Table S23. Information of candidate genes in the selected regions (Top 5% of *Fst* and *π* ratio).

Chromosome	**Start**	**End**	**Gene ID**	**Gene name**	***Fst***	***π* ratio**	**Swissprot**	**KEGG**	**TrEMBL**	**Interpro**	**GO**
chr01	10323356	10329651	Cil_01G_00471V2	NA	0.202	1.537	NA	NA	NA	NA	NA
	10332020	10348935	Cil_01G_00472V2	groEL			Q8W486/252/Y1491_ARATH Uncharacterized protein At1g04910 OS=Arabidopsis thaliana GN=At1g04910 PE=2 SV=1	K04077/groEL,/chaperonin	W9SH14/377/W9SH14_9ROSA Uncharacterized protein OS=Morus notabilis GN=L484_004969 PE=4 SV=1	1/1/IPR019378; GDP-fucose protein O-fucosyltransferase	NA
chr02	7100290	7105352	Cil_02G_00494V2	OXR1	0.185	1.885	A8KBE0/869/OXR1_XENTR Oxidation resistance protein 1 OS=Xenopus tropicalis GN=oxr1 PE=2 SV=2	K20409/WDR59/repeat-containing	A0A067LEN3/373/A0A067LEN3_JATCU Uncharacterized protein OS=Jatropha curcas GN=JCGZ_24046 PE=4 SV=1	1/1/IPR006571; TLDc domain	NA

7107050	7116378	Cil_02G_00495V2	ASNS3/ASNB	Q9LFU1/578/ASNS3_ARATH Asparagine synthetase [glutamine-hydrolyzing] 3 OS=Arabidopsis thaliana GN=ASN3 PE=2 SV=1	K01953/asnB,/asparagine	W9QNB5/584/W9QNB5_9ROSA Glutamine-dependent asparagine synthetase 2 OS=Morus notabilis GN=L484_022115 PE=4 SV=1	3/IPR017932; Glutamine amidotransferase type 2 domain/IPR026960; Reverse transcriptase zinc-binding domain	GO:0004066; asparagine synthase (glutamine-hydrolyzing) activity; function|GO:0006529; asparagine biosynthetic process; process
7137608	7147647	Cil_02G_00496V2	CSTR5	Q8LES0/304/CSTR5_ARATH CMP-sialic acid transporter 5 OS=Arabidopsis thaliana GN=At5g65000 PE=2 SV=1	K15272/SLC35A1_2_3/carrier	K7L6H4/307/K7L6H4_SOYBN Uncharacterized protein OS=Glycine max PE=4 SV=1	1/1/IPR007271; Nucleotide-sugar transporter	GO:0000139; Golgi membrane; component|GO:0005351; sugar:proton symporter activity; function|GO:0008643; carbohydrate transport; process|GO:0016021; integral component of membrane; component

7156832	7161369	Cil_02G_00497V2	DOT3		Q9LFU0/578/DOT3_ARATH BTB/POZ domain-containing protein DOT3 OS=Arabidopsis thaliana GN=DOT3 PE=2 SV=1	K03063/PSMC4,/26S	W9QDN1/603/W9QDN1_9ROSA Putative BTB/POZ domain-containing protein DOT3 OS=Morus notabilis GN=L484_022117 PE=4 SV=1	1/1/IPR027356; NPH3 domain	NA
7162349	7167064	Cil_02G_00498V2	RAH1E/RAB6A		Q9LFT9/207/RAH1E_ARATH Ras-related protein RABH1e OS=Arabidopsis thaliana GN=RABH1E PE=2 SV=1	K07893/RAB6A/protein	M5WJX4/206/M5WJX4_PRUPE Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa011539mg PE=3 SV=1	4/IPR003579; Small GTPase superfamily, Rab type/IPR020849; Small GTPase superfamily, Ras type	GO:0005525; GTP binding; function|GO:0005622; intracellular; component|GO:0007165; signal transduction; process|GO:0007264; small GTPase mediated signal transduction; process|GO:0015031; protein transport; process|GO:00160

											20; membrane; component
	7168359	7173021	Cil_02G_00499V2	NA			NA	NA	D7T5J2/262/D7T5J2_VITVI Putative uncharacterized protein OS=Vitis vinifera GN=VIT_00s0665g00030 PE=4 SV=1	NA	NA
	34892378	34894897	Cil_02G_01594V2	NA	0.159	1.737	NA	NA	D7TCF4/185/D7TCF4_VITVI Putative uncharacterized protein OS=Vitis vinifera GN=VIT_11s0016g01150 PE=4 SV=1	NA	NA
chr03	4122512	4157469	Cil_03G_00289V2	NA	0.185	1.528	NA	K09919/K09919/protein	A0A061GEK5/468/A0A061GEK5_THECC Acyl-CoA N-acyltransferase isoform 1	1/1/IPR007434; Peptidogalycan biosysnthesis/recognition	NA

						OS=Theobroma cacao GN=TCM_026893 PE=4 SV=1		
4137084	4144042	Cil_03G_00290V2	TRM3	NA	K15333/TRM3,/tRNA	NA	NA	NA
4168068	4173679	Cil_03G_00291V2	ECM4	Q9SD53/459/Y3720_ARATH UPF0481 protein At3g47200 OS=Arabidopsis thaliana GN=At3g47200 PE=2 SV=1	K07393/ECM4,/glutathionyl-hydroquinone	B9RP72/433/B9RP72_RICCO Putative uncharacterized protein OS=Ricinus communis GN=RCOM_0924580 PE=4 SV=1	1/1/IPR004158; Protein of unknown function DUF247, plant	NA
4176411	4177643	Cil_03G_00292V2	NA	NA	K16276/K16276,/zinc	U5G7Z2/96/U5G7Z2_POPTR Uncharacterized protein OS=Populus trichocarpa GN=POPTR_0008s12240g PE=4 SV=1	NA	NA

4188827	4193219	Cil_03G_00293V2	FRS11/FHY3/FAR1	Q9SY66/680/FRS11_ARATH Protein FAR1-RELATED SEQUENCE 11 OS=Arabidopsis thaliana GN=FRS11 PE=2 SV=1	K17604/ZSWIM3/finger	M5XX99/679/M5XX99_PRUPE Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa002379mg PE=4 SV=1	5/IPR018289; MULE transposase domain/IPR031052; FHY3/FAR1 family	GO:0006355; regulation of transcription, DNA-templated; process|GO:0008270; zinc ion binding; function
4191563	4191877	Cil_03G_00294V2	NA	NA	NA	NA	NA	NA
4194716	4195888	Cil_03G_00295V2	M3K3/MAP3K3	O22042/337/M3K3_ARATH Mitogen-activated protein kinase kinase kinase 3 OS=Arabidopsis thaliana GN=ANP3 PE=1 SV=1	K04421/MAP3K3,/mitogen-activated	B9SS78/356/B9SS78_RICCO ATP binding protein, putative OS=Ricinus communis GN=RCOM_0618950 PE=4 SV=1	4/IPR008271; Serine/threonine-protein kinase, active site/IPR017441; Protein kinase, ATP binding site	GO:0004672; protein kinase activity; function|GO:0005524; ATP binding; function|GO:0006468; protein phosphorylation; process
4197053	4198240	Cil_03G_00296V2	NA	NA	NA	A0A067L202/398/A0A067L202_JATCU Uncharacterized protein	NA	NA

									OS=Jatropha curcas GN=JCGZ_00264 PE=4 SV=1		
chr05	15875804	15879906	Cil_05G_01245V2	NA	0.163	1.886	NA	NA	A2ZNX3/491/A2ZNX3_ORYSJ Uncharacterized protein OS=Oryza sativa subsp. japonica GN=OsJ_00252 PE=4 SV=1	NA	NA
	15880858	15883723	Cil_05G_01246V2	NA			O04064/377/FLLH_POPTR Floricaula/leafy homolog OS=Populus trichocarpa GN=FL PE=2 SV=2	NA	D1MLK1/385/D1MLK1_9ROSI LEAFY-like protein OS=Juglans regia PE=2 SV=3	1/1/IPR002910; Floricaula/leafy protein	GO:0003677; DNA binding; function|GO:0006355; regulation of transcription, DNA-templated; process
	15951937	15958151	Cil_05G_01247V2	BRI1/IRAK4	0.161	1.831	Q8GUQ5/463/BRI1_SOLLC Brassinosteroid LRR receptor kinase OS=Solanum	K04733/IRAK4/receptor-associated	A0A078E673/192/A0A078E673_BRANA BnaA07g31330D protein OS=Brassica	NA	NA

						lycopersicum GN=CURL3 PE=1 SV=1		napus GN=BnaA07g31330D PE=4 SV=1		
15962118	15964118	Cil_05G_01248V2	LRR receptor-like/EIX1			Q8VZG8/684/Y4885_ARATH Probable LRR receptor-like serine/threonine-protein kinase At4g08850 OS=Arabidopsis thaliana GN=At4g08850 PE=2 SV=3	K13466/EIX1_2/receptor	A0A067KG50/681/A0A067KG50_JATCU Uncharacterized protein OS=Jatropha curcas GN=JCGZ_10954 PE=4 SV=1	1/1/IPR001611; Leucine-rich repeat	GO:0005515; protein binding; function
16095491	16100046	Cil_05G_01249V2	AP4M1	0.168	2.100	NA	K12402/AP4M1/complex	M5WEH8/276/M5WEH8_PRUPE Uncharacterized protein (Fragment) OS=Prunus persica GN=PRUPE_ppa019056mg PE=4 SV=1	NA	NA

16102819	16121813	Cil_05G_01250V2	IRX10		Q940Q8/415/IX10L_ARATH Probable beta-1,4-xylosyltransferase IRX10L OS=Arabidopsis thaliana GN=IRX10L PE=2 SV=1	K20870/IRX10/beta-1,4-xylosyltransferase	A0A067F2D2/416/A0A067F2D2_CITSI Uncharacterized protein OS=Citrus sinensis GN=CISIN_1g048016mg PE=4 SV=1	1/1/IPR004263; Exostosin-like	NA
16161725	16163917	Cil_05G_01251V2	nirA		NA	K00366/nirA/reductase	B9RA53/169/B9RA53_RICCO Electron transporter, putative OS=Ricinus communis GN=RCOM_1503210 PE=4 SV=1	2/IPR024934; Rubredoxin-like domain/IPR024935; Rubredoxin domain	GO:0005506; iron ion binding; function
16165061	16169139	Cil_05G_01252V2	CRL		Q9FI46/269/CRL_ARATH Chromophore lyase CRL, chloroplastic OS=Arabidopsis thaliana GN=CRL PE=1 SV=1	NA	A0A061FZN4/269/A0A061FZN4_THECC JHL07K02.6 protein OS=Theobroma cacao	1/1/IPR010404; Chromophore lyase CpcT/CpeT	GO:0016829; lyase activity; function|GO:0017009; protein-phycocyanobilin linkage; process

