

Identifier	log2-fold LT induced	Description	log2-fold LL-HL
JCVI_11085	6.816	highly similar to (613)AT2G15020 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G64190.1); similar to hypo	5.216
EV198679	6.596	weakly similar to (176)AT2G15020 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G64190.1); similar to hypo	5.412
EX041860	6.331	weakly similar to (138)AT1G02040 Symbols: zinc finger (C2H2 type) family protein chr1:358104-359078 REVERSE [21811]	3.434
ES967782	6.217	moderately similar to (249)AT5G38700 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G02170.1); similar to i	4.874
EV103808	6.217	no similarity	
JCVI_18444	5.864	no original description	
JCVI_4881	5.609	very weakly similar to (87.0)AT5G15110 Symbols: pectate lyase family protein chr5:4895969-4897685 FORWARD no original descri	5.199
JCVI_20042	5.546	moderately similar to (349)AT5G45340 Symbols: CYP707A3 CYP707A3 (cytochrome P450, family 707, subfamily A, polypeptide 3);	4.064
JCVI_22385	5.534	moderately similar to (303)AT2G41640 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G57380.1); similar to i	4.714
JCVI_20804	5.442	weakly similar to (113)AT3G19580 Symbols: AZF2 AZF2 (ARABIDOPSIS ZINC-FINGER PROTEIN 2) chr3:6803299-6804120 RE'	3.844
JCVI_13878	5.419	moderately similar to (466)AT5G45340 Symbols: CYP707A3 CYP707A3 (cytochrome P450, family 707, subfamily A, polypeptide 3);	3.174
JCVI_36344	5.395	weakly similar to (121)AT4G14450 Symbols: Identical to Uncharacterized protein At4g14450, chloroplast precursor [Arabidopsis Thal	3.725
JCVI_10510	5.290	moderately similar to (305)AT1G64110 Symbols: AAA-type ATPase family protein chr1:23800550-23804918 REVERSE no original	3.744
AM395641	5.289	very weakly similar to (82.8)AT4G27657 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G27652.1) chr4:138	5.590
JCVI_12679	5.272	no original description	4.464
JCVI_143	5.238	moderately similar to (431)AT2G40000 Symbols: HSPRO2, ATHSPRO2 similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2	2.782
JCVI_26301	5.208	moderately similar to (240)AT1G19210 Symbols: AP2 domain-containing transcription factor, putative chr1:6626964-6627521 REVE	5.982
JCVI_4569	5.183	weakly similar to (110)AT3G17520 Symbols: late embryogenesis abundant domain-containing protein / LEA domain-containing protei	3.196
JCVI_3404	5.155	moderately similar to (384)AT3G50060 Symbols: MYB77 MYB77; DNA binding / transcription factor chr3:18569129-18570034 REV	2.935
JCVI_25760	5.132	moderately similar to (475)AT4G24570 Symbols: mitochondrial substrate carrier family protein chr4:12686556-12687497 FORWARD	2.684
JCVI_20638	5.118	weakly similar to (145)AT2G20835 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G15534.1); similar to unna	3.442
JCVI_669	5.114	moderately similar to (315)AT4G17490 Symbols: ERF-6-6, ATERF6 ATERF6 (ETHYLENE RESPONSIVE ELEMENT BINDING FA	3.990
EV158484	5.103	moderately similar to (292)AT5G57240 Symbols: oxysterol-binding family protein chr5:23210675-23212529 FORWARD [21484]	3.118
JCVI_30169	5.089	very weakly similar to (100)AT2G40000 Symbols: HSPRO2, ATHSPRO2 similar to unknown protein [Arabidopsis thaliana] (TAIR:AT	
JCVI_20373	5.057	moderately similar to (255)AT1G80390 Symbols: IAA15 IAA15 (indoleacetic acid-induced protein 15); transcription factor chr1:30220	2.348
JCVI_8461	5.048	moderately similar to (376)AT1G32450 Symbols: proton-dependent oligopeptide transport (POT) family protein chr1:11715317-1171'	2.603
EE422870	5.045	no similarity	3.710
AT000615	5.012	no similarity	2.612
DW998935	5.010	weakly similar to (165)AT1G21910 Symbols: AP2 domain-containing transcription factor family protein chr1:7696644-7697336 FOR	
EV227530	5.005	no similarity	4.019
EX138359	5.003	highly similar to (534)AT1G50090 Symbols: aminotransferase class IV family protein chr1:18558309-18560462 REVERSE [21833]	3.901
EX131720	4.993	no similarity	4.803
EV182486	4.962	very weakly similar to (100)AT5G57560 Symbols: XTH22, TCH4 TCH4 (TOUCH 4); hydrolase, acting on glycosyl bonds / xyloglucan	3.371
JCVI_17081	4.943	weakly similar to (108)AT5G17350 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G03280.1); similar to unkr	3.982
JCVI_30677	4.939	moderately similar to (417)AT1G64110 Symbols: AAA-type ATPase family protein chr1:23800550-23804918 REVERSE no original	3.455
EX126027	4.871	moderately similar to (478)AT1G68570 Symbols: proton-dependent oligopeptide transport (POT) family protein chr1:25750474-2575	2.996
EV096109	4.866	very weakly similar to (80.1)AT5G14740 Symbols: CA18, BETA CA2, CA2 CA2 (BETA CARBONIC ANHYDRASE 2) chr5:475826	5.304
EV103471	4.838	no similarity	4.871
JCVI_23438	4.834	no original description	1.839
EV218551	4.824	moderately similar to (332)AT2G40140 Symbols: CZF1, ZFAR1 CZF1/ZFAR1 chr2:16779615-16781408 FORWARD [21492] 53 73:	
JCVI_9883	4.779	weakly similar to (193)AT5G66780 Symbols: similar to unknown [Ammopiptanthus mongolicus] (GB:AAW33981.1) chr5:26680853-	3.058
JCVI_22325	4.777	weakly similar to (196)AT3G19680 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G50040.1); similar to unna	3.553
JCVI_37336	4.761	weakly similar to (146)AT4G08950 Symbols: phosphate-responsive protein, putative (EXO) chr4:5740375-5741319 FORWARD no c	4.147
ES985248	4.747	weakly similar to (157)AT3G51910 Symbols: HSFA7A, AT-HSFA7A AT-HSFA7A (Arabidopsis thaliana heat shock transcription fact	3.870
ES271272	4.700	no similarity	
EE476768	4.699	moderately similar to (254)AT5G17350 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G03280.1); similar to i	3.685
H07351	4.673	very weakly similar to (85.9)AT5G17350 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G03280.1); similar to	4.062
AM386021	4.669	no similarity	2.981
JCVI_21671	4.635	moderately similar to (271)AT3G18710 Symbols: U-box domain-containing protein chr3:6434240-6435487 REVERSE no original de	3.085
JCVI_20277	4.630	no original description	4.476
H74770	4.621	very weakly similar to (87.8)AT3G19680 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G50040.1); similar to	3.331
AM394357	4.615	weakly similar to (110)AT2G40000 Symbols: HSPRO2, ATHSPRO2 similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G5'	2.561
AM389155	4.608	moderately similar to (261)AT1G14540 Symbols: anionic peroxidase, putative chr1:4974228-4975595 REVERSEweakly similar to (	3.151
EE549718	4.589	no similarity	2.903
JCVI_3712	4.581	weakly similar to (141)AT1G75390 Symbols: ATBZIP44 ATBZIP44 (ARABIDOPSIS THALIANA BASIC LEUCINE-ZIPPER 44) ch	
EE556375	4.581	no similarity	3.293
JCVI_27911	4.581	moderately similar to (416)AT2G36800 Symbols: UGT73C5, DOGT1 DOGT1 (DON-GLUCOSYLTRANSFERASE); UDP-glycosyltra	3.111
JCVI_31122	4.579	weakly similar to (144)AT3G24750 Symbols: unknown protein chr3:9036742-9037571 FORWARD no original description	4.071
JCVI_14769	4.579	weakly similar to (171)AT5G66650 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G23790.1); similar to unna	
JCVI_24381	4.559	no original description	2.784
JCVI_5468	4.530	moderately similar to (296)AT5G67300 Symbols: ATMYBR1, ATMYB44, MYBR1 ATMYB44/ATMYBR1/MYBR1 (MYB DOMAIN	2.184
ES988910	4.530	very weakly similar to (86.3)AT3G12880 Symbols: invertase/pectin methylesterase inhibitor family protein chr3:4095570-4096109 FC	
JCVI_19002	4.527	weakly similar to (124)AT4G02075 Symbols: PIT1 PIT1 (PITCHOUN 1); protein binding / zinc ion binding chr4:913555-916414 REV	3.138
JCVI_38038	4.507	weakly similar to (136)AT5G66650 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G23790.1); similar to unna	2.925
JCVI_10857	4.500	moderately similar to (353)AT1G02700 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G02140.1); similar to l	
EV108573	4.486	no similarity	3.612
JCVI_1699	4.484	weakly similar to (148)AT5G06760 Symbols: late embryogenesis abundant group 1 domain-containing protein / LEA group 1 domain-c	
EE477048	4.472	weakly similar to (139)AT3G18710 Symbols: U-box domain-containing protein chr3:6434240-6435487 REVERSE [20157] 1 623 65:	3.504
JCVI_1995	4.459	weakly similar to (136)AT1G67856 Symbols: protein binding / zinc ion binding chr1:25446149-25446550 FORWARD no original de	3.130
JCVI_12350	4.454	weakly similar to (106)AT1G52342 Symbols: unknown protein chr1:19496109-19496372 REVERSE no original description	2.748
DT317662	4.453	very weakly similar to (80.1)AT3G19030 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G49500.1) chr3:656	4.774
EE481897	4.451	weakly similar to (154)AT4G25850 Symbols: oxysterol-binding family protein chr4:13143868-13146663 FORWARD [20154]	2.804
RC_ES968676	4.448	no similarity	3.655
JCVI_26223	4.427	moderately similar to (300)AT5G51990 Symbols: CBF4, DREB1D CBF4/DREB1D (C- REPEAT-BINDING FACTOR 4); DNA bindir	2.459
JCVI_28808	4.410	weakly similar to (106)AT3G19030 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G49500.1) chr3:6564123	4.596
EV061913	4.406	no similarity	
EX071969	4.334	moderately similar to (281)AT5G07475 Symbols: plastocyanin-like domain-containing protein chr5:2364828-2365537 REVERSEvery	
JCVI_38563	4.329	weakly similar to (138)AT3G19580 Symbols: AZF2 AZF2 (ARABIDOPSIS ZINC-FINGER PROTEIN 2) chr3:6803299-6804120 RE'	2.852
EV108083	4.313	weakly similar to (154)AT2G36800 Symbols: UGT73C5, DOGT1 DOGT1 (DON-GLUCOSYLTRANSFERASE); UDP-glycosyltransfe	3.033
EX125037	4.297	weakly similar to (126)AT4G17615 Symbols: ATCBL1, SCAP5 CBL1 (CALCINEURIN B-LIKE PROTEIN 1); calcium ion binding	3.202
JCVI_1711	4.279	weakly similar to (185)AT3G55980 Symbols: zinc finger (CCH-type) family protein chr3:20787836-20789578 FORWARD no origi	2.607

JCVI_17114	4.279	moderately similar to (344)AT1G18300 Symbols: ATNUDT4 ATNUDT4 (Arabidopsis thaliana Nudix hydrolase homolog 4); hydrolase	3.644
JCVI_11504	4.266	moderately similar to (361)AT1G18300 Symbols: ATNUDT4 ATNUDT4 (Arabidopsis thaliana Nudix hydrolase homolog 4); hydrolase	3.623
EX132042	4.252	weakly similar to (172)AT5G17350 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G03280.1); similar to unkr	4.537
JCVI_8551	4.222	moderately similar to (225)AT5G42380 Symbols: CML39, CML37 CML37/CML39; calcium ion binding chr5:16959986-16960543 R	4.057
JCVI_24649	4.215	moderately similar to (204)AT4G25490 Symbols: DREB1B, CBF1 CBF1 (C-REPEAT/DRE BINDING FACTOR 1); DNA binding / tr	4.664
JCVI_23374	4.206	no original description	3.015
JCVI_24275	4.203	highly similar to (581)AT5G42760 Symbols: similar to unknown [Populus trichocarpa] (GB:ABK95091.1); contains InterPro domain C	3.310
JCVI_25058	4.181	weakly similar to (197)AT5G59820 Symbols: ZAT12, RHL41 RHL41 (RESPONSIVE TO HIGH LIGHT 41); nucleic acid binding / tra	3.388
JCVI_25314	4.169	weakly similar to (160)AT4G15810 Symbols: chloroplast outer membrane protein, putative chr4:8989175-8992604 REVERSE no orig	2.692
EV189264	4.137	moderately similar to (215)AT4G15810 Symbols: chloroplast outer membrane protein, putative chr4:8989175-8992604 REVERSE [2	2.071
EX132070	4.124	moderately similar to (232)AT4G25810 Symbols: XTH23, XTR6 XTR6 (XYLOGLUCAN ENDOTRANSGLYCOSYLASE 6); hydrola	
ES903612	4.113	no similarity	3.433
EX042542	4.110	moderately similar to (256)AT1G02040 Symbols: zinc finger (C2H2 type) family protein chr1:358104-359078 REVERSE [21811]	
JCVI_15634	4.109	moderately similar to (419)AT4G17615 Symbols: ATCBL1, SCABP5 CBL1 (CALCINEURIN B-LIKE PROTEIN 1); calcium ion bindi	2.218
JCVI_28290	4.104	weakly similar to (119)AT1G02820 Symbols: late embryogenesis abundant 3 family protein / LEA3 family protein chr1:623933-6243	3.404
JCVI_27796	4.104	weakly similar to (107)AT4G27657 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G27652.1) chr4:1381313	4.153
JCVI_29276	4.097	weakly similar to (172)AT3G21890 Symbols: zinc finger (B-box type) family protein chr3:7709305-7709670 REVERSE no original d	3.349
JCVI_32745	4.083	moderately similar to (427)AT4G21200 Symbols: ATGA2OX8 ATGA2OX8 (GIBBERELLIN 2-OXIDASE 8); gibberellin 2-beta-dioxy	2.895
JCVI_29480	4.079	no original description	
EE419156	4.052	moderately similar to (215)AT1G64110 Symbols: AAA-type ATPase family protein chr1:23800550-23804918 REVERSE [20146]	3.430
JCVI_40407	4.045	highly similar to (523)AT5G57560 Symbols: XTH22, TCH4 TCH4 (TOUCH 4); hydrolase, acting on glycosyl bonds / xyloglucan:xylo	
EV207068	4.036	no similarity	3.035
JCVI_26042	4.032	moderately similar to (338)AT5G66520 Symbols: pentatricopeptide (PPR) repeat-containing protein chr5:26569105-26570967 FORW	
JCVI_21687	4.032	moderately similar to (311)AT4G01470 Symbols: GAMMA-TIP3, TIP1;3 GAMMA-TIP3/TIP1;3 (tonoplast intrinsic protein 1;3); wate	3.464
JCVI_13720	4.020	no original description	2.367
EV028754	4.013	no similarity	
JCVI_7693	4.009	moderately similar to (225)AT5G54490 Symbols: PBP1 PBP1 (PINOID-BINDING PROTEIN 1); calcium ion binding chr5:22138684-	3.374
CD830269	4.006	moderately similar to (323)AT4G17490 Symbols: ERF-6-6, ATERF6 ATERF6 (ETHYLENE RESPONSIVE ELEMENT BINDING FA	3.408
JCVI_34980	3.999	no original description	3.387
JCVI_40963	3.991	weakly similar to (156)AT5G57240 Symbols: oxysterol-binding family protein chr5:23210675-23212529 FORWARD no original des	2.974
JCVI_33365	3.991	no original description	
JCVI_26705	3.989	highly similar to (633)AT2G38470 Symbols: ATWRKY33, WRKY33 WRKY33 (WRKY DNA-binding protein 33); transcription facto	2.146
JCVI_14519	3.982	highly similar to (871)AT5G45340 Symbols: CYP707A3 CYP707A3 (cytochrome P450, family 707, subfamily A, polypeptide 3); oxyg	3.631
JCVI_38370	3.975	moderately similar to (416)AT4G29780 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G12010.1); similar to i	2.720
JCVI_20498	3.971	no original description	
ES966758	3.953	no similarity	3.192
JCVI_15880	3.947	moderately similar to (234)AT3G56290 Symbols: similar to hypothetical protein [Vitis vinifera] (GB:CAN75527.1) chr3:20889722-20	2.979
JCVI_31716	3.941	weakly similar to (105)AT5G41130 Symbols: catalytic chr5:16476942-16480469 REVERSE no original description	
EV217148	3.936	no similarity	
JCVI_15796	3.933	moderately similar to (311)AT1G65480 Symbols: FT FT (FLOWERING LOCUS T) chr1:24335173-24337352 FORWARDweakly sin	4.445
JCVI_33149	3.930	highly similar to (659)AT5G15500 Symbols: ankyrin repeat family protein chr5:5031794-5033446 REVERSE no original description	
JCVI_30459	3.916	no original description	3.324
JCVI_4715	3.911	moderately similar to (329)AT5G64660 Symbols: U-box domain-containing protein chr5:25859345-25860607 REVERSE no original	3.394
EV177185	3.892	no similarity	1.662
ES979866	3.891	no similarity	
EX130622	3.888	moderately similar to (210)AT2G01300 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G15010.1); similar to i	3.126
JCVI_7161	3.882	moderately similar to (337)AT3G50060 Symbols: MYB77 MYB77; DNA binding / transcription factor chr3:18569129-18570034 REV	3.255
EE409984	3.881	no similarity	3.202
EE440983	3.873	moderately similar to (239)AT1G02700 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G02140.1); similar to i	
EL591180	3.872	moderately similar to (210)AT1G70780 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G23150.1); similar to i	
CX271990	3.869	moderately similar to (206)AT5G64660 Symbols: U-box domain-containing protein chr5:25859345-25860607 REVERSE [16815]	3.423
ES902870	3.865	no similarity	
JCVI_12059	3.850	moderately similar to (328)AT1G23710 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G70420.1); similar to i	2.520
JCVI_12579	3.839	weakly similar to (182)AT4G27360 Symbols: dynein light chain, putative chr4:13694038-13694523 FORWARD no original descripti	3.362
JCVI_12357	3.835	no original description	2.786
JCVI_21944	3.821	no original description	
DN961610	3.819	moderately similar to (278)AT3G55980 Symbols: zinc finger (CCCH-type) family protein chr3:20787836-20789578 FORWARD [17	1.987
CN727255	3.818	no similarity	
JCVI_40666	3.816	moderately similar to (299)AT1G72200 Symbols: zinc finger (C3HC4-type RING finger) family protein chr1:27173597-27174811 RE	
JCVI_32644	3.812	moderately similar to (345)AT3G28340 Symbols: GATL10 GATL10 (Galacturonosyltransferase-like 10); polygalacturonate 4-alpha-gal	3.522
JCVI_32406	3.802	moderately similar to (274)AT3G24460 Symbols: ATPURM, PUR5 ATPURM/PUR5; phosphoribosylformylglycinamide cyclo-ligase	2.499
EV165884	3.782	weakly similar to (126)AT4G38170 Symbols: FRS9 FRS9 (FAR1-related sequence 9); zinc ion binding chr4:17904607-17906433 FOF	
EV202611	3.781	moderately similar to (238)AT2G36750 Symbols: UGT72C1 UGT72C1 (UDP-GLUCOSYL TRANSFERASE 72C1); UDP-glycosyltra	5.300
ES963726	3.773	no similarity	3.024
EE433603	3.758	weakly similar to (107)AT1G44830 Symbols: AP2 domain-containing transcription factor TINY, putative chr1:16936232-16936867 F	4.143
JCVI_2735	3.753	weakly similar to (136)AT4G09600 Symbols: GASA3 GASA3 (GAST1 PROTEIN HOMOLOG 3) chr4:6073011-6073513 REVERSE	3.113
JCVI_1908	3.742	moderately similar to (395)AT3G55980 Symbols: zinc finger (CCCH-type) family protein chr3:20787836-20789578 FORWARD no c	2.591
JCVI_17029	3.741	weakly similar to (111)AT4G27350 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G54240.1); similar to unkn	
JCVI_9598	3.736	highly similar to (962)AT3G15880 Symbols: WSIP2, TPR4 TPR4/WSIP2 (TOPLESS-RELATED 4) chr3:5364460-5371875 REVERS	
JCVI_16210	3.736	moderately similar to (386)AT3G55010 Symbols: ATPURM, PUR5 ATPURM/PUR5; phosphoribosylformylglycinamide cyclo-ligase	
JCVI_11822	3.733	weakly similar to (179)AT5G24260 Symbols: prolyl oligopeptidase family protein chr5:8234868-8237813 REVERSE no original desc	
JCVI_15991	3.732	weakly similar to (172)AT1G28370 Symbols: ERF11, ATERF11 ATERF11/ERF11 (ERF domain protein 11); DNA binding / transcript	
AM060617	3.730	moderately similar to (415)AT3G24020 Symbols: disease resistance-responsive family protein chr3:8678834-8679565 FORWARD [1	2.654
JCVI_3116	3.727	moderately similar to (321)AT5G01640 Symbols: prenylated rab acceptor (PRA1) family protein chr5:241439-242110 REVERSE no	2.369
EX122776	3.726	no similarity	3.104
DN237910	3.725	no similarity	
JCVI_41332	3.722	no original description	
JCVI_22598	3.713	moderately similar to (280)AT1G30860 Symbols: protein binding / zinc ion binding chr1:10986677-10989227 REVERSE no original	
EV114051	3.704	no similarity	
JCVI_36270	3.702	moderately similar to (300)AT2G38470 Symbols: ATWRKY33, WRKY33 WRKY33 (WRKY DNA-binding protein 33); transcription	2.147
JCVI_15747	3.696	weakly similar to (148)AT4G27280 Symbols: calcium-binding EF hand family protein chr4:13663776-13664168 REVERSE no origin	3.053
EX125877	3.694	weakly similar to (130)AT5G21930 Symbols: PAA2, HMA8 HMA8/PAA2 (P-TYPE ATPASE OF ARABIDOPSIS 2); ATPase, couple	2.808
JCVI_40327	3.679	moderately similar to (227)AT1G64340 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G41810.1); similar to .	2.725

JCVI_31757	3.677	no original description	2.764
JCVI_40353	3.676	weakly similar to (128)AT1G01060 Symbols: LHY1, LHY LHY (LATE ELONGATED HYPOCOTYL) chr1:33992-37061 REVERSE	2.044
BQ704574	3.673	no similarity	
JCVI_40374	3.671	no original description	2.492
EE471788	3.670	very weakly similar to (99.4)AT5G21930 Symbols: PAA2, HMA8 HMA8/PAA2 (P-TYPE ATPASE OF ARABIDOPSIS 2); ATPase, cc	3.055
JCVI_29031	3.667	weakly similar to (127)AT3G56290 Symbols: similar to hypothetical protein [Vitis vinifera] (GB:CAN75527.1) chr3:20889722-20890	2.655
JCVI_39808	3.662	highly similar to (623)AT1G24530 Symbols: transducin family protein / WD-40 repeat family protein chr1:8693274-8694530 FORW	2.388
JCVI_37841	3.652	no original description	2.779
ES911751	3.648	weakly similar to (186)AT1G70230 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G01430.1); similar to Os0	2.352
CX194101	3.638	no similarity	
AM394346	3.630	moderately similar to (306)AT3G28340 Symbols: GATL10 GATL10 (Galacturonosyltransferase-like 10); polygalacturonate 4-alpha-gal	3.352
JCVI_37625	3.618	moderately similar to (381)AT1G60470 Symbols: ATGOLS4 ATGOLS4 (ARABIDOPSIS THALIANA GALACTINOL SYNTHASE 4	
JCVI_37355	3.614	moderately similar to (313)AT1G64065 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G44000.1); similar to	
EE509254	3.598	moderately similar to (289)AT2G30900 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G42570.1); similar to	
JCVI_19043	3.591	moderately similar to (421)AT2G38470 Symbols: ATWRKY33, WRKY33 WRKY33 (WRKY DNA-binding protein 33); transcription	2.218
JCVI_32996	3.589	no original description	1.543
EVI75794	3.571	very weakly similar to (83.6)AT1G55960 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G13062.2); similar to	2.603
JCVI_34901	3.569	no original description	1.943
RC_EE566317	3.568	no similarity	
EV116513	3.564	weakly similar to (150)AT1G19770 Symbols: ATPUP14 ATPUP14 (Arabidopsis thaliana purine permease 14); purine transmembrane t	
EE417832	3.562	no similarity	
JCVI_33185	3.560	weakly similar to (145)AT5G62520 Symbols: SRO5 SRO5 (SIMILAR TO RCD ONE 5); NAD+ ADP-ribosyltransferase chr5:251152	2.781
JCVI_18362	3.559	weakly similar to (192)AT4G15550 Symbols: IAGLU IAGLU (INDOLE-3-ACETATE BETA-D-GLUCOSYLTRANSFERASE); UDP-	
JCVI_35037	3.555	no original description	2.291
JCVI_20824	3.551	weakly similar to (120)AT4G28460 Symbols: unknown protein chr4:14066090-14066308 FORWARD no original description	2.846
JCVI_28244	3.541	moderately similar to (244)AT5G37770 Symbols: CML24, TCH2 TCH2 (TOUCH 2); calcium ion binding chr5:15016305-15016790 F	3.011
AT000719	3.540	no similarity	1.956
JCVI_6560	3.533	moderately similar to (316)AT3G21380 Symbols: similar to MBP1 (MYOSINASE-BINDING PROTEIN 1) [Arabidopsis thaliana] (T	4.678
EE413000	3.519	no similarity	1.796
ES929348	3.519	weakly similar to (170)AT2G36610 Symbols: ATHB22 ATHB22 (ARABIDOPSIS THALIANA HOMEBOX PROTEIN 22); DNA bi	
ES968676	3.518	no similarity	3.282
JCVI_16840	3.516	weakly similar to (163)AT1G27100 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G69900.1); similar to hypc	2.060
EE559467	3.516	no similarity	
JCVI_20274	3.501	weakly similar to (182)AT2G30020 Symbols: protein phosphatase 2C, putative / PP2C, putative chr2:12821514-12822981 FORWAR	3.466
ES907288	3.493	moderately similar to (262)AT2G39180 Symbols: protein kinase family protein chr2:16351356-16353686 REVERSEweakly similar to	3.666
JCVI_32474	3.488	moderately similar to (221)AT3G19595 Symbols: phosphoprotein phosphatase chr3:6808591-6809514 REVERSE no original descript	3.843
EE481297	3.486	very weakly similar to (86.7)AT4G28460 Symbols: unknown protein chr4:14066090-14066308 FORWARD [20154] 1 595 631	2.814
JCVI_14554	3.483	moderately similar to (319)AT1G19770 Symbols: ATPUP14 ATPUP14 (Arabidopsis thaliana purine permease 14); purine transmembra	
JCVI_16974	3.483	very weakly similar to (84.7)AT3G19680 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G50040.1); similar to	3.490
JCVI_4245	3.479	moderately similar to (369)AT5G13170 Symbols: nodulin MtN3 family protein chr5:4181334-4183174 REVERSE no original descrip	2.792
DY003886	3.479	weakly similar to (140)AT3G63350 Symbols: HSFA7B, AT-HSFA7B AT-HSFA7B (Arabidopsis thaliana heat shock transcription facto	3.126
JCVI_25396	3.477	weakly similar to (113)AT4G23870 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G11020.1) chr4:1241441	3.862
JCVI_734	3.472	highly similar to (652)AT1G67830 Symbols: ATFXG1 ATFXG1 (ALPHA-FUCOSIDASE 1); alpha-L-fucosidase/ carboxylesterase ch	
JCVI_21093	3.471	moderately similar to (204)AT3G27540 Symbols: glycosyl transferase family 17 protein chr3:10206726-10208125 FORWARD no ori	1.996
EV066486	3.466	moderately similar to (407)AT3G50940 Symbols: AAA-type ATPase family protein chr3:18945067-18946509 FORWARD [21443]	
BG543167	3.460	no similarity	
EE450166	3.458	moderately similar to (283)AT1G04350 Symbols: 2-oxoglutarate-dependent dioxygenase, putative chr1:1165295-1166537 FORWARD	2.324
JCVI_34258	3.458	weakly similar to (117)AT1G73965 Symbols: CLE13 CLE13 (CLAVATA3/ESR-RELATED 13); receptor binding chr1:27819483-278	2.032
JCVI_38371	3.457	moderately similar to (228)AT1G74930 Symbols: ORA47 ORA47; DNA binding / transcription factor chr1:28147900-28148487 FOR	4.050
JCVI_36119	3.455	weakly similar to (115)AT3G13062 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G55960.1); similar to unkn	2.214
EV058378	3.454	moderately similar to (322)AT4G26200 Symbols: ACS7 ACS7 (1-Amino-cyclopropane-1-carboxylate synthase 7); 1-aminocyclopropan	2.538
JCVI_41856	3.454	moderately similar to (224)AT1G74930 Symbols: ORA47 ORA47; DNA binding / transcription factor chr1:28147900-28148487 FOR	4.314
EV015453	3.450	very weakly similar to (92.4)AT4G25990 Symbols: CIL CIL chr4:13191946-13193552 REVERSE [21440]	
EVI18150	3.450	moderately similar to (274)AT2G40000 Symbols: HSPRO2, ATHSPRO2 similar to unknown protein [Arabidopsis thaliana] (TAIR:AT	3.009
JCVI_19330	3.446	weakly similar to (107)AT1G32920 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G32928.1) chr1:1192888	3.865
JCVI_13423	3.445	highly similar to (545)AT4G21320 Symbols: HSA32 HSA32 (HEAT-STRESS-ASSOCIATED 32); catalytic chr4:11340502-11341742	
EVI30725	3.444	no similarity	2.937
JCVI_32123	3.438	weakly similar to (103)AT2G23810 Symbols: TET8 TET8 (TETRASPANIN8) chr2:10142939-10144432 REVERSE no original descr	
EL590902	3.437	weakly similar to (146)AT3G61110 Symbols: ARS27A ARS27A (ARABIDOPSIS RIBOSOMAL PROTEIN S27); structural constituen	
JCVI_1343	3.436	moderately similar to (468)AT5G22250 Symbols: CCR4-NOT transcription complex protein, putative chr5:7365608-7366444 REVEF	2.381
JCVI_22268	3.435	moderately similar to (213)AT3G19580 Symbols: AZF2 AZF2 (ARABIDOPSIS ZINC-FINGER PROTEIN 2) chr3:6803299-6804120	
JCVI_26936	3.431	moderately similar to (243)AT3G21150 Symbols: zinc finger (B-box type) family protein chr3:7412719-7413396 REVERSE no origi	2.350
JCVI_1210	3.428	moderately similar to (295)AT2G47770 Symbols: benzodiazepine receptor-related chr2:19575771-19576361 FORWARD no original	
JCVI_1953	3.425	moderately similar to (234)AT4G25200 Symbols: ATHSP23.6-MITO ATHSP23.6-MITO (MITOCHONDRION-LOCALIZED SMALL	3.536
EV209060	3.418	weakly similar to (151)AT4G15810 Symbols: chloroplast outer membrane protein, putative chr4:8989175-8992604 REVERSE [21491]	1.901
AM058651	3.417	moderately similar to (301)AT4G30810 Symbols: SCPL29 SCPL29 (serine carboxypeptidase-like 29); serine carboxypeptidase chr4:1	
EX121530	3.416	no similarity	
JCVI_21020	3.413	weakly similar to (141)AT2G40000 Symbols: HSPRO2, ATHSPRO2 similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G5	3.003
EX015383	3.413	no similarity	1.808
JCVI_20770	3.399	weakly similar to (145)AT2G20835 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G15534.1); similar to unkn	3.082
JCVI_1347	3.399	moderately similar to (346)AT3G52400 Symbols: ATSPY122, SYP122 SYP122 (syntaxin 122); SNAP receptor chr3:19436813-19438	
JCVI_34633	3.391	weakly similar to (122)AT3G05936 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO17316.1) chr3:1774068-17	
JCVI_18790	3.390	moderately similar to (342)AT3G14680 Symbols: CYP72A14 CYP72A14 (cytochrome P450, family 72, subfamily A, polypeptide 14);	
JCVI_36253	3.388	moderately similar to (437)AT4G11280 Symbols: ACS6 (1-AMINOCYCLOPROPANE-1-CARBOXYLIC ACID (ACC) SYNTHASE	2.579
JCVI_16841	3.387	weakly similar to (181)AT4G14805 Symbols: protease inhibitor/seed storage/lipid transfer protein (LTP)-related chr4:8502369-85031	
JCVI_28384	3.382	moderately similar to (336)AT4G11660 Symbols: HSF2B2, AT-HSF2B2 AT-HSF2B2 (Arabidopsis thaliana heat shock transcription f	2.027
EE549228	3.377	very weakly similar to (91.3)AT3G50060 Symbols: MYB77 MYB77; DNA binding / transcription factor chr3:18569129-18570034 RE	
EE567489	3.373	no similarity	
JCVI_40345	3.369	moderately similar to (259)AT5G47230 Symbols: ATERF-5, ATERF5, ERF5 ERF5 (ETHYLENE RESPONSIVE ELEMENT BINDIN	1.837
EE439539	3.366	weakly similar to (109)AT4G01960 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G02380.1); similar to unkn	2.107
EV213527	3.365	very weakly similar to (86.7)AT5G50360 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G63350.1); similar to	
EX042807	3.365	no similarity	2.909
EX108444	3.362	weakly similar to (169)AT3G56290 Symbols: similar to hypothetical protein [Vitis vinifera] (GB:CAN75527.1) chr3:20889722-20890	2.446

EX036618	3.359	weakly similar to (112)AT4G30830 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G24140.1); similar to unkn	
JCVI_36421	3.359	no original description	2.642
EV160261	3.354	weakly similar to (107)AT1G32920 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G32928.1) chr1:1192888	3.694
EV142990	3.346	weakly similar to (119)AT2G40000 Symbols: HSPRO2, ATHSPRO2 similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G5	3.002
JCVI_15939	3.344	highly similar to (608)AT5G14700 Symbols: cinnamoyl-CoA reductase-related chr5:4740505-4743330 REVERSEvery weakly similar	2.563
EV120770	3.341	weakly similar to (195)AT3G44260 Symbols: CCR4-NOT transcription complex protein, putative chr3:15963200-15964042 REVERS	2.206
JCVI_11759	3.339	weakly similar to (125)AT4G21020 Symbols: late embryogenesis abundant domain-containing protein / LEA domain-containing protei	
JCVI_231	3.337	highly similar to (515)AT4G25810 Symbols: XTH23, XTR6 XTR6 (XYLOGLUCAN ENDOTRANSGLYCOSYLASE 6); hydrolase, a	
JCVI_3132	3.337	moderately similar to (321)AT2G27080 Symbols: harpin-induced protein-related / HIN1-related / harpin-responsive protein-related ch	2.473
ES938263	3.335	no similarity	
EV227409	3.331	moderately similar to (385)AT1G32450 Symbols: proton-dependent oligopeptide transport (POT) family protein chr1:11715317-1171	2.820
EV115961	3.329	weakly similar to (164)AT5G13490 Symbols: AAC2 AAC2 (ADP/ATP CARRIER 2); binding chr5:4336037-4337382 FORWARDwe	
JCVI_32987	3.329	moderately similar to (204)AT5G62520 Symbols: SRO5 SRO5 (SIMILAR TO RCD ONE 5); NAD+ ADP-ribosyltransferase chr5:251	
JCVI_28478	3.329	weakly similar to (135)AT3G19680 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G50040.1); similar to unkn	2.581
JCVI_31731	3.321	weakly similar to (196)AT4G02920 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G03340.1); similar to hyc	
EE524509	3.320	moderately similar to (215)AT2G19710 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G29440.1); similar to i	
JCVI_42207	3.317	no original description	3.087
JCVI_35716	3.316	moderately similar to (408)AT4G36030 Symbols: armadillo/beta-catenin repeat family protein chr4:17045087-17047099 REVERSE n	2.075
JCVI_35706	3.316	moderately similar to (309)AT5G15100 Symbols: PIN8 PIN8 (PIN-FORMED 8); auxin:hydrogen symporter/ transporter chr5:4892162	1.770
JCVI_21991	3.311	no original description	
CD825949	3.310	weakly similar to (172)AT3G28030 Symbols: UVR1, UVH3 UVH3 (ULTRAVIOLET HYPERSENSITIVE 3); nuclease chr3:1042555	3.080
EX102092	3.306	moderately similar to (314)AT4G29780 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G12010.1); similar to i	2.567
JCVI_9483	3.305	moderately similar to (338)AT3G20810 Symbols: transcription factor jumonji (mjC) domain-containing protein chr3:7275820-72781	
EV109707	3.304	no similarity	
EX040796	3.303	weakly similar to (198)AT3G22050 Symbols: receptor-like protein kinase-related chr3:7764138-7765150 FORWARD [21811] 20 521	
ES902008	3.302	weakly similar to (144)AT2G40080 Symbols: ELF4 ELF4 (EARLY FLOWERING 4) chr2:16741623-16741958 REVERSE [21428] 1	2.464
EV137114	3.296	no similarity	
EV173184	3.292	weakly similar to (135)AT3G14680 Symbols: CYP72A14 CYP72A14 (cytochrome P450, family 72, subfamily A, polypeptide 14); oxy	2.231
EE508763	3.292	moderately similar to (229)AT4G29890 Symbols: choline monooxygenase, putative (CMO-like) chr4:14608874-14610911 FORWAR	
EX113607	3.288	weakly similar to (177)AT2G40080 Symbols: ELF4 ELF4 (EARLY FLOWERING 4) chr2:16741623-16741958 REVERSE [21827] 5	2.615
ES969123	3.288	no similarity	3.043
EV190074	3.280	moderately similar to (249)AT2G41640 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G57380.1); similar to i	3.628
CV433416	3.259	very weakly similar to (97.8)AT3G02410 Symbols: similar to ATPCME (PRENYLCYSTEINE METHYLESTERASE), prenylcysteine	2.947
EV147360	3.254	no similarity	
JCVI_20339	3.249	very weakly similar to (89.4)AT1G65510 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G65490.1) chr1:243	
JCVI_35682	3.248	no original description	
EV100456	3.243	no similarity	
JCVI_36013	3.243	very weakly similar to (88.6)AT1G51990 Symbols: O-methyltransferase family 2 protein chr1:19334618-19336336 FORWARDvery v	
JCVI_5107	3.243	weakly similar to (141)AT3G47430 Symbols: PEX11B PEX11B chr3:17491783-17492677 FORWARD no original description	3.514
CV432238	3.241	weakly similar to (109)AT3G46620 Symbols: zinc finger (C3HC4-type RING finger) family protein chr3:17189822-17191009 REVE	2.684
EV191785	3.240	weakly similar to (131)AT4G01090 Symbols: extra-large G-protein-related chr4:470834-473248 REVERSE [21489]	
JCVI_40884	3.239	weakly similar to (146)AT4G29780 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G12010.1); similar to unkn	3.113
JCVI_3719	3.237	weakly similar to (164)AT3G29000 Symbols: calcium-binding EF hand family protein chr3:11007028-11007612 FORWARD no origi	3.731
ES965872	3.235	no similarity	
JCVI_20887	3.235	no original description	2.828
EV109361	3.230	no similarity	
JCVI_40125	3.229	weakly similar to (156)AT2G11810 Symbols: MGD3, ATMGD3, MGDC MGDC (monogalactosyldiacylglycerol synthase type C) chr	
JCVI_39508	3.223	no original description	
EE408753	3.219	weakly similar to (179)AT3G03620 Symbols: MATE efflux family protein chr3:873911-876259 REVERSE [16817] 1 642 671	2.834
L46575	3.215	no similarity	
JCVI_37858	3.215	no original description	
JCVI_6313	3.205	very weakly similar to (97.4)AT3G23170 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G14450.1) chr3:826	1.780
EV102814	3.199	weakly similar to (196)AT3G12320 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G06980.1); similar to hyc	1.962
JCVI_15314	3.198	moderately similar to (387)AT2G31380 Symbols: STH STH (salt tolerance homologue); transcription factor/ zinc ion binding chr2:133	2.666
EV128635	3.196	no similarity	2.637
JCVI_4571	3.195	moderately similar to (266)AT5G59820 Symbols: ZAT12, RHL14 RHL14 (RESPONSIVE TO HIGH LIGHT 41); nucleic acid binding	
JCVI_28902	3.194	moderately similar to (271)AT2G40140 Symbols: CZF1, ZFAR1 CZF1/ZFAR1 chr2:16779615-16781408 FORWARD no original des	
JCVI_925	3.194	weakly similar to (140)AT3G15670 Symbols: late embryogenesis abundant protein, putative / LEA protein, putative chr3:5310148-53	
JCVI_39089	3.193	moderately similar to (216)AT2G01300 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G15010.1); similar to i	2.522
DY011298	3.190	no similarity	
JCVI_22191	3.189	weakly similar to (194)AT4G01090 Symbols: extra-large G-protein-related chr4:470834-473248 REVERSE no original description	
EX136337	3.189	weakly similar to (145)AT5G18580 Symbols: TON2, EMB40, FS1, GDO, FASS FASS (FASS 1) chr5:6175156-6178216 FORWARD	
AM393934	3.180	no similarity	3.187
JCVI_15179	3.178	highly similar to (517)AT1G01540 Symbols: protein kinase family protein chr1:195980-198383 FORWARDmoderately similar to (2	2.029
JCVI_14336	3.175	weakly similar to (125)AT2G42560 Symbols: late embryogenesis abundant domain-containing protein / LEA domain-containing protei	3.980
JCVI_22226	3.175	moderately similar to (303)AT4G35240 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G17110.1); similar to i	1.773
EV224869	3.171	very weakly similar to (96.3)AT1G74930 Symbols: ORA47 ORA47; DNA binding / transcription factor chr1:28147900-28148487 FOF	5.241
JCVI_25673	3.169	moderately similar to (376)AT3G60420 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G60450.1); similar to i	
DW997843	3.167	no similarity	
AT000502	3.161	no similarity	
JCVI_14546	3.158	moderately similar to (310)AT3G46620 Symbols: zinc finger (C3HC4-type RING finger) family protein chr3:17189822-17191009 RE	2.150
JCVI_151	3.157	moderately similar to (259)AT5G04340 Symbols: CZF2, ZAT6, C2H2 C2H2 (ZINC FINGER OF ARABIDOPSIS THALIANA 6); nuc	2.878
JCVI_2085	3.152	moderately similar to (258)AT3G22840 Symbols: ELIP, ELIP1 ELIP1 (EARLY LIGHT-INDUCABLE PROTEIN); chlorophyll binding	
EE568085	3.151	no similarity	
JCVI_14921	3.149	moderately similar to (303)AT5G64430 Symbols: octicosapeptide/Phox/Bem1p (PB1) domain-containing protein chr5:25779766-257	2.067
ES993537	3.147	moderately similar to (306)AT1G01540 Symbols: protein kinase family protein chr1:195980-198383 FORWARDweakly similar to (1	1.749
JCVI_38161	3.146	no original description	
JCVI_26910	3.141	no original description	
JCVI_16211	3.141	moderately similar to (250)AT1G12020 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G62422.1); similar to i	
EE559860	3.138	no similarity	
EX109901	3.137	moderately similar to (231)AT1G06160 Symbols: ethylene-responsive factor, putative chr1:1883045-1883779 FORWARDvery weak	
EV197730	3.133	no similarity	2.750
EE507700	3.130	no similarity	

