Gene	Gene Full Name	B73v2 GRMZM	GenBank ID	Chromosome	Local duplicates	Subgenome	Gene Comments, JS	Sorghum Ortholog	Rice Ortholog
a1	anthocyaninless1	GRMZM2G026930	X05068	chr3		1	Good	Sb03g028890	Os01g44260
a2	anthocyaninless2	GRMZM2G345717	X55314	chr5		1	Good	Sb04g000260	chr2:0-600403
a4	anthocyaninless4	GRMZM2G013726	Y16040	chr8		2	Good|inverted repeats surround gene	Sb03g028890	Os01g44260
abp1	auxin binding protein1	GRMZM2G116204	L08425	chr3		2	Good	Sb08g016760	too big a gap
abp4	auxin binding protein homolog4	GRMZM2G064371	L08426	chr10	GRMZM2G078508	1	Good	Sb08g016760	Os12g34450
abph1	aberrant phyllotaxy1	GRMZM2G035688	AB042260	chr2		1	Good	Sb06g022960	Os04g44280
acc1	acetyl-coenzyme A carboxylase1	GRMZM5G858094	Z24449	chr2		NA	Good	no synteny	no synteny
act1	actin1	GRMZM2G126010	J01238	chr8	GRMZM2G126069	2	Good	Sb09g021660	Os05g36290
add1	alternative discordia1	GRMZM2G120178-GRMZM2G050800	FJ469779			2	Gene split by maizesequence.org|exons completely lost	Sb09g003830	Os05g05710
adf1	actin depolymerizing factor1	GRMZM2G117603	X80820	chr7		1	Good	Sb02g033380	Os07g30090
adh1	alcohol dehydrogenase1	GRMZM2G442658	X00580	chr1		1	Good	Sb01g008730	chr3:30154185-30678637
adh2	alcohol dehydrogenase2	GRMZM2G098346	X02915	chr4		1	Good	Sb05g009360	Os11g10480
ae1	amylose extender1	GRMZM2G032628	L08065	chr5		1	Good	Sb04g021540	Os02g32660
afd1	absence of first division1	GRMZM2G059037	AY788900	chr6		1	Good	Sb09g029640	Os05g50410
ahh1	adenosyl homocysteine hydrolase1	GRMZM2G015295	AW424691	chr4	GRMZM2G494688	1	Can't proof	too big a gap	Os11g26850
akh1	aspartate kinase-homoserine dehydrogenase1	GRMZM2G365423-GRMZM2G389303-GRMZM2G437977	L33912	chr4		2	Gene split by maizesequence.org three genes	too big a gap	no synteny
akh2	aspartate kinase homoserine dehydrogenase2	GRMZM2G104546	L33913	chr2		2	Good	Sb02g019450	no synteny
ald1	aldolase1	GRMZM2G057823	X12872	chr3		1	Good	Sb03g043140	Os01g67860
am1	ameiotic1	GRMZM5G883855	DQ663482	chr5		2	Good	Sb01g013215	Os03g44760
amya3	alpha amylase3	GRMZM2G138468	L25805	chr2	GRMZM2G566151	2	Good	Sb02g026610	Os09g28400
amyb5	beta amylase5	GRMZM2G058310	Z25871	chr7	GRMZM2G358467	1	Good	Sb02g035600	Os07g35940
an1	anther ear1	GRMZM2G081554	L37750	chr1		1	Good	Sb01g021990	chr10:13517249-14258420
ane1	androgenic embryo1	GRMZM2G039942	AJ011559	chr4		NA	Good	no synteny	no synteny
ane3	androgenic embryo3	GRMZM2G372553	AJ307880	chr10		1	Can't proof	Sb07g003415	chr8:2932877-3054776
ant2	adenine nucleotide translocator2	GRMZM2G135186	X15712	chr4		2	Good	Sb04g029750	Os02g48720
apt1	aberrant pollen transmission1	GRMZM2G448687	DQ020097	chr9		2	Good	Sb01g035230	Os03g23030
arpp1a	acidic ribosomal protein P1a	GRMZM2G032315	U62752	chr6		1	Good	Sb07g001570	Os08g02340
arpp2a	acidic ribosomal protein P2a	GRMZM2G119809	X86553	chr8	GRMZM2G102891||GRMZM2G105712	2	Good	Sb09g029390	chr5:28584191-29087363
atp1	ATPase1	GRMZM2G101020	M95063	chr3		2	Good	Sb08g004390	Os12g07140
b1	colored plant1	GRMZM2G172795	X57276	chr2		1	Missing internal exon (gene model and pseudomolecule)	Sb06g025060	Os04g47059
ba1	barren stalk1	GRMZM2G397518	AY753892	chr3		1	Good	Sb03g038820	Os01g61480
bap2	basal layer antifungal protein2	GRMZM2G152655	AJ133529	chr4	GRMZM2G027472	2	Good	Sb07g003420	too big a gap
bd1	branched silkless1	GRMZM2G307119	AY196003	chr7		1	Good	Sb02g042400	Os07g47330
bde1	bearded-ear1	GRMZM2G160565	L46397	chr5		1	Good	Sb04g031750	Os02g45770
betl3	basal endosperm transfer layer3	GRMZM2G175976	AJ133530	chr3		2	Good	too big a gap	no synteny
bif2	barren inflorescence2	GRMZM2G171822	EF532402	chr1		1	deletion within first exon	Sb08g021520	Os12g42050
bip1	Binding protein homolog1	GRMZM2G114793	U58208	chr5		1	Good	Sb04g001140	Os02g02410
bm1	brown midrib1	GRMZM5G844562	AJ005702	chr5	GRMZM5G868202	1	Good	Sb04g005950	Os02g09490
bm3	brown midrib3	AC196475.3_FG004	M73235	chr4		2	Good	Sb07g003860	Os08g06100
brk1	brick1	GRMZM5G842058	AY093614	chr5		1	Good	Sb04g038300	Os02g58320
bsd2	bundle sheath defective2	GRMZM2G062788	AF126742	chr1		1	Good	chr8:49843172-50129204	chr12:23768068-24054915
bt1	brittle endosperm1	GRMZM2G144081	M79333	chr5		1	Good	Sb04g007010	no synteny
bt2	brittle endosperm2	GRMZM2G068506	AF544167	chr4		2	Good|potentially missing upstream exons	too big a gap	no synteny
bx1	benzoxazinless1	GRMZM2G085381	X76713	chr4		1	Good	chr5:58868109-59571565	chr11:25708564-25959495
bx2	benzoxazinone synthesis2	GRMZM2G085661	X81831	chr4		1	Good	Sb05g026080	Os11g41710
bx3	benzoxazinone synthesis3	GRMZM2G167549	X81829	chr4	GRMZM2G172491||GRMZM2G473480||GRMZM5G855537||GRMZM5G899181	1	Good	Sb05g026065	chr11:25708564-25959495
bx4	benzoxazinone synthesis4	GRMZM2G172491	X81827	chr4	GRMZM2G473480||GRMZM5G855537||GRMZM5G899181	1	Good	Sb05g026065	chr11:25708564-25959495
bx5	benzoxazinone synthesis5	GRMZM2G063756	X81830	chr4	GRMZM2G167549||GRMZM2G172491||GRMZM2G473480||GRMZM5G855537||GRMZM5G899181	1	Good	Sb05g026080	chr11:25708564-25959495
bz1	defective kernel1	GRMZM2G165390	X07937	chr9		1	Good	Sb10g006140	Os06g09240
bz2	bronze2	GRMZM2G016241	U14599	chr1		1	Good	Sb01g022080	chr10:13445230-14195619
c1	colored aleurone1	GRMZM2G005066	X52201	chr9		1	Missing 3' UTR in maizesequence.org	Sb10g006700	Os06g10350

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c2	colorless2	GRMZM2G422750	X60205	chr4		1	Good	Sb05g020150	Os11g32650
caf2	crs2 associated factor2	AC199526.5_FG003	AY264369	chr3		1	Good	Sb03g013160	Os01g21990
cal1	calmodulin1	GRMZM2G117582	X74490	chr6		1	Good	Sb09g024030	Os05g41270
cal2	calmodulin2	GRMZM2G067511	X77397	chr3		1	Good	chr3:10895034-11088655	Os01g16240
cal3	calmodulin3	GRMZM2G152891	X77396	chr1	GRMZM2G452760	1	Good	Sb01g037010	Os03g20370
cap1	calcium pump1	GRMZM2G056014	AF096871	chr8		2	Good	Sb09g001850	Os05g02940