								GN=TCM_014774 PE=3 SV=1		
16210339	16211361	Cil_05G_01253V2	SDAF2/SDHAF2	0.174	1.976	Q9FI44/188/SDAF2_ARATH Succinate dehydrogenase assembly factor 2, mitochondrial OS=Arabidopsis thaliana GN=SDHAF2 PE=1 SV=1	K18168/SDHAF2,/succinate	A0A061G020/178/A0A061G020_THECC Uncharacterized protein OS=Theobroma cacao GN=TCM_014776 PE=4 SV=1	1/1/IPR005631; Flavinator of succinate dehydrogenase	NA
16429328	16431276	Cil_05G_01256V2	CAB39	0.172	1.986	NA	K08272/CAB39,/calcium	U5CX01/417/U5CX01_AMBTC Uncharacterized protein (Fragment) OS=Amborella trichopoda GN=AMTR_s04653p00000520 PE=4 SV=1	NA	NA
16450437	16451043	Cil_05G_01257V2	NA			NA	NA	NA	NA	NA

	16483748	16487053	Cil_05G_01258V2	GL111			Q2R352/203/GL111_ORYSJ Germin-like protein 11-1 OS=Oryza sativa subsp. japonica GN=Os11g0537300 PE=2 SV=1	NA	E0CV43/203/E0CV43_VITVI Putative uncharacterized protein OS=Vitis vinifera GN=VIT_16s0098g01910 PE=4 SV=1	3/IPR006045; Cupin 1/IPR019780; Germin, manganese binding site	GO:0030145; manganese ion binding; function|GO:0045735; nutrient reservoir activity; function
	16486639	16486977	Cil_05G_01259V2	NA			NA	NA	A0A059B940/56/A0A059B940_EUCGR Uncharacterized protein OS=Eucalyptus grandis GN=EUGRSUZ_G00032 PE=4 SV=1	NA	NA
	16499981	16525276	Cil_05G_01260V2	NA			NA	NA	NA	NA	NA
chr06	11615668	11617907	Cil_06G_00580V2	NA	0.168	1.535	NA	NA	NA	NA	NA

11631390	11639084	Cil_06G_00581V2	RNHX1		P0C2F6/610/RNHX1_ARATH Putative ribonuclease H protein At1g65750 OS=Arabidopsis thaliana GN=At1g65750 PE=3 SV=1	K01188/E3.2.1.21/3.2.1.21	M5VP36/450/M5VP36_PRUPE Uncharacterized protein (Fragment) OS=Prunus persica GN=PRUPE_ppa014760mg PE=4 SV=1	1/1/IPR026960; Reverse transcriptase zinc-binding domain	NA
11640735	11642495	Cil_06G_00582V2	UPF1		NA	K14326/UPF1,/regulator	U5FTI0/443/U5FTI0_POPTR Uncharacterized protein (Fragment) OS=Populus trichocarpa GN=POPTR_0012s046402g PE=4 SV=1	1/1/IPR007021; Domain of unknown function DUF659	NA
11674044	11679664	Cil_06G_00583V2	QQRX/NADPH2		Q53FA7/328/QORX_HUMAN Quinone oxidoreductase PIG3 OS=Homo sapiens	K00344/qor,/NADPH2:quinone	W9RDH2/325/W9RDH2_9ROSA Quinone oxidoreductase PIG3 OS=Morus notabilis	4/IPR013154; Alcohol dehydrogenase, N-terminal/IPR020843; Polyketide	GO:0008270; zinc ion binding; function|GO:0016491; oxidoreductase activity; function|GO:00551

						GN=TP53I3 PE=1 SV=2		GN=L484_006383 PE=4 SV=1	synthase, enoylreductase domain	14; oxidation-reduction process; process
20398042	20411347	Cil_06G_00970V2	SSY3	0.265	1.789	Q43846/1228/SSY3_SOLTU Soluble starch synthase 3, chloroplastic/amyloplastic OS=Solanum tuberosum GN=SS3 PE=1 SV=1	K00703/glgA/synthase	B9H112/1092/B9H112_POPTR Starch synthase family protein OS=Populus trichocarpa GN=POPTR_0004s01410g PE=3 SV=2	3/IPR005085; Carbohydrate binding module family 25/IPR013534; Starch synthase, catalytic domain	GO:2001070; starch binding; function
20438367	20439491	Cil_06G_00971V2	ATPG			P29790/376/ATPG_TOBAC ATP synthase gamma chain, chloroplastic OS=Nicotiana tabacum GN=ATPC PE=1 SV=1	K02115/ATPF1G,/F-type	A0A061GFT3/374/A0A061GFT3_THECC ATPase, F1 complex, gamma subunit protein OS=Theobroma cacao GN=TCM_030229 PE=3 SV=1	2/IPR000131; ATPase, F1 complex, gamma subunit/IPR023632; ATPase, F1 complex, gamma subunit conserved site	GO:0015986; ATP synthesis coupled proton transport; process|GO:0045261; proton-transporting ATP synthase complex, catalytic core F(1); component|GO:0046933; proton-transporting ATP synthase activity, rotational

								mechanism; function|GO:0046961; proton-transporting ATPase activity, rotational mechanism; function
20446358	20451165	Cil_06G_00972V2	petH	P0C2F6/513/RNHX1_ARATH Putative ribonuclease H protein At1g65750 OS=Arabidopsis thaliana GN=At1g65750 PE=3 SV=1	K02641/petH/reductase	A0A061EPI0/2775/A0A061EPI0_THECC Uncharacterized protein OS=Theobroma cacao GN=TCM_021522 PE=4 SV=1	NA	NA
20452144	20459034	Cil_06G_00973V2	GSTZ1	P28342/166/GSTZ1_DIACA Glutathione S-transferase 1 OS=Dianthus caryophyllus GN=GST1 PE=2 SV=1	K01800/maiA,/maleylacetoacetate	A0A0D2T4S0/182/A0A0D2T4S0_GOSRA Uncharacterized protein OS=Gossypium raimondii GN=B456_011G0	2/IPR004045; Glutathione S-transferase, N-terminal/IPR010987; Glutathione S-transferase, C-terminal-like	GO:0005515; protein binding; function

						90100 PE=4 SV=1		
20462316	20478903	Cil_06G_00974V2	ATPF1G	NA	K02115/ATPF1G,/F-type	A0A061GFS8/816/A0A061GFS8_THECC Homeodomain-like superfamily protein, putative isoform 1 OS=Theobroma cacao GN=TCM_030225 PE=4 SV=1	1/1/IPR000131; ATPase, F1 complex, gamma subunit	GO:0015986; ATP synthesis coupled proton transport; process|GO:0045261; proton-transporting ATP synthase complex, catalytic core F(1); component|GO:0046933; proton-transporting ATP synthase activity, rotational mechanism; function|GO:0046961; proton-transporting ATPase activity, rotational mechanism; function
20478979	20479923	Cil_06G_00975V2	ATPase	NA	NA	W9RS11/300/W9RS11_9ROSA Uncharacterized	1/1/IPR000131; ATPase, F1	GO:0015986; ATP synthesis coupled proton transport;

							protein OS=Morus notabilis GN=L484_011305 PE=4 SV=1	complex, gamma subunit	process|GO:0045261; proton-transporting ATP synthase complex, catalytic core F(1); component|GO:0046933; proton-transporting ATP synthase activity, rotational mechanism; function|GO:0046961; proton-transporting ATPase activity, rotational mechanism; function
20482545	20483007	Cil_06G_00976V2	MYBP		O22059/76/CPC_ARATH Transcription factor CPC OS=Arabidopsis thaliana GN=CPC PE=1 SV=1	K09422/MYBP/factor	A0A059DGB6/73/A0A059DGB6_EUCGR Uncharacterized protein OS=Eucalyptus grandis GN=EUGRSUZ_	2/IPR001005; SANT/Myb domain/IPR017877; Myb-like domain	NA

								A01720 PE=4 SV=1		
20497007	20498709	Cil_06G_00977V2	PER42			Q9SB81/330/PER42_ARATH Peroxidase 42 OS=Arabidopsis thaliana GN=PER42 PE=1 SV=2	K00430/E1.11.1.7/1.11.1.7	A0A067JMN0/331/A0A067JMN0_JATCU Peroxidase OS=Jatropha curcas GN=JCGZ_21220 PE=3 SV=1	2/IPR000823; Plant peroxidase/IPR002016; Haem peroxidase, plant/fungal/bacterial	GO:0004601; peroxidase activity; function|GO:0006979; response to oxidative stress; process|GO:0020037; heme binding; function|GO:0055114; oxidation-reduction process; process
29711110	29712618	Cil_06G_01383V2	MIMR1_2	0.180	1.705	NA	K18081/MTMR1_2/--	A0A0A0L0Z9/490/A0A0A0L0Z9_CUCSA Uncharacterized protein OS=Cucumis sativus GN=Csa_4G296260 PE=4 SV=1	2/IPR007700; Protein of unknown function DUF668/IPR021864; Protein of unknown function DUF3475	NA
29746960	29749069	Cil_06G_01384V2	DHX37			NA	K14780/DHX37,/ATP-dependent	B9HBV0/505/B9HBV0_POPTR Uncharacterized	1/1/IPR006740; Protein of	NA

								protein OS=Populus trichocarpa GN=POPTR_0006s09010g PE=4 SV=2	unknown function DUF604	
29759828	29766152	Cil_06G_01385V2	LHWL1			P0C7P8/707/LHWL1_ARATH Transcription factor EMB1444 OS=Arabidopsis thaliana GN=EMB1444 PE=2 SV=1	K08867/WNK,/WNK	D7THI8/692/D7THI8_VITVI Putative uncharacterized protein OS=Vitis vinifera GN=VIT_08s0007g00940 PE=4 SV=1	2/IPR011598; Myc-type, basic helix-loop-helix (bHLH) domain/IPR025610; Transcription factor MYC/MYB N-terminal	GO:0046983; protein dimerization activity; function
29784401	29785530	Cil_06G_01386V2	NA			NA	NA	NA	NA	NA
31109232	31135059	Cil_06G_01462V2	PSD7B	0.161	1.857	Q9C774/308/PSD7B_ARATH 26S proteasome non-ATPase regulatory subunit 7 homolog B OS=Arabidopsis thaliana	K03038/PSMD7,/26S	A0A061ERJ9/310/A0A061ERJ9_THECC RP non-ATPase subunit 8A OS=Theobroma cacao	3/IPR002877; Ribosomal RNA methyltransferase FtsJ domain/IPR024969; Rpn11/EIF3F, C-terminal	GO:0005515; protein binding; function|GO:0008168; methyltransferase activity; function|GO:00322

