138422	pza02040	AY110033, CL15683_1, pza02040, rs128282708, rs55625702 , ss196416197	
4164	pza02044		GRMZM2G087612	B73 RefGen_v3	Gene	Chr1	291937388	291941593	pza02044	PZA02044, rs131175374, ss196414876	
4165	pza02128		GRMZM2G023194	B73 RefGen_v3	Gene	Chr10	111795775	111798782	pza02128	PZA02128, rs128284359, ss196417413	
4166	pza02182		GRMZM2G369931	B73 RefGen_v3	Gene	Chr3	225852909	225856380	pza02182	rs128281869, ss196415656	

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4167	pza02266		GRMZM2G150383	B73 RefGen_v3	Gene	Chr2	229529084	229531382	pza02266	rs128283838, ss196415281	
4168	pza02291		GRMZM2G088849	B73 RefGen_v3	Gene	Chr7	85907159	85909631	pza02291	rs128281683, rs55624168 , ss196416619	
4169	pza02337		GRMZM2G125494	B73 RefGen_v3	Gene	Chr2	15582030	15592514	pza02337	pza02337, rs131175402, ss196415002	
4170	pza02344		GRMZM2G455568	B73 RefGen_v3	Gene	Chr9	13777074	13777439	pza02344	rs131175924, ss196417103	
4171	pza02365		GRMZM2G467907	B73 RefGen_v3	Gene	Chr7	127179179	127184226	pza02365	rs131175815, ss196416647	
4172	pza02373		GRMZM2G158021	B73 RefGen_v3	Gene	Chr7	167373185	167379694	pza02373	rs130684930, rs55626160 , ss196416739	
4173	pza02386		GRMZM2G072526	B73 RefGen_v3	Gene	Chr7	160271657	160276364	pza02386	rs128282233, rs55622744 , ss196416714	
4174	pza02388		GRMZM2G081127	B73 RefGen_v3	Gene	Chr8	167824	174330	pza02388	rs128283514, ss196416787	
4175	pza02402		GRMZM2G110398	B73 RefGen_v3	Gene	Chr3	171486954	171491966	pza02402	rs131175524, ss196415522	
4176	pza02411		GRMZM2G098800	B73 RefGen_v3	Gene	Chr4	153223584	153226721	pza02411	PHM1558, rs128281376, rs128281377, rs55622367 , ss196416249, ss196416251	
4177	pza02421		GRMZM2G073199	B73 RefGen_v3	Gene	Chr4	199962521	199966536	pza02421	PZA02421, rs128283802, rs55622127 , ss196415907	
4178	pza02423		GRMZM2G000660	B73 RefGen_v3	Gene	Chr3	230830536	230833871	pza02423	PHM13174, rs128282492, rs55624253 , ss196415660	
4179	pza02427		GRMZM2G054050	B73 RefGen_v3	Gene	Chr3	24354426	24358548	pza02427	rs131392373, rs55625030 , ss196415341	
4180	pza02450		GRMZM2G005346	B73 RefGen_v3	Gene	Chr2	47788105	47793199	pza02450	PZA02450, rs129061847, rs55624658 , ss196415077	
4181	pza02457		GRMZM2G070639	B73 RefGen_v3	Gene	Chr4	29197166	29201100	pza02457	rs131175579, ss196415704	
4182	pza02462		GRMZM2G072658	B73 RefGen_v3	Gene	Chr5	6866349	6870062	pza02462	PZA02462, rs128283674, rs55626666 , ss196415983	
4183	pza02472		GRMZM2G106218	B73 RefGen_v3	Gene	Chr6	149672083	149678650	pza02472	PZA02472, rs131175766, ss196416471	
4184	pza02478		GRMZM2G141760	B73 RefGen_v3	Gene	Chr6	141098824	141107819	pza02478	rs131175763, rs55625053 , ss196416445	
4185	pza02479		GRMZM2G026442	B73 RefGen_v3	Gene	Chr4	213260027	213287363	pza02479	rs128282030, rs55625893 , ss196415925	
4186	pza02480		GRMZM2G013981	B73 RefGen_v3	Gene	Chr5	215883771	215886889	pza02480	PHM13639, rs130207006, rs131175732, ss196416303, ss196416305	
4187	pza02487		GRMZM2G119104	B73 RefGen_v3	Gene	Chr1	22583820	22595788	pza02487	PHM3226, PZA02487, rs128395065, rs55626525 , ss196414416	
4188	pza02514		GRMZM2G114444	B73 RefGen_v3	Gene	Chr3	218561885	218567450	pza02514	PZA02514, rs128283034, rs55622990 , ss196415639	
4189	pza02527		GRMZM2G104658	B73 RefGen_v3	Gene	Chr10	148410228	148419253	pza02527	PHM1506, rs128645869, ss196417490	
4190	pza02549		GRMZM2G325762	B73 RefGen_v3	Gene	Chr2	107818821	107820874	pza02549	PHM4880, rs131927219, rs55623050 , ss196415108	
4191	pza02554		GRMZM2G152007	B73 RefGen_v3	Gene	Chr10	2454333	2457858	pza02554	rs128281805, ss196417305	
4192	pza02619		GRMZM2G073750	B73 RefGen_v3	Gene	Chr3	123881899	123888098	pza02619	PHM2142, PZA02619, rs132026013, rs55625441 , ss196415415	
4193	pza02676		GRMZM2G116434	B73 RefGen_v3	Gene	Chr5	60798603	60803937	pza02676	rs128282321, rs55623245 , ss196416082	
4194	pza02727		GRMZM2G372180	B73 RefGen_v3	Gene	Chr2	231598423	231605113	pza02727	PZA02727, rs128282151, rs55622439 , ss196415283	
4195	pza02791		GRMZM2G410479	B73 RefGen_v3	Gene	Chr1	67529480	67539492	pza02791	rs131175291, ss196414538	
4196	pza02818		GRMZM2G102845	B73 RefGen_v3	Gene	Chr5	78415886	78423936	pza02818	rs131175688, ss196416136	
4197	pza02861		GRMZM2G465169	B73 RefGen_v3	Gene	Chr9	43841651	43847738	pza02861	rs128282380, rs131719050, ss196417167, ss196417169	
4198	pza02939		GRMZM2G163769	B73 RefGen_v3	Gene	Chr2	160620927	160623348	pza02939	rs128283289, rs131175443, ss196415165, ss196415167	
4199	pza02941		GRMZM2G106590	B73 RefGen_v3	Gene	Chr10	71371828	71375270	pza02941	rs128283280, rs128283281, rs131175991, rs55624498 , ss196417369, ss196417371, ss196417373	
4200	pza02948		GRMZM2G137930	B73 RefGen_v3	Gene	Chr6	35680636	35684873	pza02948	rs128283306, ss196416517	
4201	pza02957		GRMZM2G068028	B73 RefGen_v3	Gene	Chr1	282860846	282864657	pza02957	PHM595, rs131175358, ss196414827	
4202	pza02961		GRMZM2G181251	B73 RefGen_v3	Gene	Chr10	16210496	16218008	pza02961	pco093080, rs131175979, ss196417323	
4203	pza02982		GRMZM2G129675	B73 RefGen_v3	Gene	Chr4	149303644	149309556	pza02982	rs129816335, rs129816336, rs55625377 , ss196415828, ss196415830	
4204	pza02992		GRMZM2G100716	B73 RefGen_v3	Gene	Chr4	150491358	150496840	pza02992	rs131175615, rs131175616, rs131175617, ss196415834, ss196415836, ss196415838	
4205	pza03047		GRMZM2G099186	B73 RefGen_v3	Gene	Chr6	31411941	31415710	pza03047	rs130241141, rs131175738, ss196416325, ss196416327	
4206	pza03049		GRMZM2G058252	B73 RefGen_v3	Gene	Chr5	89351903	89357717	pza03049	rs128284872, rs128284873, ss196416146, ss196416148	
4207	pza03057		GRMZM2G018619	B73 RefGen_v3	Gene	Chr9	77764194	77768544	pza03057	rs131175944, ss196417182	
4208	pza03063		GRMZM2G037140	B73 RefGen_v3	Gene	Chr6	35896141	35897813	pza03063	rs131559217, ss196416329	
4209	pza03069		GRMZM2G126361	B73 RefGen_v3	Gene	Chr6	83126966	83131041	pza03069	rs130329516, rs130329517, rs55624858 , ss196416365, ss196416367	
4210	pza03070		GRMZM2G003883	B73 RefGen_v3	Gene	Chr3	44224072	44229612	pza03070	PHM15899, rs131403365, ss196415368	
4211	pza03073		GRMZM2G080917	B73 RefGen_v3	Gene	Chr3	170149613	170154226	pza03073	phm1959, pza03073, rs128285025, rs132056255, ss196415514, ss196415516	
4212	pza03081		GRMZM2G106424	B73 RefGen_v3	Gene	Chr4	209972408	209975654	pza03081	PHM4117, rs131175639, rs131175640, ss196415916, ss196415918	
4213	pza03092		GRMZM2G130927	B73 RefGen_v3	Gene	Chr5	12044175	12049812	pza03092	rs131175662, ss196416015	
4214	pza03120		GRMZM2G102790	B73 RefGen_v3	Gene	Chr6	57696052	57697795	pza03120	rs128283396, rs128283398, rs55625636 , ss196416336, ss196416338	
4215	pza03121		GRMZM2G048295	B73 RefGen_v3	Gene	Chr2	30170679	30172939	pza03121	PZA03121, rs131175420, ss196415057	

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1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
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4217	pza03152		GRMZM2G111045	B73 RefGen_v3	Gene	Chr4	147942670	147945039	pza03152	PZA03152, rs128284005, rs55623375 , ss196415826	
4218	pza03154		GRMZM2G088783	B73 RefGen_v3	Gene	Chr3	204223730	204225741	pza03154	PZA03154, rs131175551, rs55625327 , ss196415609	
4219	pza03155		GRMZM2G419239	B73 RefGen_v3	Probed Site	Chr4	217140381	217141824	pza03155	myb42, rs128281798, rs55625103 , ss196415931	
4220	pza03167		GRMZM2G159547	B73 RefGen_v3	Gene	Chr5	208398128	208399748	pza03167	rs131175730, ss196416285	
4221	pza03168		GRMZM2G070849	B73 RefGen_v3	Gene	Chr1	51395397	51397668	pza03168	PZA03168, rs128284835, rs128284839, rs55623622 , ss196414502, ss196414504	
4222	pza03178		GRMZM2G096358	B73 RefGen_v3	Gene	Chr8	11486302	11488135	pza03178	rs128282169, rs55622463 , ss196416797	
4223	pza03182		GRMZM2G003406	B73 RefGen_v3	Gene	Chr8	153001174	153002887	pza03182	rs128283625, rs55626608 , ss196417000	
4224	pza03191		GRMZM2G139688	B73 RefGen_v3	Gene	Chr3	187060539	187064561	pza03191	rs128282975, rs128282976, rs55622920 , ss196415567, ss196415569	
4225	pza03193		GRMZM2G131937	B73 RefGen_v3	Gene	Chr1	212948280	212949607	pza03193	PZA03193, rs128282955, rs55626395 , ss196414669	
4226	pza03196		GRMZM2G173633	B73 RefGen_v3	Gene	Chr10	124346736	124348421	pza03196	rs131176006, ss196417435	
4227	pza03203		GRMZM2G111117	B73 RefGen_v3	Gene	Chr4	82918804	82920269	pza03203	PZA03203, rs131175600, rs55625754 , ss196415770	
4228	pza03205		GRMZM2G017268	B73 RefGen_v3	Gene	Chr4	197249760	197251014	pza03205	rs128284429, rs55626509 , ss196415903	
4229	pza03226		GRMZM2G070523	B73 RefGen_v3	Gene	Chr5	20219035	20221972	pza03226	rs128283635, rs55626621 , ss196416033	
4230	pza03227		GRMZM2G048136	B73 RefGen_v3	Gene	Chr4	1269236	1270429	pza03227	rs128283983, rs55623351 , ss196415688	
4231	pza03240		GRMZM2G053720	B73 RefGen_v3	Gene	Chr1	88349118	88351781	pza03240	rs131276204, ss196414567	
4232	pza03243		GRMZM2G107867	B73 RefGen_v3	Gene	Chr1	44371887	44378439	pza03243	PZA03243, rs128427716, rs131175272, ss196414466, ss196414470	
4233	pza03254		GRMZM2G365423	B73 RefGen_v3	Gene	Chr4	65845329	65852416	pza03254	PZA03254, rs129719130, rs129719131, rs131175592, rs55625101 , ss196415744, ss196415746, ss196415748	
4234	pza03274		GRMZM2G070523	B73 RefGen_v3	Gene	Chr5	20219035	20221972	pza03274	rs128284954, rs55624058 , ss196416035	
4235	pza03344		GRMZM2G176175	B73 RefGen_v3	Gene	Chr7	22015365	22026546	pza03344	PZA03343, PZA03345, rs130489480, rs131175269, ss196414453, ss196416568	
4236	pza03344		GRMZM2G372398	B73 RefGen_v3	Gene	Chr1	36501767	36518959	pza03344	PZA03343, PZA03345, rs130489480, rs131175269, ss196414453, ss196416568	
4237	pza03391		GRMZM2G028037	B73 RefGen_v3	Gene	Chr3	221519554	221524903	pza03391	PZA03391, rs131175563, ss196415648	
4238	pza03409		GRMZM2G020409	B73 RefGen_v3	Gene	Chr4	129844141	129848910	pza03409	rs131175605, rs131175606, ss196415798, ss196415800	
4239	pza03459		GRMZM2G407044	B73 RefGen_v3	Gene	Chr4	135184888	135190339	pza03459	PZA01541, rs129798483 , rs131175613, ss196415822	
4240	pza03469		GRMZM2G465169	B73 RefGen_v3	Gene	Chr9	43841651	43847738	pza03469	rs131175941, ss196417171	
4241	pza03491		GRMZM2G472703	B73 RefGen_v3	Gene	Chr10	36254235	36258217	pza03491	rs128314024, ss196417349	
4242	pza03527		GRMZM2G077197	B73 RefGen_v3	Gene	Chr3	5983469	5988309	pza03527	rs129553996, rs55623229 , ss196415323, umc1814, ZmTRAF21	
4243	pza03529		GRMZM2G112165	B73 RefGen_v3	Gene	Chr2	190093038	190097209	pza03529	PZA03528, rs129194081, rs131175455, rs131175456, ss196415213, ss196415215, ss196415217	
4244	pza03531		GRMZM2G024668	B73 RefGen_v3	Gene	Chr1	184272689	184277348	pza03531	PZA03530, PZA03532, rs128285185, rs131175311, rs131176056, rs131176057, rs55625342 , ss196414628, ss196414630, ss196417603, ss196417606	
4245	pza03536		GRMZM2G156105	B73 RefGen_v3	Gene	Chr4	108960369	108961386	pza03536	PZA03535, rs131175601, ss196415778	
4246	pza03612		GRMZM2G065599	B73 RefGen_v3	Gene	Chr8	129490869	129493053	pza03612	rs128284533, rs131175882, rs132469112, rs55626733 , ss196416948, ss196416950, ss196416952	
4247	pza03723		GRMZM2G077361	B73 RefGen_v3	Gene	Chr7	45162309	45167457	pza03723	PZA03722, rs131175797, rs131175798, rs131175799, rs131175800, ss196416584, ss196416587, ss196416589, ss196416591	
4248	pza03728		GRMZM2G048170	B73 RefGen_v3	Gene	Chr7	142818487	142819699	pza03728	PZA03727, rs128282415, ss196416672	
4249	pza03733		GRMZM2G084465	B73 RefGen_v3	Gene	Chr3	182334242	182336143	pza03733	PZA03734, PZA03735, rs129450382 , rs131175533, rs131175534, ss196415550, ss196415552	
4250	pza03735		GRMZM2G084465	B73 RefGen_v3	Gene	Chr3	182334242	182336143	pza03735	PZA03733, PZA03734, rs131175534, rs131175535, rs55625178 , ss196415552, ss196415556	
4251	pza03742		GRMZM2G107867	B73 RefGen_v3	Gene	Chr1	44371887	44378439	pza03742	rs128282074, rs55626247 , ss196414472	
4252	pza03747		GRMZM2G164400	B73 RefGen_v3	Gene	Chr2	7519489	7528034	pza03747	PZA03748, rs131175392, rs131175393, rs131175394, rs55626034 , ss196414964, ss196414966, ss196414968	
4253	pzb00079		GRMZM2G024973	B73 RefGen_v3	Gene	Chr5	11793473	11795945	pzb00079	rs128284367, ss196416011	
4254	pzb00093		GRMZM2G104262	B73 RefGen_v3	Gene	Chr4	124002463	124006407	pzb00093	rs129780080, ss196415794	
4255	pzb00221		GRMZM2G102161	B73 RefGen_v3	Gene	Chr9	146936987	146945281	pzb00221	PHM18887, PZB00221, PZB00222, rs128282610, rs55624780 , ss196417269	
4256	pzb00232		GRMZM2G145041	B73 RefGen_v3	Gene	Chr5	64145458	64148638	pzb00232	PZB00232, rs128281489, rs128281491, rs55623109 , ss196416106, ss196416108	
4257	pzb00752		GRMZM2G143955	B73 RefGen_v3	Gene	Chr7	136898993	136902620	pzb00752	rs131175817, ss196416664	
4258	pzb00761		GRMZM2G022558	B73 RefGen_v3	Gene	Chr9	87869349	87871737	pzb00761	rs128283386, rs55625622 , ss196417193	
4259	pzb00869		GRMZM2G126988	B73 RefGen_v3	Gene	Chr5	33070313	33085769	pzb00869	rs128281517, rs55623142 , ss196416056	
4260	pzb00901		GRMZM2G080054	B73 RefGen_v3	Gene	Chr2	9449250	9451125	pzb00901	PZB00901, rs131175398, ss196414979	
4261	pzb00942		GRMZM2G090905	B73 RefGen_v3	Gene	Chr6	144755799	144758179	pzb00942	rs130414504, rs55626785 , ss196416451	
4262	pzb01009		GRMZM2G365961	B73 RefGen_v3	Gene	Chr6	85959826	85961557	pzb01009	rs130332620, rs131175746, rs55623166 , ss196416369, ss196416371	
4263	pzb01021		GRMZM2G002652	B73 RefGen_v3	Gene	Chr4	210865185	210868144	pzb01021	rs131175641, ss196415920	
4264	pzb01103		GRMZM2G171707	B73 RefGen_v3	Gene	Chr2	203572465	203578306	pzb01103	rs128284001, rs131175468, rs55623371 , ss196415253, ss196415255	

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
4265	pzb01110		GRMZM2G082855	B73 RefGen_v3	Gene	Chr9	24074354	24081173	pzb01110	rs128282137, rs128282142, rs55622423 , ss196417134, ss196417136	
4266	pzb01111		GRMZM2G016939	B73 RefGen_v3	Gene	Chr10	134434838	134438537	pzb01111	rs128281896, ss196417450	
4267	pzb01112		GRMZM2G020366	B73 RefGen_v3	Gene	Chr5	69147384	69150733	pzb01112	PZB01112, rs128283011, rs55622962 , ss196416126	
4268	pzb01227		GRMZM2G474685	B73 RefGen_v3	Gene	Chr1	289615706	289619063	pzb01227	CLAVATA3/ESR (CLE)-related protein 25, PZB01226, PZB01227, rs131175371, rs55624243 , ss196414870, ZmCLE4A	candidate for clavata3 (CLV3) ortholog
4269	pzb01233		GRMZM2G047448	B73 RefGen_v3	Gene	Chr2	3392385	3393860	pzb01233	rs131175387, rs55626862 , ss196414945	
4270	pzb01301		GRMZM2G046284	B73 RefGen_v3	Gene	Chr10	10198909	10200857	pzb01301	rs128488507, rs128488510, ss196417315, ss196417317	
4271	pzb01308		GRMZM2G090905	B73 RefGen_v3	Gene	Chr6	144755799	144758179	pzb01308	PZB01308, rs130414506, ss196416453	
4272	pzb01358		GRMZM2G313162	B73 RefGen_v3	Gene	Chr9	111007594	111013702	pzb01358	rs131175951, ss196417221	
4273	pzb01647		GRMZM2G107629	B73 RefGen_v3	Gene	Chr1	231759993	231766222	pzb01647	rs128282253, ss196414698	
4274	pzb01662		GRMZM2G102347	B73 RefGen_v3	Gene	Chr1	34409866	34413485	pzb01662	rs128282333, rs131175267, rs55623261 , ss196414442, ss196414445	
4275	pzb01957		GRMZM2G079823	B73 RefGen_v3	Gene	Chr1	26198119	26204511	pzb01957	rs131175265, ss196414428	
4276	pzb02155		GRMZM2G058745	B73 RefGen_v3	Gene	Chr8	124182497	124187982	pzb02155	rs128283866, rs55622801 , ss196416916	
4277	pzb02179		GRMZM2G471529	B73 RefGen_v3	Gene	Chr3	158932008	158938325	pzb02179	hk2, PZB02188, rs128281771, rs129394726, rs131175517, rs55624674 , ss196415481, ss196415483, ss196415485	
4278	qm1	QM1 homolog1	GRMZM2G087233	B73 RefGen_v3	Gene	Chr5	19458986	19461229	qm1	60S ribosomal protein L10 homolog, L10, qm1, Zea QM1 homolog1, zqm1	cDNA sequence homologous to human tumor suppressor QM1 protein
4279	qsox1	thiol oxidoreductase1	GRMZM2G113216	B73 RefGen_v3	Gene	Chr6	163118403	163123994	qsox1	PCO146570, PCO146570(520), qsox1, tel1, TEL1, uaz43e, ZmQSOXL1	
4280	r1	colored1	GRMZM5G822829	B73 RefGen_v3	Gene	Chr10	138489998	138498818	r1	colored1, gsy64(rs), r1, red, RS, umc182, umc182(r1), ZmbHLH1	dominants represented by R1-r or r1-r (P element) confer function in anthers, leaf tip, brace roots, etc.
4281	ra1	ramosa1	GRMZM2G003927	B73 RefGen_v3	Gene	Chr7	110359182	110359930	ra1	ra1, ramosa1	ear and tassel many-branched; tassel branches taper to tip
4282	ra2	ramosa2	AC233943.1_FG002	B73 RefGen_v3	Gene	Chr3	12890068	12890853	ra2	ra2, ramosa2, ZmLBD16	tassel many-branched, upright, not conical like ra1; irregular kernel placement
4283	ra3	ramosa3	GRMZM2G014729	B73 RefGen_v3	Gene	Chr7	166895789	166900274	ra3	fae1, fea1, ra3, ramosa3, trehalose-6-phosphate phosphatase, ZmTPP10(RA3)	branched inflorescence; mutant ears have abnormal long branches at their bases; trehalose biosynthesis
4284	rab15	responsive to abscisic acid15	GRMZM2G165901	B73 RefGen_v3	Gene	Chr5	14084193	14085595	rab15	CHEM1, csic, csic(mah9), MA16, phi008, phi008a, pMAH9, rab15, responsive to abscisic acid15	nucleolar; cDNA and genomic sequence, cDNA isolated from dry embryo; SSR phi008
4285	rab28	abscisic acid-responsive28	GRMZM2G091535	B73 RefGen_v3	Gene	Chr5	5622016	5622902	rab28	abscisic acid-responsive28, late embryogenesis abundant protein D-34-like, rab28	cDNA and genomic clones, inducible by ABA in embryos and young leaves and by water-stress in leaves; similar to cotton LeaD-34
4286	rab30	responsive to abscisic acid30	GRMZM2G472236	B73 RefGen_v3	Gene	Chr1	12246354	12247358	rab30	csic, csic(rab30), late embryogenesis abundant protein D-34, PZA03551, PZA03552, rab28, rab28b, rab30, responsive to abscisic acid30	cDNA and protein elicited by ABA
4287	rack1	receptor for activated C kinase1	GRMZM2G038032	B73 RefGen_v3	Gene	Chr6	163078693	163081080	rack1	gpm583(6), rack1, rs130447334	plant disease resistance; interacts with maize homologs of RAC1, RAR1 and SGT1 in yeast two-hybrid assay (Wang 2014)
4288	rack2	receptor for activated C kinase2	GRMZM2G040477	B73 RefGen_v3	Gene	Chr8	65264847	65267084	rack2	gnp_QCB11e11, gpm583, gpm583(8), rack2, receptor for activated C kinase2	
4289	rad51a	recombination protein51 gene a	GRMZM2G121543	B73 RefGen_v3	Gene	Chr7	160178520	160182662	rad51a	CL542_1, cl542_1(577), rad51, rad51a, Rad51a1, recombination protein51 gene a, recombination protein subunit a, ZmRad51a	one of two loci producing cDNA homologous to yeast protein required with Dmc1 protein for meiotic homologous recombination
4290	rad51b	recombination protein51 gene b	GRMZM2G084762	B73 RefGen_v3	Gene	Chr3	135467784	135471240	rad51b	IDP19, IDPrad51b, Rad51a2, rad51b, recombination protein	one of two loci producing cDNA homologous to yeast protein required with Dmc1 protein for meiotic homologous recombination
4291	rad51c	recombination protein51 gene c	GRMZM2G123089	B73 RefGen_v3	Gene	Chr3	220254011	220258502	rad51c	rad51c	Homolog of rad51
4292	rad51d	recombination protein51 gene d	GRMZM2G055464	B73 RefGen_v3	Gene	Chr7	170060949	170067054	rad51d	rad51d, si486083c08, si486083c08(579)	Homolog of rad51
4293	rad51e	recombination protein51 gene e	AC219006.2_FG007	B73 RefGen_v3	Gene	Chr8	131503426	131513533	rad51e	Rad51b, rad51e	Homolog of rad51
4294	raf1	Rubisco Assembly Factor 1	GRMZM2G457621	B73 RefGen_v3	Gene	Chr2	1361783	1363354	raf1	raf1	bundle sheath chloroplasts. Rubisco Accumulation Factor1; promotes Rubisco assembly. (A. Barkan, 2015)
4295	raf2	rubisco accumulation factor2	GRMZM2G139123	B73 RefGen_v3	Gene	Chr1	295100635	295101482	raf2	raf2	mutant is seedling-lethal, Rubisco-deficient. Rubisco Accumulation Factor2; promotes Rubisco assembly. (A. Barkan, 2015)
4296	rap2	rap2.7 orthologue	GRMZM2G700665	B73 RefGen_v3	Gene	Chr8	131576889	131580316	rap2	rap2, rap2.7 orthologue, RELATED TO APETALA2 7, ZmEREB110, ZmRap2.7	negative regulator of flowering time; vgt1 acts as an enhancer (Salvi et al. 2007)
4297	raptor1		GRMZM2G048067	B73 RefGen_v3	Gene	Chr10	1411349	1423184	raptor1	raptor1	
4298	ras1	ras related protein1	GRMZM2G330430	B73 RefGen_v3	Gene	Chr2	40054092	40056877	ras1	related protein1, "RAt Sarcoma" protein-like, rs129051522, rs129051527, rs129051545, Zm-Rab2-A, ZmRab2-A, ZmRab2A1	rab2-homologous cDNA
4299	ras11B2	ras-related protein11B2	GRMZM2G144008	B73 RefGen_v3	Gene	Chr5	2259767	2263658	ras11B2	Rab11A, ras11B2, umc1496, ZmRab11B2	
4300	ras11E2	ras-related protein11E2	GRMZM2G019119	B73 RefGen_v3	Gene	Chr2	172384492	172387622	ras11E2	PCO103364, ras11E2, RGP1, umc2254, ZmRab11E2	
4301	ras18A1	ras-related protein18A1	GRMZM2G176677	B73 RefGen_v3	Gene	Chr2	27056209	27064181	ras18A1	nactf120, ras18A1, ZmRab18A1	
4302	ras2	Ras-related protein2	GRMZM2G173878	B73 RefGen_v3	Gene	Chr10	124319406	124322173	ras2	protein, ras2, Ras-related protein Rab-2-B, ras"-U22433, "RAt Sarcoma" protein-like, Zm-Rab2-B, ZmRab2-B	Homolog of mammalian binding GTP rab2 proteins
4303	ras8B1	ras related protein8B1	GRMZM2G149847	B73 RefGen_v3	Gene	Chr2	233015891	233019721	ras8B1	ARA-3, PCO128668, PCO128668(195), ras8B1, ZmRab8B1	
4304	rbap1	WD-repeat protein RBAP1	GRMZM2G316113	B73 RefGen_v3	Gene	Chr8	153994750	154008418	rbap1	nfc102, nfc105, rbap1, WD-repeat protein RBAP1, ZmRbAp1	sequence, GenBank Acc# AF384037, that encodes nucleosome /chromatin assembly factor C; has functional homology to yeast MSI1 gene, and encodes a protein that binds acetylated H3
4305	rbap2	WD-repeat protein RBAP2	GRMZM2G137965	B73 RefGen_v3	Gene	Chr3	204143323	204150370	rbap2	nfc101, NURF complex component (RBBBp4/Caf1 homologs), rbap2, WD-repeat protein RBAP2, ZmRbap2	first reported as a partial cDNA clone, AF250048, showing high sequence homology with genes rbap1 and rbap3.
4306	rbd1	RNA-binding domain1	GRMZM2G093815	B73 RefGen_v3	Gene	Chr7	11492262	11493481	rbd1	rbd1, YlmG homolog protein 1-2 chloroplastic	
4307	rboh1	respiratory burst oxidase1	GRMZM2G426953	B73 RefGen_v3	Gene	Chr3	182095773	182101296	rboh1	pco107390, pco107390(255), roothair defective5, roothairless5, rth5, ZmrbohA	mutant displays defects in root hair initiation and elongation manifested by a reduced density and length of root hairs.
4308	rboh2	respiratory burst oxidase2	GRMZM2G138152	B73 RefGen_v3	Gene	Chr3	200364162	200384941	rboh2	cl562_1, ZmrbohB	
4309	rboh3	respiratory burst oxidase3	GRMZM2G043435	B73 RefGen_v3	Gene	Chr6	160040811	160052133	rboh3	rboh3	
4310	rboh4	respiratory burst oxidase4	GRMZM2G441541	B73 RefGen_v3	Gene	Chr4	191928760	191933957	rboh4	umc1051, ZmrbohD	
4311	rca1	RUBISCO activase1	GRMZM2G162200	B73 RefGen_v3	Gene	Chr4	693736	696087	rca1	CL1146_1, csu901, csuh00901, csuh901, rca1, rs129616587 , rs129616588, rs129616590 , RUBISCO activase1	encodes the beta form of RUBISCO activase. single copy leaf cDNA csu901 smilar to RUBISCO activase
4312	rca2	RUBISCO activase2	GRMZM2G162200	B73 RefGen_v3	Gene	Chr4	693736	696087	rca2	CL1146_1, csu901, csuh00901, csuh901, rca2, ribulose 1,5-bisphosphate carboxylase/oxygenase activase, RUBISCO activase2	encodes the beta form of RUBISCO activase
4313	rca3	RUBISCO activase3	GRMZM2G162282	B73 RefGen_v3	Gene	Chr4	691410	693139	rca3	rca3	encodes alpha form of RUBISCO activase

