

Identifier	log2-fold LL induced	Description	log2-fold LT-HT
JCVI_4003	10.823	no original description	
JCVI_27160	7.157	no original description	
JCVI_30920	6.017	very weakly similar to (97.4)AT4G22460 Symbols: protease inhibitor/seed storage/lipid transfer protein (LTP) family protein chr4:11	
JCVI_37606	5.844	no original description	
EE568426	5.474	no similarity	
AM385398	5.312	no similarity	
DY002991	5.299	no similarity	4.410
CD843990	5.281	no similarity	5.208
JCVI_18611	5.192	moderately similar to (381)AT1G04780 Symbols: ankyrin repeat family protein chr1:1340890-1342964 REVERSE no original desc	
JCVI_28808	5.100	weakly similar to (106)AT3G19030 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G49500.1) chr3:65641:	
JCVI_41372	5.049	no original description	
JCVI_26301	5.015	moderately similar to (240)AT1G19210 Symbols: AP2 domain-containing transcription factor, putative chr1:6626964-6627521 RE	
RC_EE564899	5.013	no similarity	
JCVI_33125	5.013	moderately similar to (229)AT4G32900 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G03010.1); similar t	4.453
ES906294	4.970	moderately similar to (293)AT1G62660 Symbols: beta-fructosidase (BFRUCT3) / beta-fructofuranosidase / invertase, vacuolar chr1	3.171
EV161824	4.953	weakly similar to (122)AT4G17510 Symbols: UCH3 UCH3; ubiquitin thiolesterase chr4:9767127-9768661 REVERSE [21484]	
EV176011	4.905	no similarity	
DT317662	4.891	very weakly similar to (80.1)AT3G19030 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G49500.1) chr3:6:	
EV224869	4.882	very weakly similar to (96.3)AT1G74930 Symbols: ORA47 ORA47; DNA binding / transcription factor chr1:28147900-28148487 F	5.609
H07416	4.808	no similarity	2.138
EE505143	4.796	no similarity	
CX191734	4.737	no similarity	
JCVI_31442	4.646	weakly similar to (144)AT1G59910 Symbols: formin homology 2 domain-containing protein / FH2 domain-containing protein chr1:	5.289
ES89985	4.637	no similarity	
JCVI_4881	4.541	very weakly similar to (87.0)AT5G15110 Symbols: pectate lyase family protein chr5:4895969-4897685 FORWARD no original des	4.252
EV218294	4.492	moderately similar to (322)AT4G37610 Symbols: BT5 BT5 (BTB and TAZ domain protein 5); protein binding / transcription regulat	
JCVI_27237	4.471	highly similar to (593)AT5G53570 Symbols: RabGAP/TBC domain-containing protein chr5:21778150-21780308 REVERSE no or	
RC_H07284	4.469	no similarity	2.801
AM395641	4.467	very weakly similar to (82.8)AT4G27657 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G27652.1) chr4:1:	2.550
JCVI_33577	4.465	no original description	
EX132042	4.465	weakly similar to (172)AT5G17350 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G03280.1); similar to un	
EE554963	4.464	weakly similar to (175)AT5G52860 Symbols: ABC transporter family protein chr5:21437002-21438771 REVERSE [20184] 1 382	5.546
EV183787	4.422	no similarity	
RC_EE556375	4.415	no similarity	
EE521586	4.415	no similarity	
JCVI_14413	4.415	no original description	
JCVI_33843	4.415	no original description	
CN728417	4.402	no similarity	
RC_H07168	4.393	no similarity	
JCVI_20042	4.368	moderately similar to (349)AT5G45340 Symbols: CYP707A3 CYP707A3 (cytochrome P450, family 707, subfamily A, polypeptide :	
JCVI_29313	4.333	no original description	
EE567997	4.319	no similarity	
EE502320	4.319	weakly similar to (108)AT1G09010 Symbols: glycoside hydrolase family 2 protein chr1:2895262-2899290 REVERSEweakly simil.	
JCVI_17766	4.310	weakly similar to (178)AT4G38060 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G65480.1); similar to un	
JCVI_33410	4.275	moderately similar to (209)AT1G12800 Symbols: S1 RNA-binding domain-containing protein chr1:4361776-4365187 REVERSE r	
JCVI_13118	4.241	moderately similar to (205)AT1G06900 Symbols: metalloendopeptidase chr1:2115154-2120634 REVERSE no original description	6.217
JCVI_2853	4.220	moderately similar to (246)AT4G26420 Symbols: GAMT1 GAMT1 chr4:13351210-13352459 REVERSE no original description	1.986
EV152439	4.208	no similarity	
DT317685	4.182	no similarity	
ES907514	4.181	weakly similar to (177)AT2G46750 Symbols: FAD-binding domain-containing protein chr2:19215513-19217979 REVERSE [2143	
JCVI_32334	4.172	no original description	
EX123581	4.161	no similarity	
RC_ES965433	4.146	no similarity	
EE559982	4.137	no similarity	
EX088739	4.137	moderately similar to (224)AT5G19190 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G06070.1); similar t	
ES967782	4.130	moderately similar to (249)AT5G38700 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G02170.1); similar t	4.630
JCVI_13314	4.115	highly similar to (554)AT4G37610 Symbols: BT5 BT5 (BTB and TAZ domain protein 5); protein binding / transcription regulator ch	
EV193345	4.115	no similarity	
JCVI_4014	4.114	no original description	
JCVI_25215	4.113	no original description	
JCVI_26377	4.107	moderately similar to (350)AT5G60390 Symbols: elongation factor 1-alpha / EF-1-alpha chr5:24306452-24307901 FORWARDmo	
JCVI_33491	4.100	highly similar to (629)AT5G25900 Symbols: CYP701A3, GA3 GA3 (GA REQUIRING 3); oxygen binding chr5:9036076-9038281	
EV111846	4.096	no similarity	
JCVI_40573	4.096	no original description	
DY021387	4.091	weakly similar to (183)AT2G47220 Symbols: 3' exoribonuclease family domain 1 protein-related chr2:19391129-19393542 FORW	
EE474947	4.088	no similarity	
EE421759	4.079	no similarity	
JCVI_20277	4.068	no original description	
JCVI_8342	4.039	moderately similar to (408)AT4G32480 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G20670.1); similar t	
EX068239	4.038	weakly similar to (122)AT1G29120 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G25770.1); similar to un	
JCVI_3842	4.013	moderately similar to (246)AT1G13880 Symbols: ELM2 domain-containing protein chr1:4749600-4750964 FORWARD no origina	
JCVI_8946	4.012	moderately similar to (247)AT4G16265 Symbols: DNA-directed RNA polymerase II, putative chr4:9202545-9203991 REVERSE n	
EV214441	4.000	weakly similar to (118)AT2G33380 Symbols: RD20 RD20 (RESPONSIVE TO DESSICATION 20); calcium ion binding chr2:1415	
AM385947	3.987	no similarity	
JCVI_23559	3.981	weakly similar to (135)AT1G72110 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G38995.1); similar to un	
JCVI_9210	3.977	weakly similar to (196)AT2G21790 Symbols: R1, RNR1 R1/RNR1 (RIBONUCLEOTIDE REDUCTASE 1); ribonucleoside-diphosp	4.761
CV546620	3.965	no similarity	
JCVI_21499	3.965	no original description	
JCVI_38610	3.952	no original description	3.454
EV157970	3.951	weakly similar to (115)AT1G75910 Symbols: EXL4 EXL4 (extracellular lipase 4); acyltransferase/ carboxylesterase/ lipase chr1:285	
EV062201	3.951	no similarity	

JCVI_36371	3.926	weakly similar to (174)AT1G04645 Symbols: self-incompatibility protein-related chr1:1293852-1294238 REVERSE no original de	
JCVI_29256	3.915	no original description	
JCVI_36938	3.915	weakly similar to (129)AT1G15140 Symbols: oxidoreductase NAD-binding domain-containing protein chr1:5210637-5212132 REV	
EE543852	3.905	no similarity	
JCVI_7003	3.891	weakly similar to (134)AT5G22875 Symbols: similar to Os04g0165500 [Oryza sativa (japonica cultivar-group)] (GB:NP_001052132	
JCVI_28578	3.889	no original description	
EE468019	3.878	weakly similar to (104)AT2G20670 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G32480.1); similar to un	1.842
EV184492	3.877	no similarity	
EV167245	3.868	no similarity	
EX120603	3.859	weakly similar to (155)AT5G10100 Symbols: trehalose-6-phosphate phosphatase, putative chr5:3157981-3160276 FORWARD [21	
EX037832	3.830	no similarity	
JCVI_7320	3.830	no original description	
JCVI_30258	3.818	no original description	3.175
EV220855	3.817	no similarity	
JCVI_18251	3.805	moderately similar to (256)AT4G30640 Symbols: F-box family protein (FBL19) chr4:14952676-14953688 FORWARD no original	3.457
JCVI_39781	3.804	moderately similar to (389)AT3G54800 Symbols: pleckstrin homology (PH) domain-containing protein / lipid-binding START doma	
EV140410	3.803	no similarity	
JCVI_37336	3.798	weakly similar to (146)AT4G08950 Symbols: phosphate-responsive protein, putative (EXO) chr4:5740375-5741319 FORWARD m	
JCVI_35228	3.782	no original description	
EV206048	3.777	no similarity	1.925
EV135474	3.774	no similarity	
JCVI_41856	3.763	moderately similar to (224)AT1G74930 Symbols: ORA47 ORA47; DNA binding / transcription factor chr1:28147900-28148487 FC	
H07737	3.757	no similarity	
BQ704822	3.753	no similarity	
EE567293	3.751	no similarity	
JCVI_36016	3.748	no original description	
JCVI_822	3.747	moderately similar to (237)AT1G72510 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G09970.1); similar t	3.982
JCVI_21629	3.744	no original description	
EV225281	3.739	weakly similar to (193)AT1G10790 Symbols: similar to hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] (TAI	
RC_EX127879	3.722	no similarity	
JCVI_23445	3.719	moderately similar to (381)AT5G15110 Symbols: pectate lyase family protein chr5:4895969-4897685 FORWARDmoderately simil	
CD814264	3.717	no similarity	
EX015947	3.715	no similarity	5.005
JCVI_31632	3.708	no original description	
EX047708	3.708	weakly similar to (153)AT3G25940 Symbols: transcription factor S-II (TFIIS) domain-containing protein chr3:9496341-9497179 FC	
JCVI_5431	3.705	moderately similar to (449)AT4G37610 Symbols: BT5 BT5 (BTB and TAZ domain protein 5); protein binding / transcription regulat	3.488
JCVI_42542	3.701	moderately similar to (217)AT2G32070 Symbols: CCR4-NOT transcription complex protein, putative chr2:13647906-13648733 RI	
EV155581	3.695	no similarity	
JCVI_23584	3.690	no original description	
EV098651	3.680	very weakly similar to (97.4)AT1G79380 Symbols: copine-related chr1:29865705-29867916 FORWARD [21477]	4.279
EV170843	3.646	no similarity	
EX136223	3.623	no similarity	
EX092440	3.623	no similarity	
EV211780	3.608	no similarity	
JCVI_14336	3.606	weakly similar to (125)AT2G42560 Symbols: late embryogenesis abundant domain-containing protein / LEA domain-containing prot	
ES968179	3.602	no similarity	
JCVI_38371	3.597	moderately similar to (228)AT1G74930 Symbols: ORA47 ORA47; DNA binding / transcription factor chr1:28147900-28148487 FC	
JCVI_36473	3.595	no original description	
EV142173	3.588	no similarity	
RC_ES960896	3.586	no similarity	
JCVI_15742	3.579	weakly similar to (175)AT1G09370 Symbols: enzyme inhibitor/ pectinesterase chr1:3024903-3025427 FORWARD no original desc	
JCVI_22116	3.565	no original description	
EE491125	3.561	no similarity	
EV218517	3.553	moderately similar to (248)AT4G37610 Symbols: BT5 BT5 (BTB and TAZ domain protein 5); protein binding / transcription regulat	
JCVI_36509	3.548	no original description	
EE554371	3.547	no similarity	
JCVI_39141	3.536	no original description	
JCVI_245	3.534	moderately similar to (202)AT5G20230 Symbols: BCB, ATBCB ATBCB (ARABIDOPSIS BLUE-COPPER-BINDING PROTEIN);	-5.903
JCVI_39139	3.529	highly similar to (502)AT4G00290 Symbols: mechanosensitive ion channel domain-containing protein / MS ion channel domain-cont	
EV110172	3.522	no similarity	
JCVI_14519	3.522	highly similar to (871)AT5G45340 Symbols: CYP707A3 CYP707A3 (cytochrome P450, family 707, subfamily A, polypeptide 3); o	2.437
JCVI_621	3.515	moderately similar to (377)AT3G53280 Symbols: CYP71B5 CYP71B5 (CYTOCHROME P450 71B5); oxygen binding chr3:19766	
JCVI_40564	3.511	very weakly similar to (82.0)AT1G10740 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G23330.1); similar	
EV065101	3.506	no similarity	
JCVI_29891	3.500	no original description	
EV116639	3.487	weakly similar to (152)AT5G17920 Symbols: ATMETS, ATMS1, ATCIMS ATCIMS (COBALAMIN-INDEPENDENT METHIONI	
JCVI_1677	3.487	moderately similar to (310)AT5G02040 Symbols: prenylated rab acceptor (PRA1) family protein chr5:401160-402468 FORWARD	
CO749260	3.479	no similarity	3.035
JCVI_42541	3.478	no original description	3.280
EV227530	3.476	no similarity	
EE517585	3.476	weakly similar to (115)AT2G32930 Symbols: ZFN2 ZFN2 (ZINC FINGER PROTEIN 2); nucleic acid binding chr2:13973067-1397	
DY005416	3.474	no similarity	
JCVI_32474	3.474	moderately similar to (221)AT3G19595 Symbols: phosphoprotein phosphatase chr3:6808591-6809514 REVERSE no original descri	
JCVI_32631	3.467	no original description	
JCVI_22123	3.466	no original description	
JCVI_8332	3.465	moderately similar to (267)AT1G14345 Symbols: oxidoreductase chr1:4899171-4899761 FORWARD no original description	
JCVI_17114	3.465	moderately similar to (344)AT1G18300 Symbols: ATNUDT4 ATNUDT4 (Arabidopsis thaliana Nudix hydrolase homolog 4); hydrol	
EV109854	3.465	very weakly similar to (95.9)AT4G32910 Symbols: similar to nucleoporin [Lotus japonicus] (GB:BAF45348.1); similar to putative nu	
JCVI_30009	3.465	weakly similar to (131)AT3G12830 Symbols: auxin-responsive family protein chr3:4079124-4079522 REVERSE no original descri	
JCVI_21587	3.459	weakly similar to (160)AT2G15580 Symbols: zinc finger (C3HC4-type RING finger) family protein chr2:6804769-6805897 FORW	
EV066619	3.453	no similarity	
EX055317	3.453	no similarity	
JCVI_6276	3.453	moderately similar to (264)AT2G01110 Symbols: UNE3, PGA2, TATC, APG2 APG2 (ALBINO AND PALE GREEN 2) chr2:8378	

H74559	3.449	weakly similar to (124)AT4G18780 Symbols: CESA8, IRX1, ATCESA8, LEW2 CESA8 (CELLULOSE SYNTHASE 8); cellulose sy	
JCVI_258	3.442	highly similar to (521)AT2G37250 Symbols: ADK, ATPADK1 ADK/ATPADK1 (ADENOSINE KINASE); adenylate kinase/ nucleo	
JCVI_20374	3.441	weakly similar to (177)AT2G25420 Symbols: similar to TPR4/WSIP2 (TOPLESS-RELATED 4) [Arabidopsis thaliana] (TAIR:AT3C	
JCVI_691	3.441	weakly similar to (190)AT1G47200 Symbols: WPP2 WPP2 (WPP domain protein 2) chr1:17300621-17301163 REVERSE no origi	
EV225615	3.438	no similarity	
EE556267	3.435	no similarity	
CV973936	3.428	no similarity	
JCVI_40410	3.415	no original description	
JCVI_11803	3.415	highly similar to (753)AT4G20850 Symbols: TPP2 TPP2 (TRIPEPTIDYL PEPTIDASE II); subtilase chr4:11160946-11169900 RE	
CD827268	3.415	moderately similar to (215)AT5G12120 Symbols: ubiquitin-associated (UBA)/TS-N domain-containing protein chr5:3916230-3918	
AM395338	3.413	no similarity	
EE560203	3.403	weakly similar to (107)AT1G62740 Symbols: stress-inducible protein, putative chr1:23234691-23237045 FORWARDvery weakly s	
EV145756	3.402	no similarity	
JCVI_39793	3.394	moderately similar to (230)AT5G19190 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G06070.1); similar t	
EE458789	3.393	no similarity	
EV134778	3.391	no similarity	
JCVI_2073	3.390	moderately similar to (209)AT5G19190 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G06070.1); similar t	
EV068783	3.390	no similarity	
EV220406	3.386	weakly similar to (177)AT5G23450 Symbols: ATLCBK1 ATLCBK1 (A. THALIANA LONG-CHAIN BASE (LCB) KINASE 1); dia	5.395
JCVI_3072	3.384	moderately similar to (312)AT3G22640 Symbols: cupin family protein chr3:8011909-8013890 REVERSEweakly similar to (129)\	
EV098037	3.381	weakly similar to (166)AT5G07200 Symbols: GA20OX3, ATGA20OX3 YAP169 (GIBBERELLIN 20 OXIDASE 3); gibberellin 20-	
EE559752	3.376	weakly similar to (167)AT5G10630 Symbols: elongation factor 1-alpha, putative / EF-1-alpha, putative chr5:3360562-3364415 FOI	
EE567148	3.376	no similarity	4.581
RC_EE566066	3.374	no similarity	
EV171552	3.373	no similarity	
JCVI_25231	3.368	no original description	
EE562045	3.368	weakly similar to (151)AT2G38400 Symbols: AGT3 AGT3 (ALANINE:GLYOXYLATE AMINOTRANSFERASE 3); alanine-glyox	
EL589415	3.362	very weakly similar to (99.4)AT3G13800 Symbols: metallo-beta-lactamase family protein chr3:4539379-4541373 FORWARD [208	
EV176799	3.361	no similarity	
JCVI_41073	3.357	weakly similar to (196)AT5G16260 Symbols: RNA recognition motif (RRM)-containing protein chr5:5311366-5315499 FORWAR	
RC_ES917680	3.357	no similarity	
JCVI_13622	3.356	no original description	
JCVI_37026	3.347	highly similar to (521)AT3G10030 Symbols: aspartate/glutamate/uridylate kinase family protein chr3:3092623-3094836 REVERSE	
AM394323	3.345	no similarity	
EV141354	3.343	no similarity	
EV190074	3.343	moderately similar to (249)AT2G41640 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G57380.1); similar t	
JCVI_15308	3.342	moderately similar to (240)AT4G29340 Symbols: PRF4 PRF4 (PROFILIN 4); actin binding chr4:14447724-14448473 FORWARD	
EV130893	3.333	no similarity	
JCVI_23734	3.333	no original description	
ES939469	3.333	no similarity	
JCVI_38985	3.330	weakly similar to (108)AT5G16590 Symbols: leucine-rich repeat transmembrane protein kinase, putative chr5:5431865-5433924 FC	
JCVI_23932	3.329	no original description	
JCVI_878	3.321	no original description	
EE560052	3.319	no similarity	
EE549860	3.318	no similarity	3.773
EV104652	3.317	no similarity	
JCVI_32464	3.315	no original description	
JCVI_26603	3.315	no original description	
EV123720	3.313	moderately similar to (315)AT5G65530 Symbols: protein kinase, putative chr5:26208070-26210052 REVERSEvery weakly similar	
EE418549	3.313	no similarity	3.239
JCVI_29432	3.308	very weakly similar to (99.0)AT4G08670 Symbols: protease inhibitor/seed storage/lipid transfer protein (LTP) family protein chr4:5	
EX104774	3.307	weakly similar to (124)AT1G06870 Symbols: signal peptidase, putative chr1:2108831-2110641 FORWARD [21826]	
JCVI_14218	3.306	moderately similar to (406)AT1G01050 Symbols: ATPPA1 ATPPA1 (ARABIDOPSIS THALIANA PYROPHOSPHORYLASE 1); i	
JCVI_31922	3.304	highly similar to (568)AT5G13670 Symbols: nodulin MtN21 family protein chr5:4407208-4408958 REVERSE no original descript	
EV178873	3.304	moderately similar to (277)AT4G27500 Symbols: PPI1 PPI1 (PROTON PUMP INTERACTOR 1) chr4:13743620-13745906 FORV	
EV008705	3.304	very weakly similar to (96.7)AT5G13470 Symbols: similar to hypothetical protein [Vitis vinifera] (GB:CAN76949.1) chr5:4318565-	
EV006275	3.296	no similarity	2.053
ES965867	3.292	no similarity	
JCVI_29354	3.285	very weakly similar to (94.0)AT5G38820 Symbols: amino acid transporter family protein chr5:15560711-15562412 FORWARD no	
L33507	3.284	weakly similar to (127)AT1G11410 Symbols: S-locus protein kinase, putative chr1:3841286-3844284 FORWARD [132]	
JCVI_13550	3.279	moderately similar to (233)AT3G07350 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G25240.1); similar t	
JCVI_37596	3.279	no original description	
EV134134	3.278	no similarity	
RC_ES966233	3.276	no similarity	
ES905207	3.275	weakly similar to (125)AT1G15170 Symbols: MATE efflux family protein chr1:5220685-5222751 FORWARD [21432]	
RC_EV090085	3.273	no similarity	
EX131063	3.271	no similarity	
JCVI_28495	3.270	weakly similar to (136)AT4G03090 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO22433.1); contains InterP	3.446
EV130706	3.269	no similarity	
JCVI_32412	3.268	moderately similar to (419)AT5G28680 Symbols: protein kinase family protein chr5:10719441-10722017 REVERSEvery weakly si	
JCVI_4664	3.261	no original description	
ES983718	3.257	no similarity	
EV119333	3.257	no similarity	
EV178393	3.257	no similarity	
EV124923	3.257	moderately similar to (367)AT1G11080 Symbols: SCPL31 SCPL31 (serine carboxypeptidase-like 31); serine carboxypeptidase chr1:	
H07278	3.248	no similarity	
EV146828	3.242	no similarity	
EV091201	3.237	no similarity	
JCVI_11606	3.236	moderately similar to (352)AT1G66080 Symbols: similar to hypothetical protein [Vitis vinifera] (GB:CAN77663.1); contains InterPr	4.215
EV096022	3.235	weakly similar to (134)AT5G42070 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO69519.1) chr5:1683634	
JCVI_36344	3.231	weakly similar to (121)AT4G14450 Symbols: Identical to Uncharacterized protein At4g14450, chloroplast precursor [Arabidopsis Th	
RC_ES969110	3.224	no similarity	
EX092285	3.220	no similarity	

JCVI_6476	3.219	no original description	
ES265746	3.218	very weakly similar to (97.4)AT4G28700 Symbols: ammonium transporter, putative chr4:14161687-14163201 FORWARD [21031]	
EE556375	3.218	no similarity	
ES983821	3.217	no similarity	
EX053177	3.212	no similarity	
CX189498	3.212	no similarity	
RC_EE557251	3.211	no similarity	
JCVI_10861	3.211	no original description	
EV203559	3.210	no similarity	
JCVI_5976	3.208	moderately similar to (398)AT2G37130 Symbols: peroxidase 21 (PER21) (P21) (PRXR5) chr2:15605304-15606813 REVERSE	
JCVI_37665	3.207	weakly similar to (166)AT5G47910 Symbols: ATRBOHD, RBOHD RBOHD (RESPIRATORY BURST OXIDASE PROTEIN D) c	
CD827326	3.202	moderately similar to (216)AT1G27040 Symbols: nitrate transporter, putative chr1:9386880-9390005 REVERSE [13979]	
EX083667	3.198	no similarity	3.237
RC_T18376	3.195	no similarity	
RC_ES967186	3.195	no similarity	
JCVI_35832	3.193	moderately similar to (237)AT3G21910 Symbols: receptor-like protein kinase-related chr3:7717379-7718412 FORWARD	no origir
JCVI_25170	3.189	no original description	
EE444936	3.184	weakly similar to (108)AT3G61550 Symbols: zinc finger (C3HC4-type RING finger) family protein chr3:22787419-22788057 FOF	
JCVI_4727	3.181	moderately similar to (258)AT1G10500 Symbols: ATCPISCA ATCPISCA (CHLOROPLAST-LOCALIZED ISCA-LIKE PROTEIN)	
DY016083	3.180	no similarity	
JCVI_31874	3.173	weakly similar to (101)AT5G11480 Symbols: GTP binding chr5:3669351-3671472 REVERSE	no original description
JCVI_38399	3.172	no original description	
AM386974	3.172	no similarity	
EV149893	3.165	no similarity	
DY023218	3.162	weakly similar to (122)AT5G54320 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G54330.1); contains Inte	
JCVI_39779	3.156	moderately similar to (259)AT1G79010 Symbols: NADH-ubiquinone oxidoreductase 23 kDa subunit, mitochondrial (TYKY) chr1:2	
EE451938	3.154	no similarity	
RC_EX133020	3.152	no similarity	
JCVI_8603	3.152	very weakly similar to (99.0)AT2G42580 Symbols: TTL3 TTL3 (TETRATRICOPETIDE-REPEAT THIOREDOXIN-LIKE 3); protei	
JCVI_40501	3.151	no original description	
ES963726	3.149	no similarity	4.124
JCVI_36285	3.146	highly similar to (723)AT2G30800 Symbols: ATVT-1, HVT1 HVT1 (HELICASE IN VASCULAR TISSUE AND TAPETUM); ATP	
JCVI_39477	3.141	no original description	
ES959392	3.141	weakly similar to (137)AT1G52930 Symbols: brix domain-containing protein chr1:19714929-19716771 FORWARD [21423]	1 415
EV118479	3.138	no similarity	
JCVI_40884	3.136	weakly similar to (146)AT4G29780 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G12010.1); similar to un	
EV102837	3.135	moderately similar to (201)AT3G15870 Symbols: fatty acid desaturase family protein chr3:5363124-5364431 FORWARD [21477]	
EV143562	3.135	no similarity	
H07682	3.134	no similarity	
EV035805	3.130	no similarity	
JCVI_38476	3.130	no original description	
EE557464	3.130	no similarity	
EV201717	3.130	no similarity	
JCVI_40442	3.128	no original description	
JCVI_33744	3.126	no original description	
EE558266	3.125	no similarity	
H07235	3.123	no similarity	
EV123208	3.116	no similarity	
EV088046	3.113	no similarity	
BQ792023	3.113	moderately similar to (214)AT3G28340 Symbols: GATL10 GATL10 (Galacturonosyltransferase-like 10); polygalacturonate 4-alpha-g	
CX266483	3.113	no similarity	
EV127293	3.111	no similarity	
ES967428	3.111	no similarity	4.943
RC_ES966572	3.110	no similarity	
EV109388	3.107	no similarity	
EV058563	3.107	weakly similar to (192)AT4G22540 Symbols: oxysterol-binding family protein chr4:11860980-11863897 REVERSE [21442]	
EE470787	3.104	no similarity	
ES906042	3.103	moderately similar to (249)AT1G72130 Symbols: proton-dependent oligopeptide transport (POT) family protein chr1:27141425-27	
RC_CD838931	3.102	no similarity	5.419
EV062941	3.100	no similarity	
AM387385	3.099	no similarity	
EV129042	3.096	no similarity	
JCVI_40989	3.096	no original description	
JCVI_19330	3.096	weakly similar to (107)AT1G32920 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G32928.1) chr1:119288	
RC_EE565485	3.096	no similarity	
EE455325	3.093	moderately similar to (283)AT4G21630 Symbols: subtilase family protein chr4:11492260-11495512 REVERSE [20178]	
DY009530	3.093	weakly similar to (146)AT1G10020 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G29310.1); similar to un	
JCVI_116	3.092	moderately similar to (444)AT4G23920 Symbols: UGE2 UGE2 (UDP-D-GLUCOSE/UDP-D-GALACTOSE 4-EPIMERASE 2); UD	
EV221567	3.090	moderately similar to (204)AT1G24510 Symbols: T-complex protein 1 epsilon subunit, putative / TCP-1-epsilon, putative / chaperon	
JCVI_15779	3.090	weakly similar to (119)AT3G27640 Symbols: transducin family protein / WD-40 repeat family protein chr3:10233544-10236704 F	
JCVI_39723	3.082	very weakly similar to (84.7)AT1G12940 Symbols: ATNRT2.5 ATNRT2.5 (NITRATE TRANSPORTER2.5); nitrate transmembrane	
EX019133	3.082	moderately similar to (266)AT5G05970 Symbols: transducin family protein / WD-40 repeat family protein chr5:1795465-1799314	
JCVI_4883	3.081	moderately similar to (253)AT1G47980 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G62730.1); similar t	
H07167	3.081	no similarity	
ES934693	3.080	no similarity	
L37981	3.076	no similarity	
RC_EE562785	3.076	no similarity	
JCVI_7486	3.076	moderately similar to (255)AT5G30495 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G54770.1); similar t	
ES985657	3.076	moderately similar to (345)AT1G25240 Symbols: epsin N-terminal homology (ENTH) domain-containing protein / clathrin assembly	
EX108697	3.075	moderately similar to (386)AT1G13300 Symbols: myb family transcription factor chr1:4556974-4558588 FORWARD [21827]	
EV063849	3.074	no similarity	3.089
JCVI_24649	3.071	moderately similar to (204)AT4G25490 Symbols: DREB1B, CBF1 CBF1 (C-REPEAT/DRE BINDING FACTOR 1); DNA binding /	5.442
JCVI_24545	3.070	moderately similar to (311)AT1G18370 Symbols: HIK HIK (HINKEL); microtubule motor chr1:6319725-6323813 REVERSE	no o

H07236	3.064	no similarity	
JCVI_13066	3.057	moderately similar to (216)AT4G30130 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G19090.1); similar t	
JCVI_30387	3.057	no original description	
EV197141	3.056	no similarity	
RC_ES902576	3.055	no similarity	
JCVI_10033	3.053	moderately similar to (312)AT2G28250 Symbols: NCRK protein kinase family protein chr2:12051081-12053416 FORWARD no or	
EV225682	3.051	no similarity	
JCVI_11929	3.051	weakly similar to (189)AT1G17920 Symbols: HDG12 HDG12 (HOMEODOMAIN GLABROUS12); transcription factor chr1:6162	
EE558921	3.050	no similarity	
JCVI_40231	3.039	weakly similar to (175)AT5G13200 Symbols: GRAM domain-containing protein / ABA-responsive protein-related chr5:4207084-4;	
EE569167	3.035	no similarity	
JCVI_15806	3.034	moderately similar to (238)AT1G05180 Symbols: AXR1 AXR1 (AUXIN RESISTANT 1); small protein activating enzyme chr1:149	
EE502065	3.032	weakly similar to (155)AT3G11930 Symbols: universal stress protein (USP) family protein chr3:3776377-3777399 FORWARD [20	
AT001747	3.031	no similarity	
JCVI_5276	3.031	weakly similar to (150)AT4G00780 Symbols: meprin and TRAF homology domain-containing protein / MATH domain-containing p	
JCVI_18058	3.030	weakly similar to (194)AT1G76990 Symbols: ACR3 ACR3 (ACT Domain Repeat 3) chr1:28938281-28940073 FORWARD no orig	
EV107976	3.029	no similarity	
AM395367	3.028	no similarity	
JCVI_35707	3.028	highly similar to (540)AT5G22760 Symbols: PHD finger family protein chr5:7571638-7577665 FORWARD no original descriptor	
RC_EE505338	3.026	no similarity	
EV210657	3.026	no similarity	
RC_EE567017	3.026	no similarity	
JCVI_23023	3.025	very weakly similar to (99.0)AT5G57990 Symbols: UBP23 UBP23 (UBIQUITIN-SPECIFIC PROTEASE 23); ubiquitin-specific prot	2.413
EE558102	3.024	no similarity	
EV089328	3.024	no similarity	
JCVI_25666	3.023	highly similar to (599)AT1G79630 Symbols: protein phosphatase 2C family protein / PP2C family protein chr1:29967824-2996981	
JCVI_3719	3.018	weakly similar to (164)AT3G29000 Symbols: calcium-binding EF hand family protein chr3:11007028-11007612 FORWARD no or	
EV143537	3.017	no similarity	
ES942636	3.015	no similarity	
RC_JCVI_42160	3.013	no original description	
JCVI_20571	3.013	weakly similar to (117)AT3G07940 Symbols: zinc finger and C2 domain protein, putative chr3:2529548-2531374 FORWARD no c	
CD819340	3.012	no similarity	
EX016181	3.011	no similarity	
JCVI_32543	3.011	weakly similar to (107)AT1G60720 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G33710.1); similar to pu	
EV131863	3.010	very weakly similar to (94.7)AT4G24380 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G65400.1); similar	
JCVI_38228	3.001	no original description	2.783
EE392272	3.000	no similarity	
ES265006	3.000	moderately similar to (219)AT5G11820 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G26050.1); contains	
EV145403	2.998	no similarity	
JCVI_35083	2.998	no original description	
JCVI_33374	2.996	no original description	
EV066024	2.993	moderately similar to (244)AT1G78400 Symbols: glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protei	4.777
CN729994	2.992	no similarity	
CV433774	2.991	no similarity	
JCVI_5052	2.989	moderately similar to (496)AT3G21560 Symbols: UGT84A2 UGT84A2; UDP-glycosyltransferase/ sinapate 1-glucosyltransferase ch	4.673
EV151455	2.988	no similarity	
JCVI_30257	2.988	no original description	
EV151244	2.987	no similarity	
JCVI_16434	2.987	no original description	
EX112711	2.985	weakly similar to (118)AT3G14690 Symbols: CYP72A15 CYP72A15 (cytochrome P450, family 72, subfamily A, polypeptide 15); o	
JCVI_16400	2.984	moderately similar to (201)AT5G54850 Symbols: unknown protein chr5:22297981-22298589 REVERSE no original description	
EE568357	2.984	weakly similar to (119)AT3G57870 Symbols: EMB1637, SCE1, AHUS5 AHUS5 (SUMO CONJUGATION ENZYME 1); ubiquitin-	3.059
DY009096	2.984	no similarity	
EV130798	2.980	no similarity	
JCVI_4761	2.978	moderately similar to (341)AT1G01980 Symbols: SEC1A, ATSEC1A ATSEC1A; electron carrier chr1:340374-341999 REVERSE	
EV200335	2.977	very weakly similar to (96.7)AT5G43100 Symbols: aspartyl protease family protein chr5:17316492-17319946 FORWARD [21490]	3.196
EV138423	2.977	no similarity	
EE521171	2.977	no similarity	
JCVI_28651	2.977	weakly similar to (171)AT1G66120 Symbols: acyl-activating enzyme 11 (AAE11) chr1:24616303-24618353 FORWARD no origin	
EV006648	2.976	no similarity	
EX132070	2.975	moderately similar to (232)AT4G25810 Symbols: XTH23, XTR6 XTR6 (XYLOGLUCAN ENDOTRANSGLYCOSYLASE 6); hydr	
EV132473	2.974	no similarity	
JCVI_21519	2.972	highly similar to (503)AT4G21326 Symbols: ATSBT3.12 ATSBT3.12; subtilase chr4:11346991-11349664 FORWARD no original	3.975
EX125813	2.969	weakly similar to (164)AT5G45280 Symbols: pectinacetylesterase, putative chr5:18364089-18366715 FORWARD [21831]	
ES961646	2.969	no similarity	
JCVI_38197	2.967	no original description	
JCVI_38756	2.965	moderately similar to (404)AT5G15130 Symbols: ATWRKY72, WRKY72 WRKY72 (WRKY DNA-binding protein 72); transcriptic	
CD840069	2.962	no similarity	
RC_EX044727	2.959	no similarity	
DW997719	2.955	no similarity	
EV028688	2.955	no similarity	
EV125134	2.955	no similarity	
EV225683	2.951	no similarity	3.483
EV165309	2.946	moderately similar to (215)AT1G22380 Symbols: ATUGT85A3 ATUGT85A3 (UDP-GLUCOSYL TRANSFERASE 85A3); glucuro	
EX098294	2.946	moderately similar to (276)AT1G27100 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G69900.1); similar t	
JCVI_39943	2.946	moderately similar to (214)AT5G24860 Symbols: FPF, FPF1 FPF1 (FLOWERING PROMOTING FACTOR 1) chr5:8541825-8542	
JCVI_11930	2.946	moderately similar to (236)AT2G01080 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G54200.1); similar t	
JCVI_17080	2.946	weakly similar to (136)AT4G04780 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G15690.1); similar to pr	
JCVI_10679	2.946	weakly similar to (187)AT4G34790 Symbols: auxin-responsive family protein chr4:16594544-16594870 FORWARDvery weakly s	
EE556656	2.944	no similarity	4.962
CX192412	2.943	moderately similar to (208)AT1G28130 Symbols: GH3.17 GH3.17 chr1:9826366-9827870 FORWARDweakly similar to (107)GH.	
JCVI_26441	2.943	highly similar to (635)AT5G59160 Symbols: PPO, TOPP2 TOPP2 (Type one serine/threonine protein phosphatase 2); protein serine/t	4.993
EX044341	2.943	weakly similar to (112)AT3G58850 Symbols: PAR2 PAR2 (PHY RAPIDLY REGULATED 2); transcription regulator chr3:217705.	