cat1	catalase1	GRMZM2G088212	X60135	chr5		1	Good	Sb10g030840	Os06g51150
cat2	catalase2	GRMZM2G090568	X54819	chr1		1	Good	Sb01g048280	Os03g03910
cat3	catalase3	GRMZM2G079348	L05934	chr4		2	Good	Sb04g001130	Os02g02400
ccp1	cysteine protease1	GRMZM2G098298	D45402	chr5		1	Good	too big a gap	too big a gap
ccp2	cysteine protease2	GRMZM2G038636	X99936	chr7		1	Good	Sb02g025920	Os09g27030
cdj2	chaperone DNA J2	GRMZM2G364069	AF053468	chr1		1	Good	Sb01g013390	Os03g44620
cesa1	cellulose synthase1	GRMZM2G112336	AF200525	chr8		2	Good	Sb09g005280	too big a gap
cesa2	cellulose synthase2	GRMZM2G027723	AF200526	chr6		1	Good	Sb09g005280	Os05g08370
cesa3	cellulose synthase3	GRMZM2G039454	AF200527	chr3		1	Good	Sb03g004310	chr1:3437238-3858481
cesa5	cellulose synthase5	GRMZM2G111642	AF200529	chr1	GRMZM2G111837	1	Good	Sb01g004210	Os03g59340
cesa6	cellulose synthase6	GRMZM2G113137	AF200530	chr1		1	Good	Sb01g002050	Os03g62090
cesa7	cellulose synthase7	GRMZM2G025231	AF200531	chr7		1	Good	Sb02g010110	Os07g24190
cesa8	cellulose synthase8	GRMZM2G177631	AF200532	chr7		1	Good	Sb02g007810	too big a gap
cesa9	cellulose synthase9	GRMZM2G018241	AF200533	chr2	GRMZM2G150404||GRMZM2G319836||GRMZM2G452739	2	partial identical duplicate:GRMZM2G150404 |assembly errors?	Sb02g006290	Os07g10770
cf1	camouflage1	GRMZM2G026117	BT042702	chr5		1	Good	Sb04g004630	Os02g07230
chi1	chalcone flavanone isomerase1	GRMZM2G155329	Z22760	chr1		1	Good	Sb01g003330	Os03g60509
chn2	chitinase2	GRMZM2G145461	L00973		GRMZM2G145518||GRMZM2G447967	2	Good	chr10:59525238-60462013	Os06g51050
chn3	chitinase3	GRMZM2G389582	L16798	chr5	GRMZM2G064360	1	Good	chr10:60362013-60952691	Os06g51050
cip1	cytokinin inducible protease1	GRMZM2G009443	T14785	chr10		1	Can't proof	chr8:15672577-16127244	no synteny
cka1	CK2 protein kinase alpha 1	GRMZM2G143602	X61387	chr2		2	Good	Sb02g001110	Os07g02350
cka2	CK2 protein kinase alpha 2	GRMZM2G047855	Y11526	chr1		1	Good	Sb01g007270	Os03g55389
cko1	cytokinin oxidase1	GRMZM2G146644	Y18377	chr3		1	wrong exons in middle of transcript-real ones missing	Sb03g003300	Os01g09246
conz1	constans1	GRMZM2G405368	EU098139	chr9	GRMZM2G545607	1	Good	Sb10g010050	Os06g16370
cpn1	chaperonin 1	GRMZM2G458208-GRMZM2G111477	L21007	chr5		2	Gene split by maizesequence.org	Sb01g020010	Os10g32550
cr4	crinkly4	GRMZM2G051637	U67422	chr10		1	Good	Sb08g003290	chr12:2558011-3036894
crp1	chloroplast RNA processing1	GRMZM2G083950	AF073522	chr7		1	Good	Sb02g035800	Os07g36390
crr2	cytokinin response regulator2	GRMZM2G392101	AB031012	chr10		2	Good	Sb06g032600	Os04g57720
crs1	chloroplast RNA splicing1	GRMZM2G078412	AY109620	chr1		1	Good	no synteny	Os08g27150
crs2	chloroplast RNA splicing2	GRMZM2G132021	AF225708	chr8		2	Good	Sb03g007130	Os01g04130
crt2	calreticulin2	GRMZM2G358059	X89813	chr7		1	Good	Sb02g007480	Os07g14270
csy1	chloroplast SecY-1	GRMZM5G809546	AF039304	chr10		NA	Good	no synteny	no synteny
cta1	chitinase A1	GRMZM2G051943	M84164	chr2	GRMZM2G051921||GRMZM2G052175||GRMZM2G122708	1	Good	Sb06g021230	Os04g41680
cyc1	cyclin1	GRMZM2G034647	U10078	chr8	GRMZM5G804421	2	Good	Sb09g024180	Os05g41390
cyc2	cyclin2	chr3:41183262	U10077	chr3			No gene model		
cyc3	cyclin3	GRMZM2G073671	U10076	chr6		2	Good	Sb10g030790	Os06g51110
cyc4b	cyclin4	GRMZM2G310115	U10079	chr8		2	Good	Sb03g037470	Os01g59130
cyp1	cytochrome P450 homolog1	GRMZM5G899349	T12664	chr3		2	Can't proof	Sb08g002250	no synteny
cyp8	cytochrome P-450 8	GRMZM2G167986	L23209	chr1	GRMZM5G825885	1	Good	Sb01g022690	Os10g26340
d3	dwarf plant3	GRMZM2G093195	U32579	chr9		1	Good	Sb10g000920	Os06g02019
d8	dwarf plant8	GRMZM2G144744	AY103865	chr1		1	Good	Sb01g010660	Os03g49990
d9	dwarf plant9	GRMZM2G024973	DQ903073	chr5		2	Good	Sb01g010660	Os03g49990
dbf3	DRE-binding protein3	GRMZM2G124037	AY964718		GRMZM2G124011	2	Good	Sb02g030320	Os09g35020
dcd1	discordia1	GRMZM2G083459	FJ469780	chr10		1	Good	Sb09g003830	Os05g05710
dek1	defective kernel1	GRMZM2G321753	AY061806	chr1		1	Good	Sb01g037910	chr3:10491680-10834228
dgat1	diacyglycerol acyltransferase1	GRMZM2G169089	EU039830	chr6		2	Good	Sb10g022270	too big a gap
dhn1	dehydrin1	GRMZM2G079440	X15290	chr6		1	Good	Sb09g018420	chr5:17019836-17955366
dlf1	delayed flowering1	GRMZM2G067921	EF093789	chr7	GRMZM5G858064	NA	Good	no synteny	Os09g36910
dmt101	DNA methyl transferase1	GRMZM2G333916	AF229183	chr7		1	Good	Sb02g004680	Os07g08500
dof2	DNA binding with one finger2	GRMZM2G009406	X79934	chr2		2	Good	Sb02g027480	Os09g29960
dsc1	discolored kernel1	chr4:47715993	AF006498	chr4			Not gene model		
du1	dull endosperm1	GRMZM2G141399	AF023159	chr10		1	Good	Sb07g005400	Os08g09230
dwf1	DWF1 like1	GRMZM2G057000	AY523572	chr5	GRMZM2G358007	1	Good	Sb10g031090	no synteny
dzs18	delta zein structural18	GRMZM2G100018	U31541	chr6		2	Good	Sb10g013050	no synteny
ea1	egg apparatus1	GRMZM2G456746	AY733074	chr7		1	Good	Sb02g038820	Os07g41400
eif5	eucaryotic translation initiation factor5	GRMZM2G165917	X99517	chr4	GRMZM5G899228	2	Good	Sb04g003550	too big a gap
eif5a	elongation initiation factor5A	GRMZM2G113696	H35879	chr2		2	Can't proof	Sb02g038290	Os07g40580

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elfa1	elongation factor alpha1	AC233866.1_FG006	M95072	chr6	GRMZM5G859846||GRMZM5G896006	1	Can't proof	too big a gap	chr5:16888752-17955366
elfg1	elongation factor gamma1	GRMZM2G122871	T14690	chr6		2	Can't proof	Sb10g022570	too big a gap
elm1	elongated mesocotyl1	GRMZM5G861678	AY560384	chr8		2	Good	Sb03g045760	Os01g72090
emp2	empty pericarp 2	GRMZM2G039155	AF494285	chr2		2	Good	Sb02g023500	Os09g20830
emp4	empty pericarp4	GRMZM2G092198	DQ291135	chr1		1	Good	Sb01g009420	Os03g51840
eno1	enolase1	GRMZM2G064302	X55981	chr9		1	Good	Sb10g002460	Os06g04510