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
4314	rcc1	regulator of chromosome condensation1	GRMZM2G302245	B73 RefGen_v3	Gene	Chr3	179842136	179848015	rcc1	rcc1, rcc1-1	
4315	rcc2	regulator of chromosome condensation2	GRMZM2G003565	B73 RefGen_v3	Gene	Chr2	49685916	49690865	rcc2	rcc1-2, rcc2	
4316	rcc3	regulator of chromosome condensation3	GRMZM2G135770	B73 RefGen_v3	Gene	Chr4	81813738	81819034	rcc3	rcc1-3, rcc3	
4317	rcp1	root cap protein1	GRMZM2G074850	B73 RefGen_v3	Gene	Chr6	68972623	68974546	rcp1	AY110213, CL1225_1a, GDP-mannose 4,6 dehydratase, rc106, rcp1, root cap106, root cap protein1	
4318	rcph1	root-cap periphery1	GRMZM2G097316	B73 RefGen_v3	Gene	Chr3	145514689	145516008	rcph1	rcp1, RCP1, rcp2, root-cap periphery, siab021175, ZmRCP1	
4319	rcph2	root cap periphery gene2	GRMZM2G146502	B73 RefGen_v3	Gene	Chr4	188242843	188244300	rcph2	CL1277_1, CL1277_1(338), PZA02573, rc123A, RCP2, rcph2, root cap 123A, root cap periphery gene2, zmrcp2	
4320	rdr6	RNA-dependent RNA polymerase6	GRMZM2G082437	B73 RefGen_v3	Gene	Chr3	102502867	102504039	rdr6	rdr6	mutant seedlings with reduced fully abaxialized organs that arrest shortly after germination
4321	rdr6	RNA-dependent RNA polymerase6	GRMZM2G145201	B73 RefGen_v3	Gene	Chr3	102532883	102536036	rdr6	rdr6	mutant seedlings with reduced fully abaxialized organs that arrest shortly after germination
4322	reas1	ribosome export associated1	GRMZM2G092001	B73 RefGen_v3	Gene	Chr6	154250528	154251027	reas1	dek*-N1117, reas1, ribosome export associated1, ZmMDN1, ZmMidasin homolog1, ZmRea1	Encodes an AAA-ATPase that controls 60S ribosome export from the nucleus to the cytoplasm after ribosome maturation; mutants have a defective kernel phenotype.
4323	rel2	ramosa1 enhancer locus2	GRMZM2G042992	B73 RefGen_v3	Gene	Chr10	76650034	76659099	rel2	RAMOSA1 ENHANCER LOCUS2, ramosa enhancer locus2, rel2, topless-related3, ZmTPL3	rel2 mutants dramatically increase the formation of long branches in ears of both ra1 and ra2 mutants
4324	rem6.3	remorin6.3	GRMZM2G107774	B73 RefGen_v3	Gene	Chr1	25392624	25395149	rem6.3	mu1046469, rem6.3	
4325	rf2	restorer of fertility2	GRMZM2G058675	B73 RefGen_v3	Gene	Chr9	34129753	34143728	rf2	ALDH2B1, IDP489, PCO108969b, restorer of fertility2, rf2, rf2a	see rf1; cDNA prf2a complements E. coli mutant deficient in aldehyde dehydrogenase; mitochondrial
4326	rfa1	replication factor A homolog1	GRMZM2G086934	B73 RefGen_v3	Gene	Chr9	147128364	147131996	rfa1	DNA-binding subunit, rfa1, rs128281364, rs131160294, rs55622348 , ss196417273, ss196417275, uaz5c09d05(gfu)	endosperm cDNA 5C09D05, similar to yeast DNA binding protein
4327	rgd1	ragged seedling1	GRMZM2G020187	B73 RefGen_v3	Gene	Chr6	17165517	17171948	rgd1	lbl1, leaf bladeless1, PCO125857(521), PCO125857b, ragged seedling1, rg, rgd1	(aka lbl1) seedling leaves narrow, thread-like, have difficulty in emerging; low temperature enhances expression
4328	rgd2	ragged seedling2	GRMZM5G892991	B73 RefGen_v3	Gene	Chr1	75636094	75640439	rgd2	ago120, ago7, Argonaute7-like, GRMZM2G365589, protein argonaute 7, ragged seedling2, rgd2	mutant expression is variable from reduced midrib/moderately narrow leaf to filamentous or even radial leaves
4329	rgh3	rough endosperm3	GRMZM2G128228	B73 RefGen_v3	Gene	Chr5	173740449	173741941	rgh3	rgh3, rough endosperm3, U2AF35 Related Protein (URP), ZmURP	Mature rgh3 seeds show a rough, etched, or pitted endosperm surface as well as a reduced seed size
4330	rgh3	rough endosperm3	GRMZM5G849788	B73 RefGen_v3	Gene	Chr5	173803063	173806170	rgh3	rgh3, rough endosperm3, U2AF35 Related Protein (URP), ZmURP	Mature rgh3 seeds show a rough, etched, or pitted endosperm surface as well as a reduced seed size
4331	rgp2	ras-related protein RGP2	GRMZM2G093186	B73 RefGen_v3	Gene	Chr8	90299372	90301852	rgp2	AY105457, PCO149506, ras-related GTP-binding protein, rgp2, umc2503, ZmRab11B1	
4332	rh3	RNA helicase3	GRMZM2G415491	B73 RefGen_v3	Gene	Chr5	1933220	1947556	rh3	pco121445(428), rh3, rh3a, RNA helicase3	
4333	rh4	RNA helicase4	AC198418.3_FG005	B73 RefGen_v3	Gene	Chr1	295187054	295270267	rh4	pco121445(23), rh3b, rh4, RNA helicase4	assembly of the 50S ribosomal subunit. Associates in vivo with pre-50S ribosomal subunits and with a subset of group II introns. (A. Barkan, 2015). cp Dead box RNA helicase involved in cp
4334	rhcp1	ring hc protein1	GRMZM2G024690	B73 RefGen_v3	Gene	Chr5	11830175	11839047	rhcp1	putative RING zinc finger domain superfamily protein, rhcp1, ring zinc finger C3HC4 domain protein1	expressed during brace root initiation and regulated by abiotic stresses.
4335	rhn1	ras-related protein RHN1	GRMZM2G131254	B73 RefGen_v3	Gene	Chr1	179371866	179374965	rhn1	cl13607_1a, PCO080814, pco080814(165), rhn1, ZmRab5B1	
4336	ric1	ras-related protein RIC1	GRMZM2G106960	B73 RefGen_v3	Gene	Chr8	136938104	136941568	ric1	PCO122462, PCO122462(629), Rab1B1, related to ion channel1, ric1, ZmRab1B1, ZmRab1B2, ZmRab1B3	
4337	rif1	r-interacting factor1	GRMZM2G049155	B73 RefGen_v3	Gene	Chr7	74139858	74148720	rif1	ENT domain containing protein, rif1, r-interacting factor1	activation of the a1 promotor
4338	rip1	ribosome-inactivating protein1	GRMZM2G063536	B73 RefGen_v3	Gene	Chr8	108689439	108690609	rip1	ncrb32c3a, ncr(b32c3a), phi014, phi060, ribosome-inactivating protein1, rip1, Rip3, Rip3:1, rs130838200 , rs130838203 , SOG1678f, SOG5684p, uaz193, uaz193(rip), UAZ193(RIP3,	cytosolic, inactivates rabbit (not maize or wheat) ribosomes; cDNA ZmRIP3, SSR phi014, phi060, umc1202
4339	rip2	ribosome-inactivating protein2	GRMZM2G119705	B73 RefGen_v3	Gene	Chr7	162849640	162851038	rip2	cl1124_1(579), PCO148580, pco148580(579), ribosome-inactivating protein2, rip2, Rip3:2, rip*-L26305, umc1782	genomic sequence produces RIP protein in E. coli; cDNA, SSR umc1782
4340	ris1	iron-sulfur protein1	GRMZM2G162748	B73 RefGen_v3	Gene	Chr5	142748781	142750441	ris1	cytochrome b6-f complex iron-sulfur subunit, iron-sulfur protein1, PCO071754(424), Rieske Fe/S protein1, ris1, ris2	one of two very similar cDNAs recovered by antiserum screen from B73 seedling leaf RNA, both transcribed in leaf tissue (Barkan and Walker 1994)
4341	ris2	iron-sulfur protein2	GRMZM2G038365	B73 RefGen_v3	Gene	Chr4	226804999	226807042	ris2	csu271, csuh00271, cytochrome b6-f complex iron-sulfur subunit, iron-sulfur protein2, petC, Rieske Fe/S protein2, ris2	one of two very similar cDNAs recovered by antiserum screen from B73 seedling leaf RNA, both transcribed in leaf tissue (Barkan and Walker 1994)
4342	rld1	rolled leaf1	GRMZM2G109987	B73 RefGen_v3	Gene	Chr9	154912262	154920527	rld1	CL4357_1e, rld1, Rld*-1441, Rld*-1990, Rld1-N1990, rolled leaf1, ZmHB133	in dominant Rld1 plants, leaves are tightly rolled and tend to be entangled; ligular flaps on abaxial surface of leaf; resembles Ce1
4343	rld2	rolled leaf2	GRMZM2G042250	B73 RefGen_v3	Gene	Chr1	2791599	2798512	rld2	rld2, rs128359298, ZmHB58	paralogous locus of rld1
4344	rlsb1	rbcl rna s1-binding domain protein1	GRMZM2G087628	B73 RefGen_v3	Gene	Chr3	221649770	221652972	rlsb1	ribulose-1-5-bisphosphate carboxylase-large subunit RNA s1-binding domain protein1, rlsb1, RLSB-a, Zm-s1	Chloroplast RNA binding protein. (A. Barkan, 2015). encodes RLSB mRNA binding protein
4345	rlsb2	rbcl rna s1-binding domain protein2	GRMZM2G546254	B73 RefGen_v3	Gene	Chr6	161543914	161548356	rlsb2	ribulose-1-5-bisphosphate carboxylase-large subunit RNA s1-binding domain protein2, rlsb2, RLSB-b	encodes RLSB mRNA binding protein
4346	rmr1	required to maintain repression1	GRMZM2G154946	B73 RefGen_v3	Gene	Chr6	144471007	144478241	rmr1	required to maintain repression1, rmr1, SNF2 domain-containing protein CLASSY 4-like	
4347	rmr2	required to maintain repression 2	GRMZM2G009208	B73 RefGen_v3	Gene	Chr2	22729494	22732649	rmr2	ems96, required to maintain repression 2, rmr2, rmr4	
4348	rmr6	required to maintain repression6	GRMZM2G007681	B73 RefGen_v3	Gene	Chr1	188753176	188845235	rmr6	nuclear RNA polymerase D1, required to maintain repression6, required to maintain repression 6, rmr6, RNA polymerase D1, rpd1	recessive changes B' phenotype to dark; like mop1. Recessive rmr6 plants show reversions of paramutant pl1 and r1
4349	rnc1	ribonuclease III domain protein1	GRMZM2G035820	B73 RefGen_v3	Gene	Chr3	187230808	187235487	rnc1	idp1680, ribonuclease III domain protein1, RNAase III, si614043c10	albino to pale green seedling lethal; RNA splicing
4350	rnp1	RNA binding protein 1	GRMZM2G158835	B73 RefGen_v3	Gene	Chr7	167862249	167864329	rnp1	csu17, csu17a(rnp), csu17c, PCO130298, ribonucleoprotein A, RNA binding protein 1, rnp1, Rnpr, rs131181955, umc314	leaf cDNA csu17, similar to RNA binding proteins
4351	roa1	replication origin activator1	GRMZM2G100639	B73 RefGen_v3	Gene	Chr6	153935909	153940922	roa1	replication origin activator1, roa1, roa2, roa3, roa4, umc1341	cDNA Z29368, homology with yeast and vertebrate DNA licensing activity; orthologs in barley and Arabidopsis, highly conserved
4352	rop1	Rho-related protein from plants 1	GRMZM2G415327	B73 RefGen_v3	Gene	Chr5	206201286	206210007	rop1	PCO077615, rac1, RACA, RAC GTPase11, Rho-related protein from plants 1, rop1, umc2198	cDNA sequence; expression in mammalian cells associated with superoxide production
4353	rop2	Rho-related protein from plants2	GRMZM5G846811	B73 RefGen_v3	Gene	Chr4	238592881	238596701	rop2	gnp_QBM10a03a, gpm538a, PCO091374b, rac2, RACB, RAC GTPase2, Rho-related protein from plants 2, rop2, umc1699	ROP2 protein interacts with PAN1 to polaize asymmetric cell division; SSR umc1699
4354	rop3	Rho-related protein from plants 3	GRMZM2G100505	B73 RefGen_v3	Gene	Chr6	133009256	133012520	rop3	CL1205_2(506), CL1205_2d, rac3, RACC, RAC GTPase3, Rho-related protein from plants 3, rop3	cDNA sequence; expression in mammalian cells associated with superoxide production
4355	rop4	Rho-related protein from plants 4	GRMZM2G375002	B73 RefGen_v3	Gene	Chr5	217656047	217664941	rop4	gnp_QCI15c02a, gpm665a, rac4, RACD, RAC GTPase1, Rho-related protein from plants 4, rop4	cDNA sequence; expression in mammalian cells associated with superoxide production
4356	rop5	Rho-related protein from plants 5	GRMZM2G102946	B73 RefGen_v3	Gene	Chr9	3063132	3080500	rop5	PCO099720(649), PCO099720b, Rho-related protein from plants 5, rop5	
4357	rop6	Rho-related protein6	GRMZM2G176217	B73 RefGen_v3	Gene	Chr6	158645247	158647592	rop6	CL1205_2e, IDP3782, rac-like GTP-binding protein 2 , Rho-related protein6, rop6	
4358	rop7	Rho-related protein from plants 7	AC209819.3_FG012	B73 RefGen_v3	Gene	Chr8	122478251	122480444	rop7	Rho gene7, Rho-related protein from plants 7, rop7, rs130856863, rs131179793 , umc1950	cDNA, plasma membrane targeting, SSR umc1950. In Maize Genetics Conference Abstracts rop7 was called rop1. These abstracts are indeed discussing rop7.
4359	rop8	Rho-related protein from plants 8	GRMZM2G001953	B73 RefGen_v3	Gene	Chr4	182363663	182367487	rop8	Rho-related protein from plants 8, rop8	
4360	rop9	Rho-related protein from plants 9	GRMZM5G803949	B73 RefGen_v3	Gene	Chr5	70912027	70915976	rop9	PCO091374c, Rho-related protein from plants 9, rop9	ROP9 protein interact with PAN1 to polarize asymmetric cell division
4361	rp1	resistance to Puccinia sorghi1	AC152495.1_FG002	B73 RefGen_v3	Gene	Chr10	3283523	3287419	rp1	163K15.14 putative disease resistance protein RGA3, resistance to Puccinia sorghi1, rp1	dominant Rp1 resistant
4362	rp3	resistance to Puccinia sorghi3	AC230011.2_FG002	B73 RefGen_v3	Gene	Chr3	113913960	113920267	rp3	IDP826, PIC13, pic13b, putative disease resistance protein RGA1, resistance to Puccinia sorghi3, rp3	dominant Rp3 resistant

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
4363	rpd3	RPD3 histone deacetylase homolog	GRMZM2G172883	B73 RefGen_v3	Gene	Chr4	231335846	231342828	rpd3	hda, hda1, hda101, histone deacetylase, rpd3, RPD3 histone deacetylase homolog, umc1173, ZmRpd3/101	cDNA complements yeast rpd3, multiple copy, SSR umc1173.
4364	rph1	RNase PH homolog	GRMZM2G345039	B73 RefGen_v3	Gene	Chr8	67242630	67250938	rph1	CL1582_7, CL1582_7(595), RNase PH homolog, rph1, uaz313, uaz313(gfu)	endosperm cDNA 5C06F11 similar to E. coli tRNA processing enzyme
4365	rpl10	ribosomal protein L10 homolog	GRMZM2G467086	B73 RefGen_v3	Gene	Chr3	229627953	229630162	rpl10	CL12280_1(280), CL12280_1b, ribosomal protein L10 homolog, rpl10, uaz198, uaz198a(rpL10), uaz198(L10e)	endosperm cDNA 5C01D03 (uaz198), similar to yeast acidic ribosomal protein
4366	rpl15b	60S ribosomal protein L15	GRMZM2G180724	B73 RefGen_v3	Gene	Chr7	149310459	149313123	rpl15b	60S ribosomal protein L15 b, CL3259_2(571), CL3259_2b, csu364(gfu), L15, rgpc1122b(rpL15), rpl15b	leaf cDNA csu364 similar to eucaryotic 60S ribosomal protein L15 (L10, YL10)
4367	rpl17a	ribosomal protein L17a	GRMZM2G119169	B73 RefGen_v3	Gene	Chr8	92685793	92690815	rpl17a	60S ribosomal protein L17, CL9529_1c, PCO123564, PCO123564(603), ribosomal protein L17, rpl17a, uaz297, uaz297(gfu), umi4	endosperm cDNA 5C05G01, similar to barley ribosomal protein
4368	rpl17b	ribosomal protein L17b	GRMZM2G702426	B73 RefGen_v3	Gene	Chr4	44088617	44091066	rpl17b	60S ribosomal protein L17, rpl17b	
4369	rpl17c	ribosomal protein L17c	GRMZM2G148744	B73 RefGen_v3	Gene	Chr1	193824436	193827413	rpl17c	60S ribosomal protein L17, csu590(rpL17), rpl17c	
4370	rpl19	ribosomal protein L19	GRMZM2G171444	B73 RefGen_v3	Gene	Chr5	190804914	190807760	rpl19	50S ribosomal protein L19, csu566, PCO121693, PCO121693(440), ribosomal protein L19, rpl19	single copy cDNA
4371	rpl29	ribosomal protein L29	GRMZM2G028216	B73 RefGen_v3	Gene	Chr4	180610547	180612241	rpl29	L29, PCO125868, PCO125868(332), ribosomal protein L29, rpl29	cDNA sequence
4372	rpl30	ribosomal protein L30	GRMZM2G027728	B73 RefGen_v3	Gene	Chr8	2349748	2352938	rpl30	csu891(rpL30), PCO142140, ribosomal protein L30, rpl30, uaz5c02f01(gfu)	endosperm cDNA 5C02F01 similar to yeast ribosomal protein gene
4373	rpl32	ribosomal protein L32 homolog32	GRMZM2G145758	B73 RefGen_v3	Gene	Chr2	44796341	44798676	rpl32	cl1797_1(306), cl1797_1c, ribosomal protein L32 homolog32, rpl32, rpl32*-X75646	partial cDNA sequence homologous to ribosomal protein L32
4374	rpl39	ribosomal protein L39	GRMZM2G100467	B73 RefGen_v3	Gene	Chr5	213868446	213869401	rpl39	60S ribosomal protein L39, rpl39, zmec2	
4375	rpl40	50S ribosomal protein L40	GRMZM2G157007	B73 RefGen_v3	Gene	Chr8	1830837	1832237	rpl40	cl3822_1(648), cl3822_1b, npi220a, rpl40, rs131176178 , rs131176180 , rs131186990, rs131639711	npi220b was called npi553 but is listed in the database as npi220b
4376	rpl44	ribosomal protein L44	GRMZM2G009412	B73 RefGen_v3	Gene	Chr7	153856520	153858758	rpl44	60S ribosomal protein, L36, L36a/L44, ribosomal protein L44, RPL36aA, rpl44	vegetative meristem cDNA 7C02A07
4377	rpl5a	60S ribosomal protein L5-1 homolog a	GRMZM5G815894	B73 RefGen_v3	Gene	Chr3	168275428	168278435	rpl5a	rgpc385b(rpL5), rpl5a, rpl5a*(uaz189, uaz189, uaz189(L5), uaz189(rpL5), uaz260a, uaz260a(rpL5)	endosperm cDNA 5C05D11 (uaz189), similar to ribosomal protein
4378	rpl5b	60S ribosomal protein L5-1 homolog b	GRMZM2G163081	B73 RefGen_v3	Gene	Chr8	163737203	163740608	rpl5b	rpl5b	
4379	rpl7	ribosomal protein L7	GRMZM2G174919	B73 RefGen_v3	Gene	Chr2	135231574	135241133	rpl7	csu201, csu201(gfu), IDP1967, IDP601, ribosomal protein L7, rpl7	leaf cDNA csu201, similar to ribosomal protein
4380	rplp1	ribosomal large subunit pseudouridine s)	GRMZM2G018080	B73 RefGen_v3	Gene	Chr1	11692597	11694219	rplp1	rplp1, umc1160	
4381	rplp1	ribosomal large subunit pseudouridine s)	GRMZM2G315806	B73 RefGen_v3	Gene	Chr1	11687866	11691260	rplp1	rplp1, umc1160	
4382	rpo2	RNA polymerase2	GRMZM2G115564	B73 RefGen_v3	Gene	Chr9	105489333	105500736	rpo2	Ama gene encoding single-subunit RNA polymerase , RNA polymerase2, rpo2, rpo71, rpot, Rpot, T7-like RNA polymerase (rpoT2)	single copy, isolated by sequence homology and function confirmed by antibodies
4383	rpot1	RNA polymerase T phage-like 1	GRMZM2G381395	B73 RefGen_v3	Gene	Chr7	166160578	166175495	rpot1	CL1552_1b, RNA polymerase T phage-like 1, rpo3, RPO97, rpot1, rpoTm, ZEAma;RpoT;1	single copy, isolated by homology to rice gene with homology to yeast rpo41, function confirmed with antibodies
4384	rps1	Ribosomal protein S1-like1	GRMZM5G895282	B73 RefGen_v3	Gene	Chr7	16680018	16682350	rps1	CL57927_1, gnp_QCL1g11, gpm890, Ribosomal protein S1-like1, rpl39 , rps1, RpsA, RRP5 homolog	cDNA
4385	rps10	ribosomal protein S10	GRMZM2G095511	B73 RefGen_v3	Gene	Chr1	274598475	274600271	rps10	CL1073_2, CL1073_2(89), ribosomal protein S10, ribosomal protein S10 gene, rps10	
4386	rps11	ribosomal protein S11	GRMZM2G019325	B73 RefGen_v3	Gene	Chr10	141493143	141495837	rps11	CL2091_1, gsy53(rps11), IDP250, ribosomal protein S11, rps11, RS11, sc53, SC53, uaz251c(rpS11)	cDNA sequenced; homology to rps11; two bands hybridize in Southerns
4387	rps12	ribosomal proteinS12 (homolog)	GRMZM2G063340	B73 RefGen_v3	Gene	Chr7	21287558	21290256	rps12	ribosomal proteinS12 (homolog), rps12, uaz351a, uaz351a(rpS12), uaz5c08c03(gfu), uor1c, uor1c(rpS12)	endosperm cDNA 5C08C03 similar to rodent ribosomal protein
4388	rps13	ribosomal protein13	GRMZM2G158034	B73 RefGen_v3	Gene	Chr4	37626157	37628934	rps13	40S ribosomal protein S13, cytoplasmic ribosomal protein S13, PCO090232, PCO090232(470), ribosomal protein13, rps13, rps13*-X62455	cytoplasmic, complete amino acid sequence, deduced from cDNA, has 73% homology with rat cytoplasmic RPS13, small muligene family
4389	rps21a	40S ribosomal protein S21a	GRMZM2G093574	B73 RefGen_v3	Gene	Chr6	137097719	137100951	rps21a	40S ribosomal protein S21, IDP2457, IDP2560, rps21a, uaz2c01g06(gfu)	endosperm cDNA, similar to rice 40S ribosomal protein S21
4390	rps22a	ribosomal protein S22 homolog	GRMZM2G067303	B73 RefGen_v3	Gene	Chr9	142752102	142755422	rps22a	ribosomal protein S10p/S20e, ribosomal protein S22 homolog, rps22, rps22a, rps22*(M95062), umc320	multiple copies; leaf cDNA csu28 similar to Xenopus ribosomal protein
4391	rps24	ribosomal protein S24	GRMZM2G091383	B73 RefGen_v3	Gene	Chr5	151669661	151671447	rps24	40S ribosomal protein S24, PCO106630, ribosomal protein S24, rps24, uaz5c01e10(gfu)	endosperm cDNA 5C01E10, similar to animal ribosomal protein
4392	rps25	ribosomal protein S25	GRMZM2G084868	B73 RefGen_v3	Gene	Chr4	51745820	51747254	rps25	40S ribosomal protein S25-1 , csu974, PCO108152, ribosomal protein S25, rps25	single copy leaf cDNA, similar to tomato ribosomal protein
4393	rps27	ribosomal protein S27	GRMZM2G066222	B73 RefGen_v3	Gene	Chr4	218054500	218057037	rps27	PCO122603, ribosomal protein S27, rps27, uaz5c09a02(gfu)	endosperm cDNA 5C09A02
4394	rps27b	ribosomal protein S27b	GRMZM2G377600	B73 RefGen_v3	Gene	Chr5	160795273	160797497	rps27b	PCO122601, PCO122601(425), rps27b, rps27b(425)	
4395	rps27c	ribosomal protein S27c	GRMZM2G132121	B73 RefGen_v3	Gene	Chr5	7529197	7531742	rps27c	PCO122602b, rgpc975(rpS27), rps27c	
4396	rps3	ribosomal protein S3	GRMZM2G099352	B73 RefGen_v3	Gene	Chr10	75709393	75711864	rps3	40S ribosomal protein S3, PCO108959, ribosomal protein S3, rps3, TIDP2739, umc1179	cDNA clone contains SSR umc1179
4397	rps4	ribosomal protein S4	GRMZM2G125271	B73 RefGen_v3	Gene	Chr5	1489127	1491854	rps4	ribosomal protein S4, rps4	vegetative meristem cDNA 7C02E04 similar to cytoplasm ribosomal protein
4398	rps5	ribosomal protein S5	GRMZM2G156673	B73 RefGen_v3	Gene	Chr8	6591423	6593377	rps5	PCO091587, PCO091587(582), ribosomal protein S5, rps5, uaz5c06a11(gfu)	endosperm cDNA 5C06A11 similar to ribosomal protein
4399	rps6	ribosomal proteinS6	GRMZM2G054136	B73 RefGen_v3	Gene	Chr7	166416769	166429948	rps6	ribosomal proteinS6, rps6, rps6*-U92045, uaz119, uaz119b, uaz119b(rpS6), UAZ119B(S6)	mature mRNA stored in embryo axes
4400	rps8	ribosomal protein S8 homolog	GRMZM2G336875	B73 RefGen_v3	Gene	Chr4	232843893	232846622	rps8	csu34, csu34b(rpS8), csu34(rps8), csu361(rpS8), csuh34, ribosomal protein S8 homolog, rps8, rps8*(M95064), rps8*-U64436, umc326	multiple copies; leaf cDNA csu34 similar to ribosomal protein
4401	rps8 (cp)	30S ribosomal protein S8 gene	GRMZM5G845244	B73 RefGen_v3	Gene	ChrPt	78488	78898	rps8 (cp)	30S ribosomal protein S8 gene, rps8, rpS8, rps8 (cp)	
4402	rrb1	related to retinoblastoma1	GRMZM2G003043	B73 RefGen_v3	Gene	Chr2	224644895	224652148	rrb1	homolog1, retinoblastoma protein, retinoblastomarelated1, rrb1, uaz191, uaz191(gfu), zmrb1, ZmRb-1	nuclear, low copy, ubiquitous expression; phosphorylation dependent role in cell division
4403	rrb2	related to retinoblastoma2	GRMZM2G153150	B73 RefGen_v3	Gene	Chr4	192376709	192383877	rrb2	CL1187_-3, CL1187_-3(342), PZA00193, RB, rbr2, related to retinoblastoma2, rrb2, RRB2a, RRB2b, rs128284455, rs55626540 , ss196415897	alternatively spliced cDNAs, ubiquitous, see rrb1
4404	rrb3	retinoblastoma family3	GRMZM2G033828	B73 RefGen_v3	Gene	Chr1	196158449	196165691	rrb3	rbr3, RBR3, retinoblastoma family3, rrb3	
4405	rrph1	RAR1 disease resistance protein homolo	GRMZM5G868908	B73 RefGen_v3	Gene	Chr5	169710822	169727140	rrph1	RAR1, rrph1	
4406	rs1	rough sheath1	GRMZM2G028041	B73 RefGen_v3	Gene	Chr7	3667975	3674168	rs1	hb132, Homeobox-transcription factor 132, IDP1962, K-4, kn2, PCO135030, pge(E7), rough sheath1, rs1	shoot meristem and developing stem specific; dominant Rs1 plants have extreme ligule disorganization (aka kn2)
4407	rs2	rough sheath2	GRMZM2G403620	B73 RefGen_v3	Gene	Chr1	154968134	154972600	rs2	rough sheath2, rs2, umc1124, umc1124(rs2), umc1703, ZmMYB143	short, zigzag plants with warty, distorted sheaths and leaves
4408	rtcl1	RTCS-like1	AC149818.2_FG009	B73 RefGen_v3	Gene	Chr9	152747407	152748234	rtcl1	rtcl1, ZmLBD43	homologous to rtcs1
4409	rtcs1	rootless concerning crown and seminal r	GRMZM2G092542	B73 RefGen_v3	Gene	Chr1	10824798	10826042	rtcs1	Lob Domain Protein, root deficient1, rootless concerning crown and seminal roots1, rtcs1, ZmLBD2	root system reduced solely to a primary root yet plants can be carried to seed; cyclin cDNAs absent; naphthalene acetic acid induces adventitious roots
4410	rte1	rotten ear1	GRMZM2G166159	B73 RefGen_v3	Gene	Chr1	149321818	149326540	rte1	BOR1, boron transporter1, pco111657(44), pco111657a, rotten ear1, rs131804744 , rs131804751, rte, rte1	mutants show distinct defects in vegetative and reproductive development, eventually causing widespread sterility in its tassel and ear.
4411	rth1	roothair defective1	GRMZM2G099056	B73 RefGen_v3	Gene	Chr1	253953554	253966804	rth1	exocyst complex component SEC3A, IDPrth1, roothair defective1, rth1	roothairs do not elongate in rth1 homozygotes; plants are dwarfed and appear nutrient deficient; genomic sequence

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
4412	rth3	roothair defective3	GRMZM2G377215	B73 RefGen_v3	Gene	Chr1	47509017	47511525	rth3	AY112035, roothair defective3, rth3	like rth1, but "stocking cap" roothair initials under electron microscope
4413	rth6	roothairless6	GRMZM2G436299	B73 RefGen_v3	Gene	Chr1	104617335	104621459	rth6	cellulose synthase-like protein D1, rth6	mutant roothairs do not elongate; encodes a D-type cellulose synthase
4414	rtl1	reversion-to-ethylene sensitivity1 like1	GRMZM5G832994	B73 RefGen_v3	Gene	Chr8	154129622	154132963	rtl1	rtl1, ZmRTL1	Over-expression reduces ethylene responses
4415	rtl2	reversion-to-ethylene sensitivity1 like2	GRMZM2G077293	B73 RefGen_v3	Gene	Chr3	203830116	203833100	rtl2	AY105849, IDP745, PCO098078, rtl2, ZmRTL2	Over-expression reduces ethylene responses
4416	rtl3	reversion-to-ethylene sensitivity1 like3	GRMZM2G121208	B73 RefGen_v3	Gene	Chr6	161903231	161906492	rtl3	rtl3, ZmRTL3	Over-expression reduces ethylene responses
4417	rtl4	reversion-to-ethylene sensitivity1 like4	GRMZM2G039592	B73 RefGen_v3	Gene	Chr1	288924643	288926264	rtl4	rtl4, TIDP3380, ZmRTL4	Over-expression reduces ethylene responses
4418	rtp1	root preferential1	GRMZM2G017557	B73 RefGen_v3	Gene	Chr4	11930712	11932207	rtp1	CL2555_1, O-methyltransferase ZRP4, OMT, rtp1, Zea root preferential4, zrp4	cDNA, 1.4kb, preferentially accumulates in roots of young plants; likely in suberin pathway
4419	rul1	rum1-like1	GRMZM2G163848	B73 RefGen_v3	Gene	Chr8	150095586	150100818	rul1	auxin-responsive Aux/IAA family member, IAA5, rul1, ZmIAA10, ZmIAA29, ZmIAA39	
4420	rum1	rootless with undetectable meristems1	GRMZM2G037368	B73 RefGen_v3	Gene	Chr3	209176237	209179599	rum1	iaa13, rs129403618, rum1, ZmIAA10	primordia for seminal roots and for laterals on the primary root absent
4421	rws1	RNA recognition water-stress protein1	GRMZM2G019919	B73 RefGen_v3	Gene	Chr2	21882159	21886917	rws1	PCO118630, PCO118630(122), RNA recognition water-stress protein1, rws1, ws1	water-stress protein, with RNA recognition motif
4422	rxo1	reaction to X. oryzae1	GRMZM2G334584	B73 RefGen_v3	Gene	Chr6	8100151	8105044	rxo1	disease resistance protein RPM1-like, pic19, rba1, reaction to X. oryzae1, rxo1, si606060H09b	necrotic or hypersensitive reaction to inoculant
4423	rz474a(dnaj)		GRMZM2G134980	B73 RefGen_v3	Gene	Chr5	16340013	16344789	rz474a(dnaj)	rs130000309 , rs130000312 , rs131176955 , rz474a, rz474a(dnaj)	NCBI: putative dnaJ chaperone family protein
4424	rzfl1	RING zinc finger protein-like1	GRMZM2G113295	B73 RefGen_v3	Gene	Chr9	147635621	147639545	rzfl1	PCO119899, PCO119899(703), PZA01715, RING zinc finger protein-like, rs131161027, rs55622745 , rzfl1, ss196417282	
4425	s1fa1	S1Fa-like-transcription factor 1	GRMZM2G056929	B73 RefGen_v3	Gene	Chr2	59385197	59387466	s1fa1		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4426	sacd1	stearoyl-acyl-carrier-protein desaturase1	GRMZM5G852502	B73 RefGen_v3	Gene	Chr3	160709513	160714196	sacd1	gnp_QAN3e02a, gpm375a, PCO105183, PCO105183(244), PZA01383, sacd1, ZmSAD1	encodes Stearoyl-acyl carrier protein desaturase
4427	sacd10	stearoyl-acyl-carrier-protein desaturase1(	GRMZM2G119305	B73 RefGen_v3	Gene	Chr10	61689660	61692217	sacd10	sacd10	
4428	sacd11	stearoyl-acyl-carrier-protein desaturase1'	AC215690.3_FG002	B73 RefGen_v3	Gene	Chr10	106806918	106810315	sacd11	AC2156903_FG002, csu333, sacd11	
4429	sacd2	stearoyl-acyl-carrier-protein desaturase2	GRMZM2G180399	B73 RefGen_v3	Gene	Chr8	161386924	161390467	sacd2	acyl-desaturase, cl3036_1, cl3036_1(640), sacd2, ZmSAD, ZmSAD2	encodes Stearoyl-acyl carrier protein desaturase
4430	sacd3	stearoyl-acyl-carrier-protein desaturase3	GRMZM2G143625	B73 RefGen_v3	Gene	Chr1	107371746	107373355	sacd3	acyl-desaturase, pco112439, PHM3463, pza01254, rs131175300, rs55625411 , sacd3, ss196414590	
4431	sacd4	stearoyl-acyl-carrier-protein desaturase4	GRMZM2G003368	B73 RefGen_v3	Gene	Chr1	120854790	120856675	sacd4	sacd4	
4432	sacd5	stearoyl-acyl-carrier-protein desaturase5	GRMZM2G026793	B73 RefGen_v3	Gene	Chr2	74671225	74675172	sacd5	sacd5	
4433	sacd6	stearoyl-acyl-carrier-protein desaturase6	GRMZM2G027673	B73 RefGen_v3	Gene	Chr4	102114754	102116797	sacd6	sacd6	
4434	sacd7	stearoyl-acyl-carrier-protein desaturase7	GRMZM2G073540	B73 RefGen_v3	Gene	Chr5	48865287	48866779	sacd7	sacd7	
4435	sacd8	stearoyl-acyl-carrier-protein desaturase8	GRMZM5G883417	B73 RefGen_v3	Gene	Chr7	136213370	136214936	sacd8	sacd8	
4436	sacd9	stearoyl-acyl-carrier-protein desaturase9	GRMZM2G316362	B73 RefGen_v3	Gene	Chr8	164731500	164733879	sacd9	cl27608_1, cl27608_1(641), sacd9	
4437	sad1	shikimate dehydrogenase1	GRMZM2G014376	B73 RefGen_v3	Gene	Chr10	25983459	25988271	sad1	PCO083519, PCO083519(724), PZA02853, rz261a(sad), sad1, shikimate dehydrogenase1	electrophoretic mobility; plastidial; monomeric
4438	saf1	safener induced1	GRMZM2G042639	B73 RefGen_v3	Gene	Chr1	43124855	43126948	saf1	In2-1, saf1, safener induced1	
4439	sal1	supernumerary aleurone1	GRMZM2G117935	B73 RefGen_v3	Gene	Chr9	95580781	95583611	sal1	sal1, superal1, supernumerary aleurone1	Mutant allele contains up to seven layers of aleurone cells
4440	sam1	S-adenosylmethionine decarboxylase1	GRMZM2G125635	B73 RefGen_v3	Gene	Chr10	128008870	128011887	sam1	csu217, csu217(gfu), csu6B, csu6b(sam), csuh6, S-adenosylmethione decarboxylase1, S-adenosylmethionine decarboxylase1, sam1, stm*-csu217, umc305	single copy leaf cDNA csu217; aka csu6b
4441	sam2	S-adenosyl methionine decarboxylase2	GRMZM2G154397	B73 RefGen_v3	Gene	Chr2	33120217	33123687	sam2	AY103590, csu6a, csu6a(sam), csu6(gutr), gnp_QAW2d11a, gpm411a, gsy108(gutr), MZ2G1, PCO098412, sam2, sam*-mz6g1, sam*-Y07767, umc1326	leaf cDNA, csu6
4442	sar1	SAR homolog1	GRMZM2G038356	B73 RefGen_v3	Gene	Chr3	63530359	63532921	sar1	05c03g12, sar1, SAR homolog1, uaz151, uaz151(GTPB), uaz151(sar)	endosperm cDNA 5C03G12 (uaz151), similar to Arabidopsis sar1 homologue
4443	sat1	serine acetyltransferase1	GRMZM2G069203	B73 RefGen_v3	Gene	Chr8	155020473	155021850	sat1	PCO145512, sat1, satase isoform I	
4444	sat2	serine acetyltransferase2	GRMZM2G013430	B73 RefGen_v3	Gene	Chr1	24049836	24051294	sat2	sat2, satase isoform II	
4445	sat3	serine acetyltransferase3	GRMZM5G816110	B73 RefGen_v3	Gene	Chr6	159594188	159596729	sat3	sat3, satase isoform III	
4446	saur1	small auxin up RNA1	GRMZM2G466908	B73 RefGen_v3	Gene	Chr6	86723314	86724099	saur1	saur1, small auxin up RNA1, umc1818	early auxin responsive cDNA, transgenic expression; SSR umc1818
4447	sbe1	starch branching enzyme1	GRMZM2G088753	B73 RefGen_v3	Gene	Chr5	63346023	63352952	sbe1	1,4-alpha-glucan branching enzyme, branching enzyme1, bre1, PCO072723, sbe1, Sbe1, sbe1a, spe1, starch branching enzyme1	maize kernel cDNA sequence is similar to starch branching enzyme I of bacteria, encodes a putative 64-amino acid plastid transit peptide (aka sbe1)
4448	sbe3	starch branching enzyme3	GRMZM2G073054	B73 RefGen_v3	Gene	Chr2	59216710	59226937	sbe3	sbe2a, sbe3, starch branching enzyme 2a, starch branching enzyme3, starch branching enzyme IIa, umc1997	
4449	sbip1a	small basic membrane intrinsic protein1a	GRMZM2G113470	B73 RefGen_v3	Gene	Chr4	9896475	9902642	sbip1a	PCO144704, PCO144704(288), sbip1a, small basic membrane intrinsic protein1a, ZmSIP1-1	
4450	sbip1b	small basic membrane intrinsic protein1b	GRMZM2G060922	B73 RefGen_v3	Gene	Chr8	106815228	106820100	sbip1b	aquaporin SIP1-2, sbip1b, small basic membrane intrinsic protein1b, ZmSIP1-2	
4451	sbip2a	small basic membrane intrinsic protein2a	GRMZM2G175038	B73 RefGen_v3	Gene	Chr1	52193686	52196261	sbip2a	sbip2a, small basic membrane intrinsic protein2, ZmSIP2-1	
4452	sbp1	SBP-domain protein1	GRMZM2G111136	B73 RefGen_v3	Gene	Chr5	88828896	88831814	sbp1	sbp1, sbp10, SBP-domain protein1, SBP-transcription factor 10, Squamosa promoter Binding Protein, umc1575, umc1624, ZMSBP1	cDNA sequence, SSR's umc1575, umc1624
4453	sbp11	SBP-transcription factor 11	GRMZM2G109354	B73 RefGen_v3	Gene	Chr8	106259354	106278403	sbp11		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4454	sbp12	SBP-transcription factor 12	GRMZM2G126827	B73 RefGen_v3	Gene	Chr5	86820671	86824256	sbp12		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4455	sbp13	SBP-transcription factor 13	GRMZM2G113779	B73 RefGen_v3	Gene	Chr2	202626703	202628534	sbp13		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4456	sbp16	SBP-transcription factor16	GRMZM2G169270	B73 RefGen_v3	Gene	Chr1	189617226	189623070	sbp16	rs128283441 , rs131183511 , rs131183512 , rs131183513 , rs131183514 , rs131183515 , rs131826952 , rs131826954, rs55625692 , sbp16, umc1398	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.. NCBI: squamosa promoter-binding-like protein 15
4457	sbp17	SBP-transcription factor 17	GRMZM2G156756	B73 RefGen_v3	Gene	Chr1	295502079	295509029	sbp17		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4458	sbp18	SBP-transcription factor 18	GRMZM2G371033	B73 RefGen_v3	Gene	Chr8	161072193	161075285	sbp18		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4459	sbp19	SBP-transcription factor 19	GRMZM2G163813	B73 RefGen_v3	Gene	Chr4	236142134	236146366	sbp19		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4460	sbp2	SBP-domain protein2	GRMZM2G168229	B73 RefGen_v3	Gene	Chr4	235838405	235842060	sbp2	sbp2, sbp26, SBP-domain protein2, SBP-transcription factor 26, Squamosa promoter Binding Protein, umc1573, umc1574, umc1623, ZMSBP2	cDNA sequence; SSR's umc1573, umc1574, umc1623