JCVI_3834	2.942	moderately similar to (402)AT1G70710 Symbols: CEL1, AtGH9B1 AtGH9B1 (ARABIDOPSIS THALIANA GLYCOSYL HYDRO	2.045
EX091671	2.939	very weakly similar to (97.4)AT4G34430 Symbols: ATSWI3D, CHB3 CHB3 (Arabidopsis thaliana switch 3D); DNA binding / transcr	
EV184017	2.939	no similarity	
ES264932	2.929	weakly similar to (168)AT5G55060 Symbols: catalytic chr5:22359305-22363626 FORWARD [15723]	3.501
EV025072	2.928	no similarity	
RC_ES967621	2.927	no similarity	
JCVI_29369	2.927	highly similar to (504)AT5G25510 Symbols: serine/threonine protein phosphatase 2A (PP2A) regulatory subunit B', putative chr5:8f	
JCVI_36732	2.926	moderately similar to (398)AT4G01950 Symbols: ATGPAT3, GPAT3 ATGPAT3/GPAT3 (GLYCEROL-3-PHOSPHATE ACYLTR	
JCVI_31135	2.925	no original description	
JCVI_18331	2.919	highly similar to (928)AT1G68560 Symbols: ATXYL1, XYL1 ATXYL1/XYL1 (ALPHA-XYLOSIDASE 1); alpha-N-arabinofurano:	
EV225843	2.915	weakly similar to (125)AT1G22710 Symbols: SUT1, ATSUC2, SUC2 SUC2 (SUCROSE-PROTON SYMPORTER 2); carbohydrate	
JCVI_33140	2.915	no original description	
ES269078	2.915	moderately similar to (213)AT4G19230 Symbols: CYP707A1 CYP707A1 (cytochrome P450, family 707, subfamily A, polypeptide	
EV090893	2.915	moderately similar to (214)ATCG01000 Symbols: YCF1.1 hypothetical protein chrC:109405-110436 FORWARDweakly similar to	
EV179477	2.915	moderately similar to (234)AT1G67830 Symbols: ATFXG1 ATFXG1 (ALPHA-FUCOSIDASE 1); alpha-L-fucosidase/ carboxylester	
JCVI_17081	2.915	weakly similar to (108)AT5G17350 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G03280.1); similar to un	
EV069452	2.914	weakly similar to (147)AT5G25470 Symbols: DNA binding chr5:8865857-8867237 REVERSE [21443]	3.346
ES954165	2.912	no similarity	
JCVI_13878	2.912	moderately similar to (466)AT5G45340 Symbols: CYP707A3 CYP707A3 (cytochrome P450, family 707, subfamily A, polypeptide	
CD815798	2.912	weakly similar to (105)AT1G13730 Symbols: nuclear transport factor 2 (NTF2) family protein / RNA recognition motif (RRM)-cont	
EE554795	2.903	weakly similar to (116)AT1G80790 Symbols: XH/XS domain-containing protein / XS zinc finger domain-containing protein chr1:3f	
JCVI_40146	2.902	moderately similar to (229)AT1G33240 Symbols: AT-GTL2 AT-GTL1 (Arabidopsis thaliana GT2-like 1); transcription factor chr1:1	
JCVI_31926	2.901	no original description	
EE502096	2.900	weakly similar to (195)AT5G55050 Symbols: GDSL-motif lipase/hydrolase family protein chr5:22354971-22356967 FORWARDw	
ES950157	2.900	no similarity	
EE526539	2.898	no similarity	
EX119892	2.897	no similarity	
EV145334	2.895	weakly similar to (199)AT3G15990 Symbols: SULTR3;4 SULTR3;4; sulfate transmembrane transporter chr3:5427087-5430685 FO	
JCVI_29889	2.893	no original description	3.057
EV211227	2.890	very weakly similar to (99.0)AT3G26460 Symbols: major latex protein-related / MLP-related chr3:9685290-9685844 REVERSE [2	
EV144897	2.889	no similarity	
JCVI_27048	2.889	moderately similar to (367)AT1G69940 Symbols: ATPPME1 ATPPME1; pectinesterase chr1:26347212-26348634 REVERSEweak	
JCVI_23849	2.888	no original description	
EE567864	2.887	no similarity	
EE561199	2.886	no similarity	
EX091761	2.882	moderately similar to (260)AT1G08990 Symbols: PGSIP5 PGSIP5 (PLANT GLYCOGENIN-LIKE STARCH INITIATION PROTEI	
JCVI_34276	2.882	weakly similar to (172)AT1G52680 Symbols: late embryogenesis abundant protein-related / LEA protein-related chr1:19622087-19	
ES988392	2.878	weakly similar to (150)AT2G32460 Symbols: MYB101, AtM1, AtMYB101 AtM1/AtMYB101/MYB101 (myb domain protein 101)	
EV103809	2.876	weakly similar to (153)AT4G13540 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G23930.1); similar to un	
JCVI_19414	2.875	no original description	
JCVI_40938	2.875	no original description	
JCVI_33601	2.873	no original description	
EX066487	2.872	no similarity	
CX190441	2.868	no similarity	
ES911338	2.868	no similarity	
EX016747	2.868	no similarity	
EE554692	2.860	no similarity	
EX103459	2.860	moderately similar to (301)AT4G33730 Symbols: pathogenesis-related protein, putative chr4:16185101-16185619 FORWARDweal	
JCVI_31867	2.858	no original description	
JCVI_23644	2.852	weakly similar to (120)AT4G29780 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G12010.1); similar to un	
EV224979	2.850	weakly similar to (182)AT5G64370 Symbols: BETA-UP BETA-UP (BETA-UREIDOPROPIONASE); beta-ureidopropionase chr5:2	
JCVI_20804	2.848	weakly similar to (113)AT3G19580 Symbols: AZF2 AZF2 (ARABIDOPSIS ZINC-FINGER PROTEIN 2) chr3:6803299-6804120 F	
JCVI_27647	2.848	weakly similar to (171)AT3G20520 Symbols: glycerophosphoryl diester phosphodiesterase family protein chr3:7162851-7165748 F	
RC_JCVI_41988	2.842	no original description	
EX137129	2.840	no similarity	2.226
CB617591	2.839	no similarity	3.317
ES969249	2.838	no similarity	
EX103165	2.838	weakly similar to (148)AT3G52960 Symbols: peroxiredoxin type 2, putative chr3:19650677-19651381 FORWARD [21826]	
EE568624	2.838	no similarity	
JCVI_37878	2.837	no original description	4.222
JCVI_26070	2.836	no original description	
CV973925	2.835	no similarity	
EL590006	2.833	no similarity	
EX130669	2.833	no similarity	
AM062480	2.833	weakly similar to (134)AT1G43040 Symbols: auxin-responsive protein, putative chr1:16186649-16186963 FORWARD [17712] 1	
ES986655	2.832	no similarity	
JCVI_35330	2.831	no original description	
RC_EE542508	2.830	no similarity	
BG543659	2.830	no similarity	
EV179248	2.830	moderately similar to (211)AT1G67230 Symbols: LINC1 LINC1 (LITTLE NUCLEI1) chr1:25155224-25159695 REVERSE [2148	
EV135166	2.829	weakly similar to (148)AT3G55280 Symbols: 60S ribosomal protein L23A (RPL23aB) chr3:20511644-20512496 FORWARDweal	
JCVI_33988	2.829	no original description	
JCVI_39493	2.828	moderately similar to (375)AT4G21640 Symbols: subtilase family protein chr4:11496846-11500630 REVERSE no original descrip	
JCVI_34341	2.825	very weakly similar to (82.4)AT1G62020 Symbols: coatomer protein complex, subunit alpha, putative chr1:22923479-22927393 FO	
EV125286	2.825	weakly similar to (174)AT1G02900 Symbols: RALFL1 RALFL1 (RALF-LIKE 1) chr1:653976-654338 REVERSE [21479]	
EV194079	2.824	moderately similar to (226)AT1G55620 Symbols: ATCLC-F, CLC-F CLC-F (CHLORIDE CHANNEL F); voltage-gated chloride cha	
DY030160	2.822	no similarity	
EV211479	2.818	no similarity	
BQ704860	2.815	no similarity	
BG543383	2.814	weakly similar to (105)AT5G61460 Symbols: MIM MIM (HYPERSENSITIVE TO MMS, IRRADIATION AND MMC); ATP bindir	
JCVI_7633	2.814	moderately similar to (213)AT3G54190 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G38630.1); similar t	
JCVI_17406	2.813	highly similar to (858)AT1G74960 Symbols: KAS2, FAB1 FAB1 (FATTY ACID BIOSYNTHESIS 1); fatty-acid synthase chr1:281	
ES947718	2.813	no similarity	

JCVI_3227	2.810	no original description	
JCVI_19496	2.809	weakly similar to (110)AT5G50460 Symbols: protein transport protein SEC61 gamma subunit, putative chr5:20569394-20569735 F	
EV112414	2.809	no similarity	
JCVI_3208	2.808	no original description	
CV545114	2.808	moderately similar to (223)AT5G09590 Symbols: HSC70-5, mtHSC70-2 mtHSC70-2 (HEAT SHOCK PROTEIN 70); ATP binding ,	
ES898193	2.807	no similarity	
EV130046	2.806	no similarity	
DY001809	2.806	no similarity	
EE564722	2.804	no similarity	
EV197862	2.804	no similarity	
EV216622	2.804	no similarity	
JCVI_13374	2.804	moderately similar to (303)AT1G70260 Symbols: nodulin MtN21 family protein chr1:26460730-26463001 REVERSE no original d	
EE560668	2.803	no similarity	
JCVI_23275	2.803	moderately similar to (218)AT1G21280 Symbols: similar to hypothetical protein [Vitis vinifera] (GB:CAN81001.1); contains InterPr	
JCVI_20749	2.800	moderately similar to (497)AT4G35850 Symbols: pentatricopeptide (PPR) repeat-containing protein chr4:16983641-16986684 FOR	
JCVI_7567	2.798	no original description	3.413
JCVI_20088	2.794	moderately similar to (441)AT4G19540 Symbols: similar to HCF101 (HIGH-CHLOROPHYLL-FLUORESCENCE 101), ATP bindi	
EV143743	2.791	no similarity	
EV126936	2.791	no similarity	-1.053
EV147210	2.790	no similarity	
JCVI_41628	2.790	moderately similar to (229)AT5G18460 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G23340.1); similar t	
EE529933	2.790	moderately similar to (211)AT1G66880 Symbols: serine/threonine protein kinase family protein chr1:24950591-24959101 FORWA	-1.029
JCVI_19284	2.790	very weakly similar to (88.6)AT1G23550 Symbols: SRO2 SRO2 (SIMILAR TO RCD ONE 2); NAD+ ADP-ribosyltransferase chr1:f	
JCVI_9252	2.788	highly similar to (693)AT1G29980 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G34510.1); similar to unl	
JCVI_735	2.787	no original description	
RC_EE564048	2.787	no similarity	
EE420291	2.786	no similarity	
JCVI_33906	2.786	highly similar to (771)AT2G32860 Symbols: glycosyl hydrolase family 1 protein chr2:13947310-13950673 FORWARDmoderately	
JCVI_37840	2.784	no original description	
JCVI_888	2.784	moderately similar to (386)AT4G00040 Symbols: chalcone and stilbene synthase family protein chr4:14653-15897 FORWARDwea	
JCVI_38737	2.782	moderately similar to (435)AT4G12420 Symbols: SKU5 SKU5 (skewed 5); copper ion binding chr4:7349938-7352865 REVERSEn	
EV219578	2.782	moderately similar to (335)AT2G30210 Symbols: LAC3 LAC3 (laccase 3); copper ion binding / oxidoreductase chr2:12894812-128	
EV128384	2.782	no similarity	
JCVI_33673	2.782	very weakly similar to (92.0)AT3G44870 Symbols: S-adenosyl-L-methionine:carboxyl methyltransferase family protein chr3:163932	
H07270	2.780	no similarity	
JCVI_39393	2.778	weakly similar to (186)AT1G75140 Symbols: Identical to Uncharacterized membrane protein At1g75140 [Arabidopsis Thaliana] (GE	
CN728444	2.778	weakly similar to (120)AT5G15470 Symbols: GAUT14 GAUT14 (Galacturonosyltransferase 14); polygalacturonate 4-alpha-galactur	
EE408514	2.774	no similarity	
EV165860	2.774	no similarity	
JCVI_26896	2.774	moderately similar to (436)AT1G68020 Symbols: TPS6, ATTPS6 ATTPS6 (Arabidopsis thaliana trehalose phosphatase/synthase 6); t	
EE530227	2.773	no similarity	3.812
EE567771	2.773	no similarity	
JCVI_32957	2.773	moderately similar to (270)AT3G09230 Symbols: ATMYB1 ATMYB1 (MYB DOMAIN PROTEIN 1); DNA binding / transcription	
JCVI_22325	2.767	weakly similar to (196)AT3G19680 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G50040.1); similar to un	
EE558033	2.767	no similarity	
JCVI_22321	2.767	no original description	
ES968425	2.761	no similarity	
EE534462	2.760	no similarity	
H07351	2.759	very weakly similar to (85.9)AT5G17350 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G03280.1); similar	
CD836896	2.757	weakly similar to (155)AT3G29670 Symbols: transferase family protein chr3:11530431-11531786 FORWARD [13981]	
JCVI_2034	2.755	no original description	4.045
EE565488	2.753	no similarity	
ES966938	2.751	no similarity	
EE560192	2.751	no similarity	
JCVI_20970	2.751	no original description	
JCVI_33737	2.751	no original description	
JCVI_5358	2.750	weakly similar to (169)AT1G30120 Symbols: PDH-E1 BETA PDH-E1 BETA (PYRUVATE DEHYDROGENASE E1 BETA); pyru	
AM058692	2.750	weakly similar to (179)AT4G22250 Symbols: zinc finger (C3HC4-type RING finger) family protein chr4:11767697-11768341 REV	
JCVI_16557	2.747	moderately similar to (273)AT3G50060 Symbols: MYB77 MYB77; DNA binding / transcription factor chr3:18569129-18570034 R	
EX116638	2.743	no similarity	
JCVI_33378	2.743	moderately similar to (445)AT1G22760 Symbols: PAB3 PAB3 (POLY(A) BINDING PROTEIN 3); RNA binding chr1:8055588-80	
EE501925	2.737	no similarity	2.738
JCVI_19644	2.734	weakly similar to (128)AT1G48140 Symbols: dolichol-phosphate mannosyltransferase-related chr1:17787071-17787583 FORWAR	
EV083865	2.734	no similarity	
EV128635	2.732	no similarity	2.819
CO749390	2.732	no similarity	
EV112275	2.732	no similarity	
EV226371	2.731	no similarity	
CD819972	2.731	no similarity	
JCVI_16590	2.729	moderately similar to (372)AT3G10480 Symbols: ANAC050 ANAC050 chr3:3264415-3266786 FORWARDweakly similar to (18	
JCVI_32778	2.729	weakly similar to (180)AT5G45970 Symbols: ROP7, ATRAC2, ARAC2, ATROP7 ARAC2 (RHO-RELATED PROTEIN FROM PL	
CD840408	2.727	very weakly similar to (84.3)AT5G07550 Symbols: ATGRP19, GRP19 GRP19 (Glycine rich protein 19) chr5:2388619-2389185 RE	
JCVI_24817	2.721	weakly similar to (188)AT2G37980 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G01100.1); similar to un	
JCVI_38370	2.720	moderately similar to (416)AT4G29780 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G12010.1); similar t	
DY004458	2.717	moderately similar to (308)AT4G20200 Symbols: terpene synthase/cyclase family protein chr4:10908682-10911161 REVERSEwea	
EE460675	2.716	no similarity	
EV066585	2.712	weakly similar to (148)AT3G15810 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G80120.1); similar to un	
EE562412	2.711	no similarity	
JCVI_28897	2.710	weakly similar to (101)AT1G67030 Symbols: ZFP6 ZFP6 (ZINC FINGER PROTEIN 6); nucleic acid binding / transcription factor/ z	
JCVI_32592	2.709	moderately similar to (294)AT2G46960 Symbols: CYP709B1 CYP709B1 (cytochrome P450, family 709, subfamily B, polypeptide 1	
RC_EX083955	2.709	no similarity	
RC_EV010251	2.708	no similarity	
EV174730	2.707	very weakly similar to (95.9)CYB_SPEAN [21486] 62 439 786	3.344

EV131193	2.701	very weakly similar to (95.9)AT2G19880 Symbols: ceramide glucosyltransferase, putative chr2:8588660-8592200 FORWARD [214	
EX056651	2.701	no similarity	
JCVI_12359	2.696	moderately similar to (457)AT4G01810 Symbols: protein transport protein-related chr4:776734-779802 REVERSE no original desc	
EV111301	2.692	no similarity	2.674
EV018309	2.690	no similarity	
ES901996	2.688	weakly similar to (137)AT1G04590 Symbols: similar to pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] (TA	
JCVI_16560	2.688	weakly similar to (112)AT5G10660 Symbols: calmodulin-binding protein-related chr5:3370554-3371777 FORWARD no original d	
EE478991	2.687	moderately similar to (278)AT5G25170 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G25190.1); similar t	
ES967033	2.685	no similarity	5.132
JCVI_25518	2.684	highly similar to (528)AT5G15130 Symbols: ATWRKY72, WRKY72 WRKY72 (WRKY DNA-binding protein 72); transcription fac	
EE561031	2.683	no similarity	
JCVI_16974	2.681	very weakly similar to (84.7)AT3G19680 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G50040.1); similar	
JCVI_30949	2.680	no original description	3.888
ES954371	2.678	no similarity	
CD840090	2.677	no similarity	
EE551115	2.676	no similarity	
JCVI_40144	2.676	no original description	
EV194343	2.675	weakly similar to (140)AT4G32551 Symbols: RON2, LUG LUG (LEUNIG) chr4:15707869-15713365 FORWARD [21489] 21 705	5.118
RC_ES954436	2.675	no similarity	3.067
CD816610	2.674	moderately similar to (218)AT2G24220 Symbols: ATPUP5 ATPUP5 (Arabidopsis thaliana purine permease 5); purine transmembran	
EE466624	2.672	weakly similar to (101)AT1G52695 Symbols: phospholipase/carboxylesterase family protein chr1:19625079-19627056 REVERSE	
EV101236	2.672	no similarity	
EV182486	2.672	very weakly similar to (100)AT5G57560 Symbols: XTH22, TCH4 TCH4 (TOUCH 4); hydrolase, acting on glycosyl bonds / xylogluc	
JCVI_21618	2.672	weakly similar to (168)AT5G02240 Symbols: binding / catalytic/ coenzyme binding chr5:451500-452982 FORWARD no original d	
EV170947	2.671	moderately similar to (311)AT1G76130 Symbols: ATAMY2, AMY2 AMY2/ATAMY2 (ALPHA-AMYLASE-LIKE 2); alpha-amylase	
JCVI_38749	2.669	moderately similar to (348)AT5G04710 Symbols: aspartyl aminopeptidase, putative chr5:1357274-1360129 REVERSE no original	
JCVI_40532	2.669	moderately similar to (297)AT2G21790 Symbols: R1, RNR1 R1/RNR1 (RIBONUCLEOTIDE REDUCTASE 1); ribonucleoside-diphosph	1.773
EX131720	2.665	no similarity	5.534
CX270831	2.665	no similarity	
ES942692	2.663	no similarity	
EX078964	2.663	no similarity	
JCVI_21884	2.663	weakly similar to (108)AT4G00730 Symbols: AHDP, ANL2 ANL2 (ANTHOCYANINLESS 2) chr4:301071-304103 REVERSE no	
EV166537	2.662	no similarity	
EE502315	2.661	no similarity	
EV177552	2.661	no similarity	
JCVI_27398	2.661	very weakly similar to (100)AT1G63670 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G45900.1); similar	
EV141703	2.661	very weakly similar to (92.0)AT3G44870 Symbols: S-adenosyl-L-methionine:carboxyl methyltransferase family protein chr3:163932	
EV091861	2.661	no similarity	
DY029976	2.660	no similarity	
JCVI_20274	2.659	weakly similar to (182)AT2G30020 Symbols: protein phosphatase 2C, putative / PP2C, putative chr2:12821514-12822981 FORWA	
ES984449	2.658	no similarity	
CD821578	2.657	very weakly similar to (86.7)AT2G23148 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G23142.1); contain	
ES968363	2.653	no similarity	
JCVI_18078	2.653	weakly similar to (194)AT4G30070 Symbols: LCR59 LCR59 (Low-molecular-weight cysteine-rich 59) chr4:14697555-14698321 F	
JCVI_32239	2.653	no original description	
EX065570	2.649	no similarity	4.486
EV015620	2.649	no similarity	
EV098177	2.648	moderately similar to (248)AT5G53490 Symbols: thylakoid luminal 17.4 kDa protein, chloroplast chr5:21740714-21741847 REVE	3.916
EV148318	2.648	no similarity	
EE563880	2.646	no similarity	
JCVI_32289	2.646	moderately similar to (329)AT5G54280 Symbols: ATATM2, ATMYOS1, ATM4, ATM2 ATM2 (ARABIDOPSIS THALIANA MYO	
JCVI_37760	2.643	no original description	
EV142725	2.642	moderately similar to (259)AT4G26870 Symbols: aspartyl-tRNA synthetase, putative / aspartate--tRNA ligase, putative chr4:135053	
EE561569	2.642	no similarity	3.758
JCVI_1715	2.642	weakly similar to (196)AT1G54010 Symbols: myosinase-associated protein, putative chr1:20162522-20164415 REVERSE no orig	
EE549460	2.641	no similarity	
JCVI_18525	2.641	weakly similar to (125)AT3G61980 Symbols: serine protease inhibitor, Kazal-type family protein chr3:22967319-22967672 REVEI	
JCVI_33576	2.641	moderately similar to (322)AT4G27480 Symbols: glycosyltransferase family 14 protein / core-2/L-branching enzyme family protein	
EV142990	2.635	weakly similar to (119)AT2G40000 Symbols: HSPRO2, ATHSPRO2 similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3C	
RC_EE560830	2.633	no similarity	
EV160672	2.632	moderately similar to (346)AT4G19170 Symbols: NCED4 NCED4 (NINE-CIS-EPOXYCAROTENOID DIOXYGENASE 4) chr4:1	
EV153595	2.632	very weakly similar to (100)AT5G07670 Symbols: F-box family protein chr5:2430422-2432066 FORWARD [21484]	
JCVI_30766	2.630	no original description	
EV223305	2.629	moderately similar to (207)AT1G02310 Symbols: glycosyl hydrolase family protein 5 / cellulase family protein / (1-4)-beta-mannan e	
ES998196	2.629	no similarity	
ES913930	2.628	moderately similar to (285)AT3G25560 Symbols: NIK2 NIK2 (NSP-INTERACTING KINASE 2); protein kinase chr3:9280919-928	2.529
EV059775	2.626	no similarity	
EX106682	2.626	no similarity	
JCVI_36799	2.626	no original description	
JCVI_38738	2.626	weakly similar to (185)AT1G20870 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G54850.1); similar to un	
RC_EV146547	2.625	no similarity	
ES264508	2.625	no similarity	
EX072529	2.625	moderately similar to (259)AT4G17220 Symbols: ATMAP70-5 ATMAP70-5 (microtubule-associated proteins 70-5); microtubule bir	
EV000049	2.625	no similarity	
JCVI_29724	2.623	weakly similar to (174)AT1G05000 Symbols: tyrosine specific protein phosphatase family protein chr1:1425659-1428392 FORWA	
JCVI_35306	2.623	very weakly similar to (89.4)AT1G18610 Symbols: kelch repeat-containing protein chr1:6405771-6408823 FORWARD no original	
EV200364	2.623	no similarity	
EV066988	2.622	no similarity	
EE501957	2.621	weakly similar to (142)AT5G25610 Symbols: RD22 RD22 (RESPONSIVE TO DESSICATION 22) chr5:8914501-8916687 REVEI	
JCVI_16483	2.620	moderately similar to (310)AT3G48080 Symbols: lipase class 3 family protein / disease resistance protein-related chr3:17764089-17	
JCVI_40900	2.619	highly similar to (572)AT5G64120 Symbols: peroxidase, putative chr5:25676777-25678172 REVERSEmoderately similar to (393)	
EV181783	2.616	weakly similar to (187)AT1G12200 Symbols: flavin-containing monooxygenase family protein / FMO family protein chr1:4137625	
JCVI_11277	2.616	moderately similar to (379)AT3G23250 Symbols: MYB15, AtY19, AtMYB15 AtMYB15/AtY19/MYB15 (myb domain protein 15);	

JCVI_32712	2.615	no original description	
EV218651	2.615	moderately similar to (422)AT3G53480 Symbols: PDR9, ATPDR9 ATPDR9/PDR9 (PLEIOTROPIC DRUG RESISTANCE 9); ATP	
AM390906	2.614	no similarity	
EV109714	2.612	no similarity	
EX118712	2.611	no similarity	
JCVI_8780	2.609	moderately similar to (455)AT5G61820 Symbols: similar to MtN19-like protein [Pisum sativum] (GB:AAU14999.2); contains InterP	
CD814116	2.609	moderately similar to (350)AT1G43860 Symbols: transcription factor chr1:16624684-16626825 REVERSE [13977]	
EV135073	2.609	moderately similar to (240)AT4G28680 Symbols: tyrosine decarboxylase, putative chr4:14155254-14158552 FORWARDweakly si	
EV123693	2.608	no similarity	4.427
EE402903	2.605	no similarity	
JCVI_33190	2.605	no original description	
EV105906	2.604	no similarity	
EV175012	2.603	no similarity	2.019
JCVI_18635	2.602	moderately similar to (225)AT1G14420 Symbols: AT59 AT59 (Arabidopsis homolog of tomato LAT59); lyase/ pectate lyase chr1:4	-3.239
RC_EE568847	2.602	no similarity	
CD828816	2.601	weakly similar to (123)AT4G30210 Symbols: AR2, ATR2 ATR2 (ARABIDOPSIS P450 REDUCTASE 2) chr4:14796906-1480058	
JCVI_15552	2.599	weakly similar to (134)AT5G65490 Symbols: Identical to SGT1 protein homolog At5g65490 [Arabidopsis Thaliana] (GB:Q9LSM5)	
JCVI_2697	2.599	moderately similar to (263)AT4G23600 Symbols: JR2, CORI3 CORI3 (CORONATINE INDUCED 1, JASMONIC ACID RESPON	3.306
EE565377	2.599	no similarity	
JCVI_17709	2.597	moderately similar to (349)AT5G58430 Symbols: ATEXO70B1 ATEXO70B1 (exocyst subunit EXO70 family protein B1); protein b	
EV204447	2.596	no similarity	
EE567461	2.596	very weakly similar to (83.2)AT5G58375 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G14602.1); similar	
JCVI_4347	2.596	weakly similar to (155)AT1G21090 Symbols: hydroxyproline-rich glycoprotein family protein chr1:7384843-7386188 FORWARD	
EV225681	2.596	no similarity	
EV111282	2.596	no similarity	
RC_H74834	2.593	no similarity	
ES991417	2.589	no similarity	
EE505236	2.587	no similarity	
JCVI_42567	2.586	very weakly similar to (88.6)TRAC9_MAIZE no original description	
JCVI_11379	2.586	no original description	
EV197309	2.584	no similarity	
AM386194	2.582	no similarity	1.873
EX079964	2.579	weakly similar to (171)AT4G31115 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G04440.1); similar to pr	
EX089596	2.579	no similarity	
JCVI_35042	2.579	no original description	
ES967274	2.578	no similarity	
JCVI_29618	2.576	no original description	
JCVI_8926	2.575	very weakly similar to (84.3)AT4G09030 Symbols: ATAGP10, AGP10 AGP10 (Arabinogalactan protein 10) chr4:5792246-5792625	
JCVI_14001	2.574	no original description	3.670
RC_EE567222	2.573	no similarity	
CV546475	2.573	no similarity	
EE564626	2.572	weakly similar to (200)AT3G28570 Symbols: AAA-type ATPase family protein chr3:10711771-10713126 FORWARD [20153] 62	
AT000748	2.572	no similarity	
JCVI_26942	2.570	moderately similar to (279)AT2G46960 Symbols: CYP709B1 CYP709B1 (cytochrome P450, family 709, subfamily B, polypeptide 1	
EV147827	2.569	no similarity	
JCVI_26015	2.566	moderately similar to (391)AT1G61360 Symbols: S-locus lectin protein kinase family protein chr1:22641532-22644639 REVERSE	
JCVI_7955	2.563	moderately similar to (319)AT1G25280 Symbols: AtTLP10 AtTLP10 (TUBBY LIKE PROTEIN 10) chr1:8865663-8866595 FORV	
EE504791	2.563	weakly similar to (103)AT5G56670 Symbols: 40S ribosomal protein S30 (RPS30C) chr5:22952639-22953207 REVERSE [20159]	
EE552012	2.561	no similarity	2.413
JCVI_6555	2.559	moderately similar to (339)AT5G55530 Symbols: C2 domain-containing protein chr5:22511665-22512882 FORWARD no original	
EV209618	2.556	no similarity	
EE567593	2.556	no similarity	
CD820975	2.556	moderately similar to (298)AT1G63090 Symbols: ATPP2-A11 ATPP2-A11 (Phloem protein 2-A11); carbohydrate binding chr1:233	
JCVI_26699	2.556	weakly similar to (157)AT3G50240 Symbols: KICP-02 KICP-02; microtubule motor chr3:18634362-18639766 REVERSE no origi	
JCVI_10706	2.553	moderately similar to (434)AT5G20710 Symbols: BGAL7 BGAL7 (beta-galactosidase 7); beta-galactosidase chr5:7010538-7013996	
L38061	2.551	no similarity	
JCVI_5171	2.551	no original description	
EX016624	2.550	no similarity	
EV227113	2.550	no similarity	
EX123468	2.550	very weakly similar to (84.7)AT4G09060 Symbols: structural molecule chr4:5797778-5800250 REVERSE [21830]	
DN961174	2.550	moderately similar to (218)AT4G16260 Symbols: glycosyl hydrolase family 17 protein chr4:9200310-9201457 REVERSEweakly s	
EV189060	2.549	no similarity	
JCVI_20438	2.548	no original description	
JCVI_12687	2.548	no original description	
JCVI_35269	2.543	no original description	
RC_ES968472	2.541	no similarity	2.562
JCVI_19090	2.540	highly similar to (602)AT3G50270 Symbols: transferase family protein chr3:18646908-18648260 FORWARDvery weakly similar t	
JCVI_38132	2.536	no original description	
JCVI_42207	2.536	no original description	
CV546580	2.536	weakly similar to (113)AT5G40010 Symbols: AATP1 AATP1 (AAA-ATPASE 1); ATP binding / ATPase chr5:16037446-16038996	
EE567670	2.534	no similarity	1.736
RC_EV010268	2.534	no similarity	3.010
ES937722	2.534	weakly similar to (107)AT4G21050 Symbols: Dof-type zinc finger domain-containing protein chr4:11238452-11239084 FORWAR	
JCVI_25351	2.532	no original description	
EX135989	2.530	moderately similar to (209)AT5G07050 Symbols: nodulin MtN21 family protein chr5:2191534-2193417 REVERSE [21833] 1 622	
JCVI_8551	2.527	moderately similar to (225)AT5G42380 Symbols: CML39, CML37 CML37/CML39; calcium ion binding chr5:16959986-16960543	
ES968335	2.526	no similarity	
JCVI_38998	2.524	moderately similar to (214)AT2G37430 Symbols: zinc finger (C2H2 type) family protein (ZAT11) chr2:15713533-15714069 FORV	
EX055496	2.523	moderately similar to (286)AT4G28500 Symbols: ANAC073 ANAC073 (Arabidopsis NAC domain containing protein 73); transcript	
RC_ES998081	2.522	no similarity	
EE438838	2.521	no similarity	
EE505147	2.519	no similarity	3.882
JCVI_35	2.518	moderately similar to (318)AT1G27730 Symbols: ZAT10, STZ STZ (SALT TOLERANCE ZINC FINGER); nucleic acid binding / tr	

EV081248	2.514	no similarity	
CD836392	2.512	no similarity	
EE565961	2.511	no similarity	
JCVI_41847	2.511	moderately similar to (360)AT5G40250 Symbols: zinc finger (C3HC4-type RING finger) family protein chr5:16103284-16104414	
EE520604	2.511	weakly similar to (107)AT2G36695 Symbols: unknown protein chr2:15389781-15390377 FORWARD [20185] 1 412 466	
JCVI_36083	2.510	no original description	
JCVI_22141	2.510	moderately similar to (290)AT5G42240 Symbols: SCPL42 SCPL42 (serine carboxypeptidase-like 42); serine carboxypeptidase chr5	
EV222836	2.510	weakly similar to (112)AT3G15450 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G27450.1); similar to un	
EV108550	2.506	very weakly similar to (95.9)AT4G21060 Symbols: galactosyltransferase family protein chr4:11240741-11244871 FORWARD [214	
AM395149	2.506	no similarity	
JCVI_23592	2.505	no original description	
ES968374	2.504	no similarity	
EE566355	2.502	no similarity	
CB617607	2.501	no similarity	
EV052696	2.500	no similarity	
EV108926	2.499	no similarity	
EX117651	2.499	no similarity	
JCVI_37499	2.497	weakly similar to (166)AT1G11260 Symbols: STP1 STP1 (SUGAR TRANSPORTER 1); carbohydrate transmembrane transporter/ st	
JCVI_35120	2.496	no original description	
JCVI_40364	2.496	very weakly similar to (86.7)AT1G04100 Symbols: IAA10 IAA10 (indoleacetic acid-induced protein 10); transcription factor chr1:10	
EE411223	2.496	moderately similar to (251)AT2G21410 Symbols: VHA-A2 VHA-A2 (VACUOLAR PROTON ATPASE A2); ATPase chr2:916978	
RC_EX039565	2.494	no similarity	
RC_EV086118	2.493	no similarity	
JCVI_16640	2.493	moderately similar to (359)AT1G74000 Symbols: SS3 SS3 (STRICTOSIDINE SYNTHASE 3) chr1:27832927-27835062 REVERS	
ES937886	2.493	weakly similar to (115)AT2G34400 Symbols: pentatricopeptide (PPR) repeat-containing protein chr2:14523317-14525265 FORWA	
EV148460	2.492	no similarity	
CA992539	2.491	no similarity	
JCVI_28795	2.491	weakly similar to (130)AT3G53500 Symbols: RSZ32 RSZ32; nucleic acid binding chr3:19845535-19847485 REVERSE no original	
JCVI_39852	2.491	moderately similar to (238)AT4G28980 Symbols: CDKF;1, CAK1AT CAK1AT/CDKF;1 (CDK-ACTIVATING KINASE 1AT); cycl	3.288
EV207489	2.489	no similarity	
ES992292	2.489	no similarity	
RC_H07491	2.489	no similarity	
EV128764	2.487	no similarity	
EE411627	2.484	no similarity	
ES956265	2.484	no similarity	
AM394984	2.481	no similarity	
EX101229	2.481	no similarity	
EV170707	2.480	no similarity	
JCVI_11944	2.479	moderately similar to (479)AT3G16430 Symbols: jacalin lectin family protein chr3:5581836-5582965 FORWARD no original desc	3.354
EE530249	2.479	weakly similar to (137)AT3G51290 Symbols: proline-rich family protein chr3:19050959-19053416 FORWARD [16815]	
ES968293	2.479	no similarity	
JCVI_23109	2.478	highly similar to (830)AT1G14610 Symbols: VALRS, TWN2 TWN2 (TWIN 2); ATP binding / aminoacyl-tRNA ligase chr1:500845	
JCVI_10308	2.477	no original description	
EE462905	2.476	no similarity	
EE566253	2.476	no similarity	
RC_ES965015	2.475	no similarity	
EE519672	2.474	weakly similar to (167)AT1G13570 Symbols: F-box family protein chr1:4642525-4643927 REVERSE [20185]	
JCVI_10627	2.474	moderately similar to (206)AT3G57860 Symbols: UVI4-LIKE UVI4-LIKE (UV-B-INSENSITIVE 4-LIKE) chr3:21437710-214387	
JCVI_39807	2.474	very weakly similar to (89.0)AT1G61310 Symbols: disease resistance protein (CC-NBS-LRR class), putative chr1:22616831-226196	
JCVI_6755	2.472	highly similar to (610)AT1G19640 Symbols: JMT JMT (JASMONIC ACID CARBOXYL METHYLTRANSFERASE); jasmonate O	
EE567417	2.470	no similarity	
EE567519	2.467	no similarity	
EV110425	2.467	no similarity	
ES923362	2.465	no similarity	
JCVI_24975	2.465	no original description	-1.978
JCVI_18683	2.465	no original description	
JCVI_23743	2.465	no original description	
JCVI_3775	2.465	moderately similar to (384)AT2G02790 Symbols: IQD29 IQD29 (IQ-domain 29); calmodulin binding chr2:788707-790945 FORW/	2.102
JCVI_25743	2.465	weakly similar to (119)AT5G23610 Symbols: similar to SWI1 (SWITCH1), phospholipase C [Arabidopsis thaliana] (TAIR:AT5G51:	
EV218262	2.464	no similarity	
CV432107	2.462	very weakly similar to (100)AT4G14130 Symbols: XTR7 XTR7 (XYLOGLUCAN ENDOTRANSGLYCOSYLASE 7); hydrolase, ac	4.266
EX136112	2.461	no similarity	
JCVI_21020	2.461	weakly similar to (141)AT2G40000 Symbols: HSPRO2, ATHSPRO2 similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3C	
DY003910	2.460	no similarity	
EV127421	2.460	weakly similar to (115)AT1G74930 Symbols: ORA47 ORA47; DNA binding / transcription factor chr1:28147900-28148487 FORW	3.516
BG543778	2.459	weakly similar to (140)NIA1_BRANA [8791]	
EV041604	2.456	no similarity	
EV109384	2.455	no similarity	
JCVI_3778	2.454	very weakly similar to (87.0)AT2G37980 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G01100.1); similar	
JCVI_30202	2.454	weakly similar to (118)AT5G02490 Symbols: heat shock cognate 70 kDa protein 2 (HSC70-2) (HSP70-2) chr5:550294-552563 RE	
RC_ES969166	2.454	no similarity	
ES966630	2.454	no similarity	
JCVI_34162	2.453	highly similar to (551)AT1G05500 Symbols: SYTE, ATSYTE, NTMC2TYPE2.1, NTMC2T2.1 ATSYTE/NTMC2T2.1/NTMC2TYF	
EV223131	2.453	no similarity	
EE446048	2.450	weakly similar to (130)AT5G36290 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G25520.1); similar to un	1.841
AM395058	2.448	no similarity	
ES991160	2.448	no similarity	
CX189649	2.448	moderately similar to (211)AT5G09920 Symbols: ATRPB15.9, RPB15.9.9, RPB15.9 RPB15.9 (RNA polymerase II 15.9) chr5:309	
JCVI_17461	2.446	no original description	
JCVI_21988	2.445	moderately similar to (332)AT3G60830 Symbols: ARP7, ATARP7 ATARP7 (ACTIN-RELATED PROTEIN 7); structural constituen	
JCVI_12908	2.444	weakly similar to (176)ATMG00310 Symbols: ORF154 hypothetical protein chrM:90883-91347 REVERSE no original description	
EV098664	2.444	no similarity	
JCVI_26516	2.441	weakly similar to (196)AT2G17440 Symbols: leucine-rich repeat family protein chr2:7578413-7580488 FORWARD no original des	

