Accession1	ID1	Species1	Accession2	Species2	ID2	Gene	Coding Identity	BLASTN score	E value	CNS blocks	CNS %	Total Length	Function
S69616	778	HV	AF434703	TA	607	A1	88.5			7.0	50.2		structural gene/enzymes
U70541	827	OS	S69616	HV	778	A1	82.8			0.0	0.0		structural gene/enzymes
U70541	827	OS	AF010283	SB	531	A1	84.4			0.0	0.0		structural gene/enzymes
U70541	827	OS	AF434703	TA	607	A1	77.0			0.0	0.0		structural gene/enzymes
AF010283	531	SB	S69616	HV	778	A1	86.9			0.0	0.0		structural gene/enzymes
AF010283	531	SB	AF434703	TA	607	A1	81.1			0.0	0.0		structural gene/enzymes
X05068	376	ZM	S69616	HV	778	A1	82.5			1.0	1.9		structural gene/enzymes
X05068	376	ZM	AF434703	HV	607	A1	76.8			0.0	0.0		structural gene/enzymes
X05068	376	ZM	U70541	OS	827	A1	81.9	159	4E-84	15.1	15.7	3053	structural genes/enzymes
X05068	376	ZM	AF010283	SB	531	A1	85.2			2.0	7.1		structural gene/enzymes
AF055898	35	ZM	AB007404	OS	805	Alanine aminotransferase	93.6	101	9E-48	17.5	22.4	4523	nitrogen metabolism
AF172282	808	OS	AF253472	HV	708	alcohol dehydrogenase1 (Adh1)	97.6			3.0	7.7		structural gene/enzymes
AF172282	808	OS	X04049	SB	470	alcohol dehydrogenase1 (Adh1)	97.6			5.0	9.7		structural gene/enzymes
X04049	470	SB	AF253472	HV	708	alcohol dehydrogenase1 (Adh1)	97.9			3.0	6.4		structural gene/enzymes
X04049	470	ZM	AF253472	HV	708	alcohol dehydrogenase1 (Adh1)	97.9			3.0	7.5		structural gene/enzymes
X04049	470	ZM	AF172282	OS	808	alcohol dehydrogenase1 (Adh1)	97.6	184	7E-99	16.3	22.4	4774	structural genes/enzymes
X04049	470	ZM	X04049	SB	470	alcohol dehydrogenase1 (Adh1)	100.0			8.0	45.5		structural gene/enzymes
X12733	868	HV		TA	#N/A	Alcohol dehydrogenase2 (Adh2)	96.7			8.0	78.5		structural gene/enzymes
AF172282	808	OS	X12733	HV	868	Alcohol dehydrogenase2 (Adh2)	90.8			0.0	0.0		structural gene/enzymes
X02915	469	ZM	X12733	HV	868	Alcohol dehydrogenase2 (Adh2)	79.7			0.0	0.0		structural gene/enzymes
X02915	469	ZM	AF172282	OS	808	Alcohol dehydrogenase2 (Adh2)	83.1	210	0	23.4	33.2	2007	structural genes/enzymes
AF215823	53	ZM	AC084766	OS	810	aldehyde dehydrogenase Rf2	84.3	210	2E-50	1.1	1.1	15744	structural genes/enzymes
AF348418	497	ZM	AF462029	OS	811	aldehyde dehydrogenase rf2B	81.9	230	2E-56	3.4	3.2	2649	structural genes/enzymes
X55314	870	ZM	AP003199	OS	812	Anthocyaninless2 (A2)	72.8	211	0	9.7	10.4	1650	structural genes/enzymes
AJ301645	865	HV		TA	#N/A	Beta-amylase (Amy2)	98.0			1.0	38.3		starch metabolism
L10345	836	OS	AJ301645	HV	865	Beta-amylase (Amy2)	85.2			1.0	3.1		starch metabolism