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
4461	sbp20	SBP-transcription factor 20	GRMZM2G065451	B73 RefGen_v3	Gene	Chr4	238318275	238321628	sbp20		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4462	sbp21	SBP-transcription factor 21	GRMZM2G148467	B73 RefGen_v3	Gene	Chr10	139106686	139109641	sbp21		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4463	sbp22	SBP-transcription factor 22	GRMZM5G878561	B73 RefGen_v3	Gene	Chr3	159420552	159425244	sbp22		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4464	sbp23	SBP-transcription factor 23	GRMZM2G126018	B73 RefGen_v3	Gene	Chr2	190489085	190493109	sbp23		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4465	sbp24	SBP-transcription factor 24	GRMZM2G133646	B73 RefGen_v3	Gene	Chr3	50944910	50952180	sbp24		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4466	sbp25	SBP-transcription factor 25	GRMZM2G414805	B73 RefGen_v3	Gene	Chr5	58084257	58088916	sbp25		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4467	sbp27	SBP-transcription factor 27	GRMZM2G097275	B73 RefGen_v3	Gene	Chr5	77973223	77978271	sbp27		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4468	sbp28	SBP-transcription factor 28	GRMZM2G058588	B73 RefGen_v3	Gene	Chr10	145726895	145730461	sbp28		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4469	sbp29	SBP-transcription factor 29	GRMZM2G067624	B73 RefGen_v3	Gene	Chr7	151254398	151256086	sbp29		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4470	sbp3	SBP-domain protein3	GRMZM2G101499	B73 RefGen_v3	Gene	Chr6	95232272	95235580	sbp3	sbp14, sbp3, sbp3 (Cardon), SBP-domain protein3, SBP-transcription factor 14, Squamosa promoter Binding Protein, umc1572, umc1595, ZMSBP3	cDNA sequence with SSR's umc1572, umc1595
4471	sbp3 (GRASSIUS	SBP-transcription factor 3	GRMZM2G106798	B73 RefGen_v3	Gene	Chr4	17511896	17523810	sbp3 (GRASS	sbp3, sbp3 (GRASSIUS), squamosa promoter-binding protein-like (SBP domain) transcription factor family protein	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4472	sbp31	SBP-transcription factor 31	GRMZM2G156621	B73 RefGen_v3	Gene	Chr5	131224969	131228486	sbp31		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4473	sbp4	SBP-domain protein4	Zm00001d046906	Zm-B73-REFERENCE-G	Gene	Chr9	109930589	109934102	sbp4	sbp4, sbp4 (Cardon), SBP-domain protein4, Squamosa promoter Binding Protein, umc1570, umc1571, ZMSBP4	cDNA sequence includes SSR's umc1571 and umc1570
4474	sbp4 (GRASSIUS	SBP-transcription factor 4	GRMZM2G110742	B73 RefGen_v3	Gene	Chr7	57077560	57082391	sbp4 (GRASS	sbp4 (GRASSIUS)	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4475	sbp5	SBP-transcription factor 5	GRMZM2G061734	B73 RefGen_v3	Gene	Chr2	192807845	192812893	sbp5		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4476	sbp6	SBP-transcription factor 6	GRMZM2G138421	B73 RefGen_v3	Gene	Chr5	1846096	1853085	sbp6		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4477	sbp7	SBP-transcription factor 7	GRMZM2G098557	B73 RefGen_v3	Gene	Chr4	200132272	200137588	sbp7		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4478	sbp9	SBP-transcription factor 9	GRMZM2G081127	B73 RefGen_v3	Gene	Chr8	167824	174330	sbp9		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4479	sbt1	subtilisin1	GRMZM2G437435	B73 RefGen_v3	Gene	Chr10	15035904	15038278	sbt1	sbt1, zmsbt1	expressed exclusively in the in the aleurone layer of the maize kernel within a short developmental time frame
4480	sbt2	subtilisin2	GRMZM2G039538	B73 RefGen_v3	Gene	Chr2	207706084	207708708	sbt2	sbt2, zmsbt2	expressed in the in the basal kernel in very early stages of development; also weakly expressed in unpollinated female flowers.
4481	sbt3	subtilisin3	GRMZM2G363552	B73 RefGen_v3	Gene	Chr7	160351370	160353986	sbt3	sbt3, zmsbt2	paralog of sbt2
4482	sca1	short chain alcohol dehydrogenase1	GRMZM2G332976	B73 RefGen_v3	Gene	Chr5	3146074	3147825	sca1	csu149, csu149a, csu149(sca), gnp_QAL11a02, gpm351, pco109491, pco109491(458), sca1, sex determination protein tasselseed-2, short chain alcohol dehydrogenase1, umc382, ZmABA2	single copy leaf cDNA, csu149, similar to ts2
4483	sci1	subtilisin-chymotrypsin inhibitor homolo	GRMZM2G028393	B73 RefGen_v3	Gene	Chr8	133996633	133997534	sci1	CI-ms, maize proteinase inhibitor, MPI, PCO087322, PCO087322(631), pis7, sci1, serine proteinase inhbitor, subtilisin-chymotrypsin inhibitor homolog1	cDNA from germinating embryo infected with Fusarium moniliforme; similar to subtilisin-chymotrypsin inhibitor
4484	scl1	scarecrow-like1	GRMZM2G023872	B73 RefGen_v3	Gene	Chr8	72494685	72496501	scl1	CL1220_-2, CL1220_-2(613), DELLA protein gibberellin-insensitive (GAI)-like, gras20, GRAS-transcription factor 20, scarecrow-like1, scl1	cDNA sequence
4485	scp1	serine carboxypeptidase1	GRMZM2G075676	B73 RefGen_v3	Gene	Chr10	120298584	120303328	scp1	pco137899, scp1, ZmSCP	may play at role in the disease resistance response
4486	scro1	scarecrow1	GRMZM2G131516	B73 RefGen_v3	Gene	Chr4	185481408	185484991	scro1	SCARECROW, scarecrow1, SCR, scr1, scro1, siaf263457(336), siaf263457a, ZmGRAS78, ZmSCR	mRNA expressed in endodermis and quiescent center of root, influencing radial pattern
4487	sda1	severe depolymerization of actin1	GRMZM2G121074	B73 RefGen_v3	Gene	Chr2	7661318	7666576	sda1	sda1	
4488	sdg104	SET domain-containing protein SET104	GRMZM2G021044	B73 RefGen_v3	Probed Site	Chr2	21907392	21910615	sdg104	PZA03633, PZA03634, PZA03635, PZA03636, rs129029312, sdg104, set104, SET domain-containing protein SET104, ss196415027	
4489	sdg105a		GRMZM2G140577	B73 RefGen_v3	Probed Site	Chr8	119356309	119359897	sdg105a	rs131175872, rs55626689 , sdg105a, ss196416898, ss196416900, ss196416902, ss196416904, ss196416906	
4490	sdg110b		GRMZM2G033694	B73 RefGen_v3	Gene	Chr2	174419091	174436402	sdg110b	PZA03644, rs128285184, rs55625341 , ss196415199	
4491	sdg113		GRMZM2G139710	B73 RefGen_v3	Probed Site	Chr3	187087134	187091766	sdg113	PZA03647, PZA03648, PZA03649, rs131175540, rs131175541, rs131175542, sdg113, set113, ss196415571, ss196415573, ss196415575	
4492	sdg119		GRMZM2G300955	B73 RefGen_v3	Probed Site	Chr2	177370536	177375918	sdg119	PZA03659, PZA03660, PZA03661, rs129176023, rs129176024, rs131175453, rs131175454, rs55624185 , sdg119, set119, ss196415203, ss196415205, ss196415207, ss196415209	
4493	sdg123	SET domain protein123	GRMZM2G080462	B73 RefGen_v3	Gene	Chr1	242199385	242208360	sdg123	AY110349, sdg123, set123, SET domain protein123	histone methylation; one of 3 with disrupted (S-ET) domains among 22 SET domain proteins
4494	sdg136		GRMZM2G034288	B73 RefGen_v3	Gene	Chr7	38217966	38231106	sdg136	PZA03687, PZA03688, rs131175795, rs55625925 , ss196416578	
4495	sdg137		GRMZM2G025924	B73 RefGen_v3	Gene	Chr2	170175284	170177778	sdg137	PZA03690, PZA03692, rs131175449, rs131953786, ss196415185, ss196415187	
4496	sdg140		GRMZM2G164277	B73 RefGen_v3	Gene	Chr2	7527529	7531928	sdg140	PZA03699, PZA03700, PZA03701, rs129008749, rs131175395, rs131175396, ss196414970, ss196414972, ss196414975	
4497	sdg140		GRMZM2G164400	B73 RefGen_v3	Gene	Chr2	7519489	7528034	sdg140	PZA03699, PZA03700, PZA03701, rs129008749, rs131175395, rs131175396, ss196414970, ss196414972, ss196414975	
4498	se1	sugary-enhancer1	AC217415.3_FG004	B73 RefGen_v3	Gene	Chr2	230653379	230653900	se1	se1, sugary-enhancer1	high sugar content with su1; light yellow endosperm; freely wrinkled in Ill677a
4499	see2a	senescence enhanced2a	GRMZM2G081626	B73 RefGen_v3	Gene	Chr8	137286214	137293588	see2a	legumain-like protease, see2a, senescence enhanced2a	
4500	see2b	senescence enhanced2b	GRMZM2G093032	B73 RefGen_v3	Gene	Chr3	225910755	225916465	see2b	legumain-like protease, PCO131778a, see2b, senescence enhanced2b	
4501	ser2	seryl-tRNA synthetase	GRMZM2G169160	B73 RefGen_v3	Gene	Chr4	5670956	5682556	ser2	cdo520(ser), ser2, seryl-tRNA synthetase2, siy13053, siy13053(371)	complements E. coli mutant; organellar, possibly mitochondrial
4502	serk1	somatic embryogenesis receptor-like kin	GRMZM5G870959	B73 RefGen_v3	Gene	Chr10	121772419	121777860	serk1	rs131176003, rs131176004, serk1, somatic embryogenesis receptor-like kinase1, ss196417423, ss196417425, ss196417427, ss196417429, ss196417431, ZmSERK1	single copy cDNA with 79% sequence identity with serk2, and significant sequence homology to carrot and Arabidopsis SERK genes;
4503	serk2	somatic embryogenesis receptor-like kin	GRMZM2G115420	B73 RefGen_v3	Gene	Chr5	176261637	176267226	serk2	rs131175707, rs131175708, rs131175709, serk2, somatic embryogenesis receptor-like kinase2, ss196416209, ss196416211, ss196416213, ss196416215, umc2304, ZmSERK2	a single copy DNA with homology to carrot and Arabidopsis SERK genes;SSR umc2304
4504	serk3	somatic embryogenesis receptor-like kin	GRMZM2G150024	B73 RefGen_v3	Gene	Chr4	124660672	124667062	serk3	serk3, somatic embryogenesis receptor-like kinase3, ZmSERK3	a single copy cDNA;
4505	sfb1	SF1 binding protein candidate1	GRMZM2G147424	B73 RefGen_v3	Gene	Chr10	113732417	113734756	sfb1	DNA-binding protein S1FA2, PCO095455, PCO095455(746), S1FA, s1fa2, S1Fa-like-transcription factor 2, SF1 binding protein candidate1, sfb1, uaz5c09c08(gfu)	endosperm cDNA 5C09C08 similar to spinach transcription factor
4506	sfp1	sulfate permease1	GRMZM2G159632	B73 RefGen_v3	Gene	Chr1	24403203	24407782	sfp1	sfp1, ST1, sulfate permease1, ZmST1-701	
4507	sgb101	silencing gene B101	GRMZM2G106245	B73 RefGen_v3	Probed Site	Chr2	6988977	6991901	sgb101	sgb101, silencing gene B, ZmHAG10	
4508	sgb102	silencing gene B 102	GRMZM2G123159	B73 RefGen_v3	Gene	Chr1	264230117	264233270	sgb102	CL19754_1, GNAT19, GNAT transcription factor (GNAT19), sgb102, silencing gene B 102, umc2028, ZmHAG5	
4509	sgo1	shugoshin centromeric cohesion1	GRMZM2G074082	B73 RefGen_v3	Gene	Chr7	18531204	18535522	sgo1	AY109536, CL5684_1, gnp_AW055587, gpm134, sgo1, shugoshin centromeric cohesion1	male and female sterile; meiosis; centromere cohesion; segregation of sister chromatids.

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
4510	sh1	shrunken1	GRMZM2G089713	B73 RefGen_v3	Gene	Chr9	11500926	11507687	sh1	phi033, phi044, PHM1218, rs130965549, rs130965561, rs131175922, rs131175923, sc66, SC66SS1, sh1, SH-1 sucrose synthase, shrunken1, ss196417091, ss196417093,	inflated endosperm collapses on drying, forming smoothly indented kernels; sucrose synthase-sh1 of endosperm (compare sus1 and sus2); homotetramer; SSRs phi028, 044, 033
4511	sh2	shrunken2	GRMZM2G429899	B73 RefGen_v3	Gene	Chr3	216495981	216505345	sh2	Agp5, agplen, gsy59a(sh2), rs131175558, rs131175559, sc58, sh2, shrunken2, ss196415630, ss196415633, ZmAGPL1	endosperm ADPG pyrophosphorylase subunit (compare bt2); application: "supersweet" sweet corn - kernels sugar-sweet for long period
4512	shbp1	sedoheptulose bisphosphatase1	GRMZM6G741210	B73 RefGen_v3	Gene	Chr3	178865444	178897469	shbp1	csu813, csuh00813, csuh813, PCO078556(250), PCO078556a, sbp1, sedoheptulose bisphosphatase1, shbp1	leaf cDNA csu813 similar to plant Calvin cycle enzyme
4513	shpl1	shepherd-like1	GRMZM2G399073	B73 RefGen_v3	Gene	Chr5	61555816	61564735	shpl1	PCO098403, shpl1	
4514	si1	silky1	GRMZM2G139073	B73 RefGen_v3	Gene	Chr6	84949624	84954298	si1	at1, ms-si, PZD00072, si1, si1-at, silky1, ts8, ZmMADS11	(aka ts8, ms-si) multiple silks in ear; sterile tassel with silks
4515	si605085g01		GRMZM2G462062	B73 RefGen_v3	Probed Site	Chr7	47411204	47423386	si605085g01	PZA03363, rs130530777, rs55625443 , si605085g01(547), ss196416597	
4516	si606065d12		GRMZM2G149481	B73 RefGen_v3	Gene	Chr1	33322465	33326460	si606065d12	Auxin transporter-like protein 3, si606065d12(14)	
4517	si683005e02		GRMZM2G082007	B73 RefGen_v3	Gene	Chr4	169989717	169993675	si683005e02	si683005e02(328), ZmCOMT2	
4518	si946003e12		GRMZM2G378452	B73 RefGen_v3	Gene	Chr3	23844186	23847768	si946003e12	si946003e12, si946003e12(208)	
4519	sid1	sister of indeterminate spikelet1	GRMZM2G176175	B73 RefGen_v3	Gene	Chr7	22015365	22026546	sid1	ereb121, pza03344, rs130489474, rs130489478, sid1, sister of indeterminate spikelet1, sister of tasselseed6	inflorescence architecture, apparent target of tasselseed4 microRNA (Chuck et al 2008),
4520	sig1	Sigma70-like-transcription factor 1	GRMZM2G100086	B73 RefGen_v3	Gene	Chr1	39680080	39682830	sig1		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4521	sig1A	sigma factor 1A	GRMZM2G006736	B73 RefGen_v3	Gene	Chr10	75590751	75594655	sig1A	CL1542_1b, RNA polymerase sigma factor sigA, sig1, sig1A, sig9, ZmSig1A	
4522	sig1B	sigma factor 1B	GRMZM2G543629	B73 RefGen_v3	Gene	Chr4	30954610	30958718	sig1B	cl1542_1(299), cl1542_1a, gnp_QAE25f10a, gpm287a, sig1B, sig2, sig5, Sigma70-like-transcription factor 5, sigma factor of plastid RNA polymerase, ZmSig1B	
4523	sig2	Sigma70-like-transcription factor 2	GRMZM2G164084	B73 RefGen_v3	Gene	Chr1	264527252	264530002	sig2		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4524	sig2A	sigma factor sig2A	GRMZM2G143392	B73 RefGen_v3	Gene	Chr4	17349492	17354543	sig2A	AY110573, CL1596_1, gnp_QCA7c06a, gpm580a, sig1, sig2A, sigma factor sig2a, ZmSig1, ZmSig2A, ZmSIG4	
4525	sig2B	sigma-like factor2B	GRMZM2G100086	B73 RefGen_v3	Gene	Chr1	39680080	39682830	sig2B	siaf099111, sig1, sig2, sig2B, Sigma70-like-transcription factor 1, ZmSig2, ZmSig2B	
4526	sig3	Sigma70-like-transcription factor 3	GRMZM2G003182	B73 RefGen_v3	Gene	Chr2	231692547	231695297	sig3		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4527	sig5	Sigma70-like-transcription factor 5	GRMZM2G543629	B73 RefGen_v3	Gene	Chr4	30954610	30958718	sig5	sig1B	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4528	sig6	sigma-like factor6	GRMZM2G144196	B73 RefGen_v3	Gene	Chr5	647402	650238	sig6	siaf099112(402), siaf099112a, sig3, sig6, Sigma70-like-transcription factor 6, sigma-like factor6, ZmSig3, ZmSig6	
4529	sig7	Sigma70-like-transcription factor 7	GRMZM5G830932	B73 RefGen_v3	Gene	Chr6	168024789	168028473	sig7		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4530	sig8	Sigma70-like-transcription factor 8	GRMZM2G077436	B73 RefGen_v3	Gene	Chr6	168300149	168302190	sig8		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4531	sig9	Sigma70-like-transcription factor 9	GRMZM2G006736	B73 RefGen_v3	Gene	Chr10	75590751	75594655	sig9	sig1A	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4532	simk1	salt-induced MAP kinase1	GRMZM2G127141	B73 RefGen_v3	Gene	Chr9	125383956	125388954	simk1	MAGI_107464, MAPK, PCO138354, rs131129233, rs131129234, rs131183716 , rs131183717, salt-induced MAP kinase1, simk1	
4533	sin1	sin homolog1	GRMZM2G319104	B73 RefGen_v3	Gene	Chr6	46506476	46518999	sin1	sin1, sin homolog1, uaz5c01e06(gfu)	endosperm cDNA 5C01E06, similar to yeast SIN3
4534	sip1	stress-induced protein1	GRMZM2G374971	B73 RefGen_v3	Gene	Chr7	160254708	160256026	sip1	antifungal zeamatin-like protein, chem4, sip1, stress-induced protein1	cDNA sequence homologous to thaumatin-like protein
4535	sir1	sulfite reductase1	GRMZM2G090338	B73 RefGen_v3	Gene	Chr6	157217904	157222724	sir1	CL122_1, CL122_1(519), ferredoxin-sulfite reductase, sir1, sulfite reductase1	
4536	sk1	silkless ears1	GRMZM2G021786	B73 RefGen_v3	Gene	Chr2	27602064	27606189	sk1	silkless ears1, sk1	pistils abort, no silks
4537	sln1	sister of liguleless narrow1	GRMZM2G009506	B73 RefGen_v3	Gene	Chr5	201993077	201996818	sln1	serine/threonine-protein kinase receptor, sln1	A paralog of the lgn1 gene
4538	sm1	salmon silks1	GRMZM2G031311	B73 RefGen_v3	Gene	Chr6	133839846	133843446	sm1	pco142331, RHM1, salmon silks1, sm1	silks salmon color with P1-rr and P1-wr, brown with P1-ww
4539	sm2	salmon silk2	GRMZM2G180283	B73 RefGen_v3	Gene	Chr2	202536125	202537725	sm2	salmon silk2, sm2, UGT91L1	like sm1; silks salmon color with P1-rr and P1-wr, brown with P1-ww
4540	smh1	single myb histone1	GRMZM2G136887	B73 RefGen_v3	Gene	Chr8	139912821	139920531	smh1	CL35804_1c, fsu1a(smh), hon107, pUT3449 MYB-related transcription factor (MYBR101), single myb histone1, smh1, smh101	expressed in leaf tissue; member of small gene family; SMF protein binds telomere DNA repeats in vitro
4541	smh3	single myb histone3	GRMZM2G023667	B73 RefGen_v3	Gene	Chr8	153685211	153695652	smh3	CL22088_1, single myb histone3, smh103, smh3	
4542	smh4	single myb histone4	GRMZM2G108424	B73 RefGen_v3	Gene	Chr3	204430351	204438078	smh4	histone one (H1), hon108, single myb histone4, smh104, smh4, ZmMYBR7	
4543	smh5	single myb histone5	GRMZM2G163291	B73 RefGen_v3	Gene	Chr3	14476929	14481586	smh5	hon109, single myb histone5, smh105, smh5	
4544	smh6	single myb histone6	GRMZM2G095239	B73 RefGen_v3	Gene	Chr5	17123432	17138841	smh6	single myb histone6, smh106, smh6, ZmMYBR27	
4545	smk1	small kernel1	GRMZM2G030148	B73 RefGen_v3	Gene	Chr2	216076499	216078010	smk1	pentatricopeptide repeat-containing protein At3g46790, chloroplastic-like, smk1, ZmPPR134	encodes a pentatricopeptide repeat protein required for mitochondrial nad7 transcript editing
4546	smk2	small kernel2	GRMZM2G023528	B73 RefGen_v3	Gene	Chr4	239684932	239688530	smk2	AY109859, CL21031_1, pyridoxal 5'-phosphate synthase subunit PDX2, smk2	mutants are recessive embryo-lethal small kernel
4547	smt1	sterol methyltransferase1	GRMZM2G122810	B73 RefGen_v3	Gene	Chr7	18150408	18159227	smt1	PCO072714, PCO072714(541), smt1, SMT (S)-adenosyl-L-methionine:delta 24-sterol methyltransferase, sterol methyltransferase1	endosperm cDNA
4548	smt2	sterol methyl transferase2	GRMZM2G075701	B73 RefGen_v3	Gene	Chr1	8025216	8027013	smt2	smt2, sterol methyl transferase2, umc1547	cDNA sequences, SSR umc1547
4549	smu2	suppressors of mec-8 and unc-52 (C.eleg	GRMZM2G430745	B73 RefGen_v3	Gene	Chr10	1679131	1681892	smu2	smu, smu2, suppressors of mec-8 and unc-52 (C.elegans)	non-organellar pre-mRNA splicing
4550	snrk1a1	SNF1-related kinase alpha1-like1	GRMZM2G077278	B73 RefGen_v3	Gene	Chr6	159785916	159790437	snrk1a1	snrk1a1	
4551	snrk1a2	SNF1-related kinase alpha1-like2	GRMZM2G180704	B73 RefGen_v3	Gene	Chr2	154579939	154587570	snrk1a2	snrk1a2	
4552	snrk1a3	SNF1-related kinase alpha1-like3	GRMZM2G138814	B73 RefGen_v3	Gene	Chr1	52072966	52083007	snrk1a3	snrk1a3	
4553	snrkII1	SnRK2 serine threonine protein kinase1	GRMZM2G035809	B73 RefGen_v3	Gene	Chr9	121136691	121141166	snrkII1	pco069505, SNRK2.1, snrkII1, ZmSNRK2.1	
4554	snrkII10	SnRK2 serine threonine kinase10	GRMZM2G066867	B73 RefGen_v3	Gene	Chr5	18469442	18472522	snrkII10	IDP6588, SnRK2.10, snrkII10, ZmSnRK2.10	
4555	snrkII11	SnRK2 serine threonine protein kinase 11	GRMZM2G063961	B73 RefGen_v3	Gene	Chr6	150654910	150660102	snrkII11	pco126351, pco126351(515), SnRK2.11, snrkII11, ZmSnRK2.11	
4556	snrkII2	SnRK2 serine threonine protein kinase2	GRMZM2G056732	B73 RefGen_v3	Gene	Chr7	166410296	166416118	snrkII2	pco105841, pco105841(579), snrkII2, ZmSnRK2.2	induced by cold, salt and ABA
4557	snrkII3	SnRK2 serine threonine protein kinase3	GRMZM2G180916	B73 RefGen_v3	Gene	Chr1	94897504	94901091	snrkII3	pco083155b, SnRK2.3, ZmSnRK2.3	
4558	snrkII4	SnRK2 serine threonine protein kinase 4	GRMZM2G110922	B73 RefGen_v3	Gene	Chr3	174813369	174818806	snrkII4	pco126350(251), pco126350a, SnRK2.4, ZmSnRK2.4	

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
4559	snrkII5	SnRK2 serine threonine kinase5	GRMZM2G110908	B73 RefGen_v3	Gene	Chr10	148736929	148738463	snrkII5	si707044h04, si707044h04(761), SnRK2.5, ZmSnRK2.5	
4560	snrkII6	SnRK2 serine threonine protein kinase6	GRMZM2G130018	B73 RefGen_v3	Gene	Chr4	115177727	115188805	snrkII6	gnp_QBI10f12b, gpm476b, PCO075814, PCO075814(316), rs132128544, serine/threonine-protein kinase SAPK6, SnRK2.6, snrkII6, spk1, ZmSnRK2.6	
4561	snrkII7	SnRK2 serine threonine protein kinase7	GRMZM2G155593	B73 RefGen_v3	Gene	Chr2	51441153	51446361	snrkII7	gnp_QAE53d07, gpm300, PCO096414, PCO096414(134), SnRK2.7, snrkII7, ZmSnRK2.7	
4562	snrkII8	SnRK2 serine threonine protein kinase8	GRMZM2G138861	B73 RefGen_v3	Gene	Chr1	280356771	280364881	snrkII8	OST1, SAPK8, SnRK2.8, snrkII8, ZmSnRK2.8	salt tolerance expressed in Arabidopsis host (Vilela 2013)
4563	so1	sulfite oxidase1	GRMZM2G114739	B73 RefGen_v3	Gene	Chr1	193898445	193902203	so1	pco137761(58), so1, ZmSO	
4564	sod2	superoxide dismutase2	GRMZM2G025992	B73 RefGen_v3	Gene	Chr7	171775019	171778224	sod2	gnp_QBI25a07a, gpm488a, ncr(sod2), npi419a(sod2), npi419-sod2, PCO107770, pco107770(579), PZA01278, sod2, SodCc, superoxide dismutase2	electrophoretic mobility; cytosolic; Cu-Zn dimeric
4565	sod3	superoxide dismutase3	GRMZM2G059991	B73 RefGen_v3	Gene	Chr6	136070517	136074741	sod3	ncr(sod3a), sod3, SodA, superoxide dismutase3	electrophoretic mobility; mitochondrial; Mn tetrameric; intralocus hybrid bands occur; cDNA complements yeast mutant;
4566	sod4	superoxide dismutase4	GRMZM2G169890	B73 RefGen_v3	Gene	Chr1	60147420	60151012	sod4	npi412-Sod4, npi462, npi(sod4), sc304, sod4, SodCc, sod*-csu182, superoxide dismutase4, umc1169	electrophoretic mobility; cytosolic; Cu-Zn dimeric; intralocus hybrid bands occur; two similar sequences X17564 (sod4), X17565(sod4A)
4567	sod9	superoxide dismutase9	GRMZM2G058522	B73 RefGen_v3	Gene	Chr9	129535000	129538722	sod9	IDP3812, magi5472, sod*-4A, Sod4A, sod9, SodCc, superoxide dismutase9, superoxide dismutase candidate4A, umc1094	cytosolic Cu/Zn enzyme, cDNA and genomic clones; SSR umc1094
4568	sodh1	sorbitol dehydrogenase homolog1	GRMZM2G175423	B73 RefGen_v3	Gene	Chr1	197301249	197304338	sodh1	05c04a01, PCO126824, sdh1, sodh1, sorbitol dehydrogenase homolog1, uaz152, uaz152(sdh), umc1499	endosperm cDNA 5C04A01 (uaz152), similar to sorbitol dehydrogenases
4569	spi1	sparse inflorescence1	GRMZM2G025222	B73 RefGen_v3	Gene	Chr3	69968705	69970558	spi1	fmo, sparse inflorescence1, spi1, ZmYucca-like(spi1), ZmYuc-like(spi1)	mutant tassels have fewer branches and spikelets, and its ears are small, with fewer kernels
4570	spk1	stress-induced protein kinase1	GRMZM2G000278	B73 RefGen_v3	Gene	Chr5	171731069	171736269	spk1	gnp_QBI10f12a, gpm476a , IDP6801, rs131176990, SnRK2b, SnRK2 serine threonine protein kinase, spk1, SPK1	
4571	spo1	topoisomerase-like enzyme1	GRMZM2G129913	B73 RefGen_v3	Gene	Chr5	7125276	7129809	spo1	spo1, SPO11-1	Homolog of SPO11, which generates double-stranded breaks along meiotic chromosomes
4572	spo2	topoisomerase-like enzyme2	GRMZM5G890820	B73 RefGen_v3	Gene	Chr4	32840049	32842275	spo2	SPO11-2, spo2	Homolog of SPO11, which generates double-stranded breaks along meiotic chromosomes
4573	spo3	topoisomerase-like enzyme3	GRMZM2G052581	B73 RefGen_v3	Gene	Chr1	43509811	43512799	spo3	cl3138_1, cl3138_1(18), IDP1632, RHL2, SPO11-3, spo3	Homolog of SPO11, which generates double-stranded breaks along meiotic chromosomes
4574	spp1	sucrose-phosphatase1	GRMZM2G055489	B73 RefGen_v3	Gene	Chr8	115832232	115838487	spp1	CL1134_1, spp1, sucrose-6F-phosphate phosphohydrolase, sucrose-phosphatase1	
4575	spp2	sucrose-phosphatase2	GRMZM2G097641	B73 RefGen_v3	Gene	Chr10	89431021	89434146	spp2	spp2	
4576	spr1	signal recognition particle receptor homo	GRMZM2G060296	B73 RefGen_v3	Gene	Chr1	1960833	1968021	spr1	PCO122908, PCO122909, PZA01271, rs128358275 , signal recognition particle receptor homolog1, spr1, uaz8, uaz8a(spr1), uaz8(gfu)	endosperm cDNA 2C07F04(uaz8) similar to alpha subunit of animal signal recognition particle receptor
4577	spr9	signal recognition particle protein subuni	GRMZM2G046576	B73 RefGen_v3	Gene	Chr6	121303197	121311768	spr9	signal recognition particle protein subunit 9, signal recognition protein 9, spr9, srp9	
4578	sps1	sucrose phosphate synthase1	GRMZM5G875238	B73 RefGen_v3	Gene	Chr8	161465833	161471194	sps1	csu328, gsy224b(sps), sps1, SPSb, sucrose phosphate synthase1	cDNA encodes a 1068 amino acid leaf protein; transgenic (E. coli) directs sucrose phosphate synthesis
4579	sps2	sucrose phosphate synthase2	GRMZM2G140107	B73 RefGen_v3	Gene	Chr3	161295516	161301138	sps2	csu328(gfu), gsy224a(sps), sc224a, sps2, SPSa, sps*-csu328, sucrose phosphate synthase2	leaf cDNA csu328, sequence similar to sps1
4580	sqs1	squalene synthase1	GRMZM2G108225	B73 RefGen_v3	Gene	Chr5	3667095	3677998	sqs1	sqs1, squalene synthase1, ZmSS-4	
4581	sqsh1	squalene synthase homolog1	GRMZM2G029396	B73 RefGen_v3	Gene	Chr1	290074104	290082929	sqsh1	PCO094214, PCO094214(99), sqsh1*	Designation as sqsh1 based on high homology to sqs1 sequence; existence of several cDNAs indicates a functional gene (EHC Jan 2011)
4582	srk1	S-receptor kinase1	AC217293.3_FG007	B73 RefGen_v3	Gene	Chr2	232381878	232388093	srk1	csu811, csuh00811, csuh811, PCO103575, S-receptor kinase1, srk1	single copy leaf cDNA, csu811, similar to S-receptor kinase of Brassica; locus is absent from inbred GT119
4583	srph1	SGT1 disease resistance protein homolo	GRMZM2G105019	B73 RefGen_v3	Gene	Chr3	217545398	217552377	srph1	IDP1602, PCO098564, PCO098564(275), SGT1, suppressor of G2 allele of skp1	interacts with RACK1 protein involved in disease resistance (Wang et al 2014)
4584	srs1	SHI/STY (SRS)-transcription factor 1	GRMZM2G042407	B73 RefGen_v3	Gene	Chr1	207433916	207443393	srs1	lateral root primordia like3, LRL3	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4585	srs2	SHI/STY (SRS)-transcription factor 2	GRMZM2G080295	B73 RefGen_v3	Gene	Chr2	196299773	196301206	srs2	lateral root primordia like5, LRL5	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4586	srs3	SHI/STY (SRS)-transcription factor 3	GRMZM2G017606	B73 RefGen_v3	Gene	Chr4	216534703	216536379	srs3	lateral root primordia like2, LRL2	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4587	srs4	SHI/STY (SRS)-transcription factor 4	GRMZM2G097683	B73 RefGen_v3	Gene	Chr5	60161264	60163883	srs4	lateral root primordia like6, LRL6	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4588	srs5	SHI/STY (SRS)-transcription factor 5	GRMZM2G108798	B73 RefGen_v3	Gene	Chr6	85368896	85371594	srs5	lateral root primordia like7, LRL7	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4589	srs6	SHI/STY (SRS)-transcription factor 6	GRMZM2G450459	B73 RefGen_v3	Gene	Chr6	143217455	143220101	srs6	lateral root primordia like1, LRL1	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4590	srs7	SHI/STY (SRS)-transcription factor 7	GRMZM2G135783	B73 RefGen_v3	Gene	Chr7	142938485	142940360	srs7	lateral root primordia like4, LRL4	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4591	srs8	SHI/STY (SRS)-transcription factor 8	GRMZM2G179021	B73 RefGen_v3	Gene	Chr7	143145425	143146225	srs8	lateral root primordia like8, LRL8	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4592	ss1	starch synthase I	GRMZM2G129451	B73 RefGen_v3	Gene	Chr9	17640522	17651342	ss1	gnp_QBJ17c03, gpm502, PCO152066, PCO152066(661), ss1, starch synthase I	single copy endosperm specific cDNA; encoded-protein cross-reacts with antibody to granule associated starch synthase I
4593	ss4	starch synthase4	GRMZM2G044744	B73 RefGen_v3	Gene	Chr8	124838621	124847166	ss4	ss4, starch synthase IV, ZmSSIV	
4594	ss5	starch synthase5	GRMZM2G130043	B73 RefGen_v3	Gene	Chr4	172635729	172706662	ss5	ss5, starch synthase V, ZmSSV	
4595	ssp1	seed specific protein1	GRMZM2G090935	B73 RefGen_v3	Gene	Chr4	233478819	233482558	ssp1	IDP2451, PCO121205, PZA00513, seed specific protein1, ssp1, umc1740	
4596	ssu1	ribulose bisphosphate carboxylase small	GRMZM2G098520	B73 RefGen_v3	Gene	Chr4	190228051	190230534	ssu1	rbcs1, ribulose bisphosphate carboxylase small subunit1, rpa9b-ssu, sms1, ssu1, ssu2, ssu*-D00170, umc210b(ssu), uox, uox(ssu1a)	probed locus; SSRs phi092,phi093
4597	ssu1	ribulose bisphosphate carboxylase small	GRMZM2G113033	B73 RefGen_v3	Gene	Chr2	143429392	143430581	ssu1	rbcs1, ribulose bisphosphate carboxylase small subunit1, rpa9b-ssu, sms1, ssu1, ssu2, ssu*-D00170, umc210b(ssu), uox, uox(ssu1a)	probed locus; SSRs phi092,phi093
4598	ssu2	ribulose bisphosphate carboxylase small	GRMZM2G113033	B73 RefGen_v3	Gene	Chr2	143429392	143430581	ssu2	bnl(ssu), npi331-ssu2, phi092b(ssu), rbcS, rbcS2, ribulose bisphosphate carboxylase small subunit2, rpa9a-ssu, ssu1, ssu2, umc210a(ssu), uox, uox(ssu1b)	probed locus
4599	stc1	sesquiterpene cyclase1	GRMZM2G177098	B73 RefGen_v3	Gene	Chr9	11745997	11754981	stc1	60S ribosomal protein L35A (Rpl35A), CL570_1c, rpl35A, sesquiterpene cyclase1, stc1, tac6067, tac6087, umc2093	single copy; insect defense reponse; encodes a sesquiterpene cyclase involved in terpenoid biosynthesis
4600	stk1	serine threonine kinase1	GRMZM2G165433	B73 RefGen_v3	Gene	Chr9	11782450	11785572	stk1	serine threonine kinase1, stk1	
4601	stk2	serine-threonine kinase2	GRMZM2G179268	B73 RefGen_v3	Gene	Chr2	41122571	41124341	stk2	stk2	Sequence orthologous to rice stk2, in maize BAC contig overlapping b0178l03 and b0004G18 (Alleman 2006)
4602	stk3	serine-threonine kinase3	GRMZM2G301647	B73 RefGen_v3	Gene	Chr4	175306259	175309558	stk3	putative protein kinase superfamily protein, stk3, ZmSTK2_USP, ZmUPRK2	pollen-specific expression
4603	stm1	stomatin1	GRMZM2G023073	B73 RefGen_v3	Gene	Chr10	77758100	77774208	stm1	PCO142888(732), PCO142888b, stm1, stomatin1, Zm-stm1	cDNA
4604	stp1	sugar transport1	GRMZM2G097768	B73 RefGen_v3	Gene	Chr8	73418620	73424707	stp1	csu142, csu142(stp), csu142(sutp), csuh142, ERD6, PCO120720, PCO120720613), sc179, stp1, sugar transport1, sugar transport homolog1, umc376(gfu)	leaf cDNA csu142 similar to yeast plasma membrane sugar transport protein, single copy
4605	su1	sugary1	GRMZM2G138060	B73 RefGen_v3	Gene	Chr4	41396390	41405179	su1	gsy315(su1), isa1, iso1, isoamylase1, isoamylase-type starch-dbe1, isoamylase-type starch-debranching enzyme1, rs131175585, ss196415719, su1, sugary1	developing endosperm, phytoglycogen but no debranching enzyme in germinating seeds; su1-am sugary-amylaceous; su1-st recessive starchy; application: the "sweet corn" gene - recessive
4606	su2	sugary2	GRMZM2G348551	B73 RefGen_v3	Gene	Chr6	113414100	113419156	su2	IDP202, IDP584, soluble starch synthase 2-3, chloroplastic/amyloplastic, SSIIa, STSII-1, su2, sugary2, zSTSII-1	endosperm glassy, translucent, sometimes wrinkled
4607	su4	sugary4	GRMZM2G090905	B73 RefGen_v3	Gene	Chr6	144755799	144758179	su4	isa2, iso2, isoamylase2, isoamylase-type starch-dbe2, isoamylase-type starch-debranching enzyme2, isoamylase-type starch debranching enzyme ISO2, su3B, su4, sugary4	duplicate factor: in combination with su3 gives sugary endosperm phenotype.

