

Suppl. Table 1

Identifier	UV-control	Induced - Description
EV108519	5.153	moderately similar to (278)AT1G10340   Symbols:   ankyrin repeat family protein
JCVI_40837	4.852	very weakly similar to (91.7)AT2G14610   Symbols: PR-1, PR1   PR1 (PATHOGENESIS-RELATED GENE 1)
JCVI_20479	4.728	moderately similar to (328)AT1G64970   Symbols: TMT1, VTE4, G-TMT   G-TMT (GAMMA-TOCOPHEROL METHYLTRANSFERASE)
JCVI_33787	4.625	moderately similar to (320)AT3G11340   Symbols:   UDP-glucuronosyl/UDP-glucosyl transferase family protein
JCVI_24991	4.308	moderately similar to (372)AT3G57260   Symbols: PR2, BG2, PR-2, BGL2   glucan 1,3-beta-glucosidase/ hydrolase, hydrolyzing O-glycosyl compounds
AI352858	4.302	weakly similar to (112)AT2G14610   Symbols: PR-1, PR1   PR1 (PATHOGENESIS-RELATED GENE 1)
JCVI_26210	4.134	moderately similar to (333)AT1G14040   Symbols:   ATP binding / ATPase, coupled to transmembrane movement of substances
JCVI_37786	4.086	-
EV146444	4.058	-
JCVI_16762	3.991	moderately similar to (348)AT3G13080   Symbols: EST2, MRP3, ATM3P3   ATM3P3 (Arabidopsis thaliana multidrug resistance-associated protein 3)
JCVI_19327	3.813	moderately similar to (490)AT3G57240   Symbols: BG3   BG3 (BETA-1,3-GLUCANASE 3); hydrolase, hydrolyzing O-glycosyl compounds
JCVI_9816	3.812	very weakly similar to (100)AT2G47520   Symbols:   AP2 domain-containing transcription factor, putative
JCVI_291	3.767	moderately similar to (276)AT4G11650   Symbols: ATOSM34   ATOSM34 (OSMOTIN 34)
DN963737	3.668	-
EV116790	3.642	moderately similar to (304)AT5G13320   Symbols: GGD1, WIN3, PBS3   PBS3 (AVRPPHB SUSCEPTIBLE 3)
EV197431	3.612	-
JCVI_9951	3.561	moderately similar to (255)AT3G60140   Symbols: SRG2, DIN2   DIN2 (DARK INDUCIBLE 2); hydrolase, hydrolyzing O-glycosyl compounds
H07446	3.525	-
EV108419	3.457	very weakly similar to (81.3)AT3G60140   Symbols: SRG2, DIN2   DIN2 (DARK INDUCIBLE 2); hydrolase, hydrolyzing O-glycosyl compounds
JCVI_35049	3.450	weakly similar to (154)AT4G34135   Symbols: UGT73B2   UGT73B2; UDP-glycosyltransferase (flavonol 3-O-glucosyltransferase activity)
JCVI_15239	3.404	moderately similar to (298)AT1G19320   Symbols:   pathogenesis-related thaumatin family protein
JCVI_5125	3.375	moderately similar to (300)AT2G16060   Symbols: ARATH GLB1, GLB1, NSHB1, ATGLB1, AHB1   AHB1 (ARABIDOPSIS HEMOGLOBIN 1)
EE422466	3.369	-
JCVI_18994	3.296	moderately similar to (394)AT2G43570   Symbols:   chitinase, putative
JCVI_9441	3.278	moderately similar to (455)AT3G57260   Symbols: PR2, BG2, PR-2, BGL2   glucan 1,3-beta-glucosidase/ hydrolase, hydrolyzing O-glycosyl compounds
EV108922	3.262	moderately similar to (307)AT1G10340   Symbols:   ankyrin repeat family protein
DY027083	3.248	-
JCVI_29399	3.244	-
JCVI_12816	3.228	-
JCVI_18272	3.201	-
JCVI_8263	3.147	moderately similar to (475)AT2G43000   Symbols: ANAC042   ANAC042 (Arabidopsis NAC domain containing protein 42); transcription factor
EE444296	3.099	weakly similar to (175)AT1G45145   Symbols: ATH5, LIV1, ATTRX5   ATTRX5 (thioredoxin H-type 5); thiol-disulfide exchange intermediate
JCVI_29699	3.072	-
H07467	3.070	-
JCVI_12718	3.066	-
JCVI_39172	3.038	-
JCVI_35251	2.994	moderately similar to (490)AT1G03790   Symbols:   zinc finger (CCCH-type) family protein
JCVI_40707	2.973	weakly similar to (147)AT3G25882   Symbols: NIMIN-2   NIMIN-2 (NIM1-INTERACTING 2)
JCVI_18478	2.946	moderately similar to (400)AT1G53990   Symbols: GLIP3   GLIP3 (GDSL-motif lipase 3); carboxylesterase/ lipase
JCVI_16583	2.926	weakly similar to (128)AT3G04720   Symbols: HEL, PR-4, PR4   PR4 (PATHOGENESIS-RELATED 4)
EE518139	2.918	weakly similar to (195)AT2G20800   Symbols: NDB4   NDB4 (NAD(P)H DEHYDROGENASE B4); NADH dehydrogenase
EV108983	2.906	weakly similar to (157)AT1G14080   Symbols: ATFUT6, FUT6   FUT6 (fucosyltransferase 6); fucosyltransferase/ transferase, transferring glycosyl groups
JCVI_12338	2.887	very weakly similar to (89.7)AT5G65207   Symbols:   similar to unknown protein [Arabidopsis thaliana] [AT5G10040.1]
JCVI_7995	2.881	moderately similar to (393)AT3G60140   Symbols: SRG2, DIN2   DIN2 (DARK INDUCIBLE 2); hydrolase, hydrolyzing O-glycosyl compounds
JCVI_40406	2.843	moderately similar to (380)AT3G57260   Symbols: PR2, BG2, PR-2, BGL2   glucan 1,3-beta-glucosidase/ hydrolase, hydrolyzing O-glycosyl compounds
JCVI_15854	2.815	weakly similar to (140)AT2G14610   Symbols: PR-1, PR1   PR1 (PATHOGENESIS-RELATED GENE 1)
AM386985	2.788	weakly similar to (127)AT5G37990   Symbols:   S-adenosylmethionine-dependent methyltransferase
EE434928	2.786	weakly similar to (174)AT1G76680   Symbols: OPR1   OPR1 (12-oxophytodienoate reductase 1); 12-oxophytodienoate reductase
JCVI_5035	2.786	moderately similar to (429)AT5G38100   Symbols:   methyltransferase-related
AM391914	2.785	-
JCVI_8351	2.760	moderately similar to (219)AT5G24530   Symbols:   oxidoreductase, 2OG-Fe(II) oxygenase family protein
JCVI_30	2.749	moderately similar to (364)AT2G02930   Symbols: GST16, ATGSTF3   ATGSTF3 (GLUTATHIONE S-TRANSFERASE 16); glutathione transferase
EE561948	2.735	weakly similar to (130)AT4G1730   Symbols:   similar to unknown protein [AT5G24640.1]
CD824937	2.733	weakly similar to (163)AT5G09680   Symbols:   cytochrome b5 domain-containing protein
JCVI_33065	2.726	weakly similar to (131)AT3G10040   Symbols:   transcription factor
JCVI_36664	2.721	highly similar to (822)AT4G37370   Symbols: CYP81D8   CYP81D8 (cytochrome P450, family 81, subfamily D, polypeptide 8); oxygen binding
H07491	2.721	-
JCVI_27712	2.720	moderately similar to (298)AT3G55230   Symbols:   disease resistance-responsive family protein
JCVI_13432	2.714	moderately similar to (392)AT1G17180   Symbols: ATGSTU25   (Arabidopsis thaliana Glutathione S-transferase (class tau) 25); glutathione transferase
JCVI_37398	2.708	-
JCVI_5462	2.694	weakly similar to (172)AT5G01750   Symbols:   Uncharacterized protein At5g01750; similar to unknown protein [AT3G11740.1]; DUF567 (InterPro:IPR007612)
JCVI_11279	2.692	moderately similar to (262)AT1G04350   Symbols:   2-oxoglutarate-dependent dioxygenase, putative   UV-B responsive
JCVI_41553	2.684	-
EE473027	2.669	very weakly similar to (91.3)AT1G02450   Symbols: NIMIN-1, NIMIN-1   NIMIN-1/NIMIN1; protein binding
EV162033	2.648	moderately similar to (217)AT1G75050   Symbols:   ATLP-3 (Thaumatococcus-like protein 3) [AT1G75030.1]; Thaumatococcus pathogenesis-related (InterPro:IPR01938)
JCVI_798	2.646	moderately similar to (297)AT3G44840   Symbols:   S-adenosyl-L-methionine:carboxyl methyltransferase family protein
EH418095	2.639	moderately similar to (248)AT2G41790   Symbols:   peptidase M16 family protein / insulinase family protein
JCVI_12072	2.632	highly similar to (613)AT3G27060   Symbols: TSO2   TSO2 (TSO MEANING 'UGLY' IN CHINESE); ribonucleoside-diphosphate reductase
JCVI_8068	2.618	weakly similar to (194)AT4G12480   Symbols: pEARLI 1   pEARLI 1; lipid binding
JCVI_8465	2.607	moderately similar to (397)AT1G11330   Symbols:   S-locus lectin protein kinase family protein
DV643299	2.581	moderately similar to (463)AT3G60120   Symbols:   glycosyl hydrolase family 1 protein
JCVI_27211	2.577	highly similar to (692)AT5G67360   Symbols: ARA12   ARA12; subtilase
JCVI_794	2.567	moderately similar to (398)AT4G02850   Symbols:   phenazine biosynthesis PhzC/PhzF family protein
JCVI_36377	2.564	highly similar to (611)AT3G60120   Symbols:   glycosyl hydrolase family 1 protein
EV224604	2.561	-
JCVI_9165	2.560	-
EV169895	2.550	-
JCVI_24173	2.542	highly similar to (774)AT3G60140   Symbols: SRG2, DIN2   DIN2 (DARK INDUCIBLE 2); hydrolase, hydrolyzing O-glycosyl compounds
JCVI_36485	2.536	moderately similar to (353)AT3G11340   Symbols:   UDP-glucuronosyl/UDP-glucosyl transferase family protein
JCVI_10776	2.535	highly similar to (781)AT1G26420   Symbols:   FAD-binding domain-containing protein
JCVI_35521	2.527	moderately similar to (305)AT3G09270   Symbols: ATGSTU8   (Arabidopsis thaliana Glutathione S-transferase (class tau) 8); glutathione transferase
JCVI_24772	2.520	moderately similar to (227)AT2G16900   Symbols:   similar to unknown protein [AT4G35110.2]; InterPro domain Phospholipase-like (InterPro:IPR007942)
EV227118	2.507	weakly similar to (115)AT2G45220   Symbols:   pectinesterase family protein
JCVI_36804	2.499	moderately similar to (285)AT4G31800   Symbols: WRKY18   WRKY18 (WRKY DNA-binding protein 18); transcription factor
JCVI_27491	2.484	moderately similar to (307)AT4G35180   Symbols: LHT7   LHT7 (LYS/HIS TRANSPORTER 7); amino acid transmembrane transporter
JCVI_14946	2.478	moderately similar to (356)AT3G07800   Symbols:   thymidine kinase, putative
JCVI_26368	2.476	moderately similar to (469)AT5G24530   Symbols:   oxidoreductase, 2OG-Fe(II) oxygenase family protein
EX133091	2.450	very weakly similar to (80.9)AT3G14990   Symbols:   4-methyl-5(b-hydroxyethyl)-thiazole monophosphate biosynthesis protein, putative
JCVI_85	2.450	moderately similar to (432)AT3G15356   Symbols:   legume lectin family protein
JCVI_30017	2.448	-
JCVI_20291	2.444	-
JCVI_41280	2.430	-
AM387841	2.424	-
JCVI_28788	2.418	very weakly similar to (99.0)AT5G43570   Symbols:   serine-type endopeptidase inhibitor
JCVI_2406	2.408	moderately similar to (369)AT2G02930   Symbols: GST16, ATGSTF3   ATGSTF3 (GLUTATHIONE S-TRANSFERASE 16); glutathione transferase
ES902140	2.395	weakly similar to (149)AT4G25110   Symbols: ATMC2   ATMC2 (METACASPASE 2); caspase
CX191026	2.393	-
JCVI_8461	2.370	moderately similar to (376)AT1G32450   Symbols:   proton-dependent oligopeptide transport (POT) family protein
ES900687	2.366	moderately similar to (305)AT5G67450   Symbols: AZF1   AZF1 (ZINC-FINGER PROTEIN 1); nucleic acid binding/transcription factor/zinc ion binding
JCVI_16492	2.358	moderately similar to (330)AT4G27670   Symbols: HSP21   HSP21 (HEAT SHOCK PROTEIN 21)

Identifier	UV-control	Reduced - Description
EV226148	-4.006	very weakly similar to (85.9)AT1G12610  Symbols: DDF1   DDF1 (DWARF AND DELAYED FLOWERING 1); DNA binding / transcription factor
JCVI_11950	-3.761	weakly similar to (103)AT1G12610  Symbols: DDF1   DDF1 (DWARF AND DELAYED FLOWERING 1); DNA binding / transcription factor
JCVI_21273	-3.422	weakly similar to (189)AT4G34410  Symbols:   AP2 domain-containing transcription factor, putative
EV205209	-3.403	-
EE549228	-3.341	very weakly similar to (91.3)AT3G50060  Symbols: MYB77   MYB77; DNA binding / transcription factor
EV101357	-3.322	weakly similar to (173)AT2G20790  Symbols:   protein binding / protein transporter
JCVI_11230	-3.221	highly similar to (841)AT5G23050  Symbols:   acyl-activating enzyme 17 (AAE17)
EV169330	-3.194	-
EE561702	-3.191	-
JCVI_41856	-3.056	moderately similar to (224)AT1G74930  Symbols: ORA47   ORA47; DNA binding / transcription factor  original descriptor
JCVI_12658	-2.992	weakly similar to (170)AT5G52300  Symbols: RD29B, LTI65   LTI65/RD29B (RESPONSIVE TO DESSICATION 29B)   no original descriptor
JCVI_16557	-2.887	moderately similar to (273)AT3G50060  Symbols: MYB77   DNA binding / transcription factor  similar to (102)MYBA1_ORYSA no original descriptor
EV142036	-2.794	-
JCVI_6654	-2.781	moderately similar to (272)AT4G32800  Symbols:   AP2 domain-containing transcription factor TINY, putative
JCVI_10390	-2.695	moderately similar to (476)AT5G62520  Symbols: SRO5   SRO5 (SIMILAR TO RCD ONE 5); NAD+ ADP-ribosyltransferase
EE443906	-2.688	weakly similar to (152)AT2G02240  Symbols: MEE66   MEE66 (maternal effect embryo arrest 66)
JCVI_11582	-2.644	highly similar to (734)AT1G63420  Symbols:   similar to unknown protein (AT5G23850.1); contains domain DUF821, CAP10-like (InterPro:IPR008539)
JCVI_40140	-2.605	moderately similar to (340)AT1G10090  Symbols:   similar to RXW8 (AT1G58520.1); contains domain of unknown function DUF221; (InterPro:IPR003864)
JCVI_20197	-2.605	-
JCVI_18770	-2.593	very weakly similar to (89.0)AT5G52300  Symbols: RD29B, LTI65   LTI65/RD29B (RESPONSIVE TO DESSICATION 29B)
JCVI_17105	-2.591	very weakly similar to (97.1)AT5G52300  Symbols: RD29B, LTI65   LTI65/RD29B (RESPONSIVE TO DESSICATION 29B)
H74571	-2.589	-
JCVI_14413	-2.565	-
JCVI_26301	-2.513	moderately similar to (240)AT1G19210  Symbols:   AP2 domain-containing transcription factor, putative
JCVI_13070	-2.463	-
H74394	-2.450	weakly similar to (115)AT1G12630  Symbols:   DNA binding / transcription activator/ transcription factor
RC_BQ704694	-2.436	-
JCVI_38370	-2.382	moderately similar to (416)AT4G29780  Symbols:   similar to unknown protein (AT5G12010.1); contains domain PTHR22930 (PTHR22930)
EX135872	-2.373	moderately similar to (384)AT1G10090  Symbols:   similar to RXW8 (AT1G58520.1); contains InterPro domain DUF221; (InterPro:IPR003864)
JCVI_20564	-2.367	weakly similar to (144)AT5G62520  Symbols: SRO5   SRO5 (SIMILAR TO RCD ONE 5); NAD+ ADP-ribosyltransferase
JCVI_32755	-2.363	moderately similar to (259)AT4G01360  Symbols:   similar to BPS1 (BYPASS 1) (AT1G01550.2)
EE455964	-2.360	very weakly similar to (89.4)AT5G44005  Symbols:   unknown protein
H74709	-2.331	very weakly similar to (93.6)AT3G57010  Symbols:   strictosidine synthase family protein
JCVI_34763	-2.296	weakly similar to (118)AT3G19170  Symbols: BCAT4   (BRANCHED-CHAIN AMINOTRANSFERASE4); catalytic/ methionine-oxo-acid transaminase
EE434350	-2.286	-
JCVI_32987	-2.281	moderately similar to (204)AT5G62520  Symbols: SRO5   SRO5 (SIMILAR TO RCD ONE 5); NAD+ ADP-ribosyltransferase
JCVI_6514	-2.269	moderately similar to (318)AT3G57010  Symbols:   strictosidine synthase family protein
JCVI_7541	-2.251	very weakly similar to (93.6)AT1G62510  Symbols:   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein
JCVI_20042	-2.246	moderately similar to (349)AT5G45340  Symbols: CYP707A3   CYP707A3 (cytochrome P450, family 707, subfamily A, polypeptide 3); oxygen binding
JCVI_41582	-2.224	very weakly similar to (85.5)AT3G49370  Symbols:   calcium-dependent protein kinase, putative / CDPK, putative
JCVI_22998	-2.200	-
EV169436	-2.200	weakly similar to (133)AT2G16660  Symbols:   nodulin family protein
JCVI_15401	-2.164	weakly similar to (111)AT2G02240  Symbols: MEE66   MEE66 (maternal effect embryo arrest 66)
EV117567	-2.108	very weakly similar to (91.3)AT3G06760  Symbols:   identical to DEHYDRATION-INDUCED 19 (DI19-4); similar to HRB1 (AT5G49230.1)
EE524030	-2.098	very weakly similar to (80.1)AT3G46620  Symbols:   zinc finger (C3HC4-type RING finger) family protein
JCVI_18326	-2.097	moderately similar to (384)AT4G01360  Symbols:   similar to BPS1 (BYPASS 1) (AT1G01550.2); similar to BPS1 (BYPASS 1) (TAIR:AT1G01550.1)
JCVI_4859	-2.091	moderately similar to (210)AT1G65980  Symbols: TPX1   TPX1 (THIOREDOXIN-DEPENDENT PEROXIDASE 1); antioxidant
JCVI_31515	-2.088	moderately similar to (356)AT1G13560  Symbols: AAPT1   AAPT1 (AMINOALCOHOLPHOSPHOTRANSFERASE 1); phosphatidyltransferase
ES978129	-2.078	very weakly similar to (91.3)AT5G63350  Symbols:   similar to unknown protein (AT3G48510.1)
JCVI_669	-2.072	moderately similar to (315)AT4G17490  Symbols: ERF-6-6, ATERF6   (ETHYLENE RESPONSIVE FACTOR 6); DNA binding / transcription factor
AM386021	-2.070	-
JCVI_1043	-2.043	-
JCVI_1570	-2.035	moderately similar to (495)AT3G57010  Symbols:   strictosidine synthase family protein
JCVI_23374	-2.016	-
JCVI_39109	-2.010	moderately similar to (201)AT5G23130  Symbols:   peptidoglycan-binding LysM domain-containing protein
JCVI_36253	-2.001	moderately similar to (437)AT4G11280  Symbols:   ACS6 (1-AMINOCYCLOPROPANE-1-CARBOXYLIC ACID (ACC) SYNTHASE 6)
DT317662	-1.998	very weakly similar to (80.1)AT3G19030  Symbols:   similar to unknown protein (AT1G49500.1)
JCVI_27977	-1.968	moderately similar to (384)AT5G23130  Symbols:   peptidoglycan-binding LysM domain-containing protein
JCVI_3132	-1.964	moderately similar to (321)AT2G27080  Symbols:   harpin-induced protein-related / HIN1-related / harpin-responsive protein-related
JCVI_36420	-1.950	-
EX100533	-1.950	weakly similar to (167)AT1G09950  Symbols:   transcription factor-related
JCVI_34761	-1.940	weakly similar to (129)AT2G34600  Symbols: JAZ7, TIFY5B   JAZ7/TIFY5B (IASMONATE-ZIM-DOMAIN PROTEIN 7)
JCVI_38038	-1.938	weakly similar to (136)AT5G66650  Symbols:   similar to unknown protein (AT2G23790.1); domain of unknown function DUF607 (InterPro:IPR006769)
EV133613	-1.934	-
H07351	-1.932	very weakly similar to (85.9)AT5G17350  Symbols:   similar to unknown protein (AT3G03280.1)
JCVI_40884	-1.918	weakly similar to (146)AT4G29780  Symbols:   similar to unknown protein (AT5G12010.1); contains domain PTHR22930 (PTHR22930)
JCVI_5550	-1.917	highly similar to (577)AT5G14200  Symbols:   3-isopropylmalate dehydrogenase, chloroplast, putative
EX142036	-1.906	weakly similar to (143)AT5G64260  Symbols:   phosphate-responsive protein, putative
JCVI_16456	-1.903	moderately similar to (367)AT3G15540  Symbols: MSG2, IAA19   IAA19 (indoleacetic acid-induced protein 19); transcription factor
EX125776	-1.900	moderately similar to (435)AT5G40800  Symbols:   similar to unknown protein (AT3G27250.1)
JCVI_2577	-1.897	moderately similar to (264)AT5G05270  Symbols:   chalcone-flavanone isomerase family protein
JCVI_8892	-1.895	moderately similar to (261)AT2G15970  Symbols: WCOR413, ATCOR413-PM1, FL3-5A3   COR413-PM1 (cold regulated 413 plasma membrane 1)
JCVI_17114	-1.895	moderately similar to (344)AT1G18300  Symbols: ATNUDT4   ATNUDT4 (Arabidopsis thaliana Nudix hydrolase homolog 4); hydrolase
