

Gene no.	GeneBank accession number of identified EST's	E-value and % of identities of ESTs and corresponding transcripts predicted by AUGUSTUS	GeneBank accession number of identified mRNA	Genome locus
1.1	ES700631	0, 100	NM_001154387 BRASSINOSTEROID INSENSITIVE 1- associated receptor kinase 1	LOC100281469 (umc1292)
1.2	DR789872	1.55e-105, 97.8	NM_001151597	LOC100278265 (umc2523)
1.3	EE173725	0, 100	NM_001154387 BRASSINOSTEROID INSENSITIVE 1- associated receptor kinase 1	LOC100281469 (umc1292)
2.1	FL133048	1.52e-151, 100	NM_001149410	LOC100275291
2.2	DY687486	0, 100		
2.3	EE295362	0, 99.8		
3.1	FK992155	0, 96.5	NM_001138663	LOC100193552
3.2	EE013166	0, 86.9		
3.3	CF675154	9.00e-163, 93.4		
4.1	AI586830	0, 100	NM_001111911 Phytoene desaturase (pds1)	No data found
4.2	FL431278	0, 98.9		
4.3	DV516499	5.58e-133, 99.6		
5.1	DN219456	0, 95.5	NM_001147392	LOC100272940
5.2	CO459182	0, 94.8		
5.3	DV492877	0, 91		
6.1	CD441348	0, 100	NM_001150745	LOC100277079
6.2	DY397626	0, 97.7		
6.3	CD440514	1.49e-150, 100		
7.1	CF032355	0, 92.2	NM_001154468 Serine palmitoyltransferase 1	LOC100281549
7.2	DT641341	2.63e-176, 99.7		
7.3	BM498806	2.31e-101, 96.1		
8.1	FL458621	0, 98.9	NM_001152336	LOC100279315 (umc2185)
8.2	FL182719	0, 99.5		
8.3	DY686105	0, 100		
9.1	CD433356	0, 94.6	NM_001175269	LOC100382534
9.2	FL452101	1.07e-158, 97		
9.3	CD433356	0, 94.6		
10.1	FL452100	0, 95.6	NM_001196985	LOC100502507
10.2	AI065585	0, 92.4		
10.3	FL470663	0, 95.3		
11.1	BE051540	6.85e-108, 93.1	No matching sequences	
11.2	AI737422	0, 88.8		
11.3	DV492877	0, 88.2		
12.1	DV503653	0, 94.8	NM_001196821	LOC100502343

12.2	DN230491	6.24e-166, 97.2		
12.3	DV503652	0, 95.2		
13.1	CO451512	2.97e-136, 90.8	NM_001175269	LOC100382534
13.2	DV171091	0, 96.7		
13.3	CO451512	3.99e-138, 90.4		
14.1	FL041027	0, 95.4	No matching sequences	
14.2	FL460501	0, 95.2		
14.3	FL103940	0, 92.9		
15.1	CD437703	0, 94.7	NM_001175269	LOC100382534
15.2	CF384417	0, 88.6		
15.3	AI770397	0, 96.1		
16.1	FL449334	0, 92.7	NM_001151416	LOC100277992
16.2	CF92014	0, 94.9		
16.3	CD526614	0, 91.2		
17.1	EE036851	1.35e-153, 100	NM_001157149 Tesmin/TSO1-like CXC domain containing protein	LOC100284254
17.2	EE159977	0, 100		
17.3	CO525111	0, 100		
18.1	EB705358	0, 97.7	NM_001137956	LOC100192758
18.2	CO456711	0, 98.8		
18.3	EB707230	1.92e-135, 100		
19.1	CF021246	0, 99.5	NM_001154263 BGGP Beta-1-3-galactosyl-O- glycosyl-glycoprotein	LOC100281345
19.2	DR803317	0, 99.8		
19.3	EB822172	0, 100		
20.1	EE153174	0, 99.2	NM_001147885	LOC100273448
20.2	EC878750	0, 100		
20.3	EE187811	3.33e-153, 100		
21.1	FL071738	0, 96.2	No matching sequences	
21.2	FL071761	0, 95.9		
21.3	DN219554	0, 88.8		
22.1	FL470298	0, 95.5	NM_001196821	LOC100502343
22.2	BG265396	0, 95		
22.3	DV492877	0, 95.7		
23.1	EB819056	1.72e-125, 100	NM_001112440	LOC732830
23.2	FL475343	0, 97.9		
23.3	EE178254	0, 99		
24.1	DT939585	0, 95	NM_001156438 Cyclin delta-2	LOC100283538
24.2	DV518063	0, 96.8		
24.3	DR964496	2.10e-146, 92	NM_001196029	LOC100501266
25.1	CA405225	0, 92.4	No matching sequences	
25.2	CK701087	1.08e-173, 91.7		
25.3	AI861641	0, 93		
26.1	FL183072	0, 100	NM_001148535	LOC100274157
26.2	FL183076	0, 99.8		
26.3	DY688374	2.19e-160, 100		
27.1	DR962736	0, 100	NM_001177286	LOC100384850
27.2	FL155278	0, 99.7		
27.3	FL119451	4.00e-158, 100		
28.1	FL071743	0, 94.6	NM_001147983	LOC100273565
28.2	EE045605	8.26e-140, 100		

28.3	FL071759	0, 94.2		
29.1	DV522358	0, 100	NM_001143521	LOC100217156
29.2	DT939972	0, 97.4		
29.3	EE042896	0, 100		
30.1	FL043545	0, 91.7	No matching sequences	
30.2	CK701087	0, 97.5		
30.3	FL470298	2.99e-154, 87.4		
31.1	EE038035	0, 99.8	NM_001137175	LOC100191748
31.2	EC886908	0, 100		
31.3	EB816122	0, 99.3		
32.1	FL451896	0, 92.6	No matching sequences	
32.2	FL163211	1.03e-166, 95.4		
32.3	FL192768	0, 94.6		
33.1	EE158277	0, 99.8	NM_001196539	LOC100501900
33.2	EE188625	0, 100		
33.3	EE158276	0, 95.4		
34.1	FL346542	0, 99.6	NM_001143225	LOC100216831
34.2	FL347070	0, 99.8	NM_001156490	LOC100283589
34.3	DN228312	0, 100		
35.1	AW017875	0, 97.3	No matching sequences	
35.2	CF631655	0, 99.5		
35.3	EE680983	0, 100		
36.1	EB405807	1.34e-100, 99.5	NM_001176131	LOC100383483
36.2	BM032586	0, 98.1		
36.3	BM417288	0, 99.2		
37.1	CK368211	0, 94.4	NM_001157319 Verprolin	LOC100284424
37.2	BG841552	0, 99.7		
37.3	DV020738	5.13e-148, 100	NM_001150808	LOC100277159
38.1	DV026704	0, 100	NM_001139290	LOC100194249
38.2	DR813331	0, 100		
38.3	DR803682	0, 99.8		
39.1	CF675160	0, 87.8	No matching sequences	
39.2	CA405225	0, 98.4		
39.3	BG265653	0, 97.7		
40.1	DY234241	0, 100	NM_001149596	LOC100275540
40.2	FL418346	0, 86.8		
40.3	DV025759	0, 99.4		
41.1	FL062547	0, 99.5	NM_001158454 ATPase	LOC100285563
41.2	FL062554	0, 95.4		
41.3	FL069420	0, 100	NM_001149278	LOC100275095
42.1	DN230491	9.70e-120, 94.7	NM_001196821	LOC100502343
42.2	GH201244	0, 89.4		
42.3	BG265649	0, 88.7		