ES932617	2.439	no similarity	
JCVI_42191	2.438	weakly similar to (112)AT5G23570 Symbols: SGS3 SGS3 (SUPPRESSOR OF GENE SILENCING 3) chr5:7943624-7945877 FOR	
EE505116	2.438	no similarity	
JCVI_17690	2.437	weakly similar to (164)AT4G37650 Symbols: SGR7, SHR SHR (SHORT ROOT); transcription factor chr4:17691865-17693460 FC	
JCVI_38436	2.436	moderately similar to (314)AT5G11350 Symbols: endonuclease/exonuclease/phosphatase family protein chr5:3621584-3625413 FC	
ES968067	2.436	no similarity	
JCVI_32393	2.435	moderately similar to (259)AT2G45760 Symbols: BAL, BAP2 BAP2 (BON ASSOCIATION PROTEIN 2) chr2:18854199-1885482	
EV174995	2.435	no similarity	5.155
EX115617	2.434	no similarity	2.240
EV106869	2.434	no similarity	
JCVI_12231	2.434	moderately similar to (334)AT4G20130 Symbols: PTAC14 PTAC14 (PLASTID TRANSCRIPTIONALLY ACTIVE14) chr4:10878	
EE546376	2.434	weakly similar to (153)AT1G51990 Symbols: O-methyltransferase family 2 protein chr1:19334618-19336336 FORWARD [20128]	
EX088769	2.434	weakly similar to (180)AT4G26830 Symbols: hydrolase, hydrolyzing O-glycosyl compounds chr4:13494732-13496493 REVERSE	
JCVI_35155	2.432	no original description	
EX092993	2.432	no similarity	
RC_CD843352	2.431	no similarity	
EX126068	2.429	weakly similar to (144)AT2G29670 Symbols: binding chr2:12689386-12691822 REVERSE [21831] 1 664 683	
EX131397	2.429	no similarity	
EV138028	2.425	no similarity	
JCVI_40297	2.424	moderately similar to (486)AT2G44830 Symbols: protein kinase, putative chr2:18497473-18499854 FORWARDweakly similar to (	
JCVI_40943	2.423	moderately similar to (275)AT3G17920 Symbols: similar to leucine-rich repeat family protein [Arabidopsis thaliana] (TAIR:AT1G48	
AM058773	2.421	weakly similar to (124)AT2G43190 Symbols: ribonuclease P family protein chr2:17963297-17964910 FORWARD [17712]	
EV088129	2.420	no similarity	
EX045444	2.419	weakly similar to (157)AT3G21580 Symbols: cobalt ion transmembrane transporter chr3:7602015-7603727 REVERSE [21811] 1 5	
JCVI_21564	2.418	no original description	
JCVI_32644	2.418	moderately similar to (345)AT3G28340 Symbols: GATL10 GATL10 (Galacturonosyltransferase-like 10); polygalacturonate 4-alpha-γ	
EX066516	2.417	no similarity	
JCVI_21982	2.417	moderately similar to (313)AT2G41960 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G58050.1); similar t	
JCVI_30655	2.417	moderately similar to (294)AT2G44560 Symbols: ATGH9B11 ATGH9B11 (ARABIDOPSIS THALIANA GLYCOSYL HYDROLA	
JCVI_33032	2.416	very weakly similar to (90.5)AT1G05805 Symbols: basic helix-loop-helix (bHLH) family protein chr1:1744842-1747426 FORWAR	
EV191476	2.416	weakly similar to (121)AT1G77760 Symbols: GNR1, NR1, NIA1 NIA1 (NITRATE REDUCTASE 1) chr1:29240899-29244261 RE	1.120
RC_EE484085	2.415	no similarity	
EV107135	2.415	no similarity	
EX038291	2.415	no similarity	
JCVI_11680	2.415	no original description	
EE455949	2.415	very weakly similar to (98.6)AT2G20340 Symbols: tyrosine decarboxylase, putative chr2:8786885-8789571 FORWARDvery weakl	
EE533202	2.415	weakly similar to (157)AT3G59200 Symbols: F-box family protein chr3:21898461-21900191 FORWARD [20175]	
JCVI_16660	2.414	moderately similar to (213)AT5G39420 Symbols: CDC2CAT CDC2CAT (ARABIDOPSIS THALIANA CDC2C); kinase chr5:1578	
RC_EE438795	2.413	no similarity	
EX094012	2.413	moderately similar to (360)AT5G47100 Symbols: CBL9 CBL9 (Calcineurin B-like protein 9); calcium ion binding chr5:19147123-1	
EE421886	2.413	no similarity	
CV973866	2.413	no similarity	
EE563018	2.411	no similarity	
JCVI_1641	2.410	weakly similar to (129)AT4G28610 Symbols: ATPHR1, PHR1 PHR1 (PHOSPHATE STARVATION RESPONSE 1); transcription f	
EV060076	2.410	very weakly similar to (83.6)AT2G23220 Symbols: CYP81D6 CYP81D6 (cytochrome P450, family 81, subfamily D, polypeptide 6);	
ES978243	2.409	no similarity	
CX193134	2.409	no similarity	
CN730171	2.409	no similarity	
RC_EE565639	2.408	no similarity	
JCVI_40407	2.407	highly similar to (523)AT5G57560 Symbols: XTH22, TCH4 TCH4 (TOUCH 4); hydrolase, acting on glycosyl bonds / xyloglucan:xy	
EV190703	2.406	no similarity	
JCVI_14028	2.406	highly similar to (509)AT2G28780 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G09450.1); similar to un	
EV104190	2.405	moderately similar to (266)AT4G29010 Symbols: AIM1 AIM1 (ABNORMAL INFLORESCENCE MERISTEM); enoyl-CoA hydrat	
JCVI_41986	2.405	no original description	
JCVI_35443	2.405	no original description	
JCVI_39843	2.404	no original description	
EV220439	2.404	no similarity	
JCVI_20037	2.404	moderately similar to (262)AT3G47940 Symbols: DNAJ heat shock protein, putative chr3:17699217-17700387 REVERSE no origi	
EE525061	2.403	moderately similar to (230)AT3G59490 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO64819.1) chr3:2199	
EV205088	2.402	no similarity	
JCVI_23616	2.401	no original description	
JCVI_38904	2.400	moderately similar to (219)AT5G07500 Symbols: PEI1 PEI1; nucleic acid binding / transcription factor chr5:2372717-2373454 FOF	
CX278854	2.400	moderately similar to (252)AT1G52030 Symbols: MBP1.2, F-ATMBP, MBP2 MBP2 (MYROSINASE-BINDING PROTEIN 2) chr	
JCVI_29265	2.400	weakly similar to (129)AT5G05340 Symbols: peroxidase, putative chr5:1579143-1580820 REVERSEweakly similar to (126)PERI	
EX117947	2.398	no similarity	
JCVI_31778	2.397	weakly similar to (110)AT5G66600 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G23700.1); similar to un	
JCVI_22917	2.396	no original description	
BG543536	2.395	no similarity	
EE481088	2.390	no similarity	2.067
ES968160	2.389	no similarity	
JCVI_41074	2.389	no original description	
JCVI_11033	2.389	no original description	
EE569252	2.389	no similarity	3.399
JCVI_26891	2.388	moderately similar to (427)AT1G12640 Symbols: membrane bound O-acyl transferase (MBOAT) family protein chr1:4303584-430	
JCVI_41728	2.387	no original description	
EV091863	2.386	no similarity	
JCVI_27789	2.384	no original description	2.872
EV131203	2.384	no similarity	
JCVI_14004	2.384	moderately similar to (203)AT3G61680 Symbols: lipase class 3 family protein chr3:22835605-22837901 FORWARD no original d	
JCVI_32588	2.384	moderately similar to (471)AT5G49520 Symbols: ATWRKY48, WRKY48 WRKY48 (WRKY DNA-binding protein 48); transcripti	
JCVI_33886	2.384	weakly similar to (147)AT3G05490 Symbols: RALFL22 RALFL22 (RALF-LIKE 22) chr3:1591387-1591746 FORWARD no origi	
JCVI_19223	2.383	moderately similar to (268)AT4G04750 Symbols: carbohydrate transmembrane transporter/ sugar:hydrogen ion symporter chr4:2411	
EX102546	2.383	weakly similar to (200)AT4G01670 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G62070.1); similar to un	

JCVI_19679	2.383	moderately similar to (419)AT4G05050 Symbols: UBQ11 UBQ11 (UBIQUITIN 11) chr4:2588269-2588958 REVERSE	weakly sim
AM395435	2.382	weakly similar to (115)RRPO_OENBE [20346]	
JCVI_28305	2.381	no original description	
EE558622	2.381	no similarity	2.530
EE556619	2.379	no similarity	
JCVI_33213	2.379	no original description	
JCVI_4463	2.378	weakly similar to (138)AT5G01520 Symbols: zinc finger (C3HC4-type RING finger) family protein chr5:206796-208398 FORWARD	
CX270301	2.378	weakly similar to (167)AT2G24700 Symbols: transcriptional factor B3 family protein chr2:10520128-10522367 REVERSE [16815]	
JCVI_2589	2.377	no original description	2.662
EE566497	2.376	no similarity	
EV190711	2.375	very weakly similar to (89.7)AT1G29724 Symbols: protein binding chr1:10397726-10400438 REVERSE [21489] 34 802 802	
EV150955	2.374	no similarity	
EX065809	2.373	very weakly similar to (85.5)AT5G02110 Symbols: CYCD7;1, CYCD7 CYCD7/CYCD7;1 (CYCLIN D7;1); cyclin-dependent protei	
EV204290	2.373	no similarity	
JCVI_23159	2.372	weakly similar to (157)AT4G18620 Symbols: similar to Bet v I allergen family protein [Arabidopsis thaliana] (TAIR:AT5G45870.1);	
EV131705	2.371	no similarity	3.782
ES944040	2.370	no similarity	
EV079131	2.367	no similarity	
JCVI_32793	2.367	moderately similar to (218)AT3G62680 Symbols: ATPRP3, PRP3 PRP3 (PROLINE-RICH PROTEIN 3); structural constituent of cel	
EV215803	2.365	weakly similar to (157)AT2G34430 Symbols: LHCB1.4, LHB1B1 LHB1B1 (Photosystem II light harvesting complex gene 1.4); chlo	
EV166697	2.364	no similarity	
JCVI_7324	2.363	no original description	
JCVI_34932	2.363	very weakly similar to (98.6)AT1G01260 Symbols: basic helix-loop-helix (bHLH) family protein chr1:109595-111367 FORWARD	1.697
JCVI_10086	2.363	moderately similar to (256)AT3G08720 Symbols: ATS6K2, S6K2, ATPK2, ATPK19 ATPK19 (ARABIDOPSIS THALIANA PROT	
EV163212	2.361	very weakly similar to (99.4)AT5G47620 Symbols: heterogeneous nuclear ribonucleoprotein, putative / hnRNP, putative chr5:19319	
RC_H07215	2.361	no similarity	
EV127009	2.361	no similarity	
JCVI_1692	2.361	very weakly similar to (100)AT1G62780 Symbols: similar to hypothetical protein [Vitis vinifera] (GB:CAN83165.1) chr1:2325301-	
ES997948	2.361	weakly similar to (167)AT1G53710 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO68485.1); contains InterP	
EE392422	2.359	no similarity	
JCVI_16801	2.357	moderately similar to (216)AT4G32600 Symbols: zinc finger (C3HC4-type RING finger) family protein chr4:15724016-15725743	
RC_EE558820	2.355	no similarity	
EE568965	2.355	no similarity	
EV137343	2.354	no similarity	
EV187017	2.353	no similarity	
CD811951	2.352	no similarity	
JCVI_4844	2.351	no original description	
JCVI_39097	2.351	no original description	
JCVI_21471	2.350	weakly similar to (104)AT1G69170 Symbols: squamosa promoter-binding protein-like 6 (SPL6) chr1:26009289-26010704 FORW/	
H07447	2.349	no similarity	
JCVI_6023	2.349	moderately similar to (388)AT3G54150 Symbols: embryo-abundant protein-related chr3:20061780-20063720 REVERSE no origin;	
JCVI_30610	2.348	weakly similar to (189)AT2G40150 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G55990.1); similar to un	
EE468068	2.347	no similarity	
EV098616	2.347	weakly similar to (116)AT3G55260 Symbols: HEXO1, ATHEX2 ATHEX2/HEXO1 (BETA-HEXOSAMINIDASE 1); beta-N-acetyl	
JCVI_38231	2.345	no original description	
JCVI_37463	2.343	very weakly similar to (98.2)AT5G53890 Symbols: leucine-rich repeat transmembrane protein kinase, putative chr5:21894461-21897	2.878
JCVI_15939	2.342	highly similar to (608)AT5G14700 Symbols: cinnamoyl-CoA reductase-related chr5:4740505-4743330 REVERSE	very weakly simi
EE525908	2.341	no similarity	
JCVI_8746	2.339	no original description	
DN964770	2.339	moderately similar to (228)AT2G35930 Symbols: U-box domain-containing protein chr2:15090180-15091415 REVERSE [17359]	
EE478859	2.339	weakly similar to (106)AT1G50510 Symbols: indigoidine synthase A family protein chr1:18720246-18722728 FORWARD [20132]	
EV055041	2.339	no similarity	
JCVI_16092	2.339	moderately similar to (236)AT5G46830 Symbols: basic helix-loop-helix (bHLH) family protein chr5:19019946-19021481 FORWA	0.694
ES901052	2.338	weakly similar to (193)AT5G18070 Symbols: DRT101 (DNA-DAMAGE-REPAIR/TOLERATION 101); intramolecular transferase,	
RC_EE568158	2.336	no similarity	
EV127579	2.335	moderately similar to (207)AT5G18120 Symbols: ATAPRL7 ATAPRL7 (APR-LIKE 7) chr5:5991387-5993698 FORWARD [2148]	
CD817457	2.334	no similarity	
JCVI_37219	2.334	no original description	
EV106022	2.333	no similarity	
ES904917	2.333	moderately similar to (203)AT1G30270 Symbols: SnRK3.23, ATCIPK23, LKS1, CIPK23 CIPK23 (CBL-INTERACTING PROTEIN	
CV973980	2.333	no similarity	
JCVI_5055	2.332	moderately similar to (394)AT1G69930 Symbols: ATGSTU11 ATGSTU11 (Arabidopsis thaliana Glutathione S-transferase (class tau	
JCVI_17862	2.332	moderately similar to (403)AT5G13200 Symbols: GRAM domain-containing protein / ABA-responsive protein-related chr5:420708	
EV223079	2.331	no similarity	2.511
JCVI_9907	2.330	moderately similar to (286)AT1G76650 Symbols: CML38 CML38 chr1:28771803-28772336 REVERSE	Every weakly similar to (82.
JCVI_26200	2.329	moderately similar to (385)AT2G03760 Symbols: RAR047, ST ST (steroid sulfotransferase); sulfotransferase chr2:1149472-115045	
JCVI_24700	2.328	no original description	
EV165777	2.326	moderately similar to (201)AT4G20200 Symbols: terpene synthase/cyclase family protein chr4:10908682-10911161 REVERSE	Every
JCVI_4224	2.325	very weakly similar to (96.3)AT2G13770 Symbols: similar to ribosomal protein-like [Oryza sativa (japonica cultivar-group)] (GB:BA	
CX191063	2.324	no similarity	
EV039389	2.324	moderately similar to (249)AT1G27080 Symbols: transporter chr1:9400651-9403776 FORWARD [21442]	
EE417789	2.323	moderately similar to (232)AT5G07200 Symbols: GA20OX3, ATGA20OX3 YAP169 (GIBBERELLIN 20 OXIDASE 3); gibberellin	
JCVI_5855	2.322	moderately similar to (252)AT1G27190 Symbols: leucine-rich repeat transmembrane protein kinase, putative chr1:9446910-944871	
JCVI_24153	2.322	no original description	-2.559
RC_ES947980	2.320	no similarity	
ES962072	2.320	no similarity	
JCVI_39122	2.320	no original description	
JCVI_25760	2.319	moderately similar to (475)AT4G24570 Symbols: mitochondrial substrate carrier family protein chr4:12686556-12687497 FORWA	2.173
EV221283	2.319	no similarity	
EE464425	2.318	weakly similar to (130)AT1G68790 Symbols: LINC3 LINC3 (LITTLE NUCLEI3) chr1:25838595-25842820 REVERSE [20171]	4.329
EE472183	2.317	no similarity	
EV100262	2.314	no similarity	
EV136479	2.312	no similarity	2.671

EE559838	2.310	no similarity	
EX130622	2.310	moderately similar to (210)AT2G01300 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G15010.1); similar t	2.169
EE545610	2.310	weakly similar to (138)AT5G46930 Symbols: invertase/pectin methylesterase inhibitor family protein chr5:19073882-19074418 RE	
EV104577	2.310	no similarity	
JCVI_32877	2.310	no original description	
EV217196	2.310	moderately similar to (270)AT2G36880 Symbols: MAT3 MAT3 (METHIONINE ADENOSYLTRANSFERASE 3) chr2:15486800-	
JCVI_23583	2.310	no original description	
JCVI_16158	2.309	no original description	
JCVI_8360	2.308	moderately similar to (367)AT2G32240 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G05320.1); similar t	
JCVI_8722	2.306	moderately similar to (295)AT2G34500 Symbols: CYP710A1 CYP710A1 (cytochrome P450, family 710, subfamily A, polypeptide	
JCVI_4114	2.305	moderately similar to (387)AT2G22300 Symbols: ethylene-responsive calmodulin-binding protein, putative (SR1) chr2:9478679-94	
JCVI_20638	2.305	weakly similar to (145)AT2G20835 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G15534.1); similar to un	
EV142911	2.304	no similarity	
JCVI_6893	2.304	weakly similar to (151)AT3G50800 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G66580.1); similar to un	
JCVI_17037	2.304	weakly similar to (166)AT1G78080 Symbols: RAP2.4 RAP2.4 (related to AP2 4); DNA binding / transcription factor chr1:2936968.	
EV004192	2.303	no similarity	
JCVI_2174	2.302	no original description	
AM391923	2.302	very weakly similar to (100)AT5G58000 Symbols: CPL4 (C-TERMINAL DOMAIN PHOSPHATASE-LIKE 4) chr5:23494642-23-	2.689
L38213	2.301	no similarity	
EV223686	2.301	no similarity	
EV087750	2.300	no similarity	
EV121875	2.300	no similarity	
EV000534	2.299	no similarity	
EX025522	2.299	very weakly similar to (97.1)AT3G25720 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G10613.1); similar	1.916
JCVI_29006	2.299	moderately similar to (236)AT2G03980 Symbols: GDSL-motif lipase/hydrolase family protein chr2:1260904-1262405 FORWARD	
JCVI_1841	2.298	moderately similar to (223)AT4G37260 Symbols: MYB73, AtMYB73 AtMYB73/MYB73 (myb domain protein 73); DNA binding /	
EV015332	2.297	no similarity	
JCVI_530	2.296	highly similar to (611)AT2G26200 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G54650.1); similar to un	
JCVI_29421	2.296	very weakly similar to (89.4)AT1G35435 Symbols: Encodes a defensin-like (DEFL) family protein. chr1:13032784-13033225 REV	
BG543634	2.296	weakly similar to (127)AT3G45850 Symbols: kinesin motor protein-related chr3:16866799-16871935 REVERSE [8791] 1 444 458	
JCVI_14437	2.296	moderately similar to (248)AT4G20140 Symbols: GSO1 leucine-rich repeat transmembrane protein kinase, putative chr4:10884230-	
EV141857	2.296	weakly similar to (160)AT5G60170 Symbols: RNA binding chr5:24245404-24249620 FORWARD [21482] 1 600 736	
JCVI_36962	2.293	weakly similar to (110)AT3G01250 Symbols: unknown protein chr3:79411-79905 FORWARD no original description	
EE546514	2.292	no similarity	
JCVI_9412	2.291	highly similar to (551)AT4G14130 Symbols: XTR7 XTR7 (XYLOGLUCAN ENDOTRANSGLYCOSYLASE 7); hydrolase, acting c	
JCVI_31006	2.291	no original description	
EV152303	2.291	no similarity	
JCVI_22385	2.288	moderately similar to (303)AT2G41640 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G57380.1); similar t	
JCVI_13338	2.288	moderately similar to (223)AT2G37500 Symbols: arginine biosynthesis protein ArgJ family chr2:15746982-15749508 REVERSE n	
EE465917	2.287	no similarity	
JCVI_9514	2.286	moderately similar to (334)AT1G04770 Symbols: male sterility MS5 family protein chr1:1336563-1337766 REVERSE no original	
JCVI_7505	2.286	moderately similar to (355)AT1G18980 Symbols: germin-like protein, putative chr1:6557355-6558017 REVERSEmoderately simil	
RC_EE402513	2.285	no similarity	
EV053773	2.285	weakly similar to (104)AT2G13770 Symbols: similar to ribosomal protein-like [Oryza sativa (japonica cultivar-group)] (GB:BAD375	
JCVI_3148	2.284	moderately similar to (240)AT1G06280 Symbols: LBD2 LBD2 (LOB DOMAIN-CONTAINING PROTEIN 2) chr1:1920326-19205	
EE527347	2.284	no similarity	
CV973934	2.284	no similarity	2.165
EX035886	2.282	no similarity	
EG019381	2.282	weakly similar to (173)AT3G11830 Symbols: chaperonin, putative chr3:3732740-3736162 FORWARD [20440] 1 459 475	
ES914598	2.282	no similarity	
ES964741	2.282	no similarity	
RC_CD823283	2.280	no similarity	
JCVI_39875	2.280	no original description	
EE535482	2.280	moderately similar to (317)AT1G04150 Symbols: C2 domain-containing protein chr1:1081207-1084245 REVERSE [20150]	
JCVI_31263	2.280	weakly similar to (117)AT1G10000 Symbols: nucleic acid binding / ribonuclease H chr1:3263879-3264790 REVERSE no original	
EE559930	2.280	weakly similar to (102)AT1G27120 Symbols: galactosyltransferase family protein chr1:9421376-9423897 FORWARD [20153] 21	
EV171267	2.279	very weakly similar to (95.5)AT2G45200 Symbols: ATGOS12, GOS12 GOS12 (GOLGI SNARE 12); SNARE binding chr2:1864471	
ES962911	2.278	no similarity	
RC_JCVI_29195	2.277	no original description	
EE556745	2.277	no similarity	
EE504784	2.276	no similarity	
RC_ES965361	2.276	no similarity	
EE410680	2.276	no similarity	
RC_EX016639	2.276	no similarity	
EV141922	2.275	no similarity	
EV209165	2.274	very weakly similar to (95.9)ATCG00740 Symbols: RPOA RNA polymerase alpha subunit chrC:77901-78890 REVERSEvery weakl	2.894
JCVI_33562	2.273	no original description	1.624
EE535370	2.273	very weakly similar to (100)AT1G06420 Symbols: unknown protein chr1:1958986-1959651 FORWARD [20150]	
JCVI_38766	2.272	highly similar to (932)AT2G21540 Symbols: SEC14 cytosolic factor, putative / phosphoglyceride transfer protein, putative chr2:922	
ES956956	2.270	no similarity	
JCVI_15271	2.269	moderately similar to (255)AT3G47580 Symbols: leucine-rich repeat transmembrane protein kinase, putative chr3:17543672-17546	
EE541187	2.269	no similarity	
EV121879	2.269	no similarity	
EV108573	2.269	no similarity	
EV146452	2.268	no similarity	
JCVI_30459	2.263	no original description	
EV223098	2.263	no similarity	
EE392342	2.263	very weakly similar to (81.3)AT3G51190 Symbols: 60S ribosomal protein L8 (RPL8B) chr3:19027585-19028526 REVERSEvery w	
EE566653	2.263	no similarity	
JCVI_17725	2.263	no original description	
EE558644	2.262	no similarity	
JCVI_15099	2.262	no original description	
EE527375	2.259	no similarity	

JCVI_15636	2.259	moderately similar to (255)AT3G09910 Symbols: AtRab18C, AtRABC2b AtRABC2b/AtRab18C (Arabidopsis Rab GTPase homolog)	
JCVI_35641	2.258	no original description	
H06422	2.257	no similarity	
EX066286	2.257	moderately similar to (221)AT2G19050 Symbols: GDSL-motif lipase/hydrolase family protein chr2:8260498-8262616 FORWARD	
JCVI_9810	2.257	moderately similar to (477)AT3G29670 Symbols: transferase family protein chr3:11530431-11531786 FORWARD no original desc	
H07256	2.256	no similarity	
EE433603	2.256	weakly similar to (107)AT1G44830 Symbols: AP2 domain-containing transcription factor TINY, putative chr1:16936232-16936867	
CD841406	2.255	weakly similar to (150)AT5G61610 Symbols: glycine-rich protein / oleosin chr5:24787325-24788139 FORWARD [13982]	
ES966738	2.252	no similarity	
EV219168	2.251	no similarity	
EV021400	2.251	weakly similar to (189)AT2G18600 Symbols: RUB1-conjugating enzyme, putative chr2:8080419-8081647 REVERSE [21441]	2.749
JCVI_26031	2.248	weakly similar to (116)AT4G37610 Symbols: BT5 BT5 (BTB and TAZ domain protein 5); protein binding / transcription regulator c	3.630
ES900145	2.247	no similarity	2.783
AB012650	2.246	no similarity	
EE450743	2.246	no similarity	
JCVI_37168	2.246	no original description	
ES996255	2.246	moderately similar to (259)AT5G60600 Symbols: ISPG, CSB3, CLB4, GcpE GcpE (CHLOROPLAST BIOGENESIS 4) chr5:24376	
EV194609	2.246	weakly similar to (192)AT4G28820 Symbols: zinc finger (HIT type) family protein chr4:14230821-14232293 REVERSE [21489]	
EX073155	2.245	no similarity	1.250
EV126887	2.245	no similarity	4.009
EE442803	2.244	no similarity	
AM395139	2.242	no similarity	
ES993840	2.240	no similarity	
JCVI_1399	2.239	moderately similar to (244)AT5G11270 Symbols: OCP3 OCP3 (OVEREXPRESSOR OF CATIONIC PEROXIDASE 3) chr5:35955	
EV112898	2.239	no similarity	
CK991425	2.237	no similarity	
JCVI_24047	2.237	moderately similar to (371)AT1G07630 Symbols: PLL5 PLL5 (POL-like 5); protein serine/threonine phosphatase chr1:2349186-235	
EV177226	2.237	no similarity	
JCVI_39766	2.237	no original description	
EV098633	2.235	no similarity	1.798
EV186706	2.233	weakly similar to (128)AT2G26600 Symbols: glycosyl hydrolase family 17 protein chr2:11324292-11325293 FORWARD [21488]	1.281
JCVI_15437	2.233	moderately similar to (456)AT2G43770 Symbols: transducin family protein / WD-40 repeat family protein chr2:18141349-1814238	2.040
EV164663	2.232	moderately similar to (202)AT2G38370 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G51720.1); similar t	
CX189791	2.231	moderately similar to (259)AT2G13570 Symbols: CCAAT-box binding transcription factor, putative chr2:5662924-5663571 REVE	
EE402854	2.230	moderately similar to (210)AT5G16460 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G29760.1); similar t	4.297
JCVI_32857	2.228	moderately similar to (258)AT3G28980 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G28810.1); contains	
EV165339	2.227	no similarity	
EX137311	2.225	moderately similar to (323)AT1G14370 Symbols: APK2A APK2A (PROTEIN KINASE 2A); kinase chr1:4915854-4917954 FORW	
CV545055	2.225	weakly similar to (184)AT3G49670 Symbols: BAM2 BAM2 (big apical meristem 2); ATP binding / protein serine/threonine kinase c	2.155
JCVI_16916	2.225	moderately similar to (270)AT1G73540 Symbols: ATNUDT21 ATNUDT21 (Arabidopsis thaliana Nudix hydrolase homolog 21); hyc	
JCVI_38126	2.224	very weakly similar to (91.3)AT4G18570 Symbols: proline-rich family protein chr4:10231450-10234545 FORWARD no original de	
JCVI_12318	2.223	highly similar to (550)AT2G03800 Symbols: GEK1 GEK1 (GEKO1) chr2:1156779-1158692 FORWARD no original description	4.113
EV135372	2.223	weakly similar to (122)AT3G60750 Symbols: transketolase, putative chr3:22464979-22467799 FORWARDweakly similar to (123	
EV118798	2.222	no similarity	
EV161446	2.222	no similarity	
EV210107	2.222	moderately similar to (294)AT1G44760 Symbols: universal stress protein (USP) family protein chr1:16899334-16900867 REVERS	
EV109671	2.222	very weakly similar to (89.0)AT4G15530 Symbols: PPKK PPKK (PYRUVATE ORTHOPHOSPHATE DIKINASE) chr4:8864826-t	
EE421652	2.221	no similarity	
JCVI_34463	2.220	no original description	4.589
EV131594	2.219	no similarity	
JCVI_21172	2.218	no original description	
JCVI_40529	2.218	no original description	
JCVI_15094	2.217	weakly similar to (101)AT2G40900 Symbols: nodulin MtN21 family protein chr2:17070474-17072592 REVERSE no original desc	
EE563168	2.217	no similarity	
EV087239	2.215	no similarity	3.316
JCVI_2696	2.215	moderately similar to (260)AT1G17470 Symbols: ATDRG, ATDRG1 ATDRG1 (ARABIDOPSIS THALIANA DEVELOPMENTAL	
JCVI_14811	2.214	no original description	2.431
JCVI_34427	2.211	moderately similar to (343)AT1G73020 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO45737.1); similar to l	
EV108841	2.211	no similarity	
JCVI_23960	2.211	no original description	
EE548612	2.211	no similarity	2.652
JCVI_14606	2.208	moderately similar to (448)AT2G37700 Symbols: similar to CER1 protein, putative [Arabidopsis thaliana] (TAIR:AT1G02190.1); si	
EE555323	2.208	no similarity	
EE549729	2.208	no similarity	
EV163200	2.208	moderately similar to (307)AT2G40850 Symbols: phosphatidylinositol 3- and 4-kinase family protein chr2:17058653-17060338 FO	
JCVI_21273	2.207	weakly similar to (189)AT4G34410 Symbols: AP2 domain-containing transcription factor, putative chr4:16451996-16452802 FOR	4.104
EV071596	2.207	no similarity	
JCVI_23351	2.204	moderately similar to (333)AT1G60980 Symbols: ATGA20OX4 ATGA20OX4 (GIBBERELLIN 20-OXIDASE 4); gibberellin 20-ox	
JCVI_2286	2.204	moderately similar to (217)AT4G27170 Symbols: 2S seed storage protein 4 / 2S albumin storage protein / NWMU2-2S albumin 4 cl	
EV205494	2.204	no similarity	
JCVI_37300	2.203	weakly similar to (198)AT4G19230 Symbols: CYP707A1 CYP707A1 (cytochrome P450, family 707, subfamily A, polypeptide 1); o	
JCVI_31904	2.203	no original description	
JCVI_38051	2.201	moderately similar to (234)AT5G41330 Symbols: potassium channel tetramerisation domain-containing protein chr5:16553680-165	
JCVI_24324	2.200	no original description	
JCVI_38962	2.200	weakly similar to (166)AT3G02080 Symbols: 40S ribosomal protein S19 (RPS19A) chr3:364145-365168 REVERSEweakly similar	
EV180517	2.200	weakly similar to (107)AT3G49430 Symbols: SRP34A SRP34A (SER/ARG-RICH PROTEIN 34A) chr3:18343653-18345602 FOR	
EE502208	2.198	no similarity	
EV098884	2.197	no similarity	3.377
EV194141	2.196	no similarity	
JCVI_16333	2.195	weakly similar to (183)AT5G17710 Symbols: EMB1241 EMB1241 (EMBRYO DEFECTIVE 1241); adenylyl-nucleotide exchange fac	
JCVI_28458	2.195	highly similar to (704)AT5G26310 Symbols: UGT72E3 UGT72E3; UDP-glycosyltransferase/ coniferyl-alcohol glucosyltransferase/ t	
JCVI_17548	2.195	moderately similar to (292)AT1G78815 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G16910.1); similar t	
EV146975	2.194	no similarity	