JCVI_11394	3.129	moderately similar to (421)AT1G70170 Symbols: MMP MMP (MATRIX METALLOPROTEINASE); metalloendopeptidase chr1:264	
JCVI_36976	3.127	moderately similar to (362)AT3G55840 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G40000.1); similar to u	1.964
EX134698	3.126	weakly similar to (179)AT4G30830 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G24140.1); similar to unkn	
EV140755	3.119	moderately similar to (203)AT3G14950 Symbols: TTL2 TTL2 (TETRATRICOPETIDE-REPEAT THIOREDOXIN-LIKE 2); binding	3.229
DN965490	3.116	no similarity	
JCVI_4934	3.114	no original description	
EE406707	3.112	no similarity	2.152
JCVI_3622	3.110	moderately similar to (306)AT3G19380 Symbols: U-box domain-containing protein chr3:6714608-6715873 REVERSEweakly similar	2.699
EE559806	3.098	no similarity	1.604
JCVI_29566	3.097	weakly similar to (174)AT1G18265 Symbols: contains InterPro domain Protein of unknown function DUF593 (InterPro:IPR007656) c	3.135
EV125502	3.096	moderately similar to (298)AT4G33920 Symbols: protein phosphatase 2C family protein / PP2C family protein chr4:16260881-16262	2.125
JCVI_15246	3.094	moderately similar to (300)AT3G57530 Symbols: ATCPK32, CDPK32, CPK32 CPK32 (CALCIUM-DEPENDENT PROTEIN KINASE)	
JCVI_33840	3.092	no original description	
JCVI_40911	3.091	moderately similar to (446)AT1G13110 Symbols: CYP71B7 CYP71B7 (cytochrome P450, family 71, subfamily B, polypeptide 7); oxy	
JCVI_23644	3.089	weakly similar to (120)AT4G29780 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G12010.1); similar to unkn	2.928
RC_EE564068	3.083	no similarity	
EV103862	3.081	moderately similar to (310)AT1G70170 Symbols: MMP MMP (MATRIX METALLOPROTEINASE); metalloendopeptidase chr1:264	
JCVI_9015	3.079	weakly similar to (174)AT5G47320 Symbols: RPS19 RPS19 (40S ribosomal protein S19); RNA binding chr5:19221028-1922178 FO	2.229
JCVI_5733	3.078	moderately similar to (204)AT1G21910 Symbols: AP2 domain-containing transcription factor family protein chr1:7696644-7697336 f	
JCVI_9589	3.076	moderately similar to (421)AT1G27100 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G69900.1); similar to l	1.967
CN728830	3.074	no similarity	
DY010300	3.071	weakly similar to (131)AT5G10695 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G57123.1); similar to unkn	
JCVI_8881	3.070	no original description	
EX084336	3.070	moderately similar to (343)AT2G42900 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO70018.1); contains Inte	
DW997751	3.069	very weakly similar to (98.6)AT3G61640 Symbols: ATAGP20, AGP20 AGP20 (ARABINOGLACTAN PROTEIN 20) chr3:2282125	1.787
JCVI_34219	3.068	no original description	2.340
JCVI_16259	3.068	moderately similar to (491)AT4G02300 Symbols: pectinesterase family protein chr4:1009366-1013034 REVERSEmoderately similar	
JCVI_6893	3.067	weakly similar to (151)AT3G50800 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G66580.1); similar to unkn	
JCVI_28622	3.062	highly similar to (546)AT3G28340 Symbols: GATL10 GATL10 (Galacturonosyltransferase-like 10); polygalacturonate 4-alpha-galactur	3.103
JCVI_4850	3.062	weakly similar to (197)AT3G12320 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G06980.1); similar to hypc	
EE539186	3.061	moderately similar to (211)AT1G71000 Symbols: DNAJ heat shock N-terminal domain-containing protein chr1:26772998-26773773	1.740
JCVI_8403	3.060	moderately similar to (268)AT5G05410 Symbols: DREB2, DREB2A DREB2A (DRE-BINDING PROTEIN 2A); DNA binding / transcr	
JCVI_16557	3.059	moderately similar to (273)AT3G50060 Symbols: MYB77 MYB77; DNA binding / transcription factor chr3:18569129-18570034 REV	
EV107830	3.057	no similarity	
JCVI_11277	3.057	moderately similar to (379)AT3G23250 Symbols: MYB15, AtY19, AtMYB15 AtMYB15/AtY19/MYB15 (myb domain protein 15); DN	
JCVI_9832	3.056	highly similar to (582)AT1G64500 Symbols: glutaredoxin family protein chr1:23956933-23958039 FORWARD no original descriptio	2.103
JCVI_26540	3.054	moderately similar to (490)AT5G52300 Symbols: RD29B, LTI65 LTI65/RD29B (RESPONSIVE TO DESSICATION 29B) chr5:2125-	3.339
AM058038	3.053	weakly similar to (106)AT3G30580 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G38790.1) chr3:1217024	2.671
EV175274	3.050	no similarity	
EV175339	3.046	no similarity	2.469
JCVI_9836	3.046	highly similar to (828)AT3G01120 Symbols: CGS, ATCYS1, CGS1, MTO1 MTO1 (METHIONINE OVERACCUMULATION 1) chr	
BQ704951	3.046	no similarity	1.831
JCVI_34138	3.045	moderately similar to (311)AT3G07250 Symbols: nuclear transport factor 2 (NTF2) family protein / RNA recognition motif (RRM)-coi	
ES966108	3.044	no similarity	
ES968570	3.041	no similarity	
EV111322	3.040	no similarity	
EV111066	3.038	no similarity	
EV153307	3.036	weakly similar to (101)AT3G26100 Symbols: regulator of chromosome condensation (RCC1) family protein chr3:9539695-9541386 f	
JCVI_22827	3.035	highly similar to (518)AT1G21790 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO61872.1); contains InterPro	
AM394323	3.035	no similarity	3.039
EE545244	3.030	no similarity	
JCVI_8272	3.030	moderately similar to (256)AT1G05560 Symbols: UGT75B1, UGT1 UGT1 (UDP-glucosyl transferase 75B1); UDP-glycosyltransferase	2.528
BQ790750	3.029	weakly similar to (181)AT4G10250 Symbols: ATHSP22.0 ATHSP22.0 (Arabidopsis thaliana heat shock protein 22.0) chr4:6370533-6	
EX122617	3.028	moderately similar to (347)AT5G22380 Symbols: ANAC090 ANAC090 (Arabidopsis NAC domain containing protein 90); transcriptio	
ES969090	3.028	no similarity	
CX278676	3.026	no similarity	
JCVI_894	3.024	moderately similar to (423)AT3G21380 Symbols: similar to MBP1 (MYOSINASE-BINDING PROTEIN 1) [Arabidopsis thaliana] (T	3.447
JCVI_28463	3.021	moderately similar to (257)AT3G09020 Symbols: alpha 1,4-glycosyltransferase family protein / glycosyltransferase sugar-binding DXI	
JCVI_41678	3.020	highly similar to (507)AT3G09450 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G28780.1); similar to unna	3.940
JCVI_14049	3.019	moderately similar to (226)AT3G26980 Symbols: MUB4 MUB4 (MEMBRANE-ANCHORED UBIQUITIN-FOLD PROTEIN 4 PREC	
JCVI_4734	3.014	moderately similar to (397)AT1G06260 Symbols: cysteine proteinase, putative chr1:1916448-1917584 FORWARDweakly similar to (	2.013
JCVI_42470	3.010	weakly similar to (171)AT3G28200 Symbols: peroxidase, putative chr3:10519319-10520269 FORWARD no original description	
JCVI_2152	3.008	very weakly similar to (100)AT5G22650 Symbols: HDT02, HDT2, ATHD2B, HDA4, HD2, HD2B HD2B (HISTONE DEACETYLASE	1.877
JCVI_2702	3.006	no original description	
JCVI_4875	3.004	highly similar to (576)AT5G04950 Symbols: nicotianamine synthase, putative chr5:1457877-1458839 REVERSEmoderately similar to	
JCVI_4490	2.999	moderately similar to (320)AT4G40010 Symbols: SNRK2-7, SNRK2.7, SRK2F SNRK2-7/SNRK2.7/SRK2F (SNF1-RELATED PROTI	
EE524030	2.997	very weakly similar to (82.0)AT3G46620 Symbols: zinc finger (C3HC4-type RING finger) family protein chr3:17189822-17191009 R	2.810
JCVI_14678	2.990	moderately similar to (346)AT4G24660 Symbols: ATHB22, MEE68 ATHB22/MEE68 (ARABIDOPSIS THALIANA HOMEBOX PF	2.963
JCVI_7022	2.988	moderately similar to (243)AT5G12020 Symbols: HSP17.6II HSP17.6II (17.6 KDA CLASS II HEAT SHOCK PROTEIN) chr5:38824	
JCVI_13680	2.988	moderately similar to (207)AT1G09520 Symbols: similar to PHD finger family protein [Arabidopsis thaliana] (TAIR:AT3G17460.1); s	
JCVI_38283	2.986	moderately similar to (231)AT4G01090 Symbols: extra-large G-protein-related chr4:470834-473248 REVERSE no original descriptio	
JCVI_15052	2.983	moderately similar to (230)AT3G21300 Symbols: RNA methyltransferase family protein chr3:7493660-7496263 REVERSE no origin	1.927
JCVI_36240	2.982	moderately similar to (355)AT3G60420 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G60450.1); similar to l	
JCVI_16530	2.978	highly similar to (636)AT5G14700 Symbols: cinnamoyl-CoA reductase-related chr5:4740505-4743330 REVERSEvery weakly similar	3.718
JCVI_3413	2.975	moderately similar to (290)AT3G22840 Symbols: ELIP, ELIP1 ELIP1 (EARLY LIGHT-INDUCIBLE PROTEIN); chlorophyll binding	
JCVI_2015	2.972	moderately similar to (300)AT3G21710 Symbols: unknown protein chr3:7648387-7649540 FORWARD no original description	
JCVI_11681	2.968	weakly similar to (182)AT5G23730 Symbols: nucleotide binding chr5:8005289-8006395 FORWARD no original description	2.705
JCVI_16668	2.965	weakly similar to (111)AT3G15357 Symbols: unknown protein chr3:5187171-5187602 FORWARD no original description	
JCVI_31954	2.964	weakly similar to (124)AT1G26320 Symbols: NADP-dependent oxidoreductase, putative chr1:9105227-9107016 FORWARD no orig	
JCVI_25854	2.964	no original description	
JCVI_16510	2.964	weakly similar to (180)AT5G04340 Symbols: CZF2, ZAT6, C2H2 C2H2 (ZINC FINGER OF ARABIDOPSIS THALIANA 6); nucleic	2.840
CD831059	2.964	no similarity	1.480
RC_EV111589	2.963	no similarity	2.477

JCVI_23775	2.963	highly similar to (641)AT3G24460 Symbols: TMS membrane family protein / tumour differentially expressed (TDE) family protein cl	
EV151697	2.961	very weakly similar to (93.2)AT5G22020 Symbols: strictonine synthase family protein chr5:7287881-7289360 REVERSE [21483]	
EV177509	2.961	weakly similar to (185)AT1G23130 Symbols: Bet v I allergen family protein chr1:8200423-8200986 FORWARD [21487]	
JCVI_35980	2.960	moderately similar to (489)AT1G28230 Symbols: ATPUP1, PUP1 PUP1 (PURINE PERMEASE 1); purine transmembrane transporter	
EX120951	2.958	weakly similar to (113)AT1G43910 Symbols: AAA-type ATPase family protein chr1:16658490-16660068 REVERSE [21829] 49 475	
JCVI_40355	2.956	moderately similar to (250)AT5G46830 Symbols: basic helix-loop-helix (bHLH) family protein chr5:19019946-19021481 FORWARD	2.014
JCVI_32708	2.948	no original description	
JCVI_32703	2.948	moderately similar to (350)AT1G29340 Symbols: PUB17 PUB17 (PLANT U-BOX17); ubiquitin-protein ligase chr1:10264398-102661	1.987
JCVI_1521	2.947	moderately similar to (246)AT3G17520 Symbols: late embryogenesis abundant domain-containing protein / LEA domain-containing pr	
EX083488	2.945	no similarity	
JCVI_19446	2.943	weakly similar to (161)AT1G69890 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G27100.1); similar to unkr	1.721
JCVI_24715	2.942	weakly similar to (189)AT2G39980 Symbols: transferase family protein chr2:16695515-16696963 REVERSE no original description	2.870
JCVI_29935	2.941	moderately similar to (314)AT4G38960 Symbols: zinc finger (B-box type) family protein chr4:18162294-18163039 FORWARD no o	1.957
JCVI_34936	2.940	moderately similar to (360)AT1G78160 Symbols: APUM7 APUM7 (ARABIDOPSIS PUMILIO 7); RNA binding chr1:29412793-2941	
EE566364	2.939	no similarity	
RC_EE557564	2.938	no similarity	
EV108354	2.931	weakly similar to (141)AT2G36780 Symbols: UDP-glucuronosyl/UDP-glucosyl transferase family protein chr2:15424697-15426187 I	
EV078290	2.928	no similarity	1.275
DY009544	2.923	weakly similar to (105)AT1G30860 Symbols: protein binding / zinc ion binding chr1:10986677-10989227 REVERSE [18969] 15 316	1.882
JCVI_40879	2.923	very weakly similar to (83.6)AT5G46910 Symbols: transcription factor jumonji (jmi) family protein chr5:19065007-19068107 FORW	
RC_EE567343	2.916	no similarity	
JCVI_21121	2.914	no original description	4.155
EV136565	2.912	no similarity	2.792
ES966278	2.911	no similarity	2.952
ES902248	2.909	moderately similar to (286)AT1G28230 Symbols: ATPUP1, PUP1 PUP1 (PURINE PERMEASE 1); purine transmembrane transporter	
EE505148	2.908	no similarity	
JCVI_4252	2.906	moderately similar to (446)AT3G11320 Symbols: organic anion transmembrane transporter chr3:3547023-3548545 REVERSE no ori	
CB686059	2.906	no similarity	2.080
JCVI_10884	2.902	moderately similar to (467)AT1G07040 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G27030.1); similar to i	
EX092288	2.900	weakly similar to (179)AT1G69840 Symbols: band 7 family protein chr1:26297595-26298813 REVERSE [21823]	2.726
DW999620	2.896	weakly similar to (113)AT3G22840 Symbols: ELIP, ELIP1 ELIP1 (EARLY LIGHT-INDUCIBLE PROTEIN); chlorophyll binding ch	
EX041857	2.896	weakly similar to (193)AT3G11510 Symbols: 40S ribosomal protein S14 (RPS14B) chr3:3623763-3624872 REVERSEweakly similar	
JCVI_32755	2.894	moderately similar to (259)AT4G01360 Symbols: similar to BPS1 (BYPASS 1) [Arabidopsis thaliana] (TAIR:AT1G01550.2); similar t	2.619
EV126970	2.892	no similarity	
JCVI_12599	2.888	moderately similar to (252)AT5G13170 Symbols: nodulin MtN3 family protein chr5:4181334-4183174 REVERSE no original descrip	2.880
JCVI_31606	2.887	weakly similar to (151)AT2G26770 Symbols: plectin-related chr2:11411335-11414821 REVERSE no original description	2.278
EV149994	2.887	no similarity	
ES957422	2.886	no similarity	
JCVI_8830	2.883	moderately similar to (352)AT4G33920 Symbols: protein phosphatase 2C family protein / PP2C family protein chr4:16260881-16262	
JCVI_37351	2.881	moderately similar to (229)AT2G19710 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G29440.1); similar to i	
JCVI_13330	2.880	highly similar to (693)AT1G69790 Symbols: protein kinase, putative chr1:26270501-26272481 FORWARDmoderately similar to (21	
JCVI_24437	2.878	moderately similar to (296)AT4G33920 Symbols: protein phosphatase 2C family protein / PP2C family protein chr4:16260881-16262	2.305
EX064199	2.875	no similarity	2.075
EV130300	2.874	no similarity	
JCVI_4685	2.872	moderately similar to (277)AT5G11160 Symbols: APT5 APT5 (ADENINE PHOSPHORIBOSYLTRANSFERASE 5); adenine phospho	2.652
EG020213	2.867	no similarity	
EX065455	2.866	no similarity	
CD811973	2.860	no similarity	
JCVI_6977	2.858	moderately similar to (333)AT5G43700 Symbols: IAA4, ATAUX2-11 ATAUX2-11 (indoleacetic acid-induced protein 4); transcription	2.621
CD828717	2.857	no similarity	
EE563641	2.851	no similarity	
RC_JCVI_37047	2.849	no original description	
JCVI_39461	2.847	moderately similar to (230)AT4G29890 Symbols: choline monooxygenase, putative (CMO-like) chr4:14608874-14610911 FORWAR	
EV120033	2.847	moderately similar to (287)AT1G65310 Symbols: ATXTH17 ATXTH17 (XYLOGUCAN ENDOTRANSGLUCOSYLASE/HYDROL	3.176
JCVI_13959	2.842	weakly similar to (113)AT5G39670 Symbols: calcium-binding EF hand family protein chr5:15900498-15901112 FORWARD no origi	1.870
EV096758	2.839	weakly similar to (181)AT1G69523 Symbols: UbiE/COQ5 methyltransferase family protein chr1:26133490-26134820 FORWARD [2	
JCVI_10583	2.838	moderately similar to (278)AT3G50770 Symbols: calmodulin-related protein, putative chr3:18884968-18885585 FORWARDvery wei	
H74834	2.833	no similarity	2.780
CD835542	2.831	weakly similar to (180)AT3G62720 Symbols: ATXT1 ATXT1; transferase/ transferase, transferring glycosyl groups chr3:23212302-23	1.756
ES965824	2.827	no similarity	
JCVI_33886	2.819	weakly similar to (147)AT3G05490 Symbols: RALFL22 RALFL22 (RALF-LIKE 22) chr3:1591387-1591746 FORWARD no original	3.350
EV111641	2.817	no similarity	
JCVI_30402	2.817	highly similar to (629)AT3G19270 Symbols: CYP707A4 CYP707A4 (cytochrome P450, family 707, subfamily A, polypeptide 4); oxyg	2.564
EV175334	2.816	no similarity	2.899
JCVI_14789	2.816	moderately similar to (326)AT2G40140 Symbols: CZF1, ZFAR1 CZF1/ZFAR1 chr2:16779615-16781408 FORWARD no original des	
EE531628	2.813	no similarity	2.455
JCVI_25976	2.813	moderately similar to (271)AT4G33720 Symbols: pathogenesis-related protein, putative chr4:16182816-16183307 FORWARDmoder	
JCVI_37942	2.813	highly similar to (725)AT4G24550 Symbols: clathrin adaptor complexes medium subunit family protein chr4:12675883-12678913 FO	
JCVI_11454	2.810	moderately similar to (247)AT2G11810 Symbols: MGD3, ATMGD3, MGDC MGDC (monogalactosyldiacylglycerol synthase type C)	
RC_ES929155	2.806	no similarity	
JCVI_38257	2.806	no original description	
JCVI_20204	2.803	weakly similar to (163)AT1G13710 Symbols: CYP78A5 CYP78A5 (cytochrome P450, family 78, subfamily A, polypeptide 5); oxygen	1.712
RC_EH424674	2.802	no similarity	
RC_EE556375	2.801	no similarity	2.866
EV103993	2.801	moderately similar to (333)AT1G70170 Symbols: MMP MMP (MATRIX METALLOPROTEINASE); metalloendopeptidase chr1:264	
JCVI_36313	2.800	moderately similar to (228)AT3G02840 Symbols: immediate-early fungal elicitor family protein chr3:618487-619626 FORWARD no	
EV217098	2.799	very weakly similar to (100)AT1G50910 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO68056.1) chr1:18870	
EX076183	2.799	no similarity	2.021
JCVI_40617	2.797	very weakly similar to (94.4)AT1G70170 Symbols: MMP MMP (MATRIX METALLOPROTEINASE); metalloendopeptidase chr1:26	
RC_EE560638	2.796	no similarity	
EV112555	2.794	very weakly similar to (98.6)AT2G46790 Symbols: PRR9, TL1, APRR9 APRR9 (PSEUDO-RESPONSE REGULATOR 9); transcrip	
JCVI_2166	2.793	moderately similar to (375)AT2G40000 Symbols: HSPRO2, ATHSPRO2 similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2	2.136
EV205882	2.791	no similarity	

JCVI_27852	2.790	no original description	
EX097178	2.789	moderately similar to (236)AT2G40000 Symbols: HSPRO2, ATHSPRO2 similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G40000.1)	2.170
AM386327	2.788	moderately similar to (224)AT4G37320 Symbols: CYP81D5 CYP81D5 (cytochrome P450, family 81, subfamily D, polypeptide 5); oxy	
JCVI_7932	2.783	very weakly similar to (87.0)AT5G64310 Symbols: ATAGP1, AGP1 AGP1 (ARABINOGLACTAN-PROTEIN 1) chr5:25739244-25	2.884
EV128384	2.783	no similarity	2.259
JCVI_7475	2.782	moderately similar to (453)AT5G23660 Symbols: MTN3 MTN3 (ARABIDOPSIS HOMOLOG OF MEDICAGO TRUNCATULA MTN3)	
JCVI_7746	2.782	moderately similar to (205)AT5G13100 Symbols: oxidoreductase chr5:4156792-4158238 FORWARD no original description	2.240
EV218325	2.781	weakly similar to (142)AT2G40140 Symbols: CZF1, ZFAR1 CZF1/ZFAR1 chr2:16779615-16781408 FORWARD [21492]	
JCVI_30149	2.779	no original description	3.540
JCVI_17491	2.779	highly similar to (581)AT1G30370 Symbols: lipase class 3 family protein chr1:10719151-10720740 REVERSE no original description	
EE558512	2.777	no similarity	
JCVI_21233	2.776	no original description	
JCVI_32502	2.774	moderately similar to (386)AT5G56080 Symbols: nicotianamine synthase, putative chr5:22728628-22729590 REVERSEweakly simil	2.380
EX039472	2.773	weakly similar to (147)AT5G05490 Symbols: SYN1, DIF1 DIF1/SYN1 chr5:1624713-1629145 FORWARD [21811] 20 300 300	
EV112617	2.772	no similarity	
CV546572	2.770	no similarity	
JCVI_6116	2.769	moderately similar to (271)AT1G76600 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G21010.1); similar to	1.973
EV193118	2.768	weakly similar to (147)AT4G18210 Symbols: ATPUP10 ATPUP10 (Arabidopsis thaliana purine permease 10); purine transmembrane t	
JCVI_30704	2.764	very weakly similar to (83.6)AT3G62130 Symbols: epimerase-related chr3:23015969-23017333 FORWARD no original description	
JCVI_4382	2.764	moderately similar to (220)AT1G54050 Symbols: 17.4 kDa class III heat shock protein (HSP17.4-CIII) chr1:20183226-20183790 RE	1.949
AM060704	2.763	no similarity	
EX028970	2.763	weakly similar to (108)AT3G21400 Symbols: similar to unknown [Populus trichocarpa] (GB:ABK93428.1) chr3:7534830-7536299 R	
JCVI_22427	2.762	moderately similar to (257)AT1G59590 Symbols: ZCF37 ZCF37 chr1:21891525-21892160 FORWARD no original description	
JCVI_7689	2.762	moderately similar to (400)AT3G24550 Symbols: ATPERK1 ATPERK1 (PROLINE EXTENSIN-LIKE RECEPTOR KINASE 1); ATP	1.558
JCVI_13339	2.761	moderately similar to (437)AT2G29090 Symbols: CYP707A2 CYP707A2 (cytochrome P450, family 707, subfamily A, polypeptide 2);	1.876
JCVI_18124	2.761	no original description	1.874
JCVI_1097	2.761	moderately similar to (439)AT3G46600 Symbols: scarecrow transcription factor family protein chr3:17169037-17170784 FORWARE	1.632
JCVI_18406	2.759	moderately similar to (444)AT3G49810 Symbols: U-box domain-containing protein chr3:18485921-18487267 REVERSE no original	
JCVI_32775	2.757	moderately similar to (377)AT4G36670 Symbols: mannitol transporter, putative chr4:17287684-17289487 REVERSEweakly similar t	
EV093388	2.749	no similarity	
JCVI_30401	2.746	no original description	
JCVI_28693	2.746	moderately similar to (318)AT3G27250 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G40800.1); similar to	
EX131452	2.742	weakly similar to (181)AT5G59870 Symbols: HTA6 HTA6; DNA binding chr5:24132831-24133370 REVERSEweakly similar to (15	2.256
EV131203	2.738	no similarity	3.184
JCVI_32596	2.733	moderately similar to (316)AT5G46910 Symbols: transcription factor jumonji (jmi) family protein chr5:19065007-19068107 FORWA	
EX140135	2.732	weakly similar to (102)AT1G19770 Symbols: ATPUP14 ATPUP14 (Arabidopsis thaliana purine permease 14); purine transmembrane t	
JCVI_32120	2.732	very weakly similar to (86.7)AT5G08150 Symbols: unknown protein chr5:2622165-2622599 REVERSE no original description	
EV156297	2.731	moderately similar to (229)AT3G19380 Symbols: U-box domain-containing protein chr3:6714608-6715873 REVERSE [21484] 70 77	2.334
EV128921	2.729	moderately similar to (221)AT1G77380 Symbols: AAP3 AAP3 (amino acid permease 3); amino acid transmembrane transporter chr1:2	1.843
CX281139	2.728	no similarity	2.322
JCVI_38799	2.727	moderately similar to (219)AT5G01880 Symbols: zinc finger (C3HC4-type RING finger) family protein chr5:339014-339493 FORW	
EE559501	2.727	no similarity	
JCVI_26071	2.726	moderately similar to (273)AT2G40140 Symbols: CZF1, ZFAR1 CZF1/ZFAR1 chr2:16779615-16781408 FORWARD no original des	
JCVI_30046	2.726	moderately similar to (322)AT1G70170 Symbols: MMP MMP (MATRIX METALLOPROTEINASE); metalloendopeptidase chr1:264	
JCVI_34039	2.724	weakly similar to (138)AT2G46790 Symbols: PRR9, TL1, APRR9 APRR9 (PSEUDO-RESPONSE REGULATOR 9); transcription reg	1.432
JCVI_21646	2.723	weakly similar to (115)AT3G22880 Symbols: DMC1, ARLM15, ATDMC1 ATDMC1 (RECA-LIKE GENE); ATP binding / DNA-dep	
JCVI_40704	2.722	very weakly similar to (100)AT5G46295 Symbols: unknown protein chr5:18797131-18797346 REVERSE no original description	2.586
JCVI_20968	2.719	moderately similar to (235)AT3G49810 Symbols: U-box domain-containing protein chr3:18485921-18487267 REVERSEvery weakly	
JCVI_26106	2.716	moderately similar to (366)AT1G29340 Symbols: PUB17 PUB17 (PLANT U-BOX17); ubiquitin-protein ligase chr1:10264398-10266	1.661
JCVI_8440	2.715	no original description	2.640
JCVI_31045	2.715	moderately similar to (260)AT5G11090 Symbols: serine-rich protein-related chr5:3524797-3525450 FORWARD no original descripti	
JCVI_20	2.714	moderately similar to (293)AT1G27730 Symbols: ZAT10, STZ STZ (SALT TOLERANCE ZINC FINGER); nucleic acid binding / tran	2.788
JCVI_21446	2.713	no original description	
JCVI_21265	2.710	moderately similar to (251)AT1G21550 Symbols: calcium-binding protein, putative chr1:7553306-7553773 REVERSEvery weakly si	
EE448760	2.706	no similarity	2.618
EV107639	2.705	no similarity	
JCVI_31237	2.698	weakly similar to (172)AT2G40080 Symbols: ELF4 ELF4 (EARLY FLOWERING 4) chr2:16741623-16741958 REVERSE no origina	
EV199204	2.695	very weakly similar to (85.9)AT2G34720 Symbols: CCAAT-binding transcription factor (CBF-B/NF-YA) family protein chr2:146570	
AT000768	2.695	no similarity	
EX137378	2.691	moderately similar to (466)AT1G61360 Symbols: S-locus lectin protein kinase family protein chr1:22641532-22644639 REVERSEwe	
JCVI_14397	2.690	moderately similar to (237)AT1G01250 Symbols: AP2 domain-containing transcription factor, putative chr1:104731-105309 REVER	2.247
AM393924	2.689	no similarity	3.027
EX105137	2.688	weakly similar to (128)AT1G75770 Symbols: unknown protein chr1:28453683-28454632 FORWARD [21826]	
JCVI_802	2.687	moderately similar to (272)AT3G24500 Symbols: MBF1C, ATMBF1C ATMBF1C/MBF1C (MULTIPROTEIN BRIDGING FACTOR	1.699
EE425481	2.686	moderately similar to (298)AT3G06145 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CA071096.1) chr3:186012	3.572
ES957953	2.685	no similarity	2.594
ES945101	2.685	weakly similar to (114)AT1G09840 Symbols: shaggy-related protein kinase kappa / ASK-kappa (ASK10) chr1:3196116-3199526 RE	2.892
EX095727	2.684	weakly similar to (111)AT2G40000 Symbols: HSPRO2, ATHSPRO2 similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G5	2.357
ES911468	2.683	moderately similar to (454)AT3G15354 Symbols: SPA3 SPA3 (SPA1-RELATED 3); signal transducer chr3:5169334-5172487 REVE	1.843
JCVI_4818	2.683	moderately similar to (238)AT3G16720 Symbols: ATL2 ATL2 (Arabidopsis T?xicos en Levadura 2); protein binding / zinc ion binding	
EX130490	2.682	no similarity	2.328
EV191125	2.680	weakly similar to (186)AT4G08450 Symbols: disease resistance protein (TIR-NBS-LRR class), putative chr4:5365607-5371098 FOR	
JCVI_11330	2.680	weakly similar to (135)AT4G18880 Symbols: HSFA4A, AT-HSFA4A AT-HSFA4A (Arabidopsis thaliana heat shock transcription fact	1.746
JCVI_21968	2.677	no original description	
EX028275	2.675	moderately similar to (429)AT5G01550 Symbols: lectin protein kinase, putative chr5:214516-216582 REVERSEweakly similar to (1	
EE447525	2.674	no similarity	
JCVI_9907	2.674	moderately similar to (286)AT1G76650 Symbols: CML38 CML38 chr1:28771803-28772336 REVERSEvery weakly similar to (82.4)C	3.144
JCVI_13591	2.671	weakly similar to (184)AT2G30020 Symbols: protein phosphatase 2C, putative / PP2C, putative chr2:12821514-12822981 FORWAR	2.145
JCVI_39390	2.671	moderately similar to (315)AT3G12700 Symbols: aspartyl protease family protein chr3:4037143-4039050 FORWARD no original de	
EV090704	2.670	weakly similar to (147)AT1G72890 Symbols: disease resistance protein (TIR-NBS class), putative chr1:27433608-27435378 FORWA	
EE551050	2.666	weakly similar to (112)AT5G18370 Symbols: disease resistance protein (TIR-NBS-LRR class), putative chr5:6085038-6088928 REVE	
EV160381	2.665	moderately similar to (228)AT2G39980 Symbols: transferase family protein chr2:16695515-16696963 REVERSE [21484] 64 800 800	2.967
EE424279	2.664	moderately similar to (339)AT1G11050 Symbols: protein kinase family protein chr1:3681892-3683769 FORWARDweakly similar to	

CD828081	2.662	no similarity	
EE550074	2.657	no similarity	
JCVI_10466	2.653	weakly similar to (142)AT1G76900 Symbols: AtTLP1 AtTLP1 (TUBBY LIKE PROTEIN 1); phosphoric diester hydrolase/ transcriptio	
JCVI_18326	2.652	moderately similar to (384)AT4G01360 Symbols: similar to BPS1 (BYPASS 1) [Arabidopsis thaliana] (TAIR:AT1G01550.2); similar t	
JCVI_4558	2.646	moderately similar to (209)AT1G71000 Symbols: DNAJ heat shock N-terminal domain-containing protein chr1:26772998-26773773	
EV226676	2.646	very weakly similar to (91.3)AT3G16510 Symbols: C2 domain-containing protein chr3:5617118-5618200 REVERSE [21493] 1 637 7	
JCVI_22143	2.646	no original description	
EE474581	2.645	weakly similar to (118)AT3G12320 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G06980.1); similar to hypc	1.447
JCVI_35317	2.644	no original description	
JCVI_37131	2.644	moderately similar to (236)AT3G46900 Symbols: COPT2 COPT2 (Copper transporter 2); copper ion transmembrane transporter chr3:	
EE546160	2.643	moderately similar to (286)AT2G40000 Symbols: HSPRO2, ATHSPRO2 similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3	1.857
JCVI_12489	2.642	weakly similar to (154)AT3G23930 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G13540.1); similar to hypc	
JCVI_24827	2.641	highly similar to (686)AT4G12010 Symbols: disease resistance protein (TIR-NBS-LRR class), putative chr4:7197319-7201387 REVE	
ES962263	2.639	no similarity	
JCVI_40401	2.638	no original description	
JCVI_10133	2.637	weakly similar to (167)AT5G57180 Symbols: CIA2 CIA2 (CHLOROPLAST IMPORT APPARATUS 2) chr5:23185619-23186749 FC	2.034
EX132818	2.637	moderately similar to (221)AT5G66070 Symbols: zinc finger (C3HC4-type RING finger) family protein chr5:26439149-26440259 FC	
JCVI_29717	2.633	moderately similar to (305)AT4G00050 Symbols: UNE10 UNE10 (unfertilized embryo sac 10); DNA binding / transcription factor chr	2.463
RC_EX130490	2.632	no similarity	2.512
JCVI_35	2.632	moderately similar to (318)AT1G27730 Symbols: ZAT10, STZ STZ (SALT TOLERANCE ZINC FINGER); nucleic acid binding / tran	2.825
JCVI_14587	2.631	highly similar to (590)AT3G22880 Symbols: DMC1, ARLIM15, ATDMC1 ATDMC1 (RECA-LIKE GENE); ATP binding / DNA-depe	
ES987173	2.631	no similarity	
CV546797	2.629	no similarity	
CD842657	2.629	very weakly similar to (80.1)AT2G22470 Symbols: ATAGP2, AGP2 AGP2 (ARABINOGLACTAN-PROTEIN 2) chr2:9545480-954	
CX192125	2.623	weakly similar to (179)AT2G39800 Symbols: ATP5CS, P5CS1 P5CS1 (DELTA1-PYRROLINE-5-CARBOXYLATE SYNTHASE 1)	
JCVI_7050	2.620	moderately similar to (467)AT5G44730 Symbols: haloacid dehalogenase-like hydrolase family protein chr5:18062815-18063746 REV	2.380
EV133520	2.620	moderately similar to (308)AT3G54800 Symbols: pleckstrin homology (PH) domain-containing protein / lipid-binding START domain-	
JCVI_34508	2.619	moderately similar to (221)AT4G19450 Symbols: nodulin-related chr4:10606549-10609229 FORWARD no original description	2.169
EV129366	2.615	weakly similar to (119)AT4G12970 Symbols: similar to uncloned protein product [Vitis vinifera] (GB:CAO17947.1) chr4:7586241-75	1.752
EX037889	2.614	moderately similar to (289)AT4G15320 Symbols: CSLB06, ATCSLB6, ATCSLB06 ATCSLB06 (Cellulose synthase-like B6); transfera	
AM387181	2.613	no similarity	
JCVI_4467	2.613	very weakly similar to (82.0)AT5G14970 Symbols: amine oxidase/ copper ion binding / quinone binding chr5:4847371-4848763 FOR	
JCVI_32381	2.610	moderately similar to (229)AT3G08040 Symbols: MAN1, FRD3 FRD3 (FERRIC REDUCTASE DEFECTIVE 3); antiporter chr3:256	
JCVI_13251	2.609	weakly similar to (134)AT5G53590 Symbols: auxin-responsive family protein chr5:21789333-21789761 FORWARD no original desc	
JCVI_22207	2.604	no original description	
JCVI_1821	2.602	very weakly similar to (98.2)AT1G14180 Symbols: unknown protein chr1:4847972-4848801 FORWARD no original description	1.720
JCVI_31508	2.601	moderately similar to (235)AT5G43400 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G13210.1); similar to i	
JCVI_16182	2.600	moderately similar to (300)AT1G67590 Symbols: remorin family protein chr1:25336918-25338135 REVERSE no original description	
JCVI_20074	2.600	weakly similar to (171)AT1G72430 Symbols: auxin-responsive protein-related chr1:27268812-27269171 REVERSE no original descr	
JCVI_6244	2.598	highly similar to (742)AT2G35710 Symbols: glycogenin glucosyltransferase (glycogenin)-related chr2:15018004-15019330 REVERS	
EV066504	2.597	weakly similar to (101)AT5G15950 Symbols: adenosylmethionine decarboxylase family protein chr5:5206709-5207797 FORWARDv	
CV544507	2.596	weakly similar to (114)AT2G40000 Symbols: HSPRO2, ATHSPRO2 similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G5	1.848
JCVI_10442	2.596	moderately similar to (486)AT5G62520 Symbols: SRO5 SRO5 (SIMILAR TO RCD ONE 5); NAD+ ADP-ribosyltransferase chr5:251	2.103
JCVI_21126	2.594	moderately similar to (216)AT1G04040 Symbols: acid phosphatase class B family protein chr1:1042563-1043818 REVERSE no origi	3.431
AT000526	2.592	no similarity	
EV124143	2.588	very weakly similar to (89.4)AT3G16720 Symbols: ATL2 ATL2 (Arabidopsis T?xicos en Levadura 2); protein binding / zinc ion binding	
JCVI_616	2.582	moderately similar to (429)AT5G59550 Symbols: zinc finger (C3HC4-type RING finger) family protein chr5:24015648-24016871 RE	2.271
JCVI_33076	2.578	weakly similar to (117)AT1G05690 Symbols: BT3 BT3 (BTB and TAZ domain protein 3); protein binding / transcription regulator chr	
JCVI_30803	2.577	moderately similar to (318)AT3G52060 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G22070.1); similar to i	2.017
EE460220	2.574	weakly similar to (125)AT5G10930 Symbols: SnRK3.24, CIPK5 CIPK5 (CBL-INTERACTING PROTEIN KINASE 5); kinase chr5:3-	
JCVI_30647	2.573	no original description	2.365
JCVI_12701	2.573	moderately similar to (268)AT2G21320 Symbols: zinc finger (B-box type) family protein chr2:9133583-9134733 FORWARD no orig	
BG543660	2.572	weakly similar to (122)AT2G01190 Symbols: octicosapeptide/Phox/Bem1p (PB1) domain-containing protein chr2:115022-117295 FC	
ES897719	2.571	no similarity	
JCVI_5043	2.570	moderately similar to (261)AT2G41010 Symbols: ATCAMPB25 ATCAMPB25 (ARABIDOPSIS THALIANA CALMODULIN (CAM)	
EV224419	2.570	no similarity	
JCVI_41139	2.567	no original description	1.472
JCVI_4958	2.567	no original description	1.365
JCVI_30564	2.565	no original description	
JCVI_1306	2.565	highly similar to (546)AT1G09130 Symbols: ATP-dependent Clp protease proteolytic subunit, putative chr1:2940065-2942219 REVE	
EX016630	2.565	weakly similar to (131)AT1G06170 Symbols: basic helix-loop-helix (bHLH) family protein chr1:1885145-1886563 REVERSE [2180	2.722
RC_AM056987	2.564	no similarity	
EE562117	2.562	no similarity	
EV150359	2.561	no similarity	
JCVI_39405	2.559	moderately similar to (236)AT3G62090 Symbols: PIF6, PIL2 PIL2 (PHYTOCHROME INTERACTING FACTOR 3-LIKE 2) chr3:23	
JCVI_35156	2.558	moderately similar to (327)AT5G22250 Symbols: CCR4-NOT transcription complex protein, putative chr5:7365608-7366444 REVEF	1.716
JCVI_16109	2.558	weakly similar to (113)AT1G76900 Symbols: AtTLP1 AtTLP1 (TUBBY LIKE PROTEIN 1); phosphoric diester hydrolase/ transcriptio	
JCVI_16715	2.558	moderately similar to (205)AT5G15110 Symbols: pectate lyase family protein chr5:4895969-4897685 FORWARDvery weakly simila	
EH430231	2.558	no similarity	1.697
AM390828	2.557	no similarity	2.294
JCVI_27435	2.555	no original description	
JCVI_42224	2.555	no original description	2.595
JCVI_22974	2.554	weakly similar to (118)AT3G02840 Symbols: immediate-early fungal elicitor family protein chr3:618487-619626 FORWARD no orig	2.423
JCVI_14413	2.550	no original description	4.969
JCVI_41635	2.549	no original description	
EV121602	2.548	weakly similar to (102)AT1G67590 Symbols: remorin family protein chr1:25336918-25338135 REVERSE [21479]	1.685
JCVI_24850	2.546	no original description	
JCVI_28178	2.546	very weakly similar to (99.0)AT5G26760 Symbols: similar to hypothetical protein OsI_017683 [Oryza sativa (indica cultivar-group)] (C	
JCVI_29711	2.545	weakly similar to (155)AT1G75770 Symbols: unknown protein chr1:28453683-28454632 FORWARD no original description	
EE441912	2.545	no similarity	
EE538236	2.545	moderately similar to (214)AT5G47590 Symbols: heat shock protein-related chr5:19315171-19316325 REVERSE [20161] 14 665 66	
JCVI_9144	2.544	very weakly similar to (100)AT3G23170 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G14450.1) chr3:826	
DY004157	2.543	no similarity	2.964