et1	etched1	GRMZM2G157574	AJ507104	chr3	GRMZM5G887575	1	Good	Sb03g027210	Os01g42050
expa1	alpha expansin1	GRMZM2G339122	AY104146	chr3		1	Good	Sb03g038290	Os01g60770
fdx3	ferredoxin3	GRMZM2G053458	AB001387	chr1		1	Good	Sb01g002180	Os03g61960
fea2	fasciated ear2	GRMZM2G104925	AY055124	chr4		2	Good	Sb04g025240	Os02g39100
fer1	ferritin1	GRMZM2G325575	X61391	chr4		1	Good	Sb05g000530	Os11g01530
fer2	ferritin homolog2	GRMZM2G147266	X61392		GRMZM2G066165||GRMZM5G854762	1	CDS wrong|real gene is annotated as only 3' UTR	too big a gap	no synteny
fgs1	ferredoxin-dependent glutamate synthase1	GRMZM2G036609	M59190	chr7		1	Good	Sb02g041740	Os07g46460
fht1	flavanone 3-hydroxylase1	GRMZM2G062396	U04434	chr2		1	Good	Sb06g031790	Os04g56700
fie1	fertilization independent endosperm1	GRMZM2G118205	AY061964	chr4		2	Good	Sb07g002820	Os08g04290
fie2	fertilization independent endosperm2	GRMZM2G148924	AY061965	chr10		1	Good	Sb07g002820	Os08g04290
fl2	floury2	GRMZM2G397687	L34340	chr4	GRMZM2G397678	1	Good	too big a gap	too big a gap
fps1	farnesyl pyrophosphate synthase1	GRMZM2G168681	AF330036	chr8		2	Good	Sb09g027190	Os05g46580
g2	golden plant2	GRMZM2G087804	AF298118	chr3	GRMZM2G087961	1	Good	Sb03g000400	Os01g13740
gdh1	glutamic dehydrogenase1	GRMZM2G178415	AY106054	chr1		1	Good	Sb01g005370	Os03g58040
gl1	glossy1	GRMZM2G114642	U37428	chr7		1	Good	Sb02g025220	Os09g25850
gl15	glossy15	GRMZM2G160730	U41466	chr9		1	Good|neither transcript completely accurate	Sb10g025053	Os06g43220
gl2	glossy2	GRMZM2G098239	AY109951	chr2	GRMZM5G867147	1	Good	Sb06g028160	Os04g52164
gl8	glossy8	AC205703.4_FG006	U89509	chr5		1	Good	Sb04g025020	Os02g38440
glb1	globulin1	GRMZM2G067919	U28017	chr1		1	Good	Sb01g012640	Os03g46100
glb2	globulin2	GRMZM2G026703	X53715	chr1		1	Good	Sb01g005440	Os03g57960
gln1	glutamine synthetase1	GRMZM2G098290	X65931	chr10		2	Good	Sb06g031460	Os04g56400
gln2	glutamine synthetase2	GRMZM2G024104	X65927	chr1		1	Good	Sb01g010270	Os03g50490
gln3	glutamine synthetase3	GRMZM2G046601	X65930	chr9	GRMZM5G887009	2	Good	Sb01g042450	Os03g12290
gln4	glutamine synthetase4	GRMZM5G872068	X65928	chr5		1	Good	Sb04g028690	Os02g50240
gln5	glutamine synthetase5	GRMZM2G036464	X65929	chr4		2	Good	Sb04g028690	Os02g50240
gln6	glutamine synthetase6	GRMZM2G050514	X65926	chr1		1	Good	Sb01g042450	Os03g12290
glu1	beta glucosidase1	GRMZM2G016890	U33816	chr10	GRMZM2G014844||GRMZM2G119460	1	Good	Sb08g007586	no synteny
glu2	beta-glucosidase2	GRMZM2G008247	U44087	chr10		1	Good	no synteny	chr12:7256295-7525701
gn1	gnarley1	GRMZM2G452178	AY312168	chr2		2	Good	Sb02g002200	Os03g56110
gol1	goliath1	GRMZM2G080079	T18797.1	chr4		2	Can't proof	Sb04g028130	Os02g50990
got2	glutamate-oxaloacetate transaminase2	GRMZM5G836910	AY105250	chr5		1	Good	Sb04g036060	Os02g55420
gpa1	glyceraldehyde-3-phosphate dehydrogenase1	GRMZM2G337113	X07157	chr2	GRMZM2G337196	1	Good	Sb06g018880	Os04g38600
gpc1	glyceraldehyde-3-phosphate dehydrogenase1	GRMZM2G046804	X15596	chr4		2	Good	Sb07g002220	Os08g03290
gpc2	glyceraldehyde-3-phosphate dehydrogenase2	GRMZM2G180625	U45858	chr6		1	Good	Sb07g002220	Os08g03290
gpc3	glyceraldehyde-3-phosphate dehydrogenase3	GRMZM2G071630	L13431	chr4	GRMZM2G072119	2	Good	Sb04g025120	Os02g38920
grf1	general regulatory factor1	GRMZM2G102499	AY110485	chr2		1	Good	Sb06g019100	Os04g38870
grp1	glycine-rich protein1	GRMZM2G080603	X61121	chr1	GRMZM5G836166	1	Good	too big a gap	no synteny
grp3	glycine-rich protein3	GRMZM2G154954	Y07781	chr5		2	Good	too big a gap	too big a gap
gsr1	glutathione reductase1	GRMZM2G172322	T12723	chr1		1	Good	Sb01g046260	Os03g06740
gst1	glutathione-S-transferase1	GRMZM2G116273	X06754	chr8		2	Good	Sb03g035420	Os01g55830
gst4	glutathione S-transferase4	GRMZM2G146246	W49853	chr3	GRMZM5G849767	1	Good	Sb03g044980	Os01g70770
gzr1	gamma zein modifier1	GRMZM2G138727	S78780	chr7	GRMZM2G438538	1	Good|identical to 27-kDa zein protein	Sb02g025510	chr9:15882395-16462627
hcf106	high chlorophyll fluorescence106	GRMZM5G898735	AF027808	chr2		1	Good	Sb06g014410	chr4:19032798-19318750
hcf106c	high chlorophyll fluorescence106c	GRMZM2G151529	AF237945	chr10	GRMZM2G002911||GRMZM2G151566||GRMZM2G484851	2	Good	Sb06g014410	chr4:19177617-19798474
hda108	histone deacetylase	GRMZM2G136067	AF440226	chr4		2	Good	too big a gap	no synteny
hir1	hypersensitive induced reaction1	GRMZM2G117755	AF236373	chr4		2	Good	Sb07g019760	Os08g30790
his2a1	histone2A1	GRMZM2G305046	U08225	chr9	GRMZM2G305035	2	Good	Sb01g039240	Os03g17100
his2b1	histone2b1	GRMZM2G071959	X57312	chr7		1	Good	Sb02g025410	chr9:15818244-16396427
his2b2	histone2b2	GRMZM2G119071	X57313	chr4	GRMZM2G553422	2	Good	Sb07g022370	chr8:22231845-22466035
hm1	Helminthosporium carbonum susceptibility1	GRMZM5G881887	L02540	chr1		1	Good	Sb07g023130	too big a gap
hm2	Helminthosporium carbonum susceptibility2	GRMZM2G086773	AF041047	chr9		1	Good	Sb10g025770	Os06g44180
hmg1	high mobility group protein1	GRMZM5G834758	X66077	chr5		1	Good	Sb10g030910	Os06g51220
hopi1	hopi r1/b1 family member1	GRMZM5G822829	AJ251719	chr10		2	Good|lc1	Sb06g025060	Os04g47059
hrg1	hydroxyproline rich glycoprotein1	GRMZM2G168651	X63134	chr2		1	Good	Sb06g016310	Os04g34170
hsbp1	herbicide safener binding protein1	GRMZM2G085924	AF033496	chr2	GRMZM2G385313||GRMZM2G506270		Good	no synteny	no synteny

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hsk1	high-sulfur keratin homolog1	GRMZM5G844723	T14673	chr9		2	Can't proof	chr1:58795354-59707921	chr3:12522642-13228664
hsp1	heat shock protein1	GRMZM2G310431	X03697	chr8		2	Good	Sb03g039360	Os01g62290
hsp101	heat-shock protein 101	GRMZM2G360681	AF077337	chr6		1	Good	Sb09g025900	Os05g44340
hsp18c	heat shock protein18c	GRMZM2G034157	X54075	chr8		2	Upstream UTR missing	too big a gap	too big a gap