							GN=RPN8B PE=1 SV=1		GN=TCM_021739 PE=4 SV=1		59; methylation; process
	31196658	31202632	Cil_06G_01463V2	PRT29			O80436/453/PTR29_ARATH Protein NRT1/ PTR FAMILY 5.5 OS=Arabidopsis thaliana GN=NPF5.5 PE=2 SV=1	K14638/SLC15A3_4,/solute	A0A068UD64/465/A0A068UD64_COFCA Uncharacterized protein OS=Coffea canephora GN=GSCOC_T00023378001 PE=4 SV=1	1/1/IPR000109; Proton-dependent oligopeptide transporter family	GO:0005215; transporter activity; function|GO:0006810; transport; process|GO:0016020; membrane; component
chr07	18107824	18109409	Cil_07G_01193V2	RLP12	0.167	1.678	Q9C9H7/390/RLP12_ARATH Receptor-like protein 12 OS=Arabidopsis thaliana GN=RLP12 PE=2 SV=2	K13470/CF4/resistance	A0A0D2RD52/335/A0A0D2RD52_GOSRA Uncharacterized protein (Fragment) OS=Gossypium raimondii GN=B456_002G264400 PE=4 SV=1	2/IPR001611; Leucine-rich repeat/IPR013210; Leucine-rich repeat-containing N-terminal, plant-type	GO:0005515; protein binding; function
	18123621	18136247	Cil_07G_01194V2	GSO2/FLS2			Q9FIZ3/748/GSO2_ARATH LRR receptor-like	K13420/FLS2/receptor-like	M5W7H7/626/M5W7H7_PRUPE Uncharacterized	1/1/IPR001611; Leucine-rich repeat	GO:0005515; protein binding; function

							serine/threonine-protein kinase GSO2 OS=Arabidopsis thaliana GN=GSO2 PE=2 SV=2		protein OS=Prunus persica GN=PRUPE_ppa026755mg PE=4 SV=1		
	18177192	18180451	Cil_07G_01195V2	RLP12			Q9C9H7/834/RLP12_ARATH Receptor-like protein 12 OS=Arabidopsis thaliana GN=RLP12 PE=2 SV=2	K13468/K13468,/disease	A0A061ER57/1045/A0A061ER57_THECC LRR receptor-like serine/threonine-protein kinase GSO1, putative OS=Theobroma cacao GN=TCM_021646 PE=4 SV=1	3/IPR003591; Leucine-rich repeat, typical subtype/IPR013210; Leucine-rich repeat-containing N-terminal, plant-type	GO:0005515; protein binding; function
chr09	3107180	3110238	Cil_09G_00194V2	NA	0.208	2.879	NA	NA	A0A061EQX7/129/A0A061EQX7_THECC 5\'-3\' exonuclease family protein isoform 2 (Fragment) OS=Theobroma	NA	NA

							cacao GN=TCM_019883 PE=4 SV=1		
3110293	3141222	Cil_09G_00195V2	POLA		NA	K02335/polA/polymerase	D7T2D6/441/D7T2D6_VITVI Putative uncharacterized protein OS=Vitis vinifera GN=VIT_05s0094g00430 PE=4 SV=1	2/IPR002421; 5'-3' exonuclease, N-terminal/IPR020046; 5'-3' exonuclease, alpha-helical arch, N-terminal	GO:0003677; DNA binding; function
3144134	3150489	Cil_09G_00196V2	NA		NA	NA	A0A0A0K988/228/A0A0A0K988_CUCSA Uncharacterized protein OS=Cucumis sativus GN=Csa_6G086160 PE=4 SV=1	1/1/IPR008881; Trigger factor, ribosome-binding, bacterial	GO:0006457; protein folding; process|GO:0015031; protein transport; process
3151494	3153161	Cil_09G_00197V2	SRP14		O04421/111/SRP14_ARATH Signal recognition particle 14 kDa protein	K03104/SRP14/recognition	I3SA11/120/I3SA11_LOTJA Uncharacterized protein OS=Lotus	1/1/IPR003210; Signal recognition particle, SRP14 subunit	GO:0005786; signal recognition particle, endoplasmic reticulum

					OS=Arabidopsis thaliana GN=SRP14 PE=2 SV=2		japonicus PE=2 SV=1		targeting; component|GO:0006614; SRP-dependent cotranslational protein targeting to membrane; process|GO:0008312; 7S RNA binding; function|GO:0030942; endoplasmic reticulum signal peptide binding; function
3159113	3159838	Cil_09G_00198V2	MER		E7C196/97/MER_ERYCB Methylecgonone reductase OS=Erythroxylum coca PE=1 SV=1	K22374/DMAS1/reductase	Q5Y381/100/Q5Y381_FRAAN Aldo/keto reductase OS=Fragaria ananassa GN=AKR PE=2 SV=1	2/IPR001395; Aldo/keto reductase/potassium channel subunit beta/IPR023210; NADP-dependent oxidoreductase domain	NA
3163413	3164451	Cil_09G_00199V2	CHI5		Q9M2U5/273/CHI5_ARATH Endochitinase	K01183/E3.2.1.14/3.2.1.14	F6HB09/274/F6HB09_VITVI Putative	3/IPR001002; Chitin-binding, type	GO:0004568; chitinase activity; function|GO:00060

						EP3 OS=Arabidopsis thaliana GN=EP3 PE=1 SV=1		uncharacterized protein OS=Vitis vinifera GN=VIT_05s0094g00220 PE=4 SV=1	1/IPR018371; Chitin-binding, type 1, conserved site	32; chitin catabolic process; process|GO:0008061; chitin binding; function|GO:0016998; cell wall macromolecule catabolic process; process
3189870	3190821	Cil_09G_00200V2	CHI5			Q9M2U5/171/CHI5_ARATH Endochitinase EP3 OS=Arabidopsis thaliana GN=EP3 PE=1 SV=1	K01183/E3.2.1.14/3.2.1.14	F6HAW1/172/F6HAW1_VITVI Putative uncharacterized protein OS=Vitis vinifera GN=VIT_05s0094g00260 PE=4 SV=1	2/IPR000726; Glycoside hydrolase, family 19, catalytic/IPR001002; Chitin-binding, type 1	GO:0004568; chitinase activity; function|GO:0006032; chitin catabolic process; process|GO:0008061; chitin binding; function|GO:0016998; cell wall macromolecule catabolic process; process
21903147	21911642	Cil_09G_01375V2	ABCB1	0.166	1.585	Q9M3B9/1408/AB20B_ARATH ABC transporter B family member 20	K05658/ABCB1,/ATP-binding	A0A097P9R0/1404/A0A097P9R0_HEVBR ABC transporter family protein	3/IPR003593; AAA+ ATPase domain/IPR011527; ABC transporter type 1,	GO:0005524; ATP binding; function|GO:0006810; transport; process|GO:00160

					OS=Arabidopsis thaliana GN=ABCB20 PE=1 SV=1		OS=Hevea brasiliensis GN=ABCB20 PE=2 SV=1	transmembrane domain	21; integral component of membrane; component|GO:0016887; ATPase activity; function|GO:0042626; ATPase activity, coupled to transmembrane movement of substances; function|GO:0055085; transmembrane transport; process
21917649	21922668	Cil_09G_01376V2	ABCB1		Q9M3B9/280/AB20B_ARATH ABC transporter B family member 20 OS=Arabidopsis thaliana GN=ABCB20 PE=1 SV=1	K05658/ABCB1,/ATP-binding	A0A0A0KS59/269/A0A0A0KS59_CUCSA Uncharacterized protein OS=Cucumis sativus GN=Csa_5G505770 PE=4 SV=1	1/1/IPR011527; ABC transporter type 1, transmembrane domain	GO:0005524; ATP binding; function|GO:0006810; transport; process|GO:0016021; integral component of membrane; component|GO:0042626; ATPase activity, coupled to

21927874	21933714	Cil_09G_01377V2	RPL23a	Q9AT35/152/RL23A_DAUCA 60S ribosomal protein L23a OS=Daucus carota GN=RPL23A PE=2 SV=1	K02893/RP-L23Ae,/large	A0A067FK20/151/A0A067FK20_CITSI Uncharacterized protein OS=Citrus sinensis GN=CISIN_1g031766mg PE=3 SV=1	3/IPR007750; Protein of unknown function DUF674/IPR013025; Ribosomal protein L25/L23	transmembrane movement of substances; function|GO:0055085; transmembrane transport; process GO:0003735; structural constituent of ribosome; function|GO:0005840; ribosome; component|GO:0006412; translation; process
21941776	21942743	Cil_09G_01378V2	NA	NA	NA	A0A059A962/234/A0A059A962_EUCGR Uncharacterized protein OS=Eucalyptus grandis GN=EUGRSUZ_J00059 PE=4 SV=1	1/1/IPR007750; Protein of unknown function DUF674	NA

21944787	21947961	Cil_09G_01379V2	MKP1	Q9C5S1/784/MKP1_ARATH Protein-tyrosine-phosphatase MKP1 OS=Arabidopsis thaliana GN=MKP1 PE=1 SV=1	K04459/DUSP,/--	A0A061FMQ2/849/A0A061FMQ2_THECC Mitogen-activated protein kinase phosphatase 1 OS=Theobroma cacao GN=TCM_042956 PE=4 SV=1	6/IPR020422; Dual specificity protein phosphatase domain/IPR024950; Dual specificity phosphatase	GO:0003779; actin binding; function|GO:0004725; protein tyrosine phosphatase activity; function|GO:0006470; protein dephosphorylation; process|GO:0008138; protein tyrosine/serine/threonine phosphatase activity; function|GO:0016311; dephosphorylation; process|GO:0016791; phosphatase activity; function
21954383	21958633	Cil_09G_01380V2	MTP11	O80632/359/MTP11_ARATH Metal tolerance protein 11 OS=Arabidopsis	K12448/UXE,/UDP-arabinose	W9R2I1/359/W9R2I1_9ROSA Metal tolerance protein 5 OS=Morus	2/IPR002524; Cation efflux protein/IPR027470; Cation efflux protein,	GO:0006812; cation transport; process|GO:0008324; cation transmembrane

					thaliana GN=MTP11 PE=2 SV=1		notabilis GN=L484_025418 PE=4 SV=1	cytoplasmic domain	transporter activity; function|GO:0016021; integral component of membrane; component|GO:0055085; transmembrane transport; process
21972260	21973961	Cil_09G_01381V2	ENPP1_3		NA	K01513/ENPP1_3,/--	B9SAL5/94/B9SAL5_RICCO Putative uncharacterized protein OS=Ricinus communis GN=RCOM_1103690 PE=4 SV=1	1/1/IPR006476; Conserved hypothetical protein CHP01589, plant	NA
21976984	21981485	Cil_09G_01382V2	DHAR2		Q9FRL8/211/DHAR2_ARATH Glutathione S-transferase DHAR2 OS=Arabidopsis thaliana	K21888/DHAR/--	J9WN12/210/J9WN12_POPTO Dehydroascorbate reductase (Fragment) OS=Populus tomentosa	2/IPR004045; Glutathione S-transferase, N-terminal/IPR010987; Glutathione S-transferase, C-terminal-like	GO:0005515; protein binding; function

