Supplemental Table 4. *C. unshiu* specific gene groups

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0019413	0	3	0	Hypothetical protein (2); Putative DNA/RNA polymerases superfamily protein-like (1)	nucleic acid binding [GO:0003676 molecular_function] (3); DNA integration [GO:0015074 biological_process] (1)	Ribonuclease H-like domain [IPR012337] (3); Integrase, catalytic core [IPR001584] (1)	-	C_unshiu_00928_mRNA_5.1,C_unshiu_01628_mRNA_2.1,C_unshiu_02433_mRNA_5.1	-
GF0025479	0	2	0	NB-ARC domain-containing disease resistance protein (2)	ADP binding [GO:0043531 molecular_function] (2)	NB-ARC [IPR002182] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2)	-	C_unshiu_00340_mRNA_24.1,C_unshiu_00950_mRNA_3.1	-
GF0043265	0	1	0	Hypothetical protein (1)			-	C_unshiu_03147_mRNA_1.1	-
GF0043264	0	1	0	ABC transporter G family member 16 (1)	ATPase activity, coupled to transmembrane movement of substances [GO:0042626 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1); transport [GO:0006810 biological_process] (1); membrane [GO:0016020 cellular_component] (1)	ABC-2 type transporter [IPR013525] (1); CDR ABC transporter [IPR010929] (1)	-	C_unshiu_03142_mRNA_2.1	-
GF0043263	0	1	0	Hypothetical protein (1)			-	C_unshiu_03142_mRNA_1.1	-
GF0043262	0	1	0	Hypothetical protein (1)			-	C_unshiu_03135_mRNA_1.1	-
GF0043261	0	1	0	Hypothetical protein (1)			-	C_unshiu_03134_mRNA_1.1	-
GF0043260	0	1	0	Ankyrin repeat protein (1)		PGG domain [IPR026961] (1); Ankyrin repeat-containing domain [IPR020683] (1)	-	C_unshiu_03133_mRNA_1.1	-
GF0043259	0	1	0	Hypothetical protein (1)			-	C_unshiu_03132_mRNA_1.1	-
GF0043258	0	1	0	Hypothetical protein (1)			-	C_unshiu_03122_mRNA_1.1	-
GF0043257	0	1	0	DNA-directed RNA polymerase, alpha subunit (1)	transcription, DNA-templated [GO:0006351 biological_process] (1); protein dimerization activity [GO:0046983 molecular_function] (1); DNA-directed RNA polymerase activity [GO:0003899 molecular_function] (1)	DNA-directed RNA polymerase, RBP11-like dimerisation domain [IPR009025] (1); DNA-directed RNA polymerase, insert domain [IPR011262] (1); DNA-directed RNA polymerase, RpoA/D/Rpb3-type [IPR011263] (1)	-	C_unshiu_03120_mRNA_1.1	-
GF0043256	0	1	0	Hypothetical protein (1)			-	C_unshiu_03112_mRNA_1.1	-
GF0043255	0	1	0	Hypothetical protein (1)			-	C_unshiu_03110_mRNA_1.1	-
GF0043254	0	1	0	Metacaspase 3, putative isoform 2 (1)		Caspase-like domain [IPR029030] (1)	-	C_unshiu_03108_mRNA_1.1	-
GF0043253	0	1	0	CDNA clone:002-110-H12, full insert sequence (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_03106_mRNA_2.1	-
GF0043252	0	1	0	Hypothetical protein (1)			-	C_unshiu_03106_mRNA_1.1	-
GF0043251	0	1	0	Hypothetical protein (1)	intracellular [GO:0005622 cellular_component] (1); zinc ion binding [GO:0008270 molecular_function] (1)	B-box-type zinc finger [IPR000315] (1)	-	C_unshiu_03104_mRNA_1.1	-
GF0043250	0	1	0	Hypothetical protein (1)			-	C_unshiu_03102_mRNA_2.1	-
GF0043249	0	1	0	Hypothetical protein (1)			-	C_unshiu_03102_mRNA_1.1	-
GF0043248	0	1	0	Sec14 cytosolic factor (1)		CRAL-TRIO lipid binding domain [IPR001251] (1); CRAL/TRIO, N-terminal domain [IPR011074] (1)	-	C_unshiu_03096_mRNA_1.1	-
GF0043247	0	1	0	Hypothetical protein (1)			-	C_unshiu_03093_mRNA_2.1	-
GF0043246	0	1	0	Hypothetical protein (1)		Bulb-type lectin domain [IPR001480] (1)	-	C_unshiu_03092_mRNA_1.1	-
GF0043245	0	1	0	Hypothetical protein (1)			-	C_unshiu_03091_mRNA_1.1	-
GF0043244	0	1	0	LRR receptor-like kinase (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_03090_mRNA_1.1	-
GF0043243	0	1	0	Mutator-like transposase (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Transposase, MuDR, plant [IPR004332] (1); MULE transposase domain [IPR018289] (1); Zinc finger, PMZ-type [IPR006564] (1); Zinc finger, SWIM-type [IPR007527] (1)	-	C_unshiu_03089_mRNA_2.1	-
GF0043242	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_03088_mRNA_2.1	-
GF0043241	0	1	0	Hypothetical protein (1)			-	C_unshiu_03088_mRNA_1.1	-
GF0043240	0	1	0	Hypothetical protein (1)			-	C_unshiu_03086_mRNA_2.1	-
GF0043239	0	1	0	Hypothetical protein (1)			-	C_unshiu_03084_mRNA_1.1	-
GF0043238	0	1	0	Hypothetical protein (1)			-	C_unshiu_03082_mRNA_1.1	-
GF0043237	0	1	0	Hypothetical protein (1)			-	C_unshiu_03080_mRNA_1.1	-
GF0043236	0	1	0	Hypothetical protein (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1)	Glycoside hydrolase, catalytic domain [IPR013781] (1)	-	C_unshiu_03074_mRNA_1.1	-
GF0043235	0	1	0	Hypothetical protein (1)			-	C_unshiu_03069_mRNA_1.1	-
GF0043234	0	1	0	Hypothetical protein (1)		Alpha/Beta hydrolase fold [IPR029058] (1)	-	C_unshiu_03067_mRNA_2.1	-
GF0043233	0	1	0	Disease resistance-responsive, dirigent domain protein (1)		Plant disease resistance response protein [IPR004265] (1)	-	C_unshiu_03063_mRNA_1.1	-
GF0043232	0	1	0	C globular stage, putative (1)		Aminotransferase-like, plant mobile domain [IPR019557] (1); Protein of unknown function DUF716 (TMEM45) [IPR006904] (1)	-	C_unshiu_03061_mRNA_2.1	-
GF0043231	0	1	0	Hypothetical protein (1)			-	C_unshiu_03059_mRNA_2.1	-
GF0043230	0	1	0	Hypothetical protein (1)			-	C_unshiu_03059_mRNA_1.1	-
GF0043229	0	1	0	Hypothetical protein (1)			-	C_unshiu_03058_mRNA_2.1	-
GF0043228	0	1	0	Hypothetical protein (1)			-	C_unshiu_03057_mRNA_2.1	-
GF0043227	0	1	0	Probably inactive leucine-rich repeat receptor-like protein kinase (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_03051_mRNA_1.1	-
GF0043226	0	1	0	Hypothetical protein (1)		Retroviral aspartyl protease [IPR013242] (1)	-	C_unshiu_03050_mRNA_2.1	-
GF0043225	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); nucleotide binding [GO:0000166 molecular_function] (1)	Nucleotide-binding alpha-beta plait domain [IPR012677] (1); RNA recognition motif domain [IPR000504] (1)	-	C_unshiu_03047_mRNA_2.1	-
GF0043224	0	1	0	COBW domain-containing protein 1 (1)		CobW/HypB/UreG domain [IPR003495] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_03046_mRNA_1.1	-
GF0043223	0	1	0	Hypothetical protein (1)		P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_03045_mRNA_1.1	-
GF0043222	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF1985 [IPR015410] (1)	-	C_unshiu_03042_mRNA_1.1	-
GF0043221	0	1	0	Hypothetical protein (1)		Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_03039_mRNA_1.1	-
GF0043220	0	1	0	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_03038_mRNA_1.1	-
GF0043219	0	1	0	Ankyrin repeat family protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat-containing domain [IPR020683] (1); Ankyrin repeat [IPR002110] (1)	-	C_unshiu_03034_mRNA_3.1	-
GF0043218	0	1	0	Hypothetical protein (1)			-	C_unshiu_03034_mRNA_1.1	-
GF0043217	0	1	0	Hypothetical protein (1)			-	C_unshiu_03033_mRNA_2.1	-
GF0043216	0	1	0	Polygalacturonase (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1); polygalacturonase activity [GO:0004650 molecular_function] (1)	Pectin lyase fold [IPR012334] (1); Pectin lyase fold/virulence factor [IPR011050] (1); Glycoside hydrolase, family 28 [IPR000743] (1); Parallel beta-helix repeat [IPR006626] (1)	-	C_unshiu_03033_mRNA_1.1	-
GF0043215	0	1	0	Hypothetical protein (1)		Arabidopsis retrotransposon Orf1 [IPR004312] (1)	-	C_unshiu_03031_mRNA_1.1	-
GF0043214	0	1	0	Hypothetical protein (1)			-	C_unshiu_03027_mRNA_2.1	-
GF0043213	0	1	0	Hypothetical protein (1)		Alpha/Beta hydrolase fold [IPR029058] (1)	-	C_unshiu_03027_mRNA_1.1	-
GF0043212	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	WD40/YVTN repeat-like-containing domain [IPR015943] (1); WD40-repeat-containing domain [IPR017986] (1)	-	C_unshiu_03025_mRNA_2.1	-
GF0043211	0	1	0	Hypothetical protein (1)			-	C_unshiu_03022_mRNA_1.1	-
GF0043210	0	1	0	Defective in cullin neddylation protein (1)		Potentiating neddylation domain [IPR005176] (1); Defective-in-cullin neddylation protein [IPR014764] (1)	-	C_unshiu_03019_mRNA_2.1	-
GF0043209	0	1	0	Miraculin (1)	endopeptidase inhibitor activity [GO:0004866 molecular_function] (1)	Kunitz inhibitor ST1-like [IPR011065] (1); Proteinase inhibitor I3, Kunitz legume [IPR002160] (1)	-	C_unshiu_03016_mRNA_1.1	-
GF0043208	0	1	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	-	C_unshiu_03012_mRNA_3.1	-
GF0043207	0	1	0	Putative GMP synthase (glutamine-hydrolyzing) (1)	DNA-3-methyladenine glycosylase activity [GO:0008725 molecular_function] (1); catalytic activity [GO:0003824 molecular_function] (1); DNA repair [GO:0006281 biological_process] (1); base-excision repair [GO:0006284 biological_process] (1)	Methyladenine glycosylase [IPR005019] (1); DNA glycosylase [IPR011257] (1)	-	C_unshiu_03011_mRNA_2.1	-
GF0043206	0	1	0	Hypothetical protein (1)			-	C_unshiu_03005_mRNA_4.1	-
GF0043205	0	1	0	Hypothetical protein (1)			-	C_unshiu_03005_mRNA_1.1	-
GF0043204	0	1	0	Hypothetical protein (1)			-	C_unshiu_03004_mRNA_1.1	-
GF0043203	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_03003_mRNA_1.1	-
GF0043202	0	1	0	Hypothetical protein (1)		Major facilitator superfamily domain [IPR020846] (1)	-	C_unshiu_03000_mRNA_1.1	-
GF0043201	0	1	0	Hypothetical protein (1)		Rab-GTPase-TBC domain [IPR000195] (1)	-	C_unshiu_02998_mRNA_1.1	-
GF0043200	0	1	0	Hypothetical protein (1)			-	C_unshiu_02996_mRNA_1.1	-
GF0043199	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, SWIM-type [IPR007527] (1); Transposase, MuDR, plant [IPR004332] (1); Zinc finger, PMZ-type [IPR006564] (1)	-	C_unshiu_02993_mRNA_1.1	-
GF0043198	0	1	0	Hypothetical protein (1)			-	C_unshiu_02991_mRNA_1.1	-
GF0043197	0	1	0	Hypothetical protein (1)	iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Cytochrome P450 [IPR001128] (1); Cytochrome P450, conserved site [IPR017972] (1); Cytochrome P450, E-class, group I [IPR002401] (1)	-	C_unshiu_02988_mRNA_2.1	-
GF0043196	0	1	0	Hypothetical protein (1)			-	C_unshiu_02988_mRNA_1.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0043195	0	1	0	Hypothetical protein (1)	transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1); endoplasmic reticulum [GO:0005783 cellular_component] (1); integral component of membrane [GO:0016021 cellular_component] (1)	Glycosyltransferase, ALG3 [IPR007873] (1)	-	C_unshiu_02985_mRNA_1.1	-
GF0043194	0	1	0	SH3 domain protein (1)			-	C_unshiu_02984_mRNA_1.1	-
GF0043193	0	1	0	Ubiquitin-like protein ATG12 (1)	cytoplasm [GO:0005737 cellular_component] (1); autophagosome assembly [GO:0000045 biological_process] (1)	Ubiquitin-related domain [IPR029071] (1); Ubiquitin-like protein Atg12 [IPR007242] (1)	-	C_unshiu_02983_mRNA_1.1	-
GF0043192	0	1	0	Disease resistance protein (TIR-NBS-LRR class) (1)	signal transduction [GO:0007165 biological_process] (1); protein binding [GO:0005515 molecular_function] (1)	Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1)	-	C_unshiu_02982_mRNA_1.1	-
GF0043191	0	1	0	Hypothetical protein (1)		Protein-tyrosine phosphatase-like [IPR029021] (1); Myotubularin family [IPR030564] (1); Myotubularin-like phosphatase domain [IPR010569] (1)	-	C_unshiu_02981_mRNA_2.1	-
GF0043190	0	1	0	Hypothetical protein (1)			-	C_unshiu_02979_mRNA_2.1	-
GF0043189	0	1	0	Retinitis pigmentosa 1-like 1 protein, putative (1)			-	C_unshiu_02977_mRNA_2.1	-
GF0043188	0	1	0	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_02976_mRNA_3.1	-
GF0043187	0	1	0	Hypothetical protein (1)	transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); sequence-specific DNA binding [GO:0043565 molecular_function] (1)	Basic-leucine zipper domain [IPR004827] (1)	-	C_unshiu_02975_mRNA_4.1	-
GF0043186	0	1	0	Hypothetical protein (1)			-	C_unshiu_02975_mRNA_2.1	-
GF0043185	0	1	0	Monosacharide transport protein (1)			-	C_unshiu_02975_mRNA_1.1	-
GF0043184	0	1	0	Fructokinase (1)	phosphotransferase activity, alcohol group as acceptor [GO:0016773 molecular_function] (1)	Carbohydrate kinase PfkB [IPR011611] (1); Carbohydrate/puine kinase, PfkB, conserved site [IPR002173] (1); Ribokinase-like [IPR029056] (1)	-	C_unshiu_02973_mRNA_1.1	-
GF0043183	0	1	0	Hypothetical protein (1)			-	C_unshiu_02968_mRNA_4.1	-
GF0043182	0	1	0	Lipid transfer protein (1)	lipid binding [GO:0008289 molecular_function] (1); lipid transport [GO:0006869 biological_process] (1)	Plant lipid transfer protein/Par allergen [IPR000528] (1); Bifunctional inhibitor/plant lipid transfer protein/seed storage helical domain [IPR016140] (1)	-	C_unshiu_02968_mRNA_2.1	-
GF0043181	0	1	0	Hypothetical protein (1)			-	C_unshiu_02966_mRNA_3.1	-
GF0043180	0	1	0	Hypothetical protein (1)			-	C_unshiu_02965_mRNA_3.1	-
GF0043179	0	1	0	Hypothetical protein (1)		Plant disease resistance response protein [IPR004265] (1)	-	C_unshiu_02965_mRNA_2.1	-
GF0043178	0	1	0	Hypothetical protein (1)	transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (1)	Chloramphenicol acetyltransferase-like domain [IPR023213] (1); Transferase [IPR003480] (1)	-	C_unshiu_02961_mRNA_1.1	-
GF0043177	0	1	0	Hypothetical protein (1)			-	C_unshiu_02960_mRNA_1.1	-
GF0043176	0	1	0	Hypothetical protein (1)			-	C_unshiu_02958_mRNA_1.1	-
GF0043175	0	1	0	Hypothetical protein (1)	cellulose microfibril organization [GO:0010215 biological_process] (1); anchored component of membrane [GO:0031225 cellular_component] (1); cell growth [GO:0016049 biological_process] (1)	COBRA, plant [IPR006918] (1)	-	C_unshiu_02955_mRNA_3.1	-
GF0043174	0	1	0	Hypothetical protein (1)			-	C_unshiu_02955_mRNA_2.1	-
GF0043173	0	1	0	Neutral alpha-glucosidase (1)	hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1)	Glycoside hydrolase family 31 [IPR000322] (1); Glycoside hydrolase superfamily [IPR017853] (1)	-	C_unshiu_02954_mRNA_1.1	-
GF0043172	0	1	0	Hypothetical protein (1)			-	C_unshiu_02950_mRNA_2.1	-
GF0043171	0	1	0	Hypothetical protein (1)			-	C_unshiu_02949_mRNA_1.1	-
GF0043170	0	1	0	Hypothetical protein (1)			-	C_unshiu_02947_mRNA_2.1	-
GF0043169	0	1	0	Hypothetical protein (1)	phosphoric ester hydrolase activity [GO:0042578 molecular_function] (1)	SAC domain [IPR002013] (1)	-	C_unshiu_02947_mRNA_1.1	-
GF0043168	0	1	0	FATTY ACID BIOSYNTHESIS 1 family protein (1)	metabolic process [GO:0008152 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1)	Beta-ketoacyl synthase, N-terminal [IPR014030] (1); Beta-ketoacyl synthase, active site [IPR018201] (1); Polyketide synthase, beta-ketoacyl synthase domain [IPR020841] (1); Thiolase-like [IPR016039] (1)	-	C_unshiu_02944_mRNA_3.1	-
GF0043167	0	1	0	Hypothetical protein (1)			-	C_unshiu_02942_mRNA_1.1	-
GF0043166	0	1	0	Hypothetical protein (1)		Myb/SANT-like domain [IPR024752] (1)	-	C_unshiu_02940_mRNA_2.1	-
GF0043165	0	1	0	Hypothetical protein (1)			-	C_unshiu_02940_mRNA_1.1	-
GF0043164	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1); ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein serine/threonine kinase activity [GO:0004674 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1)	EGF-like domain [IPR000742] (1); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); EGF-like, conserved site [IPR013032] (1); Wall-associated receptor kinase [IPR013695] (1)	-	C_unshiu_02939_mRNA_1.1	-
GF0043163	0	1	0	Hypothetical protein (1)			-	C_unshiu_02937_mRNA_3.1	-
GF0043162	0	1	0	Hypothetical protein (1)	histone binding [GO:0042393 molecular_function] (1)	SRA-YDG [IPR003105] (1); PUA-like domain [IPR015947] (1)	-	C_unshiu_02937_mRNA_2.1	-
GF0043161	0	1	0	Hypothetical protein (1)		Expansin/pollen allergen, DPBB domain [IPR007112] (1); RlpA-like double-psi beta-barrel domain [IPR009009] (1)	-	C_unshiu_02937_mRNA_1.1	-
GF0043160	0	1	0	Carboxypeptidase (1)	proteolysis [GO:0006508 biological_process] (1); serine-type carboxypeptidase activity [GO:0004185 molecular_function] (1)	Peptidase S10, serine carboxypeptidase [IPR001563] (1); Serine carboxypeptidases, histidine active site [IPR033124] (1); Alpha/Beta hydrolase fold [IPR029058] (1); Serine carboxypeptidase, serine active site [IPR018202] (1)	-	C_unshiu_02935_mRNA_1.1	-
GF0043159	0	1	0	Ankyrin repeat family protein, putative (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat [IPR002110] (1); Ankyrin repeat-containing domain [IPR020683] (1)	-	C_unshiu_02933_mRNA_1.1	-
GF0043158	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	F-box domain [IPR001810] (1)	-	C_unshiu_02932_mRNA_2.1	-
GF0043157	0	1	0	Protein phosphatase 1 regulatory subunit 7 (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_02932_mRNA_1.1	-
GF0043156	0	1	0	Hypothetical protein (1)			-	C_unshiu_02931_mRNA_1.1	-
GF0043155	0	1	0	Hypothetical protein (1)	nucleus [GO:0005634 cellular_component] (1); DNA binding [GO:0003677 molecular_function] (1)	Methyl-CpG DNA binding [IPR001739] (1); DNA-binding domain [IPR016177] (1)	-	C_unshiu_02930_mRNA_3.1	-
GF0043154	0	1	0	CCD (1)	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen [GO:0016702 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Carotenoid oxygenase [IPR004294] (1)	-	C_unshiu_02929_mRNA_1.1	-
GF0043153	0	1	0	Hypothetical protein (1)			-	C_unshiu_02924_mRNA_1.1	-
GF0043152	0	1	0	Hypothetical protein (1)			-	C_unshiu_02923_mRNA_1.1	-
GF0043151	0	1	0	Hypothetical protein (1)			-	C_unshiu_02922_mRNA_1.1	-
GF0043150	0	1	0	Hypothetical protein (1)			-	C_unshiu_02921_mRNA_5.1	-
GF0043149	0	1	0	Hypothetical protein (1)			-	C_unshiu_02921_mRNA_4.1	-
GF0043148	0	1	0	Hypothetical protein (1)			-	C_unshiu_02921_mRNA_1.1	-
GF0043147	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_02917_mRNA_2.1	-
GF0043146	0	1	0	Putative disease resistance protein RGA4 (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_02917_mRNA_1.1	-
GF0043145	0	1	0	Hypothetical protein (1)			-	C_unshiu_02916_mRNA_1.1	-
GF0043144	0	1	0	Hypothetical protein (1)		Gag-polypeptide of LTR copia-type [IPR029472] (1)	-	C_unshiu_02914_mRNA_1.1	-
GF0043143	0	1	0	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_02912_mRNA_1.1	-
GF0043142	0	1	0	Hypothetical protein (1)			-	C_unshiu_02909_mRNA_1.1	-
GF0043141	0	1	0	G-type lectin S-receptor-like serine/threonine-protein kinase RLK1 (1)	ATP binding [GO:0005524 molecular_function] (1); recognition of pollen [GO:0048544 biological_process] (1)	PAN/Apple domain [IPR003609] (1); Bulb-type lectin domain [IPR001480] (1); S-locus glycoprotein domain [IPR000858] (1); Protein kinase, ATP binding site [IPR017441] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_02905_mRNA_1.1	-
GF0043140	0	1	0	Hypothetical protein (1)			-	C_unshiu_02904_mRNA_3.1	-
GF0043139	0	1	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Peptidase A2A, retrovirus, catalytic [IPR001995] (1); Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_02904_mRNA_1.1	-
GF0043138	0	1	0	Hypothetical leucine rich repeat protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_02903_mRNA_1.1	-
GF0043137	0	1	0	Hypothetical protein (1)	nucleus [GO:0005634 cellular_component] (1)	YLP motif-containing protein 1 [IPR026314] (1)	-	C_unshiu_02902_mRNA_1.1	-
GF0043136	0	1	0	Hypothetical protein (1)			-	C_unshiu_02900_mRNA_1.1	-
GF0043135	0	1	0	Hypothetical protein (1)			-	C_unshiu_02899_mRNA_1.1	-
GF0043134	0	1	0	Hypothetical protein (1)			-	C_unshiu_02897_mRNA_1.1	-
GF0043133	0	1	0	Hypothetical protein (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1); phosphotransferase activity, alcohol group as acceptor [GO:0016773 molecular_function] (1)	Carbohydrate kinase, FGGY, N-terminal [IPR018484] (1); Carbohydrate kinase, FGGY, C-terminal [IPR018485] (1)	-	C_unshiu_02896_mRNA_2.1	-
GF0043132	0	1	0	UPF0481 plant-like protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	C_unshiu_02894_mRNA_2.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0043131	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_02890_mRNA_1.1	-
GF0043130	0	1	0	Hypothetical protein (1)	extracellular region [GO:0005576 cellular_component] (1); growth factor activity [GO:0008083 molecular_function] (1); cell proliferation [GO:0008283 biological_process] (1)	Phytosulfokine [IPR009438] (1)	-	C_unshiu_02889_mRNA_4.1	-
GF0043129	0	1	0	Transcriptional activator DEMETER-like protein (1)	4 iron, 4 sulfur cluster binding [GO:0051539 molecular_function] (1)	Endonuclease III-like, iron-sulphur cluster loop motif [IPR003651] (1); Demeter, RRM-fold domain [IPR028925] (1); Helix-turn-helix, base-excision DNA repair, C-terminal [IPR023170] (1); Permuted single zf-CXXC unit [IPR028924] (1)	-	C_unshiu_02889_mRNA_1.1	-
GF0043128	0	1	0	Hypothetical protein (1)			-	C_unshiu_02887_mRNA_1.1	-
GF0043127	0	1	0	Wall-associated receptor kinase 2 (1)	polysaccharide binding [GO:0030247 molecular_function] (1)	Wall-associated receptor kinase, galacturonan-binding domain [IPR025287] (1)	-	C_unshiu_02886_mRNA_2.1	-
GF0043126	0	1	0	Hypothetical protein (1)	hydrolase activity [GO:0016787 molecular_function] (1)	Survival protein SurE-like phosphatase/nucleotidase [IPR002828] (1)	-	C_unshiu_02883_mRNA_1.1	-
GF0043125	0	1	0	Hypothetical protein (1)		Glycosyl transferase, family 1 [IPR001296] (1)	-	C_unshiu_02881_mRNA_1.1	-
GF0043124	0	1	0	Hypothetical protein (1)	nucleotide binding [GO:0000166 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1); metal ion binding [GO:0046872 molecular_function] (1)	P-type ATPase, transmembrane domain [IPR023298] (1); Cation-transporting P-type ATPase, C-terminal [IPR006068] (1); P-type ATPase, cytoplasmic domain N [IPR023299] (1); P-type ATPase [IPR001757] (1); P-type ATPase, phosphorylation site [IPR018303] (1); P-type ATPase, A domain [IPR008250] (1)	-	C_unshiu_02879_mRNA_1.1	-
GF0043123	0	1	0	Hypothetical protein (1)			-	C_unshiu_02877_mRNA_3.1	-
GF0043122	0	1	0	Hypothetical protein (1)			-	C_unshiu_02877_mRNA_1.1	-
GF0043121	0	1	0	Hypothetical protein (1)			-	C_unshiu_02875_mRNA_1.1	-
GF0043120	0	1	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_02873_mRNA_2.1	-
GF0043119	0	1	0	Putative mitochondrial chaperone BCS1-B (1)	ATP binding [GO:0005524 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); AAA-type ATPase, N-terminal domain [IPR025753] (1); ATPase, AAA-type, core [IPR003959] (1); AAA+ ATPase domain [IPR003593] (1)	-	C_unshiu_02871_mRNA_1.1	-
GF0043118	0	1	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_02870_mRNA_1.1	-
GF0043117	0	1	0	Hypothetical protein (1)	metabolic process [GO:0008152 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1)	Alkaline phosphatase-like, alpha/beta/alpha [IPR017849] (1); Alkaline-phosphatase-like, core domain [IPR017850] (1)	-	C_unshiu_02869_mRNA_1.1	-
GF0043116	0	1	0	Hypothetical protein (1)			-	C_unshiu_02868_mRNA_1.1	-
GF0043115	0	1	0	Hypothetical protein (1)			-	C_unshiu_02867_mRNA_2.1	-
GF0043114	0	1	0	Hypothetical protein (1)			-	C_unshiu_02867_mRNA_1.1	-
GF0043113	0	1	0	Putative class I peptide chain release factor-like (1)	translation release factor activity [GO:0003747 molecular_function] (1); translational termination [GO:0006415 biological_process] (1)	Peptide chain release factor class I/class II [IPR000352] (1); Double-stranded RNA-binding domain [IPR014720] (1)	-	C_unshiu_02866_mRNA_1.1	-
GF0043112	0	1	0	Hypothetical protein (1)			-	C_unshiu_02865_mRNA_1.1	-
GF0043111	0	1	0	UPF0481 protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	C_unshiu_02864_mRNA_1.1	-
GF0043110	0	1	0	Hypothetical protein (1)	microtubule motor activity [GO:0003777 molecular_function] (1); microtubule-based movement [GO:0007018 biological_process] (1)	NPK1-activating kinesin-like protein, C-terminal [IPR021881] (1); Kinesin-like protein [IPR027640] (1)	-	C_unshiu_02863_mRNA_4.1	-
GF0043109	0	1	0	Hypothetical protein (1)			-	C_unshiu_02863_mRNA_3.1	-
GF0043108	0	1	0	Hypothetical protein (1)			-	C_unshiu_02863_mRNA_1.1	-
GF0043107	0	1	0	Hypothetical protein (1)			-	C_unshiu_02860_mRNA_2.1	-
GF0043106	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			-	C_unshiu_02860_mRNA_1.1	-
GF0043105	0	1	0	Hypothetical protein (1)			-	C_unshiu_02858_mRNA_1.1	-
GF0043104	0	1	0	Hypothetical protein (1)			-	C_unshiu_02857_mRNA_3.1	-
GF0043103	0	1	0	Miraculin (1)	endopeptidase inhibitor activity [GO:0004866 molecular_function] (1)	Proteinase inhibitor I3, Kunitz legume [IPR002160] (1); Kunitz inhibitor ST1-like [IPR011065] (1)	-	C_unshiu_02855_mRNA_3.1	-
GF0043102	0	1	0	Hypothetical protein (1)			-	C_unshiu_02855_mRNA_2.1	-
GF0043101	0	1	0	Hypothetical protein (1)			-	C_unshiu_02855_mRNA_1.1	-
GF0043100	0	1	0	Hypothetical protein (1)		EF-hand domain pair [IPR011992] (1)	-	C_unshiu_02854_mRNA_1.1	-
GF0043099	0	1	0	Hypothetical protein (1)			-	C_unshiu_02851_mRNA_1.1	-
GF0043098	0	1	0	Hypothetical protein (1)			-	C_unshiu_02847_mRNA_1.1	-
GF0043097	0	1	0	Pentatricopeptide (PPR) repeat protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	C_unshiu_02846_mRNA_2.1	-
GF0043096	0	1	0	Hypothetical protein (1)			-	C_unshiu_02841_mRNA_2.1	-
GF0043095	0	1	0	Disease resistance protein RPS2 (1)	ADP binding [GO:0043531 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_02840_mRNA_1.1	-
GF0043094	0	1	0	MFS transporter (1)	molybdate ion transmembrane transporter activity [GO:0015098 molecular_function] (1); molybdate ion transport [GO:0015689 biological_process] (1); integral component of membrane [GO:0016021 cellular_component] (1)	Molybdate-anion transporter [IPR008509] (1); Major facilitator superfamily domain [IPR020846] (1)	-	C_unshiu_02839_mRNA_1.1	-
GF0043093	0	1	0	Hypothetical protein (1)			-	C_unshiu_02832_mRNA_3.1	-
GF0043092	0	1	0	Mitotic checkpoint protein, putative (1)	protein serine/threonine kinase activity [GO:0004674 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Protein kinase-like domain [IPR011009] (1); S-locus receptor kinase, C-terminal [IPR021820] (1); WD40/YVTN repeat-like-containing domain [IPR015943] (1); WD40-repeat-containing domain [IPR017986] (1)	-	C_unshiu_02831_mRNA_1.1	-
GF0043091	0	1	0	Anaphase-promoting complex subunit 6 (1)	protein binding [GO:0005515 molecular_function] (1)	Tetratricopeptide repeat 2 [IPR013105] (1); Tetratricopeptide-like helical domain [IPR011990] (1); Tetratricopeptide repeat-containing domain [IPR013026] (1); Tetratricopeptide repeat [IPR019734] (1)	-	C_unshiu_02830_mRNA_2.1	-
GF0043090	0	1	0	Hypothetical protein (1)			-	C_unshiu_02826_mRNA_2.1	-
GF0043089	0	1	0	Hypothetical protein (1)		ER membrane protein complex subunit 10 [IPR029615] (1)	-	C_unshiu_02826_mRNA_1.1	-
GF0043088	0	1	0	Hypothetical protein (1)		HotDog domain [IPR029069] (1)	-	C_unshiu_02825_mRNA_4.1	-
GF0043087	0	1	0	Hypothetical protein (1)			-	C_unshiu_02825_mRNA_3.1	-
GF0043086	0	1	0	Hypothetical protein (1)			-	C_unshiu_02825_mRNA_1.1	-
GF0043085	0	1	0	Hypothetical protein (1)			-	C_unshiu_02824_mRNA_3.1	-
GF0043084	0	1	0	Hypothetical protein (1)			-	C_unshiu_02823_mRNA_2.1	-
GF0043083	0	1	0	Hypothetical protein (1)			-	C_unshiu_02821_mRNA_1.1	-
GF0043082	0	1	0	Hypothetical protein (1)			-	C_unshiu_02820_mRNA_3.1	-
GF0043081	0	1	0	Hypothetical protein (1)			-	C_unshiu_02818_mRNA_2.1	-
GF0043080	0	1	0	Hypothetical protein (1)			-	C_unshiu_02818_mRNA_1.1	-
GF0043079	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			-	C_unshiu_02816_mRNA_1.1	-
GF0043078	0	1	0	Hypothetical protein (1)			-	C_unshiu_02815_mRNA_3.1	-
GF0043077	0	1	0	Acetyltransferase (GNAT) domain protein (1)	N-acetyltransferase activity [GO:0008080 molecular_function] (1)	Acyl-CoA N-acyltransferase [IPR016181] (1); GNAT domain [IPR000182] (1)	-	C_unshiu_02815_mRNA_1.1	-
GF0043076	0	1	0	Hypothetical protein (1)			-	C_unshiu_02814_mRNA_1.1	-
GF0043075	0	1	0	Hypothetical protein (1)			-	C_unshiu_02812_mRNA_2.1	-
GF0043074	0	1	0	Hypothetical protein (1)			-	C_unshiu_02812_mRNA_1.1	-
GF0043073	0	1	0	Zinc knuckle family protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_02811_mRNA_1.1	-
GF0043072	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, PMZ-type [IPR006564] (1); Zinc finger, SWIM-type [IPR007527] (1)	-	C_unshiu_02810_mRNA_3.1	-
GF0043071	0	1	0	Hypothetical protein (1)			-	C_unshiu_02810_mRNA_1.1	-
GF0043070	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_02809_mRNA_3.1	-
GF0043069	0	1	0	Hypothetical protein (1)			-	C_unshiu_02809_mRNA_2.1	-
GF0043068	0	1	0	Hypothetical protein (1)			-	C_unshiu_02806_mRNA_1.1	-
GF0043067	0	1	0	Hypothetical protein (1)			-	C_unshiu_02805_mRNA_1.1	-
GF0043066	0	1	0	Hypothetical protein (1)			-	C_unshiu_02801_mRNA_2.1	-
GF0043065	0	1	0	Hypothetical protein (1)			-	C_unshiu_02801_mRNA_1.1	-
GF0043064	0	1	0	Hypothetical protein (1)			-	C_unshiu_02799_mRNA_3.1	-
GF0043063	0	1	0	Hypothetical protein (1)			-	C_unshiu_02798_mRNA_2.1	-
GF0043062	0	1	0	Hypothetical protein (1)			-	C_unshiu_02798_mRNA_1.1	-
GF0043061	0	1	0	Hypothetical protein (1)		Agenet-like domain [IPR008395] (1)	-	C_unshiu_02797_mRNA_1.1	-
GF0043060	0	1	0	Hypothetical protein (1)	calcium-dependent phospholipid binding [GO:0005544 molecular_function] (1); negative regulation of cell death [GO:0060548 biological_process] (1)	Copine [IPR010734] (1); Protein BONZAI [IPR031116] (1)	-	C_unshiu_02796_mRNA_2.1	-
GF0043059	0	1	0	Disease resistance protein RPS2 (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_02796_mRNA_1.1	-
GF0043058	0	1	0	Hypothetical protein (1)			-	C_unshiu_02794_mRNA_1.1	-
GF0043057	0	1	0	Hypothetical protein (1)			-	C_unshiu_02793_mRNA_2.1	-
GF0043056	0	1	0	Hypothetical protein (1)			-	C_unshiu_02793_mRNA_1.1	-
GF0043055	0	1	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_02792_mRNA_2.1	-
GF0043054	0	1	0	Hypothetical protein (1)			-	C_unshiu_02792_mRNA_1.1	-
GF0043053	0	1	0	Hypothetical protein (1)			-	C_unshiu_02791_mRNA_1.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0043052	0	1	0	LRR receptor-like kinase family protein (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1); protein tyrosine kinase activity [GO:0004713 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Protein kinase-like domain [IPR011009] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Tyrosine-protein kinase, catalytic domain [IPR020635] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Protein kinase domain [IPR000719] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Leucine-rich repeat [IPR001611] (1); Protein kinase, ATP binding site [IPR017441] (1)	-	C_unshiu_02789_mRNA_3.1	-
GF0043051	0	1	0	Hypothetical protein (1)			-	C_unshiu_02789_mRNA_2.1	-
GF0043050	0	1	0	Hypothetical protein (1)			-	C_unshiu_02784_mRNA_1.1	-
GF0043049	0	1	0	Hypothetical protein (1)			-	C_unshiu_02783_mRNA_2.1	-
GF0043048	0	1	0	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	-	C_unshiu_02783_mRNA_1.1	-
GF0043047	0	1	0	Hypothetical protein (1)			-	C_unshiu_02782_mRNA_6.1	-
GF0043046	0	1	0	Hypothetical protein (1)			-	C_unshiu_02782_mRNA_3.1	-
GF0043045	0	1	0	Hypothetical protein (1)			-	C_unshiu_02782_mRNA_2.1	-
GF0043044	0	1	0	Hypothetical protein (1)			-	C_unshiu_02782_mRNA_1.1	-
GF0043043	0	1	0	Hypothetical protein (1)			-	C_unshiu_02780_mRNA_1.1	-
GF0043042	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF1977, DnaJ-like [IPR015399] (1)	-	C_unshiu_02778_mRNA_1.1	-
GF0043041	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	WD40-repeat-containing domain [IPR017986] (1); WD40 repeat [IPR001680] (1); WD40/YVTN repeat-like-containing domain [IPR015943] (1)	-	C_unshiu_02776_mRNA_2.1	-
GF0043040	0	1	0	Hypothetical protein (1)			-	C_unshiu_02771_mRNA_1.1	-
GF0043039	0	1	0	Hypothetical protein (1)			-	C_unshiu_02770_mRNA_8.1	-
GF0043038	0	1	0	Hypothetical protein (1)			-	C_unshiu_02770_mRNA_3.1	-
GF0043037	0	1	0	Hypothetical protein (1)			-	C_unshiu_02768_mRNA_2.1	-
GF0043036	0	1	0	Hypothetical protein (1)		Phox-associated domain [IPR003114] (1)	-	C_unshiu_02767_mRNA_2.1	-
GF0043035	0	1	0	Hypothetical protein (1)			-	C_unshiu_02766_mRNA_2.1	-
GF0043034	0	1	0	Hypothetical protein (1)			-	C_unshiu_02766_mRNA_1.1	-
GF0043033	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, PMZ-type [IPR006564] (1); Zinc finger, SWIM-type [IPR007527] (1)	-	C_unshiu_02765_mRNA_2.1	-
GF0043032	0	1	0	Hypothetical protein (1)			-	C_unshiu_02765_mRNA_1.1	-
GF0043031	0	1	0	Cytochrome P450 76C2 (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); monooxygenase activity [GO:0004497 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1)	Cytochrome P450 [IPR001128] (1); Cytochrome P450, E-class, group IV [IPR002403] (1); Cytochrome P450, conserved site [IPR017972] (1)	-	C_unshiu_02764_mRNA_2.1	-
GF0043030	0	1	0	Geraniol 10-hydroxylase-like protein (1)	iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1)	Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450, conserved site [IPR017972] (1); Cytochrome P450 [IPR001128] (1)	-	C_unshiu_02764_mRNA_1.1	-
GF0043029	0	1	0	Hypothetical protein (1)			-	C_unshiu_02762_mRNA_3.1	-
GF0043028	0	1	0	Hypothetical protein (1)			-	C_unshiu_02762_mRNA_2.1	-
GF0043027	0	1	0	Sulfotransferase (1)	sulfotransferase activity [GO:0008146 molecular_function] (1)	Sulfotransferase domain [IPR000863] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_02761_mRNA_2.1	-
GF0043026	0	1	0	Hypothetical protein (1)			-	C_unshiu_02761_mRNA_1.1	-
GF0043025	0	1	0	Receptor like protein 21 (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	-	C_unshiu_02760_mRNA_2.1	-
GF0043024	0	1	0	Hypothetical protein (1)	nucleotide binding [GO:0000166 molecular_function] (1)	Nucleotide-binding alpha-beta plait domain [IPR012677] (1)	-	C_unshiu_02760_mRNA_1.1	-
GF0043023	0	1	0	Putative Leucine Rich Repeat Protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1)	-	C_unshiu_02757_mRNA_2.1	-
GF0043022	0	1	0	Bnr asp-box repeat family protein (1)		Sialidases [IPR011040] (1)	-	C_unshiu_02756_mRNA_1.1	-
GF0043021	0	1	0	Hypothetical protein (1)		LysM domain [IPR018392] (1)	-	C_unshiu_02755_mRNA_1.1	-
GF0043020	0	1	0	Hypothetical protein (1)			-	C_unshiu_02754_mRNA_3.1	-
GF0043019	0	1	0	Hypothetical protein (1)			-	C_unshiu_02754_mRNA_2.1	-
GF0043018	0	1	0	Hypothetical protein (1)			-	C_unshiu_02754_mRNA_1.1	-
GF0043017	0	1	0	Hypothetical protein (1)			-	C_unshiu_02752_mRNA_2.1	-
GF0043016	0	1	0	Plasma membrane ATPase (1)	nucleotide binding [GO:0000166 molecular_function] (1); ATP biosynthetic process [GO:0006754 biological_process] (1); metal ion binding [GO:0046872 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1); ATPase activity [GO:0016887 molecular_function] (1)	Cation-transporting P-type ATPase, N-terminal [IPR004014] (1); HAD-like domain [IPR023214] (1); P-type ATPase, A domain [IPR008250] (1); P-type ATPase, transmembrane domain [IPR023298] (1); P-type ATPase, cytoplasmic domain N [IPR023299] (1); P-type ATPase [IPR001757] (1); P-type ATPase, phosphorylation site [IPR018303] (1); P-type ATPase, subfamily IIIA [IPR006534] (1)	-	C_unshiu_02750_mRNA_1.1	-
GF0043015	0	1	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	-	C_unshiu_02746_mRNA_2.1	-
GF0043014	0	1	0	Hypothetical protein (1)			-	C_unshiu_02742_mRNA_2.1	-
GF0043013	0	1	0	Serine/threonine protein phosphatase 2A 57 kDa regulatory subunit B' alpha isoform (1)	protein phosphatase type 2A regulator activity [GO:0008601 molecular_function] (1); protein phosphatase type 2A complex [GO:0000159 cellular_component] (1); binding [GO:0005488 molecular_function] (1); signal transduction [GO:0007165 biological_process] (1)	Armadillo-type fold [IPR016024] (1); Protein phosphatase 2A, regulatory B subunit, B56 [IPR002554] (1)	-	C_unshiu_02741_mRNA_1.1	-
GF0043012	0	1	0	Hypothetical protein (1)	heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Cytochrome P450 [IPR001128] (1)	-	C_unshiu_02739_mRNA_2.1	-
GF0043011	0	1	0	Hypothetical protein (1)	nutrient reservoir activity [GO:0045735 molecular_function] (1)	RmlC-like jelly roll fold [IPR014710] (1); Cupin 1 [IPR006045] (1); RmlC-like cupin domain [IPR011051] (1)	-	C_unshiu_02738_mRNA_2.1	-
GF0043010	0	1	0	Hypothetical protein (1)			-	C_unshiu_02737_mRNA_8.1	-
GF0043009	0	1	0	Hypothetical protein (1)			-	C_unshiu_02737_mRNA_5.1	-
GF0043008	0	1	0	Hypothetical protein (1)			-	C_unshiu_02737_mRNA_4.1	-
GF0043007	0	1	0	Hypothetical protein (1)			-	C_unshiu_02737_mRNA_2.1	-
GF0043006	0	1	0	Hypothetical protein (1)			-	C_unshiu_02737_mRNA_1.1	-
GF0043005	0	1	0	Hypothetical protein (1)			-	C_unshiu_02736_mRNA_2.1	-
GF0043004	0	1	0	Hypothetical protein (1)			-	C_unshiu_02733_mRNA_1.1	-
GF0043003	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_02732_mRNA_5.1	-
GF0043002	0	1	0	Hypothetical protein (1)			-	C_unshiu_02732_mRNA_2.1	-
GF0043001	0	1	0	Hypothetical protein (1)			-	C_unshiu_02732_mRNA_1.1	-
GF0043000	0	1	0	Hypothetical protein (1)	Ino80 complex [GO:0031011 cellular_component] (1); chromatin remodeling [GO:0006338 biological_process] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	Vps72/YL1, C-terminal [IPR013272] (1); INO80 complex, subunit Ies6 [IPR029525] (1)	-	C_unshiu_02728_mRNA_1.1	-
GF0042999	0	1	0	Hypothetical protein (1)			-	C_unshiu_02727_mRNA_2.1	-
GF0042998	0	1	0	Hypothetical protein (1)			-	C_unshiu_02726_mRNA_2.1	-
GF0042997	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_02725_mRNA_1.1	-
GF0042996	0	1	0	Hypothetical protein (1)			-	C_unshiu_02723_mRNA_3.1	-
GF0042995	0	1	0	Hypothetical protein (1)			-	C_unshiu_02723_mRNA_2.1	-
GF0042994	0	1	0	Hypothetical protein (1)			-	C_unshiu_02722_mRNA_4.1	-
GF0042993	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			-	C_unshiu_02722_mRNA_3.1	-
GF0042992	0	1	0	Hypothetical protein (1)			-	C_unshiu_02722_mRNA_2.1	-
GF0042991	0	1	0	Hypothetical protein (1)			-	C_unshiu_02722_mRNA_1.1	-
GF0042990	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_02721_mRNA_2.1	-
GF0042989	0	1	0	Putative RNA-directed DNA polymerase (1)	nucleic acid binding [GO:0003676 molecular_function] (1); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1)	Ribonuclease H domain [IPR002156] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_02721_mRNA_1.1	-
GF0042988	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_02720_mRNA_4.1	-
GF0042987	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_02720_mRNA_3.1	-
GF0042986	0	1	0	Putative retroelement pol polyprotein (1)			-	C_unshiu_02718_mRNA_1.1	-
GF0042985	0	1	0	Hypothetical protein (1)		Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	-	C_unshiu_02716_mRNA_4.1	-
GF0042984	0	1	0	Hypothetical protein (1)			-	C_unshiu_02714_mRNA_2.1	-
GF0042983	0	1	0	Hypothetical protein (1)			-	C_unshiu_02710_mRNA_5.1	-
GF0042982	0	1	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	-	C_unshiu_02709_mRNA_1.1	-
GF0042981	0	1	0	Defective in meristem silencing protein (1)			-	C_unshiu_02708_mRNA_4.1	-

ID	**Num. in *C. celementine***	**Num in *C. unshiu***	**Num in *P.trifoliata***	**Note**	**GO**	**InterPro**	**Members in *C.clementine***	**Members in *C.unshiu***	**Members in *P.trifoliata***
GF0042980	0	1	0	Transcription elongation factor S-II (1)	transcription, DNA-templated [GO:0006351 biological_process] (1); zinc ion binding [GO:0008270 molecular_function] (1); regulation of DNA-templated transcription, elongation [GO:0032784 biological_process] (1); DNA binding [GO:0003677 molecular_function] (1); nucleus [GO:0005634 cellular_component] (1); regulation of transcription from RNA polymerase II promoter [GO:0006357 biological_process] (1)	Transcription elongation factor S-IIM [IPR017890] (1); Transcription factor IIS, N-terminal [IPR017923] (1); Transcription elongation factor, TFIIS/CRSP70, N-terminal, sub-type [IPR003617] (1); Transcription elongation factor, TFIIS-related [IPR016492] (1); Transcription elongation factor S-II, central domain [IPR003618] (1)	-	C_unshiu_02708_mRNA_2.1	-
GF0042979	0	1	0	Orf258 protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1); Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	C_unshiu_02707_mRNA_4.1	-
GF0042978	0	1	0	Hypothetical protein (1)			-	C_unshiu_02705_mRNA_2.1	-
GF0042977	0	1	0	Hypothetical protein (1)			-	C_unshiu_02703_mRNA_4.1	-
GF0042976	0	1	0	Hypothetical protein (1)			-	C_unshiu_02703_mRNA_3.1	-
GF0042975	0	1	0	Hypothetical protein (1)			-	C_unshiu_02703_mRNA_2.1	-
GF0042974	0	1	0	Ankyrin repeat and protein kinase domain-containing protein 1 (1)			-	C_unshiu_02702_mRNA_3.1	-
GF0042973	0	1	0	Hypothetical protein (1)			-	C_unshiu_02701_mRNA_3.1	-
GF0042972	0	1	0	RNA-directed DNA polymerase ; Ribonuclease H, putative (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	C_unshiu_02701_mRNA_1.1	-
GF0042971	0	1	0	Hypothetical protein (1)	metabolic process [GO:0008152 biological_process] (1); transferase activity, transferring acyl groups [GO:0016746 molecular_function] (1)	Phospholipid/glycerol acyltransferase [IPR002123] (1)	-	C_unshiu_02699_mRNA_1.1	-
GF0042970	0	1	0	Hypothetical protein (1)			-	C_unshiu_02697_mRNA_2.1	-
GF0042969	0	1	0	Hypothetical protein (1)			-	C_unshiu_02697_mRNA_1.1	-
GF0042968	0	1	0	Hypothetical protein (1)			-	C_unshiu_02696_mRNA_2.1	-
GF0042967	0	1	0	Hypothetical protein (1)			-	C_unshiu_02695_mRNA_1.1	-
GF0042966	0	1	0	Hypothetical protein (1)			-	C_unshiu_02694_mRNA_2.1	-
GF0042965	0	1	0	Hypothetical protein (1)			-	C_unshiu_02694_mRNA_1.1	-
GF0042964	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_02693_mRNA_1.1	-
GF0042963	0	1	0	Hypothetical protein (1)			-	C_unshiu_02688_mRNA_3.1	-
GF0042962	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_02688_mRNA_2.1	-
GF0042961	0	1	0	Hypothetical protein (1)			-	C_unshiu_02685_mRNA_1.1	-
GF0042960	0	1	0	Hypothetical protein (1)			-	C_unshiu_02684_mRNA_2.1	-
GF0042959	0	1	0	Hypothetical protein (1)			-	C_unshiu_02684_mRNA_1.1	-
GF0042958	0	1	0	Hypothetical protein (1)			-	C_unshiu_02683_mRNA_3.1	-
GF0042957	0	1	0	Hypothetical protein (1)			-	C_unshiu_02683_mRNA_2.1	-
GF0042956	0	1	0	Hypothetical protein (1)			-	C_unshiu_02683_mRNA_1.1	-
GF0042955	0	1	0	Putative disease resistance protein RGA3 (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_02682_mRNA_2.1	-
GF0042954	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_02682_mRNA_1.1	-
GF0042953	0	1	0	ABC transporter A family protein, putative (1)	transporter activity [GO:0005215 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1); transport [GO:0006810 biological_process] (1)	ABC transporter A, ABCA [IPR026082] (1)	-	C_unshiu_02680_mRNA_1.1	-
GF0042952	0	1	0	Heat shock 70 kDa protein (1)		Heat shock protein 70 family [IPR013126] (1); Heat shock protein 70, conserved site [IPR018181] (1); Heat shock protein 70kD, C-terminal domain [IPR029048] (1); Heat shock protein 70kD, peptide-binding domain [IPR029047] (1)	-	C_unshiu_02677_mRNA_3.1	-
GF0042951	0	1	0	Heat shock 70kDa protein 1/8 (1)		Heat shock protein 70 family [IPR013126] (1); Heat shock protein 70, conserved site [IPR018181] (1)	-	C_unshiu_02677_mRNA_2.1	-
GF0042950	0	1	0	Hypothetical protein (1)			-	C_unshiu_02676_mRNA_2.1	-
GF0042949	0	1	0	Hypothetical protein (1)			-	C_unshiu_02676_mRNA_1.1	-
GF0042948	0	1	0	F-box/FBD/LRR-repeat protein At5g56420 (1)	protein binding [GO:0005515 molecular_function] (1)	F-box domain [IPR001810] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); FBD domain [IPR006566] (1)	-	C_unshiu_02674_mRNA_2.1	-
GF0042947	0	1	0	Hypothetical protein (1)			-	C_unshiu_02674_mRNA_1.1	-
GF0042946	0	1	0	Hypothetical protein (1)			-	C_unshiu_02671_mRNA_2.1	-
GF0042945	0	1	0	Hypothetical protein (1)			-	C_unshiu_02670_mRNA_3.1	-
GF0042944	0	1	0	Hypothetical protein (1)			-	C_unshiu_02670_mRNA_1.1	-
GF0042943	0	1	0	Hypothetical protein (1)	metal ion binding [GO:0046872 molecular_function] (1); nucleotide binding [GO:0000166 molecular_function] (1)	P-type ATPase, transmembrane domain [IPR023298] (1); P-type ATPase, A domain [IPR008250] (1)	-	C_unshiu_02669_mRNA_2.1	-
GF0042942	0	1	0	Two-component response regulator ARR9 (1)	phosphorelay signal transduction system [GO:0000160 biological_process] (1)	CheY-like superfamily [IPR011006] (1); Signal transduction response regulator, receiver domain [IPR001789] (1)	-	C_unshiu_02669_mRNA_1.1	-
GF0042941	0	1	0	Hypothetical protein (1)			-	C_unshiu_02667_mRNA_3.1	-
GF0042940	0	1	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); metallocarboxypeptidase activity [GO:0004181 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Peptidase M14, carboxypeptidase A [IPR000834] (1)	-	C_unshiu_02667_mRNA_2.1	-
GF0042939	0	1	0	Hypothetical protein (1)		DNA-binding pseudobarrel domain [IPR015300] (1)	-	C_unshiu_02667_mRNA_1.1	-
GF0042938	0	1	0	Phenazine biosynthesis PhzC/PhzF family protein (1)	biosynthetic process [GO:0009058 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1)	Phenazine biosynthesis PhzF protein [IPR003719] (1)	-	C_unshiu_02666_mRNA_1.1	-
GF0042937	0	1	0	Hypothetical protein (1)			-	C_unshiu_02665_mRNA_3.1	-
GF0042936	0	1	0	Hypothetical protein (1)	catalytic activity [GO:0003824 molecular_function] (1)	Pyridoxal phosphate-dependent transferase, major region, subdomain 2 [IPR015422] (1); Pyridoxal phosphate-dependent transferase [IPR015424] (1)	-	C_unshiu_02665_mRNA_1.1	-
GF0042935	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_02662_mRNA_4.1	-
GF0042934	0	1	0	Hypothetical protein (1)			-	C_unshiu_02662_mRNA_3.1	-
GF0042933	0	1	0	S-adenosylmethionine synthase 2 (1)	methionine adenosyltransferase activity [GO:0004478 molecular_function] (1); S-adenosylmethionine biosynthetic process [GO:0006556 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	S-adenosylmethionine synthetase superfamily [IPR022636] (1); S-adenosylmethionine synthetase, conserved site [IPR022631] (1); Ribonuclease H-like domain [IPR012337] (1); S-adenosylmethionine synthetase, N-terminal [IPR022628] (1); S-adenosylmethionine synthetase, C-terminal [IPR022630] (1); S-adenosylmethionine synthetase, central domain [IPR022629] (1); S-adenosylmethionine synthetase [IPR002133] (1)	-	C_unshiu_02662_mRNA_2.1	-
GF0042932	0	1	0	O-Glycosyl hydrolases family 17 protein (1)		X8 domain [IPR012946] (1)	-	C_unshiu_02662_mRNA_1.1	-
GF0042931	0	1	0	Hypothetical protein (1)			-	C_unshiu_02661_mRNA_1.1	-
GF0042930	0	1	0	Hypothetical protein (1)			-	C_unshiu_02660_mRNA_3.1	-
GF0042929	0	1	0	Hypothetical protein (1)			-	C_unshiu_02660_mRNA_2.1	-
GF0042928	0	1	0	Hypothetical protein (1)		MAGE homology domain [IPR002190] (1)	-	C_unshiu_02659_mRNA_1.1	-
GF0042927	0	1	0	Protein UNUSUAL FLORAL ORGANS (1)	protein binding [GO:0005515 molecular_function] (1)	Kelch-type beta propeller [IPR015915] (1); F-box domain [IPR001810] (1); Galactose oxidase/kelch, beta-propeller [IPR011043] (1)	-	C_unshiu_02658_mRNA_3.1	-