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
4608	sudh1	succinate dehydrogenase1	GRMZM2G064799	B73 RefGen_v3	Gene	Chr7	4239369	4244199	sudh1	sdh, sdh1, sudh1, TIDP3457	
4609	sudh10	succinate dehydrogenase10	GRMZM2G076524	B73 RefGen_v3	Gene	Chr5	13264659	13269113	sudh10	sdh, sudh10	
4610	sudh11	succinate dehydrogenase11	GRMZM2G306945	B73 RefGen_v3	Gene	Chr1	64881015	64884264	sudh11	sdh, sudh11	
4611	sudh12	succinate dehydrogenase12	GRMZM2G146965	B73 RefGen_v3	Gene	Chr1	262265889	262269879	sudh12	sdh, sudh12	
4612	sudh2	succinate dehydrogenase2	GRMZM2G302259	B73 RefGen_v3	Gene	Chr4	37053697	37057117	sudh2	csu474(rpS14), iron sulfur subunit of succinate dehydrogenase and ribosomal protein S14 Precursor, rps14, sdh2, succinate dehydrogenase iron-sulfur protein,mitochondrial , sudh2	chimeric protein, succinate dehydrogenase iron-sulfur protein and ribosomal protein S14, mitochondrial
4613	sudh3	succinate dehydrogenase3	GRMZM2G056912	B73 RefGen_v3	Gene	Chr8	22054607	22060804	sudh3	sdh, succinate dehydrogenase [ubiquinone] flavoprotein subunit 1, mitochondrial-like, sudh3	
4614	sudh4	succinate dehydrogenase4	GRMZM2G079888	B73 RefGen_v3	Gene	Chr2	237069904	237075210	sudh4	sdh, sudh4	
4615	sudh5	succinate dehydrogenase5	GRMZM2G109271	B73 RefGen_v3	Gene	Chr1	62981705	63005931	sudh5	sdh, sudh5	
4616	sudh6	succinate dehydrogenase6	GRMZM2G398876	B73 RefGen_v3	Gene	Chr10	115607469	115611338	sudh6	sdh, sudh6	
4617	sudh7	succinate dehydrogenase7	GRMZM2G134134	B73 RefGen_v3	Gene	Chr6	6270568	6274593	sudh7	csu474, csu474(rpS14), sdh, sudh7	
4618	sudh8	succinate dehydrogenase8	GRMZM2G023760	B73 RefGen_v3	Gene	Chr9	14624670	14625146	sudh8	sdh, succinate dehydrogenase [ubiquinone] iron-sulfur subunit 1, mitochondrial-like, sudh8	
4619	sudh9	succinate dehydrogenase9	GRMZM2G160685	B73 RefGen_v3	Gene	Chr6	154876071	154884333	sudh9	sdh, sudh9	
4620	sum1	siroheme uroporphyrinogen methyltransf	GRMZM2G105604	B73 RefGen_v3	Gene	Chr3	216674441	216678588	sum1	CL942_1, siroheme uroporphyrinogen methyltransferase1, sum1, uroporphyrinogen III methyltransferase, ZmSUMT1	
4621	sumo1a	small ubiquitin-related modifier1a	GRMZM2G053898	B73 RefGen_v3	Gene	Chr8	161569233	161573399	sumo1a	sumo1a	
4622	sumo1b	small ubiquitin-related modifier1b	GRMZM2G082390	B73 RefGen_v3	Gene	Chr8	161721257	161724576	sumo1b	pco135487, sumo1b, sumo1b(640)	
4623	sumo2	small ubiquitin-related modifier2	GRMZM2G305196	B73 RefGen_v3	Gene	Chr7	159960915	159961570	sumo2	sumo2	
4624	sumov1	small ubiquitin-related modifier-variant1	GRMZM2G073404	B73 RefGen_v3	Gene	Chr8	141677418	141681979	sumov1	cl7313_1, sumov1, sumov1(646)	
4625	sun1	SUN domain protein1	GRMZM2G109818	B73 RefGen_v3	Gene	Chr5	88695793	88701952	sun1	cl9166_1, cl9166_1(411), Sad1p, UNC-84 (snRNP assembly-defective [SAD]; uncoordinated [UNC] = SUN), sun1, SUN domain protein1	canonical C-terminal SUN-domain (CCSD) type nuclear envelope protein
4626	sun2	SUN domain protein2	GRMZM2G440614	B73 RefGen_v3	Gene	Chr3	38600230	38605885	sun2	cl44325_1, cl44325_1(219), Sad1p, UNC-84 (snRNP assembly-defective [SAD]; uncoordinated [UNC] = SUN), sun2, SUN domain protein2	
4627	sun4	SUN domain protein4	GRMZM2G005483	B73 RefGen_v3	Gene	Chr8	165131574	165135243	sun4	CL6008_1(641), CL6008_1b, Sad1p, UNC-84 (snRNP assembly-defective [SAD]; uncoordinated [UNC] = SUN), sun4, SUN domain protein4	
4628	sun5	SUN domain protein5	AC194341.4_FG003	B73 RefGen_v3	Gene	Chr8	140924162	140926362	sun5	Sad1p, UNC-84 (snRNP assembly-defective [SAD]; uncoordinated [UNC] = SUN), sun5	plant-prevalent mid-SUN 3 transmembrane (PM3) type nuclear envelope protein; may be pollen specific
4629	sus1	sucrose synthase1	GRMZM2G152908	B73 RefGen_v3	Gene	Chr9	122479052	122485725	sus1	bnl(css), css1, gsy67(sus2), IDP2527, npi121-css1, PCO112537, pco112537(686), phi016, phi032, phi042, ss2, sucrose synthase1, sus1, Sus1, sus2, umc190(css)	(was sus2, css1) sucrose synthase-1 (SUS1) of embryo and other tissues, compare sh1; SSRs phi016, 032, 042
4630	sus2	sucrose synthase2	GRMZM2G318780	B73 RefGen_v3	Gene	Chr1	56787028	56794227	sus2	gnp_AW061973c, gnp_QAM24h06d, gpm139c, gpm363d, pco079420, PCO079420(23), sucrose synthase2, sucrose synthase 3, sus2, Sus2, sus3	Encodes sucrose synthase-2 (SUS2), one of 3 loci defined for this function; compare sh1 and sus1.
4631	sut1	sucrose transporter1	GRMZM2G034302	B73 RefGen_v3	Gene	Chr1	15069084	15074473	sut1	gnp_QAT3g07b, gpm403a, sucrose transporter1, sut1, umc2347, umc2347 paralog, Zmsut1	mutant plants are deficient in leaf sucrose unloading to pholem; mature leaves hyperaccumulate carbohydrates and display leaf chlorosis with premature senescence
4632	sut2	sucrose transporter2	GRMZM2G307561	B73 RefGen_v3	Gene	Chr3	94809651	94815766	sut2	rs132017424, sut2, sut4, sut4 sucrose transporter 4, ZmSut2	mutants grow slower and have increased sugar content in leaves
4633	sut3	sucrose transporter3	GRMZM2G083248	B73 RefGen_v3	Gene	Chr1	243274177	243277640	sut3	cl62012_1, cl62012_1(78), sut3	
4634	sut4	sucrose transporter4	GRMZM2G145107	B73 RefGen_v3	Gene	Chr5	216637674	216642140	sut4	sut2, sut2 sucrose transporter 2, SUT4	
4635	sut5	sucrose transporter5	GRMZM2G081589	B73 RefGen_v3	Gene	Chr5	176533898	176537221	sut5	sucrose transporter BoSUT1, sut5	
4636	sut6	sucrose transporter6	GRMZM2G106741	B73 RefGen_v3	Gene	Chr4	124976888	124980047	sut6	sut6	
4637	sut7	sucrose transporter7	GRMZM2G087901	B73 RefGen_v3	Gene	Chr9	151514437	151518716	sut7	gnp_QAT3g07a, gpm403b, PCO103031, sucrose transport protein SUT1-like, sut7, umc2347	reproductive stage in various tissues including leaf sheaths, culms, husks, pedicels, with little transcript detected in silks and developing kernels.
4638	sweet11	sugars will eventually be exported transp	GRMZM2G368827	B73 RefGen_v3	Gene	Chr1	194965437	194968347	sweet11	pco137991, pco137991(59), sweet11	
4639	sweet12a	sugars will eventually be exported transp	GRMZM2G133322	B73 RefGen_v3	Gene	Chr1	59182679	59185966	sweet12a	sweet12a	
4640	sweet12b	sugars will eventually be exported transp	GRMZM2G099609	B73 RefGen_v3	Gene	Chr9	130027643	130030345	sweet12b	sweet12b	
4641	sweet13a	sugars will eventually be exported transp	GRMZM2G173669	B73 RefGen_v3	Gene	Chr10	14767640	14770295	sweet13a	MTN3, sweet13a	
4642	sweet13b	sugars will eventually be exported transp	GRMZM2G021706	B73 RefGen_v3	Gene	Chr10	14648064	14650932	sweet13b	sweet13b	
4643	sweet13c	sugars will eventually be exported transp	GRMZM2G179349	B73 RefGen_v3	Gene	Chr3	108721006	108722375	sweet13c	sweet13c	
4644	sweet14a	sugars will eventually be exported transp	GRMZM2G094955	B73 RefGen_v3	Gene	Chr2	223375329	223377937	sweet14a	sweet14a	
4645	sweet14b	sugars will eventually be exported transp	GRMZM2G015976	B73 RefGen_v3	Gene	Chr4	21691924	21695433	sweet14b	mtN3-like protein, sweet14b	
4646	sweet15a	sugars will eventually be exported transp	GRMZM2G168365	B73 RefGen_v3	Gene	Chr4	96336663	96338566	sweet15a	sweet15a, umc1791	
4647	sweet15b	sugars will eventually be exported transp	GRMZM5G872392	B73 RefGen_v3	Gene	Chr5	164895210	164898398	sweet15b	sweet15b	
4648	sweet16	sugars will eventually be exported transp	GRMZM2G107597	B73 RefGen_v3	Gene	Chr1	57248463	57251591	sweet16	bidirectional sugar transporter SWEET16, sweet16	
4649	sweet17a	sugars will eventually be exported transp	GRMZM2G106462	B73 RefGen_v3	Gene	Chr3	56813678	56821576	sweet17a	bidirectional sugar transporter SWEET17-like, sweet17a	
4650	sweet17b	sugars will eventually be exported transp	GRMZM2G111926	B73 RefGen_v3	Gene	Chr8	33368351	33373788	sweet17b	bidirectional sugar transporter SWEET17-like, sweet17b	
4651	sweet1a	sugars will eventually be exported transp	GRMZM2G039365	B73 RefGen_v3	Gene	Chr3	171792049	171795701	sweet1a	sweet1a, TIDP3416	
4652	sweet1b	sugars will eventually be exported transp	GRMZM2G153358	B73 RefGen_v3	Gene	Chr6	148107348	148110301	sweet1b	seven-transmembrane-domain protein 1, sweet1b	
4653	sweet2	sugars will eventually be exported transp	GRMZM2G324903	B73 RefGen_v3	Gene	Chr8	58837906	58840227	sweet2	sweet2	
4654	sweet3a	sugars will eventually be exported transp	GRMZM2G179679	B73 RefGen_v3	Gene	Chr8	112056618	112058331	sweet3a	sweet3a	
4655	sweet3b	sugars will eventually be exported transp	GRMZM2G060974	B73 RefGen_v3	Gene	Chr3	2955821	2957584	sweet3b	sweet3b	
4656	sweet4a	sugars will eventually be exported transp	GRMZM2G000812	B73 RefGen_v3	Gene	Chr5	126853038	126855915	sweet4a	sweet4a	

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
4657	sweet4b	sugars will eventually be exported transp	GRMZM2G144581	B73 RefGen_v3	Gene	Chr5	127638855	127642404	sweet4b	sweet4b, umc2406	
4658	sweet4c	sugars will eventually be exported transp	GRMZM2G137954	B73 RefGen_v3	Gene	Chr5	127500983	127504476	sweet4c	sweet4c, umc2302	Mutants are defective in seed filling
4659	sweet6a	sugars will eventually be exported transp	GRMZM2G157675	B73 RefGen_v3	Gene	Chr3	223847899	223851013	sweet6a	IDP152, sweet6a	
4660	sweet6b	sugars will eventually be exported transp	GRMZM2G416965	B73 RefGen_v3	Gene	Chr8	141481938	141485043	sweet6b	seven-transmembrane-domain protein 1, sweet6b	
4661	sxd1	sucrose export defective1	GRMZM2G009785	B73 RefGen_v3	Gene	Chr5	133540574	133557141	sxd1	PCO145578, PZB00968.1, PZB02491.1, sed1, si945027b01, sucrose export defective1, sut1, sut*-51333, sxd1, sxd1-1, vitamin E synthesis1, vte1, VTE1	vitamin E synthesis; anthocyanin accumulates in a non-clonal pattern at tip and margins of leaves soon after emergence from whorl; reduced plant height
4662	syd1	SPLAYED ATPase1	GRMZM2G387890	B73 RefGen_v3	Gene	Chr6	118452039	118460501	syd1	SPLAYED ATPase, SPLAYED ATPase1, syd1	
4663	tab2	translation chloroplast psaB mRNA2 hom	GRMZM2G081955	B73 RefGen_v3	Gene	Chr5	183533765	183536017	tab2	PsaB RNA binding protein, tab2	accumulation but is not necessary for synthesis of plastid-encoded PSI subunits in maize. (A. Barkan, 2015). required for photosystem I accumulation; ortholog of ATAB2 in Arabidopsis and
4664	tacs1	terminal acidic SANT 1	GRMZM2G111906	B73 RefGen_v3	Gene	Chr6	82660395	82663470	tacs1	cl42008_-1(187), CL42008_-1a, IDP3792, SANT 1, tacs1, terminal acidic SANT 1	cDNA expressed in meristems; similar to rice anther indehiscence1 (aid1) gene
4665	taf1	transcription associated factor1	GRMZM2G002276	B73 RefGen_v3	Gene	Chr3	179837079	179842136	taf1	csu38, csu38a(taf), csuh38, taf1, transcription associated factor1, umc329	low copy, leaf cDNA csu38 similar to human transcription initiation factor subunit
4666	tan1	tangled1	GRMZM2G039113	B73 RefGen_v3	Gene	Chr6	142758475	142760706	tan1	pigmy1, pigmy plant1, py1, rs132337008, tan1, tangled1	(was py1) leaves short, pointed, fine white streaks; displays abnormally oriented cell divisions and altered growth and development throughout the plant
4667	tap1	translocon-associated protein homolog1	GRMZM2G075844	B73 RefGen_v3	Gene	Chr5	61239228	61243371	tap1	tap1, translocon-associated protein homolog1	vegetative meristem cDNA 7C02D06, similar to endoplasmic reticulum protein
4668	tar1	tryptophan aminotransferase related1	GRMZM2G127160	B73 RefGen_v3	Gene	Chr6	123615202	123618258	tar1	tar1, umc2319	
4669	tar3	tryptophan aminotransferase related3	GRMZM2G141810	B73 RefGen_v3	Gene	Chr6	129844054	129847591	tar3	pco099468, ZmAlliinase	
4670	tat1	tyrosine aminotransferase homolog1	GRMZM2G139813	B73 RefGen_v3	Gene	Chr2	225968332	225976565	tat1	tat1, tyrosine transaminase homolog	
4671	tb1	teosinte branched1	AC233950.1_FG002	B73 RefGen_v3	Gene	Chr1	265811311	265813044	tb1	tb1, teosinte branched1, umc1082, ZmTCP1	GRASSIUS: TCP transcription factor (TCP1) . many tillers; ear branches tassel-like; affects apical dominance
4672	tbp1	TATA-binding protein1	GRMZM2G149238	B73 RefGen_v3	Gene	Chr1	259016743	259021894	tbp1	miid1, TATA-binding protein1, tbp1, tbp*-L13301, TFIID	Maize TATA-binding protein component of TFIID transcription initiation factor
4673	tbp2	TATA-binding protein2	GRMZM2G161418	B73 RefGen_v3	Gene	Chr5	15340632	15345558	tbp2	TATA-binding protein2, tbp2, TIIF	cDNA clone; encodes a TBP that functions in yeast; maps to chromosome 5 near pgm2
4674	tcp1	thiamine diphosphate carrier protein1	GRMZM2G118515	B73 RefGen_v3	Gene	Chr8	159216940	159224411	tcp1	pco141010(639), pco141010b, tcp1	complements yeast null TCP1 mutant
4675	tcp2	thiamine diphosphate carrier protein2	GRMZM2G124911	B73 RefGen_v3	Gene	Chr3	154750579	154774482	tcp2	pco141010a, tcp2	
4676	tcptf10	TCP-transcription factor 10	GRMZM2G142751	B73 RefGen_v3	Gene	Chr6	112768227	112770230	tcptf10	tcp10	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4677	tcptf11	TCP-transcription factor 11	GRMZM2G166687	B73 RefGen_v3	Gene	Chr1	214354391	214355375	tcptf11	tcp11	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4678	tcptf12	TCP-transcription factor 12	GRMZM2G093895	B73 RefGen_v3	Gene	Chr10	10294382	10296488	tcptf12	tcp12	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4679	tcptf13	TCP-transcription factor 13	GRMZM2G359599	B73 RefGen_v3	Gene	Chr4	612258	614155	tcptf13	tcp13	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4680	tcptf14	TCP-transcription factor 14	GRMZM2G465091	B73 RefGen_v3	Gene	Chr10	132055803	132056847	tcptf14	tcp14	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4681	tcptf15	TCP-transcription factor 15	GRMZM2G060319	B73 RefGen_v3	Gene	Chr4	82385034	82386103	tcptf15	tcp15	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4682	tcptf16	TCP-transcription factor 16	GRMZM2G178603	B73 RefGen_v3	Gene	Chr5	188505434	188506555	tcptf16	tcp16	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4683	tcptf17	TCP-transcription factor 17	GRMZM2G458087	B73 RefGen_v3	Gene	Chr10	110222622	110224294	tcptf17	tcp17	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4684	tcptf18	TCP-transcription factor 18	GRMZM2G064628	B73 RefGen_v3	Gene	Chr7	110809038	110810529	tcptf18	tcp18	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4685	tcptf19	TCP-transcription factor 19	AC199782.5_FG003	B73 RefGen_v3	Gene	Chr2	195005257	195006904	tcptf19	tcp19	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4686	tcptf2	TCP-transcription factor 2	GRMZM2G003944	B73 RefGen_v3	Gene	Chr4	205135012	205137037	tcptf2	rs129898608 , tcp2, tcptf2, Transcription factor TCP8 , umc52, umc52a, umc52(ext)	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4687	tcptf20	TCP-transcription factor 20	GRMZM2G034638	B73 RefGen_v3	Gene	Chr8	160527351	160529186	tcptf20	tcp20	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4688	tcptf21	TCP-transcription factor 21	GRMZM2G107031	B73 RefGen_v3	Gene	Chr1	197227445	197228576	tcptf21	tcp21	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4689	tcptf22	TCP-transcription factor 22	GRMZM2G135461	B73 RefGen_v3	Gene	Chr4	142954944	142956691	tcptf22	tcp22	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4690	tcptf23	TCP-transcription factor 23	GRMZM2G120151	B73 RefGen_v3	Gene	Chr6	158563456	158566518	tcptf23	tcp23	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4691	tcptf24	TCP-transcription factor 24	GRMZM2G015037	B73 RefGen_v3	Gene	Chr8	24477984	24481369	tcptf24	tcp24	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4692	tcptf25	TCP-transcription factor 25	GRMZM2G078077	B73 RefGen_v3	Gene	Chr4	145641628	145642678	tcptf25	tcp25	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4693	tcptf26	TCP-transcription factor 26	GRMZM2G077755	B73 RefGen_v3	Gene	Chr5	207185179	207187500	tcptf26	tcp26	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4694	tcptf27	TCP-transcription factor 27	GRMZM2G414114	B73 RefGen_v3	Gene	Chr2	225192935	225197146	tcptf27	tcp27	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4695	tcptf28	TCP-transcription factor 28	GRMZM2G062711	B73 RefGen_v3	Gene	Chr4	55947182	55947871	tcptf28	tcp28	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4696	tcptf29	TCP-transcription factor 29	GRMZM2G148022	B73 RefGen_v3	Gene	Chr8	173529415	173541170	tcptf29	tcp29	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4697	tcptf3	TCP-transcription factor 3	GRMZM2G110242	B73 RefGen_v3	Gene	Chr2	180630151	180631609	tcptf3	tcp3, wab1	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4698	tcptf30	TCP-transcription factor 30	GRMZM2G166946	B73 RefGen_v3	Gene	Chr3	194948766	194951387	tcptf30	tcp30	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4699	tcptf31	TCP-transcription factor 31	GRMZM2G089638	B73 RefGen_v3	Gene	Chr3	140859692	140861716	tcptf31	tcp31	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4700	tcptf32	TCP-transcription factor 32	GRMZM2G031905	B73 RefGen_v3	Gene	Chr6	27463599	27465214	tcptf32	tcp32	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4701	tcptf33	TCP-transcription factor 33	AC205574.3_FG006	B73 RefGen_v3	Gene	Chr3	3475925	3478586	tcptf33	tcp33	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4702	tcptf34	TCP-transcription factor 34	AC234521.1_FG006	B73 RefGen_v3	Gene	Chr2	22891424	22892551	tcptf34	tcp34	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4703	tcptf35	TCP-transcription factor 35	GRMZM2G055024	B73 RefGen_v3	Gene	Chr4	2551378	2555043	tcptf35	tcp35	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4704	tcptf36	TCP-transcription factor 36	GRMZM2G424261	B73 RefGen_v3	Gene	Chr10	112133491	112135588	tcptf36	tcp36	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4705	tcptf37	TCP-transcription factor 37	GRMZM2G088440	B73 RefGen_v3	Gene	Chr2	182307219	182309604	tcptf37	tcp37	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
4706	tcptf38	TCP-transcription factor 38	GRMZM2G180568	B73 RefGen_v3	Gene	Chr7	168258012	168259093	tcptf38	tcp38	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4707	tcptf39	TCP-transcription factor 39	GRMZM2G170232	B73 RefGen_v3	Gene	Chr4	36959864	36961776	tcptf39	tcp39	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4708	tcptf4	TCP-transcription factor 4	GRMZM2G445944	B73 RefGen_v3	Gene	Chr5	216656588	216657717	tcptf4	tcp4	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4709	tcptf40	TCP-transcription factor 40	GRMZM2G096610	B73 RefGen_v3	Gene	Chr10	100088723	100089636	tcptf40	tcp40	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4710	tcptf41	TCP-transcription factor 41	GRMZM2G416524	B73 RefGen_v3	Gene	Chr2	136203178	136208519	tcptf41	tcp41	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4711	tcptf42	TCP-transcription factor 42	AC213524.3_FG003	B73 RefGen_v3	Gene	Chr1	193546929	193548421	tcptf42	tcp42	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4712	tcptf43	TCP-transcription factor 43	GRMZM2G020805	B73 RefGen_v3	Gene	Chr2	235465951	235472063	tcptf43	php200581a, php20581b, php20581b(ext), php20581b(tb), pio200581B, pio20581, tcp43, tcptf43	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.. Mapped upper band to this site.. simiiar to Arabidosis transcription
4713	tcptf44	TCP-transcription factor 44	GRMZM2G089361	B73 RefGen_v3	Gene	Chr5	4945651	4947211	tcptf44	tcp44	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4714	tcptf5	TCP-transcription factor 5	GRMZM2G115516	B73 RefGen_v3	Gene	Chr1	285381000	285385544	tcptf5	tcp5	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4715	tcptf6	TCP-transcription factor 6	AC190734.2_FG003	B73 RefGen_v3	Gene	Chr5	11858801	11859880	tcptf6	tcp6	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4716	tcptf7	TCP-transcription factor 7	GRMZM2G035944	B73 RefGen_v3	Gene	Chr8	122433073	122435587	tcptf7	tcp7	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4717	tcptf8	TCP-transcription factor 8	GRMZM2G092214	B73 RefGen_v3	Gene	Chr3	158493312	158495256	tcptf8	tcp8	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4718	tcptf9	TCP-transcription factor 9	GRMZM2G113888	B73 RefGen_v3	Gene	Chr9	5004014	5006205	tcptf9	tcp9	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4719	tcrr1	transfer cell response regulator1	GRMZM2G016145	B73 RefGen_v3	Gene	Chr4	70600591	70601871	tcrr1	aberrant phyllotaxy1, orphans transcription factor (Orphan123), tcrr1, tcrr-1, transfer cell response regulator1, two-component response regulator ARR3-like, ZmOrphan123	basal endosperm transfer cell specific transcript; encoded protein is found other cells, the conducting cells above the transfer layer, and immature cells adjacent to the transfer layer
4720	tct1	translationally controlled tumor1	GRMZM2G075624	B73 RefGen_v3	Gene	Chr5	67851004	67853565	tct1	tct1, translationally controlled tumor1, uaz7c02c06(gfu)	vegetative meristem cDNA 7C02C06 similar to protein conserved in yeast, plants and mammals
4721	td1	thick tassel dwarf1	GRMZM2G300133	B73 RefGen_v3	Gene	Chr5	61698661	61702214	td1	td1, thick tassel dwarf1, ttd1	shortened plants, fasciated ears, increased spikelet density in tassel
4722	tdpk1	thiamin diphosphokinase1	GRMZM2G055458	B73 RefGen_v3	Gene	Chr3	66270831	66282839	tdpk1	tdpk1	
4723	tdpk2	thiamin diphosphokinase2	GRMZM5G864815	B73 RefGen_v3	Gene	Chr6	137792544	137795002	tdpk2	tdpk2, tpk1	
4724	tdy1	tie-dyed1	GRMZM2G321778	B73 RefGen_v3	Gene	Chr6	166836363	166837893	tdy1	tdy1	Leaf blades develop variegated chlorotic and green regions; chlorotic regions hyperaccumulate carbohydrates.(Braun 2008)
4725	tdy2	tie-dyed2	GRMZM5G840560	B73 RefGen_v3	Gene	Chr5	217413183	217431897	tdy2	tdy2, Tie-dyed2 callose synthase	leaves yellow in patches simulating tie-dyed or zebra patterns
4726	te1	terminal ear1	GRMZM2G085113	B73 RefGen_v3	Gene	Chr3	165216844	165220769	te1	rs132051064, siAF047852b, ss196415503, te1, te*-Galinat, terminal ear1, umc1209, umc1219	stalked ear appendages at tip; varying to infolded ears
4727	tel2	telomere maintenance2	GRMZM2G144166	B73 RefGen_v3	Gene	Chr5	181264982	181272627	tel2	tel2, telomere length regulation protein TEL2 homolog, TELomere maintenance2	
4728	tena1	thiaminase1	GRMZM2G078283	B73 RefGen_v3	Gene	Chr4	48570462	48572773	tena1	tena1, Thiaminase II	
4729	tena2	thiaminase2	GRMZM2G148896	B73 RefGen_v3	Gene	Chr1	201771782	201775619	tena2	tena2, Thiaminase II	
4730	tena3	thiaminase3	GRMZM2G080501	B73 RefGen_v3	Gene	Chr9	135600972	135602731	tena3	pco111209, pco111209(694), tena3, Thiaminase II homolog	
4731	tfIIB1	transcription initiation factor1	GRMZM2G017831	B73 RefGen_v3	Gene	Chr9	148929810	148933147	tfIIB1	pBrp, TFIIB, tfIIB1, transcription initiation factor	
4732	tga1	teosinte glume architecture1	GRMZM2G101511	B73 RefGen_v3	Gene	Chr4	44534815	44539478	tga1	mga1, squamosa promoter-binding-like protein 16, teosinte glume architecture1, tga1, ZmSBP1	glumes indurated, erect, long, boat-shaped; factor transferred from teosinte
4733	tgd1	dTDP-glucose dehydratase homolog csu1	GRMZM2G044027	B73 RefGen_v3	Gene	Chr1	41473411	41478103	tgd1	csu219, csu219(gfu), dTDP-glucose dehydratase homolog csu219, gnp_QAY3d07a, gpm418a, PCO092342, tgd1	leaf cDNA csu219, 5' sequence similar to DTDP-glucose dehydratase
4734	tgz15a	transglutaminase15a	GRMZM2G025054	B73 RefGen_v3	Gene	Chr10	125323532	125327383	tgz15a	pco063924, pco063924(750), tgz15a	
4735	tgz21	transglutaminase21	GRMZM2G045005	B73 RefGen_v3	Gene	Chr2	38044187	38048031	tgz21	tgz21, transglutaminase 21	
4736	tha1	thylakoid assembly1	GRMZM2G090086	B73 RefGen_v3	Gene	Chr2	128922840	128930111	tha1	tha1, thylakoid assembly1	pathway. Required for thylakoid protein targeting via the cpSec pathway. SecA homolog. (A. Barkan, 2015)
4737	tha4	thylakoid assembly4	GRMZM2G472651	B73 RefGen_v3	Gene	Chr1	253336039	253339554	tha4	CL1403_-2a, IDP7317, rs128929822, rs131185980, tha4	pale green seedling lethal; thlakoid protein targeting: tat pathway . Required for thylakoid protein targeting via the TAT pathway. Ortholog of bacterial TatA. (A. Barkan, 2015)
4738	tha5	thylakoid assembly5	GRMZM2G300408	B73 RefGen_v3	Gene	Chr9	14541001	14542356	tha5	GRMZM2G300408, tha5, thylakoid assembly5	Required for thylakoid protein targeting via the cpSec pathway. SecE homolog. (A. Barkan, 2015)
4739	tha8	thylakoid assembly8	AC217965.2_FG012	B73 RefGen_v3	Gene	Chr8	15108789	15109580	tha8		Chloroplast PPR protein. Required for splicing chloroplast ycf3-int2 and trnA introns and is bound to those introns in vivo. (A. Barkan, 2015)
4740	tha9	thylakoid assembly 9	GRMZM2G128454	B73 RefGen_v3	Gene	Chr5	17372076	17374433	tha9	tha9, thylakoid assembly 9	
4741	thi1	thiamine biosynthesis1	GRMZM2G018375	B73 RefGen_v3	Gene	Chr8	137677256	137679026	thi1	gnp_QCB2h02, gpm589, iger2b(thi), sed2, thi1, thiamine biosynthesis1, uiu1c(pog), uiu4, uiu4(pog1c), uiu(pog1C)	low copy, thiazole biosynthesis, cDNA complements yeast thi4
4742	thi2	thiamine biosynthesis2	GRMZM2G074097	B73 RefGen_v3	Gene	Chr3	218917243	218918947	thi2	senescence-diminished2, thi1-2, thi2, thiamine biosynthesis2, thi*-U17351, uiu1a(pog), uiu2, uiu2(pog1a)	progressive elimination of leaf blade, successive younger leaves most affected; generally tasselless
4743	thi3	thiamine synthesis3	GRMZM2G401934	B73 RefGen_v3	Gene	Chr3	138804559	138811009	thi3	bth1, phosphomethylpyrimidine kinase/thiamin-phosphate pyrophosphorylase, rs129344302, rs129417467, th1, thi3, thiamine synthesis3	enzymatic function confirmed assay of recombinant protein (Rapala-Kozik et al 2007)
4744	thic1	hydroxymethylpyrimidine phosphate syn	GRMZM2G027663	B73 RefGen_v3	Gene	Chr1	256626740	256633146	thic1	cl574_1(29), thic1	
4745	thim1	thiamin thiazole kinase M1	GRMZM2G094558	B73 RefGen_v3	Gene	Chr8	47311260	47314747	thim1	hetk, hydroxyethylthiazole kinase, thim1, THZ kinase M1	thiamin salvage enzyme
4746	thl1	thiolase1	GRMZM2G085474	B73 RefGen_v3	Gene	Chr1	180427789	180433544	thl1	acetyl-CoA acetyltransferase, cytosolic 1, PCO140839, PCO140839(662), thiolase1, thl1	cDNA
4747	tho1	THO complex subunit 7B-like1	GRMZM2G473389	B73 RefGen_v3	Gene	Chr1	4284638	4287038	tho1	rs131185915, ss196525906 , tho1, umc94a	
4748	thr1	threonine synthase1	GRMZM2G050570	B73 RefGen_v3	Gene	Chr3	206609421	206611387	thr1	CL120_1, csu189, csu189(gfu), csu189(thr), thr1, threonine synthase1	leaf cDNA csu189 similar to bacterial threonine synthase
4749	thx1	Trihelix-transcription factor 1	GRMZM2G157219	B73 RefGen_v3	Gene	Chr6	164397872	164405814	thx1		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4750	thx10	Trihelix-transcription factor 10	GRMZM2G415229	B73 RefGen_v3	Gene	Chr10	140445959	140448997	thx10		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4751	thx12	Trihelix-transcription factor 12	GRMZM2G016649	B73 RefGen_v3	Gene	Chr2	22414453	22418920	thx12		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4752	thx13	Trihelix-transcription factor 13	GRMZM2G134439	B73 RefGen_v3	Gene	Chr5	98309006	98312767	thx13		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4753	thx14	Trihelix-transcription factor 14	GRMZM2G163157	B73 RefGen_v3	Gene	Chr8	149680318	149681806	thx14		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4754	thx15	Trihelix-transcription factor 15	GRMZM2G021831	B73 RefGen_v3	Gene	Chr2	46408460	46410063	thx15		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
4755	thx16	Trihelix-transcription factor 16	GRMZM2G063203	B73 RefGen_v3	Gene	Chr4	149923554	149927268	thx16		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4756	thx17	Trihelix-transcription factor 17	GRMZM2G080583	B73 RefGen_v3	Gene	Chr3	209815458	209817472	thx17		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4757	thx18	Trihelix-transcription factor 18	GRMZM2G314660	B73 RefGen_v3	Gene	Chr1	3070619	3075128	thx18		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4758	thx19	Trihelix-transcription factor 19	GRMZM2G414159	B73 RefGen_v3	Gene	Chr5	22121290	22125541	thx19		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4759	thx2	Trihelix-transcription factor 2	GRMZM2G392168	B73 RefGen_v3	Gene	Chr10	119936505	119938289	thx2		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4760	thx20	Trihelix-transcription factor 20	GRMZM2G169580	B73 RefGen_v3	Gene	Chr5	190292136	190295846	thx20		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4761	thx21	Trihelix-transcription factor 21	GRMZM2G037128	B73 RefGen_v3	Gene	Chr4	241077710	241081030	thx21		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4762	thx22	Trihelix-transcription factor 22	GRMZM2G111760	B73 RefGen_v3	Gene	Chr5	67208649	67211604	thx22		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4763	thx23	Trihelix-transcription factor 23	GRMZM2G156348	B73 RefGen_v3	Gene	Chr2	12103921	12107093	thx23		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4764	thx24	Trihelix-transcription factor 24	GRMZM2G380094	B73 RefGen_v3	Gene	Chr5	175099364	175100572	thx24		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4765	thx25	Trihelix-transcription factor 25	GRMZM2G047370	B73 RefGen_v3	Gene	Chr10	126511889	126515647	thx25		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4766	thx26	Trihelix-transcription factor 26	GRMZM2G002978	B73 RefGen_v3	Gene	Chr2	59987056	59992370	thx26		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4767	thx27	Trihelix-transcription factor 27	AC209784.3_FG011	B73 RefGen_v3	Gene	Chr3	181029394	181032191	thx27		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4768	thx28	Trihelix-transcription factor 28	GRMZM2G428470	B73 RefGen_v3	Gene	Chr9	114575016	114577006	thx28		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4769	thx29	Trihelix-transcription factor 29	GRMZM2G326783	B73 RefGen_v3	Gene	Chr9	134290370	134296361	thx29		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4770	thx3	Trihelix-transcription factor 3	GRMZM5G850092	B73 RefGen_v3	Gene	Chr4	197161489	197162856	thx3		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4771	thx4	Trihelix-transcription factor 4	GRMZM2G481163	B73 RefGen_v3	Gene	Chr1	94888973	94890564	thx4		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4772	thx5	Trihelix-transcription factor 5	GRMZM2G016637	B73 RefGen_v3	Gene	Chr6	25703021	25704825	thx5		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4773	thx6	Trihelix-transcription factor 6	GRMZM2G339957	B73 RefGen_v3	Gene	Chr8	154781227	154784741	thx6		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4774	thx7	Trihelix-transcription factor 7	GRMZM2G023119	B73 RefGen_v3	Gene	Chr1	122587640	122590008	thx7		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4775	thx8	Trihelix-transcription factor 8	GRMZM2G379179	B73 RefGen_v3	Gene	Chr1	182381758	182383378	thx8		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4776	thx9	Trihelix-transcription factor 9	GRMZM2G037493	B73 RefGen_v3	Gene	Chr1	186502389	186506512	thx9		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4777	TIDP3683		GRMZM2G073535	B73 RefGen_v3	Gene	Chr6	156713541	156715788	TIDP3683	pco141133	
4778	tif1	translation initiation factor1	GRMZM5G835323	B73 RefGen_v3	Gene	Chr7	154305680	154308577	tif1	csu209, csu209(gfu), gos2, homolog to rice gos2, sui1, SUI1, tif1, translation initiation factor1	Was gos2, leaf cDNA csu209, single copy, 5' sequence similar to constitutive rice gos2, ? translation factor, SUI1 family.
4779	tif5A	eukaryotic translation initiation factor 5A	GRMZM2G144030	B73 RefGen_v3	Gene	Chr7	163041712	163045353	tif5A	csu154b, csu154c(eif5A), csu175d(eif5A), csu203a(eif5A), eIF-5A, S1_eIF5A, tif5A, umc384c	
4780	tip1	tonoplast intrinsic protein1	Zm00001d027652	Zm-B73-REFERENCE-G	Gene	Chr1	10150836	10152891	tip1	PCO114899, PCO114899(749), tip1, tonoplast intrinsic protein1, ZmTIP1, ZmTIP1-1	tip1 cDNA is 1097 bp long, including the 93 bp leader sequence. Its derived amino acid sequence has 76% identity with the tonoplast aquaporin from Arabidopsis.
4781	tip2	tonoplast intrinsic protein2	GRMZM2G168439	B73 RefGen_v3	Gene	Chr8	156113368	156114570	tip2	aquaporin TIP1.2, CL24208_1(636), CL24208_1b, tip1b, tip2, tonoplast intrinsic protein1, tonoplast intrinsic protein2, ZmTIP1-2	
4782	tip2a	tonoplast intrinsic protein2	GRMZM2G027098	B73 RefGen_v3	Gene	Chr4	152458301	152459746	tip2a	PCO137646, tip2a, tonoplast intrinsic protein2, ZmTIP2-1	
4783	tip2b	tonoplast intrinsic protein2	GRMZM2G056908	B73 RefGen_v3	Gene	Chr5	191963084	191964288	tip2b	CL43160_1, tip2b, tonoplast intrinsic protein2, ZmTIP2-2	
4784	tip3a	tonoplast intrinsic protein3	GRMZM2G305446	B73 RefGen_v3	Gene	Chr5	25531005	25532346	tip3a	tip3a, tonoplast intrinsic protein3, ZmTIP3-1	
4785	tip3b	tonoplast intrinsic protein3	GRMZM2G103983	B73 RefGen_v3	Gene	Chr1	228464359	228465647	tip3b	tip3b, tonoplast intrinsic protein3, ZmTIP3-2	
4786	tip4a	tonoplast intrinsic protein4	GRMZM2G103945	B73 RefGen_v3	Gene	Chr6	133537405	133539720	tip4a	tip4a, tonoplast intrinsic protein4, ZmTIP4-1	
4787	tip4b	tonoplast intrinsic protein4	GRMZM2G108273	B73 RefGen_v3	Gene	Chr8	110236661	110239074	tip4b	aquaporin TIP4.1, aquaporin TIP4-2, tip4b, tonoplast intrinsic protein4, ZmTIP4-2	
4788	tip4c	tonoplast intrinsic protein4	GRMZM2G146627	B73 RefGen_v3	Gene	Chr3	13536786	13539654	tip4c	TIP4-3, tip4c, tonoplast intrinsic protein4, ZmTIP4-3	
4789	tip4d	tonoplast intrinsic protein4	GRMZM2G093090	B73 RefGen_v3	Gene	Chr3	1847706	1848827	tip4d	aquaporin TIP4.1, tip4d, tonoplast intrinsic protein4, ZmTIP4-4	
4790	tip5	tonoplast intrinsic protein5	GRMZM2G125023	B73 RefGen_v3	Gene	Chr10	139149943	139152962	tip5	por2, tip5, tip5a, tonoplast intrinsic protein5, tonoplast membrane integral protein ZmTIP5-1, umc2122, ZmTIP5-1	cDNA sequence similar to tonoplast aquaporin; SSR umc2122
4791	tk1	transketolase 1	GRMZM2G033208	B73 RefGen_v3	Gene	Chr9	22790749	22795294	tk1	tk1, transketolase 1	
4792	tla1	transparent leaf area1	Zm00008a009742	Zm-PH207-REFERENCE	Gene	chr2	214970306	214971076	tla1	tla1, transparent leaf area1	
4793	tlk1	tousled-like protein kinase1	GRMZM2G016671	B73 RefGen_v3	Gene	Chr1	276396791	276429710	tlk1	CL1888_1a, MTK-1, tlk1, tousled-like protein kinase1, tousled protein kinase1, tpk1, uaz130, uaz130a(tlk)	endosperm cDNA 5C04A03 (uaz130), similar to Arabidopsis protein kinase, TOUSLED
4794	tlk2	tousled-like protein kinase2	GRMZM2G172132	B73 RefGen_v3	Gene	Chr5	7231744	7248155	tlk2	MTK-4, tlk2, tousled-like protein kinase2, uaz130c, uaz130c(tlk)	
4795	tls1	tasselless1	GRMZM2G176209	B73 RefGen_v3	Gene	Chr1	223906865	223910808	tls1	nip3a, NOD26-like membrane intrinsic protein3, PCO070928, PCO070928(70), rs131856224 , tassel-less, tasselless1, tls1, ZmNIP3, ZmNIP3-1	variable ranging from no seed set to a few kernels on a small ball-shaped cob; in some backgrounds, pubescent, leathery at 4-8 leaf stage; similar to bs1 of Woodworth and Micu.
4796	tm20	transmembrane protein20	GRMZM2G036564	B73 RefGen_v3	Gene	Chr6	120315469	120319622	tm20	CL1457_1, defective kernel34, dek34, DekB, lac1, lachrima, lachrima1, tm20, transmembrane protein20	genomic and cDNA sequences near Ac insertion into lachrima, aka dek34. reduced kernel
4797	tms5	thermosensitive male-sterile5	GRMZM2G147727	B73 RefGen_v3	Gene	Chr4	223366764	223369176	tms5	si618065b11, si618065b11(371) , tms5	mutants were fertile at 24C, but male sterile at 32C; exhibit fertility transition at 28C
4798	toc34	translocon at outer membrane of chlorop	GRMZM2G159777	B73 RefGen_v3	Gene	Chr9	144054835	144061089	toc34	AY107292, pco067487(654), toc34, toc34-1, toc34A, translocon at outer membrane of chloroplast34	cDNA sequence, transgenic expression
4799	toc35	translocon of outer membrane of chlorop	GRMZM2G157157	B73 RefGen_v3	Gene	Chr1	32202204	32208281	toc35	toc34-2, toc34b, toc34B, toc35, translocon of outer membrane of chloroplast35	
4800	tola1	tola protein homolog1	AC185226.4_FG001	B73 RefGen_v3	Gene	Chr4	162608157	162617862	tola1	clustered mitochondria protein-like, tola1, tola protein homolog1, ToleranceA ortholog, uaz254, uaz254(gfu)	endosperm cDNA 5C05A03 (uaz254) similar to E. coli TOLA protein, an inner membrane, colicin transport protein
4801	tom1	transporter of mugineic acid1	GRMZM2G063306	B73 RefGen_v3	Gene	Chr3	112059631	112065432	tom1	tom1, transporter of mugineic acid family phytosiderophores1, zinc induced facilitator-like1	homolog of rice tom1; expression level significantly decreased in the ys3 mutant
4802	tom3	transporter of mugineic acid3	GRMZM2G141081	B73 RefGen_v3	Gene	Chr2	149197052	149201004	tom3	carbohydrate transporter/ sugar porter/ transporter, tom3	induced in the roots under Fe-deficient conditions
4803	tpi1	triose phosphate isomerase1	GRMZM2G305211	B73 RefGen_v3	Gene	Chr7	159951153	159960399	tpi1	tpi1, triose phosphate isomerase1	electrophoretic mobility; plastidial; dimeric; intra/interlocus hybrids occur with Tpi2