JCVI_11726	-1.895	highly similar to (898)AT1G30360  Symbols: ERD4   ERD4 (EARLY-RESPONSIVE TO DEHYDRATION 4)
JCVI_30455	-1.881	moderately similar to (415)AT5G23010  Symbols: IMS3, MAM1   MAM1 (2-isopropylmalate synthase 3); 2-isopropylmalate synthase
EX056879	-1.873	very weakly similar to (84)AT1G16410  Symbols: BUS1, SP51, BUSHY 1, CYP79F1, SUPERSHOOT 1, CYTOCHROME P450 79F:
JCVI_8258	-1.856	weakly similar to (144)AT2G46490  Symbols:   similar to unknown protein [Arabidopsis thaliana] [AT5G35110.1]
JCVI_2436	-1.852	moderately similar to (377)AT1G54040  Symbols: ESR, TASTY, ESP   ESP (EPITHIOSPECIFIER PROTEIN)
EV008234	-1.849	weakly similar to (145)AT3G59350  Symbols:   serine/threonine protein kinase, putative
JCVI_14524	-1.847	moderately similar to (243)AT3G11410  Symbols: ATPP2CA, AHG3   (PROTEIN PHOSPHATASE 2CA); protein binding / serine/threonine phosphatase
EV108573	-1.839	-
JCVI_18666	-1.839	weakly similar to (136)AT2G17660  Symbols:   nitrate-responsive NOI protein, putative
JCVI_20622	-1.834	-
JCVI_36200	-1.831	weakly similar to (108)AT2G16660  Symbols:   nodulin family protein
JCVI_17081	-1.828	weakly similar to (108)AT5G17350  Symbols:   similar to unknown protein (AT3G03280.1)
JCVI_81	-1.825	moderately similar to (409)AT1G80840  Symbols: ATWRKY40, WRKY40   WRKY40 (WRKY DNA-binding protein 40); transcription factor
CV545450	-1.824	moderately similar to (218)AT4G17970  Symbols:   similar to unknown protein (AT5G46600.1; AT5G46610.1); contains UPF0005 (InterPro:IPR006214)
JCVI_11504	-1.818	moderately similar to (361)AT1G18300  Symbols: ATNUDT4   ATNUDT4 (Arabidopsis thaliana Nudix hydrolase homolog 4); hydrolase
JCVI_7373	-1.817	moderately similar to (264)AT3G11930  Symbols:   universal stress protein (USP) family protein
JCVI_31468	-1.815	moderately similar to (469)AT5G67480  Symbols: BT4   BT4 (BTB AND TAZ DOMAIN PROTEIN 4); protein binding
JCVI_38563	-1.799	weakly similar to (138)AT3G19580  Symbols: AZF2   AZF2 (ARABIDOPSIS ZINC-FINGER PROTEIN 2)
JCVI_20274	-1.780	weakly similar to (182)AT2G30020  Symbols:   protein phosphatase 2C, putative / PP2C, putative
EE567609	-1.774	-
EE401951	-1.770	weakly similar to (169)AT5G23010  Symbols: IMS3, MAM1   MAM1 (2-isopropylmalate synthase 3); 2-isopropylmalate synthase
JCVI_3974	-1.768	moderately similar to (380)AT5G13930  Symbols: CHS, TT4, ATCHS   ATCHS/CHS/TT4 (CHALCONE SYNTHASE); naringenin-chalcone synthase
JCVI_23235	-1.767	moderately similar to (379)AT5G14950  Symbols: GMII, ATGMII   ATGMII/GMII (GOLGI ALPHA-MANNOSIDASE II); alpha-mannosidase
JCVI_32566	-1.759	highly similar to (712)AT1G30360  Symbols: ERD4   ERD4 (EARLY-RESPONSIVE TO DEHYDRATION 4)
EX131720	-1.744	-
JCVI_17662	-1.737	moderately similar to (475)AT4G32480  Symbols:   similar to unknown protein (AT2G20670.1); contains domain DUF506, plant (InterPro:IPR006502)
EV215033	-1.735	-

Identifier	UV-control	Flavonoide - Description
ex131200	1.801	moderately similar to (446)AT5G49690   Symbols:   UDP-glucuronosyl/UDP-glucosyl transferase family protein
jcv1_30937	1.130	weakly similar to (137)AT5G39080   Symbols:   transferase family protein
ev009114	1.085	moderately similar to (375)AT4G10490   Symbols:   oxidoreductase, 2OG-Fe(II) oxygenase family protein
am062005	0.855	moderately similar to (264)AT3G29635   Symbols:   transferase family protein
jcv1_13173	0.696	moderately similar to (455)AT1G80820   Symbols: CCR2   CCR2 (CINNAMOYL COA REDUCTASE)
jcv1_27419	0.666	moderately similar to (356)AT5G39080   Symbols:   transferase family protein
jcv1_4502	0.644	highly similar to (560)AT1G80820   Symbols: CCR2   CCR2 (CINNAMOYL COA REDUCTASE)
es910915	0.603	moderately similar to (347)AT3G29680   Symbols:   transferase family protein
am056777	0.581	moderately similar to (272)AT3G29670   Symbols:   transferase family protein
jcv1_809	0.579	moderately similar to (258)AT3G29635   Symbols:   transferase family protein
jcv1_5913	0.510	highly similar to (571)AT5G58490   Symbols:   cinnamoyl-CoA reductase family
jcv1_7599	0.505	moderately similar to (262)AT3G10340   Symbols: PAL4   phenylalanine ammonia-lyase, putative
jcv1_243	0.483	moderately similar to (426)AT1G19540   Symbols:   isoflavone reductase, putative
jcv1_5637	0.407	highly similar to (626)AT3G29635   Symbols:   transferase family protein
cd826733	0.382	moderately similar to (227)AT4G10490   Symbols:   oxidoreductase, 2OG-Fe(II) oxygenase family protein
es917670	0.330	moderately similar to (333)AT1G78550   Symbols:   oxidoreductase, 2OG-Fe(II) oxygenase family protein
cx280917	0.326	weakly similar to (131)AT1G78550   Symbols:   oxidoreductase, 2OG-Fe(II) oxygenase family protein
jcv1_814	0.315	highly similar to (602)AT1G15950   Symbols: IRX4, ATCCR1, CCR1   CCR1 (CINNAMOYL COA REDUCTASE 1)
jcv1_811	0.303	highly similar to (608)AT1G68540   Symbols:   oxidoreductase family protein
jcv1_27081	0.302	highly similar to (736)AT4G34850   Symbols:   chalcone and stilbene synthase family protein
ex131530	0.255	weakly similar to (131)AT3G55120   Symbols: TT5, A11, CFI   A11/CFI/TT5 (TRANSPARENT TESTA 5); chalcone isomerase
jcv1_5348	0.253	moderately similar to (393)AT4G27250   Symbols:   dihydroflavonol 4-reductase family / dihydrokaempferol 4-reductase family
jcv1_7597	0.219	moderately similar to (435)AT1G75280   Symbols:   isoflavone reductase, putative
jcv1_28194	0.215	highly similar to (590)AT5G39080   Symbols:   transferase family protein
jcv1_24927	0.205	moderately similar to (305)AT5G39050   Symbols:   transferase family protein
jcv1_14166	0.183	highly similar to (504)AT1G59950   Symbols:   aldo/keto reductase, putative
ev046864	0.167	weakly similar to (101)AT5G63590   Symbols: FLS   FLS (Flavonol synthase); flavonol synthase
jcv1_13093	0.161	moderately similar to (479)AT3G29635   Symbols:   transferase family protein
el589299	0.142	moderately similar to (254)AT3G29670   Symbols:   transferase family protein
jcv1_15733	0.125	moderately similar to (260)AT4G00040   Symbols:   chalcone and stilbene synthase family protein
jcv1_9569	0.124	moderately similar to (442)AT1G75280   Symbols:   isoflavone reductase, putative
jcv1_3751	0.118	moderately similar to (281)AT3G11180   Symbols:   oxidoreductase, 2OG-Fe(II) oxygenase family protein
cn829121	0.103	weakly similar to (163)AT4G10490   Symbols:   oxidoreductase, 2OG-Fe(II) oxygenase family protein
dy029766	0.094	moderately similar to (234)AT3G49620   Symbols: DIN11   DIN11 (DARK INDUCIBLE 11); oxidoreductase
jcv1_15782	0.079	moderately similar to (263)AT4G00040   Symbols:   chalcone and stilbene synthase family protein
ev137509	0.070	weakly similar to (184)AT4G35420   Symbols:   dihydroflavonol 4-reductase family / dihydrokaempferol 4-reductase family
jcv1_512	0.062	moderately similar to (355)AT1G53520   Symbols:   chalcone-flavanone isomerase-related
ex140051	0.057	weakly similar to (153)AT4G10500   Symbols:   oxidoreductase, 2OG-Fe(II) oxygenase family protein
ev151622	0.056	moderately similar to (265)AT4G35420   Symbols:   dihydroflavonol 4-reductase family / dihydrokaempferol 4-reductase family
jcv1_19465	0.055	weakly similar to (136)AT5G08640   Symbols: FLS   FLS (FLAVONOL SYNTHASE)
jcv1_15212	0.046	highly similar to (863)AT2G37040   Symbols: PAL1   PAL1 (PHE AMMONIA LYASE 1); phenylalanine ammonia-lyase
jcv1_3980	0.037	moderately similar to (386)AT4G34540   Symbols:   isoflavone reductase family protein
jcv1_35449	0.032	weakly similar to (174)AT4G35420   Symbols:   dihydroflavonol 4-reductase family / dihydrokaempferol 4-reductase family
ee502236	0.031	weakly similar to (129)AT5G08640   Symbols: FLS   FLS (FLAVONOL SYNTHASE)
jcv1_39687	0.029	weakly similar to (176)AT5G63590   Symbols: FLS   FLS (Flavonol synthase); flavonol synthase
ev103250	0.027	moderately similar to (288)AT3G29670   Symbols:   transferase family protein
jcv1_11314	0.027	moderately similar to (360)AT3G29670   Symbols:   transferase family protein
ev002180	0.023	moderately similar to (273)AT5G13930   Symbols: CHS, TT4, ATCHS   ATCHS/CHS/TT4 (CHALCONE SYNTHASE); naringenin-chalcone synthase
jcv1_17935	0.022	moderately similar to (358)AT5G13930   Symbols: CHS, TT4, ATCHS   ATCHS/CHS/TT4 (CHALCONE SYNTHASE); naringenin-chalcone synthase
jcv1_10248	0.021	moderately similar to (450)AT3G49620   Symbols: DIN11   DIN11 (DARK INDUCIBLE 11); oxidoreductase
ev005315	0.021	weakly similar to (169)AT5G13930   Symbols: CHS, TT4, ATCHS   ATCHS/CHS/TT4 (CHALCONE SYNTHASE); naringenin-chalcone synthase
jcv1_10836	0.018	weakly similar to (199)AT4G34850   Symbols:   chalcone and stilbene synthase family protein
jcv1_888	0.017	moderately similar to (386)AT4G00040   Symbols:   chalcone and stilbene synthase family protein
es947547	0.015	moderately similar to (262)AT5G42800   Symbols: TT3, M318, DFR   DFR (DIHYDROFLAVONOL 4-REDUCTASE); dihydrokaempferol 4-reductase
jcv1_37282	0.012	moderately similar to (479)AT1G35190   Symbols:   oxidoreductase, 2OG-Fe(II) oxygenase family protein
jcv1_34084	0.012	moderately similar to (343)AT1G78550   Symbols:   oxidoreductase, 2OG-Fe(II) oxygenase family protein
eg020925	0.010	weakly similar to (111)AT3G29680   Symbols:   transferase family protein
jcv1_9810	0.006	moderately similar to (477)AT3G29670   Symbols:   transferase family protein
jcv1_20556	0.000	moderately similar to (224)AT2G39980   Symbols:   transferase family protein
ev227471	-0.001	weakly similar to (115)AT1G75290   Symbols:   isoflavone reductase, putative
ex125779	-0.005	moderately similar to (201)AT1G75280   Symbols:   isoflavone reductase, putative
jcv1_18538	-0.007	moderately similar to (293)AT3G55120   Symbols: TT5, A11, CFI   A11/CFI/TT5 (TRANSPARENT TESTA 5); chalcone isomerase
jcv1_19635	-0.010	moderately similar to (281)AT4G33360   Symbols:   terpene cyclase/mutase-related
jcv1_19635	-0.010	moderately similar to (281)AT4G33360   Symbols:   terpene cyclase/mutase-related
ex132195	-0.010	moderately similar to (229)AT3G29670   Symbols:   transferase family protein
jcv1_8954	-0.014	moderately similar to (336)AT5G49690   Symbols:   UDP-glucuronosyl/UDP-glucosyl transferase family protein
jcv1_8954	-0.014	moderately similar to (336)AT5G49690   Symbols:   UDP-glucuronosyl/UDP-glucosyl transferase family protein
cd814611	-0.018	moderately similar to (262)AT1G50580   Symbols:   glycosyltransferase family protein
ev216381	-0.024	weakly similar to (194)AT5G63590   Symbols: FLS   FLS (Flavonol synthase); flavonol synthase
jcv1_31142	-0.025	moderately similar to (363)AT3G55120   Symbols: TT5, A11, CFI   A11/CFI/TT5 (TRANSPARENT TESTA 5); chalcone isomerase
ex130280	-0.027	weakly similar to (163)AT3G29670   Symbols:   transferase family protein
jcv1_6971	-0.028	moderately similar to (314)AT1G61720   Symbols: BAN   BAN (BANYULS)
jcv1_14319	-0.030	moderately similar to (303)AT5G39080   Symbols:   transferase family protein
ev055145	-0.031	moderately similar to (211)AT3G29670   Symbols:   transferase family protein
ev043129	-0.033	weakly similar to (105)AT4G27250   Symbols:   dihydroflavonol 4-reductase family / dihydrokaempferol 4-reductase family
ex138257	-0.036	moderately similar to (436)AT3G46490   Symbols:   oxidoreductase, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor
jcv1_1900	-0.037	highly similar to (538)AT4G33360   Symbols:   terpene cyclase/mutase-related
ev103220	-0.041	weakly similar to (122)AT1G75290   Symbols:   isoflavone reductase, putative
ee517895	-0.051	moderately similar to (283)AT1G78550   Symbols:   oxidoreductase, 2OG-Fe(II) oxygenase family protein
jcv1_15361	-0.053	moderately similar to (367)AT3G49620   Symbols: DIN11   DIN11 (DARK INDUCIBLE 11); oxidoreductase
ev206420	-0.059	weakly similar to (124)AT4G01070   Symbols: GT72B1   GT72B1: UDP-glucosyltransferase/UDP-glucosyltransferase
ex035802	-0.060	moderately similar to (275)AT3G11180   Symbols:   oxidoreductase, 2OG-Fe(II) oxygenase family protein
ex035802	-0.060	moderately similar to (275)AT3G11180   Symbols:   oxidoreductase, 2OG-Fe(II) oxygenase family protein
cd836896	-0.062	weakly similar to (155)AT3G29670   Symbols:   transferase family protein
ev092581	-0.070	weakly similar to (145)AT3G49620   Symbols: DIN11   DIN11 (DARK INDUCIBLE 11); oxidoreductase
ev141692	-0.073	weakly similar to (137)AT4G34850   Symbols:   chalcone and stilbene synthase family protein
ee502168	-0.074	weakly similar to (192)AT4G27560   Symbols:   glycosyltransferase family protein
jcv1_38573	-0.080	weakly similar to (177)AT4G35420   Symbols:   dihydroflavonol 4-reductase family / dihydrokaempferol 4-reductase family
jcv1_18743	-0.080	moderately similar to (327)AT4G25300   Symbols:   oxidoreductase, 2OG-Fe(II) oxygenase family protein
jcv1_6646	-0.081	moderately similar to (434)AT5G39080   Symbols:   transferase family protein
ee477750	-0.083	weakly similar to (197)AT3G13610   Symbols:   oxidoreductase, 2OG-Fe(II) oxygenase family protein
jcv1_8547	-0.084	moderately similar to (301)AT4G35420   Symbols:   dihydroflavonol 4-reductase family / dihydrokaempferol 4-reductase family
jcv1_9319	-0.085	weakly similar to (166)AT1G32100   Symbols:   pinorensinol-laricresinol reductase, putative
jcv1_10710	-0.089	nearly identical (1101)AT3G53260   Symbols: PAL2   PAL2 (phenylalanine ammonia-lyase 2); phenylalanine ammonia-lyase
es954613	-0.089	moderately similar to (209)AT1G53520   Symbols:   chalcone-flavanone isomerase-related
ev160950	-0.093	moderately similar to (206)AT4G00040   Symbols:   chalcone and stilbene synthase family protein
ex028955	-0.093	moderately similar to (222)AT3G29635   Symbols:   transferase family protein
ev227494	-0.100	weakly similar to (191)AT1G75280   Symbols:   isoflavone reductase, putative
jcv1_14420	-0.100	highly similar to (503)AT1G61720   Symbols: BAN   BAN (BANYULS)
jcv1_21743	-0.102	weakly similar to (183)AT4G34850   Symbols:   chalcone and stilbene synthase family protein
ex090926	-0.115	moderately similar to (327)AT3G29680   Symbols:   transferase family protein
jcv1_22524	-0.116	weakly similar to (136)AT4G35420   Symbols:   dihydroflavonol 4-reductase family / dihydrokaempferol 4-reductase family
jcv1_2460	-0.123	moderately similar to (387)AT1G02050   Symbols:   chalcone and stilbene synthase family protein
ev092986	-0.129	moderately similar to (321)AT1G25460   Symbols:   oxidoreductase family protein
jcv1_3312	-0.131	moderately similar to (367)AT2G18570   Symbols:   UDP-glucuronosyl/UDP-glucosyl transferase family protein
jcv1_5	-0.136	moderately similar to (415)AT1G02050   Symbols:   chalcone and stilbene synthase family protein
jcv1_25102	-0.144	moderately similar to (235)AT4G35420   Symbols:   dihydroflavonol 4-reductase family / dihydrokaempferol 4-reductase family
jcv1_23968	-0.146	highly similar to (549)AT1G32100   Symbols:   pinorensinol-laricresinol reductase, putative
jcv1_26671	-0.147	moderately similar to (262)AT4G39230   Symbols:   isoflavone reductase, putative
ee435741	-0.150	weakly similar to (155)AT1G01390   Symbols:   UDP-glucuronosyl/UDP-glucosyl transferase family protein
jcv1_26515	-0.161	weakly similar to (136)AT5G13930   Symbols: CHS, TT4, ATCHS   ATCHS/CHS/TT4 (CHALCONE SYNTHASE); naringenin-chalcone synthase
jcv1_17602	-0.162	moderately similar to (279)AT3G53260   Symbols: PAL2   PAL2 (phenylalanine ammonia-lyase 2); phenylalanine ammonia-lyase
jcv1_14094	-0.208	highly similar to (582)AT2G02400   Symbols:   cinnamoyl-CoA reductase family
jcv1_20189	-0.210	moderately similar to (279)AT3G55120   Symbols: TT5, A11, CFI   A11/CFI/TT5 (TRANSPARENT TESTA 5); chalcone isomerase
jcv1_26257	-0.210	moderately similar to (431)AT1G25460   Symbols:   oxidoreductase family protein
am394517	-0.211	weakly similar to (105)AT4G35420   Symbols:   dihydroflavonol 4-reductase family / dihydrokaempferol 4-reductase family

ee421317	-0.213	moderately similar to ( 226)AT3G29670	Symbols:   transferase family protein
jvci_10975	-0.236	moderately similar to ( 387)AT3G53260	Symbols: PAL2   PAL2 (phenylalanine ammonia-lyase 2); phenylalanine ammonia-lyase
jvci_37761	-0.245	highly similar to ( 549)AT4G39230	Symbols:   isoflavone reductase, putative
jvci_19663	-0.283	highly similar to ( 697)AT3G53260	Symbols: PAL2   PAL2 (phenylalanine ammonia-lyase 2); phenylalanine ammonia-lyase
jvci_20382	-0.287	moderately similar to ( 385)AT1G53520	Symbols:   chalcone-flavanone isomerase-related
jvci_32380	-0.292	moderately similar to ( 428)AT3G53260	Symbols: PAL2   PAL2 (phenylalanine ammonia-lyase 2); phenylalanine ammonia-lyase
cd819938	-0.300	weakly similar to ( 140)AT2G45400	Symbols: BEN1   BEN1; oxidoreductase, acting on CH-OH group of donors
dt317691	-0.312	weakly similar to ( 104)AT3G53260	Symbols: PAL2   PAL2 (phenylalanine ammonia-lyase 2); phenylalanine ammonia-lyase
jvci_23208	-0.335	moderately similar to ( 491)AT1G35190	Symbols:   oxidoreductase_2OG-Fe(II) oxygenase family protein
am389689	-0.345	weakly similar to ( 147)AT2G29730	Symbols:   UDP-glucuronosyl/UDP-glucosyl transferase family protein
jvci_14516	-0.355	weakly similar to ( 170)AT1G19540	Symbols:   isoflavone reductase, putative
jvci_41972	-0.358	moderately similar to ( 312)AT5G63580	Symbols:   flavonol synthase, putative
jvci_9433	-0.393	moderately similar to ( 444)AT2G33590	Symbols:   cinnamoyl-CoA reductase family
jvci_31462	-0.402	moderately similar to ( 216)AT2G37040	Symbols: PAL1   PAL1 (PHE AMMONIA LYASE 1); phenylalanine ammonia-lyase