AF068119	38	ZM	AJ301645	HV	865	Beta-amylase (Amy2)	76.3			1.0	2.1		starch metabolism
AF068119	38	ZM	L10345	OS	836	Beta-amylase (Amy2)	89.3	195	0	10.0	14.9	3695	starch metabolism
AF334959	67	ZM	M31616	OS	837	Brittle2 (Bt2)	88.7	174	3E-91	10.0	11.5	1105	starch metabolism
U14599	348	ZM	AC092749	OS	813	Bronze-2 glutathione-S-transferase	74.3	416	1E-113	13.6	14.3	809	structural genes/enzymes
L27484	310	ZM	AP003073	OS	850	Calcium-dependent protein kinase (CDPK)	76.8	202	0	10.8	11.6	2490	regulatory
AY061804	489	ZM	AP004161	OS	#N/A	calpain-like protein (dek1)		477	0	7.3	7.7	3388	regulatory
L05934	307	ZM	D29966	OS	816	Catalase (Cat3)	90.9	319	0	7.2	8.4	4292	structural genes/enzymes
X60135	380	ZM	D64013	OS	814	Catalase1 (Cat1)	97.4	434	0	16.6	23.0	4158	structural genes/enzymes
Z54358	389	ZM	AF162665	OS	797	catalase2 (Cat2)	93.5	291	1E-74	11.7	14.6	2135	structural genes/enzymes
AF043347	32	ZM	AF155121	OS	838	Cell wall invertase (incw4)	82.8	241	0	7.9	8.0	3282	starch metabolism
X58339	867	HV		TA	#N/A	chalcone synthase	78.8			4.0	59.6		structural gene/enzymes
AP003380	818	OS	X58339	HV	867	chalcone synthase	95.2			1.0	1.3		structural gene/enzymes
X60204	478	ZM	X58339	HV	867	chalcone synthase	90.8			0.0	0.0		structural gene/enzymes
X60205	381	ZM	AC087723	OS	817	Chalcone synthase (C2)	64.9	69	7E-29	28.1	33.8	962	structural genes/enzymes
X60204	478	ZM	AP003380	OS	818	chalcone synthase, white pollen locus	74.3	198	6E-47	14.1	16.6	2553	structural genes/enzymes
X12735	869	HV	M10144	TA	#N/A	chlorophyll a/b binding protein (cab1)	89.9			0.0	0.0		photosynthesis
AF162665	797	OS	X12735	HV	869	chlorophyll a/b binding protein (cab1)	88.8			0.0	0.0		photosynthesis
AF162665	797	OS	M10144	TA	#N/A	chlorophyll a/b binding protein (cab1)	89.0			0.0	0.0		photosynthesis
X14794	472	ZM	X12735	HV	869	chlorophyll a/b binding protein (cab1)	90.6			1.0	11.6		photosynthesis
X14794	472	ZM	M10144	HV	#N/A	chlorophyll a/b binding protein (cab1)	89.8			0.0	0.0		photosynthesis
X14794	472	ZM	AF162665	OS	797	chlorophyll a/b binding protein (cab1)	85.5	117	1E-22	14.1	16.6	2553	photosynthesis
X68678	393	ZM	L29469	OS	783	Cyclophilin.	91.3	213	0	4.2	4.6	3571	housekeeping
AF007786	20	ZM	U38199	OS	819	cystathionine gamma-synthase	90.1	557	1E-155	16.0	17.9	5450	structural genes/enzymes
D63342	302	ZM	M29259	OS	820	Cysteine proteinase inhibitor	78.6	61	3E-24	11.6	12.5	1809	structural genes/enzymes
AF063403	36	ZM	AC092388	OS	830	cytosine-5 DNA methyltransferase ZMET1	73.8	86	1E-13	26.6	20.8	3388	structural genes/enzymes