hsp18f	heat shock protein18f	GRMZM2G083810	X54076	chr3		1	Good	Sb03g003530	Os01g08860
hsp70-4	heat shock protein70-4	GRMZM2G340251	X78414	chr3	GRMZM5G817178	2	Good	Sb08g018750	Os12g38180
hyp1	hybrid proline-rich protein1	GRMZM2G304378	X60432	chr9	GRMZM2G304385	1	Good	Sb10g004790	Os06g07220
ibp2	initiator-binding protein2	GRMZM2G110309	X79086	chr1		1	Good	Sb01g039650	Os03g16700
id1	indeterminate growth1	GRMZM2G011357	AF058757	chr1		1	Good	Sb01g021480	Os10g28330
ig1	indeterminate gametophyte1	GRMZM2G118250	EF081454	chr3	GRMZM2G419929	1	Good	Sb03g042310	Os01g66590
igl1	indole-3-glycerol phosphate lyase1	GRMZM2G046191	NM_001111532	chr1		1	Assignment corrected by maizesequence.org		
ij1	iojap striping1	GRMZM2G004583	Z15063	chr7		1	Good	Sb02g028720	Os09g32030
im30p1	IM30 protein homolog1	GRMZM2G017077	T12745	chr3		1	Can't proof	Sb03g042550	Os01g67000
in1	intensifier1	GRMZM2G042733	U57899	chr7		1	Good	Sb02g006390	Os07g11020
incw1	cell wall invertase1	GRMZM2G139300	U17695	chr5		1	Good	Sb04g021810	Os02g33110
incw3	invertase cell wall3	GRMZM2G123633	AF043346	chr10	GRMZM2G095725	2	Good	too big a gap	Os04g33740
isr1	inhibitor of striate1	GRMZM5G803874	AF296824	chr10		2	Good	Sb06g025010	Os04g47020
ivr1	invertase1	GRMZM2G394450	U16123	chr2		1	Good	Sb06g023760	Os04g45290
ivr2	invertase2	GRMZM2G089836	AJ563384	chr5	GRMZM5G863665||GRMZM5G890000	1	Good	Sb04g000620	Os02g01590
kan1	KANADI1	GRMZM2G056400	EU935003	chr1		1	Good	Sb07g020820	Os08g33050
kan3	kanadi3	GRMZM2G175827	EU925399	chr4		2	Good	Sb07g020820	Os08g33050
kch2	potassium channel2	AC234152.1_FG007-AC234152.1_FG002	AJ132686	chr8		2	Gene split by maizesequence.org	Sb09g021210	chr5:20322584-21033855
kch3	potassium channel3	GRMZM2G081666	AY461584	chr4		2	Good	Sb04g008780	Os02g14840
kip1	knotted interacting protein1	GRMZM2G163761	AY082396	chr1	GRMZM2G011588	1	Good	Sb01g011970	Os03g47730
kn1	knotted1	GRMZM2G017087	X61308	chr1		1	Missing 5' UTR	Sb01g009480	Os03g51690
knox3	knotted related homeobox3	GRMZM2G000743	DQ056238	chr1		1	Can't proof	Sb01g009480	Os03g51710
lc1	red leaf color1	GRMZM5G822829	M26227	chr10		2	Good|lc1	Sb06g025060	Os04g47059
lec1	leafy cotyledon	GRMZM2G011789	AF410176	chr5		1	Good	Sb04g029350	Os02g49370
lem1	lethal embryo mutant1	AC234157.1_FG002	AF332374	chr1		1	Good	Sb01g006910	Os03g55930
les22	lesion22	GRMZM2G044074	AF058763	chr1		1	Good	Sb01g036030	Os03g22060
lg1	liguleless1	GRMZM2G036297	AF451895	chr2		1	Good|upstream sequence on wrong contig	Sb06g031290	Os04g56170
lg2	liguleless2	GRMZM2G060216	AY180106	chr3		1	Good	Sb03g040530	Os01g64020
lg3	liguleless3	GRMZM2G087741	AF100455	chr3		1	Good	Sb03g012480	Os01g19694
lg4	liguleless4	GRMZM2G094241	AF457118	chr8		2	Good	Sb09g002520	Os05g03884
lhcb1	light harvesting chlorophyll a/b binding protein1	GRMZM2G351977	M87020	chr8		2	Can't proof	too big a gap	Os01g41710
lhcb2	light harvesting chlorophyll a/b binding protein2	AC207722.2_FG009	X14794	chr7	GRMZM2G353753	1	Good	Sb02g032040	no synteny
lhcb3	light harvesting chlorophyll a/b binding protein3	GRMZM2G155216	X55892	chr8		2	Good	Sb09g028720	chr5:28058352-28684191
lhcb7	light harvesting complex mesophyll7	GRMZM2G402936	X53398	chr6		1	Good	Sb09g028720	chr5:28081764-28748003
lhcb9	light harvesting chlorophyll binding protein9	GRMZM2G018627	X68682	chr1	GRMZM2G321320||GRMZM2G414192||GRMZM2G414195	1	Good|near identical paralog: GRMZM2G414192	Sb01g015400	Os03g39610
lkrsdh1	lysine-ketoglutarate reductase / saccharopine dehydrogenase1	GRMZM2G181362	AF271636	chr4		2	Good	Sb04g035220	Os02g54254
lls1	lethal leaf spot1	GRMZM2G339563	U77345	chr1		1	Good	Sb01g047120	Os03g05310
lop1	lo1 pI allergen homolog1	GRMZM2G072886	AY197352	chr9		2	Good	Sb01g029880	Os10g40090
lox1	lipoxygenase1	GRMZM2G156861	DQ335760	chr3	GRMZM2G458554	1	Two tandem duplicates merged into one gene by maizesequence.org?	Sb03g042440	chr1:38780116-39263267
lox3	lipoxygenase3	GRMZM2G109130	AF465643	chr1		1	Good	Sb01g011040	Os03g49260
lpa1	low phytic acid1	GRMZM2G155242	AF323175	chr1		1	Good	Sb01g044290	Os03g09250
lpa2	low phytic acid2	GRMZM2G456626	AY172635	chr1		1	Good	Sb01g028090	Os10g42550
lyce1	lycopene epsilon cyclase1	GRMZM2G012966	EU924262	chr8		2	Good	Sb03g026020	Os01g39960
mads1	MADS1	GRMZM2G171365	AF112148	chr9		2	Good	Sb01g049020	Os03g03100
mbf1	multi-protein bridging factor homolog1	GRMZM2G101480	T14752	chr4		2	Good	Sb07g014940	no synteny
mdh2	malate dehydrogenase2	GRMZM2G154595	AY103861	chr6		1	Good	Sb09g029240	Os05g49880
mdh4	malate dehydrogenase4	GRMZM2G415359	AA051891	chr1		1	Can't proof	Sb01g019280	Os10g33800
me3	NADP malic enzyme3	GRMZM2G085019	J05130	chr3		1	Good	Sb03g003220	Os01g09320
meg1	maternally expressed gene1	GRMZM2G354335	AY536120	chr7	GRMZM2G116212||GRMZM2G137959||GRMZM2G145466||GRMZM2G175896||GRMZM2G175912||GRMZM2G181051||GRMZM2G573952||GRMZM2G573956	1	Maizesequence.org adds to extra exons	too big a gap	chr7:4506584-4989949

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mez1	enhancer of zeste1	GRMZM2G157820	AF443596	chr6		2	Good	Sb10g004560	too big a gap
mgs1	male-gametophyte specific1	GRMZM2G317406	S44171	chr10		2	weird	Sb06g014740	Os04g32680
mha1	membrane H(+)-ATPase1	GRMZM2G104325	U08985	chr7		1	Good	Sb02g005440	Os07g09340
mha2	plasma-membrane H+ATPase2	GRMZM2G019404	X85805	chr2	GRMZM2G314079	1	Good	Sb06g031240	Os04g56160
mir1	maize insect resistance1	GRMZM2G150276	AF019145	chr6	GRMZM2G150256	2	Good	Sb10g027980	chr6:28229592-28756822
mlg3	lea protein group3	GRMZM2G096475	U05226	chr6		1	Good	Sb09g027110	Os05g46480
mn1	miniature seed1	GRMZM2G119689	AF050631	chr2		1	Good|probably	too big a gap	Os04g33740
mop1	mediator of paramutation1	GRMZM2G042443	DQ417755	chr2	GRMZM2G042532	1	Can't proof	Sb06g019330	Os04g39160