GF0042926	0	1	0	RING/FYVE/PHD zinc finger protein (1)	protein binding [GO:0005515 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1); N-acetyltransferase activity [GO:0008080 molecular_function] (1)	Jas TPL-binding domain [IPR032308] (1); Zinc finger, PHD-finger [IPR019787] (1); Zinc finger, PHD-type [IPR001965] (1); GNAT domain [IPR000182] (1); Zinc finger, RING/FYVE/PHD-type [IPR013083] (1); Zinc finger, PHD-type, conserved site [IPR019786] (1); Acyl-CoA N-acyltransferase [IPR016181] (1); Zinc finger, FYVE/PHD-type [IPR011011] (1)	-	C_unshiu_02658_mRNA_2.1	-
GF0042925	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Tetratricopeptide-like helical domain [IPR011990] (1)	-	C_unshiu_02658_mRNA_1.1	-
GF0042924	0	1	0	Hypothetical protein (1)			-	C_unshiu_02657_mRNA_5.1	-
GF0042923	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_02657_mRNA_4.1	-
GF0042922	0	1	0	Zinc finger NUTCRACKER-like protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	C_unshiu_02655_mRNA_1.1	-
GF0042921	0	1	0	Hypothetical protein (1)			-	C_unshiu_02652_mRNA_3.1	-
GF0042920	0	1	0	Reticulocyte-binding 2 a (1)			-	C_unshiu_02649_mRNA_2.1	-
GF0042919	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_02648_mRNA_1.1	-
GF0042918	0	1	0	Hypothetical protein (1)			-	C_unshiu_02647_mRNA_2.1	-
GF0042917	0	1	0	Lipid transfer protein (1)		Hydrophobic seed protein [IPR027923] (1); Bifunctional inhibitor/plant lipid transfer protein/seed storage helical domain [IPR016140] (1)	-	C_unshiu_02646_mRNA_1.1	-
GF0042916	0	1	0	Hypothetical protein (1)			-	C_unshiu_02645_mRNA_1.1	-
GF0042915	0	1	0	Monosacharide transport protein (1)			-	C_unshiu_02643_mRNA_2.1	-
GF0042914	0	1	0	Hypothetical protein (1)			-	C_unshiu_02643_mRNA_1.1	-
GF0042913	0	1	0	Hypothetical protein (1)		Protein-only RNase P, C-terminal [IPR031595] (1)	-	C_unshiu_02642_mRNA_2.1	-
GF0042912	0	1	0	Hypothetical protein (1)			-	C_unshiu_02641_mRNA_1.1	-
GF0042911	0	1	0	Hypothetical protein (1)			-	C_unshiu_02640_mRNA_1.1	-
GF0042910	0	1	0	Hypothetical protein (1)			-	C_unshiu_02635_mRNA_3.1	-
GF0042909	0	1	0	Hypothetical protein (1)			-	C_unshiu_02635_mRNA_2.1	-
GF0042908	0	1	0	Hypothetical protein (1)			-	C_unshiu_02630_mRNA_1.1	-
GF0042907	0	1	0	Hypothetical protein (1)			-	C_unshiu_02629_mRNA_2.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0042906	0	1	0	3-ketoacyl-CoA synthase 4 (1)	fatty acid biosynthetic process [GO:0006633 biological_process] (1); transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (1); catalytic activity [GO:0003824 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1); membrane [GO:0016020 cellular_component] (1)	Very-long-chain 3-ketoacyl-CoA synthase [IPR012392] (1); Thiolase-like [IPR016039] (1); FAE1/Type III polyketide synthase-like protein [IPR013601] (1)	-	C_unshiu_02628_mRNA_1.1	-
GF0042905	0	1	0	Hypothetical protein (1)			-	C_unshiu_02626_mRNA_4.1	-
GF0042904	0	1	0	Receptor like protein 33 (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	-	C_unshiu_02626_mRNA_3.1	-
GF0042903	0	1	0	Hypothetical protein (1)	hydrolase activity [GO:0016787 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Alpha/beta hydrolase fold-3 [IPR013094] (1); Alpha/Beta hydrolase fold [IPR029058] (1)	-	C_unshiu_02622_mRNA_1.1	-
GF0042902	0	1	0	Hypothetical protein (1)			-	C_unshiu_02620_mRNA_1.1	-
GF0042901	0	1	0	Hypothetical protein (1)			-	C_unshiu_02618_mRNA_1.1	-
GF0042900	0	1	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); ClpA/B, conserved site 1 [IPR018368] (1)	-	C_unshiu_02617_mRNA_5.1	-
GF0042899	0	1	0	Hypothetical protein (1)			-	C_unshiu_02617_mRNA_4.1	-
GF0042898	0	1	0	Hypothetical protein (1)			-	C_unshiu_02617_mRNA_3.1	-
GF0042897	0	1	0	Hypothetical protein (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_02615_mRNA_1.1	-
GF0042896	0	1	0	Hypothetical protein (1)			-	C_unshiu_02611_mRNA_2.1	-
GF0042895	0	1	0	Hypothetical protein (1)		Arabidopsis retrotransposon Orf1 [IPR004312] (1)	-	C_unshiu_02610_mRNA_2.1	-
GF0042894	0	1	0	Hypothetical protein (1)			-	C_unshiu_02610_mRNA_1.1	-
GF0042893	0	1	0	Long-chain-alcohol oxidase FAO4A (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); flavin adenine dinucleotide binding [GO:0050660 molecular_function] (1); oxidoreductase activity, acting on CH-OH group of donors [GO:0016614 molecular_function] (1)	FAD/NAD(P)-binding domain [IPR023753] (1); Glucose-methanol-choline oxidoreductase, N-terminal [IPR000172] (1)	-	C_unshiu_02609_mRNA_5.1	-
GF0042892	0	1	0	Hypothetical protein (1)			-	C_unshiu_02609_mRNA_4.1	-
GF0042891	0	1	0	E3 ubiquitin-protein ligase BAH1 (1)	metal ion binding [GO:0046872 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Zinc finger, RING/FYVE/PHD-type [IPR013083] (1); Zinc finger, C3HC4 RING-type [IPR018957] (1); Zinc finger, RING-type, conserved site [IPR017907] (1); Zinc finger, RING-type [IPR001841] (1)	-	C_unshiu_02609_mRNA_2.1	-
GF0042890	0	1	0	Glutathione gamma-glutamylcysteinyltransferase (1)	response to metal ion [GO:0010038 biological_process] (1); phytochelatin biosynthetic process [GO:0046938 biological_process] (1); glutathione gamma-glutamylcysteinyltransferase activity [GO:0016756 molecular_function] (1); metal ion binding [GO:0046872 molecular_function] (1)	Phytochelatin synthase, C-terminal [IPR015407] (1); Phytochelatin synthase [IPR007719] (1)	-	C_unshiu_02609_mRNA_1.1	-
GF0042889	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	G-patch domain [IPR000467] (1)	-	C_unshiu_02608_mRNA_1.1	-
GF0042888	0	1	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase, ATP binding site [IPR017441] (1)	-	C_unshiu_02607_mRNA_2.1	-
GF0042887	0	1	0	Polyol transporter 5 (1)	transmembrane transport [GO:0055085 biological_process] (1); transporter activity [GO:0005215 molecular_function] (1); transmembrane transporter activity [GO:0022857 molecular_function] (1); membrane [GO:0016020 cellular_component] (1); integral component of membrane [GO:0016021 cellular_component] (1); substrate-specific transmembrane transporter activity [GO:0022891 molecular_function] (1)	Sugar/inositol transporter [IPR003663] (1); Major facilitator, sugar transporter-like [IPR005828] (1); Major facilitator superfamily domain [IPR020846] (1); Sugar transporter, conserved site [IPR005829] (1)	-	C_unshiu_02606_mRNA_3.1	-
GF0042886	0	1	0	Hypothetical protein (1)			-	C_unshiu_02606_mRNA_2.1	-
GF0042885	0	1	0	Hypothetical protein (1)			-	C_unshiu_02606_mRNA_1.1	-
GF0042884	0	1	0	LRR receptor-like kinase plant (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1); Malectin-like carbohydrate-binding domain [IPR024788] (1)	-	C_unshiu_02604_mRNA_3.1	-
GF0042883	0	1	0	Hypothetical protein (1)		Malectin-like carbohydrate-binding domain [IPR024788] (1)	-	C_unshiu_02604_mRNA_1.1	-
GF0042882	0	1	0	Phytophthora resistance protein RpsYD29-1 (1)	ADP binding [GO:0043531 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	C_unshiu_02603_mRNA_3.1	-
GF0042881	0	1	0	Phospholipase A2 family protein (1)	calcium ion binding [GO:0005509 molecular_function] (1); phospholipase A2 activity [GO:0004623 molecular_function] (1); lipid catabolic process [GO:0016042 biological_process] (1)	Phospholipase A2 domain [IPR016090] (1); Phospholipase A2 [IPR001211] (1)	-	C_unshiu_02600_mRNA_2.1	-
GF0042880	0	1	0	Thylakoid lumenal 17.4 kDa protein, chloroplastic (1)		Pentapeptide repeat [IPR001646] (1)	-	C_unshiu_02600_mRNA_1.1	-
GF0042879	0	1	0	Hypothetical protein (1)			-	C_unshiu_02598_mRNA_3.1	-
GF0042878	0	1	0	Epidermis-specific secreted glycoprotein EP1 (1)		Bulb-type lectin domain [IPR001480] (1)	-	C_unshiu_02596_mRNA_1.1	-
GF0042877	0	1	0	Hypothetical protein (1)			-	C_unshiu_02593_mRNA_2.1	-
GF0042876	0	1	0	Disease resistance protein RPS2 (1)			-	C_unshiu_02592_mRNA_1.1	-
GF0042875	0	1	0	Hypothetical protein (1)	intracellular [GO:0005622 cellular_component] (1); translation [GO:0006412 biological_process] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1); ribosome [GO:0005840 cellular_component] (1)	Ribosomal protein S3Ae [IPR001593] (1)	-	C_unshiu_02589_mRNA_6.1	-
GF0042874	0	1	0	Hypothetical protein (1)			-	C_unshiu_02589_mRNA_2.1	-
GF0042873	0	1	0	Hypothetical protein (1)			-	C_unshiu_02588_mRNA_2.1	-
GF0042872	0	1	0	Hypothetical protein (1)			-	C_unshiu_02586_mRNA_2.1	-
GF0042871	0	1	0	Hypothetical protein (1)			-	C_unshiu_02585_mRNA_5.1	-
GF0042870	0	1	0	Hypothetical protein (1)			-	C_unshiu_02585_mRNA_4.1	-
GF0042869	0	1	0	Hypothetical protein (1)			-	C_unshiu_02581_mRNA_2.1	-
GF0042868	0	1	0	Proline-rich receptor-like protein kinase PERK13 (1)	ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	-	C_unshiu_02581_mRNA_1.1	-
GF0042867	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1); ATP-dependent DNA helicase activity [GO:0004003 molecular_function] (1); ATP-dependent helicase activity [GO:0008026 molecular_function] (1); nucleobase-containing compound metabolic process [GO:0006139 biological_process] (1); hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides [GO:0016818 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); ATP-dependent helicase, C-terminal [IPR006555] (1); Helicase superfamily 1/2, ATP-binding domain, DinG/Rad3-type [IPR014013] (1); DEAD2 [IPR010614] (1)	-	C_unshiu_02579_mRNA_4.1	-
GF0042866	0	1	0	Mutator-like transposase (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); MULE transposase domain [IPR018289] (1); Zinc finger, PMZ-type [IPR006564] (1); Transposase, MuDR, plant [IPR004332] (1); Zinc finger, SWIM-type [IPR007527] (1)	-	C_unshiu_02578_mRNA_4.1	-
GF0042865	0	1	0	Putative nitrate transporter 1.2-like (1)	transporter activity [GO:0005215 molecular_function] (1); transport [GO:0006810 biological_process] (1); membrane [GO:0016020 cellular_component] (1)	Proton-dependent oligopeptide transporter family [IPR000109] (1)	-	C_unshiu_02578_mRNA_1.1	-
GF0042864	0	1	0	Transcription factor (1)	protein dimerization activity [GO:0046983 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	Myc-type, basic helix-loop-helix (bHLH) domain [IPR011598] (1); Myb domain, plants [IPR006447] (1); Homeodomain-like [IPR009057] (1)	-	C_unshiu_02576_mRNA_1.1	-
GF0042863	0	1	0	Hypothetical protein (1)			-	C_unshiu_02575_mRNA_4.1	-
GF0042862	0	1	0	Hypothetical protein (1)			-	C_unshiu_02574_mRNA_4.1	-
GF0042861	0	1	0	Disease resistance protein family, putative isoform 2 (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1); Domain of unknown function DUF4220 [IPR025315] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_02574_mRNA_2.1	-
GF0042860	0	1	0	Class III homeodomain leucine zipper protein (1)		MEKHLA [IPR013978] (1)	-	C_unshiu_02574_mRNA_1.1	-
GF0042859	0	1	0	O-acyltransferase WSD1 (1)	diacylglycerol O-acyltransferase activity [GO:0004144 molecular_function] (1)	O-acyltransferase WSD1, C-terminal [IPR009721] (1)	-	C_unshiu_02573_mRNA_1.1	-
GF0042858	0	1	0	Plasma membrane fusion PRM1 (1)			-	C_unshiu_02572_mRNA_4.1	-
GF0042857	0	1	0	Hypothetical protein (1)			-	C_unshiu_02572_mRNA_3.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0042856	0	1	0	Hypothetical protein (1)		Galactose oxidase, beta-propeller [IPR015916] (1)	-	C_unshiu_02570_mRNA_3.1	-
GF0042855	0	1	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat [IPR001611] (1); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_02569_mRNA_1.1	-
GF0042854	0	1	0	Hypothetical protein (1)			-	C_unshiu_02568_mRNA_3.1	-
GF0042853	0	1	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	-	C_unshiu_02566_mRNA_2.1	-
GF0042852	0	1	0	Hypothetical protein (1)		Isopenicillin N synthase-like [IPR027443] (1)	-	C_unshiu_02566_mRNA_1.1	-
GF0042851	0	1	0	Hypothetical protein (1)			-	C_unshiu_02565_mRNA_4.1	-
GF0042850	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			-	C_unshiu_02563_mRNA_5.1	-
GF0042849	0	1	0	Hypothetical protein (1)			-	C_unshiu_02563_mRNA_4.1	-
GF0042848	0	1	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_02563_mRNA_3.1	-
GF0042847	0	1	0	Hypothetical protein (1)			-	C_unshiu_02563_mRNA_2.1	-
GF0042846	0	1	0	DEAD-box ATP-dependent RNA helicase 57 (1)	ATP binding [GO:0005524 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	RNA helicase, DEAD-box type, Q motif [IPR014014] (1); Helicase superfamily 1/2, ATP-binding domain [IPR014001] (1); DEAD/DEAH box helicase domain [IPR011545] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); ATP-dependent RNA helicase DEAD-box, conserved site [IPR000629] (1); Helicase, C-terminal [IPR001650] (1)	-	C_unshiu_02562_mRNA_2.1	-
GF0042845	0	1	0	Caffeic acid 3-O-methyltransferase (1)	O-methyltransferase activity [GO:0008171 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1); methyltransferase activity [GO:0008168 molecular_function] (1)	S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); O-methyltransferase, family 2 [IPR001077] (1); O-methyltransferase COMT-type [IPR016461] (1); Plant methyltransferase dimerisation [IPR012967] (1)	-	C_unshiu_02559_mRNA_4.1	-
GF0042844	0	1	0	Hypothetical protein (1)			-	C_unshiu_02559_mRNA_3.1	-
GF0042843	0	1	0	Hypothetical protein (1)			-	C_unshiu_02559_mRNA_2.1	-
GF0042842	0	1	0	Hypothetical protein (1)			-	C_unshiu_02558_mRNA_1.1	-
GF0042841	0	1	0	Caffeic acid O-methyltransferase (1)	methyltransferase activity [GO:0008168 molecular_function] (1); O-methyltransferase activity [GO:0008171 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	O-methyltransferase COMT-type [IPR016461] (1); Plant methyltransferase dimerisation [IPR012967] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); O-methyltransferase, family 2 [IPR001077] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	C_unshiu_02555_mRNA_2.1	-
GF0042840	0	1	0	Hypothetical protein (1)		SGNH hydrolase-type esterase domain [IPR013830] (1)	-	C_unshiu_02555_mRNA_1.1	-
GF0042839	0	1	0	Hypothetical protein (1)		Zinc finger, TTF-type [IPR006580] (1); Domain of unknown function DUF4371 [IPR025398] (1)	-	C_unshiu_02554_mRNA_1.1	-
GF0042838	0	1	0	Disease resistance protein (CC-NBS-LRR class) family protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_02553_mRNA_3.1	-
GF0042837	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_02551_mRNA_2.1	-
GF0042836	0	1	0	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_02551_mRNA_1.1	-
GF0042835	0	1	0	Hypothetical protein (1)			-	C_unshiu_02550_mRNA_4.1	-
GF0042834	0	1	0	Hypothetical protein (1)			-	C_unshiu_02547_mRNA_2.1	-
GF0042833	0	1	0	Ferrochelatase (1)	heme biosynthetic process [GO:0006783 biological_process] (1); ferrochelatase activity [GO:0004325 molecular_function] (1)	Chlorophyll a/b binding protein domain [IPR023329] (1); Ferrochelatase [IPR001015] (1); Chlorophyll A-B binding protein [IPR022796] (1); Ferrochelatase, active site [IPR019772] (1)	-	C_unshiu_02546_mRNA_1.1	-
GF0042832	0	1	0	Hypothetical protein (1)	membrane [GO:0016020 cellular_component] (1)	ABC-transporter extracellular N-terminal domain [IPR029481] (1); ABC-2 type transporter [IPR013525] (1); Plant PDR ABC transporter associated [IPR013581] (1)	-	C_unshiu_02543_mRNA_3.1	-
GF0042831	0	1	0	Hypothetical protein (1)			-	C_unshiu_02543_mRNA_2.1	-
GF0042830	0	1	0	Hypothetical protein (1)			-	C_unshiu_02542_mRNA_2.1	-
GF0042829	0	1	0	Hypothetical protein (1)			-	C_unshiu_02542_mRNA_1.1	-
GF0042828	0	1	0	CST complex subunit CTC1 (1)			-	C_unshiu_02541_mRNA_1.1	-
GF0042827	0	1	0	MORC family CW-type zinc finger protein 3 isoform 2 (1)		Histidine kinase-like ATPase, C-terminal domain [IPR003594] (1)	-	C_unshiu_02539_mRNA_2.1	-
GF0042826	0	1	0	Hypothetical protein (1)			-	C_unshiu_02537_mRNA_5.1	-
GF0042825	0	1	0	Hypothetical protein (1)	carboxylic acid metabolic process [GO:0019752 biological_process] (1); carboxy-lyase activity [GO:0016831 molecular_function] (1); pyridoxal phosphate binding [GO:0030170 molecular_function] (1); catalytic activity [GO:0003824 molecular_function] (1)	Pyridoxal phosphate-dependent decarboxylase [IPR002129] (1); Pyridoxal phosphate-dependent transferase [IPR015424] (1); Pyridoxal phosphate-dependent transferase, major region, subdomain 2 [IPR015422] (1)	-	C_unshiu_02537_mRNA_4.1	-
GF0042824	0	1	0	Hypothetical protein (1)			-	C_unshiu_02537_mRNA_3.1	-
GF0042823	0	1	0	Hypothetical protein (1)		Transcription factor GRAS [IPR005202] (1)	-	C_unshiu_02536_mRNA_6.1	-
GF0042822	0	1	0	Hypothetical protein (1)			-	C_unshiu_02535_mRNA_6.1	-
GF0042821	0	1	0	Hypothetical protein (1)			-	C_unshiu_02535_mRNA_1.1	-
GF0042820	0	1	0	Hypothetical protein (1)			-	C_unshiu_02533_mRNA_2.1	-
GF0042819	0	1	0	Pentatricopeptide repeat-containing family protein (1)	protein binding [GO:0005515 molecular_function] (1)	Pentatricopeptide repeat [IPR002885] (1); Tetratricopeptide-like helical domain [IPR011990] (1)	-	C_unshiu_02533_mRNA_1.1	-
GF0042818	0	1	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1)	Myc-type, basic helix-loop-helix (bHLH) domain [IPR011598] (1)	-	C_unshiu_02532_mRNA_4.1	-
GF0042817	0	1	0	Hypothetical protein (1)			-	C_unshiu_02532_mRNA_3.1	-
GF0042816	0	1	0	Carboxypeptidase (1)	proteolysis [GO:0006508 biological_process] (1); serine-type carboxypeptidase activity [GO:0004185 molecular_function] (1)	Serine carboxypeptidases, histidine active site [IPR033124] (1); Peptidase S10, serine carboxypeptidase [IPR001563] (1); Serine carboxypeptidase, serine active site [IPR018202] (1); Alpha/Beta hydrolase fold [IPR029058] (1)	-	C_unshiu_02532_mRNA_1.1	-
GF0042815	0	1	0	Hypothetical protein (1)			-	C_unshiu_02531_mRNA_2.1	-
GF0042814	0	1	0	Hypothetical protein (1)			-	C_unshiu_02529_mRNA_6.1	-
GF0042813	0	1	0	Purple acid phosphatase 23 (1)	metal ion binding [GO:0046872 molecular_function] (1); acid phosphatase activity [GO:0003993 molecular_function] (1)	Purple acid phosphatase, N-terminal [IPR015914] (1); Purple acid phosphatase-like, N-terminal [IPR008963] (1)	-	C_unshiu_02529_mRNA_1.1	-
GF0042812	0	1	0	Hypothetical protein (1)			-	C_unshiu_02527_mRNA_3.1	-
GF0042811	0	1	0	Hypothetical protein (1)			-	C_unshiu_02525_mRNA_1.1	-
GF0042810	0	1	0	Hypothetical protein (1)			-	C_unshiu_02523_mRNA_1.1	-
GF0042809	0	1	0	Hypothetical protein (1)			-	C_unshiu_02514_mRNA_7.1	-
GF0042808	0	1	0	Hypothetical protein (1)			-	C_unshiu_02514_mRNA_2.1	-
GF0042807	0	1	0	Gibberellin 20 oxidase 2 (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Oxoglutarate/iron-dependent dioxygenase [IPR005123] (1); Isopenicillin N synthase-like [IPR027443] (1)	-	C_unshiu_02513_mRNA_2.1	-
GF0042806	0	1	0	Hypothetical protein (1)			-	C_unshiu_02512_mRNA_1.1	-
GF0042805	0	1	0	Hypothetical protein (1)			-	C_unshiu_02511_mRNA_4.1	-
GF0042804	0	1	0	Hypothetical protein (1)			-	C_unshiu_02511_mRNA_3.1	-
GF0042803	0	1	0	Hypothetical protein (1)			-	C_unshiu_02510_mRNA_3.1	-
GF0042802	0	1	0	Putative ternary complex factor MIP1 (1)		Ternary complex factor MIP1, leucine-zipper [IPR025757] (1); Domain of unknown function DUF547 [IPR006869] (1)	-	C_unshiu_02510_mRNA_2.1	-
GF0042801	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Tetratricopeptide-like helical domain [IPR011990] (1); Tetratricopeptide repeat-containing domain [IPR013026] (1); Tetratricopeptide repeat [IPR019734] (1)	-	C_unshiu_02510_mRNA_1.1	-
GF0042800	0	1	0	Hypothetical protein (1)			-	C_unshiu_02509_mRNA_2.1	-
GF0042799	0	1	0	Putative WRKY transcription factor 19-like protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_02509_mRNA_1.1	-
GF0042798	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1)	-	C_unshiu_02508_mRNA_3.1	-
GF0042797	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_02508_mRNA_2.1	-
GF0042796	0	1	0	Hypothetical protein (1)			-	C_unshiu_02507_mRNA_3.1	-
GF0042795	0	1	0	Hypothetical protein (1)			-	C_unshiu_02506_mRNA_5.1	-
GF0042794	0	1	0	Hypothetical protein (1)			-	C_unshiu_02506_mRNA_4.1	-
GF0042793	0	1	0	Hypothetical protein (1)			-	C_unshiu_02506_mRNA_3.1	-
GF0042792	0	1	0	X intrinsic protein (1)	transport [GO:0006810 biological_process] (1); membrane [GO:0016020 cellular_component] (1); transporter activity [GO:0005215 molecular_function] (1)	Aquaporin-like [IPR023271] (1); Major intrinsic protein [IPR000425] (1)	-	C_unshiu_02506_mRNA_1.1	-
GF0042791	0	1	0	Putative serine/threonine-protein kinase NAK (1)	ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_02505_mRNA_2.1	-
GF0042790	0	1	0	Hypothetical leucine rich repeat protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1)	-	C_unshiu_02504_mRNA_2.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0042789	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Pentatricopeptide repeat [IPR002885] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_02504_mRNA_1.1	-
GF0042788	0	1	0	Rhamnogalacturonate lyase (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1); carbohydrate binding [GO:0030246 molecular_function] (1)	Rhamnogalacturonate lyase [IPR010325] (1); Rhamnogalacturonan lyase, domain III [IPR029411] (1); Galactose mutarotase-like domain [IPR011013] (1); Galactose-binding domain-like [IPR008979] (1)	-	C_unshiu_02503_mRNA_1.1	-
GF0042787	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4371 [IPR025398] (1)	-	C_unshiu_02502_mRNA_1.1	-
GF0042786	0	1	0	Hypothetical protein (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase, ATP binding site [IPR017441] (1); Bulb-type lectin domain [IPR001480] (1); Protein kinase domain [IPR000719] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_02499_mRNA_2.1	-
GF0042785	0	1	0	Hypothetical protein (1)			-	C_unshiu_02498_mRNA_2.1	-
GF0042784	0	1	0	Hypothetical protein (1)			-	C_unshiu_02498_mRNA_1.1	-
GF0042783	0	1	0	Hypothetical protein (1)			-	C_unshiu_02497_mRNA_1.1	-
GF0042782	0	1	0	Glucose-6-phosphate 1-dehydrogenase, cytoplasmic isoform (1)	glucose metabolic process [GO:0006006 biological_process] (1); oxidation-reduction process [GO:0055114 biological_process] (1); glucose-6-phosphate dehydrogenase activity [GO:0004345 molecular_function] (1); NADP binding [GO:0050661 molecular_function] (1)	Glucose-6-phosphate dehydrogenase [IPR001282] (1); NAD(P)-binding domain [IPR016040] (1); Glucose-6-phosphate dehydrogenase, C-terminal [IPR022675] (1); Glucose-6-phosphate dehydrogenase, NAD-binding [IPR022674] (1)	-	C_unshiu_02495_mRNA_3.1	-
GF0042781	0	1	0	NB-ARC domain disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_02495_mRNA_1.1	-
GF0042780	0	1	0	Hypothetical protein (1)			-	C_unshiu_02494_mRNA_2.1	-
GF0042779	0	1	0	Hypothetical protein (1)			-	C_unshiu_02493_mRNA_3.1	-
GF0042778	0	1	0	Hypothetical protein (1)			-	C_unshiu_02493_mRNA_2.1	-
GF0042777	0	1	0	Hypothetical protein (1)			-	C_unshiu_02492_mRNA_2.1	-
GF0042776	0	1	0	Hypothetical protein (1)			-	C_unshiu_02491_mRNA_1.1	-
GF0042775	0	1	0	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	C_unshiu_02490_mRNA_1.1	-
GF0042774	0	1	0	Hypothetical protein (1)	ribosome [GO:0005840 cellular_component] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1); translation [GO:0006412 biological_process] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1)	Ribosomal protein S5 domain 2-type fold [IPR020568] (1); Ribosomal protein S9 [IPR000754] (1); NAD(P)-binding domain [IPR016040] (1); Short-chain dehydrogenase/reductase SDR [IPR002198] (1); Glucose/ribitol dehydrogenase [IPR002347] (1); Ribosomal protein S5 domain 2-type fold, subgroup [IPR014721] (1)	-	C_unshiu_02489_mRNA_5.1	-
GF0042773	0	1	0	Hypothetical protein (1)		DNA-binding pseudobarrel domain [IPR015300] (1)	-	C_unshiu_02489_mRNA_4.1	-
GF0042772	0	1	0	Hypothetical protein (1)			-	C_unshiu_02489_mRNA_3.1	-
GF0042771	0	1	0	Hypothetical protein (1)			-	C_unshiu_02488_mRNA_2.1	-
GF0042770	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1); signal transduction [GO:0007165 biological_process] (1); ADP binding [GO:0043531 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	NB-ARC [IPR002182] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Protein kinase, ATP binding site [IPR017441] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Protein kinase-like domain [IPR011009] (1); Leucine-rich repeat 3 [IPR011713] (1); Protein kinase domain [IPR000719] (1); Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1)	-	C_unshiu_02488_mRNA_1.1	-
GF0042769	0	1	0	Hypothetical protein (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Short-chain dehydrogenase/reductase SDR [IPR002198] (1); NAD(P)-binding domain [IPR016040] (1)	-	C_unshiu_02487_mRNA_3.1	-
GF0042768	0	1	0	LRR receptor-like kinase family protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_02485_mRNA_3.1	-
GF0042767	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1); signal transduction [GO:0007165 biological_process] (1); ADP binding [GO:0043531 molecular_function] (1)	Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	C_unshiu_02484_mRNA_1.1	-
GF0042766	0	1	0	Hypothetical protein (1)		TB2/DP1/HVA22-related protein [IPR004345] (1); Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_02483_mRNA_3.1	-
GF0042765	0	1	0	Hypothetical protein (1)			-	C_unshiu_02482_mRNA_3.1	-
GF0042764	0	1	0	Hypothetical protein (1)			-	C_unshiu_02482_mRNA_2.1	-
GF0042763	0	1	0	Hypothetical protein (1)			-	C_unshiu_02481_mRNA_4.1	-
GF0042762	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_02481_mRNA_2.1	-
GF0042761	0	1	0	Hypothetical protein (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Serine/threonine-protein kinase, active site [IPR008271] (1)	-	C_unshiu_02480_mRNA_3.1	-
GF0042760	0	1	0	Hypothetical protein (1)			-	C_unshiu_02479_mRNA_2.1	-
GF0042759	0	1	0	Hypothetical protein (1)			-	C_unshiu_02479_mRNA_1.1	-
GF0042758	0	1	0	Hypothetical protein (1)			-	C_unshiu_02476_mRNA_1.1	-
GF0042757	0	1	0	Hypothetical protein (1)			-	C_unshiu_02475_mRNA_2.1	-
GF0042756	0	1	0	Hypothetical protein (1)			-	C_unshiu_02474_mRNA_3.1	-
GF0042755	0	1	0	17.5 kDa class I heat shock protein (1)		Small heat shock protein HSP20 [IPR031107] (1); Alpha crystallin/Hsp20 domain [IPR002068] (1); HSP20-like chaperone [IPR008978] (1)	-	C_unshiu_02473_mRNA_1.1	-
GF0042754	0	1	0	Hypothetical protein (1)			-	C_unshiu_02472_mRNA_1.1	-
GF0042753	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_02471_mRNA_2.1	-
GF0042752	0	1	0	Hypothetical protein (1)			-	C_unshiu_02471_mRNA_1.1	-
GF0042751	0	1	0	Hypothetical protein (1)			-	C_unshiu_02470_mRNA_1.1	-
GF0042750	0	1	0	Chitinase (1)	chitin catabolic process [GO:0006032 biological_process] (1); chitinase activity [GO:0004568 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1); chitin binding [GO:0008061 molecular_function] (1); cell wall macromolecule catabolic process [GO:0016998 biological_process] (1)	Chitin-binding, type 1, conserved site [IPR018371] (1); Chitin-binding, type 1 [IPR001002] (1); Glycoside hydrolase, family 19 [IPR016283] (1); Lysozyme-like domain [IPR023346] (1); Glycoside hydrolase, family 19, catalytic [IPR000726] (1)	-	C_unshiu_02466_mRNA_3.1	-
GF0042749	0	1	0	Hypothetical protein (1)		Protein of unknown function DUF241, plant [IPR004320] (1)	-	C_unshiu_02466_mRNA_1.1	-
GF0042748	0	1	0	Hypothetical protein (1)			-	C_unshiu_02465_mRNA_4.1	-
GF0042747	0	1	0	Hypothetical protein (1)			-	C_unshiu_02464_mRNA_2.1	-
GF0042746	0	1	0	Hypothetical protein (1)		LysM domain [IPR018392] (1)	-	C_unshiu_02463_mRNA_3.1	-
GF0042745	0	1	0	Hypothetical protein (1)		LysM domain [IPR018392] (1)	-	C_unshiu_02463_mRNA_1.1	-
GF0042744	0	1	0	Leucine-rich repeat protein kinase family protein, putative (1)	ATP binding [GO:0005524 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1)	Protein kinase domain [IPR000719] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Malectin-like carbohydrate-binding domain [IPR024788] (1); Protein kinase-like domain [IPR011009] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase, ATP binding site [IPR017441] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1)	-	C_unshiu_02462_mRNA_1.1	-
GF0042743	0	1	0	Hypothetical protein (1)			-	C_unshiu_02461_mRNA_2.1	-
GF0042742	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Zinc knuckle CX2CX4HX4C [IPR025836] (1)	-	C_unshiu_02461_mRNA_1.1	-
GF0042741	0	1	0	Hypothetical protein (1)			-	C_unshiu_02460_mRNA_3.1	-
GF0042740	0	1	0	Putative AC9 transposase (1)	DNA binding [GO:0003677 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Zinc finger, BED-type [IPR003656] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	-	C_unshiu_02458_mRNA_2.1	-
GF0042739	0	1	0	Hypothetical protein (1)			-	C_unshiu_02457_mRNA_3.1	-
GF0042738	0	1	0	Hypothetical protein (1)			-	C_unshiu_02454_mRNA_1.1	-
GF0042737	0	1	0	Hypothetical protein (1)			-	C_unshiu_02453_mRNA_4.1	-
GF0042736	0	1	0	Hypothetical protein (1)			-	C_unshiu_02452_mRNA_3.1	-
GF0042735	0	1	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	YEATS [IPR005033] (1)	-	C_unshiu_02449_mRNA_3.1	-
GF0042734	0	1	0	Hypothetical protein (1)			-	C_unshiu_02448_mRNA_4.1	-
GF0042733	0	1	0	Hypothetical protein (1)			-	C_unshiu_02448_mRNA_3.1	-
GF0042732	0	1	0	Hypothetical protein (1)		Ribosomal protein L2 domain 2 [IPR014722] (1)	-	C_unshiu_02448_mRNA_2.1	-
GF0042731	0	1	0	Hypothetical protein (1)		RmlC-like jelly roll fold [IPR014710] (1)	-	C_unshiu_02447_mRNA_1.1	-
GF0042730	0	1	0	Hypothetical protein (1)			-	C_unshiu_02446_mRNA_6.1	-
GF0042729	0	1	0	Hypothetical protein (1)			-	C_unshiu_02446_mRNA_4.1	-
GF0042728	0	1	0	Hypothetical protein (1)			-	C_unshiu_02446_mRNA_3.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0042727	0	1	0	Hypothetical protein (1)			-	C_unshiu_02446_mRNA_2.1	-
GF0042726	0	1	0	RNA-directed DNA polymerase (Reverse transcriptase) (1)		Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_02446_mRNA_1.1	-
GF0042725	0	1	0	Hypothetical protein (1)			-	C_unshiu_02445_mRNA_6.1	-
GF0042724	0	1	0	Hypothetical protein (1)			-	C_unshiu_02445_mRNA_5.1	-
GF0042723	0	1	0	Hypothetical protein (1)			-	C_unshiu_02445_mRNA_2.1	-
GF0042722	0	1	0	Hypothetical protein (1)			-	C_unshiu_02441_mRNA_5.1	-
GF0042721	0	1	0	Hypothetical protein (1)			-	C_unshiu_02441_mRNA_4.1	-
GF0042720	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	DEAD/DEAH box helicase domain [IPR011545] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Helicase superfamily 1/2, ATP-binding domain [IPR014001] (1)	-	C_unshiu_02441_mRNA_2.1	-
GF0042719	0	1	0	Hypothetical protein (1)			-	C_unshiu_02440_mRNA_1.1	-
GF0042718	0	1	0	Hypothetical protein (1)			-	C_unshiu_02439_mRNA_2.1	-
GF0042717	0	1	0	Hypothetical protein (1)			-	C_unshiu_02439_mRNA_1.1	-
GF0042716	0	1	0	Monosacharide transport protein (1)			-	C_unshiu_02438_mRNA_4.1	-
GF0042715	0	1	0	Hypothetical protein (1)			-	C_unshiu_02438_mRNA_2.1	-
GF0042714	0	1	0	Hypothetical protein (1)			-	C_unshiu_02436_mRNA_1.1	-
GF0042713	0	1	0	Hypothetical protein (1)			-	C_unshiu_02435_mRNA_3.1	-
GF0042712	0	1	0	Hypothetical protein (1)			-	C_unshiu_02434_mRNA_1.1	-
GF0042711	0	1	0	Hypothetical protein (1)	protein serine/threonine phosphatase activity [GO:0004722 molecular_function] (1); protein dephosphorylation [GO:0006470 biological_process] (1); cation binding [GO:0043169 molecular_function] (1); catalytic activity [GO:0003824 molecular_function] (1)	Protein phosphatase 2C family [IPR015655] (1); PPM-type phosphatase domain [IPR001932] (1); PPM-type phosphatase, divalent cation binding [IPR000222] (1)	-	C_unshiu_02433_mRNA_4.1	-
GF0042710	0	1	0	Hypothetical protein (1)			-	C_unshiu_02433_mRNA_2.1	-
GF0042709	0	1	0	Hypothetical protein (1)			-	C_unshiu_02432_mRNA_4.1	-
GF0042708	0	1	0	Hypothetical protein (1)			-	C_unshiu_02432_mRNA_2.1	-
GF0042707	0	1	0	Hypothetical protein (1)			-	C_unshiu_02431_mRNA_1.1	-
GF0042706	0	1	0	Hypothetical protein (1)			-	C_unshiu_02430_mRNA_3.1	-
GF0042705	0	1	0	Hypothetical protein (1)	O-methyltransferase activity [GO:0008171 molecular_function] (1)	S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); O-methyltransferase, family 3 [IPR002935] (1)	-	C_unshiu_02430_mRNA_2.1	-
GF0042704	0	1	0	Hypothetical protein (1)			-	C_unshiu_02429_mRNA_3.1	-
GF0042703	0	1	0	Hypothetical protein (1)			-	C_unshiu_02429_mRNA_1.1	-
GF0042702	0	1	0	Hypothetical protein (1)			-	C_unshiu_02427_mRNA_1.1	-
GF0042701	0	1	0	Hypothetical protein (1)			-	C_unshiu_02426_mRNA_3.1	-
GF0042700	0	1	0	Hypothetical protein (1)			-	C_unshiu_02425_mRNA_4.1	-
GF0042699	0	1	0	Hypothetical protein (1)			-	C_unshiu_02425_mRNA_3.1	-
GF0042698	0	1	0	Hypothetical protein (1)	integral component of membrane [GO:0016021 cellular_component] (1); cholestenol delta-isomerase activity [GO:0047750 molecular_function] (1); sterol metabolic process [GO:0016125 biological_process] (1)	Emopamil-binding protein [IPR007905] (1)	-	C_unshiu_02425_mRNA_2.1	-
GF0042697	0	1	0	Hypothetical protein (1)			-	C_unshiu_02425_mRNA_1.1	-
GF0042696	0	1	0	Hypothetical protein (1)			-	C_unshiu_02424_mRNA_1.1	-
GF0042695	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	WD40-repeat-containing domain [IPR017986] (1); WD40 repeat [IPR001680] (1); WD40/YVTN repeat-like-containing domain [IPR015943] (1); WD40 repeat, conserved site [IPR019775] (1)	-	C_unshiu_02422_mRNA_2.1	-
GF0042694	0	1	0	Hypothetical protein (1)			-	C_unshiu_02421_mRNA_4.1	-
GF0042693	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); calcium ion binding [GO:0005509 molecular_function] (1); nuclease activity [GO:0004518 molecular_function] (1); DNA repair [GO:0006281 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); EF-hand domain [IPR002048] (1); AP endonuclease 1 [IPR004808] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase, ATP binding site [IPR017441] (1); Endonuclease/exonuclease/phosphatase [IPR005135] (1); EF-Hand 1, calcium-binding site [IPR018247] (1); Protein kinase domain [IPR000719] (1); EF-hand domain pair [IPR011992] (1); Zinc finger, GRF-type [IPR010666] (1); Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_02420_mRNA_3.1	-
GF0042692	0	1	0	Hypothetical protein (1)		SGNH hydrolase-type esterase domain [IPR013830] (1)	-	C_unshiu_02419_mRNA_1.1	-
GF0042691	0	1	0	Phosphoprotein phosphatase (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_02418_mRNA_3.1	-
GF0042690	0	1	0	Hypothetical protein (1)			-	C_unshiu_02418_mRNA_1.1	-
GF0042689	0	1	0	Hypothetical protein (1)			-	C_unshiu_02416_mRNA_1.1	-
GF0042688	0	1	0	Hypothetical protein (1)			-	C_unshiu_02415_mRNA_3.1	-
GF0042687	0	1	0	Hypothetical protein (1)			-	C_unshiu_02415_mRNA_1.1	-
GF0042686	0	1	0	Hypothetical protein (1)			-	C_unshiu_02413_mRNA_4.1	-
GF0042685	0	1	0	Hypothetical protein (1)			-	C_unshiu_02413_mRNA_3.1	-
GF0042684	0	1	0	Hypothetical protein (1)			-	C_unshiu_02413_mRNA_2.1	-
GF0042683	0	1	0	Hypothetical protein (1)			-	C_unshiu_02412_mRNA_5.1	-
GF0042682	0	1	0	Hypothetical protein (1)	deadenylation-dependent decapping of nuclear-transcribed mRNA [GO:0000290 biological_process] (1); positive regulation of catalytic activity [GO:0043085 biological_process] (1); enzyme activator activity [GO:0008047 molecular_function] (1)	mRNA-decapping enzyme subunit 1 [IPR010334] (1)	-	C_unshiu_02412_mRNA_1.1	-
GF0042681	0	1	0	Hypothetical protein (1)			-	C_unshiu_02411_mRNA_5.1	-
GF0042680	0	1	0	Hypothetical protein (1)			-	C_unshiu_02411_mRNA_3.1	-
GF0042679	0	1	0	Hypothetical protein (1)			-	C_unshiu_02410_mRNA_1.1	-
GF0042678	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_02409_mRNA_3.1	-
GF0042677	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_02409_mRNA_2.1	-
GF0042676	0	1	0	Hypothetical protein (1)			-	C_unshiu_02409_mRNA_1.1	-
GF0042675	0	1	0	Hypothetical protein (1)			-	C_unshiu_02408_mRNA_1.1	-
GF0042674	0	1	0	Hypothetical protein (1)			-	C_unshiu_02407_mRNA_5.1	-
GF0042673	0	1	0	Hypothetical protein (1)			-	C_unshiu_02407_mRNA_4.1	-
GF0042672	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_02406_mRNA_6.1	-
GF0042671	0	1	0	Hypothetical protein (1)	transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	-	C_unshiu_02404_mRNA_1.1	-
GF0042670	0	1	0	Hypothetical protein (1)			-	C_unshiu_02403_mRNA_9.1	-
GF0042669	0	1	0	Hypothetical protein (1)			-	C_unshiu_02403_mRNA_4.1	-
GF0042668	0	1	0	Hypothetical protein (1)			-	C_unshiu_02403_mRNA_2.1	-
GF0042667	0	1	0	Hypothetical protein (1)			-	C_unshiu_02403_mRNA_1.1	-
GF0042666	0	1	0	Glucose-methanol-choline (GMC) oxidoreductase family protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); flavin adenine dinucleotide binding [GO:0050660 molecular_function] (1); oxidoreductase activity, acting on CH-OH group of donors [GO:0016614 molecular_function] (1)	FAD/NAD(P)-binding domain [IPR023753] (1); Glucose-methanol-choline oxidoreductase, N-terminal [IPR000172] (1); Glucose-methanol-choline oxidoreductase, C-terminal [IPR007867] (1)	-	C_unshiu_02401_mRNA_2.1	-
GF0042665	0	1	0	Hypothetical protein (1)			-	C_unshiu_02400_mRNA_3.1	-
GF0042664	0	1	0	Hypothetical protein (1)			-	C_unshiu_02399_mRNA_2.1	-
GF0042663	0	1	0	Hypothetical protein (1)			-	C_unshiu_02399_mRNA_1.1	-
GF0042662	0	1	0	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein, putative isoform 2 (1)		S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); Methyltransferase domain [IPR025714] (1)	-	C_unshiu_02396_mRNA_4.1	-
GF0042661	0	1	0	Hypothetical protein (1)	host cell surface receptor binding [GO:0046789 molecular_function] (1); fusion of virus membrane with host plasma membrane [GO:0019064 biological_process] (1); viral envelope [GO:0019031 cellular_component] (1)	Haemagglutinin, stalk [IPR013829] (1)	-	C_unshiu_02392_mRNA_1.1	-
GF0042660	0	1	0	Hypothetical protein (1)			-	C_unshiu_02390_mRNA_2.1	-
GF0042659	0	1	0	Hypothetical protein (1)			-	C_unshiu_02390_mRNA_1.1	-
GF0042658	0	1	0	Hypothetical protein (1)			-	C_unshiu_02388_mRNA_3.1	-
GF0042657	0	1	0	Hypothetical protein (1)			-	C_unshiu_02388_mRNA_2.1	-
GF0042656	0	1	0	Monosacharide transport protein (1)			-	C_unshiu_02388_mRNA_1.1	-
GF0042655	0	1	0	Hypothetical protein (1)			-	C_unshiu_02387_mRNA_2.1	-
GF0042654	0	1	0	Hypothetical protein (1)	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds [GO:0016810 molecular_function] (1); nitrogen compound metabolic process [GO:0006807 biological_process] (1)	Carbon-nitrogen hydrolase [IPR003010] (1)	-	C_unshiu_02386_mRNA_3.1	-
GF0042653	0	1	0	Hypothetical protein (1)	polysaccharide binding [GO:0030247 molecular_function] (1); calcium ion binding [GO:0005509 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Gag-polypeptide of LTR copia-type [IPR029472] (1); EGF-like calcium-binding domain [IPR001881] (1); EGF-type aspartate/asparagine hydroxylation site [IPR000152] (1); EGF-like domain [IPR000742] (1); EGF-like calcium-binding, conserved site [IPR018097] (1); Wall-associated receptor kinase, galacturonan-binding domain [IPR025287] (1)	-	C_unshiu_02386_mRNA_2.1	-
GF0042652	0	1	0	Hypothetical protein (1)			-	C_unshiu_02384_mRNA_1.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0042651	0	1	0	Hypothetical protein (1)		Nucleophile aminohydrolases, N-terminal [IPR029055] (1); Glutamine amidotransferase type 2 domain [IPR017932] (1)	-	C_unshiu_02383_mRNA_4.1	-
GF0042650	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1); Zinc knuckle CX2CX4HX4C [IPR025836] (1)	-	C_unshiu_02383_mRNA_2.1	-
GF0042649	0	1	0	Hypothetical protein (1)			-	C_unshiu_02380_mRNA_5.1	-
GF0042648	0	1	0	Hypothetical protein (1)			-	C_unshiu_02380_mRNA_3.1	-
GF0042647	0	1	0	Hypothetical protein (1)			-	C_unshiu_02380_mRNA_2.1	-
GF0042646	0	1	0	Hypothetical protein (1)			-	C_unshiu_02377_mRNA_5.1	-
GF0042645	0	1	0	Hypothetical protein (1)	transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (1)	Chloramphenicol acetyltransferase-like domain [IPR023213] (1); Transferase [IPR003480] (1)	-	C_unshiu_02377_mRNA_2.1	-
GF0042644	0	1	0	Hypothetical protein (1)			-	C_unshiu_02376_mRNA_3.1	-
GF0042643	0	1	0	Cytochrome P450 (1)	heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1)	Cytochrome P450 [IPR001128] (1); Cytochrome P450, conserved site [IPR017972] (1); Cytochrome P450, E-class, group I [IPR002401] (1)	-	C_unshiu_02376_mRNA_1.1	-
GF0042642	0	1	0	Hypothetical protein (1)			-	C_unshiu_02375_mRNA_3.1	-
GF0042641	0	1	0	Hypothetical protein (1)			-	C_unshiu_02375_mRNA_2.1	-
GF0042640	0	1	0	Hypothetical protein (1)			-	C_unshiu_02373_mRNA_1.1	-
GF0042639	0	1	0	Hypothetical protein (1)			-	C_unshiu_02372_mRNA_5.1	-
GF0042638	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_02371_mRNA_1.1	-
GF0042637	0	1	0	Amino acid permease family protein (1)	membrane [GO:0016020 cellular_component] (1); amino acid transmembrane transport [GO:0003333 biological_process] (1); amino acid transmembrane transporter activity [GO:0015171 molecular_function] (1)	Amino acid/polyamine transporter I [IPR002293] (1)	-	C_unshiu_02370_mRNA_2.1	-
GF0042636	0	1	0	Hypothetical protein (1)			-	C_unshiu_02369_mRNA_4.1	-
GF0042635	0	1	0	Hypothetical protein (1)			-	C_unshiu_02369_mRNA_2.1	-
GF0042634	0	1	0	Hypothetical protein (1)			-	C_unshiu_02368_mRNA_3.1	-
GF0042633	0	1	0	OTU-like cysteine protease (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FAR1 DNA binding domain [IPR004330] (1); FHY3/FAR1 family [IPR031052] (1)	-	C_unshiu_02368_mRNA_1.1	-
GF0042632	0	1	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	C_unshiu_02367_mRNA_1.1	-
GF0042631	0	1	0	Histone-lysine N-methyltransferase EZ1 (1)	protein binding [GO:0005515 molecular_function] (1)	SET domain [IPR001214] (1)	-	C_unshiu_02365_mRNA_2.1	-
GF0042630	0	1	0	PLC-like phosphodiesterase superfamily protein (1)	lipid metabolic process [GO:0006629 biological_process] (1); phosphoric diester hydrolase activity [GO:0008081 molecular_function] (1)	PLC-like phosphodiesterase, TIM beta/alpha-barrel domain [IPR017946] (1)	-	C_unshiu_02365_mRNA_1.1	-
GF0042629	0	1	0	Hypothetical protein (1)			-	C_unshiu_02364_mRNA_4.1	-
GF0042628	0	1	0	Isoaspartyl peptidase/L-asparaginase (1)	hydrolase activity [GO:0016787 molecular_function] (1)	Nucleophile aminohydrolases, N-terminal [IPR029055] (1); Peptidase T2, asparaginase 2 [IPR000246] (1)	-	C_unshiu_02363_mRNA_1.1	-
GF0042627	0	1	0	Hypothetical protein (1)			-	C_unshiu_02362_mRNA_6.1	-
GF0042626	0	1	0	Hypothetical protein (1)			-	C_unshiu_02362_mRNA_5.1	-
GF0042625	0	1	0	Hypothetical protein (1)			-	C_unshiu_02362_mRNA_4.1	-
GF0042624	0	1	0	Hypothetical protein (1)			-	C_unshiu_02362_mRNA_1.1	-
GF0042623	0	1	0	Hypothetical protein (1)	photoperiodism, flowering [GO:0048573 biological_process] (1); phosphatidylethanolamine binding [GO:0008429 molecular_function] (1); regulation of flower development [GO:0009909 biological_process] (1)	Phosphatidylethanolamine-binding protein PEBP [IPR008914] (1); Phosphatidylethanolamine-binding, conserved site [IPR001858] (1); Protein FLOWERING LOCUS T [IPR031095] (1)	-	C_unshiu_02361_mRNA_1.1	-
GF0042622	0	1	0	Hypothetical protein (1)			-	C_unshiu_02360_mRNA_3.1	-
GF0042621	0	1	0	Hypothetical protein (1)			-	C_unshiu_02360_mRNA_1.1	-
GF0042620	0	1	0	Hypothetical protein (1)	integral component of membrane [GO:0016021 cellular_component] (1); inorganic anion exchanger activity [GO:0005452 molecular_function] (1); membrane [GO:0016020 cellular_component] (1); anion transport [GO:0006820 biological_process] (1)	Bicarbonate transporter, eukaryotic [IPR003020] (1); Bicarbonate transporter, C-terminal [IPR011531] (1)	-	C_unshiu_02359_mRNA_1.1	-
GF0042619	0	1	0	Hypothetical protein (1)			-	C_unshiu_02357_mRNA_2.1	-
GF0042618	0	1	0	UPF0481 protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	C_unshiu_02357_mRNA_1.1	-
GF0042617	0	1	0	Hypothetical protein (1)			-	C_unshiu_02356_mRNA_5.1	-
GF0042616	0	1	0	Hypothetical protein (1)		Leucine-rich repeat 3 [IPR011713] (1)	-	C_unshiu_02356_mRNA_2.1	-
GF0042615	0	1	0	Hypothetical protein (1)		Gag-polypeptide of LTR copia-type [IPR029472] (1)	-	C_unshiu_02356_mRNA_1.1	-
GF0042614	0	1	0	RNA-directed DNA polymerase (Reverse transcriptase) (1)		Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_02355_mRNA_1.1	-
GF0042613	0	1	0	Hypothetical protein (1)			-	C_unshiu_02354_mRNA_1.1	-
GF0042612	0	1	0	Ribonuclease H (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_02353_mRNA_5.1	-
GF0042611	0	1	0	Hypothetical protein (1)			-	C_unshiu_02353_mRNA_4.1	-
GF0042610	0	1	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_02353_mRNA_3.1	-
GF0042609	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Zinc knuckle CX2CX4HX4C [IPR025836] (1)	-	C_unshiu_02353_mRNA_2.1	-
GF0042608	0	1	0	Hypothetical protein (1)			-	C_unshiu_02353_mRNA_1.1	-
GF0042607	0	1	0	Disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	AAA+ ATPase domain [IPR003593] (1); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_02351_mRNA_4.1	-
GF0042606	0	1	0	Hypothetical protein (1)			-	C_unshiu_02351_mRNA_2.1	-
GF0042605	0	1	0	Phosphoprotein phosphatase (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_02351_mRNA_1.1	-
GF0042604	0	1	0	Hypothetical protein (1)			-	C_unshiu_02350_mRNA_4.1	-
GF0042603	0	1	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1)	-	C_unshiu_02350_mRNA_3.1	-
GF0042602	0	1	0	Hypothetical protein (1)			-	C_unshiu_02349_mRNA_1.1	-
GF0042601	0	1	0	Hypothetical protein (1)			-	C_unshiu_02346_mRNA_5.1	-
GF0042600	0	1	0	Hypothetical protein (1)			-	C_unshiu_02346_mRNA_2.1	-
GF0042599	0	1	0	Hypothetical protein (1)			-	C_unshiu_02346_mRNA_1.1	-
GF0042598	0	1	0	Hypothetical protein (1)			-	C_unshiu_02345_mRNA_4.1	-
GF0042597	0	1	0	Hypothetical protein (1)			-	C_unshiu_02345_mRNA_3.1	-
GF0042596	0	1	0	Hypothetical protein (1)			-	C_unshiu_02342_mRNA_2.1	-
GF0042595	0	1	0	Hypothetical protein (1)			-	C_unshiu_02342_mRNA_1.1	-
GF0042594	0	1	0	Hypothetical protein (1)			-	C_unshiu_02341_mRNA_3.1	-
GF0042593	0	1	0	Hypothetical protein (1)			-	C_unshiu_02341_mRNA_2.1	-
GF0042592	0	1	0	NF-kappa-B inhibitor cactus (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat [IPR002110] (1); Ankyrin repeat-containing domain [IPR020683] (1)	-	C_unshiu_02341_mRNA_1.1	-
GF0042591	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	C_unshiu_02340_mRNA_3.1	-
GF0042590	0	1	0	Hypothetical protein (1)			-	C_unshiu_02339_mRNA_4.1	-
GF0042589	0	1	0	Hypothetical protein (1)	serine-type carboxypeptidase activity [GO:0004185 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Peptidase S10, serine carboxypeptidase [IPR001563] (1); Alpha/Beta hydrolase fold [IPR029058] (1)	-	C_unshiu_02339_mRNA_2.1	-