JCVI_12056	2.542	weakly similar to (107)AT5G66985 Symbols: unknown protein chr5:26760638-26760889 FORWARD no original description	
JCVI_34623	2.541	no original description	
EE450348	2.539	weakly similar to (105)AT5G17300 Symbols: myb family transcription factor chr5:5690437-5692437 REVERSE [20170] 1 428 455	2.213
ES908712	2.537	moderately similar to (269)AT1G21326 Symbols: VQ motif-containing protein chr1:7468990-7469709 REVERSE [21430]	
EE502099	2.533	no similarity	
EX096129	2.532	no similarity	1.972
JCVI_30427	2.530	moderately similar to (234)AT1G18740 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G74450.1); similar to i	
EE445350	2.530	no similarity	2.993
JCVI_16916	2.529	moderately similar to (270)AT1G73540 Symbols: ATNUDT21 ATNUDT21 (Arabidopsis thaliana Nudix hydrolase homolog 21); hydro	
JCVI_26735	2.529	moderately similar to (358)AT1G05560 Symbols: UGT75B1, UGT1 UGT1 (UDP-glucosyl transferase 75B1); UDP-glycosyltransferase	1.870
ES912597	2.527	no similarity	
JCVI_38066	2.527	moderately similar to (232)AT5G59550 Symbols: zinc finger (C3HC4-type RING finger) family protein chr5:24015648-24016871 RE	2.329
JCVI_468	2.524	highly similar to (721)AT1G70740 Symbols: protein kinase family protein chr1:26677509-26679349 REVERSEmoderately similar to	1.668
JCVI_31741	2.523	moderately similar to (249)AT3G24520 Symbols: HSFC1, AT-HSFC1 AT-HSFC1 (Arabidopsis thaliana heat shock transcription factor	2.365
EE423578	2.522	moderately similar to (201)AT5G38150 Symbols: PMI15 PMI15 (plastid movement impaired 15) chr5:15240346-15242165 REVERSI	2.036
RC_CV433289	2.520	no similarity	1.211
JCVI_14130	2.518	moderately similar to (359)AT5G49330 Symbols: AtMYB111 AtMYB111 (myb domain protein 111); DNA binding / transcription fact	
EE559412	2.517	moderately similar to (296)AT5G10930 Symbols: SnRK3.24, CIPK5 CIPK5 (CBL-INTERACTING PROTEIN KINASE 5); kinase chu	
ES961878	2.516	weakly similar to (147)AT4G26430 Symbols: CSN6B CSN6B (COP9 SIGNALOSOME SUBUNIT 6B) chr4:13355237-13357334 FOI	
JCVI_9781	2.516	weakly similar to (154)AT1G29640 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G34340.1); similar to unkr	
JCVI_3294	2.513	moderately similar to (209)AT3G21300 Symbols: RNA methyltransferase family protein chr3:7493660-7496263 REVERSE no origin	1.679
ES905653	2.513	very weakly similar to (82.0)AT5G63370 Symbols: protein kinase family protein chr5:25402180-25403616 REVERSE [21429]	
JCVI_31056	2.511	weakly similar to (126)AT4G05010 Symbols: F-box family protein chr4:2567472-2568160 FORWARD no original description	2.742
JCVI_6659	2.510	moderately similar to (444)AT2G23810 Symbols: TET8 TET8 (TETRASPANIN8) chr2:10142939-10144432 REVERSE no original d	
JCVI_23576	2.509	moderately similar to (232)AT3G16720 Symbols: ATL2 ATL2 (Arabidopsis T?xicos en Levadura 2); protein binding / zinc ion binding	1.344
JCVI_12897	2.508	no original description	2.415
EV213568	2.506	moderately similar to (248)AT2G15300 Symbols: leucine-rich repeat transmembrane protein kinase, putative chr2:6656712-6659092 I	1.914
JCVI_16980	2.506	moderately similar to (376)AT1G12500 Symbols: phosphate translocator-related chr1:4263540-4264955 REVERSE no original descri	
JCVI_29716	2.504	weakly similar to (105)AT5G17230 Symbols: PSY PSY (PHYTOENE SYNTHASE) chr5:5659841-5662089 REVERSEvery weakly s	1.447
JCVI_34766	2.502	moderately similar to (288)AT4G37260 Symbols: MYB73, AtMYB73 AtMYB73/MYB73 (myb domain protein 73); DNA binding / tra	
CD821801	2.501	weakly similar to (101)AT4G34600 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G16385.1) chr4:1652928	
JCVI_23539	2.501	moderately similar to (291)AT1G66840 Symbols: Identical to Protein PLASTID MOVEMENT IMPAIRED 2 (PMI2) [Arabidopsis The	2.029
JCVI_34618	2.501	moderately similar to (371)AT5G66210 Symbols: CPK28 CPK28 (calcium-dependent protein kinase 28) chr5:26474371-26476660 RE	1.782
EX039879	2.500	moderately similar to (310)AT1G01520 Symbols: myb family transcription factor chr1:190596-192139 FORWARD [21811]	
JCVI_30847	2.499	weakly similar to (109)AT2G25735 Symbols: unknown protein chr2:10982423-10982782 REVERSE no original description	
JCVI_42505	2.498	moderately similar to (300)AT1G25400 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G68440.1); similar to i	
EV132889	2.497	no similarity	1.853
EE557380	2.496	no similarity	2.008
EV082737	2.496	no similarity	2.548
RC_H74690	2.495	no similarity	2.567
JCVI_3653	2.492	moderately similar to (473)AT1G26480 Symbols: GF14 IOTA, GRF12 GRF12 (GENERAL REGULATORY FACTOR 12); protein ph	3.259
EV066279	2.491	no similarity	
JCVI_5377	2.488	moderately similar to (240)AT2G04680 Symbols: DC1 domain-containing protein chr2:1640185-1642158 FORWARD no original de	
DY029300	2.488	no similarity	
JCVI_22830	2.487	weakly similar to (168)AT2G34340 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G29640.1); similar to unkr	
EV124854	2.485	moderately similar to (414)AT4G23190 Symbols: AT-RLK3, CRK11 CRK11 (CYSTEINE-RICH RLK11); kinase chr4:12141208-121	
JCVI_40185	2.485	weakly similar to (194)AT1G74890 Symbols: ARR15 ARR15 (RESPONSE REGULATOR 15); transcription regulator chr1:28135251	
JCVI_36250	2.483	very weakly similar to (92.8)AT3G61640 Symbols: ATAGP20, AGP20 AGP20 (ARABINOGALACTAN PROTEIN 20) chr3:2282125	
JCVI_21619	2.478	no original description	2.283
EV132187	2.478	no similarity	
EE462195	2.478	very weakly similar to (100)AT3G24255 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G23910.1); similar to	
EE543569	2.475	weakly similar to (191)AT1G73066 Symbols: protein binding chr1:27485446-27487242 FORWARDweakly similar to (120)RPK1_IF	
JCVI_21877	2.475	weakly similar to (102)AT1G32928 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G32920.1) chr1:1193131	2.337
JCVI_5269	2.474	weakly similar to (168)AT1G14200 Symbols: zinc finger (C3HC4-type RING finger) family protein chr1:4854527-4855066 REVERSI	2.142
EE554654	2.471	weakly similar to (185)AT3G11020 Symbols: DREB2, DREB2B DREB2B (DRE-binding protein 2B); DNA binding / transcription acti	
EV198526	2.467	no similarity	
JCVI_23772	2.466	weakly similar to (141)AT5G42660 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G02910.1); similar to unne	
EV214080	2.463	moderately similar to (237)AT3G15115 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G53180.1) chr3:5086	
JCVI_37519	2.463	weakly similar to (129)AT1G26590 Symbols: zinc finger (C2H2 type) family protein chr1:9189611-9190696 FORWARD no original	
JCVI_19864	2.462	moderately similar to (402)AT1G24140 Symbols: matrixin family protein chr1:8536120-8537274 REVERSEweakly similar to (185)h	
JCVI_19926	2.457	no original description	
JCVI_23713	2.455	highly similar to (593)AT1G13710 Symbols: CYP78A5 CYP78A5 (cytochrome P450, family 78, subfamily A, polypeptide 5); oxygen l	
EV137277	2.454	no similarity	1.457
JCVI_37887	2.452	weakly similar to (188)AT4G21895 Symbols: similar to AT hook motif-containing protein [Arabidopsis thaliana] (TAIR:AT5G52890.1	
EV103398	2.451	no similarity	
H74690	2.449	no similarity	2.436
JCVI_4015	2.448	weakly similar to (159)AT4G02740 Symbols: Identical to F-box protein At4g02740 [Arabidopsis Thaliana] (GB:Q0WRC9;GB:Q683B)	
JCVI_11272	2.447	highly similar to (514)AT2G46070 Symbols: ATMPK12 ATMPK12 (Arabidopsis thaliana MAP kinase 12); MAP kinase/ kinase chr2:	1.769
ES900133	2.443	weakly similar to (167)AT5G45960 Symbols: GDSL-motif lipase/hydrolase family protein chr5:18654401-18657546 REVERSEvery	2.195
JCVI_12498	2.443	very weakly similar to (94.7)AT2G16005 Symbols: MD-2-related lipid recognition domain-containing protein / ML domain-containing	
RC_EE566066	2.437	no similarity	3.353
DN961108	2.437	moderately similar to (265)AT3G26220 Symbols: CYP71B3 CYP71B3 (cytochrome P450, family 71, subfamily B, polypeptide 3); oxy	
CD837899	2.436	no similarity	
EV170912	2.436	weakly similar to (191)AT5G25900 Symbols: CYP701A3, GA3 GA3 (GA REQUIRING 3); oxygen binding chr5:9036076-9038281 FI	
JCVI_20622	2.436	no original description	2.048
EV091268	2.435	moderately similar to (214)AT5G39530 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G39520.1); similar to i	
JCVI_19317	2.434	weakly similar to (189)AT4G30880 Symbols: protease inhibitor/seed storage/lipid transfer protein (LTP) family protein chr4:1503523	
EE547032	2.434	weakly similar to (107)AT5G55620 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G09950.1); similar to unne	1.583
EX089219	2.433	weakly similar to (110)AT5G40230 Symbols: nodulin-related chr5:16097042-16098963 REVERSE [21823]	
ES969208	2.433	weakly similar to (140)AT1G15890 Symbols: disease resistance protein (CC-NBS-LRR class), putative chr1:5461400-5463955 FORV	
JCVI_35549	2.431	no original description	
JCVI_28155	2.431	weakly similar to (177)AT4G24700 Symbols: unknown protein chr4:12744817-12745248 REVERSE no original description	1.491
JCVI_37808	2.431	weakly similar to (111)AT1G33990 Symbols: hydrolase, alpha/beta fold family protein chr1:12355889-12357874 FORWARD no orig	3.250

JCVI_28194	2.430	highly similar to (590)AT5G39080 Symbols: transferase family protein chr5:15658909-15660300 FORWARD no original description	2.848
EV095717	2.429	no similarity	
EV120020	2.429	no similarity	
EX135350	2.427	weakly similar to (146)AT3G61850 Symbols: DAG1 DAG1 (DOF AFFECTING GERMINATION 1) chr3:22906470-22908125 FORW	2.109
EV150514	2.423	moderately similar to (269)AT4G14080 Symbols: MEE48 MEE48 (maternal effect embryo arrest 48); hydrolase, hydrolyzing O-glycos	
EV167695	2.423	weakly similar to (181)AT5G05190 Symbols: Identical to Uncharacterized protein At5g05190 (Y-1) [Arabidopsis Thaliana] (GB:Q9FH	
CX268655	2.420	weakly similar to (102)AT5G17790 Symbols: VAR3 VAR3 (VARIEGATED 3); binding chr5:5869812-5872673 REVERSE [16816] 1	
JCVI_12229	2.419	moderately similar to (328)AT3G21870 Symbols: CYCP2;1 CYCP2;1 (cyclin p2;1); cyclin-dependent protein kinase chr3:7703934-77	2.436
EV132939	2.418	no similarity	
EV165235	2.418	weakly similar to (155)AT1G24530 Symbols: transducin family protein / WD-40 repeat family protein chr1:8693274-8694530 FORW	2.110
EX123750	2.415	very weakly similar to (99.4)AT5G54300 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G61260.1); similar to	
EE564839	2.415	very weakly similar to (81.3)AT1G07010 Symbols: calcineurin-like phosphoesterase family protein chr1:2152948-2154967 FORWAR	
EV116241	2.414	moderately similar to (283)AT5G39670 Symbols: calcium-binding EF hand family protein chr5:15900498-15901112 FORWARD [21	
DY026840	2.414	no similarity	1.784
JCVI_22811	2.413	moderately similar to (202)AT4G14690 Symbols: ELIP2 ELIP2 (EARLY LIGHT-INDUCIBLE PROTEIN 2); chlorophyll binding chr-	2.354
EE561389	2.413	moderately similar to (299)AT2G27210 Symbols: kelch repeat-containing serine/threonine phosphoesterase family protein chr2:11637	
JCVI_13374	2.413	moderately similar to (303)AT1G70260 Symbols: nodulin MtN21 family protein chr1:26460730-26463001 REVERSE no original des	2.750
EV090686	2.413	weakly similar to (176)AT3G24420 Symbols: hydrolase, alpha/beta fold family protein chr3:8863118-8864890 REVERSE [21476] 10	2.488
EX042931	2.413	moderately similar to (333)AT4G38960 Symbols: zinc finger (B-box type) family protein chr4:18162294-18163039 FORWARD [218	
JCVI_4284	2.411	no original description	
EV130781	2.409	no similarity	
JCVI_7784	2.409	moderately similar to (235)AT4G37260 Symbols: MYB73, AtMYB73 AtMYB73/MYB73 (myb domain protein 73); DNA binding / tra	
CD825311	2.405	weakly similar to (145)AT3G24255 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G23910.1); similar to unna	
JCVI_24635	2.403	moderately similar to (280)AT2G38160 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G40070.1); similar to i	2.245
JCVI_18765	2.401	moderately similar to (290)AT1G07615 Symbols: GTP binding chr1:2342274-2344197 REVERSE no original description	
CX194043	2.399	moderately similar to (337)AT3G55060 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G39300.1); similar to i	
JCVI_32817	2.393	moderately similar to (396)AT4G01950 Symbols: ATGPAT3, GPAT3 ATGPAT3/GPAT3 (GLYCEROL-3-PHOSPHATE ACYLTRAN	
JCVI_3997	2.393	highly similar to (504)AT5G15900 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G15890.1); similar to unna	
EE450982	2.391	moderately similar to (317)AT1G75100 Symbols: JAC1 JAC1 (J-DOMAIN PROTEIN REQUIRED FOR CHLOROPLAST ACCUMUI	
JCVI_17257	2.390	moderately similar to (318)AT5G15300 Symbols: pentatricopeptide (PPR) repeat-containing protein chr5:4968387-4970033 REVERS	
JCVI_33958	2.388	moderately similar to (317)AT4G32860 Symbols: similar to unknown [Populus trichocarpa x Populus deltoides] (GB:ABK96753.1) cl	
EV177936	2.387	weakly similar to (161)AT4G16550 Symbols: heat shock protein-related chr4:9318464-9324276 REVERSE [21487] 142 919 919	
EE423815	2.386	weakly similar to (140)AT4G19400 Symbols: actin binding chr4:10581048-10581920 REVERSE [20158]	2.031
JCVI_31295	2.385	weakly similar to (136)AT5G44005 Symbols: unknown protein chr5:17722436-17722720 REVERSE no original description	
JCVI_38427	2.383	no original description	
EE404663	2.382	no similarity	1.340
JCVI_29410	2.379	moderately similar to (338)AT2G26190 Symbols: calmodulin-binding family protein chr2:11154979-11157160 REVERSE no original	
JCVI_28898	2.378	no original description	
JCVI_13323	2.378	moderately similar to (271)AT5G06690 Symbols: (THIOREDOXIN-LIKE 5); thiol-disulfide exchange intermediate chr5:2060853-20	2.279
JCVI_2658	2.378	weakly similar to (134)AT3G56880 Symbols: VQ motif-containing protein chr3:21071023-21071760 FORWARD no original descrip	
JCVI_514	2.376	moderately similar to (383)AT3G15354 Symbols: SPA3 SPA3 (SPA1-RELATED 3); signal transducer chr3:5169334-5172487 REVEE	1.740
RC_AM387464	2.375	no similarity	
JCVI_39744	2.375	weakly similar to (199)AT1G31740 Symbols: BGAL15 BGAL15 (beta-galactosidase 15); beta-galactosidase chr1:11365266-11369885	
EX135021	2.372	weakly similar to (109)AT2G46400 Symbols: ATWRKY46, WRKY46 WRKY46 (WRKY DNA-binding protein 46); transcription facto	
JCVI_34717	2.370	moderately similar to (459)AT4G31020 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G24320.1); similar to i	
JCVI_28085	2.364	moderately similar to (207)AT4G21200 Symbols: ATGA2OX8 ATGA2OX8 (GIBBERELLIN 2-OXIDASE 8); gibberellin 2-beta-dioxy	2.360
EV145867	2.364	no similarity	
JCVI_36064	2.363	moderately similar to (320)AT2G17040 Symbols: ANAC036 ANAC036 (Arabidopsis NAC domain containing protein 36); transcription	
EX119365	2.363	moderately similar to (361)AT3G55580 Symbols: regulator of chromosome condensation (RCC1) family protein chr3:20623745-2062	
EV173310	2.363	no similarity	1.440
EE513584	2.362	no similarity	2.422
EX125631	2.359	no similarity	
JCVI_24165	2.356	moderately similar to (305)AT1G07010 Symbols: calcineurin-like phosphoesterase family protein chr1:2152948-2154967 FORWARD	1.403
JCVI_41748	2.354	no original description	
AM057705	2.354	weakly similar to (119)AT2G43470 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G03320.1); similar to unna	
EV124770	2.354	weakly similar to (169)AT4G23190 Symbols: AT-RLK3, CRK11 CRK11 (CYSTEINE-RICH RLK11); kinase chr4:12141208-121437	
JCVI_34254	2.352	very weakly similar to (84.3)AT3G15357 Symbols: unknown protein chr3:5187171-5187602 FORWARD no original description	
JCVI_22252	2.350	moderately similar to (406)AT3G19970 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G18245.1); similar to i	
EE404244	2.349	moderately similar to (236)AT3G22410 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G05370.1); similar to i	
EV225869	2.348	very weakly similar to (86.3)AT1G47128 Symbols: RD21A, RD21 RD21 (RESPONSIVE TO DEHYDRATION 21); cysteine-type pepti	
JCVI_22813	2.348	no original description	
JCVI_15274	2.348	weakly similar to (145)AT1G72390 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO45587.1) chr1:27249117-2	
JCVI_18512	2.347	weakly similar to (187)AT1G52250 Symbols: dynein light chain type 1 family protein chr1:19462513-19462904 REVERSE no origin	
EL589385	2.347	moderately similar to (346)AT5G46910 Symbols: transcription factor jumonji (jmi) family protein chr5:19065007-19068107 FORWA	
EE555489	2.346	no similarity	
EX062936	2.343	weakly similar to (121)AT4G23160 Symbols: protein kinase family protein chr4:12129496-12134097 FORWARD [21814] 15 594 59	
JCVI_35452	2.342	no original description	3.296
JCVI_27061	2.341	very weakly similar to (86.3)AT4G34150 Symbols: C2 domain-containing protein chr4:16355039-16356959 FORWARD no original d	
EV098668	2.341	no similarity	
EG019920	2.339	very weakly similar to (82.8)AT2G34720 Symbols: CCAAT-binding transcription factor (CBF-B/NF-YA) family protein chr2:146570	1.953
DY001046	2.337	moderately similar to (269)AT3G06145 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO71096.1) chr3:186012	3.615
JCVI_10088	2.337	no original description	
ES952471	2.336	no similarity	2.133
RC_JCVI_20887	2.335	no original description	
JCVI_27603	2.333	moderately similar to (309)AT4G38960 Symbols: zinc finger (B-box type) family protein chr4:18162294-18163039 FORWARD no o	1.394
EE568852	2.331	very weakly similar to (83.6)AT1G44160 Symbols: DNAJ chaperone C-terminal domain-containing protein chr1:16797472-16798716	
JCVI_17306	2.331	moderately similar to (250)AT5G13770 Symbols: pentatricopeptide (PPR) repeat-containing protein chr5:4445464-4447293 FORWA	1.737
ES902908	2.330	moderately similar to (244)AT2G35380 Symbols: peroxidase 20 (PER20) (P20) chr2:14900188-14901037 FORWARDweakly similar	
JCVI_39496	2.330	weakly similar to (127)AT3G56290 Symbols: similar to hypothetical protein [Vitis vinifera] (GB:CAN75527.1) chr3:20889722-2089	3.442
JCVI_19361	2.325	moderately similar to (399)AT3G28910 Symbols: ATMYB30, MYB30 MYB30 (myb domain protein 30); DNA binding / transcription	
EE568032	2.324	weakly similar to (112)AT5G42240 Symbols: SCPL42 SCPL42 (serine carboxypeptidase-like 42); serine carboxypeptidase chr5:16905	
AT001877	2.324	no similarity	1.805
CD817870	2.324	moderately similar to (248)AT5G42630 Symbols: KAN4, ATS ATS/KAN4 (ABERRANT TESTA SHAPE) chr5:17091808-17092975	

JCVI_6789	2.324	no original description	
JCVI_34189	2.322	moderately similar to (246)AT5G50530 Symbols: CBS domain-containing protein / octicosapeptide/Phox/Bemp1 (PB1) domain-contain	
JCVI_27468	2.322	moderately similar to (324)AT5G15890 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G15900.1); similar to l	
DY015590	2.322	very weakly similar to (87.8)AT5G59350 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO21684.1) chr5:23958	
JCVI_12037	2.322	moderately similar to (353)AT3G16510 Symbols: C2 domain-containing protein chr3:5617118-5618200 REVERSE no original descri	
EV197575	2.319	moderately similar to (285)AT3G13030 Symbols: hAT dimerisation domain-containing protein chr3:4169682-4171424 REVERSE [21	1.704
EV110835	2.317	no similarity	
DY008941	2.317	no similarity	
JCVI_38912	2.316	moderately similar to (422)AT3G15354 Symbols: SPA3 SPA3 (SPA1-RELATED 3); signal transducer chr3:5169334-5172487 REVEF	1.814
EE455707	2.315	weakly similar to (139)AT5G55890 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G55880.1); contains Interf	
JCVI_11064	2.314	very weakly similar to (89.4)AT5G22460 Symbols: esterase/lipase/thioesterase family protein chr5:7443662-7445272 REVERSE no oi	
EV137742	2.314	no similarity	1.888
JCVI_29720	2.313	moderately similar to (249)AT5G17780 Symbols: hydrolase, alpha/beta fold family protein chr5:5867431-5868978 REVERSE no orig	1.349
JCVI_1823	2.312	moderately similar to (269)AT3G14200 Symbols: DNAJ heat shock N-terminal domain-containing protein chr3:4712888-4714368 RE	1.874
JCVI_15084	2.310	moderately similar to (212)AT3G16720 Symbols: ATL2 ATL2 (Arabidopsis Thaliana Leucine-Responsive Elongation Factor 2); protein binding / zinc ion binding	
EV182475	2.310	weakly similar to (176)AT2G18240 Symbols: RER1 protein, putative chr2:7942548-7943546 FORWARD [21487]	
EE475842	2.309	weakly similar to (157)AT1G75100 Symbols: JAC1 JAC1 (J-DOMAIN PROTEIN REQUIRED FOR CHLOROPLAST ACCUMULAT	1.556
EX115234	2.309	moderately similar to (251)AT3G60420 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G60450.1); similar to i	
JCVI_26208	2.307	moderately similar to (322)AT5G61380 Symbols: APRR1, PRR1, TOC1 TOC1 (TIMING OF CAB EXPRESSION 1); transcription reg	2.179
EV182967	2.305	no similarity	
JCVI_16649	2.305	weakly similar to (113)AT5G40810 Symbols: cytochrome c1, putative chr5:16357428-16359555 FORWARDweakly similar to (111)	
DY025805	2.304	moderately similar to (333)AT3G48270 Symbols: CYP71A26 CYP71A26 (cytochrome P450, family 71, subfamily A, polypeptide 26);	
JCVI_18755	2.304	weakly similar to (113)AT3G14595 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G17080.1); similar to unkr	
JCVI_39284	2.304	weakly similar to (125)AT5G15430 Symbols: calmodulin-binding protein-related chr5:5010183-5011619 FORWARD no original des	
JCVI_7087	2.302	moderately similar to (210)AT5G48220 Symbols: indole-3-glycerol phosphate synthase, putative chr5:19567665-19569272 FORWAR	1.450
ES999466	2.302	moderately similar to (225)AT3G14080 Symbols: small nuclear ribonucleoprotein, putative / snRNP, putative / Sm protein, putative cl	1.552
EV226406	2.301	no similarity	
JCVI_29048	2.301	no original description	
JCVI_42194	2.300	no original description	
EV020693	2.298	weakly similar to (109)AT2G45760 Symbols: BAL, BAP2 BAP2 (BON ASSOCIATION PROTEIN 2) chr2:18854199-18854822 REV	
JCVI_26518	2.297	moderately similar to (340)AT2G47650 Symbols: UXS4 UXS4 (UDP-XYLOSE SYNTHASE 4); catalytic chr2:19545821-19548434 R	
EV108938	2.297	very weakly similar to (88.6)CYSA_CUCSA [21478]	
JCVI_34125	2.297	moderately similar to (499)AT2G30020 Symbols: protein phosphatase 2C, putative / PP2C, putative chr2:12821514-12822981 FORW	
DW999792	2.296	no similarity	1.934
EV091965	2.296	weakly similar to (167)AT3G59400 Symbols: GUN4 GUN4 (Genomes uncoupled 4) chr3:21959858-21960655 REVERSE [21476]	2.432
ES957665	2.294	no similarity	
DY020656	2.293	moderately similar to (214)AT3G24520 Symbols: HSFC1, AT-HSFC1 AT-HSFC1 (Arabidopsis thaliana heat shock transcription factor	
JCVI_10560	2.293	moderately similar to (210)AT5G06530 Symbols: ABC transporter family protein chr5:1990335-1994606 REVERSE no original desc	1.761
JCVI_1578	2.292	very weakly similar to (87.4)AT3G59940 Symbols: kelch repeat-containing F-box family protein chr3:22153986-22155242 FORWAR	
JCVI_33192	2.291	weakly similar to (132)AT1G28370 Symbols: ERF11, ATERF11 ATERF11/ERF11 (ERF domain protein 11); DNA binding / transcript	
JCVI_21367	2.289	moderately similar to (299)AT2G32030 Symbols: GCN5-related N-acetyltransferase (GNAT) family protein chr2:13639752-1364031	
JCVI_4747	2.289	moderately similar to (298)AT3G19184 Symbols: DNA binding chr3:6637561-6639041 FORWARD no original description	
JCVI_17360	2.289	moderately similar to (459)AT3G51860 Symbols: ATHCX1, CAX1-LIKE, ATCAX3, CAX3 CAX3 (cation exchanger 3); cation:cation	
CV433836	2.289	no similarity	
EV142995	2.288	no similarity	
JCVI_16772	2.287	moderately similar to (254)AT1G70420 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G23710.1); similar to i	2.136
EE482280	2.285	no similarity	
JCVI_12276	2.284	moderately similar to (325)AT2G37970 Symbols: SOUL-1 SOUL-1; binding chr2:15898105-15898782 FORWARD no original descri	
CB686367	2.283	no similarity	
ES967756	2.282	very weakly similar to (87.4)AT5G58570 Symbols: unknown protein chr5:23690096-23690356 REVERSE [20153] 1 505 518	
EV135776	2.279	no similarity	
JCVI_25479	2.278	highly similar to (582)AT4G22100 Symbols: glycosyl hydrolase family 1 protein chr4:11707382-11709944 REVERSEmoderately sim	
EV057520	2.273	no similarity	
JCVI_36889	2.273	moderately similar to (282)AT4G36550 Symbols: binding / ubiquitin-protein ligase chr4:17245403-17247721 REVERSEvery weakly	
JCVI_875	2.273	weakly similar to (166)AT1G28370 Symbols: ERF11, ATERF11 ATERF11/ERF11 (ERF domain protein 11); DNA binding / transcript	
ES271655	2.272	moderately similar to (328)AT1G31740 Symbols: BGAL15 BGAL15 (beta-galactosidase 15); beta-galactosidase chr1:11365266-11365	
JCVI_9499	2.272	weakly similar to (139)AT5G27770 Symbols: 60S ribosomal protein L22 (RPL22C) chr5:9836170-9837117 FORWARD no original c	
JCVI_18505	2.271	moderately similar to (487)AT4G33050 Symbols: EDA39 EDA39 (embryo sac development arrest 39) chr4:15945238-15946739 REV	
JCVI_37060	2.270	highly similar to (558)AT1G42550 Symbols: PM11 PM11 (PLASTID MOVEMENT IMPAIRED1) chr1:15979976-15982174 FORWA	
JCVI_32916	2.270	moderately similar to (263)AT5G27420 Symbols: zinc finger (C3HC4-type RING finger) family protein chr5:9684122-9685228 FOR'	1.732
JCVI_31517	2.266	highly similar to (706)AT1G28130 Symbols: GH3.17 GH3.17 chr1:9826366-9827870 FORWARDmoderately similar to (439)GH311	2.565
JCVI_41437	2.264	moderately similar to (203)AT5G27420 Symbols: zinc finger (C3HC4-type RING finger) family protein chr5:9684122-9685228 FOR'	1.540
EV202472	2.263	moderately similar to (322)AT3G14920 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G05480.1); similar to i	
JCVI_23112	2.262	weakly similar to (113)AT3G24600 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G35170.1); similar to unne	
JCVI_487	2.262	highly similar to (586)AT1G18740 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G74450.1); similar to unna	1.651
JCVI_35336	2.259	weakly similar to (151)AT5G48657 Symbols: defense protein-related chr5:19751346-19752742 REVERSE no original description	
ES919907	2.252	moderately similar to (280)AT1G17145 Symbols: protein binding / zinc ion binding chr1:5860344-5862234 REVERSE [15718]	1.453
JCVI_35793	2.252	highly similar to (829)AT2G36190 Symbols: ATCWINV4 ATCWINV4 (ARABIDOPSIS THALIANA CELL WALL INVERTASE 4); i	
EX056114	2.251	weakly similar to (192)AT3G02380 Symbols: COL2 COL2 (CONSTANS-LIKE 2); transcription factor/ zinc ion binding chr3:487445-	2.443
JCVI_42329	2.251	weakly similar to (138)AT1G80760 Symbols: NIP6;1, NLM7, NIP6 NIP6;1 (NOD26-like intrinsic protein 6;1); water channel chr1:30	
JCVI_10712	2.250	moderately similar to (315)AT5G24120 Symbols: SIG5, SIGE SIGE (RNA polymerase sigma subunit E); DNA binding / DNA-directed	
JCVI_13791	2.249	moderately similar to (358)AT5G62140 Symbols: similar to unknown [Populus trichocarpa] (GB:ABK94834.1) chr5:24971789-24972	2.108
JCVI_21574	2.249	weakly similar to (139)AT1G58520 Symbols: RXW8 RXW8 chr1:21737208-21741830 FORWARD no original description	
ES953055	2.246	no similarity	
ES949089	2.244	weakly similar to (152)AT3G13020 Symbols: hAT dimerisation domain-containing protein chr3:4167002-4168924 REVERSE [21393]	1.796
EV141934	2.244	no similarity	
JCVI_42114	2.242	no original description	2.305
EV226520	2.242	weakly similar to (143)AT5G54600 Symbols: 50S ribosomal protein L24, chloroplast (CL24) chr5:22200272-22201629 FORWARD	
JCVI_8092	2.241	weakly similar to (173)AT5G55620 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G09950.1); similar to unna	1.452
ES906146	2.240	moderately similar to (362)AT2G17080 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G17070.1); similar to un	2.608
JCVI_37786	2.239	no original description	
JCVI_26525	2.239	moderately similar to (339)AT1G07010 Symbols: calcineurin-like phosphoesterase family protein chr1:2152948-2154967 FORWARD	
JCVI_16615	2.238	moderately similar to (454)AT4G12400 Symbols: stress-inducible protein, putative chr4:7338863-7341236 REVERSEmoderately sim	2.201

ES966375	2.238	no similarity	
JCVI_5109	2.237	moderately similar to (385)AT5G15850 Symbols: COL1 COL1 (CONSTANS-LIKE 1); transcription factor/ zinc ion binding chr5:517	
AM391388	2.237	moderately similar to (312)AT3G50560 Symbols: short-chain dehydrogenase/reductase (SDR) family protein chr3:18772228-1877481	2.082
EE556723	2.237	no similarity	
JCVI_6722	2.235	weakly similar to (135)AT5G65300 Symbols: unknown protein chr5:26112492-26112944 REVERSE no original description	1.914
EX027155	2.234	moderately similar to (293)AT1G14480 Symbols: protein binding chr1:4956399-4957883 FORWARD [21810]	
JCVI_20559	2.234	no original description	
JCVI_18985	2.232	moderately similar to (330)AT1G77380 Symbols: AAP3 AAP3 (amino acid permease 3); amino acid transmembrane transporter chr1:2	
JCVI_8434	2.231	moderately similar to (236)AT5G61490 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G25170.1); similar to i	1.238
JCVI_16435	2.230	moderately similar to (354)AT1G70090 Symbols: GATL9, LGT8 GATL9/LGT8 (Galacturonosyltransferase-like 9) chr1:26404590-26	1.963
JCVI_30712	2.229	weakly similar to (167)AT4G15248 Symbols: DNA binding / zinc ion binding chr4:8708881-8709234 FORWARD no original descrip	1.808
JCVI_2425	2.227	moderately similar to (339)AT2G41860 Symbols: CPK14 CPK14 (calcium-dependent protein kinase 14); calmodulin-dependent protein	
JCVI_9329	2.226	moderately similar to (317)AT1G70090 Symbols: GATL9, LGT8 GATL9/LGT8 (Galacturonosyltransferase-like 9) chr1:26404590-26	
JCVI_35269	2.226	no original description	
JCVI_11814	2.226	no original description	
JCVI_20419	2.225	very weakly similar to (84.0)AT3G17609 Symbols: HYH HYH (HY5-HOMOLOG) chr3:6023977-6024591 FORWARD no original de	1.625
RC_ES957953	2.225	no similarity	2.906
CN727151	2.224	no similarity	1.222
RC_EE557217	2.223	no similarity	
JCVI_38669	2.222	moderately similar to (302)AT1G32640 Symbols: RD22BP1, JAI1, JIN1, MYC2, ZBF1, ATMYC2 ATMYC2 (JASMONATE INSENS	
ES956130	2.222	no similarity	
ES266382	2.221	moderately similar to (255)AT3G60680 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G45260.1); similar to i	
EX095680	2.219	moderately similar to (275)AT3G02840 Symbols: immediate-early fungal elicitor family protein chr3:618487-619626 FORWARD [21	
JCVI_35880	2.219	highly similar to (697)AT1G23030 Symbols: armadillo/beta-catenin repeat family protein / U-box domain-containing protein chr1:815	
JCVI_10244	2.219	very weakly similar to (90.1)AT1G07985 Symbols: Expressed protein chr1:2475505-2475939 FORWARD no original description	
ES936687	2.218	no similarity	
JCVI_22426	2.217	very weakly similar to (96.7)AT4G29280 Symbols: LCR22 LCR22 (Low-molecular-weight cysteine-rich 22) chr4:14427907-14428271	2.528
EE459037	2.217	very weakly similar to (88.2)AT1G12800 Symbols: S1 RNA-binding domain-containing protein chr1:4361776-4365187 REVERSE [21	
JCVI_14465	2.216	moderately similar to (207)AT5G23280 Symbols: TCP family transcription factor, putative chr5:7843020-7843772 FORWARD no or	
JCVI_8027	2.215	moderately similar to (449)AT1G05690 Symbols: BT3 BT3 (BTB and TAZ domain protein 3); protein binding / transcription regulator	
JCVI_10630	2.213	weakly similar to (111)AT5G23130 Symbols: peptidoglycan-binding LysM domain-containing protein chr5:7781478-7783336 FORW	
JCVI_31620	2.213	weakly similar to (119)AT1G28640 Symbols: GDSL-motif lipase, putative chr1:10067549-10069095 REVERSE no original descripti	2.389
EV054282	2.212	weakly similar to (101)AT2G45740 Symbols: PEX11D PEX11D chr2:18846939-18848176 FORWARD [21442]	
JCVI_4831	2.212	weakly similar to (179)AT3G46600 Symbols: scarecrow transcription factor family protein chr3:17169037-17170784 FORWARD no	
JCVI_10851	2.212	moderately similar to (315)AT4G18010 Symbols: IP5PII IP5PII (INOSITOL POLYPHOSPHATE 5-PHOSPHATASE II); inositol-poly	
EX085956	2.211	very weakly similar to (92.8)AT2G04790 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO23994.1) chr2:16795	1.933
JCVI_15429	2.211	weakly similar to (113)AT5G19875 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G31940.1); similar to hypc	
JCVI_34442	2.211	weakly similar to (176)AT4G36500 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G18210.1); similar to hypc	1.891
AM060665	2.210	no similarity	
EV211246	2.210	moderately similar to (276)AT4G37340 Symbols: CYP81D3 CYP81D3 (cytochrome P450, family 81, subfamily D, polypeptide 3); oxy	1.896
DN964921	2.209	weakly similar to (136)AT3G12320 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G06980.1); similar to hypc	
JCVI_14581	2.208	no original description	
JCVI_40058	2.208	weakly similar to (192)AT5G20710 Symbols: BGAL7 BGAL7 (beta-galactosidase 7); beta-galactosidase chr5:7010538-7013996 FOR'	
JCVI_20780	2.206	weakly similar to (169)AT2G31990 Symbols: exostosin family protein chr2:13618577-13620628 REVERSEvery weakly similar to (9	
EE533169	2.206	no similarity	
EX039688	2.206	very weakly similar to (95.9)AT4G38960 Symbols: zinc finger (B-box type) family protein chr4:18162294-18163039 FORWARD [21	1.538
JCVI_24307	2.203	moderately similar to (256)AT5G60530 Symbols: late embryogenesis abundant protein-related / LEA protein-related chr5:24351423-2	
JCVI_5154	2.203	very weakly similar to (82.8)AT5G64310 Symbols: ATAGP1, AGP1 AGP1 (ARABINOGLACTAN-PROTEIN 1) chr5:25739244-25	2.287
JCVI_20847	2.202	moderately similar to (215)AT3G12560 Symbols: ATTB2P, TRFL9 TRFL9 (TRF-LIKE 9); DNA binding chr3:3982279-3984855 REV	
BG543935	2.202	weakly similar to (144)AT1G61340 Symbols: F-box family protein chr1:22632191-22633406 FORWARD [8791]	2.245
CD835918	2.201	weakly similar to (196)AT3G08040 Symbols: MAN1, FRD3 FRD3 (FERRIC REDUCTASE DEFECTIVE 3); antiporter chr3:2566595	
RC_ES960556	2.198	no similarity	
JCVI_40054	2.197	no original description	
EX086329	2.196	very weakly similar to (82.8)AT2G40085 Symbols: unknown protein chr2:16743612-16743970 REVERSE [21823] 1 611 623	
JCVI_20213	2.195	no original description	
JCVI_20305	2.194	moderately similar to (305)AT3G23210 Symbols: basic helix-loop-helix (bHLH) family protein chr3:8283262-8284922 REVERSE nc	
EE455190	2.194	weakly similar to (118)AT4G15430 Symbols: similar to early-responsive to dehydration protein-related / ERD protein-related [Arabido	
AM391952	2.194	moderately similar to (333)AT1G07520 Symbols: scarecrow transcription factor family protein chr1:2309715-2311802 REVERSEEver	
EE504270	2.192	no similarity	
JCVI_41123	2.192	moderately similar to (445)AT1G55920 Symbols: SAT5, SAT1, AtSerat2;1 AtSerat2;1 (SERINE ACETYLTRANSFERASE 1) chr1:2(	
EE549186	2.191	no similarity	
JCVI_19123	2.191	weakly similar to (113)AT3G10930 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G05300.1) chr3:3420471	2.140
EE560233	2.190	no similarity	
JCVI_26483	2.189	weakly similar to (172)AT1G78600 Symbols: zinc finger (B-box type) family protein chr1:29572263-29573555 FORWARD no origir	1.580
H74879	2.188	no similarity	
RC_EX015383	2.187	no similarity	
ES906388	2.186	moderately similar to (336)AT5G66210 Symbols: CPK28 CPK28 (calcium-dependent protein kinase 28) chr5:26474371-26476660 RE	
EV048397	2.185	weakly similar to (127)AT4G20880 Symbols: ethylene-responsive nuclear protein / ethylene-regulated nuclear protein (ERT2) chr4:11	
JCVI_16093	2.185	moderately similar to (450)AT1G30370 Symbols: lipase class 3 family protein chr1:10719151-10720740 REVERSE no original descr	
JCVI_37273	2.184	moderately similar to (273)AT1G70740 Symbols: protein kinase family protein chr1:26677509-26679349 REVERSE no original desc	
JCVI_19289	2.184	weakly similar to (181)AT1G44414 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO61874.1) chr1:16850221-1	
AM385180	2.184	no similarity	
JCVI_20441	2.182	highly similar to (737)AT3G28740 Symbols: CYP81D1 cytochrome P450 family protein chr3:10790001-10791789 REVERSEmodera	2.224
EV027089	2.179	weakly similar to (187)AT4G09820 Symbols: TT8 TT8 (TRANSPARENT TESTA 8); DNA binding / transcription factor chr4:618206	
JCVI_30628	2.178	weakly similar to (194)AT1G42550 Symbols: PMI1 PMI1 (PLASTID MOVEMENT IMPAIRED1) chr1:15979976-15982174 FORW/	1.304
JCVI_370	2.178	no original description	2.261
EX064352	2.176	no similarity	
EV033740	2.174	no similarity	
EX094943	2.173	very weakly similar to (81.6)AT1G19770 Symbols: ATPUP14 ATPUP14 (Arabidopsis thaliana purine permease 14); purine transmembr	
EX077836	2.172	moderately similar to (401)AT2G38010 Symbols: ceramidase family protein chr2:15913940-15916945 FORWARD [21818]	
DE443822	2.171	weakly similar to (129)AT1G61960 Symbols: mitochondrial transcription termination factor-related / mTERF-related chr1:22905904-	
YY022380	2.170	no similarity	
JCVI_6399	2.169	moderately similar to (269)AT1G19770 Symbols: ATPUP14 ATPUP14 (Arabidopsis thaliana purine permease 14); purine transmembra	