mrp1	Myb related protein1	GRMZM2G111306	AJ318518	chr8		2	Good	too big a gap	chr5:1836622-2596437
mrpa3	multidrug resistance-associated protein3	GRMZM2G111903	AY609318	chr9		1	Good	Sb10g004070	Os06g06440
ms26	male sterile26	GRMZM2G091822	AF366297	chr1		1	Good	Sb01g045960	Os03g07250
ms45	male sterile45	GRMZM2G307906	AF360356	chr9		2	CDS wrong	Sb01g040250	Os03g15700
mta1	ribosomal protein	GRMZM2G090422	T14712	chr1		1	Can't proof	Sb01g007690	Os03g54860
mwp1	milkweed pod1	GRMZM2G082264	EU925398	chr7		1	Good	Sb02g024110	Os09g23200
myb2	myb2	AC203535.4_FG001	AF458962	chr3	GRMZM5G826686||GRMZM5G882384	1	Good	Sb03g044450	chr1:40516492-40965296
nac1	NaCl stress protein1	GRMZM2G015605	T14760	chr10		1	Good	Sb09g003060	Os05g04700
nbp1	nucleic acid binding protein1	GRMZM2G011129	M74566	chr7		1	Good	Sb02g011330	no synteny
ndk1	nucleotide diphosphate kinase1	GRMZM2G134797	T18831	chr7		1	Can't proof	Sb02g033710	Os07g30970
nnr1	nitrate reductase(NADH)1	GRMZM2G568636	M77792	chr4		2	Good	Sb07g022750	Os08g36480
ns1	narrow sheath1	GRMZM2G069028	AJ536578	chr2		2	Good	Sb05g003490	no synteny
o2	opaque endosperm2	GRMZM2G015534	X15544	chr7		1	Good	Sb02g004590	Os07g08420
ocl1	outer cell layer1	GRMZM2G026643	Y17898	chr3		1	Good	Sb03g008090	no synteny
ocl2	outer cell layer2	AC235534.1_FG007	AJ250984	chr10		2	Good	Sb06g025750	Os04g48070
ocl3	outer cell layer3	GRMZM2G116658	AJ250985	chr7		1	Good	Sb02g030470	Os09g35760
ocl4	outer cell layer4	GRMZM2G123140	AJ250986	chr1	GRMZM5G875327	1	Good	Sb01g028160	Os10g42490
ocl5a	outer cell layer5a	GRMZM2G130442	AJ250987	chr4		2	Good	Sb07g005180	Os08g08820
ohp1	opaque2 heterodimerizing protein1	GRMZM2G016150	L00623	chr1	GRMZM2G019446	1	Good	Sb01g005170	Os03g58250
ohp2	opaque2 heterodimerizing protein2	GRMZM2G007063	L06478	chr5		2	Good	Sb01g005170	Os03g58250
ole1	oleosin1	GRMZM2G337229	U13701	chr2		1	Good	Sb06g024350	Os04g46200
ole3	oleosin3	AC206941.2_FG002	J05212	chr5		2	3' UTR split into separate gene model	Sb01g011120	Os03g49190
orp1	orange pericarp1	GRMZM2G169593	M76684	chr4	GRMZM5G896346	2	Good	Sb07g002770	Os08g04180
orp2	orange pericarp2	GRMZM2G005024	M76685	chr10		1	Split into two transcripts?	Sb07g002770	Os08g04180
oy1	oil yellow1	GRMZM2G419806	DQ084025	chr10		1	Good	Sb08g004300	chr12:3388067-4083733
p1	pericarp color1	GRMZM2G084799	U57002	chr1		1	3' UTR missing	Sb01g037670	Os03g19120
p2	pericarp color2	GRMZM2G057027	AF210617	chr1		1	duplicate of P1	Sb01g037690	Os03g19120
pac1	pale aleurone color1	GRMZM2G058292	AY115485	chr5	GRMZM5G872691	1	Good|maizesequence.org includes more 5' UTR	Sb04g031730	Os02g45810
pal1	phenylalanine ammonia lyase homolog1	GRMZM2G074604	M95077	chr5	GRMZM2G029048||GRMZM2G170692||GRMZM2G334655||GRMZM2G334660	1	Can't proof	Sb04g026530	Os02g41680
pcna1	proliferating cell nuclear antigen1	GRMZM2G030523	X79065	chr5		1	Good	Sb04g036440	Os02g56130
pdc2	pyruvate decarboxylase2	GRMZM2G038821	D14456	chr8		2	Good	Sb03g005240	Os01g06660
pdc3	pyruvate decarboxylase3	GRMZM2G087186	D14457	chr1	GRMZM5G841025	1	Good	Sb01g038360	Os03g18220
pdi1	protein disulfide isomerase1	GRMZM2G091481	AY739284	chr4	GRMZM2G393320	1	Good	Sb05g006150	Os11g09280
pep1	phosphoenolpyruvate carboxylase1	GRMZM2G083841	X15238	chr9		1	Good	Sb10g021330	chr6:19969223-20504683
pep4	phosphoenolpyruvate carboxylase4	GRMZM2G473001	X61489	chr7		1	Good	Sb02g021090	Os09g14670
pex1	pollen extensin-like1	GRMZM5G841015	Z34465	chr2	GRMZM2G453012	2	Good	too big a gap	no synteny
pgd2	6-phosphogluconate dehydrogenase2	GRMZM2G145715	AF061837	chr3		1	Good	Sb03g045216	chr1:41194784-41479544
pgl2	polygalacturonase2	GRMZM2G320175	X57628	chr6	GRMZM2G058033||GRMZM2G153666||GRMZM2G160526||GRMZM2G160626||GRMZM2G162384||GRMZM2G306693||GRMZM5G880653	2	Good	Sb10g024010	Os06g40890
pgl8	exopolygalacturonase8	GRMZM2G394259	X64408	chr6		2	Good	Sb10g024010	Os06g40890
phot1	blue-light receptor phototropin 1	GRMZM2G001457	AF033263	chr3		2	Good	Sb08g000260	Os11g01140
phyA1	phytochromeA1	GRMZM2G157727	AY234826	chr1	GRMZM5G895731	1	Good	Sb01g009920	Os03g51030
phyB1	phytochromeB1	GRMZM2G124532	DQ307579	chr1		1	maizesequence.org CDS starts too late (insertion into B73 exon?)	Sb01g037340	Os03g19590
phyB2	phytochromeB2	GRMZM2G092174	AY234828	chr9		2	Good	Sb01g037340	Os03g19590
phyC1	phytochromeC1	GRMZM2G057935	AY234829	chr1	GRMZM2G357074	1	Good	Sb01g007850	Os03g54084
phyC2	phytochromeC2	GRMZM2G129889	AY234830	chr5		2	Good	Sb01g007850	Os03g54084
piip1	physical impedance induced protein1	AC234161.1_FG001	AF001634	chr9	AC234161.1_FG002	2	Good	Sb01g029630	Os10g40420

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pip1b	plasma membrane intrinsic protein1	AC209208.3_FG002	AF131201	chr5		1	maizesequence.org skips 3' UTR	Sb04g032430	Os02g44630
pip1c	plasma membrane intrinsic protein1	GRMZM2G392975	AF326487	chr4		2	Good	Sb04g032430	Os02g44630
pip1e	plasma membrane intrinsic protein1	GRMZM2G081843	AF326489	chr4		2	Good	Sb04g037800	Os02g57720
pip1f	plasma membrane intrinsic protein1	GRMZM2G136032	AF326490	chr9		1	Good	Sb10g007610	chr6:5814961-6206831
pip2a	plasma membrane intrinsic protein2	GRMZM2G178693	AF130975	chr2		1	Good	Sb06g023240	Os04g44570
pip2b	plasma membrane intrinsic protein2	GRMZM2G092125	AF326492	chr2		2	Good	Sb02g010760	too big a gap
pip2c	plasma membrane intrinsic protein2	GRMZM2G081192	AF326493	chr4	GRMZM2G081333	2	Good	Sb04g026650	Os02g41860
pip2d	plasma membrane intrinsic protein2	GRMZM2G154628	AF326494	chr5		1	Good	Sb04g032430	Os02g44630
pip2e	plasma membrane intrinsic protein2	GRMZM2G014914	AF326491	chr7	GRMZM2G047368	1	Good	Sb02g010760	too big a gap
pip2f	plasma membrane intrinsic protein2	GRMZM2G047368	AF326495	chr7		1	Good	too big a gap	too big a gap
pk4	protein kinase4	GRMZM2G014833	AF141378	chr3		1	Good	Sb03g035170	Os01g55450