GF0042588	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_02338_mRNA_4.1	-
GF0042587	0	1	0	Hypothetical protein (1)			-	C_unshiu_02338_mRNA_2.1	-
GF0042586	0	1	0	Hypothetical protein (1)			-	C_unshiu_02338_mRNA_1.1	-
GF0042585	0	1	0	Hypothetical protein (1)			-	C_unshiu_02336_mRNA_2.1	-
GF0042584	0	1	0	Hypothetical protein (1)			-	C_unshiu_02336_mRNA_1.1	-
GF0042583	0	1	0	Calcium-dependent protein kinase 17 (1)	calcium ion binding [GO:0005509 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	EF-hand domain pair [IPR011992] (1); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); EF-hand domain [IPR002048] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); EF-Hand 1, calcium-binding site [IPR018247] (1)	-	C_unshiu_02335_mRNA_1.1	-
GF0042582	0	1	0	Transcription factor bHLH131 (1)	protein dimerization activity [GO:0046983 molecular_function] (1)	Myc-type, basic helix-loop-helix (bHLH) domain [IPR011598] (1)	-	C_unshiu_02333_mRNA_3.1	-
GF0042581	0	1	0	Early nodulin 75-like protein (1)			-	C_unshiu_02333_mRNA_2.1	-
GF0042580	0	1	0	Hypothetical protein (1)		P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_02330_mRNA_5.1	-
GF0042579	0	1	0	Hypothetical protein (1)			-	C_unshiu_02328_mRNA_2.1	-
GF0042578	0	1	0	Hypothetical protein (1)			-	C_unshiu_02327_mRNA_6.1	-
GF0042577	0	1	0	Hypothetical protein (1)			-	C_unshiu_02327_mRNA_5.1	-
GF0042576	0	1	0	Hypothetical protein (1)			-	C_unshiu_02327_mRNA_4.1	-
GF0042575	0	1	0	G-type lectin S-receptor-like serine/threonine-protein kinase RLK1 (1)	protein tyrosine kinase activity [GO:0004713 molecular_function] (1); recognition of pollen [GO:0048544 biological_process] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	PAN/Apple domain [IPR003609] (1); Bulb-type lectin domain [IPR001480] (1); S-locus glycoprotein domain [IPR000858] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Tyrosine-protein kinase, catalytic domain [IPR020635] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	-	C_unshiu_02327_mRNA_1.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0042574	0	1	0	Hypothetical protein (1)	metabolic process [GO:0008152 biological_process] (1)	Aconitase A/isopropylmalate dehydratase small subunit, swivel domain [IPR000573] (1); Aconitase/3-isopropylmalate dehydratase, swivel [IPR015928] (1); Aconitase/isopropylmalate dehydratase [IPR015937] (1)	-	C_unshiu_02324_mRNA_4.1	-
GF0042573	0	1	0	Hypothetical protein (1)			-	C_unshiu_02324_mRNA_3.1	-
GF0042572	0	1	0	Hypothetical protein (1)			-	C_unshiu_02324_mRNA_1.1	-
GF0042571	0	1	0	Hypothetical protein (1)			-	C_unshiu_02323_mRNA_1.1	-
GF0042570	0	1	0	Caffeic acid O-methyltransferase (1)	protein dimerization activity [GO:0046983 molecular_function] (1); O-methyltransferase activity [GO:0008171 molecular_function] (1); methyltransferase activity [GO:0008168 molecular_function] (1)	S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); O-methyltransferase, family 2 [IPR001077] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Plant methyltransferase dimerisation [IPR012967] (1); O-methyltransferase COMT-type [IPR016461] (1)	-	C_unshiu_02321_mRNA_3.1	-
GF0042569	0	1	0	Polynucleotidyl transferase, Ribonuclease H fold (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc knuckle CX2CX4HX4C [IPR025836] (1); Ribonuclease H-like domain [IPR012337] (1); Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_02321_mRNA_2.1	-
GF0042568	0	1	0	TSA: Wollemia nobilis transcribed RNA sequence (1)		Uncharacterised protein family, basic secretory protein [IPR007541] (1)	-	C_unshiu_02320_mRNA_4.1	-
GF0042567	0	1	0	Hypothetical protein (1)			-	C_unshiu_02319_mRNA_2.1	-
GF0042566	0	1	0	SH3 domain protein (1)			-	C_unshiu_02319_mRNA_1.1	-
GF0042565	0	1	0	Hypothetical protein (1)			-	C_unshiu_02318_mRNA_2.1	-
GF0042564	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_02318_mRNA_1.1	-
GF0042563	0	1	0	Methyl esterase 10, putative (1)		Alpha/Beta hydrolase fold [IPR029058] (1); Alpha/beta hydrolase fold-1 [IPR000073] (1)	-	C_unshiu_02316_mRNA_2.2	-
GF0042562	0	1	0	Hypothetical protein (1)			-	C_unshiu_02316_mRNA_1.1	-
GF0042561	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_02314_mRNA_6.1	-
GF0042560	0	1	0	Hypothetical protein (1)			-	C_unshiu_02314_mRNA_5.1	-
GF0042559	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_02314_mRNA_2.1	-
GF0042558	0	1	0	Hypothetical protein (1)			-	C_unshiu_02313_mRNA_7.1	-
GF0042557	0	1	0	Hypothetical protein (1)			-	C_unshiu_02313_mRNA_5.1	-
GF0042556	0	1	0	Hypothetical protein (1)			-	C_unshiu_02313_mRNA_1.1	-
GF0042555	0	1	0	Hypothetical protein (1)			-	C_unshiu_02312_mRNA_2.1	-
GF0042554	0	1	0	Lustrin A-like, putative (1)		PC-Esterase [IPR026057] (1); Trichome birefringence-like family [IPR029962] (1); PMR5 N-terminal domain [IPR025846] (1)	-	C_unshiu_02312_mRNA_1.1	-
GF0042553	0	1	0	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	C_unshiu_02311_mRNA_4.1	-
GF0042552	0	1	0	Hypothetical protein (1)		GH3 family [IPR004993] (1)	-	C_unshiu_02311_mRNA_1.1	-
GF0042551	0	1	0	Hypothetical protein (1)			-	C_unshiu_02310_mRNA_3.1	-
GF0042550	0	1	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_02309_mRNA_2.1	-
GF0042549	0	1	0	Hypothetical protein (1)			-	C_unshiu_02307_mRNA_3.1	-
GF0042548	0	1	0	LRR receptor-like kinase (1)		Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Protein kinase-like domain [IPR011009] (1); Malectin [IPR021720] (1)	-	C_unshiu_02306_mRNA_2.1	-
GF0042547	0	1	0	Seipin (1)	lipid storage [GO:0019915 biological_process] (1)	Seipin family [IPR009617] (1)	-	C_unshiu_02306_mRNA_1.1	-
GF0042546	0	1	0	12-oxophytodienoate reductase 2 (1)	FMN binding [GO:0010181 molecular_function] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1)	Aldolase-type TIM barrel [IPR013785] (1); NADH:flavin oxidoreductase/NADH oxidase, N-terminal [IPR001155] (1)	-	C_unshiu_02305_mRNA_5.1	-
GF0042545	0	1	0	Hypothetical protein (1)			-	C_unshiu_02305_mRNA_1.1	-
GF0042544	0	1	0	Hypothetical protein (1)	transporter activity [GO:0005215 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1)	Purine permease, plant [IPR030182] (1)	-	C_unshiu_02304_mRNA_5.1	-
GF0042543	0	1	0	Hypothetical protein (1)	drug transmembrane transport [GO:0006855 biological_process] (1); membrane [GO:0016020 cellular_component] (1); drug transmembrane transporter activity [GO:0015238 molecular_function] (1); antiporter activity [GO:0015297 molecular_function] (1); transmembrane transport [GO:0055085 biological_process] (1)	Multi antimicrobial extrusion protein [IPR002528] (1)	-	C_unshiu_02304_mRNA_3.1	-
GF0042542	0	1	0	Hypothetical protein (1)		Aspartate/glutamate/uridylate kinase [IPR001048] (1)	-	C_unshiu_02303_mRNA_4.1	-
GF0042541	0	1	0	Hypothetical protein (1)			-	C_unshiu_02303_mRNA_1.1	-
GF0042540	0	1	0	Hypothetical protein (1)			-	C_unshiu_02302_mRNA_1.1	-
GF0042539	0	1	0	Hypothetical protein (1)		Thaumatin [IPR001938] (1)	-	C_unshiu_02301_mRNA_3.1	-
GF0042538	0	1	0	Hypothetical protein (1)			-	C_unshiu_02300_mRNA_3.1	-
GF0042537	0	1	0	Hypothetical protein (1)			-	C_unshiu_02299_mRNA_4.1	-
GF0042536	0	1	0	Hypothetical protein (1)			-	C_unshiu_02299_mRNA_2.1	-
GF0042535	0	1	0	Hypothetical protein (1)			-	C_unshiu_02294_mRNA_1.1	-
GF0042534	0	1	0	Hypothetical protein (1)			-	C_unshiu_02293_mRNA_9.1	-
GF0042533	0	1	0	Hypothetical protein (1)			-	C_unshiu_02293_mRNA_7.1	-
GF0042532	0	1	0	Hypothetical protein (1)			-	C_unshiu_02293_mRNA_6.1	-
GF0042531	0	1	0	Hypothetical protein (1)			-	C_unshiu_02293_mRNA_5.1	-
GF0042530	0	1	0	Hypothetical protein (1)			-	C_unshiu_02293_mRNA_1.1	-
GF0042529	0	1	0	Hypothetical protein (1)		Bulb-type lectin domain [IPR001480] (1)	-	C_unshiu_02292_mRNA_3.1	-
GF0042528	0	1	0	NBS-LRR type disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_02290_mRNA_5.1	-
GF0042527	0	1	0	Disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	C_unshiu_02290_mRNA_2.1	-
GF0042526	0	1	0	Hypothetical protein (1)			-	C_unshiu_02290_mRNA_1.1	-
GF0042525	0	1	0	Hypothetical protein (1)			-	C_unshiu_02289_mRNA_3.1	-
GF0042524	0	1	0	Hypothetical protein (1)			-	C_unshiu_02286_mRNA_2.1	-
GF0042523	0	1	0	Single hybrid motif superfamily protein isoform 1 (1)		Single hybrid motif [IPR011053] (1)	-	C_unshiu_02285_mRNA_5.1	-
GF0042522	0	1	0	Hypothetical protein (1)	methyltransferase activity [GO:0008168 molecular_function] (1); protein methylation [GO:0006479 biological_process] (1)	Protein arginine N-methyltransferase [IPR025799] (1)	-	C_unshiu_02284_mRNA_1.1	-
GF0042521	0	1	0	Hypothetical protein (1)			-	C_unshiu_02280_mRNA_1.1	-
GF0042520	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_02279_mRNA_4.1	-
GF0042519	0	1	0	Hypothetical protein (1)		MULE transposase domain [IPR018289] (1)	-	C_unshiu_02279_mRNA_3.1	-
GF0042518	0	1	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1)	-	C_unshiu_02279_mRNA_1.1	-
GF0042517	0	1	0	Hypothetical protein (1)			-	C_unshiu_02278_mRNA_5.1	-
GF0042516	0	1	0	Hypothetical protein (1)			-	C_unshiu_02276_mRNA_6.1	-
GF0042515	0	1	0	Hypothetical protein (1)			-	C_unshiu_02273_mRNA_2.1	-
GF0042514	0	1	0	Hypothetical protein (1)			-	C_unshiu_02272_mRNA_4.1	-
GF0042513	0	1	0	Hypothetical protein (1)			-	C_unshiu_02272_mRNA_3.1	-
GF0042512	0	1	0	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	-	C_unshiu_02272_mRNA_1.1	-
GF0042511	0	1	0	Ubiquitin carboxyl-terminal hydrolase 12 (1)	protein binding [GO:0005515 molecular_function] (1)	TRAF-like [IPR008974] (1); MATH/TRAF domain [IPR002083] (1)	-	C_unshiu_02271_mRNA_4.1	-
GF0042510	0	1	0	Hypothetical protein (1)			-	C_unshiu_02270_mRNA_1.1	-
GF0042509	0	1	0	Hypothetical protein (1)			-	C_unshiu_02269_mRNA_2.1	-
GF0042508	0	1	0	DUF2351 family protein (1)	response to stress [GO:0006950 biological_process] (1); response to water [GO:0009415 biological_process] (1)	Ubiquitin-conjugating enzyme E2-binding protein [IPR019193] (1); Dehydrin, conserved site [IPR030513] (1); Dehydrin [IPR000167] (1)	-	C_unshiu_02267_mRNA_3.1	-
GF0042507	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Gag-polypeptide of LTR copia-type [IPR029472] (1)	-	C_unshiu_02266_mRNA_4.1	-
GF0042506	0	1	0	Hypothetical protein (1)			-	C_unshiu_02266_mRNA_3.1	-
GF0042505	0	1	0	Hypothetical protein (1)			-	C_unshiu_02266_mRNA_1.1	-
GF0042504	0	1	0	Hypothetical protein (1)			-	C_unshiu_02265_mRNA_4.1	-
GF0042503	0	1	0	Hypothetical protein (1)			-	C_unshiu_02264_mRNA_1.1	-
GF0042502	0	1	0	E3 ubiquitin-protein ligase (1)	ubiquitin-dependent protein catabolic process [GO:0006511 biological_process] (1); multicellular organismal development [GO:0007275 biological_process] (1); nucleus [GO:0005634 cellular_component] (1); protein binding [GO:0005515 molecular_function] (1)	TRAF-like [IPR008974] (1); E3 ubiquitin-protein ligase SIN-like [IPR004162] (1); Seven-in-absentia protein, TRAF-like domain [IPR018121] (1)	-	C_unshiu_02263_mRNA_2.1	-
GF0042501	0	1	0	Hypothetical protein (1)	phosphoric ester hydrolase activity [GO:0042578 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	WW domain [IPR001202] (1); SAC domain [IPR002013] (1)	-	C_unshiu_02262_mRNA_3.1	-
GF0042500	0	1	0	Ubiquitin carboxyl-terminal hydrolase family protein (1)		Plant organelle RNA recognition domain [IPR021099] (1)	-	C_unshiu_02259_mRNA_4.1	-
GF0042499	0	1	0	Hypothetical protein (1)			-	C_unshiu_02258_mRNA_1.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0042498	0	1	0	Putative ternary complex factor MIP1 (1)		Domain of unknown function DUF547 [IPR006869] (1); Ternary complex factor MIP1, leucine-zipper [IPR025757] (1)	-	C_unshiu_02257_mRNA_3.1	-
GF0042497	0	1	0	Hypothetical protein (1)			-	C_unshiu_02256_mRNA_4.1	-
GF0042496	0	1	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	-	C_unshiu_02256_mRNA_3.1	-
GF0042495	0	1	0	Hypothetical protein (1)			-	C_unshiu_02255_mRNA_3.1	-
GF0042494	0	1	0	Hypothetical protein (1)			-	C_unshiu_02255_mRNA_1.1	-
GF0042493	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Tetratricopeptide-like helical domain [IPR011990] (1); Elongated TPR repeat-containing domain [IPR023114] (1)	-	C_unshiu_02252_mRNA_7.1	-
GF0042492	0	1	0	Hypothetical protein (1)			-	C_unshiu_02252_mRNA_1.1	-
GF0042491	0	1	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_02251_mRNA_3.1	-
GF0042490	0	1	0	Hypothetical protein (1)			-	C_unshiu_02250_mRNA_1.1	-
GF0042489	0	1	0	Hypothetical protein (1)			-	C_unshiu_02248_mRNA_2.1	-
GF0042488	0	1	0	Hypothetical protein (1)			-	C_unshiu_02248_mRNA_1.1	-
GF0042487	0	1	0	Hypothetical protein (1)			-	C_unshiu_02247_mRNA_4.1	-
GF0042486	0	1	0	Hypothetical protein (1)			-	C_unshiu_02247_mRNA_3.1	-
GF0042485	0	1	0	Hypothetical protein (1)	endopeptidase inhibitor activity [GO:0004866 molecular_function] (1)	Proteinase inhibitor I3, Kunitz legume [IPR002160] (1); Kunitz inhibitor ST1-like [IPR011065] (1)	-	C_unshiu_02247_mRNA_1.1	-
GF0042484	0	1	0	Hypothetical protein (1)			-	C_unshiu_02246_mRNA_4.1	-
GF0042483	0	1	0	Hypothetical protein (1)			-	C_unshiu_02246_mRNA_2.1	-
GF0042482	0	1	0	Hypothetical protein (1)			-	C_unshiu_02245_mRNA_3.1	-
GF0042481	0	1	0	Putative disease resistance RGA1 (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_02245_mRNA_2.1	-
GF0042480	0	1	0	Hypothetical protein (1)			-	C_unshiu_02245_mRNA_1.1	-
GF0042479	0	1	0	Isopenicillin N epimerase (1)	catalytic activity [GO:0003824 molecular_function] (1)	Pyridoxal phosphate-dependent transferase, major region, subdomain 1 [IPR015421] (1); Pyridoxal phosphate-dependent transferase [IPR015424] (1)	-	C_unshiu_02244_mRNA_1.1	-
GF0042478	0	1	0	Hypothetical protein (1)			-	C_unshiu_02243_mRNA_3.1	-
GF0042477	0	1	0	Hypothetical protein (1)		Ribosomal protein S5 domain 2-type fold [IPR020568] (1); Ribosomal protein S5 domain 2-type fold, subgroup [IPR014721] (1)	-	C_unshiu_02243_mRNA_1.1	-
GF0042476	0	1	0	Sugar transporter (1)	transmembrane transport [GO:0055085 biological_process] (1); transporter activity [GO:0005215 molecular_function] (1); membrane [GO:0016020 cellular_component] (1); transmembrane transporter activity [GO:0022857 molecular_function] (1); substrate-specific transmembrane transporter activity [GO:0022891 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1)	Major facilitator, sugar transporter-like [IPR005828] (1); Sugar/inositol transporter [IPR003663] (1); Sugar transporter, conserved site [IPR005829] (1); Major facilitator superfamily domain [IPR020846] (1)	-	C_unshiu_02242_mRNA_1.1	-
GF0042475	0	1	0	Hypothetical protein (1)			-	C_unshiu_02240_mRNA_6.1	-
GF0042474	0	1	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_02240_mRNA_1.1	-
GF0042473	0	1	0	Hypothetical protein (1)		Nop domain [IPR002687] (1)	-	C_unshiu_02239_mRNA_4.1	-
GF0042472	0	1	0	Hypothetical protein (1)			-	C_unshiu_02239_mRNA_1.1	-
GF0042471	0	1	0	Hypothetical protein (1)			-	C_unshiu_02238_mRNA_2.1	-
GF0042470	0	1	0	Leucine-rich repeat protein kinase family protein (1)		Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	-	C_unshiu_02238_mRNA_1.1	-
GF0042469	0	1	0	Hypothetical protein (1)			-	C_unshiu_02237_mRNA_1.1	-
GF0042468	0	1	0	Hypothetical protein (1)		Ribosomal protein S5 domain 2-type fold, subgroup [IPR014721] (1)	-	C_unshiu_02235_mRNA_2.1	-
GF0042467	0	1	0	Hypothetical protein (1)			-	C_unshiu_02235_mRNA_1.1	-
GF0042466	0	1	0	Hypothetical protein (1)			-	C_unshiu_02233_mRNA_1.1	-
GF0042465	0	1	0	Hypothetical protein (1)		Transposase, MuDR, plant [IPR004332] (1)	-	C_unshiu_02230_mRNA_3.1	-
GF0042464	0	1	0	Hypothetical protein (1)			-	C_unshiu_02230_mRNA_1.1	-
GF0042463	0	1	0	Hypothetical protein (1)			-	C_unshiu_02229_mRNA_5.1	-
GF0042462	0	1	0	Putative retroelement pol polyprotein (1)		Gag-polypeptide of LTR copia-type [IPR029472] (1)	-	C_unshiu_02229_mRNA_2.1	-
GF0042461	0	1	0	Hypothetical protein (1)			-	C_unshiu_02228_mRNA_2.1	-
GF0042460	0	1	0	Disease resistance protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_02228_mRNA_1.1	-
GF0042459	0	1	0	Hypothetical protein (1)			-	C_unshiu_02227_mRNA_3.1	-
GF0042458	0	1	0	Hypothetical protein (1)			-	C_unshiu_02227_mRNA_2.1	-
GF0042457	0	1	0	Hypothetical protein (1)			-	C_unshiu_02225_mRNA_2.1	-
GF0042456	0	1	0	Leucine-rich repeat receptor-like serine/threonine/tyrosine-protein kinase SOBIR1 (1)	ATP binding [GO:0005524 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Serine/threonine-protein kinase, active site [IPR008271] (1)	-	C_unshiu_02225_mRNA_1.1	-
GF0042455	0	1	0	Hypothetical protein (1)			-	C_unshiu_02223_mRNA_2.1	-
GF0042454	0	1	0	Hypothetical protein (1)	translation release factor activity [GO:0003747 molecular_function] (1); translational termination [GO:0006415 biological_process] (1)	Double-stranded RNA-binding domain [IPR014720] (1); Peptide chain release factor class I/class II [IPR000352] (1)	-	C_unshiu_02223_mRNA_1.1	-
GF0042453	0	1	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	-	C_unshiu_02222_mRNA_1.1	-
GF0042452	0	1	0	Hypothetical protein (1)			-	C_unshiu_02221_mRNA_1.1	-
GF0042451	0	1	0	Hypothetical protein (1)		Protein of unknown function DUF966 [IPR010369] (1)	-	C_unshiu_02220_mRNA_4.1	-
GF0042450	0	1	0	Hypothetical protein (1)			-	C_unshiu_02218_mRNA_3.1	-
GF0042449	0	1	0	Phosphoprotein phosphatase (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_02218_mRNA_2.1	-
GF0042448	0	1	0	Hypothetical protein (1)			-	C_unshiu_02217_mRNA_2.1	-
GF0042447	0	1	0	RNA polymerase II ctd phosphatase-like protein (1)		HAD-like domain [IPR023214] (1); BRCT domain [IPR001357] (1); FCP1 homology domain [IPR004274] (1)	-	C_unshiu_02217_mRNA_1.1	-
GF0042446	0	1	0	Hypothetical protein (1)			-	C_unshiu_02213_mRNA_3.1	-
GF0042445	0	1	0	Hypothetical protein (1)			-	C_unshiu_02213_mRNA_1.1	-
GF0042444	0	1	0	Hypothetical protein (1)			-	C_unshiu_02212_mRNA_6.1	-
GF0042443	0	1	0	Hypothetical protein (1)			-	C_unshiu_02212_mRNA_5.1	-
GF0042442	0	1	0	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_02212_mRNA_4.1	-
GF0042441	0	1	0	Hypothetical protein (1)			-	C_unshiu_02211_mRNA_8.1	-
GF0042440	0	1	0	Hypothetical protein (1)			-	C_unshiu_02211_mRNA_7.1	-
GF0042439	0	1	0	Hypothetical protein (1)	membrane [GO:0016020 cellular_component] (1); ammonium transport [GO:0015696 biological_process] (1); ammonium transmembrane transporter activity [GO:0008519 molecular_function] (1); ammonium transmembrane transport [GO:0072488 biological_process] (1)	Ammonium transporter [IPR001905] (1); Ammonium transporter, conserved site [IPR018047] (1); Ammonium/urea transporter [IPR029020] (1); Ammonium transporter AmtB-like domain [IPR024041] (1)	-	C_unshiu_02210_mRNA_1.1	-
GF0042438	0	1	0	Oleosin (1)	monolayer-surrounded lipid storage body [GO:0012511 cellular_component] (1); integral component of membrane [GO:0016021 cellular_component] (1)	Oleosin [IPR000136] (1)	-	C_unshiu_02209_mRNA_3.1	-
GF0042437	0	1	0	Hypothetical protein (1)			-	C_unshiu_02208_mRNA_3.1	-
GF0042436	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Post-SET domain [IPR003616] (1); SET domain [IPR001214] (1)	-	C_unshiu_02207_mRNA_3.1	-
GF0042435	0	1	0	Elongation factor 2 (1)	GTP binding [GO:0005525 molecular_function] (1)	Ribosomal protein S5 domain 2-type fold, subgroup [IPR014721] (1); Translation elongation factor EFG, V domain [IPR000640] (1); Translation protein, beta-barrel domain [IPR009000] (1); Translation elongation factor EFG/EF2, domain IV [IPR005517] (1); Ribosomal protein S5 domain 2-type fold [IPR020568] (1); Translation elongation factor EFTu/EF1A, domain 2 [IPR004161] (1); Elongation factor G, III-V domain [IPR009022] (1)	-	C_unshiu_02207_mRNA_1.1	-
GF0042434	0	1	0	Hypothetical protein (1)			-	C_unshiu_02206_mRNA_4.1	-
GF0042433	0	1	0	Hypothetical protein (1)			-	C_unshiu_02205_mRNA_3.1	-
GF0042432	0	1	0	Hypothetical protein (1)			-	C_unshiu_02204_mRNA_5.1	-
GF0042431	0	1	0	Hypothetical protein (1)			-	C_unshiu_02204_mRNA_4.1	-
GF0042430	0	1	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1)	Chaperonin Cpn60/TCP-1 family [IPR002423] (1); GroEL-like equatorial domain [IPR027413] (1); Chaperone tailless complex polypeptide 1 (TCP-1) [IPR017998] (1)	-	C_unshiu_02204_mRNA_3.1	-
GF0042429	0	1	0	Hypothetical protein (1)			-	C_unshiu_02201_mRNA_2.1	-
GF0042428	0	1	0	Hypothetical protein (1)	metal ion binding [GO:0046872 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger C2H2-type/integrase DNA-binding domain [IPR013087] (1); Zinc finger, C2H2-like [IPR015880] (1); Zinc finger, C2H2 [IPR007087] (1)	-	C_unshiu_02200_mRNA_6.1	-
GF0042427	0	1	0	Hypothetical protein (1)	metal ion binding [GO:0046872 molecular_function] (1)	Zinc finger, C2H2 [IPR007087] (1)	-	C_unshiu_02200_mRNA_5.1	-
GF0042426	0	1	0	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	C_unshiu_02200_mRNA_4.1	-
GF0042425	0	1	0	Putative pentatricopeptide repeat domain containing protein (1)	protein binding [GO:0005515 molecular_function] (1)	Pentatricopeptide repeat [IPR002885] (1); Tetratricopeptide-like helical domain [IPR011990] (1)	-	C_unshiu_02200_mRNA_3.1	-
GF0042424	0	1	0	Hypothetical protein (1)	ATPase activity [GO:0016887 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Anion-transporting ATPase-like domain [IPR025723] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Arsenical pump ATPase, ArsA/GET3 [IPR016300] (1)	-	C_unshiu_02200_mRNA_1.1	-
GF0042423	0	1	0	Hypothetical protein (1)			-	C_unshiu_02199_mRNA_1.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0042422	0	1	0	Pectin acetylesterase (1)	hydrolase activity [GO:0016787 molecular_function] (1)	Alpha/Beta hydrolase fold [IPR029058] (1); Pectinacetylesterase/NOTUM [IPR004963] (1)	-	C_unshiu_02197_mRNA_2.1	-
GF0042421	0	1	0	Calcium-binding protein CML38 (1)	calcium ion binding [GO:0005509 molecular_function] (1)	EF-hand domain pair [IPR011992] (1); EF-Hand 1, calcium-binding site [IPR018247] (1); EF-hand domain [IPR002048] (1)	-	C_unshiu_02196_mRNA_5.1	-
GF0042420	0	1	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	-	C_unshiu_02196_mRNA_4.1	-
GF0042419	0	1	0	Kinase family protein / peptidoglycan-binding LysM domain-containing protein, putative (1)		Concanavalin A-like lectin/glucanase domain [IPR013320] (1); LysM domain [IPR018392] (1)	-	C_unshiu_02196_mRNA_3.1	-
GF0042418	0	1	0	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); ADP binding [GO:0043531 molecular_function] (1); binding [GO:0005488 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Armadillo [IPR000225] (1); Amine oxidase [IPR002937] (1); Armadillo-like helical [IPR011989] (1); FAD/NAD(P)-binding domain [IPR023753] (1); NB-ARC [IPR002182] (1); Armadillo-type fold [IPR016024] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_02195_mRNA_1.1	-
GF0042417	0	1	0	Hypothetical protein (1)			-	C_unshiu_02193_mRNA_2.1	-
GF0042416	0	1	0	Hypothetical protein (1)			-	C_unshiu_02193_mRNA_1.1	-
GF0042415	0	1	0	Hypothetical protein (1)			-	C_unshiu_02192_mRNA_2.1	-
GF0042414	0	1	0	Hypothetical protein (1)			-	C_unshiu_02191_mRNA_4.1	-
GF0042413	0	1	0	Hypothetical protein (1)			-	C_unshiu_02191_mRNA_3.1	-
GF0042412	0	1	0	Hypothetical protein (1)			-	C_unshiu_02188_mRNA_1.1	-
GF0042411	0	1	0	Hypothetical protein (1)			-	C_unshiu_02187_mRNA_1.1	-
GF0042410	0	1	0	Hypothetical protein (1)			-	C_unshiu_02186_mRNA_7.1	-
GF0042409	0	1	0	Hypothetical protein (1)			-	C_unshiu_02186_mRNA_5.1	-
GF0042408	0	1	0	Hypothetical protein (1)			-	C_unshiu_02186_mRNA_4.1	-
GF0042407	0	1	0	Hypothetical protein (1)			-	C_unshiu_02186_mRNA_3.1	-
GF0042406	0	1	0	Hypothetical protein (1)			-	C_unshiu_02186_mRNA_1.1	-
GF0042405	0	1	0	Hypothetical protein (1)			-	C_unshiu_02185_mRNA_7.1	-
GF0042404	0	1	0	Hypothetical protein (1)			-	C_unshiu_02185_mRNA_4.1	-
GF0042403	0	1	0	Hypothetical protein (1)			-	C_unshiu_02185_mRNA_1.1	-
GF0042402	0	1	0	Hypothetical protein (1)			-	C_unshiu_02183_mRNA_4.1	-
GF0042401	0	1	0	Hypothetical protein (1)			-	C_unshiu_02183_mRNA_1.1	-
GF0042400	0	1	0	Hypothetical protein (1)			-	C_unshiu_02180_mRNA_2.1	-
GF0042399	0	1	0	Hypothetical protein (1)			-	C_unshiu_02179_mRNA_1.1	-
GF0042398	0	1	0	Hypothetical protein (1)			-	C_unshiu_02178_mRNA_5.1	-
GF0042397	0	1	0	Hypothetical protein (1)			-	C_unshiu_02178_mRNA_2.1	-
GF0042396	0	1	0	Hypothetical protein (1)	GTP biosynthetic process [GO:0006183 biological_process] (1); CTP biosynthetic process [GO:0006241 biological_process] (1); UTP biosynthetic process [GO:0006228 biological_process] (1); nucleoside diphosphate phosphorylation [GO:0006165 biological_process] (1); nucleoside diphosphate kinase activity [GO:0004550 molecular_function] (1)	Nucleoside diphosphate kinase [IPR001564] (1)	-	C_unshiu_02178_mRNA_1.1	-
GF0042395	0	1	0	Hypothetical protein (1)			-	C_unshiu_02177_mRNA_4.1	-
GF0042394	0	1	0	Hypothetical protein (1)			-	C_unshiu_02177_mRNA_3.1	-
GF0042393	0	1	0	Hypothetical protein (1)			-	C_unshiu_02177_mRNA_2.1	-
GF0042392	0	1	0	Hypothetical protein (1)			-	C_unshiu_02175_mRNA_4.1	-
GF0042391	0	1	0	Hypothetical protein (1)	hydrolase activity, acting on ester bonds [GO:0016788 molecular_function] (1)	Harbinger transposase-derived protein [IPR006912] (1)	-	C_unshiu_02175_mRNA_2.1	-
GF0042390	0	1	0	Hypothetical protein (1)		Gag-polypeptide of LTR copia-type [IPR029472] (1)	-	C_unshiu_02174_mRNA_1.1	-
GF0042389	0	1	0	Hypothetical protein (1)			-	C_unshiu_02170_mRNA_6.1	-
GF0042388	0	1	0	Hypothetical protein (1)	O-methyltransferase activity [GO:0008171 molecular_function] (1); methyltransferase activity [GO:0008168 molecular_function] (1)	S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); O-methyltransferase COMT-type [IPR016461] (1); O-methyltransferase, family 2 [IPR001077] (1)	-	C_unshiu_02170_mRNA_2.1	-
GF0042387	0	1	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	-	C_unshiu_02169_mRNA_4.1	-
GF0042386	0	1	0	Hypothetical protein (1)		Transposase, MuDR, plant [IPR004332] (1)	-	C_unshiu_02169_mRNA_3.1	-
GF0042385	0	1	0	Hypothetical protein (1)			-	C_unshiu_02169_mRNA_1.1	-
GF0042384	0	1	0	Hypothetical protein (1)			-	C_unshiu_02168_mRNA_8.1	-
GF0042383	0	1	0	Hypothetical protein (1)			-	C_unshiu_02168_mRNA_7.1	-
GF0042382	0	1	0	Hypothetical protein (1)			-	C_unshiu_02168_mRNA_3.1	-
GF0042381	0	1	0	Serine/threonine-protein kinase Nek4 , related (1)	ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Protein kinase, ATP binding site [IPR017441] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	-	C_unshiu_02167_mRNA_6.1	-
GF0042380	0	1	0	Hypothetical protein (1)			-	C_unshiu_02167_mRNA_4.1	-
GF0042379	0	1	0	Hypothetical protein (1)			-	C_unshiu_02167_mRNA_2.1	-
GF0042378	0	1	0	Hypothetical protein (1)			-	C_unshiu_02165_mRNA_3.1	-
GF0042377	0	1	0	Hypothetical protein (1)			-	C_unshiu_02165_mRNA_2.1	-
GF0042376	0	1	0	Hypothetical protein (1)			-	C_unshiu_02165_mRNA_1.1	-
GF0042375	0	1	0	Hypothetical protein (1)			-	C_unshiu_02163_mRNA_3.1	-
GF0042374	0	1	0	Hypothetical protein (1)			-	C_unshiu_02163_mRNA_2.1	-
GF0042373	0	1	0	Hypothetical protein (1)			-	C_unshiu_02163_mRNA_1.1	-
GF0042372	0	1	0	Hypothetical protein (1)	terpene synthase activity [GO:0010333 molecular_function] (1); lyase activity [GO:0016829 molecular_function] (1); magnesium ion binding [GO:0000287 molecular_function] (1)	Isoprenoid synthase domain [IPR008949] (1); Terpene synthase, metal-binding domain [IPR005630] (1)	-	C_unshiu_02162_mRNA_3.1	-
GF0042371	0	1	0	Putative disease resistance gene NBS-LRR family protein (1)	ADP binding [GO:0043531 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_02160_mRNA_5.1	-
GF0042370	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_02159_mRNA_3.1	-
GF0042369	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_02159_mRNA_2.1	-
GF0042368	0	1	0	Hypothetical protein (1)	recognition of pollen [GO:0048544 biological_process] (1)	S-locus glycoprotein domain [IPR000858] (1)	-	C_unshiu_02158_mRNA_4.1	-
GF0042367	0	1	0	Hypothetical protein (1)			-	C_unshiu_02158_mRNA_3.1	-
GF0042366	0	1	0	Hypothetical protein (1)	recognition of pollen [GO:0048544 biological_process] (1)	PAN/Apple domain [IPR003609] (1); Bulb-type lectin domain [IPR001480] (1); S-locus glycoprotein domain [IPR000858] (1)	-	C_unshiu_02158_mRNA_2.1	-
GF0042365	0	1	0	Hypothetical protein (1)			-	C_unshiu_02157_mRNA_4.1	-
GF0042364	0	1	0	Exo-polygalacturonase, family GH28 (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1); polygalacturonase activity [GO:0004650 molecular_function] (1)	Pectin lyase fold/virulence factor [IPR011050] (1); Pectin lyase fold [IPR012334] (1); Parallel beta-helix repeat [IPR006626] (1); Glycoside hydrolase, family 28 [IPR000743] (1)	-	C_unshiu_02157_mRNA_2.1	-
GF0042363	0	1	0	Hypothetical protein (1)			-	C_unshiu_02157_mRNA_1.1	-
GF0042362	0	1	0	Hypothetical protein (1)			-	C_unshiu_02156_mRNA_1.1	-
GF0042361	0	1	0	Hypothetical protein (1)			-	C_unshiu_02155_mRNA_4.1	-
GF0042360	0	1	0	Hypothetical protein (1)			-	C_unshiu_02155_mRNA_1.1	-
GF0042359	0	1	0	Disease resistance family protein / LRR family protein, putative (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_02153_mRNA_2.1	-
GF0042358	0	1	0	Disease resistance family protein / LRR family protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1)	-	C_unshiu_02153_mRNA_1.1	-
GF0042357	0	1	0	Hypothetical protein (1)			-	C_unshiu_02152_mRNA_1.1	-
GF0042356	0	1	0	Hypothetical protein (1)	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1)	Cytochrome P450 [IPR001128] (1)	-	C_unshiu_02151_mRNA_3.1	-
GF0042355	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, SWIM-type [IPR007527] (1); Transposase, MuDR, plant [IPR004332] (1); Zinc finger, PMZ-type [IPR006564] (1); MULE transposase domain [IPR018289] (1)	-	C_unshiu_02151_mRNA_2.1	-
GF0042354	0	1	0	Hypothetical protein (1)			-	C_unshiu_02151_mRNA_1.1	-
GF0042353	0	1	0	60S ribosomal protein L36 (1)	ribosome [GO:0005840 cellular_component] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1); translation [GO:0006412 biological_process] (1); intracellular [GO:0005622 cellular_component] (1)	Ribosomal protein L36e [IPR000509] (1)	-	C_unshiu_02150_mRNA_2.1	-
GF0042352	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat-containing domain [IPR020683] (1); Ankyrin repeat [IPR002110] (1)	-	C_unshiu_02149_mRNA_4.1	-
GF0042351	0	1	0	BURP domain-containing protein (1)		BURP domain [IPR004873] (1)	-	C_unshiu_02149_mRNA_2.1	-
GF0042350	0	1	0	Hypothetical protein (1)			-	C_unshiu_02148_mRNA_1.1	-
GF0042349	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	C_unshiu_02147_mRNA_2.1	-
GF0042348	0	1	0	Hypothetical protein (1)			-	C_unshiu_02147_mRNA_1.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0042347	0	1	0	4-hydroxy-3-methylbut-2-enyl diphosphate reductase (1)	4-hydroxy-3-methylbut-2-en-1-yl diphosphate reductase activity [GO:0051745 molecular_function] (1); isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway [GO:0019288 biological_process] (1); metal ion binding [GO:0046872 molecular_function] (1); dimethylallyl diphosphate biosynthetic process [GO:0050992 biological_process] (1)	4-hydroxy-3-methylbut-2-enyl diphosphate reductase [IPR003451] (1)	-	C_unshiu_02145_mRNA_3.1	-
GF0042346	0	1	0	Hypothetical protein (1)			-	C_unshiu_02143_mRNA_2.1	-
GF0042345	0	1	0	Hypothetical protein (1)			-	C_unshiu_02142_mRNA_2.1	-
GF0042344	0	1	0	Hypothetical protein (1)			-	C_unshiu_02142_mRNA_1.1	-
GF0042343	0	1	0	PsbA protein (1)	photosynthetic electron transport in photosystem II [GO:0009772 biological_process] (1); electron transporter, transferring electrons within the cyclic electron transport pathway of photosynthesis activity [GO:0045156 molecular_function] (1); photosynthesis, light reaction [GO:0019684 biological_process] (1)	Photosynthetic reaction centre, L/M [IPR000484] (1)	-	C_unshiu_02140_mRNA_1.1	-
GF0042342	0	1	0	Hypothetical protein (1)			-	C_unshiu_02139_mRNA_3.1	-
GF0042341	0	1	0	Hypothetical protein (1)			-	C_unshiu_02138_mRNA_3.1	-
GF0042340	0	1	0	Hypothetical protein (1)			-	C_unshiu_02138_mRNA_1.1	-
GF0042339	0	1	0	Hypothetical protein (1)		Protein of unknown function DUF866, eukaryotic [IPR008584] (1)	-	C_unshiu_02137_mRNA_2.1	-
GF0042338	0	1	0	Hypothetical protein (1)			-	C_unshiu_02136_mRNA_2.1	-
GF0042337	0	1	0	Hypothetical protein (1)			-	C_unshiu_02136_mRNA_1.1	-
GF0042336	0	1	0	Hypothetical protein (1)			-	C_unshiu_02134_mRNA_2.1	-
GF0042335	0	1	0	Hypothetical protein (1)			-	C_unshiu_02131_mRNA_7.1	-
GF0042334	0	1	0	Hypothetical protein (1)			-	C_unshiu_02131_mRNA_6.1	-
GF0042333	0	1	0	Hypothetical protein (1)			-	C_unshiu_02131_mRNA_3.1	-
GF0042332	0	1	0	Hypothetical protein (1)			-	C_unshiu_02131_mRNA_2.1	-
GF0042331	0	1	0	Hypothetical protein (1)			-	C_unshiu_02131_mRNA_1.1	-
GF0042330	0	1	0	Hypothetical protein (1)			-	C_unshiu_02130_mRNA_6.1	-
GF0042329	0	1	0	Hypothetical protein (1)			-	C_unshiu_02130_mRNA_5.1	-
GF0042328	0	1	0	Putative non-LTR retroelement reverse transcriptase (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_02130_mRNA_4.1	-
GF0042327	0	1	0	Hypothetical protein (1)			-	C_unshiu_02130_mRNA_2.1	-
GF0042326	0	1	0	Hypothetical protein (1)			-	C_unshiu_02129_mRNA_4.1	-
GF0042325	0	1	0	Hypothetical protein (1)			-	C_unshiu_02126_mRNA_3.1	-
GF0042324	0	1	0	Disease resistance protein (CC-NBS-LRR class) family protein (1)	ADP binding [GO:0043531 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1); AAA+ ATPase domain [IPR003593] (1)	-	C_unshiu_02125_mRNA_3.1	-
GF0042323	0	1	0	Hypothetical protein (1)			-	C_unshiu_02124_mRNA_6.1	-
GF0042322	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); DNA integration [GO:0015074 biological_process] (1)	Integrase, catalytic core [IPR001584] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_02124_mRNA_4.1	-
GF0042321	0	1	0	Hypothetical protein (1)			-	C_unshiu_02123_mRNA_5.1	-
GF0042320	0	1	0	Hypothetical protein (1)			-	C_unshiu_02123_mRNA_4.1	-
GF0042319	0	1	0	Hypothetical protein (1)	metal ion binding [GO:0046872 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1); nucleotide binding [GO:0000166 molecular_function] (1)	P-type ATPase, A domain [IPR008250] (1); P-type ATPase, transmembrane domain [IPR023298] (1); P-type ATPase [IPR001757] (1); P-type ATPase, phosphorylation site [IPR018303] (1)	-	C_unshiu_02123_mRNA_3.1	-
GF0042318	0	1	0	Hypothetical protein (1)		HAD-like domain [IPR023214] (1)	-	C_unshiu_02123_mRNA_2.1	-
GF0042317	0	1	0	Hypothetical protein (1)			-	C_unshiu_02121_mRNA_7.1	-
GF0042316	0	1	0	Hypothetical protein (1)			-	C_unshiu_02121_mRNA_6.1	-
GF0042315	0	1	0	Caffeic acid 3-O-methyltransferase (1)	O-methyltransferase activity [GO:0008171 molecular_function] (1); methyltransferase activity [GO:0008168 molecular_function] (1)	O-methyltransferase, family 2 [IPR001077] (1); O-methyltransferase COMT-type [IPR016461] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	C_unshiu_02120_mRNA_3.1	-
GF0042314	0	1	0	Dolichyl-diphosphooligosaccharide-protein glycotransferase (1)	integral component of membrane [GO:0016021 cellular_component] (1); protein N-linked glycosylation [GO:0006487 biological_process] (1); oligosaccharyltransferase complex [GO:0008250 cellular_component] (1)	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit Swp1 [IPR008814] (1)	-	C_unshiu_02120_mRNA_2.1	-
GF0042313	0	1	0	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	NAD(P)-binding domain [IPR016040] (1); Alcohol dehydrogenase superfamily, zinc-type [IPR002085] (1); GroES-like [IPR011032] (1)	-	C_unshiu_02119_mRNA_4.1	-
GF0042312	0	1	0	Hypothetical protein (1)	solute:proton antiporter activity [GO:0015299 molecular_function] (1); cation transport [GO:0006812 biological_process] (1); integral component of membrane [GO:0016021 cellular_component] (1)	Cation/H+ exchanger, CPA1 family [IPR018422] (1)	-	C_unshiu_02119_mRNA_3.1	-
GF0042311	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1)	Alcohol dehydrogenase superfamily, zinc-type [IPR002085] (1); GroES-like [IPR011032] (1)	-	C_unshiu_02119_mRNA_1.1	-
GF0042310	0	1	0	Delta-cadinene synthase isozyme XC14 (1)	terpene synthase activity [GO:0010333 molecular_function] (1); lyase activity [GO:0016829 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (1); Terpene synthase, N-terminal domain [IPR001906] (1)	-	C_unshiu_02118_mRNA_4.1	-
GF0042309	0	1	0	Hypothetical protein (1)			-	C_unshiu_02117_mRNA_5.1	-
GF0042308	0	1	0	Hypothetical protein (1)			-	C_unshiu_02117_mRNA_1.1	-
GF0042307	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Endonuclease/exonuclease/phosphatase [IPR005135] (1); Zinc finger, SWIM-type [IPR007527] (1); MULE transposase domain [IPR018289] (1); Zinc finger, PMZ-type [IPR006564] (1); Transposase, MuDR, plant [IPR004332] (1)	-	C_unshiu_02116_mRNA_1.1	-
GF0042306	0	1	0	Hypothetical protein (1)			-	C_unshiu_02115_mRNA_4.1	-
GF0042305	0	1	0	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1); Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_02115_mRNA_3.1	-
GF0042304	0	1	0	Disease resistance protein RGA2 (1)		Protein RETICULATA-related [IPR021825] (1)	-	C_unshiu_02114_mRNA_2.1	-
GF0042303	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_02114_mRNA_1.1	-
GF0042302	0	1	0	Hypothetical protein (1)			-	C_unshiu_02108_mRNA_3.1	-
GF0042301	0	1	0	Hypothetical protein (1)			-	C_unshiu_02105_mRNA_6.1	-
GF0042300	0	1	0	Hypothetical protein (1)			-	C_unshiu_02104_mRNA_2.1	-
GF0042299	0	1	0	Hypothetical protein (1)			-	C_unshiu_02104_mRNA_1.1	-
GF0042298	0	1	0	Hypothetical protein (1)			-	C_unshiu_02103_mRNA_2.1	-
GF0042297	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1); Probable transposase, Ptta/En/Spm, plant [IPR004252] (1)	-	C_unshiu_02103_mRNA_1.1	-
GF0042296	0	1	0	Hypothetical protein (1)			-	C_unshiu_02102_mRNA_6.1	-
GF0042295	0	1	0	Hypothetical protein (1)			-	C_unshiu_02102_mRNA_2.1	-
GF0042294	0	1	0	Hypothetical protein (1)			-	C_unshiu_02102_mRNA_1.1	-
GF0042293	0	1	0	Rapid alkalinization factor (1)		Rapid ALkalinization Factor [IPR008801] (1)	-	C_unshiu_02101_mRNA_5.1	-
GF0042292	0	1	0	Ankyrin repeat family protein, putative (1)	protein binding [GO:0005515 molecular_function] (1)	PGG domain [IPR026961] (1); Ankyrin repeat-containing domain [IPR020683] (1); Ankyrin repeat [IPR002110] (1)	-	C_unshiu_02100_mRNA_7.1	-
GF0042291	0	1	0	Ankyrin repeat family protein, putative (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat-containing domain [IPR020683] (1); Ankyrin repeat [IPR002110] (1)	-	C_unshiu_02100_mRNA_5.1	-
GF0042290	0	1	0	Hypothetical protein (1)		Ankyrin repeat-containing domain [IPR020683] (1)	-	C_unshiu_02100_mRNA_4.1	-
GF0042289	0	1	0	Hypothetical protein (1)			-	C_unshiu_02099_mRNA_6.1	-
GF0042288	0	1	0	Hypothetical protein (1)			-	C_unshiu_02099_mRNA_4.1	-
GF0042287	0	1	0	Acetyltransferase component of pyruvate dehydrogenase complex (1)	transferase activity, transferring acyl groups [GO:0016746 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Chloramphenicol acetyltransferase-like domain [IPR023213] (1); Biotin/lipoyl attachment [IPR000089] (1); Single hybrid motif [IPR011053] (1); 2-oxoacid dehydrogenase acyltransferase, catalytic domain [IPR001078] (1)	-	C_unshiu_02099_mRNA_3.1	-
GF0042286	0	1	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	-	C_unshiu_02098_mRNA_3.1	-
GF0042285	0	1	0	Hypothetical protein (1)			-	C_unshiu_02097_mRNA_9.1	-
GF0042284	0	1	0	Hypothetical protein (1)			-	C_unshiu_02097_mRNA_8.1	-
GF0042283	0	1	0	Hypothetical protein (1)			-	C_unshiu_02097_mRNA_7.1	-
GF0042282	0	1	0	Hypothetical protein (1)			-	C_unshiu_02097_mRNA_6.1	-
GF0042281	0	1	0	Hypothetical protein (1)			-	C_unshiu_02097_mRNA_4.1	-
GF0042280	0	1	0	Hypothetical protein (1)			-	C_unshiu_02097_mRNA_3.1	-
GF0042279	0	1	0	Hypothetical protein (1)			-	C_unshiu_02097_mRNA_10.1	-
GF0042278	0	1	0	Hypothetical protein (1)			-	C_unshiu_02097_mRNA_1.1	-
GF0042277	0	1	0	Hypothetical protein (1)			-	C_unshiu_02096_mRNA_6.1	-
GF0042276	0	1	0	Hypothetical protein (1)			-	C_unshiu_02096_mRNA_5.1	-
GF0042275	0	1	0	Hypothetical protein (1)			-	C_unshiu_02096_mRNA_4.1	-
GF0042274	0	1	0	Hypothetical protein (1)			-	C_unshiu_02096_mRNA_2.1	-
GF0042273	0	1	0	Hypothetical protein (1)			-	C_unshiu_02094_mRNA_7.1	-
GF0042272	0	1	0	Hypothetical protein (1)			-	C_unshiu_02094_mRNA_6.1	-
GF0042271	0	1	0	Hypothetical protein (1)			-	C_unshiu_02094_mRNA_5.1	-
GF0042270	0	1	0	Hypothetical protein (1)			-	C_unshiu_02094_mRNA_4.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0042269	0	1	0	Hypothetical protein (1)			-	C_unshiu_02094_mRNA_2.1	-
GF0042268	0	1	0	Hypothetical protein (1)			-	C_unshiu_02093_mRNA_5.1	-
GF0042267	0	1	0	Hypothetical protein (1)			-	C_unshiu_02093_mRNA_4.1	-
GF0042266	0	1	0	Hypothetical protein (1)			-	C_unshiu_02093_mRNA_3.1	-
GF0042265	0	1	0	Hypothetical protein (1)			-	C_unshiu_02093_mRNA_2.1	-
GF0042264	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_02093_mRNA_1.1	-
GF0042263	0	1	0	DNA mismatch repair protein MutS2-like (1)			-	C_unshiu_02092_mRNA_2.1	-
GF0042262	0	1	0	Hypothetical protein (1)	ribosome [GO:0005840 cellular_component] (1); nucleic acid binding [GO:0003676 molecular_function] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1); intracellular [GO:0005622 cellular_component] (1); translation [GO:0006412 biological_process] (1)	Ribosomal protein L15, conserved site [IPR001196] (1); Ribosomal protein L18e/L15P [IPR021131] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_02092_mRNA_1.1	-
GF0042261	0	1	0	Hypothetical protein (1)			-	C_unshiu_02091_mRNA_1.1	-
GF0042260	0	1	0	Hypothetical protein (1)			-	C_unshiu_02090_mRNA_1.1	-
GF0042259	0	1	0	Hypothetical protein (1)			-	C_unshiu_02089_mRNA_5.1	-
GF0042258	0	1	0	Histone H2A (1)	DNA binding [GO:0003677 molecular_function] (1); nucleus [GO:0005634 cellular_component] (1); protein heterodimerization activity [GO:0046982 molecular_function] (1); nucleosome [GO:0000786 cellular_component] (1)	Histone H2A conserved site [IPR032458] (1); Histone H2A/H2B/H3 [IPR007125] (1); Histone-fold [IPR009072] (1); Histone H2A [IPR002119] (1)	-	C_unshiu_02089_mRNA_1.1	-
GF0042257	0	1	0	Hypothetical protein (1)			-	C_unshiu_02088_mRNA_1.1	-
GF0042256	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_02087_mRNA_2.1	-
GF0042255	0	1	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); nucleus [GO:0005634 cellular_component] (1)	DNA-binding domain [IPR016177] (1); Methyl-CpG DNA binding [IPR001739] (1)	-	C_unshiu_02087_mRNA_1.1	-
GF0042254	0	1	0	GDSL esterase/lipase 7 (1)	hydrolase activity, acting on ester bonds [GO:0016788 molecular_function] (1)	GDSL lipase/esterase [IPR001087] (1); SGNH hydrolase-type esterase domain [IPR013830] (1)	-	C_unshiu_02085_mRNA_1.1	-
GF0042253	0	1	0	Hypothetical protein (1)			-	C_unshiu_02084_mRNA_5.1	-
GF0042252	0	1	0	Hypothetical protein (1)			-	C_unshiu_02084_mRNA_4.1	-
GF0042251	0	1	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_02084_mRNA_3.1	-
GF0042250	0	1	0	Hypothetical protein (1)			-	C_unshiu_02083_mRNA_5.1	-
GF0042249	0	1	0	Hypothetical protein (1)			-	C_unshiu_02083_mRNA_3.1	-
GF0042248	0	1	0	Sesquiterpene synthase (1)	DNA binding [GO:0003677 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1); terpene synthase activity [GO:0010333 molecular_function] (1); lyase activity [GO:0016829 molecular_function] (1); magnesium ion binding [GO:0000287 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (1); Zinc finger, BED-type [IPR003656] (1); Terpene synthase, N-terminal domain [IPR001906] (1); Ribonuclease H-like domain [IPR012337] (1); Terpene synthase, metal-binding domain [IPR005630] (1); Isoprenoid synthase domain [IPR008949] (1)	-	C_unshiu_02083_mRNA_2.1	-
GF0042247	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_02082_mRNA_3.1	-
GF0042246	0	1	0	Probable xyloglucan endotransglucosylase/hydrolase protein 23 (1)	cellular glucan metabolic process [GO:0006073 biological_process] (1); apoplast [GO:0048046 cellular_component] (1); xyloglucan:xyloglucosyl transferase activity [GO:0016762 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1); cell wall [GO:0005618 cellular_component] (1); hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (1)	Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Glycoside hydrolase family 16 [IPR000757] (1); Xyloglucan endo-transglycosylase, C-terminal [IPR010713] (1)	-	C_unshiu_02081_mRNA_3.1	-
GF0042245	0	1	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	-	C_unshiu_02081_mRNA_2.1	-
GF0042244	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	C_unshiu_02080_mRNA_4.1	-
GF0042243	0	1	0	Hypothetical protein (1)			-	C_unshiu_02079_mRNA_9.1	-
GF0042242	0	1	0	Hypothetical protein (1)			-	C_unshiu_02079_mRNA_6.1	-
GF0042241	0	1	0	Hypothetical protein (1)			-	C_unshiu_02079_mRNA_3.1	-
GF0042240	0	1	0	Non-LTR retroelement reverse transcriptase-like (1)	nucleic acid binding [GO:0003676 molecular_function] (1); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1)	Ribonuclease H domain [IPR002156] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H-like domain [IPR012337] (1); Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_02079_mRNA_2.1	-
GF0042239	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Endonuclease/exonuclease/phosphatase [IPR005135] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_02079_mRNA_1.1	-
GF0042238	0	1	0	Hypothetical protein (1)			-	C_unshiu_02078_mRNA_2.1	-
GF0042237	0	1	0	LRR receptor-like kinase family protein (1)	protein binding [GO:0005515 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Protein kinase, ATP binding site [IPR017441] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Protein kinase-like domain [IPR011009] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Protein kinase domain [IPR000719] (1)	-	C_unshiu_02077_mRNA_5.1	-
GF0042236	0	1	0	Leucine-rich repeat protein kinase family protein (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase-like domain [IPR011009] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Protein kinase domain [IPR000719] (1)	-	C_unshiu_02077_mRNA_3.1	-
GF0042235	0	1	0	4-methyl-5(B-hydroxyethyl)-thiazole monophosphate biosynthesis (1)		DJ-1/PfpI [IPR002818] (1); Class I glutamine amidotransferase-like [IPR029062] (1); DJ-1 [IPR006287] (1)	-	C_unshiu_02077_mRNA_2.1	-
GF0042234	0	1	0	Chaperone protein dnaJ 8, chloroplastic (1)		DnaJ domain [IPR001623] (1)	-	C_unshiu_02073_mRNA_4.1	-