21983113	21985709	Cil_09G_01383V2	DHAR2			GN=DHAR2 PE=1 SV=1 Q9FRL8/213/DHAR2_ARATH Glutathione S-transferase DHAR2 OS=Arabidopsis thaliana GN=DHAR2 PE=1 SV=1	K21888/DHAR/--	GN=DHAR2 PE=2 SV=1 J9WN12/212/J9WN12_POPTO Dehydroascorbate reductase (Fragment) OS=Populus tomentosa GN=DHAR2 PE=2 SV=1	2/IPR004045; Glutathione S-transferase, N-terminal/IPR010987; Glutathione S-transferase, C-terminal-like	GO:0005515; protein binding; function
21996397	21999766	Cil_09G_01384V2	NA			NA	NA	F6HRR2/663/F6HRR2_VITVI Putative uncharacterized protein OS=Vitis vinifera GN=VIT_00s0317g00060 PE=4 SV=1	3/IPR025486; Domain of unknown function DUF4378/IPR032795; DUF3741-associated sequence motif	NA
54869301	54963593	Cil_09G_02990V2	MYBP	0.218	1.567	NA	K09422/MYBP/factor	NA	NA	NA
54915008	54915619	Cil_09G_02991V2	NA			NA	NA	A0A061DT80/194/A0A061DT80_THECC UvrABC	1/1/IPR025322; Protein of	NA

								system protein C OS=Theobroma cacao GN=TCM_005045 PE=4 SV=1	unknown function DUF4228, plant	
54978931	54980358	Cil_09G_02992V2	NAC43			Q84WP6/344/NAC43_ARATH NAC domain-containing protein 43 OS=Arabidopsis thaliana GN=NAC043 PE=2 SV=2	K00521/E1.16.1.7/reductase	A0A061E007/366/A0A061E007_THECC Transcription factor OS=Theobroma cacao GN=TCM_005047 PE=4 SV=1	1/1/IPR003441; NAC domain	GO:0003677; DNA binding; function|GO:0006355; regulation of transcription, DNA-templated; process
54997792	55002826	Cil_09G_02993V2	RNHX1	0.251	1.779	P0C2F6/461/RNHX1_ARATH Putative ribonuclease H protein At1g65750 OS=Arabidopsis thaliana GN=At1g65750 PE=3 SV=1	K17535/TNNI3K/kinase	M5W5F3/911/M5W5F3_PRUPE Uncharacterized protein (Fragment) OS=Prunus persica GN=PRUPE_ppa026368mg PE=4 SV=1	2/IPR025558; Domain of unknown function DUF4283/IPR026960; Reverse transcriptase zinc-binding domain	NA

	55041820	55044801	Cil_09G_02994V2	NA			NA	NA	NA	NA	NA
	55072669	55083638	Cil_09G_02995V2	KIF11			Q9FT92/331/Y5843_ARATH Uncharacterized protein At5g08430 OS=Arabidopsis thaliana GN=At5g08430 PE=1 SV=2	K10398/KIF11,/kinesin	A0A067JU74/568/A0A067JU74_JATCU Uncharacterized protein OS=Jatropha curcas GN=JCGZ_01655 PE=4 SV=1	3/IPR004343; Plus-3 domain/IPR018144; Plus-3 domain, subgroup	GO:0003677; DNA binding; function|GO:0005515; protein binding; function|GO:0005634; nucleus; component|GO:0006352; DNA-templated transcription, initiation; process|GO:0016570; histone modification; process
chr10	13704151	13721974	Cil_10G_00533V2	NA	0.178	1.563	NA	K15407/QTRTD1/tRNA-ribosyltransferase	A0A067JEC4/353/A0A067JEC4_JATCU Uncharacterized protein OS=Jatropha curcas	1/1/IPR011016; Zinc finger, RING-CH-type	GO:0008270; zinc ion binding; function

							GN=JCGZ_21589 PE=4 SV=1		
13744762	13753008	Cil_10G_00534V2	AAT1/GOT2		P46643/429/AAT1_ARATH Aspartate aminotransferase, mitochondrial OS=Arabidopsis thaliana GN=ASP1 PE=1 SV=1	K14455/GOT2/aminotransferase,	A0A059DHE5/425/A0A059DHE5_EUCGR Aspartate aminotransferase OS=Eucalyptus grandis GN=EUGRSUZ_A01927 PE=3 SV=1	3/IPR004838; Aminotransferases, class-I, pyridoxal-phosphate-binding site/IPR004839; Aminotransferase, class I/classII	GO:0003824; catalytic activity; function|GO:0006520; cellular amino acid metabolic process; process|GO:0008483; transaminase activity; function|GO:0009058; biosynthetic process; process|GO:0030170; pyridoxal phosphate binding; function
13758069	13763917	Cil_10G_00535V2	HSPA1		NA	K03283/HSPA1s/shock	M5VP36/435/M5VP36_PRUPE Uncharacterized protein (Fragment) OS=Prunus persica GN=PRUPE_ppa	NA	NA

							014760mg PE=4 SV=1		
13778612	13780962	Cil_10G_00536V2	DTX41		Q9LYT3/502/DTX41_ARATH Protein DETOXIFICATION 41 OS=Arabidopsis thaliana GN=DTX41 PE=2 SV=1	K03327/TC.MATE,/norM,	A0A061DSU4/550/A0A061DSU4_THECC Protein DETOXIFICATION OS=Theobroma cacao GN=TCM_001905 PE=3 SV=1	1/1/IPR002528; Multi antimicrobial extrusion protein	GO:0006855; drug transmembrane transport; process|GO:0015238; drug transmembrane transporter activity; function|GO:0015297; antiporter activity; function|GO:0016020; membrane; component|GO:0055085; transmembrane transport; process
13782264	13786905	Cil_10G_00537V2	NCL		NA	K11294/NCL,/nucleolin	A0A061ELV8/341/A0A061ELV8_THECC Uncharacterized protein OS=Theobroma cacao	2/IPR025558; Domain of unknown function DUF4283/IPR025836; Zinc knuckle CX2CX4HX4C	NA

16530137	16534634	Cil_10G_00597V2	RSLE1	0.201	1.991	B9FJG3/653/RSLE1_ORYSJ Zinc finger BED domain-containing protein RICESLEEPER 1 OS=Oryza sativa subsp. japonica GN=Os05g0239150 PE=3 SV=1	K03283/HSPA1s/shock	GN=TCM_020721 PE=4 SV=1 A0A0D2NCJ1/525/A0A0D2NCJ1_GOSRA Uncharacterized protein OS=Gossypium raimondii GN=B456_005G140200 PE=4 SV=1	2/IPR008906; HAT, C-terminal dimerisation domain/IPR025525; hAT-like transposase, RNase-H fold	GO:0003677; DNA binding; function|GO:0046983; protein dimerization activity; function
16550504	16555061	Cil_10G_00598V2	NA			NA	NA	NA	NA	NA
16600749	16601265	Cil_10G_00599V2	NA			NA	NA	NA	NA	NA
16621565	16622050	Cil_10G_00600V2	NA	0.285	1.764	NA	NA	B9N9R1/148/B9N9R1_POPTR Uncharacterized protein OS=Populus trichocarpa GN=POPTR_001	NA	NA

16649020	16651051	Cil_10G_00601V2	PTM		F4JYC8/469/PTM_ARATH DDT domain-containing protein PTM OS=Arabidopsis thaliana GN=PTM PE=1 SV=1	K08881/TRIM24,/tripartite	1s08290g PE=4 SV=1 F6HA06/651/F6HA06_VITVI Putative uncharacterized protein OS=Vitis vinifera GN=VIT_06s0009g03800 PE=4 SV=1	1/1/IPR001965; Zinc finger, PHD-type	GO:0005515; protein binding; function|GO:0008270; zinc ion binding; function
16662647	16683812	Cil_10G_00602V2	PPP5		Q84K11/537/PPP5_SOLLC Serine/threonine-protein phosphatase 5 OS=Solanum lycopersicum GN=PP5 PE=1 SV=1	K04460/PPP5C/phosphatase	K7LA10/521/K7LA10_SOYBN Uncharacterized protein OS=Glycine max PE=4 SV=1	8/IPR013235; PPP domain/IPR019734; Tetratricopeptide repeat	GO:0004721; phosphoprotein phosphatase activity; function|GO:0005515; protein binding; function|GO:0005634; nucleus; component|GO:0005737; cytoplasm; component|GO:0006470; protein dephosphorylation; process|GO:00167

29403167	29406167	Cil_10G_01364V2	PPI1	0.208	1.562	O23144/339/PPI1_ARATH Proton pump-interactor 1 OS=Arabidopsis thaliana GN=PPI1 PE=1 SV=2	NA	A0A0A0K9L8/382/A0A0A0K9L8_CUCSA Uncharacterized protein OS=Cucumis sativus GN=Csa_6G094680 PE=4 SV=1	1/1/IPR029669; Proton pump-interactor	87; hydrolase activity; function GO:0005783; endoplasmic reticulum; component|GO:0005886; plasma membrane; component|GO:0010155; regulation of proton transport; process
29408532	29412549	Cil_10G_01365V2	THF1			Q7XAB8/289/THF1_SOLTU Protein THYLAKOID FORMATION1, chloroplastic OS=Solanum tuberosum GN=THF1 PE=2 SV=1	NA	A0A061E4M4/294/A0A061E4M4_THECC Photosystem II reaction center PSB29 protein OS=Theobroma cacao GN=TCM_007929 PE=3 SV=1	1/1/IPR017499; Protein Thf1	GO:0010207; photosystem II assembly; process|GO:0015979; photosynthesis; process
29434901	29435098	Cil_10G_01366V2	USP39			NA	K12847/USP39, /U4/U6.U5	NA	NA	NA

29467103	29474023	Cil_10G_01367V2	NA			NA	NA	A0A0B2P9L5/82/A0A0B2P9L5_GLYSO Uncharacterized protein OS=Glycine soja GN=glysoja_037967 PE=4 SV=1	1/1/IPR022251; Protein of unknown function wound-induced	NA
29615907	29616751	Cil_10G_01374V2	NA			NA	NA	NA	NA	NA
29620962	29623964	Cil_10G_01375V2	VAP42	0.172	2.389	Q8VYN2/294/VAP42_ARATH Vesicle-associated protein 4-2 OS=Arabidopsis thaliana GN=PVA42 PE=1 SV=1	K01681/ACO,/aconitate	I3SHF4/265/I3SHF4_LOTJA Uncharacterized protein OS=Lotus japonicus PE=2 SV=1	2/IPR000535; Major sperm protein (MSP) domain/IPR016763; Vesicle-associated membrane-protein-associated protein	GO:0005789; endoplasmic reticulum membrane; component
29630040	29630342	Cil_10G_01376V2	NA			NA	NA	A0A061EBE5/1057/A0A061EBE5_THECC Uncharacterized protein OS=Theobroma	NA	NA

								cacao GN=TCM_011923 PE=4 SV=1		
29667023	29667802	Cil_10G_01377V2	NA			NA	NA	NA	NA	NA
29685756	29709235	Cil_10G_01378V2	VPS18			P59015/971/VPS18_DANRE Vacuolar protein sorting-associated protein 18 homolog OS=Danio rerio GN=vps18 PE=2 SV=2	K20181/VPS18, /vacuolar	M5WX82/985/M5WX82_PRUPE Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa000832mg PE=4 SV=1	3/IPR002885; Pentatricopeptide repeat/IPR007810; Pep3/Vps18/deep orange	GO:0006886; intracellular protein transport; process|GO:0016192; vesicle-mediated transport; process
32500194	32501924	Cil_10G_01474V2	NA			NA	NA	NA	NA	NA
32506000	32507142	Cil_10G_01475V2	NA	0.206	2.547	NA	NA	NA	NA	NA
32523460	32535938	Cil_10G_01476V2	SCPL-II			NA	K16297/SCPL-II/carboxypeptidase-like	NA	1/1/IPR004252; Probable transposase, Ptta/En/Spm, plant	NA