pki1	protein kinase inhibitor1	GRMZM2G018728	Z29643	chr1		1	Good	Sb01g036830	Os03g20630
pl1	purple plant1	GRMZM2G701063	AF015268	chr6		2	Good	Sb10g006700	Os06g10350
plt1	phospholipid transfer protein homolog1	GRMZM2G101958	J04176	chr10		1	Good	Sb08g002670	no synteny
plt2	phospholipid transfer protein homolog2	GRMZM2G010868	U66105	chr3		2	Good	Sb08g002670	Os11g02424
pmg1	phosphoglycerate mutase1	GRMZM5G833389	Z33612	chr8		2	Good	Sb03g038020	Os01g60190
ppp1	pyrophosphate-energized proton pump1	GRMZM2G090718	T18800	chr5		1	3' end half of gene sequence missing	Sb04g034340	Os02g52940
ppr5	pentatricopeptide repeat 5	GRMZM2G025409	EU037901	chr4		2	Good	Sb04g027800	Os02g51480
prc1	proteasome C9 1	GRMZM2G120047	T14766	chr6		2	Can't proof	Sb10g004740	Os06g07140
prf1	profilin homolog1	GRMZM2G074361	X73279	chr6		1	Good	Sb09g026120	chr5:25962071-26565743
prh1	ser/thr protein phosphatase1	GRMZM2G112240	M60215	chr4		2	Good	Sb04g037500	Os02g57450
prp1	pathogenesis-related protein1	AC205274.3_FG001	X54325	chr8			UTRs unannotated	no synteny	no synteny
prp2	pathogenesis-related protein2	GRMZM2G102356	T18697	chr2	GRMZM5G809105	1	Good	Sb06g019320	Os04g39150
ps1	pink scutellum1	GRMZM5G849107	AY206862	chr5	GRMZM2G403196	1	Good	Sb04g006120	Os02g09750
psei1	cystatin1	GRMZM2G438551	AM055630	chr3	GRMZM5G858738	1	Good	Sb03g037370	Os01g58890
psei2	cystatin2	GRMZM2G012160	D63342	chr8		2	Good	Sb03g037370	Os01g58890
ptk1	protein kinase1	GRMZM2G328785	X52384	chr6	GRMZM2G328772	1	Good	Sb09g008070	no synteny
qm1	QM1 homolog1	GRMZM2G087233	U06108	chr5		2	Good	Sb01g015470	no synteny
r1	colored1	GRMZM5G822829	X15806	chr10		2	Good||lc1	Sb06g025060	Os04g47059
ra1	ramosa1	GRMZM2G003927	AY957396	chr7		1	Good	Sb02g024400	chr9:14417584-14918349
ra2	ramosa2	AC233943.1_FG002	BT035538	chr3		1	UTR exon skipped my maizesequence.org	Sb03g004590	Os01g07480
ra3	ramosa3	GRMZM2G014729	DQ436920	chr7		1	Good	Sb02g039820	Os07g43160
rab15	responsive to abscisic acid15	GRMZM2G165901	X12564	chr5	GRMZM2G166026	2	Good	Sb01g012300	Os03g46770
rbap1	WD-repeat protein RBAP1	GRMZM2G316113	AF250047	chr8		2	Good	Sb03g032630	Os01g51300
rel2	ramosa1 enhancer locus2	GRMZM2G042992	GQ927145	chr10		1	Good	Sb07g004180	Os08g06480
rf2	restorer of fertility2	GRMZM2G058675	U43082	chr9		1	Good	Sb10g009790	Os06g15990
rgd1	ragged seedling1	GRMZM2G020187	DQ832257	chr6			Good	no synteny	no synteny
ris2	iron-sulfur protein2	GRMZM2G162748	W49887		GRMZM2G162805	1	Can't proof	chr4:10212873-10952629	Os02g15560
rld1	rolled leaf1	GRMZM2G109987	AY501430	chr9		2	Good	Sb01g050000	Os03g01890
rmr1	required to maintain repression1	GRMZM2G154946	EU155001	chr6	GRMZM2G453655	1	Good	Sb09g019410	Os05g32610
rnc1	ribonuclease III domain protein1	GRMZM2G035820	EU971053	chr3		1	Good	Sb03g037610	Os01g59510
rop2	Rho-related protein from plants2	GRMZM5G846811	AY163379	chr4		2	Good	Sb04g001690	Os02g02840
rp1	resistance to Puccinia sorghi1	AC152495.1_FG002	AF107293	chr10	AC152495.1_FG003||GRMZM2G003625||GRMZM2G005134||GRMZM2G061742||GRMZM2G069382||GRMZM2G083246||GRMZM2G083258||GRMZM2G165720||GRMZM5G833046	1	5' and 3' UTR exons missed by maizesequence.org	Sb08g002410	no synteny
rpl17	ribosomal protein L17	GRMZM2G702426	AF034948	chr4		2	Good	Sb07g026305	Os08g41810
rpot1	RNA polymerase T phage-like 1	GRMZM2G381395	AF127021	chr7		1	Good	Sb02g039520	chr7:25585675-26175382
rps11	ribosomal protein S11	GRMZM2G019325	X55967	chr10		2	Good	Sb06g028330	Os04g52354
rps4	ribosomal protein S4	GRMZM2G035017	AF015522	chr1		1	Good	Sb01g001850	chr3:35199453-35652824
rrb1	related to retinoblastoma1	GRMZM2G003043	AF007793	chr2		2	Good	Sb05g020280	Os11g32900
rs1	rough sheath1	GRMZM2G028041	L44133	chr7		1	Good	Sb02g002200	Os07g03770
rs2	rough sheath2	GRMZM2G403620	AF143447	chr1		1	Good	Sb08g018840	Os12g38400
rtcs1	rootless concerning crown and seminal roots1	GRMZM2G092542	EF051732	chr1	GRMZM2G092483	1	Good	Sb01g046990	Os03g05510
rth1	roothair defective1	GRMZM2G099056	AY265854	chr1		1	Good	Sb01g014290	Os03g42750
rth3	roothair defective3	GRMZM2G377215	AY265855	chr1		1	Good	Sb01g037850	Os03g18910
rtp1	Zea root preferential4	GRMZM2G017557	L14063	chr4		1	Good	Sb05g006910	too big a gap
sal1	supernumerary aleurone1	GRMZM2G117935	AY243475	chr9		1	Good	Sb10g025200	Os06g43590
sam2	S-adenosyl methionine decarboxylase2	GRMZM2G154397	W99255	chr2		1	Can't proof	Sb06g021540	Os04g42090
sar1	SAR homolog1	GRMZM2G038356	T14655	chr3		1	Good	Sb03g013550	Os01g23620
sbe1	starch branching enzyme1	GRMZM2G088753	D11081	chr5		1	Good	Sb10g030776	Os06g51084

Gene	Gene Full Name	B73v2 GRMZM	GenBank ID	Chromosome	Local duplicates	Subgenome	Gene Comments, JS	Sorghum Ortholog	Rice Ortholog
sbe3	starch branching enzyme3	GRMZM2G073054	U65948	chr2		1	Good	Sb06g015360	Os04g33460
sci1	subtilisin-chymotrypsin inhibitor homolog1	GRMZM2G028393	X69972	chr8	GRMZM2G028656||GRMZM2G042789	2	Good	too big a gap	too big a gap
scm1	self-colored marbled1	GRMZM5G822829	AF135458	chr10		2	can't proof|lc1	Sb06g025060	Os04g47059
sdh1	sorbitol dehydrogenase homolog1	GRMZM2G175423	DQ191049	chr1		1	Good	Sb07g025220	Os08g43190
sgo1	shugoshin centromeric cohesion1	GRMZM2G074082	AY964185	chr7		1	Good	Sb02g006220	too big a gap
sh1	shrunken1	GRMZM2G089713	X02400	chr9	GRMZM2G090962||GRMZM2G090974	1	Extra 5' UTR in maizesequence.org	Sb10g006330	Os06g09450
sh2	shrunken2	GRMZM2G429899	M81603	chr3		1	extra (coding)exons in maizesequence.org	Sb03g028850	Os01g44220
si1	silky1	GRMZM2G139073	AF181479	chr6		2	Good	Sb10g029810	Os06g49840
Smh1	Single Myb Histone1	GRMZM2G136887	AY271659	chr8		2	Good	Sb03g026470	Os01g40670
Smh2	Single Myb Histone2	GRMZM2G087817		chr3		1	No GenBank Record|personal communication	Sb03g026470	Os01g40670
Smh3	Single Myb Histone3	GRMZM2G023667	AY280629	chr8		2	Good	Sb03g032540	Os01g51170