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
4804	tpi2	triose phosphate isomerase2	GRMZM2G002807	B73 RefGen_v3	Gene	Chr2	196570628	196574505	tpi2	gpm397a, tpi2, triose phosphate isomerase2	electrophoretic mobility; plastidial; dimeric; intra/interlocus hybrids occur with Tpi1
4805	tpi3	triose phosphate isomerase3	GRMZM2G018177	B73 RefGen_v3	Gene	Chr8	14391800	14395986	tpi3	gsy326(tpi), npi344-tpi3, tpi3, triose phosphate isomerase3, triosephosphate isomerase, cytosolic, uaz93a(tpi)	electrophoretic mobility; cytosolic; dimeric; intra/interlocus hybrids occur with Tpi4 & Tpi5
4806	tpi4	triose phosphate isomerase4	GRMZM2G030784	B73 RefGen_v3	Gene	Chr3	17832286	17836567	tpi4	csu301, mzeTPF1, nc030, nc30, npi344A, npi345-tpi3, npi(tpi), PCO130270, pco130270(214), phi029, phi29, tpi4, tpi*D00012, triose phosphate isomerase4	electrophoretic mobility; cytosolic; dimeric; intra/interlocus hybrids occur with Tpi3 & Tpi5; leaf cDNA csu301 single copy, SSRs phi029, nc030
4807	tpi5	triose phosphate isomerase5	GRMZM2G146206	B73 RefGen_v3	Gene	Chr8	168296435	168300637	tpi5	tpi5, triose phosphate isomerase5	electrophoretic mobility; cytosolic; dimeric intra/interlocus hybrids occur with Tpi3 & Tpi4
4808	tpl1	topless-related1	GRMZM2G316967	B73 RefGen_v3	Gene	Chr3	35794787	35804261	tpl1	topless-related protein 2, tpl1	
4809	tpl2	topless-related2	GRMZM2G030422	B73 RefGen_v3	Gene	Chr1	35244552	35255551	tpl2	tpl2	
4810	tps1	terpene synthase1	GRMZM2G049538	B73 RefGen_v3	Gene	Chr2	10602719	10611664	tps1	csu186, csu186(gfu), eks1, KS, terpene synthase1, tps1, ZmKS2.1, ZmTPS1	possible plant defense gene
4811	tps10	terpene synthase10	GRMZM2G179092	B73 RefGen_v3	Gene	Chr10	74488739	74492309	tps10	sesquiterpene synthase10, terpene synthase10, tps10	
4812	tps11	terpene synthase11	GRMZM2G127087	B73 RefGen_v3	Gene	Chr10	55612816	55765958	tps11	bisabolene synthase, macrocarpene synthase, sesquiterpene cyclase (Umi3) , sesquiterpene synthase11, terpene synthase11, tps11, umi3	
4813	tps17	terpene synthase17	GRMZM2G010356	B73 RefGen_v3	Gene	Chr2	113211755	113214535	tps17	terpene synthase 7, tps17	
4814	tps2	terpene synthase2	GRMZM2G046615	B73 RefGen_v3	Gene	Chr5	71292782	71295610	tps2	S-linalool synthase, terpene synthase2, tps2	
4815	tps23	terpene synthase23	GRMZM2G127336	B73 RefGen_v3	Gene	Chr10	57658111	57664789	tps23	(E)-beta-caryophyllene synthase, sesquiterpene synthase23, terpene synthase23, tps23	part of defense response to herbivory by western maize rootworm and Spodoptera littoralis but not expressed highly in most North American maize
4816	tps26	terpene synthase26	GRMZM2G030583	B73 RefGen_v3	Gene	Chr6	107478552	107483274	tps26	terpene synthase26, tps26	orthologous to stc1 but function in insect herbivory not clear
4817	tps3	terpene synthase3	GRMZM2G064406	B73 RefGen_v3	Gene	Chr5	71410033	71413111	tps3	S-linalool synthase, terpene synthase3, tps3	
4818	tps4	terpene synthase4	GRMZM2G117319	B73 RefGen_v3	Gene	Chr10	74022933	74026069	tps4	sesquiterpene synthase4, terpene synthase4, tps4	gene product raised in E. coli forms same mixture of sesquiterpene olefins as tsp5 but with quantitative differences.
4819	tps5	terpene synthase5	GRMZM2G074309	B73 RefGen_v3	Gene	Chr10	74248611	74251874	tps5	sesquiterpene synthase5, terpene synthase5, tps5, TPS5 inactive sesquithujene synthase-like	
4820	tps6	terpene synthase6	GRMZM2G127087	B73 RefGen_v3	Gene	Chr10	55612816	55765958	tps6	bisabolene synthase, macrocarpene synthase, sequiterpene synthase6, sesquiterpene cyclase2, stc2, terpene synthase6, tps6, umi2, Ustilago maydis induced 2	
4821	tps7	terpene synthase7	AC217050.4_FG007	B73 RefGen_v3	Gene	Chr1	214936884	214943430	tps7	gnp_QCD28c06, gpm852, terpene synthase7, tps7	
4822	tps8	terpene synthase8	GRMZM2G038153	B73 RefGen_v3	Gene	Chr1	61014839	61021281	tps8	IDP1979, terpene synthase8, tps8, umc2217	
4823	tps9	terpene synthase9	GRMZM2G465812	B73 RefGen_v3	Gene	Chr10	73850131	73851474	tps9	IDP70, PCO101634b, terpene synthase9, tps9	
4824	tre1	trehalase1	GRMZM2G162690	B73 RefGen_v3	Gene	Chr1	80003683	80008544	tre1	tre1, ZmTRE1.1, ZmTRE1.2, ZmTRE1.3	
4825	trh1	thioredoxin h homolog1	GRMZM2G424053	B73 RefGen_v3	Gene	Chr6	157965018	157969757	trh1	csu727(trh), thioredoxin h homolog1, thioredoxin H-type, trh1, trxh1, uaz5c05b02(gfu)	endosperm cDNA 5c05b02 similar to plant and yeast thioredoxin
4826	trh2	thioredoxin h homolog2	GRMZM2G144653	B73 RefGen_v3	Gene	Chr7	13181810	13184354	trh2	PCO064560(538), PCO064560b, trh2, trxh2	
4827	trh3	thioredoxin h homolog3	GRMZM2G079089	B73 RefGen_v3	Gene	Chr3	219419739	219421147	trh3	histone H2B.2, trh3	
4828	trm1	thioredoxin M1	GRMZM2G181258	B73 RefGen_v3	Gene	Chr10	16218811	16219788	trm1	PCO147105, PCO147105(721), pTHRm, pza02961 , rs131175979, ss196417323, thioredoxin M1, trm1	cDNA with conserved active site
4829	trm2	thioredoxin M2	GRMZM2G358009	B73 RefGen_v3	Gene	Chr3	138151050	138152140	trm2	csu439(trm), trm2	
4830	trm3	thioredoxin M3	GRMZM2G131202	B73 RefGen_v3	Gene	Chr2	51853125	51854807	trm3	trm3	
4831	trpp1	trehalose-6-phosphate phosphatase1	GRMZM2G347280	B73 RefGen_v3	Gene	Chr1	217833921	217836445	trpp1	trpp1, ZmTPP1	
4832	trpp10	trehalose-6-phosphate phosphatase10	GRMZM2G080354	B73 RefGen_v3	Gene	Chr9	5654774	5657748	trpp10	trpp10, ZmTPP11	
4833	trpp11	trehalose-6-phosphate phosphatase11	GRMZM2G178546	B73 RefGen_v3	Gene	Chr9	117179608	117183243	trpp11	trpp11, ZmTPP12	
4834	trpp2	trehalose-6-phosphate phosphatase2	GRMZM2G140078	B73 RefGen_v3	Gene	Chr2	177921904	177924464	trpp2	trpp2, ZmTPP2	
4835	trpp3	trehalose-6-phosphate phosphatase3	GRMZM2G117564	B73 RefGen_v3	Gene	Chr2	213142636	213145421	trpp3	trpp3, ZmTPP3	
4836	trpp4	trehalose-6-phosphate phosphatase4	GRMZM2G151044	B73 RefGen_v3	Gene	Chr4	180916055	180919097	trpp4	trpp4, ZmTPP4	
4837	trpp5	trehalose-6-phosphate phosphatase5	GRMZM2G059840	B73 RefGen_v3	Gene	Chr4	183294232	183295877	trpp5	trpp5, ZmTPP5	
4838	trpp6	trehalose-6-phosphate phosphatase6	GRMZM2G112830	B73 RefGen_v3	Gene	Chr5	192358347	192362866	trpp6	trpp6, ZmTPP6	
4839	trpp7	trehalose-6-phosphate phosphatase7	GRMZM2G055150	B73 RefGen_v3	Gene	Chr5	208220125	208222639	trpp7	trehalose-6-phosphate phosphatase7, trpp7, ZmTPP7	
4840	trpp8	trehalose-6-phosphate phosphatase8	GRMZM2G174396	B73 RefGen_v3	Gene	Chr7	100351591	100353678	trpp8	trpp8, ZmTPP8	
4841	trpp9	trehalose-6-phosphate phosphatase9	GRMZM5G840145	B73 RefGen_v3	Gene	Chr7	166884741	166887809	trpp9	rs132438174, si603015d01b, sister of ramosa3, sra, trehalose-6-phosphate phosphatase9, trpp9, ZmTPP9	
4842	trps1	trehalose-6-phosphate synthase1	GRMZM2G068943	B73 RefGen_v3	Gene	Chr8	123130508	123138783	trps1	tps1, trehalose-6-phosphate synthase1, trps1, ZmTPS1, ZmTPS14.1	
4843	trps10	trehalose-6-phosphate synthase10	GRMZM2G312521	B73 RefGen_v3	Gene	Chr4	174991784	174996304	trps10	trps10, ZmTPS9	
4844	trps11	trehalose-6-phosphate synthase11	GRMZM2G122231	B73 RefGen_v3	Gene	Chr5	213103736	213107678	trps11	trps11, ZmTPS10	
4845	trps12	trehalose-6-phosphate synthase12	GRMZM2G001304	B73 RefGen_v3	Gene	Chr6	159446662	159451841	trps12	trps12, ZmTPS11.1	
4846	trps13	trehalose-6-phosphate synthase13	GRMZM2G019183	B73 RefGen_v3	Gene	Chr7	107954189	107958866	trps13	trps13, ZmTPS12.2	
4847	trps14	trehalose-6-phosphate synthase14	GRMZM2G416836	B73 RefGen_v3	Gene	Chr8	5488159	5500321	trps14	trps14, ZmTPS13.1	
4848	trps15	trehalose-6-phosphate synthase15	GRMZM2G118462	B73 RefGen_v3	Gene	Chr8	173973120	173978270	trps15	trps15, ZmTPS15	
4849	trps2	trehalose-6-phosphate synthase2	GRMZM2G099860	B73 RefGen_v3	Gene	Chr1	28446754	28451214	trps2	trps2, ZmTPS1.1	
4850	trps3	trehalose-6-phosphate synthase3	GRMZM2G079928	B73 RefGen_v3	Gene	Chr1	210710797	210714526	trps3	trps3, ZmTPS2	
4851	trps4	trehalose-6-phosphate synthase4	GRMZM2G008226	B73 RefGen_v3	Gene	Chr1	218618199	218623790	trps4	trps4, ZmTPS3	
4852	trps5	trehalose-6-phosphate synthase5	GRMZM2G527891	B73 RefGen_v3	Gene	Chr2	178595620	178602402	trps5	trps5, ZmTPS4	

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
4853	trps6	trehalose-6-phosphate synthase6	GRMZM2G304274	B73 RefGen_v3	Gene	Chr3	197959792	197974963	trps6	trps6, ZmTPS5	
4854	trps7	trehalose-6-phosphate synthase7	GRMZM2G123277	B73 RefGen_v3	Gene	Chr3	198017608	198022549	trps7	trps7, ZmTPS6	
4855	trps8	trehalose-6-phosphate synthase8	GRMZM2G007736	B73 RefGen_v3	Gene	Chr4	61432557	61437544	trps8	trps8, ZmTPS7.2	
4856	trps9	trehalose-6-phosphate synthase9	GRMZM2G366659	B73 RefGen_v3	Gene	Chr4	76359450	76362880	trps9	trps9, ZmTPS8	
4857	tru1	tassels replace upper ears1	GRMZM2G039867	B73 RefGen_v3	Gene	Chr3	150088574	150091550	tru1	regulatory protein NPR5-like, tassels replace upper ears1, tru1	upper ear branches tassel-like, tillers bear ears
4858	ts1	tassel seed1	GRMZM2G104843	B73 RefGen_v3	Gene	Chr2	45820737	45825105	ts1	lipoxygenase8, lox8, tassel seed1, ts1	tassel pistillate and pendant; if removed, small ear with irregular kernel placement develops
4859	ts2	tassel seed2	GRMZM2G455809	B73 RefGen_v3	Gene	Chr1	46683464	46684885	ts2	microsatellite ynh(ts2), phi001, tassel seed2, ts2, ynh, ynh(ts2)	like ts1, but tassel branches variably pistillate and staminate; sequence homologous to short chain alcohol dehydrogenases; SSR phi001
4860	ts4	tasselseed4	GRMZM5G803935	B73 RefGen_v3	Gene	Chr3	144918011	144918720	ts4	mir172, miR172e, Sorghum Tassel, tasselseed4, tassel seed4, ts4, zma-MIR172e	encodes miRNA that targets ts6 and sid1; tassel compact silky mass, upright, with pistillate and staminate florets; ear silky and proliferated
4861	ts6	tasselseed6	GRMZM5G862109	B73 RefGen_v3	Gene	Chr1	292966682	292970925	ts6	rs128281361, rs131175377, ss196414883, ss196414885, tasselseed6, tassel seed6, ts6, umc1009, ZmEREB11	Recessive alleles have more than two florets per spikelet, and reversed germ orientation. Dominant Ts6 tassels are compact, pistillate to mixed and ears have irregular kernel placement.
4862	tsa1	tryptophan synthase alpha subunit1	GRMZM5G841619	B73 RefGen_v3	Gene	Chr7	10780313	10784254	tsa1	PCO145511(535), PCO145511a, TIDP5250, tsa1	With products of orp1 and orp2 genes, forms tryptophan synthase. Plastidic.
4863	tsah1	tryptophan synthase A homolog1	GRMZM2G046191	B73 RefGen_v3	Gene	Chr1	288331936	288337173	tsah1	csu868(trp), tryptophan synthase A homolog1, tsah1, tsalike	Homologous to tryptophan synthase alpha subunit but does occur as part of native tryptophan synthase. Localized in the cytosol (Kriechbaumer et al 2008). Function unknown.
4864	tsh1	tassel sheath1	GRMZM2G325850	B73 RefGen_v3	Gene	Chr6	166277494	166278842	tsh1	GATA transcription factor 19, tassel sheath1, tsh1, tsh*-50330, ZmGATA20	Whipple et al, 2010. It was initially mapped between umc2059 and bnlg1740. The position was narrowed using a larger population, synteny with rice provided two candidate genes, one was
4865	tsh4	tassel sheath4	GRMZM2G307588	B73 RefGen_v3	Gene	Chr7	133202776	133206423	tsh4	sbp6, SBP-box transcription factor, SBP-domain protein , siaj011619(566), siaj011619a, Squamosa promoter Binding Protein, tassel sheath4, tsh4, ZmSBP2, ZMSBP6	mutant W22. In place of tassel branches, long bract leaves were present, clustered at the base of the tassel.
4866	tti1	tel2-interacting protein1	GRMZM2G056403	B73 RefGen_v3	Gene	Chr5	43832034	43852685	tti1	ARM repeat superfamily protein, Tel2 interacting protein 1, tti1	
4867	tu1	tunicate1	GRMZM2G370777	B73 RefGen_v3	Gene	Chr4	178918189	178925234	tu1	corn, PZD00029, PZD00030, PZD00031, rs128284880, rs131175628, rs131175629, ss196415874, ss196415876, ss196415878, tu1, tunicate1, Zea mays MADS19, zmm19,	coarse glumes and sex reversal; both inflorescences become grossly vegetative and sterile in homozygotes
4868	tua1	alpha tubulin1	GRMZM2G153292	B73 RefGen_v3	Gene	Chr1	271172696	271181023	tua1	alpha tubulin1, Atub, bnl17.04(tua), bnl17.21(tua), csu272a(tua), csu399a(tua), gsy56(tua1), IDP2525, SC56, SC58, tua1, tua1(445), tua1(608), tua7, tub1, TubA	mRNA expressed primarily in root tips and pollen; member of tandem repeat (see tua2); gene specific cDNA probe
4869	tua2	alpha tubulin2	GRMZM2G153292	B73 RefGen_v3	Gene	Chr1	271172696	271181023	tua2	alpha tubulin2, IDP2525, rs131176914, rs131892013, tua2, tub2, TubA, Tubalpha2	in radicles, root tips and coleoptiles; 6 alpha tubulin genes identified; gene specific cDNA probe and SNPs
4870	tua3	alpha tubulin3	AC195340.3_FG001	B73 RefGen_v3	Gene	Chr5	5434731	5437116	tua3	alpha tubulin3, PCO151041, tua3, TubA, Tubalpha3, uaz201(tua)	alpha tubulin family; mRNA expressed in all dividing cells examined; gene specific cDNA probe
4871	tua4	alpha tubulin4	GRMZM2G152466	B73 RefGen_v3	Gene	Chr5	9481738	9485476	tua4	alpha tubulin4, csu272b(tua), csu399b(tua), csu662(tua), PCO076329, PCO076329(378), tua4, TubA	belongs to alpha tubulin subfamily I, with tua1 and tua2; gene specific cDNA probe
4872	tua5	alpha tubulin5	GRMZM2G099167	B73 RefGen_v3	Gene	Chr2	207291939	207295620	tua5	alpha tubulin5, PCO104685a, pZMA3, tua5, tua*-L27815, TubA	alpha tubulin subfamily II with tua6; gene specific cDNA probe
4873	tua6	alpha tubulin6	GRMZM2G083243	B73 RefGen_v3	Gene	Chr7	160071867	160075599	tua6	alpha tubulin6, csu581a(tua), pco104685(577), PCO104685b, tua6, TubA	alpha tubulin subfamily II, gene specific cDNA probe
4874	tub1	beta tubulin1	GRMZM2G164696	B73 RefGen_v3	Gene	Chr1	2035661	2037950	tub1	beta tubulin1, CL2242_8a, phi056, phi056(tub1), phi097, rs131191473, rs131191482, tub1, TubB	genomic clones sequenced; gene-specific probe (by Southern blot) hybridizes to a single transcript size; SSRs phi056, 097
4875	tub2	beta tubulin2	GRMZM2G334899	B73 RefGen_v3	Gene	Chr8	104292707	104296183	tub2	beta tubulin2, TIDP2849, tub2, TubB	cDNA sequenced; single copy (Southern blots)
4876	tub3	beta tubulin3	GRMZM2G108766	B73 RefGen_v3	Gene	Chr1	258611047	258615106	tub3	beta tubulin3, tub3, TubB, tubulin beta-8 chain , umc1181	cDNA sequence, gene specific probe; SSR umc1181
4877	tub4	beta tubulin4	GRMZM2G066191	B73 RefGen_v3	Gene	Chr5	14869913	14874139	tub4	beta tubulin4, CL2242_8f, rs131495788 , rs726195318 , tub4, TubB, tub*-L10635	cDNA sequence, gene specific probe
4878	tub5	beta tubulin5	GRMZM2G133802	B73 RefGen_v3	Gene	Chr3	47738975	47742300	tub5	beta tubulin5, tub5, tub8, TubB, TUBB5, TUBB5 beta-5 tubulin, tub*-L10636	cDNA sequence, gene specific probe
4879	tub6	beta tubulin6	GRMZM2G172932	B73 RefGen_v3	Gene	Chr8	170881296	170884640	tub6	beta tubulin6, CL2242_8k, IDP2378, PCO095713, PCO095713(644), tub6, tub6a	
4880	tubb6	beta tubulin6b	GRMZM2G071790	B73 RefGen_v3	Gene	Chr3	187499362	187503653	tubb6	beta-6 tubulin, beta tubulin6, CL2242_8d, tub6, tub6b, tubb6, tub*-L10633, tubulin beta-4 chain	cDNA sequence, gene specific probe
4881	tubg1	gamma-tubulin1	GRMZM2G073888	B73 RefGen_v3	Gene	Chr8	78798124	78804134	tubg1	CL2076_-3(606), CL2076_-3c, tubg1, tubg3	
4882	tubg2	gamma-tubulin2	GRMZM2G085970	B73 RefGen_v3	Gene	Chr6	126762125	126766341	tubg2	gamma-tubulin1, tubg1, tubg2, tubg*-X78891, Zmtubg1	full-length cDNA; deduced amino acid sequence shows high similarity to this tubulin of Arabidopsis and others
4883	tubtf1	TUB-transcription factor 1	GRMZM2G068586	B73 RefGen_v3	Gene	Chr8	149813540	149818967	tubtf1	tub1, ZmTLP4	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4884	tubtf10	TUB-transcription factor 10	GRMZM2G129288	B73 RefGen_v3	Gene	Chr6	150264620	150270514	tubtf10	pentatricopeptide repeat-containing protein At3g42630-like, tub10, tubby-like F-box protein 8, ZmTLP7	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4885	tubtf11	TUB-transcription factor 11	GRMZM2G378907	B73 RefGen_v3	Gene	Chr1	60094998	60103977	tubtf11	tub11, ZmTLP11	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4886	tubtf12	TUB-transcription factor 12	GRMZM5G871407	B73 RefGen_v3	Gene	Chr8	167438145	167440601	tubtf12	tub12, ZmTLP15	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4887	tubtf13	TUB-transcription factor 13	GRMZM2G349376	B73 RefGen_v3	Gene	Chr9	112038910	112042465	tubtf13	tub13, tubby-like F-box protein 11, ZmTLP10	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4888	tubtf14	TUB-transcription factor 14	GRMZM2G001272	B73 RefGen_v3	Gene	Chr10	8789860	8796975	tubtf14	AY109994, CL768_1, tub14, tubby-like protein, tubtf14, ZmTLP1	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4889	tubtf15	TUB-transcription factor 15	GRMZM2G062154	B73 RefGen_v3	Gene	Chr3	209720836	209725600	tubtf15	tub15, tubtf15, umc1140, ZmTLP3	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4890	tubtf2	TUB-transcription factor 2	GRMZM5G866954	B73 RefGen_v3	Gene	Chr3	175734269	175738021	tubtf2	TIDP3098, tub2, tubtf2, ZmTLP14	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4891	tubtf3	TUB-transcription factor 3	GRMZM2G046816	B73 RefGen_v3	Gene	Chr4	214907581	214912733	tubtf3	tub3, ZmTLP2	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4892	tubtf4	TUB-transcription factor 4	GRMZM2G108228	B73 RefGen_v3	Gene	Chr2	25431508	25435921	tubtf4	tub4, tubtf4, umc1555, ZmTLP5	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4893	tubtf5	TUB-transcription factor 5	GRMZM2G435445	B73 RefGen_v3	Gene	Chr6	158666528	158671070	tubtf5	tub5, ZmTLP12	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4894	tubtf6	TUB-transcription factor 6	GRMZM2G176340	B73 RefGen_v3	Gene	Chr4	160005783	160009342	tubtf6	tub6, ZmTLP9	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4895	tubtf7	TUB-transcription factor 7	GRMZM2G163726	B73 RefGen_v3	Gene	Chr4	195960621	195964652	tubtf7	cl11715_1, cl11715_1(343), tub7, tubtf7, ZmTLP8	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4896	tubtf8	TUB-transcription factor 8	GRMZM2G472945	B73 RefGen_v3	Gene	Chr5	90798763	90801363	tubtf8	tub8, ZmTLP13	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4897	tubtf9	TUB-transcription factor 9	GRMZM2G115701	B73 RefGen_v3	Gene	Chr5	200962624	200966193	tubtf9	pco071899(446), pco071899b, tub9, tubtf9, ZmTLP6	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
4898	tufm1	elongation factor TU mitochondrial1	GRMZM2G022269	B73 RefGen_v3	Gene	Chr1	298487571	298492926	tufm1	elongation factor TU mitochondrial1, tufM, tufm1, umc2100	genomic sequence, low copy numberl SSR umc2100
4899	uaz237a(prc)		GRMZM2G005080	B73 RefGen_v3	Probed Site	Chr9	16001659	16002927	uaz237a(prc)	PCO106817, pco106817(660), ptc1, uaz237, uaz237a(prc), UAZ237A(Pros), uaz237a(ser), uaz237(pros)	endosperm cDNA 5C02A05 (uaz237), similar to proteasome subunit
4900	uaz265b(sbe)		GRMZM2G169073	B73 RefGen_v3	Probed Site	Chr6	82869841	82888278	uaz265b(sbe)	uaz265b, uaz265b(sbe)	
4901	ub2	unbranched2	GRMZM2G160917	B73 RefGen_v3	Gene	Chr1	188215376	188219483	ub2	sbp5, sbp8, SBP-domain protein5, SBP-transcription factor 8, squamosa promoter-binding-like protein 14 [Zea mays] , TC305612, ub2, ZMSBP5	double mutant shows decrease in tassel branch number