32545856	32547635	Cil_10G_01477V2	NA			NA	NA	U5FVV7/296/U5FVV7_POPTR Uncharacterized protein OS=Populus trichocarpa GN=POPTR_0013s13350g PE=4 SV=1	1/1/IPR006502; Protein of unknown function PDDEXK-like	NA
32695463	32702898	Cil_10G_01478V2	SMC6	0.214	2.793	P93295/148/M310_ARATH Uncharacterized mitochondrial protein AtMg00310 OS=Arabidopsis thaliana GN=AtMg00310 PE=4 SV=1	K22804/SMC6/maintenance	M5XSK0/979/M5XSK0_PRUPE Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa016553mg PE=4 SV=1	3/IPR025836; Zinc knuckle CX2CX4HX4C/IPR026960; Reverse transcriptase zinc-binding domain	NA
42305779	42307955	Cil_10G_01934V2	RPS15	0.163	1.889	P62302/141/RS13_SOYBN 40S ribosomal protein S13 OS=Glycine max GN=RPS13 PE=2 SV=1	K02953/RP-S13e,/small	A0A0D2LZT7/161/A0A0D2LZT7_GOSRA Uncharacterized protein (Fragment) OS=Gossypium	2/IPR000589; Ribosomal protein S15/IPR012606; Ribosomal protein S13/S15, N-terminal	GO:0003735; structural constituent of ribosome; function|GO:0005622; intracellular; component|GO:00

							raimondii GN=B456_001G174200 PE=3 SV=1		05840; ribosome; component|GO:0006412; translation; process
42321883	42328803	Cil_10G_01935V2	RPS10		Q9LVA7/207/ICLN_ARATH Chloride conductance regulatory protein ICln OS=Arabidopsis thaliana GN=At5g62290 PE=2 SV=1	K05019/CLNS1A/channel,	B9I4K9/210/B9I4K9_POPTR Nucleotide-sensitive chloride conductance regulator family protein OS=Populus trichocarpa GN=POPTR_0012s14450g PE=4 SV=1	3/IPR018268; Ribosomal protein S10, conserved site/IPR027486; Ribosomal protein S10 domain	GO:0003723; RNA binding; function|GO:0003735; structural constituent of ribosome; function|GO:0005622; intracellular; component|GO:0005840; ribosome; component|GO:0006412; translation; process
42349737	42353275	Cil_10G_01936V2	RPS10		P49200/124/RS201_ARATH 40S ribosomal protein S20-1 OS=Arabidopsis thaliana GN=RPS20A PE=2 SV=2	K02969/RP-S20e,/small	A0A0B0N2B4/122/A0A0B0N2B4_GOSAR 40S ribosomal S20-2-like protein OS=Gossypium arboreum GN=F383_33121 PE=3 SV=1	3/IPR018268; Ribosomal protein S10, conserved site/IPR027486; Ribosomal protein S10 domain	GO:0003723; RNA binding; function|GO:0003735; structural constituent of ribosome; function|GO:0005622; intracellular; component|GO:00

								05840; ribosome; component|GO:0006412; translation; process
42366719	42367750	Cil_10G_01937V2	EXOL3	Q9FHM9/337/EXOL3_ARATH Protein EXORDIUM-like 3 OS=Arabidopsis thaliana GN=EXL3 PE=2 SV=1	NA	A0A061G0K8/338/A0A061G0K8_THECC EXORDIUM like 3 OS=Theobroma cacao GN=TCM_014962 PE=4 SV=1	1/1/IPR006766; Phosphate-induced protein 1	NA
42380004	42381574	Cil_10G_01938V2	BES1/BZR1	Q5Z9E5/84/BZR3_ORYSJ Protein BZR1 homolog 3 OS=Oryza sativa subsp. japonica GN=BZR3 PE=2 SV=1	K14503/BZR1_2/resistant	U5CW90/85/U5CW90_AMBTC Uncharacterized protein OS=Amborella trichopoda GN=AMTR_s00059p00136790 PE=4 SV=1	1/1/IPR008540; BES1/BZR1 plant transcription factor, N-terminal	NA
42382722	42395408	Cil_10G_01939V2	IRE	Q9LE81/1164/IRE_ARATH Probable serine/threonine protein kinase	K08789/MAST/serine/threonine	M5XM13/1198/M5XM13_PRUPE Uncharacterized protein OS=Prunus	4/IPR002290; Serine/threonine/dual specificity protein kinase, catalytic	GO:0004672; protein kinase activity; function|GO:0004674; protein

						IRE OS=Arabidopsis thaliana GN=IRE PE=2 SV=1		persica GN=PRUPE_ppa000414mg PE=4 SV=1	domain/IPR008271; Serine/threonine-protein kinase, active site	serine/threonine kinase activity; function|GO:0005524; ATP binding; function|GO:0006468; protein phosphorylation; process
	42397748	42399441	Cil_10G_01940V2	MYB26		Q50EX6/271/ODO1_PETHY Protein ODORANT1 OS=Petunia hybrida GN=ODO1 PE=2 SV=1	K09422/MYBP/factor	V5K8K7/249/V5K8K7_9ROSI MYB transcription factor 2 OS=Betula luminifera GN=MYB2 PE=2 SV=1	2/IPR001005; SANT/Myb domain/IPR017930; Myb domain	NA
chr11	16401106	16404803	Cil_11G_01297V2	UTR3		Q9M9S6/330/UTR3_ARATH UDP-galactose/UDP-glucose transporter 3 OS=Arabidopsis thaliana	K15275/SLC35B1/carrier	A0A061EBJ3/330/A0A061EBJ3_THECC UDP-galactose transporter 3 isoform 1 OS=Theobroma cacao	1/1/IPR013657; UAA transporter	GO:0055085; transmembrane transport; process

						GN=UTR3 PE=1 SV=1		GN=TCM_011775 PE=4 SV=1		
16424669	16433184	Cil_11G_01298V2	APK2B			O49840/426/APK2B_ARATH Protein kinase 2B, chloroplastic OS=Arabidopsis thaliana GN=APK2B PE=2 SV=1	K04733/IRAK4/receptor-associated	A0A061EAP5/419/A0A061EAP5_THECC Kinase 2B isoform 1 OS=Theobroma cacao GN=TCM_011774 PE=3 SV=1	4/IPR008271; Serine/threonine-protein kinase, active site/IPR017441; Protein kinase, ATP binding site	GO:0004672; protein kinase activity; function|GO:0005524; ATP binding; function|GO:0006468; protein phosphorylation; process
16491495	16492382	Cil_11G_01299V2	NCL			NA	K11294/NCL,/nucleolin	A0A061ELV8/263/A0A061ELV8_THECC Uncharacterized protein OS=Theobroma cacao GN=TCM_020721 PE=4 SV=1	2/IPR025558; Domain of unknown function DUF4283/IPR025836; Zinc knuckle CX2CX4HX4C	NA
16550950	16553401	Cil_11G_01300V2	pvadh	0.167	2.202	NA	K05889/pvadh/alcohol	U5FPF8/500/U5FPF8_POPTR Uncharacterized protein (Fragment) OS=Populus	2/IPR002372; Pyrrolo-quinoline quinone repeat/IPR018391; Pyrrolo-quinoline quinone	NA

						trichocarpa GN=POPTR_0016s14620g PE=4 SV=1	beta-propeller repeat	
16564754	16565020	Cil_11G_01301V2	NA	NA	NA	NA	NA	NA
16572998	16575893	Cil_11G_01302V2	E2.7.1.-/2.7	Q9M9S4/721/Y1143_ARATH Probable LRR receptor-like serine/threonine-protein kinase At1g14390 OS=Arabidopsis thaliana GN=At1g14390 PE=2 SV=1	K00924/E2.7.1.-/2.7.1.-	A0A059BG47/735/A0A059BG47_EUCGR Uncharacterized protein OS=Eucalyptus grandis GN=EUGRSUZ_G02533 PE=4 SV=1	3/IPR001245; Serine-threonine/tyrosine-protein kinase catalytic domain/IPR016251; Tyrosine-protein kinase, non-receptor Jak/Tyk2	GO:0004672; protein kinase activity; function|GO:0004715; non-membrane spanning protein tyrosine kinase activity; function|GO:0005524; ATP binding; function|GO:0006468; protein phosphorylation; process|GO:0016020; membrane; component|GO:0035556; intracellular signal

										transduction; process
17401747	17403180	Cil_11G_01344V2	KIFC2_3	0.168	1.717	NA	K10406/KIFC2_3/family	A0A0A9A291/118/A0A0A9A291_ARUDO Uncharacterized protein OS=Arundo donax PE=4 SV=1	1/1/IPR025836; Zinc knuckle CX2CX4HX4C	NA
17417757	17422592	Cil_11G_01345V2	HIPL1/TAF1A			Q9SSG3/651/HIPL1_ARATH HIPL1 protein OS=Arabidopsis thaliana GN=HIPL1 PE=1 SV=2	K15212/TAF1A,/TATA	D7TNG9/659/D7TNG9_VITVI Putative uncharacterized protein OS=Vitis vinifera GN=VIT_01s0026g01300 PE=4 SV=1	1/1/IPR012938; Glucose/Sorbosone dehydrogenase	GO:0005975; carbohydrate metabolic process; process|GO:0016901; oxidoreductase activity, acting on the CH-OH group of donors, quinone or similar compound as acceptor; function|GO:0048038; quinone binding; function