jvci_22515	-0.431	highly similar to ( 882)AT3G10340	Symbols: PAL4   phenylalanine ammonia-lyase, putative
jvci_27862	-0.529	moderately similar to ( 306)AT2G45400	Symbols: BEN1   BEN1; oxidoreductase, acting on CH-OH group of donors
ee418726	-0.567	moderately similar to ( 307)AT2G37040	Symbols: PAL1   PAL1 (PHE AMMONIA LYASE 1); phenylalanine ammonia-lyase
jvci_2239	-0.622	weakly similar to ( 196)AT5G63590	Symbols: FLS   FLS (Flavonol synthase); flavonol synthase
jvci_13216	-0.647	highly similar to ( 868)AT2G37040	Symbols: PAL1   PAL1 (PHE AMMONIA LYASE 1); phenylalanine ammonia-lyase
ee515919	-0.703	weakly similar to ( 149)AT2G45400	Symbols: BEN1   BEN1; oxidoreductase, acting on CH-OH group of donors
jvci_26334	-0.797	highly similar to ( 535)AT1G75280	Symbols:   isoflavone reductase, putative
ev152862	-0.805	moderately similar to ( 381)AT2G37040	Symbols: PAL1   PAL1 (PHE AMMONIA LYASE 1); phenylalanine ammonia-lyase
cd834583	-0.817	moderately similar to ( 283)AT3G55120	Symbols: TT5, A11, CFI   A11/CFI/TT5 (TRANSPARENT TESTA 5); chalcone isomerase
jvci_12895	-0.864	moderately similar to ( 358)AT5G54010	Symbols:   glycosyltransferase family protein
dy010548	-0.929	weakly similar to ( 109)AT4G01070	Symbols: GT72B1   GT72B1; UDP-glucosyltransferase/ UDP-glucosyltransferase/ transferase
dy025170	-0.955	moderately similar to ( 404)AT5G54060	Symbols: UF3GT   UF3GT (UDP-GLUCOSE:FLAVONOID 3-O-GLUCOSYLTRANSFERASE); transferase
jvci_17031	-0.959	moderately similar to ( 444)AT3G51240	Symbols: TT6, F3H, F3H   F3H (TRANSPARENT TESTA 6); naringenin 3-dioxygenase
jvci_38481	-0.965	moderately similar to ( 288)AT1G75280	Symbols:   isoflavone reductase, putative
jvci_11889	-1.089	moderately similar to ( 307)AT5G42800	Symbols: TT3, M318, DFR   DFR (DIHYDROFLAVONOL 4-REDUCTASE); dihydrokaempferol 4-reductase
jvci_18158	-1.092	moderately similar to ( 219)AT4G22880	Symbols: TDS4, TT18, ANS, LDOX   LDOX (TANNIN DEFICIENT SEED 4)
jvci_1334	-1.115	weakly similar to ( 172)AT5G13930	Symbols: CHS, TT4, ATCHS   ATCHS/CHS/TT4 (CHALCONE SYNTHASE); naringenin-chalcone synthase
jvci_2411	-1.195	moderately similar to ( 468)AT5G13930	Symbols: CHS, TT4, ATCHS   ATCHS/CHS/TT4 (CHALCONE SYNTHASE); naringenin-chalcone synthase
jvci_13996	-1.204	weakly similar to ( 171)AT4G01070	Symbols: GT72B1   GT72B1; UDP-glucosyltransferase/ UDP-glucosyltransferase/ transferase
jvci_6210	-1.460	moderately similar to ( 303)AT5G13930	Symbols: CHS, TT4, ATCHS   ATCHS/CHS/TT4 (CHALCONE SYNTHASE); naringenin-chalcone synthase
jvci_2058	-1.573	moderately similar to ( 454)AT5G13930	Symbols: CHS, TT4, ATCHS   ATCHS/CHS/TT4 (CHALCONE SYNTHASE); naringenin-chalcone synthase
jvci_2414	-1.597	moderately similar to ( 441)AT5G13930	Symbols: CHS, TT4, ATCHS   ATCHS/CHS/TT4 (CHALCONE SYNTHASE); naringenin-chalcone synthase
jvci_2934	-1.632	highly similar to ( 589)AT5G08640	Symbols: FLS   FLS (FLAVONOL SYNTHASE)
jvci_3974	-1.768	moderately similar to ( 380)AT5G13930	Symbols: CHS, TT4, ATCHS   ATCHS/CHS/TT4 (CHALCONE SYNTHASE); naringenin-chalcone synthase
jvci_2577	-1.897	moderately similar to ( 264)AT5G05270	Symbols:   chalcone-flavanone isomerase family protein

Identifier	UV-control	Glucosinolates - Description
JCVI_13139	1.852	moderately similar to (317)AT1G12140  Symbols: FMO GS-OX5, FLAVIN-MONOOXYGENASE GLUCOSINOLATE S-OXYGENASE 5
AM388472	1.680	weakly similar to (181)AT5G57220  Symbols: CYP81F2, CYTOCHROME P450 81F2
EX121009	1.393	moderately similar to (237)AT1G18570  Symbols: HIG1, MYB51, MYB DOMAIN PROTEIN 51, HIGH INDOLIC GLUCOSINOLATE 1
JCVI_18417	1.320	moderately similar to (351)AT5G57220  Symbols: CYP81F2, CYTOCHROME P450 81F2
EV175932	0.881	weakly similar to (105)AT4G37410  Symbols: CYP81F4, CYTOCHROME P450 81F4
JCVI_16363	0.855	moderately similar to (203)AT1G12140  Symbols: FMO GS-OX5, FLAVIN-MONOOXYGENASE GLUCOSINOLATE S-OXYGENASE 5
EV217091	0.797	moderately similar to (238)AT4g39950  Symbols: CYP79B2, CYTOCHROME P450 79B2
JCVI_8389	0.776	moderately similar to (230)AT5G23010  Symbols: IMS3, MAM1   MAM1 (2-isopropylmalate synthase 3); 2-isopropylmalate synthase
JCVI_40366	0.686	weakly similar to (197)AT4G03060-CV1  Symbols: AOP2-CV1, ALKENYL HYDROXALKYL PRODUCING 2 - CAPE VERDE ISLANDS
JCVI_531	0.639	highly similar to (653)AT2g20610  Symbols: ALF1, RTY1, SUR1, ROOTY 1, SUPERROOT 1, ABERRANT LATERAL ROOT FORMATION 1
JCVI_33391	0.628	highly similar to (988)AT4g39950  Symbols: CYP79B2, CYTOCHROME P450 79B2
JCVI_24334	0.623	highly similar to (764)AT4g39950  Symbols: CYP79B2, CYTOCHROME P450 79B2
JCVI_16379	0.560	highly similar to (563)AT4g39950  Symbols: CYP79B2, CYTOCHROME P450 79B2
EX132986	0.509	weakly similar to (195)AT1G18570  Symbols: HIG1, MYB51, MYB DOMAIN PROTEIN 51, HIGH INDOLIC GLUCOSINOLATE 1
EV125432	0.508	moderately similar to (246)AT4G37410  Symbols: CYP81F4, CYTOCHROME P450 81F4
JCVI_109	0.507	highly similar to (541)AT4g31500  Symbols: ATR4, RNT1, SUR2, CYP83B1, SUPERROOT 2, ALTERED TRYPTOPHAN REGULATION 4, CYTOCHROME P450 83B1
ES903348	0.506	moderately similar to (242)AT1G18570  Symbols: HIG1, MYB51, MYB DOMAIN PROTEIN 51, HIGH INDOLIC GLUCOSINOLATE 1
JCVI_38759	0.471	moderately similar to (251)AT1G18570  Symbols: HIG1, MYB51, MYB DOMAIN PROTEIN 51, HIGH INDOLIC GLUCOSINOLATE 1
JCVI_4650	0.439	moderately similar to (398)AT4g31500  Symbols: ATR4, RNT1, SUR2, CYP83B1, SUPERROOT 2, ALTERED TRYPTOPHAN REGULATION 4, CYTOCHROME P450 83B1
JCVI_32420	0.436	weakly similar to (177)AT5G23010  Symbols: IMS3, MAM1   MAM1 (2-isopropylmalate synthase 3); 2-isopropylmalate synthase
JCVI_17153	0.371	moderately similar to (204)AT1G18570  Symbols: HIG1, MYB51, MYB DOMAIN PROTEIN 51, HIGH INDOLIC GLUCOSINOLATE 1
JCVI_37074	0.357	highly similar to (614)AT1g74100  Symbols: SOT16, ATST5A, ATST16, SULFOTRANSFERASE 16, ARABIDOPSIS SULFOTRANSFERASE 5A
CV432363	0.325	highly similar to (183)AT1g74100  Symbols: SOT16, ATST5A, ATST16, SULFOTRANSFERASE 16, ARABIDOPSIS SULFOTRANSFERASE 5A
JCVI_35732	0.284	weakly similar to (184)AT1g65880  Symbols: BZO1, BENZOYLOXYGLUCOSINOLATE 1
JCVI_29531	0.279	weakly similar to (147)AT2g25450  Symbols: AIGS-OH, encodes a protein whose sequence is similar to ACC oxidase
JCVI_37597	0.261	weakly similar to (146)AT3G49680  Symbols: BCAT3   BCAT3 (BRANCHED-CHAIN AMINOTRANSFERASE3); catalytic/ methionine-oxo-acid transaminase
JCVI_6128	0.255	moderately similar to (276)AT2g31790  Symbols: UGT74C, UDP-GLUCOSYL TRANSFERASE
JCVI_7218	0.224	moderately similar to (357)AT4G37410  Symbols: CYP81F4, CYTOCHROME P450 81F4
JCVI_212	0.208	moderately similar to (462)AT2g25450  Symbols: AIGS-OH, encodes a protein whose sequence is similar to ACC oxidase
EV048610	0.164	weakly similar to (174)AT1g74090  Symbols: SOT18, ATST5B, ATST18, ARABIDOPSIS SULFOTRANSFERASE 5B
EX092364	0.141	moderately similar to (209)AT5G07700  Symbols: MYB76, MYB DOMAIN PROTEIN 76
JCVI_15872	0.121	moderately similar to (338)AT3G49680  Symbols: BCAT3   BCAT3 (BRANCHED-CHAIN AMINOTRANSFERASE3); catalytic/ methionine-oxo-acid transaminase
JCVI_28651	0.112	highly similar to (136)AT1g65880  Symbols: BZO1, BENZOYLOXYGLUCOSINOLATE 1
JCVI_14388	0.091	moderately similar to (205)AT2g31790  Symbols: UGT74C, UDP-GLUCOSYL TRANSFERASE
JCVI_31655	0.075	highly similar to (517)AT5G60890  Symbols: ATR1, MYB34, MYB DOMAIN PROTEIN 34, ALTERED TRYPTOPHAN REGULATION 1
EV172987	0.072	moderately similar to (324)AT2g25450  Symbols: AIGS-OH, encodes a protein whose sequence is similar to ACC oxidase
CNT37571	0.059	moderately similar to (372)AT1G12140  Symbols: FMO GS-OX5, FLAVIN-MONOOXYGENASE GLUCOSINOLATE S-OXYGENASE 5
JCVI_3824	0.057	highly similar to (522)AT1g74090  Symbols: SOT18, ATST5B, ATST18, ARABIDOPSIS SULFOTRANSFERASE 5B
JCVI_32185	0.056	moderately similar to (219)AT2g20610  Symbols: ALF1, RTY1, SUR1, ROOTY 1, SUPERROOT 1, ABERRANT LATERAL ROOT FORMATION 1
EV036453	0.056	highly similar to (580)AT5g05260  Symbols: CYP79A2, CYTOCHROME P450 79A2
JCVI_32618	0.048	moderately similar to (213)AT5G23020  Symbols: MS2, MAM3, MAM-L (2-ISOPROPYLMALATE SYNTHASE 2, METHYLTHIOALKYLMALATE SYNTHASE-LIKE)
EV121242	0.048	moderately similar to (371)AT4G37410  Symbols: CYP81F4, CYTOCHROME P450 81F4
JCVI_32659	0.047	moderately similar to (325)AT5G57220  Symbols: CYP81F2, CYTOCHROME P450 81F2
EV152669	0.032	moderately similar to (254)AT5G57220  Symbols: CYP81F2, CYTOCHROME P450 81F2
EV136236	0.030	moderately similar to (244)AT1g65880  Symbols: BZO1, BENZOYLOXYGLUCOSINOLATE 1
JCVI_6034	0.028	highly similar to (633)AT1g74100  Symbols: SOT16, ATST5A, ATST16, SULFOTRANSFERASE 16, ARABIDOPSIS SULFOTRANSFERASE 5A
JCVI_14950	0.024	highly similar to (820)AT4g13770  Symbols: REF2, CYP83A1, REDUCED EPIDERMAL FLUORESCENCE 2, CYTOCHROME P450 83A1
JCVI_7952	0.018	highly similar to (516)AT1g74090  Symbols: SOT18, ATST5B, ATST18, ARABIDOPSIS SULFOTRANSFERASE 5B
EV042571	0.011	weakly similar to (133)AT1g07640  Symbols: OBP2, a member of the DOF transcription factors
JCVI_24252	-0.001	highly similar to (585)AT5G57220  Symbols: CYP81F2, CYTOCHROME P450 81F2
EV066556	-0.009	weakly similar to (127)AT1g65880  Symbols: BZO1, BENZOYLOXYGLUCOSINOLATE 1
DY009740	-0.015	moderately similar to (249)AT5G23010  Symbols: IMS3, MAM1   MAM1 (2-isopropylmalate synthase 3); 2-isopropylmalate synthase
EV107979	-0.016	moderately similar to (223)AT1g24100  Symbols: UGT74B1, UDP-GLUCOSYL TRANSFERASE 74B1
JCVI_9709	-0.023	highly similar to (550)AT3G49680  Symbols: BCAT3   BCAT3 (BRANCHED-CHAIN AMINOTRANSFERASE3); catalytic/ methionine-oxo-acid transaminase
DY009319	-0.025	moderately similar to (273)AT1G12140  Symbols: FMO GS-OX5, FLAVIN-MONOOXYGENASE GLUCOSINOLATE S-OXYGENASE 5
JCVI_32569	-0.026	moderately similar to (315)AT1g07640  Symbols: OBP2, a member of the DOF transcription factors
JCVI_19089	-0.029	moderately similar to (438)AT2g20610  Symbols: ALF1, RTY1, SUR1, ROOTY 1, SUPERROOT 1, ABERRANT LATERAL ROOT FORMATION 1
EV215478	-0.033	weakly similar to (126)AT1g07640  Symbols: OBP2, a member of the DOF transcription factors
JCVI_18356	-0.033	highly similar to (730)AT1G12140  Symbols: FMO GS-OX5, FLAVIN-MONOOXYGENASE GLUCOSINOLATE S-OXYGENASE 5
EV166394	-0.033	moderately similar to (498)AT5G57220  Symbols: CYP81F2, CYTOCHROME P450 81F2
JCVI_863	-0.048	moderately similar to (344)AT2g25450  Symbols: AIGS-OH, encodes a protein whose sequence is similar to ACC oxidase
JCVI_40856	-0.055	moderately similar to (401)AT2g20610  Symbols: ALF1, RTY1, SUR1, ROOTY 1, SUPERROOT 1, ABERRANT LATERAL ROOT FORMATION 1
ES901674	-0.060	weakly similar to (189)AT5G60890  Symbols: ATR1, MYB34, MYB DOMAIN PROTEIN 34, ALTERED TRYPTOPHAN REGULATION 1
ES948269	-0.065	weakly similar to (216)AT1g18590  Symbols: SOT17, ATST5C, ATST17, SULFOTRANSFERASE 17, ARABIDOPSIS SULFOTRANSFERASE 5C
JCVI_1293	-0.065	moderately similar to (397)AT2g25450  Symbols: AIGS-OH, encodes a protein whose sequence is similar to ACC oxidase
EX112446	-0.068	moderately similar to (399)AT2g20610  Symbols: ALF1, RTY1, SUR1, ROOTY 1, SUPERROOT 1, ABERRANT LATERAL ROOT FORMATION 1
EV226338	-0.073	moderately similar to (271)AT2g20610  Symbols: ALF1, RTY1, SUR1, ROOTY 1, SUPERROOT 1, ABERRANT LATERAL ROOT FORMATION 1
ES902202	-0.074	moderately similar to (251)AT5G60890  Symbols: ATR1, MYB34, MYB DOMAIN PROTEIN 34, ALTERED TRYPTOPHAN REGULATION 1
JCVI_37729	-0.080	highly similar to (539)AT1g18590  Symbols: SOT17, ATST5C, ATST17, SULFOTRANSFERASE 17, ARABIDOPSIS SULFOTRANSFERASE 5C
JCVI_31546	-0.087	moderately similar to (456)AT4G37410  Symbols: CYP81F4, CYTOCHROME P450 81F4
JCVI_6517	-0.094	moderately similar to (331)AT5G07690  Symbols: MYB29, PMG2, MYB DOMAIN PROTEIN 29, PRODUCTION OF METHIONINE-DERIVED GLUCOSINOLATE 2
EX059080	-0.096	moderately similar to (359)AT5G23010  Symbols: IMS3, MAM1   MAM1 (2-isopropylmalate synthase 3); 2-isopropylmalate synthase
JCVI_24441	-0.109	weakly similar to (173)AT5G61420  Symbols: MYB28, HAG1, MYB DOMAIN PROTEIN 28, HIGH ALIPHATIC GLUCOSINOLATE 1
JCVI_22996	-0.113	weakly similar to (229)AT1g74090  Symbols: SOT18, ATST5B, ATST18, ARABIDOPSIS SULFOTRANSFERASE 5B
JCVI_36433	-0.121	weakly similar to (181)AT4G03060-CV1  Symbols: AOP2-CV1, ALKENYL HYDROXALKYL PRODUCING 2 - CAPE VERDE ISLANDS
JCVI_24921	-0.125	moderately similar to (346)AT1g74090  Symbols: SOT18, ATST5B, ATST18, ARABIDOPSIS SULFOTRANSFERASE 5B
CD837066	-0.141	moderately similar to (383)AT2g31790  Symbols: UGT74C, UDP-GLUCOSYL TRANSFERASE
JCVI_19574	-0.147	weakly similar to (187)AT4G03050  Symbols: AOP3, the transcribed allele in ecotype Ler encodes a 2-oxoglutarate-dependent dioxygenase
JCVI_19574	-0.147	weakly similar to (181)AT4G03060-CV1  Symbols: AOP2-CV1, ALKENYL HYDROXALKYL PRODUCING 2 - CAPE VERDE ISLANDS
DN961030	-0.151	moderately similar to (245)AT2g20610  Symbols: ALF1, RTY1, SUR1, ROOTY 1, SUPERROOT 1, ABERRANT LATERAL ROOT FORMATION 1
JCVI_14975	-0.154	moderately similar to (291)AT4G37410  Symbols: CYP81F4, CYTOCHROME P450 81F4
JCVI_26799	-0.160	moderately similar to (438)AT4g13770  Symbols: REF2, CYP83A1, REDUCED EPIDERMAL FLUORESCENCE 2, CYTOCHROME P450 83A1
EX019177	-0.188	weakly similar to (147)AT5G23010  Symbols: IMS3, MAM1   MAM1 (2-isopropylmalate synthase 3); 2-isopropylmalate synthase
JCVI_12709	-0.240	moderately similar to (410)AT3G19710  Symbols: BCAT4   BCAT4 (BRANCHED-CHAIN AMINOTRANSFERASE4); catalytic/ methionine-oxo-acid transaminase
JCVI_31290	-0.241	moderately similar to (458)AT1g24100  Symbols: UGT74B1, UDP-GLUCOSYL TRANSFERASE 74B1
EE480029	-0.280	moderately similar to (293)AT1g74090  Symbols: SOT18, ATST5B, ATST18, ARABIDOPSIS SULFOTRANSFERASE 5B
ES917650	-0.285	weakly similar to (122)AT5G23010  Symbols: IMS3, MAM1   MAM1 (2-isopropylmalate synthase 3); 2-isopropylmalate synthase
EX059882	-0.301	moderately similar to (368)AT2g31790  Symbols: UGT74C, UDP-GLUCOSYL TRANSFERASE
JCVI_39476	-0.306	moderately similar to (262)AT5G60890  Symbols: ATR1, MYB34, MYB DOMAIN PROTEIN 34, ALTERED TRYPTOPHAN REGULATION 1
JCVI_40221	-0.307	moderately similar to (400)AT1G12140  Symbols: FMO GS-OX5, FLAVIN-MONOOXYGENASE GLUCOSINOLATE S-OXYGENASE 5
JCVI_5227	-0.346	moderately similar to (384)AT1G62540  Symbols: FMO GS-OX2, FLAVIN-MONOOXYGENASE GLUCOSINOLATE S-OXYGENASE 2
JCVI_32160	-0.421	moderately similar to (316)AT1g74090  Symbols: SOT18, ATST5B, ATST18, ARABIDOPSIS SULFOTRANSFERASE 5B
JCVI_33924	-0.427	moderately similar to (464)AT5G60890  Symbols: ATR1, MYB34, MYB DOMAIN PROTEIN 34, ALTERED TRYPTOPHAN REGULATION 1
JCVI_2638	-0.535	moderately similar to (431)AT3G49680  Symbols: BCAT3   BCAT3 (BRANCHED-CHAIN AMINOTRANSFERASE3); catalytic/ methionine-oxo-acid transaminase
JCVI_40613	-0.554	moderately similar to (445)AT5G07690  Symbols: MYB29, PMG2, MYB DOMAIN PROTEIN 29, PRODUCTION OF METHIONINE-DERIVED GLUCOSINOLATE 2
EE468053	-0.583	moderately similar to (241)AT1g74090  Symbols: SOT18, ATST5B, ATST18, ARABIDOPSIS SULFOTRANSFERASE 5B
JCVI_17243	-0.591	moderately similar to (354)AT1g74090  Symbols: SOT18, ATST5B, ATST18, ARABIDOPSIS SULFOTRANSFERASE 5B
JCVI_15640	-0.599	weakly similar to (197)AT1G65880  Symbols: FMO GS-OX1, FLAVIN-MONOOXYGENASE GLUCOSINOLATE S-OXYGENASE 1
JCVI_5112	-0.652	moderately similar to (434)AT4g13770  Symbols: REF2, CYP83A1, REDUCED EPIDERMAL FLUORESCENCE 2, CYTOCHROME P450 83A1
EX043693	-0.755	moderately similar to (200)AT5G07690  Symbols: MYB29, PMG2, MYB DOMAIN PROTEIN 29, PRODUCTION OF METHIONINE-DERIVED GLUCOSINOLATE 2
JCVI_33047	-0.886	moderately similar to (324)AT4G03060-CV1  Symbols: AOP2-CV1, ALKENYL HYDROXALKYL PRODUCING 2 - CAPE VERDE ISLANDS
JCVI_17335	-0.970	moderately similar to (351)AT1g16410  Symbols: BUS1, SPS1, BUSHY 1, CYP79F1, SUPERSHOOT 1, CYTOCHROME P450 79F1
JCVI_6771	-1.217	highly similar to (726)AT2g31790  Symbols: UGT74C, UDP-GLUCOSYL TRANSFERASE
JCVI_9973	-1.237	moderately similar to (297)AT2g25450  Symbols: AIGS-OH, encodes a protein whose sequence is similar to ACC oxidase
JCVI_18213	-1.479	highly similar to (565)AT3G19710  Symbols: BCAT4   BCAT4 (BRANCHED-CHAIN AMINOTRANSFERASE4); catalytic/ methionine-oxo-acid transaminase
EE401951	-1.770	weakly similar to (197)AT5G23010  Symbols: IMS3, MAM1   MAM1 (2-isopropylmalate synthase 3); 2-isopropylmalate synthase
EX066879	-1.873	very highly similar to (84)AT1g16410  Symbols: BUS1, SPS1, BUSHY 1, CYP79F1, SUPERSHOOT 1, CYTOCHROME P450 79F1
JCVI_30455	-1.881	highly similar to (519)AT5G23020  Symbols: MS2, MAM3, MAM-L (2-ISOPROPYLMALATE SYNTHASE 2, METHYLTHIOALKYLMALATE SYNTHASE-LIKE)
JCVI_34763	-2.296	weakly similar to (187)AT3G19710  Symbols: BCAT4   BCAT4 (BRANCHED-CHAIN AMINOTRANSFERASE4); catalytic/ methionine-oxo-acid transaminase

Identifier	UV-control	Isoprenoids - Description
jvci_20479	4.728	moderately similar to (328)AT1G64970  Symbols: TMT1, VTE4, G-TMT   G-TMT (GAMMA-TOCOPHEROL METHYLTRANSFERASE)
jvci_2005	1.409	moderately similar to (218)AT1G74470  Symbols:   geranylgeranyl reductase
jvci_4210	1.388	moderately similar to (488)AT2G26930  Symbols: PDE27, ISPE, ATCDPMK   PIGMENT DEFECTIVE 277; 4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol kinase
jvci_9534	1.067	highly similar to (795)AT4G34350  Symbols: ISPH, CLB6   CLB6 (CHLOROPLAST BIOGENESIS 6); 4-hydroxy-3-methylbut-2-en-1-yl diphosphate reductase
jvci_5099	0.871	weakly similar to (116)AT1G78955  Symbols: CAMS1   CAMS1 (CAMELLIOL C SYNTHASE 1); beta-amyrin synthase