JCVI_27993	2.194	weakly similar to (117)AT1G56560 Symbols: beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fruct	
EV178209	2.193	no similarity	
ES938309	2.191	no similarity	
JCVI_38772	2.189	no original description	2.762
EV144440	2.189	no similarity	
JCVI_26223	2.189	moderately similar to (300)AT5G51990 Symbols: CBF4, DREB1D CBF4/DREB1D (C- REPEAT-BINDING FACTOR 4); DNA bin	
EE562569	2.189	no similarity	
JCVI_22409	2.189	no original description	
JCVI_11605	2.189	moderately similar to (230)AT1G79340 Symbols: ATMC4 ATMC4 (METACASPASE 4); caspase/ cysteine-type peptidase chr1:29f	
ES266187	2.189	moderately similar to (361)AT2G33100 Symbols: CSLD1, ATCSLD1 ATCSLD1 (Cellulose synthase-like D1); cellulose synthase/ tra	
CX189187	2.189	no similarity	
JCVI_696	2.185	no original description	
JCVI_2054	2.185	no original description	
JCVI_30284	2.184	no original description	
JCVI_20083	2.184	no original description	
EX087049	2.183	very weakly similar to (100)AT1G12290 Symbols: disease resistance protein (CC-NBS-LRR class), putative chr1:4178591-418124f	2.436
JCVI_9348	2.182	no original description	
JCVI_38243	2.182	no original description	
JCVI_18453	2.182	moderately similar to (258)AT1G17620 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G11890.1); similar t	
EH430271	2.180	no similarity	
EV219606	2.180	weakly similar to (180)AT2G26690 Symbols: nitrate transporter (NTP2) chr2:11354425-11357994 REVERSE [21492] 52 704 704	
EX089551	2.179	no similarity	
EV111696	2.178	no similarity	
JCVI_5240	2.176	moderately similar to (272)AT3G03950 Symbols: ECT1 ECT1 chr3:1021509-1023774 FORWARD no original description	
JCVI_21087	2.175	moderately similar to (217)AT3G53190 Symbols: pectate lyase family protein chr3:19725149-19728515 FORWARD no original de	
EV218736	2.175	no similarity	
EV088740	2.174	no similarity	
EE534620	2.172	no similarity	
ES950859	2.172	no similarity	
H74438	2.172	no similarity	
EX102092	2.172	moderately similar to (314)AT4G29780 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G12010.1); similar t	
JCVI_14845	2.172	moderately similar to (471)ATCG01110 Symbols: NDHH Encodes the 49KDa plastid NAD(P)H dehydrogenase subunit H protein. It	
JCVI_24538	2.172	weakly similar to (103)AT1G12000 Symbols: pyrophosphate--fructose-6-phosphate 1-phosphotransferase beta subunit, putative / pyr	
EV098641	2.172	weakly similar to (169)AT5G10450 Symbols: AFT1, GRF6 GRF6 (G-BOX REGULATING FACTOR 6); protein phosphorylated am	
EV151827	2.172	no similarity	
EV221722	2.172	very weakly similar to (87.0)AT2G37180 Symbols: PIP2;3, PIP2C, RD28 RD28 (plasma membrane intrinsic protein 2;3); water chann	4.699
AM059925	2.172	no similarity	
EE559738	2.172	no similarity	
EX046962	2.172	no similarity	
JCVI_31746	2.172	no original description	
JCVI_11988	2.170	no original description	
ES968632	2.169	no similarity	
EX071243	2.168	weakly similar to (139)AT2G39855 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G55646.1); similar to un	
JCVI_14937	2.167	no original description	
JCVI_27655	2.167	no original description	
JCVI_15016	2.166	no original description	
EH415296	2.166	no similarity	
CV432076	2.166	no similarity	
EE556297	2.165	no similarity	
JCVI_19674	2.162	no original description	
AT002205	2.162	no similarity	
EV167224	2.162	no similarity	
EE504774	2.161	no similarity	
JCVI_37340	2.161	moderately similar to (249)AT5G58580 Symbols: ATL63 ATL63; protein binding / zinc ion binding chr5:23694132-23695058 REV	
JCVI_32803	2.161	no original description	
DY029251	2.160	no similarity	
CX189531	2.158	weakly similar to (121)AT3G22040 Symbols: receptor-like protein kinase-related chr3:7761814-7762682 FORWARD [16807]	
RC_ES958682	2.158	no similarity	
EE424329	2.156	weakly similar to (106)AT1G24460 Symbols: myosin-related chr1:8666060-8672346 FORWARD [20158]	
JCVI_42319	2.155	no original description	
DN964809	2.155	weakly similar to (188)AT5G50420 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G53770.1); similar to un	2.187
EV100550	2.155	weakly similar to (189)AT1G11440 Symbols: similar to glycine-rich protein [Arabidopsis thaliana] (TAIR:AT3G29075.1); similar to	
RC_EE567818	2.154	no similarity	
EX130042	2.153	weakly similar to (127)AT5G14940 Symbols: proton-dependent oligopeptide transport (POT) family protein chr5:4831751-483431f	
EV147401	2.152	no similarity	
CN735960	2.152	no similarity	
JCVI_38623	2.150	highly similar to (556)AT3G55840 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G40000.1); similar to un	
RC_ES962063	2.150	no similarity	4.530
JCVI_35611	2.149	moderately similar to (235)AT3G61150 Symbols: HDG1 HDG1 (HOMEODOMAIN GLABROUS1); DNA binding / transcription fa	
JCVI_28996	2.148	no original description	
JCVI_32830	2.148	highly similar to (592)AT5G18525 Symbols: WD-40 repeat family protein chr5:6146934-6149732 REVERSE no original descripti	
DY021832	2.147	no similarity	
JCVI_29379	2.147	no original description	
EV144812	2.146	no similarity	
EV059840	2.146	no similarity	
ES266564	2.146	no similarity	
RC_EV032029	2.146	no similarity	
EV135225	2.146	no similarity	
JCVI_2317	2.146	no original description	
CD830742	2.145	no similarity	
JCVI_24387	2.145	moderately similar to (241)AT5G07070 Symbols: SnRK3.2, CIPK2 CIPK2 (CBL-INTERACTING PROTEIN KINASE 2); kinase cl	
ES966580	2.145	no similarity	
BG544771	2.143	no similarity	

JCVI_4691	2.143	no original description	
EV087233	2.143	no similarity	
EE471788	2.142	very weakly similar to (99.4)AT5G21930 Symbols: PAA2, HMA8 HMA8/PAA2 (P-TYPE ATPASE OF ARABIDOPSIS 2); ATPase,	
JCVI_14317	2.141	no original description	
BG544701	2.141	no similarity	1.562
JCVI_21363	2.141	highly similar to (690)AT2G22400 Symbols: NOL1/NOP2/sun family protein chr2:9511903-9515868 REVERSE no original descri	
RC_CV973903	2.140	no similarity	
DN965542	2.140	no similarity	
ES966406	2.139	no similarity	
JCVI_16044	2.138	moderately similar to (225)AT3G21175 Symbols: TIFY2B, ZML1 ZML1 (ZIM-LIKE 1) chr3:7422838-7423771 FORWARD no ori	3.479
EE551761	2.137	no similarity	
JCVI_28686	2.137	no original description	3.195
JCVI_18700	2.137	moderately similar to (423)AT1G70590 Symbols: F-box family protein chr1:26622066-26623822 FORWARD no original descripti	
JCVI_7142	2.136	moderately similar to (377)AT2G42810 Symbols: PAPP5, PP5 PAPP5/PP5 (PROTEIN PHOSPHATASE 5); phosphoprotein phosph	
EE557970	2.136	very weakly similar to (82.4)AT5G10010 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G64910.1); similar	2.923
JCVI_41173	2.136	weakly similar to (181)AT5G02900 Symbols: CYP96A13 CYP96A13 (cytochrome P450, family 96, subfamily A, polypeptide 13); o	
JCVI_17336	2.136	no original description	
JCVI_21850	2.135	moderately similar to (239)AT1G29090 Symbols: peptidase C1A papain family protein chr1:10163089-10164371 REVERSEvery v	
AM387464	2.135	no similarity	
JCVI_33167	2.135	no original description	
EV088344	2.135	no similarity	
EV091831	2.134	no similarity	
EE561329	2.134	no similarity	
EV193910	2.132	no similarity	
JCVI_8771	2.132	highly similar to (862)AT5G18840 Symbols: sugar transporter, putative chr5:6282956-6286401 FORWARDweakly similar to (166	4.527
JCVI_21979	2.130	weakly similar to (169)AT3G60800 Symbols: zinc finger (DHHC type) family protein chr3:22478461-22480248 REVERSE no origi	
DN961328	2.129	no similarity	
EV090686	2.128	weakly similar to (176)AT3G24420 Symbols: hydrolase, alpha/beta fold family protein chr3:8863118-8864890 REVERSE [21476]	
JCVI_38500	2.127	weakly similar to (124)AT5G14130 Symbols: peroxidase, putative chr5:4558864-4560030 REVERSEvery weakly similar to (82.8)	
JCVI_33648	2.126	moderately similar to (290)AT2G42450 Symbols: lipase class 3 family protein chr2:17679503-17681932 REVERSE no original de	
JCVI_18452	2.126	no original description	
JCVI_42141	2.126	no original description	
JCVI_29693	2.126	moderately similar to (337)AT1G08630 Symbols: THA1 THA1 (THREONINE ALDOLASE 1) chr1:2743951-2745688 REVERSE	2.632
EE569691	2.126	no similarity	
JCVI_21714	2.125	weakly similar to (147)AT4G39840 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO21162.1); similar to unna	
EX047424	2.124	no similarity	
ES912517	2.123	highly similar to (565)AT3G19820 Symbols: DIM, EVE1, DW1, DIM1, CBB1, DWF1 DWF1 (DIMINUTO 1); catalytic chr3:68791	
JCVI_29229	2.122	weakly similar to (119)AT5G52510 Symbols: scarecrow-like transcription factor 8 (SCL8) chr5:21324422-21326344 FORWARD r	
EV150562	2.116	no similarity	
JCVI_3065	2.115	moderately similar to (443)AT5G04180 Symbols: carbonic anhydrase family protein chr5:1147908-1149238 REVERSE no original	
CX279977	2.115	moderately similar to (235)AT2G42560 Symbols: late embryogenesis abundant domain-containing protein / LEA domain-containing	
RC_EE567416	2.115	no similarity	
JCVI_40915	2.115	no original description	
JCVI_26660	2.115	moderately similar to (467)AT5G61510 Symbols: NADP-dependent oxidoreductase, putative chr5:24754310-24756201 REVERSE	
JCVI_40041	2.114	moderately similar to (234)AT2G39400 Symbols: hydrolase, alpha/beta fold family protein chr2:16459797-16461728 FORWARD	
JCVI_38816	2.113	no original description	
DY026036	2.113	weakly similar to (154)AT3G16490 Symbols: IQD26 IQD26 (IQ-domain 26); calmodulin binding chr3:5603968-5605495 REVERS	
EE494544	2.113	no similarity	
EV149501	2.112	no similarity	
JCVI_16662	2.111	moderately similar to (224)AT5G21170 Symbols: 5'-AMP-activated protein kinase beta-2 subunit, putative chr5:7205721-7208242	
JCVI_22827	2.111	highly similar to (518)AT1G21790 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO61872.1); contains InterPr	
JCVI_30122	2.110	no original description	
RC_EE563070	2.109	no similarity	
CX269865	2.107	moderately similar to (231)AT4G10400 Symbols: F-box family protein chr4:6446331-6447711 REVERSE [16815]	
CD843764	2.107	no similarity	3.564
EV138924	2.106	no similarity	
EV111582	2.106	no similarity	
ES993543	2.106	no similarity	2.121
EL590485	2.106	weakly similar to (146)AT1G70770 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G23170.1); similar to hy	
EV130012	2.105	no similarity	
EV140465	2.104	no similarity	
JCVI_21809	2.104	no original description	
EX134202	2.103	no similarity	1.739
EE567286	2.103	no similarity	
CV546780	2.102	no similarity	
EV218215	2.101	no similarity	
JCVI_8099	2.101	no original description	
JCVI_26192	2.101	moderately similar to (438)AT3G21090 Symbols: ABC transporter family protein chr3:7391503-7394939 REVERSE no original de	
H07242	2.101	no similarity	
EE562117	2.100	no similarity	2.733
JCVI_33113	2.099	no original description	
EE472195	2.099	no similarity	1.277
EV159783	2.098	weakly similar to (145)AT4G30810 Symbols: SCPL29 SCPL29 (serine carboxypeptidase-like 29); serine carboxypeptidase chr4:150	
RC_ES962408	2.097	no similarity	
EV132861	2.097	no similarity	
ES917057	2.097	moderately similar to (208)AT5G22920 Symbols: zinc finger (C3HC4-type RING finger) family protein chr5:7665146-7667034 FC	2.262
EV112391	2.097	no similarity	
EX091753	2.096	no similarity	
JCVI_33259	2.096	weakly similar to (191)AT1G62120 Symbols: mitochondrial transcription termination factor-related / mTERF-related chr1:2296399	3.079
JCVI_19706	2.095	no original description	
EE565674	2.094	no similarity	
JCVI_1184	2.093	moderately similar to (280)AT2G35960 Symbols: NHL12 NHL12 (NDR1/HIN1-like 12) chr2:15114229-15114861 FORWARD no	
EV098433	2.093	no similarity	

JCVI_34493	2.090	weakly similar to (150)AT3G26910 Symbols: hydroxyproline-rich glycoprotein family protein chr3:9916541-9919748 REVERSE r	
EE545727	2.089	no similarity	
EV132933	2.088	no similarity	
JCVI_113	2.087	moderately similar to (371)AT2G43130 Symbols: AtRab11F, AtRABA5c, Ara-4 ARA4 (Arabidopsis Rab GTPase homolog A5c); G	
JCVI_42470	2.087	weakly similar to (171)AT3G28200 Symbols: peroxidase, putative chr3:10519319-10520269 FORWARD no original description	
JCVI_6426	2.087	moderately similar to (240)AT1G80830 Symbols: PMIT1, ATNRAMP1, NRAMP1 NRAMP1 (NRAMP metal ion transporter 1); ma	
CD843729	2.085	no similarity	
EV199280	2.085	no similarity	
EV165341	2.085	moderately similar to (261)AT5G57190 Symbols: PSD2 PSD2 (PHOSPHATIDYLSERINE DECARBOXYLASE 2); phosphatidylser	
RC_EE543346	2.084	no similarity	
EE562825	2.084	no similarity	
JCVI_8102	2.082	moderately similar to (235)AT3G17850 Symbols: protein kinase, putative chr3:6109860-6116251 REVERSE no original description	
EV111479	2.082	very weakly similar to (96.7)AT4G23700 Symbols: CHX17, ATCHX17 ATCHX17 (CATION/H+ EXCHANGER 17); monovalent c	2.348
EX023620	2.082	weakly similar to (182)AT1G04830 Symbols: RabGAP/TBC domain-containing protein chr1:1359086-1361843 REVERSE [21809	
EX086430	2.080	very weakly similar to (99.0)AT5G36228 Symbols: nucleic acid binding / zinc ion binding chr5:14288921-14290006 FORWARD [2	
JCVI_35107	2.080	weakly similar to (191)AT3G62170 Symbols: VGDH2 VGDH2 (VANGUARD 1 HOMOLOG 2); pectinesterase chr3:23027470-23	
RC_EX055797	2.078	no similarity	2.546
RC_EE559778	2.077	no similarity	
ES930022	2.077	weakly similar to (132)AT5G18800 Symbols: NADH-ubiquinone oxidoreductase 19 kDa subunit (NDUFA8) family protein chr5:62	
JCVI_9869	2.076	moderately similar to (326)AT2G34590 Symbols: transketolase family protein chr2:14576035-14577923 REVERSEmoderately sim	
CN733031	2.076	no similarity	
EE548763	2.076	no similarity	
JCVI_28834	2.076	highly similar to (689)AT4G28650 Symbols: leucine-rich repeat transmembrane protein kinase, putative chr4:14144161-14147282 I	
JCVI_41666	2.076	weakly similar to (151)AT2G45120 Symbols: zinc finger (C2H2 type) family protein chr2:18610755-18611699 FORWARD no ori	
JCVI_40985	2.076	weakly similar to (159)AT3G59080 Symbols: aspartyl protease family protein chr3:21847789-21849396 FORWARD no original de	
JCVI_25460	2.076	weakly similar to (157)AT5G23700 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G48860.2); similar to hy	
EV110529	2.075	no similarity	
EE561790	2.075	no similarity	
EE419429	2.075	no similarity	
JCVI_31482	2.074	no original description	
JCVI_21105	2.073	very weakly similar to (84.7)AT2G35765 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G19500.1) chr2:15	
JCVI_23169	2.073	no original description	
JCVI_18757	2.073	weakly similar to (196)AT1G24260 Symbols: AGL9, SEP3 SEP3 (SEPALATA3); transcription factor chr1:8593779-8595851 RE	
EX096357	2.072	no similarity	
JCVI_25363	2.070	moderately similar to (324)AT1G18460 Symbols: lipase family protein chr1:6352675-6355964 FORWARD no original description	
EE565238	2.070	no similarity	
EE427194	2.069	no similarity	
EV019444	2.069	weakly similar to (122)AT1G69290 Symbols: pentatricopeptide (PPR) repeat-containing protein chr1:26051035-26053011 REVER	
EV144814	2.068	no similarity	
JCVI_24568	2.068	no original description	
EV141577	2.067	weakly similar to (132)AT4G37990 Symbols: ELI3, ELI3-2 ELI3-2 (ELICITOR-ACTIVATED GENE 3) chr4:17855958-17857382	
CX267764	2.067	no similarity	3.541
CD828534	2.067	no similarity	3.078
JCVI_30997	2.066	moderately similar to (420)AT1G15210 Symbols: PDR7, ATPDR7 ATPDR7/PDR7 (PLEIOTROPIC DRUG RESISTANCE 7); ATP	
EV219183	2.066	no similarity	
ES269370	2.065	no similarity	
CX267453	2.064	no similarity	
JCVI_30388	2.064	no original description	
JCVI_13509	2.064	highly similar to (671)AT5G63930 Symbols: leucine-rich repeat transmembrane protein kinase, putative chr5:25600232-25603618 I	
AM389116	2.064	no similarity	
EV046827	2.061	no similarity	
JCVI_7161	2.061	moderately similar to (337)AT3G50060 Symbols: MYB77 MYB77; DNA binding / transcription factor chr3:18569129-18570034 R	
EE563466	2.061	no similarity	
JCVI_37344	2.060	moderately similar to (421)AT2G44220 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G44240.1); similar t	3.696
JCVI_11305	2.059	highly similar to (827)AT3G22520 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G14840.1); similar to unr	
CX270847	2.059	no similarity	
EX131682	2.058	weakly similar to (163)AT5G44730 Symbols: haloacid dehalogenase-like hydrolase family protein chr5:18062815-18063746 REVE	
JCVI_35972	2.057	very weakly similar to (93.2)AT2G31945 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G05575.1); similar	
EV215352	2.056	no similarity	
JCVI_32780	2.053	no original description	
JCVI_41102	2.053	no original description	
RC_EE558774	2.053	no similarity	
CD819016	2.051	moderately similar to (204)AT5G04530 Symbols: beta-ketoacyl-CoA synthase family protein chr5:1292223-1293617 REVERSE [1	
CV432234	2.051	very weakly similar to (87.4)AT2G01450 Symbols: ATPMK17 ATPMK17 (Arabidopsis thaliana MAP kinase 17); MAP kinase chr2:	
JCVI_29355	2.050	no original description	
JCVI_13749	2.049	moderately similar to (340)AT1G80070 Symbols: EMB158, EMB33, EMB177, EMB14, SUS2 SUS2 (ABNORMAL SUSPENSOR	
EV064850	2.049	no similarity	
EV173253	2.048	moderately similar to (432)AT3G27970 Symbols: exonuclease chr3:10390846-10392781 FORWARD [21486] 102 877 877	
ES269021	2.048	no similarity	
JCVI_35831	2.048	weakly similar to (103)AT4G15280 Symbols: UDP-glucuronosyl/UDP-glucosyl transferase family protein chr4:8719182-8720618 I	
EE559030	2.047	no similarity	
EV164136	2.045	weakly similar to (172)AT4G27080 Symbols: ATPDIL5-4 ATPDIL5-4 (PDI-LIKE 5-4) chr4:13589162-13593341 FORWARD [21	
JCVI_23106	2.045	no original description	
EE438020	2.045	weakly similar to (102)AT5G51210 Symbols: OLEO3 OLEO3 (OLEOSIN3) chr5:20837397-20837932 FORWARDvery weakly sin	
EE439045	2.043	no similarity	
EE547503	2.043	no similarity	1.198
EV150094	2.042	weakly similar to (151)AT5G51220 Symbols: ubiquinol-cytochrome C chaperone family protein chr5:20838631-20840351 REVER	2.021
RC_L46444	2.042	no similarity	
EV113522	2.041	moderately similar to (210)AT4G17800 Symbols: DNA-binding protein-related chr4:9895562-9896440 REVERSE [21479]	
JCVI_9305	2.040	highly similar to (692)AT4G19120 Symbols: ERD3 ERD3 (EARLY-RESPONSIVE TO DEHYDRATION 3) chr4:10460676-10462	
JCVI_21660	2.039	weakly similar to (148)ATMG01360 Symbols: COX1 cytochrome c oxidase subunit 1 chrM:349830-351413 REVERSEweakly simi	
JCVI_26941	2.039	moderately similar to (248)AT5G02960 Symbols: 40S ribosomal protein S23 (RPS23B) chr5:693278-694394 REVERSEmoderate	
EX088920	2.038	moderately similar to (303)AT2G31580 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G32320.1); similar t	

JCVI_12862	2.038	moderately similar to (211)AT5G37790 Symbols: protein kinase family protein chr5:15025663-15028255 REVERSE no original de	
JCVI_25462	2.037	no original description	
JCVI_13618	2.037	moderately similar to (227)AT4G01280 Symbols: myb family transcription factor chr4:535288-536854 FORWARD no original des	
JCVI_37995	2.037	highly similar to (508)AT4G24250 Symbols: ATMLO13, MLO13 MLO13 (MILDEW RESISTANCE LOCUS O 13); calmodulin bin	
EV194567	2.036	no similarity	
EV090075	2.036	no similarity	
H07212	2.035	no similarity	2.695
JCVI_21495	2.035	weakly similar to (140)AT1G24160 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G70100.3); similar to un	
JCVI_21658	2.035	no original description	
JCVI_19565	2.034	no original description	
RC_EV064436	2.033	no similarity	
EL589202	2.033	moderately similar to (373)AT1G55810 Symbols: uracil phosphoribosyltransferase, putative / UMP pyrophosphorylase, putative / UF	
ES269387	2.033	moderately similar to (473)AT2G25600 Symbols: AKT6, SPIK SPIK (SHAKER POLLEN INWARD K+ CHANNEL); cyclic nucleo	
JCVI_25123	2.033	weakly similar to (176)AT5G20380 Symbols: transporter-related chr5:6887938-6892360 REVERSE no original description	
EE559382	2.033	very weakly similar to (92.4)AT3G60040 Symbols: F-box family protein chr3:22186914-22190705 REVERSE [20153] 18 563 563	
EX088005	2.032	no similarity	
EV163883	2.032	no similarity	
JCVI_4292	2.031	moderately similar to (205)AT4G14420 Symbols: lesion inducing protein-related chr4:8302167-8303734 REVERSE no original des	
JCVI_18863	2.031	weakly similar to (150)AT3G58850 Symbols: PAR2 PAR2 (PHY RAPIDLY REGULATED 2); transcription regulator chr3:217705	
JCVI_3379	2.031	moderately similar to (469)AT5G39320 Symbols: UDP-glucose 6-dehydrogenase, putative chr5:15760482-15761924 FORWARDn	
CX266960	2.028	no similarity	
EB041738	2.027	no similarity	
JCVI_21520	2.027	no original description	
EE431349	2.027	moderately similar to (222)AT1G47600 Symbols: glycosyl hydrolase family 1 protein chr1:17494211-17497029 FORWARDweakl	
JCVI_27606	2.027	moderately similar to (270)AT1G59660 Symbols: nucleoporin family protein chr1:21928358-21932898 FORWARD no original de	
JCVI_6200	2.027	moderately similar to (432)AT3G15450 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G27450.1); similar t	
JCVI_20045	2.027	moderately similar to (399)AT4G38530 Symbols: ATPLC1 ATPLC1 (PHOSPHOLIPASE C 1); phospholipase C chr4:18020702-18	
EV216785	2.027	no similarity	
JCVI_40202	2.026	very weakly similar to (83.6)AT4G27657 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G27652.1) chr4:1:	
JCVI_19632	2.025	moderately similar to (421)AT5G12080 Symbols: mechanosensitive ion channel domain-containing protein / MS ion channel domain	
JCVI_12561	2.024	no original description	
EE448803	2.024	weakly similar to (150)AT1G11480 Symbols: eukaryotic translation initiation factor-related chr1:3864368-3866707 REVERSE [20	4.507
EE453480	2.022	no similarity	
JCVI_21756	2.022	moderately similar to (263)AT1G72520 Symbols: lipoxygenase, putative chr1:27312273-27316251 FORWARDweakly similar to (	
EV132818	2.022	no similarity	
JCVI_38351	2.022	no original description	
JCVI_6543	2.022	very weakly similar to (96.3)AT3G24080 Symbols: KRR1 family protein chr3:8695198-8697114 REVERSE no original description	
JCVI_30203	2.019	no original description	
AM057474	2.019	no similarity	
JCVI_27328	2.018	moderately similar to (269)AT1G78160 Symbols: APUM7 APUM7 (ARABIDOPSIS PUMILIO 7); RNA binding chr1:29412793-2'	
RC_ES951332	2.018	no similarity	
ES938339	2.018	weakly similar to (173)AT3G12820 Symbols: AtMYB10 AtMYB10 (myb domain protein 10); DNA binding / transcription factor ch	
JCVI_13863	2.017	moderately similar to (398)AT5G13050 Symbols: 5-FCL 5-FCL; 5-formyltetrahydrofolate cyclo-ligase chr5:4137265-4138714 REV	
EB041739	2.017	no similarity	
EV182652	2.016	no similarity	
EE485895	2.015	no similarity	
EV088245	2.014	weakly similar to (129)AT4G35600 Symbols: CONNEXIN 32 CONNEXIN 32; kinase chr4:16896453-16898719 FORWARD [214	
EE558058	2.014	no similarity	
EV109748	2.013	no similarity	
EV222413	2.013	no similarity	
ES962947	2.012	no similarity	
JCVI_42135	2.012	moderately similar to (356)AT1G59900 Symbols: AT-E1 ALPHA AT-E1 ALPHA (pyruvate dehydrogenase complex E1 alpha subun	
RC_EE462682	2.011	no similarity	
RC_JCVI_19560	2.011	no original description	
ES998460	2.011	no similarity	
EE531816	2.011	very weakly similar to (96.3)AT4G29090 Symbols: reverse transcriptase, putative / RNA-dependent DNA polymerase, putative chr4:	
EX086786	2.010	moderately similar to (283)AT3G28940 Symbols: avirulence-responsive protein, putative / avirulence induced gene (AIG) protein, pu	
EX045585	2.010	no similarity	
CX270567	2.009	weakly similar to (109)AT5G15540 Symbols: EMB2773 EMB2773 (EMBRYO DEFECTIVE 2773); binding / protein binding / zinc	
JCVI_10122	2.009	weakly similar to (171)AT5G57790 Symbols: unknown protein chr5:23429469-23430668 REVERSE no original description	
EV068125	2.008	no similarity	
EV129846	2.008	no similarity	
JCVI_38684	2.007	no original description	
ES969123	2.007	no similarity	
JCVI_3752	2.006	moderately similar to (307)AT1G31880 Symbols: NIP3;1, NLM9, BRX BRX/NIP3;1/NLM9 (BREVIS RADIX); identical protein bi	
EE524530	2.006	moderately similar to (202)AT3G26780 Symbols: catalytic chr3:9849984-9851514 FORWARD [20143]	
EH419213	2.005	no similarity	
JCVI_29307	2.005	weakly similar to (125)AT5G13300 Symbols: VAN3, SFC SFC (SCARFACE) chr5:4255926-4262021 REVERSE no original descr	
ES959432	2.005	very weakly similar to (100)AT1G08520 Symbols: PDE166, CHLD CHLD/PDE166 (PIGMENT DEFECTIVE 166); magnesium che	
RC_JCVI_24506	2.004	no original description	
H07426	2.004	no similarity	
EV226604	2.004	no similarity	
JCVI_36867	2.003	very weakly similar to (94.7)AT2G26850 Symbols: F-box family protein chr2:11456447-11457967 REVERSE no original descripti	
EV192330	2.002	no similarity	
EE473381	2.001	weakly similar to (130)AT1G72570 Symbols: DNA binding / transcription factor chr1:27335043-27337360 FORWARD [20163]	2.714
JCVI_23621	1.999	no original description	3.157
EX137551	1.999	moderately similar to (236)AT3G04370 Symbols: Identical to Cysteine-rich repeat secretory protein 39 precursor (CRRSP39) [Arabid	
EE508434	1.998	weakly similar to (111)AT3G03410 Symbols: calmodulin-related protein, putative chr3:8111331-811726 REVERSE [15718] 1 490	
JCVI_35686	1.998	no original description	
BG543161	1.997	no similarity	
CN727560	1.995	very weakly similar to (99.0)AT1G08750 Symbols: GPI-anchor transamidase, putative chr1:2801286-2804395 FORWARD [15722]	
EX119983	1.995	no similarity	2.573
JCVI_13982	1.994	no original description	

JCVI_18023	1.994	weakly similar to (186)AT3G24550 Symbols: ATPERK1 ATPERK1 (PROLINE EXTENSIN-LIKE RECEPTOR KINASE 1); ATP t	
EX016696	1.994	no similarity	
JCVI_36742	1.994	no original description	
EV160261	1.993	weakly similar to (107)AT1G32920 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G32928.1) chr1:11928t	
ES968137	1.991	no similarity	
EV094248	1.991	very weakly similar to (82.4)AT3G57260 Symbols: PR2, BG2, PR-2, BGL2 BGL2 (PATHOGENESIS-RELATED PROTEIN 2); glu	
DY009744	1.991	no similarity	
JCVI_4868	1.991	moderately similar to (325)AT1G67730 Symbols: YBR159 YBR159; ketoreductase/ oxidoreductase chr1:25395339-25397028 FOR	
JCVI_3657	1.989	moderately similar to (240)AT2G46030 Symbols: UBC6 UBC6 (UBIQUITIN-CONJUGATING ENZYME 6); ubiquitin-protein ligas	
EV060838	1.988	moderately similar to (209)AT1G71070 Symbols: glycosyltransferase family 14 protein / core-2/I-branching enzyme family protein	
JCVI_7741	1.986	no original description	
RC_JCVI_42038	1.985	no original description	
AM396053	1.985	no similarity	
JCVI_171	1.984	moderately similar to (229)AT5G67420 Symbols: LBD37 LBD37 (LOB DOMAIN-CONTAINING PROTEIN 37) chr5:26921802-2	
CD815607	1.984	weakly similar to (181)AT4G24970 Symbols: ATP-binding region, ATPase-like domain-containing protein chr4:12831135-128354t	
EX093682	1.984	no similarity	
EV191670	1.983	no similarity	
EE423429	1.983	no similarity	
JCVI_14630	1.983	no original description	
JCVI_42282	1.982	weakly similar to (162)AT3G25585 Symbols: AAPT2 AAPT2 (AMINOALCOHOLPHOSPHOTRANSFERASE); phosphatidyltransf	
JCVI_39310	1.982	no original description	2.019
EV091050	1.981	moderately similar to (203)AT1G14620 Symbols: DECOY DECOY (endoxylglucan transferase A2) chr1:5014943-5016496 REVE	
CN727410	1.980	moderately similar to (262)AT5G64190 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G40390.1); similar t	2.341
EE534969	1.980	no similarity	
EX083822	1.977	very weakly similar to (91.7)AT1G54040 Symbols: ESR, TASTY, ESP ESP (EPITHIOSPECIFIER PROTEIN) chr1:20174663-2017	
EV134209	1.977	no similarity	
EV197150	1.977	no similarity	
EV108126	1.977	weakly similar to (127)AT3G03100 Symbols: NADH:ubiquinone oxidoreductase family protein chr3:705571-707585 REVERSE [2	
JCVI_23044	1.977	weakly similar to (155)AT1G13390 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G68490.1); similar to un	
RC_ES967962	1.977	no similarity	
ES965114	1.975	no similarity	
ES967006	1.975	no similarity	
EE568004	1.975	no similarity	
EE569332	1.975	weakly similar to (129)AT1G54070 Symbols: dormancy/auxin associated protein-related chr1:20186351-20186910 FORWARD [2(	
JCVI_33502	1.973	moderately similar to (450)AT4G31940 Symbols: CYP82C4 CYP82C4 (cytochrome P450, family 82, subfamily C, polypeptide 4); o	
JCVI_10773	1.973	no original description	
ES967676	1.973	no similarity	
EV105096	1.971	no similarity	
EE557906	1.971	no similarity	
JCVI_7498	1.971	no original description	
EV193158	1.971	moderately similar to (206)AT1G09932 Symbols: phosphoglycerate/bisphosphoglycerate mutase-related chr1:3230718-3232926 RE	
EV100424	1.969	moderately similar to (385)AT1G60590 Symbols: polygalacturonase, putative / pectinase, putative chr1:22318091-22320532 REVE	
AM394903	1.968	no similarity	3.560
RC_JCVI_40485	1.968	no original description	
JCVI_32942	1.967	no original description	
EV170896	1.967	moderately similar to (254)AT5G25900 Symbols: CYP701A3, GA3 GA3 (GA REQUIRING 3); oxygen binding chr5:9036076-903t	
EV085654	1.966	no similarity	2.081
EV209930	1.966	no similarity	
EX040735	1.966	weakly similar to (160)AT2G17800 Symbols: ARAC1, ATGP2, ATRAC1, RAC1, ROP3, AtROP3 ARAC1/ATGP2/ATRAC1/AtRO	
EX097145	1.966	weakly similar to (144)AT5G41690 Symbols: RNA binding chr5:16687354-16691417 REVERSE [21824]	
JCVI_16727	1.965	moderately similar to (207)AT1G19730 Symbols: ATH4, ATTRX4 ATTRX4 (thioredoxin H-type 4); thiol-disulfide exchange interm	
CV432081	1.964	no similarity	2.596
JCVI_30734	1.964	moderately similar to (208)AT1G71400 Symbols: disease resistance family protein / LRR family protein chr1:26913567-26916110	
JCVI_31836	1.964	no original description	
CV973910	1.964	no similarity	
CV973916	1.964	no similarity	
EV098722	1.964	moderately similar to (270)AT1G14740 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G63500.2); similar t	
JCVI_11504	1.963	moderately similar to (361)AT1G18300 Symbols: ATNUDT4 ATNUDT4 (Arabidopsis thaliana Nudix hydrolase homolog 4); hydroly	
JCVI_22028	1.962	highly similar to (506)AT1G61130 Symbols: SCPL32 SCPL32; serine carboxypeptidase chr1:22532689-22535449 REVERSEmode	
EV208608	1.961	no similarity	
JCVI_15928	1.961	weakly similar to (103)AT3G12750 Symbols: ZIP1 ZIP1 (ZINC TRANSPORTER 1 PRECURSOR); zinc ion transmembrane transpo	1.672
ES936686	1.958	no similarity	
JCVI_16840	1.957	weakly similar to (163)AT1G27100 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G69900.1); similar to hy	
JCVI_17852	1.955	moderately similar to (461)AT3G22104 Symbols: phototropic-responsive NPH3 protein-related chr3:7789821-7792186 FORWARD	1.775
EE467749	1.954	no similarity	2.632
JCVI_34813	1.954	no original description	
EE550610	1.953	no similarity	
EV142231	1.953	no similarity	
JCVI_10689	1.953	no original description	4.871
JCVI_5423	1.951	moderately similar to (325)AT3G61880 Symbols: CYP78A9 CYP78A9 (CYTOCHROME P450 78A9); oxygen binding chr3:22917	
JCVI_28609	1.951	no original description	
JCVI_12043	1.950	weakly similar to (164)AT4G32090 Symbols: galactosyltransferase chr4:15509996-15510826 REVERSE no original description	
EV063153	1.948	no similarity	
JCVI_13279	1.948	moderately similar to (385)AT1G10010 Symbols: AAP8 AAP8 (amino acid permease 8); amino acid transmembrane transporter chr:	
ES997598	1.948	no similarity	
EV109865	1.947	no similarity	
EX067093	1.946	no similarity	2.732
JCVI_20223	1.946	no original description	3.518
JCVI_10128	1.946	no original description	
EV100308	1.946	weakly similar to (189)AT5G59660 Symbols: leucine-rich repeat protein kinase, putative chr5:24052913-24057205 FORWARDver	
DY015548	1.946	weakly similar to (192)AT1G09570 Symbols: FHY2, FRE1, HY8, PHYA PHYA (PHYTOCHROME A) chr1:3095500-3098894 RI	1.724
EE568833	1.946	weakly similar to (103)AT5G06070 Symbols: RAB, RBE RBE (RABBIT EARS); nucleic acid binding / transcription factor/ zinc ion	
AM386883	1.945	weakly similar to (191)AT1G76600 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G21010.1); similar to hy	