GF0042233	0	1	0	Hypothetical protein (1)			-	C_unshiu_02072_mRNA_4.1	-
GF0042232	0	1	0	Hypothetical protein (1)			-	C_unshiu_02072_mRNA_3.1	-
GF0042231	0	1	0	Hypothetical protein (1)			-	C_unshiu_02072_mRNA_1.1	-
GF0042230	0	1	0	Hypothetical protein (1)			-	C_unshiu_02071_mRNA_2.1	-
GF0042229	0	1	0	Hypothetical protein (1)		P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_02071_mRNA_1.1	-
GF0042228	0	1	0	Hypothetical protein (1)			-	C_unshiu_02070_mRNA_6.1	-
GF0042227	0	1	0	Hypothetical protein (1)			-	C_unshiu_02070_mRNA_4.1	-
GF0042226	0	1	0	Aldo/keto reductase family oxidoreductase (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1)	Aldo/keto reductase/potassium channel subunit beta [IPR001395] (1); NADP-dependent oxidoreductase domain [IPR023210] (1); Aldo/keto reductase, conserved site [IPR018170] (1)	-	C_unshiu_02069_mRNA_5.1	-
GF0042225	0	1	0	NADPH-dependent codeinone reductase-like protein (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Aldo/keto reductase/potassium channel subunit beta [IPR001395] (1); Aldo/keto reductase [IPR020471] (1); Aldo/keto reductase, conserved site [IPR018170] (1); NADP-dependent oxidoreductase domain [IPR023210] (1)	-	C_unshiu_02069_mRNA_4.1	-
GF0042224	0	1	0	Hyoscyamine 6-dioxygenase, putative isoform 1 (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Oxoglutarate/iron-dependent dioxygenase [IPR005123] (1); Isopenicillin N synthase-like [IPR027443] (1)	-	C_unshiu_02069_mRNA_2.1	-
GF0042223	0	1	0	Hypothetical protein (1)	transporter activity [GO:0005215 molecular_function] (1); membrane [GO:0016020 cellular_component] (1); transport [GO:0006810 biological_process] (1)	Proton-dependent oligopeptide transporter family [IPR000109] (1)	-	C_unshiu_02066_mRNA_7.1	-
GF0042222	0	1	0	Hypothetical protein (1)		Gag-polypeptide of LTR copia-type [IPR029472] (1)	-	C_unshiu_02066_mRNA_5.1	-
GF0042221	0	1	0	Hypothetical protein (1)			-	C_unshiu_02066_mRNA_3.1	-
GF0042220	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_02066_mRNA_2.1	-
GF0042219	0	1	0	Hypothetical protein (1)			-	C_unshiu_02065_mRNA_1.1	-
GF0042218	0	1	0	Hypothetical protein (1)			-	C_unshiu_02064_mRNA_3.1	-
GF0042217	0	1	0	TIR-NBS-LRR class disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_02064_mRNA_1.1	-
GF0042216	0	1	0	Hypothetical protein (1)			-	C_unshiu_02063_mRNA_7.1	-
GF0042215	0	1	0	Hypothetical protein (1)			-	C_unshiu_02063_mRNA_6.1	-
GF0042214	0	1	0	Hypothetical protein (1)			-	C_unshiu_02063_mRNA_2.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0042213	0	1	0	Cation/H(+) antiporter 4 (1)	transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1); cation transport [GO:0006812 biological_process] (1); zinc ion binding [GO:0008270 molecular_function] (1); sequence-specific DNA binding [GO:0043565 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); transmembrane transport [GO:0055085 biological_process] (1); solute:proton antiporter activity [GO:0015299 molecular_function] (1)	Cation/H+ exchanger [IPR006153] (1); Zinc finger, NHR/GATA-type [IPR013088] (1); Zinc finger, GATA-type [IPR000679] (1)	-	C_unshiu_02062_mRNA_3.1	-
GF0042212	0	1	0	Hypothetical protein (1)	metal ion binding [GO:0046872 molecular_function] (1)	Metallothionein, family 15, plant [IPR000347] (1)	-	C_unshiu_02062_mRNA_1.1	-
GF0042211	0	1	0	Hypothetical protein (1)			-	C_unshiu_02061_mRNA_4.1	-
GF0042210	0	1	0	Hypothetical protein (1)			-	C_unshiu_02060_mRNA_2.1	-
GF0042209	0	1	0	Hypothetical protein (1)			-	C_unshiu_02059_mRNA_3.1	-
GF0042208	0	1	0	Hypothetical protein (1)		Gag-polypeptide of LTR copia-type [IPR029472] (1)	-	C_unshiu_02059_mRNA_1.1	-
GF0042207	0	1	0	Hypothetical protein (1)			-	C_unshiu_02058_mRNA_5.1	-
GF0042206	0	1	0	Hypothetical protein (1)			-	C_unshiu_02058_mRNA_4.1	-
GF0042205	0	1	0	Leucine-rich repeat protein kinase family protein, putative (1)	protein binding [GO:0005515 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Protein kinase-like domain [IPR011009] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Protein kinase domain [IPR000719] (1); Leucine-rich repeat [IPR001611] (1); Protein kinase, ATP binding site [IPR017441] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1)	-	C_unshiu_02058_mRNA_2.1	-
GF0042204	0	1	0	Hypothetical leucine rich repeat protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_02058_mRNA_1.1	-
GF0042203	0	1	0	Hypothetical protein (1)			-	C_unshiu_02057_mRNA_9.1	-
GF0042202	0	1	0	Hypothetical protein (1)			-	C_unshiu_02057_mRNA_6.1	-
GF0042201	0	1	0	Hypothetical protein (1)			-	C_unshiu_02057_mRNA_5.1	-
GF0042200	0	1	0	Monosacharide transport protein (1)			-	C_unshiu_02057_mRNA_3.1	-
GF0042199	0	1	0	Hypothetical protein (1)			-	C_unshiu_02056_mRNA_2.1	-
GF0042198	0	1	0	LRR receptor-like kinase family protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase, ATP binding site [IPR017441] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Protein kinase-like domain [IPR011009] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Protein kinase domain [IPR000719] (1)	-	C_unshiu_02055_mRNA_2.1	-
GF0042197	0	1	0	Hypothetical protein (1)			-	C_unshiu_02055_mRNA_1.1	-
GF0042196	0	1	0	Hypothetical protein (1)			-	C_unshiu_02054_mRNA_8.1	-
GF0042195	0	1	0	Hypothetical protein (1)			-	C_unshiu_02054_mRNA_6.1	-
GF0042194	0	1	0	Hypothetical protein (1)			-	C_unshiu_02054_mRNA_4.1	-
GF0042193	0	1	0	Hypothetical protein (1)			-	C_unshiu_02054_mRNA_10.1	-
GF0042192	0	1	0	Hypothetical protein (1)			-	C_unshiu_02054_mRNA_1.1	-
GF0042191	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat-containing domain [IPR020683] (1); Ankyrin repeat [IPR002110] (1); Regulatory protein NPR, central domain [IPR024228] (1)	-	C_unshiu_02053_mRNA_7.1	-
GF0042190	0	1	0	Hypothetical protein (1)		Regulatory protein NPR, central domain [IPR024228] (1); NPR1/NIM1-like, C-terminal [IPR021094] (1)	-	C_unshiu_02053_mRNA_6.1	-
GF0042189	0	1	0	Nonexpressor of pathogenesis-related protein 1 (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat-containing domain [IPR020683] (1); NPR1/NIM1-like, C-terminal [IPR021094] (1); BTB/POZ domain [IPR000210] (1); Ankyrin repeat [IPR002110] (1); Regulatory protein NPR, central domain [IPR024228] (1); SKP1/BTB/POZ domain [IPR011333] (1)	-	C_unshiu_02053_mRNA_1.1	-
GF0042188	0	1	0	Hypothetical protein (1)	chromatin binding [GO:0003682 molecular_function] (1)	Bromo adjacent homology (BAH) domain [IPR001025] (1)	-	C_unshiu_02052_mRNA_3.1	-
GF0042187	0	1	0	Hypothetical protein (1)			-	C_unshiu_02051_mRNA_2.1	-
GF0042186	0	1	0	Hypothetical protein (1)			-	C_unshiu_02050_mRNA_5.1	-
GF0042185	0	1	0	Disease resistance protein family, putative (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_02050_mRNA_2.1	-
GF0042184	0	1	0	Hypothetical protein (1)			-	C_unshiu_02050_mRNA_1.1	-
GF0042183	0	1	0	LRR receptor-like kinase family protein (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Protein kinase-like domain [IPR011009] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase, ATP binding site [IPR017441] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_02049_mRNA_6.1	-
GF0042182	0	1	0	Hypothetical protein (1)			-	C_unshiu_02049_mRNA_4.1	-
GF0042181	0	1	0	Hypothetical protein (1)			-	C_unshiu_02049_mRNA_3.1	-
GF0042180	0	1	0	LRR receptor-like kinase family protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_02049_mRNA_1.1	-
GF0042179	0	1	0	Hypothetical protein (1)			-	C_unshiu_02048_mRNA_3.1	-
GF0042178	0	1	0	Hypothetical protein (1)			-	C_unshiu_02048_mRNA_2.1	-
GF0042177	0	1	0	Hypothetical protein (1)			-	C_unshiu_02048_mRNA_1.1	-
GF0042176	0	1	0	Hypothetical protein (1)	transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (1)	Transferase [IPR003480] (1); Chloramphenicol acetyltransferase-like domain [IPR023213] (1)	-	C_unshiu_02047_mRNA_9.1	-
GF0042175	0	1	0	Hypothetical protein (1)			-	C_unshiu_02046_mRNA_5.1	-
GF0042174	0	1	0	Hypothetical protein (1)			-	C_unshiu_02046_mRNA_4.1	-
GF0042173	0	1	0	Hypothetical protein (1)			-	C_unshiu_02046_mRNA_2.1	-
GF0042172	0	1	0	Hypothetical protein (1)			-	C_unshiu_02045_mRNA_2.1	-
GF0042171	0	1	0	Hypothetical protein (1)			-	C_unshiu_02044_mRNA_4.1	-
GF0042170	0	1	0	Hypothetical protein (1)			-	C_unshiu_02044_mRNA_1.1	-
GF0042169	0	1	0	Cc-nbs-lrr resistance protein, putative isoform 2 (1)	ADP binding [GO:0043531 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_02043_mRNA_5.1	-
GF0042168	0	1	0	Hypothetical protein (1)			-	C_unshiu_02042_mRNA_2.1	-
GF0042167	0	1	0	Hypothetical protein (1)			-	C_unshiu_02042_mRNA_1.1	-
GF0042166	0	1	0	AT1G32200 protein (1)			-	C_unshiu_02041_mRNA_5.1	-
GF0042165	0	1	0	Hypothetical protein (1)	small GTPase mediated signal transduction [GO:0007264 biological_process] (1); GTP binding [GO:0005525 molecular_function] (1); protein transport [GO:0015031 biological_process] (1)	Small GTPase superfamily, Rab type [IPR003579] (1); Small GTPase superfamily [IPR001806] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_02040_mRNA_5.1	-
GF0042164	0	1	0	Disease resistance protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_02040_mRNA_2.1	-
GF0042163	0	1	0	Hypothetical protein (1)	small GTPase mediated signal transduction [GO:0007264 biological_process] (1); GTP binding [GO:0005525 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Small GTPase superfamily [IPR001806] (1)	-	C_unshiu_02040_mRNA_1.1	-
GF0042162	0	1	0	Sesquiterpene synthase (1)	terpene synthase activity [GO:0010333 molecular_function] (1); lyase activity [GO:0016829 molecular_function] (1); magnesium ion binding [GO:0000287 molecular_function] (1)	Terpene synthase, metal-binding domain [IPR005630] (1); Isoprenoid synthase domain [IPR008949] (1)	-	C_unshiu_02039_mRNA_1.1	-
GF0042161	0	1	0	Hypothetical protein (1)			-	C_unshiu_02037_mRNA_4.1	-
GF0042160	0	1	0	Disease resistance protein (CC-NBS-LRR class) family protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_02036_mRNA_3.1	-
GF0042159	0	1	0	Hypothetical protein (1)			-	C_unshiu_02034_mRNA_1.1	-
GF0042158	0	1	0	Hypothetical protein (1)			-	C_unshiu_02033_mRNA_2.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0042157	0	1	0	Wall-associated receptor kinase 5 (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1)	-	C_unshiu_02032_mRNA_1.1	-
GF0042156	0	1	0	Hypothetical protein (1)			-	C_unshiu_02030_mRNA_5.1	-
GF0042155	0	1	0	Hypothetical protein (1)			-	C_unshiu_02030_mRNA_2.1	-
GF0042154	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Tetratricopeptide-like helical domain [IPR011990] (1)	-	C_unshiu_02029_mRNA_5.1	-
GF0042153	0	1	0	Hypothetical protein (1)			-	C_unshiu_02029_mRNA_2.1	-
GF0042152	0	1	0	Cactus-binding carboxy-terminal, cactin protein (1)	protein binding [GO:0005515 molecular_function] (1)	Cactin, central domain [IPR018816] (1); Cactin, C-terminal [IPR019134] (1)	-	C_unshiu_02027_mRNA_4.1	-
GF0042151	0	1	0	Hypothetical protein (1)			-	C_unshiu_02026_mRNA_6.1	-
GF0042150	0	1	0	Hypothetical protein (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase, ATP binding site [IPR017441] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_02023_mRNA_4.1	-
GF0042149	0	1	0	Hypothetical protein (1)		Eukaryotic translation initiation factor 3 subunit G, N-terminal [IPR024675] (1)	-	C_unshiu_02023_mRNA_1.1	-
GF0042148	0	1	0	Hypothetical protein (1)	metabolic process [GO:0008152 biological_process] (1); membrane [GO:0016020 cellular_component] (1); fatty acid biosynthetic process [GO:0006633 biological_process] (1); transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (1); catalytic activity [GO:0003824 molecular_function] (1)	Very-long-chain 3-ketoacyl-CoA synthase [IPR012392] (1); Thiolase-like [IPR016039] (1); FAE1/Type III polyketide synthase-like protein [IPR013601] (1)	-	C_unshiu_02022_mRNA_5.1	-
GF0042147	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_02022_mRNA_3.1	-
GF0042146	0	1	0	Hypothetical protein (1)			-	C_unshiu_02021_mRNA_3.1	-
GF0042145	0	1	0	Hypothetical protein (1)	double-stranded RNA binding [GO:0003725 molecular_function] (1)	YrdC-like domain [IPR006070] (1); DHBP synthase RibB-like alpha/beta domain [IPR017945] (1)	-	C_unshiu_02021_mRNA_11.1	-
GF0042144	0	1	0	Hypothetical protein (1)			-	C_unshiu_02021_mRNA_1.1	-
GF0042143	0	1	0	Hypothetical protein (1)			-	C_unshiu_02020_mRNA_1.1	-
GF0042142	0	1	0	Hypothetical protein (1)	U2AF [GO:0089701 cellular_component] (1); metal ion binding [GO:0046872 molecular_function] (1); RNA binding [GO:0003723 molecular_function] (1); mRNA splicing, via spliceosome [GO:0000398 biological_process] (1)	Alpha/Beta hydrolase fold [IPR029058] (1); U2 auxiliary factor small subunit [IPR009145] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Zinc finger, CCCH-type [IPR000571] (1)	-	C_unshiu_02019_mRNA_1.1	-
GF0042141	0	1	0	Hypothetical protein (1)			-	C_unshiu_02018_mRNA_2.1	-
GF0042140	0	1	0	Putative potassium transporter 13 (1)	potassium ion transmembrane transporter activity [GO:0015079 molecular_function] (1); potassium ion transmembrane transport [GO:0071805 biological_process] (1); membrane [GO:0016020 cellular_component] (1)	Potassium transporter [IPR003855] (1)	-	C_unshiu_02017_mRNA_1.1	-
GF0042139	0	1	0	Hypothetical protein (1)	ubiquitin-dependent protein catabolic process [GO:0006511 biological_process] (1); multicellular organismal development [GO:0007275 biological_process] (1); nucleus [GO:0005634 cellular_component] (1)	E3 ubiquitin-protein ligase SIN-like [IPR004162] (1)	-	C_unshiu_02016_mRNA_3.1	-
GF0042138	0	1	0	Hypothetical protein (1)	orotidine-5'-phosphate decarboxylase activity [GO:0004590 molecular_function] (1); 'de novo' pyrimidine nucleobase biosynthetic process [GO:0006207 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Ribulose-phosphate binding barrel [IPR011060] (1); Orotidine 5'-phosphate decarboxylase domain [IPR001754] (1); Aldolase-type TIM barrel [IPR013785] (1)	-	C_unshiu_02016_mRNA_2.1	-
GF0042137	0	1	0	Hypothetical protein (1)		Polyprenyl synthetase-related [IPR017446] (1); Isoprenoid synthase domain [IPR008949] (1)	-	C_unshiu_02016_mRNA_1.1	-
GF0042136	0	1	0	Hypothetical protein (1)			-	C_unshiu_02015_mRNA_4.1	-
GF0042135	0	1	0	Hypothetical protein (1)			-	C_unshiu_02015_mRNA_3.1	-
GF0042134	0	1	0	Hypothetical protein (1)			-	C_unshiu_02015_mRNA_1.1	-
GF0042133	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_02014_mRNA_3.1	-
GF0042132	0	1	0	Hypothetical protein (1)			-	C_unshiu_02014_mRNA_1.1	-
GF0042131	0	1	0	Zinc finger containing preotein, putative (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Zinc finger, PMZ-type [IPR006564] (1); Zinc finger, SWIM-type [IPR007527] (1)	-	C_unshiu_02013_mRNA_5.1	-
GF0042130	0	1	0	Mads box protein, putative (1)	DNA binding [GO:0003677 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	Transcription factor, MADS-box [IPR002100] (1)	-	C_unshiu_02013_mRNA_1.1	-
GF0042129	0	1	0	Hypothetical protein (1)			-	C_unshiu_02012_mRNA_2.1	-
GF0042128	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_02011_mRNA_6.1	-
GF0042127	0	1	0	Histone deacetylase 15 (1)		Histone deacetylase superfamily [IPR000286] (1); Histone deacetylase domain [IPR023801] (1)	-	C_unshiu_02011_mRNA_5.1	-
GF0042126	0	1	0	Hypothetical protein (1)			-	C_unshiu_02010_mRNA_2.1	-
GF0042125	0	1	0	Hypothetical protein (1)			-	C_unshiu_02008_mRNA_1.1	-
GF0042124	0	1	0	Hypothetical protein (1)			-	C_unshiu_02007_mRNA_5.1	-
GF0042123	0	1	0	Hypothetical protein (1)			-	C_unshiu_02007_mRNA_3.1	-
GF0042122	0	1	0	Hypothetical protein (1)			-	C_unshiu_02007_mRNA_1.1	-
GF0042121	0	1	0	Hypothetical protein (1)	Piccolo NuA4 histone acetyltransferase complex [GO:0032777 cellular_component] (1); regulation of transcription from RNA polymerase II promoter [GO:0006357 biological_process] (1); NuA4 histone acetyltransferase complex [GO:0035267 cellular_component] (1)	Enhancer of polycomb protein [IPR024943] (1)	-	C_unshiu_02003_mRNA_4.1	-
GF0042120	0	1	0	Hypothetical protein (1)	translation release factor activity [GO:0003747 molecular_function] (1); translational termination [GO:0006415 biological_process] (1)	Double-stranded RNA-binding domain [IPR014720] (1); MULE transposase domain [IPR018289] (1); Peptide chain release factor class I/class II [IPR000352] (1)	-	C_unshiu_02003_mRNA_2.1	-
GF0042119	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_02003_mRNA_1.1	-
GF0042118	0	1	0	Hypothetical protein (1)		GAG-pre-integrase domain [IPR025724] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Leucine-rich repeat 3 [IPR011713] (1)	-	C_unshiu_02002_mRNA_2.1	-
GF0042117	0	1	0	Hypothetical protein (1)			-	C_unshiu_02001_mRNA_4.1	-
GF0042116	0	1	0	Hypothetical protein (1)			-	C_unshiu_02001_mRNA_1.1	-
GF0042115	0	1	0	Hypothetical protein (1)		Transposon, En/Spm-like [IPR004242] (1)	-	C_unshiu_02000_mRNA_1.1	-
GF0042114	0	1	0	Hypothetical protein (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Glycoside hydrolase, catalytic domain [IPR013781] (1); Chitinase insertion domain [IPR029070] (1)	-	C_unshiu_01999_mRNA_4.1	-
GF0042113	0	1	0	Hypothetical protein (1)			-	C_unshiu_01999_mRNA_3.1	-
GF0042112	0	1	0	Hypothetical protein (1)			-	C_unshiu_01999_mRNA_2.1	-
GF0042111	0	1	0	Hypothetical protein (1)			-	C_unshiu_01999_mRNA_1.1	-
GF0042110	0	1	0	Hypothetical protein (1)			-	C_unshiu_01998_mRNA_3.1	-
GF0042109	0	1	0	Hypothetical protein (1)	serine-type carboxypeptidase activity [GO:0004185 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Peptidase S10, serine carboxypeptidase [IPR001563] (1); Alpha/Beta hydrolase fold [IPR029058] (1)	-	C_unshiu_01997_mRNA_1.1	-
GF0042108	0	1	0	Hypothetical protein (1)			-	C_unshiu_01994_mRNA_6.1	-
GF0042107	0	1	0	Hypothetical protein (1)		Calycin-like [IPR011038] (1); Lipocalin/cytosolic fatty-acid binding domain [IPR000566] (1); Calycin [IPR012674] (1)	-	C_unshiu_01994_mRNA_1.1	-
GF0042106	0	1	0	Putative disease resistance protein RGA1 (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	C_unshiu_01993_mRNA_6.1	-
GF0042105	0	1	0	Hypothetical protein (1)			-	C_unshiu_01993_mRNA_5.1	-
GF0042104	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, PMZ-type [IPR006564] (1); Zinc finger, SWIM-type [IPR007527] (1)	-	C_unshiu_01993_mRNA_1.1	-
GF0042103	0	1	0	Hypothetical protein (1)			-	C_unshiu_01992_mRNA_2.1	-
GF0042102	0	1	0	Cytochrome P450 76C4 (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1)	Cytochrome P450 [IPR001128] (1); Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450, conserved site [IPR017972] (1)	-	C_unshiu_01991_mRNA_4.1	-
GF0042101	0	1	0	Hypothetical protein (1)			-	C_unshiu_01991_mRNA_3.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0042100	0	1	0	G-type lectin S-receptor-like serine/threonine-protein kinase (1)	ATP binding [GO:0005524 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); recognition of pollen [GO:0048544 biological_process] (1)	S-locus glycoprotein domain [IPR000858] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); PAN/Apple domain [IPR003609] (1); Bulb-type lectin domain [IPR001480] (1); Protein kinase domain [IPR000719] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_01991_mRNA_2.1	-
GF0042099	0	1	0	Hypothetical protein (1)			-	C_unshiu_01991_mRNA_1.1	-
GF0042098	0	1	0	Hypothetical protein (1)			-	C_unshiu_01989_mRNA_3.1	-
GF0042097	0	1	0	MuDR family transposase isoform 1 (1)		MULE transposase domain [IPR018289] (1); Transposase, MuDR, plant [IPR004332] (1)	-	C_unshiu_01987_mRNA_5.1	-
GF0042096	0	1	0	Hypothetical protein (1)		HAD-like domain [IPR023214] (1); FCP1 homology domain [IPR004274] (1)	-	C_unshiu_01987_mRNA_4.1	-
GF0042095	0	1	0	Hypothetical protein (1)	ribosome [GO:0005840 cellular_component] (1); translation [GO:0006412 biological_process] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1)	Ribosomal protein S8 [IPR000630] (1)	-	C_unshiu_01987_mRNA_1.1	-
GF0042094	0	1	0	Hypothetical protein (1)			-	C_unshiu_01986_mRNA_4.1	-
GF0042093	0	1	0	Hypothetical protein (1)			-	C_unshiu_01986_mRNA_3.1	-
GF0042092	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_01986_mRNA_2.1	-
GF0042091	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_01985_mRNA_3.1	-
GF0042090	0	1	0	Hypothetical protein (1)			-	C_unshiu_01985_mRNA_2.1	-
GF0042089	0	1	0	Hypothetical protein (1)		10TM putative phosphate transporter, cytosolic domain [IPR027815] (1); Calcium permeable stress-gated cation channel 1, N-terminal transmembrane domain [IPR032880] (1)	-	C_unshiu_01984_mRNA_5.1	-
GF0042088	0	1	0	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); glutathione peroxidase activity [GO:0004602 molecular_function] (1); response to oxidative stress [GO:0006979 biological_process] (1)	Glutathione peroxidase conserved site [IPR029760] (1); Glutathione peroxidase [IPR000889] (1); Thioredoxin-like fold [IPR012336] (1); Glutathione peroxidase active site [IPR029759] (1); PWWP domain [IPR000313] (1)	-	C_unshiu_01984_mRNA_1.1	-
GF0042087	0	1	0	Hypothetical protein (1)			-	C_unshiu_01983_mRNA_5.1	-
GF0042086	0	1	0	Hypothetical protein (1)			-	C_unshiu_01983_mRNA_4.1	-
GF0042085	0	1	0	SLG-Sc and SLA-Sc genes and Melmoth retrotransposon sequence (1)			-	C_unshiu_01983_mRNA_3.1	-
GF0042084	0	1	0	Hypothetical protein (1)			-	C_unshiu_01982_mRNA_8.1	-
GF0042083	0	1	0	Hypothetical protein (1)		PIN domain-like [IPR029060] (1)	-	C_unshiu_01982_mRNA_6.1	-
GF0042082	0	1	0	Amidophosphoribosyltransferase (1)	nucleoside metabolic process [GO:0009116 biological_process] (1)	Phosphoribosyltransferase-like [IPR029057] (1); Phosphoribosyltransferase domain [IPR000836] (1)	-	C_unshiu_01982_mRNA_5.1	-
GF0042081	0	1	0	Hypothetical protein (1)		Phosphoribosyltransferase-like [IPR029057] (1)	-	C_unshiu_01982_mRNA_4.1	-
GF0042080	0	1	0	Ta11 non-LTR retroelement protein-like (1)		Zinc knuckle CX2CX4HX4C [IPR025836] (1); Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_01982_mRNA_3.1	-
GF0042079	0	1	0	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	C_unshiu_01982_mRNA_2.1	-
GF0042078	0	1	0	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_01982_mRNA_1.1	-
GF0042077	0	1	0	Hypothetical protein (1)			-	C_unshiu_01981_mRNA_1.1	-
GF0042076	0	1	0	Hypothetical protein (1)			-	C_unshiu_01980_mRNA_5.1	-
GF0042075	0	1	0	Hypothetical protein (1)			-	C_unshiu_01980_mRNA_3.1	-
GF0042074	0	1	0	Hypothetical protein (1)			-	C_unshiu_01980_mRNA_2.1	-
GF0042073	0	1	0	Hypothetical protein (1)			-	C_unshiu_01980_mRNA_1.1	-
GF0042072	0	1	0	Hypothetical protein (1)			-	C_unshiu_01979_mRNA_4.1	-
GF0042071	0	1	0	LRR receptor-like kinase (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01978_mRNA_3.1	-
GF0042070	0	1	0	Hypothetical protein (1)			-	C_unshiu_01978_mRNA_1.1	-
GF0042069	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_01976_mRNA_5.1	-
GF0042068	0	1	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_01976_mRNA_4.1	-
GF0042067	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1)	-	C_unshiu_01975_mRNA_2.1	-
GF0042066	0	1	0	Hypothetical protein (1)			-	C_unshiu_01974_mRNA_5.1	-
GF0042065	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1); Zinc finger, PMZ-type [IPR006564] (1); Zinc finger, SWIM-type [IPR007527] (1)	-	C_unshiu_01974_mRNA_4.1	-
GF0042064	0	1	0	LRR receptor-like kinase (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	-	C_unshiu_01972_mRNA_2.1	-
GF0042063	0	1	0	Hypothetical protein (1)			-	C_unshiu_01971_mRNA_5.1	-
GF0042062	0	1	0	Hypothetical protein (1)			-	C_unshiu_01971_mRNA_4.1	-
GF0042061	0	1	0	Hypothetical protein (1)			-	C_unshiu_01971_mRNA_1.1	-
GF0042060	0	1	0	Hypothetical protein (1)			-	C_unshiu_01970_mRNA_2.1	-
GF0042059	0	1	0	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_01970_mRNA_1.1	-
GF0042058	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_01969_mRNA_3.1	-
GF0042057	0	1	0	Hypothetical protein (1)			-	C_unshiu_01969_mRNA_2.1	-
GF0042056	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_01969_mRNA_1.1	-
GF0042055	0	1	0	Hypothetical protein (1)			-	C_unshiu_01968_mRNA_4.1	-
GF0042054	0	1	0	Hypothetical protein (1)		High mobility group box domain [IPR009071] (1)	-	C_unshiu_01968_mRNA_2.1	-
GF0042053	0	1	0	Hypothetical protein (1)			-	C_unshiu_01968_mRNA_1.1	-
GF0042052	0	1	0	Cc-nbs-lrr resistance protein, putative isoform 1 (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01967_mRNA_4.1	-
GF0042051	0	1	0	Hypothetical protein (1)			-	C_unshiu_01967_mRNA_2.1	-
GF0042050	0	1	0	Hypothetical protein (1)			-	C_unshiu_01966_mRNA_3.1	-
GF0042049	0	1	0	Hypothetical protein (1)			-	C_unshiu_01966_mRNA_2.1	-
GF0042048	0	1	0	Hypothetical protein (1)			-	C_unshiu_01965_mRNA_4.1	-
GF0042047	0	1	0	Hypothetical protein (1)			-	C_unshiu_01965_mRNA_3.1	-
GF0042046	0	1	0	Hypothetical protein (1)			-	C_unshiu_01965_mRNA_2.1	-
GF0042045	0	1	0	Hypothetical protein (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Protein kinase-like domain [IPR011009] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Serine/threonine-protein kinase, active site [IPR008271] (1)	-	C_unshiu_01965_mRNA_1.1	-
GF0042044	0	1	0	Hypothetical protein (1)		P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_01963_mRNA_5.1	-
GF0042043	0	1	0	ABC transporter F family member 1 (1)	ATP binding [GO:0005524 molecular_function] (1); ATPase activity [GO:0016887 molecular_function] (1)	ABC-transporter extension domain [IPR032781] (1); ABC transporter, conserved site [IPR017871] (1); ABC transporter-like [IPR003439] (1); AAA+ ATPase domain [IPR003593] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_01963_mRNA_4.1	-
GF0042042	0	1	0	Hypothetical protein (1)		Rossmann-like alpha/beta/alpha sandwich fold [IPR014729] (1)	-	C_unshiu_01963_mRNA_1.1	-
GF0042041	0	1	0	Protein prenyltransferase alpha subunit repeat-containing protein 1-B (1)	protein prenyltransferase activity [GO:0008318 molecular_function] (1); protein prenylation [GO:0018342 biological_process] (1)	Protein prenyltransferase, alpha subunit [IPR002088] (1)	-	C_unshiu_01961_mRNA_2.1	-
GF0042040	0	1	0	Hypothetical protein (1)			-	C_unshiu_01961_mRNA_1.1	-
GF0042039	0	1	0	Hypothetical protein (1)			-	C_unshiu_01960_mRNA_5.1	-
GF0042038	0	1	0	Hypothetical protein (1)			-	C_unshiu_01960_mRNA_4.1	-
GF0042037	0	1	0	Hypothetical protein (1)			-	C_unshiu_01959_mRNA_4.1	-
GF0042036	0	1	0	Glucan endo-1,3-beta-glucosidase 7 (1)	hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1)	X8 domain [IPR012946] (1); Glycoside hydrolase family 17 [IPR000490] (1); Glycoside hydrolase superfamily [IPR017853] (1); Glycoside hydrolase, catalytic domain [IPR013781] (1)	-	C_unshiu_01959_mRNA_1.1	-
GF0042035	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF632 [IPR006867] (1)	-	C_unshiu_01958_mRNA_2.1	-
GF0042034	0	1	0	Glutathione S-transferase L3 (1)	protein binding [GO:0005515 molecular_function] (1)	Thioredoxin-like fold [IPR012336] (1); Glutathione S-transferase, C-terminal-like [IPR010987] (1); Glutathione S-transferase, N-terminal [IPR004045] (1)	-	C_unshiu_01956_mRNA_2.1	-
GF0042033	0	1	0	Lambda class glutathione S-transferase (1)	protein binding [GO:0005515 molecular_function] (1)	Thioredoxin-like fold [IPR012336] (1); Glutathione S-transferase, C-terminal-like [IPR010987] (1); Glutathione S-transferase, N-terminal [IPR004045] (1)	-	C_unshiu_01956_mRNA_1.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0042032	0	1	0	Hypothetical protein (1)		Ribonuclease H1, N-terminal [IPR011320] (1); Ribosomal protein L9/RNase H1, N-terminal [IPR009027] (1); Metallo-dependent phosphatase-like [IPR029052] (1)	-	C_unshiu_01955_mRNA_5.1	-
GF0042031	0	1	0	Hypothetical protein (1)			-	C_unshiu_01955_mRNA_3.1	-
GF0042030	0	1	0	Hypothetical protein (1)			-	C_unshiu_01955_mRNA_2.1	-
GF0042029	0	1	0	Hypothetical protein (1)			-	C_unshiu_01954_mRNA_4.1	-
GF0042028	0	1	0	Hypothetical protein (1)	fatty acid biosynthetic process [GO:0006633 biological_process] (1)	Acyl carrier protein-like [IPR009081] (1); Acyl carrier protein (ACP) [IPR003231] (1); Phosphopantetheine attachment site [IPR006162] (1)	-	C_unshiu_01954_mRNA_2.1	-
GF0042027	0	1	0	Hypothetical protein (1)			-	C_unshiu_01954_mRNA_1.1	-
GF0042026	0	1	0	Hypothetical protein (1)			-	C_unshiu_01952_mRNA_1.1	-
GF0042025	0	1	0	Hypothetical protein (1)			-	C_unshiu_01950_mRNA_5.1	-
GF0042024	0	1	0	Hypothetical protein (1)			-	C_unshiu_01950_mRNA_1.1	-
GF0042023	0	1	0	Hypothetical protein (1)			-	C_unshiu_01949_mRNA_1.1	-
GF0042022	0	1	0	Hypothetical protein (1)			-	C_unshiu_01948_mRNA_2.1	-
GF0042021	0	1	0	Hypothetical protein (1)			-	C_unshiu_01948_mRNA_1.1	-
GF0042020	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Domain of unknown function DUF4371 [IPR025398] (1)	-	C_unshiu_01947_mRNA_5.1	-
GF0042019	0	1	0	LRR receptor-like serine/threonine-protein kinase FLS2 (1)	protein binding [GO:0005515 molecular_function] (1)	Protein kinase-like domain [IPR011009] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_01947_mRNA_1.1	-
GF0042018	0	1	0	Hypothetical protein (1)			-	C_unshiu_01946_mRNA_3.1	-
GF0042017	0	1	0	Pentatricopeptide repeat-containing family protein (1)	protein binding [GO:0005515 molecular_function] (1)	Pentatricopeptide repeat [IPR002885] (1); Tetratricopeptide-like helical domain [IPR011990] (1)	-	C_unshiu_01946_mRNA_2.1	-
GF0042016	0	1	0	LRR receptor-like kinase (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1)	-	C_unshiu_01944_mRNA_3.1	-
GF0042015	0	1	0	Hypothetical protein (1)			-	C_unshiu_01943_mRNA_4.1	-
GF0042014	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_01943_mRNA_3.1	-
GF0042013	0	1	0	Hypothetical protein (1)			-	C_unshiu_01942_mRNA_1.1	-
GF0042012	0	1	0	Hypothetical protein (1)			-	C_unshiu_01941_mRNA_7.1	-
GF0042011	0	1	0	Hypothetical protein (1)			-	C_unshiu_01941_mRNA_4.1	-
GF0042010	0	1	0	Hypothetical leucine rich repeat protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_01940_mRNA_4.1	-
GF0042009	0	1	0	Hypothetical protein (1)			-	C_unshiu_01940_mRNA_3.1	-
GF0042008	0	1	0	Hypothetical protein (1)			-	C_unshiu_01940_mRNA_2.1	-
GF0042007	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Zinc knuckle CX2CX4HX4C [IPR025836] (1); Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	C_unshiu_01940_mRNA_1.1	-
GF0042006	0	1	0	Hypothetical protein (1)			-	C_unshiu_01939_mRNA_5.1	-
GF0042005	0	1	0	Hypothetical protein (1)			-	C_unshiu_01939_mRNA_2.1	-
GF0042004	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF1985 [IPR015410] (1)	-	C_unshiu_01938_mRNA_3.1	-
GF0042003	0	1	0	Vinorine synthase (1)	transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (1)	Transferase [IPR003480] (1); Chloramphenicol acetyltransferase-like domain [IPR023213] (1)	-	C_unshiu_01935_mRNA_3.1	-
GF0042002	0	1	0	Hypothetical protein (1)			-	C_unshiu_01935_mRNA_2.1	-
GF0042001	0	1	0	Flavonoid 3',5'-hydroxylase (1)	iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Cytochrome P450, conserved site [IPR017972] (1); Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450 [IPR001128] (1)	-	C_unshiu_01934_mRNA_2.1	-
GF0042000	0	1	0	Flavonoid 3',5'-hydroxylase (1)	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1)	Cytochrome P450, conserved site [IPR017972] (1); Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450 [IPR001128] (1)	-	C_unshiu_01934_mRNA_1.1	-
GF0041999	0	1	0	Hypothetical protein (1)			-	C_unshiu_01933_mRNA_5.1	-
GF0041998	0	1	0	Hypothetical protein (1)			-	C_unshiu_01933_mRNA_4.1	-
GF0041997	0	1	0	Hypothetical protein (1)			-	C_unshiu_01933_mRNA_2.1	-
GF0041996	0	1	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1)	Reverse transcriptase domain [IPR000477] (1); Peptidase A2A, retrovirus, catalytic [IPR001995] (1)	-	C_unshiu_01933_mRNA_15.1	-
GF0041995	0	1	0	Hypothetical protein (1)			-	C_unshiu_01933_mRNA_12.1	-
GF0041994	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_01932_mRNA_6.1	-
GF0041993	0	1	0	Hypothetical protein (1)			-	C_unshiu_01932_mRNA_5.1	-
GF0041992	0	1	0	Hypothetical protein (1)			-	C_unshiu_01932_mRNA_4.1	-
GF0041991	0	1	0	Hypothetical protein (1)			-	C_unshiu_01931_mRNA_4.1	-
GF0041990	0	1	0	Hypothetical protein (1)			-	C_unshiu_01931_mRNA_3.1	-
GF0041989	0	1	0	Hypothetical protein (1)			-	C_unshiu_01930_mRNA_8.1	-
GF0041988	0	1	0	Ribonuclease H protein, putative (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_01930_mRNA_5.1	-
GF0041987	0	1	0	Random slug protein 5 (1)		CRAL/TRIO, N-terminal domain [IPR011074] (1); CRAL-TRIO lipid binding domain [IPR001251] (1)	-	C_unshiu_01930_mRNA_4.1	-
GF0041986	0	1	0	Chaperone protein dnaJ 49 (1)		Domain of unknown function DUF1977, DnaJ-like [IPR015399] (1)	-	C_unshiu_01930_mRNA_1.1	-
GF0041985	0	1	0	Hypothetical protein (1)			-	C_unshiu_01929_mRNA_4.1	-
GF0041984	0	1	0	Translation machinery associated TMA7 (1)		Translation machinery associated TMA7 [IPR015157] (1)	-	C_unshiu_01929_mRNA_2.1	-
GF0041983	0	1	0	RNI-like/FBD-like domains (1)	protein binding [GO:0005515 molecular_function] (1)	F-box domain [IPR001810] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01929_mRNA_10.1	-
GF0041982	0	1	0	Hypothetical protein (1)			-	C_unshiu_01929_mRNA_1.1	-
GF0041981	0	1	0	Hypothetical protein (1)	polysaccharide binding [GO:0030247 molecular_function] (1)	Wall-associated receptor kinase, galacturonan-binding domain [IPR025287] (1)	-	C_unshiu_01928_mRNA_8.1	-
GF0041980	0	1	0	Hypothetical protein (1)			-	C_unshiu_01928_mRNA_7.1	-
GF0041979	0	1	0	Hypothetical protein (1)			-	C_unshiu_01928_mRNA_4.1	-
GF0041978	0	1	0	Hypothetical protein (1)			-	C_unshiu_01928_mRNA_3.1	-
GF0041977	0	1	0	Hypothetical protein (1)		Retroviral aspartyl protease [IPR013242] (1)	-	C_unshiu_01928_mRNA_2.2	-
GF0041976	0	1	0	Hypothetical protein (1)			-	C_unshiu_01928_mRNA_1.1	-
GF0041975	0	1	0	Hypothetical protein (1)			-	C_unshiu_01927_mRNA_1.1	-
GF0041974	0	1	0	Hypothetical protein (1)			-	C_unshiu_01926_mRNA_6.1	-
GF0041973	0	1	0	Hypothetical protein (1)			-	C_unshiu_01926_mRNA_1.1	-
GF0041972	0	1	0	Hypothetical protein (1)		Histidine phosphatase superfamily, clade-1 [IPR013078] (1); Histidine phosphatase superfamily [IPR029033] (1)	-	C_unshiu_01924_mRNA_6.1	-
GF0041971	0	1	0	Hypothetical protein (1)			-	C_unshiu_01924_mRNA_5.1	-
GF0041970	0	1	0	Hypothetical protein (1)		Chromo domain-like [IPR016197] (1)	-	C_unshiu_01923_mRNA_5.1	-
GF0041969	0	1	0	Hypothetical protein (1)			-	C_unshiu_01923_mRNA_1.1	-
GF0041968	0	1	0	Hypothetical protein (1)			-	C_unshiu_01919_mRNA_1.1	-
GF0041967	0	1	0	Hypothetical protein (1)			-	C_unshiu_01918_mRNA_2.1	-
GF0041966	0	1	0	Hypothetical protein (1)			-	C_unshiu_01917_mRNA_2.1	-
GF0041965	0	1	0	Hypothetical protein (1)			-	C_unshiu_01917_mRNA_1.1	-
GF0041964	0	1	0	NBS-LRR class resistance protein Fy1-Ry1 (1)	ADP binding [GO:0043531 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_01916_mRNA_4.1	-
GF0041963	0	1	0	Hypothetical protein (1)		Protein of unknown function DUF594 [IPR007658] (1)	-	C_unshiu_01916_mRNA_1.1	-
GF0041962	0	1	0	Hypothetical protein (1)			-	C_unshiu_01915_mRNA_2.1	-
GF0041961	0	1	0	Hypothetical protein (1)			-	C_unshiu_01915_mRNA_1.1	-
GF0041960	0	1	0	Hypothetical protein (1)			-	C_unshiu_01912_mRNA_4.1	-
GF0041959	0	1	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_01912_mRNA_1.1	-
GF0041958	0	1	0	Hypothetical protein (1)		Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01911_mRNA_6.1	-
GF0041957	0	1	0	Hypothetical protein (1)		Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01911_mRNA_5.1	-
GF0041956	0	1	0	Hypothetical protein (1)			-	C_unshiu_01910_mRNA_2.1	-
GF0041955	0	1	0	Putative non-LTR reverse transcriptase (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_01910_mRNA_1.1	-
GF0041954	0	1	0	Hypothetical protein (1)			-	C_unshiu_01909_mRNA_3.1	-
GF0041953	0	1	0	Hypothetical protein (1)			-	C_unshiu_01909_mRNA_2.1	-
GF0041952	0	1	0	Hypothetical protein (1)			-	C_unshiu_01909_mRNA_1.1	-
GF0041951	0	1	0	Hypothetical protein (1)		Ankyrin repeat-containing domain [IPR020683] (1)	-	C_unshiu_01908_mRNA_5.1	-
GF0041950	0	1	0	Hypothetical protein (1)			-	C_unshiu_01907_mRNA_4.1	-
GF0041949	0	1	0	Hypothetical protein (1)			-	C_unshiu_01907_mRNA_2.1	-
GF0041948	0	1	0	Hypothetical protein (1)			-	C_unshiu_01907_mRNA_1.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0041947	0	1	0	Isoprene synthase (1)	protein binding [GO:0005515 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1); lyase activity [GO:0016829 molecular_function] (1); terpene synthase activity [GO:0010333 molecular_function] (1); magnesium ion binding [GO:0000287 molecular_function] (1)	Terpene synthase, N-terminal domain [IPR001906] (1); Terpene synthase, metal-binding domain [IPR005630] (1); Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (1); Ubiquitin-related domain [IPR029071] (1); UBX domain [IPR001012] (1); Isoprenoid synthase domain [IPR008949] (1)	-	C_unshiu_01906_mRNA_5.1	-
GF0041946	0	1	0	Hypothetical protein (1)			-	C_unshiu_01906_mRNA_2.1	-
GF0041945	0	1	0	Hypothetical protein (1)			-	C_unshiu_01904_mRNA_6.1	-
GF0041944	0	1	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); serine-type exopeptidase activity [GO:0070008 molecular_function] (1); serine-type endopeptidase activity [GO:0004252 molecular_function] (1)	Peptidase S9A, N-terminal domain [IPR023302] (1); Peptidase S9A, prolyl oligopeptidase [IPR002470] (1)	-	C_unshiu_01904_mRNA_1.1	-
GF0041943	0	1	0	Hypothetical protein (1)			-	C_unshiu_01903_mRNA_1.1	-
GF0041942	0	1	0	Disease resistance protein RPM1 (1)	proteolysis [GO:0006508 biological_process] (1); peptidase activity [GO:0008233 molecular_function] (1); ADP binding [GO:0043531 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Peptidase C13, legumain [IPR001096] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	C_unshiu_01902_mRNA_1.1	-
GF0041941	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01900_mRNA_6.1	-
GF0041940	0	1	0	LRR receptor-like kinase family protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_01900_mRNA_2.1	-
GF0041939	0	1	0	DUF3049 family protein (1)		The fantastic four family [IPR021410] (1)	-	C_unshiu_01899_mRNA_3.1	-
GF0041938	0	1	0	Hypothetical protein (1)			-	C_unshiu_01899_mRNA_2.1	-
GF0041937	0	1	0	Caffeic acid O-methyltransferase (1)	O-methyltransferase activity [GO:0008171 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1); methyltransferase activity [GO:0008168 molecular_function] (1)	Plant methyltransferase dimerisation [IPR012967] (1); O-methyltransferase COMT-type [IPR016461] (1); O-methyltransferase, family 2 [IPR001077] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	C_unshiu_01897_mRNA_1.1	-
GF0041936	0	1	0	Hypothetical protein (1)			-	C_unshiu_01894_mRNA_2.1	-
GF0041935	0	1	0	Hypothetical protein (1)			-	C_unshiu_01894_mRNA_1.1	-
GF0041934	0	1	0	Hypothetical protein (1)			-	C_unshiu_01893_mRNA_5.1	-
GF0041933	0	1	0	Hypothetical protein (1)			-	C_unshiu_01893_mRNA_3.1	-
GF0041932	0	1	0	Hypothetical protein (1)			-	C_unshiu_01893_mRNA_15.1	-
GF0041931	0	1	0	Putative nitronate monooxygenase (1)	nitronate monooxygenase activity [GO:0018580 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1)	Nitronate monooxygenase [IPR004136] (1); Aldolase-type TIM barrel [IPR013785] (1)	-	C_unshiu_01891_mRNA_2.1	-
GF0041930	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Piwi domain [IPR003165] (1); Argonaute linker 2 domain [IPR032472] (1); Ribonuclease H-like domain [IPR012337] (1); Argonaute, linker 1 domain [IPR014811] (1)	-	C_unshiu_01889_mRNA_6.1	-
GF0041929	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_01888_mRNA_1.1	-
GF0041928	0	1	0	Hypothetical protein (1)	hydrolase activity [GO:0016787 molecular_function] (1); isopentenyl-diphosphate delta-isomerase activity [GO:0004452 molecular_function] (1); isoprenoid biosynthetic process [GO:0008299 biological_process] (1)	NUDIX hydrolase domain-like [IPR015797] (1); Isopentenyl-diphosphate delta-isomerase, type 1 [IPR011876] (1)	-	C_unshiu_01887_mRNA_7.1	-
GF0041927	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1); binding [GO:0005488 molecular_function] (1)	MIF4G-like domain [IPR016021] (1); Armadillo-type fold [IPR016024] (1); W2 domain [IPR003307] (1)	-	C_unshiu_01887_mRNA_6.1	-
GF0041926	0	1	0	Hypothetical protein (1)			-	C_unshiu_01883_mRNA_5.1	-
GF0041925	0	1	0	Hypothetical protein (1)			-	C_unshiu_01883_mRNA_4.1	-
GF0041924	0	1	0	Hypothetical protein (1)			-	C_unshiu_01883_mRNA_2.1	-
GF0041923	0	1	0	Aldehyde oxidase (1)	catalytic activity [GO:0003824 molecular_function] (1); oxidoreductase activity, acting on CH-OH group of donors [GO:0016614 molecular_function] (1); electron carrier activity [GO:0009055 molecular_function] (1); metal ion binding [GO:0046872 molecular_function] (1); iron-sulfur cluster binding [GO:0051536 molecular_function] (1); flavin adenine dinucleotide binding [GO:0050660 molecular_function] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Molybdopterin dehydrogenase, FAD-binding [IPR002346] (1); Aldehyde oxidase/xanthine dehydrogenase, a/b hammerhead [IPR000674] (1); Aldehyde oxidase/xanthine dehydrogenase, molybdopterin binding [IPR008274] (1); Beta-grasp domain [IPR012675] (1); FAD-binding, type 2 [IPR016166] (1); CO dehydrogenase flavoprotein, C-terminal [IPR005107] (1); 2Fe-2S ferredoxin-type iron-sulfur binding domain [IPR001041] (1); [2Fe-2S]-binding [IPR002888] (1); CO dehydrogenase flavoprotein-like, FAD-binding, subdomain 2 [IPR016169] (1)	-	C_unshiu_01882_mRNA_3.1	-
GF0041922	0	1	0	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	C_unshiu_01881_mRNA_6.1	-
GF0041921	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	C_unshiu_01881_mRNA_4.1	-
GF0041920	0	1	0	Hypothetical protein (1)		Plant disease resistance response protein [IPR004265] (1)	-	C_unshiu_01880_mRNA_3.1	-
GF0041919	0	1	0	Hypothetical protein (1)		Plant disease resistance response protein [IPR004265] (1)	-	C_unshiu_01880_mRNA_2.1	-
GF0041918	0	1	0	Hypothetical protein (1)			-	C_unshiu_01880_mRNA_1.1	-
GF0041917	0	1	0	Putative rRNA methyltransferase (1)	nucleus [GO:0005634 cellular_component] (1); rRNA methylation [GO:0031167 biological_process] (1); rRNA processing [GO:0006364 biological_process] (1); methyltransferase activity [GO:0008168 molecular_function] (1); RNA methylation [GO:0001510 biological_process] (1); rRNA methyltransferase activity [GO:0008649 molecular_function] (1)	Ribosomal RNA methyltransferase, Spb1, C-terminal [IPR012920] (1); AdoMet-dependent rRNA methyltransferase, Spb1 [IPR028589] (1); Ribosomal RNA large subunit methyltransferase E [IPR015507] (1); Ribosomal RNA methyltransferase Spb1, domain of unknown function DUF3381 [IPR024576] (1)	-	C_unshiu_01879_mRNA_6.1	-
GF0041916	0	1	0	Hypothetical protein (1)	terpene synthase activity [GO:0010333 molecular_function] (1); lyase activity [GO:0016829 molecular_function] (1); magnesium ion binding [GO:0000287 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1); zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (1); Terpene synthase, metal-binding domain [IPR005630] (1); Terpene synthase, N-terminal domain [IPR001906] (1); Zinc finger, CCHC-type [IPR001878] (1); Isoprenoid synthase domain [IPR008949] (1)	-	C_unshiu_01878_mRNA_3.1	-
GF0041915	0	1	0	Hypothetical protein (1)			-	C_unshiu_01877_mRNA_6.1	-
GF0041914	0	1	0	Hypothetical protein (1)			-	C_unshiu_01877_mRNA_5.1	-
GF0041913	0	1	0	Hypothetical protein (1)			-	C_unshiu_01877_mRNA_4.1	-
GF0041912	0	1	0	Hypothetical protein (1)			-	C_unshiu_01877_mRNA_3.1	-
GF0041911	0	1	0	Ankyrin repeat family protein, putative (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat [IPR002110] (1); PGG domain [IPR026961] (1); Ankyrin repeat-containing domain [IPR020683] (1)	-	C_unshiu_01876_mRNA_1.1	-
GF0041910	0	1	0	Hypothetical protein (1)		Peroxisome membrane protein, Pex16 [IPR013919] (1)	-	C_unshiu_01874_mRNA_1.1	-
GF0041909	0	1	0	Hypothetical protein (1)	ubiquitin-dependent protein catabolic process [GO:0006511 biological_process] (1)	SKP1 component, dimerisation [IPR016072] (1)	-	C_unshiu_01873_mRNA_8.1	-
GF0041908	0	1	0	Hypothetical protein (1)			-	C_unshiu_01873_mRNA_6.1	-
GF0041907	0	1	0	Hypothetical protein (1)			-	C_unshiu_01873_mRNA_5.1	-
GF0041906	0	1	0	Hypothetical protein (1)			-	C_unshiu_01873_mRNA_3.1	-
GF0041905	0	1	0	Hypothetical protein (1)			-	C_unshiu_01873_mRNA_2.1	-
GF0041904	0	1	0	Hypothetical protein (1)			-	C_unshiu_01873_mRNA_1.1	-
GF0041903	0	1	0	Hypothetical protein (1)			-	C_unshiu_01872_mRNA_6.1	-
GF0041902	0	1	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1)	Aspartic peptidase domain [IPR021109] (1); Retropepsins [IPR018061] (1); Aspartic peptidase, active site [IPR001969] (1)	-	C_unshiu_01871_mRNA_5.1	-
GF0041901	0	1	0	Caffeic acid 3-O-methyltransferase (1)	methyltransferase activity [GO:0008168 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1); O-methyltransferase activity [GO:0008171 molecular_function] (1)	O-methyltransferase COMT-type [IPR016461] (1); Plant methyltransferase dimerisation [IPR012967] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); O-methyltransferase, family 2 [IPR001077] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	C_unshiu_01871_mRNA_1.1	-
GF0041900	0	1	0	Hypothetical protein (1)			-	C_unshiu_01870_mRNA_6.1	-
GF0041899	0	1	0	LRR receptor-like kinase family protein (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein binding [GO:0005515 molecular_function] (1)	Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Protein kinase-like domain [IPR011009] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01869_mRNA_6.1	-
GF0041898	0	1	0	Hypothetical protein (1)			-	C_unshiu_01869_mRNA_5.1	-
GF0041897	0	1	0	Hypothetical protein (1)			-	C_unshiu_01867_mRNA_7.1	-
GF0041896	0	1	0	Hypothetical protein (1)			-	C_unshiu_01867_mRNA_6.1	-
GF0041895	0	1	0	Hypothetical protein (1)			-	C_unshiu_01867_mRNA_5.1	-
GF0041894	0	1	0	Hypothetical protein (1)			-	C_unshiu_01867_mRNA_3.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0041893	0	1	0	Hypothetical protein (1)			-	C_unshiu_01867_mRNA_2.1	-
GF0041892	0	1	0	Gag protease polyprotein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Retrotransposon gag domain [IPR005162] (1); Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_01866_mRNA_8.1	-