jvci_2706	0.833	moderately similar to (355)AT5G17230  Symbols: PSY   PSY (PHYTOENE SYNTHASE)
jvci_14575	0.631	highly similar to (506)AT5G57030  Symbols: LUT2   LUT2 (LUTEIN DEFICIENT 2); lycopene epsilon cyclase
jvci_14396	0.602	moderately similar to (369)AT3G05500  Symbols:   rubber elongation factor (REF) family protein
jvci_29126	0.587	highly similar to (521)AT1G78510  Symbols: SPS1   SPS1 (SOLANESYL DIPHOSPHATE SYNTHASE 1)
jvci_8419	0.563	moderately similar to (348)AT3G54250  Symbols:   mevalonate diphosphate decarboxylase, putative
jvci_5261	0.546	moderately similar to (424)AT4G25700  Symbols: B1, CHY1, BETA-OHASE 1   BETA-OHASE 1 (BETA-HYDROXYLASE 1)
jvci_11442	0.536	highly similar to (585)AT5G48230  Symbols: EMB1276, ACAT2   ACAT2/EMB1276 (ACETOACETYL-COA THIOLEASE 2); acetyl-CoA C-acetyltransferase
jvci_36369	0.528	weakly similar to (155)AT1G08500  Symbols: AVDE1   NPQ1 (NON-PHOTOCHEMICAL QUENCHING 1)
ev128620	0.509	moderately similar to (344)AT5G62790  Symbols: PDE129, DXR   DXR (1-DEOXY-D-XYLULOSE 5-PHOSPHATE REDUCTOISOMERASE)
ei592527	0.470	weakly similar to (155)AT3G02780  Symbols: IPP2, IPIAT1, IDI2   IDI2/IPIAT1/IPP2 (ISOPENTENYL DIPHOSPHATE ISOMERASE 2)
jvci_36090	0.466	moderately similar to (461)AT2G02500  Symbols: ATMEPCT, MCT, ISPD   ISPD (2-C-METHYL-D-ERYTHRITOL 4-PHOSPHATE CYTIIDYLTRANSFERASE)
jvci_156	0.463	moderately similar to (341)AT2G47780  Symbols:   terpene elongation factor (REF) protein-related
jvci_27803	0.447	moderately similar to (281)AT2G24210  Symbols: TPS10   TPS10 (TERPENE SYNTHASE 10); myrcene/(E)-beta-ocimene synthase
jvci_3310	0.442	moderately similar to (328)AT3G02780  Symbols: IPP2, IPIAT1, IDI2   IDI2/IPIAT1/IPP2 (ISOPENTENYL DIPHOSPHATE ISOMERASE 2)
jvci_12969	0.371	moderately similar to (351)AT5G17230  Symbols: PSY   PSY (PHYTOENE SYNTHASE)
jvci_29425	0.362	highly similar to (623)AT1G06820  Symbols: CCR2, CRTISO   CRTISO (CAROTENOID ISOMERASE); carotenoid isomerase
dy023560	0.347	moderately similar to (404)AT2G17570  Symbols:   undecaprenyl pyrophosphate synthetase family protein / UPP synthetase family protein
jvci_37079	0.346	highly similar to (624)AT3G11945  Symbols: ATHST   ATHST; prenyltransferase
jvci_33771	0.320	moderately similar to (496)AT5G27450  Symbols: MVK, MK   MK/MVK; mevalonate kinase
jvci_22503	0.311	highly similar to (592)AT2G24210  Symbols: TPS10   TPS10 (TERPENE SYNTHASE 10); myrcene/(E)-beta-ocimene synthase
jvci_11039	0.298	moderately similar to (263)AT5G17230  Symbols: PSY   PSY (PHYTOENE SYNTHASE)
ex086464	0.278	moderately similar to (395)AT5G52570  Symbols: B2, CHY2, BETA-OHASE 2   BETA-OHASE 2 (BETA-CAROTENE HYDROXYLASE 2)
jvci_12663	0.277	moderately similar to (447)AT1G76490  Symbols: HMGR1, HMG1   HMG1 (3-HYDROXY-3-METHYLGLUTARYL COA REDUCTASE)
ex137163	0.276	moderately similar to (306)AT5G44630  Symbols:   terpene synthase/cyclase family protein
jvci_28866	0.256	moderately similar to (315)AT3G54250  Symbols:   mevalonate diphosphate decarboxylase, putative
jvci_25775	0.252	highly similar to (531)AT5G47770  Symbols: FSP1   FSP1 (FARNESYL DIPHOSPHATE SYNTHASE 1); dimethylallyltransferase/geranyltransferase
jvci_25537	0.232	highly similar to (595)AT4G24490  Symbols:   protein binding / protein prenyltransferase
jvci_24842	0.230	moderately similar to (239)AT5G57030  Symbols: LUT2   LUT2 (LUTEIN DEFICIENT 2); lycopene epsilon cyclase
jvci_19477	0.229	highly similar to (527)AT5G12210  Symbols:   geranylgeranyl transferase type II beta subunit, putative / RAB geranylgeranyltransferase beta subunit, putative
jvci_3655	0.224	moderately similar to (302)AT1G31910  Symbols:   GHMP kinase family protein
jvci_38872	0.215	moderately similar to (350)AT3G54250  Symbols:   mevalonate diphosphate decarboxylase, putative
jvci_3137	0.214	moderately similar to (439)AT1G76490  Symbols: HMGR1, HMG1   HMG1 (3-HYDROXY-3-METHYLGLUTARYL COA REDUCTASE)
jvci_34321	0.212	weakly similar to (168)AT4G16740  Symbols: ATTPS03   ATTPS03 (Arabidopsis thaliana terpene synthase 03)
jvci_4212	0.211	highly similar to (597)AT1G79460  Symbols: KS, ATKS, GA2   GA2 (GA REQUIRING 2); ent-kaurene synthase
jvci_5891	0.198	moderately similar to (328)AT1G63970  Symbols: MECPS, ISPF   ISPF (Homolog of E. coli ispF (isoprenoids F)); 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase
jvci_4351	0.195	moderately similar to (343)AT4G36810  Symbols: GGPS1   GGPS1 (GERANYLPYROPHOSPHATE SYNTHASE 1); farnesyltransferase
ee427949	0.194	moderately similar to (289)AT4G20200  Symbols:   terpene synthase/cyclase family protein
ee518275	0.182	moderately similar to (411)AT2G07050  Symbols: CAS1   CAS1 (CYCLOARTENOL SYNTHASE 1); cycloartenol synthase
jvci_38479	0.177	moderately similar to (447)AT3G63410  Symbols: VTE3, APG1   APG1 (ALBINO OR PALE GREEN MUTANT 1); methyltransferase
ev101195	0.167	moderately similar to (252)AT1G74470  Symbols:   geranylgeranyl reductase
dy021078	0.154	moderately similar to (232)AT1G76490  Symbols: HMGR1, HMG1   HMG1 (3-HYDROXY-3-METHYLGLUTARYL COA REDUCTASE)
jvci_18225	0.148	moderately similar to (399)AT4G15560  Symbols: DEF, CLA, DXS, DXPS2, CLA1   CLA1 (CLOROPLASTOS ALTERADOS 1)
jvci_17595	0.147	weakly similar to (125)AT1G06570  Symbols: HPD, PDS1   PDS1 (PHYTOENE DESATURATION 1)
jvci_3377	0.144	weakly similar to (141)AT5G60600  Symbols: ISPG, CSB3, CLB4, GcpE   GcpE (CHLOROPLAST BIOGENESIS 4)
jvci_27449	0.139	highly similar to (885)AT4G15560  Symbols: DEF, CLA, DXS, DXPS2, CLA1   CLA1 (CLOROPLASTOS ALTERADOS 1)
ev165777	0.137	moderately similar to (201)AT4G20200  Symbols:   terpene synthase/cyclase family protein
ex103290	0.132	weakly similar to (105)AT5G57030  Symbols: LUT2   LUT2 (LUTEIN DEFICIENT 2); lycopene epsilon cyclase
jvci_10823	0.131	highly similar to (685)AT1G17050  Symbols: SPS2   SPS2 (SOLANESYL DIPHOSPHATE SYNTHASE 2); dimethylallyltransferase/trans-octaprenyltransferase
jvci_18605	0.130	highly similar to (568)AT4G34350  Symbols: ISPH, CLB6   CLB6 (CHLOROPLAST BIOGENESIS 6); 4-hydroxy-3-methylbut-2-en-1-yl diphosphate reductase
jvci_39154	0.130	moderately similar to (353)AT2G17370  Symbols: HMGR2, HMG2   HMG2 (3-HYDROXY-3-METHYLGLUTARYL-COA REDUCTASE 2)
jvci_41100	0.126	weakly similar to (184)AT5G48230  Symbols: EMB1276, ACAT2   ACAT2/EMB1276 (ACETOACETYL-COA THIOLEASE 2); acetyl-CoA C-acetyltransferase
jvci_29560	0.120	highly similar to (561)AT1G78960  Symbols: ATLUP2   ATLUP2 (Arabidopsis thaliana lupeol synthase 2); lupeol synthase
ex039035	0.112	weakly similar to (159)AT1G60600  Symbols: ABC4   ABC4 (ABERRANT CHLOROPLAST DEVELOPMENT 4)
jvci_34157	0.110	moderately similar to (383)AT5G36160  Symbols:   aminotransferase-related
jvci_3911	0.102	moderately similar to (464)AT4G25700  Symbols: B1, CHY1, BETA-OHASE 1   BETA-OHASE 1 (BETA-HYDROXYLASE 1)
jvci_6367	0.097	weakly similar to (182)AT1G76490  Symbols: HMGR1, HMG1   HMG1 (3-HYDROXY-3-METHYLGLUTARYL COA REDUCTASE)
jvci_12963	0.079	weakly similar to (108)AT1G61120  Symbols:   terpene synthase/cyclase family protein
jvci_35093	0.076	moderately similar to (417)AT5G16440  Symbols: IPP1, IDI1   IPP1 (ISOPENTENYL DIPHOSPHATE ISOMERASE 1); isopentenyl-diphosphate delta-isomerase
jvci_19174	0.076	highly similar to (691)AT5G42500  Symbols:   mevalonate diphosphate decarboxylase, putative
ev148909	0.074	moderately similar to (221)AT1G78955  Symbols: CAMS1   CAMS1 (CAMELLIOL C SYNTHASE 1); beta-amyrin synthase
jvci_34730	0.071	weakly similar to (102)AT3G10230  Symbols: LYC   LYC (LYCOPENE CYCLASE)
ex097077	0.068	moderately similar to (292)AT3G29110  Symbols:   terpene synthase/cyclase family protein
cv545646	0.064	weakly similar to (120)AT1G76490  Symbols: HMGR1, HMG1   HMG1 (3-HYDROXY-3-METHYLGLUTARYL COA REDUCTASE)
ex041264	0.063	moderately similar to (185)AT1G78955  Symbols: CAMS1   CAMS1 (CAMELLIOL C SYNTHASE 1); beta-amyrin synthase
jvci_20625	0.054	highly similar to (714)AT2G07050  Symbols: CAS1   CAS1 (CYCLOARTENOL SYNTHASE 1); cycloartenol synthase
jvci_32699	0.051	moderately similar to (224)AT5G62790  Symbols: PDE129, DXR   DXR (1-DEOXY-D-XYLULOSE 5-PHOSPHATE REDUCTOISOMERASE)
jvci_12214	0.050	weakly similar to (106)AT2G34630  Symbols: GGPS, GPS1   GGPS/GPS1 (GERANYLPYROPHOSPHATE SYNTHASE); dimethylallyltransferase
jvci_12014	0.048	weakly similar to (130)AT5G23960  Symbols:   terpene synthase/cyclase family protein
jvci_11281	0.038	moderately similar to (331)AT1G06570  Symbols: HPD, PDS1   PDS1 (PHYTOENE DESATURATION 1)
ev214032	0.034	weakly similar to (127)AT4G34350  Symbols: ISPH, CLB6   CLB6 (CHLOROPLAST BIOGENESIS 6); 4-hydroxy-3-methylbut-2-en-1-yl diphosphate reductase
ev009533	0.032	moderately similar to (257)AT2G18620  Symbols:   geranylgeranyl pyrophosphate synthetase, putative / GGPP synthetase, putative / farnesyltransferase, putative
ev097529	0.030	weakly similar to (179)AT4G15560  Symbols: DEF, CLA, DXS, DXPS2, CLA1   CLA1 (CLOROPLASTOS ALTERADOS 1)
es913880	0.028	moderately similar to (215)AT3G25830  Symbols: ATTPS-CIN   ATTPS-CIN (TERPENE SYNTHASE-LIKE SEQUENCE-1.8-CINEOLE); myrcene/(E)-beta-ocimene synthase
ee403740	0.026	weakly similar to (181)AT1G63970  Symbols: MECPS, ISPF   ISPF (Homolog of E. coli ispF (isoprenoids F)); 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase
ev177417	0.025	moderately similar to (431)AT5G62790  Symbols: PDE129, DXR   DXR (1-DEOXY-D-XYLULOSE 5-PHOSPHATE REDUCTOISOMERASE)
jvci_9314	0.025	moderately similar to (334)AT1G76490  Symbols: HMGR1, HMG1   HMG1 (3-HYDROXY-3-METHYLGLUTARYL COA REDUCTASE)
ee532266	0.021	moderately similar to (305)AT3G14490  Symbols:   terpene synthase/cyclase family protein
jvci_25321	0.018	moderately similar to (215)AT1G06560  Symbols:   NOL1/NOP2/sun family protein
ee509744	0.016	weakly similar to (188)AT1G78960  Symbols: ATLUP2   ATLUP2 (Arabidopsis thaliana lupeol synthase 2); lupeol synthase
ev124192	0.015	weakly similar to (116)AT4G23590  Symbols:   aminotransferase class I and II family protein
jvci_35581	0.013	highly similar to (572)AT5G27450  Symbols: MVK, MK   MK/MVK; mevalonate kinase
es860774	0.012	weakly similar to (114)AT2G18620  Symbols:   geranylgeranyl pyrophosphate synthetase, putative / GGPP synthetase, putative / farnesyltransferase, putative
jvci_10559	0.009	weakly similar to (117)AT5G57030  Symbols: LUT2   LUT2 (LUTEIN DEFICIENT 2); lycopene epsilon cyclase
jvci_29716	0.008	weakly similar to (105)AT5G17230  Symbols: PSY   PSY (PHYTOENE SYNTHASE)
ev133412	0.007	moderately similar to (290)AT4G24490  Symbols:   protein binding / protein prenyltransferase
cx196105	0.005	moderately similar to (382)AT3G11950  Symbols:   homogenitase farnesyltransferase / homogenitase geranyltransferase / homogenitase solanesyltransferase
ev186096	0.000	weakly similar to (166)AT4G14210  Symbols: PDS, PDE226, PDS3   PDS3 (PHYTOENE DESATURASE)
jvci_2997	-0.001	moderately similar to (353)AT1G78955  Symbols: CAMS1   CAMS1 (CAMELLIOL C SYNTHASE 1); beta-amyrin synthase
jvci_27349	-0.001	moderately similar to (133)AT3G29410  Symbols:   terpene synthase/cyclase family protein
jvci_17063	-0.004	highly similar to (502)AT1G60600  Symbols: ABC4   ABC4 (ABERRANT CHLOROPLAST DEVELOPMENT 4)
es903218	-0.006	moderately similar to (409)AT3G25830  Symbols: ATTPS-CIN   ATTPS-CIN (TERPENE SYNTHASE-LIKE SEQUENCE-1.8-CINEOLE); myrcene/(E)-beta-ocimene synthase
jvci_18484	-0.009	moderately similar to (347)AT5G58784  Symbols:   dehydrodicholyl diphosphate synthase, putative / DEDOL-PP synthase, putative
jvci_26262	-0.010	moderately similar to (405)AT5G23960  Symbols:   terpene synthase/cyclase family protein
es952658	-0.011	weakly similar to (156)AT2G17570  Symbols:   undecaprenyl pyrophosphate synthetase family protein / UPP synthetase family protein
dy028331	-0.012	moderately similar to (281)AT5G49555  Symbols:   amine oxidase-related
dy004458	-0.012	moderately similar to (308)AT4G20200  Symbols:   terpene synthase/cyclase family protein
jvci_1694	-0.013	weakly similar to (163)AT2G34630  Symbols: GGPS, GPS1   GGPS/GPS1 (GERANYLPYROPHOSPHATE SYNTHASE); dimethylallyltransferase
ee471142	-0.014	weakly similar to (168)AT3G25830  Symbols: ATTPS-CIN   ATTPS-CIN (TERPENE SYNTHASE-LIKE SEQUENCE-1.8-CINEOLE); myrcene/(E)-beta-ocimene synthase
ev165861	-0.015	moderately similar to (273)AT3G29110  Symbols:   terpene synthase/cyclase family protein
jvci_23316	-0.016	moderately similar to (416)AT1G78500  Symbols:   pentacyclic triterpene synthase, putative
jvci_2752	-0.017	moderately similar to (288)AT4G11820  Symbols: HMGS, EMB2778, MVA1   MVA1 (HYDROXYMETHYLGLUTARYL-COA SYNTHASE)
jvci_40121	-0.020	moderately similar to (228)AT5G57030  Symbols: LUT2   LUT2 (LUTEIN DEFICIENT 2); lycopene epsilon cyclase
jvci_31309	-0.022	highly similar to (823)AT4G14210  Symbols: PDS, PDE226, PDS3   PDS3 (PHYTOENE DESATURASE)
jvci_21434	-0.024	moderately similar to (255)AT5G57030  Symbols: LUT2   LUT2 (LUTEIN DEFICIENT 2); lycopene epsilon cyclase
jvci_24718	-0.027	moderately similar to (225)AT5G12210  Symbols:   geranylgeranyl transferase type II beta subunit, putative / RAB geranylgeranyltransferase beta subunit, putative
es906255	-0.028	moderately similar to (259)AT5G60600  Symbols: ISPG, CSB3, CLB4, GcpE   GcpE (CHLOROPLAST BIOGENESIS 4)
ev214637	-0.029	weakly similar to (149)AT1G74470  Symbols:   geranylgeranyl reductase
ex137765	-0.032	weakly similar to (173)AT5G44630  Symbols:   terpene synthase/cyclase family protein
ex092640	-0.036	weakly similar to (103)AT1G78960  Symbols: ATLUP2   ATLUP2 (Arabidopsis thaliana lupeol synthase 2); lupeol synthase
jvci_15620	-0.043	moderately similar to (416)AT4G32770  Symbols: ATSDX1, VTE1   VTE1 (VITAMIN E DEFICIENT 1)
ee422476	-0.046	weakly similar to (139)AT4G20200  Symbols:   terpene synthase/cyclase family protein

cd827634	-0.046	weakly similar to ( 140)AT2G18640	Symbols: GGPS4   GGPS4 (GERANYLGERANYL PYROPHOSPHATE SYNTHASE 4); farnesyltransferase
cd834687	-0.048	moderately similar to ( 229)AT1G48800	Symbols:   terpene synthase/cyclase family protein
ex106389	-0.048	weakly similar to ( 105)AT5G57030	Symbols: LUT2   LUT2 (LUTEIN DEFICIENT 2); lycopene epsilon cyclase
ev218406	-0.050	moderately similar to ( 405)AT2G18950	Symbols: TPT1, ATHPT, HPT, VTE2, HPT1   HPT1 (HOMOGENITISATE PHYTYLTRANSFERASE 1); prenilyltransferase
ex097042	-0.050	moderately similar to ( 305)AT1G76490	Symbols: HMG1   HMG1 (3-HYDROXY-3-METHYLGLUTARYL COA REDUCTASE)
jcvi_12917	-0.052	moderately similar to ( 452)AT2G34630	Symbols: GPPS, GPS1   GPPS/GPS1 (GERANYLPYROPHOSPHATE SYNTHASE); dimethylallyltransferase
ee517739	-0.052	moderately similar to ( 219)AT2G26930	Symbols: PDE226, PDS3   PDE226, PDS3 (1-DEOXY-D-XYLULOSE 5-PHOSPHATE SYNTHASE 3); 4-(cytidine 5-diphospho)-2-C-methyl-D-erythritol kinase
ev120968	-0.054	moderately similar to ( 274)AT4G15870	Symbols: ATTS1   ATTS1 (Arabidopsis thaliana terpene synthase 1); lyase/magnesium ion binding
jcvi_961	-0.058	moderately similar to ( 341)AT1G74470	Symbols:   geranylgeranyl reductase
jcvi_1053	-0.058	moderately similar to ( 204)AT3G63520	Symbols: ATCCD1, ATNCED1, NCED1, CCD1   CCD1 (CAROTENOID CLEAVAGE DIOXYGENASE 1)
ev225118	-0.060	moderately similar to ( 222)AT3G25810	Symbols:   myrcene/ocimene synthase, putative
cd835924	-0.061	moderately similar to ( 288)AT4G20230	Symbols:   terpene synthase/cyclase family protein
cd836704	-0.062	moderately similar to ( 363)AT5G11380	Symbols: DXPS3   DXPS3 (1-DEOXY-D-XYLULOSE 5-PHOSPHATE SYNTHASE 3)
jcvi_28404	-0.064	moderately similar to ( 287)AT2G26250	Symbols: FDH   FDH (FIDDLEHEAD); acyltransferase
jcvi_33856	-0.067	moderately similar to ( 454)AT2G07050	Symbols: CAS1   CAS1 (CYCLOARTENOL SYNTHASE 1); cycloartenol synthase
ev189544	-0.068	weakly similar to ( 163)AT1G74470	Symbols:   geranylgeranyl reductase
jcvi_18575	-0.071	moderately similar to ( 389)AT3G25830	Symbols: ATTPS-CIN   ATTPS-CIN (TERPENE SYNTHASE-LIKE SEQUENCE-1,8-CINEOLE); myrcene/(E)-beta-ocimene synthase
es906763	-0.073	moderately similar to ( 377)AT3G29110	Symbols:   terpene synthase/cyclase family protein
jcvi_26986	-0.073	moderately similar to ( 395)AT4G15560	Symbols: DEF, CLA, DXS, DXPS2, CLA1   CLA1 (CLOROPLASTOS ALTERADOS 1)
ev193301	-0.079	moderately similar to ( 289)AT4G14210	Symbols: PDS, PDE226, PDS3   PDS3 (PHYTOENE DESATURASE)
jcvi_42043	-0.084	weakly similar to ( 138)AT1G50890	Symbols:   binding
ev197471	-0.087	weakly similar to ( 163)AT5G17230	Symbols: PSY   PSY (PHYTOENE SYNTHASE)
cx193227	-0.088	weakly similar to ( 111)AT5G23960	Symbols:   terpene synthase/cyclase family protein
jcvi_40299	-0.089	weakly similar to ( 161)AT1G61120	Symbols:   terpene synthase/cyclase family protein
ev209368	-0.091	moderately similar to ( 228)AT5G60600	Symbols: ISPG, CSB3, CLB4, GcpE   GcpE (CHLOROPLAST BIOGENESIS 4)
jcvi_40815	-0.093	moderately similar to ( 429)AT5G11380	Symbols: DXPS3   DXPS3 (1-DEOXY-D-XYLULOSE 5-PHOSPHATE SYNTHASE 3)
jcvi_123	-0.094	highly similar to ( 655)AT1G74470	Symbols:   geranylgeranyl reductase
cd819976	-0.095	moderately similar to ( 260)AT3G11950	Symbols:   homogenitise farnesyltransferase/ homogenitise geranylgeranyltransferase/ homogenitise solanesyltransferase
jcvi_27069	-0.097	moderately similar to ( 249)AT5G23960	Symbols:   terpene synthase/cyclase family protein
jcvi_39823	-0.097	weakly similar to ( 144)AT1G66020	Symbols:   terpene synthase/cyclase family protein