CD828547	1.945	no similarity	
EE392293	1.943	weakly similar to (131)AT2G42480 Symbols: meprin and TRAF homology domain-containing protein / MATH domain-containing p	
EV176999	1.943	very weakly similar to (95.9)AT5G23630 Symbols: (MALE GAMETOGENESIS IMPAIRED ANTHERS); cation-transporting ATPa	
EX101625	1.943	no similarity	
JCVI_4372	1.943	moderately similar to (303)AT4G26720 Symbols: EP124, PPX-1, EP129, PPX1 PPX1 (protein phosphatase x-1); protein serine/threo	
JCVI_30567	1.942	weakly similar to (166)AT2G43810 Symbols: small nuclear ribonucleoprotein F, putative / U6 snRNA-associated Sm-like protein, pu	
EV089696	1.942	no similarity	
EV134137	1.942	no similarity	
EE413685	1.940	moderately similar to (277)AT1G27020 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G27030.1); similar t	
EV192716	1.940	weakly similar to (198)AT5G02490 Symbols: heat shock cognate 70 kDa protein 2 (HSC70-2) (HSP70-2) chr5:550294-552563 RE	
CD823627	1.940	no similarity	
ES938422	1.940	no similarity	
EE568889	1.939	no similarity	
EE445726	1.939	no similarity	
RC_ES899340	1.939	no similarity	3.337
JCVI_7980	1.938	no original description	
JCVI_35395	1.936	no original description	
EV144299	1.935	no similarity	
EE530127	1.934	no similarity	
DY025489	1.934	moderately similar to (467)AT5G51810 Symbols: GA20OX2, AT2353, ATGA20OX2 AT2353/ATGA20OX2/GA20OX2 (GIBBERI	
CX268053	1.933	weakly similar to (127)AT1G60830 Symbols: U2 snRNP auxiliary factor large subunit, putative chr1:22398723-22399268 REVER'	
EE471019	1.933	no similarity	2.554
ES914604	1.932	no similarity	
EV163400	1.931	no similarity	
JCVI_21881	1.929	no original description	2.722
H74867	1.927	no similarity	
CD830177	1.926	no similarity	
EE454397	1.926	moderately similar to (207)AT3G11460 Symbols: pentatricopeptide (PPR) repeat-containing protein chr3:3608256-3610127 FORW	
JCVI_7542	1.925	very weakly similar to (82.0)AT2G24450 Symbols: FLA3 FLA3 (FASCICLIN-LIKE ARABINOGALACTAN PROTEIN 3 PRECUR	
JCVI_24052	1.925	moderately similar to (215)AT1G09660 Symbols: KH domain-containing quaking protein, putative chr1:3128207-3130793 REVER	
RC_DY014259	1.925	no similarity	
EE561338	1.924	no similarity	
ES965210	1.923	no similarity	1.897
EV151707	1.923	no similarity	
JCVI_11805	1.922	highly similar to (863)AT5G40270 Symbols: metal-dependent phosphohydrolase HD domain-containing protein chr5:16110622-16'	4.838
EV147666	1.920	no similarity	
JCVI_15183	1.920	highly similar to (608)AT3G52200 Symbols: LTA3 LTA3 (Dihydrolipoamide S-acetyltransferase 3); dihydrolipoyllysine-residue acet	
EV142230	1.920	moderately similar to (246)AT3G47610 Symbols: transcription regulator/ zinc ion binding chr3:17560163-17562189 FORWARD	
JCVI_34418	1.920	weakly similar to (169)AT2G21470 Symbols: ATSAE2, EMB2764, SAE2 SAE2 (SUMO-ACTIVATING ENZYME 2) chr2:92058'	
JCVI_11409	1.920	no original description	
CX193796	1.919	no similarity	
JCVI_6677	1.919	moderately similar to (387)AT4G29700 Symbols: type I phosphodiesterase/nucleotide pyrophosphatase family protein chr4:145437-	
ES901797	1.919	moderately similar to (467)AT5G09640 Symbols: SCPL19, SNG2 SNG2 (SINAPOYLGLUCOSE ACCUMULATOR 2); serine carb	
JCVI_32770	1.918	no original description	
JCVI_34440	1.917	moderately similar to (214)AT4G13350 Symbols: human Rev interacting-like protein-related / hRIP protein-related chr4:7770166-7	
EX055332	1.916	moderately similar to (228)AT5G18880 Symbols: glucose transmembrane transporter chr5:6300537-6301424 REVERSE [21813]	
EV220133	1.916	no similarity	
EE442548	1.916	no similarity	
EE560050	1.915	no similarity	
EV127979	1.915	no similarity	
ES906146	1.915	moderately similar to (362)AT2G17080 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G17070.1); similar t	
JCVI_28934	1.915	moderately similar to (376)AT2G29740 Symbols: UDP-glucuronosyl/UDP-glucosyl transferase family protein chr2:12713824-1271	
JCVI_3404	1.915	moderately similar to (384)AT3G50060 Symbols: MYB77 MYB77; DNA binding / transcription factor chr3:18569129-18570034 R	
JCVI_23195	1.914	weakly similar to (177)AT4G23550 Symbols: WRKY29 WRKY29 (WRKY DNA-binding protein 29); transcription factor chr4:122	
RC_H07302	1.912	no similarity	
JCVI_6241	1.912	highly similar to (521)AT4G37320 Symbols: CYP81D5 CYP81D5 (cytochrome P450, family 81, subfamily D, polypeptide 5); oxyge	
JCVI_39267	1.912	highly similar to (649)AT4G00660 Symbols: DEAD/DEAH box helicase, putative chr4:274638-277438 FORWARDweakly similar	
JCVI_16889	1.912	weakly similar to (103)AT4G23496 Symbols: SP1L5 SP1L5 (SPIRAL1-LIKE5) chr4:12257924-12258307 REVERSE no original d	2.202
EV032701	1.911	no similarity	
EX043377	1.911	weakly similar to (118)AT3G09530 Symbols: ATEXO70H3 ATEXO70H3 (exocyst subunit EXO70 family protein H3); protein bindi	
EV026904	1.908	moderately similar to (317)AT2G37700 Symbols: similar to CER1 protein, putative [Arabidopsis thaliana] (TAIR:AT1G02190.1); sii	
EV146041	1.908	no similarity	
JCVI_39230	1.908	no original description	
EE564724	1.908	no similarity	
ES899313	1.907	no similarity	
EE532266	1.906	moderately similar to (305)AT3G14490 Symbols: terpene synthase/cyclase family protein chr3:4863638-4865956 REVERSEweakl'	
JCVI_35529	1.904	no original description	3.477
JCVI_25830	1.903	moderately similar to (248)AT1G07570 Symbols: APK1, APK1A APK1A (Arabidopsis protein kinase 1A); kinase chr1:2331366-23	
EX135316	1.903	no similarity	2.964
EV108280	1.903	no similarity	
EE558691	1.902	no similarity	
EV152555	1.902	no similarity	
EV130895	1.902	no similarity	
JCVI_15023	1.902	moderately similar to (262)AT4G14350 Symbols: protein kinase family protein chr4:8256349-8259930 REVERSE no original desc	-1.952
EV092671	1.902	moderately similar to (264)AT2G24765 Symbols: ARF3, ARL1, ATARL1 ARF3/ARL1/ATARL1 (ADP-RIBOSYLATION FACTOI	
ES968428	1.901	no similarity	
EV142567	1.900	no similarity	
EE565008	1.899	no similarity	
EE474833	1.899	no similarity	
EE559048	1.898	no similarity	
EE550318	1.898	weakly similar to (101)AT1G74680 Symbols: exostosin family protein chr1:28063189-28064645 FORWARD [20184] 1 349 407	
JCVI_42268	1.897	no original description	
CN729010	1.897	no similarity	

RC_CO750204	1.896	no similarity	2.769
JCVI_42216	1.894	no original description	
EV075089	1.894	no similarity	
ES920481	1.894	weakly similar to (182)AT5G49330 Symbols: AtMYB111 AtMYB111 (myb domain protein 111); DNA binding / transcription factor	
EE558707	1.893	no similarity	
JCVI_16518	1.893	moderately similar to (232)AT1G75450 Symbols: ATCKX5, ATCKX6, CKX5 CKX5 (CYTOKININ OXIDASE 5); cytokinin dehyd	
EE502213	1.892	weakly similar to (199)AT2G04520 Symbols: eukaryotic translation initiation factor 1A, putative / eIF-1A, putative / eIF-4C, putative	
JCVI_23825	1.890	no original description	
ES968980	1.890	no similarity	
EX016437	1.890	weakly similar to (115)AT5G59510 Symbols: RTFL5, DVL18 DVL18/RTFL5 (ROTUNDIFOLIA LIKE 5) chr5:24007315-240077.	
JCVI_36328	1.890	nearly identical (1134)AT5G41770 Symbols: crooked neck protein, putative / cell cycle protein, putative chr5:16735249-16738164 F	
EE561047	1.889	no similarity	
DR697814	1.889	no similarity	
EE557936	1.889	no similarity	
JCVI_27478	1.888	weakly similar to (117)AT3G22270 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G14990.1); similar to un	
EV110410	1.887	no similarity	
JCVI_5721	1.887	moderately similar to (332)AT1G17810 Symbols: BETA-TIP BETA-TIP (BETA-TONOPLAST INTRINSIC PROTEIN); water chan	
EX030008	1.887	no similarity	
EV212682	1.887	no similarity	
EE566996	1.886	no similarity	
EV198952	1.884	weakly similar to (127)AT3G57810 Symbols: OTU-like cysteine protease family protein chr3:21427313-21428786 FORWARD [21	
ES968507	1.882	no similarity	
EV002408	1.882	no similarity	
EL587213	1.882	no similarity	
AM059211	1.882	no similarity	
EE567172	1.881	no similarity	
EE561058	1.881	no similarity	
EE559320	1.880	no similarity	
EE441925	1.880	no similarity	-1.496
EV091905	1.880	no similarity	
EV224947	1.880	moderately similar to (281)AT5G56190 Symbols: WD-40 repeat family protein chr5:22759880-22762135 FORWARD [21493] 16	1.502
JCVI_2893	1.880	moderately similar to (402)AT5G62180 Symbols: ATCXE20 ATCXE20 (ARABIDOPSIS THALIANA CARBOXYESTERASE 20);	
JCVI_29162	1.880	highly similar to (594)AT1G24530 Symbols: transducin family protein / WD-40 repeat family protein chr1:8693274-8694530 FOR	
JCVI_33081	1.880	moderately similar to (238)AT1G29900 Symbols: CARB CARB (CARBAMOYL PHOSPHATE SYNTHETASE B); ATP binding / e	
CN827556	1.879	moderately similar to (350)AT1G30810 Symbols: transcription factor jumonji (jmj) family protein / zinc finger (C5HC2 type) family	
RC_EV169393	1.879	no similarity	
JCVI_35396	1.878	no original description	
EE555609	1.877	no similarity	
EE535427	1.877	no similarity	
RC_L38119	1.875	no similarity	1.290
DY006402	1.875	weakly similar to (115)AT5G08260 Symbols: SCPL35 SCPL35 (serine carboxypeptidase-like 35); serine carboxypeptidase chr5:265	
JCVI_8107	1.875	no original description	
JCVI_15635	1.874	moderately similar to (275)AT5G62020 Symbols: HSFB2A, AT-HSFB2A AT-HSFB2A (Arabidopsis thaliana heat shock transcriptio	
EV116513	1.873	weakly similar to (150)AT1G19770 Symbols: ATPUP14 ATPUP14 (Arabidopsis thaliana purine permease 14); purine transmembran	
EX067845	1.871	weakly similar to (150)AT5G67010 Symbols: AP2 domain-containing transcription factor, putative chr5:26766284-26766842 REV	
JCVI_40120	1.871	no original description	
RC_ES969136	1.870	no similarity	
JCVI_23844	1.869	no original description	
EV165796	1.866	no similarity	
DY024008	1.865	no similarity	
JCVI_11671	1.865	no original description	
EX020287	1.865	weakly similar to (133)AT1G09420 Symbols: G6PD4 G6PD4 (GLUCOSE-6-PHOSPHATE DEHYDROGENASE 4); glucose-6-pho	
JCVI_39013	1.865	weakly similar to (177)AT1G69935 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G33780.1); similar to un	
EV145554	1.864	no similarity	2.527
EV091919	1.864	weakly similar to (123)AT1G14410 Symbols: ATWHY1, PTAC1 ATWHY1/PTAC1 (A. THALIANA WHIRLY 1); DNA binding / t	
RC_EV001684	1.864	no similarity	
RC_L46581	1.864	no similarity	
EV095136	1.863	no similarity	2.508
EV101256	1.861	no similarity	
EV226837	1.861	no similarity	
JCVI_20838	1.860	no original description	
JCVI_23101	1.860	no original description	
EV136808	1.860	no similarity	
ES911858	1.858	moderately similar to (461)AT4G19680 Symbols: IRT2 IRT2 (iron-responsive transporter 2); iron ion transmembrane transporter/ zinc	
JCVI_26452	1.858	weakly similar to (184)AT3G26120 Symbols: TEL1 TEL1 (TERMINAL EAR1-LIKE 1); RNA binding chr3:9547635-9550423 FOI	
ES901851	1.858	moderately similar to (390)AT5G05570 Symbols: transducin family protein / WD-40 repeat family protein chr5:1656767-1663729	
JCVI_592	1.856	moderately similar to (252)AT1G15860 Symbols: calcium ion binding chr1:5455050-5456735 FORWARD no original description	
EE556882	1.856	no similarity	
EX032619	1.856	no similarity	
JCVI_35354	1.855	no original description	
JCVI_14118	1.855	moderately similar to (284)AT4G23050 Symbols: protein kinase, putative chr4:12080123-12083719 FORWARD no original descri	
EE564522	1.854	no similarity	
EV065223	1.853	no similarity	
EV157628	1.852	weakly similar to (182)AT1G14460 Symbols: DNA polymerase-related chr1:4948957-4952745 REVERSE [21484]	
JCVI_41752	1.852	weakly similar to (135)AT3G13350 Symbols: high mobility group (HMG1/2) family protein / ARID/BRIGHT DNA-binding domain	
CX272501	1.852	no similarity	4.669
JCVI_31911	1.851	no original description	
JCVI_25083	1.851	no original description	
JCVI_5217	1.851	moderately similar to (223)AT5G04150 Symbols: BHLH101 BHLH101; DNA binding / transcription factor chr5:1138560-1139477	1.185
EV068666	1.849	moderately similar to (313)AT3G09090 Symbols: DEX1 DEX1 (DEFECTIVE IN EXINE FORMATION 1) chr3:2783170-2787557	
EE566491	1.848	no similarity	
JCVI_23973	1.847	no original description	
JCVI_31530	1.846	no original description	2.297

JCVI_18647	1.845	weakly similar to (179)AT3G02550 Symbols: LBD41 LBD41 (LOB DOMAIN-CONTAINING PROTEIN 41) chr3:536754-537657	
JCVI_17337	1.845	moderately similar to (210)AT1G32750 Symbols: TAF1, HAF1, HAC13, GTD1, HAF01 HAF01 (HISTONE ACETYLTRANSFERASE 1) chr1:1007028-11007612 FORWARD [21487] 80 1092 109	2.302
JCVI_5778	1.845	moderately similar to (392)AT2G37210 Symbols: Encodes a protein of unknown function. It has been crystallized and shown to be similar to the protein encoded by the human gene HSP70.	
EE502373	1.844	no similarity	
EV135177	1.843	weakly similar to (144)AT4G16530 Symbols: binding chr4:9311378-9315576 FORWARD [21481] 1 461 751	
JCVI_1506	1.843	weakly similar to (181)AT3G02470 Symbols: SAMDC SAMDC (S-ADENOSYLMETHIONINE DECARBOXYLASE) chr3:51023	
CD817935	1.843	no similarity	
ES982268	1.843	no similarity	
EV146998	1.842	no similarity	
JCVI_20973	1.841	weakly similar to (150)AT2G45140 Symbols: vesicle-associated membrane protein, putative / VAMP, putative chr2:18618104-18621104 FORWARD [21487] 16 547 73	
ES982756	1.839	no similarity	
JCVI_37318	1.838	moderately similar to (267)AT5G63370 Symbols: protein kinase family protein chr5:25402180-25403616 REVERSE [21487] 80 1092 109	
ES930133	1.838	very weakly similar to (100)AT4G20880 Symbols: ethylene-responsive nuclear protein / ethylene-regulated nuclear protein (ERT2) chr4:9865364-9866730 FORWARD [21487] 16 547 73	
EX099443	1.838	no similarity	
CN827568	1.838	moderately similar to (252)AT5G23720 Symbols: PHS1 PHS1 (PROPYLAMIDE-HYPERSENSITIVE 1); protein tyrosine/serine/threonine kinase	
EV221042	1.837	no similarity	
EV205064	1.837	no similarity	
JCVI_32240	1.836	no original description	
JCVI_14542	1.836	no original description	3.435
EV112284	1.836	no similarity	2.498
EE560671	1.835	no similarity	
H07703	1.833	no similarity	3.341
JCVI_7791	1.832	no original description	
CD815331	1.831	no similarity	
JCVI_36009	1.831	no original description	
JCVI_23709	1.830	moderately similar to (301)AT2G36020 Symbols: HVA22J HVA22J (HVA22-LIKE PROTEIN J) chr2:15130503-15132219 REVERSE [21487] 80 1092 109	3.316
ES267439	1.829	no similarity	
JCVI_15545	1.829	no original description	
EE557056	1.828	no similarity	3.742
JCVI_12764	1.828	moderately similar to (265)AT4G17730 Symbols: ATSYP23, SYP23 SYP23 (syntaxin 23) chr4:9865364-9866730 FORWARD [21487] 16 547 73	
JCVI_24351	1.828	no original description	
EE559717	1.827	no similarity	
RC_EV109019	1.827	no similarity	
CD839772	1.827	weakly similar to (140)AT2G22170 Symbols: lipid-associated family protein chr2:9434090-9434822 REVERSE [13982]	
EV159377	1.827	moderately similar to (420)AT3G28430 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO69571.1); similar to the protein encoded by the human gene HSP70.	
EE463115	1.827	no similarity	3.436
EV144905	1.826	no similarity	
EV130759	1.826	no similarity	2.779
ES939515	1.824	moderately similar to (231)AT1G76250 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO62018.1) chr1:2861	
JCVI_18184	1.824	no original description	
AM394657	1.824	no similarity	
JCVI_11535	1.824	moderately similar to (447)AT2G22490 Symbols: CYCD2;1 CYCD2;1 (CYCLIN D2;1); cyclin-dependent protein kinase regulator/ phosphatase	
EV146941	1.823	no similarity	
H74903	1.822	no similarity	
EX127610	1.822	no similarity	
EV123932	1.821	moderately similar to (412)AT2G26440 Symbols: pectinesterase family protein chr2:11254485-11256485 FORWARD [21487] 16 547 73	
EV176822	1.820	moderately similar to (347)AT5G11490 Symbols: adaptin family protein chr5:3671965-3676145 FORWARD [21487] 80 1092 109	
EV101497	1.818	no similarity	-1.186
JCVI_27423	1.818	weakly similar to (149)AT1G14910 Symbols: epsin N-terminal homology (ENTH) domain-containing protein chr1:5139923-514351 FORWARD [21487] 16 547 73	
JCVI_37307	1.818	very weakly similar to (100)AT3G29000 Symbols: calcium-binding EF hand family protein chr3:11007028-11007612 FORWARD [21487] 16 547 73	
JCVI_29635	1.817	moderately similar to (327)AT3G47360 Symbols: ATHSD3 ATHSD3 (HYDROXYSTEROID DEHYDROGENASE 3); oxidoreductase	
EE413535	1.817	very weakly similar to (82.0)AT3G17520 Symbols: late embryogenesis abundant domain-containing protein / LEA domain-containing protein	2.782
ES933407	1.816	weakly similar to (119)AT5G47690 Symbols: binding chr5:19335125-19344240 FORWARD [20143] 1 357 371	
EE439537	1.815	no similarity	
EE563418	1.814	no similarity	
EX089824	1.814	no similarity	2.195
JCVI_34109	1.814	no original description	
BQ704694	1.813	no similarity	
JCVI_38866	1.812	no original description	1.893
EE502258	1.812	no similarity	
EV180758	1.812	weakly similar to (144)AT1G21890 Symbols: nodulin MtN21 family protein chr1:7682797-7685570 REVERSE [21487] 16 547 73	
EV223885	1.811	weakly similar to (105)AT5G13820 Symbols: ATBP-1, ATBP1, ATTBP1, HPPBF-1, TBP1 TBP1 (TELOMERIC DNA BINDING PROTEIN 1)	
H07316	1.811	no similarity	
EV098557	1.811	no similarity	3.483
JCVI_16389	1.811	weakly similar to (142)AT4G08670 Symbols: protease inhibitor/seed storage/lipid transfer protein (LTP) family protein chr4:553671	
JCVI_29569	1.810	moderately similar to (296)AT4G26720 Symbols: EP124, PPX-1, EP129, PPX1 PPX1 (protein phosphatase x-1); protein serine/threonine phosphatase	
CX271936	1.810	moderately similar to (222)AT3G58820 Symbols: F-box family protein chr3:21763937-21765592 FORWARD [16815]	
ES968707	1.809	no similarity	
JCVI_20770	1.809	weakly similar to (145)AT2G20835 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G15534.1); similar to the protein encoded by the human gene HSP70.	
RC_ES967741	1.808	no similarity	
JCVI_28364	1.808	moderately similar to (461)AT5G45780 Symbols: leucine-rich repeat transmembrane protein kinase, putative chr5:18584173-18586173 FORWARD [21487] 16 547 73	4.279
RC_EE558983	1.808	no similarity	
EE426054	1.808	weakly similar to (179)AT1G72570 Symbols: DNA binding / transcription factor chr1:27335043-27337360 FORWARD [20189]	
JCVI_10440	1.807	weakly similar to (198)AT1G47270 Symbols: AtTLP6 AtTLP6 (TUBBY LIKE PROTEIN 6); phosphoric diester hydrolase/ transcriptase	
CO750001	1.807	moderately similar to (217)AT4G04570 Symbols: protein kinase family protein chr4:2290043-2292253 FORWARD [16161]	
JCVI_21051	1.806	no original description	
JCVI_9657	1.804	moderately similar to (355)AT3G03420 Symbols: Ku70-binding family protein chr3:812534-813651 FORWARD [21487] 16 547 73	
EE527123	1.801	no similarity	
JCVI_4685	1.801	moderately similar to (277)AT5G11160 Symbols: APT5 APT5 (ADENINE PHOSPHORIBOSYLTRANSFERASE 5); adenine phosphatase	
JCVI_27186	1.801	weakly similar to (199)AT4G27280 Symbols: calcium-binding EF hand family protein chr4:13663776-13664168 REVERSE [21487] 16 547 73	
RC_JCVI_34456	1.801	no original description	
JCVI_15360	1.800	weakly similar to (155)AT5G01960 Symbols: zinc finger (C3HC4-type RING finger) family protein chr5:370808-372772 FORWARD [21487] 16 547 73	
EE559149	1.799	no similarity	-1.554

JCVI_10145	1.799	highly similar to (831)AT3G25840 Symbols: protein kinase family protein chr3:9454230-9457559 REVERSEweakly similar to (12	
JCVI_3479	1.799	moderately similar to (325)AT2G25150 Symbols: transferase family protein chr2:10709661-10711345 REVERSE no original descr	
RC_EE501888	1.798	no similarity	
EV063739	1.798	no similarity	
JCVI_27803	1.798	moderately similar to (281)AT2G24210 Symbols: TPS10 TPS10 (TERPENE SYNTHASE 10); myrcene/(E)-beta-ocimene synthase	
RC_CN735168	1.798	no similarity	
EE547059	1.794	no similarity	2.271
EE546377	1.793	no similarity	
JCVI_22353	1.792	very weakly similar to (85.5)AT5G48140 Symbols: polygalacturonase, putative / pectinase, putative chr5:19536133-19537638 REV1	
EV110965	1.792	no similarity	
EE558884	1.791	no similarity	
JCVI_545	1.791	no original description	
RC_AM057182	1.790	no similarity	
JCVI_30427	1.788	moderately similar to (234)AT1G18740 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G74450.1); similar t	
JCVI_4001	1.787	highly similar to (642)AT5G62790 Symbols: PDE129, DXR DXR (1-DEOXY-D-XYLULOSE 5-PHOSPHATE REDUCTOISOME)	
EX038628	1.786	moderately similar to (364)AT1G51410 Symbols: cinnamyl-alcohol dehydrogenase, putative (CAD) chr1:19063553-19065092 FOR	
EE502143	1.783	moderately similar to (277)AT4G02080 Symbols: ATSARA1C, ATSAR2, ASAR1 ASAR1 (Arabidopsis thaliana secretion-associated	1.774
JCVI_31190	1.783	no original description	
EE392256	1.783	moderately similar to (216)AT1G02690 Symbols: importin alpha-2 subunit, putative chr1:584397-587036 FORWARDweakly simil	3.133
EV047330	1.782	no similarity	
EV226389	1.782	no similarity	
EE568299	1.781	no similarity	1.751
CD828081	1.781	no similarity	
JCVI_9944	1.780	very weakly similar to (95.9)AT2G33520 Symbols: similar to proline-rich family protein [Arabidopsis thaliana] (TAIR:AT1G12810.1	
EE473185	1.780	no similarity	
JCVI_15249	1.779	moderately similar to (325)AT3G17810 Symbols: dihydroorotate dehydrogenase family protein / dihydroorotate oxidase family prote	
JCVI_39917	1.779	weakly similar to (121)AT1G70410 Symbols: carbonic anhydrase, putative / carbonate dehydratase, putative chr1:26537830-265411	
EV135881	1.778	no similarity	
JCVI_29424	1.777	no original description	
EV149959	1.777	no similarity	2.858
CD812606	1.777	weakly similar to (129)AT3G44110 Symbols: ATJ, ATJ3 ATJ3 (Arabidopsis thaliana DnaJ homologue 3) chr3:15880166-15882046	
EE564414	1.776	no similarity	
JCVI_27747	1.776	moderately similar to (425)AT5G25430 Symbols: anion exchange protein family chr5:8851254-8854262 FORWARD no original d	
EE568267	1.776	no similarity	
ES954012	1.775	no similarity	
AM387291	1.774	no similarity	
JCVI_10057	1.773	moderately similar to (396)AT5G48100 Symbols: LAC15, TT10 TT10 (TRANSPARENT TESTA 10); laccase chr5:19506756-1950	
JCVI_32184	1.771	weakly similar to (135)AT2G28430 Symbols: similar to unknown [Populus trichocarpa] (GB:ABK94614.1) chr2:12166813-121674	
JCVI_12087	1.770	no original description	
JCVI_630	1.770	no original description	
EV215200	1.768	no similarity	
EV151095	1.768	no similarity	
JCVI_27431	1.766	no original description	
JCVI_41634	1.765	no original description	
EV075020	1.765	no similarity	
JCVI_32346	1.764	moderately similar to (456)AT5G37020 Symbols: ARF8 ARF8 (AUXIN RESPONSE FACTOR 8) chr5:14647381-14651146 FORV	4.621
EE559769	1.763	no similarity	
AM394870	1.763	no similarity	
EV165884	1.763	weakly similar to (126)AT4G38170 Symbols: FRS9 FRS9 (FAR1-related sequence 9); zinc ion binding chr4:17904607-17906433 F	
EE502259	1.762	no similarity	
EE567435	1.761	weakly similar to (117)AT5G22880 Symbols: H2B, HTB2 H2B/HTB2 (HISTONE H2B); DNA binding chr5:7652133-7652570 RE	
JCVI_12315	1.760	moderately similar to (216)AT1G05600 Symbols: pentatricopeptide (PPR) repeat-containing protein chr1:1672160-1673674 FORW	
ES964533	1.760	no similarity	
JCVI_12680	1.760	moderately similar to (327)AT1G52600 Symbols: signal peptidase, putative chr1:19594281-19596155 FORWARD no original desc	
EV128496	1.759	no similarity	
ES966380	1.758	no similarity	
CD826220	1.758	no similarity	
JCVI_31755	1.757	moderately similar to (391)AT1G18800 Symbols: NRP2 NRP2 (NAP1-RELATED PROTEIN 2); DNA binding / chromatin binding /	
EE564779	1.757	no similarity	
JCVI_11316	1.756	weakly similar to (130)AT5G44540 Symbols: tapetum-specific protein-related chr5:17958514-17958873 REVERSE no original des	
JCVI_38387	1.755	moderately similar to (225)AT2G36460 Symbols: fructose-bisphosphate aldolase, putative chr2:15304008-15304811 REVERSEmo	2.523
RC_AT000660	1.754	no similarity	
EX019686	1.753	weakly similar to (169)AT1G02730 Symbols: CSLD5, ATCSLD5 ATCSLD5 (CELLULOSE SYNTHASE-LIKE D5); 1,4-beta-D-xy	
EE491541	1.752	no similarity	
JCVI_11306	1.752	moderately similar to (466)AT1G17840 Symbols: WBC11, ABCG11, DSO, COF1 ABCG11/COF1/DSO/WBC11 (DESPERADO); ;	
EE562280	1.751	no similarity	2.478
EE479477	1.751	no similarity	
H06424	1.751	no similarity	
CD825434	1.751	no similarity	
JCVI_32964	1.751	no original description	
JCVI_21823	1.750	no original description	
JCVI_41609	1.750	weakly similar to (155)AT4G04614 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO22561.1); similar to hypo	1.279
EV225197	1.750	no similarity	
EX045323	1.749	moderately similar to (296)AT3G05580 Symbols: serine/threonine protein phosphatase, putative chr3:1618222-1619856 REVERSE	
EE449338	1.749	no similarity	
EV060159	1.749	no similarity	
EV125321	1.748	moderately similar to (464)AT2G22070 Symbols: pentatricopeptide (PPR) repeat-containing protein chr2:9390682-9393042 FORW	
CV546087	1.748	no similarity	
EV085386	1.748	no similarity	
EV147391	1.748	no similarity	
ES947980	1.747	no similarity	
EV103116	1.746	no similarity	
EE403898	1.745	weakly similar to (119)AT5G10820 Symbols: integral membrane transporter family protein chr5:3420877-3423167 REVERSE [16f	

JCVI_11723	1.744	no original description	
EV176810	1.744	no similarity	
EV057037	1.744	moderately similar to (234)AT4G11850 Symbols: MEE54 PLDGAMMA1 (maternal effect embryo arrest 54); phospholipase D chr4	
AM387499	1.743	no similarity	1.791
JCVI_292	1.742	moderately similar to (284)AT2G17480 Symbols: ATMLO8, MLO8 MLO8 (MILDEW RESISTANCE LOCUS O 8); calmodulin bin	
EE468849	1.741	very weakly similar to (95.9)AT4G23160 Symbols: protein kinase family protein chr4:12129496-12134097 FORWARD [20156]	
JCVI_40662	1.740	moderately similar to (253)AT5G24470 Symbols: PRR5, APRR5 APRR5 (PSEUDO-RESPONSE REGULATOR 5); transcription re	
JCVI_23700	1.739	no original description	
JCVI_29668	1.737	no original description	
EV091712	1.737	weakly similar to (182)AT1G72050 Symbols: zinc finger (C2H2 type) family protein chr1:27119470-27120890 FORWARD [2147]	
EE562464	1.735	no similarity	
EE568820	1.734	no similarity	
EV178478	1.734	no similarity	
JCVI_41484	1.733	no original description	
EV108402	1.733	no similarity	3.158
EV101393	1.732	moderately similar to (201)AT4G02500 Symbols: ATXT2 ATXT2; UDP-xylosyltransferase/ transferase/ transferase, transferring glyc	
EE533412	1.732	no similarity	
JCVI_4697	1.732	weakly similar to (193)AT2G47460 Symbols: MYB12, ATMYB12 ATMYB12/MYB12 (MYB DOMAIN PROTEIN 12); DNA bind	2.682
EE563050	1.732	no similarity	
EV104299	1.731	no similarity	
EV104369	1.731	weakly similar to (113)AT1G77920 Symbols: bZIP family transcription factor chr1:29303853-29305501 FORWARD [21478] 1 38	
RC_EE462179	1.730	no similarity	
ES979266	1.730	no similarity	
JCVI_3468	1.730	moderately similar to (499)AT1G68530 Symbols: CER6, G2, POP1, CUT1 CUT1 (CUTICULAR 1); catalytic chr1:2571263-2571	
JCVI_12686	1.728	very weakly similar to (92.0)AT3G18295 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G48770.1); similar	
CD832055	1.727	no similarity	
ES992740	1.727	very weakly similar to (95.5)AT5G51150 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G34630.1); similar	
H07440	1.727	no similarity	
EX044792	1.726	weakly similar to (144)AT4G13710 Symbols: pectate lyase family protein chr4:7962546-7966008 FORWARDvery weakly similar t	
CX188493	1.726	no similarity	
EV033347	1.726	no similarity	
JCVI_19655	1.723	no original description	
JCVI_13277	1.723	no original description	
ES904390	1.722	moderately similar to (331)AT3G51340 Symbols: pepsin A chr3:19067992-19070767 REVERSE [21432]	
EE561202	1.722	no similarity	
EV152311	1.722	no similarity	
EE502361	1.722	no similarity	
JCVI_33258	1.721	moderately similar to (204)AT3G07150 Symbols: similar to hypothetical protein [Vitis vinifera] (GB:CAN68821.1) chr3:2263812-;	
EE562017	1.721	no similarity	
JCVI_20854	1.721	moderately similar to (416)AT3G27170 Symbols: ATCLC-B, CLC-B CLC-B (chloride channel protein B); anion channel/ voltage-gai	
RC_EV171149	1.720	no similarity	
JCVI_36881	1.720	very weakly similar to (83.6)AT4G20870 Symbols: fatty acid hydroxylase, putative chr4:11174631-11175889 REVERSE no origina	
EE469983	1.720	no similarity	
ES912522	1.719	weakly similar to (103)AT4G22640 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G22666.1); similar to un	
EV217391	1.719	no similarity	
EV145829	1.719	no similarity	
EV227344	1.718	very weakly similar to (94.0)AT3G57050 Symbols: CBL CBL (CYSTATHIONINE BETA-LYASE) chr3:21122918-21125500 REV	
EV115639	1.717	weakly similar to (170)AT2G46860 Symbols: ATPPA3 ATPPA3 (ARABIDOPSIS THALIANA PYROPHOSPHORYLASE 3); inorg	
RC_CV974015	1.717	no similarity	
H07193	1.717	no similarity	
EV024333	1.717	no similarity	
EV102580	1.716	no similarity	
JCVI_40354	1.715	no original description	
EV189801	1.714	moderately similar to (217)AT1G18420 Symbols: similar to ATALMT9 (ALUMINUM-ACTIVATED MALATE TRANSPORTER)	
CN728159	1.712	no similarity	
EV223123	1.712	no similarity	
JCVI_29879	1.712	moderately similar to (253)AT2G17510 Symbols: EMB2763 EMB2763 (EMBRYO DEFECTIVE 2763); RNA binding / ribonucleas	
EV043014	1.711	no similarity	1.780
EE557448	1.711	no similarity	
JCVI_12956	1.710	no original description	2.235
JCVI_25865	1.708	weakly similar to (154)AT5G22070 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G52060.2); similar to un	
JCVI_29079	1.707	no original description	
JCVI_448	1.707	moderately similar to (362)AT3G23080 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G14500.1); similar t	
DY014788	1.707	very weakly similar to (99.0)AT1G03830 Symbols: guanylate-binding family protein chr1:962127-966621 REVERSE [18966]	
JCVI_32596	1.707	moderately similar to (316)AT5G46910 Symbols: transcription factor jumonji (jmi) family protein chr5:19065007-19068107 FORV	
JCVI_8823	1.706	weakly similar to (182)AT5G20830 Symbols: SUS1, ASUS1, ATSUS1 SUS1 (SUCROSE SYNTHASE 1); UDP-glycosyltransferase/	
RC_CD836255	1.706	no similarity	1.402
JCVI_1810	1.705	moderately similar to (416)AT3G07680 Symbols: emp24/gp25L/p24 family protein chr3:2455633-2456658 FORWARD no origina	
EV191047	1.705	no similarity	
JCVI_12735	1.704	moderately similar to (457)AT4G28520 Symbols: CRC, CRU3 CRU3 (CRUCIFERIN 3) chr4:14087602-14089235 FORWARDhig	
JCVI_8469	1.703	moderately similar to (401)AT4G38160 Symbols: PDE191 PDE191 (PIGMENT DEFECTIVE 191) chr4:17902406-17903778 FOR	
BG544144	1.701	very weakly similar to (97.1)AT5G05670 Symbols: signal recognition particle binding chr5:1695917-1697535 REVERSE [8791] 1 .	
JCVI_24437	1.700	moderately similar to (296)AT4G33920 Symbols: protein phosphatase 2C family protein / PP2C family protein chr4:16260881-162	
CX192092	1.700	weakly similar to (125)AT2G33690 Symbols: late embryogenesis abundant protein, putative / LEA protein, putative chr2:14259275-	
EE559528	1.700	no similarity	
EE559687	1.699	no similarity	
JCVI_10809	1.698	moderately similar to (253)AT1G28590 Symbols: lipase, putative chr1:10047495-10049286 REVERSEvery weakly similar to (84.0	2.475
CX270121	1.698	weakly similar to (176)AT1G18190 Symbols: GC2 GC2 (GOLGIN CANDIDATE 2) chr1:6257956-6261318 REVERSE [16815] 1!	
EX132152	1.698	moderately similar to (242)AT1G80820 Symbols: CCR2 CCR2 (CINNAMOYL COA REDUCTASE) chr1:30375538-30377352 FC	
EV089702	1.697	weakly similar to (114)AT3G19170 Symbols: ATPREP1, ATZNMP ATPREP1/ATZNMP (PRESEQUENCE PROTEASE 1); metall	
EE502180	1.697	weakly similar to (193)AT5G51040 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO23083.1); contains InterP	
JCVI_38753	1.695	moderately similar to (479)AT4G26010 Symbols: peroxidase, putative chr4:13200662-13201697 FORWARDmoderately similar to	
EB041761	1.694	no similarity	