GF0041891	0	1	0	Hypothetical protein (1)	GTP binding [GO:0005525 molecular_function] (1)	AIG1-type guanine nucleotide-binding (G) domain [IPR006703] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_01866_mRNA_5.1	-
GF0041890	0	1	0	Hypothetical protein (1)	GTP binding [GO:0005525 molecular_function] (1)	AIG1-type guanine nucleotide-binding (G) domain [IPR006703] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_01866_mRNA_4.1	-
GF0041889	0	1	0	Hypothetical protein (1)	GTP binding [GO:0005525 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); AIG1-type guanine nucleotide-binding (G) domain [IPR006703] (1)	-	C_unshiu_01866_mRNA_2.1	-
GF0041888	0	1	0	Hypothetical protein (1)			-	C_unshiu_01866_mRNA_1.1	-
GF0041887	0	1	0	Cysteine/histidine-rich C1 domain protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); protein-disulfide reductase activity [GO:0047134 molecular_function] (1)	C1-like [IPR011424] (1)	-	C_unshiu_01865_mRNA_5.1	-
GF0041886	0	1	0	Hypothetical protein (1)			-	C_unshiu_01864_mRNA_6.1	-
GF0041885	0	1	0	Disease resistance RPS5-like protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_01864_mRNA_5.1	-
GF0041884	0	1	0	Hypothetical protein (1)			-	C_unshiu_01864_mRNA_4.1	-
GF0041883	0	1	0	Phosphoprotein phosphatase (1)	binding [GO:0005488 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Armadillo-like helical [IPR011989] (1); Armadillo-type fold [IPR016024] (1)	-	C_unshiu_01864_mRNA_3.1	-
GF0041882	0	1	0	Hypothetical protein (1)			-	C_unshiu_01862_mRNA_7.1	-
GF0041881	0	1	0	Hypothetical protein (1)		Alpha crystallin/Hsp20 domain [IPR002068] (1); HSP20-like chaperone [IPR008978] (1)	-	C_unshiu_01860_mRNA_6.1	-
GF0041880	0	1	0	Hypothetical protein (1)		HSP20-like chaperone [IPR008978] (1); Alpha crystallin/Hsp20 domain [IPR002068] (1)	-	C_unshiu_01860_mRNA_5.1	-
GF0041879	0	1	0	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	-	C_unshiu_01860_mRNA_2.1	-
GF0041878	0	1	0	Hypothetical protein (1)			-	C_unshiu_01860_mRNA_1.1	-
GF0041877	0	1	0	Hypothetical protein (1)			-	C_unshiu_01859_mRNA_5.1	-
GF0041876	0	1	0	Hypothetical protein (1)			-	C_unshiu_01858_mRNA_3.1	-
GF0041875	0	1	0	LRR receptor-like serine/threonine-protein kinase GSO1 (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01857_mRNA_5.1	-
GF0041874	0	1	0	Hypothetical protein (1)	catalytic activity [GO:0003824 molecular_function] (1)	Pyridoxal phosphate-dependent transferase, major region, subdomain 1 [IPR015421] (1); Pyridoxal phosphate-dependent transferase [IPR015424] (1); Aminotransferase class V domain [IPR000192] (1)	-	C_unshiu_01857_mRNA_4.1	-
GF0041873	0	1	0	Hypothetical protein (1)	catalytic activity [GO:0003824 molecular_function] (1)	Pyridoxal phosphate-dependent transferase, major region, subdomain 1 [IPR015421] (1); Pyridoxal phosphate-dependent transferase [IPR015424] (1)	-	C_unshiu_01857_mRNA_3.1	-
GF0041872	0	1	0	Hypothetical protein (1)	catalytic activity [GO:0003824 molecular_function] (1); DNA integration [GO:0015074 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Integrase, catalytic core [IPR001584] (1); Pyridoxal phosphate-dependent transferase, major region, subdomain 1 [IPR015421] (1); Aminotransferase class V domain [IPR000192] (1); GAG-pre-integrase domain [IPR025724] (1); Pyridoxal phosphate-dependent transferase [IPR015424] (1)	-	C_unshiu_01857_mRNA_12.1	-
GF0041871	0	1	0	Aspartic proteinase (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); lipid metabolic process [GO:0006629 biological_process] (1); proteolysis [GO:0006508 biological_process] (1)	Saposin-like type B, region 1 [IPR007856] (1); Aspartic peptidase, active site [IPR001969] (1); Saposin-like [IPR011001] (1); Aspartic peptidase A1 family [IPR001461] (1); Peptidase family A1 domain [IPR033121] (1); Aspartic peptidase domain [IPR021109] (1); Saposin B type, region 2 [IPR008138] (1); Saposin B type domain [IPR008139] (1)	-	C_unshiu_01857_mRNA_1.1	-
GF0041870	0	1	0	Hypothetical protein (1)			-	C_unshiu_01856_mRNA_2.1	-
GF0041869	0	1	0	Hypothetical protein (1)			-	C_unshiu_01856_mRNA_1.1	-
GF0041868	0	1	0	Hypothetical protein (1)			-	C_unshiu_01855_mRNA_3.1	-
GF0041867	0	1	0	Hypothetical protein (1)			-	C_unshiu_01855_mRNA_2.1	-
GF0041866	0	1	0	Hypothetical protein (1)			-	C_unshiu_01855_mRNA_1.1	-
GF0041865	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat-containing domain [IPR020683] (1); Ankyrin repeat [IPR002110] (1)	-	C_unshiu_01854_mRNA_7.1	-
GF0041864	0	1	0	Hypothetical protein (1)		Ankyrin repeat-containing domain [IPR020683] (1)	-	C_unshiu_01854_mRNA_6.1	-
GF0041863	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	PGG domain [IPR026961] (1); Ankyrin repeat-containing domain [IPR020683] (1); Ankyrin repeat [IPR002110] (1)	-	C_unshiu_01854_mRNA_2.1	-
GF0041862	0	1	0	Phenylcoumaran benzylic ether reductase (1)		NAD(P)-binding domain [IPR016040] (1); NmrA-like domain [IPR008030] (1)	-	C_unshiu_01853_mRNA_2.1	-
GF0041861	0	1	0	Hypothetical protein (1)			-	C_unshiu_01852_mRNA_2.1	-
GF0041860	0	1	0	Hypothetical protein (1)			-	C_unshiu_01852_mRNA_1.1	-
GF0041859	0	1	0	Hypothetical protein (1)	fatty acid metabolic process [GO:0006631 biological_process] (1); acyl-[acyl-carrier-protein] desaturase activity [GO:0045300 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1)	Ribonucleotide reductase-related [IPR012348] (1); Ferritin-like superfamily [IPR009078] (1); Fatty acid desaturase, type 2 [IPR005067] (1)	-	C_unshiu_01851_mRNA_3.1	-
GF0041858	0	1	0	Hypothetical protein (1)	nucleus [GO:0005634 cellular_component] (1); DNA binding [GO:0003677 molecular_function] (1)	Methyl-CpG DNA binding [IPR001739] (1); DNA-binding domain [IPR016177] (1)	-	C_unshiu_01851_mRNA_2.1	-
GF0041857	0	1	0	Hypothetical protein (1)			-	C_unshiu_01850_mRNA_3.1	-
GF0041856	0	1	0	Hypothetical protein (1)			-	C_unshiu_01850_mRNA_2.1	-
GF0041855	0	1	0	C2 calcium/lipid-binding plant phosphoribosyltransferase family protein isoform 2 (1)	protein binding [GO:0005515 molecular_function] (1)	C2 domain [IPR000008] (1); Phosphoribosyltransferase C-terminal [IPR013583] (1)	-	C_unshiu_01850_mRNA_1.1	-
GF0041854	0	1	0	LRR receptor-like kinase family protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein binding [GO:0005515 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Protein kinase-like domain [IPR011009] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Protein kinase, ATP binding site [IPR017441] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_01849_mRNA_5.1	-
GF0041853	0	1	0	Hypothetical protein (1)			-	C_unshiu_01849_mRNA_1.1	-
GF0041852	0	1	0	Clp protease ATP binding subunit (1)	ATP binding [GO:0005524 molecular_function] (1)	ClpA/B family [IPR001270] (1); ClpA/B, conserved site 1 [IPR018368] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Clp ATPase, C-terminal [IPR019489] (1); ATPase, AAA-type, core [IPR003959] (1); AAA+ ATPase domain [IPR003593] (1)	-	C_unshiu_01848_mRNA_7.1	-
GF0041851	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	WD40/YVTN repeat-like-containing domain [IPR015943] (1)	-	C_unshiu_01848_mRNA_1.1	-
GF0041850	0	1	0	Chaperonin CPN60-2 (1)		GroEL-like apical domain [IPR027409] (1)	-	C_unshiu_01847_mRNA_1.1	-
GF0041849	0	1	0	Putative disease resistance protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01846_mRNA_5.1	-
GF0041848	0	1	0	Hypothetical protein (1)			-	C_unshiu_01846_mRNA_4.1	-
GF0041847	0	1	0	Phosphoprotein phosphatase (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_01846_mRNA_3.1	-
GF0041846	0	1	0	Hypothetical protein (1)			-	C_unshiu_01845_mRNA_1.1	-
GF0041845	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_01843_mRNA_4.1	-
GF0041844	0	1	0	Hypothetical protein (1)			-	C_unshiu_01843_mRNA_3.1	-
GF0041843	0	1	0	Hypothetical protein (1)			-	C_unshiu_01843_mRNA_1.1	-
GF0041842	0	1	0	Hypothetical protein (1)			-	C_unshiu_01842_mRNA_2.1	-
GF0041841	0	1	0	Putative non-LTR retroelement reverse transcriptase (1)		Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_01841_mRNA_5.1	-
GF0041840	0	1	0	Disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); VQ [IPR008889] (1)	-	C_unshiu_01841_mRNA_4.1	-
GF0041839	0	1	0	Hypothetical protein (1)			-	C_unshiu_01841_mRNA_3.1	-
GF0041838	0	1	0	Hypothetical protein (1)			-	C_unshiu_01840_mRNA_7.1	-
GF0041837	0	1	0	Hypothetical protein (1)			-	C_unshiu_01840_mRNA_6.1	-
GF0041836	0	1	0	Hypothetical protein (1)			-	C_unshiu_01839_mRNA_4.1	-
GF0041835	0	1	0	Hypothetical protein (1)			-	C_unshiu_01839_mRNA_2.1	-
GF0041834	0	1	0	Disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_01837_mRNA_2.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0041833	0	1	0	Hexosyltransferase (1)	transferase activity, transferring glycosyl groups [GO:0016757 molecular_function] (1)	Nucleotide-diphospho-sugar transferases [IPR029044] (1); Glycosyl transferase, family 8 [IPR002495] (1)	-	C_unshiu_01837_mRNA_1.1	-
GF0041832	0	1	0	Hypothetical protein (1)	protein serine/threonine kinase activity [GO:0004674 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	WD40/YVTN repeat-like-containing domain [IPR015943] (1); S-locus receptor kinase, C-terminal [IPR021820] (1); WD40-repeat-containing domain [IPR017986] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_01836_mRNA_3.1	-
GF0041831	0	1	0	Hypothetical protein (1)		Protein kinase-like domain [IPR011009] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1)	-	C_unshiu_01836_mRNA_2.1	-
GF0041830	0	1	0	30S ribosomal protein S11, chloroplastic (1)	structural constituent of ribosome [GO:0003735 molecular_function] (1); translation [GO:0006412 biological_process] (1); ribosome [GO:0005840 cellular_component] (1)	Ribosomal protein S11 [IPR001971] (1); Ribosomal S11, conserved site [IPR018102] (1)	-	C_unshiu_01835_mRNA_3.1	-
GF0041829	0	1	0	DNA-directed RNA polymerase, alpha subunit (1)	protein dimerization activity [GO:0046983 molecular_function] (1); DNA-directed RNA polymerase activity [GO:0003899 molecular_function] (1); transcription, DNA-templated [GO:0006351 biological_process] (1)	DNA-directed RNA polymerase, RBP11-like dimerisation domain [IPR009025] (1); DNA-directed RNA polymerase, insert domain [IPR011262] (1); DNA-directed RNA polymerase, RpoA/D/Rpb3-type [IPR011263] (1)	-	C_unshiu_01835_mRNA_2.1	-
GF0041828	0	1	0	Hypothetical protein (1)			-	C_unshiu_01835_mRNA_1.1	-
GF0041827	0	1	0	Hypothetical protein (1)			-	C_unshiu_01833_mRNA_5.1	-
GF0041826	0	1	0	Hypothetical protein (1)			-	C_unshiu_01833_mRNA_4.1	-
GF0041825	0	1	0	Hypothetical protein (1)			-	C_unshiu_01833_mRNA_3.1	-
GF0041824	0	1	0	Hypothetical protein (1)			-	C_unshiu_01832_mRNA_2.1	-
GF0041823	0	1	0	Hypothetical protein (1)			-	C_unshiu_01831_mRNA_3.1	-
GF0041822	0	1	0	Pleiotropic drug resistance protein 3 (1)	ATP binding [GO:0005524 molecular_function] (1); membrane [GO:0016020 cellular_component] (1); ATPase activity [GO:0016887 molecular_function] (1)	ABC-transporter extracellular N-terminal domain [IPR029481] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); AAA+ ATPase domain [IPR003593] (1); ABC transporter-like [IPR003439] (1); ABC-2 type transporter [IPR013525] (1)	-	C_unshiu_01830_mRNA_4.1	-
GF0041821	0	1	0	P-loop nucleoside triphosphate hydrolase superfamily protein (1)		P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_01829_mRNA_7.1	-
GF0041820	0	1	0	Hypothetical protein (1)		P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_01829_mRNA_5.1	-
GF0041819	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_01829_mRNA_3.1	-
GF0041818	0	1	0	Monosacharide transport protein (1)			-	C_unshiu_01829_mRNA_1.1	-
GF0041817	0	1	0	LRR receptor-like kinase (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_01828_mRNA_6.1	-
GF0041816	0	1	0	Hypothetical protein (1)			-	C_unshiu_01827_mRNA_5.1	-
GF0041815	0	1	0	Hypothetical protein (1)			-	C_unshiu_01827_mRNA_2.1	-
GF0041814	0	1	0	RING/U-box superfamily protein, putative isoform 3 (1)	ubiquitin-protein transferase activity [GO:0004842 molecular_function] (1); protein ubiquitination [GO:0016567 biological_process] (1)	IBR domain [IPR002867] (1); E3 ubiquitin ligase RBR family [IPR031127] (1)	-	C_unshiu_01826_mRNA_4.1	-
GF0041813	0	1	0	Hypothetical protein (1)			-	C_unshiu_01826_mRNA_3.1	-
GF0041812	0	1	0	Hypothetical protein (1)			-	C_unshiu_01825_mRNA_3.1	-
GF0041811	0	1	0	Hypothetical protein (1)	metabolic process [GO:0008152 biological_process] (1); lyase activity [GO:0016829 molecular_function] (1); terpene synthase activity [GO:0010333 molecular_function] (1)	Terpene synthase, N-terminal domain [IPR001906] (1); Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (1)	-	C_unshiu_01825_mRNA_2.1	-
GF0041810	0	1	0	Hypothetical protein (1)			-	C_unshiu_01824_mRNA_2.1	-
GF0041809	0	1	0	Hypothetical protein (1)			-	C_unshiu_01824_mRNA_1.1	-
GF0041808	0	1	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1); Xylanase inhibitor, C-terminal [IPR032799] (1)	-	C_unshiu_01823_mRNA_7.1	-
GF0041807	0	1	0	Abhydrolase domain-containing protein (1)		Alpha/beta hydrolase fold-5 [IPR029059] (1); Alpha/Beta hydrolase fold [IPR029058] (1)	-	C_unshiu_01823_mRNA_6.1	-
GF0041806	0	1	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Protein kinase, ATP binding site [IPR017441] (1)	-	C_unshiu_01821_mRNA_5.1	-
GF0041805	0	1	0	Hypothetical protein (1)			-	C_unshiu_01821_mRNA_2.1	-
GF0041804	0	1	0	Hypothetical protein (1)			-	C_unshiu_01820_mRNA_4.1	-
GF0041803	0	1	0	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_01820_mRNA_2.1	-
GF0041802	0	1	0	Hypothetical protein (1)			-	C_unshiu_01819_mRNA_3.1	-
GF0041801	0	1	0	Hypothetical protein (1)			-	C_unshiu_01819_mRNA_2.1	-
GF0041800	0	1	0	Hypothetical protein (1)			-	C_unshiu_01819_mRNA_1.1	-
GF0041799	0	1	0	Hypothetical protein (1)			-	C_unshiu_01818_mRNA_1.1	-
GF0041798	0	1	0	Hypothetical protein (1)			-	C_unshiu_01817_mRNA_5.1	-
GF0041797	0	1	0	Hypothetical protein (1)		Protein of unknown function DUF3537 [IPR021924] (1)	-	C_unshiu_01817_mRNA_4.1	-
GF0041796	0	1	0	Hypothetical protein (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Aspartic peptidase, active site [IPR001969] (1); Peptidase A2A, retrovirus, catalytic [IPR001995] (1); Retropepsins [IPR018061] (1)	-	C_unshiu_01816_mRNA_2.1	-
GF0041795	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1); zinc ion binding [GO:0008270 molecular_function] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1)	Peptidase A2A, retrovirus, catalytic [IPR001995] (1); Aspartic peptidase, active site [IPR001969] (1); Retropepsins [IPR018061] (1); Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_01816_mRNA_1.1	-
GF0041794	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_01811_mRNA_7.1	-
GF0041793	0	1	0	Hypothetical protein (1)			-	C_unshiu_01811_mRNA_5.1	-
GF0041792	0	1	0	Hypothetical protein (1)			-	C_unshiu_01811_mRNA_4.1	-
GF0041791	0	1	0	Hypothetical protein (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1)	Protein kinase-like domain [IPR011009] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1)	-	C_unshiu_01811_mRNA_10.1	-
GF0041790	0	1	0	Hypothetical protein (1)			-	C_unshiu_01811_mRNA_1.1	-
GF0041789	0	1	0	Chloroplast thylakoid membrane, putative isoform 3 (1)			-	C_unshiu_01810_mRNA_9.1	-
GF0041788	0	1	0	Hypothetical protein (1)			-	C_unshiu_01809_mRNA_7.1	-
GF0041787	0	1	0	Hypothetical protein (1)		Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_01809_mRNA_6.1	-
GF0041786	0	1	0	Hypothetical protein (1)			-	C_unshiu_01809_mRNA_5.1	-
GF0041785	0	1	0	Gibberellin receptor GID1, putative (1)	hydrolase activity [GO:0016787 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Alpha/Beta hydrolase fold [IPR029058] (1); Alpha/beta hydrolase fold-3 [IPR013094] (1)	-	C_unshiu_01809_mRNA_2.1	-
GF0041784	0	1	0	Hypothetical protein (1)			-	C_unshiu_01808_mRNA_4.1	-
GF0041783	0	1	0	Hypothetical protein (1)			-	C_unshiu_01807_mRNA_4.1	-
GF0041782	0	1	0	Hypothetical protein (1)			-	C_unshiu_01807_mRNA_3.1	-
GF0041781	0	1	0	Hypothetical protein (1)			-	C_unshiu_01807_mRNA_2.1	-
GF0041780	0	1	0	Hypothetical protein (1)			-	C_unshiu_01807_mRNA_1.1	-
GF0041779	0	1	0	Phosphoprotein phosphatase (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01806_mRNA_4.1	-
GF0041778	0	1	0	NADP specific isocitrate dehydrogenase (1)	isocitrate dehydrogenase (NADP+) activity [GO:0004450 molecular_function] (1); oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor [GO:0016616 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); isocitrate metabolic process [GO:0006102 biological_process] (1)	Isopropylmalate dehydrogenase-like domain [IPR024084] (1); Isocitrate dehydrogenase NADP-dependent [IPR004790] (1)	-	C_unshiu_01804_mRNA_1.1	-
GF0041777	0	1	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1)	Peptidase A2A, retrovirus, catalytic [IPR001995] (1); Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_01803_mRNA_7.1	-
GF0041776	0	1	0	Hypothetical protein (1)			-	C_unshiu_01803_mRNA_6.1	-
GF0041775	0	1	0	Hypothetical protein (1)			-	C_unshiu_01803_mRNA_11.1	-
GF0041774	0	1	0	Transcription factor Pcc1 (1)		CTAG/Pcc1 family [IPR015419] (1)	-	C_unshiu_01802_mRNA_4.1	-
GF0041773	0	1	0	Mitogen-activated protein kinase kinase (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase, ATP binding site [IPR017441] (1)	-	C_unshiu_01802_mRNA_1.1	-
GF0041772	0	1	0	Hypothetical protein (1)			-	C_unshiu_01800_mRNA_1.1	-
GF0041771	0	1	0	Hypothetical protein (1)	transport [GO:0006810 biological_process] (1)	Transposase, MuDR, plant [IPR004332] (1); Longin-like domain [IPR011012] (1)	-	C_unshiu_01799_mRNA_7.1	-
GF0041770	0	1	0	Caffeoyl CoA O-methyltransferase (1)	O-methyltransferase activity [GO:0008171 molecular_function] (1)	S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); O-methyltransferase, family 3 [IPR002935] (1)	-	C_unshiu_01799_mRNA_4.1	-
GF0041769	0	1	0	Hypothetical protein (1)			-	C_unshiu_01799_mRNA_3.1	-
GF0041768	0	1	0	Caffeoyl CoA O-methyltransferase (1)	O-methyltransferase activity [GO:0008171 molecular_function] (1)	S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); O-methyltransferase, family 3 [IPR002935] (1)	-	C_unshiu_01799_mRNA_2.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0041767	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, SWIM-type [IPR007527] (1); Zinc finger, PMZ-type [IPR006564] (1)	-	C_unshiu_01799_mRNA_1.1	-
GF0041766	0	1	0	Piriformospora indica-insensitive protein 2 (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01798_mRNA_7.1	-
GF0041765	0	1	0	WD repeat-containing protein 55 like (1)	protein binding [GO:0005515 molecular_function] (1)	WD40-repeat-containing domain [IPR017986] (1); WD40/YVTN repeat-like-containing domain [IPR015943] (1)	-	C_unshiu_01798_mRNA_3.1	-
GF0041764	0	1	0	Hypothetical protein (1)			-	C_unshiu_01798_mRNA_2.1	-
GF0041763	0	1	0	Hypothetical protein (1)			-	C_unshiu_01797_mRNA_5.1	-
GF0041762	0	1	0	Hypothetical protein (1)			-	C_unshiu_01797_mRNA_2.1	-
GF0041761	0	1	0	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	C_unshiu_01796_mRNA_6.1	-
GF0041760	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_01796_mRNA_2.1	-
GF0041759	0	1	0	Hypothetical protein (1)	metal ion binding [GO:0046872 molecular_function] (1); nucleotide binding [GO:0000166 molecular_function] (1)	P-type ATPase, transmembrane domain [IPR023298] (1); P-type ATPase, A domain [IPR008250] (1)	-	C_unshiu_01793_mRNA_2.1	-
GF0041758	0	1	0	Hypothetical protein (1)			-	C_unshiu_01791_mRNA_1.1	-
GF0041757	0	1	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_01790_mRNA_4.1	-
GF0041756	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01790_mRNA_3.1	-
GF0041755	0	1	0	Phosphoprotein phosphatase (1)	ATP binding [GO:0005524 molecular_function] (1); ADP binding [GO:0043531 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); ATPase domain [IPR011579] (1); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_01790_mRNA_2.1	-
GF0041754	0	1	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01790_mRNA_1.1	-
GF0041753	0	1	0	Hypothetical protein (1)			-	C_unshiu_01789_mRNA_8.1	-
GF0041752	0	1	0	Hypothetical protein (1)		Gag-polypeptide of LTR copia-type [IPR029472] (1)	-	C_unshiu_01789_mRNA_7.1	-
GF0041751	0	1	0	Hypothetical protein (1)			-	C_unshiu_01789_mRNA_2.1	-
GF0041750	0	1	0	Flavonoid 3'-monooxygenase (1)	iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450, conserved site [IPR017972] (1); Cytochrome P450 [IPR001128] (1)	-	C_unshiu_01789_mRNA_1.1	-
GF0041749	0	1	0	Hypothetical protein (1)			-	C_unshiu_01787_mRNA_4.1	-
GF0041748	0	1	0	Hypothetical protein (1)			-	C_unshiu_01787_mRNA_3.1	-
GF0041747	0	1	0	Hypothetical protein (1)		Malectin [IPR021720] (1)	-	C_unshiu_01787_mRNA_2.1	-
GF0041746	0	1	0	Hypothetical protein (1)			-	C_unshiu_01786_mRNA_7.1	-
GF0041745	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_01786_mRNA_6.1	-
GF0041744	0	1	0	Hypothetical protein (1)			-	C_unshiu_01786_mRNA_4.1	-
GF0041743	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_01786_mRNA_2.1	-
GF0041742	0	1	0	Hypothetical protein (1)			-	C_unshiu_01786_mRNA_1.1	-
GF0041741	0	1	0	Hypothetical protein (1)			-	C_unshiu_01783_mRNA_4.1	-
GF0041740	0	1	0	Hypothetical protein (1)			-	C_unshiu_01783_mRNA_1.1	-
GF0041739	0	1	0	Hypothetical protein (1)			-	C_unshiu_01782_mRNA_1.4	-
GF0041738	0	1	0	Hypothetical protein (1)			-	C_unshiu_01781_mRNA_7.1	-
GF0041737	0	1	0	Hypothetical protein (1)			-	C_unshiu_01781_mRNA_6.1	-
GF0041736	0	1	0	Hypothetical protein (1)			-	C_unshiu_01781_mRNA_3.1	-
GF0041735	0	1	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1)	Peptidase A2A, retrovirus, catalytic [IPR001995] (1)	-	C_unshiu_01781_mRNA_2.1	-
GF0041734	0	1	0	Hypothetical protein (1)			-	C_unshiu_01781_mRNA_1.1	-
GF0041733	0	1	0	Hypothetical protein (1)			-	C_unshiu_01780_mRNA_1.1	-
GF0041732	0	1	0	Hypothetical protein (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1); phosphotransferase activity, alcohol group as acceptor [GO:0016773 molecular_function] (1)	Carbohydrate kinase, FGGY, N-terminal [IPR018484] (1)	-	C_unshiu_01779_mRNA_5.1	-
GF0041731	0	1	0	Hypothetical protein (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1); phosphotransferase activity, alcohol group as acceptor [GO:0016773 molecular_function] (1)	Carbohydrate kinase, FGGY, C-terminal [IPR018485] (1)	-	C_unshiu_01779_mRNA_4.1	-
GF0041730	0	1	0	Hypothetical protein (1)	phosphotransferase activity, alcohol group as acceptor [GO:0016773 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1)	Carbohydrate kinase, FGGY, C-terminal [IPR018485] (1)	-	C_unshiu_01779_mRNA_2.1	-
GF0041729	0	1	0	Hypothetical protein (1)			-	C_unshiu_01776_mRNA_5.1	-
GF0041728	0	1	0	Hypothetical protein (1)			-	C_unshiu_01776_mRNA_2.1	-
GF0041727	0	1	0	Hypothetical protein (1)			-	C_unshiu_01774_mRNA_5.1	-
GF0041726	0	1	0	Putative disease resistance RPP13-like protein 1 (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01773_mRNA_2.1	-
GF0041725	0	1	0	UDP-glycosyltransferase 74E1 (1)	transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	-	C_unshiu_01773_mRNA_1.1	-
GF0041724	0	1	0	Hypothetical protein (1)			-	C_unshiu_01772_mRNA_1.1	-
GF0041723	0	1	0	Hypothetical protein (1)			-	C_unshiu_01771_mRNA_9.1	-
GF0041722	0	1	0	Hypothetical protein (1)	recognition of pollen [GO:0048544 biological_process] (1)	S-locus glycoprotein domain [IPR000858] (1)	-	C_unshiu_01771_mRNA_7.1	-
GF0041721	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_01771_mRNA_5.1	-
GF0041720	0	1	0	Hypothetical protein (1)			-	C_unshiu_01771_mRNA_10.1	-
GF0041719	0	1	0	S locus glycoprotein (1)	recognition of pollen [GO:0048544 biological_process] (1)	S-locus glycoprotein domain [IPR000858] (1); Bulb-type lectin domain [IPR001480] (1); PAN/Apple domain [IPR003609] (1)	-	C_unshiu_01771_mRNA_1.1	-
GF0041718	0	1	0	Hypothetical protein (1)			-	C_unshiu_01770_mRNA_5.1	-
GF0041717	0	1	0	Hypothetical protein (1)			-	C_unshiu_01770_mRNA_2.1	-
GF0041716	0	1	0	Hypothetical protein (1)		Arabidopsis retrotransposon Orf1 [IPR004312] (1)	-	C_unshiu_01770_mRNA_1.1	-
GF0041715	0	1	0	Hypothetical protein (1)			-	C_unshiu_01769_mRNA_1.1	-
GF0041714	0	1	0	Hypothetical protein (1)			-	C_unshiu_01768_mRNA_3.1	-
GF0041713	0	1	0	Hypothetical protein (1)			-	C_unshiu_01767_mRNA_2.1	-
GF0041712	0	1	0	Hypothetical protein (1)			-	C_unshiu_01766_mRNA_1.1	-
GF0041711	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_01765_mRNA_5.1	-
GF0041710	0	1	0	Hypothetical protein (1)			-	C_unshiu_01765_mRNA_4.1	-
GF0041709	0	1	0	Hypothetical protein (1)			-	C_unshiu_01764_mRNA_5.1	-
GF0041708	0	1	0	Hypothetical protein (1)			-	C_unshiu_01764_mRNA_3.1	-
GF0041707	0	1	0	Hypothetical protein (1)			-	C_unshiu_01764_mRNA_2.1	-
GF0041706	0	1	0	Putative calcium-binding protein CML16 (1)	calcium ion binding [GO:0005509 molecular_function] (1)	EF-hand domain pair [IPR011992] (1); EF-hand domain [IPR002048] (1); EF-Hand 1, calcium-binding site [IPR018247] (1)	-	C_unshiu_01763_mRNA_2.1	-
GF0041705	0	1	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); cytoplasm [GO:0005737 cellular_component] (1); DNA binding [GO:0003677 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1); helicase activity [GO:0004386 molecular_function] (1); nuclear-transcribed mRNA catabolic process, nonsense-mediated decay [GO:0000184 biological_process] (1)	RNA helicase UPF1, UPF2-interacting domain [IPR018999] (1)	-	C_unshiu_01763_mRNA_1.1	-
GF0041704	0	1	0	Hypothetical protein (1)			-	C_unshiu_01762_mRNA_4.1	-
GF0041703	0	1	0	Hypothetical protein (1)			-	C_unshiu_01762_mRNA_2.1	-
GF0041702	0	1	0	Hypothetical protein (1)	phospholipid-translocating ATPase activity [GO:0004012 molecular_function] (1); metal ion binding [GO:0046872 molecular_function] (1); phospholipid transport [GO:0015914 biological_process] (1); integral component of membrane [GO:0016021 cellular_component] (1); magnesium ion binding [GO:0000287 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1); nucleotide binding [GO:0000166 molecular_function] (1)	P-type ATPase, subfamily IV [IPR006539] (1); P-type ATPase, A domain [IPR008250] (1)	-	C_unshiu_01762_mRNA_1.1	-
GF0041701	0	1	0	Hypothetical protein (1)			-	C_unshiu_01761_mRNA_5.1	-
GF0041700	0	1	0	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	C_unshiu_01761_mRNA_4.1	-
GF0041699	0	1	0	Retrotransposon protein, putative, unclassified (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_01761_mRNA_3.1	-
GF0041698	0	1	0	Cytochrome P450 716B2 (1)	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1)	Cytochrome P450, conserved site [IPR017972] (1); Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450 [IPR001128] (1)	-	C_unshiu_01760_mRNA_5.1	-
GF0041697	0	1	0	Hypothetical protein (1)			-	C_unshiu_01760_mRNA_3.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0041696	0	1	0	Caffeic acid 3-O-methyltransferase (1)	methyltransferase activity [GO:0008168 molecular_function] (1); O-methyltransferase activity [GO:0008171 molecular_function] (1)	Winged helix-turn-helix DNA-binding domain [IPR011991] (1); O-methyltransferase, family 2 [IPR001077] (1); O-methyltransferase COMT-type [IPR016461] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	C_unshiu_01760_mRNA_2.1	-
GF0041695	0	1	0	Hypothetical protein (1)			-	C_unshiu_01760_mRNA_1.1	-
GF0041694	0	1	0	Hypothetical protein (1)			-	C_unshiu_01759_mRNA_3.1	-
GF0041693	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_01759_mRNA_2.1	-
GF0041692	0	1	0	Hypothetical protein (1)		PAP/25A-associated [IPR002058] (1)	-	C_unshiu_01758_mRNA_6.1	-
GF0041691	0	1	0	Hypothetical protein (1)			-	C_unshiu_01758_mRNA_5.1	-
GF0041690	0	1	0	Hypothetical protein (1)			-	C_unshiu_01758_mRNA_11.1	-
GF0041689	0	1	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	-	C_unshiu_01758_mRNA_10.1	-
GF0041688	0	1	0	Hypothetical protein (1)	nucleotidyltransferase activity [GO:0016779 molecular_function] (1)	Polymerase, nucleotidyl transferase domain [IPR002934] (1)	-	C_unshiu_01758_mRNA_1.1	-
GF0041687	0	1	0	Cytochrome P450 82A4 (1)	heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1)	Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450 [IPR001128] (1)	-	C_unshiu_01756_mRNA_9.1	-
GF0041686	0	1	0	N(2),N(2)-dimethylguanosine tRNA methyltransferase Trm1 (1)	tRNA processing [GO:0008033 biological_process] (1); RNA binding [GO:0003723 molecular_function] (1); tRNA (guanine-N2-)-methyltransferase activity [GO:0004809 molecular_function] (1)	tRNA methyltransferase, Trm1 [IPR002905] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	C_unshiu_01756_mRNA_2.1	-
GF0041685	0	1	0	Hypothetical protein (1)			-	C_unshiu_01755_mRNA_5.1	-
GF0041684	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_01755_mRNA_2.1	-
GF0041683	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	DEAD/DEAH box helicase domain [IPR011545] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Helicase superfamily 1/2, ATP-binding domain [IPR014001] (1)	-	C_unshiu_01755_mRNA_1.1	-
GF0041682	0	1	0	Disease resistance protein RPS2 (1)	ADP binding [GO:0043531 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); NB-ARC [IPR002182] (1); Leucine-rich repeat [IPR001611] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_01754_mRNA_4.1	-
GF0041681	0	1	0	UPF0481 protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	C_unshiu_01753_mRNA_7.1	-
GF0041680	0	1	0	Hypothetical protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	C_unshiu_01753_mRNA_6.1	-
GF0041679	0	1	0	Hypothetical protein (1)			-	C_unshiu_01753_mRNA_5.1	-
GF0041678	0	1	0	Mitogen-activated protein kinase kinase (1)	ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase, ATP binding site [IPR017441] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1)	-	C_unshiu_01753_mRNA_2.1	-
GF0041677	0	1	0	Hypothetical protein (1)			-	C_unshiu_01752_mRNA_9.1	-
GF0041676	0	1	0	Hypothetical protein (1)			-	C_unshiu_01752_mRNA_7.1	-
GF0041675	0	1	0	Wall-associated receptor kinase 2 (1)	polysaccharide binding [GO:0030247 molecular_function] (1)	Wall-associated receptor kinase, galacturonan-binding domain [IPR025287] (1)	-	C_unshiu_01751_mRNA_3.1	-
GF0041674	0	1	0	Hypothetical protein (1)			-	C_unshiu_01750_mRNA_2.1	-
GF0041673	0	1	0	Hypothetical protein (1)			-	C_unshiu_01749_mRNA_5.1	-
GF0041672	0	1	0	Hypothetical protein (1)			-	C_unshiu_01749_mRNA_4.1	-
GF0041671	0	1	0	Hypothetical protein (1)			-	C_unshiu_01748_mRNA_5.1	-
GF0041670	0	1	0	Hypothetical protein (1)			-	C_unshiu_01747_mRNA_4.1	-
GF0041669	0	1	0	Hypothetical protein (1)			-	C_unshiu_01747_mRNA_3.1	-
GF0041668	0	1	0	Disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01747_mRNA_2.1	-
GF0041667	0	1	0	Hypothetical protein (1)			-	C_unshiu_01747_mRNA_1.1	-
GF0041666	0	1	0	Hypothetical protein (1)	asparagine-tRNA ligase activity [GO:0004816 molecular_function] (1); aminoacyl-tRNA ligase activity [GO:0004812 molecular_function] (1); asparaginyl-tRNA aminoacylation [GO:0006421 biological_process] (1); tRNA aminoacylation for protein translation [GO:0006418 biological_process] (1); cytoplasm [GO:0005737 cellular_component] (1); nucleotide binding [GO:0000166 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Asparagine-tRNA ligase [IPR004522] (1); Aminoacyl-tRNA synthetase, class II (D/K/N) [IPR004364] (1); Aminoacyl-tRNA synthetase, class II (D/K/N)-like [IPR018150] (1); OB-fold nucleic acid binding domain, AA-tRNA synthetase-type [IPR004365] (1); Nucleic acid-binding, OB-fold [IPR012340] (1)	-	C_unshiu_01746_mRNA_1.1	-
GF0041665	0	1	0	Mutant xyloglucan endotransglycosylase/hydrolase (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1); hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (1)	Glycoside hydrolase family 16 [IPR000757] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1)	-	C_unshiu_01745_mRNA_9.1	-
GF0041664	0	1	0	NAC domain protein NAC5 (1)	DNA binding [GO:0003677 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	NAC domain [IPR003441] (1)	-	C_unshiu_01745_mRNA_6.1	-
GF0041663	0	1	0	Mutant xyloglucan endotransglycosylase/hydrolase (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1); hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (1)	Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Glycoside hydrolase family 16 [IPR000757] (1)	-	C_unshiu_01745_mRNA_5.1	-
GF0041662	0	1	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1)	Plant methyltransferase dimerisation [IPR012967] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1)	-	C_unshiu_01745_mRNA_3.1	-
GF0041661	0	1	0	Hypothetical protein (1)			-	C_unshiu_01745_mRNA_2.1	-
GF0041660	0	1	0	Xyloglucan endotransglucosylase/hydrolase protein 22 (1)	apoplast [GO:0048046 cellular_component] (1); cellular glucan metabolic process [GO:0006073 biological_process] (1); cell wall [GO:0005618 cellular_component] (1); hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1); xyloglucan:xyloglucosyl transferase activity [GO:0016762 molecular_function] (1)	Xyloglucan endo-transglycosylase, C-terminal [IPR010713] (1); Glycoside hydrolase family 16 [IPR000757] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1)	-	C_unshiu_01745_mRNA_10.1	-
GF0041659	0	1	0	Hypothetical protein (1)	methyltransferase activity [GO:0008168 molecular_function] (1); O-methyltransferase activity [GO:0008171 molecular_function] (1)	S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); O-methyltransferase COMT-type [IPR016461] (1); O-methyltransferase, family 2 [IPR001077] (1)	-	C_unshiu_01745_mRNA_1.1	-
GF0041658	0	1	0	Mavicyanin (1)	electron carrier activity [GO:0009055 molecular_function] (1)	Cupredoxin [IPR008972] (1); Phytocyanin domain [IPR003245] (1); Blue (type 1) copper protein, binding site [IPR028871] (1)	-	C_unshiu_01744_mRNA_2.1	-
GF0041657	0	1	0	Haloacid dehalogenase-like hydrolase (1)	metabolic process [GO:0008152 biological_process] (1); hydrolase activity [GO:0016787 molecular_function] (1)	HAD hydrolase, subfamily IA [IPR006439] (1); Pyrimidine 5-nucleotidase [IPR010237] (1); HAD-like domain [IPR023214] (1)	-	C_unshiu_01743_mRNA_5.1	-
GF0041656	0	1	0	Putative muDR family transposase-like (1)	DNA binding [GO:0003677 molecular_function] (1); transposase activity [GO:0004803 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1); transposition, DNA-mediated [GO:0006313 biological_process] (1)	Transposase, mutator type [IPR001207] (1); MULE transposase domain [IPR018289] (1); Zinc finger, SWIM-type [IPR007527] (1)	-	C_unshiu_01743_mRNA_4.1	-
GF0041655	0	1	0	Hypothetical protein (1)			-	C_unshiu_01742_mRNA_1.1	-
GF0041654	0	1	0	Hypothetical protein (1)		Chromo domain-like [IPR016197] (1); Chromo domain [IPR023780] (1)	-	C_unshiu_01741_mRNA_3.1	-
GF0041653	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_01741_mRNA_2.1	-
GF0041652	0	1	0	Hypothetical protein (1)			-	C_unshiu_01740_mRNA_2.1	-
GF0041651	0	1	0	Hypothetical protein (1)			-	C_unshiu_01740_mRNA_1.1	-
GF0041650	0	1	0	Hypothetical protein (1)			-	C_unshiu_01739_mRNA_9.1	-
GF0041649	0	1	0	Hypothetical protein (1)			-	C_unshiu_01739_mRNA_6.1	-
GF0041648	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_01739_mRNA_3.1	-
GF0041647	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_01739_mRNA_2.1	-
GF0041646	0	1	0	Hypothetical protein (1)			-	C_unshiu_01739_mRNA_1.1	-
GF0041645	0	1	0	Hypothetical protein (1)	calcium ion binding [GO:0005509 molecular_function] (1)	EF-hand domain pair [IPR011992] (1); EF-hand domain [IPR002048] (1)	-	C_unshiu_01738_mRNA_7.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0041644	0	1	0	Adenylate kinase (1)	ATP binding [GO:0005524 molecular_function] (1); nucleobase-containing compound kinase activity [GO:0019205 molecular_function] (1); nucleobase-containing compound metabolic process [GO:0006139 biological_process] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Adenylate kinase/UMP-CMP kinase [IPR000850] (1)	-	C_unshiu_01738_mRNA_4.1	-
GF0041643	0	1	0	Hypothetical protein (1)			-	C_unshiu_01738_mRNA_3.1	-
GF0041642	0	1	0	Hypothetical protein (1)			-	C_unshiu_01738_mRNA_2.1	-
GF0041641	0	1	0	Adenylate kinase (1)	nucleobase-containing compound kinase activity [GO:0019205 molecular_function] (1); nucleobase-containing compound metabolic process [GO:0006139 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1)	Adenylate kinase/UMP-CMP kinase [IPR000850] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_01738_mRNA_1.1	-
GF0041640	0	1	0	Hypothetical protein (1)			-	C_unshiu_01736_mRNA_4.1	-
GF0041639	0	1	0	Hypothetical protein (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Oxoglutarate/iron-dependent dioxygenase [IPR005123] (1); Isopenicillin N synthase-like [IPR027443] (1)	-	C_unshiu_01734_mRNA_5.1	-
GF0041638	0	1	0	Oxidoreductase, 2OG-Fe oxygenase family protein, expressed (1)		Isopenicillin N synthase-like [IPR027443] (1); Non-haem dioxygenase N-terminal domain [IPR026992] (1)	-	C_unshiu_01734_mRNA_4.1	-
GF0041637	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_01733_mRNA_7.1	-
GF0041636	0	1	0	Hypothetical protein (1)			-	C_unshiu_01733_mRNA_4.1	-
GF0041635	0	1	0	Hypothetical protein (1)			-	C_unshiu_01733_mRNA_2.1	-
GF0041634	0	1	0	MAP kinase kinase 2 (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase, ATP binding site [IPR017441] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	-	C_unshiu_01733_mRNA_1.1	-
GF0041633	0	1	0	Protein WAX2 (1)			-	C_unshiu_01732_mRNA_4.1	-
GF0041632	0	1	0	Hypothetical protein (1)			-	C_unshiu_01732_mRNA_1.1	-
GF0041631	0	1	0	Sugar transport protein 13 (1)	transporter activity [GO:0005215 molecular_function] (1); transmembrane transport [GO:0055085 biological_process] (1); substrate-specific transmembrane transporter activity [GO:0022891 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1); transmembrane transporter activity [GO:0022857 molecular_function] (1); membrane [GO:0016020 cellular_component] (1)	Major facilitator superfamily domain [IPR020846] (1); Sugar transporter, conserved site [IPR005829] (1); Sugar/inositol transporter [IPR003663] (1); Major facilitator, sugar transporter-like [IPR005828] (1)	-	C_unshiu_01731_mRNA_2.1	-
GF0041630	0	1	0	Hypothetical protein (1)			-	C_unshiu_01731_mRNA_1.1	-
GF0041629	0	1	0	Hypothetical protein (1)			-	C_unshiu_01730_mRNA_3.1	-
GF0041628	0	1	0	Hypothetical protein (1)			-	C_unshiu_01730_mRNA_2.1	-
GF0041627	0	1	0	Hypothetical protein (1)			-	C_unshiu_01730_mRNA_1.1	-
GF0041626	0	1	0	Hypothetical protein (1)			-	C_unshiu_01729_mRNA_11.1	-
GF0041625	0	1	0	Truncated verticillium wilt resistance-like protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	-	C_unshiu_01728_mRNA_2.1	-
GF0041624	0	1	0	Hypothetical protein (1)			-	C_unshiu_01727_mRNA_3.1	-
GF0041623	0	1	0	Hypothetical protein (1)			-	C_unshiu_01727_mRNA_2.1	-
GF0041622	0	1	0	LRR receptor-like kinase family protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_01727_mRNA_1.1	-
GF0041621	0	1	0	Hypothetical protein (1)			-	C_unshiu_01726_mRNA_7.1	-
GF0041620	0	1	0	Hypothetical protein (1)			-	C_unshiu_01726_mRNA_3.1	-
GF0041619	0	1	0	Hypothetical protein (1)			-	C_unshiu_01724_mRNA_9.1	-
GF0041618	0	1	0	Hypothetical protein (1)			-	C_unshiu_01724_mRNA_8.1	-
GF0041617	0	1	0	Hypothetical protein (1)			-	C_unshiu_01724_mRNA_5.1	-
GF0041616	0	1	0	Hypothetical protein (1)			-	C_unshiu_01724_mRNA_4.1	-
GF0041615	0	1	0	Hypothetical protein (1)			-	C_unshiu_01724_mRNA_3.1	-
GF0041614	0	1	0	Hypothetical protein (1)			-	C_unshiu_01724_mRNA_2.1	-
GF0041613	0	1	0	Hypothetical protein (1)			-	C_unshiu_01724_mRNA_16.1	-
GF0041612	0	1	0	Phenylcoumaran benzylic ether reductase (1)		NmrA-like domain [IPR008030] (1); NAD(P)-binding domain [IPR016040] (1)	-	C_unshiu_01724_mRNA_14.1	-
GF0041611	0	1	0	Hypothetical protein (1)			-	C_unshiu_01724_mRNA_13.1	-
GF0041610	0	1	0	Hypothetical protein (1)			-	C_unshiu_01724_mRNA_12.1	-
GF0041609	0	1	0	Hypothetical protein (1)			-	C_unshiu_01723_mRNA_1.1	-
GF0041608	0	1	0	Hypothetical protein (1)			-	C_unshiu_01719_mRNA_4.1	-
GF0041607	0	1	0	E3 ubiquitin-protein ligase KEG-like protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1)	Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1)	-	C_unshiu_01717_mRNA_1.2	-
GF0041606	0	1	0	Hypothetical protein (1)			-	C_unshiu_01714_mRNA_3.1	-
GF0041605	0	1	0	General transcription factor 2-related zinc finger protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Domain of unknown function DUF4371 [IPR025398] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_01714_mRNA_2.1	-
GF0041604	0	1	0	Hypothetical protein (1)			-	C_unshiu_01713_mRNA_5.1	-
GF0041603	0	1	0	DNA sequence with open reading frame (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	-	C_unshiu_01713_mRNA_3.1	-
GF0041602	0	1	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	C_unshiu_01712_mRNA_5.1	-
GF0041601	0	1	0	Monosacharide transport protein (1)			-	C_unshiu_01712_mRNA_3.1	-
GF0041600	0	1	0	Hypothetical protein (1)			-	C_unshiu_01712_mRNA_2.1	-
GF0041599	0	1	0	Retrotransposon protein, putative, Ty1-copia subclass (1)			-	C_unshiu_01710_mRNA_5.1	-
GF0041598	0	1	0	Ubiquitin thioesterase OTU1 (1)			-	C_unshiu_01709_mRNA_2.1	-
GF0041597	0	1	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Helicase superfamily 1/2, ATP-binding domain, DinG/Rad3-type [IPR014013] (1)	-	C_unshiu_01708_mRNA_9.1	-
GF0041596	0	1	0	Hypothetical protein (1)	peroxidase activity [GO:0004601 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); response to oxidative stress [GO:0006979 biological_process] (1); heme binding [GO:0020037 molecular_function] (1)	Haem peroxidase, plant/fungal/bacterial [IPR002016] (1); Plant peroxidase [IPR000823] (1); Haem peroxidase [IPR010255] (1)	-	C_unshiu_01708_mRNA_6.1	-
GF0041595	0	1	0	Hypothetical protein (1)			-	C_unshiu_01707_mRNA_2.1	-
GF0041594	0	1	0	GTP cyclohydrolase 1 (1)		Myb/SANT-like domain [IPR024752] (1)	-	C_unshiu_01706_mRNA_2.1	-
GF0041593	0	1	0	Hypothetical protein (1)			-	C_unshiu_01705_mRNA_6.1	-
GF0041592	0	1	0	Hypothetical protein (1)			-	C_unshiu_01703_mRNA_4.1	-
GF0041591	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_01703_mRNA_2.1	-
GF0041590	0	1	0	Hypothetical protein (1)			-	C_unshiu_01703_mRNA_1.1	-
GF0041589	0	1	0	Hypothetical protein (1)			-	C_unshiu_01701_mRNA_3.1	-
GF0041588	0	1	0	Hypothetical protein (1)			-	C_unshiu_01699_mRNA_6.1	-
GF0041587	0	1	0	Phytosulfokine receptor (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	-	C_unshiu_01698_mRNA_7.1	-
GF0041586	0	1	0	LRR receptor-like kinase family protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	-	C_unshiu_01698_mRNA_5.1	-
GF0041585	0	1	0	Hypothetical protein (1)			-	C_unshiu_01697_mRNA_2.1	-
GF0041584	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_01697_mRNA_1.1	-
GF0041583	0	1	0	Hypothetical protein (1)			-	C_unshiu_01696_mRNA_4.1	-
GF0041582	0	1	0	Hypothetical protein (1)	heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1)	Cytochrome P450 [IPR001128] (1)	-	C_unshiu_01696_mRNA_3.1	-
GF0041581	0	1	0	Hypothetical protein (1)			-	C_unshiu_01696_mRNA_2.1	-
GF0041580	0	1	0	Hypothetical protein (1)			-	C_unshiu_01696_mRNA_1.1	-
GF0041579	0	1	0	Hypothetical protein (1)			-	C_unshiu_01695_mRNA_8.1	-
GF0041578	0	1	0	Hypothetical protein (1)			-	C_unshiu_01695_mRNA_12.1	-
GF0041577	0	1	0	Hypothetical protein (1)			-	C_unshiu_01695_mRNA_1.1	-
GF0041576	0	1	0	Hypothetical protein (1)		Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01694_mRNA_7.1	-
GF0041575	0	1	0	Hypothetical protein (1)			-	C_unshiu_01694_mRNA_5.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0041574	0	1	0	Hypothetical protein (1)	deadenylation-dependent decapping of nuclear-transcribed mRNA [GO:0000290 biological_process] (1); positive regulation of catalytic activity [GO:0043085 biological_process] (1); enzyme activator activity [GO:0008047 molecular_function] (1)	PH domain-like [IPR011993] (1); mRNA-decapping enzyme subunit 1 [IPR010334] (1)	-	C_unshiu_01694_mRNA_3.1	-
GF0041573	0	1	0	Phytosulfokine receptor 2-like protein (1)		Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01694_mRNA_1.1	-
GF0041572	0	1	0	Hypothetical protein (1)	heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1)	Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1); Cytochrome P450 [IPR001128] (1)	-	C_unshiu_01693_mRNA_4.1	-
GF0041571	0	1	0	Hypothetical protein (1)			-	C_unshiu_01693_mRNA_1.1	-
GF0041570	0	1	0	TMV resistance N (1)			-	C_unshiu_01692_mRNA_5.1	-
GF0041569	0	1	0	Hypothetical protein (1)		Bulb-type lectin domain [IPR001480] (1)	-	C_unshiu_01692_mRNA_4.1	-
GF0041568	0	1	0	Hypothetical protein (1)		GAG-pre-integrase domain [IPR025724] (1)	-	C_unshiu_01692_mRNA_3.1	-
GF0041567	0	1	0	Hypothetical protein (1)			-	C_unshiu_01692_mRNA_1.1	-
GF0041566	0	1	0	Hypothetical protein (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Reverse transcriptase domain [IPR000477] (1); Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_01691_mRNA_7.1	-
GF0041565	0	1	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1)	Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1)	-	C_unshiu_01691_mRNA_6.1	-
GF0041564	0	1	0	Hypothetical protein (1)			-	C_unshiu_01691_mRNA_4.1	-
GF0041563	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_01691_mRNA_2.1	-
GF0041562	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	SH3 domain [IPR001452] (1)	-	C_unshiu_01691_mRNA_1.1	-
GF0041561	0	1	0	Hypothetical protein (1)			-	C_unshiu_01690_mRNA_8.1	-
GF0041560	0	1	0	Hypothetical protein (1)			-	C_unshiu_01690_mRNA_1.1	-
GF0041559	0	1	0	Hypothetical protein (1)		DJ-1/PfpI [IPR002818] (1); Class I glutamine amidotransferase-like [IPR029062] (1)	-	C_unshiu_01688_mRNA_6.1	-
GF0041558	0	1	0	LRR receptor-like kinase family protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Protein kinase-like domain [IPR011009] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01688_mRNA_4.1	-
GF0041557	0	1	0	4-methyl-5(B-hydroxyethyl)-thiazole monophosphate biosynthesis (1)		Class I glutamine amidotransferase-like [IPR029062] (1); DJ-1/PfpI [IPR002818] (1)	-	C_unshiu_01688_mRNA_3.1	-