jcvi_25994	-0.100	moderately similar to ( 285)AT4G15870	Symbols: ATTS1   ATTS1 (Arabidopsis thaliana terpene synthase 1); lyase/magnesium ion binding
jcvi_39717	-0.101	moderately similar to ( 291)AT2G23800	Symbols: GGPS5, GGPS2   GGPS2 (GERANYLGERANYL PYROPHOSPHATE SYNTHASE 2); farnesyltransferase
ex086652	-0.104	weakly similar to ( 116)AT3G25830	Symbols: ATTPS-CIN   ATTPS-CIN (TERPENE SYNTHASE-LIKE SEQUENCE-1,8-CINEOLE); myrcene/(E)-beta-ocimene synthase
jcvi_14579	-0.109	moderately similar to ( 427)AT2G23800	Symbols: GGPS5, GGPS2   GGPS2 (GERANYLGERANYL PYROPHOSPHATE SYNTHASE 2); farnesyltransferase
jcvi_17388	-0.109	moderately similar to ( 288)AT4G14210	Symbols: PDS, PDE226, PDS3   PDS3 (PHYTOENE DESATURASE)
jcvi_2950	-0.110	weakly similar to ( 194)AT4G11820	Symbols: HMGS, MVA1   MVA1 (HYDROXYMETHYLGLUTARYL-COA SYNTHASE)
jcvi_42543	-0.110	moderately similar to ( 483)AT1G78960	Symbols: ATLUP2   ATLUP2 (Arabidopsis thaliana lupeol synthase 2); lupeol synthase
ev178595	-0.111	moderately similar to ( 218)AT4G36810	Symbols: GGP51   GGP51 (GERANYLGERANYL PYROPHOSPHATE SYNTHASE 1); farnesyltransferase
jcvi_2410	-0.111	moderately similar to ( 293)AT4G16740	Symbols: ATTPS03   ATTPS03 (Arabidopsis thaliana terpene synthase 03)
jcvi_16311	-0.113	moderately similar to ( 324)AT1G08550	Symbols: AVDE1   NPO1 (NON-PHOTOCHEMICAL QUENCHING 1)
es97679	-0.117	weakly similar to ( 102)AT5G27450	Symbols: MVK, MK   MK/MVK; mevalonate kinase
ev206464	-0.117	moderately similar to ( 308)AT1G06570	Symbols: HPD, PDS1   PDS1 (PHYTOENE DESATURATION 1)
jcvi_18580	-0.125	moderately similar to ( 222)AT5G57030	Symbols: LUT2   LUT2 (LUTEIN DEFICIENT 2); lycopene epsilon cyclase
jcvi_32269	-0.127	moderately similar to ( 447)AT1G06570	Symbols: HPD, PDS1   PDS1 (PHYTOENE DESATURATION 1)
ev078086	-0.127	weakly similar to ( 157)AT4G14210	Symbols: PDS, PDE226, PDS3   PDS3 (PHYTOENE DESATURASE)
am060327	-0.130	weakly similar to ( 195)AT3G11950	Symbols:   homogenitise farnesyltransferase/ homogenitise geranylgeranyltransferase/ homogenitise solanesyltransferase
es935671	-0.132	moderately similar to ( 247)AT3G14550	Symbols: GGPS3   GGPS3 (GERANYLGERANYL PYROPHOSPHATE SYNTHASE 3); farnesyltransferase
jcvi_1328	-0.133	moderately similar to ( 318)AT1G31910	Symbols:   GHMP kinase family protein
jcvi_300735	-0.133	moderately similar to ( 300)AT5G23960	Symbols:   terpene synthase/cyclase family protein
ev224011	-0.133	weakly similar to ( 167)AT5G60600	Symbols: ISPG, CSB3, CLB4, GcpE   GcpE (CHLOROPLAST BIOGENESIS 4)
jcvi_14909	-0.134	moderately similar to ( 263)AT5G57030	Symbols: LUT2   LUT2 (LUTEIN DEFICIENT 2); lycopene epsilon cyclase
jcvi_1929	-0.137	moderately similar to ( 462)AT5G47720	Symbols:   acetyl-CoA C-acyltransferase, putative / 3-ketoacyl-CoA thiolase, putative
jcvi_12947	-0.146	moderately similar to ( 231)AT1G76490	Symbols: HMGR1, HMG1   HMG1 (3-HYDROXY-3-METHYLGLUTARYL COA REDUCTASE)
jcvi_25489	-0.147	moderately similar to ( 281)AT2G18620	Symbols:   geranylgeranyl pyrophosphate synthase, putative / GPP synthetase, putative / farnesyltransferase, putative
ev225436	-0.152	weakly similar to ( 150)AT3G25810	Symbols:   myrcene/ocimene synthase, putative
jcvi_19077	-0.159	highly similar to ( 737)AT3G25830	Symbols: ATTPS-CIN   ATTPS-CIN (TERPENE SYNTHASE-LIKE SEQUENCE-1,8-CINEOLE); myrcene/(E)-beta-ocimene synthase
jcvi_28617	-0.160	weakly similar to ( 194)AT1G78955	Symbols: CAMS1   CAMS1 (CAMELLIOL C SYNTHASE 1); beta-amyrin synthase
jcvi_1390	-0.167	moderately similar to ( 396)AT4G14210	Symbols: PDS, PDE226, PDS3   PDS3 (PHYTOENE DESATURASE)
jcvi_11050	-0.167	moderately similar to ( 429)AT4G15560	Symbols: DEF, CLA, DXS, DXPS2, CLA1   CLA1 (CLOROPLASTOS ALTERADOS 1)
eh429199	-0.168	moderately similar to ( 304)AT2G21860	Symbols:   violaxanthin de-epoxidase-related
jcvi_21874	-0.173	highly similar to ( 550)AT2G39550	Symbols: PGGT-I, GGB, ATGGT-IB   (GERANYLGERANYLTRANSFERASE-I BETA SUBUNIT); CAAX-protein geranylgeranyltransferase
ee544890	-0.181	moderately similar to ( 235)AT5G11380	Symbols: DXPS3   DXPS3 (1-DEOXY-D-XYLULOSE 5-PHOSPHATE SYNTHASE 3)
jcvi_37199	-0.185	weakly similar to ( 151)AT5G57030	Symbols: LUT2   LUT2 (LUTEIN DEFICIENT 2); lycopene epsilon cyclase
jcvi_15638	-0.186	highly similar to ( 508)AT4G24490	Symbols:   protein binding / protein prenilyltransferase
jcvi_39785	-0.188	moderately similar to ( 258)AT2G18950	Symbols: TPT1, ATHPT, VTE2, HPT1   HPT1 (HOMOGENITISATE PHYTYLTRANSFERASE 1); prenilyltransferase
jcvi_26708	-0.192	moderately similar to ( 379)AT5G60510	Symbols:   undecaprenyl pyrophosphate synthetase family protein / UPP synthetase family protein
jcvi_2339	-0.198	moderately similar to ( 201)AT5G48230	Symbols: EMB1276, ACAT2   ACAT2/EMB1276 (ACETOACETYL-COA THIOLASE 2); acetyl-CoA C-acetyltransferase
jcvi_17564	-0.199	weakly similar to ( 143)AT2G07050	Symbols: CAS1   CAS1 (CYCLOARTENOL SYNTHASE 1); cycloartenol synthase
jcvi_7482	-0.200	moderately similar to ( 400)AT5G49555	Symbols:   amine oxidase-related
jcvi_7179	-0.218	moderately similar to ( 367)AT5G48230	Symbols: EMB1276, ACAT2   ACAT2/EMB1276 (ACETOACETYL-COA THIOLASE 2); acetyl-CoA C-acetyltransferase
eh429196	-0.231	moderately similar to ( 226)AT2G21860	Symbols:   violaxanthin de-epoxidase-related
jcvi_42310	-0.234	moderately similar to ( 273)AT2G17370	Symbols: HMGR2, HMG2   HMG2 (3-HYDROXY-3-METHYLGLUTARYL-COA REDUCTASE 2)
jcvi_25684	-0.237	weakly similar to ( 138)AT1G06570	Symbols: HPD, PDS1   PDS1 (PHYTOENE DESATURATION 1)
jcvi_4755	-0.253	moderately similar to ( 347)AT1G76490	Symbols: HMGR1, HMG1   HMG1 (3-HYDROXY-3-METHYLGLUTARYL COA REDUCTASE)
jcvi_5723	-0.262	moderately similar to ( 348)AT5G36160	Symbols:   aminotransferase-related
jcvi_11826	-0.280	highly similar to ( 612)AT3G10230	Symbols: LYC   LYC (LYCOPENE CYCLASE)
dy009108	-0.286	moderately similar to ( 340)AT4G34350	Symbols: ISPH, CLB6   CLB6 (CHLOROPLAST BIOGENESIS 6); 4-hydroxy-3-methylbut-2-en-1-yl diphosphate reductase
es264628	-0.286	moderately similar to ( 348)AT3G11950	Symbols:   homogenitise farnesyltransferase/ homogenitise geranylgeranyltransferase/ homogenitise solanesyltransferase
dy018306	-0.293	weakly similar to ( 104)AT5G27450	Symbols: MVK, MK   MK/MVK; mevalonate kinase
jcvi_10896	-0.304	highly similar to ( 664)AT3G04870	Symbols: PDE181, ZDS   ZDS (ZETA-CAROTENE DESATURASE); carotene 7,8-desaturase
ev127419	-0.306	weakly similar to ( 143)AT3G04870	Symbols: PDE181, ZDS   ZDS (ZETA-CAROTENE DESATURASE); carotene 7,8-desaturase
es932498	-0.316	moderately similar to ( 330)AT3G11950	Symbols:   homogenitise farnesyltransferase/ homogenitise geranylgeranyltransferase/ homogenitise solanesyltransferase
jcvi_4538	-0.343	weakly similar to ( 182)AT5G60600	Symbols: ISPG, CSB3, CLB4, GcpE   GcpE (CHLOROPLAST BIOGENESIS 4)
jcvi_2864	-0.371	moderately similar to ( 320)AT4G38460	Symbols: GGR   GGR (GERANYLGERANYL REDUCTASE); farnesyltransferase
jcvi_9289	-0.371	highly similar to ( 536)AT5G60600	Symbols: ISPG, CSB3, CLB4, GcpE   GcpE (CHLOROPLAST BIOGENESIS 4)
es987043	-0.376	moderately similar to ( 383)AT4G24490	Symbols:   protein binding / protein prenilyltransferase
jcvi_6145	-0.378	moderately similar to ( 454)AT5G48230	Symbols: EMB1276, ACAT2   ACAT2/EMB1276 (ACETOACETYL-COA THIOLASE 2); acetyl-CoA C-acetyltransferase
jcvi_7811	-0.381	moderately similar to ( 349)AT4G32770	Symbols: ATSDX1, VTE1   VTE1 (VITAMIN E DEFICIENT 1)
ev053661	-0.409	weakly similar to ( 187)AT5G27450	Symbols: MVK, MK   MK/MVK; mevalonate kinase
jcvi_9750	-0.428	moderately similar to ( 359)AT3G10230	Symbols: LYC   LYC (LYCOPENE CYCLASE)
ex108959	-0.432	moderately similar to ( 415)AT5G58782	Symbols:   dehydrodicolyl diphosphate synthase, putative / DEDOL-PP synthase, putative
gy024944	-0.437	weakly similar to ( 101)AT3G01050	Symbols: MUB1   MUB1 (MEMBRANE-ANCHORED UBIQUITIN-FOLD PROTEIN 1 PRECURSOR)
jcvi_2741	-0.567	moderately similar to ( 381)AT3G04870	Symbols: PDE181, ZDS   ZDS (ZETA-CAROTENE DESATURASE); carotene 7,8-desaturase
jcvi_2090	-0.748	moderately similar to ( 308)AT1G67360	Symbols:   rubber elongation factor (REF) family protein
ex056312	-0.787	weakly similar to ( 196)AT4G32770	Symbols: ATSDX1, VTE1   VTE1 (VITAMIN E DEFICIENT 1)
ee423907	-0.789	moderately similar to ( 223)AT3G20160	Symbols:   geranylgeranyl pyrophosphate synthase, putative / GPP synthetase, putative / farnesyltransferase, putative
jcvi_27760	-0.899	highly similar to ( 553)AT4G15560	Symbols: DEF, CLA, DXS, DXPS2, CLA1   CLA1 (CLOROPLASTOS ALTERADOS 1)
ee459992	-0.997	weakly similar to ( 138)AT4G23600	Symbols: JR2, COR13   COR13 (CORONATINE INDUCED 1, JASMONIC ACID RESPONSIVE 2); transaminase
jcvi_38125	-1.131	moderately similar to ( 271)AT1G78970	Symbols: ATLUP1, LUP1   LUP1 (LUPEOL SYNTHASE 1); lupeol synthase
jcvi_263	-1.223	moderately similar to ( 460)AT5G58770	Symbols:   dehydrodicolyl diphosphate synthase, putative / DEDOL-PP synthase, putative
jcvi_40215	-1.324	moderately similar to ( 310)AT1G78960	Symbols: ATLUP2   ATLUP2 (Arabidopsis thaliana lupeol synthase 2); lupeol synthase
cx194269	-1.354	moderately similar to ( 272)AT1G78960	Symbols: ATLUP2   ATLUP2 (Arabidopsis thaliana lupeol synthase 2); lupeol synthase

Identifier	UV-control	cytochrome P450 - Description
jcvi_36664	2.721	highly similar to ( 822)AT4G37370   Symbols: CYP81D8   CYP81D8 (cytochrome P450, family 81, subfamily D, polypeptide 8); oxygen binding
jcvi_19911	2.118	moderately similar to ( 292)AT2G30750   Symbols: CYP71A12   CYTOCHROME P450, FAMILY 71, SUBFAMILY A, POLYPEPTIDE 12; oxygen binding
jcvi_41233	1.931	very weakly similar to ( 97.4)ATS5G57220   Symbols: CYP81F2   CYP81F2 (cytochrome P450, family 81, subfamily F, polypeptide 2); oxygen binding
dy019565	1.862	weakly similar to ( 188)ATS5G25180   Symbols: CYP71B14   CYP71B14 (cytochrome P450, family 71, subfamily B, polypeptide 14); oxygen binding
jcvi_8726	1.791	moderately similar to ( 329)AT1G01190   Symbols: CYP78A8   CYP78A8 (cytochrome P450, family 78, subfamily A, polypeptide 8); oxygen binding
jcvi_37166	1.776	highly similar to ( 756)AT2G45570   Symbols: CYP76C2   CYP76C2 (cytochrome P450, family 76, subfamily C, polypeptide 2); oxygen binding
jcvi_11703	1.688	highly similar to ( 652)AT4G22710   Symbols: CYP706A2   CYP706A2 (cytochrome P450, family 706, subfamily A, polypeptide 2); oxygen binding
am388472	1.680	weakly similar to ( 172)ATS5G57220   Symbols: CYP81F2   CYP81F2 (cytochrome P450, family 81, subfamily F, polypeptide 2); oxygen binding
cn731885	1.666	moderately similar to ( 215)AT3G48300   Symbols: CYP71A23   CYP71A23 (cytochrome P450, family 71, subfamily A, polypeptide 23); oxygen binding
es911851	1.643	moderately similar to ( 329)AT5G24960   Symbols: CYP71A14   CYP71A14 (cytochrome P450, family 71, subfamily A, polypeptide 14); oxygen binding
jcvi_12863	1.621	weakly similar to ( 142)ATS5G42590   Symbols: CYP71A16   CYP71A16 (cytochrome P450, family 71, subfamily A, polypeptide 16); oxygen binding
ev166431	1.495	moderately similar to ( 232)AT5G42590   Symbols: CYP71A16   CYP71A16 (cytochrome P450, family 71, subfamily A, polypeptide 16); oxygen binding
am388966	1.394	moderately similar to ( 331)AT3G26170   Symbols: CYP71B19   CYP71B19 (cytochrome P450, family 71, subfamily B, polypeptide 19); oxygen binding
jcvi_18417	1.320	moderately similar to ( 301)ATS5G57220   Symbols: CYP81F2   CYP81F2 (cytochrome P450, family 81, subfamily F, polypeptide 2); oxygen binding
jcvi_13667	1.233	moderately similar to ( 249)AT5G24960   Symbols: CYP71A14   CYP71A14 (cytochrome P450, family 71, subfamily A, polypeptide 14); oxygen binding
jcvi_5209	1.203	moderately similar to ( 374)AT3G26210   Symbols: CYP71B23   CYP71B23 (cytochrome P450, family 71, subfamily B, polypeptide 23); oxygen binding
ee535363	1.196	moderately similar to ( 343)AT3G26230   Symbols: CYP71B24   CYP71B24 (cytochrome P450, family 71, subfamily B, polypeptide 24); oxygen binding
jcvi_18353	1.128	moderately similar to ( 406)AT3G53130   Symbols: CYP97C1, LUT1   LUT1 (LUTEIN DEFICIENT 1); oxygen binding
jcvi_8640	0.992	moderately similar to ( 397)AT4G22690   Symbols: CYP706A1   CYP706A1 (cytochrome P450, family 706, subfamily A, polypeptide 1); oxygen binding
jcvi_18435	0.910	moderately similar to ( 383)AT4G19230   Symbols: CYP707A1   CYP707A1 (cytochrome P450, family 707, subfamily A, polypeptide 1); oxygen binding
jcvi_34711	0.908	moderately similar to ( 223)AT2G45550   Symbols: CYP76C4   CYP76C4 (cytochrome P450, family 76, subfamily C, polypeptide 4); oxygen binding
cd813547	0.878	moderately similar to ( 254)AT3G26170   Symbols: CYP71B19   CYP71B19 (cytochrome P450, family 71, subfamily B, polypeptide 19); oxygen binding
jcvi_1241	0.832	highly similar to ( 948)AT4G22690   Symbols: CYP706A1   CYP706A1 (cytochrome P450, family 706, subfamily A, polypeptide 1); oxygen binding
jcvi_3629	0.822	highly similar to ( 571)AT4G22690   Symbols: CYP706A1   CYP706A1 (cytochrome P450, family 706, subfamily A, polypeptide 1); oxygen binding
jcvi_16635	0.771	highly similar to ( 836)AT2G3190   Symbols: CYP81D7   CYP81D7 (cytochrome P450, family 81, subfamily D, polypeptide 7); oxygen binding
jcvi_17274	0.752	moderately similar to ( 245)AT4G36220   Symbols: CYP84A1, FAH1   FAH1 (FERULATE-5-HYDROXYLASE 1); ferulate 5-hydroxylase
jcvi_32341	0.729	moderately similar to ( 333)AT4G37310   Symbols: CYP81H1   CYP81H1 (cytochrome P450, family 81, subfamily H, polypeptide 1); oxygen binding
ex133161	0.723	moderately similar to ( 325)AT1G13110   Symbols: CYP71B7   CYP71B7 (cytochrome P450, family 71, subfamily B, polypeptide 7); oxygen binding
jcvi_18334	0.705	moderately similar to ( 417)AT2G30490   Symbols: ATCAH, CAH, CYP73A5   [(CINNAMATE-4-HYDROXYLASE)]; trans-cinnamate 4-monooxygenase
am386327	0.696	moderately similar to ( 224)AT4G37320   Symbols: CYP81D5   CYP81D5 (cytochrome P450, family 81, subfamily D, polypeptide 5); oxygen binding
jcvi_18951	0.688	moderately similar to ( 312)AT3G14680   Symbols: CYP72A14   CYP72A14 (cytochrome P450, family 72, subfamily A, polypeptide 14); oxygen binding
jcvi_25119	0.652	moderately similar to ( 221)AT1G57750   Symbols: MAH1, CYP96A15   CYP96A15 (MID-CHAIN ALKANE HYDROXYLASE 1)
jcvi_33391	0.628	highly similar to ( 630)AT4G39950   Symbols: CYP79B2   CYP79B2 (cytochrome P450, family 79, subfamily B, polypeptide 2); oxygen binding
jcvi_24334	0.623	highly similar to ( 719)AT2G22330   Symbols: CYP79B3   CYP79B3 (cytochrome P450, family 79, subfamily B, polypeptide 3); oxygen binding
jcvi_13253	0.618	highly similar to ( 551)AT4G36220   Symbols: CYP84A1, FAH1   FAH1 (FERULATE-5-HYDROXYLASE 1); ferulate 5-hydroxylase
ex020887	0.615	weakly similar to ( 133)ATS5G25120   Symbols: CYP71B11   CYP71B11 (cytochrome P450, family 71, subfamily B, polypeptide 11); oxygen binding
jcvi_12930	0.613	highly similar to ( 756)AT4G37430   Symbols: CYP81F1, CYP91A2   CYP91A2 (CYTOCHROME P450 MONOOXYGENASE 91A2); oxygen binding
jcvi_15156	0.593	moderately similar to ( 293)AT3G26200   Symbols: CYP71B22   CYP71B22 (cytochrome P450, family 71, subfamily B, polypeptide 22); oxygen binding
jcvi_40829	0.571	moderately similar to ( 452)AT2G45510   Symbols: CYP704A2   CYP704A2 (cytochrome P450, family 704, subfamily A, polypeptide 2); oxygen binding
jcvi_32691	0.563	highly similar to ( 626)AT4G39510   Symbols: CYP96A12   CYP96A12 (cytochrome P450, family 96, subfamily A, polypeptide 12); oxygen binding
jcvi_16379	0.560	highly similar to ( 564)AT4G39950   Symbols: CYP79B2   CYP79B2 (cytochrome P450, family 79, subfamily B, polypeptide 2); oxygen binding
jcvi_18851	0.531	highly similar to ( 854)AT3G26170   Symbols: CYP71B19   CYP71B19 (cytochrome P450, family 71, subfamily B, polypeptide 19); oxygen binding
jcvi_4639	0.523	highly similar to ( 546)AT3G14680   Symbols: CYP72A14   CYP72A14 (cytochrome P450, family 72, subfamily A, polypeptide 14); oxygen binding
jcvi_34819	0.522	moderately similar to ( 211)ATS5G57260   Symbols: CYP71B10   CYP71B10 (cytochrome P450, family 71, subfamily B, polypeptide 10); oxygen binding
jcvi_8948	0.517	moderately similar to ( 299)AT4G36220   Symbols: CYP84A1, FAH1   FAH1 (FERULATE-5-HYDROXYLASE 1); ferulate 5-hydroxylase
ee540603	0.513	weakly similar to ( 137)AT4G37320   Symbols: CYP81D5   CYP81D5 (cytochrome P450, family 81, subfamily D, polypeptide 5); oxygen binding
ex137858	0.512	moderately similar to ( 276)AT2G30490   Symbols: ATCAH, CAH, CYP73A5   [(CINNAMATE-4-HYDROXYLASE)]; trans-cinnamate 4-monooxygenase
ev125432	0.508	moderately similar to ( 240)AT4G37410   Symbols: CYP81F4   CYP81F4 (cytochrome P450, family 81, subfamily F, polypeptide 4); oxygen binding
jcvi_109	0.507	moderately similar to ( 493)AT4G31500   Symbols: SUR2, RNT1, ATR4, CYP83B1   [(CYTOCHROME P450 MONOOXYGENASE 83B1)]; oxygen binding
jcvi_34193	0.507	moderately similar to ( 244)AT1G13080   Symbols: CYP71B2   CYP71B2 (CYTOCHROME P450 71B2); oxygen binding
es904596	0.505	weakly similar to ( 123)AT4G27710   Symbols: CYP709B3   CYP709B3 (cytochrome P450, family 709, subfamily B, polypeptide 3); oxygen binding
jcvi_24359	0.495	moderately similar to ( 328)AT3G26200   Symbols: CYP71B22   CYP71B22 (cytochrome P450, family 71, subfamily B, polypeptide 22); oxygen binding
jcvi_1512	0.494	highly similar to ( 535)AT3G14690   Symbols: CYP72A15   CYP72A15 (cytochrome P450, family 72, subfamily A, polypeptide 15); oxygen binding