17424962	17427217	Cil_11G_01346V2	PPR12		Q0WVK7/734/PPR12_ARATH Pentatricopeptide repeat-containing protein At1g05670, mitochondrial OS=Arabidopsis thaliana GN=At1g05670 PE=2 SV=1	K17710/PTCD1/repeat	F6HPH4/748/F6HPH4_VITVI Putative uncharacterized protein OS=Vitis vinifera GN=VIT_01s0026g01280 PE=4 SV=1	2/IPR000048; IQ motif, EF-hand binding site/IPR002885; Pentatricopeptide repeat	GO:0005515; protein binding; function
17453084	17460970	Cil_11G_01347V2	IRAK4		NA	K04733/IRAK4/receptor-associated	F6HPH5/292/F6HPH5_VITVI Putative uncharacterized protein OS=Vitis vinifera GN=VIT_01s0026g01250 PE=4 SV=1	2/IPR025287; Wall-associated receptor kinase, galacturonan-binding domain/IPR032872; Wall-associated receptor kinase, C-terminal	GO:0030247; polysaccharide binding; function
17467017	17471548	Cil_11G_01348V2	B3GTI		Q8RX55/622/B3GTI_ARATH Probable beta-1,3-galactosyltransferase 18 OS=Arabidopsis	K20843/GALT2S/O-galactosyltransferase	A5AJ66/628/A5AJ66_VITVI Putative uncharacterized protein OS=Vitis vinifera	2/IPR001079; Galectin, carbohydrate recognition domain/IPR002659; Glycosyl	GO:0006486; protein glycosylation; process|GO:0008378; galactosyltransfera

				thaliana GN=B3GALT18 PE=2 SV=1		GN=VITISV_023073 PE=4 SV=1	transferase, family 31	se activity; function|GO:0016020; membrane; component|GO:0030246; carbohydrate binding; function
17490651	17492692	Cil_11G_01349V2	GPAT6	O80437/494/GPAT6_ARATH Glycerol-3-phosphate 2-O-acyltransferase 6 OS=Arabidopsis thaliana GN=GPAT6 PE=1 SV=1	K13508/GPAT/--	B9IIF1/501/B9IIF1_POPTR Uncharacterized protein OS=Populus trichocarpa GN=POPTR_0016s06390g PE=4 SV=2	1/1/IPR002123; Phospholipid/glycerol acyltransferase	GO:0008152; metabolic process; process|GO:0016746; transferase activity, transferring acyl groups; function
17496404	17506386	Cil_11G_01350V2	NA	NA	NA	V4SP43/96/V4SP43_9ROSI Uncharacterized protein (Fragment) OS=Citrus clementina GN=CICLE_v10033320mg PE=4 SV=1	NA	NA

17711650	17718316	Cil_11G_01353V2	LRRC8			Q40392/899/TMVRN_NICGU TMV resistance protein N OS=Nicotiana glutinosa GN=N PE=1 SV=1	K22038/LRRC8/anion	M5XSP1/1372/M5XSP1_PRUPE Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa000268mg PE=4 SV=1	4/IPR002182; NB-ARC/IPR003591; Leucine-rich repeat, typical subtype	GO:0005515; protein binding; function|GO:0007165; signal transduction; process|GO:0043531; ADP binding; function
17746173	17751821	Cil_11G_01354V2	LOX1	0.230	1.988	NA	K15718/LOX1_5/9S-lipoxygenase	M0TLR3/420/M0TLR3_MUSAM Uncharacterized protein OS=Musa acuminata subsp. malaccensis PE=4 SV=1	NA	NA
17776014	17782799	Cil_11G_01355V2	SNC1/ERN1			O23530/1060/SNC1_ARATH Protein SUPPRESSOR OF npr1-1, CONSTITUTIVE 1 OS=Arabidopsis thaliana GN=SNC1 PE=1 SV=4	K08852/ERN1/--	F6HPI4/1404/F6HPI4_VITVI Putative uncharacterized protein OS=Vitis vinifera GN=VIT_01s0026g01120 PE=4 SV=1	4/IPR003591; Leucine-rich repeat, typical subtype/IPR003593; AAA+ ATPase domain	GO:0005515; protein binding; function|GO:0007165; signal transduction; process|GO:0043531; ADP binding; function

23110482	23119361	Cil_11G_01521V2	PTR2			P46032/570/PTR2_ARATH Protein NRT1/ PTR FAMILY 8.3 OS=Arabidopsis thaliana GN=NPF8.3 PE=1 SV=1	K14638/SLC15A3_4,/solute	A0A061EA41/570/A0A061EA41_THECC Peptide transporter 2 isoform 1 OS=Theobroma cacao GN=TCM_011173 PE=3 SV=1	2/IPR000109; Proton-dependent oligopeptide transporter family/IPR018456; PTR2 family proton/oligopeptide symporter, conserved site	GO:0005215; transporter activity; function|GO:0006810; transport; process|GO:0006857; oligopeptide transport; process|GO:0016020; membrane; component
23154223	23154567	Cil_11G_01522V2	RRP5	0.162	1.527	NA	K14792/RRP5,/rRNA	NA	NA	NA
23190999	23196615	Cil_11G_01523V2	PTR2			P46032/584/PTR2_ARATH Protein NRT1/ PTR FAMILY 8.3 OS=Arabidopsis thaliana GN=NPF8.3 PE=1 SV=1	K14638/SLC15A3_4,/solute	A0A061EA41/583/A0A061EA41_THECC Peptide transporter 2 isoform 1 OS=Theobroma cacao GN=TCM_011173 PE=3 SV=1	2/IPR000109; Proton-dependent oligopeptide transporter family/IPR018456; PTR2 family proton/oligopeptide symporter, conserved site	GO:0005215; transporter activity; function|GO:0006810; transport; process|GO:0006857; oligopeptide transport; process|GO:0016020; membrane; component

23234314	23241077	Cil_11G_01524V2	NA	0.204	1.767	NA	NA	D7SMG7/226/D7SMG7_VITVI Putative uncharacterized protein OS=Vitis vinifera GN=VIT_01s0137g00060 PE=4 SV=1	NA	NA
28413279	28417965	Cil_11G_01686V2	SMC6	0.174	1.844	NA	K22804/SMC6/maintenance	S8D5C6/767/S8D5C6_9LAMI Uncharacterized protein (Fragment) OS=Genlisea aurea GN=M569_02121 PE=4 SV=1	1/1/IPR025836; Zinc knuckle CX2CX4HX4C	NA
28435290	28466439	Cil_11G_01687V2	FHY3/FAR1			Q9LIE5/661/FHY3_ARATH Protein FAR-RED ELONGATED HYPOCOTYL 3 OS=Arabidopsis thaliana	K17604/ZSWIM3/finger	M0TWQ5/140/M0TWQ5_MUSAM Uncharacterized protein OS=Musa acuminata subsp. malaccensis PE=4 SV=1	3/IPR007527; Zinc finger, SWIM-type/IPR031052; FHY3/FAR1 family	GO:0006355; regulation of transcription, DNA-templated; process|GO:0008270; zinc ion binding; function

						GN=FHY3 PE=1 SV=1				
28441450	28444401	Cil_11G_01688V2	VINSY			Q70PR7/409/VINSY_RAUSE Vinorine synthase OS=Rauvolfia serpentina GN=ACT PE=1 SV=2	K13065/E2.3.1.133,/shikimate	B9HTD4/403/B9HTD4_POPTR Transferase family protein OS=Populus trichocarpa GN=POPTR_0010s06390g PE=4 SV=2	1/1/IPR003480; Transferase	GO:0016747; transferase activity, transferring acyl groups other than amino-acyl groups; function
28470692	28478978	Cil_11G_01689V2	NA			NA	NA	NA	NA	NA
28497602	28499869	Cil_11G_01690V2	COIL			NA	K13150/COIL,/coilin	A0A072V2N3/405/A0A072V2N3_MEDTR DUF630 family protein OS=Medicago truncatula GN=MTR_3g115120 PE=4 SV=1	1/1/IPR006867; Domain of unknown function DUF632	NA
28544173	28550698	Cil_11G_01691V2	VINSY	0.160	1.765	Q70PR7/415/VINSY_RAUSE Vinorine synthase OS=Rauvolfia	K13065/E2.3.1.133,/shikimate	A0A061E719/423/A0A061E719_THECC HXXXD-type acyl-	1/1/IPR003480; Transferase	GO:0016747; transferase activity, transferring acyl

						serpentina GN=ACT PE=1 SV=2		transferase family protein, putative OS=Theobroma cacao GN=TCM_010714 PE=4 SV=1		groups other than amino-acyl groups; function
28599784	28603692	Cil_11G_01692V2	NA			NA	NA	NA	NA	NA
30269056	30302994	Cil_11G_01766V2	MED23	0.155	1.723	F4I4P3/1512/MED23_ARATH Mediator of RNA polymerase II transcription subunit 23 OS=Arabidopsis thaliana GN=MED23 PE=1 SV=1	K15166/MED23/of	M5XL69/1504/M5XL69_PRUPE Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa000154mg PE=4 SV=1	1/1/IPR021629; Mediator complex, subunit Med23	NA
30306368	30317496	Cil_11G_01767V2	MED23			F4I4P3/399/MED23_ARATH Mediator of RNA polymerase II transcription subunit 23 OS=Arabidopsis	K15166/MED23/of	A0A059D7Q6/317/A0A059D7Q6_EUCGR Uncharacterized protein OS=Eucalyptus grandis	NA	NA

					thaliana GN=MED23 PE=1 SV=1		GN=EUGRSUZ_B02949 PE=4 SV=1		
30330028	30334544	Cil_11G_01768V2	DYL		Q86A88/89/DYL_DICDI Dynein light chain, cytoplasmic OS=Dictyostelium discoideum GN=dlcB PE=3 SV=1	K10418/DYNLL/light	A0A061E8U7/128/A0A061E8U7_THECC Dynein light chain type 1 family protein OS=Theobroma cacao GN=TCM_011012 PE=4 SV=1	1/1/IPR001372; Dynein light chain, type 1/2	GO:0005875; microtubule associated complex; component|GO:0007017; microtubule-based process; process
30350760	30353867	Cil_11G_01769V2	PCR2		Q9LQU4/152/PCR2_ARATH Protein PLANT CADMIUM RESISTANCE 2 OS=Arabidopsis thaliana GN=PCR2 PE=1 SV=1	NA	B9HW36/193/B9HW36_POPTR Uncharacterized protein OS=Populus trichocarpa GN=POPTR_0010s11910g PE=4 SV=1	1/1/IPR006461; PLAC8 motif-containing protein	NA
30356989	30358191	Cil_11G_01770V2	PCR2		Q9LQU4/152/PCR2_ARATH Protein PLANT CADMIUM RESISTANCE 2	K11153/RDH12/dehydrogenase	B9HW36/193/B9HW36_POPTR Uncharacterized protein OS=Populus	1/1/IPR006461; PLAC8 motif-containing protein	NA

chr12					0.195	2.619	OS=Arabidopsis thaliana GN=PCR2 PE=1 SV=1		trichocarpa GN=POPTR_0010s11910g PE=4 SV=1		
	1675692	1703337	Cil_12G_00091V2	CHR28/TTF2			Q94BR5/610/CHR28_ARATH Helicase-like transcription factor CHR28 OS=Arabidopsis thaliana GN=CHR28 PE=1 SV=1	K15173/TTF2/termination	A0A061E9R6/651/A0A061E9R6_THECC SNF2 domain-containing protein / helicase domain-containing protein / zinc finger protein-related isoform 4 OS=Theobroma cacao GN=TCM_007664 PE=4 SV=1	4/IPR014001; Helicase superfamily 1/2, ATP-binding domain/IPR017907; Zinc finger, RING-type, conserved site	GO:0005524; ATP binding; function
	1735934	1737673	Cil_12G_00092V2	FLS2			Q9LZV7/567/PXC2_ARATH Leucine-rich repeat receptor-like protein kinase PXC2 OS=Arabidopsis thaliana	K13420/FLS2/receptor-like	V4W6J1/600/V4W6J1_9ROSI Uncharacterized protein OS=Citrus clementina GN=CICLE_v10014664mg PE=4 SV=1	3/IPR003591; Leucine-rich repeat, typical subtype/IPR013210; Leucine-rich repeat-containing N-terminal, plant-type	GO:0005515; protein binding; function