EE501998	1.694	weakly similar to (137)AT2G23090 Symbols: Identical to Uncharacterized protein At2g23090 [Arabidopsis thaliana] (GB:O64818);	-1.959
RC_ES948491	1.694	no similarity	
JCVI_27817	1.694	moderately similar to (362)AT3G44050 Symbols: kinesin motor protein-related chr3:15829725-15835779 FORWARD no original d	
EX138069	1.693	moderately similar to (471)AT4G08040 Symbols: ACS11 ACS11 (1-Amino-cyclopropane-1-carboxylate synthase 11); 1-aminocyclo	
EV128803	1.693	no similarity	1.910
EE566677	1.691	no similarity	
EV207729	1.691	no similarity	
RC_EE559934	1.691	no similarity	2.191
EE561150	1.690	no similarity	6.596
CO749673	1.689	no similarity	
JCVI_36133	1.689	moderately similar to (416)AT3G49600 Symbols: UBP26 UBP26 (ubiquitin-specific protease 26); ubiquitin-specific protease chr3:1	
EV132438	1.689	no similarity	
RC_JCVI_42214	1.689	no original description	
JCVI_15454	1.688	weakly similar to (163)AT2G18300 Symbols: basic helix-loop-helix (bHLH) family protein chr2:7960104-7961528 REVERSE no o	
EE563413	1.688	no similarity	2.896
EV054789	1.688	no similarity	
H74693	1.688	no similarity	
EV227465	1.687	no similarity	
EV226810	1.686	weakly similar to (167)AT4G25630 Symbols: ATFIB2, FIB2 FIB2 (FIBRILLARIN 2) chr4:13074248-13076214 FORWARD [2149	
JCVI_25142	1.686	no original description	
JCVI_2540	1.686	very weakly similar to (84.0)AT5G59960 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO21698.1) chr5:241:	
CX267699	1.686	weakly similar to (156)AT1G11880 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO22037.1); contains InterP	
DN962582	1.684	no similarity	
DN961527	1.683	moderately similar to (243)AT5G48790 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G73060.1); similar t	
RC_EX016781	1.683	no similarity	
JCVI_39273	1.682	no original description	
EE415349	1.682	no similarity	
JCVI_6044	1.681	no original description	
EV111606	1.681	no similarity	
JCVI_38215	1.679	moderately similar to (228)AT3G54770 Symbols: RNA recognition motif (RRM)-containing protein chr3:20284841-20286709 RE	
EE567363	1.677	no similarity	5.290
JCVI_32610	1.676	weakly similar to (184)AT2G25360 Symbols: zinc finger protein-related chr2:10811328-10812840 FORWARD no original descript	
JCVI_1222	1.674	highly similar to (583)AT1G13260 Symbols: RAV1 RAV1 (Related to ABI3/VP1 1); DNA binding / transcription factor chr1:45423	
JCVI_27148	1.674	moderately similar to (218)AT4G21710 Symbols: EMB1989, RPB2, NRPB2 NRPB2 (EMBRYO DEFECTIVE 1989); DNA binding	-1.574
JCVI_41873	1.673	weakly similar to (110)AT3G13677 Symbols: similar to unknown [Populus trichocarpa] (GB:ABK93532.1) chr3:4476303-4477099	
JCVI_6876	1.672	moderately similar to (283)AT3G46550 Symbols: SOS5 SOS5 (SALT OVERLY SENSITIVE 5) chr3:17147597-17148859 REVER	
EV122790	1.671	very weakly similar to (82.4)AT2G03120 Symbols: signal peptide peptidase family protein chr2:937551-940080 FORWARD [2147:	
JCVI_31056	1.671	weakly similar to (126)AT4G05010 Symbols: F-box family protein chr4:2567472-2568160 FORWARD no original description	
EV218355	1.669	no similarity	
JCVI_9205	1.669	weakly similar to (106)AT2G14900 Symbols: gibberellin-regulated family protein chr2:6411292-6412125 FORWARD no original d	
JCVI_40876	1.667	no original description	
EE566526	1.666	no similarity	
JCVI_17594	1.666	weakly similar to (132)AT3G01500 Symbols: CA1 CA1 (CARBONIC ANHYDRASE 1); carbonate dehydratase/ zinc ion binding cl	
ES993383	1.665	no similarity	1.274
EX025934	1.664	moderately similar to (264)AT5G38100 Symbols: methyltransferase-related chr5:15217014-15218398 REVERSE [21810] 1 661 67	
ES980004	1.664	no similarity	
JCVI_23839	1.663	weakly similar to (137)AT1G65020 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO62149.1); contains InterP	
CD822668	1.662	no similarity	
CX280196	1.662	no similarity	
EV005095	1.661	weakly similar to (129)AT3G19100 Symbols: calcium-dependent protein kinase, putative / CDPK, putative chr3:6605687-6608986	
EV099418	1.661	moderately similar to (211)AT1G74170 Symbols: protein binding chr1:27895216-27899102 REVERSE [21477]	2.601
JCVI_18828	1.661	moderately similar to (350)AT2G35610 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G70630.1); similar t	
AM390087	1.661	weakly similar to (130)ATMG00730 Symbols: COX3 Encodes cytochrome c oxidase subunit 3. chrM:218280-219077 FORWARDv	
EV159516	1.661	moderately similar to (318)AT2G35320 Symbols: ATEYA ATEYA (ARABIDOPSIS THALIANA EYES ABSENT HOMOLOG); pr	
EV056990	1.661	weakly similar to (127)AT5G01860 Symbols: zinc finger (C2H2 type) family protein chr5:335627-336274 FORWARD [21442]	
JCVI_31810	1.655	moderately similar to (241)AT5G61170 Symbols: 40S ribosomal protein S19 (RPS19C) chr5:24628384-24629428 FORWARDwea	
JCVI_10781	1.655	moderately similar to (294)AT1G20816 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G76405.2); similar t	
EE564467	1.654	no similarity	
RC_EE567283	1.653	no similarity	
JCVI_20231	1.653	weakly similar to (101)AT3G10800 Symbols: BZIP28 BZIP28; DNA binding / transcription factor chr3:3379331-3381435 FORWA	
ES980826	1.653	weakly similar to (118)AT5G08460 Symbols: GDSL-motif lipase/hydrolase family protein chr5:2733221-2735352 FORWARD [21	
EV099882	1.652	weakly similar to (119)AT1G31810 Symbols: actin binding chr1:11399903-11405742 REVERSE [21477]	
AT000440	1.652	no similarity	
EV165402	1.652	no similarity	
EV213685	1.651	moderately similar to (210)AT4G24500 Symbols: hydroxyproline-rich glycoprotein family protein chr4:12658742-12660221 FORV	3.189
JCVI_27326	1.649	moderately similar to (406)AT3G33530 Symbols: transducin family protein / WD-40 repeat family protein chr3:14096340-1410443	
EV166336	1.648	moderately similar to (235)AT5G57100 Symbols: transporter-related chr5:23123789-23125666 REVERSE [21486]	
EE450638	1.648	weakly similar to (155)AT3G07340 Symbols: basic helix-loop-helix (bHLH) family protein chr3:2341194-2343294 REVERSE [20	
JCVI_31999	1.648	no original description	
JCVI_36145	1.646	weakly similar to (166)AT5G08460 Symbols: GDSL-motif lipase/hydrolase family protein chr5:2733221-2735352 FORWARD no	2.049
JCVI_3357	1.646	moderately similar to (236)AT5G20130 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO21131.1) chr5:6797	
EV172610	1.645	no similarity	
RC_ES965115	1.644	no similarity	
JCVI_17427	1.644	moderately similar to (230)AT4G37240 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G23690.1); similar t	
EV225312	1.643	weakly similar to (148)AT2G39720 Symbols: RHC2A RHC2A (RING-H2 finger C2A); protein binding / zinc ion binding chr2:1657	
JCVI_5701	1.643	highly similar to (815)AT3G05910 Symbols: pectinacetylsterase, putative chr3:1764515-1767246 REVERSE no original descripti	
JCVI_1424	1.643	weakly similar to (101)AT3G54360 Symbols: protein binding / zinc ion binding chr3:20139548-20142559 REVERSE no original d	
EX063324	1.641	very weakly similar to (81.6)AT1G60500 Symbols: dynamin family protein chr1:22295247-22297487 FORWARD [21814]	
JCVI_24368	1.641	no original description	
EV213935	1.641	no similarity	
JCVI_1046	1.641	no original description	
JCVI_27292	1.640	highly similar to (504)AT1G20150 Symbols: subtilase family protein chr1:6987323-6990352 REVERSE no original description	2.496
JCVI_487	1.638	highly similar to (586)AT1G18740 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G74450.1); similar to unr	1.220

DY030758	1.637	weakly similar to (111)AT1G17360 Symbols: COP1-interacting protein-related chr1:5947434-5951210 FORWARD [18973]	
JCVI_23476	1.637	moderately similar to (312)AT4G18050 Symbols: PGP9 PGP9 (P-GLYCOPROTEIN 9); ATPase, coupled to transmembrane movem	2.150
EE529641	1.637	weakly similar to (104)AT5G59710 Symbols: ATVIP2, VIP2 VIP2 (VIRE2 INTERACTING PROTEIN2); transcription regulator ch	3.096
JCVI_5942	1.637	moderately similar to (296)AT5G01160 Symbols: e-cadherin binding protein-related chr5:54279-55726 FORWARD no original des	
EX134973	1.636	very weakly similar to (92.8)AT5G17920 Symbols: ATMETS, ATMS1, ATCIMS ATCIMS (COBALAMIN-INDEPENDENT METH	
RC_EE557370	1.635	no similarity	2.225
JCVI_32278	1.635	no original description	
RC_EE566596	1.635	no similarity	
EX094943	1.635	very weakly similar to (81.6)AT1G19770 Symbols: ATPUP14 ATPUP14 (Arabidopsis thaliana purine permease 14); purine transmem	2.582
ES952392	1.634	no similarity	
EV109547	1.634	no similarity	
EE565219	1.633	no similarity	
RC_JCVI_22611	1.632	no original description	
EV099239	1.632	weakly similar to (135)AT3G55110 Symbols: ABC transporter family protein chr3:20435743-20437869 REVERSE [21477]	
EE568265	1.631	no similarity	
RC_EE565891	1.631	no similarity	
JCVI_33452	1.630	moderately similar to (234)AT1G68580 Symbols: agenet domain-containing protein / bromo-adjacent homology (BAH) domain-cont	
EV187726	1.630	no similarity	
JCVI_38563	1.630	weakly similar to (138)AT3G19580 Symbols: AZF2 AZF2 (ARABIDOPSIS ZINC-FINGER PROTEIN 2) chr3:6803299-6804120 F	
JCVI_35689	1.629	weakly similar to (104)AT1G17970 Symbols: zinc finger (C3HC4-type RING finger) family protein chr1:6185025-6187195 FORW	
AM058095	1.624	weakly similar to (113)AT1G16130 Symbols: WAKL2 WAKL2 (WALL ASSOCIATED KINASE-LIKE 2); kinase chr1:5525628-5	1.831
EE449463	1.624	no similarity	
JCVI_15891	1.624	no original description	
JCVI_7849	1.623	no original description	
JCVI_17175	1.623	no original description	
RC_EX018585	1.623	no similarity	
JCVI_27236	1.622	moderately similar to (234)AT3G05960 Symbols: sugar transporter, putative chr3:1783593-1785340 REVERSEmoderately similar	
RC_ES967426	1.622	no similarity	1.161
JCVI_19599	1.620	weakly similar to (133)AT2G35880 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G32330.3); similar to un	2.524
JCVI_25017	1.620	nearly identical (1139)AT1G50200 Symbols: ACD, ALATS ALATS (ALANYL-TRNA SYNTHETASE); ATP binding / alanine-tRN,	
JCVI_14685	1.620	no original description	
JCVI_24319	1.619	no original description	
JCVI_38747	1.618	no original description	
EE561010	1.616	no similarity	
RC_JCVI_41110	1.616	no original description	
RC_JCVI_30899	1.615	no original description	
ES949733	1.614	weakly similar to (102)AT2G34320 Symbols: nucleic acid binding chr2:14492038-14492916 FORWARD [21393] 1 528 543	
CD842452	1.614	no similarity	
JCVI_13591	1.614	weakly similar to (184)AT2G30020 Symbols: protein phosphatase 2C, putative / PP2C, putative chr2:12821514-12822981 FORWA	1.692
JCVI_9015	1.614	weakly similar to (174)AT5G47320 Symbols: RPS19 RPS19 (40S ribosomal protein S19); RNA binding chr5:19221028-19222178	
EE567109	1.613	no similarity	
EE408517	1.612	no similarity	3.702
JCVI_6399	1.609	moderately similar to (269)AT1G19770 Symbols: ATPUP14 ATPUP14 (Arabidopsis thaliana purine permease 14); purine transmemt	2.378
JCVI_42480	1.609	no original description	
EV178524	1.608	no similarity	
EE562863	1.606	no similarity	
JCVI_35554	1.606	moderately similar to (483)AT3G16630 Symbols: ATKINESIN-13A, KINESIN-13A ATKINESIN-13A/KINESIN-13A; microtubule	
DN961326	1.605	moderately similar to (297)AT2G27600 Symbols: SKD1, VPS4 SKD1/VPS4; ATP binding chr2:11788303-11790807 FORWARDv	
EV013733	1.605	weakly similar to (157)AT5G54650 Symbols: ATFH5, Fh5 Fh5 (FORMIN HOMOLOG5); actin binding chr5:22215082-2221887	
JCVI_491	1.604	moderately similar to (202)AT3G48860 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G23700.1); similar t	
CV973973	1.603	no similarity	
JCVI_27908	1.602	no original description	
EE483198	1.601	no similarity	
JCVI_41234	1.601	moderately similar to (376)AT4G31910 Symbols: transferase family protein chr4:15441131-15443702 FORWARD no original desc	
JCVI_33249	1.601	weakly similar to (186)AT2G42110 Symbols: similar to unknown [Populus trichocarpa] (GB:ABK94541.1); similar to unknown [Po]	
EE556047	1.600	no similarity	
EV142282	1.600	no similarity	
JCVI_25794	1.600	no original description	3.388
EV132091	1.600	no similarity	
RC_AM395286	1.598	no similarity	
EE465690	1.597	no similarity	
ES956530	1.597	no similarity	
CX188266	1.597	no similarity	
JCVI_13557	1.597	no original description	
EV146460	1.597	no similarity	
JCVI_37999	1.597	no original description	
JCVI_32042	1.596	highly similar to (572)AT4G10710 Symbols: SPT16 SPT16 (GLOBAL TRANSCRIPTION FACTOR C); metalloexopeptidase chr4:	
JCVI_22377	1.596	no original description	
JCVI_41374	1.596	no original description	
EV107977	1.595	no similarity	
JCVI_35945	1.595	no original description	1.634
ES941720	1.594	no similarity	2.185
JCVI_37468	1.594	very weakly similar to (81.6)AT5G60710 Symbols: zinc finger (C3HC4-type RING finger) family protein chr5:24428179-24432075	
JCVI_6962	1.593	moderately similar to (324)AT3G16840 Symbols: ATP-dependent helicase chr3:5738026-5743048 REVERSE no original descripti	
CD813496	1.593	no similarity	
EV160049	1.593	weakly similar to (186)AT3G19360 Symbols: zinc finger (CCCH-type) family protein chr3:6707550-6708870 FORWARD [21484]	
JCVI_22420	1.592	no original description	
JCVI_37547	1.592	no original description	
EX094245	1.592	no similarity	
ES902651	1.590	weakly similar to (142)AT3G05490 Symbols: RALFL22 RALFL22 (RALF-LIKE 22) chr3:1591387-1591746 FORWARD [21432]	
EE502207	1.589	moderately similar to (246)AT3G60820 Symbols: PBF1 PBF1 (20S proteasome beta subunit F1); peptidase chr3:22483013-2248478	
EV041949	1.588	no similarity	1.205
EV104580	1.587	no similarity	

EV221331	1.587	weakly similar to (178)AT3G08530 Symbols: clathrin heavy chain, putative chr3:2587177-2595417 REVERSE [21492]	
EE558473	1.587	no similarity	
JCVI_24542	1.587	very weakly similar to (85.1)AT3G05480 Symbols: cell cycle checkpoint control protein family chr3:1585389-1588244 FORWARD	
JCVI_35960	1.584	highly similar to (612)AT3G54090 Symbols: pfkB-type carbohydrate kinase family protein chr3:20039123-20040813 FORWARDv	
EE445045	1.582	no similarity	
DQ023570	1.582	moderately similar to (268)AT3G06483 Symbols: ATPDHK, PDK PDK (PYRUVATE DEHYDROGENASE KINASE); ATP bindin	
RC_EE561263	1.581	no similarity	
EE459120	1.581	no similarity	
JCVI_22446	1.579	moderately similar to (271)AT4G22050 Symbols: aspartyl protease family protein chr4:11683877-11685518 FORWARDmoderatel	
EV150296	1.579	no similarity	2.449
EV215705	1.579	no similarity	
JCVI_34831	1.579	no original description	2.501
EE562727	1.579	no similarity	
JCVI_22260	1.578	no original description	
EV109961	1.578	no similarity	
CV973968	1.578	no similarity	1.246
JCVI_41216	1.578	no original description	
EV069942	1.575	no similarity	2.939
JCVI_9130	1.574	highly similar to (517)AT1G62280 Symbols: SLAH1 SLAH1 (SLAC1 HOMOLOGUE 1); transporter chr1:23010974-23012205 RE	
EE563043	1.574	no similarity	
EV008788	1.574	no similarity	
EE446245	1.574	no similarity	
JCVI_42231	1.574	no original description	
CX279538	1.574	no similarity	
EV107311	1.574	moderately similar to (230)AT3G11080 Symbols: disease resistance family protein chr3:3470487-3473318 FORWARD [21478] 51	
EE472497	1.572	no similarity	
JCVI_41664	1.571	no original description	
JCVI_20891	1.571	moderately similar to (250)AT1G05230 Symbols: HDG2 homeobox-leucine zipper family protein / lipid-binding START domain-cor	
EE561932	1.571	no similarity	2.129
AM393924	1.570	no similarity	2.557
EE568263	1.570	no similarity	
EV178531	1.570	no similarity	
JCVI_30630	1.570	highly similar to (520)AT1G14040 Symbols: ATP binding / ATPase, coupled to transmembrane movement of substances chr1:4810	
EX047601	1.570	no similarity	
EV106366	1.570	no similarity	
EV094759	1.569	no similarity	
DY020476	1.568	no similarity	2.961
RC_H07300	1.568	no similarity	
EE431728	1.568	very weakly similar to (82.4)AT4G08395 Symbols: unknown protein chr4:5319631-5320709 FORWARD [20151]	
CX272790	1.567	no similarity	
JCVI_38889	1.567	moderately similar to (264)AT1G17620 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G11890.1); similar t	
EB041727	1.566	no similarity	
RC_EV141714	1.566	no similarity	
EX119499	1.566	no similarity	
EX079614	1.565	moderately similar to (239)AT2G22260 Symbols: oxidoreductase, 2OG-Fe(II) oxygenase family protein chr2:9468422-9470133 FO	
JCVI_39775	1.565	weakly similar to (171)AT1G29350 Symbols: similar to kinase-related [Arabidopsis thaliana] (TAIR:AT1G29370.1); similar to unnai	
JCVI_665	1.565	very weakly similar to (83.2)AT2G41260 Symbols: ATM17, M17 M17 chr2:17213619-17214570 FORWARD no original descriptio	
RC_JCVI_25003	1.563	no original description	1.707
EE489964	1.563	no similarity	1.819
CD835540	1.562	weakly similar to (194)AT4G15240 Symbols: fringe-related protein chr4:8703518-8705378 REVERSE [13981]	
JCVI_18612	1.561	moderately similar to (336)AT5G59520 Symbols: ZIP2 ZIP2 (ZINC TRANSPORTER 2 PRECURSOR); transferase, transferring glyco	1.713
JCVI_25257	1.561	no original description	
ES962397	1.560	no similarity	
EV105033	1.559	no similarity	
AM057728	1.557	no similarity	
EV140579	1.557	no similarity	3.953
JCVI_7222	1.557	weakly similar to (115)AT5G22650 Symbols: HDT02, HDT2, ATHD2B, HDA4, HD2, HD2B HD2B (HISTONE DEACETYLASE 2)	
EX117630	1.557	very weakly similar to (88.2)AT3G57520 Symbols: AT5IP2 AT5IP2 (ARABIDOPSIS THALIANA SEED IMBIBITION 2); hydrolase	
EV206812	1.556	no similarity	
EV108197	1.556	no similarity	
EV104958	1.556	no similarity	
JCVI_3284	1.556	no original description	
JCVI_25402	1.556	moderately similar to (233)AT1G75510 Symbols: transcription initiation factor IIF beta subunit (TFIIF-beta) family protein chr1:285	
CD840477	1.556	weakly similar to (126)AT4G37610 Symbols: BT5 BT5 (BTB and TAZ domain protein 5); protein binding / transcription regulator c	
JCVI_21215	1.556	weakly similar to (127)AT3G21160 Symbols: mannosyl-oligosaccharide 1,2-alpha-mannosidase, putative chr3:7414135-7418334 R	
JCVI_4933	1.555	moderately similar to (407)AT5G55240 Symbols: caleosin-related family protein / embryo-specific protein, putative chr5:22423189	
JCVI_10739	1.555	moderately similar to (263)AT1G73500 Symbols: ATMKK9 ATMKK9 (Arabidopsis thaliana MAP kinase kinase 9); kinase chr1:271	
JCVI_24886	1.554	weakly similar to (169)AT1G24330 Symbols: armadillo/beta-catenin repeat family protein / U-box domain-containing family protein	
JCVI_6423	1.554	moderately similar to (385)AT5G25060 Symbols: RNA recognition motif (RRM)-containing protein chr5:8634222-8639987 REVE	
ES952546	1.553	no similarity	
EE532855	1.553	no similarity	
ES967248	1.551	no similarity	
JCVI_18064	1.551	no original description	
JCVI_18420	1.551	moderately similar to (253)AT1G77840 Symbols: eukaryotic translation initiation factor 5, putative / eIF-5, putative chr1:29273981-	
EE559789	1.550	no similarity	4.052
JCVI_14836	1.550	no original description	2.083
JCVI_6820	1.548	no original description	
EE562330	1.547	no similarity	
EE438788	1.547	no similarity	
EE558591	1.547	no similarity	
RC_EV035662	1.546	no similarity	1.704
EX133841	1.546	no similarity	
JCVI_42244	1.544	no original description	

CD843660	1.544	weakly similar to (191)AT2G19070 Symbols: transferase family protein chr2:8267267-8269040 REVERSE [13982]	
EV000713	1.542	moderately similar to (223)AT5G46420 Symbols: 16S rRNA processing protein RimM family chr5:18847226-18850120 FORWARD	2.217
JCVI_27020	1.540	weakly similar to (134)AT5G62090 Symbols: similar to SLK1 (SEUSS-LIKE 1), transcription regulator [Arabidopsis thaliana] (TAIR	
EV144618	1.540	no similarity	
EV142183	1.539	no similarity	
EV173421	1.539	no similarity	
EE565935	1.539	no similarity	
EV226774	1.537	no similarity	3.259
RC_EV141915	1.537	no similarity	
RC_EE564588	1.536	no similarity	
JCVI_169	1.535	moderately similar to (256)AT3G26070 Symbols: plastid-lipid associated protein PAP / fibrillin family protein chr3:9528141-95294	
JCVI_40949	1.534	no original description	
DW997333	1.533	no similarity	
RC_EE568828	1.533	no similarity	
EV078734	1.533	no similarity	3.329
JCVI_41494	1.533	no original description	
EE406554	1.532	no similarity	
EV064568	1.531	no similarity	2.238
EX055179	1.531	weakly similar to (134)AT2G32360 Symbols: ubiquitin family protein chr2:13744096-13744623 REVERSE [21812]	
JCVI_38972	1.530	no original description	
JCVI_42289	1.529	weakly similar to (137)AT5G12380 Symbols: annexin, putative chr5:4009224-4010688 FORWARDvery weakly similar to (94.0)A	
EV040325	1.528	no similarity	
RC_EV128855	1.527	no similarity	
ES216611	1.526	no similarity	
JCVI_24995	1.526	no original description	
ES979003	1.526	no similarity	
JCVI_40220	1.526	no original description	
JCVI_21007	1.525	no original description	
RC_EE557313	1.524	no similarity	
CD835852	1.523	no similarity	
JCVI_24854	1.522	moderately similar to (273)AT2G40940 Symbols: ERS, ERS1 ERS1 (ETHYLENE RESPONSE SENSOR 1); receptor chr2:170917	
ES907952	1.522	weakly similar to (142)AT5G41761 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G55570.1); similar to un	2.742
JCVI_35060	1.521	moderately similar to (410)AT5G55050 Symbols: GDSL-motif lipase/hydrolase family protein chr5:22354971-22356967 FORWARD	
EV192239	1.520	moderately similar to (298)AT3G10540 Symbols: 3-phosphoinositide-dependent protein kinase, putative chr3:3289921-3292434 FC	
JCVI_12379	1.520	no original description	
EV110091	1.520	no similarity	
EV221831	1.520	moderately similar to (328)AT3G61240 Symbols: DEAD/DEAH box helicase, putative (RH12) chr3:22677565-22680129 FORWARD	3.094
EV013227	1.519	no similarity	
EV185534	1.518	no similarity	3.141
EX038903	1.517	moderately similar to (363)AT1G06250 Symbols: lipase class 3 family protein chr1:1913338-1914849 REVERSE [21811]	
RC_EH425397	1.517	no similarity	
RC_CX188526	1.517	no similarity	
JCVI_36167	1.516	weakly similar to (127)AT5G14090 Symbols: similar to hypothetical protein [Vitis vinifera] (GB:CAN72196.1) chr5:4547232-4549	
EE457779	1.514	moderately similar to (270)AT3G04480 Symbols: endoribonuclease chr3:1193994-1197326 REVERSE [20179]	
JCVI_13327	1.514	moderately similar to (266)AT1G73180 Symbols: eukaryotic translation initiation factor-related chr1:27521996-27524675 FORWARD	
JCVI_32326	1.513	weakly similar to (152)AT5G24400 Symbols: EMB2024 EMB2024 (EMBRYO DEFECTIVE 2024); catalytic chr5:8330535-83317	
H07192	1.512	no similarity	
JCVI_14371	1.511	moderately similar to (244)AT4G34490 Symbols: CAP 1, CAP1, ATCAP1 ATCAP1 (CYCLASE ASSOCIATED PROTEIN 1) chr2	2.881
RC_EX125674	1.511	no similarity	
ES906075	1.510	moderately similar to (390)AT3G14260 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G53870.1); similar t	
EE415842	1.509	no similarity	
EV107180	1.507	no similarity	
EE484017	1.506	weakly similar to (119)AT5G39220 Symbols: hydrolase, alpha/beta fold family protein chr5:15723141-15725267 FORWARD [201	
EV103018	1.504	no similarity	
EV129642	1.503	no similarity	
EV178946	1.503	moderately similar to (390)AT3G59770 Symbols: SAC9 SAC9 (suppressor of actin 9) chr3:22090258-22095762 REVERSE [21487	
RC_ES965522	1.503	no similarity	
JCVI_40706	1.502	no original description	
EE433092	1.502	moderately similar to (225)AT1G21340 Symbols: Dof-type zinc finger domain-containing protein chr1:7476075-7476857 FORWARD	
EV177360	1.502	moderately similar to (204)AT2G21390 Symbols: coatomer protein complex, subunit alpha, putative chr2:9159508-9163657 FORWARD	
EX118448	1.502	moderately similar to (252)AT1G03220 Symbols: extracellular dermal glycoprotein, putative / EDGP, putative chr1:787143-788444	
EV107159	1.502	no similarity	
CV546376	1.501	no similarity	
DY017085	1.500	no similarity	
ES271455	1.500	weakly similar to (168)AT4G32630 Symbols: ARF GTPase activator/ zinc ion binding chr4:15738321-15741418 FORWARD [210	
EV000620	1.500	moderately similar to (353)AT3G14630 Symbols: CYP72A9 CYP72A9 (cytochrome P450, family 72, subfamily A, polypeptide 9); c	
ES958185	1.499	no similarity	
AT000633	1.499	no similarity	3.835
JCVI_30925	1.499	moderately similar to (323)AT2G41340 Symbols: eukaryotic rpb5 RNA polymerase subunit family protein chr2:17236104-1723752	
JCVI_13859	1.498	moderately similar to (210)AT4G08670 Symbols: protease inhibitor/seed storage/lipid transfer protein (LTP) family protein chr4:55	
JCVI_26057	1.497	moderately similar to (303)AT5G60390 Symbols: elongation factor 1-alpha / EF-1-alpha chr5:24306452-24307901 FORWARDdmo	
AT000459	1.496	no similarity	2.297
ES918306	1.496	weakly similar to (156)AT2G02170 Symbols: remorin family protein chr2:556594-558609 REVERSE [15718]	
JCVI_5783	1.495	moderately similar to (342)AT1G04640 Symbols: LIP2 LIP2 (LIPOYLTRANSFERASE 2) chr1:1292540-1293247 FORWARD no	
JCVI_31055	1.494	highly similar to (631)AT5G08280 Symbols: HEMC HEMC (HYDROXYMETHYLBILANE SYNTHASE); hydroxymethylbilane sy	
JCVI_36426	1.493	moderately similar to (209)AT2G23200 Symbols: protein kinase family protein chr2:9886431-9888935 FORWARD no original des	
EX136226	1.493	weakly similar to (108)AT3G13720 Symbols: prenylated rab acceptor (PRA1) family protein chr3:4495209-4495775 REVERSE [2	
CX190389	1.491	weakly similar to (194)AT5G58400 Symbols: peroxidase, putative chr5:23622583-23624193 REVERSEweakly similar to (159)PE	
EV090258	1.490	very weakly similar to (87.4)AT3G17120 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G01960.1); similar	-1.130
JCVI_29503	1.490	very weakly similar to (86.3)AT1G16850 Symbols: unknown protein chr1:5765055-5765611 REVERSE no original description	-1.896
JCVI_32755	1.489	moderately similar to (259)AT4G01360 Symbols: similar to BPS1 (BYPASS 1) [Arabidopsis thaliana] (TAIR:AT1G01550.2); simila	1.520
EV111104	1.488	no similarity	
JCVI_11120	1.488	very weakly similar to (92.4)AT5G44510 Symbols: disease resistance protein (TIR-NBS-LRR class), putative chr5:17946900-17951	

JCVI_36219	1.488	no original description	
RC_EE556547	1.487	no similarity	1.849
EE509045	1.487	no similarity	
CX189964	1.487	weakly similar to (126)AT1G30820 Symbols: CTP synthase, putative / UTP--ammonia ligase, putative chr1:10945232-10948806 R	
EE556555	1.486	no similarity	
CD833602	1.486	no similarity	
JCVI_10814	1.485	moderately similar to (387)AT5G36260 Symbols: aspartyl protease family protein chr5:14302298-14305409 REVERSE no original	
JCVI_39869	1.485	no original description	
ES909140	1.484	moderately similar to (329)AT2G41700 Symbols: similar to ATATH11 (ABC2 homolog 11), ATPase, coupled to transmembrane mc	
JCVI_8380	1.483	no original description	
ES967290	1.483	no similarity	
EV110348	1.483	no similarity	
EX070150	1.482	no similarity	
RC_JCVI_42143	1.482	no original description	
JCVI_28003	1.481	moderately similar to (377)AT5G13680 Symbols: ELO2, ABO1 ABO1/ELO2 (ABA-OVERLY SENSITIVE 1); transcription elongat	1.504
EV130288	1.479	weakly similar to (138)AT3G58780 Symbols: AGL1, SHP1 SHP1 (SHATTERPROOF 1) chr3:21750127-21752743 FORWARDve	
EV084867	1.478	moderately similar to (237)AT1G03080 Symbols: kinase interacting family protein chr1:731794-737332 REVERSE [21444]	
AM060558	1.477	no similarity	
JCVI_11707	1.477	moderately similar to (317)AT1G10870 Symbols: AGD4 AGD4 (ARF-GAP DOMAIN 4); ARF GTPase activator/ protein binding / z	
EV103854	1.477	no similarity	
JCVI_22538	1.476	moderately similar to (258)AT5G26830 Symbols: threonyl-tRNA synthetase / threonine--tRNA ligase (THRRS) chr5:9437354-9441	
JCVI_20186	1.475	no original description	
EV130305	1.475	no similarity	
EV111694	1.475	no similarity	
JCVI_32927	1.475	moderately similar to (390)AT3G14040 Symbols: exopolysaccharuronase / galacturan 1,4-alpha-galacturonidase / pectinase chr3:4648	3.555
EE467127	1.474	moderately similar to (261)AT1G51640 Symbols: ATEXO70G2 ATEXO70G2 (exocyst subunit EXO70 family protein G2); protein t	
EL590556	1.474	weakly similar to (134)AT2G18193 Symbols: AAA-type ATPase family protein chr2:7924703-7926266 REVERSE [20863]	
EV051986	1.473	weakly similar to (103)AT2G46240 Symbols: BAG6, ATBAG6 BAG6 (ARABIDOPSIS THALIANA BCL-2-ASSOCIATED ATHA	
JCVI_23286	1.469	very weakly similar to (81.6)AT1G03850 Symbols: glutaredoxin family protein chr1:977232-977684 REVERSE no original descri	
EE557335	1.469	no similarity	
JCVI_34163	1.468	weakly similar to (132)AT3G56910 Symbols: PSRP5 PSRP5 (PLASTID-SPECIFIC 50S RIBOSOMAL PROTEIN 5) chr3:2108053	
EV221306	1.467	moderately similar to (290)AT5G53320 Symbols: leucine-rich repeat transmembrane protein kinase, putative chr5:21653679-21655	
ES978384	1.467	no similarity	
CA992531	1.466	no similarity	
JCVI_40057	1.465	no original description	
EV197949	1.465	no similarity	
JCVI_13973	1.463	no original description	
CD842998	1.463	no similarity	
RC_EH429864	1.463	no similarity	
EE566128	1.462	no similarity	
JCVI_36756	1.461	highly similar to (561)AT2G34357 Symbols: binding chr2:14506315-14512634 FORWARD no original description	
ES915996	1.461	weakly similar to (169)AT1G04990 Symbols: zinc finger (CCCH-type) family protein chr1:1419367-1421453 REVERSEvery weak	
EH429137	1.461	no similarity	-2.615
EE567756	1.461	no similarity	
JCVI_33816	1.460	no original description	
JCVI_4603	1.458	no original description	
AT000953	1.457	no similarity	
EH430386	1.457	weakly similar to (107)AT1G29120 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G25770.1); similar to un	
ES956344	1.457	no similarity	4.109
JCVI_26037	1.456	moderately similar to (475)AT1G06250 Symbols: lipase class 3 family protein chr1:1913338-1914849 REVERSE no original descr	
EV099378	1.455	no similarity	
CD822982	1.455	no similarity	
JCVI_8059	1.455	very weakly similar to (91.3)AT4G28990 Symbols: RNA-binding protein-related chr4:14291211-14293024 FORWARD no original	
EX055974	1.455	no similarity	
JCVI_26814	1.454	moderately similar to (333)AT5G55090 Symbols: MAPKKK15 MAPKKK15 (Mitogen-activated protein kinase kinase kinase 15); ki	
JCVI_23536	1.453	weakly similar to (193)AT3G17350 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G50290.1); similar to un	
EE559322	1.453	no similarity	
EV028305	1.452	moderately similar to (279)AT5G12350 Symbols: Ran GTPase binding / chromatin binding / zinc ion binding chr5:3995790-40005	
RC_EV151856	1.452	no similarity	
EV098567	1.451	moderately similar to (256)AT4G17530 Symbols: ATRAB1C, ATRABD2C, RAB1C RAB1C; GTP binding chr4:9773734-9775437	
JCVI_20203	1.451	moderately similar to (245)AT4G37670 Symbols: GCN5-related N-acetyltransferase (GNAT) family protein / amino acid kinase fam	-1.794
EE567709	1.449	moderately similar to (318)AT4G15040 Symbols: subtilase family protein chr4:8581368-8584117 REVERSE [20153] 16 639 639	
CD827731	1.448	no similarity	
EV145901	1.448	no similarity	
JCVI_35650	1.448	no original description	
EX125576	1.448	moderately similar to (332)AT4G35860 Symbols: ATRABB1B, ATGB2, ATRAB2C ATGB2/ATRAB2C/ATRABB1B (GTP-BINDI	
EV186410	1.448	weakly similar to (115)AT1G08200 Symbols: AXS2 AXS2 (UDP-D-APIOSE/UDP-D-XYLOSE SYNTHASE 2) chr1:2574256-257	
JCVI_36160	1.448	weakly similar to (188)AT5G67620 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G62900.1); similar to un	
JCVI_32997	1.448	no original description	
JCVI_26862	1.447	weakly similar to (163)AT5G14370 Symbols: similar to CIL [Arabidopsis thaliana] (TAIR:AT4G25990.1); similar to unnamed prote	
JCVI_27777	1.446	moderately similar to (213)AT2G40030 Symbols: DRD3, ATNRPD1B, NRPD1b NRPD1b (nuclear RNA polymerase D 1b); DNA b	
JCVI_4641	1.445	very weakly similar to (99.0)AT1G12970 Symbols: leucine-rich repeat family protein chr1:4423725-4425630 FORWARD no origin	
H07209	1.445	no similarity	
EE407583	1.444	no similarity	
RC_EV069141	1.444	no similarity	
JCVI_26895	1.443	no original description	
EX135527	1.441	no similarity	
JCVI_1129	1.440	moderately similar to (278)AT2G39960 Symbols: microsomal signal peptidase 25 kDa subunit, putative (SPC25) chr2:16688744-16	
AM060232	1.438	no similarity	
AT000698	1.438	no similarity	
JCVI_9908	1.436	no original description	
EV147742	1.436	no similarity	
JCVI_40930	1.434	no original description	