JCVI_18534	2.168	weakly similar to (178)AT2G32530 Symbols: CSLB03, ATCSLB3, ATCSLB03 ATCSLB03 (Cellulose synthase-like B3); transferase/ t	1.973
JCVI_17506	2.168	highly similar to (699)AT4G18010 Symbols: IP5PII IP5PII (INOSITOL POLYPHOSPHATE 5-PHOSPHATASE II); inositol-polyphosp	
JCVI_784	2.168	highly similar to (506)AT1G13470 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G13520.1); similar to unna	
EV192533	2.168	weakly similar to (123)AT3G06670 Symbols: binding chr3:2105914-2113142 REVERSE [21489] 1 742 757	
EX068443	2.167	weakly similar to (160)AT1G22630 Symbols: heat shock protein binding / unfolded protein binding chr1:8003476-8004156 FORWAF	
JCVI_6434	2.167	weakly similar to (187)AT2G20825 Symbols: ULT2 ULT2 (ULTRAPETALA 2); DNA binding chr2:8972926-8973876 REVERSE no	
ES986055	2.166	no similarity	2.674
RC_EE557313	2.165	no similarity	
JCVI_31600	2.164	moderately similar to (213)AT2G41290 Symbols: strictosidine synthase family protein chr2:17217677-17219982 REVERSE no origin	2.180
H07702	2.164	no similarity	
EX027590	2.163	no similarity	1.513
EX125453	2.162	weakly similar to (187)AT3G61190 Symbols: BAP1 BAP1 (BON ASSOCIATION PROTEIN 1) chr3:22661812-22662390 REVERSE	
JCVI_22687	2.161	no original description	
ES901454	2.159	no similarity	
EV123347	2.159	weakly similar to (120)AT4G30780 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G24100.1); similar to unna	
ES944059	2.158	no similarity	
JCVI_19049	2.158	no original description	2.441
JCVI_26486	2.157	moderately similar to (313)AT1G26800 Symbols: zinc finger (C3HC4-type RING finger) family protein chr1:9285563-9286177 REV	
JCVI_33539	2.156	weakly similar to (119)AT4G10300 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G04300.1); similar to unkr	2.178
JCVI_22350	2.155	moderately similar to (327)AT5G12900 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G12330.1); similar to i	
JCVI_5957	2.154	weakly similar to (101)AT3G59400 Symbols: GUN4 GUN4 (Genomes uncoupled 4) chr3:21959858-21960655 REVERSE no original	2.197
JCVI_26589	2.152	moderately similar to (295)AT5G58660 Symbols: oxidoreductase, 2OG-Fe(II) oxygenase family protein chr5:23718735-23721028 FC	
EV148639	2.150	no similarity	
JCVI_8766	2.150	no original description	
JCVI_23299	2.150	moderately similar to (364)AT1G69540 Symbols: AGL94 AGL94; DNA binding / transcription factor chr1:26148969-26150822 REV	1.666
EV136519	2.148	no similarity	
JCVI_22381	2.144	very weakly similar to (95.1)AT1G71000 Symbols: DNAJ heat shock N-terminal domain-containing protein chr1:26772998-26773773	
JCVI_1991	2.142	moderately similar to (416)AT2G39650 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G14620.1); similar to i	
JCVI_5473	2.139	moderately similar to (231)AT5G51460 Symbols: ATTPPA ATTPPA (Arabidopsis thaliana trehalose-6-phosphate phosphatase); trehalc	2.227
EV218294	2.138	moderately similar to (322)AT4G37610 Symbols: BT5 BT5 (BTB and TAZ domain protein 5); protein binding / transcription regulator	3.609
ES981144	2.138	weakly similar to (125)AT3G52820 Symbols: ATPAP22, PAP22 ATPAP22/PAP22 (purple acid phosphatase 22); acid phosphatase/ pro	
EE466210	2.137	weakly similar to (181)AT4G25480 Symbols: CBF3, DREB1, DREB1A DREB1A (DEHYDRATION RESPONSE ELEMENT B1A); I	2.463
EV142318	2.137	no similarity	
CV544654	2.135	no similarity	
JCVI_14524	2.135	moderately similar to (243)AT3G11410 Symbols: ATPP2CA, AHG3 AHG3/ATPP2CA (ARABIDOPSIS THALIANA PROTEIN PHOS	
EE475848	2.133	very weakly similar to (91.7)AT2G22440 Symbols: similar to reverse transcriptase, putative / RNA-dependent DNA polymerase, putativ	
CD837184	2.131	weakly similar to (186)AT1G21150 Symbols: mitochondrial transcription termination factor family protein / mTERF family protein ch	
JCVI_15245	2.130	moderately similar to (244)AT1G26800 Symbols: zinc finger (C3HC4-type RING finger) family protein chr1:9285563-9286177 REV	
EE419793	2.129	weakly similar to (110)AT3G58690 Symbols: protein kinase family protein chr3:21720346-2172223 FORWARD [20149]	
JCVI_38510	2.129	very weakly similar to (83.2)AT1G59910 Symbols: formin homology 2 domain-containing protein / FH2 domain-containing protein ch	
AM061459	2.126	no similarity	2.153
JCVI_39207	2.125	moderately similar to (210)AT3G29130 Symbols: similar to unknown [Populus trichocarpa] (GB:ABK93868.1); contains domain PTHI	
EV091988	2.124	moderately similar to (360)AT2G32530 Symbols: CSLB03, ATCSLB3, ATCSLB03 ATCSLB03 (Cellulose synthase-like B3); transfera	
JCVI_10987	2.122	weakly similar to (173)AT4G21870 Symbols: 26.5 kDa class P-related heat shock protein (HSP26.5-P) chr4:11603768-11604297 REV	1.933
ES930133	2.121	very weakly similar to (100)AT4G20880 Symbols: ethylene-responsive nuclear protein / ethylene-regulated nuclear protein (ERT2) ch	
CV432094	2.118	no similarity	
EV110864	2.117	no similarity	
EE565545	2.116	very weakly similar to (84.7)AT5G44720 Symbols: molybdenum cofactor sulfurase family protein chr5:18060313-18062502 FORWA	
JCVI_27077	2.114	no original description	
CV546383	2.111	very weakly similar to (88.6)AT1G27730 Symbols: ZAT10, STZ STZ (SALT TOLERANCE ZINC FINGER); nucleic acid binding / tra	2.495
JCVI_13044	2.110	moderately similar to (288)AT2G28200 Symbols: nucleic acid binding / transcription factor/ zinc ion binding chr2:12031398-1203225	
JCVI_17264	2.110	moderately similar to (345)AT1G10010 Symbols: AAP8 AAP8 (amino acid permease 8); amino acid transmembrane transporter chr1:3	
EV049297	2.110	moderately similar to (320)AT3G55450 Symbols: protein kinase, putative chr3:20569106-20570940 FORWARDweakly similar to (1	1.498
JCVI_36422	2.109	no original description	
JCVI_18855	2.109	moderately similar to (383)AT3G21670 Symbols: nitrate transporter (NTP3) chr3:7626949-7628961 REVERSE no original descriptio	1.331
JCVI_20774	2.109	highly similar to (560)AT3G53230 Symbols: cell division cycle protein 48, putative / CDC48, putative chr3:19734394-19737467 FOF	
EE469173	2.107	weakly similar to (188)AT2G01870 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO21902.1) chr2:389845-39C	2.059
JCVI_26083	2.107	very weakly similar to (94.7)AT4G27310 Symbols: zinc finger (B-box type) family protein chr4:13675859-13676622 FORWARD no	2.570
JCVI_41701	2.106	no original description	
JCVI_10924	2.105	highly similar to (522)AT1G56600 Symbols: ATGOLS2 ATGOLS2 (ARABIDOPSIS THALIANA GALACTINOL SYNTHASE 2); tra	
EV008996	2.105	no similarity	
JCVI_7992	2.104	very weakly similar to (87.8)AT4G19390 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G13720.1); similar to	
JCVI_34217	2.104	weakly similar to (150)AT5G05900 Symbols: UDP-glucuronosyl/UDP-glucosyl transferase family protein chr5:1774514-1776382 FO	
EV215868	2.104	no similarity	
EV076981	2.103	no similarity	1.335
RC_JCVI_40485	2.102	no original description	
JCVI_38611	2.100	no original description	1.555
JCVI_8271	2.099	no original description	
JCVI_26710	2.097	moderately similar to (281)AT5G39670 Symbols: calcium-binding EF hand family protein chr5:15900498-15901112 FORWARD no	
JCVI_32367	2.097	no original description	
EE450080	2.097	weakly similar to (156)AT1G44100 Symbols: AAP5 AAP5 (amino acid permease 5); amino acid transmembrane transporter chr1:1676	
RC_EE522201	2.095	no similarity	
JCVI_11679	2.095	moderately similar to (352)AT1G73480 Symbols: hydrolase, alpha/beta fold family protein chr1:27632927-27636147 FORWARD no	
JCVI_14292	2.093	weakly similar to (117)AT4G11660 Symbols: HSF2B2, AT-HSF2B2 AT-HSF2B2 (Arabidopsis thaliana heat shock transcription facto	
EX120516	2.093	no similarity	
EH429196	2.093	moderately similar to (226)AT2G21860 Symbols: violaxanthin de-epoxidase-related chr2:9325413-9327070 REVERSE [20767]	
JCVI_16378	2.093	moderately similar to (248)AT1G14480 Symbols: protein binding chr1:4956399-4957883 FORWARD no original description	
EV136896	2.093	no similarity	
JCVI_34264	2.092	no original description	
JCVI_25211	2.092	weakly similar to (125)AT5G62770 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G27880.1); similar to hypc	
JCVI_40260	2.091	weakly similar to (151)AT4G12970 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO17947.1) chr4:7586241-75	
JCVI_14484	2.090	moderately similar to (266)AT4G30280 Symbols: ATXTH18, XTH18 ATXTH18/XTH18 (XYLOGLUCAN ENDOTRANSGLYCOSY	3.028
RC_EH424469	2.089	no similarity	

EE417055	2.086	no similarity	
EV143922	2.085	no similarity	
EE479654	2.085	no similarity	
JCVI_13766	2.085	moderately similar to (261)AT5G67300 Symbols: ATMYB1, ATMYB44, MYB1 ATMYB44/ATMYB1/MYB1 (MYB DOMAIN)	1.687
JCVI_30808	2.085	moderately similar to (324)AT2G16430 Symbols: PAP10, ATPAP10 ATPAP10/PAP10; acid phosphatase/ protein serine/threonine phosphatase	2.019
DY027899	2.083	no similarity	
JCVI_38636	2.083	no original description	1.497
ES907374	2.082	moderately similar to (375)AT4G01450 Symbols: nodulin MtN21 family protein chr4:608586-610127 FORWARD [21429]	
JCVI_39109	2.081	moderately similar to (201)AT5G23130 Symbols: peptidoglycan-binding LysM domain-containing protein chr5:7781478-7783336 FORWARD	1.452
ES906142	2.081	moderately similar to (228)AT5G06790 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G57950.1); similar to	
EX133779	2.081	weakly similar to (196)AT1G49405 Symbols: integral membrane protein, putative chr1:18288003-18288615 REVERSE [21833] 1 68;	
EV054296	2.080	weakly similar to (103)AT3G09740 Symbols: ATSP71, SYP71 SYP71 (SYNTAXIN OF PLANTS 71) chr3:2989620-2991359 FORWARD	
JCVI_10530	2.080	moderately similar to (308)AT1G21670 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G21680.1); similar to	2.177
JCVI_26872	2.078	moderately similar to (241)AT1G66160 Symbols: U-box domain-containing protein chr1:24640881-24642176 FORWARD no original description	2.128
JCVI_29680	2.078	moderately similar to (222)AT2G32530 Symbols: CSLB03, ATCSLB3, ATCSLB03 ATCSLB03 (Cellulose synthase-like B3); transferase	1.320
ES945473	2.078	very weakly similar to (85.9)AT4G29900 Symbols: ATACA10, ACA10 ACA10 (autoinhibited Ca ²⁺ -ATPase 10); calcium-transporting	
JCVI_20208	2.077	moderately similar to (211)AT1G15260 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G16070.1) chr1:5249	1.275
JCVI_28406	2.076	weakly similar to (186)AT5G05220 Symbols: similar to hypothetical protein [Vitis vinifera] (GB:CAN82940.1) chr5:1550274-155082	
JCVI_12923	2.076	very weakly similar to (80.9)AT3G23170 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G14450.1) chr3:826	
JCVI_19551	2.076	weakly similar to (191)AT1G44414 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO61874.1) chr1:16850221-1	
JCVI_10486	2.074	weakly similar to (169)AT4G10300 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G04300.1); similar to unknown	2.230
JCVI_19373	2.074	no original description	3.150
JCVI_37800	2.073	no original description	
ES919101	2.070	no similarity	
JCVI_11538	2.068	moderately similar to (224)AT4G20380 Symbols: LSD1 LSD1 (LESION SIMULATING DISEASE) chr4:11005023-11006449 FORWARD	
EV180758	2.067	weakly similar to (144)AT1G21890 Symbols: nodulin MtN21 family protein chr1:7682797-7685570 REVERSE [21487] 16 547 739	
EX100333	2.066	moderately similar to (360)AT1G07520 Symbols: scarecrow transcription factor family protein chr1:2309715-2311802 REVERSE weakly similar to	
JCVI_40192	2.066	weakly similar to (140)AT5G48990 Symbols: kelch repeat-containing F-box family protein chr5:19879566-19880684 FORWARD no original description	1.388
EV124296	2.065	no similarity	
JCVI_8448	2.065	moderately similar to (300)AT5G52420 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G23920.1); similar to	
JCVI_19719	2.063	moderately similar to (299)AT3G28740 Symbols: CYP81D1 cytochrome P450 family protein chr3:10790001-10791789 REVERSE weakly similar to	2.183
EV165943	2.062	weakly similar to (146)AT2G32020 Symbols: GCN5-related N-acetyltransferase (GNAT) family protein chr2:13638270-13638821 REVERSE	
EE501966	2.061	weakly similar to (117)AT5G56670 Symbols: 40S ribosomal protein S30 (RPS30C) chr5:22952639-22953207 REVERSE [20193] 35	
JCVI_19433	2.060	no original description	
EH429199	2.059	moderately similar to (304)AT2G21860 Symbols: violaxanthin de-epoxidase-related chr2:9325413-9327070 REVERSE [20767]	1.356
AM388297	2.058	weakly similar to (181)AT1G66500 Symbols: zinc finger (C2H2-type) family protein chr1:24814925-24816175 REVERSE [20118]	
EE490643	2.057	moderately similar to (225)AT5G05580 Symbols: SH1, FAD8 FAD8 (FATTY ACID DESATURASE 8); omega-3 fatty acid desaturase	2.461
JCVI_16910	2.055	no original description	
EV197013	2.055	moderately similar to (204)AT4G19450 Symbols: nodulin-related chr4:10606549-10609229 FORWARD [21490]	1.634
EV055334	2.054	no similarity	
BQ792023	2.053	moderately similar to (214)AT3G28340 Symbols: GATL10 GATL10 (Galacturonosyltransferase-like 10); polygalacturonate 4-alpha-galacturonidase	2.534
EX064182	2.053	very weakly similar to (83.2)AT4G13670 Symbols: PTAC5 PTAC5 (PLASTID TRANSCRIPTIONALLY ACTIVE5); heat shock protein	1.754
JCVI_33411	2.052	moderately similar to (379)AT2G03550 Symbols: hydrolase chr2:1077077-1078015 FORWARD weakly similar to (115)GID1_ORYZA SATIVA	
JCVI_23724	2.052	moderately similar to (402)AT1G30860 Symbols: protein binding / zinc ion binding chr1:10986677-10989227 REVERSE no original description	
JCVI_40415	2.052	moderately similar to (496)AT4G36870 Symbols: SAW1, BLH2 BLH2 (BEL1-LIKE HOMEODOMAIN 2, SAWTOOTH 1); DNA binding	
JCVI_18054	2.052	weakly similar to (190)AT4G23570 Symbols: SGT1A SGT1A (Suppressor of G2 (Two) 1A) chr4:12300025-12302503 FORWARD no original description	
JCVI_14672	2.049	no original description	
ES994226	2.049	weakly similar to (131)AT2G01180 Symbols: PAP1, LPP1, ATLPP1, ATPAP1 ATPAP1 (PHOSPHATIDIC ACID PHOSPHATASE 1)	1.520
EE409683	2.048	no similarity	
JCVI_29302	2.048	moderately similar to (219)AT1G04380 Symbols: 2-oxoglutarate-dependent dioxygenase, putative chr1:1177141-1178383 REVERSE	
EV036222	2.047	weakly similar to (145)AT4G37480 Symbols: DNAJ heat shock N-terminal domain-containing protein chr4:17619255-17621396 FORWARD	
JCVI_15889	2.047	moderately similar to (306)AT1G65690 Symbols: harpin-induced protein-related / HIN1-related / harpin-responsive protein-related chr1:10986677-10989227 REVERSE	
EV115465	2.046	moderately similar to (233)AT1G30370 Symbols: lipase class 3 family protein chr1:10719151-10720740 REVERSE [21479]	
JCVI_26544	2.045	moderately similar to (343)AT1G74650 Symbols: AtY13, AtMYB31 AtMYB31/AtY13 (myb domain protein 31); DNA binding / transcription factor	
EX078964	2.045	no similarity	
DY019163	2.043	moderately similar to (270)AT1G14480 Symbols: protein binding chr1:4956399-4957883 FORWARD [18966]	
JCVI_36695	2.041	moderately similar to (234)AT5G66310 Symbols: kinesin motor family protein chr5:26503012-26507530 REVERSE no original description	
DN962793	2.040	weakly similar to (128)AT2G40000 Symbols: HSPRO2, ATHSPRO2 similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G57950.1)	
JCVI_20460	2.040	very weakly similar to (96.3)AT3G57450 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO40798.1) chr3:21273	
EE457288	2.039	no similarity	
EX036296	2.039	very weakly similar to (95.5)AT4G13690 Symbols: similar to hypothetical protein MtrDRAFT_AC161864g11v2 [Medicago truncatula]	1.669
EV135969	2.038	weakly similar to (191)AT1G18330 Symbols: EPR1 EPR1 (EARLY-PHYTOCHROME-RESPONSIVE1) chr1:6306189-6307711 REVERSE	1.832
JCVI_41843	2.036	no original description	
EE540603	2.036	weakly similar to (137)AT4G37320 Symbols: CYP81D5 CYP81D5 (cytochrome P450, family 81, subfamily D, polypeptide 5); oxygen	
JCVI_27566	2.035	moderately similar to (390)AT3G28960 Symbols: amino acid transporter family protein chr3:10985482-10987004 REVERSE no original description	
JCVI_30619	2.035	no original description	
JCVI_4805	2.035	moderately similar to (216)AT1G71000 Symbols: DNAJ heat shock N-terminal domain-containing protein chr1:26772998-26773773 FORWARD	
JCVI_32919	2.035	no original description	
ES962556	2.033	weakly similar to (104)AT2G20562 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G31090.1); similar to unnamed	
AM394555	2.031	weakly similar to (143)AT2G31800 Symbols: ankyrin protein kinase, putative chr2:13527682-13530723 REVERSE [20346]	
JCVI_36638	2.030	no original description	
JCVI_7390	2.029	weakly similar to (194)AT5G24120 Symbols: SIG5, SIGE SIGE (RNA polymerase sigma subunit E); DNA binding / DNA-directed RNA polymerase	
RC_ES948251	2.028	no similarity	
JCVI_34303	2.027	weakly similar to (103)AT5G48820 Symbols: KRP3, ICK6 ICK6/KRP3 (KIP-RELATED PROTEIN 3); cyclin binding / cyclin-dependent kinase	
JCVI_14969	2.027	highly similar to (853)AT3G61880 Symbols: CYP78A9 CYP78A9 (CYTOCHROME P450 78A9); oxygen binding chr3:22917089-22917100 FORWARD	1.584
RC_EV010845	2.026	no similarity	
JCVI_11608	2.026	moderately similar to (347)AT5G43730 Symbols: disease resistance protein (CC-NBS-LRR class), putative chr5:17577494-17580040	
JCVI_3621	2.025	highly similar to (593)AT4G26530 Symbols: fructose-bisphosphate aldolase, putative chr4:13391573-13392944 FORWARD highly similar to	
JCVI_28980	2.025	weakly similar to (168)AT2G40080 Symbols: ELF4 ELF4 (EARLY FLOWERING 4) chr2:16741623-16741958 REVERSE no original description	
ES938920	2.023	no similarity	
EV041837	2.022	weakly similar to (144)AT5G17400 Symbols: ER-ANT1 ADP, ATP carrier protein, mitochondrial, putative / ADP/ATP translocase, putative	
EV194156	2.022	very weakly similar to (100)AT2G46830 Symbols: CCA1 CCA1 (CIRCADIAN CLOCK ASSOCIATED 1); transcription factor chr2:1	
EV068998	2.022	very weakly similar to (92.4)AT1G70740 Symbols: protein kinase family protein chr1:26677509-26679349 REVERSE [21443]	

EV088843	2.021	weakly similar to (124)AT1G70780 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G23150.1); similar to unna	
EV107694	2.021	no similarity	1.890
JCVI_27977	2.019	moderately similar to (384)AT5G23130 Symbols: peptidoglycan-binding LysM domain-containing protein chr5:7781478-7783336 FO	1.466
JCVI_18453	2.019	moderately similar to (258)AT1G17620 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G11890.1); similar to i	2.112
AT002133	2.019	no similarity	1.654
JCVI_21467	2.018	weakly similar to (190)AT3G14075 Symbols: lipase class 3 family protein chr3:4663826-4666345 REVERSE no original description	1.560
EL588022	2.016	no similarity	2.173
JCVI_41245	2.016	no original description	
EV123214	2.016	no similarity	
EV226929	2.015	no similarity	
JCVI_16337	2.013	weakly similar to (136)AT1G74370 Symbols: zinc finger (C3HC4-type RING finger) family protein chr1:27961861-27962646 REVE	
EE567498	2.013	no similarity	1.305
EX062935	2.012	no similarity	1.732
EV100364	2.010	moderately similar to (285)AT3G15354 Symbols: SPA3 SPA3 (SPA1-RELATED 3); signal transducer chr3:5169334-5172487 REVE	
JCVI_18772	2.010	moderately similar to (499)AT5G11650 Symbols: hydrolase, alpha/beta fold family protein chr5:3745070-3746817 FORWARD no or	
JCVI_1443	2.009	moderately similar to (351)AT1G72030 Symbols: GCN5-related N-acetyltransferase (GNAT) family protein chr1:27114549-2711548	
EE508362	2.009	weakly similar to (102)AT2G39940 Symbols: COI1 COI1 (CORONATINE INSENSITIVE 1); ubiquitin-protein ligase chr2:16679926-	
CV544883	2.009	very weakly similar to (90.1)AT2G15480 Symbols: UGT73B5 UGT73B5 (UDP-GLUCOSYL TRANSFERASE 73B5); UDP-glycosyltra	
JCVI_804	2.007	weakly similar to (135)AT1G28370 Symbols: ERF11, ATERF11 ATERF11/ERF11 (ERF domain protein 11); DNA binding / transcript	
EE546123	2.005	very weakly similar to (93.2)AT3G45640 Symbols: MPK3, ATMPK3 ATMPK3 (MITOGEN-ACTIVATED PROTEIN KINASE 3); MA	
AM391473	2.003	weakly similar to (103)AT1G25400 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G68440.1); similar to unna	
EV205399	2.003	no similarity	
JCVI_28482	2.002	moderately similar to (433)AT1G49780 Symbols: U-box domain-containing protein chr1:18432692-18433957 REVERSE no original	
EV121574	2.001	very weakly similar to (100)AT2G26530 Symbols: AR781 AR781 chr2:11290114-11291067 REVERSE [21479]	1.847
JCVI_25449	2.000	moderately similar to (374)AT2G39920 Symbols: acid phosphatase class B family protein chr2:16670279-16671383 REVERSE no or	
JCVI_23523	2.000	moderately similar to (229)AT3G24190 Symbols: ABC1 family protein chr3:8743326-8747710 FORWARD no original description	
EE472897	1.998	weakly similar to (102)AT2G37460 Symbols: nodulin MtN21 family protein chr2:15733745-15736088 REVERSE [20163]	
JCVI_27098	1.996	no original description	
JCVI_14196	1.995	weakly similar to (112)AT2G17300 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G35320.1) chr2:7529547-	2.112
ES931762	1.993	moderately similar to (283)AT3G04890 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G46100.1); similar to i	1.829
EV177438	1.991	weakly similar to (132)AT4G15800 Symbols: RALFL33 RALFL33 (RALF-LIKE 33) chr4:8984923-8985273 FORWARD [21487] 1 1	1.978
AT000573	1.991	very weakly similar to (91.3)AT1G62300 Symbols: WRKY6 WRKY6 (WRKY DNA-binding protein 6); transcription factor chr1:2302	
JCVI_35371	1.989	moderately similar to (274)AT1G69900 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G27100.1); similar to l	
JCVI_2940	1.989	moderately similar to (251)AT1G01250 Symbols: AP2 domain-containing transcription factor, putative chr1:104731-105309 REVER	
JCVI_25076	1.988	weakly similar to (105)AT1G69490 Symbols: ANAC029, ATNAP, NAP NAP (NAC-LIKE, ACTIVATED BY AP3/PI); transcription fa	
ES945435	1.987	weakly similar to (160)AT1G44100 Symbols: AAP5 AAP5 (amino acid permease 5); amino acid transmembrane transporter chr1:1676	
EV163061	1.987	weakly similar to (118)AT5G15770 Symbols: ATGNA1 ATGNA1 (ARABIDOPSIS THALIANA GLUCOSE-6-PHOSPHATE ACETY	
JCVI_2292	1.987	no original description	
AM388881	1.987	moderately similar to (246)AT1G14780 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G24290.2); similar to i	
JCVI_34173	1.986	moderately similar to (278)AT1G73480 Symbols: hydrolase, alpha/beta fold family protein chr1:27632927-27636147 FORWARD no	
JCVI_1247	1.986	weakly similar to (126)AT4G10340 Symbols: LHCB5 LHCB5 (LIGHT HARVESTING COMPLEX OF PHOTOSYSTEM II 5); chloro	2.003
JCVI_13314	1.986	highly similar to (554)AT4G37610 Symbols: BT5 BT5 (BTB and TAZ domain protein 5); protein binding / transcription regulator chr	3.479
AM056987	1.984	no similarity	
JCVI_6146	1.983	moderately similar to (319)AT4G23990 Symbols: CSLG3, ATCSLG3 ATCSLG3 (Cellulose synthase-like G3); transferase/ transferase,	2.153
JCVI_30499	1.983	moderately similar to (366)AT2G17040 Symbols: ANAC036 ANAC036 (Arabidopsis NAC domain containing protein 36); transcrip	
DY026607	1.981	weakly similar to (190)AT3G08760 Symbols: ATSIK ATSIK; kinase chr3:2658135-2659990 REVERSE [18978]	
JCVI_38471	1.981	moderately similar to (263)AT3G05410 Symbols: similar to hypothetical protein Osl_004967 [Oryza sativa (indica cultivar-group)] (Gl	1.611
EX105012	1.981	moderately similar to (297)AT3G05410 Symbols: similar to hypothetical protein Osl_004967 [Oryza sativa (indica cultivar-group)] (Gl	1.662
JCVI_11039	1.980	moderately similar to (263)AT5G17230 Symbols: PSY PSY (PHYTOENE SYNTHASE) chr5:5659841-5662089 REVERSEweakly sir	1.361
JCVI_28230	1.979	weakly similar to (134)AT2G47440 Symbols: DNAJ heat shock N-terminal domain-containing protein chr2:19476982-19478730 FOR	
JCVI_20526	1.979	weakly similar to (149)AT5G62200 Symbols: embryo-specific protein-related chr5:25001689-25002900 REVERSE no original descri	2.173
JCVI_22168	1.977	weakly similar to (101)AT1G67195 Symbols: MIR414 MIR414 chr1:25141041-25141307 REVERSE no original description	1.836
JCVI_19667	1.976	very weakly similar to (88.2)AT2G03830 Symbols: unknown protein chr2:1171223-1172144 FORWARD no original description	1.911
JCVI_8338	1.976	no original description	1.583
JCVI_4089	1.976	weakly similar to (120)AT3G27210 Symbols: Identical to Uncharacterized protein At3g27210 (Y-2) [Arabidopsis Thaliana] (GB:Q9LK	
EX114202	1.976	moderately similar to (342)AT5G01540 Symbols: lectin protein kinase, putative chr5:211284-213332 REVERSEweakly similar to (1	
JCVI_22128	1.975	moderately similar to (383)AT4G35190 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G37210.1); similar to i	
EV191421	1.974	weakly similar to (129)AT1G51480 Symbols: disease resistance protein (CC-NBS-LRR class), putative chr1:19094515-19097974 RE	
ES969031	1.973	no similarity	
EV076037	1.973	no similarity	
EV105899	1.973	no similarity	
JCVI_39178	1.970	moderately similar to (330)AT1G10460 Symbols: GLP7 GLP7 (GERMIN-LIKE PROTEIN 7); manganese ion binding / metal ion bindi	
ES957548	1.969	no similarity	1.231
CD831313	1.969	weakly similar to (175)AT3G52740 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G44450.1); similar to unna	2.105
EV108697	1.968	no similarity	
JCVI_18991	1.968	weakly similar to (101)AT1G67195 Symbols: MIR414 MIR414 chr1:25141041-25141307 REVERSE no original description	1.936
JCVI_2215	1.968	highly similar to (663)AT2G39800 Symbols: ATP5CS, P5CS1 P5CS1 (DELTA1-PYRROLINE-5-CARBOXYLATE SYNTHASE 1) c	1.485
EV153292	1.968	moderately similar to (271)AT2G42890 Symbols: AML2 AML2 chr2:17857709-17861282 FORWARD [21484] 61 1033 1033	
JCVI_20788	1.967	no original description	
JCVI_20267	1.967	weakly similar to (114)AT3G14395 Symbols: unknown protein chr3:4811051-4811278 FORWARD no original description	
EV185924	1.967	moderately similar to (343)AT1G27480 Symbols: lecithin:cholesterol acyltransferase family protein / LACT family protein chr1:9544	1.426
EE567412	1.967	no similarity	
EE561149	1.967	no similarity	
JCVI_36644	1.967	highly similar to (538)AT3G14850 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G29050.1); similar to unna	
JCVI_33485	1.967	moderately similar to (258)AT1G26750 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO68449.1); similar to hy	
EV141196	1.966	moderately similar to (271)AT3G14950 Symbols: TTL2 TTL2 (TETRATRICOPETIDE-REPEAT THIOREDOXIN-LIKE 2); binding	
JCVI_17343	1.966	moderately similar to (275)AT1G60190 Symbols: armadillo/beta-catenin repeat family protein / U-box domain-containing protein chr	
ES979962	1.965	no similarity	
JCVI_16357	1.964	no original description	
JCVI_40181	1.963	weakly similar to (171)AT5G42610 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G23790.1); similar to hypc	
EV199111	1.961	moderately similar to (329)AT5G59580 Symbols: UDP-glucuronosyl/UDP-glucosyl transferase family protein chr5:24023465-240249	1.682
EE531069	1.961	weakly similar to (163)AT2G18460 Symbols: LCV3 LCV3 (LIKE COV 3) chr2:8008720-8009936 FORWARD [20175]	
ES949482	1.960	no similarity	

JCVI_21975	1.960	no original description	2.114
JCVI_33709	1.959	moderately similar to (229)AT2G29750 Symbols: UDP-glucuronosyl/UDP-glucosyl transferase family protein chr2:12716979-127184	1.856
EE496340	1.959	no similarity	
JCVI_10897	1.959	highly similar to (539)AT5G46800 Symbols: BOU BOU (A BOUT DE SOUFFLE); binding chr5:19006006-19007037 REVERSE	very
JCVI_5926	1.958	moderately similar to (426)AT2G41290 Symbols: strictosidine synthase family protein chr2:17217677-17219982 REVERSE	weakly si 2.276
EE405584	1.957	weakly similar to (115)AT5G44310 Symbols: late embryogenesis abundant domain-containing protein / LEA domain-containing protei	
ES955034	1.955	weakly similar to (187)AT4G28703 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G04300.1); similar to unnn	1.415
EX133918	1.954	no similarity	
JCVI_263	1.954	moderately similar to (460)AT5G58770 Symbols: dehydrololichyl diphosphate synthase, putative / DEDOL-PP synthase, putative chr	2.416
JCVI_3676	1.953	moderately similar to (274)AT3G22840 Symbols: ELIP, ELIP1 ELIP1 (EARLY LIGHT-INDUCABLE PROTEIN); chlorophyll binding	
RC_ES968318	1.953	no similarity	
JCVI_18986	1.952	weakly similar to (192)AT3G16570 Symbols: RALFL23 RALFL23 (RALF-LIKE 23) chr3:5644754-5645170 FORWARD	no original
EV189797	1.951	moderately similar to (219)AT5G37260 Symbols: RVE2, CIR1 CIR1/RVE2 (CIRCADIAN 1); DNA binding / transcription factor chr5	2.320
EL587715	1.951	moderately similar to (384)AT2G26150 Symbols: HSFA2, ATHSFA2 ATHSFA2 (Arabidopsis thaliana heat shock transcription factor /	
JCVI_37195	1.948	weakly similar to (131)AT5G18370 Symbols: disease resistance protein (TIR-NBS-LRR class), putative chr5:6085038-6088928 REVE	
EV189169	1.947	no similarity	
EV098127	1.946	no similarity	
JCVI_31983	1.946	no original description	1.483
JCVI_10332	1.945	weakly similar to (162)AT4G11390 Symbols: DC1 domain-containing protein chr4:6927887-6930373 FORWARD	no original descrip
EV201538	1.945	weakly similar to (186)AT1G01060 Symbols: LHY1, LHY LHY (LATE ELONGATED HYPOCOTYL) chr1:33992-37061 REVERSE	
DY026197	1.944	no similarity	
JCVI_8096	1.944	moderately similar to (488)AT1G48260 Symbols: SnRK3.21, CIPK17 CIPK17 (SNF1-RELATED PROTEIN KINASE 3.21); kinase cl	
EE473052	1.944	no similarity	
EV225634	1.943	weakly similar to (104)AT2G23810 Symbols: TET8 TET8 (TETRASPANIN8) chr2:10142939-10144432 REVERSE [21493] 69 740 7	1.454
ES907954	1.942	no similarity	
CV545835	1.942	no similarity	
JCVI_38191	1.942	no original description	
JCVI_30458	1.942	no original description	2.163
EV135810	1.940	weakly similar to (130)AT1G46768 Symbols: RAP2.1 RAP2.1 (related to AP2 1); DNA binding / transcription factor chr1:17268486-1	
CV544813	1.940	no similarity	
JCVI_8749	1.939	no original description	
EV038543	1.939	no similarity	
EX107105	1.939	very weakly similar to (98.2)AT4G01090 Symbols: extra-large G-protein-related chr4:470834-473248 REVERSE [21827]	
JCVI_26904	1.938	moderately similar to (301)AT3G61320 Symbols: Identical to UPF0187 protein At3g61320, chloroplast precursor [Arabidopsis Thalian	1.528
EX096733	1.937	no similarity	
EV050576	1.936	weakly similar to (140)AT3G13340 Symbols: WD-40 repeat family protein chr3:4332377-4334610 FORWARD [21442]	1.863
RC_EX042891	1.936	no similarity	
EV107773	1.936	no similarity	1.601
JCVI_9043	1.935	moderately similar to (314)AT3G27540 Symbols: glycosyl transferase family 17 protein chr3:10206726-10208125 FORWARD	no ori
EV112327	1.934	no similarity	1.782
JCVI_27151	1.934	weakly similar to (187)AT5G59350 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO21684.1) chr5:23958358-2	1.902
EE412990	1.933	weakly similar to (175)AT4G21060 Symbols: galactosyltransferase family protein chr4:11240741-11244871 FORWARD [20145] 1 5	
JCVI_16826	1.933	moderately similar to (256)AT5G52870 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G64080.1); similar to i	
EX051964	1.929	no similarity	
JCVI_41544	1.928	moderately similar to (452)AT5G61900 Symbols: CPN1, BON, BON1 BON1 (BONZAI1); calcium-dependent phospholipid binding c	
JCVI_23547	1.928	highly similar to (525)AT5G43630 Symbols: zinc knuckle (CCHC-type) family protein chr5:17544488-17547434 FORWARD	no orig
JCVI_28502	1.928	weakly similar to (125)AT1G80610 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G15800.1); similar to hycp	
AM058972	1.927	weakly similar to (111)AT5G66630 Symbols: LIM domain-containing protein chr5:26609946-26612917 FORWARD [17712]	
EX043867	1.927	moderately similar to (316)AT5G62430 Symbols: CDF1 CDF1 (CYCLING DOF FACTOR 1); DNA binding / protein binding / transcri	1.507
JCVI_39669	1.925	weakly similar to (112)AT1G22470 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G72240.1) chr1:7932897-	
EX050276	1.925	moderately similar to (341)AT5G41890 Symbols: GDSL-motif lipase/hydrolase family protein chr5:16781520-16784128 REVERSE	
EV218517	1.925	moderately similar to (248)AT4G37610 Symbols: BT5 BT5 (BTB and TAZ domain protein 5); protein binding / transcription regulator	3.308
JCVI_14498	1.925	moderately similar to (498)AT4G28740 Symbols: similar to LPA1 (LOW PSII ACCUMULATION1), binding [Arabidopsis thaliana] (T	
RC_EV086676	1.925	no similarity	
EE555777	1.924	weakly similar to (177)AT3G15990 Symbols: SULTR3;4 SULTR3;4; sulfate transmembrane transporter chr3:5427087-5430685 FORV	2.073
JCVI_36110	1.924	highly similar to (587)AT2G15880 Symbols: leucine-rich repeat family protein / extensin family protein chr2:6925121-6927401 REV	
JCVI_19785	1.922	moderately similar to (276)AT5G43630 Symbols: zinc knuckle (CCHC-type) family protein chr5:17544488-17547434 FORWARD	nc
EE462190	1.919	weakly similar to (176)AT1G75100 Symbols: JAC1 JAC1 (J-DOMAIN PROTEIN REQUIRED FOR CHLOROPLAST ACCUMULAT	
JCVI_17512	1.918	moderately similar to (328)AT3G20050 Symbols: ATTCP-1 ATTCP-1 (Arabidopsis thaliana T-complex protein 1 alpha subunit); ATP	
JCVI_22790	1.918	very weakly similar to (88.2)AT1G60060 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G53900.2); similar to	
EV199230	1.918	moderately similar to (248)AT4G18880 Symbols: HSFA4A, AT-HSFA4A AT-HSFA4A (Arabidopsis thaliana heat shock transcription f	
AM389200	1.918	very weakly similar to (85.5)AT3G50810 Symbols: integral membrane protein, putative chr3:18898595-18900849 REVERSE [20118]	
JCVI_18514	1.916	weakly similar to (131)AT3G57450 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO40798.1) chr3:21273005-2	1.762
JCVI_38889	1.916	moderately similar to (264)AT1G17620 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G11890.1); similar to i	2.118
JCVI_24738	1.916	highly similar to (965)AT5G08570 Symbols: pyruvate kinase, putative chr5:2778434-2780301 FORWARD	highly similar to (887)KP
EX110829	1.915	weakly similar to (180)AT4G04830 Symbols: methionine sulfoxide reductase domain-containing protein / SeIR domain-containing prot	
JCVI_15186	1.915	no original description	
CD833252	1.914	weakly similar to (115)AT4G30830 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G24140.1); similar to unnn	
EX016523	1.913	no similarity	
JCVI_35079	1.913	moderately similar to (278)AT3G54390 Symbols: transcription factor chr3:20148890-20149841 REVERSE	no original description
JCVI_30317	1.912	very weakly similar to (94.0)AT1G57820 Symbols: VIM1, ORTH2 ORTH2/VIM1 (VARIANT IN METHYLATION 1); DNA binding	
EV194015	1.910	very weakly similar to (88.6)AT1G69295 Symbols: beta-1,3-glucanase-related chr1:26054155-26055506 REVERSE [21489]	1.877
JCVI_7521	1.910	moderately similar to (261)AT4G01000 Symbols: ubiquitin family protein chr4:432186-433727 REVERSE	no original description
JCVI_34187	1.910	moderately similar to (357)AT2G34650 Symbols: ABR, PID PID (PINOID); kinase chr2:14597013-14598636 REVERSE	weakly simil
JCVI_207	1.909	moderately similar to (464)AT1G69490 Symbols: ANAC029, ATNAP, NAP NAP (NAC-LIKE, ACTIVATED BY AP3/PI); transcrip	
JCVI_23006	1.908	moderately similar to (271)AT5G19330 Symbols: armadillo/beta-catenin repeat family protein / BTB/POZ domain-containing protein	
JCVI_27007	1.907	moderately similar to (283)AT4G24660 Symbols: ATHB22, MEE68 ATHB22/MEE68 (ARABIDOPSIS THALIANA HOMEBOX PF	
ES966044	1.907	no similarity	
EE446682	1.907	no similarity	
EV085501	1.907	no similarity	
EV157418	1.906	moderately similar to (208)AT4G26850 Symbols: VTC2 VTC2 (VITAMIN C DEFECTIVE 2) chr4:13499268-13501151 REVERSE [	
JCVI_1705	1.904	moderately similar to (418)AT2G41250 Symbols: haloacid dehalogenase-like hydrolase family protein chr2:17207940-17209629 REV	1.371
JCVI_33161	1.903	weakly similar to (187)AT4G23530 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G11300.1); similar to hycp	