				GN=PXC2 PE=2 SV=1				
1755276	1759187	Cil_12G_00093V2	SH3YL1	NA	K20523/SH3YL1/domain-containing	A0A061E1V8/566/A0A061E1V8_THECC E3 ubiquitin-protein ligase RNF25 OS=Theobroma cacao GN=TCM_007657 PE=4 SV=1	NA	NA
1777767	1785080	Cil_12G_00094V2	TRA1	P08770/376/TRA1_MAIZE Putative AC transposase OS=Zea mays PE=2 SV=2	NA	D0UIX2/259/D0UIX2_CUCME Putative transposase OS=Cucumis melo PE=4 SV=1	NA	NA
1785881	1789813	Cil_12G_00095V2	PPCEL/PTRB	Q5ZKL5/400/PPCEL_CHICK Prolyl endopeptidase-like OS=Gallus gallus GN=PREPL PE=2 SV=1	K01354/ptrB/B	M5XB32/492/M5XB32_PRUPE Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa001738mg PE=4 SV=1	2/IPR002470; Peptidase S9A, prolyl oligopeptidase/IPR023302; Peptidase S9A, N-terminal domain	GO:0004252; serine-type endopeptidase activity; function|GO:0006508; proteolysis; process|GO:0070008; serine-type

										exopeptidase activity; function
1791185	1798405	Cil_12G_00096V2	NA			NA	NA	W9RP25/136/W9RP25_9ROSA Uncharacterized protein OS=Morus notabilis GN=L484_008713 PE=4 SV=1	NA	NA
10194840	10201441	Cil_12G_00571V2	CAMTA	0.164	1.554	Q9SZL7/435/FRS9_ARATH Protein FAR1-RELATED SEQUENCE 9 OS=Arabidopsis thaliana GN=FRS9 PE=2 SV=2	K17604/ZSWIM3/finger	V4T962/124/V4T962_9ROSI Uncharacterized protein OS=Citrus clementina GN=CICLE_v10003142mg PE=4 SV=1	3/IPR007527; Zinc finger, SWIM-type/IPR031052; FHY3/FAR1 family	GO:0006355; regulation of transcription, DNA-templated; process|GO:0008270; zinc ion binding; function
10215307	10216300	Cil_12G_00572V2	FRS9/FHY3/FAR1			NA	NA	B9GNX6/207/B9GNX6_POPTR Uncharacterized protein OS=Populus trichocarpa GN=POPTR_000	NA	NA

								2s12930g PE=4 SV=1		
10217434	10220102	Cil_12G_00573V2	SDH5			Q9SX77/257/SDH5_ARATH Succinate dehydrogenase subunit 5, mitochondrial OS=Arabidopsis thaliana GN=SDH5 PE=1 SV=1	NA	A0A0A0LP60/241/A0A0A0LP60_CUCSA Uncharacterized protein OS=Cucumis sativus GN=Csa_2G360050 PE=4 SV=1	1/1/IPR025397; Protein of unknown function DUF4370	NA
10228960	10232664	Cil_12G_00574V2	HIDH			Q5NUF3/240/HIDH_SOYBN 2-hydroxyisoflavanone dehydratase OS=Glycine max GN=HIDH PE=1 SV=1	K20506/TCEA/A-converting	A0A061FC92/324/A0A061FC92_THECC Alpha/beta-Hydrolases superfamily protein OS=Theobroma cacao GN=TCM_033878 PE=4 SV=1	1/1/IPR013094; Alpha/beta hydrolase fold-3	GO:0008152; metabolic process; process|GO:0016787; hydrolase activity; function
10234961	10238696	Cil_12G_00575V2	PTGES3			Q6ID70/150/Y3377_ARATH Uncharacterized	K15730/PTGES3/prostaglandin-E	C6T4G0/150/C6T4G0_SOYBN Uncharacterized	1/1/IPR007052; CS domain	NA

				protein At3g03773 OS=Arabidopsis thaliana GN=At3g03773 PE=1 SV=1		protein OS=Glycine max PE=2 SV=1		
10248171	10249151	Cil_12G_00576V2	CXE2	Q9SX78/311/CXE2_ARATH Probable carboxylesterase 2 OS=Arabidopsis thaliana GN=CXE2 PE=2 SV=1	K20506/TCEA/A-converting	A0A0D2RIU8/320/A0A0D2RIU8_GOSRA Uncharacterized protein OS=Gossypium raimondii GN=B456_005G103700 PE=4 SV=1	1/1/IPR013094; Alpha/beta hydrolase fold-3	GO:0008152; metabolic process; process|GO:0016787; hydrolase activity; function
10282602	10284705	Cil_12G_00577V2	PLP2	O48723/403/PLP2_ARATH Patatin-like protein 2 OS=Arabidopsis thaliana GN=PLP2 PE=1 SV=1	K06900/K06900/protein	F6H012/406/F6H012_VITVI Patatin OS=Vitis vinifera GN=VIT_18s0001g10910 PE=3 SV=1	1/1/IPR002641; Patatin/Phospholipase A2-related	GO:0006629; lipid metabolic process; process

10293436	10297799	Cil_12G_00578V2	NCL			NA	K11294/NCL,/nucleolin	B8ADJ3/310/B8ADJ3_ORYSI Putative uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI_00627 PE=4 SV=1	1/1/IPR025836; Zinc knuckle CX2CX4HX4C	NA
24716000	24717152	Cil_12G_01043V2	CAMTA	0.208	1.625	Q8GXC7/423/FBK50_ARATH F-box/kelch-repeat protein At3g06240 OS=Arabidopsis thaliana GN=At3g06240 PE=2 SV=1	K21596/CAMTA/transcription	A0A0D2USP1/366/A0A0D2USP1_GOSRA Uncharacterized protein OS=Gossypium raimondii GN=B456_011G135900 PE=4 SV=1	2/IPR001810; F-box domain/IPR006527; F-box associated domain, type 1	GO:0005515; protein binding; function
24778621	24779799	Cil_12G_01044V2	CAMTA			Q8GXC7/423/FBK50_ARATH F-box/kelch-repeat protein At3g06240 OS=Arabidopsis thaliana	K21596/CAMTA/transcription	K4CEQ0/362/K4CEQ0_SOLLC Uncharacterized protein OS=Solanum lycopersicum	2/IPR001810; F-box domain/IPR006527; F-box associated domain, type 1	GO:0005515; protein binding; function

							GN=At3g06240 PE=2 SV=1		GN=Solyc07g044920.1 PE=4 SV=1		
chr14	19197627	19202589	Cil_14G_01385V2	NA			NA	K15032/MTERFD/domain-containing	V4TSZ3/276/V4TSZ3_9ROSI Uncharacterized protein OS=Citrus clementina GN=CICLE_v10021599mg PE=4 SV=1	NA	NA
	19236922	19238038	Cil_14G_01386V2	MYB26	0.161	1.978	Q9SPG3/127/MYB26_ARATH Transcription factor MYB26 OS=Arabidopsis thaliana GN=MYB26 PE=2 SV=1	K09422/MYBP/factor	A0A067L7B1/312/A0A067L7B1_JATCU MYB family protein OS=Jatropha curcas GN=JCGZ_26656 PE=4 SV=1	2/IPR001005; SANT/Myb domain/IPR017930; Myb domain	NA
	19254731	19264286	Cil_14G_01387V2	SRP68			Q00004/618/SRP68_CANLF Signal recognition particle subunit SRP68 OS=Canis lupus familiaris GN=SRP68 PE=1 SV=1	K03107/SRP68/recognition	A0A061FYN7/601/A0A061FYN7_THECC Signal recognition particle subunit SRP68 OS=Theobroma cacao	1/1/IPR026258; Signal recognition particle subunit SRP68	GO:0005047; signal recognition particle binding; function|GO:0005786; signal recognition particle, endoplasmic

									GN=TCM_014748 PE=3 SV=1		reticulum targeting; component|GO:0006614; SRP-dependent cotranslational protein targeting to membrane; process|GO:0008312; 7S RNA binding; function|GO:0030942; endoplasmic reticulum signal peptide binding; function
chr15	299503	304946	Cil_15G_00015V2	GLR36/GRIP	0.174	1.623	Q84W41/895/GLR36_ARATH Glutamate receptor 3.6 OS=Arabidopsis thaliana GN=GLR3.6 PE=2 SV=1	K05387/GRIP/receptor,	M5WEL2/935/M5WEL2_PRUPE Glutamate receptor OS=Prunus persica GN=PRUPE_ppa000995mg PE=3 SV=1	3/IPR001638; Solute-binding protein family 3/N-terminal domain of MltF/IPR001828; Receptor, ligand binding region	GO:0004970; ionotropic glutamate receptor activity; function|GO:0016020; membrane; component