EV105948	1.430	no similarity	
JCVI_39709	1.429	no original description	
EV134099	1.429	no similarity	
EE439107	1.429	no similarity	
JCVI_5282	1.429	moderately similar to (270)AT3G62300 Symbols: agenet domain-containing protein chr3:23065222-23068056 FORWARD no orig	
EV140700	1.427	no similarity	
JCVI_10013	1.427	moderately similar to (292)AT1G73260 Symbols: trypsin and protease inhibitor family protein / Kunitz family protein chr1:2755107	
JCVI_41334	1.427	weakly similar to (195)AT3G53750 Symbols: ACT3 ACT3 (ACTIN 3); structural constituent of cytoskeleton chr3:19926902-19928	
EV024953	1.426	weakly similar to (192)AT1G63730 Symbols: disease resistance protein (TIR-NBS-LRR class), putative chr1:23645433-23648795 I	2.567
EV092812	1.425	weakly similar to (121)AT5G67420 Symbols: LBD37 LBD37 (LOB DOMAIN-CONTAINING PROTEIN 37) chr5:26921802-2692	
ES900535	1.424	moderately similar to (349)AT4G32650 Symbols: KAT3, ATKC1 ATKC1 (ARABIDOPSIS THALIANA K+ RECTIFYING CHAN	
ES945936	1.424	no similarity	
H07240	1.424	no similarity	
EV109794	1.424	weakly similar to (116)AT4G29480 Symbols: mitochondrial ATP synthase g subunit family protein chr4:14486271-14487263 REV	
EL590531	1.424	weakly similar to (196)AT3G11060 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G06545.1) chr3:34663	
JCVI_22813	1.423	no original description	
JCVI_30785	1.421	no original description	
CD822362	1.421	no similarity	
JCVI_2457	1.421	weakly similar to (185)AT5G54170 Symbols: similar to CP5 [Arabidopsis thaliana] (TAIR:AT1G64720.1); similar to putative nodule	
EV015734	1.421	no similarity	
EE561281	1.420	no similarity	
EV136405	1.420	weakly similar to (118)AT3G13400 Symbols: SKS13 SKS13 (SKU5 Similar 13); copper ion binding / oxidoreductase chr3:4355264	
EE450741	1.419	weakly similar to (105)AT3G07350 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G25240.1); similar to un	
JCVI_31903	1.419	weakly similar to (148)AT2G45460 Symbols: forkhead-associated domain-containing protein / FHA domain-containing protein chr2	
JCVI_20194	1.418	moderately similar to (452)AT3G55250 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO14780.1) chr3:2049	
JCVI_38968	1.417	weakly similar to (150)AT5G59950 Symbols: RNA and export factor-binding protein, putative chr5:24157461-24158636 FORWA	
JCVI_33747	1.416	moderately similar to (208)AT3G28790 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G28830.1); contains	
EL590055	1.415	moderately similar to (335)AT1G09580 Symbols: emp24/gp25L/p24 family protein chr1:3104659-3106094 FORWARD [20863]	
ES969282	1.415	no similarity	
JCVI_11321	1.414	no original description	
JCVI_32388	1.414	moderately similar to (330)AT5G01890 Symbols: leucine-rich repeat transmembrane protein kinase, putative chr5:341658-344647 F	
JCVI_31189	1.414	weakly similar to (104)AT1G43722 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G28730.1); similar to hy	2.036
EV093388	1.414	no similarity	
JCVI_27345	1.414	moderately similar to (211)AT5G04420 Symbols: kelch repeat-containing protein chr5:1246868-1249456 REVERSE no original de	
CX187929	1.414	no similarity	
ES966917	1.411	no similarity	
RC_EX070870	1.411	no similarity	
EV089036	1.410	no similarity	
ES921286	1.410	no similarity	
JCVI_38310	1.409	no original description	
EX015585	1.408	no similarity	
RC_ES979021	1.408	no similarity	2.761
EV118247	1.408	no similarity	
CB617669	1.407	no similarity	
DT469162	1.407	very weakly similar to (81.6)AT1G76580 Symbols: transcription factor chr1:28740222-28743345 FORWARD [17811]	
AM394346	1.407	moderately similar to (306)AT3G28340 Symbols: GATL10 GATL10 (Galacturonosyltransferase-like 10); polygalacturonate 4-alpha-g	1.019
EV122886	1.406	no similarity	
EV220108	1.406	no similarity	
JCVI_7932	1.406	very weakly similar to (87.0)AT5G64310 Symbols: ATAGP1, AGP1 AGP1 (ARABINO GALACTAN-PROTEIN 1) chr5:25739244-	
EV150383	1.406	very weakly similar to (97.8)AT5G15640 Symbols: mitochondrial substrate carrier family protein chr5:5087593-5089680 FORWAR	
EV170073	1.406	moderately similar to (352)AT4G21990 Symbols: PRH-26, PRH26, ATPR3, APR3 APR3 (APS REDUCTASE 3) chr4:11657296-	1.672
EV116362	1.405	no similarity	
JCVI_37124	1.405	weakly similar to (107)AT3G31430 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G18636.1); similar to 80	2.602
JCVI_25347	1.405	no original description	
EV098586	1.405	weakly similar to (112)AT2G35860 Symbols: FLA16 FLA16 (FASCICLIN-LIKE ARABINO GALACTAN PROTEIN 16 PRECURS	
RC_ES968445	1.404	no similarity	
EX055334	1.404	no similarity	
JCVI_19533	1.404	no original description	
EV186109	1.402	very weakly similar to (98.2)AT2G15620 Symbols: NIR, ATHNIR, NIR1 NIR1 (NITRITE REDUCTASE); ferredoxin-nitrate reducta	
EV105960	1.402	no similarity	3.413
JCVI_40367	1.401	no original description	
RC_ES966556	1.401	no similarity	
ES900108	1.400	weakly similar to (157)AT2G45430 Symbols: DNA-binding protein-related chr2:18734922-18735875 FORWARD [21428] 1 678 7	
RC_EE565489	1.399	no similarity	
ES937199	1.399	weakly similar to (124)AT3G09360 Symbols: RNA polymerase II transcription factor chr3:2873802-2878438 FORWARD [16815]	
EE559472	1.398	no similarity	
CV433373	1.398	very weakly similar to (85.9)AT3G21510 Symbols: AHP1 AHP1 (HISTIDINE-CONTAINING PHOSPHOTRANSMITTER 3); histid	
EV177441	1.398	moderately similar to (283)AT1G06890 Symbols: transporter-related chr1:2111727-2114037 REVERSE [21487]	
CX194834	1.397	no similarity	
DY019070	1.397	no similarity	
JCVI_7693	1.396	moderately similar to (225)AT5G54490 Symbols: PBP1 PBP1 (PINOID-BINDING PROTEIN 1); calcium ion binding chr5:221386i	
EX093528	1.396	weakly similar to (130)AT5G13340 Symbols: similar to F-box family protein [Arabidopsis thaliana] (TAIR:AT1G10890.1); similar t	
JCVI_30328	1.395	moderately similar to (270)AT1G44750 Symbols: ATPUP11 ATPUP11 (Arabidopsis thaliana purine permease 11) chr1:16896697-1	1.423
EX110845	1.394	no similarity	
EV086171	1.393	no similarity	
EV098661	1.393	very weakly similar to (85.5)TRAC9_MAIZE [21477]	
ES898836	1.392	no similarity	
EV131945	1.392	no similarity	
EE566632	1.392	no similarity	
EE567536	1.392	no similarity	
JCVI_26497	1.391	no original description	
JCVI_40060	1.391	no original description	2.532
EE513336	1.390	no similarity	

EV223121	1.390	no similarity	
EE562204	1.389	no similarity	
EE423276	1.389	no similarity	
ES995596	1.389	no similarity	
EV220623	1.388	no similarity	
EV174416	1.388	weakly similar to (121)AT3G15450 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G27450.1); similar to un	
EV091063	1.388	no similarity	
ETG10_236652	1.387	no similarity	
ES966626	1.387	no similarity	
CD843597	1.387	no similarity	
JCVI_622	1.386	moderately similar to (464)AT2G34770 Symbols: FAH1 FAH1 (FATTY ACID HYDROXYLASE 1); catalytic chr2:14673855-1467	
EV067830	1.385	no similarity	
JCVI_38585	1.384	no original description	
JCVI_31383	1.384	weakly similar to (199)AT2G40600 Symbols: appr-1-p processing enzyme family protein chr2:16954090-16955615 REVERSE no	1.693
ES910429	1.384	weakly similar to (174)AT1G34010 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G22790.2); similar to un	
JCVI_29049	1.384	weakly similar to (130)AT1G58360 Symbols: NAT2, AAP1 AAP1 (AMINO ACID PERMEASE 1); amino acid transmembrane trans	
JCVI_2595	1.384	highly similar to (646)AT1G71770 Symbols: PAB5 PAB5 (POLY(A)-BINDING PROTEIN); RNA binding chr1:26994439-269971	
EE501845	1.383	no similarity	
DY011593	1.383	very weakly similar to (86.3)AT4G30240 Symbols: protein binding chr4:14808365-14809751 REVERSE [18980]	
EV146475	1.382	weakly similar to (147)AT4G21120 Symbols: CAT1 AAT1 (CATIONIC AMINO ACID TRANSPORTER 1); cationic amino acid tra	
ES960234	1.382	no similarity	
JCVI_35527	1.382	moderately similar to (261)AT5G23190 Symbols: CYP86B1 CYP86B1 (cytochrome P450, family 86, subfamily B, polypeptide 1); o	
EV096246	1.382	no similarity	
JCVI_33758	1.380	moderately similar to (354)AT1G69940 Symbols: ATPPME1 ATPPME1; pectinesterase chr1:26347212-26348634 REVERSEvery	
EX103391	1.380	weakly similar to (155)AT3G05920 Symbols: heavy-metal-associated domain-containing protein chr3:1768997-1769528 REVERSI	
RC_CV973879	1.380	no similarity	
EV183877	1.379	weakly similar to (130)AT1G11880 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO22037.1); contains InterP	
AM395320	1.379	no similarity	
RC_EV167123	1.379	no similarity	
JCVI_6453	1.378	no original description	
BQ791333	1.377	no similarity	1.770
JCVI_4244	1.377	moderately similar to (261)AT3G20740 Symbols: FIS3, FIE1, FIE FIE (FERTILIZATION-INDEPENDENT ENDOSPERM 1); nucle	
CX266638	1.377	moderately similar to (230)AT1G55550 Symbols: microtubule motor chr1:20752581-20756528 FORWARD [16816] 26 522 522	
CO750216	1.377	no similarity	1.715
JCVI_3837	1.374	moderately similar to (326)AT2G23640 Symbols: reticulon family protein (RTNLB13) chr2:10064634-10066122 FORWARD no o	
JCVI_181	1.371	highly similar to (524)AT5G67400 Symbols: peroxidase 73 (PER73) (P73) (PRXR11) chr5:26912122-26913526 FORWARDmode	1.278
EE558079	1.371	no similarity	
DN962793	1.370	weakly similar to (128)AT2G40000 Symbols: HSPRO2, ATHSPRO2 similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3C	
EV165539	1.370	moderately similar to (228)AT2G46140 Symbols: late embryogenesis abundant protein, putative / LEA protein, putative chr2:18966	
EE531349	1.369	no similarity	
JCVI_25169	1.369	weakly similar to (199)AT2G43900 Symbols: endonuclease/exonuclease/phosphatase family protein chr2:18185910-18190899 REV	
EE547386	1.369	no similarity	
JCVI_6384	1.367	no original description	
ES265492	1.367	weakly similar to (108)AT4G16745 Symbols: exostosin family protein chr4:9412207-9414075 FORWARD [21031]	
JCVI_28178	1.366	very weakly similar to (99.0)AT5G26760 Symbols: similar to hypothetical protein OsI_017683 [Oryza sativa (indica cultivar-group)]	
JCVI_4494	1.364	no original description	
EV145751	1.363	no similarity	
DY009187	1.363	no similarity	
EV049289	1.361	no similarity	
RC_EV216502	1.361	no similarity	2.065
EE552225	1.361	no similarity	
RC_EV017894	1.361	no similarity	
EE471402	1.361	moderately similar to (252)AT4G24790 Symbols: ATP binding / DNA binding / DNA-directed DNA polymerase chr4:12778232-12	
EX125037	1.359	weakly similar to (126)AT4G17615 Symbols: ATCBL1, SCABP5 CBL1 (CALCINEURIN B-LIKE PROTEIN 1); calcium ion bindin	
EV177542	1.359	no similarity	
JCVI_11488	1.358	moderately similar to (364)AT4G29240 Symbols: leucine-rich repeat family protein / extensin family protein chr4:14418832-14420	
EV135306	1.357	no similarity	
JCVI_33127	1.356	moderately similar to (334)AT1G80410 Symbols: EMB2753 EMB2753 (EMBRYO DEFECTIVE 2753); binding chr1:30232855-30	
AM389713	1.356	no similarity	
JCVI_7609	1.354	weakly similar to (137)AT1G12390 Symbols: comichon family protein chr1:4220345-4221479 FORWARD no original description	
JCVI_33753	1.354	no original description	
EV065424	1.353	no similarity	
EE521237	1.352	no similarity	
JCVI_47	1.352	moderately similar to (246)AT1G77640 Symbols: AP2 domain-containing transcription factor, putative chr1:29183690-29184424 F	
RC_JCVI_29494	1.351	no original description	2.068
JCVI_40366	1.350	moderately similar to (435)AT4G03070 Symbols: AOP, AOP1.1, AOP1 AOP1 (2-oxoglutarate?dependent dioxygenase 1.1); oxidore	
ES948565	1.350	no similarity	
RC_EE565901	1.349	no similarity	
JCVI_25786	1.348	no original description	
JCVI_39967	1.348	moderately similar to (397)AT2G18480 Symbols: mannitol transporter, putative chr2:8016664-8018325 REVERSEweakly similar t	
JCVI_22350	1.347	moderately similar to (327)AT5G12900 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G12330.1); similar t	
EV090195	1.346	weakly similar to (176)AT3G52340 Symbols: SPP2 SPP2; sucrose-phosphatase chr3:19418390-19420160 FORWARD [21444]	
DY028090	1.346	no similarity	1.769
ES903612	1.344	no similarity	
JCVI_24754	1.344	very weakly similar to (89.0)AT1G02720 Symbols: GATL5 GATL5; transferase, transferring glycosyl groups / transferase, transferring	
JCVI_32832	1.343	weakly similar to (145)AT1G14510 Symbols: PHD finger family protein chr1:4962166-4964149 REVERSE no original description	
EE565995	1.343	no similarity	-1.715
EE501795	1.343	weakly similar to (120)AT1G70260 Symbols: nodulin MtN21 family protein chr1:26460730-26463001 REVERSE [20133]	
JCVI_32977	1.343	weakly similar to (101)AT2G28390 Symbols: SAND family protein chr2:12146913-12150452 REVERSE no original description	
CD825490	1.341	no similarity	
JCVI_25567	1.341	moderately similar to (295)AT5G44560 Symbols: VPS2.2 VPS2.2 chr5:17963743-17965449 FORWARD no original description	3.892
ES960175	1.341	no similarity	
JCVI_30718	1.340	moderately similar to (293)AT5G59340 Symbols: WOX2 WOX2 (WUSCHEL-related homeobox 2); transcription factor chr5:23950	

EE550965	1.340	no similarity	
JCVI_41811	1.340	weakly similar to (140)AT4G27470 Symbols: zinc finger (C3HC4-type RING finger) family protein chr4:13735582-13736313 FOF	
JCVI_1372	1.340	moderately similar to (322)AT1G47600 Symbols: glycosyl hydrolase family 1 protein chr1:17494211-17497029 FORWARDweakl	
JCVI_18975	1.338	highly similar to (511)AT1G31440 Symbols: SH3 domain-containing protein 1 (SH3P1) chr1:11256131-11258460 REVERSE no o	
RC_EB041735	1.336	no similarity	
EV110999	1.336	no similarity	
JCVI_8848	1.336	no original description	1.622
EE560278	1.334	no similarity	
EV109636	1.334	no similarity	1.781
EX047794	1.332	no similarity	
EV106052	1.332	no similarity	
JCVI_12010	1.332	weakly similar to (197)AT3G48800 Symbols: sterile alpha motif (SAM) domain-containing protein chr3:18106810-18107646 REV	1.251
RC_AM394852	1.332	no similarity	
ES963527	1.331	no similarity	
EV018052	1.330	no similarity	
JCVI_38459	1.330	moderately similar to (374)AT3G60320 Symbols: DNA binding chr3:22303048-22306203 REVERSE no original description	2.114
EE549718	1.330	no similarity	
EH424674	1.329	no similarity	
RC_JCVI_40422	1.329	no original description	
EE526882	1.329	no similarity	
JCVI_28456	1.329	no original description	
CV973884	1.328	no similarity	
JCVI_34878	1.328	weakly similar to (175)AT5G59670 Symbols: leucine-rich repeat protein kinase, putative chr5:24058764-24062704 FORWARD no	3.178
DN965455	1.327	no similarity	
JCVI_27380	1.327	moderately similar to (232)AT3G53020 Symbols: RPL24B, RPL24, STV1 STV1 (SHORT VALVE1); structural constituent of ribosc	1.500
JCVI_6966	1.326	moderately similar to (343)AT1G01360 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G01026.1); similar t	
JCVI_7640	1.325	moderately similar to (384)AT3G47500 Symbols: CDF3 CDF3 (CYCLING DOF FACTOR 3); DNA binding / protein binding / trans	2.716
EV147794	1.324	no similarity	
EX133335	1.324	weakly similar to (127)AT4G23460 Symbols: beta-adaptin, putative chr4:12243909-12248908 REVERSE [21833] 20 585 585	
JCVI_41079	1.323	highly similar to (893)AT5G39590 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO61019.1); contains InterPr	
ES967608	1.322	no similarity	
JCVI_9461	1.321	highly similar to (503)AT3G50100 Symbols: exonuclease chr3:18589394-18591577 FORWARD no original description	
RC_ES960829	1.321	no similarity	
EV173566	1.320	moderately similar to (439)AT1G66830 Symbols: leucine-rich repeat transmembrane protein kinase, putative chr1:24934363-24936	
EX092831	1.320	moderately similar to (297)AT5G56370 Symbols: F-box family protein chr5:22853426-22854845 REVERSE [21823] 18 852 852	
EE558537	1.320	no similarity	
EE565726	1.319	no similarity	1.130
JCVI_27002	1.318	no original description	
DY003536	1.317	very weakly similar to (99.8)AT5G25540 Symbols: CID6 CID6 (CTC-Interacting Domain 6); protein binding chr5:8891773-8892365	
EE567175	1.316	no similarity	
JCVI_23541	1.316	very weakly similar to (99.0)AT4G34410 Symbols: AP2 domain-containing transcription factor, putative chr4:16451996-16452802	
JCVI_5591	1.314	moderately similar to (334)AT1G74820 Symbols: cupin family protein chr1:28115543-28116226 REVERSEweakly similar to (15'	
JCVI_38439	1.314	no original description	
EL591783	1.313	moderately similar to (353)AT1G08340 Symbols: rac GTPase activating protein, putative chr1:2631305-2632666 FORWARD [208	
RC_EE563974	1.313	no similarity	2.230
EE505235	1.313	no similarity	1.228
JCVI_35716	1.313	moderately similar to (408)AT4G36030 Symbols: armadillo/beta-catenin repeat family protein chr4:17045087-17047099 REVERSI	
EE543610	1.312	no similarity	
EV171540	1.312	no similarity	
JCVI_12486	1.311	moderately similar to (263)AT3G48080 Symbols: lipase class 3 family protein / disease resistance protein-related chr3:17764089-17	
JCVI_35549	1.311	no original description	
JCVI_34556	1.310	moderately similar to (316)AT5G02370 Symbols: kinesin motor protein-related chr5:503442-506386 FORWARD no original descr	
EV163857	1.310	weakly similar to (109)AT2G33810 Symbols: SPL3 SPL3 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 3); transcription	
JCVI_28643	1.309	weakly similar to (105)AT5G56460 Symbols: protein kinase, putative chr5:22882735-22885092 FORWARD no original description	
ES953772	1.309	no similarity	
EE569283	1.309	no similarity	
EV221837	1.308	no similarity	
JCVI_15874	1.308	no original description	
JCVI_34123	1.306	moderately similar to (234)AT5G04010 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G03920.1); similar t	
JCVI_27017	1.306	weakly similar to (180)AT1G17530 Symbols: ATTIM23-1 ATTIM23-1 (TRANSLOCASE OF INNER MITOCHONDRIAL MEMB)	
EX093418	1.306	weakly similar to (183)AT1G65160 Symbols: ubiquitin carboxyl-terminal hydrolase family protein chr1:24209887-24211401 FOR	
JCVI_31159	1.305	highly similar to (580)AT2G46750 Symbols: FAD-binding domain-containing protein chr2:19215513-19217979 REVERSE no orig	
EE546195	1.305	no similarity	
JCVI_33419	1.305	very weakly similar to (95.9)AT5G11810 Symbols: similar to Os02g0135600 [Oryza sativa (japonica cultivar-group)] (GB:NP_00104	
JCVI_11741	1.303	no original description	
JCVI_958	1.303	no original description	
JCVI_9018	1.302	weakly similar to (169)AT5G23860 Symbols: TUB8 TUB8 (tubulin beta-8) chr5:8042965-8044531 FORWARDweakly similar to (	
EE567384	1.302	no similarity	
JCVI_18326	1.300	moderately similar to (384)AT4G01360 Symbols: similar to BPS1 (BYPASS 1) [Arabidopsis thaliana] (TAIR:AT1G01550.2); simila	
JCVI_195	1.300	no original description	
EV006157	1.300	weakly similar to (105)AT5G58640 Symbols: selenoprotein-related chr5:23715222-23716731 FORWARD [21427]	
JCVI_18920	1.300	no original description	
JCVI_32318	1.299	moderately similar to (206)AT3G18440 Symbols: ATALMT9 ATALMT9 (ALUMINUM-ACTIVATED MALATE TRANSPORTER	
JCVI_39291	1.299	moderately similar to (226)AT5G16890 Symbols: exostosin family protein chr5:5551667-5554744 FORWARD no original descript	
EE559994	1.298	no similarity	
EX125056	1.297	weakly similar to (167)AT3G57010 Symbols: strictosidine synthase family protein chr3:21106833-21108295 REVERSE [21830]	
EV223015	1.297	no similarity	4.448
ES908593	1.296	weakly similar to (139)AT4G05150 Symbols: octicosapeptide/Phox/Bem1p (PB1) domain-containing protein chr4:2660337-266267	
RC_EE565714	1.295	no similarity	
EV217656	1.294	no similarity	
H07284	1.294	no similarity	
ES961512	1.294	no similarity	2.110
ES996702	1.293	no similarity	

RC_JCVI_42381	1.292	no original description	
EV190691	1.292	no similarity	
ES939524	1.292	no similarity	
EV150322	1.290	very weakly similar to (100)AT5G14995 Symbols: Encodes a ECA1 gametogenesis related family protein chr5:4853416-4853721 F	
JCVI_27796	1.289	weakly similar to (107)AT4G27657 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G27652.1) chr4:13813	
EE417919	1.289	no similarity	
EE558422	1.288	no similarity	
JCVI_18930	1.288	weakly similar to (170)AT3G16000 Symbols: MFP1 MFP1 (MAR BINDING FILAMENT-LIKE PROTEIN 1) chr3:5431047-54336	
EV099338	1.287	no similarity	2.066
JCVI_38236	1.287	weakly similar to (159)AT1G14860 Symbols: ATNUDT18 ATNUDT18 (Arabidopsis thaliana Nudix hydrolase homolog 18); hydroly	
CX278446	1.287	moderately similar to (298)AT4G37050 Symbols: PLP4, PLA V PLA V/PLP4 (Patatin-like protein 4); nutrient reservoir chr4:17457	1.324
JCVI_13997	1.285	no original description	
JCVI_15772	1.285	weakly similar to (177)AT4G30180 Symbols: transcription factor/ transcription regulator chr4:14769034-14769510 FORWARD no	
EV128968	1.283	no similarity	
JCVI_35464	1.283	moderately similar to (334)AT4G33210 Symbols: F-box family protein (FBL15) chr4:16015974-16020700 REVERSE no original d	
EE419268	1.283	no similarity	1.862
JCVI_26806	1.283	no original description	
EV148098	1.282	no similarity	
JCVI_7083	1.282	no original description	
JCVI_12330	1.282	weakly similar to (148)AT5G50915 Symbols: basic helix-loop-helix (bHLH) family protein chr5:20727990-20729478 REVERSE n	
JCVI_5729	1.281	no original description	
EV107221	1.280	no similarity	
EE569647	1.279	no similarity	
EV175792	1.279	weakly similar to (148)AT5G27150 Symbols: ATNHX, AT-NHX1, ATNHX1, NHX1 NHX1 (NA ⁺ /H ⁺ EXCHANGER); sodium ion	1.355
EE449364	1.277	weakly similar to (144)AT1G12540 Symbols: basic helix-loop-helix (bHLH) family protein chr1:4273135-4273978 FORWARD [2	
EE566939	1.275	no similarity	
EV178131	1.275	no similarity	
EE472687	1.274	no similarity	
RC_ES955688	1.273	no similarity	
RC_EE569610	1.273	no similarity	
EV064370	1.273	no similarity	
EV224957	1.272	very weakly similar to (99.8)AT5G57800 Symbols: FLP1, YRE, CER3, WAX2 CER3/FLP1/WAX2/YRE (ECERIFERUM 3); catalyt	
EE438184	1.272	moderately similar to (257)AT4G13310 Symbols: CYP71A20 CYP71A20 (cytochrome P450, family 71, subfamily A, polypeptide 2)	
JCVI_18418	1.271	highly similar to (579)AT4G13020 Symbols: MHK MHK chr4:7603944-7606729 FORWARDweakly similar to (189)CDC2_MAI2	
EE549228	1.270	very weakly similar to (91.3)AT3G50060 Symbols: MYB77 MYB77; DNA binding / transcription factor chr3:18569129-18570034 I	
RC_EE461708	1.270	no similarity	
JCVI_3627	1.270	moderately similar to (330)AT4G03960 Symbols: tyrosine specific protein phosphatase family protein chr4:1887671-1888998 FOR	
RC_EV015302	1.270	no similarity	
JCVI_27951	1.269	moderately similar to (202)AT4G33400 Symbols: dem protein-related / defective embryo and meristems protein-related chr4:16078	
JCVI_218	1.269	moderately similar to (365)AT5G27390 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO17664.1); contains In	
JCVI_10805	1.269	weakly similar to (134)AT1G51650 Symbols: ATP synthase epsilon chain, mitochondrial chr1:19156348-19157309 FORWARDwe	
JCVI_16808	1.268	weakly similar to (152)AT1G76740 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G76840.1); similar to ce	
JCVI_39221	1.267	no original description	
EE408376	1.267	weakly similar to (162)AT2G03520 Symbols: ATUPS4 ATUPS4 (ARABIDOPSIS THALIANA UREIDE PERMEASE 4) chr2:106	
JCVI_28642	1.267	no original description	
EE518209	1.267	very weakly similar to (89.0)AT1G63100 Symbols: scarecrow transcription factor family protein chr1:23403056-23405032 REVER	
AM394544	1.266	no similarity	
EE560298	1.266	no similarity	5.045
CO750106	1.266	no similarity	
EE446770	1.265	no similarity	
RC_ES958812	1.265	no similarity	
CV544986	1.265	no similarity	
EX037129	1.264	weakly similar to (183)AT1G03050 Symbols: epsin N-terminal homology (ENTH) domain-containing protein / clathrin assembly pro	
EV103962	1.264	weakly similar to (146)AT4G13540 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G23930.1); similar to un	
JCVI_12210	1.263	no original description	
JCVI_13709	1.263	no original description	
JCVI_38694	1.263	weakly similar to (168)AT2G34480 Symbols: 60S ribosomal protein L18A (RPL18aB) chr2:14539995-14541240 REVERSEweakl	
JCVI_34334	1.262	weakly similar to (145)AT2G35930 Symbols: U-box domain-containing protein chr2:15090180-15091415 REVERSE no original d	
DY026611	1.259	no similarity	
JCVI_38780	1.259	no original description	
EE551048	1.258	no similarity	-1.240
CD842919	1.258	no similarity	1.001
AM058087	1.257	weakly similar to (172)AT2G17550 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G02390.1); similar to un	
JCVI_36197	1.257	moderately similar to (233)AT4G00350 Symbols: MATE efflux family protein chr4:151978-153988 FORWARD no original descri	
JCVI_21009	1.257	no original description	
RC_CX272297	1.256	no similarity	2.986
JCVI_10234	1.255	moderately similar to (244)AT4G30410 Symbols: transcription factor chr4:14871315-14871857 REVERSE no original description	
EV226155	1.255	no similarity	3.589
RC_EE567596	1.255	no similarity	
JCVI_432	1.254	moderately similar to (231)AT4G04780 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G15690.1); similar t	
DW999676	1.253	very weakly similar to (89.7)AT5G12050 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO45643.1) chr5:389	
JCVI_31414	1.253	weakly similar to (191)AT4G29710 Symbols: phosphodiesterase/nucleotide pyrophosphatase-related chr4:14547007-14547408 RE	
JCVI_25393	1.253	no original description	
RC_H07474	1.253	no similarity	
JCVI_34834	1.252	moderately similar to (303)AT3G05630 Symbols: PDLZ2, PLDP2 PLDP2 (PHOSPHOLIPASE D ZETA 2); phospholipase D chr3:1	
JCVI_9651	1.252	weakly similar to (146)AT4G25760 Symbols: ATGDU2 ATGDU2 (ARABIDOPSIS THALIANA GLUTAMINE DUMPER 2) chr4	
JCVI_24883	1.251	weakly similar to (101)AT2G20100 Symbols: ethylene-responsive family protein chr2:8685266-8687997 FORWARD no original d	
EE483558	1.250	no similarity	1.667
JCVI_7689	1.250	moderately similar to (400)AT3G24550 Symbols: ATPERK1 ATPERK1 (PROLINE EXTENSIN-LIKE RECEPTOR KINASE 1); A'	
EV128726	1.249	no similarity	
EE505233	1.248	no similarity	
JCVI_2497	1.248	no original description	
EE556940	1.248	no similarity	

JCVI_40151	1.248	weakly similar to (136)AT5G22920 Symbols: zinc finger (C3HC4-type RING finger) family protein chr5:7665146-7667034 FORW	
EL586758	1.248	no similarity	
EV217824	1.247	moderately similar to (390)AT3G51360 Symbols: aspartyl protease family protein chr3:19075273-19077539 REVERSE [21492] 41	
CD832107	1.247	weakly similar to (116)AT3G33520 Symbols: ARP6, SUF3, ESD1, ATARP6 ATARP6; structural constituent of cytoskeleton chr3:1	
ES961244	1.246	no similarity	
JCVI_20201	1.246	moderately similar to (352)AT5G24400 Symbols: EMB2024 EMB2024 (EMBRYO DEFECTIVE 2024); catalytic chr5:8330535-83	
EV086515	1.245	no similarity	
EE501848	1.245	no similarity	
EV146237	1.245	weakly similar to (152)AT4G21120 Symbols: CAT1 AAT1 (CATIONIC AMINO ACID TRANSPORTER 1); cationic amino acid tra	
JCVI_41582	1.244	very weakly similar to (85.5)AT3G49370 Symbols: calcium-dependent protein kinase, putative / CDPK, putative chr3:18315939-183	
EV169287	1.243	no similarity	
EE569976	1.243	no similarity	
JCVI_27856	1.242	weakly similar to (155)AT4G31430 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO43934.1) chr4:15248511	
EE564834	1.242	no similarity	
EE566081	1.240	no similarity	
CN733443	1.240	no similarity	
CX190646	1.240	no similarity	
EE568186	1.239	very weakly similar to (89.4)AT2G42910 Symbols: ribose-phosphate pyrophosphokinase 4 / phosphoribosyl diphosphate synthetase 4	
CD829818	1.239	no similarity	-1.695
EV099841	1.239	no similarity	
EV181239	1.239	no similarity	
EE567251	1.238	no similarity	1.307
EE567468	1.238	no similarity	
DY017020	1.237	no similarity	
CX194309	1.237	no similarity	
RC_EE565477	1.237	no similarity	
CN733048	1.236	no similarity	
JCVI_21024	1.235	weakly similar to (159)AT2G30150 Symbols: UDP-glucuronosyl/UDP-glucosyl transferase family protein chr2:12881783-1288319	
JCVI_9495	1.234	moderately similar to (230)AT5G61780 Symbols: tudor domain-containing protein / nuclease family protein chr5:24839238-248438	
CD827908	1.234	no similarity	
JCVI_35754	1.233	no original description	
EE548376	1.233	no similarity	
JCVI_41169	1.233	very weakly similar to (92.0)AT4G32300 Symbols: lectin protein kinase family protein chr4:15599976-15602441 FORWARD no or	
JCVI_34278	1.232	no original description	
RC_ES957422	1.232	no similarity	
ES938120	1.232	no similarity	
DY021547	1.231	no similarity	
EB041749	1.231	no similarity	
EE453815	1.231	very weakly similar to (84.3)AT1G25350 Symbols: OVA9 OVA9 (OVULE ABORTION 9); glutamine-tRNA ligase chr1:8889267-8	
H07287	1.231	no similarity	
JCVI_39802	1.229	no original description	
EV152480	1.229	very weakly similar to (85.5)AT1G11840 Symbols: ATGLX1 ATGLX1 (GLYOXALASE I HOMOLOG); lactoylglutathione lyase ch	
JCVI_23697	1.227	moderately similar to (229)AT1G73030 Symbols: VPS46.2 VPS46.2 chr1:27477599-27478509 FORWARD no original description	
JCVI_20622	1.226	no original description	1.891
CV432552	1.226	very weakly similar to (100)AT4G25980 Symbols: cationic peroxidase, putative chr4:13189402-13191516 FORWARD [16490] 40	
EV210294	1.224	no similarity	1.490
JCVI_39874	1.224	moderately similar to (261)AT2G20030 Symbols: zinc finger (C3HC4-type RING finger) family protein chr2:8654894-8656066 FC	
EE503950	1.224	no similarity	
JCVI_35218	1.223	moderately similar to (216)AT5G67060 Symbols: HEC1 HEC1 (HECATE 1); transcription factor chr5:26783502-26784227 FORW	
JCVI_13157	1.222	moderately similar to (320)AT1G18830 Symbols: transducin family protein / WD-40 repeat family protein chr1:6489300-6494209	
ES967984	1.221	no similarity	1.320
JCVI_42478	1.220	very weakly similar to (96.3)AT5G60390 Symbols: elongation factor 1-alpha / EF-1-alpha chr5:24306452-24307901 FORWARDve	
EV101103	1.220	weakly similar to (188)AT2G34420 Symbols: LHCB1.5, LHB1B2 LHB1B2 (Photosystem II light harvesting complex gene 1.5); chlo	
JCVI_22578	1.220	nearly identical (1211)AT2G25800 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G20010.2); similar to unk	
RC_AM060878	1.219	no similarity	1.046
JCVI_21427	1.219	no original description	
ES951218	1.218	no similarity	
JCVI_22340	1.218	no original description	
EV105059	1.218	no similarity	
EV178195	1.217	moderately similar to (309)AT1G22870 Symbols: protein kinase family protein chr1:8089490-8094162 FORWARD [21487] 82 99	
EV110475	1.217	no similarity	-1.217
JCVI_3538	1.217	moderately similar to (326)AT1G75910 Symbols: EXL4 EXL4 (extracellular lipase 4); acyltransferase/ carboxylesterase/ lipase chr1:	
EE552044	1.216	very weakly similar to (81.6)RL7A_ORYSA [20184] 1 221 257	1.613
AM395789	1.216	weakly similar to (143)AT5G35930 Symbols: AMP-dependent synthetase and ligase family protein chr5:14084427-14091634 REV:	1.094
JCVI_13220	1.215	moderately similar to (252)AT3G07840 Symbols: polygalacturonase, putative / pectinase, putative chr3:2501899-2503481 REVER:	
JCVI_8900	1.214	moderately similar to (209)AT4G22310 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G14695.1); similar t	
JCVI_17093	1.214	very weakly similar to (92.0)AT5G54690 Symbols: GAUT12, LGT6, IRX8 GAUT12/IRX8/LGT6 (GALACTURONOSYLTRANSFERASE	
EV225710	1.213	no similarity	
EV090756	1.212	no similarity	
JCVI_33407	1.212	weakly similar to (187)AT1G48360 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO45274.1); contains InterP	
ES967449	1.212	no similarity	
JCVI_9638	1.211	weakly similar to (183)AT1G52415 Symbols: similar to Expressed protein [Arabidopsis thaliana] (TAIR:AT4G28405.1); contains Int	
EV037482	1.211	no similarity	
JCVI_1957	1.211	weakly similar to (117)AT5G48480 Symbols: Identical to Uncharacterized protein At5g48480 [Arabidopsis Thaliana] (GB:Q9LV66)	
EV065172	1.210	no similarity	
JCVI_36018	1.210	no original description	
JCVI_39538	1.210	moderately similar to (257)AT4G20030 Symbols: RNA recognition motif (RRM)-containing protein chr4:10846372-10847256 FOI	
JCVI_30471	1.210	no original description	
JCVI_11395	1.210	moderately similar to (217)AT3G46480 Symbols: oxidoreductase, acting on paired donors, with incorporation or reduction of molecu	
JCVI_42352	1.208	moderately similar to (342)AT3G09630 Symbols: 60S ribosomal protein L4/L1 (RPL4A) chr3:2953818-2955449 FORWARD no o	
EV157622	1.207	no similarity	
JCVI_18484	1.207	moderately similar to (347)AT5G58784 Symbols: dehydrololichyl diphosphate synthase, putative / DEDOL-PP synthase, putative c	
JCVI_3808	1.207	weakly similar to (168)AT5G59310 Symbols: LTP4 LTP4 (LIPID TRANSFER PROTEIN 4); lipid binding chr5:23942522-2394295	