AX085557	204	ZM	X91806	OS	800	Dull1-like starch-synthase	95.3	280	5E-72	19.7	25.3	609	starch metabolism
AF225411	54	ZM	AP003106	OS	821	Exoglucanase precursor (exg1)	78.9	38	2E-10	9.0	9.9	2333	structural genes/enzymes
X83076	404	ZM	AF370029	OS	#N/A	Ferrodoxin I	82.7	77	6E-35	24.8	30.6	2539	photosynthesis

AB001386	15	ZM	D30794	OS	799	Ferrodoxin VI	80.6	66	3E-27	12.6	15.3	1511	photosynthesis
Z22760	420	ZM	X91806	OS	800	Ferrodoxin-NADP reductase	94.9	256	1E-64	8.8	9.6	1245	photosynthesis
AF101045	842	OS	AF010283	SB	531	Gene X putative transcription factor (X)	76.0			0.0	0.0		regulatory
AF434193	486	ZM	AF010283	SB	531	Gene X putative transcription factor (X)	86.8			1.0	33.7		regulatory
D63956	304	ZM	D63955	OS	851	Gmlip15 (bZIP factor)	75.8	33	0.0000002	6.9	8.5	2617	transcription factor
AF298118	64	ZM	AP002855	OS	852	Golden2	56.7	94	1E-43	12.4	15.8	3787	transcription factor
U09989	345	ZM	D31843	OS	784	H(+)-transporting ATPase (Mha1)	90.1	116	2E-56	1.5	1.8	6454	housekeeping
X03714	362	ZM	AF432915	OS	822	heat shock protein 70	80.9	373	1E-99	31.4	32.9	541	structural genes/enzymes
S59780	340	ZM	Z11920	OS	823	Heat shock protein HSP82	92.7	399	0	5.3	5.8	1322	structural genes/enzymes
AB026295	785	OS	X00937	TA	595	Histone H3	100.0			0.0	0.0		housekeeping
M13379	319	ZM	X00937	HV	595	Histone H3	100.0			0.0	0.0		housekeeping
M13379	319	ZM	AB026295	OS	785	Histone H3 (H3C4)	100.0	275	0	10.5	10.8	854	housekeeping
M13370	316	ZM	AC073166	OS	786	Histone H4 (H4C14)	100.0	225	0	19.4	19.9	824	housekeeping
X63134	382	ZM	X61280	OS	824	Hydroxy-rice glycoprotein (HRGP)	54.0	51	2E-18	15.2	21.8	657	structural genes/enzymes
X61280	824	OS	X56010	SB	540	Hydroxy-rich glycoprotein (HGRP)	60.8			1.0	2.2		structural gene/enzymes
AJ131535	424	ZM	X56010	SB	540	Hydroxy-rich glycoprotein (HGRP)	87.5			6.0	10.2		structural gene/enzymes
AF048900	153	ZM	AP002861	OS	853	Indeterminate spikelet 1 (ids1)		32	0.0000004	10.5	10.7	665	transcription factor
Z11754	419	ZM	D16685	OS	787	Lactate dehydrogenase.	58.7	230	0	11.4	11.5	1936	housekeeping
AF334960	68	ZM	M31616	OS	837	Leaf ADP-glucose pyrophosphorylase small subunit	82.7	184	3E-97	12.3	15.3	4979	starch metabolism
AF451895	488	ZM	U70541	OS	827	Liguleless1 (lg1)	84.9	236	0	12.4	18.5	5944	transcription factor
AJ224847	428	ZM	AP002836	OS	863	Me gene expressed I immature embryo	79.6	46	6E-15	16.0	17.9	5450	unknown
S57628	494	ZM	U46159	OS	826	metallonthionein-like gene	77.6	66	0.0000001	19.0	19.8	1630	structural genes/enzymes
AJ238786	430	ZM	AP003047	OS	788	Mus2 for DNA mismatch repair	71.5	32	0.000003	4.8	6.4	8068	housekeeping