GF0041556	0	1	0	LRR receptor-like kinase (1)	protein binding [GO:0005515 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase-like domain [IPR011009] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Protein kinase domain [IPR000719] (1)	-	C_unshiu_01688_mRNA_1.1	-
GF0041555	0	1	0	Hypothetical protein (1)			-	C_unshiu_01687_mRNA_9.1	-
GF0041554	0	1	0	Hypothetical protein (1)			-	C_unshiu_01687_mRNA_6.1	-
GF0041553	0	1	0	Hypothetical protein (1)			-	C_unshiu_01687_mRNA_3.1	-
GF0041552	0	1	0	Hypothetical protein (1)			-	C_unshiu_01687_mRNA_2.1	-
GF0041551	0	1	0	RPS2 protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01686_mRNA_7.1	-
GF0041550	0	1	0	Hypothetical protein (1)			-	C_unshiu_01686_mRNA_5.1	-
GF0041549	0	1	0	Hypothetical protein (1)			-	C_unshiu_01686_mRNA_4.1	-
GF0041548	0	1	0	Hypothetical protein (1)			-	C_unshiu_01685_mRNA_2.1	-
GF0041547	0	1	0	Hypothetical protein (1)			-	C_unshiu_01684_mRNA_3.1	-
GF0041546	0	1	0	Superoxide dismutase [Cu-Zn] (1)	metal ion binding [GO:0046872 molecular_function] (1); superoxide metabolic process [GO:0006801 biological_process] (1); superoxide dismutase activity [GO:0004784 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Superoxide dismutase (Cu/Zn) / superoxide dismutase copper chaperone [IPR024134] (1); Superoxide dismutase, copper/zinc binding domain [IPR001424] (1); Superoxide dismutase, copper/zinc, binding site [IPR018152] (1)	-	C_unshiu_01683_mRNA_1.1	-
GF0041545	0	1	0	Leucine zipper protein (1)		Domain of unknown function DUF630 [IPR006868] (1); Domain of unknown function DUF632 [IPR006867] (1)	-	C_unshiu_01681_mRNA_8.1	-
GF0041544	0	1	0	Hypothetical protein (1)	catalytic activity [GO:0003824 molecular_function] (1); intramolecular transferase activity, phosphotransferases [GO:0016868 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1); glycolytic process [GO:0006096 biological_process] (1); phosphoglycerate mutase activity [GO:0004619 molecular_function] (1)	Phosphoglycerate/bisphosphoglycerate mutase, active site [IPR001345] (1); Histidine phosphatase superfamily, clade-1 [IPR013078] (1); Phosphoglycerate mutase 1 [IPR005952] (1); Histidine phosphatase superfamily [IPR029033] (1)	-	C_unshiu_01681_mRNA_3.1	-
GF0041543	0	1	0	Hypothetical protein (1)			-	C_unshiu_01681_mRNA_1.1	-
GF0041542	0	1	0	Hypothetical protein (1)			-	C_unshiu_01680_mRNA_8.1	-
GF0041541	0	1	0	Peroxidase 4 (1)	oxidation-reduction process [GO:0055114 biological_process] (1); peroxidase activity [GO:0004601 molecular_function] (1); response to oxidative stress [GO:0006979 biological_process] (1); heme binding [GO:0020037 molecular_function] (1)	Haem peroxidase, plant/fungal/bacterial [IPR002016] (1); Plant peroxidase [IPR000823] (1); Peroxidases heam-ligand binding site [IPR019793] (1); Peroxidase, active site [IPR019794] (1); Haem peroxidase [IPR010255] (1)	-	C_unshiu_01680_mRNA_4.1	-
GF0041540	0	1	0	Hypothetical protein (1)			-	C_unshiu_01680_mRNA_2.1	-
GF0041539	0	1	0	Hypothetical protein (1)			-	C_unshiu_01680_mRNA_13.1	-
GF0041538	0	1	0	Hypothetical protein (1)			-	C_unshiu_01680_mRNA_1.1	-
GF0041537	0	1	0	Hypothetical protein (1)			-	C_unshiu_01678_mRNA_8.1	-
GF0041536	0	1	0	Hypothetical protein (1)			-	C_unshiu_01677_mRNA_9.1	-
GF0041535	0	1	0	Hypothetical protein (1)			-	C_unshiu_01677_mRNA_5.1	-
GF0041534	0	1	0	Hypothetical protein (1)			-	C_unshiu_01677_mRNA_4.1	-
GF0041533	0	1	0	Hypothetical protein (1)			-	C_unshiu_01677_mRNA_10.1	-
GF0041532	0	1	0	Hypothetical protein (1)			-	C_unshiu_01677_mRNA_1.1	-
GF0041531	0	1	0	Hypothetical protein (1)			-	C_unshiu_01676_mRNA_3.1	-
GF0041530	0	1	0	Hypothetical protein (1)		Heat shock protein 70kD, C-terminal domain [IPR029048] (1)	-	C_unshiu_01676_mRNA_2.1	-
GF0041529	0	1	0	Heat shock protein 70 (1)		Heat shock protein 70, conserved site [IPR018181] (1); Heat shock protein 70 family [IPR013126] (1); Heat shock protein 70kD, peptide-binding domain [IPR029047] (1)	-	C_unshiu_01676_mRNA_1.1	-
GF0041528	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_01675_mRNA_1.1	-
GF0041527	0	1	0	Hypothetical protein (1)			-	C_unshiu_01674_mRNA_5.1	-
GF0041526	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Glutathione S-transferase, N-terminal [IPR004045] (1); Glutathione S-transferase, C-terminal-like [IPR010987] (1); Thioredoxin-like fold [IPR012336] (1); Glutathione S-transferase, C-terminal [IPR004046] (1)	-	C_unshiu_01674_mRNA_4.1	-
GF0041525	0	1	0	Hypothetical protein (1)			-	C_unshiu_01674_mRNA_1.1	-
GF0041524	0	1	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Zinc finger, BED-type [IPR003656] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	-	C_unshiu_01673_mRNA_3.1	-
GF0041523	0	1	0	Hypothetical protein (1)			-	C_unshiu_01673_mRNA_1.1	-
GF0041522	0	1	0	Hypothetical protein (1)			-	C_unshiu_01672_mRNA_7.1	-
GF0041521	0	1	0	Hypothetical protein (1)			-	C_unshiu_01671_mRNA_9.1	-
GF0041520	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_01671_mRNA_8.1	-
GF0041519	0	1	0	Hypothetical protein (1)			-	C_unshiu_01671_mRNA_2.1	-
GF0041518	0	1	0	Hypothetical protein (1)			-	C_unshiu_01671_mRNA_1.1	-
GF0041517	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_01670_mRNA_2.1	-
GF0041516	0	1	0	Hypothetical protein (1)			-	C_unshiu_01669_mRNA_5.1	-
GF0041515	0	1	0	Hypothetical protein (1)			-	C_unshiu_01669_mRNA_1.1	-
GF0041514	0	1	0	Hypothetical protein (1)			-	C_unshiu_01668_mRNA_3.1	-
GF0041513	0	1	0	Hypothetical protein (1)			-	C_unshiu_01668_mRNA_1.1	-
GF0041512	0	1	0	Hypothetical protein (1)		TB2/DP1/HVA22-related protein [IPR004345] (1)	-	C_unshiu_01667_mRNA_2.1	-
GF0041511	0	1	0	Hypothetical protein (1)			-	C_unshiu_01667_mRNA_1.1	-
GF0041510	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_01666_mRNA_9.1	-
GF0041509	0	1	0	Hypothetical protein (1)			-	C_unshiu_01666_mRNA_8.1	-
GF0041508	0	1	0	Hypothetical protein (1)			-	C_unshiu_01666_mRNA_4.1	-
GF0041507	0	1	0	Hypothetical protein (1)			-	C_unshiu_01666_mRNA_1.1	-
GF0041506	0	1	0	Hypothetical protein (1)			-	C_unshiu_01665_mRNA_4.1	-
GF0041505	0	1	0	ABC(Binding protein) family transporter: polyamine (1)			-	C_unshiu_01664_mRNA_5.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0041504	0	1	0	SH3 domain-containing protein 1 (1)			-	C_unshiu_01664_mRNA_3.1	-
GF0041503	0	1	0	LRR receptor-like serine/threonine-protein kinase GSO1 (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_01664_mRNA_2.1	-
GF0041502	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01664_mRNA_1.1	-
GF0041501	0	1	0	Hypothetical protein (1)			-	C_unshiu_01663_mRNA_5.1	-
GF0041500	0	1	0	Hypothetical protein (1)			-	C_unshiu_01663_mRNA_4.1	-
GF0041499	0	1	0	Hypothetical protein (1)			-	C_unshiu_01663_mRNA_3.1	-
GF0041498	0	1	0	L-type lectin-domain containing receptor kinase IX.1 (1)		Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_01662_mRNA_3.1	-
GF0041497	0	1	0	Ankyrin repeat plant-like protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Ankyrin repeat [IPR002110] (1); PGG domain [IPR026961] (1); Zinc finger, CCHC-type [IPR001878] (1); Ankyrin repeat-containing domain [IPR020683] (1); Zinc knuckle CX2CX4HX4C [IPR025836] (1)	-	C_unshiu_01661_mRNA_3.1	-
GF0041496	0	1	0	Hypothetical protein (1)			-	C_unshiu_01660_mRNA_5.1	-
GF0041495	0	1	0	Hypothetical protein (1)			-	C_unshiu_01660_mRNA_2.1	-
GF0041494	0	1	0	Hypothetical protein (1)			-	C_unshiu_01659_mRNA_8.1	-
GF0041493	0	1	0	Hypothetical protein (1)			-	C_unshiu_01659_mRNA_4.1	-
GF0041492	0	1	0	Hypothetical protein (1)			-	C_unshiu_01659_mRNA_2.1	-
GF0041491	0	1	0	Hypothetical protein (1)			-	C_unshiu_01658_mRNA_3.1	-
GF0041490	0	1	0	NBS-LRR type disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	AAA+ ATPase domain [IPR003593] (1); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_01658_mRNA_2.1	-
GF0041489	0	1	0	Disease resistance RPS5-like protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01658_mRNA_1.1	-
GF0041488	0	1	0	Hypothetical protein (1)			-	C_unshiu_01657_mRNA_5.1	-
GF0041487	0	1	0	Hypothetical protein (1)			-	C_unshiu_01657_mRNA_3.1	-
GF0041486	0	1	0	Hypothetical protein (1)	RNA-directed RNA polymerase activity [GO:0003968 molecular_function] (1)	RNA-dependent RNA polymerase, eukaryotic-type [IPR007855] (1)	-	C_unshiu_01657_mRNA_2.1	-
GF0041485	0	1	0	Hypothetical protein (1)			-	C_unshiu_01657_mRNA_1.1	-
GF0041484	0	1	0	Disease resistance protein (TIR-NBS-LRR class) (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1)	-	C_unshiu_01656_mRNA_2.1	-
GF0041483	0	1	0	Hydrolase, alpha/beta domain protein (1)		Alpha/beta hydrolase fold-1 [IPR000073] (1); Alpha/Beta hydrolase fold [IPR029058] (1)	-	C_unshiu_01656_mRNA_1.1	-
GF0041482	0	1	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Protein kinase-like domain [IPR011009] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Protein kinase domain [IPR000719] (1)	-	C_unshiu_01654_mRNA_4.1	-
GF0041481	0	1	0	Hypothetical protein (1)		HAD-like domain [IPR023214] (1); HAD-superfamily hydrolase, subfamily IG, 5'-nucleotidase [IPR008380] (1)	-	C_unshiu_01654_mRNA_2.1	-
GF0041480	0	1	0	Polycomb group RING finger protein 3 (1)	zinc ion binding [GO:0008270 molecular_function] (1); metal ion binding [GO:0046872 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Zinc finger, RING-type, conserved site [IPR017907] (1); Zinc finger, RING-type [IPR001841] (1); Zinc finger, RING/FYVE/PHD-type [IPR013083] (1); Zinc finger, C3HC4 RING-type [IPR018957] (1)	-	C_unshiu_01653_mRNA_1.1	-
GF0041479	0	1	0	Hypothetical protein (1)			-	C_unshiu_01652_mRNA_5.1	-
GF0041478	0	1	0	Hypothetical protein (1)			-	C_unshiu_01652_mRNA_1.1	-
GF0041477	0	1	0	Extracellular calcium sensing receptor (1)		Rhodanese-like domain [IPR001763] (1)	-	C_unshiu_01651_mRNA_1.1	-
GF0041476	0	1	0	Hypothetical protein (1)			-	C_unshiu_01650_mRNA_1.1	-
GF0041475	0	1	0	Hypothetical protein (1)			-	C_unshiu_01649_mRNA_8.1	-
GF0041474	0	1	0	Hypothetical protein (1)			-	C_unshiu_01649_mRNA_3.1	-
GF0041473	0	1	0	Hypothetical protein (1)			-	C_unshiu_01648_mRNA_6.1	-
GF0041472	0	1	0	Putative serine/threonine-protein kinase WNK4 (1)			-	C_unshiu_01648_mRNA_4.1	-
GF0041471	0	1	0	Hypothetical protein (1)			-	C_unshiu_01646_mRNA_9.1	-
GF0041470	0	1	0	Hypothetical protein (1)			-	C_unshiu_01646_mRNA_8.1	-
GF0041469	0	1	0	Hypothetical protein (1)			-	C_unshiu_01646_mRNA_6.1	-
GF0041468	0	1	0	LRR receptor-like serine/threonine-protein kinase GSO1 (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_01646_mRNA_12.1	-
GF0041467	0	1	0	Hypothetical protein (1)	hydrolase activity [GO:0016787 molecular_function] (1)	Pectinacetylesterase/NOTUM [IPR004963] (1)	-	C_unshiu_01646_mRNA_11.1	-
GF0041466	0	1	0	Hypothetical protein (1)			-	C_unshiu_01645_mRNA_3.1	-
GF0041465	0	1	0	Hypothetical protein (1)			-	C_unshiu_01645_mRNA_2.1	-
GF0041464	0	1	0	Hypothetical protein (1)			-	C_unshiu_01645_mRNA_1.1	-
GF0041463	0	1	0	Hypothetical protein (1)			-	C_unshiu_01644_mRNA_3.1	-
GF0041462	0	1	0	Putative polyprotein (Aspartic proteinase, reverse transcriptase, ribonuclease H) (1)		Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_01643_mRNA_2.1	-
GF0041461	0	1	0	Hypothetical protein (1)			-	C_unshiu_01641_mRNA_9.1	-
GF0041460	0	1	0	LRR receptor-like kinase family protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	-	C_unshiu_01640_mRNA_1.1	-
GF0041459	0	1	0	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	C_unshiu_01639_mRNA_3.1	-
GF0041458	0	1	0	Hypothetical protein (1)			-	C_unshiu_01638_mRNA_9.1	-
GF0041457	0	1	0	Hypothetical protein (1)			-	C_unshiu_01638_mRNA_8.1	-
GF0041456	0	1	0	Hypothetical protein (1)			-	C_unshiu_01638_mRNA_7.1	-
GF0041455	0	1	0	Ubiquitinyl hydrolase 1 (1)	thiol-dependent ubiquitin-specific protease activity [GO:0004843 molecular_function] (1); intracellular [GO:0005622 cellular_component] (1); ubiquitin-dependent protein catabolic process [GO:0006511 biological_process] (1)	Peptidase C12, ubiquitin carboxyl-terminal hydrolase [IPR001578] (1)	-	C_unshiu_01638_mRNA_6.1	-
GF0041454	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_01638_mRNA_2.1	-
GF0041453	0	1	0	Hypothetical protein (1)			-	C_unshiu_01638_mRNA_11.1	-
GF0041452	0	1	0	Hypothetical protein (1)			-	C_unshiu_01638_mRNA_10.1	-
GF0041451	0	1	0	Hypothetical protein (1)			-	C_unshiu_01637_mRNA_9.1	-
GF0041450	0	1	0	Hypothetical protein (1)			-	C_unshiu_01637_mRNA_8.1	-
GF0041449	0	1	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1)	Aspartic peptidase domain [IPR021109] (1); Reverse transcriptase domain [IPR000477] (1); Retropepsins [IPR018061] (1); Peptidase A2A, retrovirus, catalytic [IPR001995] (1)	-	C_unshiu_01637_mRNA_5.1	-
GF0041448	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			-	C_unshiu_01637_mRNA_3.1	-
GF0041447	0	1	0	Hypothetical protein (1)			-	C_unshiu_01637_mRNA_10.1	-
GF0041446	0	1	0	Hypothetical protein (1)			-	C_unshiu_01637_mRNA_1.1	-
GF0041445	0	1	0	Polyphosphoinositide phosphatase (1)	phosphatidylinositol-3-phosphate biosynthetic process [GO:0036092 biological_process] (1); phosphoric ester hydrolase activity [GO:0042578 molecular_function] (1); vacuole organization [GO:0007033 biological_process] (1)	SAC domain [IPR002013] (1); Phosphoinositide phosphatase SAC, plants [IPR030213] (1)	-	C_unshiu_01633_mRNA_3.1	-
GF0041444	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_01632_mRNA_8.1	-
GF0041443	0	1	0	Hypothetical protein (1)			-	C_unshiu_01632_mRNA_7.1	-
GF0041442	0	1	0	Hypothetical protein (1)			-	C_unshiu_01632_mRNA_6.1	-
GF0041441	0	1	0	Hypothetical protein (1)			-	C_unshiu_01632_mRNA_5.1	-
GF0041440	0	1	0	Hypothetical protein (1)			-	C_unshiu_01632_mRNA_11.1	-
GF0041439	0	1	0	Hypothetical protein (1)			-	C_unshiu_01632_mRNA_1.1	-
GF0041438	0	1	0	Hypothetical protein (1)	copper ion binding [GO:0005507 molecular_function] (1)	Cytochrome c oxidase assembly protein CtaG/Cox11, domain [IPR023471] (1); Cytochrome c oxidase assembly protein CtaG/Cox11 [IPR007533] (1)	-	C_unshiu_01631_mRNA_7.1	-
GF0041437	0	1	0	Hypothetical protein (1)			-	C_unshiu_01631_mRNA_4.1	-
GF0041436	0	1	0	Disease resistance protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01630_mRNA_4.1	-
GF0041435	0	1	0	Disease resistance protein RPS5 (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); AAA+ ATPase domain [IPR003593] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_01630_mRNA_3.1	-
GF0041434	0	1	0	Hypothetical protein (1)			-	C_unshiu_01629_mRNA_7.1	-
GF0041433	0	1	0	Hypothetical protein (1)			-	C_unshiu_01629_mRNA_4.1	-
GF0041432	0	1	0	Hypothetical protein (1)			-	C_unshiu_01629_mRNA_14.1	-
GF0041431	0	1	0	Hypothetical protein (1)			-	C_unshiu_01629_mRNA_13.1	-
GF0041430	0	1	0	Hypothetical protein (1)			-	C_unshiu_01628_mRNA_3.1	-
GF0041429	0	1	0	Putative aspartic protease (1)	proteolysis [GO:0006508 biological_process] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1)	Aspartic peptidase domain [IPR021109] (1); Peptidase family A1 domain [IPR033121] (1); Aspartic peptidase A1 family [IPR001461] (1); Xylanase inhibitor, C-terminal [IPR032799] (1); Xylanase inhibitor, N-terminal [IPR032861] (1); Aspartic peptidase, active site [IPR001969] (1)	-	C_unshiu_01626_mRNA_6.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0041428	0	1	0	LRR receptor-like kinase family protein (1)	protein binding [GO:0005515 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Protein kinase-like domain [IPR011009] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Protein kinase domain [IPR000719] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Leucine-rich repeat [IPR001611] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase, ATP binding site [IPR017441] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1)	-	C_unshiu_01625_mRNA_3.1	-
GF0041427	0	1	0	Hypothetical protein (1)			-	C_unshiu_01624_mRNA_4.1	-
GF0041426	0	1	0	Hypothetical protein (1)			-	C_unshiu_01623_mRNA_8.1	-
GF0041425	0	1	0	Hypothetical protein (1)			-	C_unshiu_01623_mRNA_4.1	-
GF0041424	0	1	0	Hypothetical protein (1)			-	C_unshiu_01621_mRNA_3.1	-
GF0041423	0	1	0	Hypothetical protein (1)			-	C_unshiu_01621_mRNA_2.1	-
GF0041422	0	1	0	LRR receptor-like serine/threonine-protein kinase EFR (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Protein kinase-like domain [IPR011009] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	-	C_unshiu_01621_mRNA_1.1	-
GF0041421	0	1	0	Hypothetical protein (1)			-	C_unshiu_01620_mRNA_9.1	-
GF0041420	0	1	0	Hypothetical protein (1)			-	C_unshiu_01620_mRNA_8.1	-
GF0041419	0	1	0	Uncharacterized mitochondrial protein AtMg00810 (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	-	C_unshiu_01620_mRNA_6.1	-
GF0041418	0	1	0	Hypothetical protein (1)			-	C_unshiu_01620_mRNA_5.1	-
GF0041417	0	1	0	Hypothetical protein (1)			-	C_unshiu_01620_mRNA_2.1	-
GF0041416	0	1	0	Disease resistance protein RPS2 (1)	protein binding [GO:0005515 molecular_function] (1); ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01620_mRNA_11.1	-
GF0041415	0	1	0	Hypothetical protein (1)			-	C_unshiu_01620_mRNA_1.1	-
GF0041414	0	1	0	Hypothetical protein (1)	response to oxidative stress [GO:0006979 biological_process] (1); heme binding [GO:0020037 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); peroxidase activity [GO:0004601 molecular_function] (1)	Peroxidases heam-ligand binding site [IPR019793] (1); Peroxidase, active site [IPR019794] (1); Haem peroxidase, plant/fungal/bacterial [IPR002016] (1); Haem peroxidase [IPR010255] (1); Protein kinase-like domain [IPR011009] (1); Plant ascorbate peroxidase [IPR002207] (1)	-	C_unshiu_01619_mRNA_6.1	-
GF0041413	0	1	0	Nitrate excretion transporter 1 (1)	oligopeptide transport [GO:0006857 biological_process] (1); transporter activity [GO:0005215 molecular_function] (1); transport [GO:0006810 biological_process] (1); membrane [GO:0016020 cellular_component] (1)	PTR2 family proton/oligopeptide symporter, conserved site [IPR018456] (1); Proton-dependent oligopeptide transporter family [IPR000109] (1); Major facilitator superfamily domain [IPR020846] (1)	-	C_unshiu_01619_mRNA_4.1	-
GF0041412	0	1	0	Hypothetical protein (1)			-	C_unshiu_01618_mRNA_2.1	-
GF0041411	0	1	0	Ankyrin repeat plant-like protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat [IPR002110] (1); Ankyrin repeat-containing domain [IPR020683] (1); PGG domain [IPR026961] (1)	-	C_unshiu_01617_mRNA_2.1	-
GF0041410	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); DNA integration [GO:0015074 biological_process] (1)	PGG domain [IPR026961] (1); GAG-pre-integrase domain [IPR025724] (1); Ribonuclease H-like domain [IPR012337] (1); Integrase, catalytic core [IPR001584] (1)	-	C_unshiu_01617_mRNA_1.1	-
GF0041409	0	1	0	Hypothetical protein (1)			-	C_unshiu_01616_mRNA_4.1	-
GF0041408	0	1	0	Hypothetical protein (1)			-	C_unshiu_01616_mRNA_1.1	-
GF0041407	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_01615_mRNA_9.1	-
GF0041406	0	1	0	Hypothetical protein (1)			-	C_unshiu_01615_mRNA_8.1	-
GF0041405	0	1	0	Hypothetical protein (1)			-	C_unshiu_01615_mRNA_7.1	-
GF0041404	0	1	0	Hypothetical protein (1)			-	C_unshiu_01615_mRNA_6.1	-
GF0041403	0	1	0	Hypothetical protein (1)			-	C_unshiu_01615_mRNA_5.1	-
GF0041402	0	1	0	Hypothetical protein (1)			-	C_unshiu_01615_mRNA_3.1	-
GF0041401	0	1	0	Hypothetical protein (1)		Chromo domain [IPR023780] (1)	-	C_unshiu_01615_mRNA_2.1	-
GF0041400	0	1	0	Hypothetical protein (1)			-	C_unshiu_01615_mRNA_1.1	-
GF0041399	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_01614_mRNA_5.1	-
GF0041398	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	-	C_unshiu_01614_mRNA_1.1	-
GF0041397	0	1	0	Hypothetical protein (1)			-	C_unshiu_01612_mRNA_6.1	-
GF0041396	0	1	0	Hypothetical protein (1)			-	C_unshiu_01612_mRNA_4.1	-
GF0041395	0	1	0	SLG-Sc and SLA-Sc genes and Melmoth retrotransposon sequence (1)			-	C_unshiu_01612_mRNA_1.1	-
GF0041394	0	1	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_01611_mRNA_5.1	-
GF0041393	0	1	0	Hypothetical protein (1)			-	C_unshiu_01611_mRNA_4.1	-
GF0041392	0	1	0	Hypothetical protein (1)			-	C_unshiu_01611_mRNA_3.1	-
GF0041391	0	1	0	Hypothetical protein (1)			-	C_unshiu_01611_mRNA_1.1	-
GF0041390	0	1	0	Hypothetical protein (1)	histone acetyltransferase complex [GO:0000123 cellular_component] (1)	KAT8 regulatory NSL complex subunit 2 [IPR026316] (1); Potential DNA-binding domain [IPR025927] (1)	-	C_unshiu_01610_mRNA_6.1	-
GF0041389	0	1	0	Hypothetical protein (1)			-	C_unshiu_01609_mRNA_3.1	-
GF0041388	0	1	0	Prefoldin chaperone subunit family protein, putative isoform 2 (1)	prefoldin complex [GO:0016272 cellular_component] (1); unfolded protein binding [GO:0051082 molecular_function] (1); protein folding [GO:0006457 biological_process] (1)	Prefoldin alpha-like [IPR004127] (1); Prefoldin alpha subunit, archaea-type [IPR011599] (1); Prefoldin [IPR009053] (1)	-	C_unshiu_01608_mRNA_4.1	-
GF0041387	0	1	0	Hypothetical protein (1)	lyase activity [GO:0016829 molecular_function] (1); terpene synthase activity [GO:0010333 molecular_function] (1); magnesium ion binding [GO:0000287 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Isoprenoid synthase domain [IPR008949] (1); Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (1); Terpene synthase, N-terminal domain [IPR001906] (1); Terpene synthase, metal-binding domain [IPR005630] (1)	-	C_unshiu_01608_mRNA_3.1	-
GF0041386	0	1	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1)	Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Plant methyltransferase dimerisation [IPR012967] (1)	-	C_unshiu_01607_mRNA_6.1	-
GF0041385	0	1	0	Hypothetical protein (1)		Transposase, MuDR, plant [IPR004332] (1)	-	C_unshiu_01606_mRNA_4.1	-
GF0041384	0	1	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_01606_mRNA_3.1	-
GF0041383	0	1	0	Carotenoid cleavage dioxygenase (1)	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen [GO:0016702 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Carotenoid oxygenase [IPR004294] (1)	-	C_unshiu_01606_mRNA_2.1	-
GF0041382	0	1	0	Disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	NB-ARC [IPR002182] (1); Leucine-rich repeat [IPR001611] (1); AAA+ ATPase domain [IPR003593] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01605_mRNA_8.1	-
GF0041381	0	1	0	Beta-1,3-N-acetylglucosaminyltransferase lunatic fringe (1)		Protein of unknown function DUF604 [IPR006740] (1)	-	C_unshiu_01604_mRNA_7.1	-
GF0041380	0	1	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Serine/threonine-protein kinase, active site [IPR008271] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	-	C_unshiu_01604_mRNA_3.1	-
GF0041379	0	1	0	Leucine-rich repeat protein kinase family protein, putative (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1)	-	C_unshiu_01603_mRNA_7.1	-
GF0041378	0	1	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1)	Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	-	C_unshiu_01603_mRNA_5.1	-
GF0041377	0	1	0	Hypothetical protein (1)			-	C_unshiu_01602_mRNA_5.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0041376	0	1	0	Cytochrome P450 (1)	iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1)	Cytochrome P450 [IPR001128] (1); Cytochrome P450, E-class, group I [IPR002401] (1)	-	C_unshiu_01602_mRNA_2.1	-
GF0041375	0	1	0	Hypothetical protein (1)			-	C_unshiu_01601_mRNA_4.1	-
GF0041374	0	1	0	Hypothetical protein (1)			-	C_unshiu_01601_mRNA_3.1	-
GF0041373	0	1	0	Hypothetical protein (1)			-	C_unshiu_01601_mRNA_1.1	-
GF0041372	0	1	0	Hypothetical protein (1)			-	C_unshiu_01599_mRNA_6.1	-
GF0041371	0	1	0	Hypothetical protein (1)			-	C_unshiu_01599_mRNA_2.1	-
GF0041370	0	1	0	Hypothetical protein (1)			-	C_unshiu_01599_mRNA_1.1	-
GF0041369	0	1	0	Hypothetical protein (1)			-	C_unshiu_01598_mRNA_9.1	-
GF0041368	0	1	0	Hypothetical protein (1)			-	C_unshiu_01598_mRNA_8.1	-
GF0041367	0	1	0	CXE carboxylesterase (1)	metabolic process [GO:0008152 biological_process] (1); hydrolase activity [GO:0016787 molecular_function] (1)	Alpha/beta hydrolase fold-3 [IPR013094] (1); Alpha/Beta hydrolase fold [IPR029058] (1)	-	C_unshiu_01598_mRNA_5.1	-
GF0041366	0	1	0	Hypothetical protein (1)		Alpha/Beta hydrolase fold [IPR029058] (1)	-	C_unshiu_01598_mRNA_4.1	-
GF0041365	0	1	0	Hypothetical protein (1)			-	C_unshiu_01597_mRNA_9.1	-
GF0041364	0	1	0	Hypothetical protein (1)			-	C_unshiu_01597_mRNA_6.1	-
GF0041363	0	1	0	Hypothetical protein (1)			-	C_unshiu_01597_mRNA_5.1	-
GF0041362	0	1	0	Hypothetical protein (1)			-	C_unshiu_01597_mRNA_2.1	-
GF0041361	0	1	0	Hypothetical protein (1)		FANCI solenoid 2 domain [IPR029315] (1)	-	C_unshiu_01597_mRNA_10.1	-
GF0041360	0	1	0	Hypothetical protein (1)			-	C_unshiu_01597_mRNA_1.1	-
GF0041359	0	1	0	Hypothetical protein (1)			-	C_unshiu_01596_mRNA_5.1	-
GF0041358	0	1	0	Disease resistance protein RPS2 (1)	protein binding [GO:0005515 molecular_function] (1); ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); Leucine-rich repeat [IPR001611] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01595_mRNA_4.1	-
GF0041357	0	1	0	Hypothetical protein (1)			-	C_unshiu_01595_mRNA_3.1	-
GF0041356	0	1	0	Hypothetical protein (1)			-	C_unshiu_01595_mRNA_2.1	-
GF0041355	0	1	0	Flavonoid 3-monooxygenase (1)	iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Cytochrome P450 [IPR001128] (1)	-	C_unshiu_01595_mRNA_1.1	-
GF0041354	0	1	0	Putative bifunctional amine oxidase (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1)	FAD/NAD(P)-binding domain [IPR023753] (1)	-	C_unshiu_01594_mRNA_7.1	-
GF0041353	0	1	0	Hypothetical protein (1)		Alpha crystallin/Hsp20 domain [IPR002068] (1); HSP20-like chaperone [IPR008978] (1)	-	C_unshiu_01594_mRNA_5.1	-
GF0041352	0	1	0	Hypothetical protein (1)			-	C_unshiu_01594_mRNA_3.1	-
GF0041351	0	1	0	Hypothetical protein (1)			-	C_unshiu_01594_mRNA_2.1	-
GF0041350	0	1	0	AT3G04670 protein (1)			-	C_unshiu_01594_mRNA_1.1	-
GF0041349	0	1	0	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1); AAA-type ATPase, N-terminal domain [IPR025753] (1)	-	C_unshiu_01593_mRNA_3.1	-
GF0041348	0	1	0	Hypothetical protein (1)			-	C_unshiu_01592_mRNA_2.1	-
GF0041347	0	1	0	Hypothetical protein (1)			-	C_unshiu_01591_mRNA_2.1	-
GF0041346	0	1	0	Hypothetical protein (1)			-	C_unshiu_01591_mRNA_14.1	-
GF0041345	0	1	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_01590_mRNA_4.1	-
GF0041344	0	1	0	Hypothetical protein (1)			-	C_unshiu_01589_mRNA_2.1	-
GF0041343	0	1	0	Hypothetical protein (1)			-	C_unshiu_01589_mRNA_1.1	-
GF0041342	0	1	0	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	C_unshiu_01588_mRNA_2.1	-
GF0041341	0	1	0	Hypothetical protein (1)			-	C_unshiu_01587_mRNA_3.1	-
GF0041340	0	1	0	Peptide chain release factor 1 (1)	translational termination [GO:0006415 biological_process] (1); translation release factor activity [GO:0003747 molecular_function] (1)	Peptide chain release factor class I/class II [IPR000352] (1); Double-stranded RNA-binding domain [IPR014720] (1)	-	C_unshiu_01587_mRNA_2.1	-
GF0041339	0	1	0	Hypothetical protein (1)			-	C_unshiu_01587_mRNA_10.1	-
GF0041338	0	1	0	Hypothetical protein (1)			-	C_unshiu_01586_mRNA_7.1	-
GF0041337	0	1	0	Hypothetical protein (1)			-	C_unshiu_01586_mRNA_5.1	-
GF0041336	0	1	0	Hypothetical protein (1)			-	C_unshiu_01586_mRNA_3.1	-
GF0041335	0	1	0	Hypothetical protein (1)			-	C_unshiu_01586_mRNA_2.1	-
GF0041334	0	1	0	Hypothetical protein (1)			-	C_unshiu_01585_mRNA_9.1	-
GF0041333	0	1	0	Hypothetical protein (1)			-	C_unshiu_01585_mRNA_6.1	-
GF0041332	0	1	0	Nonexpressor of pathogenesis-related protein 1 (1)		Regulatory protein NPR, central domain [IPR024228] (1); Ankyrin repeat-containing domain [IPR020683] (1); NPR1/NIM1-like, C-terminal [IPR021094] (1)	-	C_unshiu_01584_mRNA_9.1	-
GF0041331	0	1	0	Hypothetical protein (1)			-	C_unshiu_01584_mRNA_7.1	-
GF0041330	0	1	0	Hypothetical protein (1)			-	C_unshiu_01584_mRNA_5.1	-
GF0041329	0	1	0	Hypothetical protein (1)			-	C_unshiu_01584_mRNA_1.1	-
GF0041328	0	1	0	Hypothetical protein (1)			-	C_unshiu_01583_mRNA_4.1	-
GF0041327	0	1	0	Hypothetical protein (1)		Zinc finger, TTF-type [IPR006580] (1); Domain of unknown function DUF4371 [IPR025398] (1)	-	C_unshiu_01583_mRNA_2.1	-
GF0041326	0	1	0	Hypothetical protein (1)			-	C_unshiu_01583_mRNA_1.1	-
GF0041325	0	1	0	Hypothetical protein (1)			-	C_unshiu_01582_mRNA_2.1	-
GF0041324	0	1	0	Hypothetical protein (1)			-	C_unshiu_01581_mRNA_5.1	-
GF0041323	0	1	0	Hypothetical protein (1)			-	C_unshiu_01581_mRNA_2.1	-
GF0041322	0	1	0	Amino acid binding protein, putative (1)			-	C_unshiu_01580_mRNA_7.1	-
GF0041321	0	1	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1); Domain of unknown function DUF1985 [IPR015410] (1)	-	C_unshiu_01580_mRNA_3.1	-
GF0041320	0	1	0	E3 ubiquitin-protein ligase RNF14 (1)	protein ubiquitination [GO:0016567 biological_process] (1); ubiquitin-protein transferase activity [GO:0004842 molecular_function] (1); metal ion binding [GO:0046872 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Zinc finger, RING-type [IPR001841] (1); Zinc finger, RING-type, conserved site [IPR017907] (1); E3 ubiquitin ligase RBR family [IPR031127] (1); Zinc finger, RING/FYVE/PHD-type [IPR013083] (1); Zinc finger, C3HC4 RING-type [IPR018957] (1)	-	C_unshiu_01580_mRNA_2.1	-
GF0041319	0	1	0	RING zinc finger protein, putative (1)	protein ubiquitination [GO:0016567 biological_process] (1); ubiquitin-protein transferase activity [GO:0004842 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, RING-type, conserved site [IPR017907] (1); E3 ubiquitin ligase RBR family [IPR031127] (1); Zinc finger, RING-type [IPR001841] (1); Zinc finger, RING/FYVE/PHD-type [IPR013083] (1)	-	C_unshiu_01580_mRNA_1.1	-
GF0041318	0	1	0	Hypothetical protein (1)			-	C_unshiu_01579_mRNA_7.1	-
GF0041317	0	1	0	Hypothetical protein (1)			-	C_unshiu_01579_mRNA_1.1	-
GF0041316	0	1	0	TIR-NBS-LRR type disease resistance protein (1)	signal transduction [GO:0007165 biological_process] (1); protein binding [GO:0005515 molecular_function] (1)	Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_01578_mRNA_4.1	-
GF0041315	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1); signal transduction [GO:0007165 biological_process] (1)	Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1)	-	C_unshiu_01578_mRNA_3.1	-
GF0041314	0	1	0	Hypothetical protein (1)	translation release factor activity [GO:0003747 molecular_function] (1); translational termination [GO:0006415 biological_process] (1)	Peptide chain release factor class I/class II [IPR000352] (1); Alpha/Beta hydrolase fold [IPR029058] (1); Double-stranded RNA-binding domain [IPR014720] (1)	-	C_unshiu_01578_mRNA_2.1	-
GF0041313	0	1	0	Major pollen allergen Ory s 1, putative (1)	extracellular region [GO:0005576 cellular_component] (1)	Expansin, cellulose-binding-like domain [IPR007117] (1); Expansin/Lol pI [IPR007118] (1); RlpA-like double-psi beta-barrel domain [IPR009009] (1); Expansin/pollen allergen, DPBB domain [IPR007112] (1)	-	C_unshiu_01577_mRNA_3.1	-
GF0041312	0	1	0	G-type lectin S-receptor-like serine/threonine-protein kinase (1)	recognition of pollen [GO:0048544 biological_process] (1)	S-locus glycoprotein domain [IPR000858] (1); PAN/Apple domain [IPR003609] (1); Bulb-type lectin domain [IPR001480] (1)	-	C_unshiu_01576_mRNA_8.1	-
GF0041311	0	1	0	Hypothetical protein (1)			-	C_unshiu_01576_mRNA_7.1	-
GF0041310	0	1	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); protein heterodimerization activity [GO:0046982 molecular_function] (1); nucleosome [GO:0000786 cellular_component] (1)	Histone-fold [IPR009072] (1); Histone H3/CENP-A [IPR000164] (1)	-	C_unshiu_01576_mRNA_1.1	-
GF0041309	0	1	0	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	-	C_unshiu_01575_mRNA_3.1	-
GF0041308	0	1	0	Hypothetical protein (1)			-	C_unshiu_01573_mRNA_7.1	-
GF0041307	0	1	0	Similarity to non-LTR retroelement reverse transcriptase (1)			-	C_unshiu_01573_mRNA_4.1	-
GF0041306	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01572_mRNA_4.1	-
GF0041305	0	1	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	GPN-loop GTPase [IPR004130] (1); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01572_mRNA_3.1	-
GF0041304	0	1	0	Hypothetical protein (1)			-	C_unshiu_01570_mRNA_9.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0041303	0	1	0	Protein SRG1 (1)	nucleic acid binding [GO:0003676 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1)	Oxoglutarate/iron-dependent dioxygenase [IPR005123] (1); Isopenicillin N synthase-like [IPR027443] (1); Non-haem dioxygenase N-terminal domain [IPR026992] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_01570_mRNA_2.1	-
GF0041302	0	1	0	Hypothetical protein (1)			-	C_unshiu_01569_mRNA_6.1	-
GF0041301	0	1	0	Hypothetical protein (1)			-	C_unshiu_01569_mRNA_4.1	-
GF0041300	0	1	0	Hypothetical protein (1)			-	C_unshiu_01568_mRNA_6.1	-
GF0041299	0	1	0	Hypothetical protein (1)			-	C_unshiu_01568_mRNA_4.1	-
GF0041298	0	1	0	Hypothetical protein (1)			-	C_unshiu_01568_mRNA_3.1	-
GF0041297	0	1	0	Hypothetical protein (1)			-	C_unshiu_01568_mRNA_2.1	-
GF0041296	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_01568_mRNA_15.1	-
GF0041295	0	1	0	Hypothetical protein (1)			-	C_unshiu_01568_mRNA_14.1	-
GF0041294	0	1	0	Hypothetical protein (1)			-	C_unshiu_01568_mRNA_12.1	-
GF0041293	0	1	0	Hypothetical protein (1)			-	C_unshiu_01568_mRNA_11.1	-
GF0041292	0	1	0	Hypothetical protein (1)			-	C_unshiu_01568_mRNA_1.1	-
GF0041291	0	1	0	Hypothetical protein (1)			-	C_unshiu_01567_mRNA_8.1	-
GF0041290	0	1	0	Hypothetical protein (1)		PAN/Apple domain [IPR003609] (1)	-	C_unshiu_01567_mRNA_1.1	-
GF0041289	0	1	0	Hypothetical protein (1)		P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_01566_mRNA_8.1	-
GF0041288	0	1	0	Hypothetical protein (1)			-	C_unshiu_01566_mRNA_2.1	-
GF0041287	0	1	0	Hypothetical protein (1)			-	C_unshiu_01565_mRNA_3.1	-
GF0041286	0	1	0	Hypothetical protein (1)			-	C_unshiu_01564_mRNA_5.1	-
GF0041285	0	1	0	Hypothetical protein (1)			-	C_unshiu_01564_mRNA_4.1	-
GF0041284	0	1	0	Hypothetical protein (1)			-	C_unshiu_01564_mRNA_2.1	-
GF0041283	0	1	0	Hypothetical protein (1)			-	C_unshiu_01564_mRNA_1.1	-
GF0041282	0	1	0	Hypothetical protein (1)			-	C_unshiu_01563_mRNA_1.1	-
GF0041281	0	1	0	Hypothetical protein (1)			-	C_unshiu_01562_mRNA_1.1	-
GF0041280	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	F-box domain [IPR001810] (1)	-	C_unshiu_01561_mRNA_8.1	-
GF0041279	0	1	0	Hypothetical protein (1)			-	C_unshiu_01561_mRNA_7.1	-
GF0041278	0	1	0	Hypothetical protein (1)			-	C_unshiu_01561_mRNA_4.1	-
GF0041277	0	1	0	Protein phosphatase 1 regulatory subunit 7 (1)	protein binding [GO:0005515 molecular_function] (1)	Pectin lyase fold [IPR012334] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01561_mRNA_3.1	-
GF0041276	0	1	0	Hypothetical protein (1)			-	C_unshiu_01560_mRNA_7.1	-
GF0041275	0	1	0	Hypothetical protein (1)			-	C_unshiu_01560_mRNA_4.1	-
GF0041274	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF630 [IPR006868] (1)	-	C_unshiu_01559_mRNA_3.1	-
GF0041273	0	1	0	Serine/threonine phosphatase family, 2C domain protein (1)	catalytic activity [GO:0003824 molecular_function] (1); protein dephosphorylation [GO:0006470 biological_process] (1); cation binding [GO:0043169 molecular_function] (1); protein serine/threonine phosphatase activity [GO:0004722 molecular_function] (1)	PPM-type phosphatase, divalent cation binding [IPR000222] (1); Protein phosphatase 2C family [IPR015655] (1); PPM-type phosphatase domain [IPR001932] (1)	-	C_unshiu_01559_mRNA_2.1	-
GF0041272	0	1	0	Hypothetical protein (1)			-	C_unshiu_01558_mRNA_4.1	-
GF0041271	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_01558_mRNA_2.1	-
GF0041270	0	1	0	Hypothetical protein (1)			-	C_unshiu_01558_mRNA_1.1	-
GF0041269	0	1	0	Hypothetical protein (1)			-	C_unshiu_01557_mRNA_8.1	-
GF0041268	0	1	0	Hypothetical protein (1)			-	C_unshiu_01557_mRNA_6.1	-
GF0041267	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF641, plant [IPR006943] (1)	-	C_unshiu_01557_mRNA_5.1	-
GF0041266	0	1	0	Hypothetical protein (1)			-	C_unshiu_01557_mRNA_3.1	-
GF0041265	0	1	0	Hypothetical protein (1)			-	C_unshiu_01556_mRNA_9.1	-
GF0041264	0	1	0	Hypothetical protein (1)			-	C_unshiu_01556_mRNA_8.1	-
GF0041263	0	1	0	Hypothetical protein (1)			-	C_unshiu_01556_mRNA_6.1	-
GF0041262	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	BTB/POZ domain [IPR000210] (1)	-	C_unshiu_01556_mRNA_3.1	-
GF0041261	0	1	0	Nonexpressor of pathogenesis-related protein 1 (1)	protein binding [GO:0005515 molecular_function] (1)	Regulatory protein NPR, central domain [IPR024228] (1); SKP1/BTB/POZ domain [IPR011333] (1); Ankyrin repeat [IPR002110] (1); BTB/POZ domain [IPR000210] (1); NPR1/NIM1-like, C-terminal [IPR021094] (1); Ankyrin repeat-containing domain [IPR020683] (1)	-	C_unshiu_01556_mRNA_2.1	-
GF0041260	0	1	0	Nonexpressor of pathogenesis-related protein 1 (1)	protein binding [GO:0005515 molecular_function] (1)	SKP1/BTB/POZ domain [IPR011333] (1); Regulatory protein NPR, central domain [IPR024228] (1); Ankyrin repeat [IPR002110] (1); Ankyrin repeat-containing domain [IPR020683] (1); NPR1/NIM1-like, C-terminal [IPR021094] (1); BTB/POZ domain [IPR000210] (1)	-	C_unshiu_01556_mRNA_10.1	-
GF0041259	0	1	0	Hypothetical protein (1)			-	C_unshiu_01556_mRNA_1.1	-
GF0041258	0	1	0	Hypothetical protein (1)			-	C_unshiu_01555_mRNA_7.1	-
GF0041257	0	1	0	Hypothetical protein (1)			-	C_unshiu_01554_mRNA_2.1	-
GF0041256	0	1	0	Hypothetical protein (1)			-	C_unshiu_01553_mRNA_6.1	-
GF0041255	0	1	0	LRR receptor-like serine/threonine-protein kinase ERL1 (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01553_mRNA_1.1	-
GF0041254	0	1	0	Hypothetical protein (1)			-	C_unshiu_01552_mRNA_2.1	-
GF0041253	0	1	0	Hypothetical protein (1)			-	C_unshiu_01551_mRNA_4.1	-
GF0041252	0	1	0	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	C_unshiu_01551_mRNA_3.1	-
GF0041251	0	1	0	LRR receptor-like serine/threonine-protein kinase EFR (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1)	-	C_unshiu_01550_mRNA_5.1	-
GF0041250	0	1	0	Embryonic abundant protein-like (1)	metabolic process [GO:0008152 biological_process] (1); methyltransferase activity [GO:0008168 molecular_function] (1)	S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); Methyltransferase type 11 [IPR013216] (1)	-	C_unshiu_01549_mRNA_2.1	-
GF0041249	0	1	0	Hypothetical protein (1)			-	C_unshiu_01549_mRNA_1.1	-
GF0041248	0	1	0	Hypothetical protein (1)			-	C_unshiu_01548_mRNA_8.1	-
GF0041247	0	1	0	Hypothetical protein (1)			-	C_unshiu_01548_mRNA_7.1	-
GF0041246	0	1	0	Leucine rich repeat containing protein, putative (1)	protein binding [GO:0005515 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Leucine-rich repeat [IPR001611] (1); Protein kinase-like domain [IPR011009] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01548_mRNA_6.1	-
GF0041245	0	1	0	Hypothetical protein (1)			-	C_unshiu_01548_mRNA_5.1	-
GF0041244	0	1	0	Hypothetical protein (1)			-	C_unshiu_01548_mRNA_4.1	-
GF0041243	0	1	0	RNA-directed DNA polymerase (Reverse transcriptase), Ribonuclease H (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_01548_mRNA_3.1	-
GF0041242	0	1	0	Hypothetical protein (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1); Serine/threonine-protein kinase, active site [IPR008271] (1)	-	C_unshiu_01548_mRNA_1.1	-
GF0041241	0	1	0	Hypothetical protein (1)			-	C_unshiu_01547_mRNA_6.1	-
GF0041240	0	1	0	Hypothetical protein (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Peptidase A2A, retrovirus, catalytic [IPR001995] (1); Retropepsins [IPR018061] (1); Aspartic peptidase domain [IPR021109] (1)	-	C_unshiu_01547_mRNA_5.1	-
GF0041239	0	1	0	Hypothetical protein (1)	lipid binding [GO:0008289 molecular_function] (1); lipid transport [GO:0006869 biological_process] (1)	Plant lipid transfer protein/Par allergen [IPR000528] (1); Bifunctional inhibitor/plant lipid transfer protein/seed storage helical domain [IPR016140] (1)	-	C_unshiu_01547_mRNA_13.1	-
GF0041238	0	1	0	Hypothetical protein (1)			-	C_unshiu_01547_mRNA_12.1	-
GF0041237	0	1	0	Hypothetical protein (1)			-	C_unshiu_01546_mRNA_4.1	-
GF0041236	0	1	0	Hypothetical protein (1)			-	C_unshiu_01546_mRNA_3.1	-
GF0041235	0	1	0	Hypothetical protein (1)			-	C_unshiu_01545_mRNA_8.1	-
GF0041234	0	1	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); nucleotide binding [GO:0000166 molecular_function] (1); tRNA aminoacylation for protein translation [GO:0006418 biological_process] (1); aminoacyl-tRNA ligase activity [GO:0004812 molecular_function] (1)	Aminoacyl-tRNA synthetase, class 1a, anticodon-binding [IPR009080] (1); Cysteinyl-tRNA synthetase/mycothiol ligase [IPR024909] (1)	-	C_unshiu_01545_mRNA_7.1	-
GF0041233	0	1	0	Hypothetical protein (1)			-	C_unshiu_01544_mRNA_6.1	-
GF0041232	0	1	0	Hypothetical protein (1)			-	C_unshiu_01544_mRNA_5.1	-
GF0041231	0	1	0	Hypothetical protein (1)			-	C_unshiu_01543_mRNA_3.1	-
GF0041230	0	1	0	Hypothetical protein (1)			-	C_unshiu_01543_mRNA_1.1	-
GF0041229	0	1	0	Hypothetical protein (1)	RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Retrotransposon gag domain [IPR005162] (1); Ribonuclease H-like domain [IPR012337] (1); Ribonuclease H domain [IPR002156] (1)	-	C_unshiu_01542_mRNA_4.1	-
GF0041228	0	1	0	Putative non-LTR retroelement reverse transcriptase, related (1)			-	C_unshiu_01542_mRNA_1.1	-
GF0041227	0	1	0	Hypothetical protein (1)			-	C_unshiu_01541_mRNA_8.1	-
GF0041226	0	1	0	Hypothetical protein (1)			-	C_unshiu_01541_mRNA_6.1	-
GF0041225	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Alpha/Beta hydrolase fold [IPR029058] (1)	-	C_unshiu_01541_mRNA_5.1	-
GF0041224	0	1	0	Hypothetical protein (1)			-	C_unshiu_01541_mRNA_3.1	-
GF0041223	0	1	0	Dienelactone hydrolase family, putative (1)	hydrolase activity [GO:0016787 molecular_function] (1)	Alpha/Beta hydrolase fold [IPR029058] (1); Dienelactone hydrolase [IPR002925] (1)	-	C_unshiu_01541_mRNA_1.1	-
GF0041222	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	C_unshiu_01540_mRNA_8.1	-
GF0041221	0	1	0	Hypothetical protein (1)			-	C_unshiu_01540_mRNA_5.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0041220	0	1	0	Disease resistance family protein / LRR family protein, putative (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01539_mRNA_6.1	-
GF0041219	0	1	0	Hypothetical protein (1)			-	C_unshiu_01539_mRNA_5.1	-
GF0041218	0	1	0	Cellulose synthase-like protein H1 (1)	cellulose biosynthetic process [GO:0030244 biological_process] (1); membrane [GO:0016020 cellular_component] (1); cellulose synthase (UDP-forming) activity [GO:0016760 molecular_function] (1)	Cellulose synthase [IPR005150] (1)	-	C_unshiu_01539_mRNA_4.1	-
GF0041217	0	1	0	Hypothetical protein (1)			-	C_unshiu_01539_mRNA_2.1	-
GF0041216	0	1	0	Ankyrin repeat protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat-containing domain [IPR020683] (1); Ankyrin repeat [IPR002110] (1)	-	C_unshiu_01537_mRNA_9.1	-
GF0041215	0	1	0	Hypothetical protein (1)			-	C_unshiu_01537_mRNA_7.1	-
GF0041214	0	1	0	Hypothetical protein (1)			-	C_unshiu_01537_mRNA_4.1	-
GF0041213	0	1	0	Hypothetical protein (1)			-	C_unshiu_01537_mRNA_3.1	-
GF0041212	0	1	0	Hypothetical protein (1)			-	C_unshiu_01536_mRNA_1.1	-
GF0041211	0	1	0	Hypothetical protein (1)	binding [GO:0005488 molecular_function] (1)	MIF4G-like domain [IPR016021] (1); Armadillo-type fold [IPR016024] (1); Initiation factor eIF-4 gamma, MA3 [IPR003891] (1)	-	C_unshiu_01535_mRNA_5.1	-
GF0041210	0	1	0	Hypothetical protein (1)			-	C_unshiu_01535_mRNA_4.1	-
GF0041209	0	1	0	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (1)	methionine biosynthetic process [GO:0009086 biological_process] (1); zinc ion binding [GO:0008270 molecular_function] (1); cellular amino acid biosynthetic process [GO:0008652 biological_process] (1); 5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase activity [GO:0003871 molecular_function] (1)	Cobalamin-independent methionine synthase MetE, C-terminal/archaeal [IPR002629] (1); Cobalamin-independent methionine synthase MetE, N-terminal [IPR013215] (1)	-	C_unshiu_01535_mRNA_2.1	-
GF0041208	0	1	0	Hypothetical protein (1)			-	C_unshiu_01534_mRNA_9.1	-
GF0041207	0	1	0	Hypothetical protein (1)			-	C_unshiu_01534_mRNA_8.1	-
GF0041206	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_01533_mRNA_9.1	-
GF0041205	0	1	0	Hypothetical protein (1)			-	C_unshiu_01533_mRNA_8.1	-
GF0041204	0	1	0	Hypothetical protein (1)			-	C_unshiu_01533_mRNA_5.1	-
GF0041203	0	1	0	Hypothetical protein (1)			-	C_unshiu_01531_mRNA_8.1	-
GF0041202	0	1	0	Hypothetical protein (1)			-	C_unshiu_01531_mRNA_7.1	-
GF0041201	0	1	0	Putative disease resistance gene NBS-LRR family protein (1)	ADP binding [GO:0043531 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	C_unshiu_01531_mRNA_6.1	-
GF0041200	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_01531_mRNA_5.1	-
GF0041199	0	1	0	Hypothetical protein (1)			-	C_unshiu_01531_mRNA_2.1	-
GF0041198	0	1	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_01530_mRNA_7.1	-
GF0041197	0	1	0	Hypothetical protein (1)			-	C_unshiu_01530_mRNA_6.1	-
GF0041196	0	1	0	Hypothetical protein (1)			-	C_unshiu_01530_mRNA_4.1	-
GF0041195	0	1	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	-	C_unshiu_01530_mRNA_3.1	-
GF0041194	0	1	0	Hypothetical protein (1)			-	C_unshiu_01530_mRNA_2.1	-
GF0041193	0	1	0	Putative muDR family transposase-like (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, SWIM-type [IPR007527] (1); MULE transposase domain [IPR018289] (1); Zinc finger, PMZ-type [IPR006564] (1)	-	C_unshiu_01530_mRNA_1.1	-
GF0041192	0	1	0	Hypothetical protein (1)			-	C_unshiu_01529_mRNA_4.1	-
GF0041191	0	1	0	Hypothetical protein (1)			-	C_unshiu_01529_mRNA_3.1	-
GF0041190	0	1	0	Hypothetical protein (1)			-	C_unshiu_01529_mRNA_1.1	-
GF0041189	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_01527_mRNA_3.1	-
GF0041188	0	1	0	Hypothetical protein (1)			-	C_unshiu_01527_mRNA_2.1	-
GF0041187	0	1	0	Hypothetical protein (1)			-	C_unshiu_01526_mRNA_5.1	-
GF0041186	0	1	0	Hypothetical protein (1)			-	C_unshiu_01526_mRNA_3.1	-
GF0041185	0	1	0	Hypothetical protein (1)			-	C_unshiu_01526_mRNA_2.1	-
GF0041184	0	1	0	Hypothetical protein (1)			-	C_unshiu_01524_mRNA_3.1	-
GF0041183	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_01524_mRNA_2.1	-
GF0041182	0	1	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	-	C_unshiu_01524_mRNA_1.1	-