EV011894	1.206	no similarity	
JCVI_32121	1.206	no original description	
EX037308	1.205	moderately similar to (314)AT1G26310 Symbols: CAL1, AGL10, CAL CAL (CAULIFLOWER); DNA binding / transcription factor	
JCVI_32296	1.205	moderately similar to (224)AT3G01440 Symbols: oxygen evolving enhancer 3 (PsbQ) family protein chr3:168485-169414 FORWARD	
JCVI_16072	1.204	moderately similar to (214)AT5G66800 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G50640.1); similar t	
EE516834	1.204	weakly similar to (161)AT1G66620 Symbols: seven in absentia (SINA) protein, putative chr1:24856469-24857707 REVERSE	
AT000438	1.203	no similarity	
JCVI_36165	1.202	no original description	
EE564606	1.201	no similarity	1.813
JCVI_21906	1.200	no original description	
EE546397	1.199	no similarity	3.205
JCVI_5915	1.198	moderately similar to (228)AT3G50270 Symbols: transferase family protein chr3:18646908-18648260 FORWARD no original desc	
JCVI_27059	1.198	moderately similar to (291)AT3G56620 Symbols: integral membrane family protein / nodulin MtN21-related chr3:20983675-20985	
JCVI_12374	1.197	weakly similar to (175)AT4G30720 Symbols: oxidoreductase chr4:14972218-14975467 REVERSE no original description	
EE556970	1.197	no similarity	
DN961164	1.195	no similarity	0.308
JCVI_17941	1.194	no original description	
JCVI_28053	1.194	no original description	
ES912768	1.193	moderately similar to (248)AT5G19880 Symbols: peroxidase, putative chr5:6720580-6722413 REVERSE	
EV149614	1.193	very weakly similar to (92.8)AT5G42980 Symbols: ATH3, ATTRX3, TRX3, ATTRX3 ATTRX3 (thioredoxin H-type 3); thiol-dis	
JCVI_10422	1.193	no original description	
EV127720	1.193	no similarity	
JCVI_34489	1.191	moderately similar to (346)AT5G09540 Symbols: DNAJ heat shock N-terminal domain-containing protein chr5:2962423-2963265	
JCVI_3134	1.191	highly similar to (526)AT1G04770 Symbols: male sterility MS5 family protein chr1:1336563-1337766 REVERSE no original desc	
EE481259	1.190	weakly similar to (165)AT5G58230 Symbols: MEE70, MSI1 MSI1 (MULTICOPY SUPPRESSOR OF IRA1) chr5:23573338-235752	
JCVI_8705	1.190	moderately similar to (294)AT5G54080 Symbols: HGO HGO (HOMOGENITISATE 1,2-DIOXYGENASE); homogentisate 1,2-dioxy	2.093
JCVI_20091	1.190	weakly similar to (164)AT4G36120 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G19835.1); similar to un	
EE552450	1.190	no similarity	
EE516683	1.189	weakly similar to (115)AT2G33130 Symbols: RALFL18 RALFL18 (RALF-LIKE 18) chr2:14053598-14053909 REVERSE [20185	
JCVI_28244	1.189	moderately similar to (244)AT5G37770 Symbols: CML24, TCH2 TCH2 (TOUCH 2); calcium ion binding chr5:15016305-1501679	
JCVI_32418	1.188	very weakly similar to (80.5)AT3G28770 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G28810.1); similar	1.278
EE476768	1.188	moderately similar to (254)AT5G17350 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G03280.1); similar t	
JCVI_39321	1.188	very weakly similar to (82.0)AT5G13000 Symbols: GSL12, ATGSL12 ATGSL12 (GLUCAN SYNTHASE-LIKE 12); 1,3-beta-glucar	
EV150273	1.188	no similarity	
JCVI_22208	1.188	very weakly similar to (81.3)AT2G43710 Symbols: FAB2, SSI2 SSI2 (fatty acid biosynthesis 2); acyl-[acyl-carrier-protein] desaturase	
JCVI_27767	1.188	moderately similar to (254)AT1G22360 Symbols: ATUGT85A2 ATUGT85A2 (UDP-GLUCOSYL TRANSFERASE 85A2); UDP-gl	3.359
JCVI_5733	1.186	moderately similar to (204)AT1G21910 Symbols: AP2 domain-containing transcription factor family protein chr1:7696644-769733	
EE444230	1.186	moderately similar to (225)AT1G04110 Symbols: SDD1 SDD1 (STOMATAL DENSITY AND DISTRIBUTION); subtilase chr1:10	
JCVI_39320	1.185	weakly similar to (143)AT2G44440 Symbols: emsy N terminus domain-containing protein / ENT domain-containing protein chr2:18	
EV078713	1.185	no similarity	
JCVI_27559	1.185	highly similar to (972)AT4G33330 Symbols: PGSP3 PGSP3 (PLANT GLYCOGENIN-LIKE STARCH INITIATION PROTEIN 3)	
EV141101	1.184	no similarity	
JCVI_17229	1.183	weakly similar to (105)AT1G30090 Symbols: kelch repeat-containing F-box family protein chr1:10559730-10560926 REVERSE n	
JCVI_24981	1.183	no original description	2.685
ES930799	1.182	very weakly similar to (100)AT5G02010 Symbols: ATROPGEF7, ROPGEF7 ATROPGEF7/ROPGEF7 (KINASE PARTNER PROT	
EV092818	1.182	no similarity	
JCVI_19370	1.181	no original description	
EE460363	1.181	no similarity	
EV163624	1.179	weakly similar to (170)AT3G22270 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G14990.1); similar to un	
JCVI_21812	1.178	no original description	
JCVI_36563	1.178	no original description	1.433
EV104180	1.176	weakly similar to (160)AT2G01600 Symbols: epsin N-terminal homology (ENTH) domain-containing protein chr2:268974-272355	
JCVI_40106	1.176	moderately similar to (225)AT5G26250 Symbols: sugar transporter, putative chr5:9196761-9198684 FORWARD	
EV205459	1.175	no similarity	
EV107555	1.174	very weakly similar to (87.0)AT1G74940 Symbols: senescence-associated protein-related chr1:28149945-28150726 FORWARD [21	
JCVI_7629	1.174	moderately similar to (203)AT2G47880 Symbols: glutaredoxin family protein chr2:19612194-19612502 FORWARD no original de	
EV106984	1.173	no similarity	
JCVI_8132	1.173	moderately similar to (210)AT3G23910 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G24255.1); similar t	
CD829816	1.172	no similarity	
EV128714	1.172	no similarity	
JCVI_25373	1.171	moderately similar to (321)AT3G46960 Symbols: ATP-dependent helicase chr3:17301989-17309052 REVERSE no original descri	
RC_ES967585	1.169	no similarity	
RC_EE558216	1.168	no similarity	
L46475	1.167	no similarity	
EX131157	1.167	weakly similar to (147)AT5G42310 Symbols: pentatricopeptide (PPR) repeat-containing protein chr5:16933088-16935466 FORWA	
JCVI_22967	1.167	weakly similar to (179)AT3G58430 Symbols: similar to meprin and TRAF homology domain-containing protein / MATH domain-co	
EE414049	1.166	no similarity	
EE410226	1.166	no similarity	
EV063338	1.166	no similarity	1.720
RC_EE526833	1.166	no similarity	
JCVI_19079	1.165	weakly similar to (106)AT4G27657 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G27652.1) chr4:13813	
EV214081	1.164	weakly similar to (195)AT1G49470 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G55230.1); similar to hy	
CX192459	1.164	no similarity	
JCVI_12482	1.164	weakly similar to (129)AT2G19110 Symbols: HMA4 HMA4 (Heavy metal ATPase 4); cadmium-transporting ATPase chr2:8286560	
EV104851	1.162	no similarity	1.837
JCVI_2170	1.160	moderately similar to (332)AT5G64840 Symbols: ATGCN5 ATGCN5 (Arabidopsis thaliana general control non-repressible 5) chr5:	
EV171239	1.159	no similarity	
EV184925	1.159	no similarity	
JCVI_20977	1.159	weakly similar to (115)AT5G46370 Symbols: ATPK2, KCO2, ATKCO2 KCO2 (CA2+ ACTIVATED OUTWARD RECTIFYING	
JCVI_12760	1.158	very weakly similar to (82.0)AT5G14620 Symbols: DMT7, DRM2 DRM2 (DOMAINS REARRANGED METHYLTRANSFERASE	
EV146900	1.157	no similarity	
JCVI_17711	1.157	no original description	
JCVI_14258	1.157	very weakly similar to (85.5)AT5G05830 Symbols: zinc finger (C3HC4-type RING finger) family protein chr5:1755911-1756826 F	

EE468341	1.157	no similarity	
EE566453	1.157	weakly similar to (140)AT4G35750 Symbols: Rho-GTPase-activating protein-related chr4:16940870-16941679 REVERSE [20153]	
CD812594	1.157	weakly similar to (143)AT2G47330 Symbols: DEAD/DEAH box helicase, putative chr2:19436153-19438687 REVERSE [13976]	
EV124157	1.157	moderately similar to (216)AT1G01790 Symbols: ATKEA1, KEA1 KEA1 (K EFFLUX ANTIporter 1); potassium:hydrogen antiporter	
CX193946	1.156	weakly similar to (155)AT4G25630 Symbols: ATFIB2, FIB2 FIB2 (FIBRILLARIN 2) chr4:13074248-13076214 FORWARD [1680]	
EE470884	1.156	no similarity	
EV152808	1.156	weakly similar to (101)AT4G04690 Symbols: F-box family protein (FBX15) chr4:2373997-2375133 REVERSE [21484]	
ES951296	1.155	moderately similar to (233)AT4G10630 Symbols: glutaredoxin family protein chr4:6566621-6567625 REVERSE [21423]	
ES978926	1.155	no similarity	
EE470870	1.155	no similarity	
EV151880	1.154	weakly similar to (147)AT4G21560 Symbols: vacuolar protein sorting-associated protein 28 family protein / VPS28 family protein chr4:16940870-16941679 REVERSE [20153]	
JCVI_38305	1.154	moderately similar to (288)AT1G55870 Symbols: ATPARN, AHG2 AHG2/ATPARN chr1:20899850-20901710 FORWARD no original description	
EH426427	1.154	moderately similar to (203)AT5G20490 Symbols: ATXIK, XIK XIK (Myosin-like protein XIK); motor/ protein binding chr5:692704-692804 REVERSE [21423]	1.388
EX132052	1.153	moderately similar to (254)AT5G13590 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO41555.1) chr5:4374-4384 REVERSE [21423]	
JCVI_19138	1.153	no original description	
EV104616	1.152	no similarity	
ES968782	1.152	no similarity	
EL587353	1.151	weakly similar to (108)AT1G15790 Symbols: similar to protein binding / transcription cofactor [Arabidopsis thaliana] (TAIR:AT1G15790)	
JCVI_19076	1.151	no original description	3.098
EE561884	1.150	weakly similar to (107)AT1G22240 Symbols: APUM8 APUM8 (ARABIDOPSIS PUMILIO 8); RNA binding chr1:7853073-785491 REVERSE [21423]	-1.097
AM395567	1.150	no similarity	
EV226946	1.149	no similarity	
EE562182	1.149	no similarity	
EV130747	1.149	no similarity	
JCVI_16629	1.148	moderately similar to (248)AT3G51780 Symbols: ATBAG4 ATBAG4 (ARABIDOPSIS THALIANA BCL-2-ASSOCIATED ATHA18)	
EV210662	1.147	no similarity	
EV099499	1.146	no similarity	
EX124506	1.145	weakly similar to (144)AT4G29090 Symbols: reverse transcriptase, putative / RNA-dependent DNA polymerase, putative chr4:1433-1443 REVERSE [21423]	
EE538327	1.144	no similarity	
EV207690	1.143	no similarity	
RC_JCVI_32770	1.143	no original description	
EX036222	1.143	moderately similar to (409)AT4G22730 Symbols: leucine-rich repeat transmembrane protein kinase, putative chr4:11941395-119431 REVERSE [21423]	
RC_ES965944	1.142	no similarity	
EE563724	1.141	weakly similar to (166)AT5G60615 Symbols: Encodes a defensin-like (DEFL) family protein. chr5:24383179-24383545 REVERSE [21423]	
RC_EX015383	1.140	no similarity	
JCVI_24416	1.139	highly similar to (707)AT3G46520 Symbols: ACT12 ACT12 (ACTIN-12); structural constituent of cytoskeleton chr3:17139552-17140552 REVERSE [21423]	
EE444120	1.139	weakly similar to (186)AT3G05670 Symbols: PHD finger family protein chr3:1653894-1657028 FORWARD [20160]	
JCVI_36364	1.138	highly similar to (505)AT3G20350 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G50660.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO41555.1) chr5:4374-4384 REVERSE [21423]	
EV156212	1.134	no similarity	
EX035128	1.134	moderately similar to (393)AT2G36780 Symbols: UDP-glucuronosyl/UDP-glucosyl transferase family protein chr2:15424697-15425697 REVERSE [21423]	1.439
EX031510	1.134	no similarity	
EE546863	1.134	no similarity	
JCVI_198	1.132	moderately similar to (292)AT3G25910 Symbols: zinc ion binding chr3:9491073-9492191 FORWARD no original description	
JCVI_8079	1.132	weakly similar to (155)AT5G61880 Symbols: signaling molecule-related chr5:24867824-24868738 FORWARD no original description	
JCVI_14185	1.132	no original description	
EV111276	1.131	no similarity	
JCVI_35629	1.130	no original description	
CX191134	1.130	no similarity	
EV104642	1.129	no similarity	
EE560434	1.125	no similarity	
JCVI_34940	1.123	no original description	
RC_ES963926	1.121	no similarity	
EX089618	1.121	very weakly similar to (84.0)AT2G33000 Symbols: ubiquitin-associated (UBA)/TS-N domain-containing protein-related chr2:14013-14023 REVERSE [21423]	
AM395361	1.121	no similarity	
EE546528	1.120	no similarity	
EV166563	1.119	no similarity	
EE417103	1.118	moderately similar to (253)AT3G55720 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G05840.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO41555.1) chr5:4374-4384 REVERSE [21423]	
EX041917	1.118	no similarity	
EV035083	1.115	weakly similar to (135)AT4G31560 Symbols: HCF153 HCF153 chr4:15295225-15296034 FORWARD [21441]	
JCVI_9275	1.115	no original description	
EE410492	1.115	no similarity	
AT000499	1.115	no similarity	
JCVI_5468	1.115	moderately similar to (296)AT5G67300 Symbols: ATMYBR1, ATMYB44, MYBR1 ATMYB44/ATMYBR1/MYBR1 (MYB DOMAIN-CONTAINING PROTEIN 44) chr5:2999363-3000186 REVERSE no original description	
JCVI_39718	1.115	very weakly similar to (85.9)AT5G09680 Symbols: cytochrome b5 domain-containing protein chr5:2999363-3000186 REVERSE no original description	
EV142971	1.114	no similarity	
JCVI_28912	1.114	moderately similar to (233)AT2G45110 Symbols: EXPB4, ATHEXP BETA 1.1, ATEXPB4 ATEXPB4 (ARABIDOPSIS THALIANA EXPANSIN-BETA 1.1)	
RC_H07276	1.113	no similarity	
JCVI_8672	1.112	weakly similar to (136)AT2G25720 Symbols: similar to hypothetical protein SDM1_56t00007 [Solanum demissum] (GB:AAU90325)	
EX016787	1.111	weakly similar to (136)AT5G09630 Symbols: protein binding / zinc ion binding chr5:2986017-2987177 REVERSE [21808]	
JCVI_28425	1.111	no original description	1.256
ES264714	1.110	moderately similar to (306)AT3G13850 Symbols: LBD22 LBD22 (LOB DOMAIN-CONTAINING PROTEIN 22) chr3:4559917-4560017 REVERSE [21423]	
EE414902	1.109	no similarity	-1.004
JCVI_31954	1.109	weakly similar to (124)AT1G26320 Symbols: NADP-dependent oxidoreductase, putative chr1:9105227-9107016 FORWARD no original description	
EE518095	1.108	no similarity	
RC_JCVI_42177	1.107	no original description	
CV973890	1.107	no similarity	1.186
RC_EX083949	1.106	no similarity	
RC_EE544274	1.106	no similarity	
CX190870	1.105	weakly similar to (114)AT1G02335 Symbols: GL22 GL22 (GERMIN-LIKE PROTEIN SUBFAMILY 2 MEMBER 2 PRECURSOR)	
JCVI_10850	1.105	moderately similar to (225)AT1G15010 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G01300.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO41555.1) chr5:4374-4384 REVERSE [21423]	
RC_EE561316	1.104	no similarity	
EX073784	1.103	no similarity	
EE568516	1.102	no similarity	

JCVI_16325	1.101	no original description	
EV221580	1.101	no similarity	
EV100923	1.100	no similarity	
ES930632	1.099	no similarity	
EV144282	1.099	no similarity	
ES991430	1.099	moderately similar to (307)AT5G13600 Symbols: phototropic-responsive NPH3 family protein chr5:4380435-4382500 FORWARD	
CV546281	1.097	weakly similar to (150)AT3G10610 Symbols: 40S ribosomal protein S17 (RPS17C) chr3:3319464-3319886 FORWARD [16551] 1	
RC_JCVI_31046	1.097	no original description	
EV216499	1.095	no similarity	
JCVI_39149	1.095	no original description	2.105
ES959318	1.094	no similarity	
JCVI_37107	1.094	no original description	
CD834522	1.094	weakly similar to (185)AT4G15350 Symbols: CYP705A2 CYP705A2 (cytochrome P450, family 705, subfamily A, polypeptide 2); o	
JCVI_30071	1.093	moderately similar to (416)AT4G24150 Symbols: AtGRF8 AtGRF8 (GROWTH-REGULATING FACTOR 8) chr4:12535982-1253	
EV112906	1.092	no similarity	
EE563564	1.092	no similarity	
EV088013	1.092	weakly similar to (191)POLX_TOBAC [21444]	
JCVI_38437	1.091	weakly similar to (118)AT1G23600 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G23570.2); similar to un	
EE418004	1.090	weakly similar to (135)AT5G14670 Symbols: ATARFA1B ATARFA1B (ADP-RIBOSYLATION FACTOR A1B); GTP binding / ph	
EV205151	1.090	no similarity	
ES968154	1.089	no similarity	
EX022131	1.089	no similarity	
ES968127	1.087	no similarity	
JCVI_39772	1.087	weakly similar to (182)AT2G47270 Symbols: transcription factor/ transcription regulator chr2:19418811-19419119 REVERSE no c	
JCVI_8777	1.087	moderately similar to (234)AT1G04250 Symbols: IAA17, AXR3 AXR3 (AUXIN RESISTANT 3); transcription factor chr1:113638	
JCVI_41343	1.086	no original description	
EE563352	1.085	no similarity	
EX050638	1.085	weakly similar to (150)AT2G13770 Symbols: similar to ribosomal protein-like [Oryza sativa (japonica cultivar-group)] (GB:BAD375	
JCVI_38473	1.085	very weakly similar to (80.5)AT1G76920 Symbols: F-box family protein (FBX3) chr1:28897189-28898313 FORWARD no original	
JCVI_20996	1.085	no original description	
JCVI_22562	1.084	very weakly similar to (82.0)AT2G22440 Symbols: similar to reverse transcriptase, putative / RNA-dependent DNA polymerase, puta	
EE561437	1.084	no similarity	
RC_EL591193	1.083	no similarity	
EV110683	1.082	no similarity	
JCVI_17733	1.081	moderately similar to (218)AT4G22390 Symbols: F-box family protein-related chr4:11813769-11815086 REVERSE no original de	
ES960748	1.081	no similarity	
EE567830	1.079	no similarity	
JCVI_19775	1.079	moderately similar to (466)AT5G13530 Symbols: KEG KEG (KEEP ON GOING); protein binding / protein kinase/ ubiquitin-protein	
JCVI_28778	1.077	no original description	2.222
JCVI_21849	1.076	moderately similar to (486)AT5G41080 Symbols: glycerophosphoryl diester phosphodiesterase family protein chr5:16459217-1646	
RC_EV130845	1.075	no similarity	
CX271629	1.075	weakly similar to (118)AT1G60720 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G33710.1); similar to pu	
EV140246	1.074	no similarity	
JCVI_17398	1.073	moderately similar to (288)AT4G14210 Symbols: PDS, PDE226, PDS3 PDS3 (PHYTOENE DESATURASE) chr4:8190421-81947	
EV220592	1.073	no similarity	
JCVI_16185	1.071	weakly similar to (193)AT1G20220 Symbols: nucleic acid binding chr1:7005081-7007276 REVERSE no original description	
ES966548	1.070	no similarity	
JCVI_35557	1.070	moderately similar to (213)AT1G01260 Symbols: basic helix-loop-helix (bHLH) family protein chr1:109595-111367 FORWARD r	
JCVI_293	1.069	weakly similar to (169)AT3G12480 Symbols: transcription factor, putative chr3:3958072-3960285 FORWARD no original descript	
EV152233	1.069	no similarity	1.294
JCVI_38516	1.069	no original description	
EV194445	1.067	weakly similar to (120)AT1G31550 Symbols: GDSL-motif lipase, putative chr1:11295616-11297265 REVERSE [21489] 41 722 7.	
EE567416	1.066	no similarity	
JCVI_11761	1.065	no original description	1.254
DY003886	1.064	weakly similar to (140)AT3G63350 Symbols: HSFA7B, AT-HSFA7B AT-HSFA7B (Arabidopsis thaliana heat shock transcription fac	
ES933334	1.063	no similarity	
JCVI_4571	1.062	moderately similar to (266)AT5G59820 Symbols: ZAT12, RHL41 RHL41 (RESPONSIVE TO HIGH LIGHT 41); nucleic acid bindi	
JCVI_3696	1.062	moderately similar to (420)AT5G26110 Symbols: ATP binding / protein kinase chr5:9118242-9118993 REVERSE no original desc	
JCVI_5445	1.061	no original description	
DW997179	1.061	no similarity	
CD826637	1.060	moderately similar to (350)AT4G02350 Symbols: exocyst complex subunit Sec15-like family protein chr4:1038157-1040571 FOR	
JCVI_40879	1.060	very weakly similar to (83.6)AT5G46910 Symbols: transcription factor jumonji (jmj) family protein chr5:19065007-19068107 FOR	
DT317682	1.060	no similarity	
JCVI_16376	1.060	moderately similar to (464)AT5G65910 Symbols: BSD domain-containing protein chr5:26378818-26380567 REVERSE no origina	
JCVI_13274	1.056	moderately similar to (369)AT3G24800 Symbols: PRT1 PRT1 (PROTEOLYSIS 1); ubiquitin-protein ligase chr3:9055660-9057802	
EV134884	1.056	no similarity	
EE530681	1.055	no similarity	
CX188787	1.055	no similarity	
RC_ES978013	1.055	no similarity	
EV131420	1.054	no similarity	
EE559481	1.054	no similarity	
JCVI_15747	1.054	weakly similar to (148)AT4G27280 Symbols: calcium-binding EF hand family protein chr4:13663776-13664168 REVERSE no ori	
JCVI_31294	1.052	moderately similar to (459)AT4G38890 Symbols: dihydrouridine synthase family protein chr4:18135903-18139094 REVERSE no o	-1.448
JCVI_39499	1.052	weakly similar to (108)AT2G24650 Symbols: transcriptional factor B3 family protein chr2:10487807-10494650 REVERSE no orig	
EE567405	1.051	no similarity	
EV107687	1.050	no similarity	
JCVI_7424	1.050	no original description	
EV039920	1.049	moderately similar to (239)AT2G42550 Symbols: protein kinase family protein chr2:17720274-17721308 FORWARDvery weakly	
JCVI_14583	1.049	weakly similar to (118)AT5G24490 Symbols: 30S ribosomal protein, putative chr5:8365693-8367181 FORWARDvery weakly simi	
EE524452	1.048	weakly similar to (169)AT1G14560 Symbols: mitochondrial substrate carrier family protein chr1:4981295-4983077 FORWARD [2	
EV100862	1.048	very weakly similar to (85.9)AT1G57750 Symbols: MAH1, CYP96A15 CYP96A15/MAH1 (MID-CHAIN ALKANE HYDROXYLA	
JCVI_40	1.048	moderately similar to (432)AT1G78630 Symbols: EMB1473 EMB1473 (EMBRYO DEFECTIVE 1473); structural constituent of rib	
EE504672	1.047	no similarity	

JCVI_18195	1.047	moderately similar to (215)AT3G15210 Symbols: ATERF-4, ERF4, RAP2.5, ATERF4 ATERF-4/ATERF4/ERF4/RAP2.5 (ETHYLE	
JCVI_12621	1.044	no original description	
JCVI_30114	1.042	no original description	
EV099936	1.041	moderately similar to (241)AT1G20020 Symbols: ATLFNR2 ATLFNR2 (LEAF FNR 2); poly(U) binding chr1:6942842-6944859 F	
JCVI_33471	1.041	no original description	2.085
EV178823	1.038	no similarity	
EV098082	1.037	no similarity	1.317
JCVI_39622	1.037	weakly similar to (157)AT2G15910 Symbols: CSL zinc finger domain-containing protein chr2:6939999-6942415 REVERSE no ori	
JCVI_6413	1.037	weakly similar to (102)AT1G08920 Symbols: sugar transporter, putative chr1:2867449-2870193 FORWARD no original descriptio	
EV091597	1.035	moderately similar to (261)AT5G23890 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G52410.2); similar t	1.086
CA991582	1.035	very weakly similar to (83.6)AT4G38800 Symbols: ATMTN1 ATMTN1; catalytic/ methylthioadenosine nucleosidase chr4:18113349	
RC_JCVI_35546	1.034	no original description	
EE568839	1.034	no similarity	
JCVI_20936	1.032	no original description	
EV218157	1.032	no similarity	
BG543914	1.031	weakly similar to (102)AT4G31700 Symbols: RPS6 RPS6 (RIBOSOMAL PROTEIN S6) chr4:15346312-15347081 REVERSEvery	
JCVI_26963	1.029	very weakly similar to (88.2)AT2G38500 Symbols: similar to DTA4 (DOWNSTREAM TARGET OF AGL15-4) [Arabidopsis thaliar	
JCVI_15983	1.027	moderately similar to (394)AT1G10910 Symbols: similar to PTAC2 (PLASTID TRANSCRIPTIONALLY ACTIVE2) [Arabidopsis t	
ES965081	1.027	no similarity	
JCVI_19002	1.026	weakly similar to (124)AT4G02075 Symbols: PIT1 PIT1 (PITCHOUN 1); protein binding / zinc ion binding chr4:913555-916414 R	
CX268927	1.025	no similarity	
EV103978	1.025	no similarity	
EV208389	1.025	no similarity	
EX016865	1.024	no similarity	
JCVI_33662	1.024	no original description	
EV135772	1.024	no similarity	
EV204179	1.022	no similarity	
EE401649	1.022	weakly similar to (103)AT2G42380 Symbols: bZIP transcription factor family protein chr2:17654283-17655738 REVERSE [20197	
JCVI_20087	1.022	weakly similar to (182)AT1G19230 Symbols: respiratory burst oxidase protein E (RbohE) / NADPH oxidase chr1:6644180-664914	
EV148759	1.020	no similarity	
JCVI_18052	1.020	moderately similar to (254)AT3G11980 Symbols: MS2 MS2 (MALE STERILITY 2) chr3:3814490-3816933 FORWARD no origin.	
EV218684	1.019	no similarity	
JCVI_41904	1.018	no original description	
JCVI_29660	1.018	moderately similar to (262)AT2G44520 Symbols: COX10 COX10 (CYTOCHROME C OXIDASE 10); prenyltransferase chr2:1838	
JCVI_10099	1.018	moderately similar to (225)AT5G51750 Symbols: ATSBT1.3 ATSBT1.3; subtilase chr5:21037492-21039834 FORWARD no origin	
JCVI_18456	1.017	weakly similar to (180)AT1G07150 Symbols: MAPKKK13 MAPKKK13 (Mitogen-activated protein kinase kinase kinase 13); kinase	
RC_H07682	1.017	no similarity	
RC_EV112452	1.016	no similarity	
EV206757	1.015	weakly similar to (102)AT3G27690 Symbols: LHCB2.3, LHCB2, LHCB2:4 LHCB2:4 (Photosystem II light harvesting complex gene	
EV197442	1.015	very weakly similar to (99.0)AT4G38970 Symbols: fructose-bisphosphate aldolase, putative chr4:18163763-18165653 REVERSEve	
JCVI_39268	1.015	moderately similar to (245)AT5G41270 Symbols: similar to Os01g0541600 [Oryza sativa (japonica cultivar-group)] (GB:NP_00104	
EE472257	1.013	weakly similar to (159)AT4G11580 Symbols: F-box family protein chr4:7006642-7007732 REVERSE [20163]	
JCVI_5111	1.011	no original description	
RC_JCVI_41878	1.011	no original description	
EV222917	1.011	moderately similar to (237)AT5G60390 Symbols: elongation factor 1-alpha / EF-1-alpha chr5:24306452-24307901 FORWARDmo	
EX087640	1.009	moderately similar to (212)AT1G23380 Symbols: KNAT6L, KNAT6S, KNAT6 KNAT6 (Knotted-like Arabidopsis thaliana 6); DNA	
JCVI_39590	1.008	moderately similar to (366)AT4G23460 Symbols: beta-adaptin, putative chr4:12243909-12248908 REVERSE no original descriptio	
EX065651	1.008	moderately similar to (298)AT1G55570 Symbols: SKS12 SKS12 (SKU5 Similar 12); copper ion binding / oxidoreductase chr1:2076	
EX093982	1.007	moderately similar to (378)AT1G12260 Symbols: EMB2749, ANAC007, VND4 VND4 (VASCULAR RELATED NAC-DOMAIN I	
EV226859	1.006	moderately similar to (326)AT5G24470 Symbols: PRR5, APRR5 APRR5 (PSEUDO-RESPONSE REGULATOR 5); transcription re	
EV170364	1.004	weakly similar to (174)AT5G06950 Symbols: TGA2, AHBp-1B AHBp-1B (bZIP transcription factor HBP-1b homolog) chr5:21523	
EL590426	1.002	moderately similar to (276)AT5G02010 Symbols: ATROPGEF7, ROPGEF7 ATROPGEF7/ROPGEF7 (KINASE PARTNER PROTI	
EV058225	1.002	weakly similar to (179)AT5G25320 Symbols: ACT domain-containing protein chr5:8787406-8789533 REVERSE [21442]	
EE449456	0.999	no similarity	
EL587091	0.998	no similarity	
JCVI_14015	0.997	moderately similar to (370)AT5G37300 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G38995.1); similar t	
EV195092	0.996	very weakly similar to (97.1)AT1G69800 Symbols: CBS domain-containing protein chr1:26278079-26279988 REVERSE [21489] 3	
EV209409	0.988	weakly similar to (169)AT5G25150 Symbols: TAF5 TAF5 (TBP-ASSOCIATED FACTOR 5); nucleotide binding chr5:8677120-868	
EV158470	0.988	no similarity	
JCVI_41467	0.983	no original description	
JCVI_4595	0.979	moderately similar to (266)AT4G34970 Symbols: actin binding chr4:16653789-16654598 FORWARDweakly similar to (176)ADF	
JCVI_5890	0.977	weakly similar to (192)AT2G22500 Symbols: mitochondrial substrate carrier family protein chr2:9570611-9571552 REVERSE no o	
JCVI_12349	0.976	no original description	1.277
EE565485	0.971	no similarity	
RC_EV012511	0.967	no similarity	
EE392280	0.954	very weakly similar to (96.7)AT1G45190 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G11990.1); contain	
JCVI_2142	0.950	no original description	
JCVI_14932	0.945	no original description	
EV220691	0.943	no similarity	
EV142319	0.943	no similarity	
JCVI_27062	0.936	no original description	
JCVI_13988	0.936	moderately similar to (213)AT4G21895 Symbols: similar to AT hook motif-containing protein [Arabidopsis thaliana] (TAIR:AT5G5	
EV130062	0.932	no similarity	
EE535293	0.929	moderately similar to (240)AT5G11560 Symbols: catalytic chr5:3709735-3713995 REVERSE [20150]	
JCVI_35720	0.921	moderately similar to (305)AT4G32510 Symbols: anion exchanger chr4:15685909-15688817 REVERSE no original description	
EV098714	0.920	moderately similar to (266)AT2G35610 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G70630.1); similar t	
H07700	0.919	no similarity	
JCVI_15621	0.919	no original description	
JCVI_34192	0.914	no original description	
JCVI_25545	0.911	moderately similar to (248)AT1G11020 Symbols: zinc finger (C3HC4-type RING finger) family protein chr1:3676968-3678350 FC	
JCVI_16737	0.897	no original description	
JCVI_19949	0.896	moderately similar to (297)AT2G19050 Symbols: GDSL-motif lipase/hydrolase family protein chr2:8260498-8262616 FORWARD	
ES966296	0.878	no similarity	

RC_EV204033	0.878	no similarity
JCVI_26199	0.867	no original description
JCVI_19464	0.860	highly similar to (565)AT1G04990 Symbols: zinc finger (CCH-type) family protein chr1:1419367-1421453 REVERSEmoderately
JCVI_41069	0.859	highly similar to (556)AT2G38010 Symbols: ceramidase family protein chr2:15913940-15916945 FORWARD no original descripti
JCVI_31489	0.858	moderately similar to (308)AT2G41840 Symbols: 40S ribosomal protein S2 (RPS2C) chr2:17467094-17468476 REVERSE no orig -0.964
EE568162	0.854	no similarity
EV143884	0.853	no similarity
JCVI_23627	0.846	moderately similar to (295)AT5G67310 Symbols: CYP81G1 CYP81G1 (cytochrome P450, family 81, subfamily G, polypeptide 1); c
JCVI_23654	0.846	no original description -1.526
JCVI_15762	0.845	moderately similar to (462)AT4G18480 Symbols: CH42, CH-42, CHL11, CHLI-1, CHLI1 CHLI1 (CHLORINA 42); magnesium che
EE558080	0.842	no similarity
CV433940	0.831	no similarity
JCVI_11165	0.817	no original description
RC_EV013640	0.815	no similarity
EV127571	0.815	no similarity
JCVI_15980	0.805	weakly similar to (112)AT1G54050 Symbols: 17.4 kDa class III heat shock protein (HSP17.4-CIII) chr1:20183226-20183790 REV1
EV176914	0.802	no similarity
RC_EE565963	0.802	no similarity
JCVI_36562	0.801	no original description
EE560924	0.786	no similarity
EV123380	0.775	weakly similar to (135)AT4G00440 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G45900.1); similar to un
ES960782	0.772	no similarity
JCVI_3653	0.770	moderately similar to (473)AT1G26480 Symbols: GF14 IOTA, GRF12 GRF12 (GENERAL REGULATORY FACTOR 12); protein
ES983837	0.766	no similarity
RC_EX064898	0.765	no similarity
DY010873	0.756	no similarity
JCVI_1068	0.745	moderately similar to (212)AT3G04320 Symbols: endopeptidase inhibitor chr3:1143822-1144433 FORWARD no original descripti
JCVI_37982	0.740	no original description
CX271816	0.729	weakly similar to (102)AT1G04150 Symbols: C2 domain-containing protein chr1:1081207-1084245 REVERSE [16815]
JCVI_33335	0.728	weakly similar to (187)AT3G06390 Symbols: integral membrane family protein chr3:1938919-1939713 REVERSE no original desc
DN965438	0.723	no similarity
JCVI_33057	0.719	weakly similar to (111)AT5G60850 Symbols: OBP4 OBP4 (OBF BINDING PROTEIN 4); DNA binding / transcription factor chr5:.
RC_ES966655	0.718	no similarity
CX190760	0.706	no similarity
EE562726	0.702	very weakly similar to (93.6)AT2G01450 Symbols: ATPK17 ATPK17 (Arabidopsis thaliana MAP kinase 17); MAP kinase chr2:
JCVI_19732	0.696	moderately similar to (270)AT1G47610 Symbols: transducin family protein / WD-40 repeat family protein chr1:17507276-1750833
DY007829	0.683	weakly similar to (113)AT4G14695 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G22310.1); similar to un
EV132032	0.672	no similarity
CV432515	0.644	weakly similar to (138)AT3G10400 Symbols: RNA recognition motif (RRM)-containing protein chr3:3232641-3233426 FORWAR
JCVI_41442	0.643	no original description
EX134503	0.634	no similarity
EX133342	0.631	no similarity
JCVI_14485	0.604	no original description
EV107694	0.594	no similarity
JCVI_18802	0.577	moderately similar to (350)AT4G28040 Symbols: nodulin MtN21 family protein chr4:13940887-13942207 FORWARD no original
CD823053	0.528	no similarity
EX095814	0.509	weakly similar to (180)AT1G34220 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G35730.1); similar to hy
EX110598	0.502	no similarity
JCVI_34124	0.497	moderately similar to (370)AT5G51760 Symbols: AHG1 AHG1 (ABA-HYPERSENSITIVE GERMINATION 1); protein serine/threc
JCVI_22401	0.470	moderately similar to (340)AT5G06930 Symbols: similar to nucleolar protein gar2-related [Arabidopsis thaliana] (TAIR:AT2G42320
JCVI_39816	0.469	no original description
EX070812	0.410	no similarity
JCVI_9447	0.250	no original description
EE523558	0.206	moderately similar to (209)AT1G17890 Symbols: GER2 GER2; catalytic chr1:6154471-6155589 REVERSEweakly similar to (158
JCVI_25196	0.172	moderately similar to (272)AT2G28880 Symbols: EMB1997 EMB1997 (EMBRYO DEFECTIVE 1997); anthranilate synthase/ cataly
JCVI_35033	0.110	weakly similar to (184)AT5G56290 Symbols: PEX5 PEX5 (PEROXIN 5); peroxisome matrix targeting signal-1 binding chr5:22803
RC_ES979191	0.069	no similarity
RC_ES955671	0.033	no similarity