306970	310961	Cil_15G_00016V2	GLR36/GRIP		Q84W41/903/GLR36_ARATH Glutamate receptor 3.6 OS=Arabidopsis thaliana GN=GLR3.6 PE=2 SV=1	K05387/GRIP/receptor,	W9RW17/1006/W9RW17_9ROSA Glutamate receptor 3.6 OS=Morus notabilis GN=L484_007062 PE=4 SV=1	3/IPR001638; Solute-binding protein family 3/N-terminal domain of MltF/IPR001828; Receptor, ligand binding region	GO:0004970; ionotropic glutamate receptor activity; function|GO:0016020; membrane; component
322411	326009	Cil_15G_00017V2	GLR36/GRIP		Q84W41/901/GLR36_ARATH Glutamate receptor 3.6 OS=Arabidopsis thaliana GN=GLR3.6 PE=2 SV=1	K05387/GRIP/receptor,	D7SWB7/921/D7SWB7_VITVI Glutamate receptor OS=Vitis vinifera GN=VIT_07s0031g02170 PE=3 SV=1	3/IPR001638; Solute-binding protein family 3/N-terminal domain of MltF/IPR001828; Receptor, ligand binding region	GO:0004970; ionotropic glutamate receptor activity; function|GO:0016020; membrane; component
333303	336727	Cil_15G_00018V2	GLR36/GRIP		Q84W41/901/GLR36_ARATH Glutamate receptor 3.6 OS=Arabidopsis thaliana GN=GLR3.6 PE=2 SV=1	K05387/GRIP/receptor,	W9RW17/995/W9RW17_9ROSA Glutamate receptor 3.6 OS=Morus notabilis GN=L484_007062 PE=4 SV=1	4/IPR001638; Solute-binding protein family 3/N-terminal domain of MltF/IPR001828; Receptor, ligand binding region	GO:0004930; G-protein coupled receptor activity; function|GO:0004970; ionotropic glutamate receptor activity; function|GO:0007186; G-protein coupled receptor

										signaling pathway; process|GO:0016020; membrane; component|GO:0016021; integral component of membrane; component
358169	371918	Cil_15G_00019V2	GLR36/GRIP			Q84W41/901/GLR36_ARATH Glutamate receptor 3.6 OS=Arabidopsis thaliana GN=GLR3.6 PE=2 SV=1	K05387/GRIP/receptor,	W9RW17/1001/W9RW17_9ROSA Glutamate receptor 3.6 OS=Morus notabilis GN=L484_007062 PE=4 SV=1	3/IPR001638; Solute-binding protein family 3/N-terminal domain of MltF/IPR001828; Receptor, ligand binding region	GO:0004970; ionotropic glutamate receptor activity; function|GO:0016020; membrane; component
8951067	8958534	Cil_15G_00555V2	CC90B	0.166	1.842	Q9GZT6/252/CC90B_HUMAN Coiled-coil domain-containing protein 90B, mitochondrial OS=Homo sapiens	K22137/MCUR1/calcium	A0A0A0KZG0/258/A0A0A0KZG0_CUCSA Uncharacterized protein OS=Cucumis sativus GN=Csa_4G043920 PE=4 SV=1	1/1/IPR024461; Coiled-coil domain-containing protein 90-like	NA

				GN=CCDC90B PE=1 SV=2				
8951673	8952582	Cil_15G_00556V2	NA	NA	NA	NA	NA	NA
8973404	8975815	Cil_15G_00557V2	NA	NA	NA	B9HFD2/234/B9HFD2_POPTR Uncharacterized protein OS=Populus trichocarpa GN=POPTR_0007s13740g PE=4 SV=1	NA	NA
8977627	8985683	Cil_15G_00558V2	YELD	O14244/686/YELD_SCHPO Uncharacterized membrane protein C6F6.13c OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=SPAC6F6.13c PE=3 SV=1	K14773/UTP23/small	A0A067FUS2/658/A0A067FUS2_CITSI Uncharacterized protein OS=Citrus sinensis GN=CISIN_1g006082mg PE=4 SV=1	1/1/IPR007941; Protein of unknown function DUF726	NA

8996228	9009729	Cil_15G_00559V2	IRAK4			Q9SD33/268/U183_ARATH UPF0183 protein At3g51130 OS=Arabidopsis thaliana GN=At3g51130 PE=2 SV=2	K04733/IRAK4/receptor-associated	A0A067LH71/263/A0A067LH71_JATCU Uncharacterized protein OS=Jatropha curcas GN=JCGZ_06481 PE=4 SV=1	2/IPR005373; Uncharacterised protein family UPF0183/IPR026960; Reverse transcriptase zinc-binding domain	NA
13953938	13988180	Cil_15G_00734V2	PTAR1	0.192	1.852	Q7Z6K3/401/PTAR1_HUMAN Protein prenyltransferase alpha subunit repeat-containing protein 1 OS=Homo sapiens GN=PTAR1 PE=1 SV=2	K14137/PTAR1/prenyltransferase	M5WEZ3/417/M5WEZ3_PRUPE Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa021259mg PE=4 SV=1	1/1/IPR002088; Protein prenyltransferase, alpha subunit	GO:0008318; protein prenyltransferase activity; function|GO:0018342; protein prenylation; process
13956553	14009407	Cil_15G_00735V2	NA			NA	NA	NA	NA	NA
16656530	16661851	Cil_15G_00816V2	CBSX6	0.209	1.736	Q8GZA4/422/CBSX6_ARATH CBS domain-	NA	A0A061F5V0/424/A0A061F5V0_THECC	1/1/IPR000644; CBS domain	NA

						containing protein CBSX6 OS=Arabidopsis thaliana GN=CBSX6 PE=1 SV=1		Cystathionine beta-synthase family protein isoform 1 OS=Theobroma cacao GN=TCM_025271 PE=4 SV=1		
16663309	16690525	Cil_15G_00817V2	NA			NA	NA	NA	NA	NA
16696856	16699850	Cil_15G_00818V2	RNHX1			P0C2F6/586/RNHX1_ARATH Putative ribonuclease H protein At1g65750 OS=Arabidopsis thaliana GN=At1g65750 PE=3 SV=1	K17535/TNNI3K/kinase	M5VP36/423/M5VP36_PRUPE Uncharacterized protein (Fragment) OS=Prunus persica GN=PRUPE_ppa014760mg PE=4 SV=1	1/1/IPR026960; Reverse transcriptase zinc-binding domain	NA
18101155	18103927	Cil_15G_00863V2	LORF2/SMC6	0.190	2.776	O00370/482/LORF2_HUMAN LINE-1 retrotransposable element ORF2	K22804/SMC6/maintenance	S8D906/806/S8D906_9LAMI Uncharacterized protein (Fragment)	2/IPR025558; Domain of unknown function DUF4283/IPR025	NA

				protein OS=Homo sapiens PE=1 SV=1		OS=Genlisea aurea GN=M569_00896 PE=4 SV=1	836; Zinc knuckle CX2CX4HX4C	
18153373	18154173	Cil_15G_00864V2	BRI1/IRAK4	Q9ASS4/370/Y5838_ARATH Probably inactive leucine-rich repeat receptor-like protein kinase At5g48380 OS=Arabidopsis thaliana GN=At5g48380 PE=1 SV=1	K04733/IRAK4/receptor-associated	A5B9Q7/371/A5B9Q7_VITVI Putative uncharacterized protein OS=Vitis vinifera GN=VITISV_037939 PE=4 SV=1	NA	NA
18159341	18159832	Cil_15G_00865V2	NA	NA	NA	F6HSM6/139/F6HSM6_VITVI Putative uncharacterized protein OS=Vitis vinifera GN=VIT_14s0006g01930 PE=4 SV=1	NA	NA

18176361	18176826	Cil_15G_00866V2	NA			NA	NA	A5BB12/139/A5BB12_VITVI Putative uncharacterized protein OS=Vitis vinifera GN=VITISV_024715 PE=4 SV=1	NA	NA
18184400	18189436	Cil_15G_00867V2	NA			NA	NA	A0A067D926/225/A0A067D926_CITSI Uncharacterized protein (Fragment) OS=Citrus sinensis GN=CISIN_1g041788mg PE=4 SV=1	NA	NA
18241674	18242981	Cil_15G_00868V2	INV	0.193	2.505	Q9SD53/457/Y3720_ARATH UPF0481 protein At3g47200 OS=Arabidopsis thaliana	K01193/INV,/beta-fructofuranosidase	A0A067JDW8/339/A0A067JDW8_JATCU Uncharacterized protein OS=Jatropha curcas	1/1/IPR004158; Protein of unknown function DUF247, plant	NA

							GN=At3g47200 PE=2 SV=1		GN=JCGZ_25892 PE=4 SV=1		
	18276084	18280132	Cil_15G_00869V2	NA			NA	K03549/kup/system	M5WQE3/108/M5WQE3_PRUPE Uncharacterized protein (Fragment) OS=Prunus persica GN=PRUPE_ppa015123m2g PE=4 SV=1	1/1/IPR029480; Transposase-associated domain	NA
	18284403	18286129	Cil_15G_00870V2	NA			NA	NA	A5AEV7/1238/A5AEV7_VITVI Putative uncharacterized protein OS=Vitis vinifera GN=VITISV_018031 PE=4 SV=1	1/1/IPR004252; Probable transposase, Ptta/En/Spm, plant	NA
	23000491	23012641	Cil_15G_01037V2	GBE	0.179	1.541	O82261/607/DEGP2_ARATH Protease Do-like 2, chloroplastic OS=Arabidopsis thaliana	K00700/GBE1,/1,4-alpha-glucan	A0A061DY29/633/A0A061DY29_THECC DEGP protease 2 isoform 1 OS=Theobroma	3/IPR001478; PDZ domain/IPR015724; Serine endopeptidase DegP2	GO:0004252; serine-type endopeptidase activity; function|GO:0005515; protein

						GN=DEGP2 PE=1 SV=2		cacao GN=TCM_004530 PE=4 SV=1		binding; function|GO:0006508; proteolysis; process
	23013451	23015300	Cil_15G_01038V2	YUC10/YUCCA		Q9FVQ0/377/YUC10_ARATH Probable indole-3-pyruvate monooxygenase YUCCA10 OS=Arabidopsis thaliana GN=YUC10 PE=2 SV=1	K11816/YUCCA/monooxygenase	M5VJ66/384/M5VJ66_PRUPE Uncharacterized protein OS=Prunus persica GN=PRUPE_ppa007054mg PE=4 SV=1	1/1/IPR020946; Flavin monooxygenase-like	GO:0004499; N,N-dimethylaniline monooxygenase activity; function|GO:0050660; flavin adenine dinucleotide binding; function|GO:0050661; NADP binding; function|GO:0055114; oxidation-reduction process; process
	23021173	23024683	Cil_15G_01039V2	KIP1-like		Q66GR8/242/NET3A_ARATH Protein NETWORKED 3A OS=Arabidopsis	K20478/GOLGB1/subfamily	A0A067H6A4/289/A0A067H6A4_CITSI Uncharacterized protein OS=Citrus sinensis	1/1/IPR011684; KIP1-like	NA

					thaliana GN=NET3A PE=2 SV=1		GN=CISIN_1g048255mg PE=4 SV=1		
23088448	23104124	Cil_15G_01040V2	NHX2		Q56XP4/537/NHX2_ARATH Sodium/hydrogen exchanger 2 OS=Arabidopsis thaliana GN=NHX2 PE=2 SV=2	K14724/SLC9A8,/solute	A0A0B0NMF6/521/A0A0B0NMF6_GOSAR Sodium/hydrogen exchanger OS=Gossypium arboreum GN=F383_00537 PE=3 SV=1	4/IPR018422; Cation/H+ exchanger, CPA1 family/IPR029872; Na+/H+ exchanger NHX -type, plants	GO:0005774; vacuolar membrane; component|GO:0005886; plasma membrane; component|GO:0006812; cation transport; process|GO:0006814; sodium ion transport; process|GO:0006885; regulation of pH; process|GO:0009651; response to salt stress; process|GO:0015299; solute:proton antiporter activity; function|GO:0015385; sodium:proton

antiporter activity; function|GO:0016021; integral component of membrane; component|GO:0055075; potassium ion homeostasis; process|GO:0055085; transmembrane transport; process