ee439868	0.451	weakly similar to ( 183)AT3G26150   Symbols: CYP71B16   CYP71B16 (cytochrome P450, family 71, subfamily B, polypeptide 16); oxygen binding
jcvi_31166	0.447	highly similar to ( 644)ATS5G24910   Symbols: CYP71A41   CYP71A41 (cytochrome P450, family 71, subfamily A, polypeptide 41); oxygen binding
jcvi_8274	0.442	moderately similar to ( 350)AT3G26290   Symbols: CYP71B26   CYP71B26 (cytochrome P450, family 71, subfamily B, polypeptide 26); oxygen binding
jcvi_4650	0.439	moderately similar to ( 459)AT4G31500   Symbols: SUR2, RNT1, RED1, ATR4, CYP83B1   [(CYTOCHROME P450 MONOOXYGENASE 83B1)]; oxygen binding
jcvi_22839	0.434	moderately similar to ( 233)AT2G24180   Symbols: CYP71B6   CYP71B6 (CYTOCHROME P450 71B6); oxygen binding
jcvi_15740	0.430	moderately similar to ( 343)AT3G56630   Symbols: CYP94D2   CYP94D2 (cytochrome P450, family 94, subfamily D, polypeptide 2); oxygen binding
ex096737	0.423	moderately similar to ( 293)AT2G45570   Symbols: CYP76C2   CYP76C2 (cytochrome P450, family 76, subfamily C, polypeptide 2); oxygen binding
jcvi_4133	0.421	moderately similar to ( 404)AT3G26300   Symbols: CYP71B34   CYP71B34 (cytochrome P450, family 71, subfamily B, polypeptide 34); oxygen binding
jcvi_14696	0.414	moderately similar to ( 232)AT3G26200   Symbols: CYP71B22   CYP71B22 (cytochrome P450, family 71, subfamily B, polypeptide 22); oxygen binding
jcvi_15136	0.410	moderately similar to ( 230)AT5G07990   Symbols: CYP75B1, D501, TT7   TT7 (TRANSPARENT TESTA 7); flavonoid 3'-monooxygenase/oxygen binding
jcvi_27495	0.403	moderately similar to ( 460)AT5G67310   Symbols: CYP81G1   CYP81G1 (cytochrome P450, family 81, subfamily G, polypeptide 1); oxygen binding
ex125578	0.402	moderately similar to ( 273)AT3G26310   Symbols: CYP71B35   CYP71B35 (cytochrome P450, family 71, subfamily B, polypeptide 35); oxygen binding
jcvi_34558	0.381	moderately similar to ( 371)ATS5G25180   Symbols: CYP71B14   CYP71B14 (cytochrome P450, family 71, subfamily B, polypeptide 14); oxygen binding
jcvi_15251	0.380	moderately similar to ( 446)AT3G14610   Symbols: CYP72A7   CYP72A7 (cytochrome P450, family 72, subfamily A, polypeptide 7); oxygen binding
jcvi_8722	0.368	moderately similar to ( 295)AT2G34500   Symbols: CYP710A1   (family 710, subfamily A, polypeptide 1); C-22 sterol desaturase/oxygen binding
jcvi_20441	0.360	highly similar to ( 737)AT3G28740   Symbols: CYP81D1   cytochrome P450 family protein
jcvi_42408	0.355	moderately similar to ( 465)AT3G56630   Symbols: CYP94D2   CYP94D2 (cytochrome P450, family 94, subfamily D, polypeptide 2); oxygen binding
jcvi_28286	0.344	very weakly similar to ( 95.9)AT4G27710   Symbols: CYP709B3   CYP709B3 (cytochrome P450, family 709, subfamily B, polypeptide 3); oxygen binding
dy018071	0.334	weakly similar to ( 133)AT3G14650   Symbols: CYP72A11   CYP72A11 (cytochrome P450, family 72, subfamily A, polypeptide 11); oxygen binding
ev120534	0.284	moderately similar to ( 298)AT5G67310   Symbols: CYP81G1   CYP81G1 (cytochrome P450, family 81, subfamily G, polypeptide 1); oxygen binding
jcvi_13081	0.283	highly similar to ( 981)AT4G15110   Symbols: CYP97B3   CYP97B3 (cytochrome P450, family 97, subfamily B, polypeptide 3); oxygen binding
ev170951	0.272	weakly similar to ( 105)AT3G28740   Symbols: CYP81D1   cytochrome P450 family protein
jcvi_18572	0.266	moderately similar to ( 317)AT1G75130   Symbols: CYP721A1   CYP721A1 (cytochrome P450, family 721, subfamily A, polypeptide 1); oxygen binding
jcvi_10547	0.262	moderately similar to ( 254)AT3G03470   Symbols: CYP89A9   CYP89A9 (cytochrome P450, family 89, subfamily A, polypeptide 9); oxygen binding
cn727087	0.243	moderately similar to ( 338)AT1G13080   Symbols: CYP71B2   CYP71B2 (CYTOCHROME P450 71B2); oxygen binding
jcvi_7218	0.224	moderately similar to ( 291)AT4G37410   Symbols: CYP81F4   CYP81F4 (cytochrome P450, family 81, subfamily F, polypeptide 4); oxygen binding
en087499	0.215	moderately similar to ( 270)AT3G52970   Symbols: CYP76G1   CYP76G1 (cytochrome P450, family 76, subfamily G, polypeptide 1); oxygen binding
ex097771	0.213	moderately similar to ( 423)AT2G34500   Symbols: CYP710A3   [(family 710, subfamily A, polypeptide 1)]; C-22 sterol desaturase/oxygen binding
jcvi_11055	0.208	highly similar to ( 884)AT1G31800   Symbols: CYP97A3, LUT5   [(CYTOCHROME P450-TYPE MONOOXYGENASE 97A3)]; carotene beta-ring hydroxylase
ee445881	0.202	weakly similar to ( 127)ATS5G25120   Symbols: CYP71B11   CYP71B11 (cytochrome P450, family 71, subfamily B, polypeptide 11); oxygen binding
ee434071	0.200	moderately similar to ( 207)AT4G15300   Symbols: CYP702A2   CYP702A2 (cytochrome P450, family 702, subfamily A, polypeptide 2); oxygen binding
jcvi_844	0.193	moderately similar to ( 439)AT3G53130   Symbols: CYP97C1, LUT1   LUT1 (LUTEIN DEFICIENT 1); oxygen binding
dy002094	0.183	weakly similar to ( 117)ATS5G24960   Symbols: CYP71A14   CYP71A14 (cytochrome P450, family 71, subfamily A, polypeptide 14); oxygen binding
jcvi_35248	0.169	moderately similar to ( 201)AT1G13150   Symbols: CYP86C4   CYP86C4 (cytochrome P450, family 86, subfamily C, polypeptide 4); oxygen binding
jcvi_34585	0.164	moderately similar to ( 306)AT3G10570   Symbols: CYP77A6   CYP77A6 (cytochrome P450, family 77, subfamily A, polypeptide 6); oxygen binding
am394776	0.160	weakly similar to ( 119)AT3G20090   Symbols: CYP705A18   CYP705A18 (cytochrome P450, family 705, subfamily A, polypeptide 18); oxygen binding
ev167713	0.159	moderately similar to ( 221)AT1G13080   Symbols: CYP71B2   CYP71B2 (CYTOCHROME P450 71B2); oxygen binding
es906507	0.154	moderately similar to ( 391)AT1G12740   Symbols: CYP87A2   CYP87A2 (cytochrome P450, family 87, subfamily A, polypeptide 2); oxygen binding
jcvi_35958	0.142	highly similar to ( 683)AT1G13080   Symbols: CYP71B2   CYP71B2 (CYTOCHROME P450 71B2); oxygen binding
jcvi_40911	0.142	moderately similar to ( 446)AT1G13110   Symbols: CYP71B7   CYP71B7 (cytochrome P450, family 71, subfamily B, polypeptide 7); oxygen binding
jcvi_10629	0.140	moderately similar to ( 341)AT2G46960   Symbols: CYP709B1   CYP709B1 (cytochrome P450, family 709, subfamily B, polypeptide 1); oxygen binding
jcvi_3487	0.134	highly similar to ( 832)AT2G46950   Symbols: CYP709B2   CYP709B2 (cytochrome P450, family 709, subfamily B, polypeptide 2); oxygen binding
cn726649	0.131	moderately similar to ( 218)AT5G25140   Symbols: CYP71B13   CYP71B13 (cytochrome P450, family 71, subfamily B, polypeptide 13); oxygen binding
jcvi_37300	0.130	weakly similar to ( 198)AT4G19230   Symbols: CYP707A1   CYP707A1 (cytochrome P450, family 707, subfamily A, polypeptide 1); oxygen binding
ev063264	0.125	weakly similar to ( 182)AT1G79370   Symbols: CYP79C1   CYP79C1 (cytochrome P450, family 79, subfamily C, polypeptide 1); oxygen binding
jcvi_25553	0.120	moderately similar to ( 226)AT3G28740   Symbols: CYP81D1   cytochrome P450 family protein
jcvi_29673	0.118	moderately similar to ( 469)AT3G56630   Symbols: CYP94D2   CYP94D2 (cytochrome P450, family 94, subfamily D, polypeptide 2); oxygen binding

ev109894	0.118	moderately similar to ( 281)AT4G37330	Symbols: CYP81D4   CYP81D4 (cytochrome P450, family 81, subfamily D, polypeptide 4); oxygen binding
jcvi_38723	0.111	moderately similar to (261)AT4G39510	Symbols: CYP96A12   CYP96A12 (cytochrome P450, family 96, subfamily A, polypeptide 12); oxygen binding
jcvi_20119	0.110	moderately similar to (359)AT2G24180	Symbols: CYP71B6   CYP71B6 (CYTOCHROME P450 71B6); oxygen binding
jcvi_18271	0.108	moderately similar to (254)AT1G75130	Symbols: CYP721A1   CYP721A1 (cytochrome P450, family 721, subfamily A, polypeptide 1); oxygen binding
jcvi_35653	0.107	moderately similar to (227)AT5G42590	Symbols: CYP71A16   CYP71A16 (cytochrome P450, family 71, subfamily A, polypeptide 16); oxygen binding
jcvi_39399	0.103	moderately similar to (234)AT1G13080	Symbols: CYP71B2   CYP71B2 (CYTOCHROME P450 71B2); oxygen binding
ev193501	0.089	moderately similar to (342)AT3G56630	Symbols: CYP94D2   CYP94D2 (cytochrome P450, family 94, subfamily D, polypeptide 2); oxygen binding
es912347	0.086	moderately similar to (318)AT1G50520	Symbols: CYP705A27   CYP705A27 (cytochrome P450, family 705, subfamily A, polypeptide 27); oxygen binding
dn961108	0.086	moderately similar to (265)AT3G26220	Symbols: CYP71B3   CYP71B3 (cytochrome P450, family 71, subfamily B, polypeptide 3); oxygen binding
es999487	0.084	moderately similar to (291)AT4G19230	Symbols: CYP707A1   CYP707A1 (cytochrome P450, family 707, subfamily A, polypeptide 1); oxygen binding
jcvi_1289	0.072	moderately similar to (219)AT3G14680	Symbols: CYP72A14   CYP72A14 (cytochrome P450, family 72, subfamily A, polypeptide 14); oxygen binding
dn192514	0.068	weakly similar to (113)AT2G45510	Symbols: CYP704A2   CYP704A2 (cytochrome P450, family 704, subfamily A, polypeptide 2); oxygen binding
jcvi_36182	0.065	moderately similar to (202)AT5G23190	Symbols: CYP86B1   CYP86B1 (cytochrome P450, family 86, subfamily B, polypeptide 1); oxygen binding
jcvi_2367	0.063	weakly similar to (187)AT4G32170	Symbols: CYP96A2   CYP96A2 (cytochrome P450, family 96, subfamily A, polypeptide 2); oxygen binding
ev166291	0.063	moderately similar to (335)AT5G25900	Symbols: CYP701A3, GA3   GA3 (GA REQUIRING 3); oxygen binding
jcvi_33502	0.060	moderately similar to (450)AT4G31940	Symbols: CYP82C4   CYP82C4 (cytochrome P450, family 82, subfamily C, polypeptide 4); oxygen binding
jcvi_41946	0.059	moderately similar to (484)AT3G25180	Symbols: CYP82G1   CYP82G1 (cytochrome P450, family 82, subfamily G, polypeptide 1); oxygen binding
jcvi_21655	0.058	moderately similar to (233)AT1G17060	Symbols: SOB7, CYP72C1   CYP72C1 (cytochrome P450, family 72, subfamily C, polypeptide 1); oxygen binding
jcvi_23213	0.056	moderately similar to (400)AT1G13140	Symbols: CYP86C3   CYP86C3 (cytochrome P450, family 86, subfamily C, polypeptide 3); oxygen binding
ev036453	0.056	moderately similar to (280)AT5G05260	Symbols: CYP79A2   CYP79A2 (CYTOCHROME P450 79A2); oxygen binding
eg020568	0.055	moderately similar to (219)AT2G46960	Symbols: CYP709B1   CYP709B1 (cytochrome P450, family 709, subfamily B, polypeptide 1); oxygen binding
cd841165	0.055	weakly similar to (125)AT5G04630	Symbols: CYP77A9   CYP77A9 (cytochrome P450, family 77, subfamily A, polypeptide 9); oxygen binding
jcvi_31023	0.054	moderately similar to (483)AT5G24960	Symbols: CYP71A14   CYP71A14 (cytochrome P450, family 71, subfamily A, polypeptide 14); oxygen binding
jcvi_36402	0.053	moderately similar to (208)AT3G14680	Symbols: CYP72A14   CYP72A14 (cytochrome P450, family 72, subfamily A, polypeptide 14); oxygen binding
jcvi_15865	0.049	moderately similar to (375)AT1G24540	Symbols: CYP86C1   CYP86C1 (cytochrome P450, family 86, subfamily C, polypeptide 1); oxygen binding
jcvi_6793	0.049	moderately similar to (295)AT3G20130	Symbols: CYP705A22   CYP705A22 (cytochrome P450, family 705, subfamily A, polypeptide 22)
ev121242	0.048	moderately similar to (293)AT4G37410	Symbols: CYP81F4   CYP81F4 (cytochrome P450, family 81, subfamily F, polypeptide 4); oxygen binding
ee403440	0.047	weakly similar to (150)AT3G26160	Symbols: CYP71B17   CYP71B17 (cytochrome P450, family 71, subfamily B, polypeptide 17); oxygen binding
jcvi_32659	0.047	moderately similar to (315)AT5G57220	Symbols: CYP81F2   CYP81F2 (cytochrome P450, family 81, subfamily F, polypeptide 2); oxygen binding
jcvi_29123	0.047	weakly similar to (176)AT2G29090	Symbols: CYP707A2   CYP707A2 (cytochrome P450, family 707, subfamily A, polypeptide 2); oxygen binding
ex044579	0.042	moderately similar to (352)AT5G38450	Symbols: CYP735A1   CYP735A1 (cytochrome P450, family 735, subfamily A, polypeptide 1); oxygen binding
jcvi_40877	0.041	moderately similar to (381)AT4G37430	Symbols: CYP81F1, CYP91A2   CYP91A2 (CYTOCHROME P450 MONOOXYGENASE 91A2); oxygen binding
bg543646	0.039	weakly similar to (130)AT1G13110	Symbols: CYP71B7   CYP71B7 (cytochrome P450, family 71, subfamily B, polypeptide 7); oxygen binding
jcvi_38817	0.039	moderately similar to (243)AT2G14100	Symbols: CYP705A13   CYP705A13 (cytochrome P450, family 705, subfamily A, polypeptide 13); oxygen binding
jcvi_8970	0.038	highly similar to (684)AT3G28740	Symbols: CYP81D1   cytochrome P450 family protein
ex018812	0.037	moderately similar to (251)AT1G13080	Symbols: CYP71B2   CYP71B2 (CYTOCHROME P450 71B2); oxygen binding
jcvi_13160	0.036	moderately similar to (365)AT1G13710	Symbols: CYP78A5   CYP78A5 (cytochrome P450, family 78, subfamily A, polypeptide 5); oxygen binding
ev052709	0.033	weakly similar to (167)AT1G24540	Symbols: CYP86C1   CYP86C1 (cytochrome P450, family 86, subfamily C, polypeptide 1); oxygen binding
jcvi_19719	0.033	moderately similar to (299)AT3G28740	Symbols: CYP81D1   cytochrome P450 family protein
ev152669	0.032	moderately similar to (250)AT5G57220	Symbols: CYP81F2   CYP81F2 (cytochrome P450, family 81, subfamily F, polypeptide 2); oxygen binding
jcvi_13403	0.031	highly similar to (736)AT2G45580	Symbols: CYP76C3   CYP76C3 (cytochrome P450, family 76, subfamily C, polypeptide 3); oxygen binding
jcvi_26392	0.030	moderately similar to (292)AT4G36220	Symbols: CYP84A1, FAH1   FAH1 (FERULATE-5-HYDROXYLASE 1); ferulate 5-hydroxylase
jcvi_33109	0.029	moderately similar to (424)AT1G01280	Symbols: CYP703A2, CYP703   CYP703A2 (CYTOCHROME P450, FAMILY 703, SUBFAMILY A, POLYPEPTIDE 2)
jcvi_458	0.026	highly similar to (777)AT5G05690	Symbols: CYP90A, CYP90, CBB3, DWF3, CYP90A1, CPD   CPD (CABBAGE 3)
ex044469	0.024	moderately similar to (296)AT3G14690	Symbols: CYP72A15   CYP72A15 (cytochrome P450, family 72, subfamily A, polypeptide 15); oxygen binding
jcvi_14950	0.024	highly similar to (754)AT4G13770	Symbols: REF2, CYP83A1   CYP83A1 (CYTOCHROME P450 83A1); oxygen binding
jcvi_16866	0.023	moderately similar to (321)AT2G45550	Symbols: CYP76C4   CYP76C4 (cytochrome P450, family 76, subfamily C, polypeptide 4); oxygen binding
jcvi_19692	0.020	moderately similar to (212)AT4G37310	Symbols: CYP81H1   CYP81H1 (cytochrome P450, family 81, subfamily H, polypeptide 1); oxygen binding
ev121493	0.020	moderately similar to (263)AT5G67310	Symbols: CYP81G1   CYP81G1 (cytochrome P450, family 81, subfamily G, polypeptide 1); oxygen binding
ex106290	0.020	moderately similar to (262)AT4G37330	Symbols: CYP81D4   CYP81D4 (cytochrome P450, family 81, subfamily D, polypeptide 4); oxygen binding
ev177168	0.019	moderately similar to (216)AT4G15396	Symbols: CYP702A6   heme binding / iron ion binding / monooxygenase
jcvi_34106	0.019	moderately similar to (342)AT3G52970	Symbols: CYP76G1   CYP76G1 (cytochrome P450, family 76, subfamily G, polypeptide 1); oxygen binding
jcvi_14895	0.019	moderately similar to (336)AT4G19230	Symbols: CYP707A1   CYP707A1 (cytochrome P450, family 707, subfamily A, polypeptide 1); oxygen binding
jcvi_5423	0.018	moderately similar to (325)AT3G61880	Symbols: CYP78A9   CYP78A9 (CYTOCHROME P450 78A9); oxygen binding
jcvi_16677	0.017	moderately similar to (238)AT1G57750	Symbols: MAH1, CYP96A15   CYP96A15/MAH1 (MID-CHAIN ALKANE HYDROXYLASE 1)
jcvi_21729	0.015	weakly similar to (169)AT5G23190	Symbols: CYP86B1   CYP86B1 (cytochrome P450, family 86, subfamily B, polypeptide 1); oxygen binding
jcvi_15755	0.014	moderately similar to (347)AT5G25120	Symbols: CYP71B11   CYP71B11 (cytochrome P450, family 71, subfamily B, polypeptide 11); oxygen binding
ev077815	0.012	moderately similar to (213)AT3G26310	Symbols: CYP71B35   CYP71B35 (cytochrome P450, family 71, subfamily B, polypeptide 35); oxygen binding
ev060677	0.012	moderately similar to (318)AT1G17060	Symbols: SOB7, CYP72C1   CYP72C1 (cytochrome P450, family 72, subfamily C, polypeptide 1); oxygen binding
jcvi_28614	0.008	moderately similar to (267)AT1G78490	Symbols: CYP708A3   CYP708A3 (cytochrome P450, family 708, subfamily A, polypeptide 3); oxygen binding
jcvi_25998	0.007	weakly similar to (165)AT4G39500	Symbols: CYP96A11   CYP96A11 (cytochrome P450, family 96, subfamily A, polypeptide 11); oxygen binding
jcvi_13505	0.006	moderately similar to (388)AT3G26330	Symbols: CYP71B37   CYP71B37 (cytochrome P450, family 71, subfamily B, polypeptide 37); oxygen binding
jcvi_35470	0.004	weakly similar to (169)AT2G46960	Symbols: CYP709B1   CYP709B1 (cytochrome P450, family 709, subfamily B, polypeptide 1); oxygen binding
jcvi_2258	0.003	moderately similar to (375)AT1G74540	Symbols: CYP98A8   CYP98A8 (cytochrome P450, family 98, subfamily A, polypeptide 8); oxygen binding
jcvi_13256	0.001	moderately similar to (410)AT3G28740	Symbols: CYP81D1   cytochrome P450 family protein
jcvi_27950	0.001	moderately similar to (306)AT2G45550	Symbols: CYP76C4   CYP76C4 (cytochrome P450, family 76, subfamily C, polypeptide 4); oxygen binding
jcvi_13758	-0.001	moderately similar to (343)AT1G01600	Symbols: CYP86A4   CYP86A4 (cytochrome P450, family 86, subfamily A, polypeptide 4); oxygen binding
jcvi_24252	-0.001	highly similar to (599)AT5G57220	Symbols: CYP81F2   CYP81F2 (cytochrome P450, family 81, subfamily F, polypeptide 2); oxygen binding
ev220365	-0.002	moderately similar to (269)AT2G25160	Symbols: CYP82F1   CYP82F1 (cytochrome P450, family 82, subfamily F, polypeptide 1); oxygen binding
jcvi_2779	-0.002	moderately similar to (317)AT3G26230	Symbols: CYP71B24   CYP71B24 (cytochrome P450, family 71, subfamily B, polypeptide 24); oxygen binding