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
4902	ub3	unbranched3	GRMZM2G460544	B73 RefGen_v3	Gene	Chr4	199456664	199460958	ub3	sbp30, sbp7, sbp7 SBP-domain protein 7 [Zea mays] , SBP-domain protein7, SBP-transcription factor 30, TC282500, ub3, ZMSBP7	double mutant shows decrease in tassel branch number
4903	ubi1	ubiquitin1	GRMZM2G409726	B73 RefGen_v3	Gene	Chr5	82479947	82483338	ubi1	agr, AGR1002B, agr(ubi)1002b, csu377b(ubi), csu562b, csu562b(ubi), ubi1, Ubi-1, ubi2, ubiquitin1	genomic sequence, 7 contiguous direct ubiquitin repeats; transcript specific probe; promoter active in monocots, not in tobacco
4904	ubi2	ubiquitin2	GRMZM2G419891	B73 RefGen_v3	Gene	Chr4	237423191	237427552	ubi2	gnp_QAE23g10_PCR, gnp_QBI5d09_PCR, gpm284, gpm497, gsy257(ubi), MubG5(?), MubG9, polyubiquitin containing 7 ubiquitin monomer, uaz247(ubi), UAZ247(Ubiq), ubi1, ubi2, Ubi-2,	genomic sequence encodes 7 contiguous ubiquitin monomers; transcript specific probe
4905	ubi3	ubiquitin3	GRMZM2G014119	B73 RefGen_v3	Gene	Chr6	96004229	96006495	ubi3	qPEH6, ubi3, ubiquitin-NEDD8-like protein RUB2	candidate gene for major plant and ear height QTL
4906	ubl1	U6 biogenesis like1	GRMZM2G156575	B73 RefGen_v3	Gene	Chr5	190738089	190739754	ubl1	si945031h05(438), si945031h05a, ubl1	plays an important role in kernel and seedling development by influencing pre-mRNA splicing
4907	ubr1	ubiquitin receptor1	GRMZM2G017845	B73 RefGen_v3	Gene	Chr6	52901117	52909594	ubr1	da1, DA = "Large" in Chinese, ubr1, Zmda1	Orthologous to Arabidopsis DA1
4908	uce1	ubiquitin conjugating enzyme1	GRMZM2G018447	B73 RefGen_v3	Gene	Chr3	93201404	93219385	uce1	5c05d12, uaz102, uaz102(ubc), uaz5c05d12, ubiquitin conjugating enzyme1, uce1	endosperm cDNA 2C06C11 (uaz102), similar to plant ubiquitin conjugating enzymes
4909	uce2	ubiquitin conjugating enzyme2	GRMZM2G177276	B73 RefGen_v3	Gene	Chr9	11707996	11712257	uce2	ubiquitin-conjugating enzyme E2 J2, uce2	
4910	uce3	ubiquitin conjugating enzyme3	GRMZM2G070047	B73 RefGen_v3	Gene	Chr1	4974957	4978299	uce3	PCO142080, PCO142080(4), SCE1, std20b, std20b(uce), SUMO-conjugating enzyme SCE1, ubiquitin-conjugating enzyme E2 I , uce3, uce*-U49913	
4911	uce4	ubiquitin conjugating enzyme4	GRMZM2G102471	B73 RefGen_v3	Gene	Chr2	2808177	2811018	uce4	AY109692, CL301_1, PZA02175, rs129000554, rs55622624 , ss196414939, UBCP*, uce4, ZmUBCP	
4912	uce5	ubiquitin conjugating enzyme5	GRMZM2G022859	B73 RefGen_v3	Gene	Chr1	267922012	267928571	uce5	gnp_QBD2f01, gpm438, PCO143146, PCO143146(88), rs725353520 , ubiquitin-conjugating enzyme E2 variant 1, uce5, umc107a(croc)	
4913	uck1	UMP/CMP kinase1	GRMZM2G141009	B73 RefGen_v3	Gene	Chr6	57559271	57563575	uck1	csu612, uck1, UMP/CMP kinase1	single copy leaf cDNA, csu612, similar to Arabidopsis enzyme; pyrimidine biosynthesis
4914	udg1	uracil-DNA glycosylase1	GRMZM2G040627	B73 RefGen_v3	Gene	Chr2	2072014	2081975	udg1	udg1	
4915	ugp1	UDP-glucose pyrophosphorylase1	GRMZM6G729818	B73 RefGen_v3	Gene	Chr2	198410457	198414756	ugp1	PCO108378, uaz194, UAZ194A(UDPG), uaz194a(ugu), uaz194b, UAZ194B(UDPG), uaz194b(ugu), UDP-glucose pyrophosphorylase1, ugp1	endosperm cDNA 5C02H07 (uaz194), similar to potato UDP-glucose pyrophosphorylase
4916	ugp2	UDP-glucose pyrophosphorylase2	GRMZM2G032003	B73 RefGen_v3	Gene	Chr7	146528252	146535144	ugp2	csu815, ugp2	second locus with homology to T14797
4917	ugt1	UDP-glucosyl transferase1	GRMZM2G162755	B73 RefGen_v3	Gene	Chr6	120058984	120060863	ugt1	anthocyanidin 3-O-glucosyltransferase, ugt1	
4918	ugu1	UTP-glucose-P-uridyltransferase homolo	GRMZM2G134903	B73 RefGen_v3	Gene	Chr5	34604351	34608765	ugu1	exonuclease family protein, uazT14728(gfu), ugu1, UTP-glucose-P-uridyltransferase homolog	endosperm cDNA 5C04E10, similar to slime mold UTP--glucose-1-P uridylyltransferase
4919	umc1041		GRMZM2G448701	B73 RefGen_v3	Gene	Chr1	6148853	6149887	umc1041	umc1041	
4920	umc106a		GRMZM2G301071	B73 RefGen_v3	Gene	Chr1	274775918	274780056	umc106a	PCO146373, PCO146373(90), rs131181998, rs131181999 , umc106a	Similar to Arabidopsis CwfJ-like protein
4921	umc109		GRMZM2G136831	B73 RefGen_v3	Gene	Chr9	3310246	3313061	umc109	rs131691308, umc109	NCBI: Serine/threonine-protein kinase WNK (With No Lysine)-related
4922	umc1122		GRMZM2G016210	B73 RefGen_v3	Gene	Chr1	201673513	201678322	umc1122	PCO092830, rs131838514, umc1122	
4923	umc1147		GRMZM2G438386	B73 RefGen_v3	Gene	Chr1	225170303	225174114	umc1147	cpb1, C-terminal peptide-binding protein 1, umc1147	C-terminal peptide-binding protein 1. Similar to Monocopper oxidase-like protein SKU5 of Arabidopsis
4924	umc1149		GRMZM2G105005	B73 RefGen_v3	Gene	Chr8	159840596	159842605	umc1149	PCO081534, rs130911592, umc1149	NCBI: Glutathione S-transferase family
4925	umc115		GRMZM2G162814	B73 RefGen_v3	Gene	Chr1	14939938	14942616	umc115	rs128382382, rs131184429 , umc115	
4926	umc1177		GRMZM2G137329	B73 RefGen_v3	Gene	Chr1	2993011	2993734	umc1177	nonspecific lipid-transfer protein, PCO142716, umc1177	nonspecific lipid-transfer protein identified in CERES sequences
4927	umc1200		GRMZM2G127635	B73 RefGen_v3	Gene	Chr1	23109443	23111096	umc1200	umc1200	
4928	umc1220		GRMZM2G061626	B73 RefGen_v3	Gene	Chr1	293231711	293232742	umc1220	umc1220, ZFP16-2	
4929	umc1222		GRMZM2G056870	B73 RefGen_v3	Gene	Chr1	10989939	10997425	umc1222	cl4677_2(7), cl4677_2a, proteasome subunit alpha type 5, umc1222	
4930	umc1243		GRMZM2G085198	B73 RefGen_v3	Gene	Chr1	83531702	83533706	umc1243	rs128655266 , rs131183133, rs131183134 , rs131270942 , rs131270944 , umc1243, umc1244	similar to Arabidopsis peroxidase 3
4931	umc1245		GRMZM2G113781	B73 RefGen_v3	Gene	Chr1	229874104	229877959	umc1245	LysM domain containing protein , umc1245	
4932	umc124a(chk)		GRMZM2G087146	B73 RefGen_v3	Gene	Chr8	21151886	21155655	umc124a(chk)	rs131181608 , rs131658576, rs131658582, rs131658591 , si605019d10, si605019d10(589), umc124, umc124a, umc124a(chk), umc124(chk)	"NCBI: choline/ethanolamine kinase; putative choline kinase 2"
4933	umc1254		GRMZM2G045135	B73 RefGen_v3	Gene	Chr1	196619128	196623386	umc1254	umc1254	
4934	umc126a		Zm00001d017444	Zm-B73-REFERENCE-G	Gene	Chr5	196012063	196014634	umc126a	umc1019, umc126a	NCBI: probable WRKY transcription factor 51
4935	umc1278		GRMZM2G092595	B73 RefGen_v3	Gene	Chr1	215254512	215259644	umc1278	rs131183875, rs131849368, rs131849380, umc1278	putative 1-phosphatidylinositol-3-phosphate 5-kinase FAB1C per NCBI
4936	umc1290		GRMZM2G026780	B73 RefGen_v3	Gene	Chr1	270897979	270898979	umc1290	umc1290	
4937	umc1292		GRMZM2G176604	B73 RefGen_v3	Gene	Chr1	5401254	5405109	umc1292	CL27324_1a, umc1292	similar to Arabidopsis serine/threonine-protein kinase
4938	umc130		GRMZM2G125931	B73 RefGen_v3	Gene	Chr10	13559624	13562431	umc130	rs128492086 , rs131182150 , umc130, umc130(ntc)	
4939	umc1306		GRMZM2G153476	B73 RefGen_v3	Gene	Chr1	265241093	265242952	umc1306	umc1306	simiilar to Arabidopsis 30S ribosomal protein S13
4940	umc131		GRMZM2G024933	B73 RefGen_v3	Gene	Chr2	71740629	71768626	umc131	umc131, umc131(pext)	similar to predicted 2,3-dimethylmalate lyase-like isoform 2 of B. distachyon / phosphoenolpyruvate carboxylase-like protein of Arabidopsis
4941	umc1316		GRMZM2G116083	B73 RefGen_v3	Probed Site	Chr8	138324011	138329683	umc1316	PZA00090, rs131175889, ss196416977, umc1316	
4942	umc1323		GRMZM2G100121	B73 RefGen_v3	Gene	Chr1	170491369	170495919	umc1323	rs128802877 , rs131177885 ", rs131814405 , umc1323	NCBI: F-box/LRR-repeat protein 17-like
4943	umc132a(chk)		GRMZM2G014303	B73 RefGen_v3	Gene	Chr6	161321890	161325363	umc132a(chk)	rs132363230, umc132a, umc132a(chk)	NCBI: putative choline kinase 2
4944	umc1331		GRMZM5G874478	B73 RefGen_v3	Gene	Chr1	296282014	296284211	umc1331	rs131920648 , umc1331, umc1725	similar to glycine-rich RNA-binding protein 8 of Chlamydomonas
4945	umc1335		GRMZM2G477872	B73 RefGen_v3	Gene	Chr1	197104210	197113406	umc1335	rs128837548 , rs128837552, rs131183835 , umc1335	similar to Arabidopsis ABC transporter G family member 35
4946	umc1356		GRMZM2G112617	B73 RefGen_v3	Gene	Chr1	206507475	206509065	umc1356	rs131183000 , rs131841909 , umc1356	NCBI: NEP1-interacting protein-like 1
4947	umc1374		GRMZM2G119761	B73 RefGen_v3	Gene	Chr1	206554966	206558522	umc1374	rs128852333, umc1374	NCBI: similar to Arabidopsis 26S proteasome regulatory subunit N3
4948	umc1386b		GRMZM2G052650	B73 RefGen_v3	Gene	Chr1	170866748	170871629	umc1386b	CL12457_1b , PCO136812b, rs128803230 , rs128803237 , rs128803261, rs131180260 , rs131180261 , rs131814688	NCBI: serine/threonine-protein kinase Nek2-like
4949	umc1395		GRMZM2G329655	B73 RefGen_v3	Gene	Chr1	164572134	164574375	umc1395	rs128792479 , rs131811751 , umc1395	NCBI: cyclin-D5-2-like
4950	umc1396		GRMZM2G005652	B73 RefGen_v3	Gene	Chr1	191123119	191128083	umc1396	rs128831080 , rs128831086, rs128831093 , rs128831099, rs131181030 , umc1396	

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
4951	umc1397		GRMZM2G160506	B73 RefGen_v3	Gene	Chr1	39115112	39118417	umc1397	PCO105776, PCO105776(16), rs128419988, umc1397	similar to Arabidopsis mannose-1-phosphate guanylyltransferase
4952	umc1403		GRMZM2G108032	B73 RefGen_v3	Gene	Chr1	33126620	33130048	umc1403	pco132242, pco132242(14), umc1403	NCBI:putative glycosyl hydrolase family 10
4953	umc140a		GRMZM2G108861	B73 RefGen_v3	Gene	Chr1	258714960	258716976	umc140a	rs128938649 , umc140a	
4954	umc1411a		GRMZM6G799230	B73 RefGen_v3	Gene	scaffold_1279	2173		umc1411a	umc1411, umc1411a	NCBI: anther-specific proline-rich protein APG. NCBI: similar to Arabidopsis GDSL esterase/lipase
4955	umc1421		GRMZM2G078200	B73 RefGen_v3	Gene	Chr1	287959555	287963914	umc1421	rs128974568 , rs128974579 , ss196526992, ss196526994, umc1421	NCBI: pyruvate kinase isozyme A, chloroplastic-like
4956	umc1431		GRMZM2G004012	B73 RefGen_v3	Gene	Chr1	267212960	267213968	umc1431	rs131180591 , ss196502157 , umc1431	NCBI: similar to Arabidopsis plantacyanin
4957	umc1433		GRMZM2G001114	B73 RefGen_v3	Probed Site	Chr7	82672544	82681910	umc1433	PHM12830, PZA00418, rs130558562, ss196416613, umc1433	
4958	umc1446		GRMZM2G162508	B73 RefGen_v3	Gene	Chr1	240842179	240846321	umc1446	umc1446	NCBI: fatty acid elongase
4959	umc1452		GRMZM2G107463	B73 RefGen_v3	Gene	Chr1	53171372	53176168	umc1452	rs131184030 , rs131184042 , rs131252885 , ss196517580 , ss196517586 , ss196517634 , TIDP3188, umc1452	
4960	umc1457		GRMZM5G887068	B73 RefGen_v3	Gene	Chr8	101647239	101650151	umc1457	umc1457	NCBI: universal stress protein family
4961	umc1461		AC202185.4_FG004	B73 RefGen_v3	Gene	Chr1	122169770	122170960	umc1461	rs131796796 , ss196426833 , umc1461	
4962	umc1467		GRMZM2G134367	B73 RefGen_v3	Gene	Chr1	20418111	20419920	umc1467	rs128391396 , rs131182914 , rs131182915 , ss196512598 , ss196512600 , ss196512602 , umc1467	
4963	umc1469		GRMZM2G466982	B73 RefGen_v3	Gene	Chr1	115653428	115654009	umc1469	umc1469	
4964	umc1472		GRMZM2G124576	B73 RefGen_v3	Gene	Chr1	59672736	59676878	umc1472	pco142224, rs131177796 , ss196424257 , umc1472	NCBI: similar to Arabidopsis putative nucleolar protein 5-2
4965	umc1479		GRMZM2G042032	B73 RefGen_v3	Gene	Chr1	43137809	43141198	umc1479	IDP430, rs131176745 , rs131176746 , rs131177060 , rs131177357 , rs131183162, ss196419432 , ss196419434 , ss196420256 , ss196421024 , umc1479	
4966	umc1482		GRMZM2G037865	B73 RefGen_v3	Gene	Chr5	171020159	171021294	umc1482	NF-180, PCO090284, PCO090284(428), rs132243609, umc1482	NCBI: NF-180
4967	umc1484		GRMZM2G107532	B73 RefGen_v3	Gene	Chr1	9428005	9432250	umc1484	rs131181020 , rs131181021, rs131205701 , rs131205706 , rs131205708, TIDP3216, TIDP4603, umc1484	
4968	umc1486		GRMZM2G389567	B73 RefGen_v3	Gene	Chr1	211043052	211043783	umc1486	PCO096646, PCO096646(67), rs128859707 , rs131845826 , ss196430001 , ss196430003 , umc1486	
4969	umc1500		GRMZM2G069218	B73 RefGen_v3	Gene	Chr1	285603499	285608445	umc1500	umc1500	NCBI: DNA-binding protein HEXBP-like
4970	umc1509		GRMZM2G154523	B73 RefGen_v3	Gene	Chr4	5460337	5462342	umc1509	patatin T5, rs131428316, umc1509	NCBI: similar to Arabidopsis PATATIN-like protein 5
4971	umc1511		GRMZM2G004878	B73 RefGen_v3	Gene	Chr4	81276744	81278113	umc1511	rs131466451 , rs131466452 , umc1511	
4972	umc1538a		GRMZM5G831951	B73 RefGen_v3	Gene	Chr1	291973322	291974630	umc1538a	AP-1 complex subunit sigma-2, rs131187188 , ss196530750 , umc1538, umc1538a	
4973	umc1539		GRMZM2G109429	B73 RefGen_v3	Gene	Chr3	168533377	168536519	umc1539	PCO100914, rs129408819, umc1539	NCBI: selenoprotein family protein
4974	umc1553		GRMZM2G371210	B73 RefGen_v3	Gene	Chr1	287054286	287062461	umc1553	IDP8475, rs128973078 , rs131185474 , rs131185475 , rs131910051 , ss196523918 , ss196523926 , ss196523934 , ss196523936 , umc1553	NCBI type I inositol 1,4,5-trisphosphate 5-phosphatase CVP2-like
4975	umc1558		GRMZM2G047187	B73 RefGen_v3	Gene	Chr1	85839688	85844369	umc1558	rs128659948 , rs128659960 , rs128659968 , rs131182134 , rs131272348 , ss196425271 , ss196425273 , ss196509045 , ss196509059 , Tetracycline transporter, umc1558	NCBI: similar to Arabidopsis major facilitator protein
4976	umc1590		GRMZM2G176962	B73 RefGen_v3	Gene	Chr1	182873055	182876103	umc1590	rs131822865 , ss196429030 , umc1590	
4977	umc1601		GRMZM2G038855	B73 RefGen_v3	Gene	Chr1	166785190	166789349	umc1601	rs131812796 , rs131812807 , ss196428385, ss196428387 , umc1601	NCBI: protein trichome birefringence-like 28 . NCBI: putative DUF231 domain containing family protein
4978	umc1605		GRMZM5G821637	B73 RefGen_v3	Gene	Chr1	298766998	298771703	umc1605	ankyrin repeat domain-containing protein 2 , rs131186138 , rs131186841 , ss196526871 , ss196529790 , umc1605	NCBI: ankyrin repeat domain-containing protein 2
4979	umc1611		GRMZM2G132077	B73 RefGen_v3	Gene	Chr1	152175789	152176887	umc1611	umc1611	
4980	umc1613		GRMZM2G161560	B73 RefGen_v3	Gene	Chr1	1785557	1787537	umc1613	CL9345_1, umc1613	
4981	umc161a		GRMZM2G472827	B73 RefGen_v3	Gene	Chr1	283258252	283262785	umc161a	php4241, rs131186640 , ss196529142 , TIDP6166, umc161a, umc257	
4982	umc1626		GRMZM5G801886	B73 RefGen_v3	Gene	Chr1	157148809	157149892	umc1626	AY107682, PZA01041, rs128779484 , rs131808031 , rs131808034 , rs131808041 , ss196427924 , ss196427926 , ss196427928 , ss196427930 , umc1626	similar to Arabidopsis purple acid phosphatase 24
4983	umc1641		GRMZM2G064031	B73 RefGen_v3	Gene	Chr3	227133973	227141739	umc1641	rs132120891 , umc1641	NCBI: chaperone protein dnaJ 49-like
4984	umc1664		GRMZM2G083725	B73 RefGen_v3	Gene	Chr1	194690089	194692196	umc1664	rs128833953 , rs128833954 , rs131830801 , ss196429387 , ss196429389 , ss196523810 , umc1664, umc1668	NCBI: putative bifunctional inhibitor/LTP/seed storage protein family
4985	umc168		GRMZM2G135341	B73 RefGen_v3	Gene	Chr7	174404316	174410512	umc168	BADH-like protein, bnl7, CL53684_1, rs130697533 , rs130697535 , rs131177054 , rs131184717 , umc168, umc168b, umc1760	NCBI: similar to Arabidopsis aldehyde dehydrogenase 22A1
4986	umc1709		GRMZM2G159996	B73 RefGen_v3	Gene	Chr1	195590031	195594661	umc1709	PZA00619, rs131832121, umc1709, ZmOrphan268	
4987	umc1710		GRMZM2G008687	B73 RefGen_v3	Gene	Chr7	156539630	156543248	umc1710	rs131180253, umc1710	NCBI: similar to Arabidopsis PLAC8 family protein
4988	umc1711		GRMZM2G107815	B73 RefGen_v3	Gene	Chr1	25409169	25413691	umc1711	rs55622812 , umc1711	
4989	umc1715		GRMZM2G171559	B73 RefGen_v3	Gene	Chr1	226296202	226296963	umc1715	rs131858466 , umc1715	
4990	umc1734		GRMZM2G114667	B73 RefGen_v3	Gene	Chr1	92254266	92255946	umc1734	umc1734	
4991	umc1737		GRMZM2G082312	B73 RefGen_v3	Gene	Chr1	290377065	290381073	umc1737	rs128977405 , rs128977411 , rs131913963 , umc1737	
4992	umc1744		GRMZM2G073155	B73 RefGen_v3	Gene	Chr1	292873373	292873972	umc1744	umc1744	
4993	umc1748		GRMZM2G386209	B73 RefGen_v3	Gene	Chr1	191892986	191895008	umc1748	umc1748	Similar to Arabidopsis putative auxin-responsive protein
4994	umc1790a		GRMZM2G125304	B73 RefGen_v3	Gene	Chr1	82498393	82505931	umc1790a	p-umc1790, rs131270255 , ss196425141 , umc1790(32), umc1790a	Identified as "homerin" at NCBI
4995	umc17a		GRMZM2G057283	B73 RefGen_v3	Gene	Chr3	205369890	205371486	umc17a	rs131180669, umc17, umc17a	NCBI plasma membrane associated protein
4996	umc1811		AC187262.4_FG007	B73 RefGen_v3	Gene	Chr1	184732930	184733551	umc1811	IDP2370, umc1811	
4997	umc1812		GRMZM2G169451	B73 RefGen_v3	Gene	Chr1	180743250	180744404	umc1812	IDP9136, TIDP3585, umc1812	similar to Arabidopsis yippee-like protein
4998	umc1849		GRMZM2G069618	B73 RefGen_v3	Gene	Chr1	56894719	56897083	umc1849	cl22329_1, cl22329_1(23), rs128445684 , rs131185293, umc1849	similar to TPR (tetratricopeptide) domain containing protein
4999	umc1906		GRMZM2G041050	B73 RefGen_v3	Gene	Chr1	162601608	162610432	umc1906	pco149009, pco149009(47), umc1906	

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
5000	umc1917		AC213099.3_FG001	B73 RefGen_v3	Gene	Chr1	62921411	62922558	umc1917	pco096184, pco096184(27), umc1917	
5001	umc1919a		GRMZM2G329909	B73 RefGen_v3	Gene	Chr1	191885470	191889519	umc1919a	rs128831652, rs128831691 , rs128831697, rs128831698 , rs131186012 , rs131186013 , rs131828561 , rs131828580 , rs131828585 , umc1919, umc1919a	NCBI: type II inositol 1,4,5-trisphosphate 5-phosphatase FRA3-like
5002	umc1919a		GRMZM5G896294	B73 RefGen_v3	Gene	Chr1	191891265	191892243	umc1919a	rs128831652, rs128831691 , rs128831697, rs128831698 , rs131186012 , rs131186013 , rs131828561 , rs131828580 , rs131828585 , umc1919, umc1919a	NCBI: type II inositol 1,4,5-trisphosphate 5-phosphatase FRA3-like
5003	umc1924		GRMZM2G057173	B73 RefGen_v3	Gene	Chr1	240012334	240013819	umc1924	rs131868411, umc1924	
5004	umc1955		GRMZM2G067315	B73 RefGen_v3	Gene	Chr1	235968685	235970191	umc1955	glycine-rich cell wall structural protein 2, rs131865662, umc1955, umc2080	NCBI: glycine-rich cell wall structural protein 2
5005	umc1976		GRMZM2G162535	B73 RefGen_v3	Gene	Chr1	21567145	21568044	umc1976	IDP673, rs131220226, umc1976	
5006	umc1991		GRMZM5G842695	B73 RefGen_v3	Gene	Chr1	245369017	245372021	umc1991	transparent testa 12 protein Alex, umc1991	NCBI: transparent testa 12 protein . Similar to Arabidopsis MATE efflux family protein (multidrug and toxic compound extrusion (MATE) family)
5007	umc2047		GRMZM2G369130	B73 RefGen_v3	Gene	Chr1	258442739	258446721	umc2047	rs128938268 , rs131182092, umc2047	NCBI prediction by Gnomon: type I inositol 1,4,5-trisphosphate 5-phosphatase CVP2-like
5008	umc2067		GRMZM2G034152	B73 RefGen_v3	Probed Site	Chr10	62260920	62265303	umc2067	PZA00409, rs131175989, ss196417361, umc2067	
5009	umc21		GRMZM2G174170	B73 RefGen_v3	Gene	Chr6	121033833	121040632	umc21	PCO111935, PCO111935(499), rs131181259 , umc21	NCBI: Protein-tyrosine-phosphatase IBR5
5010	umc2145		GRMZM2G003424	B73 RefGen_v3	Gene	Chr1	54122528	54126795	umc2145	CL17071_1, CL17071_1(23), umc2145	NCBI: putative RNA-binding zinc finger family protein
5011	umc2181		GRMZM2G008290	B73 RefGen_v3	Gene	Chr1	237715096	237717332	umc2181	metal ion binding protein , rs128902732, umc2181	similar to Arabidopsis heavy metal transport/detoxification domain-containing protein
5012	umc2189		GRMZM2G401331	B73 RefGen_v3	Gene	Chr1	271379568	271381337	umc2189	rs131892231, rs131892243 , rs131892244 , umc2189	
5013	umc2224		GRMZM2G076062	B73 RefGen_v3	Gene	Chr1	12162857	12167581	umc2224	umc2224	
5014	umc2226		GRMZM2G114055	B73 RefGen_v3	Gene	Chr1	21756543	21775704	umc2226	rs131220710 , rs131220713 , transposon protein Mutator sub-class, umc2226, ZmOrphan277	
5015	umc2227		GRMZM2G412430	B73 RefGen_v3	Gene	Chr1	67856797	67858961	umc2227	rs128460206 , rs131261986 , umc2227	NCBI: similar to B. distachyon putative HLH DNA-binding domain superfamily protein
5016	umc2228		GRMZM2G125241	B73 RefGen_v3	Gene	Chr1	73974267	73976401	umc2228	glucan endo-1,3-beta-glucosidase 4 , umc2228	NCBI: glucan endo-1,3-beta-glucosidase 4
5017	umc2229		GRMZM2G093962	B73 RefGen_v3	Gene	Chr1	80329646	80332141	umc2229	IMR18, membrane protein, umc2229	
5018	umc2232		GRMZM5G836886	B73 RefGen_v3	Gene	Chr1	164519562	164522656	umc2232	calcium-transporting ATPase 1, plasma membrane-type-like, magi75799, TIDP3361, umc2232	NCBI: calcium-transporting ATPase 1, plasma membrane-type-like
5019	umc2232		GRMZM5G878058	B73 RefGen_v3	Gene	Chr1	164522853	164525776	umc2232	calcium-transporting ATPase 1, plasma membrane-type-like, magi75799, TIDP3361, umc2232	NCBI: calcium-transporting ATPase 1, plasma membrane-type-like
5020	umc2233		GRMZM2G428216	B73 RefGen_v3	Gene	Chr1	165420890	165421476	umc2233	magi14362, rs131183791, umc2233	
5021	umc2234		GRMZM2G441903	B73 RefGen_v3	Gene	Chr1	187432434	187434251	umc2234	TIDP3262, umc2234	
5022	umc2235		GRMZM2G074270	B73 RefGen_v3	Gene	Chr1	191475413	191478860	umc2235	IDP7405, methylase, rs131827949 , umc2235	
5023	umc2237		GRMZM2G133413	B73 RefGen_v3	Gene	Chr1	200759099	200762378	umc2237	cyclin-D4-2-like, rs128842854, umc2237	NCBI: cyclin-D4-2-like
5024	umc2243		GRMZM2G053299	B73 RefGen_v3	Gene	Chr1	296102632	296106489	umc2243	umc2243	NCBI: putative actin family protein
5025	umc2244		GRMZM5G876146	B73 RefGen_v3	Gene	Chr1	298813792	298816795	umc2244	TIDP5836, umc2244	like Arabidopsis pantoate--beta-alanine ligase
5026	umc2389		GRMZM2G089895	B73 RefGen_v3	Probed Site	Chr6	156785536	156787610	umc2389	PHM5794, PZA00223, rs130435158, rs55625885 , ss196416481, umc2389	
5027	umc254		GRMZM2G019916	B73 RefGen_v3	Gene	Chr7	156050388	156051083	umc254	php4238, rs130668554, umc254	
5028	umc255a		GRMZM2G452717	B73 RefGen_v3	Gene	Chr2	153139055	153143121	umc255a	AY110336, CL54827_1, php4239, rs129150608, rs129150610 , rs131947108 , rs131947126, rs131947129 , umc255, umc255a	NCBI: F-box/LRR-repeat protein 3-like
5029	umc259a		AC233888.1_FG001	B73 RefGen_v3	Gene	Chr10	127957386	127959778	umc259a	php4243, rs128623704, umc259, umc259a	
5030	umc32a		GRMZM2G123519	B73 RefGen_v3	Gene	Chr3	1726094	1729468	umc32a	PCO079942, PCO079942(199), phi049, rs131365253, umc32a, umc32a(cgn), umc32e	NCBI: putative ubiquitin-conjugating enzyme E2 25
5031	umc44a		GRMZM2G116542	B73 RefGen_v3	Gene	Chr10	137339524	137341097	umc44a	umc44a, umc44b	
5032	umc44a		GRMZM5G836567	B73 RefGen_v3	Gene	Chr10	137311826	137319567	umc44a	umc44a, umc44b	
5033	umc59a		GRMZM2G134930	B73 RefGen_v3	Gene	Chr6	86045720	86048771	umc59a	pco142103, pco142103(470), umc59a	NCBI: WAT1-related protein. NPI linkage catalog of 1/25/91 places this probe on chromosome 7.
5034	umc64a		GRMZM2G060721	B73 RefGen_v3	Gene	Chr10	85759150	85760465	umc64a	rs131781730, umc64, umc64a	NCBI: peroxidase 2-like
5035	umc7		GRMZM2G090747	B73 RefGen_v3	Gene	Chr8	171085827	171089416	umc7	umc7	Likely encodes glycerol-3-phosphate dehydrogenase per Alexandrov et al.
5036	umc83a		GRMZM2G001812	B73 RefGen_v3	Gene	Chr1	233516803	233520836	umc83a	umc83, umc83a	NCBI: probable LRR receptor-like serine/threonine-protein kinase At4g08850-like`
5037	umc85a		GRMZM2G019225	B73 RefGen_v3	Gene	Chr6	8272015	8277539	umc85a	rs130221261 , rs131552182, umc85, umc85a	NCBI: similar to Medicago CHUP1, chloroplastic-like . NCBI: Tetratricopeptide repeat (TPR)-like
5038	umc86a		GRMZM2G093776	B73 RefGen_v3	Gene	Chr1	293531158	293535465	umc86a	umc86a, ZmOrphan91	NCBI: protein phosphatase 2C 35-like
5039	umc95		GRMZM5G880028	B73 RefGen_v3	Gene	Chr9	127192292	127194925	umc95	umc95	NCBI: Putative calmodulin-binding family protein
5040	umi11	Ustilago maydis induced11	GRMZM2G450866	B73 RefGen_v3	Gene	Chr7	3889069	3891403	umi11	IDP1650, putative cyclotide family protein, umi11, ustilago maydis induced11	
5041	umi12	ustilago maydis induced12	GRMZM2G149923	B73 RefGen_v3	Gene	Chr1	275154534	275157007	umi12	rs131896300 , ss196432517 , umi12, ustilago maydis induced12	
5042	umi8	ustilago maydis induced8	GRMZM2G330302	B73 RefGen_v3	Gene	Chr3	213469252	213473397	umi8	umi8, ustilago maydis induced8	
5043	v30	virescent30	GRMZM2G121456	B73 RefGen_v3	Gene	Chr9	135397438	135401073	v30	chloroplast protease complex P1, chr9_chloroplast protease complex P5, Chr.9_ClpP5, clpp1, pco096065, v30, v*-8587, virescent30	Chloroplast ATP-dependent Clp protease subunit 5. (A. Barkan, 2015). encodes one subunit of the chloroplast Clp protease complex. like v1, but more yellow
5044	vacs1	vacuolar sorting receptor homolog1	GRMZM2G067546	B73 RefGen_v3	Gene	Chr9	131423638	131431860	vacs1	PCO087823, PCO087823(692), uaz5c06d10(gfu), urmodulin homolog1, uro1, vacs1, vacuolar sorting receptor homolog1	endosperm cDNA 5C06D10 similar to rodent uromodulin
5045	vdac1a	voltage-dependent anion channel protein	GRMZM2G150616	B73 RefGen_v3	Gene	Chr2	177290831	177294514	vdac1a	isochorismate synthase, PCO081914, PCO081914(163), pzvdac1a, vdac1a	
5046	vdac1b	voltage-dependent anion channel protein	GRMZM2G146670	B73 RefGen_v3	Gene	Chr7	97642539	97646675	vdac1b	vdac1b	
5047	vdac2	voltage-dependent anion channel protein	GRMZM2G115049	B73 RefGen_v3	Gene	Chr6	161642062	161645447	vdac2	porin, vdac2	
5048	vde1	violaxanthin de-epoxidase1	GRMZM2G027219	B73 RefGen_v3	Gene	Chr2	74716207	74718993	vde1	si605018d09, VDE, vde1, violaxanthin de-epoxidase1	Encodes violaxanthin de-epoxidase. Based on sequence similarity to Arabiodopsis gene.