ES961855	1.903	no similarity	
JCVI_21019	1.902	weakly similar to (159)AT1G11650 Symbols: ATRBP45B ATRBP45B; RNA binding chr1:3914895-3917301 FORWARD no original	
JCVI_36439	1.900	no original description	
EE456342	1.900	no similarity	
AM391559	1.898	no similarity	1.699
JCVI_33439	1.898	no original description	1.765
JCVI_15615	1.897	highly similar to (546)AT4G15430 Symbols: similar to early-responsive to dehydration protein-related / ERD protein-related [Arabidop	1.694
JCVI_38650	1.897	very weakly similar to (84.7)AT5G62200 Symbols: embryo-specific protein-related chr5:25001689-25002900 REVERSE no original d	1.962
JCVI_34540	1.896	moderately similar to (244)AT4G28270 Symbols: zinc finger (C3HC4-type RING finger) family protein chr4:14007620-14008201 RE	
JCVI_12100	1.896	no original description	
AM388362	1.896	moderately similar to (263)AT1G13520 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G13480.1); similar to	
JCVI_24968	1.895	no original description	
ES950203	1.893	no similarity	1.851
JCVI_37535	1.892	weakly similar to (171)AT4G40020 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G16730.1); similar to hypc	
JCVI_11196	1.891	weakly similar to (189)AT5G56710 Symbols: 60S ribosomal protein L31 (RPL31C) chr5:22961229-22961993 REVERSEweakly simi	2.449
EV168475	1.891	weakly similar to (120)AT2G46810 Symbols: basic helix-loop-helix (bHLH) family protein chr2:19246763-19249442 FORWARD [2	1.886
JCVI_28339	1.890	weakly similar to (154)AT4G28025 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO66511.1); contains domain	2.040
EE514308	1.889	weakly similar to (194)AT5G09820 Symbols: plastid-lipid associated protein PAP / fibrillin family protein chr5:3056091-3057381 RE	
EV031987	1.888	moderately similar to (216)AT5G05190 Symbols: Identical to Uncharacterized protein At5g05190 (Y-1) [Arabidopsis Thaliana] (GB:Q	
JCVI_20591	1.888	weakly similar to (133)AT5G57340 Symbols: similar to hypothetical protein MtrDRAFT_AC155282g59v2 [Medicago truncatula] (GB	
JCVI_24343	1.887	moderately similar to (375)AT2G41835 Symbols: zinc finger (C2H2 type, AN1-like) family protein chr2:17465098-17466492 REVEI	
EV019429	1.884	no similarity	
JCVI_15416	1.883	very weakly similar to (92.0)AT4G16141 Symbols: similar to zinc finger (GATA type) family protein [Arabidopsis thaliana] (TAIR:AT	
JCVI_33509	1.882	moderately similar to (322)AT1G48600 Symbols: phosphoethanolamine N-methyltransferase 2, putative (NMT2) chr1:17970116-179	2.229
EX126783	1.880	highly similar to (503)AT1G63440 Symbols: HMA5 HMA5 (HEAVY METAL ATPASE 5); ATPase, coupled to transmembrane mover	
JCVI_42293	1.880	no original description	
JCVI_8143	1.878	moderately similar to (209)AT1G72640 Symbols: binding / catalytic chr1:27350071-27351809 REVERSE no original description	
ES968415	1.878	no similarity	
JCVI_22085	1.877	weakly similar to (162)AT1G62250 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO21221.1) chr1:22999280-2	
EV170934	1.877	no similarity	
JCVI_654	1.877	moderately similar to (357)AT5G64840 Symbols: ATGCN5 ATGCN5 (Arabidopsis thaliana general control non-repressible 5) chr5:25	
JCVI_3170	1.876	no original description	
JCVI_27216	1.874	moderately similar to (309)AT2G26150 Symbols: HSFA2, ATHSFA2 ATHSFA2 (Arabidopsis thaliana heat shock transcription factor /	
JCVI_23230	1.873	moderately similar to (253)AT1G50450 Symbols: binding / catalytic chr1:18691570-18694016 REVERSE no original description	1.963
JCVI_38623	1.873	highly similar to (556)AT3G55840 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G40000.1); similar to unna	2.674
JCVI_33804	1.873	weakly similar to (129)AT3G61890 Symbols: ATHB12, ATHB-12 ATHB-12 (ARABIDOPSIS THALIANA HOMEBOX PROTEIN 1	
AM387827	1.872	weakly similar to (198)AT1G07520 Symbols: scarecrow transcription factor family protein chr1:2309715-2311802 REVERSE [20118	
JCVI_3138	1.872	moderately similar to (391)AT4G26850 Symbols: VTC2 VTC2 (VITAMIN C DEFECTIVE 2) chr4:13499268-13501151 REVERSE n	
EE564016	1.871	no similarity	
EX121234	1.870	very weakly similar to (94.7)AT5G05190 Symbols: Identical to Uncharacterized protein At5g05190 (Y-1) [Arabidopsis Thaliana] (GB:Q	
JCVI_29126	1.870	highly similar to (521)AT1G78510 Symbols: SPS1 SPS1 (SOLANESYL DIPHOSPHATE SYNTHASE 1) chr1:29540303-29541935 R	
JCVI_33053	1.870	no original description	1.518
JCVI_28035	1.868	weakly similar to (103)AT1G64490 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G42060.1); contains doma	
JCVI_34203	1.868	moderately similar to (208)AT4G28025 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO66511.1); contains dom	1.956
JCVI_41016	1.868	moderately similar to (241)AT1G63440 Symbols: HMA5 HMA5 (HEAVY METAL ATPASE 5); ATPase, coupled to transmembrane n	
JCVI_22361	1.868	highly similar to (727)AT3G43600 Symbols: AAO2 AAO2 (ALDEHYDE OXIDASE 2) chr3:15523766-15528363 REVERSEhighly s	
DY028827	1.867	no similarity	
DN961498	1.866	weakly similar to (122)AT2G38170 Symbols: ATCAX1, RCI4, CAX1 CAX1 (CATION EXCHANGER 1); calcium:hydrogen antiporte	
JCVI_16081	1.865	moderately similar to (207)AT1G77920 Symbols: bZIP family transcription factor chr1:29303853-29305501 FORWARD no original	
EX093366	1.865	weakly similar to (149)AT1G07050 Symbols: CONSTANS-like protein-related chr1:2164326-2165132 REVERSE [21823]	2.502
EV064718	1.865	no similarity	
EV199927	1.863	weakly similar to (189)AT3G02380 Symbols: COL2 COL2 (CONSTANS-LIKE 2); transcription factor/ zinc ion binding chr3:487445-	2.496
JCVI_18620	1.862	no original description	1.654
EV140039	1.862	no similarity	
EE514837	1.862	no similarity	1.644
DY025326	1.861	moderately similar to (221)AT1G23030 Symbols: armadillo/beta-catenin repeat family protein / U-box domain-containing protein chr	
JCVI_2320	1.860	moderately similar to (370)AT1G07450 Symbols: tropinone reductase, putative / tropine dehydrogenase, putative chr1:2288035-2289;	
JCVI_17705	1.859	moderately similar to (474)AT4G12300 Symbols: CYP706A4 CYP706A4 (cytochrome P450, family 706, subfamily A, polypeptide 4);	
ES942971	1.858	moderately similar to (213)AT5G52050 Symbols: MATE efflux protein-related chr5:21156159-21157676 FORWARD [21392]	2.034
EV117032	1.858	no similarity	1.238
JCVI_443	1.857	no original description	
JCVI_20777	1.857	weakly similar to (180)AT3G28940 Symbols: avirulence-responsive protein, putative / avirulence induced gene (AIG) protein, putative	1.576
JCVI_30270	1.857	moderately similar to (365)AT3G52380 Symbols: PDE322, CP33 CP33 (PIGMENT DEFECTIVE 322); RNA binding chr3:19432597-	
EV203422	1.857	very weakly similar to (91.3)AT2G40400 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G56140.1); similar to	2.125
EE483891	1.856	no similarity	1.478
JCVI_9783	1.855	highly similar to (633)AT5G04360 Symbols: ATPU1, ATLDA ATLDA/ATPU1 (PULLULANASE 1); alpha-amylase/ limit dextrinase	
EE409598	1.855	no similarity	
JCVI_33907	1.854	moderately similar to (417)AT5G65090 Symbols: MRH3, BST1, DER4 BST1/DER4/MRH3 (BRISTLED1) chr5:26022063-26023882	
RC_AM394013	1.853	no similarity	
JCVI_23811	1.853	no original description	
JCVI_7188	1.853	weakly similar to (164)AT2G46830 Symbols: CCA1 CCA1 (CIRCADIAN CLOCK ASSOCIATED 1); transcription factor chr2:19253	
JCVI_37905	1.853	no original description	
JCVI_29069	1.852	no original description	
DY023666	1.852	moderately similar to (207)AT1G61250 Symbols: SC3 SC3 (SECRETORY CARRIER 3); transmembrane transporter chr1:22589700-	
EV027589	1.852	weakly similar to (157)AT5G62140 Symbols: similar to unknown [Populus trichocarpa] (GB:ABK94834.1) chr5:24971789-24972602	
JCVI_5451	1.851	moderately similar to (455)AT3G52060 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G22070.1); similar to	
JCVI_22078	1.850	weakly similar to (126)AT5G23210 Symbols: SCPL34 SCPL34 chr5:7811628-7814611 FORWARD no original description	2.571
JCVI_41488	1.850	no original description	
EV128075	1.850	no similarity	
EV122995	1.849	no similarity	
JCVI_27857	1.849	weakly similar to (162)AT1G33475 Symbols: Identical to Probable VAMP-like protein At1g33475 [Arabidopsis Thaliana] (GB:Q84W)	
JCVI_16414	1.849	moderately similar to (437)AT1G80840 Symbols: ATWRKY40, WRKY40 WRKY40 (WRKY DNA-binding protein 40); transcription	
DY011268	1.848	weakly similar to (152)AT5G58320 Symbols: kinase interacting protein-related chr5:23595320-23596757 FORWARD [18980]	

JCVI_2663	1.848	moderately similar to (339)AT2G23580 Symbols: hydrolase, alpha/beta fold family protein chr2:10040440-10041390 REVERSEweak	1.575
EV092858	1.847	weakly similar to (175)AT2G15580 Symbols: zinc finger (C3HC4-type RING finger) family protein chr2:6804769-6805897 FORWA	1.581
ES937867	1.847	no similarity	
EH427320	1.845	moderately similar to (362)AT3G61320 Symbols: Identical to UPF0187 protein At3g61320, chloroplast precursor [Arabidopsis Thalian	
CB686392	1.845	no similarity	
JCVI_30176	1.844	moderately similar to (246)AT5G17400 Symbols: ER-ANT1 ADP, ATP carrier protein, mitochondrial, putative / ADP/ATP translocase	1.566
JCVI_38419	1.843	moderately similar to (469)AT2G03550 Symbols: hydrolase chr2:1077077-1078015 FORWARDweakly similar to (125)GID1_ORY	
JCVI_5431	1.842	moderately similar to (449)AT4G37610 Symbols: BT5 BT5 (BTB and TAZ domain protein 5); protein binding / transcription regulator	3.306
ES930275	1.842	weakly similar to (139)AT2G47300 Symbols: ribonuclease P chr2:19426403-19429146 FORWARD [20185]	
H07560	1.842	no similarity	
DY008536	1.842	weakly similar to (114)AT4G25980 Symbols: cationic peroxidase, putative chr4:13189402-13191516 FORWARD [18972]	
AM386883	1.841	weakly similar to (191)AT1G76600 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G21010.1); similar to hypc	2.212
EV187751	1.840	no similarity	
DY005554	1.840	weakly similar to (118)AT3G17600 Symbols: IAA31 IAA31 (indoleacetic acid-induced protein 31); transcription factor chr3:6020287-	
EE412814	1.840	no similarity	
EV108800	1.840	no similarity	
JCVI_26215	1.839	moderately similar to (408)AT2G47180 Symbols: ATGOLS1 ATGOLS1 (ARABIDOPSIS THALIANA GALACTINOL SYNTHASE 1	
JCVI_35331	1.839	no original description	
JCVI_16334	1.838	no original description	
ES904772	1.838	moderately similar to (408)AT4G37260 Symbols: MYB73, AtMYB73 AtMYB73/MYB73 (myb domain protein 73); DNA binding / tra	
EE568029	1.837	no similarity	
JCVI_32436	1.837	moderately similar to (400)AT5G62430 Symbols: CDF1 CDF1 (CYCLING DOF FACTOR 1); DNA binding / protein binding / transcri	
EX043963	1.836	moderately similar to (341)AT4G04320 Symbols: malonyl-CoA decarboxylase family protein chr4:2113563-2116523 FORWARD [2]	
CN829082	1.836	weakly similar to (102)AT2G41835 Symbols: zinc finger (C2H2 type, AN1-like) family protein chr2:17465098-17466492 REVERSE	
JCVI_36159	1.835	moderately similar to (250)AT5G39420 Symbols: CDC2CAT CDC2CAT (ARABIDOPSIS THALIANA CDC2C); kinase chr5:157894	
EV221069	1.835	weakly similar to (195)AT3G05200 Symbols: ATL6 ATL6 (Arabidopsis T?xicos en Levadura 6); protein binding / zinc ion binding chi	
JCVI_20797	1.834	moderately similar to (310)AT5G06320 Symbols: NHL3 NHL3 (NDR1/HIN1-like 3) chr5:1931017-1931712 REVERSE no original de	
EV128361	1.834	no similarity	
JCVI_4708	1.832	moderately similar to (335)AT3G51430 Symbols: YLS2 YLS2 (yellow-leaf-specific gene 2); strictosidine synthase chr3:19097527-190	
EX063012	1.832	no similarity	
JCVI_330	1.831	highly similar to (524)AT1G59725 Symbols: DNAJ heat shock protein, putative chr1:21954403-21955875 FORWARDweakly similar	1.802
ES922465	1.829	no similarity	
EV012124	1.829	no similarity	
EV102958	1.828	no similarity	
EV106031	1.827	weakly similar to (124)AT5G65300 Symbols: unknown protein chr5:26112492-26112944 REVERSE [21478] 39 606 735	
EX119983	1.827	no similarity	
EV164211	1.827	no similarity	
JCVI_37850	1.826	moderately similar to (429)AT4G25160 Symbols: protein kinase family protein chr4:12903370-12906679 REVERSEweakly similar to	
EV191999	1.826	moderately similar to (344)AT1G53090 Symbols: SPA4 SPA4 (SPA1-RELATED 4); signal transducer chr1:19787416-19790358 FOR	1.244
JCVI_13799	1.825	moderately similar to (243)AT5G05280 Symbols: zinc finger (C3HC4-type RING finger) family protein chr5:1565510-1566040 REV	
CD812196	1.824	no similarity	
JCVI_18896	1.824	moderately similar to (242)AT3G12860 Symbols: nucleolar protein Nop56, putative chr3:4091685-4093928 FORWARD no original c	
JCVI_28223	1.824	no original description	
EV161880	1.824	weakly similar to (138)AT2G40010 Symbols: 60S acidic ribosomal protein P0 (RPP0A) chr2:16715656-16717526 REVERSEweakly	
JCVI_17687	1.823	moderately similar to (227)AT3G62410 Symbols: CP12, CP12-2 CP12-2 chr3:23101982-23102377 FORWARD no original descriptio	
JCVI_3095	1.822	weakly similar to (186)AT3G54810 Symbols: BME3-ZF, BME3 BME3/BME3-ZF (BLUE MICROPYLAR END3); transcription factor	2.170
JCVI_12784	1.822	weakly similar to (117)AT1G29690 Symbols: CAD1 CAD1 (CONSTITUTIVELY ACTIVATED CELL DEATH 1) chr1:10379296-10	
ES912977	1.820	moderately similar to (358)AT1G71530 Symbols: protein kinase family protein chr1:26943428-26945241 FORWARD [21430]	
JCVI_7443	1.819	moderately similar to (223)AT4G30270 Symbols: MERI-5, SEN4, MERI5B MERI5B (MERISTEM-5); hydrolase, acting on glycosyl b	
EV191697	1.819	weakly similar to (141)AT5G41100 Symbols: DNA binding chr5:16464657-16467914 FORWARD [21489]	
CN731264	1.815	moderately similar to (261)AT2G26150 Symbols: HSF A2, ATHSFA2 ATHSFA2 (Arabidopsis thaliana heat shock transcription factor /	
JCVI_4553	1.814	moderately similar to (319)AT4G15550 Symbols: IAGLU IAGLU (INDOLE-3-ACETATE BETA-D-GLUCOSYLTRANSFERASE); U	
DY015383	1.814	no similarity	1.475
JCVI_29181	1.813	weakly similar to (120)AT4G21740 Symbols: unknown protein chr4:11545938-11546408 FORWARD no original description	
JCVI_20427	1.813	very weakly similar to (87.4)AT1G33055 Symbols: unknown protein chr1:11972316-11972516 REVERSE no original description	
EL591285	1.811	moderately similar to (368)AT1G07540 Symbols: TRFL2 TRFL2 (TRF-LIKE 2); DNA binding chr1:2318430-2321045 REVERSE [2C	
EV218940	1.810	no similarity	
JCVI_41262	1.809	no original description	
JCVI_16958	1.809	weakly similar to (195)AT1G61667 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G54530.1); similar to unn	
EV106465	1.809	no similarity	
JCVI_22326	1.809	moderately similar to (347)AT1G44100 Symbols: AAP5 AAP5 (amino acid permease 5); amino acid transmembrane transporter chr1:1	
JCVI_39829	1.808	weakly similar to (140)AT3G15115 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G53180.1) chr3:5086226	
JCVI_28144	1.808	weakly similar to (185)AT1G52000 Symbols: jacalin lectin family protein chr1:19337021-19339369 REVERSE no original descriptio	
JCVI_5485	1.807	weakly similar to (172)AT3G16870 Symbols: zinc finger (GATA type) family protein chr3:5763758-5764582 REVERSE no original	
EE524164	1.807	weakly similar to (104)AT4G18880 Symbols: HSF A4A, AT-HSF A4A AT-HSF A4A (Arabidopsis thaliana heat shock transcription fact	
JCVI_30304	1.807	moderately similar to (350)AT5G06530 Symbols: ABC transporter family protein chr5:1990335-1994606 REVERSE no original desc	1.273
JCVI_41730	1.805	weakly similar to (130)AT5G48820 Symbols: KRP3, ICK6 ICK6/KRP3 (KIP-RELATED PROTEIN 3); cyclin binding / cyclin-depende	1.230
JCVI_9800	1.802	moderately similar to (216)AT5G48655 Symbols: zinc finger (C3HC4-type RING finger) family protein chr5:19748801-19749712 RE	
JCVI_3082	1.801	no original description	
RC_JCVI_10503	1.801	no original description	
JCVI_18360	1.801	no original description	
JCVI_481	1.800	moderately similar to (250)AT4G32340 Symbols: binding chr4:15612747-15614225 REVERSE no original description	
JCVI_3716	1.800	moderately similar to (259)AT2G27100 Symbols: SE SE (SERRATE); transcription factor chr2:11579665-11583435 FORWARD no o	
ES941361	1.800	very weakly similar to (89.0)AT3G22970 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G14620.1); similar to	
BQ791333	1.798	no similarity	2.173
JCVI_28525	1.796	moderately similar to (302)AT3G22850 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G43830.1); similar to l	
EV089082	1.795	moderately similar to (334)AT4G22790 Symbols: MATE efflux family protein chr4:11975164-11976639 REVERSE [21444]	
EV027628	1.795	moderately similar to (325)AT5G24430 Symbols: calcium-dependent protein kinase, putative / CDPK, putative chr5:8339393-834291	1.476
JCVI_39382	1.791	no original description	
JCVI_13401	1.790	moderately similar to (296)AT5G37740 Symbols: C2 domain-containing protein chr5:15009378-15010661 FORWARD no original de	
JCVI_39801	1.789	no original description	
JCVI_4356	1.788	moderately similar to (467)AT3G24190 Symbols: ABC1 family protein chr3:8743326-8747710 FORWARD no original description	
EV194073	1.787	weakly similar to (150)AT2G46830 Symbols: CCA1 CCA1 (CIRCADIAN CLOCK ASSOCIATED 1); transcription factor chr2:19253	1.332

EV123018	1.786	weakly similar to (132)AT2G03120 Symbols: signal peptide peptidase family protein chr2:937551-940080 FORWARD [21479]	
EV192295	1.785	no similarity	
RC_ES216592	1.784	no similarity	
CN725800	1.784	weakly similar to (126)AT1G16770 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO41707.1) chr1:5738128-57	
EE417839	1.783	weakly similar to (104)AT1G28360 Symbols: ERF12, ATERF12 ATERF12/ERF12 (ERF domain protein 12); DNA binding / transcript	
AM392202	1.783	weakly similar to (105)AT1G25275 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO43403.1) chr1:8860706-88	
EV121615	1.782	no similarity	1.917
JCVI_161	1.781	very weakly similar to (93.2)AT3G12630 Symbols: zinc finger (AN1-like) family protein chr3:4012714-4013196 FORWARD no origi	1.321
EE552556	1.781	no similarity	
JCVI_28271	1.780	weakly similar to (172)AT3G50800 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G66580.1); similar to unn	
EL590833	1.780	moderately similar to (224)AT1G04290 Symbols: thioesterase family protein chr1:1147720-1148351 REVERSE [20863]	
EX123200	1.780	moderately similar to (477)AT5G04360 Symbols: ATPU1, ATLDA ATLDA/ATPU1 (PULLULANASE 1); alpha-amylase/ limit dextrin	
EV216677	1.780	weakly similar to (172)AT1G22770 Symbols: FB, GI GI (GIGANTEA); binding chr1:8062387-8067436 FORWARDweakly similar to	
CD817929	1.778	very weakly similar to (98.2)AT1G67195 Symbols: MIR414 MIR414 chr1:25141041-25141307 REVERSE [13978]	
JCVI_30050	1.778	moderately similar to (408)AT3G46130 Symbols: AtMYB48, MYB111 MYB111 (myb domain protein 111) chr3:16956450-16957361	
EV009199	1.778	very weakly similar to (99.8)AT5G60580 Symbols: zinc finger (C3HC4-type RING finger) family protein chr5:24371524-24373932 F	
EV205511	1.777	moderately similar to (286)AT3G27170 Symbols: ATCLC-B, CLC-B CLC-B (chloride channel protein B); anion channel/ voltage-gate	1.612
JCVI_40243	1.777	moderately similar to (340)AT2G18940 Symbols: pentatricopeptide (PPR) repeat-containing protein chr2:8210955-8213423 REVERS	
CD813571	1.777	moderately similar to (274)AT3G62260 Symbols: protein phosphatase 2C, putative / PP2C, putative chr3:23049491-23051366 REVE	
JCVI_24149	1.777	moderately similar to (310)AT3G24120 Symbols: myb family transcription factor chr3:8705932-8708155 REVERSE no original desc	1.501
JCVI_39719	1.777	moderately similar to (369)AT1G17690 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO64063.1); contains Inte	
EX116646	1.775	moderately similar to (255)AT1G51940 Symbols: protein kinase family protein / peptidoglycan-binding LysM domain-containing prote	
EV148845	1.775	weakly similar to (177)AT4G27595 Symbols: protein transport protein-related chr4:13772825-13776524 REVERSE [21483]	
JCVI_25290	1.775	weakly similar to (169)AT1G77090 Symbols: thylakoid luminal 29.8 kDa protein chr1:28965470-28966769 REVERSE no original de	
JCVI_28307	1.775	weakly similar to (190)AT1G46768 Symbols: RAP2.1 RAP2.1 (related to AP2 1); DNA binding / transcription factor chr1:1726486-1	
EX124723	1.774	moderately similar to (270)AT1G14780 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G24290.2); similar to i	
JCVI_29738	1.774	weakly similar to (182)AT4G16141 Symbols: similar to zinc finger (GATA type) family protein [Arabidopsis thaliana] (TAIR:AT3G16	
JCVI_41470	1.774	moderately similar to (254)AT4G12680 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G40640.1); similar to i	
JCVI_9412	1.773	highly similar to (551)AT4G14130 Symbols: XTR7 XTR7 (XYLOGLUCAN ENDOTRANSGLYCOSYLASE 7); hydrolase, acting on i	
JCVI_5794	1.773	moderately similar to (230)AT2G34720 Symbols: CCAAT-binding transcription factor (CBF-B/NF-YA) family protein chr2:1465709	
JCVI_36434	1.773	weakly similar to (119)AT5G50920 Symbols: ATHSP93-V, HSP93-V, CLPC, DCA1, CLPC1 CLPC (HEAT SHOCK PROTEIN 93-V)	1.449
JCVI_13951	1.772	moderately similar to (306)AT5G44120 Symbols: ATCRA1, CRU1, CRA1 CRA1 (CRUCIFERINA); nutrient reservoir chr5:17773687	
JCVI_42056	1.770	weakly similar to (173)AT5G14880 Symbols: potassium transporter, putative chr5:4814247-4817670 FORWARDweakly similar to (	1.831
AT000965	1.769	no similarity	
EV096676	1.768	weakly similar to (104)AT1G69526 Symbols: UbiE/COQ5 methyltransferase family protein chr1:26135156-26136597 FORWARD [2	
EV015756	1.768	no similarity	
JCVI_20312	1.768	no original description	1.285
EV200593	1.768	weakly similar to (160)AT4G04850 Symbols: ATKEA3, KEA3 KEA3 (K+ efflux antiporter 3); potassium:hydrogen antiporter chr4:24	
AM394479	1.765	no similarity	1.571
EE554939	1.765	weakly similar to (165)AT3G04600 Symbols: tRNA synthetase class I (W and Y) family protein chr3:1243158-1245964 FORWARD	
JCVI_27935	1.764	moderately similar to (500)AT1G21450 Symbols: SCL1 SCL1 (SCARECROW-LIKE 1); transcription factor chr1:7509710-7511491 F	
CD816426	1.764	moderately similar to (236)AT3G14075 Symbols: lipase class 3 family protein chr3:4663826-4666345 REVERSE [13977]	
CX193407	1.763	no similarity	
JCVI_32636	1.761	highly similar to (589)AT5G62570 Symbols: calmodulin-binding protein chr5:25132214-25134193 FORWARD no original descriptio	
JCVI_15575	1.760	moderately similar to (369)AT1G22770 Symbols: FB, GI GI (GIGANTEA); binding chr1:8062387-8067436 FORWARDmoderately si	
JCVI_19462	1.760	weakly similar to (186)AT2G42530 Symbols: COR15B COR15B chr2:17716269-17716951 REVERSE no original description	
JCVI_35610	1.760	no original description	1.695
JCVI_36574	1.760	weakly similar to (177)AT1G50450 Symbols: binding / catalytic chr1:18691570-18694016 REVERSE no original description	1.721
JCVI_21676	1.759	highly similar to (676)AT5G19160 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G06080.2); similar to unnai	
AM059307	1.759	no similarity	
EE462092	1.759	no similarity	
CO750244	1.758	no similarity	
ES993037	1.756	very weakly similar to (94.7)AT1G33475 Symbols: Identical to Probable VAMP-like protein At1g33475 [Arabidopsis Thaliana] (GB:Q	
JCVI_24713	1.756	weakly similar to (155)AT5G61380 Symbols: APRR1, PRR1, TOC1 TOC1 (TIMING OF CAB EXPRESSION 1); transcription regulat	1.827
EV084988	1.754	no similarity	
EE403215	1.754	very weakly similar to (84.7)AT1G74370 Symbols: zinc finger (C3HC4-type RING finger) family protein chr1:27961861-27962646 R	
JCVI_29471	1.752	no original description	
JCVI_209	1.751	moderately similar to (366)AT3G56090 Symbols: ATFER3 ATFER3 (FERRITIN 3); ferric iron binding chr3:20825329-20826963 RE	
CO750168	1.751	no similarity	
JCVI_26327	1.751	no original description	
RC_ES966207	1.750	no similarity	1.573
DY021448	1.750	moderately similar to (416)AT5G14580 Symbols: polyribonucleotide nucleotidyltransferase, putative chr5:4697615-4703016 REVER	
ES969134	1.750	very weakly similar to (84.7)AT1G34010 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G22790.2); similar to	1.855
JCVI_18933	1.749	weakly similar to (112)AT4G36550 Symbols: binding / ubiquitin-protein ligase chr4:17245403-17247721 REVERSE no original desc	
EV011579	1.749	no similarity	
ES955408	1.749	no similarity	
EE470530	1.749	moderately similar to (326)AT1G32640 Symbols: RD22BP1, JAI1, JIN1, MYC2, ZBF1, ATMYC2 ATMYC2 (JASMONATE INSENS	
JCVI_37180	1.748	moderately similar to (224)AT1G75700 Symbols: HVA22G HVA22G (HVA22-LIKE PROTEIN G) chr1:28427737-28428592 FORW	
JCVI_21279	1.748	weakly similar to (128)AT1G73390 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G17940.1); similar to unn	
EV176836	1.748	no similarity	
JCVI_27161	1.746	moderately similar to (209)AT4G27660 Symbols: similar to RIN13 (RPM1 INTERACTING PROTEIN 13) [Arabidopsis thaliana] (TA	
JCVI_9	1.746	moderately similar to (411)AT2G31380 Symbols: STH STH (salt tolerance homologue); transcription factor/ zinc ion binding chr2:133	
JCVI_34904	1.746	weakly similar to (153)AT2G32620 Symbols: CSLB02, ATCSLB2, ATCSLB02 ATCSLB02 (Cellulose synthase-like B2); transferase/ t	1.576
JCVI_18352	1.746	moderately similar to (422)AT5G66675 Symbols: Identical to UPF0496 protein At5g66675 [Arabidopsis Thaliana] (GB:Q8GW16); sin	
JCVI_27874	1.744	moderately similar to (204)AT1G76070 Symbols: Identical to Uncharacterized protein At1g76070 [Arabidopsis Thaliana] (GB:Q9SGS	1.487
EV031999	1.741	moderately similar to (354)AT5G01110 Symbols: pentatricopeptide (PPR) repeat-containing protein chr5:42113-44302 REVERSEwe	
JCVI_16079	1.740	highly similar to (651)AT5G64570 Symbols: ATBXL4, XYL4 XYL4 (beta-xylosidase 4); hydrolase, hydrolyzing O-glycosyl compound	1.621
EX022680	1.740	weakly similar to (157)AT5G46510 Symbols: disease resistance protein (TIR-NBS-LRR class), putative chr5:18877678-18882437 FO	
JCVI_31680	1.740	no original description	
JCVI_36229	1.740	highly similar to (524)AT4G31390 Symbols: ABC1 family protein chr4:15233132-15236770 FORWARD no original description	
JCVI_29537	1.740	very weakly similar to (87.0)AT4G35090 Symbols: CAT2 CAT2 (CATALASE 2); catalase chr4:16701110-16703220 REVERSEvery v	
EE441525	1.740	weakly similar to (142)AT1G18570 Symbols: AtMYB51, BW51A, BW51B, MYB51 MYB51 (MYB DOMAIN PROTEIN 51); DNA b	
EE479477	1.739	no similarity	2.103

JCVI_38469	1.739	no original description	
EV132933	1.736	no similarity	1.596
EV004763	1.736	no similarity	1.169
JCVI_24769	1.735	highly similar to (640)AT5G15950 Symbols: adenosylmethionine decarboxylase family protein chr5:5206709-5207797 FORWARD	
EV196161	1.734	moderately similar to (255)AT5G03555 Symbols: permease, cytosine/purines, uracil, thiamine, allantoin family protein chr5:898353-9	
JCVI_37170	1.734	moderately similar to (333)AT3G52080 Symbols: CHX28 CHX28 (cation/hydrogen exchanger 28); monovalent cation:proton antiporter	
JCVI_42417	1.734	no original description	
JCVI_41570	1.733	moderately similar to (233)AT1G79040 Symbols: PSBR PSBR (photosystem II subunit R) chr1:29740978-29741674 FORWARD	
JCVI_980	1.732	moderately similar to (273)AT4G26850 Symbols: VTC2 VTC2 (VITAMIN C DEFECTIVE 2) chr4:13499268-13501151 REVERSE	1.374
JCVI_15122	1.732	moderately similar to (212)AT3G12345 Symbols: similar to Os06g0484500 [Oryza sativa (japonica cultivar-group)] (GB:NP_00105761	1.804
JCVI_1201	1.731	moderately similar to (312)AT1G55210 Symbols: disease resistance response chr1:20601724-20602287 REVERSE no original descrip	2.099
EV094783	1.730	moderately similar to (317)AT5G59750 Symbols: riboflavin biosynthesis protein, putative chr5:24090623-24092637 FORWARD [21	2.056
JCVI_30695	1.729	no original description	
CD835898	1.729	no similarity	
JCVI_7717	1.728	moderately similar to (206)AT1G78995 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO41778.1) chr1:297203	1.842
JCVI_26720	1.728	moderately similar to (281)AT2G37970 Symbols: SOUL-1 SOUL-1; binding chr2:15898105-15898782 FORWARD no original descrip	
EV213654	1.727	no similarity	
JCVI_2083	1.726	moderately similar to (352)AT1G21460 Symbols: nodulin MtN3 family protein chr1:7512019-7513270 REVERSE no original descrip	2.354
EE553984	1.724	no similarity	2.437
JCVI_21128	1.724	no original description	3.025
JCVI_14346	1.723	moderately similar to (444)AT2G29630 Symbols: thiamine biosynthesis family protein / thiC family protein chr2:12674472-12676646	
JCVI_26965	1.722	highly similar to (851)AT2G41190 Symbols: amino acid transporter family protein chr2:17174639-17177223 REVERSE no original d	
EV109508	1.722	moderately similar to (306)AT2G37970 Symbols: SOUL-1 SOUL-1; binding chr2:15898105-15898782 FORWARD [21478]	
AM395389	1.721	no similarity	
EV091804	1.721	no similarity	
JCVI_29075	1.721	moderately similar to (268)AT5G08740 Symbols: NDC1 NDC1 (NAD(P)H DEHYDROGENASE C1); NADH dehydrogenase chr5:28	
JCVI_29628	1.721	moderately similar to (477)AT2G16365 Symbols: F-box family protein chr2:7082022-7086263 FORWARD no original description	2.626
JCVI_17269	1.720	moderately similar to (380)AT3G50240 Symbols: KICP-02 KICP-02; microtubule motor chr3:18634362-18639766 REVERSE no orig	
DT317711	1.720	moderately similar to (219)AT4G28270 Symbols: zinc finger (C3HC4-type RING finger) family protein chr4:14007620-14008201 RE	
JCVI_26583	1.720	moderately similar to (210)AT5G62200 Symbols: embryo-specific protein-related chr5:25001689-25002900 REVERSE no original de	1.819
JCVI_31554	1.720	very weakly similar to (92.4)AT3G27350 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G40700.1); similar to	1.921
EV193817	1.720	weakly similar to (101)AT5G12440 Symbols: zinc finger (CCCH-type) family protein chr5:4035892-4038311 REVERSE [21489] 39	
EV130420	1.719	no similarity	
JCVI_32590	1.718	moderately similar to (300)AT4G04450 Symbols: ATWRKY42, WRKY42 WRKY42 (WRKY DNA-binding protein 42); transcription	
EH419222	1.717	very weakly similar to (87.4)AT4G12300 Symbols: CYP706A4 CYP706A4 (cytochrome P450, family 706, subfamily A, polypeptide 4)	
EV076440	1.716	moderately similar to (289)AT2G41835 Symbols: zinc finger (C2H2 type, AN1-like) family protein chr2:17465098-17466492 REVEI	
EE564109	1.715	no similarity	1.452
AM394473	1.715	no similarity	
ES897894	1.714	weakly similar to (133)AT1G67370 Symbols: ASY1 ASY1 (ASYNAPTIC 1); DNA binding chr1:25243010-25247376 REVERSE [21	
ES935840	1.713	no similarity	
JCVI_35591	1.713	no original description	
EX134882	1.712	moderately similar to (266)AT1G27100 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G69900.1); similar to l	
JCVI_25817	1.711	no original description	
EX039908	1.711	moderately similar to (267)AT1G22770 Symbols: FB, GI GI (GIGANTEA); binding chr1:8062387-8067436 FORWARD	weakly simil
JCVI_37289	1.710	no original description	
JCVI_36476	1.710	highly similar to (525)AT1G78070 Symbols: WD-40 repeat family protein chr1:29360113-29363261 FORWARD no original descript	
JCVI_7459	1.708	weakly similar to (190)AT3G47650 Symbols: bundle-sheath defective protein 2 family / bsd2 family chr3:17580561-17581247 FORW	
JCVI_16417	1.708	moderately similar to (272)AT1G76500 Symbols: DNA-binding family protein chr1:28710426-28711334 FORWARD no original des	
EE477064	1.707	no similarity	
EE553905	1.707	moderately similar to (222)AT5G53080 Symbols: kinesin light chain-related chr5:21537850-21540384 FORWARD [20184] 16 488 5	
EV216760	1.707	no similarity	2.097
ES911257	1.705	weakly similar to (112)AT4G35090 Symbols: CAT2 CAT2 (CATALASE 2); catalase chr4:16701110-16703220 REVERSE	weakly sim
RC_ES965974	1.704	no similarity	
JCVI_927	1.704	moderately similar to (352)AT1G68410 Symbols: protein phosphatase 2C-related / PP2C-related chr1:25653925-25655918 REVERSI	
EX062158	1.704	weakly similar to (164)AT5G49220 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G01260.1); similar to unne	
JCVI_2263	1.704	weakly similar to (195)AT5G23750 Symbols: remorin family protein chr5:8010007-8011456 REVERSE	weakly similar to (141)REM
EV152128	1.703	weakly similar to (184)AT5G22020 Symbols: strictosidine synthase family protein chr5:7287881-7289360 REVERSE [21483]	
CN727916	1.703	weakly similar to (167)AT5G62680 Symbols: proton-dependent oligopeptide transport (POT) family protein chr5:25182656-25185044	
EX017231	1.703	weakly similar to (174)AT1G62720 Symbols: binding chr1:23231239-23232696 FORWARD [21809]	
EE566457	1.702	no similarity	
EV139849	1.702	moderately similar to (273)AT5G59750 Symbols: riboflavin biosynthesis protein, putative chr5:24090623-24092637 FORWARD [21	1.700
EE569137	1.700	no similarity	
JCVI_7479	1.700	moderately similar to (261)AT1G21010 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G76600.1); similar to i	
EV197639	1.697	moderately similar to (289)AT4G30780 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G24100.1); similar to i	1.324
JCVI_41409	1.697	weakly similar to (166)AT1G68570 Symbols: proton-dependent oligopeptide transport (POT) family protein chr1:25750474-2575377	
ES947980	1.697	no similarity	2.184
JCVI_2748	1.697	moderately similar to (364)AT4G35090 Symbols: CAT2 CAT2 (CATALASE 2); catalase chr4:16701110-16703220 REVERSE	moder
ES923548	1.696	weakly similar to (130)AT1G34010 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G22790.2); similar to unkr	
JCVI_38973	1.696	weakly similar to (147)AT1G31460 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G23270.1); similar to hypc	
EX052463	1.696	very weakly similar to (84.7)AT4G19645 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G31300.2); similar to	
ES966048	1.695	no similarity	
JCVI_4522	1.694	moderately similar to (202)AT3G51780 Symbols: ATBAG4 ATBAG4 (ARABIDOPSIS THALIANA BCL-2-ASSOCIATED ATHANO	
EX093176	1.693	weakly similar to (166)AT1G34010 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G22790.2); similar to unkr	
ES953802	1.692	no similarity	1.792
EV198684	1.691	very weakly similar to (89.7)AT2G46830 Symbols: CCA1 CCA1 (CIRCADIAN CLOCK ASSOCIATED 1); transcription factor chr2:1	
JCVI_38759	1.691	weakly similar to (124)AT1G18570 Symbols: AtMYB51, BW51A, BW51B, MYB51 MYB51 (MYB DOMAIN PROTEIN 51); DNA b	
EE448817	1.690	very weakly similar to (94.4)AT5G66675 Symbols: Identical to UPF0496 protein At5g66675 [Arabidopsis Thaliana] (GB:Q8GW16); si	1.048
EX099101	1.690	no similarity	
JCVI_27010	1.689	moderately similar to (201)AT3G02850 Symbols: SKOR SKOR (stelar K+ outward rectifier); cyclic nucleotide binding / outward rectif	2.375
AM059909	1.688	weakly similar to (135)AT4G14560 Symbols: AXR5, IAA1 IAA1 (INDOLE-3-ACETIC ACID INDUCIBLE); transcription factor chr4	2.260
JCVI_25793	1.687	no original description	
EV165005	1.687	no similarity	
JCVI_36555	1.685	weakly similar to (181)AT1G12220 Symbols: RPS5 RPS5 (RESISTANT TO P. SYRINGAE 5) chr1:4145009-4147678 FORWARD no	