jcvi_15484	-0.003	moderately similar to (341)AT1G13080	Symbols: CYP71B2   CYP71B2 (CYTOCHROME P450 71B2); oxygen binding
jcvi_35527	-0.004	moderately similar to (261)AT5G23190	Symbols: CYP86B1   CYP86B1 (cytochrome P450, family 86, subfamily B, polypeptide 1); oxygen binding
ev004703	-0.004	moderately similar to (326)AT1G17060	Symbols: SOB7, CYP72C1   CYP72C1 (cytochrome P450, family 72, subfamily C, polypeptide 1); oxygen binding
ee435302	-0.005	weakly similar to (118)AT3G26230	Symbols: CYP71B24   CYP71B24 (cytochrome P450, family 71, subfamily B, polypeptide 24); oxygen binding
jcvi_38864	-0.006	moderately similar to (429)AT3G52970	Symbols: CYP76G1   CYP76G1 (cytochrome P450, family 76, subfamily G, polypeptide 1); oxygen binding
jcvi_21903	-0.006	moderately similar to (416)AT5G05690	Symbols: CYP90A, CYP90, CBB3, DWF3, CYP90A1, CPD   CPD (CABBAGE 3)
jcvi_14640	-0.007	moderately similar to (375)AT2G42250	Symbols: CYP712A1   CYP712A1 (cytochrome P450, family 712, subfamily A, polypeptide 1); oxygen binding
ev170896	-0.007	moderately similar to (254)AT5G25900	Symbols: CYP701A3, GA3   GA3 (GA REQUIRING 3); oxygen binding
dy025805	-0.008	moderately similar to (333)AT3G48270	Symbols: CYP71A26   CYP71A26 (cytochrome P450, family 71, subfamily A, polypeptide 26); oxygen binding
ev160033	-0.008	moderately similar to (346)AT1G11600	Symbols: CYP77B1   CYP77B1 (cytochrome P450, family 77, subfamily B, polypeptide 1); oxygen binding
jcvi_12683	-0.011	moderately similar to (299)AT1G57750	Symbols: MAH1, CYP96A15   CYP96A15/MAH1 (MID-CHAIN ALKANE HYDROXYLASE 1)
cx189341	-0.011	weakly similar to (123)AT3G26280	Symbols: CYP71B4   CYP71B4 (cytochrome P450, family 71, subfamily B, polypeptide 4); oxygen binding
ev137238	-0.011	weakly similar to (172)AT3G19270	Symbols: CYP707A4   CYP707A4 (cytochrome P450, family 707, subfamily A, polypeptide 4); oxygen binding
jcvi_26942	-0.012	moderately similar to (279)AT2G46960	Symbols: CYP709B1   CYP709B1 (cytochrome P450, family 709, subfamily B, polypeptide 1); oxygen binding
jcvi_17717	-0.012	moderately similar to (351)AT2G34500	Symbols: CYP710A1   cytochrome P450, family 710, subfamily A, polypeptide 1; C-22 sterol desaturase/ oxygen binding
cn728267	-0.013	moderately similar to (300)AT5G44620	Symbols: CYP706A3   CYP706A3 (cytochrome P450, family 706, subfamily A, polypeptide 3); oxygen binding
jcvi_32868	-0.014	weakly similar to (124)AT4G12320	Symbols: CYP706A6   CYP706A6 (cytochrome P450, family 706, subfamily A, polypeptide 6); oxygen binding
jcvi_1486	-0.014	moderately similar to (377)AT5G67310	Symbols: CYP81G1   CYP81G1 (cytochrome P450, family 81, subfamily G, polypeptide 1); oxygen binding
jcvi_36410	-0.014	weakly similar to (127)AT2G23190	Symbols: CYP81D7   CYP81D7 (cytochrome P450, family 81, subfamily D, polypeptide 7); oxygen binding
jcvi_13408	-0.017	moderately similar to (457)AT1G69500	Symbols:   oxygen binding
ev216628	-0.017	weakly similar to (191)AT3G53130	Symbols: CYP97C1, LUT1   LUT1 (LUTEIN DEFICIENT 1); oxygen binding
jcvi_30612	-0.018	highly similar to (858)AT3G14630	Symbols: CYP72A9   CYP72A9 (cytochrome P450, family 72, subfamily A, polypeptide 9); oxygen binding
cx088960	-0.019	moderately similar to (295)AT3G19270	Symbols: CYP709B3   CYP709B3 (cytochrome P450, family 709, subfamily B, polypeptide 3); oxygen binding
ev122740	-0.022	weakly similar to (198)AT3G20080	Symbols: CYP705A15   CYP705A15 (cytochrome P450, family 705, subfamily A, polypeptide 15); oxygen binding
ex088251	-0.023	moderately similar to (293)AT1G01280	Symbols: CYP703A2   NADH or NADPH as one donor, and incorporation of one atom of oxygen / oxygen binding
ev207466	-0.025	moderately similar to (384)AT2G46660	Symbols: CYP78A6   CYP78A6 (cytochrome P450, family 78, subfamily A, polypeptide 6); oxygen binding
jcvi_41173	-0.026	weakly similar to (181)AT5G02900	Symbols: CYP96A13   CYP96A13 (cytochrome P450, family 96, subfamily A, polypeptide 13); oxygen binding
jcvi_13752	-0.027	moderately similar to (343)AT1G69500	Symbols:   oxygen binding
jcvi_23627	-0.028	moderately similar to (295)AT5G67310	Symbols: CYP81G1   CYP81G1 (cytochrome P450, family 81, subfamily G, polypeptide 1); oxygen binding
jcvi_21425	-0.028	weakly similar to (188)AT2G42180	Symbols: CYP71B6   CYP71B6 (CYTOCHROME P450 71B6); oxygen binding
cd836257	-0.030	moderately similar to (296)AT5G57260	Symbols: CYP71B10   CYP71B10 (cytochrome P450, family 71, subfamily B, polypeptide 10); oxygen binding

ee470757	-0.030 weakly similar to (141)AT2G42850   Symbols: CYP718   CYP718 (cytochrome P450, family 718); oxygen binding
ev211246	-0.031 moderately similar to (276)AT4G37340   Symbols: CYP81D3   CYP81D3 (cytochrome P450, family 81, subfamily D, polypeptide 3); oxygen binding
cn830062	-0.031 moderately similar to (392)AT2G45970   Symbols: LCR, CYP86A8   CYP86A8 (LACERATA); fatty acid (omega-1)-hydroxylase/ oxygen binding
ev109225	-0.031 weakly similar to (187)AT3G52970   Symbols: CYP76G1   CYP76G1 (cytochrome P450, family 76, subfamily G, polypeptide 1); oxygen binding
jcvi_18314	-0.031 moderately similar to (448)AT2G45510   Symbols: CYP704A2   CYP704A2 (cytochrome P450, family 704, subfamily A, polypeptide 2); oxygen binding
ev166394	-0.033 moderately similar to (443)AT5G57220   Symbols: CYP81F2   CYP81F2 (cytochrome P450, family 81, subfamily F, polypeptide 2); oxygen binding
ev112982	-0.034 moderately similar to (216)AT4G36220   Symbols: CYP84A1, FAH1   FAH1 (FERULATE-5-HYDROXYLASE 1); ferulate 5-hydroxylase
ee513955	-0.035 weakly similar to (174)AT3G61040   Symbols: CYP76C7   CYP76C7 (cytochrome P450, family 76, subfamily C, polypeptide 7); oxygen binding
ee438184	-0.035 moderately similar to (257)AT4G13310   Symbols: CYP71A20   CYP71A20 (cytochrome P450, family 71, subfamily A, polypeptide 20); oxygen binding
jcvi_32462	-0.036 moderately similar to (343)AT3G14650   Symbols: CYP72A11   CYP72A11 (cytochrome P450, family 72, subfamily A, polypeptide 11); oxygen binding
jcvi_26026	-0.037 moderately similar to (288)AT5G63450   Symbols: CYP94B1   CYP94B1 (cytochrome P450, family 94, subfamily B, polypeptide 1); oxygen binding
jcvi_22136	-0.038 highly similar to (839)AT3G50660   Symbols: CYP90B1, CLM, SNP2, DWF4   DWF4 (DWARF 4)
ev034065	-0.038 moderately similar to (259)AT2G23190   Symbols: CYP81D7   CYP81D7 (cytochrome P450, family 81, subfamily D, polypeptide 7); oxygen binding
jcvi_37742	-0.039 moderately similar to (206)AT1G65340   Symbols: CYP96A3   CYP96A3 (cytochrome P450, family 96, subfamily A, polypeptide 3); oxygen binding
jcvi_8984	-0.039 moderately similar to (332)AT4G27710   Symbols: CYP709B3   CYP709B3 (cytochrome P450, family 709, subfamily B, polypeptide 3); oxygen binding
jcvi_39009	-0.041 moderately similar to (288)AT5G63450   Symbols: CYP81K1   CYP81K1 (cytochrome P450, family 81, subfamily K, polypeptide 1); oxygen binding
dn192274	-0.041 moderately similar to (277)AT4G27710   Symbols: CYP709B3   CYP709B3 (cytochrome P450, family 709, subfamily B, polypeptide 3); oxygen binding
jcvi_33491	-0.041 highly similar to (629)AT5G25900   Symbols: CYP701A3, GA3   GA3 (GA REQUIRING 3); oxygen binding
ev216674	-0.042 moderately similar to (327)AT3G48270   Symbols: CYP71A26   CYP71A26 (cytochrome P450, family 71, subfamily A, polypeptide 26); oxygen binding
am062044	-0.043 moderately similar to (295)AT4G27710   Symbols: CYP709B3   CYP709B3 (cytochrome P450, family 709, subfamily B, polypeptide 3); oxygen binding
jcvi_5528	-0.044 highly similar to (753)AT3G48300   Symbols: CYP71A23   CYP71A23 (cytochrome P450, family 71, subfamily A, polypeptide 23); oxygen binding
jcvi_11758	-0.045 moderately similar to (294)AT3G14610   Symbols: CYP72A7   CYP72A7 (cytochrome P450, family 72, subfamily A, polypeptide 7); oxygen binding
jcvi_11410	-0.045 moderately similar to (297)AT1G33720   Symbols: CYP76C6   CYP76C6 (cytochrome P450, family 76, subfamily C, polypeptide 6); oxygen binding
ee473119	-0.045 moderately similar to (206)AT2G46960   Symbols: CYP709B1   CYP709B1 (cytochrome P450, family 709, subfamily B, polypeptide 1); oxygen binding
jcvi_24102	-0.046 very weakly similar to (88.2)AT3G26290   Symbols: CYP71B26   CYP71B26 (cytochrome P450, family 71, subfamily B, polypeptide 26); oxygen binding
jcvi_34056	-0.046 moderately similar to (121)AT3G26280   Symbols: CYP71B4   CYP71B4 (cytochrome P450, family 71, subfamily B, polypeptide 4); oxygen binding
jcvi_6241	-0.048 highly similar to (521)AT4G37320   Symbols: CYP81D5   CYP81D5 (cytochrome P450, family 81, subfamily D, polypeptide 5); oxygen binding
ev060076	-0.048 very weakly similar to (83.6)AT2G23220   Symbols: CYP81D6   CYP81D6 (cytochrome P450, family 81, subfamily D, polypeptide 6); oxygen binding
ex112711	-0.048 weakly similar to (118)AT3G14690   Symbols: CYP72A15   CYP72A15 (cytochrome P450, family 72, subfamily A, polypeptide 15); oxygen binding
jcvi_22400	-0.052 highly similar to (623)AT2G25160   Symbols: CYP82F1   CYP82F1 (cytochrome P450, family 82, subfamily F, polypeptide 1); oxygen binding
cx194361	-0.052 highly similar to (190)AT1G13090   Symbols: CYP71B28   CYP71B28 (cytochrome P450, family 71, subfamily B, polypeptide 28); oxygen binding
jcvi_4889	-0.053 highly similar to (757)AT4G32170   Symbols: CYP96A2   CYP96A2 (cytochrome P450, family 96, subfamily A, polypeptide 2); oxygen binding
jcvi_42596	-0.053 moderately similar to (418)AT2G23190   Symbols: CYP81D7   CYP81D7 (cytochrome P450, family 81, subfamily D, polypeptide 7); oxygen binding
jcvi_29816	-0.053 moderately similar to (470)AT5G10610   Symbols: CYP81K1   CYP81K1 (cytochrome P450, family 81, subfamily K, polypeptide 1); oxygen binding
jcvi_4637	-0.054 moderately similar to (240)AT1G74540   Symbols: CYP98A8   CYP98A8 (cytochrome P450, family 98, subfamily A, polypeptide 8); oxygen binding
jcvi_5513	-0.054 highly similar to (881)AT2G40890   Symbols: CYP98A3   monoxygenase/ p-coumarate 3-hydroxylase
jcvi_33871	-0.054 moderately similar to (277)AT2G45970   Symbols: LCR, CYP86A8   CYP86A8 (LACERATA); fatty acid (omega-1)-hydroxylase/ oxygen binding
ev121702	-0.056 moderately similar to (390)AT4G31940   Symbols: CYP82C4   CYP82C4 (cytochrome P450, family 82, subfamily C, polypeptide 4); oxygen binding
ex040060	-0.059 moderately similar to (210)AT2G45570   Symbols: CYP76C2   CYP76C2 (cytochrome P450, family 76, subfamily C, polypeptide 2); oxygen binding
es269078	-0.061 moderately similar to (213)AT4G19230   Symbols: CYP707A1   CYP707A1 (cytochrome P450, family 707, subfamily A, polypeptide 1); oxygen binding
ex037042	-0.062 moderately similar to (290)AT5G04660   Symbols: CYP77A4   CYP77A4 (cytochrome P450, family 77, subfamily A, polypeptide 4); oxygen binding
es906436	-0.062 moderately similar to (293)AT5G67310   Symbols: CYP81G1   CYP81G1 (cytochrome P450, family 81, subfamily G, polypeptide 1); oxygen binding
cd834522	-0.064 weakly similar to (185)AT4G15350   Symbols: CYP705A2   CYP705A2 (cytochrome P450, family 705, subfamily A, polypeptide 2); oxygen binding
jcvi_14008	-0.065 moderately similar to (227)AT5G63450   Symbols: CYP94B1   CYP94B1 (cytochrome P450, family 94, subfamily B, polypeptide 1); oxygen binding
jcvi_14969	-0.067 highly similar to (853)AT3G61880   Symbols: CYP78A9   CYP78A9 (CYTOCHROME P450 78A9); oxygen binding
jcvi_27964	-0.068 moderately similar to (388)AT1G13090   Symbols: CYP71B28   CYP71B28 (cytochrome P450, family 71, subfamily B, polypeptide 28); oxygen binding
jcvi_25515	-0.069 moderately similar to (451)AT3G26125   Symbols: CYP86C2   CYP86C2 (cytochrome P450, family 86, subfamily C, polypeptide 2); oxygen binding
1B5832	-0.071 weakly similar to (191)AT4G00360   Symbols: ATT1, CYP86A2   CYP86A2 (ABERRANT INDUCTION OF TYPE THREE GENES 1); oxygen binding
ev111587	-0.072 weakly similar to (106)AT3G14630   Symbols: CYP72A9   CYP72A9 (cytochrome P450, family 72, subfamily A, polypeptide 9); oxygen binding
ev153072	-0.074 weakly similar to (150)AT2G45580   Symbols: CYP76C3   CYP76C3 (cytochrome P450, family 76, subfamily C, polypeptide 3); oxygen binding
jcvi_24362	-0.074 moderately similar to (311)AT3G20130   Symbols: CYP705A22   CYP705A22 (cytochrome P450, family 705, subfamily A, polypeptide 22)
jcvi_42512	-0.075 moderately similar to (328)AT2G27690   Symbols: CYP94C1   CYP94C1 (cytochrome P450, family 94, subfamily C, polypeptide 1); oxygen binding
jcvi_32427	-0.076 moderately similar to (360)AT1G13100   Symbols: CYP71B29   CYP71B29 (cytochrome P450, family 71, subfamily B, polypeptide 29); oxygen binding
jcvi_16369	-0.081 highly similar to (550)AT4G15396   Symbols: CYP702A6   heme binding / iron ion binding / monoxygenase
1B3212	-0.083 weakly similar to (128)AT1G13150   Symbols: CYP86C4   CYP86C4 (cytochrome P450, family 86, subfamily C, polypeptide 4); oxygen binding
jcvi_18440	-0.083 moderately similar to (288)AT3G26280   Symbols: CYP71B4   CYP71B4 (cytochrome P450, family 71, subfamily B, polypeptide 4); oxygen binding
am395066	-0.083 weakly similar to (114)AT5G24960   Symbols: CYP71A14   CYP71A14 (cytochrome P450, family 71, subfamily A, polypeptide 14); oxygen binding
jcvi_20366	-0.083 moderately similar to (229)AT1G13080   Symbols: CYP71B2   CYP71B2 (CYTOCHROME P450 71B2); oxygen binding
jcvi_31546	-0.087 moderately similar to (398)AT4G37410   Symbols: CYP81F4   CYP81F4 (cytochrome P450, family 81, subfamily F, polypeptide 4); oxygen binding
jcvi_8810	-0.090 moderately similar to (218)AT2G45510   Symbols: CYP704A2   CYP704A2 (cytochrome P450, family 704, subfamily A, polypeptide 2); oxygen binding
jcvi_15265	-0.094 moderately similar to (342)AT2G42250   Symbols: CYP712A1   CYP712A1 (cytochrome P450, family 712, subfamily A, polypeptide 1); oxygen binding
cd829521	-0.095 moderately similar to (201)AT3G48310   Symbols: CYP71A22   CYP71A22 (cytochrome P450, family 71, subfamily A, polypeptide 22); oxygen binding
jcvi_36324	-0.095 moderately similar to (334)AT4G15396   Symbols: CYP702A6   heme binding / iron ion binding / monoxygenase
es993338	-0.097 weakly similar to (189)AT3G28740   Symbols: CYP81D1   cytochrome P450 family protein
ev114804	-0.097 moderately similar to (374)AT3G26330   Symbols: CYP71B37   CYP71B37 (cytochrome P450, family 71, subfamily B, polypeptide 37); oxygen binding
jcvi_39819	-0.101 moderately similar to (232)AT3G48270   Symbols: CYP71A26   CYP71A26 (cytochrome P450, family 71, subfamily A, polypeptide 26); oxygen binding
jcvi_22517	-0.103 moderately similar to (275)AT4G00360   Symbols: ATT1, CYP86A2   CYP86A2 (ABERRANT INDUCTION OF TYPE THREE GENES 1); oxygen binding
jcvi_37321	-0.104 moderately similar to (428)AT5G67310   Symbols: CYP81G1   CYP81G1 (cytochrome P450, family 81, subfamily G, polypeptide 1); oxygen binding
cd826995	-0.104 moderately similar to (280)AT2G25160   Symbols: CYP82F1   CYP82F1 (cytochrome P450, family 82, subfamily F, polypeptide 1); oxygen binding
jcvi_18323	-0.106 moderately similar to (305)AT1G65670   Symbols: CYP702A1   CYTOCHROME P450, FAMILY 702, SUBFAMILY A, POLYPEPTIDE 1; oxygen binding
ev080390	-0.108 moderately similar to (260)AT3G28740   Symbols: CYP81D1   cytochrome P450 family protein
ee531205	-0.109 weakly similar to (123)AT3G50660   Symbols: CYP90B1, CLM, SNP2, DWF4   DWF4 (DWARF 4)
cd827796	-0.110 weakly similar to (127)AT2G34500   Symbols: CYP710A1   cytochrome P450, family 710, subfamily A, polypeptide 1; C-22 sterol desaturase/ oxygen binding
ev177001	-0.111 moderately similar to (315)AT1G17060   Symbols: SOB7, CYP72C1   CYP72C1 (cytochrome P450, family 72, subfamily C, polypeptide 1); oxygen binding
jcvi_41772	-0.112 highly similar to (528)AT1G17060   Symbols: SOB7, CYP72C1   CYP72C1 (cytochrome P450, family 72, subfamily C, polypeptide 1); oxygen binding
jcvi_14270	-0.113 moderately similar to (219)AT5G67310   Symbols: CYP81G1   CYP81G1 (cytochrome P450, family 81, subfamily G, polypeptide 1); oxygen binding
jcvi_20371	-0.117 moderately similar to (338)AT1G13150   Symbols: CYP86C4   CYP86C4 (cytochrome P450, family 86, subfamily C, polypeptide 4); oxygen binding
es968427	-0.124 very weakly similar to (99.0)AT4G13310   Symbols: CYP71A20   CYP71A20 (cytochrome P450, family 71, subfamily A, polypeptide 20); oxygen binding
jcvi_10179	-0.124 moderately similar to (271)AT4G36220   Symbols: CYP84A1, FAH1   FAH1 (FERULATE-5-HYDROXYLASE 1); ferulate 5-hydroxylase
jcvi_34973	-0.128 moderately similar to (384)AT1G65340   Symbols: CYP96A3   CYP96A3 (cytochrome P450, family 96, subfamily A, polypeptide 3); oxygen binding
jcvi_8386	-0.134 moderately similar to (324)AT5G04660   Symbols: CYP77A4   CYP77A4 (cytochrome P450, family 77, subfamily A, polypeptide 4); oxygen binding
ev000620	-0.136 moderately similar to (353)AT3G14630   Symbols: CYP72A9   CYP72A9 (cytochrome P450, family 72, subfamily A, polypeptide 9); oxygen binding
jcvi_14187	-0.137 moderately similar to (401)AT1G01280   Symbols: CYP703A2   NADH or NADPH as one donor, and incorporation of one atom of oxygen / oxygen binding
jcvi_29378	-0.139 moderately similar to (244)AT2G45510   Symbols: CYP704A2   CYP704A2 (cytochrome P450, family 704, subfamily A, polypeptide 2); oxygen binding
dy080836	-0.140 weakly similar to (200)AT3G14630   Symbols: CYP72A9   CYP72A9 (cytochrome P450, family 72, subfamily A, polypeptide 9); oxygen binding