Smh4	Single Myb Histone4	GRMZM2G108424	AY280631	chr3		1	Good	Sb03g032530	Os01g51154
Smh5	Single Myb Histone5	GRMZM2G163291	AY280630	chr3		1	Good	Sb03g005080	chr1:2844116-3337953
Smh6	Single Myb Histone6	GRMZM2G095239	AY280632	chr5		2	Good	Sb01g013670	no synteny
sn1	scutellar node color1	GRMZM5G822829	X60706	chr10		2	Good|lc1	Sb06g025060	Os04g47059
sod2	superoxide dismutase2	GRMZM2G025992	M54936	chr7	GRMZM2G027777	1	Good	Sb02g042170	Os07g46990
sod3	superoxide dismutase3	GRMZM2G059991	M33119	chr6		1	Good	too big a gap	Os05g25850
sod4	superoxide dismutase4	GRMZM2G169890	X17565	chr1		1	Good	Sb01g035350	Os03g22810
sod9	superoxide dismutase9	GRMZM2G058522	X17564	chr9		2	Good	Sb01g035350	Os03g22810
spi1	sparse inflorescence1	GRMZM2G025222	EU910940	chr3		NA	5' end of CDS lost in gap	no synteny	no synteny
spp1	sucrose-phosphatase1	GRMZM2G055489	AF283564	chr8		2	Good	chr9:52109989-52638612	chr5:22388038-22888762
sps1	sucrose phosphate synthase1	GRMZM5G875238	M97550	chr8		2	Good	Sb03g043900	Os01g69030
ss1	starch synthase I	GRMZM2G129451	AF036891	chr9		1	Good	Sb10g004160	Os06g06560
ssu1	ribulose bisphosphate carboxylase small subuni	GRMZM2G098520	X06535	chr4		1	Good	Sb05g003480	too big a gap
ssu2	ribulose bisphosphate carboxylase small subuni	GRMZM2G113033	Y09214	chr2		2	Good	Sb05g003480	no synteny
stc1	sesquiterpene cyclase1	GRMZM2G177098	AF296122	chr9	GRMZM2G177211	1	Good	Sb10g006160	chr6:4114082-4703565
stk1	serine threonine kinase1	GRMZM2G165433	EF523347	chr9	GRMZM2G465296	1	Good	Sb10g006130	Os06g09230
stp1	sugar transport1	GRMZM2G097768	T12737	chr8		2	Can't proof	Sb09g029520	Os05g50280
su1	sugary1	GRMZM2G138060	U18908	chr4		2	Missing 5' coding region?	Sb07g027200	Os08g40930
su2	sugary2	GRMZM2G348551	AY499410	chr6		2	5' UTR and upsteam sequence missing	Sb10g008200	Os06g12450
Sun1	sad1-unc84-like 1 CCSD type	GRMZM2G109818	EU964563	chr5		1	personal communication	Sb04g005160	chr2:4152195-4473675
Sun2	sad1-unc84-like 2 CCSD type	GRMZM2G440614	BT055722	chr3		1	personal communication	Sb03g010590	Os01g16220
Sun4	sad1-unc84-like 4 PM3 type	GRMZM2G005483	GU453173	chr8		2	personal communication	Sb03g041510	Os01g65520
Sun5	sad1-unc84-like 5 PM3 type	AC194341.4_FG003	EU953247	chr8		2	personal communication	Sb03g026980	Os01g41600
sus1	sucrose synthase1	GRMZM2G152908	L33244	chr9		2	Good	Sb01g033060	Os03g28330
sxd1	sucrose export defective1	GRMZM2G009785	AF302187	chr5		1	Good	Sb04g010660	Os02g17650
tacs1	Terminal Acidic SANT 1	GRMZM2G111906	AY738116	chr6		2	Good	chr10:59803993-60610533	chr6:30308446-31043218
taf1	transcription associated factor1	GRMZM2G002276	T12672	chr3		1	Can't proof	Sb03g039720	Os01g62820
tan1	tangled1	GRMZM2G039113	AF305892	chr6		1	Good	Sb09g018850	chr5:18275913-19077686
tb1	teosinte branched1	AC233950.1_FG002	U94494	chr1		1	Good	Sb01g010690	Os03g49880
tbp2	TATA-binding protein2	GRMZM2G161418	L13302	chr5		2	Good	Sb01g012880	Os03g45410
tdy1	tie-dyed1	GRMZM2G321778	FJ376984	chr6		1	Good	Sb09g029660	Os05g50470
te1	terminal ear1	GRMZM2G085113	AF047852	chr3		1	Good	Sb03g043230	Os01g68000
tga1	teosinte glume architecture1	GRMZM2G101511	AY883559	chr4	AC233751.1_FG002	2	Good	Sb07g026220	Os08g41940
tha1	thylakoid assembly1	chr3:58008644	U71123	chr3			No gene model		
tif1	translation initiation factor1	GRMZM5G835323	AF034944	chr7		1	Good	Sb02g035170	Os07g34589
tif5A	eukaryotic translation initiation factor 5A	GRMZM2G144030	AF034943	chr7		1	Good	Sb02g038290	Os07g40580
tlk1	tousled-like protein kinase1	GRMZM2G016671	AY644701	chr1		1	Good	Sb01g008020	Os03g53880
tlk2	tousled-like protein kinase2	GRMZM2G172132	AF012889	chr5		2	Can't proof	Sb01g008020	Os03g53880
tm20	transmembrane protein20	GRMZM2G036564	X97570	chr6	GRMZM2G313761	2	Good	Sb10g010780	no synteny
tpi4	triose phosphate isomerase4	GRMZM2G018177	L00371	chr8		2	Good	Sb03g006130	Os01g05490
trh1	thioredoxin h homolog1	GRMZM2G424053	T15273	chr6		1	Good	Sb09g024960	chr5:25057494-25544351
ts1	tassel seed1	GRMZM2G104843	FJ360855	chr2		1	Good	Sb06g018040	Os04g37430
ts2	tassel seed2	GRMZM2G455809	L20621	chr1		1	Good	Sb01g038050	Os03g18740
ts4	tasselseed4	GRMZM5G803935	GQ905588	chr3		1	why does a microRNA have a CDS?	chr3:73688749-74313024	chr1:42689358-43324564
ts6	tasselseed6	GRMZM5G862109	AF048900	chr1	GRMZM5G880027	1	Good	Sb01g003400	Os03g60430
tsh1	tasselsheath1	GRMZM2G325850		chr6		1	No GenBank Record|gene name in publication	Sb09g029510	Os05g50270
tua1	alpha tubulin1	AC195340.3_FG001	X63176	chr5		2	Good	Sb01g006710	Os03g56810
tua4	alpha tubulin4	GRMZM2G152466	X73980	chr5		2	Good	Sb01g009560	Os03g51600
tua5	alpha tubulin5	GRMZM2G099167	X63177	chr2	GRMZM2G333258	2	Good	Sb02g037260	Os07g38730
tua6	alpha tubulin6	GRMZM2G083243	X63178	chr7	GRMZM2G083590	1	Good	Sb02g037260	Os07g38730
tub1	beta tubulin1	GRMZM2G164696	X52878	chr1		1	Good	Sb01g050310	Os03g01530

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tub2	beta tubulin2	GRMZM2G334899	X52879	chr8		2	Good	Sb09g020360	Os05g34170
tub3	beta tubulin3	GRMZM2G108766	X74654	chr1		1	Good	Sb01g012740	Os03g45920
tub4	beta tubulin4	GRMZM2G066191	X74655	chr5		2	Good	Sb01g012740	Os03g45920
tub6	beta tubulin6	GRMZM2G071790	L10633	chr3	GRMZM5G857152	1	Good	Sb03g037490	Os01g59150
ubi2	ubiquitin2	GRMZM2G419891	S94466	chr4	GRMZM2G118637||GRMZM2G419844	2	Good	Sb04g004260	Os02g06640
uce1	ubiquitin conjugating enzyme1	GRMZM2G018447	T18767	chr3		2	Good	Sb08g022990	Os12g44000
ugp1	UDP-glucose pyrophosphorylase1	GRMZM2G032003	T14797	chr7		1	Can't proof	Sb02g032250	Os09g38030
vacs1	vacuolar sorting receptor homolog1	GRMZM2G067546	AY105262	chr9		2	Good	Sb01g036170	Os03g21720
vp1	viviparous1	GRMZM2G133398	M60214	chr3		1	Good	Sb03g043480	Os01g68370
vp10	viviparous10	GRMZM2G067176	DQ231522	chr10		2	Good	Sb06g031680	Os04g56620