JCVI_23095	1.685	highly similar to (505)AT4G04020 Symbols: FIB FIB (FIBRILLIN); structural molecule chr4:1932159-1933544 FORWARDmoderate	
EV167312	1.684	moderately similar to (288)AT5G27410 Symbols: aminotransferase class IV family protein chr5:9678824-9682471 FORWARD [2148	
JCVI_14455	1.683	weakly similar to (181)AT4G37590 Symbols: phototropic-responsive NPH3 family protein chr4:17663074-17665293 REVERSEvery	
CX280442	1.683	weakly similar to (122)AT3G04080 Symbols: ATAPY1 ATAPY1 (APYRASE 1); calmodulin binding chr3:1068075-1070924 REVER	1.440
JCVI_24093	1.682	very weakly similar to (81.3)AT2G23550 Symbols: hydrolase chr2:10034893-10035847 REVERSE no original description	
EE535642	1.682	weakly similar to (124)AT5G04360 Symbols: ATPU1, ATLDA ATLDA/ATPU1 (PULLULANASE 1); alpha-amylase/ limit dextrinase	
EV041581	1.680	weakly similar to (108)AT1G22050 Symbols: MUB6 MUB6 (MEMBRANE-ANCHORED UBIQUITIN-FOLD PROTEIN 6 PRECURS	
JCVI_21086	1.680	no original description	
EV206346	1.680	very weakly similar to (86.3)AT5G08720 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G01650.2); similar to	
JCVI_18429	1.679	moderately similar to (452)AT4G22980 Symbols: similar to catalytic/ pyridoxal phosphate binding [Arabidopsis thaliana] (TAIR:AT5C	
EX027736	1.678	moderately similar to (314)AT2G33060 Symbols: leucine-rich repeat family protein chr2:14032738-14035164 FORWARDweakly sin	
JCVI_12242	1.678	nearly identical (1075)AT4G34860 Symbols: beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosid	
JCVI_40140	1.677	weakly similar to (137)AT5G44005 Symbols: unknown protein chr5:17722436-17722720 REVERSE no original description	1.817
JCVI_12819	1.676	moderately similar to (477)AT2G38170 Symbols: ATCAX1, RC14, CAX1 CAX1 (CATION EXCHANGER 1); calcium:hydrogen antip	
ES965932	1.674	no similarity	
JCVI_35746	1.674	nearly identical (1019)AT1G73680 Symbols: pathogen-responsive alpha-dioxygenase, putative chr1:27707882-27711078 REVERSE n	
EE414947	1.673	very weakly similar to (89.0)AT2G18540 Symbols: cupin family protein chr2:8049464-8052090 REVERSE [20141]	
EE482292	1.672	very weakly similar to (80.9)AT1G07135 Symbols: glycine-rich protein chr1:2190156-2190623 REVERSE [20154]	1.850
JCVI_18868	1.672	weakly similar to (150)AT4G22780 Symbols: ACR7 ACR7 (ACT Domain Repeat 7) chr4:11968707-11970967 REVERSE no original	
EV052565	1.671	moderately similar to (279)AT3G48510 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G63350.1); similar to i	
EX030491	1.671	moderately similar to (206)AT1G29690 Symbols: CAD1 CAD1 (CONSTITUTIVELY ACTIVATED CELL DEATH 1) chr1:10379290	
EE414354	1.670	moderately similar to (345)AT1G74650 Symbols: AtY13, AtMYB31 AtMYB31/AtY13 (myb domain protein 31); DNA binding / trans	
EX108966	1.670	moderately similar to (320)AT3G04890 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G46100.1); similar to i	1.689
EV108070	1.670	no similarity	
EE551684	1.668	no similarity	
EX111629	1.667	weakly similar to (115)AT5G08330 Symbols: TCP family transcription factor, putative chr5:2680829-2681548 FORWARD [21827] 1	
JCVI_30477	1.667	moderately similar to (284)AT5G62070 Symbols: IQD23 IQD23 (IQ-domain 23); calmodulin binding chr5:24947283-24949677 REVE	
EV045136	1.667	no similarity	
JCVI_13341	1.667	moderately similar to (408)AT1G01050 Symbols: ATPPA1 ATPPA1 (ARABIDOPSIS THALIANA PYROPHOSPHORYLASE 1); inoi	
JCVI_24119	1.667	very weakly similar to (86.3)AT3G62260 Symbols: protein phosphatase 2C, putative / PP2C, putative chr3:23049491-23051366 REVE	
EV177748	1.666	moderately similar to (399)AT1G44100 Symbols: AAP5 AAP5 (amino acid permease 5); amino acid transmembrane transporter chr1:1	
EV209272	1.666	no similarity	1.864
JCVI_19681	1.665	moderately similar to (314)AT1G08630 Symbols: THA1 THA1 (THREONINE ALDOLASE 1) chr1:2743951-2745688 REVERSE no	
EE535792	1.664	weakly similar to (144)AT3G52040 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO40759.1) chr3:19315346-1	
RC_CO749971	1.664	no similarity	
JCVI_28076	1.663	moderately similar to (335)AT4G22100 Symbols: glycosyl hydrolase family 1 protein chr4:11707382-11709944 REVERSEweakly sir	
RC_EX099573	1.663	no similarity	
DY024253	1.663	moderately similar to (344)AT4G34610 Symbols: BLH6 BLH6 (BELL1-LIKE HOMEODOMAIN 5) chr4:16530551-16532503 REVE	1.857
EV205067	1.662	weakly similar to (134)AT1G71810 Symbols: ABC1 family protein chr1:27006264-27011626 REVERSE [21491]	
EV042239	1.661	moderately similar to (232)AT4G37460 Symbols: binding chr4:17608617-17615528 REVERSE [21442]	1.262
JCVI_36201	1.661	no original description	
JCVI_37130	1.660	moderately similar to (293)AT1G45474 Symbols: LHCA5 LHCA5 (Photosystem I light harvesting complex gene 5) chr1:17181793-17	1.746
ES998075	1.659	very weakly similar to (87.4)AT2G41250 Symbols: haloacid dehalogenase-like hydrolase family protein chr2:17207940-17209629 RE	
EV128716	1.657	no similarity	
EV190021	1.657	no similarity	2.050
JCVI_38075	1.657	moderately similar to (214)AT3G19800 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO15360.1) chr3:687615	2.157
EE512033	1.657	very weakly similar to (85.9)AT2G34720 Symbols: CCAAT-binding transcription factor (CBF-B/NF-YA) family protein chr2:146570	
CN730708	1.657	no similarity	
JCVI_28058	1.657	highly similar to (560)AT1G75880 Symbols: family II extracellular lipase 1 (EXL1) chr1:28494225-28495959 FORWARDmoderately	
JCVI_27097	1.656	moderately similar to (313)AT3G21790 Symbols: UDP-glucuronosyl/UDP-glucosyl transferase family protein chr3:7676934-7678421	
EE532961	1.655	no similarity	
DY026490	1.654	weakly similar to (154)AT5G58660 Symbols: oxidoreductase, 2OG-Fe(II) oxygenase family protein chr5:23718735-23721028 FORW	
JCVI_17245	1.654	moderately similar to (273)AT5G50100 Symbols: similar to Pbg143 [Vigna radiata] (GB:BAB82450.1); contains InterPro domain Th	
EV047731	1.654	no similarity	
CX192067	1.654	weakly similar to (120)AT5G23750 Symbols: remorin family protein chr5:8010007-8011456 REVERSEvery weakly similar to (80.1)	
ES904856	1.653	weakly similar to (165)AT5G62130 Symbols: Per1-like protein-related chr5:24967911-24970144 REVERSE [21432] 1 605 650	
EV176230	1.653	no similarity	
JCVI_7918	1.653	moderately similar to (405)AT1G77090 Symbols: thylakoid luminal 29.8 kDa protein chr1:28965470-28966769 REVERSE no origin	
CN729294	1.653	moderately similar to (207)AT4G19450 Symbols: nodulin-related chr4:10606549-10609229 FORWARD [15725]	
JCVI_33153	1.652	moderately similar to (268)AT5G15550 Symbols: transducin family protein / WD-40 repeat family protein chr5:5059318-5062006 RE	
JCVI_13868	1.652	weakly similar to (123)AT3G12320 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G06980.1); similar to hycp	
JCVI_39183	1.649	very weakly similar to (98.2)AT5G13730 Symbols: SIGD, SIG4 SIG4 (SIGMA FACTOR 4); DNA binding / DNA-directed RNA polym	1.219
JCVI_26722	1.648	moderately similar to (331)AT2G41120 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO18305.1); contains Inte	
JCVI_5209	1.647	moderately similar to (374)AT3G26210 Symbols: CYP71B23 CYP71B23 (cytochrome P450, family 71, subfamily B, polypeptide 23);	
JCVI_39350	1.647	moderately similar to (348)AT1G67370 Symbols: ASY1 ASY1 (ASYNAPTIC 1); DNA binding chr1:25243010-25247376 REVERSE	
JCVI_813	1.646	weakly similar to (147)AT3G56880 Symbols: VQ motif-containing protein chr3:21071023-21071760 FORWARD no original descrip	
EV035703	1.646	no similarity	
EE564648	1.645	no similarity	
JCVI_29438	1.644	weakly similar to (160)AT3G14680 Symbols: CYP72A14 CYP72A14 (cytochrome P450, family 72, subfamily A, polypeptide 14); oxy	
JCVI_1254	1.644	weakly similar to (162)AT3G48240 Symbols: octicosapeptide/Phox/Bem1p (PB1) domain-containing protein chr3:17878366-1787895	
ES266449	1.644	weakly similar to (161)AT3G62260 Symbols: protein phosphatase 2C, putative / PP2C, putative chr3:23049491-23051366 REVERSE	
JCVI_34519	1.643	weakly similar to (105)AT5G64350 Symbols: ATKBP12, FKBP12 FKBP12 (FK506-binding protein 12 kD); FK506 binding / peptidy	1.705
CO749481	1.643	weakly similar to (140)AT1G75100 Symbols: JAC1 JAC1 (J-DOMAIN PROTEIN REQUIRED FOR CHLOROPLAST ACCUMULAT	
JCVI_20853	1.642	moderately similar to (278)AT1G08530 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G09995.3); similar to i	
JCVI_766	1.641	moderately similar to (374)AT4G09350 Symbols: DNAJ heat shock N-terminal domain-containing protein chr4:5931314-5932149 RE	1.735
JCVI_31156	1.641	weakly similar to (166)AT5G27600 Symbols: LACS7 LACS7 (LONG-CHAIN ACYL-COA SYNTHETASE 7) chr5:9742619-9746790	
AM395056	1.640	weakly similar to (106)AT2G32120 Symbols: HSP70T-2 HSP70T-2; ATP binding chr2:13658797-13660488 REVERSE [20346]	
JCVI_6920	1.640	highly similar to (866)AT1G53140 Symbols: dynamin family protein chr1:19802939-19806109 FORWARD no original description	
EV008362	1.640	weakly similar to (122)AT1G63470 Symbols: DNA-binding family protein chr1:23540496-23542528 REVERSE [21427] 1 605 619	
EE519214	1.640	no similarity	
H74609	1.639	no similarity	
EE569260	1.639	no similarity	
EV108331	1.639	no similarity	

JCVI_11824	1.637	moderately similar to (459)AT3G05200 Symbols: ATL6 ATL6 (Arabidopsis T?xicos en Levadura 6); protein binding / zinc ion binding	
EV146350	1.635	no similarity	
ES901040	1.635	weakly similar to (188)AT3G05165 Symbols: sugar transporter, putative chr3:1458293-1462743 REVERSE [21428]	0.995
CV546543	1.634	weakly similar to (111)AT1G17620 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G11890.1); similar to unk	1.919
JCVI_308	1.634	moderately similar to (279)AT3G52800 Symbols: zinc finger (AN1-like) family protein chr3:19580784-19581296 FORWARD	weakly
JCVI_30460	1.633	highly similar to (672)AT3G02875 Symbols: ILR1 ILR1 (IAA-LEUCINE RESISTANT 1); metalloproteinase chr3:632000-633866 FOF	
DW998864	1.632	weakly similar to (124)AT1G74450 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G18740.1); similar to unkn	
JCVI_7637	1.632	weakly similar to (147)AT3G25950 Symbols: similar to DNA-binding storekeeper protein-related [Arabidopsis thaliana] (TAIR:AT5G1	
EV006195	1.631	moderately similar to (238)AT2G45870 Symbols: Identical to UPF0187 protein At2g45870, chloroplast precursor [Arabidopsis thaliana]	
EV099861	1.631	moderately similar to (320)AT1G78070 Symbols: WD-40 repeat family protein chr1:29360113-29363261 FORWARD [21477] 104 9	
EX098994	1.631	moderately similar to (226)AT4G37590 Symbols: phototropic-responsive NPH3 family protein chr4:17663074-17665293 REVERSE	
EE462682	1.631	no similarity	
EE563089	1.631	no similarity	
JCVI_37924	1.630	weakly similar to (162)AT5G52750 Symbols: heavy-metal-associated domain-containing protein chr5:21401360-21402021 FORWAR	
JCVI_37564	1.628	weakly similar to (140)AT3G14420 Symbols: (S)-2-hydroxy-acid oxidase, peroxisomal, putative / glycolate oxidase, putative / short ch	1.628
JCVI_301	1.628	moderately similar to (328)AT2G37220 Symbols: 29 kDa ribonucleoprotein, chloroplast, putative / RNA-binding protein cp29, putative	
EV007990	1.627	moderately similar to (263)AT5G53920 Symbols: ribosomal protein L11 methyltransferase-related chr5:21909350-21911313 FORWA	
EV034359	1.627	no similarity	
EH422476	1.626	no similarity	
JCVI_6726	1.626	moderately similar to (273)AT3G21510 Symbols: AHP1 AHP1 (HISTIDINE-CONTAINING PHOSPHOTRANSMITTER 3); histidine	
ES940059	1.626	no similarity	
JCVI_16321	1.625	moderately similar to (263)AT4G34150 Symbols: C2 domain-containing protein chr4:16355039-16356959 FORWARD no original de	
EE568740	1.625	no similarity	
DY004109	1.625	weakly similar to (144)AT3G62260 Symbols: protein phosphatase 2C, putative / PP2C, putative chr3:23049491-23051366 REVERSE	
JCVI_10451	1.625	no original description	
JCVI_41295	1.624	very weakly similar to (89.4)AT1G12280 Symbols: disease resistance protein (CC-NBS-LRR class), putative chr1:4174873-417557 F	
JCVI_24647	1.624	no original description	
JCVI_11120	1.624	very weakly similar to (92.4)AT5G44510 Symbols: disease resistance protein (TIR-NBS-LRR class), putative chr5:17946900-1795141	
JCVI_6202	1.623	moderately similar to (253)AT1G76880 Symbols: trihelix DNA-binding protein, putative chr1:28870488-28872825 FORWARD no oi	
JCVI_38446	1.622	no original description	
JCVI_25466	1.622	highly similar to (675)AT1G08230 Symbols: amino acid transporter family protein chr1:2583712-2586697 REVERSE no original des	
EX131001	1.621	weakly similar to (131)AT2G37530 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G07795.1); similar to hypc	
EV077920	1.621	no similarity	
JCVI_10262	1.621	moderately similar to (291)AT1G21010 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G76600.1); similar to i	
ES983579	1.620	no similarity	
JCVI_15812	1.620	moderately similar to (218)AT4G12980 Symbols: auxin-responsive protein, putative chr4:7589667-7591071 REVERSE no original de	1.650
ES964543	1.620	no similarity	
CX189998	1.620	very weakly similar to (96.3)AT5G45400 Symbols: replication protein, putative chr5:18416217-18418871 FORWARD [16807]	
JCVI_20165	1.619	moderately similar to (436)AT1G77990 Symbols: SULTR2;2, AST56 AST56 (sulphate transporter 2;2); sulfate transmembrane transpor	
JCVI_20545	1.619	moderately similar to (435)AT4G25130 Symbols: peptide methionine sulfoxide reductase, putative chr4:12898812-12900008 REVER	
RC_ES979977	1.617	no similarity	
EV091132	1.617	no similarity	1.334
BQ704570	1.617	no similarity	2.578
JCVI_16188	1.616	moderately similar to (303)AT1G70070 Symbols: PDE317, ISE2, EMB25 EMB25 (EMBRYO DEFECTIVE 25); ATP-dependent helic	
JCVI_31665	1.615	moderately similar to (443)AT2G40730 Symbols: HEAT repeat-containing protein chr2:16997161-17003150 REVERSE no original d	
JCVI_16811	1.613	weakly similar to (162)AT4G18740 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO48031.1) chr4:10303554-1	
JCVI_34572	1.613	moderately similar to (266)AT1G15760 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G80520.1); similar to i	
JCVI_40795	1.613	moderately similar to (223)AT4G36050 Symbols: endonuclease/exonuclease/phosphatase family protein chr4:17052326-17055047 RE	
EV204270	1.613	no similarity	1.712
JCVI_18261	1.612	moderately similar to (418)AT1G21450 Symbols: SCL1 SCL1 (SCARECROW-LIKE 1); transcription factor chr1:7509710-7511491 F	
JCVI_19482	1.611	moderately similar to (488)AT1G76350 Symbols: RWP-RK domain-containing protein chr1:28645037-28647711 FORWARD no orig	
JCVI_1634	1.610	moderately similar to (312)AT1G23205 Symbols: invertase/pectin methyltransferase inhibitor family protein chr1:8234223-8234840 RE	
JCVI_28588	1.610	highly similar to (646)AT5G47910 Symbols: ATRBOHD, RBOHD RBOHD (RESPIRATORY BURST OXIDASE PROTEIN D) chr5	
EX131487	1.609	moderately similar to (252)AT4G30850 Symbols: HHP2 HHP2 (HEPTAHELICAL TRANSMEMBRANE PROTEIN2) chr4:15020546	
EV138048	1.608	no similarity	
AM394249	1.607	weakly similar to (104)AT4G06634 Symbols: zinc finger (C2H2 type) family protein chr4:3764496-3766174 REVERSE [20346] 1 42	
ES909645	1.606	weakly similar to (117)AT2G47710 Symbols: universal stress protein (USP) family protein chr2:19562115-19563026 REVERSE [214	
JCVI_32380	1.606	moderately similar to (428)AT3G53260 Symbols: PAL2 PAL2 (phenylalanine ammonia-lyase 2); phenylalanine ammonia-lyase chr3:1	
JCVI_9019	1.605	moderately similar to (361)AT4G31870 Symbols: ATGPX7 ATGPX7 (GLUTATHIONE PEROXIDASE 7); glutathione peroxidase ch	1.918
JCVI_28807	1.604	moderately similar to (420)AT3G44610 Symbols: protein kinase family protein chr3:16199253-16203094 REVERSEmoderately simil	
EV102803	1.604	moderately similar to (226)AT4G12310 Symbols: CYP706A5 CYP706A5 (cytochrome P450, family 706, subfamily A, polypeptide 5);	
JCVI_26937	1.604	no original description	
JCVI_16857	1.603	no original description	
JCVI_27837	1.602	weakly similar to (139)AT1G45230 Symbols: defective chloroplasts and leaves protein-related / DCL protein-related chr1:17172314-1	
JCVI_10733	1.602	moderately similar to (325)AT2G33310 Symbols: IAA13 IAA13 (indoleacetic acid-induced protein 13) chr2:14121646-14122834 REV	
JCVI_1603	1.601	moderately similar to (480)AT1G32240 Symbols: KAN2 KAN2 (KANADI 2); DNA binding / transcription factor chr1:11625862-116	
EL588585	1.601	very weakly similar to (94.7)AT1G09660 Symbols: KH domain-containing quaking protein, putative chr1:3128207-3130793 REVERS	1.484
JCVI_2483	1.600	moderately similar to (352)AT3G12490 Symbols: cysteine protease inhibitor, putative / cystatin, putative chr3:3960530-3961784 REV	
EV109979	1.600	very weakly similar to (92.4)AT5G66570 Symbols: PSBO-1, OEE1, OEE33, OE33, PSBO1 OE33/OEE1/OEE33/PSBO-1/PSBO1 (OXY	
EE462182	1.600	weakly similar to (176)AT1G72640 Symbols: binding / catalytic chr1:27350071-27351809 REVERSE [15722]	
EH423274	1.600	moderately similar to (259)AT4G23530 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G11300.1); similar to i	
JCVI_28743	1.598	moderately similar to (314)AT1G66390 Symbols: ATMYB90, PAP2, MYB90 PAP2 (PRODUCTION OF ANTHOCYANIN PIGMENT	
JCVI_15620	1.598	moderately similar to (416)AT4G32770 Symbols: ATSDX1, VTE1 VTE1 (VITAMIN E DEFICIENT 1) chr4:15804986-15807795 FO	
ES948420	1.597	no similarity	
JCVI_8733	1.594	moderately similar to (265)AT1G52880 Symbols: ANAC018, ATNAM, NAM NAM (Arabidopsis NAC domain containing protein 18);	
JCVI_34439	1.594	moderately similar to (343)AT3G53830 Symbols: regulator of chromosome condensation (RCC1) family protein / UVB-resistance prot	
JCVI_18541	1.593	highly similar to (504)AT1G13710 Symbols: CYP78A5 CYP78A5 (cytochrome P450, family 78, subfamily A, polypeptide 5); oxygen i	
JCVI_23598	1.593	moderately similar to (332)AT1G75180 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G19400.1); similar to i	
AM389654	1.593	no similarity	
JCVI_6904	1.592	moderately similar to (434)AT1G76110 Symbols: high mobility group (HMG1/2) family protein / ARID/BRIGHT DNA-binding domai	
JCVI_9640	1.591	moderately similar to (251)AT1G66330 Symbols: senescence-associated family protein chr1:24733543-24735807 REVERSE no origi	
EV105665	1.591	no similarity	
AM056601	1.591	moderately similar to (220)AT1G14480 Symbols: protein binding chr1:4956399-4957883 FORWARD [17712]	

EV141915	1.589	no similarity	2.031
JCVI_29448	1.589	no original description	
JCVI_8974	1.589	highly similar to (510)AT2G40900 Symbols: nodulin MtN21 family protein chr2:17070474-17072592 REVERSE no original descript	
JCVI_34522	1.589	highly similar to (553)AT3G44290 Symbols: ANAC060 ANAC060 (Arabidopsis NAC domain containing protein 60); transcription fact	
JCVI_33872	1.588	moderately similar to (289)AT5G64230 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G19920.1); similar to	
JCVI_14961	1.587	moderately similar to (232)AT1G10960 Symbols: ATFD1 ATFD1 (FERREDOXIN 1); 2 iron, 2 sulfur cluster binding / electron carrier/	
EV210544	1.586	moderately similar to (221)AT4G36550 Symbols: binding / ubiquitin-protein ligase chr4:17245403-17247721 REVERSE [21491] 51 '	
EV071811	1.585	no similarity	
JCVI_3315	1.584	moderately similar to (330)AT5G65840 Symbols: similar to antioxidant/ oxidoreductase [Arabidopsis thaliana] (TAIR:AT2G37240.1);	
JCVI_17301	1.583	moderately similar to (301)AT4G31390 Symbols: ABC1 family protein chr4:15233132-15236770 FORWARD no original description	
EV185414	1.583	no similarity	1.537
JCVI_3689	1.582	very weakly similar to (80.9)AT5G13090 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G24270.1); similar to	
BG543396	1.581	no similarity	
CX192368	1.580	very weakly similar to (99.0)AT2G42190 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G57930.1); similar to	1.301
EX063148	1.579	no similarity	
EV171189	1.578	weakly similar to (140)AT4G36550 Symbols: binding / ubiquitin-protein ligase chr4:17245403-17247721 REVERSE [21486] 96 905	
JCVI_39471	1.578	no original description	
JCVI_22248	1.577	weakly similar to (104)AT5G06520 Symbols: SWAP (Suppressor-of-White-APricot)/surp domain-containing protein chr5:1987251-19	
EX044469	1.575	moderately similar to (296)AT3G14690 Symbols: CYP72A15 CYP72A15 (cytochrome P450, family 72, subfamily A, polypeptide 15);	
ES929102	1.575	moderately similar to (204)AT5G11260 Symbols: TED 5, HY5 HY5 (ELONGATED HYPOCOTYL 5); DNA binding / transcription fa	
JCVI_16714	1.574	weakly similar to (156)AT3G14010 Symbols: CID4 CID4 (CTC-Interacting Domain 4) chr3:4637171-4640698 FORWARD no origina	
JCVI_42421	1.573	moderately similar to (246)AT2G27480 Symbols: calcium ion binding chr2:11753889-11754963 FORWARD no original description	1.497
DY020430	1.570	moderately similar to (316)AT4G22900 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G11950.1); similar to	1.886
EV073235	1.570	weakly similar to (102)AT4G12130 Symbols: aminomethyltransferase chr4:7263634-7265419 FORWARD [21443]	
CN729023	1.569	no similarity	
JCVI_20564	1.569	weakly similar to (144)AT5G62520 Symbols: SRO5 SRO5 (SIMILAR TO RCD ONE 5); NAD+ ADP-ribosyltransferase chr5:251152	
EX123618	1.569	moderately similar to (371)AT5G40160 Symbols: EMB506 EMB506 (EMBRYO DEFECTIVE 506); protein binding chr5:16079954-1	1.547
JCVI_38632	1.568	moderately similar to (457)AT5G44110 Symbols: ATPOP1, ATNAP2, POP1 POP1 chr5:17771619-17772899 REVERSE no original c	
JCVI_35560	1.568	no original description	1.809
EE424482	1.567	weakly similar to (168)AT1G17147 Symbols: similar to VQ motif-containing protein [Arabidopsis thaliana] (TAIR:AT1G78410.1); sin	1.446
JCVI_6813	1.567	moderately similar to (425)AT1G36730 Symbols: eukaryotic translation initiation factor 5, putative / eIF-5, putative chr1:13899918-1	
ES961328	1.567	moderately similar to (337)AT3G18390 Symbols: EMB1865 EMB1865 (EMBRYO DEFECTIVE 1865) chr3:6313578-6317590 FOR	
JCVI_150	1.567	moderately similar to (243)AT2G33800 Symbols: ribosomal protein S5 family protein chr2:14308001-14309428 REVERSEweakly si	
EE533089	1.567	moderately similar to (208)AT2G44270 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G76170.1); similar to	
JCVI_26539	1.567	weakly similar to (150)AT5G53590 Symbols: auxin-responsive family protein chr5:21789333-21789761 FORWARD no original desc	
JCVI_12051	1.566	weakly similar to (136)AT1G18170 Symbols: immunophilin / FKBP-type peptidyl-prolyl cis-trans isomerase family protein chr1:6254	
JCVI_23675	1.565	moderately similar to (465)AT4G34830 Symbols: binding chr4:16599981-16605999 REVERSEvery weakly similar to (100)RF1_OR	
JCVI_22859	1.564	moderately similar to (236)AT1G42540 Symbols: GLR3.3, ATGLR3.3 ATGLR3.3 (Arabidopsis thaliana glutamate receptor 3.3) chr1:	
CB686317	1.564	no similarity	
JCVI_33299	1.562	weakly similar to (165)AT2G37530 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G07795.1); similar to hypc	
JCVI_21849	1.562	moderately similar to (486)AT5G41080 Symbols: glycerophosphoryl diester phosphodiesterase family protein chr5:16459217-164610	2.002
JCVI_30588	1.562	no original description	
EX043068	1.560	no similarity	
JCVI_8753	1.560	moderately similar to (420)AT4G34680 Symbols: GATA transcription factor 3, putative (GATA-3) chr4:16553705-16554615 FORW	
JCVI_11117	1.560	moderately similar to (307)AT5G24460 Symbols: hydrolase chr5:8354818-8355720 FORWARD no original description	
RC_EX052706	1.559	no similarity	
JCVI_845	1.559	weakly similar to (178)AT2G01850 Symbols: XTH27, ATXTH27, EXGT-A3 EXGT-A3 (endo-xylglucan transferase A3); hydrolase, i	
EE481286	1.559	no similarity	1.872
JCVI_22370	1.558	highly similar to (588)AT2G30840 Symbols: 2-oxoglutarate-dependent dioxygenase, putative chr2:13142658-13143910 REVERSEmc	
JCVI_22481	1.558	moderately similar to (240)AT5G16170 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G11730.1); similar to	
EE569362	1.558	no similarity	
EE475617	1.558	no similarity	
EV223721	1.557	moderately similar to (246)AT5G13820 Symbols: ATBP-1, ATPB1, ATTBP1, HPPBF-1, TBP1 TBP1 (TELOMERIC DNA BINDING	
AM060154	1.557	no similarity	
JCVI_38745	1.555	weakly similar to (113)AT3G11170 Symbols: FADD, FAD7 FAD7 (FATTY ACID DESATURASE 7); omega-3 fatty acid desaturase	
JCVI_30892	1.555	weakly similar to (132)AT1G26230 Symbols: chaperonin, putative chr1:9072375-9075259 REVERSE no original description	1.539
EX071950	1.553	moderately similar to (229)AT5G43630 Symbols: zinc knuckle (CCHC-type) family protein chr5:17544488-17547434 FORWARD [2	
ES969062	1.551	no similarity	
EV084948	1.550	weakly similar to (105)AT5G01030 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G37930.1); similar to unnz	
CX188778	1.547	very weakly similar to (88.6)AT5G05550 Symbols: transcription factor chr5:1639530-1640551 REVERSE [16807]	
EE525877	1.547	no similarity	1.634
JCVI_4988	1.547	moderately similar to (372)AT4G12320 Symbols: CYP706A6 CYP706A6 (cytochrome P450, family 706, subfamily A, polypeptide 6);	
JCVI_30505	1.545	weakly similar to (177)AT3G59080 Symbols: aspartyl protease family protein chr3:21847789-21849396 FORWARD no original desc	
JCVI_33360	1.545	moderately similar to (251)AT5G15950 Symbols: adenosylmethionine decarboxylase family protein chr5:5206709-5207797 FORWA	
JCVI_9672	1.544	moderately similar to (375)AT2G17230 Symbols: phosphate-responsive 1 family protein chr2:7501974-7503065 REVERSE no origin	1.481
JCVI_26976	1.544	no original description	
EV209077	1.543	weakly similar to (135)AT5G56860 Symbols: GNC GNC (GATA, NITRATE-INDUCIBLE, CARBON METABOLISM-INVOLVED);	
JCVI_40453	1.543	weakly similar to (158)AT3G55646 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G39855.2) chr3:2065606	
EE567750	1.542	no similarity	
DY000135	1.541	no similarity	
EE435451	1.540	no similarity	
JCVI_38024	1.540	no original description	3.293
JCVI_5494	1.538	moderately similar to (449)AT4G10120 Symbols: ATSPS4F ATSPS4F chr4:6315029-6319781 FORWARDweakly similar to (196)SP	
JCVI_28818	1.537	moderately similar to (258)AT2G18245 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G19970.1); similar to	
JCVI_28414	1.537	no original description	1.415
JCVI_30926	1.535	no original description	
ES983022	1.534	moderately similar to (236)AT2G18940 Symbols: pentatricopeptide (PPR) repeat-containing protein chr2:8210955-8213423 REVERS	
EE534158	1.534	very weakly similar to (89.4)AT1G76590 Symbols: zinc-binding family protein chr1:28745769-28746788 FORWARD [20150] 1 540 '	
EE448615	1.534	very weakly similar to (86.7)AT1G27210 Symbols: binding chr1:9455656-9457904 REVERSE [20172]	
JCVI_25642	1.534	moderately similar to (390)AT4G23570 Symbols: SGT1A SGT1A (Suppressor of G2 (Two) 1A) chr4:12300025-12302503 FORWAR	
EX020651	1.532	moderately similar to (261)AT5G25840 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G79770.1); similar to	1.794
JCVI_15272	1.532	moderately similar to (228)AT4G24480 Symbols: serine/threonine protein kinase, putative chr4:12650420-12654765 FORWARD no	1.367
ES945788	1.532	no similarity	

EV102326	1.531	moderately similar to (342)AT4G22100 Symbols: glycosyl hydrolase family 1 protein chr4:11707382-11709944 REVERSEweakly sir	
AM386056	1.531	very weakly similar to (92.0)AT5G63630 Symbols: DEAD box RNA helicase, putative chr5:25489824-25492422 REVERSE [20118]	
JCVI_10376	1.531	weakly similar to (148)AT5G23660 Symbols: MTN3 MTN3 (ARABIDOPSIS HOMOLOG OF MEDICAGO TRUNCATULA MTN3)	1.632
JCVI_41482	1.530	no original description	
JCVI_21042	1.530	no original description	1.454
JCVI_15695	1.529	highly similar to (888)AT5G08720 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G01650.2); similar to unkn	
JCVI_3098	1.528	moderately similar to (490)AT4G24390 Symbols: F-box family protein (FBX14) chr4:12613919-12615976 REVERSE no original des	2.210
JCVI_38999	1.528	weakly similar to (193)AT4G01280 Symbols: myb family transcription factor chr4:535288-536854 FORWARD no original descriptio	
H06411	1.528	no similarity	
JCVI_15851	1.527	moderately similar to (411)AT1G29690 Symbols: CAD1 CAD1 (CONSTITUTIVELY ACTIVATED CELL DEATH 1) chr1:10379294	
JCVI_21951	1.527	no original description	
EV110700	1.527	no similarity	
EE542499	1.524	weakly similar to (172)AT4G36470 Symbols: S-adenosyl-L-methionine:carboxyl methyltransferase family protein chr4:17215131-172	
EV209810	1.524	very weakly similar to (92.8)AT5G64230 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G19920.1); similar to	
JCVI_36108	1.524	moderately similar to (483)AT3G21360 Symbols: oxidoreductase chr3:7522871-7524042 FORWARD no original description	
EV004240	1.524	moderately similar to (297)AT4G25910 Symbols: ATCNFU3, NFU3 NFU3 (NFU domain protein 3) chr4:13164137-13165103 FORW	
JCVI_26218	1.523	weakly similar to (129)AT1G43730 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G04650.1); similar to puta	
JCVI_31684	1.523	no original description	2.586
EH419365	1.522	weakly similar to (115)AT1G29720 Symbols: protein kinase family protein chr1:10393880-10395067 REVERSE [20767]	
EE545987	1.522	no similarity	
JCVI_6312	1.522	weakly similar to (193)AT1G21450 Symbols: SCL1 SCL1 (SCARECROW-LIKE 1); transcription factor chr1:7509710-7511491 FOR'	
EV122754	1.522	weakly similar to (110)AT5G48560 Symbols: basic helix-loop-helix (bHLH) family protein chr5:19701386-19704097 FORWARD [2	
EE425009	1.520	no similarity	
JCVI_42520	1.520	moderately similar to (464)AT3G08760 Symbols: ATSIK ATSIK; kinase chr3:2658135-2659990 REVERSEvery weakly similar to (87	
EE548570	1.520	no similarity	
EV106908	1.519	weakly similar to (133)AT1G75880 Symbols: family II extracellular lipase 1 (EXL1) chr1:28494225-28495959 FORWARD [21478]	
EE564714	1.519	no similarity	
ES935268	1.518	weakly similar to (119)AT4G34680 Symbols: GATA transcription factor 3, putative (GATA-3) chr4:16553705-16554615 FORWARD	
JCVI_23284	1.516	weakly similar to (130)AT5G48545 Symbols: histidine triad family protein / HIT family protein chr5:19693454-19695171 FORWARD	
EV027655	1.516	moderately similar to (314)AT3G19553 Symbols: amino acid permease family protein chr3:6790994-6792513 REVERSE [21441] 1 6	
JCVI_20309	1.514	weakly similar to (169)AT2G31370 Symbols: bZIP transcription factor (POSF21) chr2:13386525-13388114 FORWARDweakly simil	
EX096590	1.513	moderately similar to (204)AT1G68440 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G25400.1); similar to i	
JCVI_32269	1.512	moderately similar to (447)AT1G06570 Symbols: HPD, PDS1 PDS1 (PHYTOENE DESATURATION 1) chr1:2012014-2013542 REV	
EX062659	1.512	weakly similar to (149)AT4G33100 Symbols: Identical to Uncharacterized protein At4g33100 [Arabidopsis Thaliana] (GB:Q9SMZ9;G	
JCVI_17232	1.511	no original description	
EV009411	1.511	no similarity	
JCVI_34659	1.511	moderately similar to (238)AT1G28360 Symbols: ERF12, ATERF12 ATERF12/ERF12 (ERF domain protein 12); DNA binding / trans	
EE430952	1.511	no similarity	
JCVI_12278	1.507	weakly similar to (182)AT5G53970 Symbols: aminotransferase, putative chr5:21927902-21929820 FORWARD no original descriptio	
JCVI_36423	1.507	no original description	1.550
CD831977	1.506	weakly similar to (170)AT5G63350 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G48510.1); similar to unne	1.310
JCVI_27799	1.505	weakly similar to (137)AT1G29530 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G34310.1); similar to unkr	
JCVI_36711	1.504	weakly similar to (164)AT3G22120 Symbols: CWLP CWLP (CELL WALL-PLASMA MEMBRANE LINKER PROTEIN); lipid bindir	1.627
JCVI_23014	1.503	moderately similar to (306)AT4G35440 Symbols: ATCLC-E, CLC-E CLC-E (CHLORIDE CHANNEL E); voltage-gated chloride cham	
JCVI_6422	1.503	no original description	
JCVI_17662	1.502	moderately similar to (475)AT4G32480 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G20670.1); similar to i	
RC_ES967834	1.502	no similarity	1.728
JCVI_35782	1.500	moderately similar to (311)AT1G70420 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G23710.1); similar to i	2.075
ES927039	1.499	no similarity	
EX114983	1.498	no similarity	
JCVI_40824	1.497	highly similar to (560)AT5G60730 Symbols: anion-transporting ATPase family protein chr5:24440064-24442578 FORWARD no orig	
JCVI_38617	1.497	no original description	
EV227037	1.496	weakly similar to (187)AT4G22980 Symbols: similar to catalytic/ pyridoxal phosphate binding [Arabidopsis thaliana] (TAIR:AT5G519	
JCVI_41198	1.495	no original description	
JCVI_30263	1.495	moderately similar to (390)AT5G13630 Symbols: CCH, CHLH, CCH1, GUN5 GUN5 (GENOMES UNCOUPLED 5) chr5:4387923-4	
EV085499	1.495	no similarity	
JCVI_28528	1.495	moderately similar to (295)AT2G19640 Symbols: ASHR2 ASHR2 (ASH1-RELATED PROTEIN 2) chr2:8498483-8499679 FORWAF	
JCVI_6032	1.495	moderately similar to (388)AT3G01060 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO15045.1); similar to unl	
EX050363	1.493	moderately similar to (486)AT3G29400 Symbols: ATEXO70E1 ATEXO70E1 (exocyst subunit EXO70 family protein E1); protein bind	
JCVI_7388	1.493	moderately similar to (476)AT3G04650 Symbols: oxidoreductase chr3:1262023-1264349 FORWARD no original description	
EV063973	1.493	no similarity	
JCVI_25868	1.491	moderately similar to (433)AT5G22020 Symbols: strictosidine synthase family protein chr5:7287881-7289360 REVERSEweakly simi	
EV105427	1.491	weakly similar to (119)AT5G53970 Symbols: aminotransferase, putative chr5:21927902-21929820 FORWARD [21478]	
EV026824	1.491	moderately similar to (353)AT5G67385 Symbols: signal transducer chr5:26901980-26904309 FORWARDweakly similar to (142)NP	
EX092040	1.491	very weakly similar to (92.8)AT5G17780 Symbols: hydrolase, alpha/beta fold family protein chr5:5867431-5868978 REVERSE [2182	
CN727142	1.490	weakly similar to (120)AT1G07650 Symbols: leucine-rich repeat transmembrane protein kinase, putative chr1:2359814-2366420 REV	
EX134575	1.489	no similarity	
JCVI_25190	1.488	moderately similar to (219)AT1G20330 Symbols: CVP1, FRL1, SMT2 SMT2 (STEROL METHYLTRANSFERASE 2) chr1:7038958-	
JCVI_25349	1.488	weakly similar to (136)AT4G00050 Symbols: UNE10 UNE10 (unfertilized embryo sac 10); DNA binding / transcription factor chr4:1	1.847
JCVI_11590	1.487	moderately similar to (357)AT3G16770 Symbols: RAP2.3, ATEBP, ERF72 ATEBP/ERF72/RAP2.3 (RELATED TO AP2 3); DNA bin	
ES984062	1.484	no similarity	
EX129024	1.484	moderately similar to (216)AT4G07960 Symbols: CSLC12, ATCSLC12 ATCSLC12 (Cellulose synthase-like C12); transferase, transfer	
EE416669	1.484	moderately similar to (352)AT5G60540 Symbols: EMB2407, ATPDX2, PDX2 ATPDX2/EMB2407/PDX2 (PYRIDOXINE BIOSYNTI	
JCVI_32316	1.483	no original description	
JCVI_32294	1.482	highly similar to (713)AT5G27600 Symbols: LACS7 LACS7 (LONG-CHAIN ACYL-COA SYNTHETASE 7) chr5:9742619-9746798	
JCVI_22871	1.481	weakly similar to (111)AT1G32060 Symbols: PRK PRK (PHOSPHORIBULOKINASE); ATP binding / phosphoribulokinase/ protein b	1.256
EV199912	1.480	moderately similar to (219)AT3G27350 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G40700.1); similar to i	1.540
JCVI_12696	1.480	highly similar to (640)AT4G35090 Symbols: CAT2 CAT2 (CATALASE 2); catalase chr4:16701110-16703220 REVERSEhighly simil	
EE511843	1.479	moderately similar to (268)AT3G29400 Symbols: ATEXO70E1 ATEXO70E1 (exocyst subunit EXO70 family protein E1); protein bind	
JCVI_6581	1.478	moderately similar to (233)AT4G24090 Symbols: similar to hypothetical protein [Vitis vinifera] (GB:CAN62286.1) chr4:12512752-1	
JCVI_415	1.478	moderately similar to (402)AT1G80760 Symbols: NIP6.1, NLM7, NIP6 NIP6.1 (NOD26-like intrinsic protein 6.1); water channel chr1	
EV216674	1.477	moderately similar to (327)AT3G48270 Symbols: CYP71A26 CYP71A26 (cytochrome P450, family 71, subfamily A, polypeptide 26);	
JCVI_3671	1.477	moderately similar to (345)AT5G53970 Symbols: aminotransferase, putative chr5:21927902-21929820 FORWARD no original descri	