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
5049	vde2	violaxanthin de-epoxidase2	GRMZM2G701673	B73 RefGen_v3	Gene	Chr10	106812274	106812762	vde2	vde2	sequence ortholog of Arabidopsis AT1G08550 (AVDE1)
5050	vde3	violaxanthin de-epoxidase3	GRMZM2G408706	B73 RefGen_v3	Gene	Chr8	154564180	154569605	vde3	vde3	sequence ortholog of Arabidopsis AT1G08550 (AVDE1)
5051	vdl1	variegated and distorted leaf1	GRMZM2G415538	B73 RefGen_v3	Gene	Chr8	156348546	156364515	vdl1	ATP binding protein, vdl1	Required for biogenesis of plastid translation machinery
5052	vim102	variant in methylation102	GRMZM2G339151	B73 RefGen_v3	Gene	Chr8	134742942	134746904	vim102	vim102, VIM1-like102	
5053	vim103	variant in methylation103	GRMZM2G461447	B73 RefGen_v3	Gene	Chr6	44751886	44756124	vim103	vim103, VIM1-like103	
5054	vim104	variant in methylation104	AC191534.3_FG003	B73 RefGen_v3	Gene	Chr7	27685032	27687705	vim104	vim104, VIM1-like104	
5055	voz1	VOZ-transcription factor 1	GRMZM2G111696	B73 RefGen_v3	Gene	Chr6	159112392	159115898	voz1		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5056	voz2	VOZ-transcription factor 2	GRMZM2G158717	B73 RefGen_v3	Gene	Chr2	216402429	216405935	voz2		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5057	voz3	VOZ-transcription factor 3	GRMZM2G094081	B73 RefGen_v3	Gene	Chr3	98456978	98457972	voz3		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5058	voz4	VOZ-transcription factor 4	GRMZM2G156016	B73 RefGen_v3	Gene	Chr3	198983586	198990186	voz4		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5059	voz5	VOZ-transcription factor 5	GRMZM2G449165	B73 RefGen_v3	Gene	Chr8	173825142	173828292	voz5		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5060	vp1	viviparous1	GRMZM2G133398	B73 RefGen_v3	Gene	Chr3	162842569	162847653	vp1	bnl-vp1, CL1869_-1, pm, primitive sporophyte, rs128282964 , rs132050100 , rs55622910 , viviparous1, vp1, vp4, ZmABI1, ZmAFL3	embryo fails to become dormant, viable if transplanted; some alleles dormant; chlorophyll and carotenoids unaffected; anthocyanins in aleurone suppressed (aka vp4); cDNA
5061	vp10	viviparous10	GRMZM2G067176	B73 RefGen_v3	Gene	Chr10	146104115	146108434	vp10	CL43049_1, CL43049_1(761), viviparous10, vp10, vp13, vp*-2048, vp*-84-5279-29, vp*-85-3040-29, vp*-85-3339-25, vp*-86GN5	yellow endosperm, colored aleurone, green seedlings, adherent
5062	vp14	viviparous14	GRMZM2G014392	B73 RefGen_v3	Gene	Chr1	250953388	250956063	vp14	NCED1, NCED1 homolog, nine-cis-epoxycarotenoid dioxygenase1, siu95953a, siu95953a(82), ufg4, umc1218, viviparous14, vp14	viviparous; yellow endosperm; abscisic acid biosynthesis; SSR umc1218
5063	vp15	viviparous15	GRMZM2G121468	B73 RefGen_v3	Gene	Chr5	174261710	174266807	vp15	vp15	Viviporous with yellow endosperm; Vp15 encodes a plant MPT synthase small subunit (ZmCNX7)
5064	vp5	viviparous5	GRMZM2G410515	B73 RefGen_v3	Gene	Chr1	17660122	17666235	vp5	desaturase L39266, PZA02069, PZB00648, PZB00718, umc1070, viviparous5, vp5, vp5-83-3101-36, vp5-8419, y-vp*-83-3101-36, y-vp*-8419, y-vp*-85-3101-36	cDNA, strongest hybridization to this site; other sites are near o2, bnl17.25 and dup103; encodes a 2-step phytoene desaturase; SSR umc1070. like vp2
5065	vp8	viviparous8	GRMZM2G010353	B73 RefGen_v3	Gene	Chr1	286390345	286398537	vp8	viviparous8, vp8, widow's peak, wpk1	embryo fails to become dormant; chlorophyll and carotenoids unaffected; small, pointed-leaf seedlings
5066	vp9	viviparous9	GRMZM2G454952	B73 RefGen_v3	Gene	Chr7	17481578	17490013	vp9	CL78_1, cl78_1(541), viviparous9, vp9, y7, z1, zds1, zeta carotene desaturase1	(was y7, z1, zds1) like vp2; vp9-4889 dormant, pale aleurone, pale green seedling
5067	vpe1	vacuolar processing enzyme1	GRMZM2G463291	B73 RefGen_v3	Gene	Chr5	189856260	189862512	vpe1	AY110063, CL863_1, PZA02383, rs131175716, rs55622723 , ss196416245, vacuolar processing enzyme1, vpe1	gene designated based on match of AY110063 with AY062214, unpublished GenBank submission by D. B. Gruis, 01-Dec-2004, and TIGR contig
5068	vpp1	vacuolar proton pump homolog1	GRMZM2G014240	B73 RefGen_v3	Gene	Chr9	14328479	14333699	vpp1	vacuolar H+-pyrophosphatase2, MZ5C1, ovp2, PCO084888, PCO084888(500), ppp*-mz5c1, umc328, vacuolar proton pump homolog1, vpp1	glucose-starved root tip cDNA closely similar to Oryza gene (TIGR match)
5069	vpp2	vacuolar proton pump2	GRMZM2G094497	B73 RefGen_v3	Gene	Chr9	79417971	79429946	vpp2	PCO062733, uaz223, UAZ223(ATPs), uaz223(vpp), vpp2	etiolated leaf cDNA, 5' sequence similar to plant vacuolar ATPase, subunit B
5070	vpp3	vacuolar proton pump3	GRMZM2G421857	B73 RefGen_v3	Gene	Chr4	235983602	235992984	vpp3	csu848a(vpp), csuh00848, IDP1607a, IDP1607c, IDP1662, IDP2575a, IDP2575c, PCO134411, PCO134411(361), PZA00936, vacuolar proton pump3, V-ATPase, vpp3, vpp*-U36436	coleoptile tip cDNA similar to carrot homolog, including putative active site region
5071	vpp4	vacuolar proton pump4	GRMZM2G028432	B73 RefGen_v3	Gene	Chr10	9542117	9544172	vpp4	ATP synthase 16 kDa proteolipid subunit, PCO154307, PCO154307(717), vacuolar proton pump4, V-ATPase, vpp4	coleoptile tip cDNA sequences similar to other plant homologs
5072	vpp5	vacuolar-type H+-pyrophosphatase5	GRMZM2G170927	B73 RefGen_v3	Gene	Chr9	95183056	95188412	vpp5	vacuolar proton pump5, vacuolar-type H+-pyrophosphatase (H+-PPase), vpp5, ZmVPP1	variants affect drought tolerance
5073	vps1	vesicular transport protein1	GRMZM2G023858	B73 RefGen_v3	Gene	Chr5	8007214	8021382	vps1	cl1496_1(377), cl1496_1b, csu318, PCO131795(377), PCO131795g, PHM533, PZA02029, rs129986216, rs131177658, rs55626276, ss196415995, umc90, vps1	NCBI: similar to Aabidopsis Vps51/Vps67 family (components of vesicular transport) protein
5074	vpsh26	vacuolar protein sorting homolog26	GRMZM2G140737	B73 RefGen_v3	Gene	Chr10	17837806	17842618	vpsh26	PCO142195, uaz5c06f05(gfu), vacuolar protein sorting homolog26 , vpsh26, Zea mouse H58 homolog1, zmh1	endosperm cDNA 5C06F05 similar to conserved vertebrate embryogenesis protein
5075	vt2	vanishing tassel2	GRMZM2G127308	B73 RefGen_v3	Gene	Chr8	16853232	16857380	vt2	vt2	inflorescence development; TRP-depenedent auxin synthesis
5076	vte4	vitamin E synthesis4	GRMZM2G035213	B73 RefGen_v3	Gene	Chr5	200419844	200423666	vte4	cl364_1, cl364_1(446), vte4	
5077	w2	white seedling2	GRMZM2G480171	B73 RefGen_v3	Gene	Chr10	144030003	144038674	w2	chloroplast DNA polymerase, cppol, dek21, DNA polymerase I A, chloroplastic-like, msc*-1330, vpyg72, w2, white2, white seedling2, ZmDNApolA	seedling (yellow with l1); endosperm pitted and spotted (allele dek21); plastid DNA content decreased
5078	wab1	Wavy auricles in blades1	GRMZM2G110242	B73 RefGen_v3	Gene	Chr2	180630151	180631609	wab1	bad1, branch angle defective1, tcptf3, Wab, wab1, Wab1, Wavy auricles in blades, ZmTCP3	acute tassel branch angles accompanied by a significant reduction in the size of the pulvinus compared with normal plants
5079	wc1	white cap1	GRMZM2G057243	B73 RefGen_v3	Gene	Chr9	152353213	152359196	wc1	AY106323, ccd1, IDP700, PCO084517, wc1, white cap1, ZmCCD1	dominant Wc1 kernels have pale yellow endosperm if Y1 (pearly white with y1); whiteness is emphasized in soft-starch crowns
5080	wee1	wee1	GRMZM5G878541	B73 RefGen_v3	Gene	Chr4	239984257	239988267	wee1	CL587_1, umc1255, umc169, umc169a, wee1	cDNA single copy, deduced protein 50% identity to protein kinase domain of human Wee1; SSR umc1255
5081	whirly2	WHIRLY-transcription factor 2	GRMZM2G012262	B73 RefGen_v3	Gene	Chr4	237573503	237579217	whirly2		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5082	whp1	white pollen1	GRMZM2G151227	B73 RefGen_v3	Gene	Chr2	224558005	224561990	whp1	bnl17.03(whp), CL2073_1, cl2073_1(193), mpik(chs1b), umc183(c2, umc183(c2), umc198, umc198(c2), umc198(whp1), white pollen1, whp1	duplicate factor with c2 for pollen color and for anthocyanins
5083	why1	whirly1	GRMZM2G155662	B73 RefGen_v3	Gene	Chr6	71779327	71782388	why1	DNA-binding protein p24 , emb16, gnp_QBI2b09, gpm491, whirly1, why1, ZmWHIRLY1, ZmWhy1	maturation. (A. Barkan, 2015). why1-1 and why1-2 mutants exhibit albino to pale green seedling lethal, plastid ribosome deficient. why1-3 mutant arrests embryogenesis at transition stage and
5084	wip1	wound induced protein1	GRMZM2G156632	B73 RefGen_v3	Gene	Chr8	12275985	12276693	wip1	CL2068_1e, wip1, wound induced protease inhibitor, wound induced protein1	wounding-induced transcript, cDNA clone (601bp) sequenced; homologous to Bowman-Birk proteinase inhibitors
5085	wip2	wound inducible protein2	GRMZM2G112795	B73 RefGen_v3	Gene	Chr4	20529042	20532586	wip2	uaz293, uaz293(gfu), wip2, wound inducible protein2	endosperm cDNA 5C05B11 (uaz293), similar to basic wound-induced bean protein
5086	wox12a	wuschel-related homeobox12A	Zm00001d022524	Zm-B73-REFERENCE-G	Gene	Chr7	179332232	179334819	wox12a	Homeobox-transcription factor, wox12a, WUSCHEL-related homeobox 11-like, ZmWOX11/12A	cDNA ortholog of Arabidopsis wuschel-related homeobox gene
5087	wox4	wuschel-related homeobox4	GRMZM6G260565	B73 RefGen_v3	Gene	Chr10	144893352	144894218	wox4	Homeobox-transcription factor, wox4, WUSCHEL-related homeobox 4-like, ZmWOX4	cDNA ortholog of Arabidopsis wuschel-related homeobox gene
5088	wox9a	WUSCHEL related homeobox 9a	GRMZM2G133972	B73 RefGen_v3	Gene	Chr8	148836644	148840404	wox9a	hb50, Homeobox-transcription factor 50, wox9a, WUSCHEL-related homeobox 7-like, ZmWOX9A	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5089	wox9b	WUSCHEL related homeobox 9b	GRMZM2G031882	B73 RefGen_v3	Gene	Chr3	210664178	210668618	wox9b	dd9B, hb85, Homeobox-transcription factor 85, wox9b, WUSCHEL-related homeobox 7, WUSCHEL related homeobox 9b, ZmWOX9B	expressed in late embryo stages;in suspensor and also, unlike wox9c, in the shoot apical meristem (SAM)
5090	wox9c	WUSCHEL related homeobox 9c	GRMZM2G409881	B73 RefGen_v3	Gene	Chr6	164845767	164849983	wox9c	dd9, hb117, Homeobox-transcription factor 117, wox9c, WUSCHEL-related homeobox 12-like, WUSCHEL related homeobox 9c, ZmWOX9C	late embryo in outer layer of suspensor through leaf 4 stage
5091	wri1	WRI1 transcription factor1	GRMZM2G124524	B73 RefGen_v3	Gene	Chr2	149971656	149977527	wri1	EREB85, pco068306(164), wri1, WRI1 transcription factor1, wrinkled1 transcription factor, ZmEREB85	
5092	wri2	WRI1 transcription factor2	GRMZM2G174834	B73 RefGen_v3	Gene	Chr4	185907968	185912697	wri2	TIDP8813, WRI1 transcription factor2, wri2, wrinkled1 transcription factor, ZmEREB20	
5093	wrky1	WRKY-transcription factor 1	GRMZM2G398506	B73 RefGen_v3	Gene	Chr7	161329465	161340038	wrky1		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5094	wrky10	WRKY-transcription factor 10	GRMZM2G083717	B73 RefGen_v3	Gene	Chr1	299362324	299367903	wrky10		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5095	wrky100	WRKY-transcription factor 100	GRMZM2G401521	B73 RefGen_v3	Gene	Chr6	160019664	160021008	wrky100		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5096	wrky101	WRKY-transcription factor 101	GRMZM2G123387	B73 RefGen_v3	Gene	Chr2	22124688	22129615	wrky101		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5097	wrky102	WRKY-transcription factor 102	GRMZM2G070211	B73 RefGen_v3	Gene	Chr1	253562148	253565268	wrky102		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
5098	wrky103	WRKY-transcription factor 103	GRMZM2G141299	B73 RefGen_v3	Gene	Chr3	198284414	198286315	wrky103		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5099	wrky104	WRKY-transcription factor 104	GRMZM2G169149	B73 RefGen_v3	Gene	Chr7	115576479	115577711	wrky104		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5100	wrky105	WRKY-transcription factor 105	GRMZM2G102583	B73 RefGen_v3	Gene	Chr2	79911960	79914453	wrky105		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5101	wrky106	WRKY-transcription factor 106	GRMZM2G063880	B73 RefGen_v3	Gene	Chr8	71900055	71901434	wrky106		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5102	wrky107	WRKY-transcription factor 107	GRMZM2G018487	B73 RefGen_v3	Gene	Chr1	274947476	274951614	wrky107		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5103	wrky108	WRKY-transcription factor 108	GRMZM2G106560	B73 RefGen_v3	Gene	Chr2	222422824	222427359	wrky108		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5104	wrky109	WRKY-transcription factor 109	GRMZM5G880069	B73 RefGen_v3	Gene	Chr5	17336230	17338997	wrky109		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5105	wrky11	WRKY-transcription factor 11	GRMZM2G138683	B73 RefGen_v3	Gene	Chr4	158888697	158893034	wrky11		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5106	wrky110	WRKY-transcription factor 110	GRMZM2G173680	B73 RefGen_v3	Gene	Chr3	116043878	116046928	wrky110		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5107	wrky111	WRKY-transcription factor 111	GRMZM2G013391	B73 RefGen_v3	Gene	Chr8	173930578	173932078	wrky111		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5108	wrky112	WRKY-transcription factor 112	AC208110.2_FG001	B73 RefGen_v3	Gene	Chr10	140081545	140084417	wrky112		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5109	wrky113	WRKY-transcription factor 113	GRMZM2G147880	B73 RefGen_v3	Gene	Chr5	7879528	7883985	wrky113		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5110	wrky114	WRKY-transcription factor 114	AC209050.3_FG003	B73 RefGen_v3	Gene	Chr6	96492394	96493954	wrky114		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5111	wrky115	WRKY-transcription factor 115	GRMZM2G036703	B73 RefGen_v3	Gene	Chr8	169646298	169648807	wrky115		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5112	wrky116	WRKY-transcription factor 116	GRMZM2G130854	B73 RefGen_v3	Gene	Chr2	208504961	208511327	wrky116		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5113	wrky117	WRKY-transcription factor 117	GRMZM2G453571	B73 RefGen_v3	Gene	Chr6	164999993	165002960	wrky117		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5114	wrky118	WRKY-transcription factor 118	GRMZM2G003551	B73 RefGen_v3	Gene	Chr9	18108182	18111635	wrky118		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5115	wrky119	WRKY-transcription factor 119	GRMZM2G015433	B73 RefGen_v3	Gene	Chr8	124481009	124482168	wrky119		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5116	wrky12	WRKY-transcription factor 12	GRMZM2G164082	B73 RefGen_v3	Gene	Chr1	288766734	288768763	wrky12		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5117	wrky120	WRKY-transcription factor 120	AC165171.2_FG002	B73 RefGen_v3	Gene	Chr3	144777899	144779302	wrky120		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5118	wrky121	WRKY-transcription factor 121	GRMZM2G061408	B73 RefGen_v3	Gene	Chr8	109092838	109094506	wrky121		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5119	wrky122	WRKY-transcription factor 122	GRMZM2G549512	B73 RefGen_v3	Gene	Chr4	58356325	58374672	wrky122	WRKY transcription factor 4, ZmWRKY4	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5120	wrky123	WRKY-transcription factor 123	GRMZM2G105140	B73 RefGen_v3	Gene	Chr3	217543229	217545089	wrky123		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5121	wrky124	WRKY-transcription factor 124	GRMZM2G111711	B73 RefGen_v3	Gene	Chr9	104082393	104083964	wrky124		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5122	wrky125	WRKY-transcription factor 125	GRMZM2G163054	B73 RefGen_v3	Gene	Chr6	127773579	127775131	wrky125		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5123	wrky13	WRKY-transcription factor 13	GRMZM2G156529	B73 RefGen_v3	Gene	Chr6	110609946	110610865	wrky13		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5124	wrky14	WRKY-transcription factor 14	GRMZM2G091331	B73 RefGen_v3	Gene	Chr10	140695930	140697533	wrky14		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5125	wrky15	WRKY-transcription factor 15	GRMZM2G004060	B73 RefGen_v3	Gene	Chr10	12108516	12110234	wrky15		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5126	wrky16	WRKY-transcription factor 16	GRMZM2G063216	B73 RefGen_v3	Gene	Chr4	184812978	184816591	wrky16	umc2384, wrky16, ZmWRKY46	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5127	wrky17	WRKY-transcription factor 17	GRMZM2G381378	B73 RefGen_v3	Gene	Chr7	173263217	173265322	wrky17		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5128	wrky18	WRKY-transcription factor 18	GRMZM2G092694	B73 RefGen_v3	Gene	Chr8	653032	655605	wrky18		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5129	wrky19	WRKY-transcription factor 19	GRMZM2G382350	B73 RefGen_v3	Gene	Chr3	185085984	185090499	wrky19		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5130	wrky2	WRKY-transcription factor 2	GRMZM2G048450	B73 RefGen_v3	Gene	Chr5	138386996	138389124	wrky2		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5131	wrky20	WRKY-transcription factor 20	GRMZM2G414315	B73 RefGen_v3	Gene	Chr8	74420546	74421859	wrky20		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5132	wrky21	WRKY-transcription factor 21	GRMZM2G127064	B73 RefGen_v3	Gene	Chr6	135889651	135892588	wrky21		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5133	wrky22	WRKY-transcription factor 22	GRMZM2G111354	B73 RefGen_v3	Gene	Chr8	175251100	175252414	wrky22		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5134	wrky23	WRKY-transcription factor 23	GRMZM2G400559	B73 RefGen_v3	Gene	Chr2	152320522	152321739	wrky23		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5135	wrky24	WRKY-transcription factor 24	GRMZM2G099593	B73 RefGen_v3	Gene	Chr2	152369498	152370911	wrky24		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5136	wrky25	WRKY-transcription factor 25	GRMZM2G324999	B73 RefGen_v3	Gene	Chr1	216633236	216634880	wrky25		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5137	wrky26	WRKY-transcription factor 26	GRMZM2G083350	B73 RefGen_v3	Gene	Chr8	19856200	19858470	wrky26		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5138	wrky27	WRKY-transcription factor 27	GRMZM2G475984	B73 RefGen_v3	Gene	Chr3	8214258	8215483	wrky27		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5139	wrky28	WRKY-transcription factor 28	GRMZM2G145554	B73 RefGen_v3	Gene	Chr8	145062095	145064464	wrky28		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5140	wrky29	WRKY-transcription factor 29	GRMZM2G040298	B73 RefGen_v3	Gene	Chr3	201085602	201087238	wrky29	ZmWRKY14	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5141	wrky3	WRKY-transcription factor 3	GRMZM2G130374	B73 RefGen_v3	Gene	Chr1	167915436	167917645	wrky3		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5142	wrky30	WRKY-transcription factor 30	GRMZM2G143204	B73 RefGen_v3	Gene	Chr1	278228862	278232499	wrky30		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5143	wrky31	WRKY-transcription factor 31	GRMZM2G008029	B73 RefGen_v3	Gene	Chr1	278669130	278671406	wrky31		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5144	wrky32	WRKY-transcription factor 32	GRMZM2G030272	B73 RefGen_v3	Gene	Chr1	52917450	52918870	wrky32		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5145	wrky33	WRKY-transcription factor 33	GRMZM2G020254	B73 RefGen_v3	Gene	Chr10	65429005	65430793	wrky33		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5146	wrky34	WRKY-transcription factor 34	GRMZM2G057116	B73 RefGen_v3	Gene	Chr8	88471371	88472763	wrky34		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
5147	wrky35	WRKY-transcription factor 35	GRMZM2G029292	B73 RefGen_v3	Gene	Chr8	169910906	169937945	wrky35		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5148	wrky36	WRKY-transcription factor 36	GRMZM2G054125	B73 RefGen_v3	Gene	Chr4	17875436	17878321	wrky36		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5149	wrky37	WRKY-transcription factor 37	GRMZM2G139815	B73 RefGen_v3	Gene	Chr7	92417479	92419510	wrky37		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5150	wrky38	WRKY-transcription factor 38	GRMZM2G163418	B73 RefGen_v3	Gene	Chr2	176398481	176400987	wrky38		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5151	wrky39	WRKY-transcription factor 39	AC193630.3_FG003	B73 RefGen_v3	Gene	Chr9	19940858	19942697	wrky39		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5152	wrky4	WRKY-transcription factor 4	GRMZM2G501775	B73 RefGen_v3	Gene	Chr3	231953985	231957372	wrky4		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5153	wrky40	WRKY-transcription factor 40	GRMZM2G158328	B73 RefGen_v3	Gene	Chr3	184905732	184908623	wrky40		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5154	wrky41	WRKY-transcription factor 41	GRMZM2G065290	B73 RefGen_v3	Gene	Chr3	184988151	184997449	wrky41		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5155	wrky42	WRKY-transcription factor 42	GRMZM5G812272	B73 RefGen_v3	Gene	Chr8	148612740	148615433	wrky42		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5156	wrky43	WRKY-transcription factor 43	GRMZM2G148087	B73 RefGen_v3	Gene	Chr3	183944439	183947443	wrky43		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5157	wrky44	WRKY-transcription factor 44	GRMZM2G432583	B73 RefGen_v3	Gene	Chr8	118562818	118564187	wrky44		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5158	wrky45	WRKY-transcription factor 45	GRMZM2G151444	B73 RefGen_v3	Gene	Chr3	9237045	9244979	wrky45		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5159	wrky46	WRKY-transcription factor 46	GRMZM5G823157	B73 RefGen_v3	Gene	Chr5	199697223	199700885	wrky46		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5160	wrky47	WRKY-transcription factor 47	GRMZM2G149683	B73 RefGen_v3	Gene	Chr8	144765374	144766804	wrky47		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5161	wrky48	WRKY-transcription factor 48	GRMZM2G120320	B73 RefGen_v3	Gene	Chr5	92841738	92843574	wrky48		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5162	wrky49	WRKY-transcription factor 49	GRMZM2G006497	B73 RefGen_v3	Gene	Chr8	13139079	13140882	wrky49		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5163	wrky5	WRKY-transcription factor 5	AC194362.3_FG003	B73 RefGen_v3	Gene	Chr3	232080384	232081786	wrky5		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5164	wrky50	WRKY-transcription factor 50	GRMZM2G071907	B73 RefGen_v3	Gene	Chr2	11760940	11762535	wrky50		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5165	wrky51	WRKY-transcription factor 51	GRMZM2G366795	B73 RefGen_v3	Gene	Chr6	165221558	165224020	wrky51		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5166	wrky52	WRKY-transcription factor 52	GRMZM2G151407	B73 RefGen_v3	Gene	Chr7	131319563	131323434	wrky52		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5167	wrky53	WRKY-transcription factor 53	GRMZM2G125653	B73 RefGen_v3	Gene	Chr7	115336589	115338419	wrky53		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5168	wrky54	WRKY-transcription factor 54	GRMZM2G178671	B73 RefGen_v3	Gene	Chr3	180652901	180653592	wrky54		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5169	wrky55	WRKY-transcription factor 55	GRMZM2G057011	B73 RefGen_v3	Gene	Chr2	181270963	181272226	wrky55		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5170	wrky56	WRKY-transcription factor 56	GRMZM2G176489	B73 RefGen_v3	Gene	Chr3	8219105	8221465	wrky56		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5171	wrky57	WRKY-transcription factor 57	GRMZM2G169966	B73 RefGen_v3	Gene	Chr6	153458471	153461535	wrky57		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5172	wrky58	WRKY-transcription factor 58	GRMZM2G076657	B73 RefGen_v3	Gene	Chr3	134942701	134950706	wrky58		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5173	wrky59	WRKY-transcription factor 59	GRMZM2G031963	B73 RefGen_v3	Gene	Chr10	124679542	124684591	wrky59		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5174	wrky6	WRKY-transcription factor 6	GRMZM2G161411	B73 RefGen_v3	Gene	Chr5	15337856	15339461	wrky6		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5175	wrky60	WRKY-transcription factor 60	GRMZM2G383594	B73 RefGen_v3	Gene	Chr1	105958946	105960357	wrky60		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5176	wrky61	WRKY-transcription factor 61	GRMZM2G171428	B73 RefGen_v3	Gene	Chr9	124488682	124495259	wrky61		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5177	wrky62	WRKY-transcription factor 62	GRMZM2G143765	B73 RefGen_v3	Gene	Chr6	22907413	22912048	wrky62		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5178	wrky63	WRKY-transcription factor 63	GRMZM2G005207	B73 RefGen_v3	Gene	Chr10	3995050	3997307	wrky63		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5179	wrky64	WRKY-transcription factor 64	AC198725.4_FG009	B73 RefGen_v3	Gene	Chr3	217293881	217296220	wrky64		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5180	wrky65	WRKY-transcription factor 65	GRMZM2G060918	B73 RefGen_v3	Gene	Chr9	133947951	133949483	wrky65		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5181	wrky66	WRKY-transcription factor 66	GRMZM2G045560	B73 RefGen_v3	Gene	Chr8	168374785	168379461	wrky66		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5182	wrky67	WRKY-transcription factor 67	GRMZM2G090594	B73 RefGen_v3	Gene	Chr10	68737989	68739253	wrky67		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5183	wrky68	WRKY-transcription factor 68	GRMZM2G137802	B73 RefGen_v3	Gene	Chr8	135574148	135576504	wrky68		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5184	wrky69	WRKY-transcription factor 69	GRMZM2G448605	B73 RefGen_v3	Gene	Chr8	70575003	70578661	wrky69		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5185	wrky7	WRKY-transcription factor 7	GRMZM2G354384	B73 RefGen_v3	Gene	Chr3	221361951	221362634	wrky7		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5186	wrky70	WRKY-transcription factor 70	GRMZM2G024898	B73 RefGen_v3	Gene	Chr2	12806751	12811093	wrky70		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5187	wrky71	WRKY-transcription factor 71	GRMZM2G052671	B73 RefGen_v3	Gene	Chr2	189959952	189963986	wrky71		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5188	wrky72	WRKY-transcription factor 72	GRMZM5G816457	B73 RefGen_v3	Gene	Chr2	39388778	39394181	wrky72		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5189	wrky73	WRKY-transcription factor 73	GRMZM2G101405	B73 RefGen_v3	Gene	Chr3	203155290	203156282	wrky73		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5190	wrky74	WRKY-transcription factor 74	GRMZM2G408462	B73 RefGen_v3	Gene	Chr3	212821185	212822609	wrky74		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5191	wrky75	WRKY-transcription factor 75	GRMZM2G425430	B73 RefGen_v3	Gene	Chr1	75177786	75179016	wrky75		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5192	wrky76	WRKY-transcription factor 76	GRMZM2G451035	B73 RefGen_v3	Gene	Chr4	184834748	184835856	wrky76		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5193	wrky77	WRKY-transcription factor 77	GRMZM2G461648	B73 RefGen_v3	Gene	Chr4	184849931	184851199	wrky77		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5194	wrky78	WRKY-transcription factor 78	GRMZM2G073272	B73 RefGen_v3	Gene	Chr5	159271175	159272391	wrky78		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5195	wrky79	WRKY-transcription factor 79	GRMZM2G025895	B73 RefGen_v3	Gene	Chr7	93189728	93191396	wrky79		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
5196	wrky8	WRKY-transcription factor 8	GRMZM2G038158	B73 RefGen_v3	Gene	Chr4	224059974	224061852	wrky8		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5197	wrky80	WRKY-transcription factor 80	GRMZM2G516301	B73 RefGen_v3	Gene	Chr8	19839384	19840388	wrky80		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5198	wrky81	WRKY-transcription factor 81	GRMZM2G059562	B73 RefGen_v3	Gene	Chr3	184872991	184874285	wrky81		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5199	wrky82	WRKY-transcription factor 82	GRMZM5G863420	B73 RefGen_v3	Gene	Chr6	161673003	161674439	wrky82		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5200	wrky83	WRKY-transcription factor 83	GRMZM2G012724	B73 RefGen_v3	Gene	Chr6	141604322	141606522	wrky83		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5201	wrky84	WRKY-transcription factor 84	GRMZM2G304573	B73 RefGen_v3	Gene	Chr8	139485939	139486968	wrky84		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5202	wrky85	WRKY-transcription factor 85	GRMZM2G018721	B73 RefGen_v3	Gene	Chr7	1923485	1924841	wrky85		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5203	wrky86	WRKY-transcription factor 86	GRMZM2G411766	B73 RefGen_v3	Gene	Chr8	147544923	147546743	wrky86		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5204	wrky87	WRKY-transcription factor 87	GRMZM2G027972	B73 RefGen_v3	Gene	Chr4	198308636	198311250	wrky87		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5205	wrky88	WRKY-transcription factor 88	GRMZM2G029282	B73 RefGen_v3	Gene	Chr8	169904229	169907044	wrky88		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5206	wrky89	WRKY-transcription factor 89	GRMZM2G034421	B73 RefGen_v3	Gene	Chr8	118496550	118498937	wrky89		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5207	wrky9	WRKY-transcription factor 9	GRMZM2G169564	B73 RefGen_v3	Gene	Chr4	184955171	184956823	wrky9		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5208	wrky90	WRKY-transcription factor 90	GRMZM2G468056	B73 RefGen_v3	Gene	Chr8	169887391	169888449	wrky90		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5209	wrky91	WRKY-transcription factor 91	GRMZM2G441031	B73 RefGen_v3	Gene	Chr10	4035458	4036997	wrky91		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5210	wrky92	WRKY-transcription factor 92	GRMZM2G449681	B73 RefGen_v3	Gene	Chr8	109740015	109742387	wrky92		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5211	wrky93	WRKY-transcription factor 93	GRMZM5G871347	B73 RefGen_v3	Gene	Chr3	1260777	1262611	wrky93		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5212	wrky94	WRKY-transcription factor 94	GRMZM2G148561	B73 RefGen_v3	Gene	Chr4	69945001	69946217	wrky94		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5213	wrky95	WRKY-transcription factor 95	GRMZM2G151763	B73 RefGen_v3	Gene	Chr3	211059226	211062376	wrky95		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5214	wrky96	WRKY-transcription factor 96	GRMZM2G149219	B73 RefGen_v3	Gene	Chr1	259014756	259016110	wrky96		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5215	wrky97	WRKY-transcription factor 97	AC205562.3_FG002	B73 RefGen_v3	Gene	Chr4	73393297	73394259	wrky97		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5216	wrky98	WRKY-transcription factor 98	GRMZM2G377217	B73 RefGen_v3	Gene	Chr4	151097946	151109901	wrky98	rs132144412 , rs132144421 , rs132144449 , umc156a, wrky98	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.. NCBI: probable WRKY transcription factor 12 (similarity to
5217	wrky99	WRKY-transcription factor 99	GRMZM2G327349	B73 RefGen_v3	Gene	Chr3	49564575	49568298	wrky99		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5218	wtf1	what's this factor1	GRMZM2G403797	B73 RefGen_v3	Gene	Chr8	71815346	71817424	wtf1	what's this factor?1, wtf1	Founding member of PORR domain family of RNA binding proteins. Interacts with RNC1. Required for the splicing of many chloroplast group II introns and binds those introns in vivo. (A.
5219	wtf2	what's this factor2	AC210013.4_FG013	B73 RefGen_v3	Gene	Chr5	3403642	3407902	wtf2	protein ROOT PRIMORDIUM DEFECTIVE 1, wtf2	
5220	wtf4	what's this factor4	GRMZM2G350157	B73 RefGen_v3	Gene	Chr4	158327464	158329034	wtf4	wtf4	
5221	wusl1032		GRMZM2G043878	B73 RefGen_v3	Gene	Chr1	41441065	41442219	wusl1032	GFU(pZmL1032), umc217, umc217(gfu), umc217(unt), wusl1032	cDNA clone pZmL1032 (cultivar Berkeley Fast) hybridizes to mRNA with very late anaerobic accumulation
5222	wx1	waxy1	GRMZM2G024993	B73 RefGen_v3	Gene	Chr9	23267684	23271612	wx1	phi022, phi027, phi061, PZA01999, PZB00540, PZB00547, rs131709281, umc25, umc25(wx), waxy1, wx1, ZmGBSSI	extensive allelic series; application: highly branched starch has gelling properties, used for food gels, adhesives, and other industrial purposes; SSRs phi022, 027, 061. NCBI: granule-bound
5223	x1	putative transcription factor	GRMZM2G160032	B73 RefGen_v3	Gene	Chr3	216426468	216435001	x1	gnp_QAE8c02, gpm306, PCO104373(274), PCO104373a, putative transcription factor, x1	1.4kb genomic clone derived by PCR with primers from gene X in sorghum and rice, transcripts detected in leaves, cobs, and silks
5224	xet1	xyloglucan endotransglycosylase homol	GRMZM2G026980	B73 RefGen_v3	Gene	Chr5	53934855	53936718	xet1	umc1692, wusl1005, xet1, xyloglucan endotransglycosylase homolog1	cDNA clone (cultivar Berkeley Fast); continuous anaerobic accumulation of mRNA through 72 h
5225	xrcc3	X-ray repair complementing defective rep	GRMZM2G157817	B73 RefGen_v3	Gene	Chr5	174035742	174036908	xrcc3	xrcc3	Homolog of X-ray Repair Complementing defective repair in Chinese hamster cells 3
5226	xth1	xyloglucan endo-transglycosylase/hydrol	GRMZM2G119783	B73 RefGen_v3	Gene	Chr10	69098782	69100591	xth1	gnp_AW433364, PCO111647, xth1	
5227	xyl1	xylanase1	GRMZM2G170839	B73 RefGen_v3	Gene	Chr1	132575709	132578475	xyl1	CL1226_1(706), CL1226_1a, xyl1, xylanase1	encoded by one or few genes.
5228	xyn10	xylanase/glycosyl hydrolase10	GRMZM2G031004	B73 RefGen_v3	Gene	Chr3	21267432	21270193	xyn10	endo-1,4-beta-xylanase, xyn10	
5229	y1	yellow endosperm1	GRMZM2G300348	B73 RefGen_v3	Gene	Chr6	82180486	82184345	y1	pb1, Psy1, rs130328408, rs131175743, white1, y1, y1ssr, y4, yellow endosperm1	reduced carotenoid pigments in endosperm; some alleles affect chlorophyll in seedlings (e.g. y1-8549, y1-pb)
5230	y9	pale yellow9	GRMZM2G011746	B73 RefGen_v3	Gene	Chr10	13613175	13616729	y9	pale yellow9, w-Kermicle#3, y12, y9, Z-ISO	pale endosperm, slightly viviparous; green to pale green seedlings and plants; accumulates 9,15,9'-tri-cis-zeta carotene in dark
5231	yab1	C2C2-YABBY-transcription factor 1	GRMZM2G054795	B73 RefGen_v3	Gene	Chr2	23380099	23382093	yab1		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5232	yab10	yabby homolog10	GRMZM2G167824	B73 RefGen_v3	Gene	Chr1	225097097	225102315	yab10	axial regulator YABBY1, cereal shattering homolog, PCO147319, PCO147319(72), yab10, yab12, yabby homolog10, ZmSh1-1, ZmYAB10, zyb10	
5233	yab11	C2C2-YABBY-transcription factor 11	GRMZM2G141955	B73 RefGen_v3	Gene	Chr1	175665423	175671657	yab11	pco127567, umc67, umc67a, yab11	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.. UMC 1989 map places umc67a on chromosome 5, but all other
5234	yab12	C2C2-YABBY-transcription factor 12	GRMZM2G085873	B73 RefGen_v3	Gene	Chr1	260424101	260427079	yab12	C2C2-YABBY-transcription factor 12, enhancer of tb1.2, etb1.2, shattering1-like, yab5, YABBY 12, YABBY 2-like, ZmSh1-1, ZmYAB2.1	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5235	yab14	yabby14	GRMZM2G005353	B73 RefGen_v3	Gene	Chr10	133133767	133136401	yab14	yab14, yabby14, ZmYAB14, zyb14	
5236	yab15	yabby15	GRMZM2G529859	B73 RefGen_v3	Gene	Chr5	189249290	189252175	yab15	C2C2-YABBY-transcription factor 8, cl672_1(438), cl672_1c, yab15, yab8, yabby15, ZmYAB8, zyb15	
5237	yab3	C2C2-YABBY-transcription factor 3	GRMZM2G106204	B73 RefGen_v3	Gene	Chr7	6315293	6328611	yab3		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5238	yab4	C2C2-YABBY-transcription factor 4	GRMZM2G046829	B73 RefGen_v3	Gene	Chr7	159501156	159503146	yab4		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5239	yab5	C2C2-YABBY-transcription factor 5	GRMZM2G116646	B73 RefGen_v3	Gene	Chr3	89439022	89445313	yab5		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5240	yab6	C2C2-YABBY-transcription factor 6	GRMZM2G074124	B73 RefGen_v3	Gene	Chr5	16146472	16181777	yab6	C2C2-YABBY-transcription factor 6, cereal shattering homolog, IDP681, YABBY 6 homolog, ZmSh1-5.1, ZmSh1-5.1+ZmSh1-5.2, ZmSh1-5.2	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5241	yab9	yabby9	GRMZM2G074543	B73 RefGen_v3	Gene	Chr5	23592937	23597115	yab9	yab9, yabby9, ZmYAB9, zyb9	
5242	ycf54	ycf54 homolog	GRMZM2G010196	B73 RefGen_v3	Gene	Chr1	54599336	54602391	ycf54	hypothetical chloroplast open reading frame54, pco132392, pco132392(23), ycf54	cyclase. (A. Barkan, 2015). reduced levels of major light harvesting chlorophyll a/b binding proteins; ortholog of barley/cyanobacterial Ycf54, a subunit of Mg-protoporphyrin IX monomethyl
5243	ypt1	ypt homolog1	GRMZM2G086971	B73 RefGen_v3	Gene	Chr2	47740882	47746771	ypt1	CL2070_1(132), CL2070_1a, gene related to "yeast protein two", IDP3942, ras-like protein, rs131187182, X63277, ypt1, ypt homolog1, yptm1, ZmRab1A1, ZmRab1A2	cDNAs obtained by homology to GTP-binding domain of ras-protein family and mouse ypt protein
5244	ypt2	ypt homolog2	GRMZM2G097728	B73 RefGen_v3	Gene	Chr5	191132644	191136724	ypt2	PCO152592, PCO152592(439), ras-like protein, ypt2, ypt homolog2, yptm2, ZmRab1C1, ZmRab1C2	cDNA obtained by homology to GTP-binding domain of ras-protein family and mouse ypt protein