GF0041181	0	1	0	ATP-citrate synthase alpha chain protein 3 (1)		Succinyl-CoA synthetase-like [IPR016102] (1); ATP-citrate synthase, citrate-binding domain [IPR032263] (1)	-	C_unshiu_01523_mRNA_5.1	-
GF0041180	0	1	0	Hypothetical protein (1)			-	C_unshiu_01523_mRNA_3.1	-
GF0041179	0	1	0	Hypothetical protein (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1); hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (1); chitinase activity [GO:0004568 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1); chitin catabolic process [GO:0006032 biological_process] (1)	Protein kinase domain [IPR000719] (1); Chitinase II [IPR011583] (1); Glycoside hydrolase, catalytic domain [IPR013781] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Glycoside hydrolase superfamily [IPR017853] (1); Protein kinase-like domain [IPR011009] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Glycoside hydrolase family 18, catalytic domain [IPR001223] (1); Chitinase insertion domain [IPR029070] (1); Serine/threonine-protein kinase, active site [IPR008271] (1)	-	C_unshiu_01523_mRNA_1.1	-
GF0041178	0	1	0	Hypothetical protein (1)	cohesin core heterodimer [GO:0008280 cellular_component] (1); chromatin binding [GO:0003682 molecular_function] (1); DNA repair [GO:0006281 biological_process] (1); mitotic sister chromatid cohesion [GO:0007064 biological_process] (1)	RecF/RecN/SMC, N-terminal [IPR003395] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Structural maintenance of chromosomes protein 3 [IPR029685] (1)	-	C_unshiu_01522_mRNA_6.1	-
GF0041177	0	1	0	Hypothetical protein (1)		Concanavalin A-like lectin/glucanase domain [IPR013320] (1)	-	C_unshiu_01522_mRNA_5.1	-
GF0041176	0	1	0	Putative RNA-dependent RNA polymerase 2 (1)	RNA-directed RNA polymerase activity [GO:0003968 molecular_function] (1)	RNA-dependent RNA polymerase, eukaryotic-type [IPR007855] (1)	-	C_unshiu_01521_mRNA_6.1	-
GF0041175	0	1	0	Ankyrin repeat family protein (1)		PGG domain [IPR026961] (1)	-	C_unshiu_01521_mRNA_2.1	-
GF0041174	0	1	0	Hypothetical protein (1)			-	C_unshiu_01520_mRNA_6.1	-
GF0041173	0	1	0	Hypothetical protein (1)			-	C_unshiu_01520_mRNA_2.1	-
GF0041172	0	1	0	Hypothetical protein (1)			-	C_unshiu_01520_mRNA_1.1	-
GF0041171	0	1	0	Hypothetical protein (1)	calcium ion binding [GO:0005509 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	EF-Hand 1, calcium-binding site [IPR018247] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase, ATP binding site [IPR017441] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); EF-hand domain [IPR002048] (1); Protein kinase-like domain [IPR011009] (1); EF-hand domain pair [IPR011992] (1); Protein kinase domain [IPR000719] (1)	-	C_unshiu_01519_mRNA_4.1	-
GF0041170	0	1	0	Hypothetical protein (1)		Gag-polypeptide of LTR copia-type [IPR029472] (1)	-	C_unshiu_01518_mRNA_8.1	-
GF0041169	0	1	0	Polynucleotidyl transferase, Ribonuclease H fold (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_01517_mRNA_6.1	-
GF0041168	0	1	0	Hypothetical protein (1)			-	C_unshiu_01517_mRNA_4.1	-
GF0041167	0	1	0	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	C_unshiu_01517_mRNA_3.1	-
GF0041166	0	1	0	Hypothetical protein (1)			-	C_unshiu_01517_mRNA_2.1	-
GF0041165	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_01517_mRNA_1.1	-
GF0041164	0	1	0	Hypothetical protein (1)			-	C_unshiu_01516_mRNA_8.1	-
GF0041163	0	1	0	Hypothetical protein (1)			-	C_unshiu_01516_mRNA_7.1	-
GF0041162	0	1	0	Hypothetical protein (1)	lyase activity [GO:0016829 molecular_function] (1); terpene synthase activity [GO:0010333 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Terpene synthase, N-terminal domain [IPR001906] (1); Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (1)	-	C_unshiu_01516_mRNA_5.1	-
GF0041161	0	1	0	Delta-cadinene synthase isozyme XC1 (1)	magnesium ion binding [GO:0000287 molecular_function] (1); lyase activity [GO:0016829 molecular_function] (1); terpene synthase activity [GO:0010333 molecular_function] (1)	Terpene synthase, metal-binding domain [IPR005630] (1); Isoprenoid synthase domain [IPR008949] (1)	-	C_unshiu_01516_mRNA_4.1	-
GF0041160	0	1	0	Hypothetical protein (1)	lyase activity [GO:0016829 molecular_function] (1); terpene synthase activity [GO:0010333 molecular_function] (1); magnesium ion binding [GO:0000287 molecular_function] (1)	Terpene synthase, metal-binding domain [IPR005630] (1); Isoprenoid synthase domain [IPR008949] (1)	-	C_unshiu_01516_mRNA_3.1	-
GF0041159	0	1	0	Delta-cadinene synthase isozyme XC14 (1)	lyase activity [GO:0016829 molecular_function] (1); terpene synthase activity [GO:0010333 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (1); Terpene synthase, N-terminal domain [IPR001906] (1)	-	C_unshiu_01516_mRNA_2.1	-
GF0041158	0	1	0	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	C_unshiu_01515_mRNA_7.1	-
GF0041157	0	1	0	Phosphatidylinositol 4-kinase alpha 2 (1)	phosphatidylinositol-mediated signaling [GO:0048015 biological_process] (1); phosphatidylinositol phosphorylation [GO:0046854 biological_process] (1); phosphotransferase activity, alcohol group as acceptor [GO:0016773 molecular_function] (1)	Protein kinase-like domain [IPR011009] (1); Phosphatidylinositol 3-/4-kinase, catalytic domain [IPR000403] (1); Phosphatidylinositol 3/4-kinase, conserved site [IPR018936] (1); Phosphatidylinositol Kinase [IPR015433] (1)	-	C_unshiu_01515_mRNA_3.1	-
GF0041156	0	1	0	Hypothetical protein (1)			-	C_unshiu_01515_mRNA_2.1	-
GF0041155	0	1	0	Hypothetical protein (1)			-	C_unshiu_01515_mRNA_1.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0041154	0	1	0	LysM type receptor kinase (1)	ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Alkaline phosphatase D-related [IPR018946] (1); Metallo-dependent phosphatase-like [IPR029052] (1); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1)	-	C_unshiu_01514_mRNA_4.1	-
GF0041153	0	1	0	Hypothetical protein (1)			-	C_unshiu_01513_mRNA_6.1	-
GF0041152	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01513_mRNA_5.1	-
GF0041151	0	1	0	Hypothetical protein (1)			-	C_unshiu_01513_mRNA_2.1	-
GF0041150	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_01513_mRNA_1.1	-
GF0041149	0	1	0	Hypothetical protein (1)			-	C_unshiu_01512_mRNA_1.1	-
GF0041148	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_01511_mRNA_4.1	-
GF0041147	0	1	0	Hypothetical protein (1)			-	C_unshiu_01511_mRNA_16.1	-
GF0041146	0	1	0	Putative non-LTR retroelement reverse transcriptase (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Reverse transcriptase domain [IPR000477] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_01511_mRNA_13.1	-
GF0041145	0	1	0	Hypothetical protein (1)			-	C_unshiu_01511_mRNA_12.1	-
GF0041144	0	1	0	Hypothetical protein (1)			-	C_unshiu_01511_mRNA_11.1	-
GF0041143	0	1	0	Ankyrin repeat family protein, putative (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat-containing domain [IPR020683] (1); Ankyrin repeat [IPR002110] (1)	-	C_unshiu_01510_mRNA_6.1	-
GF0041142	0	1	0	Anaphase-promoting complex subunit 6 (1)	protein binding [GO:0005515 molecular_function] (1)	Tetratricopeptide-like helical domain [IPR011990] (1)	-	C_unshiu_01510_mRNA_4.1	-
GF0041141	0	1	0	Hypothetical protein (1)			-	C_unshiu_01510_mRNA_3.1	-
GF0041140	0	1	0	Hypothetical protein (1)			-	C_unshiu_01510_mRNA_2.1	-
GF0041139	0	1	0	Hypothetical protein (1)			-	C_unshiu_01510_mRNA_1.1	-
GF0041138	0	1	0	Hypothetical protein (1)			-	C_unshiu_01509_mRNA_3.1	-
GF0041137	0	1	0	Hypothetical protein (1)			-	C_unshiu_01508_mRNA_5.1	-
GF0041136	0	1	0	Hypothetical protein (1)			-	C_unshiu_01508_mRNA_4.1	-
GF0041135	0	1	0	Hypothetical protein (1)			-	C_unshiu_01508_mRNA_2.1	-
GF0041134	0	1	0	Hypothetical protein (1)		FAR1 DNA binding domain [IPR004330] (1)	-	C_unshiu_01508_mRNA_10.1	-
GF0041133	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_01508_mRNA_1.1	-
GF0041132	0	1	0	Embryonic abundant protein-like (1)	methyltransferase activity [GO:0008168 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); Methyltransferase type 11 [IPR013216] (1)	-	C_unshiu_01507_mRNA_6.1	-
GF0041131	0	1	0	Hypothetical protein (1)			-	C_unshiu_01507_mRNA_4.1	-
GF0041130	0	1	0	Hypothetical protein (1)			-	C_unshiu_01507_mRNA_3.1	-
GF0041129	0	1	0	Hypothetical protein (1)			-	C_unshiu_01506_mRNA_5.1	-
GF0041128	0	1	0	Hypothetical protein (1)		High mobility group box domain [IPR009071] (1)	-	C_unshiu_01505_mRNA_2.1	-
GF0041127	0	1	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1)	-	C_unshiu_01505_mRNA_1.1	-
GF0041126	0	1	0	Hypothetical protein (1)	RNA-directed RNA polymerase activity [GO:0003968 molecular_function] (1)	RNA-dependent RNA polymerase, eukaryotic-type [IPR007855] (1)	-	C_unshiu_01504_mRNA_2.1	-
GF0041125	0	1	0	Hypothetical protein (1)			-	C_unshiu_01504_mRNA_1.1	-
GF0041124	0	1	0	Hypothetical protein (1)			-	C_unshiu_01503_mRNA_8.1	-
GF0041123	0	1	0	Hypothetical protein (1)			-	C_unshiu_01503_mRNA_5.1	-
GF0041122	0	1	0	Hypothetical protein (1)	phosphotransferase activity, alcohol group as acceptor [GO:0016773 molecular_function] (1)	Carbohydrate kinase PfkB [IPR011611] (1); Carbohydrate/puine kinase, PfkB, conserved site [IPR002173] (1); Ribokinase-like [IPR029056] (1)	-	C_unshiu_01503_mRNA_4.1	-
GF0041121	0	1	0	Hypothetical protein (1)			-	C_unshiu_01503_mRNA_3.1	-
GF0041120	0	1	0	Hypothetical protein (1)			-	C_unshiu_01503_mRNA_2.1	-
GF0041119	0	1	0	Hypothetical protein (1)			-	C_unshiu_01502_mRNA_5.1	-
GF0041118	0	1	0	Cysteine proteinase inhibitor (1)			-	C_unshiu_01502_mRNA_1.1	-
GF0041117	0	1	0	Hypothetical protein (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1); zinc ion binding [GO:0008270 molecular_function] (1); polygalacturonase activity [GO:0004650 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Photosynthesis system II assembly factor Ycf48/Hcf136-like domain [IPR028203] (1); Glycoside hydrolase, family 28 [IPR000743] (1); Pectin lyase fold [IPR012334] (1); Zinc finger, CCHC-type [IPR001878] (1); Pectin lyase fold/virulence factor [IPR011050] (1)	-	C_unshiu_01500_mRNA_4.1	-
GF0041116	0	1	0	Hypothetical protein (1)			-	C_unshiu_01499_mRNA_4.1	-
GF0041115	0	1	0	Hypothetical protein (1)			-	C_unshiu_01498_mRNA_9.1	-
GF0041114	0	1	0	Hypothetical protein (1)			-	C_unshiu_01498_mRNA_8.1	-
GF0041113	0	1	0	Hypothetical protein (1)			-	C_unshiu_01498_mRNA_7.1	-
GF0041112	0	1	0	Hypothetical protein (1)			-	C_unshiu_01498_mRNA_6.1	-
GF0041111	0	1	0	Hypothetical protein (1)			-	C_unshiu_01498_mRNA_5.1	-
GF0041110	0	1	0	Hypothetical protein (1)			-	C_unshiu_01498_mRNA_10.1	-
GF0041109	0	1	0	Hypothetical protein (1)			-	C_unshiu_01498_mRNA_1.1	-
GF0041108	0	1	0	Hypothetical protein (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Serine/threonine-protein kinase, active site [IPR008271] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); LysM domain [IPR018392] (1); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_01497_mRNA_7.1	-
GF0041107	0	1	0	Hypothetical protein (1)	membrane [GO:0016020 cellular_component] (1)	Calcium-dependent channel, 7TM region, putative phosphate [IPR003864] (1)	-	C_unshiu_01495_mRNA_8.1	-
GF0041106	0	1	0	Hyperosmolality-gated Ca2+ permeable channel (1)	membrane [GO:0016020 cellular_component] (1)	Calcium permeable stress-gated cation channel 1, N-terminal transmembrane domain [IPR032880] (1); Calcium-dependent channel, 7TM region, putative phosphate [IPR003864] (1)	-	C_unshiu_01495_mRNA_6.1	-
GF0041105	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01494_mRNA_3.1	-
GF0041104	0	1	0	Hypothetical protein (1)			-	C_unshiu_01494_mRNA_2.1	-
GF0041103	0	1	0	Hypothetical protein (1)	transcription from RNA polymerase II promoter [GO:0006366 biological_process] (1); DNA-directed RNA polymerase activity [GO:0003899 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1); transcription, DNA-templated [GO:0006351 biological_process] (1); DNA-directed RNA polymerase II, core complex [GO:0005665 cellular_component] (1)	RNA polymerase Rpb1, domain 1 [IPR007080] (1); RNA polymerase Rpb1, domain 5 [IPR007081] (1); RNA polymerase Rpb1, domain 7 [IPR007073] (1); RNA polymerase II, heptapeptide repeat, eukaryotic [IPR000684] (1)	-	C_unshiu_01493_mRNA_9.1	-
GF0041102	0	1	0	Hypothetical protein (1)			-	C_unshiu_01492_mRNA_6.1	-
GF0041101	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_01492_mRNA_2.1	-
GF0041100	0	1	0	Putative transcriptional regulator DJ-1 (1)		Class I glutamine amidotransferase-like [IPR029062] (1); DJ-1 [IPR006287] (1); DJ-1/PfpI [IPR002818] (1)	-	C_unshiu_01491_mRNA_7.1	-
GF0041099	0	1	0	Hypothetical protein (1)		Class I glutamine amidotransferase-like [IPR029062] (1); DJ-1/PfpI [IPR002818] (1)	-	C_unshiu_01491_mRNA_6.1	-
GF0041098	0	1	0	Receptor like protein 33 (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	-	C_unshiu_01491_mRNA_5.1	-
GF0041097	0	1	0	Putative transcriptional regulator DJ-1 (1)		Class I glutamine amidotransferase-like [IPR029062] (1); DJ-1 [IPR006287] (1); DJ-1/PfpI [IPR002818] (1)	-	C_unshiu_01491_mRNA_10.1	-
GF0041096	0	1	0	Hypothetical protein (1)			-	C_unshiu_01490_mRNA_4.1	-
GF0041095	0	1	0	Ubiquitin thioesterase OTU1 (1)			-	C_unshiu_01490_mRNA_3.1	-
GF0041094	0	1	0	Hypothetical protein (1)			-	C_unshiu_01490_mRNA_2.1	-
GF0041093	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	TRAF-like [IPR008974] (1); MATH/TRAF domain [IPR002083] (1)	-	C_unshiu_01489_mRNA_3.1	-
GF0041092	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	MATH/TRAF domain [IPR002083] (1); TRAF-like [IPR008974] (1)	-	C_unshiu_01489_mRNA_1.1	-
GF0041091	0	1	0	Hypothetical protein (1)	catalytic activity [GO:0003824 molecular_function] (1)	Pyridoxal phosphate-dependent transferase [IPR015424] (1); Pyridoxal phosphate-dependent transferase, major region, subdomain 1 [IPR015421] (1)	-	C_unshiu_01488_mRNA_8.1	-
GF0041090	0	1	0	Hypothetical protein (1)	biosynthetic process [GO:0009058 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1); pyridoxal phosphate binding [GO:0030170 molecular_function] (1)	Aminotransferase, class I/classII [IPR004839] (1); Pyridoxal phosphate-dependent transferase, major region, subdomain 1 [IPR015421] (1); Pyridoxal phosphate-dependent transferase [IPR015424] (1); Pyridoxal phosphate-dependent transferase, major region, subdomain 2 [IPR015422] (1)	-	C_unshiu_01488_mRNA_7.1	-
GF0041089	0	1	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1)	Phosphoribosylglycinamide synthetase, ATP-grasp (A) domain [IPR020561] (1); ATP-grasp fold, subdomain 2 [IPR013816] (1)	-	C_unshiu_01488_mRNA_4.1	-
GF0041088	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Tetratricopeptide-like helical domain [IPR011990] (1)	-	C_unshiu_01488_mRNA_3.1	-
GF0041087	0	1	0	Hypothetical protein (1)			-	C_unshiu_01488_mRNA_1.1	-
GF0041086	0	1	0	Hypothetical protein (1)			-	C_unshiu_01487_mRNA_8.1	-
GF0041085	0	1	0	Hypothetical protein (1)			-	C_unshiu_01487_mRNA_7.1	-
GF0041084	0	1	0	Hypothetical protein (1)			-	C_unshiu_01486_mRNA_8.1	-
GF0041083	0	1	0	Hypothetical protein (1)			-	C_unshiu_01486_mRNA_7.1	-
GF0041082	0	1	0	Hypothetical protein (1)			-	C_unshiu_01486_mRNA_4.1	-
GF0041081	0	1	0	Hypothetical protein (1)			-	C_unshiu_01486_mRNA_3.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0041080	0	1	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1)	Peptidase A2A, retrovirus, catalytic [IPR001995] (1)	-	C_unshiu_01486_mRNA_14.1	-
GF0041079	0	1	0	Hypothetical protein (1)			-	C_unshiu_01486_mRNA_12.1	-
GF0041078	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_01486_mRNA_11.1	-
GF0041077	0	1	0	Hypothetical protein (1)		DnaJ domain, conserved site [IPR018253] (1); DnaJ domain [IPR001623] (1); Class I glutamine amidotransferase-like [IPR029062] (1)	-	C_unshiu_01485_mRNA_4.1	-
GF0041076	0	1	0	Hypothetical protein (1)			-	C_unshiu_01485_mRNA_3.1	-
GF0041075	0	1	0	Hypothetical protein (1)			-	C_unshiu_01484_mRNA_3.1	-
GF0041074	0	1	0	Hypothetical protein (1)			-	C_unshiu_01482_mRNA_7.1	-
GF0041073	0	1	0	Hypothetical protein (1)		Vps53-like, N-terminal [IPR007234] (1)	-	C_unshiu_01482_mRNA_6.1	-
GF0041072	0	1	0	Hypothetical protein (1)			-	C_unshiu_01482_mRNA_4.1	-
GF0041071	0	1	0	Hypothetical protein (1)			-	C_unshiu_01482_mRNA_2.1	-
GF0041070	0	1	0	Hypothetical protein (1)			-	C_unshiu_01481_mRNA_4.1	-
GF0041069	0	1	0	Hypothetical protein (1)			-	C_unshiu_01481_mRNA_3.1	-
GF0041068	0	1	0	Hypothetical protein (1)			-	C_unshiu_01480_mRNA_9.1	-
GF0041067	0	1	0	NBS-LRR type disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_01480_mRNA_8.1	-
GF0041066	0	1	0	Hypothetical protein (1)			-	C_unshiu_01480_mRNA_10.1	-
GF0041065	0	1	0	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial (1)	oxidoreductase activity, acting on the aldehyde or oxo group of donors, disulfide as acceptor [GO:0016624 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Dehydrogenase, E1 component [IPR001017] (1); Thiamin diphosphate-binding fold [IPR029061] (1)	-	C_unshiu_01479_mRNA_5.1	-
GF0041064	0	1	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	-	C_unshiu_01479_mRNA_4.1	-
GF0041063	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_01478_mRNA_8.1	-
GF0041062	0	1	0	Hypothetical protein (1)			-	C_unshiu_01478_mRNA_7.1	-
GF0041061	0	1	0	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	C_unshiu_01478_mRNA_4.1	-
GF0041060	0	1	0	Hypothetical protein (1)			-	C_unshiu_01478_mRNA_2.1	-
GF0041059	0	1	0	Pentatricopeptide (PPR) repeat protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	C_unshiu_01478_mRNA_12.1	-
GF0041058	0	1	0	Hypothetical protein (1)			-	C_unshiu_01478_mRNA_11.1	-
GF0041057	0	1	0	Putative pentatricopeptide repeat-containing protein, mitochondrial (1)		Pentatricopeptide repeat [IPR002885] (1)	-	C_unshiu_01478_mRNA_10.1	-
GF0041056	0	1	0	Hypothetical protein (1)			-	C_unshiu_01478_mRNA_1.1	-
GF0041055	0	1	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	-	C_unshiu_01477_mRNA_3.1	-
GF0041054	0	1	0	Hypothetical protein (1)			-	C_unshiu_01477_mRNA_2.1	-
GF0041053	0	1	0	Hypothetical protein (1)	transcription, DNA-templated [GO:0006351 biological_process] (1); DNA binding [GO:0003677 molecular_function] (1); DNA-directed RNA polymerase activity [GO:0003899 molecular_function] (1)	DNA-directed RNA polymerase, phage-type [IPR002092] (1)	-	C_unshiu_01476_mRNA_6.1	-
GF0041052	0	1	0	Hypothetical protein (1)			-	C_unshiu_01476_mRNA_5.1	-
GF0041051	0	1	0	Hypothetical protein (1)	heme-copper terminal oxidase activity [GO:0015002 molecular_function] (1); membrane [GO:0016020 cellular_component] (1)	Cytochrome c oxidase subunit III domain [IPR000298] (1)	-	C_unshiu_01476_mRNA_4.1	-
GF0041050	0	1	0	Hypothetical protein (1)			-	C_unshiu_01476_mRNA_2.1	-
GF0041049	0	1	0	Hypothetical protein (1)			-	C_unshiu_01476_mRNA_1.1	-
GF0041048	0	1	0	Hypothetical protein (1)			-	C_unshiu_01475_mRNA_8.1	-
GF0041047	0	1	0	Hypothetical protein (1)		Prolamin-like domain [IPR008502] (1)	-	C_unshiu_01475_mRNA_3.1	-
GF0041046	0	1	0	Receptor like protein 27 (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01475_mRNA_2.1	-
GF0041045	0	1	0	Hypothetical protein (1)			-	C_unshiu_01473_mRNA_8.1	-
GF0041044	0	1	0	Hypothetical protein (1)			-	C_unshiu_01473_mRNA_6.1	-
GF0041043	0	1	0	Hypothetical protein (1)			-	C_unshiu_01473_mRNA_5.1	-
GF0041042	0	1	0	Hypothetical protein (1)			-	C_unshiu_01473_mRNA_4.1	-
GF0041041	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF1985 [IPR015410] (1)	-	C_unshiu_01473_mRNA_2.1	-
GF0041040	0	1	0	Hypothetical protein (1)	nucleobase-containing compound metabolic process [GO:0006139 biological_process] (1); 3'-5' exonuclease activity [GO:0008408 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); 3'-5' exonuclease domain [IPR002562] (1)	-	C_unshiu_01472_mRNA_7.1	-
GF0041039	0	1	0	HD subdomain, putative isoform 2 (1)		Ppx/GppA phosphatase [IPR003695] (1)	-	C_unshiu_01472_mRNA_6.1	-
GF0041038	0	1	0	Hypothetical protein (1)			-	C_unshiu_01472_mRNA_2.1	-
GF0041037	0	1	0	Hypothetical protein (1)			-	C_unshiu_01472_mRNA_1.1	-
GF0041036	0	1	0	Pseudouridylate synthase family protein (1)	pseudouridine synthase activity [GO:0009982 molecular_function] (1); RNA modification [GO:0009451 biological_process] (1); RNA binding [GO:0003723 molecular_function] (1); pseudouridine synthesis [GO:0001522 biological_process] (1)	Pseudouridine synthase I, TruA [IPR001406] (1); Pseudouridine synthase I, TruA, C-terminal [IPR020095] (1)	-	C_unshiu_01471_mRNA_3.1	-
GF0041035	0	1	0	Hypothetical protein (1)			-	C_unshiu_01470_mRNA_4.1	-
GF0041034	0	1	0	Hypothetical protein (1)			-	C_unshiu_01469_mRNA_6.1	-
GF0041033	0	1	0	Cytochrome P450 family 71 protein (1)	iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1)	Cytochrome P450 [IPR001128] (1)	-	C_unshiu_01469_mRNA_5.1	-
GF0041032	0	1	0	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1)	Cytochrome P450 [IPR001128] (1)	-	C_unshiu_01469_mRNA_4.1	-
GF0041031	0	1	0	Hypothetical protein (1)			-	C_unshiu_01466_mRNA_6.1	-
GF0041030	0	1	0	Hypothetical protein (1)			-	C_unshiu_01466_mRNA_3.1	-
GF0041029	0	1	0	Hypothetical protein (1)			-	C_unshiu_01466_mRNA_2.1	-
GF0041028	0	1	0	Hypothetical protein (1)			-	C_unshiu_01466_mRNA_1.1	-
GF0041027	0	1	0	Hypothetical protein (1)			-	C_unshiu_01465_mRNA_3.1	-
GF0041026	0	1	0	Zinc knuckle family protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_01465_mRNA_2.1	-
GF0041025	0	1	0	Hypothetical protein (1)			-	C_unshiu_01465_mRNA_1.1	-
GF0041024	0	1	0	Hypothetical protein (1)			-	C_unshiu_01463_mRNA_8.1	-
GF0041023	0	1	0	Hypothetical protein (1)			-	C_unshiu_01463_mRNA_6.1	-
GF0041022	0	1	0	Hypothetical protein (1)			-	C_unshiu_01463_mRNA_5.1	-
GF0041021	0	1	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); DNA binding [GO:0003677 molecular_function] (1)	NAC domain [IPR003441] (1)	-	C_unshiu_01463_mRNA_12.1	-
GF0041020	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01463_mRNA_11.1	-
GF0041019	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01463_mRNA_1.1	-
GF0041018	0	1	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	-	C_unshiu_01462_mRNA_9.1	-
GF0041017	0	1	0	Hypothetical protein (1)			-	C_unshiu_01462_mRNA_14.1	-
GF0041016	0	1	0	Hypothetical protein (1)			-	C_unshiu_01462_mRNA_13.1	-
GF0041015	0	1	0	Hypothetical protein (1)			-	C_unshiu_01462_mRNA_12.1	-
GF0041014	0	1	0	Hypothetical protein (1)			-	C_unshiu_01462_mRNA_11.1	-
GF0041013	0	1	0	Hypothetical protein (1)			-	C_unshiu_01462_mRNA_1.1	-
GF0041012	0	1	0	Hypothetical protein (1)			-	C_unshiu_01461_mRNA_8.1	-
GF0041011	0	1	0	Hypothetical protein (1)			-	C_unshiu_01461_mRNA_2.1	-
GF0041010	0	1	0	Protein TSSC1 (1)	protein binding [GO:0005515 molecular_function] (1)	WD40 repeat [IPR001680] (1); WD40-repeat-containing domain [IPR017986] (1); WD40/YVTN repeat-like-containing domain [IPR015943] (1)	-	C_unshiu_01461_mRNA_1.1	-
GF0041009	0	1	0	Hypothetical protein (1)	transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); sequence-specific DNA binding [GO:0043565 molecular_function] (1)	Basic-leucine zipper domain [IPR004827] (1)	-	C_unshiu_01460_mRNA_7.1	-
GF0041008	0	1	0	Hypothetical protein (1)			-	C_unshiu_01460_mRNA_4.1	-
GF0041007	0	1	0	Hypothetical protein (1)			-	C_unshiu_01460_mRNA_3.1	-
GF0041006	0	1	0	Hypothetical protein (1)			-	C_unshiu_01460_mRNA_2.1	-
GF0041005	0	1	0	Hypothetical protein (1)			-	C_unshiu_01460_mRNA_1.1	-
GF0041004	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01459_mRNA_2.1	-
GF0041003	0	1	0	DUF247 domain protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	C_unshiu_01458_mRNA_9.1	-
GF0041002	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat [IPR002110] (1); Ankyrin repeat-containing domain [IPR020683] (1)	-	C_unshiu_01458_mRNA_1.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0041001	0	1	0	Sesquiterpene synthase (1)	magnesium ion binding [GO:0000287 molecular_function] (1); terpene synthase activity [GO:0010333 molecular_function] (1); lyase activity [GO:0016829 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Terpene synthase, N-terminal domain [IPR001906] (1); Terpene synthase, metal-binding domain [IPR005630] (1); Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (1); Isoprenoid synthase domain [IPR008949] (1)	-	C_unshiu_01457_mRNA_5.1	-
GF0041000	0	1	0	Hypothetical protein (1)			-	C_unshiu_01457_mRNA_4.1	-
GF0040999	0	1	0	Hypothetical protein (1)			-	C_unshiu_01456_mRNA_7.1	-
GF0040998	0	1	0	Hypothetical protein (1)			-	C_unshiu_01456_mRNA_2.1	-
GF0040997	0	1	0	Hypothetical protein (1)			-	C_unshiu_01455_mRNA_6.1	-
GF0040996	0	1	0	Hypothetical protein (1)			-	C_unshiu_01455_mRNA_5.1	-
GF0040995	0	1	0	Hypothetical protein (1)			-	C_unshiu_01455_mRNA_4.1	-
GF0040994	0	1	0	Hypothetical protein (1)			-	C_unshiu_01454_mRNA_4.1	-
GF0040993	0	1	0	Hypothetical protein (1)			-	C_unshiu_01454_mRNA_3.1	-
GF0040992	0	1	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, SWIM-type [IPR007527] (1); Zinc finger, PMZ-type [IPR006564] (1); FHY3/FAR1 family [IPR031052] (1)	-	C_unshiu_01453_mRNA_2.1	-
GF0040991	0	1	0	LRR receptor-like serine/threonine-protein kinase FLS2 (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); MULE transposase domain [IPR018289] (1); Leucine-rich repeat [IPR001611] (1); FAR1 DNA binding domain [IPR004330] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	-	C_unshiu_01453_mRNA_1.1	-
GF0040990	0	1	0	Protein SUPPRESSOR OF npr1-1, CONSTITUTIVE 1 (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01452_mRNA_6.1	-
GF0040989	0	1	0	Protein SUPPRESSOR OF npr1-1, CONSTITUTIVE 1 (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01452_mRNA_4.1	-
GF0040988	0	1	0	Hypothetical protein (1)			-	C_unshiu_01451_mRNA_6.1	-
GF0040987	0	1	0	Hypothetical protein (1)	phosphotransferase activity, alcohol group as acceptor [GO:0016773 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1)	Carbohydrate kinase, FGGY, C-terminal [IPR018485] (1)	-	C_unshiu_01450_mRNA_8.1	-
GF0040986	0	1	0	Hypothetical protein (1)	phosphotransferase activity, alcohol group as acceptor [GO:0016773 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1)	Carbohydrate kinase, FGGY, conserved site [IPR018483] (1)	-	C_unshiu_01450_mRNA_6.1	-
GF0040985	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_01450_mRNA_3.1	-
GF0040984	0	1	0	Hypothetical protein (1)		Histone deacetylase domain [IPR023801] (1)	-	C_unshiu_01449_mRNA_3.1	-
GF0040983	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	-	C_unshiu_01449_mRNA_1.1	-
GF0040982	0	1	0	Hypothetical protein (1)			-	C_unshiu_01448_mRNA_8.1	-
GF0040981	0	1	0	Hypothetical protein (1)			-	C_unshiu_01448_mRNA_7.1	-
GF0040980	0	1	0	Hypothetical protein (1)			-	C_unshiu_01448_mRNA_6.1	-
GF0040979	0	1	0	Hypothetical protein (1)			-	C_unshiu_01448_mRNA_4.1	-
GF0040978	0	1	0	Disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1); AAA+ ATPase domain [IPR003593] (1)	-	C_unshiu_01448_mRNA_1.1	-
GF0040977	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_01446_mRNA_6.1	-
GF0040976	0	1	0	Hypothetical protein (1)			-	C_unshiu_01446_mRNA_2.1	-
GF0040975	0	1	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1); Domain of unknown function DUF1985 [IPR015410] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01445_mRNA_7.1	-
GF0040974	0	1	0	Pentatricopeptide repeat-containing family protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	DYW domain [IPR032867] (1); Pentatricopeptide repeat [IPR002885] (1); Tetratricopeptide-like helical domain [IPR011990] (1)	-	C_unshiu_01445_mRNA_4.1	-
GF0040973	0	1	0	Hypothetical protein (1)			-	C_unshiu_01445_mRNA_2.1	-
GF0040972	0	1	0	Hus1 domain-containing protein (1)	DNA damage checkpoint [GO:0000077 biological_process] (1); checkpoint clamp complex [GO:0030896 cellular_component] (1); DNA repair [GO:0006281 biological_process] (1)	Checkpoint protein Hus1/Mec3 [IPR007150] (1)	-	C_unshiu_01445_mRNA_10.1	-
GF0040971	0	1	0	Hypothetical protein (1)			-	C_unshiu_01445_mRNA_1.1	-
GF0040970	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_01444_mRNA_7.1	-
GF0040969	0	1	0	Truncated At4g21370 (1)	recognition of pollen [GO:0048544 biological_process] (1)	Bulb-type lectin domain [IPR001480] (1); PAN/Apple domain [IPR003609] (1); S-locus glycoprotein domain [IPR000858] (1)	-	C_unshiu_01444_mRNA_10.1	-
GF0040968	0	1	0	Hypothetical protein (1)			-	C_unshiu_01444_mRNA_1.1	-
GF0040967	0	1	0	Disease resistance protein (CC-NBS-LRR class) family protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); AAA+ ATPase domain [IPR003593] (1); NB-ARC [IPR002182] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01443_mRNA_8.1	-
GF0040966	0	1	0	Hypothetical protein (1)			-	C_unshiu_01443_mRNA_7.1	-
GF0040965	0	1	0	Hypothetical protein (1)			-	C_unshiu_01443_mRNA_4.1	-
GF0040964	0	1	0	Phosphoprotein phosphatase isoform 1 (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01443_mRNA_2.1	-
GF0040963	0	1	0	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); acyl-[acyl-carrier-protein] desaturase activity [GO:0045300 molecular_function] (1); fatty acid metabolic process [GO:0006631 biological_process] (1)	Ribonucleotide reductase-related [IPR012348] (1); Ferritin-like superfamily [IPR009078] (1); Fatty acid desaturase, type 2 [IPR005067] (1)	-	C_unshiu_01442_mRNA_1.1	-
GF0040962	0	1	0	Hypothetical protein (1)			-	C_unshiu_01441_mRNA_8.1	-
GF0040961	0	1	0	CDNA clone:J013129I18, full insert sequence (1)	DNA integration [GO:0015074 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Integrase, catalytic core [IPR001584] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_01441_mRNA_4.1	-
GF0040960	0	1	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_01441_mRNA_2.1	-
GF0040959	0	1	0	Hypothetical protein (1)			-	C_unshiu_01441_mRNA_1.1	-
GF0040958	0	1	0	UDP-glycosyltransferase 83A1 (1)	metabolic process [GO:0008152 biological_process] (1); calcium ion binding [GO:0005509 molecular_function] (1); transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1)	EF-Hand 1, calcium-binding site [IPR018247] (1); EF-hand domain [IPR002048] (1); UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	-	C_unshiu_01440_mRNA_9.1	-
GF0040957	0	1	0	Monosacharide transport protein (1)			-	C_unshiu_01440_mRNA_7.1	-
GF0040956	0	1	0	Monosacharide transport protein (1)			-	C_unshiu_01440_mRNA_12.1	-
GF0040955	0	1	0	Hypothetical protein (1)			-	C_unshiu_01440_mRNA_11.1	-
GF0040954	0	1	0	Hypothetical protein (1)	kinase activity [GO:0016301 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1); metabolic process [GO:0008152 biological_process] (1); phosphoribulokinase activity [GO:0008974 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Phosphoribulokinase/uridine kinase [IPR006083] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Phosphoribulokinase [IPR006082] (1)	-	C_unshiu_01440_mRNA_1.1	-
GF0040953	0	1	0	Disease resistance protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01439_mRNA_4.1	-
GF0040952	0	1	0	Hypothetical protein (1)			-	C_unshiu_01439_mRNA_2.1	-
GF0040951	0	1	0	Disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	C_unshiu_01439_mRNA_1.1	-
GF0040950	0	1	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_01438_mRNA_9.1	-
GF0040949	0	1	0	Disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01438_mRNA_8.1	-
GF0040948	0	1	0	Hypothetical protein (1)			-	C_unshiu_01438_mRNA_5.1	-
GF0040947	0	1	0	Hypothetical protein (1)			-	C_unshiu_01438_mRNA_3.1	-
GF0040946	0	1	0	LRR and NB-ARC domains-containing disease resistance protein, putative (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01438_mRNA_2.1	-
GF0040945	0	1	0	Putative disease resistance protein RGA4 (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	C_unshiu_01438_mRNA_11.1	-
GF0040944	0	1	0	Ras-like GTP-binding protein YPT1 (1)	protein transport [GO:0015031 biological_process] (1); GTP binding [GO:0005525 molecular_function] (1); small GTPase mediated signal transduction [GO:0007264 biological_process] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Small GTPase superfamily, Rab type [IPR003579] (1); Mitochondrial Rho-like [IPR013684] (1)	-	C_unshiu_01438_mRNA_1.1	-
GF0040943	0	1	0	Hypothetical protein (1)			-	C_unshiu_01435_mRNA_6.1	-
GF0040942	0	1	0	AtpA (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, PMZ-type [IPR006564] (1); Zinc finger, SWIM-type [IPR007527] (1)	-	C_unshiu_01435_mRNA_3.1	-
GF0040941	0	1	0	Hypothetical protein (1)			-	C_unshiu_01435_mRNA_2.1	-
GF0040940	0	1	0	Hypothetical protein (1)			-	C_unshiu_01435_mRNA_1.1	-
GF0040939	0	1	0	Hypothetical protein (1)			-	C_unshiu_01432_mRNA_9.1	-
GF0040938	0	1	0	Hypothetical protein (1)			-	C_unshiu_01432_mRNA_7.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0040937	0	1	0	Hypothetical protein (1)			-	C_unshiu_01432_mRNA_4.1	-
GF0040936	0	1	0	Hypothetical protein (1)			-	C_unshiu_01432_mRNA_2.1	-
GF0040935	0	1	0	Hypothetical protein (1)			-	C_unshiu_01432_mRNA_15.1	-
GF0040934	0	1	0	Hypothetical protein (1)			-	C_unshiu_01432_mRNA_14.1	-
GF0040933	0	1	0	Hypothetical protein (1)			-	C_unshiu_01432_mRNA_13.1	-
GF0040932	0	1	0	Hypothetical protein (1)			-	C_unshiu_01432_mRNA_12.1	-
GF0040931	0	1	0	Hypothetical protein (1)			-	C_unshiu_01432_mRNA_1.1	-
GF0040930	0	1	0	Hypothetical protein (1)			-	C_unshiu_01431_mRNA_9.1	-
GF0040929	0	1	0	Ankyrin repeat family protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat-containing domain [IPR020683] (1); Ankyrin repeat [IPR002110] (1)	-	C_unshiu_01431_mRNA_6.1	-
GF0040928	0	1	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	NTF2-like domain [IPR032710] (1); Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_01431_mRNA_3.1	-
GF0040927	0	1	0	Hypothetical protein (1)			-	C_unshiu_01429_mRNA_6.1	-
GF0040926	0	1	0	Hypothetical protein (1)		Protein of unknown function DUF604 [IPR006740] (1)	-	C_unshiu_01428_mRNA_8.1	-
GF0040925	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	C_unshiu_01428_mRNA_1.1	-
GF0040924	0	1	0	Hypothetical protein (1)			-	C_unshiu_01427_mRNA_4.1	-
GF0040923	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_01427_mRNA_3.1	-
GF0040922	0	1	0	Hypothetical protein (1)			-	C_unshiu_01426_mRNA_7.1	-
GF0040921	0	1	0	Hypothetical protein (1)			-	C_unshiu_01426_mRNA_3.1	-
GF0040920	0	1	0	Putative disease resistance protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01426_mRNA_2.1	-
GF0040919	0	1	0	Hypothetical protein (1)			-	C_unshiu_01426_mRNA_1.1	-
GF0040918	0	1	0	Hypothetical protein (1)	guanyl nucleotide binding [GO:0019001 molecular_function] (1); signal transducer activity [GO:0004871 molecular_function] (1); GTPase activity [GO:0003924 molecular_function] (1); G-protein beta/gamma-subunit complex binding [GO:0031683 molecular_function] (1); signal transduction [GO:0007165 biological_process] (1); G-protein coupled receptor signaling pathway [GO:0007186 biological_process] (1)	Guanine nucleotide binding protein (G-protein), alpha subunit [IPR001019] (1); G protein alpha subunit, helical insertion [IPR011025] (1)	-	C_unshiu_01425_mRNA_3.1	-
GF0040917	0	1	0	Hypothetical protein (1)			-	C_unshiu_01424_mRNA_3.1	-
GF0040916	0	1	0	Hypothetical protein (1)			-	C_unshiu_01424_mRNA_2.1	-
GF0040915	0	1	0	Hypothetical protein (1)			-	C_unshiu_01424_mRNA_1.1	-
GF0040914	0	1	0	Hypothetical protein (1)			-	C_unshiu_01423_mRNA_1.1	-
GF0040913	0	1	0	Hypothetical protein (1)		Protein of unknown function DUF617, plant [IPR006460] (1)	-	C_unshiu_01422_mRNA_7.1	-
GF0040912	0	1	0	Hypothetical protein (1)			-	C_unshiu_01421_mRNA_5.1	-
GF0040911	0	1	0	Hypothetical protein (1)			-	C_unshiu_01420_mRNA_6.1	-
GF0040910	0	1	0	Hypothetical protein (1)			-	C_unshiu_01420_mRNA_4.1	-
GF0040909	0	1	0	Hypothetical protein (1)			-	C_unshiu_01420_mRNA_3.1	-
GF0040908	0	1	0	Hypothetical protein (1)		Transposon, En/Spm-like [IPR004242] (1)	-	C_unshiu_01420_mRNA_2.1	-
GF0040907	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	C_unshiu_01420_mRNA_1.1	-
GF0040906	0	1	0	Hypothetical protein (1)			-	C_unshiu_01419_mRNA_4.1	-
GF0040905	0	1	0	Hypothetical protein (1)			-	C_unshiu_01418_mRNA_8.1	-
GF0040904	0	1	0	Aspartic proteinase-like protein 1 (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Xylanase inhibitor, C-terminal [IPR032799] (1); Aspartic peptidase A1 family [IPR001461] (1); Aspartic peptidase domain [IPR021109] (1); Peptidase family A1 domain [IPR033121] (1)	-	C_unshiu_01418_mRNA_6.1	-
GF0040903	0	1	0	Hypothetical protein (1)	protein dephosphorylation [GO:0006470 biological_process] (1); protein serine/threonine phosphatase activity [GO:0004722 molecular_function] (1)	Protein phosphatase 2C family [IPR015655] (1)	-	C_unshiu_01418_mRNA_11.1	-
GF0040902	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_01417_mRNA_3.1	-
GF0040901	0	1	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); metallocarboxypeptidase activity [GO:0004181 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Peptidase M14, carboxypeptidase A [IPR000834] (1)	-	C_unshiu_01416_mRNA_3.1	-
GF0040900	0	1	0	Hypothetical protein (1)	membrane [GO:0016020 cellular_component] (1); potassium ion transmembrane transport [GO:0071805 biological_process] (1); potassium ion transmembrane transporter activity [GO:0015079 molecular_function] (1)	Potassium transporter [IPR003855] (1)	-	C_unshiu_01414_mRNA_9.1	-
GF0040899	0	1	0	Hypothetical protein (1)			-	C_unshiu_01414_mRNA_5.1	-
GF0040898	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_01414_mRNA_4.1	-
GF0040897	0	1	0	Hypothetical protein (1)			-	C_unshiu_01414_mRNA_1.1	-
GF0040896	0	1	0	DUF760 family protein (1)		Protein of unknown function DUF760 [IPR008479] (1)	-	C_unshiu_01413_mRNA_7.1	-
GF0040895	0	1	0	Hypothetical protein (1)			-	C_unshiu_01413_mRNA_6.1	-
GF0040894	0	1	0	Hypothetical protein (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	FAD/NAD(P)-binding domain [IPR023753] (1)	-	C_unshiu_01413_mRNA_4.1	-
GF0040893	0	1	0	Hypothetical protein (1)			-	C_unshiu_01413_mRNA_3.1	-
GF0040892	0	1	0	Hypothetical protein (1)			-	C_unshiu_01413_mRNA_1.1	-
GF0040891	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_01412_mRNA_7.1	-
GF0040890	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_01412_mRNA_6.1	-
GF0040889	0	1	0	Hypothetical protein (1)			-	C_unshiu_01412_mRNA_5.1	-
GF0040888	0	1	0	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_01412_mRNA_4.1	-
GF0040887	0	1	0	Hypothetical protein (1)			-	C_unshiu_01412_mRNA_10.1	-
GF0040886	0	1	0	Hypothetical protein (1)			-	C_unshiu_01412_mRNA_1.1	-
GF0040885	0	1	0	Hypothetical protein (1)			-	C_unshiu_01410_mRNA_7.1	-
GF0040884	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_01409_mRNA_7.1	-
GF0040883	0	1	0	Hypothetical protein (1)			-	C_unshiu_01409_mRNA_5.1	-
GF0040882	0	1	0	Phosphoprotein phosphatase (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01408_mRNA_8.1	-
GF0040881	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF1336 [IPR009769] (1)	-	C_unshiu_01408_mRNA_7.1	-
GF0040880	0	1	0	Hypothetical protein (1)			-	C_unshiu_01408_mRNA_6.1	-
GF0040879	0	1	0	Hypothetical protein (1)	metabolic process [GO:0008152 biological_process] (1); transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	-	C_unshiu_01408_mRNA_4.1	-
GF0040878	0	1	0	Hypothetical protein (1)		Casparian strip membrane protein [IPR006459] (1); Domain of unknown function DUF588 [IPR006702] (1)	-	C_unshiu_01407_mRNA_9.1	-
GF0040877	0	1	0	Hypothetical protein (1)			-	C_unshiu_01407_mRNA_2.1	-
GF0040876	0	1	0	Hypothetical protein (1)			-	C_unshiu_01407_mRNA_14.1	-
GF0040875	0	1	0	Hypothetical protein (1)			-	C_unshiu_01407_mRNA_13.1	-
GF0040874	0	1	0	Hypothetical protein (1)			-	C_unshiu_01407_mRNA_10.1	-
GF0040873	0	1	0	Hypothetical protein (1)			-	C_unshiu_01407_mRNA_1.1	-
GF0040872	0	1	0	Hypothetical protein (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1); polygalacturonase activity [GO:0004650 molecular_function] (1)	Pectin lyase fold [IPR012334] (1); Pectin lyase fold/virulence factor [IPR011050] (1); Glycoside hydrolase, family 28 [IPR000743] (1)	-	C_unshiu_01406_mRNA_3.1	-
GF0040871	0	1	0	Hypothetical protein (1)	polygalacturonase activity [GO:0004650 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1)	Pectin lyase fold/virulence factor [IPR011050] (1); Pectin lyase fold [IPR012334] (1); Glycoside hydrolase, family 28 [IPR000743] (1)	-	C_unshiu_01406_mRNA_2.1	-
GF0040870	0	1	0	Hypothetical protein (1)	polygalacturonase activity [GO:0004650 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1)	Pectin lyase fold [IPR012334] (1); Pectin lyase fold/virulence factor [IPR011050] (1); Glycoside hydrolase, family 28 [IPR000743] (1)	-	C_unshiu_01406_mRNA_1.1	-
GF0040869	0	1	0	Hypothetical protein (1)			-	C_unshiu_01405_mRNA_8.1	-
GF0040868	0	1	0	Polygalacturonase 7 (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1); polygalacturonase activity [GO:0004650 molecular_function] (1)	Glycoside hydrolase, family 28 [IPR000743] (1); Pectin lyase fold/virulence factor [IPR011050] (1); Pectin lyase fold [IPR012334] (1)	-	C_unshiu_01405_mRNA_6.1	-
GF0040867	0	1	0	Hypothetical protein (1)		PGG domain [IPR026961] (1); Ankyrin repeat-containing domain [IPR020683] (1)	-	C_unshiu_01405_mRNA_12.1	-
GF0040866	0	1	0	Hypothetical protein (1)			-	C_unshiu_01404_mRNA_8.1	-
GF0040865	0	1	0	Hypothetical protein (1)		GAG-pre-integrase domain [IPR025724] (1)	-	C_unshiu_01403_mRNA_3.1	-
GF0040864	0	1	0	Hypothetical protein (1)			-	C_unshiu_01403_mRNA_2.1	-
GF0040863	0	1	0	Sesquiterpene synthase (1)	metabolic process [GO:0008152 biological_process] (1); lyase activity [GO:0016829 molecular_function] (1); terpene synthase activity [GO:0010333 molecular_function] (1); magnesium ion binding [GO:0000287 molecular_function] (1)	Isoprenoid synthase domain [IPR008949] (1); Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (1); Terpene synthase, N-terminal domain [IPR001906] (1); Terpene synthase, metal-binding domain [IPR005630] (1)	-	C_unshiu_01403_mRNA_1.1	-
GF0040862	0	1	0	Limonene synthase (1)	magnesium ion binding [GO:0000287 molecular_function] (1); terpene synthase activity [GO:0010333 molecular_function] (1); lyase activity [GO:0016829 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (1); Terpene synthase, metal-binding domain [IPR005630] (1); Terpene synthase, N-terminal domain [IPR001906] (1); Isoprenoid synthase domain [IPR008949] (1)	-	C_unshiu_01402_mRNA_2.1	-

ID	**Num. in *C. celementine***	**Num in *C. unshiu***	**Num in *P.trifoliata***	**Note**	**GO**	**InterPro**	**Members in *C.clementine***	**Members in *C.unshiu***	**Members in *P.trifoliata***
GF0040861	0	1	0	Hypothetical protein (1)	terpene synthase activity [GO:0010333 molecular_function] (1); lyase activity [GO:0016829 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Terpene synthase, N-terminal domain [IPR001906] (1); Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (1)	-	C_unshiu_01402_mRNA_1.1	-
GF0040860	0	1	0	RNA-directed DNA polymerase (Reverse transcriptase), Polynucleotidyl transferase, Ribonuclease H fold-like protein (1)	RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H domain [IPR002156] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_01401_mRNA_8.1	-
GF0040859	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01401_mRNA_7.1	-
GF0040858	0	1	0	Tetratricopeptide repeat (TPR)-containing protein-like (1)		Clustered mitochondria protein, N-terminal [IPR028275] (1)	-	C_unshiu_01401_mRNA_3.1	-
GF0040857	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Tetratricopeptide-like helical domain [IPR011990] (1)	-	C_unshiu_01401_mRNA_1.1	-
GF0040856	0	1	0	Hypothetical protein (1)			-	C_unshiu_01400_mRNA_6.1	-
GF0040855	0	1	0	Hypothetical protein (1)			-	C_unshiu_01400_mRNA_5.1	-
GF0040854	0	1	0	Hypothetical protein (1)			-	C_unshiu_01400_mRNA_1.1	-
GF0040853	0	1	0	Hypothetical protein (1)			-	C_unshiu_01399_mRNA_7.1	-
GF0040852	0	1	0	Hypothetical protein (1)			-	C_unshiu_01399_mRNA_3.1	-
GF0040851	0	1	0	Hypothetical protein (1)			-	C_unshiu_01397_mRNA_9.1	-
GF0040850	0	1	0	Hypothetical protein (1)			-	C_unshiu_01397_mRNA_1.1	-
GF0040849	0	1	0	Hypothetical protein (1)			-	C_unshiu_01396_mRNA_9.1	-
GF0040848	0	1	0	Hypothetical protein (1)			-	C_unshiu_01396_mRNA_8.1	-
GF0040847	0	1	0	Hypothetical protein (1)			-	C_unshiu_01396_mRNA_6.1	-
GF0040846	0	1	0	Hypothetical protein (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1)	Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_01396_mRNA_5.1	-
GF0040845	0	1	0	Hypothetical protein (1)			-	C_unshiu_01396_mRNA_4.1	-
GF0040844	0	1	0	Hypothetical protein (1)			-	C_unshiu_01396_mRNA_10.1	-
GF0040843	0	1	0	Hypothetical protein (1)	recognition of pollen [GO:0048544 biological_process] (1); protein serine/threonine kinase activity [GO:0004674 molecular_function] (1)	S-locus receptor kinase, C-terminal [IPR021820] (1); S-locus glycoprotein domain [IPR000858] (1); PAN/Apple domain [IPR003609] (1); Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_01396_mRNA_1.1	-
GF0040842	0	1	0	Hypothetical protein (1)			-	C_unshiu_01395_mRNA_3.1	-
GF0040841	0	1	0	Hypothetical protein (1)			-	C_unshiu_01394_mRNA_7.1	-
GF0040840	0	1	0	Hypothetical protein (1)			-	C_unshiu_01394_mRNA_6.1	-
GF0040839	0	1	0	Hypothetical protein (1)			-	C_unshiu_01394_mRNA_2.1	-
GF0040838	0	1	0	Hypothetical protein (1)			-	C_unshiu_01394_mRNA_1.1	-
GF0040837	0	1	0	Hypothetical protein (1)			-	C_unshiu_01393_mRNA_6.1	-
GF0040836	0	1	0	Hypothetical protein (1)			-	C_unshiu_01392_mRNA_8.1	-
GF0040835	0	1	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	C_unshiu_01392_mRNA_4.1	-
GF0040834	0	1	0	Hypothetical protein (1)			-	C_unshiu_01392_mRNA_2.1	-
GF0040833	0	1	0	Hypothetical protein (1)			-	C_unshiu_01391_mRNA_4.1	-
GF0040832	0	1	0	Hypothetical protein (1)			-	C_unshiu_01390_mRNA_3.1	-
GF0040831	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_01390_mRNA_1.1	-
GF0040830	0	1	0	Hypothetical protein (1)			-	C_unshiu_01388_mRNA_5.1	-
GF0040829	0	1	0	Hypothetical protein (1)			-	C_unshiu_01388_mRNA_3.1	-
GF0040828	0	1	0	Hypothetical protein (1)			-	C_unshiu_01388_mRNA_2.1	-
GF0040827	0	1	0	Hypothetical protein (1)			-	C_unshiu_01388_mRNA_1.1	-
GF0040826	0	1	0	Hypothetical protein (1)			-	C_unshiu_01387_mRNA_4.1	-