JCVI_40178	1.476	moderately similar to (321)AT5G24120 Symbols: SIG5, SIGE SIGE (RNA polymerase sigma subunit E); DNA binding / DNA-directed	
DY023268	1.476	moderately similar to (243)AT3G16230 Symbols: RNA binding / catalytic chr3:5500569-5503309 FORWARD [18979]	
EH422740	1.475	moderately similar to (240)AT3G56630 Symbols: CYP94D2 CYP94D2 (cytochrome P450, family 94, subfamily D, polypeptide 2); oxy	
JCVI_8758	1.474	moderately similar to (358)AT1G77280 Symbols: protein kinase family protein chr1:29036362-29040776 REVERSE	Every weakly simi
RC_ES966121	1.473	no similarity	
JCVI_29171	1.473	moderately similar to (298)AT4G17350 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G47440.1); similar to l	
JCVI_14303	1.472	moderately similar to (448)AT1G06430 Symbols: FTSH8 FTSH8 (FtsH protease 8); ATP-dependent peptidase/ ATPase/ metallopeptida	
JCVI_18302	1.472	moderately similar to (215)AT4G13670 Symbols: PTAC5 PTAC5 (PLASTID TRANSCRIPTIONALLY ACTIVE5); heat shock protein	1.645
EX138021	1.471	weakly similar to (154)AT2G35510 Symbols: SRO1 SRO1 (SIMILAR TO RCD ONE 1); NAD+ ADP-ribosyltransferase chr2:149239	
AM061598	1.471	no similarity	
CV432495	1.470	weakly similar to (130)AT5G16280 Symbols: binding chr5:5323380-5331348 REVERSE [16490]	
EV200952	1.470	no similarity	
EV177166	1.469	no similarity	
EV132699	1.467	no similarity	
JCVI_7418	1.467	no original description	
JCVI_37471	1.467	weakly similar to (122)AT2G23580 Symbols: hydrolase, alpha/beta fold family protein chr2:10040440-10041390 REVERSE	Every wea
JCVI_38688	1.467	moderately similar to (348)AT3G16560 Symbols: protein phosphatase 2C-related / PP2C-related chr3:5636057-5637708 REVERSE n	
RC_EV012604	1.466	no similarity	
JCVI_8318	1.465	moderately similar to (358)AT3G10420 Symbols: sporulation protein-related chr3:3239312-3241576 FORWARD	no original descript
JCVI_32498	1.465	moderately similar to (240)AT4G32340 Symbols: binding chr4:15612747-15614225 REVERSE	no original description
JCVI_40512	1.464	moderately similar to (289)AT4G15570 Symbols: tRNA-splicing endonuclease positive effector-related chr4:8893041-8898856 FORV	
EV155598	1.464	moderately similar to (310)AT3G21690 Symbols: MATE efflux family protein chr3:7638757-7641868 FORWARD [21484]	57 775 7 1.948
EX055263	1.464	no similarity	
EV033230	1.464	moderately similar to (203)AT1G20860 Symbols: phosphate transporter family protein chr1:7253996-7258666 REVERSE [21441]	
EE476140	1.462	weakly similar to (127)AT5G64800 Symbols: CLE21 CLE21 (CLAVATA3/ESR-RELATED 21); receptor binding chr5:25923309-259	
JCVI_26040	1.461	weakly similar to (142)AT4G09690 Symbols: DC1 domain-containing protein chr4:6124894-6126117 FORWARD	no original descrip 1.643
DY015573	1.461	no similarity	
EE402507	1.460	weakly similar to (157)AT1G19490 Symbols: bZIP transcription factor family protein chr1:6751944-6753950 REVERSE [16820]	
JCVI_31136	1.460	no original description	
JCVI_27274	1.459	weakly similar to (187)AT5G43260 Symbols: chaperone protein dnaJ-related chr5:17374921-17375214 REVERSE	no original descrip 1.239
JCVI_25059	1.458	highly similar to (729)AT2G42890 Symbols: AML2 AML2 chr2:17857709-17861282 FORWARD	very weakly similar to (98.2)PLA2
JCVI_36088	1.458	moderately similar to (481)AT2G01850 Symbols: XTH27, ATXTH27, EXGT-A3 EXGT-A3 (endo-xyloglucan transferase A3); hydroly	
EV090755	1.458	weakly similar to (181)AT1G15760 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G80520.1); similar to unna	
JCVI_7186	1.457	weakly similar to (179)AT5G18140 Symbols: DNAJ heat shock N-terminal domain-containing protein chr5:5998237-5999701 FORW	
JCVI_31769	1.456	weakly similar to (139)AT5G02120 Symbols: OHP OHP (ONE HELIX PROTEIN) chr5:419141-419630 FORWARD	no original desc 1.402
DY006660	1.456	weakly similar to (197)AT2G41705 Symbols: camphor resistance CrcB family protein chr2:17405161-17406988 FORWARD [18976]	
EV066649	1.455	weakly similar to (158)AT4G16690 Symbols: esterase/lipase/thioesterase family protein chr4:9392427-9393446 REVERSE [21443]	
JCVI_26264	1.455	highly similar to (949)AT4G00370 Symbols: ANTR2 ANTR2 (anion transporter 2); organic anion transmembrane transporter chr4:163	
AM385820	1.455	weakly similar to (117)AT3G19760 Symbols: eukaryotic translation initiation factor 4A, putative / eIF-4A, putative / DEAD box RNA	
JCVI_7963	1.454	weakly similar to (171)AT2G33250 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO71510.1) chr2:14104531-1	
JCVI_2616	1.454	moderately similar to (208)AT5G16830 Symbols: PEP12P, SYP21, ATSP21, PEP12, ATPEP12 SYP21 (syntaxin 21); SNAP receptor	
JCVI_32353	1.453	moderately similar to (455)AT5G18570 Symbols: GTP1/OBG family protein chr5:6171841-6174825 REVERSE	no original descriptic
JCVI_16807	1.453	highly similar to (856)AT3G30775 Symbols: AT-POX, ATPOX, ATPDH, PRO1, PRODH, ERD5 ERD5 (EARLY RESPONSIVE TO I	
JCVI_4776	1.453	moderately similar to (301)AT2G29630 Symbols: thiamine biosynthesis family protein / thiC family protein chr2:12674472-12676646	
EX101867	1.452	moderately similar to (211)AT1G10820 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G60670.2); similar to l	
JCVI_2640	1.451	moderately similar to (447)AT2G17230 Symbols: phosphate-responsive 1 family protein chr2:7501974-7503065 REVERSE	no origin
EX085756	1.451	moderately similar to (407)AT4G12830 Symbols: hydrolase, alpha/beta fold family protein chr4:7531186-7533324 FORWARD [2182	1.298
ES977199	1.451	no similarity	
JCVI_5544	1.451	weakly similar to (159)AT5G59050 Symbols: unknown protein chr5:23859075-23859745 REVERSE	no original description
AT002171	1.450	no similarity	2.397
ES899115	1.449	no similarity	
EV100249	1.448	no similarity	1.738
JCVI_16858	1.448	no original description	
JCVI_30048	1.447	moderately similar to (273)AT2G46660 Symbols: CYP78A6 CYP78A6 (cytochrome P450, family 78, subfamily A, polypeptide 6); oxy	
EV148028	1.446	no similarity	
JCVI_7403	1.446	no original description	
EE468391	1.446	no similarity	
JCVI_34406	1.446	weakly similar to (144)AT5G18370 Symbols: disease resistance protein (TIR-NBS-LRR class), putative chr5:6085038-6088928 REV	
JCVI_33180	1.446	highly similar to (575)AT2G02450 Symbols: ANAC034, ANAC035 ANAC034/ANAC035 (Arabidopsis NAC domain containing protei	1.406
JCVI_35766	1.442	moderately similar to (259)AT1G26761 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO68448.1); contains dom	
JCVI_13931	1.442	weakly similar to (138)AT4G27940 Symbols: mitochondrial substrate carrier family protein chr4:13904751-13907042 FORWARD nc	
JCVI_26456	1.441	moderately similar to (362)AT1G09810 Symbols: ECT11 ECT11 (evolutionarily conserved C-terminal region 11) chr1:3181140-3183	1.263
DW998250	1.441	weakly similar to (110)AT1G54030 Symbols: GDSL-motif lipase, putative chr1:20171353-20173144 FORWARD [18977]	1 429 465
EX086464	1.441	moderately similar to (395)AT5G52570 Symbols: B2, CHY2, BETA-OHASE 2 BETA-OHASE 2 (BETA-CAROTENE HYDROXYLA	
EE490474	1.440	weakly similar to (103)AT4G28740 Symbols: similar to LPA1 (LOW PSII ACCUMULATION1), binding [Arabidopsis thaliana] (TAIF	
JCVI_23768	1.439	no original description	
ES914005	1.439	weakly similar to (122)AT1G08900 Symbols: Identical to Sugar transporter ERD6-like 2 (SUGTL3) [Arabidopsis Thaliana] (GB:Q4F	1.370
EX093767	1.439	no similarity	
EH422975	1.438	weakly similar to (126)AT3G14420 Symbols: (S)-2-hydroxy-acid oxidase, peroxisomal, putative / glycolate oxidase, putative / short ch	1.268
JCVI_1070	1.437	highly similar to (527)AT5G63140 Symbols: ATPAP29, PAP29 ATPAP29/PAP29 (purple acid phosphatase 29); acid phosphatase/ prot	
JCVI_18202	1.437	highly similar to (599)AT5G46570 Symbols: protein kinase family protein chr5:18911914-18914425 FORWARD	no original descript
JCVI_41519	1.437	very weakly similar to (81.3)AT5G65840 Symbols: similar to antioxidant/ oxidoreductase [Arabidopsis thaliana] (TAIR:AT2G37240.1)	
JCVI_19378	1.437	moderately similar to (232)AT1G17360 Symbols: COP1-interacting protein-related chr1:5947434-5951210 FORWARD	no original de
EV110855	1.436	very weakly similar to (99.4)AT4G02280 Symbols: SUS3 SUS3; UDP-glycosyltransferase/ sucrose synthase/ transferase, transferring gl	
EV012135	1.435	no similarity	
JCVI_5414	1.433	weakly similar to (161)AT2G27290 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO48682.1); contains InterPro	1.316
JCVI_21447	1.433	weakly similar to (122)AT4G33920 Symbols: protein phosphatase 2C family protein / PP2C family protein chr4:16260881-16262708	
JCVI_7513	1.432	moderately similar to (474)AT1G64860 Symbols: SIG1, SIG2, SIGB, RPOD1, SIGA SIGA (SIGMA FACTOR A); DNA binding / DN	1.178
JCVI_25849	1.431	moderately similar to (231)AT5G15070 Symbols: acid phosphatase/ oxidoreductase/ transition metal ion binding chr5:4876901-48856	
JCVI_12283	1.431	weakly similar to (162)AT5G11250 Symbols: disease resistance protein (TIR-NBS-LRR class), putative chr5:3587979-3591961 REV	
EV124080	1.427	moderately similar to (353)AT5G41550 Symbols: disease resistance protein (TIR-NBS-LRR class), putative chr5:16634460-16638013	
JCVI_17925	1.426	weakly similar to (178)AT1G23980 Symbols: zinc finger (C3HC4-type RING finger) family protein chr1:8484868-8485977 REVERS	
JCVI_35729	1.426	highly similar to (651)AT1G56500 Symbols: haloacid dehalogenase-like hydrolase family protein chr1:21163440-21170757 FORWA	

RC_EV013364	1.425	no similarity	
JCVI_18395	1.425	weakly similar to (175)AT1G04770 Symbols: male sterility MS5 family protein chr1:1336563-1337766 REVERSE no original descri	
EV089000	1.424	weakly similar to (111)AT1G49540 Symbols: nucleotide binding chr1:18337435-18341050 REVERSE [21444]	1.157
JCVI_9788	1.423	weakly similar to (161)AT4G15800 Symbols: RALFL33 RALFL33 (RALF-LIKE 33) chr4:8984923-8985273 FORWARD no original	1.551
JCVI_17262	1.423	weakly similar to (188)AT1G32710 Symbols: cytochrome c oxidase subunit VIb family chr1:11833093-11833686 FORWARD no ori	
JCVI_24163	1.423	no original description	
EE533139	1.423	moderately similar to (300)AT3G23670 Symbols: PAKRP1L, KINESIN-12B KINESIN-12B/PAKRP1L; microtubule motor chr3:8519	
JCVI_14557	1.423	moderately similar to (325)AT1G68890 Symbols: 2-oxoglutarate decarboxylase/ hydro-lyase/ magnesium ion binding / thiamin pyroph	
JCVI_22845	1.422	weakly similar to (189)AT4G01090 Symbols: extra-large G-protein-related chr4:470834-473248 REVERSE no original description	
EX043605	1.422	moderately similar to (397)AT2G44280 Symbols: similar to lactose permease-related [Arabidopsis thaliana] (TAIR:AT3G60070.1); sin	
EE564191	1.420	weakly similar to (186)AT5G15390 Symbols: tRNA/rRNA methyltransferase (SpoU) family protein chr5:4995336-4997258 FORWARD	
JCVI_13282	1.419	moderately similar to (491)AT5G15180 Symbols: peroxidase, putative chr5:4930564-4932214 FORWARDmoderately similar to (27	1.483
JCVI_11489	1.419	moderately similar to (309)AT1G78110 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G22230.1); similar to i	
ES915455	1.419	moderately similar to (288)AT2G22790 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G67020.1); similar to i	
CB686250	1.419	no similarity	
JCVI_41612	1.419	no original description	
JCVI_12728	1.418	weakly similar to (152)AT1G26761 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO68448.1); contains domain	
JCVI_4651	1.418	moderately similar to (369)AT3G28050 Symbols: nodulin MtN21 family protein chr3:10444221-10446453 FORWARD no original de	
JCVI_16543	1.418	weakly similar to (197)AT1G74950 Symbols: JAZ2, TIFY10B JAZ2/TIFY10B (JASMONATE-ZIM-DOMAIN PROTEIN 2) chr1:281	
RC_EV011386	1.417	no similarity	
JCVI_20276	1.417	moderately similar to (338)AT5G66070 Symbols: zinc finger (C3HC4-type RING finger) family protein chr5:26439149-26440259 FC	
EV223056	1.415	no similarity	
JCVI_24292	1.415	moderately similar to (490)AT1G30160 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G05540.1); contains Ir	
EV092653	1.415	moderately similar to (288)AT1G59620 Symbols: CW9 CW9; ATP binding chr1:21906292-21909192 FORWARD [21476] 104 886 8	
EV192481	1.415	weakly similar to (147)AT3G15430 Symbols: regulator of chromosome condensation (RCC1) family protein chr3:5209415-5211569 F	
JCVI_17614	1.415	moderately similar to (211)AT1G11530 Symbols: ATCXXS1 ATCXXS1 (C-TERMINAL CYSTEINE RESIDUE IS CHANGED TO A	
JCVI_41131	1.415	moderately similar to (452)AT3G10450 Symbols: SCPL7 SCPL7; serine carboxypeptidase chr3:3249775-3252325 FORWARDweakly	
JCVI_34874	1.414	highly similar to (592)AT1G12990 Symbols: glycosyl transferase family 17 protein chr1:4433971-4435550 FORWARD no original d	
JCVI_8732	1.413	moderately similar to (353)AT3G06430 Symbols: EMB2750 EMB2750 (EMBRYO DEFECTIVE 2750) chr3:1956664-1958246 REV1	
CB686228	1.412	weakly similar to (187)AT5G19500 Symbols: tryptophan/tyrosine permease family protein chr5:6579021-6581701 FORWARD [1293	
JCVI_40452	1.412	no original description	
JCVI_19953	1.412	moderately similar to (358)AT3G20300 Symbols: extracellular ligand-gated ion channel chr3:7079838-7081815 REVERSE no origina	
JCVI_31510	1.411	moderately similar to (280)AT1G66130 Symbols: oxidoreductase N-terminal domain-containing protein chr1:24618703-24620405 FC	
JCVI_37245	1.411	moderately similar to (378)AT3G58160 Symbols: ATXII, ATMYOS3, MYA3, XIJ XIJ (Myosin-like protein XIJ) chr3:21545774-2155	
EV158800	1.411	no similarity	
ES967436	1.410	no similarity	
CX281009	1.410	moderately similar to (227)AT4G25910 Symbols: ATCNFU3, NFU3 NFU3 (NFU domain protein 3) chr4:13164137-13165103 FORW	
JCVI_1695	1.409	very weakly similar to (91.7)AT4G23160 Symbols: protein kinase family protein chr4:12129496-12134097 FORWARDweakly similar	
EX061195	1.409	moderately similar to (213)AT4G21440 Symbols: ATMYB102, ATM4 ATM4/ATMYB102 (ARABIDOPSIS MYB-LIKE 102); DNA b	
CD831581	1.408	no similarity	
CX188047	1.408	weakly similar to (161)AT1G47580 Symbols: lipoyltransferase, putative chr1:17487193-17488827 FORWARD [16807]	
EV106902	1.408	weakly similar to (127)AT1G50020 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO49863.1) chr1:18523812-1	
JCVI_10478	1.407	moderately similar to (331)AT4G18010 Symbols: IP5PII IP5PII (INOSITOL POLYPHOSPHATE 5-PHOSPHATASE II); inositol-poly	
JCVI_5409	1.407	weakly similar to (178)AT5G11260 Symbols: TED 5, HY5 HY5 (ELONGATED HYPOCOTYL 5); DNA binding / transcription factor	
JCVI_30076	1.407	highly similar to (713)AT3G07130 Symbols: ATPAP15, PAP15 ATPAP15/PAP15 (purple acid phosphatase 15); acid phosphatase/ prot	
EV108959	1.406	no similarity	
EV182137	1.406	very weakly similar to (83.6)AT5G20140 Symbols: SOUL heme-binding family protein chr5:6799049-6800894 REVERSE [21487]	
JCVI_6057	1.404	weakly similar to (194)AT1G28270 Symbols: RALFL4 RALFL4 (RALF-LIKE 4) chr1:9883152-9883484 FORWARD no original des	
EE569939	1.404	no similarity	
JCVI_15193	1.403	highly similar to (562)AT1G20500 Symbols: 4-coumarate--CoA ligase family / 4-coumaroyl-CoA synthase family chr1:7101599-7102	1.810
JCVI_41689	1.402	moderately similar to (256)AT5G20110 Symbols: dynein light chain, putative chr5:6791544-6793255 REVERSE no original descripti	1.517
EV118365	1.402	moderately similar to (218)AT1G29300 Symbols: UNE1 UNE1 (unfertilized embryo sac 1) chr1:10248106-10249485 REVERSE [214	1.625
EE561826	1.401	no similarity	
JCVI_13934	1.401	moderately similar to (446)AT4G13250 Symbols: short-chain dehydrogenase/reductase (SDR) family protein chr4:7684413-7686687	
EE471256	1.401	weakly similar to (140)AT2G32540 Symbols: CSLB04, ATCSLB4, ATCSLB04 ATCSLB04 (Cellulose synthase-like B4); transferase/ t	
JCVI_14907	1.401	weakly similar to (157)AT5G37260 Symbols: RVE2, CIR1 CIR1/RVE2 (CIRCADIAN 1); DNA binding / transcription factor chr5:14	1.412
EE552941	1.400	no similarity	
ES941335	1.399	moderately similar to (219)AT5G47050 Symbols: ATP binding / protein binding / shikimate kinase/ zinc ion binding chr5:19123839-1	
RC_EX040707	1.397	no similarity	
EV092736	1.397	weakly similar to (132)AT2G16365 Symbols: F-box family protein chr2:7082022-7086263 FORWARD [21476] 45 496 896	1.955
EV139401	1.396	very weakly similar to (97.4)AT3G57370 Symbols: transcription factor IIB (TFIIB) family protein chr3:21237816-21239452 REVERS	
JCVI_12877	1.396	moderately similar to (465)AT5G02830 Symbols: pentatricopeptide (PPR) repeat-containing protein chr5:644456-648419 REVERSE	
JCVI_2120	1.396	moderately similar to (385)AT3G47730 Symbols: ATATH1 ATATH1 (ABC2 homolog 1); ATPase, coupled to transmembrane moveme	
EV193364	1.395	no similarity	
EV085735	1.394	no similarity	
ES264797	1.394	weakly similar to (152)AT5G02020 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G59080.1); similar to hypc	1.393
EE533182	1.393	moderately similar to (350)AT4G02050 Symbols: sugar transporter, putative chr4:898387-900095 REVERSEmoderately similar to (3	
AM395845	1.392	weakly similar to (120)AT4G22100 Symbols: glycosyl hydrolase family 1 protein chr4:11707382-11709944 REVERSE [20346]	
ES993667	1.390	weakly similar to (112)AT2G44190 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G60000.2); similar to unne	
JCVI_41486	1.390	moderately similar to (243)AT4G28820 Symbols: zinc finger (HIT type) family protein chr4:14230821-14232293 REVERSE no origi	
JCVI_2570	1.388	weakly similar to (144)AT3G45050 Symbols: heat shock protein binding / unfolded protein binding chr3:16487008-16488092 FORW	
EV119723	1.388	no similarity	
JCVI_38381	1.388	moderately similar to (265)AT1G69310 Symbols: ATWRKY57, WRKY57 WRKY57 (WRKY DNA-binding protein 57); transcription :	
JCVI_33475	1.388	highly similar to (526)AT2G03750 Symbols: sulfotransferase family protein chr2:1147965-1149020 REVERSE no original descriptio	2.688
ES937747	1.386	weakly similar to (181)AT1G58290 Symbols: HEMA1 HEMA1; glutamyl-tRNA reductase chr1:21627693-21629716 REVERSEweakl	
JCVI_2172	1.386	moderately similar to (379)AT3G14680 Symbols: CYP72A14 CYP72A14 (cytochrome P450, family 72, subfamily A, polypeptide 14);	
JCVI_7843	1.386	highly similar to (537)AT2G46800 Symbols: ATMTTP1, MTP1, ZAT1, ZAT ATMTTP1/MTP1/ZAT1 (ZINC TRANSPORTER OF ARA	
JCVI_7249	1.385	weakly similar to (200)AT3G16570 Symbols: RALFL23 RALFL23 (RALF-LIKE 23) chr3:5644754-5645170 FORWARD no original	
EV147259	1.385	no similarity	
JCVI_3183	1.385	highly similar to (889)AT1G57770 Symbols: amine oxidase family chr1:21398919-21401800 FORWARDweakly similar to (167)CR	
JCVI_25457	1.385	no original description	
JCVI_7433	1.385	moderately similar to (313)AT2G27680 Symbols: aldo/keto reductase family protein chr2:11811058-11813042 REVERSE no original	
JCVI_24218	1.384	moderately similar to (322)AT5G01710 Symbols: similar to methyltransferase [Arabidopsis thaliana] (TAIR:AT4G24805.1); similar to	

JCVI_36738	1.384	weakly similar to (186)AT1G77120 Symbols: ADH, ATADH, ADH1 ADH1 (ALCOHOL DEHYDROGENASE 1) chr1:28980403-28	
JCVI_18041	1.384	moderately similar to (358)AT1G33970 Symbols: avirulence-responsive protein, putative / avirulence induced gene protein, putative /	
EV176450	1.384	no similarity	
JCVI_16914	1.383	highly similar to (598)AT4G02280 Symbols: SUS3 SUS3: UDP-glycosyltransferase/ sucrose synthase/ transferase, transferring glycosyl	
JCVI_22978	1.383	moderately similar to (275)AT5G20830 Symbols: SUS1, ASUS1, ATSUS1 SUS1 (SUCROSE SYNTHASE 1); UDP-glycosyltransferase	
EV135947	1.382	no similarity	
DN962661	1.382	no similarity	
EE534878	1.381	no similarity	
JCVI_17704	1.380	weakly similar to (150)AT3G55250 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO14780.1) chr3:20490279-2	
JCVI_15680	1.380	weakly similar to (193)AT5G67385 Symbols: signal transducer chr5:26901980-26904309 FORWARD no original description	
JCVI_7971	1.379	highly similar to (760)AT4G31210 Symbols: DNA topoisomerase family protein chr4:15165286-15172540 FORWARD no original de	
JCVI_8270	1.378	moderately similar to (393)AT5G10070 Symbols: RNase L inhibitor protein-related chr5:3148685-3150325 REVERSE no original de	
CV432490	1.378	no similarity	
EV047114	1.378	weakly similar to (112)AT4G29810 Symbols: MKK2, MK1, ATMKK2 ATMKK2 (MAP KINASE KINASE 2) chr4:14593485-14595	
EX057115	1.378	weakly similar to (198)AT3G45890 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G13770.1); similar to unna	
EV209478	1.374	no similarity	
JCVI_9641	1.374	moderately similar to (395)AT2G12190 Symbols: cytochrome P450, putative chr2:4898889-4900427 REVERSEmoderately similar to	
EV056789	1.374	very weakly similar to (98.6)AT5G41010 Symbols: DNA-directed RNA polymerases I, II, and III 7 kDa subunit, putative chr5:164412	
JCVI_6728	1.374	very weakly similar to (98.2)AT1G49760 Symbols: PAB8 PAB8 (POLY(A) BINDING PROTEIN 8); RNA binding / translation initiatio	
ES917488	1.373	weakly similar to (123)AT3G06190 Symbols: ATBPM2 ATBPM2; protein binding chr3:1874583-1876581 REVERSE [15718]	
ES931175	1.372	no similarity	
JCVI_30821	1.372	moderately similar to (397)AT5G27330 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G05130.1); similar to i	
EV140116	1.371	no similarity	
JCVI_27008	1.371	moderately similar to (204)AT2G22870 Symbols: EMB2001 EMB2001 (EMBRYO DEFECTIVE 2001); GTP binding chr2:9746556-5	
JCVI_28832	1.370	moderately similar to (375)AT1G80880 Symbols: pentatricopeptide (PPR) repeat-containing protein chr1:30400086-30401813 REVE	
JCVI_7117	1.370	no original description	
EV135593	1.370	no similarity	1.799
JCVI_34535	1.370	no original description	
EV076567	1.369	weakly similar to (162)AT4G16690 Symbols: esterase/lipase/thioesterase family protein chr4:9392427-9393446 REVERSE [21443]	
JCVI_12500	1.368	moderately similar to (212)AT5G08410 Symbols: FTRA2 FTRA2 (ferredoxin/thioredoxin reductase subunit A (variable subunit) 2); fer	
JCVI_1451	1.367	moderately similar to (472)AT5G18650 Symbols: zinc finger (C3HC4-type RING finger) family protein chr5:6218262-6220376 FOR	
RC_EX119510	1.366	no similarity	
AM396151	1.366	weakly similar to (135)AT3G02990 Symbols: HSFA1E, ATHSFA1E ATHSFA1E (Arabidopsis thaliana heat shock transcription factor .	
ES265177	1.366	no similarity	
EV071876	1.366	moderately similar to (292)AT5G29000 Symbols: myb family transcription factor chr5:11023017-11024233 REVERSE [21443]	
DY023260	1.366	weakly similar to (172)AT1G68410 Symbols: protein phosphatase 2C-related / PP2C-related chr1:25653925-25655918 REVERSE [11	
JCVI_33246	1.365	highly similar to (526)AT2G02450 Symbols: ANAC034, ANAC035 ANAC034/ANAC035 (Arabidopsis NAC domain containing protei	
CD841157	1.365	weakly similar to (138)AT4G30470 Symbols: cinnamoyl-CoA reductase-related chr4:14894269-14896512 FORWARD [13982]	
JCVI_985	1.365	highly similar to (514)AT1G80760 Symbols: NIP6;1, NLM7, NIP6 NIP6;1 (NOD26-like intrinsic protein 6;1); water channel chr1:303	
DN963563	1.364	no similarity	
JCVI_41966	1.364	very weakly similar to (88.2)AT2G39170 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO68899.1); contains dor	
JCVI_28850	1.363	very weakly similar to (80.1)AT3G57062 Symbols: similar to hypothetical protein MtrDRAFT_AC153128g25v2 [Medicago truncatula]	
EV010880	1.363	no similarity	
EV040761	1.362	moderately similar to (228)AT3G23670 Symbols: PAKRP1L, KINESIN-12B KINESIN-12B/PAKRP1L; microtubule motor chr3:8519	
EE446340	1.362	weakly similar to (180)AT5G19470 Symbols: ATNUDT24 ATNUDT24 (Arabidopsis thaliana Nudix hydrolase homolog 24); hydrolase	
JCVI_30315	1.361	moderately similar to (350)AT3G54740 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G11850.1); similar to i	
JCVI_33675	1.359	weakly similar to (138)AT1G27300 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO66149.1) chr1:9483311-94	
JCVI_28793	1.359	moderately similar to (430)AT3G06510 Symbols: SFR2 SFR2 (SENSITIVE TO FREEZING 2) chr3:2016456-2019539 FORWARD no	
EV075832	1.358	weakly similar to (149)AT4G22970 Symbols: AESP AESP (ARABIDOPSIS HOMOLOG OF SEPARASE); peptidase chr4:12033714-	
EE509065	1.357	moderately similar to (310)AT1G28350 Symbols: ATP binding / aminoacyl-tRNA ligase chr1:9944470-9949564 FORWARD [15718]	
EV098240	1.356	weakly similar to (115)AT2G29310 Symbols: tropinone reductase, putative / tropine dehydrogenase, putative chr2:12597145-1259833	1.467
EV167383	1.356	weakly similar to (190)AT3G57180 Symbols: GTP binding chr3:21174642-21176985 REVERSE [21486] 82 607 607	
EL592310	1.355	no similarity	
JCVI_8592	1.355	very weakly similar to (93.6)AT5G54585 Symbols: unknown protein chr5:22192914-22193735 FORWARD no original description	2.995
EE563126	1.355	no similarity	
CX191309	1.353	weakly similar to (140)AT3G22440 Symbols: hydroxyproline-rich glycoprotein family protein chr3:7959861-7961893 FORWARD [1	
JCVI_4785	1.352	moderately similar to (337)AT4G25910 Symbols: ATCNFU3, NFU3 NFU3 (NFU domain protein 3) chr4:13164137-13165103 FORW	
BQ704527	1.351	no similarity	
JCVI_81	1.351	moderately similar to (409)AT1G80840 Symbols: ATWRKY40, WRKY40 WRKY40 (WRKY DNA-binding protein 40); transcription : 1.783	
JCVI_4100	1.351	moderately similar to (345)AT2G43235 Symbols: sugar porter chr2:17975987-17977899 REVERSE no original description	
EE532415	1.350	weakly similar to (169)AT2G41705 Symbols: camphor resistance CrcB family protein chr2:17405161-17406988 FORWARD [20175]	
JCVI_13397	1.350	moderately similar to (221)AT3G22550 Symbols: senescence-associated protein-related chr3:7991834-7992812 REVERSE no origina	1.816
EE440043	1.350	no similarity	
JCVI_27775	1.349	moderately similar to (201)AT3G52920 Symbols: hematopoietin/interferon-class (D200-domain) cytokine receptor binding chr3:1963	
ES913410	1.348	no similarity	
EV075063	1.347	weakly similar to (136)AT1G67510 Symbols: leucine-rich repeat family protein chr1:25301140-25303847 REVERSE [21443]	
ES968868	1.347	weakly similar to (184)AT5G25840 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G79770.1); similar to unna	1.906
EX032230	1.346	no similarity	
JCVI_9453	1.345	moderately similar to (204)AT3G02310 Symbols: AGL4, SEP2 SEP2 (SEPALLATA2); DNA binding / transcription factor chr3:46456	
JCVI_3494	1.345	moderately similar to (236)AT5G24314 Symbols: PDE225, PTAC7 PDE225/PTAC7 (PIGMENT DEFECTIVE 225) chr5:8277753-82	
AM057156	1.345	no similarity	
JCVI_8704	1.344	highly similar to (585)AT5G63160 Symbols: BT1 BT1 (BTB and TAZ domain protein 1); protein binding / transcription regulator chr	
JCVI_3182	1.343	weakly similar to (150)AT4G33300 Symbols: ADRI-L1 ADRI-L1 (ADRI-LIKE 1); ATP binding / protein binding chr4:16051166-16	
JCVI_14744	1.342	moderately similar to (373)AT1G09795 Symbols: H1SN1B, ATATP-PR2 ATATP-PR2 (ATP PHOSPHORIBOSYL TRANSFERASE	
JCVI_39164	1.341	no original description	
EV181486	1.341	moderately similar to (327)AT4G23990 Symbols: CSLG3, ATCSLG3 ATCSLG3 (Cellulose synthase-like G3); transferase/ transferase, 1.253	
JCVI_25822	1.341	moderately similar to (228)AT1G31460 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G23270.1); similar to i	
JCVI_11796	1.340	moderately similar to (271)AT5G19500 Symbols: tryptophan/tyrosine permease family protein chr5:6579021-6581701 FORWARD no	
JCVI_31186	1.339	no original description	
JCVI_35780	1.339	moderately similar to (211)AT5G10380 Symbols: zinc finger (C3HC4-type RING finger) family protein chr5:3267820-3268725 FOR	
EE569276	1.338	moderately similar to (422)AT2G26850 Symbols: F-box family protein chr2:11456447-11457967 REVERSE [20191] 43 821 821	
RC_EH427440	1.337	no similarity	
JCVI_8801	1.336	weakly similar to (179)AT5G64850 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G09960.1); similar to 80C	

JCVI_2868	1.335	weakly similar to (168)AT5G23440 Symbols: FTRA1 FTRA1 (ferredoxin/thioredoxin reductase subunit A (variable subunit) 1); ferredoxin	
RC_ES937978	1.334	no similarity	
EV084300	1.334	weakly similar to (152)AT3G59670 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G37440.2); similar to unkn	
JCVI_1061	1.334	moderately similar to (330)AT1G80050 Symbols: ATAPT2, APT2 APT2 (ADENINE PHOSPHORIBOSYL TRANSFERASE 2); adenine	
JCVI_8219	1.333	moderately similar to (254)AT5G66900 Symbols: disease resistance protein (CC-NBS-LRR class), putative chr5:26732157-26734983	
JCVI_26674	1.333	moderately similar to (275)AT3G61080 Symbols: fructosamine kinase family protein chr3:22618127-22619858 FORWARD no origin	
JCVI_18313	1.333	moderately similar to (452)AT2G37050 Symbols: similar to leucine-rich repeat family protein / protein kinase family protein [Arabidop	1.672
BQ704168	1.332	no similarity	
EV037401	1.331	weakly similar to (182)AT2G43235 Symbols: sugar porter chr2:17975987-17977899 REVERSE [21441] 1 615 629	
ES922541	1.330	moderately similar to (208)AT5G16560 Symbols: KAN1, KAN KAN (KANADI); transcription factor chr5:5407368-5411095 REVER	
JCVI_31308	1.329	weakly similar to (124)AT1G29530 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G34310.1); similar to unkn	
EV142036	1.327	no similarity	
JCVI_13418	1.326	highly similar to (818)AT5G48150 Symbols: PAT1 PAT1 (PHYTOCHROME A SIGNAL TRANSDUCTION 1); transcription factor c	
RC_AM385827	1.325	no similarity	
JCVI_28516	1.325	no original description	
EE417681	1.325	no similarity	
JCVI_413	1.325	moderately similar to (287)AT3G56400 Symbols: ATWRKY70, WRKY70 WRKY70 (WRKY DNA-binding protein 70); transcription	
JCVI_10298	1.325	moderately similar to (246)AT1G76110 Symbols: high mobility group (HMG1/2) family protein / ARID/BRIGHT DNA-binding domai	
JCVI_33247	1.325	moderately similar to (201)AT1G10657 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G55240.1); similar to l	
JCVI_19821	1.325	weakly similar to (158)AT1G67030 Symbols: ZFP6 ZFP6 (ZINC FINGER PROTEIN 6); nucleic acid binding / transcription factor/ zin	
JCVI_16741	1.324	moderately similar to (218)AT5G57350 Symbols: AHA3 AHA3 (Arabidopsis H(+)-ATPase 3); ATPase chr5:23248434-23253607 RE	
JCVI_14157	1.324	moderately similar to (325)AT2G01180 Symbols: PAP1, LPP1, ATLPP1, ATPAP1 ATPAP1 (PHOSPHATIDIC ACID PHOSPHATASI	
JCVI_14659	1.323	moderately similar to (296)AT1G56650 Symbols: PAP1, ATMYB75, MYB75, SIAA1 PAP1 (PRODUCTION OF ANTHOCYANIN PI	
JCVI_2836	1.322	highly similar to (688)AT5G19220 Symbols: APL1, ADG2 ADG2 (ADGP PYROPHOSPHORYLASE 2); glucose-1-phosphate adenyl	1.467
JCVI_30612	1.322	highly similar to (858)AT3G14630 Symbols: CYP72A9 CYP72A9 (cytochrome P450, family 72, subfamily A, polypeptide 9); oxygen l	
AM059821	1.322	no similarity	
EV206429	1.321	no similarity	
JCVI_3083	1.320	moderately similar to (253)AT1G16320 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G79510.2); similar to	
JCVI_39559	1.320	no original description	1.709
JCVI_15994	1.319	highly similar to (624)AT2G41670 Symbols: GTP-binding family protein chr2:17381196-17383255 FORWARD no original descripti	
JCVI_16626	1.318	weakly similar to (124)AT1G28540 Symbols: similar to Os06g0524500 [Oryza sativa (japonica cultivar-group)] (GB:NP_001057759.1	
EV148049	1.318	no similarity	
JCVI_35838	1.318	no original description	
AM059112	1.317	no similarity	
JCVI_36796	1.317	highly similar to (898)AT1G31480 Symbols: SGR2 SGR2 (SHOOT GRAVITROPISM 2) chr1:11266206-11271508 FORWARD no or	
JCVI_31825	1.317	moderately similar to (381)AT4G26220 Symbols: caffeoyl-CoA 3-O-methyltransferase, putative chr4:13284188-13285155 FORWAR	
JCVI_5679	1.316	moderately similar to (498)AT1G48460 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G63040.2); similar to	
CN726984	1.316	no similarity	
EE417743	1.316	weakly similar to (105)AT5G13650 Symbols: elongation factor family protein chr5:4397824-4402367 FORWARD [20146]	
JCVI_13970	1.315	highly similar to (678)AT1G07870 Symbols: protein kinase family protein chr1:2429930-2431840 REVERSEmoderately similar to (2	
EV209377	1.314	no similarity	
JCVI_28061	1.311	weakly similar to (199)AT1G11020 Symbols: zinc finger (C3HC4-type RING finger) family protein chr1:3676968-3678350 FORWA	
ES986386	1.311	moderately similar to (201)AT1G04920 Symbols: ATSPS3F ATSPS3F (sucrose phosphate synthase 3F); sucrose-phosphate synthase/ tr	
JCVI_7936	1.311	weakly similar to (194)AT1G29690 Symbols: CAD1 CAD1 (CONSTITUTIVELY ACTIVATED CELL DEATH 1) chr1:10379296-10	
EX066713	1.310	weakly similar to (191)AT4G34680 Symbols: GATA transcription factor 3, putative (GATA-3) chr4:16553705-16554615 FORWARD	
DY001903	1.310	no similarity	
CD834806	1.309	weakly similar to (162)AT5G52990 Symbols: vesicle-associated membrane protein-related chr5:21501414-21502232 FORWARD [13	
EV139626	1.307	no similarity	
EV201808	1.307	moderately similar to (267)AT5G24120 Symbols: SIG5, SIGE SIGE (RNA polymerase sigma subunit E); DNA binding / DNA-directed	
EV015083	1.306	no similarity	
CN735512	1.305	weakly similar to (167)AT1G69380 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G13610.1); similar to unkn	
JCVI_14434	1.305	weakly similar to (200)AT5G58760 Symbols: DDB2 DDB2 (DAMAGED DNA-BINDING 2); nucleotide binding chr5:23747967-237	
JCVI_2173	1.305	moderately similar to (406)AT5G08610 Symbols: DEAD box RNA helicase (RH26) chr5:2790342-2794060 FORWARD no original	
JCVI_36713	1.304	highly similar to (819)AT3G47090 Symbols: leucine-rich repeat transmembrane protein kinase, putative chr3:17352497-17355630 RE	
EX130945	1.303	weakly similar to (153)AT5G24430 Symbols: calcium-dependent protein kinase, putative / CDPK, putative chr5:8339393-8342916 RI	
EV185303	1.301	moderately similar to (246)AT5G43870 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G14740.1); similar to	1.118
CD827448	1.299	no similarity	
JCVI_29041	1.296	moderately similar to (315)AT2G44280 Symbols: similar to lactose permease-related [Arabidopsis thaliana] (TAIR:AT3G60070.1); sin	
CX192117	1.294	no similarity	
JCVI_3911	1.293	moderately similar to (464)AT4G25700 Symbols: B1, CHY1, BETA-OHASE 1 BETA-OHASE 1 (BETA-HYDROXYLASE 1) chr4:1	
JCVI_10808	1.293	moderately similar to (255)AT4G18820 Symbols: ATP binding / DNA binding / DNA-directed DNA polymerase/ nucleoside-triphosph	1.708
EV193644	1.293	weakly similar to (119)AT5G49730 Symbols: ATFRO6, FRO6 ATFRO6/FRO6 (FERRIC REDUCTION OXIDASE 6); ferric-chelate re	
EV131436	1.293	no similarity	
JCVI_12423	1.292	no original description	
JCVI_4242	1.291	moderately similar to (302)AT4G15540 Symbols: nodulin-related chr4:8873392-8875184 FORWARD no original description	
RC_EE562412	1.291	no similarity	
JCVI_37200	1.291	highly similar to (616)AT3G14090 Symbols: ATEXO70D3 ATEXO70D3 (exocyst subunit EXO70 family protein D3); protein binding	
JCVI_17677	1.290	moderately similar to (392)AT4G22780 Symbols: ACR7 ACR7 (ACT Domain Repeat 7) chr4:11968707-11970967 REVERSE no orig	
JCVI_20615	1.290	moderately similar to (349)AT1G79510 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G16320.1); similar to	
ES913705	1.290	weakly similar to (160)AT4G36150 Symbols: disease resistance protein (TIR-NBS-LRR class), putative chr4:17104779-17108714 FO	
JCVI_16075	1.290	moderately similar to (283)AT2G46340 Symbols: SPA1 SPA1 (SUPPRESSOR OF PHYA-105 1); signal transducer chr2:19029645-19	
JCVI_4280	1.290	no original description	1.611
JCVI_40806	1.290	no original description	
EV102134	1.288	moderately similar to (201)AT1G55340 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G03880.1); similar to	
JCVI_10872	1.288	weakly similar to (160)AT3G03920 Symbols: Gar1 RNA-binding region family protein chr3:1009130-1010386 REVERSE no origina	
RC_EX031510	1.288	no similarity	1.704
JCVI_38045	1.288	no original description	
JCVI_2171	1.288	moderately similar to (210)AT5G08130 Symbols: BIM1 BIM1 (BES1-interacting Myc-like protein 1) chr5:2606656-2609572 REVER	
EV036583	1.285	weakly similar to (140)AT3G27210 Symbols: Identical to Uncharacterized protein At3g27210 (Y-2) [Arabidopsis Thaliana] (GB:Q9LK	
JCVI_18026	1.284	weakly similar to (168)AT4G32190 Symbols: centromeric protein-related chr4:15545058-15547695 FORWARD no original descripti	
JCVI_14865	1.283	moderately similar to (334)AT4G33770 Symbols: inositol 1,3,4-trisphosphate 5/6-kinase family protein chr4:16193591-16195240 RE	
ES949525	1.283	weakly similar to (183)AT3G06510 Symbols: SFR2 SFR2 (SENSITIVE TO FREEZING 2) chr3:2016456-2019539 FORWARD [2139	
JCVI_4413	1.283	weakly similar to (140)AT2G38230 Symbols: ATPDX1.1 ATPDX1.1 (PYRIDOXINE BIOSYNTHESIS 1.1); protein heterodimerizatio	