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
5245	ypt3	ypt homolog3	GRMZM2G416142	B73 RefGen_v3	Gene	Chr4	127723181	127727534	ypt3	cdo395a(ypt), gene related to "yeast protein two", PCO103212, Rab-2-A, ypt3, yptm3, ZmRab2A3	
5246	ypt4	ypt homolog4	GRMZM2G097746	B73 RefGen_v3	Gene	Chr5	191122611	191130012	ypt4	gene related to "yeast protein two", pco152591, ypt4	
5247	ys1	yellow stripe1	GRMZM2G156599	B73 RefGen_v3	Gene	Chr5	190726052	190729182	ys1	IDP187, yellow stripe1, ys1	yellow tissue between leaf veins, reflects iron deficiency symptoms; defect in Fe-phytosiderophore uptake
5248	yuc2	Yucca2	GRMZM2G159393	B73 RefGen_v3	Gene	Chr10	98816289	98818353	yuc2	disulfide oxidoreductase/ monooxygenase/ oxidoreductase, fmo2, yuc2, ZmYuc2	
5249	yuc3	Yucca3	GRMZM2G107761	B73 RefGen_v3	Gene	Chr4	14185128	14208882	yuc3	disulfide oxidoreductase/ monooxygenase/ oxidoreductase, fmo3, yuc3, ZmYuc3	
5250	yuc4	Yucca4	GRMZM2G141383	B73 RefGen_v3	Gene	Chr2	111172433	111174381	yuc4	probable indole-3-pyruvate monooxygenase YUCCA9, yuc4	up-regulated by light irradiation in the 0-1mm tip region
5251	yuc5	Yucca5	GRMZM2G132489	B73 RefGen_v3	Gene	Chr7	38907938	38910587	yuc5	umc2526, yuc5	transcribed in the root apex (0-5mm)
5252	yuc6	Yucca6	GRMZM2G019515	B73 RefGen_v3	Gene	Chr8	2897539	2904387	yuc6	disulfide oxidoreductase/ monooxygenase/ oxidoreductase, yuc6	transcribed in the root apex (0-5mm)
5253	yy1	yin-yang1	GRMZM2G140016	B73 RefGen_v3	Gene	Chr4	115453280	115456159	yy1	siaf142322b, transcription repressor-maize 1, trm1, yin-yang1, yy1	putative transcription repressor maize TRM
5254	yz1	polypeptide: yz1	GRMZM2G114048	B73 RefGen_v3	Gene	Chr3	216399970	216403243	yz1	yz1	Like x1, is a gene found to be between a1 and sh2
5255	zag1	Zea AGAMOUS homolog1	GRMZM2G052890	B73 RefGen_v3	Gene	Chr6	132008587	132016861	zag1	MADS37 , pzd00011, pzd00012, rs128282270, rs131175762, ss196416431, ss196416433, ucsd64e, ucsd72i, ucsd78a(zag1), umc1187, zag1, Zea AGAMOUS homolog1, ZmMADS37	floral homeotic gene protein AG1; expression strong in female inflorescence; possibly pt1; SSR umc1187
5256	zag2	Zea AGAMOUS homolog2	GRMZM2G160687	B73 RefGen_v3	Gene	Chr3	137255997	137261748	zag2	rs128284543, rs131175507, rs131175508, rs131175509, ss196415439, ss196415441, ss196415443, ss196415445, ucsd81a, zag2, Zag2a, Zea AGAMOUS homolog2, ZmMADS2	amino acid sequence, deduced from cDNA sequence, has 49% identity to Arabidopsis, floral homeotic gene product; expression restricted to female inflorescence; near ts4
5257	zag4	zea agamous4	GRMZM2G531231	B73 RefGen_v3	Gene	Chr9	16806164	16814207	zag4	ucsd61h, ucsd62a(zag4), umc1183, zag4, Zag4a, zea agamous4, Zea endosperm MADS box1, zem1, ZEM2, ZEM3, ZEMa, zemC, Zemc, ZmMADS61	genomic clone: distinct leaf and endosperm transcripts attributed to alternative splicing; contains zag1-like MADS box; SSR umc1183
5258	zag5	zea agamous5	GRMZM2G003514	B73 RefGen_v3	Gene	Chr4	156111149	156118295	zag5	pzd00018, ucsd64G, ucsd72C, ucsd78c, ucsd78c(zag1), zag3, zag5, zea agamous5, ZmMADS5	MADS box, gene specific cDNA probe, expressed in carpels not stamens; SNP pzd00018
5259	zag6	agamous-like6	GRMZM2G026223	B73 RefGen_v3	Gene	Chr1	4855703	4871281	zag6	mads56, MADS-box transcription factor 56, PCO130644, PCO130644(4), rs131175250, ss196414352, zag6, zagl1, zea agamous-like1, ZmMADS56	Encodes a MADS-box transcription factor homologous to SUPPRESSOR OF OVEREXPRESSION OF CONSTANS 1 that affects flowering time in Arabidopsis.
5260	zap1	zea apetala homolog1	GRMZM2G148693	B73 RefGen_v3	Gene	Chr2	236669675	236679078	zap1	MADS-box transcription factor 15, PZD00022, ucsd106a, umc1696, zap1, zap1a, zea apetala homolog1, ZmMADS10	
5261	zar1	Zea mays ARGOS1	GRMZM2G446201	B73 RefGen_v3	Gene	Chr10	119433276	119435009	zar1	Zea mays ARGOS1, zar1, zar2, Zea mays auxin regulated gene involved in organ size, ZmARGOS1	affects yield, and response to drought
5262	zar3	Zea mays ARGOS homolog3	GRMZM2G137546	B73 RefGen_v3	Gene	Chr2	220671352	220673700	zar3	argos3, cl24227_1(192), zar3, Zea mays ARGOS homolog3, Zea mays auxin regulated gene involved in organ size	putative auxin response gene regulating organ size
5263	zar4	Zea mays ARGOS4	GRMZM2G066029	B73 RefGen_v3	Gene	Chr6	147571950	147572995	zar4	argos4, zar4, Zea mays auxin regulated gene involved in organ size	
5264	zar5	Zea mays ARGOS5	GRMZM2G175995	B73 RefGen_v3	Gene	Chr6	3976733	3977389	zar5	argos5, zar5, Zea mays auxin regulated gene involved in organ size	
5265	zar6	Zea mays ARGOS6	GRMZM2G162250	B73 RefGen_v3	Gene	Chr3	147629744	147637183	zar6	argos6, zar6, Zea mays auxin regulated gene involved in organ size	
5266	zar7	Zea mays ARGOS7	GRMZM2G113583	B73 RefGen_v3	Gene	Chr5	174393336	174397308	zar7	argos7, zar7, Zea mays auxin regulated gene involved in organ size	
5267	zar8	Zea mays ARGOS8	GRMZM2G354338	B73 RefGen_v3	Gene	Chr6	143057719	143058385	zar8	argos8, zar8, Zea mays auxin regulated gene involved in organ size, ZmARGOS8	Over-expression can lead to improved drought tolerance
5268	zar9	Zea mays ARGOS9	GRMZM2G082943	B73 RefGen_v3	Gene	Chr3	136407881	136409285	zar9	argos9, zar9, Zea mays auxin regulated gene involved in organ size	
5269	zep1	zeaxanthin epoxidase1	GRMZM2G127139	B73 RefGen_v3	Gene	Chr2	45068944	45077882	zep1	fha5, TMR41, zep1	
5270	zep2	zeaxanthin epoxidase2	GRMZM2G136344	B73 RefGen_v3	Gene	Chr10	120802689	120805284	zep2	rs132588829, zep2	
5271	zfl1	zea floricaula/leafy1	GRMZM2G098813	B73 RefGen_v3	Gene	Chr10	140276803	140279827	zfl1	FLO/LFY, LEAFY, ucsd, ucsd(lfyA), zea floricaula/leafy1, zfl1, zlfy, ZmLFY2	zfl1 and zfl2 double mutants exhibit a disruption of floral organ identity and patterning, as well as defects in inflorescence architecture and in the vegetative to reproductive phase transition.
5272	zfl2	Zea floricaula leafy2	GRMZM2G180190	B73 RefGen_v3	Gene	Chr2	12649206	12652213	zfl2	FLO/LFY, floricaula, floricula, leafy, rs131304556, ss196414994, ucsd, ucsd(lfyB), Zea floricaula leafy2, Zea floricula leafy2, zfl2, zlfy, ZmLFY1	zfl1 and zfl2 double mutants exhibit a disruption of floral organ identity and patterning, as well as defects in inflorescence architecture and in the vegetative to reproductive phase transition.
5273	zfp30	putative zinc finger protein30	GRMZM2G116079	B73 RefGen_v3	Gene	Chr4	232434818	232442130	zfp30	gnp_AI714812, gpm64, umc1328, ZF2, zfp30	
5274	zhd1	ZF-HD-transcription factor 1	GRMZM2G068330	B73 RefGen_v3	Gene	Chr4	11278503	11281332	zhd1		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5275	zhd10	ZF-HD-transcription factor 10	GRMZM2G470974	B73 RefGen_v3	Gene	Chr10	2632775	2633842	zhd10		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5276	zhd11	ZF-HD-transcription factor 11	GRMZM2G328438	B73 RefGen_v3	Gene	Chr8	73654879	73656447	zhd11		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5277	zhd12	ZF-HD-transcription factor 12	GRMZM2G417229	B73 RefGen_v3	Gene	Chr5	201282108	201284278	zhd12		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5278	zhd13	ZF-HD-transcription factor 13	GRMZM2G071112	B73 RefGen_v3	Gene	Chr7	112658777	112661470	zhd13		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5279	zhd14	ZF-HD-transcription factor 14	GRMZM2G172586	B73 RefGen_v3	Gene	Chr10	2639262	2640147	zhd14		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5280	zhd15	ZF-HD-transcription factor 15	GRMZM2G089619	B73 RefGen_v3	Gene	Chr2	50140925	50142374	zhd15		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5281	zhd16	ZF-HD-transcription factor 16	GRMZM2G389379	B73 RefGen_v3	Gene	Chr2	188271896	188273136	zhd16		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5282	zhd17	ZF-HD-transcription factor 17	GRMZM2G069365	B73 RefGen_v3	Gene	Chr4	160153804	160155930	zhd17		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5283	zhd18	ZF-HD-transcription factor 18	GRMZM2G462417	B73 RefGen_v3	Gene	Chr4	185816491	185819532	zhd18		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5284	zhd19	ZF-HD-transcription factor 19	GRMZM2G370863	B73 RefGen_v3	Gene	Chr4	85758755	85759432	zhd19		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5285	zhd2	ZF-HD-transcription factor 2	GRMZM2G161315	B73 RefGen_v3	Gene	Chr7	112903752	112905463	zhd2		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5286	zhd20	ZF-HD-transcription factor 20	GRMZM2G051955	B73 RefGen_v3	Gene	Chr2	181822882	181824556	zhd20		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5287	zhd21	ZF-HD-transcription factor 21	GRMZM5G821755	B73 RefGen_v3	Gene	Chr3	136934215	136936196	zhd21		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5288	zhd22	ZF-HD transcription factor homolog22	GRMZM5G884837	B73 RefGen_v3	Gene	Chr1	200897499	200899336	zhd22	cl50557_1, cl50557_1(61), ZF-HD transcription factor homolog22	
5289	zhd3	ZF-HD-transcription factor 3	GRMZM2G346920	B73 RefGen_v3	Gene	Chr1	200897499	200899336	zhd3		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5290	zhd4	ZF-HD-transcription factor 4	GRMZM2G425236	B73 RefGen_v3	Gene	Chr5	10223283	10224485	zhd4		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5291	zhd5	ZF-HD-transcription factor 5	GRMZM2G438438	B73 RefGen_v3	Gene	Chr1	212577817	212579728	zhd5		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5292	zhd6	ZF-HD-transcription factor 6	GRMZM2G414844	B73 RefGen_v3	Gene	Chr6	166375940	166377410	zhd6		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5293	zhd7	ZF-HD-transcription factor 7	GRMZM2G353734	B73 RefGen_v3	Gene	Chr4	85320866	85323592	zhd7		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
5294	zhd8	ZF-HD-transcription factor 8	GRMZM2G423423	B73 RefGen_v3	Gene	Chr1	269147449	269148335	zhd8		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5295	zhd9	ZF-HD-transcription factor 9	GRMZM2G353076	B73 RefGen_v3	Gene	Chr3	230480803	230481862	zhd9		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5296	zim1	ZIM-transcription factor 1	GRMZM2G126507	B73 RefGen_v3	Gene	Chr7	108871320	108874327	zim1		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5297	zim10	ZIM-transcription factor 10	GRMZM2G173596	B73 RefGen_v3	Gene	Chr5	36976140	36977007	zim10	ZmJAZ7	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5298	zim11	ZIM-transcription factor 11	GRMZM2G122160	B73 RefGen_v3	Gene	Chr4	11373950	11375953	zim11		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5299	zim12	ZIM-transcription factor 12	GRMZM2G101769	B73 RefGen_v3	Gene	Chr2	211875346	211877961	zim12	ZmJAZ11	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5300	zim13	ZIM-transcription factor 13	GRMZM2G005954	B73 RefGen_v3	Gene	Chr2	184649167	184651569	zim13		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5301	zim14	ZIM-transcription factor 14	GRMZM2G036288	B73 RefGen_v3	Gene	Chr9	150582432	150583458	zim14	umc2089, zim14, ZmJAZ3	
5302	zim15	ZIM-transcription factor 15	GRMZM2G114681	B73 RefGen_v3	Gene	Chr2	180086933	180089653	zim15		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5303	zim16	ZIM-transcription factor 16	GRMZM2G445634	B73 RefGen_v3	Gene	Chr1	16791540	16792462	zim16	ZmJAZ5	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5304	zim17	ZIM-transcription factor 17	GRMZM2G327263	B73 RefGen_v3	Gene	Chr3	231290310	231303400	zim17		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5305	zim18	ZIM-transcription factor 18	GRMZM2G145412	B73 RefGen_v3	Gene	Chr1	244885427	244886628	zim18	gnp_QCS15e03, gpm925, zim18, ZmJAZ8	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5306	zim19	ZIM-transcription factor 19	GRMZM2G382794	B73 RefGen_v3	Gene	Chr1	290452059	290455157	zim19		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5307	zim2	ZIM-transcription factor 2	GRMZM2G065896	B73 RefGen_v3	Gene	Chr5	8462838	8467789	zim2		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5308	zim20	ZIM-transcription factor 20	GRMZM2G080509	B73 RefGen_v3	Gene	Chr6	87858244	87863266	zim20	GATA transcription factor 25, ZmJAZ19	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5309	zim21	ZIM-transcription factor 21	GRMZM2G024680	B73 RefGen_v3	Gene	Chr1	244829629	244830954	zim21		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5310	zim22	ZIM-transcription factor 22	GRMZM2G110131	B73 RefGen_v3	Gene	Chr1	30037028	30039032	zim22		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5311	zim23	ZIM-transcription factor 23	GRMZM2G089736	B73 RefGen_v3	Gene	Chr7	165496239	165498650	zim23		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5312	zim24	ZIM-transcription factor 24	GRMZM2G117513	B73 RefGen_v3	Gene	Chr1	69894564	69897090	zim24		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5313	zim25	ZIM-transcription factor 25	GRMZM2G314145	B73 RefGen_v3	Gene	Chr6	107168442	107169441	zim25		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5314	zim26	ZIM-transcription factor 26	GRMZM2G343157	B73 RefGen_v3	Gene	Chr1	16776170	16777317	zim26	ZmJAZ4	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5315	zim27	ZIM-transcription factor 27	GRMZM5G838098	B73 RefGen_v3	Gene	Chr1	16782463	16783895	zim27	ZmJAZ12	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5316	zim28	ZIM-transcription factor 28	GRMZM2G116614	B73 RefGen_v3	Gene	Chr7	121257089	121259224	zim28	umc1585, zim28, ZmJAZ10	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5317	zim29	ZIM-transcription factor 29	GRMZM2G064775	B73 RefGen_v3	Gene	Chr5	36785899	36787242	zim29		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5318	zim3	ZIM-transcription factor 3	GRMZM2G145458	B73 RefGen_v3	Gene	Chr1	244892947	244893692	zim3		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5319	zim30	ZIM-transcription factor 30	AC197764.4_FG003	B73 RefGen_v3	Gene	Chr5	36853650	36854491	zim30		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5320	zim31	ZIM-transcription factor 31	GRMZM2G066020	B73 RefGen_v3	Gene	Chr7	142622294	142626934	zim31		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5321	zim32	ZIM-transcription factor 32	GRMZM2G086920	B73 RefGen_v3	Gene	Chr2	4702643	4706609	zim32		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5322	zim33	ZIM-transcription factor 33	GRMZM2G145407	B73 RefGen_v3	Gene	Chr2	65326353	65328811	zim33		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5323	zim34	ZIM-transcription factor 34	GRMZM2G143402	B73 RefGen_v3	Gene	Chr10	145369299	145373351	zim34	ZmJAZ1	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5324	zim35	ZIM-transcription factor 35	GRMZM2G151519	B73 RefGen_v3	Gene	Chr4	80927425	80930017	zim35		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5325	zim36	ZIM-transcription factor 36	GRMZM2G058479	B73 RefGen_v3	Gene	Chr5	55956384	55961158	zim36	zml2	bm3 (comt) gene. Related to wound induced lignin biosyntheses. Locus designated and assigned to a transcription factor family by the GRASSIUS project (Yilmaz et al 2009) , which
5326	zim4	ZIM-transcription factor 4	GRMZM2G036351	B73 RefGen_v3	Gene	Chr9	150514712	150515694	zim4	ZmJAZ6	(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5327	zim5	ZIM-transcription factor 5	GRMZM2G054689	B73 RefGen_v3	Gene	Chr8	64176829	64179518	zim5		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5328	zim6	ZIM-transcription factor 6	GRMZM2G036349	B73 RefGen_v3	Gene	Chr9	150518483	150519836	zim6		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5329	zim7	ZIM-transcription factor 7	GRMZM2G063632	B73 RefGen_v3	Gene	Chr5	22279974	22282078	zim7		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5330	zim8	ZIM-transcription factor 8	GRMZM2G171830	B73 RefGen_v3	Gene	Chr2	97375739	97377764	zim8		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5331	zim9	ZIM-transcription factor 9	GRMZM2G338829	B73 RefGen_v3	Gene	Chr6	14014557	14015717	zim9		(Yilmaz et al 2009) , which also provided the mappings to the B73_Reference Genome sequence v2 gene models.
5332	zmm1	Zea mays MADS1	GRMZM2G010669	B73 RefGen_v3	Gene	Chr10	30872196	30876367	zmm1	mpik21, mpik31, ov23, PZD00032, PZD00033, rs131175984, ss196417341, ucsd81b, ucsd81b(zag2), Zea mays MADS1, zmm1, ZmMADS23, ZmOV23	box genes, and zmm2 with zag1, may reflect duplications; expression restricted to female inflorescence
5333	zmm15	Zea mays MADS-box 15	GRMZM2G553379	B73 RefGen_v3	Gene	Chr5	6993294	7011505	zmm15	mads15, Zea mays MADS-box 15, zmm15	
5334	zmm16	Zea mays MADS16	GRMZM2G110153	B73 RefGen_v3	Gene	Chr3	171471054	171473646	zmm16	rs131175522, rs131175523, rs55623049 , ss196415518, ss196415520, sterile tassel silky ear1, sts1, umc1730, Zea mays MADS16, zmm16, ZMM16, ZmMADS16	single copy; orthologous to rice GLO-like gene, OSMADS2; strongly expressed in developing male and female inflorescences but wealky expressed indeveloping kernels.
5335	zmm17	zea mays MADS17	GRMZM2G130382	B73 RefGen_v3	Gene	Chr5	85114743	85115386	zmm17	mads44, mpik40, zea mays MADS17, zmm17	single copy GLOBOSA (GLO) or class B MADS box gene expressed in female inflorescences, with weak expression in male inflorescence (Becker 2002)
5336	zmm18	Zea mays MADS18	GRMZM5G805387	B73 RefGen_v3	Gene	Chr8	102542053	102545720	zmm18	cl683_1, mads18, MADS-box transcription factor 4, mpik41, Zea mays MADS18, zmm18, ZMM18	an ortholog of rice GLOBOSA-like gene, OSMADS4; expressed in male and female inflorescences and developing kernels.
5337	zmm2	Zea mays MADS2	GRMZM2G359952	B73 RefGen_v3	Gene	Chr8	22983104	22992125	zmm2	AGAMOUS-like , AGAMOUS-like protein, koln3(zmm2), MADS35, mpik16c, mpik24a(zmm2), TMZ1-7, ucsd78b, ucsd78b(zag1), Zea mays MADS2, zmm2, ZmMADS35	like zmm1 and zag2, are possibly duplications phylogenetically; expression preferentially in the tassel
5338	zmm24	Zea mays MADS24	GRMZM2G087095	B73 RefGen_v3	Gene	Chr1	277377468	277415566	zmm24	mads24, MADS-box transcription factor 34 , pco154775, pco154775(92), Zea mays MADS24, zmm24, ZmMADS24	
5339	zmm27	Zea mays MADS27	GRMZM2G129034	B73 RefGen_v3	Gene	Chr2	192877045	192885419	zmm27	BRACE9-60, koln6a, koln6a(zmm7), mads49, mpik27a(zmm7), Zea mays MADS27, zmm27	AGL2 MADS box family
5340	zmm29	Zea mays MADS29	GRMZM2G152862	B73 RefGen_v3	Gene	Chr8	102450748	102454585	zmm29	cl683_1, MADS-box transcription factor 4, mpik41, Zea mays MADS29, zmm29, ZMM29, ZmMADS29	probably an ortholog of rice GLOBOSA-like gene, OSMADS4; strongly expressed in male and female inflorescences and developing kernels.
5341	zmm3	Zea mays MADS3	AC197699.3_FG001	B73 RefGen_v3	Gene	Chr9	17021226	17024054	zmm3	MADS9 MADS-domain transcription factor, mpik25(zmm3), rs131175926, ss196417109, Zea mays MADS3, zmm3	identified by Northerns; expressed preferentially in male inflorescence
5342	zmm31	Zea mays MADS31	GRMZM2G071620	B73 RefGen_v3	Gene	Chr5	6925447	6932461	zmm31	csu137, csu137a(ap), csu137a(mads), csu137a(zap), csu137(zap1), csuh137, m31, Madsa , mpik22b(zmm4), ucsd106c, umc374, Zea mays MADS31, zmm31, ZmMADS31	

	A	B	C	D	E	F	G	H	I	J	K
1	short name (gene_symbol)	long name (gene_name)	gene_model	assembly_version	locus_type	chr	start	end	short name	synonyms (via maizegdb)	description via maizegdb
5343	zmm6	Zea mays MADS6	GRMZM2G159397	B73 RefGen_v3	Gene	Chr1	194046502	194054589	zmm6	mpik23a, mpik23a(zmm6), Zea mays MADS6, zmm6, ZmMADS6	single copy; identified by cDNA hybridization in situ; early expression in male and female inflorescences, differentially in one member of a spikelet-primordium pair
5344	zmm7	Zea mays MADS7	GRMZM2G097059	B73 RefGen_v3	Gene	Chr7	136296029	136307251	zmm7	koln6b(zmm7), mads7, mik27, mpik27b, mpik27b(zmm7), PZD00054, rs128285102, ss196416660, Zea mays MADS7, zmm7	identified by Northern analysis; expression female-specific, late onset
5345	zmm8	Zea mays MADS8	GRMZM2G102161	B73 RefGen_v3	Gene	Chr9	146936987	146945281	zmm8	IDP223, IDP549, koln4(zmm8), mads5, mpik28, mpik28a(zmm8), mpik28(zmm8), PZD00055, rs128282605, rs55624775 , ss196417271, Zea mays MADS8, zmm8, ZmMADS8	
5346	znf1	zinc finger protein1	GRMZM5G836222	B73 RefGen_v3	Gene	Chr9	102483351	102485242	znf1	A20, AN13, AN1 (animal pole1 - Xenopus), MZ2B1, prp*-mz2b1, zinc finger A20 and AN1 domains, ZmZf, znf1, ZnF-AN1	glucose starved, root tip cDNA
5347	znf2	Zinc finger nuclease2	GRMZM2G478553	B73 RefGen_v3	Gene	Chr9	11736162	11737986	znf2	umc1967, znf2	located between sh1 and bz1 (Hawkins et al., 2014)
5348	znfn1	zinc finger protein1	GRMZM2G086277	B73 RefGen_v3	Gene	Chr6	79660379	79662222	znfn1	zinc finger, C2H2 type family protein, znfn1	
5349	znod1	Zea nodulation homolog1	GRMZM2G052562	B73 RefGen_v3	Gene	Chr9	18630211	18632350	znod1	alpha-L-fucosidase 2, PCO062696, uaz6c06e02(gfu), Zea nodulation homolog1, znod1	leaf cDNA 6C06E02, similar to alfalfa early nodulation protein ENOD8
5350	zp1	zein alpha protein1	GRMZM2G008913	B73 RefGen_v3	Gene	Chr4	29963321	29964591	zp1	alpha zein pms2, phi096, phi096a, pMS2, z1A, zein alpha protein1, zp1, zp19/22(pms2)	genomic sequence pMS2, SSR phi096
5351	zp15	zein protein, 15kDa15	GRMZM2G086294	B73 RefGen_v3	Gene	Chr6	44541825	44542774	zp15	bz15, PCO154060, rs130262118, zein protein, 15kDa15, zp15	high methionine; genomic blot indicates one or two copies
5352	zp2	zein protein2	AF546188.1_FG005	B73 RefGen_v3	Gene	Chr7	18865424	18866146	zp2	z1B, zein-alpha A20-like, zp2	encodes a 19 kD alpha zein
5353	zp22.1	zein protein 22.1	GRMZM2G044625	B73 RefGen_v3	Gene	Chr4	5122439	5123472	zp22.1	phi074, zein protein 22.1, zp22.1	cDNA pZ22.1, SSR phi074
5354	zp27	27-kDa zein protein	GRMZM2G138727	B73 RefGen_v3	Gene	Chr7	120233940	120236057	zp27	modifier1, gz27, gza1, gzr1, mo2, modifier of o2, o2 modifier, opaque2 modifier, opaque2 modifier (gamma-zein A), umc1216, Zc2, zp27, zpA1	proline rich; least abundant of zeins in endosperm, not clear if all in zp27 cluster
5355	zp3	zein protein3	GRMZM2G160739	B73 RefGen_v3	Gene	Chr4	5171933	5177135	zp3	azs2-2 22 kDa type alpha zein 2-2, z1C, zp3	encodes a 22 kD alpha zein
5356	zpl2a	zein polypeptidesL2a	GRMZM2G404459	B73 RefGen_v3	Gene	Chr4	5521259	5523302	zpl2a	19kD alpha zein B1, 19kD alpha zein B2, 19kD alpha zein B5, z1A alpha zein, zein, zein polypeptidesL2a, zpl2a, zpL2a	zein protein characterized by electrophoretic mobility on isoelectric focusing gels. Maps near orp1
5357	zpl2b	zein polypeptidesL2b	AF546188.1_FG002	B73 RefGen_v3	Pseudogene	Chr7	18779575	18780300	zpl2b	az19B1, az19B2, az19b4, az19b5, z1B , z1B-1, z1B-2, zein, zein polypeptidesL2b, zpl2b, zpL2b	zein protein characterized by electrophoretic mobility on isoelectric focusing gels
5358	zpu1	pullulanase-type starch debranching enz	GRMZM2G158043	B73 RefGen_v3	Gene	Chr2	109260299	109311620	zpu1	CL128_1, pul1, pullulanase-type starch debranching enzyme1, umc1003, umc1003(zpu1), zpu1	pullulanase-type starch debranching enzyme. Analysis of plants homozygous for the zpu1-204 mutation reveal the genes role in starch catabolism. zpu1-204 endosperm accumulate
5359	zrp2	Zea root protein2	GRMZM2G106980	B73 RefGen_v3	Gene	Chr1	203686906	203693519	zrp2	siU38791, Zea root protein2, zrp2	cDNA expressed in roots and stems
5360	zyp1	synaptonemal complex protein ZIPPER1	GRMZM2G143590	B73 RefGen_v3	Gene	Chr10	121738153	121749667	zyp1	synaptonemal complex protein ZYP1, ZEP1, ZIP1, zyp1	Homlogous to Yeast ZIPPER1 (ZIP1), Arabidopsis ZYP1 and rice ZEP1.