jcvi_32592	-0.141 moderately similar to (294)AT2G46960   Symbols: CYP709B1   CYP709B1 (cytochrome P450, family 709, subfamily B, polypeptide 1); oxygen binding
ev160116	-0.146 moderately similar to (247)AT1G11600   Symbols: CYP77B1   CYP77B1 (cytochrome P450, family 77, subfamily B, polypeptide 1); oxygen binding
es901345	-0.146 moderately similar to (257)AT4G37320   Symbols: CYP81D5   CYP81D5 (cytochrome P450, family 81, subfamily D, polypeptide 5); oxygen binding
jcvi_5352	-0.148 moderately similar to (209)AT3G14640   Symbols: CYP72A10   CYP72A10 (cytochrome P450, family 72, subfamily A, polypeptide 10); oxygen binding
jcvi_32582	-0.150 moderately similar to (320)AT3G26300   Symbols: CYP71B34   CYP71B34 (cytochrome P450, family 71, subfamily B, polypeptide 34); oxygen binding
ex025947	-0.150 weakly similar to (142)AT5G58860   Symbols: CYP86, CYP86A1   CYP86A1 (cytochrome P450, family 86, subfamily A, polypeptide 1); oxygen binding
jcvi_14975	-0.154 moderately similar to (263)AT4G37410   Symbols: CYP71A4   CYP71A4 (cytochrome P450, family 81, subfamily F, polypeptide 4); oxygen binding
dn961931	-0.156 moderately similar to (369)AT2G45510   Symbols: CYP704A2   CYP704A2 (cytochrome P450, family 704, subfamily A, polypeptide 2); oxygen binding
es981427	-0.157 moderately similar to (234)AT3G50660   Symbols: CYP90B1, CLM, SNP2, DWF4   DWF4 (DWARF 4)
jcvi_26799	-0.160 moderately similar to (389)AT4G13770   Symbols: REF2, CYP83A1   CYP83A1 (CYTOCHROME P450 83A1); oxygen binding
ev202871	-0.162 weakly similar to (104)AT1G01190   Symbols: CYP78A8   CYP78A8 (cytochrome P450, family 78, subfamily A, polypeptide 8); oxygen binding
jcvi_13980	-0.162 highly similar to (507)AT2G30490   Symbols: ATC4H, C4H, CYP73A5   trans-cinnamate 4-monoxygenase
jcvi_18074	-0.163 moderately similar to (303)AT2G45970   Symbols: LCR, CYP86A8   CYP86A8 (LACERATA); fatty acid (omega-1)-hydroxylase/ oxygen binding
jcvi_621	-0.166 moderately similar to (377)AT3G53280   Symbols: CYP71B5   CYP71B5 (CYTOCHROME P450 71B5); oxygen binding
jcvi_12445	-0.166 moderately similar to (409)AT5G25140   Symbols: CYP71B13   CYP71B13 (cytochrome P450, family 71, subfamily B, polypeptide 13); oxygen binding
jcvi_9357	-0.166 highly similar to (541)AT2G40890   Symbols: CYP98A3   monoxygenase/ p-coumarate 3-hydroxylase

jcvi_13380	-0.167	moderately similar to (352)AT5G58860	Symbols: CYP86, CYP86A1   CYP86A1 (cytochrome P450, family 86, subfamily A, polypeptide 1); oxygen binding
jcvi_9799	-0.171	moderately similar to (435)AT3G26160	Symbols: CYP71B17   CYP71B17 (cytochrome P450, family 71, subfamily B, polypeptide 17); oxygen binding
ev155336	-0.172	moderately similar to (417)AT2G23180	Symbols: CYP96A1   CYP96A1 (cytochrome P450, family 96, subfamily A, polypeptide 1); oxygen binding
cd836219	-0.173	moderately similar to (306)AT4G27710	Symbols: CYP709B3   CYP709B3 (cytochrome P450, family 709, subfamily B, polypeptide 3); oxygen binding
jcvi_15282	-0.176	moderately similar to (493)AT5G07990	Symbols: CYP75B1, D501, TT7   TT7 (TRANSPARENT TESTA 7); flavonoid 3'-monooxygenase/ oxygen binding
jcvi_17170	-0.176	weakly similar to (138)AT5G36220	Symbols: CYP91A1, CYP81D1   CYP81D1 (CYTOCHROME P450 91A1); oxygen binding
cd828252	-0.180	weakly similar to (148)AT3G14610	Symbols: CYP72A7   CYP72A7 (cytochrome P450, family 72, subfamily A, polypeptide 7); oxygen binding
ev100862	-0.184	very weakly similar to (85.9)AT1G57750	Symbols: MAH1, CYP96A15   CYP96A15/MAH1 (MID-CHAIN ALKANE HYDROXYLASE 1)
ev020283	-0.188	moderately similar to (425)AT3G50660	Symbols: CYP90B1, CLM, SNP2, DWF4   DWF4 (DWARF 4)
jcvi_13111	-0.188	moderately similar to (492)AT5G58860	Symbols: CYP86, CYP86A1   CYP86A1 (cytochrome P450, family 86, subfamily A, polypeptide 1); oxygen binding
jcvi_7861	-0.190	moderately similar to (339)AT1G13110	Symbols: CYP71B7   CYP71B7 (cytochrome P450, family 71, subfamily B, polypeptide 7); oxygen binding
jcvi_10859	-0.192	very weakly similar to (100)AT1G11600	Symbols: CYP77B1   CYP77B1 (cytochrome P450, family 77, subfamily B, polypeptide 1); oxygen binding
jcvi_7322	-0.193	moderately similar to (249)AT3G26125	Symbols: CYP86C2   CYP86C2 (cytochrome P450, family 86, subfamily C, polypeptide 2); oxygen binding
jcvi_23363	-0.196	weakly similar to (166)AT1G57750	Symbols: MAH1, CYP96A15   CYP96A15/MAH1 (MID-CHAIN ALKANE HYDROXYLASE 1)
jcvi_8135	-0.201	moderately similar to (355)AT5G10600	Symbols: CYP81K2   CYP81K2 (cytochrome P450, family 81, subfamily K, polypeptide 2); oxygen binding
ex056678	-0.205	moderately similar to (339)AT3G14690	Symbols: CYP72A15   CYP72A15 (cytochrome P450, family 72, subfamily A, polypeptide 15); oxygen binding
jcvi_20750	-0.205	moderately similar to (396)AT2G30490	Symbols: ATCAH, C4H, CYP73A5   trans-cinnamate 4-monooxygenase
jcvi_33397	-0.227	moderately similar to (251)AT5G44620	Symbols: CYP706A3   CYP706A3 (cytochrome P450, family 706, subfamily A, polypeptide 3); oxygen binding
jcvi_17488	-0.228	moderately similar to (401)AT1G28430	Symbols: CYP705A24   CYP705A24 (cytochrome P450, family 705, subfamily A, polypeptide 24); oxygen binding
jcvi_7608	-0.231	moderately similar to (424)AT1G13110	Symbols: CYP71B7   CYP71B7 (cytochrome P450, family 71, subfamily B, polypeptide 7); oxygen binding
jcvi_29231	-0.234	moderately similar to (366)AT5G63450	Symbols: CYP94B1   CYP94B1 (cytochrome P450, family 94, subfamily B, polypeptide 1); oxygen binding
jcvi_8862	-0.234	moderately similar to (289)AT1G13710	Symbols: CYP78A5   CYP78A5 (cytochrome P450, family 78, subfamily A, polypeptide 5); oxygen binding
jcvi_14088	-0.236	moderately similar to (392)AT3G14690	Symbols: CYP72A15   CYP72A15 (cytochrome P450, family 72, subfamily A, polypeptide 15); oxygen binding
ex093564	-0.241	moderately similar to (426)AT2G45550	Symbols: MAH1, CYP76C4   CYP76C4 (cytochrome P450, family 76, subfamily C, polypeptide 4); oxygen binding
jcvi_24285	-0.246	highly similar to (784)AT5G04660	Symbols: CYP77A4   CYP77A4 (cytochrome P450, family 77, subfamily A, polypeptide 4); oxygen binding
jcvi_4902	-0.247	moderately similar to (350)AT1G17060	Symbols: SOB7, CYP72C1   CYP72C1 (cytochrome P450, family 72, subfamily C, polypeptide 1); oxygen binding
jcvi_30653	-0.248	moderately similar to (396)AT1G33720	Symbols: CYP76C6   CYP76C6 (cytochrome P450, family 76, subfamily C, polypeptide 6); oxygen binding
jcvi_29438	-0.249	weakly similar to (160)AT3G14680	Symbols: CYP72A14   CYP72A14 (cytochrome P450, family 72, subfamily A, polypeptide 14); oxygen binding
jcvi_38332	-0.254	moderately similar to (274)AT5G09970	Symbols: CYP78A7   CYP78A7 (cytochrome P450, family 78, subfamily A, polypeptide 7); oxygen binding
jcvi_21570	-0.257	moderately similar to (201)AT1G13080	Symbols: CYP71B2   CYP71B2 (CYTOCHROME P450 71B2); oxygen binding
ex140353	-0.258	weakly similar to (171)AT3G26280	Symbols: CYP71B4   CYP71B4 (cytochrome P450, family 71, subfamily B, polypeptide 4); oxygen binding
jcvi_1712	-0.262	moderately similar to (313)AT3G26210	Symbols: CYP71B23   CYP71B23 (cytochrome P450, family 71, subfamily B, polypeptide 23); oxygen binding
jcvi_9360	-0.263	moderately similar to (231)AT2G40890	Symbols: CYP98A3   monoxygenase/ p-coumarate 3-hydroxylase
jcvi_32769	-0.271	moderately similar to (353)AT1G13100	Symbols: CYP71B29   CYP71B29 (cytochrome P450, family 71, subfamily B, polypeptide 29); oxygen binding
jcvi_23144	-0.275	moderately similar to (202)AT1G13080	Symbols: CYP71B2   CYP71B2 (CYTOCHROME P450 71B2); oxygen binding
jcvi_10372	-0.287	moderately similar to (273)AT1G13080	Symbols: CYP71B2   CYP71B2 (CYTOCHROME P450 71B2); oxygen binding
jcvi_25804	-0.292	moderately similar to (338)AT1G13090	Symbols: CYP71B28   CYP71B28 (cytochrome P450, family 71, subfamily B, polypeptide 28); oxygen binding
es930162	-0.292	weakly similar to (122)AT4G15110	Symbols: CYP97B3   CYP97B3 (cytochrome P450, family 97, subfamily B, polypeptide 3); oxygen binding
jcvi_34518	-0.292	highly similar to (665)AT3G14690	Symbols: CYP72A15   CYP72A15 (cytochrome P450, family 72, subfamily A, polypeptide 15); oxygen binding
ev173169	-0.293	moderately similar to (281)AT3G28740	Symbols: CYP81D1   cytochrome P450 family protein
jcvi_13077	-0.300	highly similar to (766)AT3G14610	Symbols: CYP72A7   CYP72A7 (cytochrome P450, family 72, subfamily A, polypeptide 7); oxygen binding
jcvi_13339	-0.304	moderately similar to (437)AT2G29090	Symbols: CYP707A2   CYP707A2 (cytochrome P450, family 707, subfamily A, polypeptide 2); oxygen binding
jcvi_18541	-0.307	highly similar to (504)AT1G13710	Symbols: CYP78A5   CYP78A5 (cytochrome P450, family 78, subfamily A, polypeptide 5); oxygen binding
jcvi_4653	-0.315	moderately similar to (218)AT5G36220	Symbols: CYP91A1, CYP81D1   CYP81D1 (CYTOCHROME P450 91A1); oxygen binding
es900791	-0.318	moderately similar to (449)AT1G19630	Symbols: CYP722A1   CYP722A1 (cytochrome P450, family 722, subfamily A, polypeptide 1); oxygen binding
ex039068	-0.319	weakly similar to (110)AT4G31500	Symbols: SUR2, RNT1, RED1, ATR4, CYP83B1   CYTOCHROME P450 MONOOXYGENASE 83B1; oxygen binding
amb06073	-0.322	moderately similar to (260)AT5G63450	Symbols: CYP94B1   CYP94B1 (cytochrome P450, family 94, subfamily B, polypeptide 1); oxygen binding
jcvi_8488	-0.331	moderately similar to (394)AT3G14690	Symbols: CYP72A15   CYP72A15 (cytochrome P450, family 72, subfamily A, polypeptide 15); oxygen binding
jcvi_38880	-0.334	highly similar to (818)AT4G12300	Symbols: CYP706A4   CYP706A4 (cytochrome P450, family 706, subfamily A, polypeptide 4); oxygen binding
ex045165	-0.346	moderately similar to (206)AT3G03470	Symbols: CYP89A9   CYP89A9 (cytochrome P450, family 89, subfamily A, polypeptide 9); oxygen binding
jcvi_2172	-0.351	moderately similar to (379)AT3G14680	Symbols: CYP72A14   CYP72A14 (cytochrome P450, family 72, subfamily A, polypeptide 14); oxygen binding
ev216094	-0.356	moderately similar to (308)AT3G14690	Symbols: CYP72A15   CYP72A15 (cytochrome P450, family 72, subfamily A, polypeptide 15); oxygen binding
ev116895	-0.358	moderately similar to (336)AT3G53280	Symbols: CYP71B5   CYP71B5 (CYTOCHROME P450 71B5); oxygen binding
ev170929	-0.365	moderately similar to (292)AT3G28740	Symbols: CYP81D1   cytochrome P450 family protein
jcvi_25728	-0.368	moderately similar to (470)AT4G37330	Symbols: CYP81D4   CYP81D4 (cytochrome P450, family 81, subfamily D, polypeptide 4); oxygen binding
ev110073	-0.370	weakly similar to (111)AT1G66540	Symbols:   cytochrome P450, putative
jcvi_21065	-0.411	highly similar to (521)AT1G13080	Symbols: CYP71B2   CYP71B2 (CYTOCHROME P450 71B2); oxygen binding
ex134057	-0.416	highly similar to (509)AT1G73340	Symbols:   oxygen binding
jcvi_16598	-0.419	moderately similar to (466)AT4G00360	Symbols: ATT1, CYP86A2   CYP86A2 (ABERRANT INDUCTION OF TYPE THREE GENES 1); oxygen binding
jcvi_9641	-0.428	moderately similar to (395)AT2G12190	Symbols:   cytochrome P450, putative
ex081446	-0.434	weakly similar to (106)AT5G52320	Symbols: CYP96A4   CYP96A4 (cytochrome P450, family 96, subfamily A, polypeptide 4); oxygen binding
ev102803	-0.448	moderately similar to (226)AT4G12310	Symbols: CYP706A5   CYP706A5 (cytochrome P450, family 706, subfamily A, polypeptide 5); oxygen binding
eh422740	-0.458	moderately similar to (240)AT3G56630	Symbols: CYP94D2   CYP94D2 (cytochrome P450, family 94, subfamily D, polypeptide 2); oxygen binding
jcvi_16255	-0.478	weakly similar to (157)AT3G03470	Symbols: CYP89A9   CYP89A9 (cytochrome P450, family 89, subfamily A, polypeptide 9); oxygen binding
jcvi_36307	-0.503	very weakly similar to (87.8)AT1G13800	Symbols: CYP97A3, LUT5   carotene beta-ring hydroxylase/ oxygen binding
jcvi_5919	-0.507	moderately similar to (381)AT2G26710	Symbols: BAS1, CYP734A1   PHYB ACTIVATION TAGGED SUPPRESSOR 1; oxygen binding / steroid hydroxylase
jcvi_18790	-0.527	moderately similar to (342)AT3G14680	Symbols: CYP72A14   CYP72A14 (cytochrome P450, family 72, subfamily A, polypeptide 14); oxygen binding
jcvi_30048	-0.544	moderately similar to (273)AT2G46660	Symbols: CYP78A6   CYP78A6 (cytochrome P450, family 78, subfamily A, polypeptide 6); oxygen binding
jcvi_4988	-0.546	moderately similar to (372)AT4G12320	Symbols: CYP706A6   CYP706A6 (cytochrome P450, family 706, subfamily A, polypeptide 6); oxygen binding
jcvi_17705	-0.556	moderately similar to (474)AT4G12300	Symbols: CYP706A4   CYP706A4 (cytochrome P450, family 706, subfamily A, polypeptide 4); oxygen binding
ex077007	-0.556	moderately similar to (217)AT4G36380	Symbols: ROT3   ROT3 (ROTUNDIFOLIA 3); oxygen binding / steroid hydroxylase
ex098535	-0.562	moderately similar to (393)AT3G28740	Symbols: CYP81D1   cytochrome P450 family protein
ev173184	-0.576	weakly similar to (135)AT3G14680	Symbols: CYP72A14   CYP72A14 (cytochrome P450, family 72, subfamily A, polypeptide 14); oxygen binding
ee557855	-0.578	moderately similar to (326)AT1G74110	Symbols: CYP78A10   CYP78A10 (cytochrome P450, family 78, subfamily A, polypeptide 10); oxygen binding
jcvi_26571	-0.612	highly similar to (770)AT2G26170	Symbols: MAX1, CYP711A1   CYP711A1 (MORE AXILLARY BRANCHES 1); oxygen binding
jcvi_39927	-0.615	moderately similar to (460)AT1G11600	Symbols: CYP77B1   CYP77B1 (cytochrome P450, family 77, subfamily B, polypeptide 1); oxygen binding
jcvi_4773	-0.618	moderately similar to (324)AT3G26290	Symbols: CYP71B26   CYP71B26 (cytochrome P450, family 71, subfamily B, polypeptide 26); oxygen binding
jcvi_16089	-0.627	moderately similar to (248)AT3G20080	Symbols: CYP705A15   CYP705A15 (cytochrome P450, family 705, subfamily A, polypeptide 15); oxygen binding
jcvi_14772	-0.631	moderately similar to (228)AT5G67310	Symbols: CYP81G1   CYP81G1 (cytochrome P450, family 81, subfamily G, polypeptide 1); oxygen binding
eh419222	-0.634	very weakly similar to (87.4)AT4G12300	Symbols: CYP706A4   CYP706A4 (cytochrome P450, family 706, subfamily A, polypeptide 4); oxygen binding
jcvi_14153	-0.638	moderately similar to (280)AT4G12300	Symbols: CYP706A4   CYP706A4 (cytochrome P450, family 706, subfamily A, polypeptide 4); oxygen binding
ev152526	-0.639	moderately similar to (385)AT2G23180	Symbols: CYP96A1   CYP96A1 (cytochrome P450, family 96, subfamily A, polypeptide 1); oxygen binding
cd835093	-0.642	very weakly similar to (100)AT3G20960	Symbols: CYP705A33   CYP705A33 (cytochrome P450, family 705, subfamily A, polypeptide 33); oxygen binding
jcvi_12612	-0.649	moderately similar to (204)AT4G37400	Symbols: CYP81F3   CYP81F3 (cytochrome P450, family 81, subfamily F, polypeptide 3); oxygen binding
jcvi_5112	-0.652	moderately similar to (392)AT4G13770	Symbols: REF2, CYP83A1   CYP83A1 (CYTOCHROME P450 83A1); oxygen binding
jcvi_34378	-0.674	moderately similar to (398)AT5G09970	Symbols: CYP78A7   CYP78A7 (cytochrome P450, family 78, subfamily A, polypeptide 7); oxygen binding
jcvi_30128	-0.678	moderately similar to (446)AT2G32440	Symbols: CYP88A4, KAO2   KAO2 (ENT-KAUROIC ACID HYDROXYLASE 2); oxygen binding
jcvi_20204	-0.678	weakly similar to (163)AT1G13710	Symbols: CYP78A5   CYP78A5 (cytochrome P450, family 78, subfamily A, polypeptide 5); oxygen binding
jcvi_26408	-0.689	moderately similar to (410)AT5G36220	Symbols: CYP91A1, CYP81D1   CYP81D1 (CYTOCHROME P450 91A1); oxygen binding
ev041638	-0.746	moderately similar to (313)AT3G26220	Symbols: CYP71B3   CYP71B3 (cytochrome P450, family 71, subfamily B, polypeptide 3); oxygen binding
jcvi_23713	-0.748	highly similar to (593)AT1G13710	Symbols: CYP78A5   CYP78A5 (cytochrome P450, family 78, subfamily A, polypeptide 5); oxygen binding
jcvi_8225	-0.798	moderately similar to (440)AT3G26290	Symbols: CYP71B26   CYP71B26 (cytochrome P450, family 71, subfamily B, polypeptide 26); oxygen binding
jcvi_42506	-0.817	moderately similar to (391)AT3G14620	Symbols: CYP72A8   CYP72A8 (cytochrome P450, family 72, subfamily A, polypeptide 8); oxygen binding
jcvi_8990	-0.848	moderately similar to (422)AT5G36220	Symbols: CYP91A1, CYP81D1   CYP81D1 (CYTOCHROME P450 91A1); oxygen binding
jcvi_7226	-0.851	moderately similar to (355)AT1G13080	Symbols: CYP71B2   CYP71B2 (CYTOCHROME P450 71B2); oxygen binding
jcvi_17335	-0.970	moderately similar to (28)AT1G16410	Symbols: BUS1, SP51, CYP79F1   CYP79F1 (SUPERSHOOT 1)
jcvi_7931	-0.999	moderately similar to (439)AT4G39480	Symbols: CYP96A9   CYP96A9 (cytochrome P450, family 96, subfamily A, polypeptide 9); oxygen binding
jcvi_10139	-1.144	moderately similar to (304)AT4G39490	Symbols: CYP96A10   heme binding / iron ion binding / monooxygenase
jcvi_14499	-1.152	highly similar to (961)AT1G01600	Symbols: CYP86A4   CYP86A4 (cytochrome P450, family 86, subfamily A, polypeptide 4); oxygen binding
jcvi_30402	-1.155	highly similar to (629)AT3G19270	Symbols: CYP707A4   CYP707A4 (cytochrome P450, family 707, subfamily A, polypeptide 4); oxygen binding
jcvi_13878	-1.318	moderately similar to (466)AT5G45340	Symbols: CYP707A3   CYP707A3 (cytochrome P450, family 707, subfamily A, polypeptide 3); oxygen binding

jcv_i_14519	-1.669 highly similar to ( 871)AT5G45340   Symbols: CYP707A3   CYP707A3 (cytochrome P450, family 707, subfamily A, polypeptide 3); oxygen binding
jcv_i_18210	-1.693 highly similar to ( 807)AT3G48520   Symbols: CYP94B3   CYP94B3 (cytochrome P450, family 94, subfamily B, polypeptide 3); oxygen binding
jcv_i_20042	-2.246 moderately similar to ( 349)AT5G45340   Symbols: CYP707A3   CYP707A3 (cytochrome P450, family 707, subfamily A, polypeptide 3); oxygen binding