JCVI_33105	1.282	moderately similar to (490)AT1G69800 Symbols: CBS domain-containing protein chr1:26278079-26279988 REVERSE no original d	
JCVI_27708	1.281	moderately similar to (467)AT1G55850 Symbols: CSLE1, ATCSLE1 ATCSLE1 (Cellulose synthase-like E1); cellulose synthase/ trans	
CO750216	1.281	no similarity	
JCVI_8488	1.281	moderately similar to (394)AT3G14690 Symbols: CYP72A15 CYP72A15 (cytochrome P450, family 72, subfamily A, polypeptide 15);	
EV202868	1.281	moderately similar to (273)AT2G33860 Symbols: ARF3, ETT ETT (ETTIN); transcription factor chr2:14332520-14335689 REVERSE	
EH430438	1.280	weakly similar to (102)AT4G20020 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G44780.1); similar to Os1	
JCVI_5562	1.280	weakly similar to (139)AT1G29530 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G34310.1); similar to unkr	
JCVI_15958	1.280	moderately similar to (313)AT3G01440 Symbols: oxygen evolving enhancer 3 (PsbQ) family protein chr3:168485-169414 FORWARD	
JCVI_13933	1.280	moderately similar to (437)AT3G01060 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO15045.1); similar to unl	
EX099556	1.279	moderately similar to (349)AT3G23410 Symbols: alcohol oxidase-related chr3:8382867-8386031 FORWARD [21825]	
JCVI_10804	1.279	no original description	
DN961453	1.279	weakly similar to (130)AT1G11650 Symbols: ATRBP45B ATRBP45B; RNA binding chr1:3914895-3917301 FORWARD [17359]	
JCVI_22005	1.278	weakly similar to (148)AT4G30993 Symbols: similar to hypothetical protein [Vitis vinifera] (GB:CAN67945.1); contains domain Meta	
ES948897	1.278	very weakly similar to (97.8)AT5G65300 Symbols: unknown protein chr5:26112492-26112944 REVERSE [21393]	
JCVI_15672	1.278	weakly similar to (166)AT3G49601 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G37820.1); similar to unna	1.258
JCVI_42559	1.278	no original description	
EE539675	1.277	weakly similar to (179)AT3G53470 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO18045.1) chr3:19833791-1	
JCVI_20801	1.277	no original description	1.436
EV132438	1.277	no similarity	1.882
JCVI_11869	1.276	moderately similar to (284)AT5G65400 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G24380.1); similar to i	1.131
JCVI_15073	1.275	moderately similar to (258)AT3G62910 Symbols: APG3 APG3 (ALBINO AND PALE GREEN); translation release factor chr3:23268	
JCVI_21970	1.275	weakly similar to (196)AT1G49890 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G19570.1); similar to unkr	
JCVI_14017	1.275	very weakly similar to (85.1)AT3G09300 Symbols: oxysterol-binding family protein chr3:2858074-2860468 FORWARD no original d	
JCVI_15218	1.274	moderately similar to (332)AT3G10420 Symbols: sporulation protein-related chr3:3239312-3241576 FORWARD no original descript	
EX057896	1.274	moderately similar to (225)AT3G15354 Symbols: SPA3 SPA3 (SPA1-RELATED 3); signal transducer chr3:5169334-5172487 REVEF	
DY012811	1.272	no similarity	
JCVI_35571	1.271	weakly similar to (164)AT1G23550 Symbols: SRO2 SRO2 (SIMILAR TO RCD ONE 2); NAD+ ADP-ribosyltransferase chr1:835090:	
JCVI_20661	1.271	moderately similar to (283)AT3G48500 Symbols: PDE312, PTAC10 PDE312/PTAC10 (PIGMENT DEFECTIVE 312); RNA binding	
EE455964	1.269	very weakly similar to (89.4)AT5G44005 Symbols: unknown protein chr5:17722436-17722720 REVERSE [20178]	
EV068746	1.268	moderately similar to (235)AT2G20580 Symbols: RPN1A, AtRPN1a AtRPN1a/RPN1A (26S proteasome regulatory subunit S2 1A); bir	
JCVI_37764	1.267	moderately similar to (257)AT1G06070 Symbols: bZIP transcription factor, putative (bZIP69) chr1:1835200-1837115 REVERSEweal	
EX051415	1.267	weakly similar to (171)AT4G15885 Symbols: kinesin motor protein-related chr4:9016466-9016993 REVERSE [21812]	
JCVI_27458	1.265	moderately similar to (396)AT5G08620 Symbols: STRS2 STRS2 (STRESS RESPONSE SUPPRESSOR 2); ATP-dependent helicase c	
EH428672	1.265	no similarity	
ES994891	1.265	no similarity	
JCVI_36678	1.264	no original description	
EX090991	1.264	weakly similar to (109)AT1G48175 Symbols: EMB2191 EMB2191 (EMBRYO DEFECTIVE 2191); catalytic/ hydrolase/ zinc ion bind	
EX056312	1.263	weakly similar to (196)AT4G32770 Symbols: ATSDX1, VTE1 VTE1 (VITAMIN E DEFICIENT 1) chr4:15804986-15807795 FORW	
JCVI_7029	1.262	moderately similar to (310)AT5G53490 Symbols: thylakoid lumenal 17.4 kDa protein, chloroplast chr5:21740714-21741847 REVER	1.452
EE473850	1.262	weakly similar to (168)AT4G38060 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G65480.1); similar to unkr	
EV089440	1.262	moderately similar to (206)AT5G61820 Symbols: similar to MtN19-like protein [Pisum sativum] (GB:AAU14999.2); contains InterPro	
JCVI_38007	1.262	moderately similar to (279)AT4G31115 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G04440.1); similar to i	
DN962534	1.262	no similarity	1.546
BG543306	1.261	weakly similar to (147)AT2G33430 Symbols: plastid developmental protein DAG, putative chr2:14169808-14171805 FORWARD [8:	
JCVI_18962	1.259	weakly similar to (167)AT1G22160 Symbols: senescence-associated protein-related chr1:7823227-7823763 FORWARD no original d	
JCVI_28653	1.258	moderately similar to (393)AT2G01690 Symbols: binding chr2:309143-313498 REVERSE no original description	
CX195839	1.257	moderately similar to (438)AT1G74240 Symbols: mitochondrial substrate carrier family protein chr1:27921098-27923648 FORWARD	
JCVI_44459	1.257	moderately similar to (236)AT2G01480 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G14970.1); similar to i	1.506
DY001451	1.257	weakly similar to (129)AT4G24480 Symbols: serine/threonine protein kinase, putative chr4:12650420-12654765 FORWARD [18968]	1.467
JCVI_9625	1.256	moderately similar to (326)AT2G22680 Symbols: zinc finger (C3HC4-type RING finger) family protein chr2:9652513-9654564 FOR	
JCVI_26594	1.256	very weakly similar to (97.4)AT5G27320 Symbols: ATGID1C, GID1C ATGID1C/GID1C (GA INSENSITIVE DWARF1C); hydrolase	
JCVI_37296	1.256	moderately similar to (224)AT1G24400 Symbols: AATL2, LHT2 LHT2 (LYSINE HISTIDINE TRANSPORTER 2); amino acid transm	1.777
EE453092	1.256	weakly similar to (103)AT5G02840 Symbols: LCL1 LCL1 (LHY/CCA1-LIKE 1); DNA binding / transcription factor chr5:648792-651	
JCVI_19277	1.255	moderately similar to (265)AT1G67480 Symbols: kelch repeat-containing F-box family protein chr1:25280957-25282192 FORWARD	
EV091175	1.255	no similarity	
JCVI_35468	1.255	no original description	
JCVI_28692	1.254	weakly similar to (181)AT5G51720 Symbols: similar to Os07g0467200 [Oryza sativa (japonica cultivar-group)] (GB:NP_001059590.1	
JCVI_38581	1.254	very weakly similar to (95.5)AT5G07530 Symbols: ATGRP17, ATGRP-7, GRP17 GRP17 (Glycine rich protein 17) chr5:2382630-238	0.523
JCVI_7806	1.254	highly similar to (685)AT1G63180 Symbols: UGE3 UGE3 (UDP-D-GLUCOSE/UDP-D-GALACTOSE 4-EPIMERASE 3); UDP-glucos	2.025
JCVI_19728	1.254	moderately similar to (281)AT1G29690 Symbols: CAD1 CAD1 (CONSTITUTIVELY ACTIVATED CELL DEATH 1) chr1:1037929	
JCVI_17250	1.253	moderately similar to (291)AT1G12370 Symbols: UVR2, PHR1 PHR1 (PHOTOLYASE 1) chr1:4206498-4208840 REVERSE no orig	
EV194149	1.253	moderately similar to (214)AT5G62430 Symbols: CDF1 CDF1 (CYCLING DOF FACTOR 1); DNA binding / protein binding / transcri	
EV181448	1.252	moderately similar to (206)AT1G75020 Symbols: LPAT4 LPAT4; acyltransferase chr1:28175440-28177018 FORWARD [21487] 1 42	
JCVI_10494	1.252	moderately similar to (423)AT5G52450 Symbols: MATE efflux protein-related chr5:21306268-21308975 REVERSE no original desc	
RC_ES958250	1.251	no similarity	
EV105960	1.250	no similarity	
AM059731	1.250	moderately similar to (253)AT3G21760 Symbols: UDP-glucuronosyl/UDP-glucosyl transferase family protein chr3:7667106-7668563	
JCVI_5602	1.249	weakly similar to (170)AT2G04700 Symbols: ferredoxin thioredoxin reductase catalytic beta chain family protein chr2:1646958-1648	
JCVI_38340	1.249	very weakly similar to (92.8)AT5G48990 Symbols: kelch repeat-containing F-box family protein chr5:19879566-19880684 FORWARD	
JCVI_9135	1.248	weakly similar to (142)AT2G35060 Symbols: KUP11 KUP11 (K+ uptake permease 11); potassium ion transmembrane transporter chr	
CX192609	1.247	weakly similar to (156)AT1G78140 Symbols: methyltransferase-related chr1:29406830-29408771 REVERSE [16807]	1.306
JCVI_19933	1.247	weakly similar to (165)AT3G52070 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO40812.1) chr3:19323731-1	
JCVI_17663	1.246	moderately similar to (204)AT2G34300 Symbols: dehydration-responsive protein-related chr2:14480995-14483890 REVERSE no ori	
JCVI_10431	1.246	highly similar to (808)AT5G54960 Symbols: PDC2 PDC2 (PYRUVATE DECARBOXYLASE-2); pyruvate decarboxylase chr5:22328	
EX022379	1.246	no similarity	1.400
JCVI_27830	1.245	no original description	
JCVI_31713	1.244	moderately similar to (337)AT4G03070 Symbols: AOP, AOP1.1, AOP1 AOP1 (2-oxoglutarate-dependent dioxygenase 1.1); oxidoreduc	1.824
EV191225	1.244	weakly similar to (144)AT1G20640 Symbols: RWP-RK domain-containing protein chr1:7155191-7157976 FORWARD [21489] 22 8	
JCVI_28169	1.244	weakly similar to (179)AT5G26594 Symbols: ARR24 ARR24 (ARABIDOPSIS RESPONSE REGULATOR 24); two-component respon	
JCVI_23609	1.243	moderately similar to (253)AT5G60540 Symbols: EMB2407, ATPDX2, PDX2 ATPDX2/EMB2407/PDX2 (PYRIDOXINE BIOSYNTH	
JCVI_38952	1.243	moderately similar to (481)AT5G18820 Symbols: EMB3007 EMB3007 (EMBRYO DEFECTIVE 3007); ATP binding / protein binding	
JCVI_35538	1.242	moderately similar to (352)AT5G60210 Symbols: cytoplasmic linker protein-related chr5:24260755-24262858 REVERSE no original	
JCVI_10958	1.241	moderately similar to (286)AT2G37450 Symbols: nodulin MtN21 family protein chr2:15729907-15731930 REVERSE no original des	

JCVI_7352	1.240	moderately similar to (258)AT4G03150 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO22424.1) chr4:139373	
JCVI_20992	1.236	weakly similar to (196)AT2G24280 Symbols: serine carboxypeptidase S28 family protein chr2:10341702-10344007 FORWARD no o	
EV193577	1.236	weakly similar to (190)AT1G42550 Symbols: PM11 PM11 (PLASTID MOVEMENT IMPAIRED1) chr1:15979976-15982174 FORW/	
ES950166	1.234	no similarity	
JCVI_38789	1.234	highly similar to (540)AT5G10170 Symbols: inositol-3-phosphate synthase, putative / myo-inositol-1-phosphate synthase, putative / M	
JCVI_13684	1.234	weakly similar to (139)AT5G35970 Symbols: DNA-binding protein, putative chr5:14136290-14140308 REVERSE no original descrip	
CO750032	1.233	weakly similar to (187)AT1G74240 Symbols: mitochondrial substrate carrier family protein chr1:27921098-27923648 FORWARD [1	
JCVI_15644	1.232	highly similar to (660)AT1G44446 Symbols: ATCAO, CAO, CH1 CH1 (CHLOROPHYLL B BIOSYNTHESIS); chlorophyllide a oxyg	1.579
JCVI_33968	1.231	moderately similar to (441)AT5G53080 Symbols: kinesin light chain-related chr5:21537850-21540384 FORWARD no original descri	
JCVI_22038	1.231	moderately similar to (421)AT5G51130 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO65480.1); contains Inte	
EV015405	1.230	no similarity	
JCVI_699	1.228	moderately similar to (372)AT1G72150 Symbols: PATL1 PATL1 (PATELLIN 1); transporter chr1:27152220-27154314 FORWARD r	
JCVI_7811	1.225	moderately similar to (349)AT4G32770 Symbols: ATSDX1, VTE1 VTE1 (VITAMIN E DEFICIENT 1) chr4:15804986-15807795 FO	1.313
AM385827	1.224	no similarity	
JCVI_38390	1.224	moderately similar to (380)AT1G22850 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G03260.1); similar to i	
JCVI_41430	1.224	weakly similar to (186)AT1G32870 Symbols: ANAC013 ANAC013 (Arabidopsis NAC domain containing protein 13) chr1:11911725-	
JCVI_19366	1.222	moderately similar to (307)AT5G57960 Symbols: GTP-binding family protein chr5:23480359-23483707 REVERSE no original descr	1.229
JCVI_18163	1.222	moderately similar to (350)AT5G57840 Symbols: transferase family protein chr5:23450171-23452387 REVERSEweakly similar to (	
JCVI_3516	1.221	moderately similar to (234)AT2G36835 Symbols: similar to hypothetical protein [Vitis vinifera] (GB:CAN81061.1) chr2:15456918-15	
ES978120	1.221	no similarity	
EV110266	1.220	no similarity	
JCVI_42226	1.220	moderately similar to (216)AT5G11020 Symbols: kinase chr5:3486440-3488984 REVERSE no original description	
JCVI_19175	1.220	moderately similar to (214)AT5G18140 Symbols: DNAJ heat shock N-terminal domain-containing protein chr5:5998237-5999701 FO	
JCVI_8920	1.219	moderately similar to (304)AT1G06650 Symbols: 2-oxoglutarate-dependent dioxygenase, putative chr1:2035908-2037185 FORWARD	
JCVI_41388	1.218	highly similar to (565)AT1G32170 Symbols: XTH30, XTR4 XTR4 (XYLOGLUCAN ENDOTRANSGLYCOSYLASE 4); hydrolase, a	
CN731025	1.218	moderately similar to (364)AT5G12900 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G12330.1); similar to i	
EX093931	1.217	no similarity	1.298
JCVI_31014	1.217	very weakly similar to (89.4)AT1G62120 Symbols: mitochondrial transcription termination factor-related / mTERF-related chr1:22963	
JCVI_27739	1.217	moderately similar to (202)AT5G62570 Symbols: calmodulin-binding protein chr5:25132214-25134193 FORWARD no original desc	
JCVI_34031	1.216	highly similar to (853)AT1G59990 Symbols: DEAD/DEAH box helicase, putative (RH22) chr1:22094034-22096550 REVERSE no oi	
DY018222	1.215	moderately similar to (344)AT1G49580 Symbols: calcium-dependent protein kinase, putative / CDPK, putative chr1:18355279-18358	
JCVI_20522	1.215	no original description	
EE569140	1.215	no similarity	
EV180925	1.214	moderately similar to (263)AT4G21880 Symbols: pentatricopeptide (PPR) repeat-containing protein chr4:11605168-11611220 FORW	
JCVI_37411	1.214	moderately similar to (421)AT4G10120 Symbols: ATSPS4F ATSPS4F chr4:6315029-6319781 FORWARDmoderately similar to (247	
JCVI_9072	1.213	very weakly similar to (98.6)AT2G35120 Symbols: glycine cleavage system H protein, mitochondrial, putative chr2:14812992-148143	
EX041844	1.213	no similarity	
JCVI_33154	1.212	highly similar to (574)AT4G01100 Symbols: mitochondrial substrate carrier family protein chr4:477411-479590 FORWARDweakly s	
EV110599	1.212	weakly similar to (118)AT4G21910 Symbols: MATE efflux family protein chr4:11625833-11630976 REVERSE [21478] 1 367 755	
ES951500	1.211	no similarity	
JCVI_12973	1.211	moderately similar to (298)AT5G10150 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G59790.1); similar to .	
JCVI_37218	1.210	moderately similar to (360)AT5G62460 Symbols: zinc finger (C3HC4-type RING finger) family protein chr5:25092771-25094298 FC	
JCVI_12162	1.208	no original description	
ES999914	1.208	no similarity	
JCVI_7195	1.206	moderately similar to (405)AT1G10600 Symbols: similar to mov34 family protein [Arabidopsis thaliana] (TAIR:AT1G48790.1); simila	
EV195567	1.205	moderately similar to (259)AT5G59700 Symbols: protein kinase, putative chr5:24069839-24072328 REVERSE [21490] 38 769 769	
JCVI_41782	1.205	moderately similar to (429)AT3G22550 Symbols: senescence-associated protein-related chr3:7991834-7992812 REVERSE no origina	
JCVI_6142	1.202	moderately similar to (439)AT3G61320 Symbols: Identical to UPF0187 protein At3g61320, chloroplast precursor [Arabidopsis Thalian	
JCVI_27298	1.202	highly similar to (506)AT1G22180 Symbols: SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein chr1:78	
JCVI_40618	1.202	moderately similar to (468)AT1G64280 Symbols: SAI1, NIM1, NPR1 NPR1 (NONEXPRESSER OF PR GENES 1); protein binding c	
JCVI_11359	1.201	moderately similar to (226)AT5G61820 Symbols: similar to MtN19-like protein [Pisum sativum] (GB:AAU14999.2); contains InterPro	
ES900614	1.201	weakly similar to (186)AT1G60610 Symbols: protein binding / zinc ion binding chr1:22331664-22332851 REVERSE [21428] 1 481 4	
JCVI_20247	1.201	no original description	
JCVI_22076	1.200	weakly similar to (198)AT5G55710 Symbols: similar to tic20 protein-related [Arabidopsis thaliana] (TAIR:AT2G47840.1); similar to u	
ES960310	1.200	no similarity	
EE558554	1.199	moderately similar to (207)AT5G08620 Symbols: STRS2 STRS2 (STRESS RESPONSE SUPPRESSOR 2); ATP-dependent helicase c	
JCVI_31759	1.199	weakly similar to (110)AT5G17270 Symbols: tetratricopeptide repeat (TPR)-containing protein chr5:5679997-5685599 FORWARD n	
EV132032	1.198	no similarity	1.685
JCVI_21570	1.196	moderately similar to (201)AT1G13080 Symbols: CYP71B2 CYP71B2 (CYTOCHROME P450 71B2); oxygen binding chr1:4459491-	1.760
JCVI_24422	1.194	moderately similar to (320)AT3G09650 Symbols: CRM3, HCF152 HCF152 (HIGH CHLOROPHYLL FLUORESCENCE 152) chr3:2	
EV148999	1.194	no similarity	
EX045717	1.193	weakly similar to (115)AT5G49730 Symbols: ATFR06, FRO6 ATFR06/FRO6 (FERRIC REDUCTION OXIDASE 6); ferric-chelate re	
AM062443	1.193	moderately similar to (383)AT4G05090 Symbols: inositol monophosphatase family protein chr4:2609242-2611625 FORWARDweakl	
JCVI_9203	1.193	weakly similar to (137)AT4G16160 Symbols: ATOEP16-2, ATOEP16-S ATOEP16-2/ATOEP16-S; P-P-bond-hydrolysis-driven protein	
JCVI_6153	1.191	highly similar to (677)AT3G10530 Symbols: transducin family protein / WD-40 repeat family protein chr3:3286282-3288675 FORW.	
JCVI_10350	1.190	moderately similar to (288)AT3G09050 Symbols: similar to unknown [Populus trichocarpa x Populus deltoides] (GB:ABK96465.1) c	
JCVI_32540	1.189	moderately similar to (377)AT5G13650 Symbols: elongation factor family protein chr5:4397824-4402367 FORWARD no original de	
JCVI_14409	1.189	highly similar to (574)AT5G52820 Symbols: WD-40 repeat family protein / notchless protein, putative chr5:21418649-21421429 FOF	
EV150324	1.188	no similarity	
JCVI_29495	1.187	moderately similar to (360)AT1G18660 Symbols: zinc finger (C3HC4-type RING finger) family protein chr1:6421425-6425557 FOR'	
JCVI_9648	1.186	weakly similar to (167)AT3G05900 Symbols: neurofilament protein-related chr3:1761414-1763860 REVERSE no original descriptor	
EV090658	1.186	weakly similar to (107)AT3G14200 Symbols: DNAJ heat shock N-terminal domain-containing protein chr3:4712888-4714368 REVEI	
JCVI_27451	1.185	highly similar to (910)AT2G47390 Symbols: serine-type endopeptidase/ serine-type peptidase chr2:19449348-19453323 REVERSE n	
JCVI_18645	1.184	no original description	
JCVI_1073	1.182	moderately similar to (226)AT1G15890 Symbols: disease resistance protein (CC-NBS-LRR class), putative chr1:5461400-5463955 FC	
EV111535	1.181	weakly similar to (109)AT5G01410 Symbols: ATPDX1.3, RSR4, PDX1.3, PDX1 PDX1 (PYRIDOXINE BIOSYNTHESIS 1.3); protein	
ES909677	1.181	moderately similar to (497)AT5G18650 Symbols: zinc finger (C3HC4-type RING finger) family protein chr5:6218262-6220376 FOR'	
EX123017	1.179	no similarity	
JCVI_3995	1.177	moderately similar to (256)AT2G33860 Symbols: ARF3, ETT ETT (ETTIN); transcription factor chr2:14332520-14335689 REVERSI	
EV155653	1.176	moderately similar to (238)AT1G58290 Symbols: HEMA1 HEMA1; glutamyl-tRNA reductase chr1:21627693-21629716 REVERSEm	
CB617597	1.175	no similarity	
JCVI_17545	1.175	weakly similar to (119)AT2G32710 Symbols: ACK2, ICK7, KRP4 KRP4 (KIP-RELATED PROTEIN 4) chr2:13880573-13882427 FC	
EE549419	1.174	no similarity	

EX086887	1.173	weakly similar to (128)AT5G63820 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G28920.1); contains InterF	1.976
EE551212	1.173	no similarity	
JCVI_30131	1.173	very weakly similar to (88.2)AT1G66330 Symbols: senescence-associated family protein chr1:24733543-24735807 REVERSE no orig	
JCVI_13106	1.172	highly similar to (529)AT5G24150 Symbols: SQP1 SQP1 (Squalene monooxygenase 1) chr5:8172673-8175398 REVERSEhighly simi	
JCVI_32002	1.171	moderately similar to (388)AT4G05090 Symbols: inositol monophosphatase family protein chr4:2609242-2611625 FORWARDvery v	
EX020842	1.171	no similarity	
JCVI_18535	1.171	highly similar to (552)AT2G45160 Symbols: scarecrow transcription factor family protein chr2:18625185-18627107 REVERSEweakl	
CO750309	1.170	no similarity	
JCVI_7739	1.168	no original description	
EV102078	1.168	very weakly similar to (94.7)AT2G21240 Symbols: BPC4, BBR/BPC4, ATBPC4 ATBPC4/BBR/BPC4/BPC4 (BASIC PENTACYSTEI	
EV118501	1.168	moderately similar to (320)AT4G29900 Symbols: ATACA10, ACA10 ACA10 (autoinhibited Ca2+ -ATPase 10); calcium-transporting /	
ES964175	1.167	weakly similar to (129)AT1G02560 Symbols: NCLPP1, NCLPP5, CLPP5 CLPP5 (NUCLEAR ENCODED CLP PROTEASE 1); endop	
JCVI_5696	1.166	very weakly similar to (95.1)AT1G64140 Symbols: similar to loricrin-related [Arabidopsis thaliana] (TAIR:AT5G64550.1); similar to u	
AM386177	1.165	no similarity	
JCVI_24080	1.165	highly similar to (567)AT5G49990 Symbols: xanthine/uracil permease family protein chr5:20355090-20358413 REVERSE no origina	
CO750316	1.164	no similarity	
JCVI_41681	1.164	no original description	
RC_EV029606	1.163	no similarity	
EX054690	1.161	moderately similar to (201)AT3G02030 Symbols: hydrolase, alpha/beta fold family protein chr3:345031-347820 FORWARD [21812]	
JCVI_12613	1.160	moderately similar to (334)AT4G26850 Symbols: VTC2 VTC2 (VITAMIN C DEFECTIVE 2) chr4:13499268-13501151 REVERSE n	
EE191543	1.159	no similarity	
JCVI_17664	1.158	highly similar to (798)AT2G01320 Symbols: ABC transporter family protein chr2:154668-158062 REVERSEweakly similar to (181)	
JCVI_41152	1.158	weakly similar to (106)AT1G19700 Symbols: BEL10, BLH10A BEL10/BLH10A (BEL1-LIKE HOMEODOMAIN 10); DNA binding /	
JCVI_6882	1.158	weakly similar to (110)AT1G60950 Symbols: ATFD2, FED A FED A (FERREDOXIN 2); 2 iron, 2 sulfur cluster binding / electron car	
JCVI_17691	1.157	no original description	
RC_ES985508	1.155	no similarity	
JCVI_21672	1.154	weakly similar to (123)AT3G17980 Symbols: C2 domain-containing protein chr3:6152423-6153121 FORWARD no original descripti	
JCVI_31309	1.153	highly similar to (823)AT4G14210 Symbols: PDS, PDE226, PDS3 PDS3 (PHYTOENE DESATURASE) chr4:8190421-8194764 REV	
JCVI_34514	1.153	highly similar to (641)AT2G04030 Symbols: EMB1956, CR88 CR88 (EMBRYO DEFECTIVE 1956); ATP binding chr2:1281980-128	
JCVI_41912	1.152	moderately similar to (284)AT3G03950 Symbols: ECT1 ECT1 chr3:1021509-1023774 FORWARD no original description	
JCVI_26776	1.152	moderately similar to (322)AT4G31800 Symbols: WRKY18 WRKY18 (WRKY DNA-binding protein 18); transcription factor chr4:15	
JCVI_33756	1.152	moderately similar to (354)AT4G18130 Symbols: PHYE PHYE (PHYTOCHROME DEFECTIVE E); G-protein coupled photoreceptor.	
JCVI_22223	1.151	moderately similar to (337)AT5G58870 Symbols: FTSH9 FTSH9 (FtsH protease 9); ATP-dependent peptidase/ ATPase/ metallopeptida	
JCVI_1077	1.151	moderately similar to (343)AT4G09040 Symbols: RNA recognition motif (RRM)-containing protein chr4:5795072-5797190 REVERS	
EV096192	1.151	weakly similar to (103)AT5G67385 Symbols: signal transducer chr5:26901980-26904309 FORWARD [21476]	
JCVI_22000	1.150	moderately similar to (270)AT1G24490 Symbols: ALB4 ALB4 (ALBINA 4) chr1:8682352-8684954 FORWARDvery weakly similar t	
JCVI_28412	1.150	moderately similar to (427)AT5G49730 Symbols: ATFRO6, FRO6 ATFRO6/FRO6 (FERRIC REDUCTION OXIDASE 6); ferric-chela	
JCVI_3692	1.149	moderately similar to (352)AT5G11150 Symbols: VAMP713, ATVAMP713 ATVAMP713 (Arabidopsis thaliana vesicle-associated me	
JCVI_35010	1.148	highly similar to (680)AT5G63420 Symbols: EMB2746 EMB2746 (EMBRYO DEFECTIVE 2746); catalytic chr5:25417741-2542303	
CO749749	1.148	no similarity	
ES968003	1.147	weakly similar to (121)AT2G20585 Symbols: NFD6 NFD6 (NUCLEAR FUSION DEFECTIVE 6) chr2:8872303-8873178 FORWARD	
EE436595	1.147	moderately similar to (261)AT2G39940 Symbols: COI1 COI1 (CORONATINE INSENSITIVE 1); ubiquitin-protein ligase chr2:16679	
JCVI_5140	1.146	moderately similar to (426)AT5G61820 Symbols: similar to MtN19-like protein [Pisum sativum] (GB:AAU14999.2); contains InterPro	
EE566306	1.145	moderately similar to (250)AT1G56230 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G22660.2); similar to i	
JCVI_7373	1.144	moderately similar to (264)AT3G11930 Symbols: universal stress protein (USP) family protein chr3:3776377-3777399 FORWARD n	
JCVI_11755	1.144	no original description	
JCVI_5203	1.144	moderately similar to (308)AT1G64230 Symbols: UBC28 UBC28; ubiquitin-protein ligase chr1:23837455-23838883 FORWARDdweal	
JCVI_22412	1.144	highly similar to (636)AT5G66770 Symbols: scarecrow transcription factor family protein chr5:26677949-26679703 FORWARDdweal	
EV215008	1.143	no similarity	
JCVI_18292	1.143	moderately similar to (311)AT5G45370 Symbols: nodulin-related / integral membrane family protein chr5:18405638-18407509 FORV	
JCVI_21110	1.143	moderately similar to (280)AT2G41720 Symbols: EMB2654 EMB2654 (EMBRYO DEFECTIVE 2654) chr2:17410822-17414205 RE	1.274
JCVI_11000	1.141	weakly similar to (197)AT1G22630 Symbols: heat shock protein binding / unfolded protein binding chr1:8003476-8004156 FORWAF	1.374
JCVI_22009	1.140	highly similar to (664)ATCG00170 Symbols: RPOC2 RNA polymerase beta' subunit-2 chrC:15938-20068 REVERSEhighly similar to	
ES269966	1.139	no similarity	
EV100448	1.139	no similarity	
EE438735	1.138	moderately similar to (224)AT1G18660 Symbols: zinc finger (C3HC4-type RING finger) family protein chr1:6421425-6425557 FOR'	
EE418244	1.136	weakly similar to (122)AT3G06530 Symbols: BAP28-related chr3:2022602-2033643 FORWARD [20146] 1 386 426	
JCVI_20033	1.135	highly similar to (524)AT3G06483 Symbols: ATPDHK, PDK PDK (PYRUVATE DEHYDROGENASE KINASE); ATP binding / pyru	1.305
ES963435	1.135	weakly similar to (116)AT5G16420 Symbols: pentatricopeptide (PPR) repeat-containing protein chr5:5368037-5369644 FORWARD	
ES902623	1.134	moderately similar to (471)AT2G40390 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G64190.1); similar to i	
JCVI_24089	1.134	weakly similar to (115)AT3G62250 Symbols: UBQ5 UBQ5 (UBIQUITIN 5); protein binding chr3:23048113-23048586 FORWARDw	
JCVI_22106	1.133	moderately similar to (303)AT2G03670 Symbols: CDC48B CDC48B; ATPase chr2:1117592-1120358 FORWARDweakly similar to (	
EE462415	1.133	weakly similar to (110)AT1G62250 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO21221.1) chr1:22999280-2	
JCVI_35316	1.131	moderately similar to (340)AT3G20270 Symbols: lipid-binding serum glycoprotein family protein chr3:7068885-7070872 FORWARD	
JCVI_31260	1.130	moderately similar to (247)AT3G16640 Symbols: TCTP TCTP (TRANSLATIONALLY CONTROLLED TUMOR PROTEIN) chr3:56	1.359
JCVI_38082	1.129	no original description	
EE475633	1.128	weakly similar to (140)AT1G73700 Symbols: MATE efflux family protein chr1:27721215-27723291 REVERSE [20134] 1 522 535	
JCVI_36969	1.125	moderately similar to (238)AT4G37550 Symbols: formamidase, putative / formamide amidohydrolase, putative chr4:17643678-17645	
JCVI_28047	1.124	moderately similar to (364)AT3G04550 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G28500.1); similar to i	
JCVI_42166	1.124	weakly similar to (159)AT2G22490 Symbols: CYCD2;1 CYCD2;1 (CYCLIN D2;1); cyclin-dependent protein kinase regulator/ protein	
ES946106	1.124	no similarity	
EE513355	1.123	weakly similar to (125)AT1G19870 Symbols: IQD32 IQD32 (IQ-domain 32); calmodulin binding chr1:6895391-6898530 REVERSE	
EV110515	1.122	no similarity	
JCVI_4017	1.121	moderately similar to (213)AT2G17710 Symbols: similar to unnamed protein product [Vitis vinifera] (GB:CAO42932.1) chr2:770093	
JCVI_24276	1.121	moderately similar to (385)AT3G27925 Symbols: DEG1, DEG1 DEG1 (DEGP PROTEASE 1); serine-type peptidase chr3:1036789	
EV063703	1.120	moderately similar to (379)AT2G31340 Symbols: EMB1381 EMB1381 (EMBRYO DEFECTIVE 1381) chr2:13368691-13371710 FO	
JCVI_1151	1.120	moderately similar to (255)AT2G47450 Symbols: CAO CAO (CHAOS); chromatin binding chr2:19479851-19480972 FORWARDwez	
JCVI_21174	1.120	moderately similar to (360)AT2G28200 Symbols: nucleic acid binding / transcription factor/ zinc ion binding chr2:12031398-1203225	
ES952320	1.120	moderately similar to (269)AT4G31850 Symbols: PGR3 PGR3 (PROTON GRADIENT REGULATION 3) chr4:15403026-15406364	
JCVI_29162	1.120	highly similar to (594)AT1G24530 Symbols: transducin family protein / WD-40 repeat family protein chr1:8693274-8694530 FORW,	2.110
JCVI_3146	1.117	moderately similar to (358)AT1G06650 Symbols: 2-oxoglutarate-dependent dioxygenase, putative chr1:2035908-2037185 FORWARD	
JCVI_7067	1.116	moderately similar to (439)AT3G06960 Symbols: PDE320 PDE320 (PIGMENT DEFECTIVE 320) chr3:2195222-2196510 REVERSE	1.174
EV111447	1.114	no similarity	

EX065546	1.114	very weakly similar to (80.5)ERG11_BRANA [21815]	
JCVI_4355	1.113	moderately similar to (340)AT2G42490 Symbols: copper amine oxidase, putative chr2:17698678-17702604 REVERSE	Every weakly si
JCVI_11025	1.113	no original description	
EV171250	1.111	weakly similar to (152)AT4G10080 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G13530.1); similar to unkn	
JCVI_28871	1.109	moderately similar to (273)AT3G57810 Symbols: OTU-like cysteine protease family protein chr3:21427313-21428786 FORWARD	n
JCVI_1532	1.107	moderately similar to (228)AT3G52800 Symbols: zinc finger (AN1-like) family protein chr3:19580784-19581296 FORWARD	weakly
EV056658	1.107	very weakly similar to (81.6)AT3G22942 Symbols: AGG2 AGG2 (G-PROTEIN GAMMA SUBUNIT 2) chr3:8134482-8135674 FORW	
JCVI_27351	1.106	moderately similar to (222)AT5G38990 Symbols: protein kinase family protein chr5:15626054-15628696 FORWARD	no original des
JCVI_22281	1.104	moderately similar to (420)AT2G38330 Symbols: MATE efflux family protein chr2:16071649-16074396 FORWARD	no original des
JCVI_5439	1.104	moderately similar to (326)AT4G16370 Symbols: OPT3, ATOPT3 ATOPT3 (OLIGOPEPTIDE TRANSPORTER); oligopeptide transp	
JCVI_31427	1.102	moderately similar to (211)AT5G63860 Symbols: UVR8 UVR8 (UVB-RESISTANCE 8) chr5:25572047-25575813 REVERSE	no orig
ES952239	1.100	moderately similar to (298)AT5G07670 Symbols: F-box family protein chr5:2430422-2432066 FORWARD [21423]	
JCVI_28453	1.100	moderately similar to (211)AT3G08010 Symbols: ATAB2 ATAB2; RNA binding chr3:2556052-2557432 FORWARD	no original desc
JCVI_36393	1.099	no original description	
JCVI_15132	1.099	weakly similar to (173)AT1G51090 Symbols: heavy-metal-associated domain-containing protein chr1:18936653-18937415 FORWAR	
JCVI_8692	1.098	no original description	
JCVI_30678	1.096	moderately similar to (345)AT4G01037 Symbols: similar to EMB1692 (EMBRYO DEFECTIVE 1692) [Arabidopsis thaliana] (TAIR:/	
CV432588	1.096	moderately similar to (215)AT5G20350 Symbols: TIP1 TIP1 (TIP GROWTH DEFECTIVE 1) chr5:6876774-6881104 FORWARD [11	
JCVI_31822	1.095	no original description	
JCVI_40421	1.094	no original description	1.213
JCVI_23938	1.094	moderately similar to (320)AT2G03810 Symbols: 18S pre-ribosomal assembly protein gar2-related chr2:1162700-1164283 FORWAR	
JCVI_12922	1.093	weakly similar to (125)AT1G47500 Symbols: ATRBP47C' ATRBP47C' (RNA-BINDING PROTEIN 47C'); RNA binding chr1:174351	
JCVI_41907	1.093	highly similar to (538)AT5G51890 Symbols: peroxidase chr5:21108389-21109561 REVERSE	moderately similar to (241)PER1_ORY
ES901726	1.091	no similarity	
CV544312	1.090	moderately similar to (209)AT3G27330 Symbols: zinc finger (C3HC4-type RING finger) family protein chr3:10118187-10121753 RE	
EX045943	1.089	no similarity	
JCVI_8063	1.086	moderately similar to (220)AT5G64300 Symbols: ATGCH ATGCH (ARABIDOPSIS THALIANA GTP CYCLOHYDROLASE II); 3,4	
JCVI_41814	1.086	no original description	
EV217832	1.084	no similarity	
JCVI_12678	1.080	moderately similar to (479)AT2G03810 Symbols: 18S pre-ribosomal assembly protein gar2-related chr2:1162700-1164283 FORWAR	
EX090230	1.080	weakly similar to (110)AT1G35460 Symbols: basic helix-loop-helix (bHLH) family protein chr1:13040070-13041885 FORWARD [2	
JCVI_17892	1.079	moderately similar to (295)AT2G40460 Symbols: proton-dependent oligopeptide transport (POT) family protein chr2:16904201-1690	1.167
DY009503	1.078	weakly similar to (111)AT5G66470 Symbols: GTP binding / RNA binding chr5:26559212-26561528 REVERSE [18969] 1 378 455	
JCVI_11911	1.077	highly similar to (542)AT3G23700 Symbols: S1 RNA-binding domain-containing protein chr3:8531696-8533749 REVERSE	weakly s
JCVI_37793	1.077	no original description	
JCVI_42443	1.075	no original description	
JCVI_3872	1.074	moderately similar to (204)AT1G05870 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G31560.1); similar to n	2.265
JCVI_1588	1.072	moderately similar to (406)AT4G27585 Symbols: band 7 family protein chr4:13766990-13769838 REVERSE	no original description
CV433633	1.071	weakly similar to (104)AT1G34780 Symbols: ATAPRL4 ATAPRL4 (APR-LIKE 4) chr1:12748813-12750102 REVERSE [16490] 1 4	
DY015167	1.070	moderately similar to (252)AT3G08010 Symbols: ATAB2 ATAB2; RNA binding chr3:2556052-2557432 FORWARD [18966]	
JCVI_5197	1.068	moderately similar to (239)AT3G58680 Symbols: MBF1B, ATMBF1B ATMBF1B/MBF1B (MULTIPROTEIN BRIDGING FACTOR	
ES266193	1.066	moderately similar to (311)AT4G07960 Symbols: CSLC12, ATCSLC12 ATCSLC12 (Cellulose synthase-like C12); transferase, transfer	
JCVI_38503	1.065	very weakly similar to (87.0)AT2G34720 Symbols: CCAAT-binding transcription factor (CBF-B/NF-YA) family protein chr2:146570	
JCVI_7350	1.064	highly similar to (640)AT1G21780 Symbols: BTB/POZ domain-containing protein chr1:7652465-7653855 FORWARD	no original de
JCVI_10417	1.062	weakly similar to (154)AT3G10410 Symbols: SCPL49 SCPL49 (serine carboxypeptidase-like 49); serine carboxypeptidase chr3:32355	
JCVI_934	1.060	moderately similar to (370)AT3G61440 Symbols: ARATH;BSA53;1, ATCYSC1 ATCYSC1 (BETA-SUBSTITUTED ALA SYNTHAS	
JCVI_18551	1.058	no original description	
JCVI_42045	1.058	weakly similar to (174)AT5G23050 Symbols: acyl-activating enzyme 17 (AAE17) chr5:7731516-7735402 REVERSE	no original desc
JCVI_37755	1.056	no original description	
EVI67683	1.054	weakly similar to (135)AT1G50420 Symbols: SCL-3, SCL3 SCL3 (SCARECROW-LIKE 3); transcription factor chr1:18681845-1868	
JCVI_29481	1.053	moderately similar to (293)AT4G31390 Symbols: ABC1 family protein chr4:15233132-15236770 FORWARD	no original description
JCVI_4086	1.052	moderately similar to (401)AT1G49670 Symbols: ARP protein (REF) chr1:18385259-18389689 REVERSE	Every weakly similar to (90
JCVI_27019	1.051	weakly similar to (149)AT4G22770 Symbols: DNA-binding family protein chr4:11963890-11965450 REVERSE	no original descripti
JCVI_5858	1.050	highly similar to (635)AT1G53750 Symbols: RPT1A RPT1A (regulatory particle triple-A 1A); ATPase chr1:20069589-20071992 REV	
JCVI_10621	1.046	weakly similar to (159)ATCG00660 Symbols: RPL20 encodes a chloroplast ribosomal protein L20, a constituent of the large subunit of	
AM394356	1.045	very weakly similar to (97.4)AT3G60070 Symbols: lactose permease-related chr3:22194554-22196917 REVERSE [20346] 1 372 400	
RC_H74686	1.045	no similarity	
JCVI_16561	1.034	moderately similar to (282)AT1G55140 Symbols: RNA binding / ribonuclease III chr1:20576455-20577999 REVERSE	no original de
JCVI_23123	1.031	very weakly similar to (85.9)AT5G66760 Symbols: SDH1-1 SDH1-1 (Succinate dehydrogenase 1-1) chr5:26671002-26674450 FORW.	
JCVI_21113	1.031	very weakly similar to (82.8)ATCG00905 Symbols: RPS12, RPS12C chloroplast gene encoding ribosomal protein s12. The gene is locat	
BQ704934	1.029	weakly similar to (183)AT1G21780 Symbols: BTB/POZ domain-containing protein chr1:7652465-7653855 FORWARD [11009]	
EVI56226	1.027	no similarity	
RC_CD838260	1.027	no similarity	
JCVI_14373	1.027	moderately similar to (245)AT1G63680 Symbols: ATMURE, PDE316 ATMURE/PDE316 (PIGMENT DEFECTIVE EMBRYO); ATP	
JCVI_27050	1.024	moderately similar to (258)AT5G63790 Symbols: ANAC102 ANAC102 (Arabidopsis NAC domain containing protein 102); transcripti	
JCVI_19595	1.023	moderately similar to (317)AT1G68070 Symbols: zinc finger (C3HC4-type RING finger) family protein chr1:25519075-25520430 RE	
EVI69442	1.021	weakly similar to (134)AT5G02840 Symbols: LCL1 LCL1 (LHY/CCA1-LIKE 1); DNA binding / transcription factor chr5:648792-651	
JCVI_23769	1.019	weakly similar to (182)AT4G33980 Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G42900.2); similar to unkn	1.803
JCVI_4654	1.012	highly similar to (513)AT1G67800 Symbols: copine-related chr1:25424692-25426900 REVERSE	no original description
ES928296	1.009	no similarity	
JCVI_24666	1.005	weakly similar to (132)AT2G37130 Symbols: peroxidase 21 (PER21) (P21) (PRXR5) chr2:15605304-15606813 REVERSE	no origin
JCVI_16888	1.004	moderately similar to (283)AT5G24120 Symbols: SIG5, SIGE SIGE (RNA polymerase sigma subunit E); DNA binding / DNA-directed	
JCVI_7881	1.004	moderately similar to (424)AT4G08700 Symbols: ATPUP13 ATPUP13 (Arabidopsis thaliana purine permease 13); purine transmembra	
JCVI_20818	1.001	moderately similar to (312)AT1G44446 Symbols: ATCAO, CAO, CH1 CH1 (CHLOROPHYLL B BIOSYNTHESIS); chlorophyllide a	1.607
JCVI_5147	0.987	moderately similar to (335)AT3G08010 Symbols: ATAB2 ATAB2; RNA binding chr3:2556052-2557432 FORWARD	no original desc
JCVI_11350	0.969	moderately similar to (373)AT1G71870 Symbols: MATE efflux family protein chr1:27036118-27038557 REVERSE	no original desc
EV226857	0.963	weakly similar to (196)AT5G24470 Symbols: PRR5, APRR5 APRR5 (PSEUDO-RESPONSE REGULATOR 5); transcription regulator	
EVI74833	0.956	no similarity	
JCVI_38057	0.953	moderately similar to (377)AT5G20040 Symbols: ATIPT9 ATIPT9 (Arabidopsis thaliana isopentenyltransferase 9); ATP binding / tRN.	
JCVI_18310	0.935	moderately similar to (281)AT5G02830 Symbols: pentatricopeptide (PPR) repeat-containing protein chr5:644456-648419 REVERSE	
EE535812	0.932	no similarity	
JCVI_33200	0.915	no original description	
CD844622	0.845	no similarity	

EV106399	0.843	no similarity	
EV125308	0.837	no similarity	
ES938100	0.814	moderately similar to (370)AT4G33170 Symbols: pentatricopeptide (PPR) repeat-containing protein chr4:15995704-15998676 REVE	
JCVI_16366	0.811	no original description	
CD824445	0.782	moderately similar to (232)AT3G06880 Symbols: transducin family protein / WD-40 repeat family protein chr3:2169862-2175692 RE	
EV207729	0.694	no similarity	
JCVI_35222	0.648	moderately similar to (276)AT5G51700 Symbols: ATRAR1, RPR2, RAR1, PBS2 PBS2 (PPHB SUSCEPTIBLE 2); protein binding / zii	
RC_ES958174	0.630	no similarity	
EV047064	0.591	weakly similar to (145)AT2G42860 Symbols: unknown protein chr2:17840936-17841724 FORWARD [21442]	
ES927658	0.486	no similarity	
EE550774	0.480	very weakly similar to (83.2)AT2G43730 Symbols: lectin-related chr2:18131898-18132746 REVERSE [20184]	
EV087280	0.308	no similarity	1.730
JCVI_26638	0.049	no original description	