AF153448	48	ZM	X15820	OS	#N/A	Nitrate reductase1	90.1	846	0	2.3	2.3	5218	nitrogen metabolism
U43930	828	ZM	U43930	OS	828	Oleosin (ole16)	87.2	232	0	8.0	11.2	1000	structural genes/enzymes
X59546	379	ZM	U26660	OS	#N/A	Pdc mRNA for pyruvate decarboxylase	93.3	409	0	9.0	11.6	2211	housekeeping
AP003052	801	OS	X63756	SB	537	Phosphoenolpyruvate carboxylase	86.2			0.0	0.0		photosynthesis
E17154	305	ZM	X63756	SB	537	Phosphoenolpyruvate carboxylase	93.0			3.0	28.4		photosynthesis
X15239	370	ZM	AP003052	OS	801	Phosphoenolpyruvate carboxylase (PEPC1)	87.2	274	0	7.3	7.4	3168	photosynthesis
Z33611	422	ZM	AP003411	OS	791	Phosphoglycerate mutase	94.4	98	8E-47	13.1	14.5	992	housekeeping
X66422	390	ZM	AP003140	OS	829	Polygalacturonase (PG)	44.2	32	0.0000009	7.8	8.2	2828	structural genes/enzymes
S94464	465	ZM	AP003725	OS	792	polyubiquitin (Ubiqutin 1)	72.2	503	0	6.2	8.3	3251	housekeeping
S94466	466	ZM	AF184279	OS	793	polyubiquitin2	85.7	1439	0	14.1	15.4	1838	housekeeping
X79065	871	ZM	AF294427	OS	789	proliferating cell nuclear antigen (PCNA)	97.7	229	0	25.4	29.9	355	housekeeping
Y11649	417	ZM	AB036786	OS	858	Protein kinase alpha subunit (CK2)	96.4	96	1E-44	7.8	8.9	6419	regulatory
AF063403	36	ZM	AC092388	OS	830	putative cytosine-5 DNA methyltransferase ZMET1	73.8	86	1E-13	14.5	17.7	3388	regulatory
AF370004	496	ZM	AC121364	OS	#N/A	pyruvate decarboxylase2		105	7E-50	3.6	6.5	3345	housekeeping
AF370006	495	ZM	AC122144	OS	831	pyruvate decarboxylase3	94.3	262	6E-67	13.6	15.4	5960	housekeeping
X15994	374	ZM	AC092750	OS	832	RAB-17		114	5E-56	13.2	22.7	1137	structural genes/enzymes
X59138	378	ZM	AC099401	OS	833	Rab28	73.1	99	2E-48	24.7	24.3	1012	structural genes/enzymes
X67733	392	ZM	AF229199	OS	859	Receptor-like protein kinase (PK1)		35	0.00000002	13.3	13.9	2034	regulatory
AF101045	842	OS	M81603	SB	330	Shrunken2 (Sh2)	100.0			10.0	17.0		starch metabolism
M81603	330	ZM	AF101045	OS	842	Shrunken2 (Sh2)	84.9	103	7E-49	5.7	6.7	5949	starch metabolism
M81603	330	ZM	M81603	SB	330	Shrunken2 (Sh2)	93.4			2.0	63.0		starch metabolism
D10838	843	OS	AJ237897	TA	630	Starch branching enzyme (Sbe1)	80.2			2.0	2.8		starch metabolism
AF072724	439	ZM	AJ237897	HV	630	Starch branching enzyme (Sbe1)	82.2			2.0	2.6		starch metabolism
AF072724	439	ZM	D10838	OS	843	Starch branching enzyme I (Sbe1)	82.3	503	0	12.1	30.0	5363	starch metabolism
AF228486	55	ZM	AB023498	OS	844	Starch branching enzyme2a (Sbe2a)		44	7E-14	7.4	5.2	4202	starch metabolism