vp14	viviparous14	GRMZM2G014392	U95953	chr1		1	Good	Sb01g013520	Os03g44380
vp15	viviparous15	GRMZM2G121468	DQ273133	chr5	GRMZM2G421883	1	Good	Sb04g022920	Os02g35200
vp5	viviparous5	GRMZM2G410515	AF039585	chr1		1	Can't proof	Sb01g044990	Os03g08570
vp8	viviparous8	GRMZM2G010353	EU401893	chr1		1	Good	Sb01g005710	Os03g57660
vpp1	vacuolar proton pump homolog1	GRMZM2G014240	AY103622	chr9		1	Good	Sb10g005250	Os06g08080
wc1	white cap1	GRMZM2G057243	DQ100346	chr9		2	Good	Sb01g047540	too big a gap
whp1	white pollen1	GRMZM2G151227	X60204	chr2	GRMZM2G027130||GRMZM5G818346	2	Good	too big a gap	Os11g32540
why1	whirly1	GRMZM2G155662	EU595664	chr6		2	Good	Sb10g003170	no synteny
wip1	wound induced protein1	GRMZM2G156632	X71396	chr8		2	Good	Sb03g007180	Os01g04050
wtf1	what's this factor?1	GRMZM2G403797	FJ264201	chr8		2	Good	Sb09g029040	Os05g49610
wx1	waxy1	GRMZM2G024993	X03935	chr9		1	Good	Sb10g002140	Os06g04200
xyl1	xylanase1	GRMZM2G170839	AF063865	chr1			Good	no synteny	no synteny
yab10	yabby homolog10	GRMZM2G167824	AY313904	chr1		1	Good	Sb01g017560	Os10g36420
yab14	yabby14	GRMZM2G005353	AY313901	chr10		2	Good	Sb06g023770	Os04g45330
yab15	yabby15	GRMZM2G529859	AY313902	chr5		1	Good	Sb04g033590	Os02g42950
yab9	yabby9	GRMZM2G074543	AY313903	chr5		2	Good	Sb01g017560	Os10g36420
ypt1	ypt homolog1	GRMZM2G086971	X63277	chr2		1	Good	Sb06g017640	chr4:21509416-21975014
ys1	yellow stripe1	GRMZM2G156599	AF186234	chr5		1	Good	Sb04g033345	Os02g43370
yy1	yin-yang1	GRMZM2G140016	AF142322	chr4		2	Good	Sb04g022470	Os02g34680
zag1	Zea AGAMOUS homolog1	GRMZM2G052890	L18924	chr6	GRMZM2G052937	1	Good	Sb09g006360	Os05g11414
zag2	Zea AGAMOUS homolog2	GRMZM2G160687	L18925	chr3		2	Good	Sb08g006460	Os12g10540
zag4	zea agamous4	GRMZM2G531231	L46399	chr9		1	weird gene model	Sb10g004390	Os06g06750
zag5	zea agamous5	GRMZM2G003514	L46398	chr4		2	Good	Sb04g031750	Os02g45770
zap1	zea apetala homolog1	GRMZM2G148693		chr2		2	Assignment corrected by maizesequence.org		
zcn1	phosphatidylethanolamine-binding protein1	GRMZM2G092008	EU241917	chr3		2	Good	Sb08g003210	Os12g05590
zcn10	phosphatidylethanolamine-binding protein10	GRMZM2G152689	EU241926	chr3		1	Good	Sb03g008270	Os01g02120
zcn11	phosphatidylethanolamine-binding protein11	GRMZM2G117057	EU241927	chr6		2	Good	Sb10g013070	no synteny
zcn12	phosphatidylethanolamine-binding protein12	GRMZM2G103666	EU241928	chr3		1	Good	Sb03g034580	Os01g54490
zcn13	phosphatidylethanolamine-binding protein13	GRMZM2G108016	EU241904	chr5		1	Good	Sb04g008320	Os02g13830
zcn14	phosphatidylethanolamine-binding protein14	GRMZM2G373928	EU241929	chr8		2	Maybe annotated as pseudogene?	Sb03g001700	Os01g11940
zcn15	phosphatidylethanolamine-binding protein15	GRMZM2G051338	EU241930	chr6		2	5' UTR unannotated by maizesequence.org	Sb10g003940	Os06g06320
zcn16	phosphatidylethanolamine-binding protein16	GRMZM2G127121	EU241931	chr5		1	Good	Sb04g025210	Os02g39064
zcn17	phosphatidylethanolamine-binding protein17	GRMZM2G075215	EU241932	chr2		NA	Good	no synteny	no synteny
zcn18	phosphatidylethanolamine-binding protein18	GRMZM2G158809	EU241933	chr2		2	Good	Sb02g029725	Os09g33850
zcn19	phosphatidylethanolamine-binding protein19	GRMZM2G062052	EU241934	chr10		2	Good	Sb06g020850	Os04g41130
zcn2	phosphatidylethanolamine-binding protein2	GRMZM2G156079	EU241893	chr4		2	Good	too big a gap	no synteny
zcn20	phosphatidylethanolamine-binding protein20	AC214791.2_FG002	EU241935	chr10		1	3' UTR unannotated	Sb08g008180	no synteny
zcn3	phosphatidylethanolamine-binding protein3	GRMZM2G338454	EU241919	chr10		1	5' end of gene lost in a gap	Sb08g003210	Os12g05590
zcn4	phosphatidylethanolamine-binding protein4	GRMZM2G075081	EU241920	chr2		1	Good	Sb06g015490	Os04g33570
zcn5	phosphatidylethanolamine-binding protein5	AC217051.3_FG006	EU241921	chr10		2	Good	Sb06g015490	Os04g33570
zcn6	phosphatidylethanolamine-binding protein6	GRMZM2G132880	EU241922	chr4		1	Good	Sb05g003200	Os11g05470
zcn7	phosphatidylethanolamine-binding protein7	GRMZM2G141756	EU241923	chr6		1	Good	Sb09g025760	Os05g44180
zcn8	phosphatidylethanolamine-binding protein8	GRMZM2G179264	EU241924	chr8		2	Good	Sb09g025760	Os05g44180
zcn9	phosphatidylethanolamine-binding protein9	GRMZM2G021614	EU241925	chr8		2	Good	Sb03g008270	Os01g02120
zfl1	zea floricaula/leafy1	GRMZM2G098813	AY179882	chr10		2	Good	Sb06g027340	Os04g51000
zfl2	Zea floricaula leafy2	GRMZM2G180190	AY179881	chr2		1	Good	Sb06g027340	Os04g51000
zmm2	Zea mays MADS2	GRMZM2G359952	X81200	chr8		2	Good	Sb03g002525	Os01g10504
zmm24	Zea mays MADS24	GRMZM2G087095	AJ430638	chr1	GRMZM2G032339	1	Good	Sb01g007790	Os03g54160
zmm31	Zea mays MADS31	GRMZM2G071620	AJ430640	chr5	GRMZM2G553379	2	Good	Sb01g007790	Os03g54160
zmm6	Zea mays MADS6	GRMZM2G159397	AJ430692	chr1	GRMZM2G098986	1	Good	Sb07g026180	Os08g41950
zmm7	Zea mays MADS7	GRMZM2G129034	Y09302	chr2		2	Good	Sb02g029310	Os09g32948
zmm8	Zea mays MADS8	GRMZM2G102161	Y09303	chr9		2	Good	Sb01g042840	Os03g11614
znf1	zinc finger protein1	GRMZM5G836222	W99253		GRMZM5G803160	1	Good	Sb10g024060	Os06g41010

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zp1	zein alpha protein1	GRMZM2G008913	X58700	chr4		2	Good|inversion in nongene sequence downstream of gene	too big a gap	too big a gap
zp15	zein protein	GRMZM2G086294	M12147	chr6		1	Good	Sb09g000360	chr5:0-218039
zp27	27-kDa zein protein	GRMZM2G138727	M16218	chr7	GRMZM2G438538	1	Good	Sb02g025510	chr9:15882395-16462627
zpl2b	zein polypeptidesL2b	GRMZM2G404459	AF371270	chr4	GRMZM2G018193||GRMZM2G053120||GRMZM2G059620||GRMZM2G353268||GRMZM2G353272||GRMZM2G489581||GRMZM2G514379||GRMZM2G514469||GRMZM2G514479||GRMZM2G514485||GRMZM2G518465||GRMZM2G545000||GRMZM2G586611	1	Good	too big a gap	chr11:22583954-23404386