AF072725	440	ZM	From Monsanto	OS	845	Starch branching enzymeIIb (Sbe2b/Ae)	85.2	98	6E-47	7.1	13.7	6863	starch metabolism
AF234163	864	HV	AF091802	TA	633	Starch Synthase	99.1			4.0	17.7		starch metabolism
D38221	846	OS	AF234163	HV	864	Starch Synthase	80.3			1.0	20.9		starch metabolism
D38221	846	OS	AF091802	TA	633	Starch Synthase	89.9			0.0	0.0		starch metabolism
AF036891	25	ZM	AF234163	HV	864	Starch Synthase	80.6			0.0	0.0		starch metabolism
AF036891	25	ZM	AF091802	HV	633	Starch Synthase	81.7			0.0	0.0		starch metabolism
AF036891	25	ZM	D38221	OS	846	Starch synthaseI (Ss1)	86.8	811	0	16.0	22.9	1123	starch metabolism
X02382	361	ZM	X64770	OS	847	Sucrose synthase (Sh1)	96.3	138	9E-70	18.3	24.6	5562	starch metabolism

L29418	311	ZM	AC084380	OS	848	Sucrose synthase (Sus1)	97.4	175	9E-92	14.9	20.8	7305	starch metabolism
AF030882	23	ZM	AB015615	OS	849	Sugary1 (Su1)	87.5	97	1E-46	1.1	1.5	9183	starch metabolism
U34726	353	ZM	L19435	OS	834	Superoxide dismutase 4 (sod4)	92.7	81	4E-36	11.6	15.2	2671	structural genes/enzymes
AF149016	47	ZM	AP003278	OS	835	tapetum-specific endoxylanase	93.9	918	0	16.9	33.3	2722	structural genes/enzymes
AY043215	866	OS	AF466204	SB	#N/A	Teosinte branched 1 (tb1)	61.7			2.0	36.7		regulatory
AF377732	78	ZM	AF466204	SB	#N/A	Teosinte branched 1 (tb1)	79.8			4.0	37.3		regulatory
AF348319	70	ZM	AB058397	OS	860	terminal ear1	92.0	892	0	20.9	27.7	6074	regulatory
AF264877	58	ZM	AC096688	OS	#N/A	translational elongation factor EF-TuM		268	2E-68	14.4	18.1	4646	housekeeping
X15704	372	ZM	AF182523	OS	780	tubulin A2	98.7	402	0	7.2	7.7	3612	housekeeping
M60171	328	ZM	AF182523	OS	780	tubulin A3	95.1	316	0	10.4	10.7	2590	housekeeping
X15704	372	ZM	AF182523	OS	780	tubulinA1	98.7	402	0	14.4	15.0	2229	housekeeping
AJ420859	508	ZM	AF474922	OS	794	tubulinA5	82.6	208	2E-50	3.0	3.7	2326	housekeeping
AJ420858	509	ZM	D86611	OS	795	tubulinA6	50.6	1126	0	9.1	9.0	1211	housekeeping
AF486508	724	HV	AY050175	TA	578	Waxy1	95.1			0.0	0.0		starch metabolism
AF141954	840	OS	X07931	HV	#N/A	Waxy1	87.7			0.0	0.0		starch metabolism
AF141954	840	OS	AY050175	TA	578	Waxy1	84.7			0.0	0.0		starch metabolism
X03935	363	ZM	X07931	HV	#N/A	Waxy1	87.1			0.0	0.0		starch metabolism
X03935	363	ZM	AY050175	HV	578	Waxy1	84.5			0.0	0.0		starch metabolism
X03935	363	ZM	AF141954	OS	840	Waxy1	87.2	163	7E-85	5.3	6.3	3184	starch metabolism
X91883	411	ZM	AP003105	OS	861	ZEMb	23.7	95	1E-44	17.8	27.0	1853	transcription factor
AX085359	203	ZM	AF345911	OS	862	ZMADS2 MADS-box gene	53.7	53	3E-19	10.4	11.5	4335	transcription factor