GF0040825	0	1	0	Hypothetical protein (1)		Histone deacetylase domain [IPR023801] (1)	-	C_unshiu_01387_mRNA_1.1	-
GF0040824	0	1	0	Hypothetical protein (1)			-	C_unshiu_01386_mRNA_2.1	-
GF0040823	0	1	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_01385_mRNA_7.1	-
GF0040822	0	1	0	Hypothetical protein (1)			-	C_unshiu_01385_mRNA_6.1	-
GF0040821	0	1	0	Hypothetical protein (1)	nucleotide binding [GO:0000166 molecular_function] (1)	Domain of unknown function DUF4283 [IPR025558] (1); Nucleotide-binding alpha-beta plait domain [IPR012677] (1)	-	C_unshiu_01385_mRNA_5.1	-
GF0040820	0	1	0	Hypothetical protein (1)			-	C_unshiu_01385_mRNA_3.1	-
GF0040819	0	1	0	Hypothetical protein (1)			-	C_unshiu_01384_mRNA_9.1	-
GF0040818	0	1	0	Hypothetical protein (1)			-	C_unshiu_01384_mRNA_7.1	-
GF0040817	0	1	0	Hypothetical protein (1)			-	C_unshiu_01384_mRNA_6.1	-
GF0040816	0	1	0	Hypothetical protein (1)			-	C_unshiu_01384_mRNA_4.1	-
GF0040815	0	1	0	Hypothetical protein (1)			-	C_unshiu_01384_mRNA_3.1	-
GF0040814	0	1	0	Hypothetical protein (1)			-	C_unshiu_01384_mRNA_1.1	-
GF0040813	0	1	0	Hypothetical protein (1)			-	C_unshiu_01383_mRNA_5.1	-
GF0040812	0	1	0	Truncated tyrosine decarboxylase (1)	carboxy-lyase activity [GO:0016831 molecular_function] (1); carboxylic acid metabolic process [GO:0019752 biological_process] (1); cellular amino acid metabolic process [GO:0006520 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1); pyridoxal phosphate binding [GO:0030170 molecular_function] (1)	Pyridoxal phosphate-dependent transferase, major region, subdomain 1 [IPR015421] (1); Pyridoxal phosphate-dependent decarboxylase [IPR002129] (1); Pyridoxal phosphate-dependent transferase [IPR015424] (1); Aromatic-L-amino-acid decarboxylase [IPR010977] (1)	-	C_unshiu_01382_mRNA_5.1	-
GF0040811	0	1	0	Hypothetical protein (1)			-	C_unshiu_01382_mRNA_1.1	-
GF0040810	0	1	0	Hypothetical protein (1)			-	C_unshiu_01381_mRNA_1.1	-
GF0040809	0	1	0	Nucleic acid binding / zinc ion binding protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Domain of unknown function DUF4283 [IPR025558] (1); Zinc finger, CCHC-type [IPR001878] (1); Zinc knuckle CX2CX4HX4C [IPR025836] (1)	-	C_unshiu_01380_mRNA_1.1	-
GF0040808	0	1	0	Putative non-LTR retroelement reverse transcriptase (1)		Reverse transcriptase domain [IPR000477] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1); Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_01379_mRNA_5.1	-
GF0040807	0	1	0	Hypothetical protein (1)		HAD-like domain [IPR023214] (1); FCP1 homology domain [IPR004274] (1)	-	C_unshiu_01379_mRNA_3.1	-
GF0040806	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_01379_mRNA_2.1	-
GF0040805	0	1	0	Hypothetical protein (1)			-	C_unshiu_01376_mRNA_6.1	-
GF0040804	0	1	0	Hypothetical protein (1)			-	C_unshiu_01376_mRNA_4.1	-
GF0040803	0	1	0	Hypothetical protein (1)			-	C_unshiu_01376_mRNA_1.1	-
GF0040802	0	1	0	Hypothetical protein (1)			-	C_unshiu_01375_mRNA_1.1	-
GF0040801	0	1	0	Hypothetical protein (1)			-	C_unshiu_01374_mRNA_6.1	-
GF0040800	0	1	0	Hypothetical protein (1)			-	C_unshiu_01374_mRNA_3.1	-
GF0040799	0	1	0	Hypothetical protein (1)			-	C_unshiu_01374_mRNA_1.1	-
GF0040798	0	1	0	Hypothetical protein (1)			-	C_unshiu_01373_mRNA_5.1	-
GF0040797	0	1	0	Hypothetical protein (1)			-	C_unshiu_01373_mRNA_1.1	-
GF0040796	0	1	0	Hypothetical protein (1)			-	C_unshiu_01372_mRNA_7.1	-
GF0040795	0	1	0	Hypothetical protein (1)			-	C_unshiu_01372_mRNA_4.1	-
GF0040794	0	1	0	Hypothetical protein (1)			-	C_unshiu_01372_mRNA_3.1	-
GF0040793	0	1	0	Hypothetical protein (1)			-	C_unshiu_01372_mRNA_1.1	-
GF0040792	0	1	0	Hypothetical protein (1)			-	C_unshiu_01370_mRNA_8.1	-
GF0040791	0	1	0	Ubiquitin-conjugating enzyme E2 N (1)		Ubiquitin-conjugating enzyme/RWD-like [IPR016135] (1); Ubiquitin-conjugating enzyme, active site [IPR023313] (1); Ubiquitin-conjugating enzyme E2 [IPR000608] (1)	-	C_unshiu_01369_mRNA_5.1	-
GF0040790	0	1	0	Hypothetical protein (1)			-	C_unshiu_01368_mRNA_2.1	-
GF0040789	0	1	0	TAP42-like family protein, expressed (1)	regulation of signal transduction [GO:0009966 biological_process] (1)	TAP42-like protein [IPR007304] (1)	-	C_unshiu_01368_mRNA_1.1	-
GF0040788	0	1	0	Hypothetical protein (1)			-	C_unshiu_01367_mRNA_9.1	-
GF0040787	0	1	0	Hypothetical protein (1)	Ino80 complex [GO:0031011 cellular_component] (1)	Nuclear factor related to kappa-B-binding protein [IPR024867] (1)	-	C_unshiu_01367_mRNA_6.1	-
GF0040786	0	1	0	Hypothetical protein (1)			-	C_unshiu_01367_mRNA_5.1	-
GF0040785	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_01367_mRNA_3.1	-
GF0040784	0	1	0	HAT transposon superfamily (1)	zinc ion binding [GO:0008270 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Domain of unknown function DUF659 [IPR007021] (1); Ribonuclease H-like domain [IPR012337] (1); Zinc finger, GRF-type [IPR010666] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	-	C_unshiu_01367_mRNA_11.1	-
GF0040783	0	1	0	Type II peroxiredoxin (1)	oxidoreductase activity [GO:0016491 molecular_function] (1)	Redoxin [IPR013740] (1); Thioredoxin-like fold [IPR012336] (1)	-	C_unshiu_01366_mRNA_5.1	-
GF0040782	0	1	0	ADP-ribosylation factor GTPase-activating protein AGD3 (1)	protein binding [GO:0005515 molecular_function] (1)	PH domain-like [IPR011993] (1); Pleckstrin homology domain [IPR001849] (1); Ankyrin repeat-containing domain [IPR020683] (1); Arfaptin homology (AH) domain/BAR domain [IPR027267] (1); Ankyrin repeat [IPR002110] (1); Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_01366_mRNA_1.1	-
GF0040781	0	1	0	Hypothetical protein (1)			-	C_unshiu_01365_mRNA_8.1	-
GF0040780	0	1	0	Nucleic acid binding protein, putative (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_01365_mRNA_7.1	-
GF0040779	0	1	0	Ribonuclease H protein, putative (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_01365_mRNA_6.1	-
GF0040778	0	1	0	Hypothetical protein (1)			-	C_unshiu_01365_mRNA_5.1	-
GF0040777	0	1	0	Hypothetical protein (1)			-	C_unshiu_01365_mRNA_1.1	-
GF0040776	0	1	0	Hypothetical protein (1)		Heat shock protein 70kD, peptide-binding domain [IPR029047] (1); Heat shock protein 70kD, C-terminal domain [IPR029048] (1); Heat shock protein 70 family [IPR013126] (1)	-	C_unshiu_01364_mRNA_3.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0040775	0	1	0	Cytochrome P450 (1)	heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1)	Cytochrome P450 [IPR001128] (1); Cytochrome P450, conserved site [IPR017972] (1)	-	C_unshiu_01364_mRNA_2.1	-
GF0040774	0	1	0	Hypothetical protein (1)	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1)	Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450, conserved site [IPR017972] (1); Domain of unknown function DUF1985 [IPR015410] (1); Cytochrome P450 [IPR001128] (1)	-	C_unshiu_01363_mRNA_1.1	-
GF0040773	0	1	0	Hypothetical protein (1)			-	C_unshiu_01360_mRNA_8.1	-
GF0040772	0	1	0	Putative RNA-directed DNA polymerase (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_01360_mRNA_5.1	-
GF0040771	0	1	0	Hypothetical protein (1)			-	C_unshiu_01360_mRNA_3.1	-
GF0040770	0	1	0	Hypothetical protein (1)			-	C_unshiu_01360_mRNA_2.1	-
GF0040769	0	1	0	Hypothetical protein (1)			-	C_unshiu_01360_mRNA_1.1	-
GF0040768	0	1	0	Hypothetical protein (1)			-	C_unshiu_01359_mRNA_9.1	-
GF0040767	0	1	0	Hypothetical protein (1)	ATPase activity [GO:0016887 molecular_function] (1); catalytic activity [GO:0003824 molecular_function] (1); trehalose metabolic process [GO:0005991 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1); alpha,alpha-trehalase activity [GO:0004555 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); AAA+ ATPase domain [IPR003593] (1); ABC transporter-like [IPR003439] (1); ABC transporter, conserved site [IPR017871] (1); Six-hairpin glycosidase-like [IPR008928] (1); Glycoside hydrolase, family 37, conserved site [IPR018232] (1); ABC-transporter extension domain [IPR032781] (1); Glycoside hydrolase, family 37 [IPR001661] (1)	-	C_unshiu_01359_mRNA_8.1	-
GF0040766	0	1	0	Carbon-nitrogen hydrolase family protein (1)	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds [GO:0016810 molecular_function] (1); NAD+ synthase (glutamine-hydrolyzing) activity [GO:0003952 molecular_function] (1); NAD biosynthetic process [GO:0009435 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1); nitrogen compound metabolic process [GO:0006807 biological_process] (1)	NAD/GMP synthase [IPR022310] (1); Carbon-nitrogen hydrolase [IPR003010] (1); Rossmann-like alpha/beta/alpha sandwich fold [IPR014729] (1); NAD(+) synthetase [IPR003694] (1); Glutamine-dependent NAD(+) synthetase [IPR014445] (1)	-	C_unshiu_01359_mRNA_6.1	-
GF0040765	0	1	0	Importin subunit beta-1 (1)	Ran GTPase binding [GO:0008536 molecular_function] (1); protein transporter activity [GO:0008565 molecular_function] (1); intracellular protein transport [GO:0006886 biological_process] (1); binding [GO:0005488 molecular_function] (1); nucleocytoplasmic transport [GO:0006913 biological_process] (1)	Armadillo-like helical [IPR011989] (1); Importin-beta, N-terminal domain [IPR001494] (1); Importin subunit beta-1, plants [IPR027140] (1); Armadillo-type fold [IPR016024] (1)	-	C_unshiu_01359_mRNA_4.1	-
GF0040764	0	1	0	Short-chain dehydrogenase TIC 32 (1)	metabolic process [GO:0008152 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1)	Short-chain dehydrogenase/reductase SDR [IPR002198] (1); Glucose/ribitol dehydrogenase [IPR002347] (1); NAD(P)-binding domain [IPR016040] (1)	-	C_unshiu_01359_mRNA_10.1	-
GF0040763	0	1	0	Hypothetical protein (1)			-	C_unshiu_01359_mRNA_1.1	-
GF0040762	0	1	0	Hypothetical protein (1)			-	C_unshiu_01358_mRNA_4.1	-
GF0040761	0	1	0	Hypothetical protein (1)			-	C_unshiu_01357_mRNA_8.1	-
GF0040760	0	1	0	Histone H3 (1)	nucleosome [GO:0000786 cellular_component] (1); protein heterodimerization activity [GO:0046982 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	Histone-fold [IPR009072] (1); Histone H3/CENP-A [IPR000164] (1); Histone H2A/H2B/H3 [IPR007125] (1)	-	C_unshiu_01357_mRNA_6.1	-
GF0040759	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_01357_mRNA_2.1	-
GF0040758	0	1	0	Hypothetical protein (1)	endopeptidase inhibitor activity [GO:0004866 molecular_function] (1)	Proteinase inhibitor I3, Kunitz legume [IPR002160] (1); Kunitz inhibitor ST1-like [IPR011065] (1)	-	C_unshiu_01357_mRNA_10.1	-
GF0040757	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_01356_mRNA_3.1	-
GF0040756	0	1	0	Hypothetical protein (1)			-	C_unshiu_01356_mRNA_2.1	-
GF0040755	0	1	0	Hypothetical protein (1)			-	C_unshiu_01355_mRNA_4.1	-
GF0040754	0	1	0	Fasciclin-like AGP 15 family protein (1)		FAS1 domain [IPR000782] (1)	-	C_unshiu_01354_mRNA_9.1	-
GF0040753	0	1	0	Syntaxin of plants protein (1)	protein binding [GO:0005515 molecular_function] (1); membrane [GO:0016020 cellular_component] (1); intracellular protein transport [GO:0006886 biological_process] (1); SNAP receptor activity [GO:0005484 molecular_function] (1)	Syntaxin/epimorphin, conserved site [IPR006012] (1); Target SNARE coiled-coil homology domain [IPR000727] (1)	-	C_unshiu_01354_mRNA_4.1	-
GF0040752	0	1	0	Hypothetical protein (1)			-	C_unshiu_01354_mRNA_3.1	-
GF0040751	0	1	0	Ubiquitin thioesterase OTU1 (1)			-	C_unshiu_01352_mRNA_4.1	-
GF0040750	0	1	0	Hypothetical protein (1)			-	C_unshiu_01351_mRNA_7.1	-
GF0040749	0	1	0	Hypothetical protein (1)			-	C_unshiu_01351_mRNA_6.1	-
GF0040748	0	1	0	Hypothetical protein (1)			-	C_unshiu_01351_mRNA_1.1	-
GF0040747	0	1	0	Glutathione S-transferase, amino-terminal domain protein (1)	protein binding [GO:0005515 molecular_function] (1)	Glutathione S-transferase, N-terminal [IPR004045] (1); Glutathione S-transferase, C-terminal-like [IPR010987] (1); Thioredoxin-like fold [IPR012336] (1)	-	C_unshiu_01350_mRNA_8.1	-
GF0040746	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Uncharacterised protein family UPF0274 [IPR007451] (1)	-	C_unshiu_01350_mRNA_6.1	-
GF0040745	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01350_mRNA_4.1	-
GF0040744	0	1	0	TRNA-splicing ligase RtcB (1)		Domain of unknown function DUF239 [IPR004314] (1); Domain of unknown function DUF4409 [IPR025521] (1)	-	C_unshiu_01348_mRNA_4.1	-
GF0040743	0	1	0	Hypothetical protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	C_unshiu_01348_mRNA_10.1	-
GF0040742	0	1	0	Hypothetical protein (1)		Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	-	C_unshiu_01348_mRNA_1.1	-
GF0040741	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_01347_mRNA_6.1	-
GF0040740	0	1	0	Hypothetical protein (1)			-	C_unshiu_01347_mRNA_5.1	-
GF0040739	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_01347_mRNA_3.1	-
GF0040738	0	1	0	Hypothetical protein (1)			-	C_unshiu_01347_mRNA_1.1	-
GF0040737	0	1	0	Hypothetical protein (1)			-	C_unshiu_01346_mRNA_1.1	-
GF0040736	0	1	0	Hypothetical protein (1)			-	C_unshiu_01344_mRNA_9.1	-
GF0040735	0	1	0	Hypothetical protein (1)		Zinc knuckle CX2CX4HX4C [IPR025836] (1); Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_01344_mRNA_2.1	-
GF0040734	0	1	0	Hypothetical protein (1)			-	C_unshiu_01344_mRNA_13.1	-
GF0040733	0	1	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1)	-	C_unshiu_01344_mRNA_11.1	-
GF0040732	0	1	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1); FAR1 DNA binding domain [IPR004330] (1)	-	C_unshiu_01344_mRNA_10.1	-
GF0040731	0	1	0	Hypothetical protein (1)			-	C_unshiu_01344_mRNA_1.1	-
GF0040730	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_01343_mRNA_9.1	-
GF0040729	0	1	0	Hypothetical protein (1)			-	C_unshiu_01343_mRNA_7.1	-
GF0040728	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_01343_mRNA_14.1	-
GF0040727	0	1	0	Hypothetical protein (1)			-	C_unshiu_01343_mRNA_12.1	-
GF0040726	0	1	0	Hypothetical protein (1)			-	C_unshiu_01343_mRNA_10.1	-
GF0040725	0	1	0	Hypothetical protein (1)			-	C_unshiu_01342_mRNA_9.1	-
GF0040724	0	1	0	Hypothetical protein (1)			-	C_unshiu_01342_mRNA_8.1	-
GF0040723	0	1	0	Tether containing UBX domain for GLUT4, putative (1)			-	C_unshiu_01342_mRNA_1.1	-
GF0040722	0	1	0	Hypothetical protein (1)			-	C_unshiu_01341_mRNA_1.1	-
GF0040721	0	1	0	Hypothetical protein (1)			-	C_unshiu_01340_mRNA_4.1	-
GF0040720	0	1	0	Hypothetical protein (1)			-	C_unshiu_01340_mRNA_3.1	-
GF0040719	0	1	0	Hypothetical protein (1)			-	C_unshiu_01340_mRNA_2.1	-
GF0040718	0	1	0	Hypothetical protein (1)			-	C_unshiu_01340_mRNA_1.1	-
GF0040717	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); RNA binding [GO:0003723 molecular_function] (1); 'de novo' IMP biosynthetic process [GO:0006189 biological_process] (1)	K Homology domain [IPR004087] (1); Phosphoribosylaminoimidazole carboxylase PurE domain [IPR000031] (1); K Homology domain, type 1 [IPR004088] (1)	-	C_unshiu_01339_mRNA_7.1	-
GF0040716	0	1	0	Hypothetical protein (1)			-	C_unshiu_01339_mRNA_6.1	-
GF0040715	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	Zinc finger, BED-type [IPR003656] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_01339_mRNA_5.1	-
GF0040714	0	1	0	Zinc knuckle family protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_01339_mRNA_4.1	-
GF0040713	0	1	0	Hypothetical protein (1)			-	C_unshiu_01339_mRNA_2.1	-
GF0040712	0	1	0	Putative protease Do-like 14 (1)	serine-type endopeptidase activity [GO:0004252 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1); protein binding [GO:0005515 molecular_function] (1)	Peptidase S1, PA clan [IPR009003] (1); PDZ domain [IPR001478] (1); Peptidase S1C [IPR001940] (1)	-	C_unshiu_01339_mRNA_1.1	-
GF0040711	0	1	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_01338_mRNA_7.1	-
GF0040710	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_01338_mRNA_6.1	-
GF0040709	0	1	0	Hypothetical protein (1)			-	C_unshiu_01338_mRNA_5.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0040708	0	1	0	Hypothetical protein (1)			-	C_unshiu_01338_mRNA_2.1	-
GF0040707	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_01338_mRNA_1.1	-
GF0040706	0	1	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	DNA-binding pseudobarrel domain [IPR015300] (1); B3 DNA binding domain [IPR003340] (1); Protein of unknown function DUF1313 [IPR009741] (1)	-	C_unshiu_01337_mRNA_1.1	-
GF0040705	0	1	0	Hypothetical protein (1)			-	C_unshiu_01336_mRNA_5.1	-
GF0040704	0	1	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_01336_mRNA_2.1	-
GF0040703	0	1	0	Hypothetical protein (1)			-	C_unshiu_01336_mRNA_10.1	-
GF0040702	0	1	0	Hypothetical protein (1)		Pre-mRNA-splicing factor 19 [IPR013915] (1)	-	C_unshiu_01335_mRNA_3.1	-
GF0040701	0	1	0	Hypothetical protein (1)	catalytic activity [GO:0003824 molecular_function] (1)	PFTB repeat [IPR001330] (1); Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (1)	-	C_unshiu_01335_mRNA_1.1	-
GF0040700	0	1	0	Hypothetical protein (1)			-	C_unshiu_01334_mRNA_2.1	-
GF0040699	0	1	0	Hypothetical protein (1)			-	C_unshiu_01333_mRNA_7.1	-
GF0040698	0	1	0	Hypothetical protein (1)			-	C_unshiu_01333_mRNA_5.1	-
GF0040697	0	1	0	Hypothetical protein (1)			-	C_unshiu_01333_mRNA_3.1	-
GF0040696	0	1	0	Hypothetical protein (1)			-	C_unshiu_01333_mRNA_2.1	-
GF0040695	0	1	0	Hypothetical protein (1)			-	C_unshiu_01333_mRNA_1.1	-
GF0040694	0	1	0	Hypothetical protein (1)			-	C_unshiu_01332_mRNA_9.1	-
GF0040693	0	1	0	Hypothetical protein (1)			-	C_unshiu_01332_mRNA_8.1	-
GF0040692	0	1	0	Hypothetical protein (1)			-	C_unshiu_01332_mRNA_7.1	-
GF0040691	0	1	0	Hypothetical protein (1)			-	C_unshiu_01332_mRNA_6.1	-
GF0040690	0	1	0	Hypothetical protein (1)			-	C_unshiu_01331_mRNA_7.1	-
GF0040689	0	1	0	Hypothetical protein (1)			-	C_unshiu_01331_mRNA_1.1	-
GF0040688	0	1	0	Hypothetical protein (1)			-	C_unshiu_01330_mRNA_6.1	-
GF0040687	0	1	0	Hypothetical protein (1)		Domain unknown function DUF295 [IPR005174] (1)	-	C_unshiu_01329_mRNA_1.1	-
GF0040686	0	1	0	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); metal ion binding [GO:0046872 molecular_function] (1); superoxide metabolic process [GO:0006801 biological_process] (1)	Superoxide dismutase, copper/zinc binding domain [IPR001424] (1)	-	C_unshiu_01327_mRNA_4.1	-
GF0040685	0	1	0	Hypothetical protein (1)			-	C_unshiu_01327_mRNA_3.1	-
GF0040684	0	1	0	Hypothetical protein (1)			-	C_unshiu_01327_mRNA_1.1	-
GF0040683	0	1	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_01326_mRNA_5.1	-
GF0040682	0	1	0	Hypothetical protein (1)			-	C_unshiu_01326_mRNA_4.1	-
GF0040681	0	1	0	Hypothetical protein (1)			-	C_unshiu_01326_mRNA_2.1	-
GF0040680	0	1	0	Hypothetical protein (1)		EEIG1/EHBP1 N-terminal domain [IPR019448] (1)	-	C_unshiu_01325_mRNA_9.1	-
GF0040679	0	1	0	Putative muDR family transposase-like (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	MULE transposase domain [IPR018289] (1); Zinc finger, PMZ-type [IPR006564] (1); Zinc finger, SWIM-type [IPR007527] (1); Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_01325_mRNA_2.1	-
GF0040678	0	1	0	Hypothetical protein (1)	heme binding [GO:0020037 molecular_function] (1); response to oxidative stress [GO:0006979 biological_process] (1); peroxidase activity [GO:0004601 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Haem peroxidase, plant/fungal/bacterial [IPR002016] (1); Plant peroxidase [IPR000823] (1); Haem peroxidase [IPR010255] (1)	-	C_unshiu_01324_mRNA_1.1	-
GF0040677	0	1	0	Hypothetical protein (1)			-	C_unshiu_01323_mRNA_8.1	-
GF0040676	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4005 [IPR025064] (1); Gag-polypeptide of LTR copia-type [IPR029472] (1)	-	C_unshiu_01323_mRNA_7.1	-
GF0040675	0	1	0	Hypothetical protein (1)			-	C_unshiu_01323_mRNA_6.1	-
GF0040674	0	1	0	Hypothetical protein (1)			-	C_unshiu_01323_mRNA_5.1	-
GF0040673	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_01323_mRNA_10.1	-
GF0040672	0	1	0	Hypothetical protein (1)			-	C_unshiu_01322_mRNA_8.1	-
GF0040671	0	1	0	Hypothetical protein (1)			-	C_unshiu_01322_mRNA_5.1	-
GF0040670	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_01322_mRNA_3.1	-
GF0040669	0	1	0	Peroxidase 4 (1)	oxidation-reduction process [GO:0055114 biological_process] (1); peroxidase activity [GO:0004601 molecular_function] (1); response to oxidative stress [GO:0006979 biological_process] (1); heme binding [GO:0020037 molecular_function] (1)	Haem peroxidase [IPR010255] (1); Peroxidase, active site [IPR019794] (1); Plant peroxidase [IPR000823] (1); Haem peroxidase, plant/fungal/bacterial [IPR002016] (1)	-	C_unshiu_01322_mRNA_1.1	-
GF0040668	0	1	0	Hypothetical protein (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Viral movement protein [IPR028919] (1); Aspartic peptidase, active site [IPR001969] (1)	-	C_unshiu_01321_mRNA_5.1	-
GF0040667	0	1	0	Hypothetical protein (1)			-	C_unshiu_01321_mRNA_4.1	-
GF0040666	0	1	0	Dessication-induced 1VOC superfamily protein (1)		Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase [IPR029068] (1); Glyoxalase-like domain [IPR025870] (1)	-	C_unshiu_01320_mRNA_9.1	-
GF0040665	0	1	0	Hypothetical protein (1)			-	C_unshiu_01320_mRNA_8.1	-
GF0040664	0	1	0	Pathogenesis-related thaumatin family protein (1)		Thaumatin [IPR001938] (1)	-	C_unshiu_01320_mRNA_5.1	-
GF0040663	0	1	0	Hypothetical protein (1)			-	C_unshiu_01320_mRNA_13.1	-
GF0040662	0	1	0	Heat shock protein 70 (1)		Heat shock protein 70kD, C-terminal domain [IPR029048] (1); Heat shock protein 70 family [IPR013126] (1); Heat shock protein 70, conserved site [IPR018181] (1); Heat shock protein 70kD, peptide-binding domain [IPR029047] (1)	-	C_unshiu_01320_mRNA_1.1	-
GF0040661	0	1	0	Hypothetical protein (1)			-	C_unshiu_01319_mRNA_8.1	-
GF0040660	0	1	0	Hypothetical protein (1)			-	C_unshiu_01319_mRNA_6.1	-
GF0040659	0	1	0	Disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_01319_mRNA_1.1	-
GF0040658	0	1	0	Disease resistance family protein / LRR family protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_01318_mRNA_13.1	-
GF0040657	0	1	0	Hypothetical protein (1)			-	C_unshiu_01317_mRNA_3.1	-
GF0040656	0	1	0	Hypothetical protein (1)			-	C_unshiu_01316_mRNA_1.1	-
GF0040655	0	1	0	ABA 8'-hydroxylase (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1)	Cytochrome P450 [IPR001128] (1); Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450, conserved site [IPR017972] (1)	-	C_unshiu_01315_mRNA_5.1	-
GF0040654	0	1	0	Protein CYPRO4 (1)	protein binding [GO:0005515 molecular_function] (1)	Vacuolar import/degradation, Vid27-related [IPR013863] (1); WD40/YVTN repeat-like-containing domain [IPR015943] (1)	-	C_unshiu_01315_mRNA_1.1	-
GF0040653	0	1	0	Hypothetical protein (1)			-	C_unshiu_01314_mRNA_4.1	-
GF0040652	0	1	0	Hypothetical protein (1)			-	C_unshiu_01313_mRNA_9.1	-
GF0040651	0	1	0	Hypothetical protein (1)			-	C_unshiu_01313_mRNA_8.1	-
GF0040650	0	1	0	Hypothetical protein (1)			-	C_unshiu_01313_mRNA_6.1	-
GF0040649	0	1	0	Hypothetical protein (1)			-	C_unshiu_01313_mRNA_4.1	-
GF0040648	0	1	0	Hypothetical protein (1)			-	C_unshiu_01313_mRNA_10.1	-
GF0040647	0	1	0	Hypothetical protein (1)	microtubule motor activity [GO:0003777 molecular_function] (1); microtubule-based movement [GO:0007018 biological_process] (1); protein binding [GO:0005515 molecular_function] (1); microtubule binding [GO:0008017 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Calponin homology domain [IPR001715] (1); Kinesin motor domain [IPR001752] (1); Kinesin motor domain, conserved site [IPR019821] (1); Kinesin-like protein [IPR027640] (1)	-	C_unshiu_01313_mRNA_1.1	-
GF0040646	0	1	0	Hypothetical protein (1)			-	C_unshiu_01311_mRNA_1.1	-
GF0040645	0	1	0	Hypothetical protein (1)	membrane [GO:0016020 cellular_component] (1); acetylglucosaminyltransferase activity [GO:0008375 molecular_function] (1)	Glycosyl transferase, family 14 [IPR003406] (1)	-	C_unshiu_01310_mRNA_8.1	-
GF0040644	0	1	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	-	C_unshiu_01310_mRNA_4.1	-
GF0040643	0	1	0	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	-	C_unshiu_01310_mRNA_3.1	-
GF0040642	0	1	0	Hypothetical protein (1)			-	C_unshiu_01310_mRNA_1.1	-
GF0040641	0	1	0	Hypothetical protein (1)			-	C_unshiu_01309_mRNA_7.1	-
GF0040640	0	1	0	Hypothetical protein (1)	FAD binding [GO:0071949 molecular_function] (1)	FAD-binding domain [IPR002938] (1)	-	C_unshiu_01309_mRNA_3.1	-
GF0040639	0	1	0	Hypothetical protein (1)			-	C_unshiu_01309_mRNA_2.1	-
GF0040638	0	1	0	Hypothetical protein (1)	transmembrane transport [GO:0055085 biological_process] (1); metal ion transmembrane transporter activity [GO:0046873 molecular_function] (1); metal ion transport [GO:0030001 biological_process] (1); membrane [GO:0016020 cellular_component] (1)	Zinc/iron permease [IPR003689] (1)	-	C_unshiu_01309_mRNA_1.1	-
GF0040637	0	1	0	Hypothetical protein (1)			-	C_unshiu_01308_mRNA_7.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0040636	0	1	0	Hypothetical protein (1)	hydrolase activity [GO:0016787 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); HAT, C-terminal dimerisation domain [IPR008906] (1); NUDIX hydrolase domain [IPR000086] (1); NUDIX hydrolase domain-like [IPR015797] (1)	-	C_unshiu_01308_mRNA_5.1	-
GF0040635	0	1	0	Hypothetical protein (1)			-	C_unshiu_01308_mRNA_10.1	-
GF0040634	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); RNA binding [GO:0003723 molecular_function] (1)	K Homology domain [IPR004087] (1); K Homology domain, type 1 [IPR004088] (1)	-	C_unshiu_01308_mRNA_1.1	-
GF0040633	0	1	0	Hypothetical protein (1)			-	C_unshiu_01307_mRNA_5.1	-
GF0040632	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF1336 [IPR009769] (1)	-	C_unshiu_01306_mRNA_9.1	-
GF0040631	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF1336 [IPR009769] (1)	-	C_unshiu_01306_mRNA_5.1	-
GF0040630	0	1	0	Hypothetical protein (1)			-	C_unshiu_01306_mRNA_4.1	-
GF0040629	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF1336 [IPR009769] (1)	-	C_unshiu_01306_mRNA_1.1	-
GF0040628	0	1	0	Hypothetical protein (1)	serine-type peptidase activity [GO:0008236 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Peptidase S28 [IPR008758] (1)	-	C_unshiu_01305_mRNA_5.1	-
GF0040627	0	1	0	Hypothetical protein (1)			-	C_unshiu_01304_mRNA_4.1	-
GF0040626	0	1	0	Hypothetical protein (1)			-	C_unshiu_01304_mRNA_2.1	-
GF0040625	0	1	0	Hypothetical protein (1)			-	C_unshiu_01304_mRNA_1.1	-
GF0040624	0	1	0	AT1G57750 protein (1)	heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1)	Cytochrome P450 [IPR001128] (1); Cytochrome P450, E-class, group I [IPR002401] (1)	-	C_unshiu_01303_mRNA_8.1	-
GF0040623	0	1	0	Hypothetical protein (1)	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1)	Cytochrome P450 [IPR001128] (1)	-	C_unshiu_01303_mRNA_7.1	-
GF0040622	0	1	0	Hypothetical protein (1)			-	C_unshiu_01303_mRNA_5.1	-
GF0040621	0	1	0	Hypothetical protein (1)	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1)	Cytochrome P450 [IPR001128] (1)	-	C_unshiu_01303_mRNA_4.1	-
GF0040620	0	1	0	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1)	Cytochrome P450 [IPR001128] (1); Cytochrome P450, conserved site [IPR017972] (1)	-	C_unshiu_01303_mRNA_3.1	-
GF0040619	0	1	0	Hypothetical protein (1)			-	C_unshiu_01303_mRNA_11.1	-
GF0040618	0	1	0	Hypothetical protein (1)			-	C_unshiu_01303_mRNA_10.1	-
GF0040617	0	1	0	Hypothetical protein (1)			-	C_unshiu_01302_mRNA_7.1	-
GF0040616	0	1	0	Hypothetical protein (1)			-	C_unshiu_01302_mRNA_4.1	-
GF0040615	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_01302_mRNA_11.1	-
GF0040614	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4219 [IPR025314] (1)	-	C_unshiu_01301_mRNA_5.1	-
GF0040613	0	1	0	Hypothetical protein (1)			-	C_unshiu_01301_mRNA_4.1	-
GF0040612	0	1	0	Hypothetical protein (1)			-	C_unshiu_01301_mRNA_3.1	-
GF0040611	0	1	0	Hypothetical protein (1)			-	C_unshiu_01301_mRNA_1.1	-
GF0040610	0	1	0	Hypothetical protein (1)			-	C_unshiu_01300_mRNA_6.1	-
GF0040609	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_01300_mRNA_1.1	-
GF0040608	0	1	0	Hypothetical protein (1)			-	C_unshiu_01299_mRNA_5.1	-
GF0040607	0	1	0	Hypothetical protein (1)			-	C_unshiu_01299_mRNA_13.1	-
GF0040606	0	1	0	Monosacharide transport protein (1)			-	C_unshiu_01299_mRNA_12.1	-
GF0040605	0	1	0	Hypothetical protein (1)			-	C_unshiu_01298_mRNA_9.1	-
GF0040604	0	1	0	RnaseH protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_01298_mRNA_11.1	-
GF0040603	0	1	0	ATP-dependent RNA helicase (1)	nucleic acid binding [GO:0003676 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Helicase superfamily 1/2, ATP-binding domain [IPR014001] (1); RNA helicase, DEAD-box type, Q motif [IPR014014] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); DEAD/DEAH box helicase domain [IPR011545] (1); Helicase, C-terminal [IPR001650] (1)	-	C_unshiu_01298_mRNA_1.1	-
GF0040602	0	1	0	Hypothetical protein (1)			-	C_unshiu_01296_mRNA_7.1	-
GF0040601	0	1	0	Hypothetical protein (1)			-	C_unshiu_01296_mRNA_5.1	-
GF0040600	0	1	0	Hypothetical protein (1)			-	C_unshiu_01296_mRNA_4.1	-
GF0040599	0	1	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_01296_mRNA_1.1	-
GF0040598	0	1	0	Hypothetical protein (1)			-	C_unshiu_01295_mRNA_8.1	-
GF0040597	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_01295_mRNA_7.1	-
GF0040596	0	1	0	Hypothetical protein (1)			-	C_unshiu_01294_mRNA_3.1	-
GF0040595	0	1	0	Hypothetical protein (1)			-	C_unshiu_01293_mRNA_5.1	-
GF0040594	0	1	0	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	C_unshiu_01293_mRNA_4.1	-
GF0040593	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1); Zinc knuckle CX2CX4HX4C [IPR025836] (1)	-	C_unshiu_01293_mRNA_3.1	-
GF0040592	0	1	0	Hypothetical protein (1)		Cupredoxin [IPR008972] (1)	-	C_unshiu_01293_mRNA_10.1	-
GF0040591	0	1	0	Hypothetical protein (1)			-	C_unshiu_01292_mRNA_4.1	-
GF0040590	0	1	0	LRR and NB-ARC domain disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_01292_mRNA_3.1	-
GF0040589	0	1	0	Hypothetical protein (1)			-	C_unshiu_01290_mRNA_4.1	-
GF0040588	0	1	0	Hypothetical protein (1)			-	C_unshiu_01288_mRNA_3.1	-
GF0040587	0	1	0	Hypothetical protein (1)			-	C_unshiu_01287_mRNA_7.1	-
GF0040586	0	1	0	Hypothetical protein (1)			-	C_unshiu_01287_mRNA_5.1	-
GF0040585	0	1	0	Hypothetical protein (1)			-	C_unshiu_01287_mRNA_3.1	-
GF0040584	0	1	0	Hypothetical protein (1)	heme binding [GO:0020037 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1)	Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450, conserved site [IPR017972] (1); F-box domain [IPR001810] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Cytochrome P450 [IPR001128] (1)	-	C_unshiu_01287_mRNA_2.1	-
GF0040583	0	1	0	Hypothetical protein (1)			-	C_unshiu_01286_mRNA_6.1	-
GF0040582	0	1	0	Hypothetical protein (1)			-	C_unshiu_01286_mRNA_3.1	-
GF0040581	0	1	0	Hypothetical protein (1)			-	C_unshiu_01285_mRNA_7.1	-
GF0040580	0	1	0	Hypothetical protein (1)			-	C_unshiu_01284_mRNA_4.1	-
GF0040579	0	1	0	Hypothetical protein (1)			-	C_unshiu_01284_mRNA_3.1	-
GF0040578	0	1	0	Hypothetical protein (1)	protein transport [GO:0015031 biological_process] (1); GTP binding [GO:0005525 molecular_function] (1); small GTPase mediated signal transduction [GO:0007264 biological_process] (1)	Small GTPase superfamily [IPR001806] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Small GTPase superfamily, Rab type [IPR003579] (1)	-	C_unshiu_01284_mRNA_17.1	-
GF0040577	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_01284_mRNA_1.1	-
GF0040576	0	1	0	Hypothetical protein (1)			-	C_unshiu_01283_mRNA_3.1	-
GF0040575	0	1	0	Hypothetical protein (1)	phosphatidylinositol dephosphorylation [GO:0046856 biological_process] (1); protein binding [GO:0005515 molecular_function] (1)	Inositol polyphosphate-related phosphatase [IPR000300] (1); PapD-like [IPR008962] (1); WD40/YVTN repeat-like-containing domain [IPR015943] (1); WD40-repeat-containing domain [IPR017986] (1); Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	C_unshiu_01283_mRNA_10.1	-
GF0040574	0	1	0	Hypothetical protein (1)			-	C_unshiu_01282_mRNA_7.1	-
GF0040573	0	1	0	Hypothetical protein (1)			-	C_unshiu_01282_mRNA_6.1	-
GF0040572	0	1	0	Hypothetical protein (1)	protein ubiquitination [GO:0016567 biological_process] (1); ubiquitin-protein transferase activity [GO:0004842 molecular_function] (1)	E3 ubiquitin ligase RBR family [IPR031127] (1)	-	C_unshiu_01282_mRNA_4.1	-
GF0040571	0	1	0	Hypothetical protein (1)	ubiquitin-protein transferase activity [GO:0004842 molecular_function] (1); protein ubiquitination [GO:0016567 biological_process] (1)	IBR domain [IPR002867] (1); E3 ubiquitin ligase RBR family [IPR031127] (1)	-	C_unshiu_01282_mRNA_3.1	-
GF0040570	0	1	0	Hypothetical protein (1)			-	C_unshiu_01282_mRNA_11.1	-
GF0040569	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_01281_mRNA_5.1	-
GF0040568	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4219 [IPR025314] (1)	-	C_unshiu_01280_mRNA_7.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0040567	0	1	0	Hypothetical protein (1)			-	C_unshiu_01280_mRNA_2.1	-
GF0040566	0	1	0	Hypothetical protein (1)		Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase [IPR029068] (1)	-	C_unshiu_01280_mRNA_1.1	-
GF0040565	0	1	0	Hypothetical protein (1)			-	C_unshiu_01278_mRNA_8.1	-
GF0040564	0	1	0	Hypothetical protein (1)			-	C_unshiu_01278_mRNA_7.1	-
GF0040563	0	1	0	Hypothetical protein (1)			-	C_unshiu_01278_mRNA_6.1	-
GF0040562	0	1	0	Hypothetical protein (1)			-	C_unshiu_01278_mRNA_5.1	-
GF0040561	0	1	0	Hypothetical protein (1)			-	C_unshiu_01278_mRNA_4.1	-
GF0040560	0	1	0	Hypothetical protein (1)			-	C_unshiu_01278_mRNA_2.1	-
GF0040559	0	1	0	Hypothetical protein (1)			-	C_unshiu_01278_mRNA_14.1	-
GF0040558	0	1	0	Hypothetical protein (1)			-	C_unshiu_01278_mRNA_12.1	-
GF0040557	0	1	0	Hypothetical protein (1)			-	C_unshiu_01278_mRNA_11.1	-
GF0040556	0	1	0	Hypothetical protein (1)			-	C_unshiu_01278_mRNA_10.1	-
GF0040555	0	1	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	hAT-like transposase, RNase-H fold [IPR025525] (1)	-	C_unshiu_01277_mRNA_4.1	-
GF0040554	0	1	0	Hypothetical protein (1)			-	C_unshiu_01277_mRNA_3.1	-
GF0040553	0	1	0	Hypothetical protein (1)			-	C_unshiu_01276_mRNA_9.1	-
GF0040552	0	1	0	Hypothetical protein (1)			-	C_unshiu_01276_mRNA_6.1	-
GF0040551	0	1	0	Hypothetical protein (1)			-	C_unshiu_01276_mRNA_5.1	-
GF0040550	0	1	0	Hypothetical protein (1)			-	C_unshiu_01276_mRNA_15.1	-
GF0040549	0	1	0	Hypothetical protein (1)			-	C_unshiu_01275_mRNA_2.1	-
GF0040548	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF1985 [IPR015410] (1)	-	C_unshiu_01274_mRNA_5.1	-
GF0040547	0	1	0	Hypothetical protein (1)			-	C_unshiu_01274_mRNA_3.1	-
GF0040546	0	1	0	Caffeic acid 3-O-methyltransferase (1)	methyltransferase activity [GO:0008168 molecular_function] (1); O-methyltransferase activity [GO:0008171 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	Winged helix-turn-helix DNA-binding domain [IPR011991] (1); O-methyltransferase, family 2 [IPR001077] (1); Plant methyltransferase dimerisation [IPR012967] (1); O-methyltransferase COMT-type [IPR016461] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	C_unshiu_01273_mRNA_4.1	-
GF0040545	0	1	0	Lectin (1)	carbohydrate binding [GO:0030246 molecular_function] (1)	Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Lectin [IPR016363] (1); Legume lectin domain [IPR001220] (1)	-	C_unshiu_01272_mRNA_3.1	-
GF0040544	0	1	0	Hypothetical protein (1)	carbohydrate binding [GO:0030246 molecular_function] (1)	Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Legume lectin domain [IPR001220] (1)	-	C_unshiu_01272_mRNA_2.1	-
GF0040543	0	1	0	Hypothetical protein (1)			-	C_unshiu_01271_mRNA_4.1	-
GF0040542	0	1	0	Hypothetical protein (1)			-	C_unshiu_01271_mRNA_3.1	-
GF0040541	0	1	0	Hypothetical protein (1)			-	C_unshiu_01271_mRNA_1.1	-
GF0040540	0	1	0	Hypothetical protein (1)	transmembrane transport [GO:0055085 biological_process] (1); solute:proton antiporter activity [GO:0015299 molecular_function] (1); cation transport [GO:0006812 biological_process] (1); integral component of membrane [GO:0016021 cellular_component] (1)	Cation/H+ exchanger [IPR006153] (1)	-	C_unshiu_01270_mRNA_6.1	-
GF0040539	0	1	0	Hypothetical protein (1)			-	C_unshiu_01269_mRNA_2.1	-
GF0040538	0	1	0	Leucine-rich repeat protein kinase family protein, putative (1)	ATP binding [GO:0005524 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein binding [GO:0005515 molecular_function] (1)	Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase, ATP binding site [IPR017441] (1); Leucine-rich repeat [IPR001611] (1); Protein kinase domain [IPR000719] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Protein kinase-like domain [IPR011009] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1)	-	C_unshiu_01268_mRNA_6.1	-
GF0040537	0	1	0	Hypothetical protein (1)			-	C_unshiu_01268_mRNA_4.1	-
GF0040536	0	1	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); hAT-like transposase, RNase-H fold [IPR025525] (1)	-	C_unshiu_01268_mRNA_2.1	-
GF0040535	0	1	0	Hypothetical protein (1)			-	C_unshiu_01267_mRNA_7.1	-
GF0040534	0	1	0	Hypothetical protein (1)			-	C_unshiu_01267_mRNA_5.1	-
GF0040533	0	1	0	Hypothetical protein (1)			-	C_unshiu_01266_mRNA_4.1	-
GF0040532	0	1	0	Hypothetical protein (1)			-	C_unshiu_01266_mRNA_2.1	-
GF0040531	0	1	0	Hypothetical protein (1)			-	C_unshiu_01266_mRNA_1.1	-
GF0040530	0	1	0	Disease resistance family protein / LRR family protein, putative (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_01265_mRNA_9.1	-
GF0040529	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1); Leucine-rich repeat [IPR001611] (1); Ribonuclease H-like domain [IPR012337] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine rich repeat 4 [IPR025875] (1)	-	C_unshiu_01265_mRNA_3.1	-
GF0040528	0	1	0	Hypothetical protein (1)			-	C_unshiu_01265_mRNA_14.1	-
GF0040527	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1)	-	C_unshiu_01265_mRNA_10.1	-
GF0040526	0	1	0	Hypothetical protein (1)			-	C_unshiu_01264_mRNA_9.1	-
GF0040525	0	1	0	Hypothetical protein (1)			-	C_unshiu_01264_mRNA_8.1	-
GF0040524	0	1	0	Hypothetical protein (1)			-	C_unshiu_01264_mRNA_7.1	-
GF0040523	0	1	0	Hypothetical protein (1)			-	C_unshiu_01264_mRNA_10.1	-
GF0040522	0	1	0	Hypothetical protein (1)			-	C_unshiu_01263_mRNA_7.1	-
GF0040521	0	1	0	Hypothetical protein (1)	GTPase activity [GO:0003924 molecular_function] (1); cytoplasm [GO:0005737 cellular_component] (1); integral component of membrane [GO:0016021 cellular_component] (1); GTP binding [GO:0005525 molecular_function] (1)	Tubulin/FtsZ, GTPase domain [IPR003008] (1); Cell division protein FtsZ, conserved site [IPR020805] (1); Nonaspanin (TM9SF) [IPR004240] (1)	-	C_unshiu_01263_mRNA_4.1	-
GF0040520	0	1	0	Hypothetical protein (1)			-	C_unshiu_01263_mRNA_1.1	-
GF0040519	0	1	0	Pentatricopeptide (PPR) repeat protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	C_unshiu_01262_mRNA_9.1	-
GF0040518	0	1	0	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	C_unshiu_01262_mRNA_7.1	-
GF0040517	0	1	0	Pentatricopeptide (PPR) repeat protein (1)	protein binding [GO:0005515 molecular_function] (1)	Pentatricopeptide repeat [IPR002885] (1); Tetratricopeptide-like helical domain [IPR011990] (1)	-	C_unshiu_01262_mRNA_6.1	-
GF0040516	0	1	0	Hypothetical protein (1)			-	C_unshiu_01262_mRNA_3.1	-
GF0040515	0	1	0	Tetratricopeptide repeat (TPR)-like superfamily protein, putative (1)		Pentatricopeptide repeat [IPR002885] (1)	-	C_unshiu_01262_mRNA_2.1	-
GF0040514	0	1	0	Hypothetical protein (1)			-	C_unshiu_01261_mRNA_1.1	-
GF0040513	0	1	0	Hypothetical protein (1)			-	C_unshiu_01260_mRNA_7.1	-
GF0040512	0	1	0	Hypothetical protein (1)			-	C_unshiu_01260_mRNA_5.1	-
GF0040511	0	1	0	Hypothetical protein (1)			-	C_unshiu_01260_mRNA_3.1	-
GF0040510	0	1	0	Hypothetical protein (1)	BLOC-1 complex [GO:0031083 cellular_component] (1); intracellular protein transport [GO:0006886 biological_process] (1)	Snapin [IPR017246] (1); Snapin/Pallidin/Snn1 [IPR028119] (1)	-	C_unshiu_01259_mRNA_8.1	-
GF0040509	0	1	0	Hypothetical protein (1)			-	C_unshiu_01259_mRNA_7.1	-
GF0040508	0	1	0	Hypothetical protein (1)			-	C_unshiu_01259_mRNA_6.1	-
GF0040507	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_01259_mRNA_3.1	-
GF0040506	0	1	0	Hypothetical protein (1)			-	C_unshiu_01259_mRNA_12.1	-
GF0040505	0	1	0	Flavanone 3-dioxygenase (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1)	Oxoglutarate/iron-dependent dioxygenase [IPR005123] (1); Isopenicillin N synthase-like [IPR027443] (1)	-	C_unshiu_01259_mRNA_1.1	-
GF0040504	0	1	0	Hypothetical protein (1)			-	C_unshiu_01258_mRNA_7.1	-
GF0040503	0	1	0	Hypothetical protein (1)		Gag-polypeptide of LTR copia-type [IPR029472] (1)	-	C_unshiu_01258_mRNA_3.1	-
GF0040502	0	1	0	Hypothetical protein (1)			-	C_unshiu_01258_mRNA_13.1	-
GF0040501	0	1	0	Hypothetical protein (1)		Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01258_mRNA_11.1	-
GF0040500	0	1	0	Hypothetical protein (1)			-	C_unshiu_01258_mRNA_10.1	-
GF0040499	0	1	0	Hypothetical protein (1)			-	C_unshiu_01257_mRNA_9.1	-
GF0040498	0	1	0	Thiazole biosynthetic enzyme (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Thiazole biosynthetic enzyme Thi4 family [IPR002922] (1); FAD/NAD(P)-binding domain [IPR023753] (1)	-	C_unshiu_01257_mRNA_1.1	-
GF0040497	0	1	0	Hypothetical protein (1)			-	C_unshiu_01256_mRNA_7.1	-
GF0040496	0	1	0	Hypothetical protein (1)			-	C_unshiu_01256_mRNA_6.1	-
GF0040495	0	1	0	Hypothetical protein (1)			-	C_unshiu_01256_mRNA_5.1	-
GF0040494	0	1	0	Hypothetical protein (1)			-	C_unshiu_01256_mRNA_4.1	-
GF0040493	0	1	0	Cysteine-rich RLK (Receptor-like kinase) protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein serine/threonine kinase activity [GO:0004674 molecular_function] (1)	Bulb-type lectin domain [IPR001480] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); S-locus receptor kinase, C-terminal [IPR021820] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	-	C_unshiu_01256_mRNA_2.1	-
GF0040492	0	1	0	Hypothetical protein (1)			-	C_unshiu_01255_mRNA_5.1	-
GF0040491	0	1	0	Hypothetical protein (1)			-	C_unshiu_01255_mRNA_4.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0040490	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); biosynthetic process [GO:0009058 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1); pyridoxal phosphate binding [GO:0030170 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Pyridoxal phosphate-dependent transferase [IPR015424] (1); Zinc finger, CCHC-type [IPR001878] (1); Pyridoxal phosphate-dependent transferase, major region, subdomain 1 [IPR015421] (1); Zinc finger, SWIM-type [IPR007527] (1); Zinc finger, PMZ-type [IPR006564] (1); Aminotransferase, class I/classII [IPR004839] (1)	-	C_unshiu_01254_mRNA_6.1	-
GF0040489	0	1	0	22.0 kDa class IV heat shock protein (1)		Small heat shock protein HSP20 [IPR031107] (1); Alpha crystallin/Hsp20 domain [IPR002068] (1); HSP20-like chaperone [IPR008978] (1)	-	C_unshiu_01254_mRNA_4.1	-
GF0040488	0	1	0	Hypothetical protein (1)			-	C_unshiu_01254_mRNA_1.1	-
GF0040487	0	1	0	Hypothetical protein (1)			-	C_unshiu_01253_mRNA_5.1	-
GF0040486	0	1	0	Hypothetical protein (1)			-	C_unshiu_01253_mRNA_4.1	-
GF0040485	0	1	0	Hypothetical protein (1)			-	C_unshiu_01251_mRNA_9.1	-
GF0040484	0	1	0	Hypothetical protein (1)			-	C_unshiu_01251_mRNA_6.1	-
GF0040483	0	1	0	Hypothetical protein (1)			-	C_unshiu_01251_mRNA_3.1	-
GF0040482	0	1	0	Hypothetical protein (1)			-	C_unshiu_01251_mRNA_2.1	-
GF0040481	0	1	0	Hypothetical protein (1)			-	C_unshiu_01251_mRNA_10.1	-
GF0040480	0	1	0	Hypothetical protein (1)			-	C_unshiu_01251_mRNA_1.1	-
GF0040479	0	1	0	Hypothetical protein (1)			-	C_unshiu_01250_mRNA_9.1	-
GF0040478	0	1	0	Hypothetical protein (1)			-	C_unshiu_01250_mRNA_6.1	-
GF0040477	0	1	0	Hypothetical protein (1)			-	C_unshiu_01250_mRNA_11.1	-
GF0040476	0	1	0	U4/U6 small nuclear PRP4-like protein (1)	RNA splicing [GO:0008380 biological_process] (1)	Splicing factor motif [IPR003648] (1); Pre-mRNA processing factor 4 (PRP4)-like [IPR014906] (1); U4/U6 small nuclear ribonucleoprotein Prp4 [IPR027106] (1)	-	C_unshiu_01249_mRNA_8.1	-
GF0040475	0	1	0	Hypothetical protein (1)			-	C_unshiu_01249_mRNA_3.1	-
GF0040474	0	1	0	Hypothetical protein (1)			-	C_unshiu_01249_mRNA_1.1	-
GF0040473	0	1	0	ER-derived vesicles protein ERV14 (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); core TFIIH complex [GO:0000439 cellular_component] (1); membrane [GO:0016020 cellular_component] (1); intracellular signal transduction [GO:0035556 biological_process] (1); nucleotide-excision repair [GO:0006289 biological_process] (1)	Cornichon [IPR003377] (1); TFIIH subunit TTDA/Tfb5 [IPR009400] (1)	-	C_unshiu_01248_mRNA_4.1	-
GF0040472	0	1	0	Hypothetical protein (1)			-	C_unshiu_01247_mRNA_4.1	-
GF0040471	0	1	0	Hypothetical protein (1)			-	C_unshiu_01247_mRNA_12.1	-
GF0040470	0	1	0	U4/U6 small nuclear ribonucleoprotein PRP4-like protein (1)	protein binding [GO:0005515 molecular_function] (1)	U4/U6 small nuclear ribonucleoprotein Prp4 [IPR027106] (1); G-protein beta WD-40 repeat [IPR020472] (1); WD40/YVTN repeat-like-containing domain [IPR015943] (1); WD40 repeat, conserved site [IPR019775] (1); WD40 repeat [IPR001680] (1); WD40-repeat-containing domain [IPR017986] (1)	-	C_unshiu_01247_mRNA_1.1	-
GF0040469	0	1	0	Hypothetical protein (1)			-	C_unshiu_01246_mRNA_3.1	-
GF0040468	0	1	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1)	Peptidase A2A, retrovirus, catalytic [IPR001995] (1)	-	C_unshiu_01245_mRNA_8.1	-
GF0040467	0	1	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_01245_mRNA_7.1	-
GF0040466	0	1	0	Hypothetical protein (1)			-	C_unshiu_01245_mRNA_5.1	-
GF0040465	0	1	0	Hypothetical protein (1)			-	C_unshiu_01245_mRNA_3.1	-
GF0040464	0	1	0	Hypothetical protein (1)			-	C_unshiu_01245_mRNA_14.1	-
GF0040463	0	1	0	Hypothetical protein (1)			-	C_unshiu_01245_mRNA_13.1	-
GF0040462	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_01245_mRNA_12.1	-
GF0040461	0	1	0	Hypothetical protein (1)			-	C_unshiu_01245_mRNA_1.1	-
GF0040460	0	1	0	Hypothetical protein (1)			-	C_unshiu_01244_mRNA_2.1	-
GF0040459	0	1	0	Ankyrin repeat protein (1)		PGG domain [IPR026961] (1)	-	C_unshiu_01242_mRNA_11.1	-
GF0040458	0	1	0	Hypothetical protein (1)			-	C_unshiu_01241_mRNA_3.1	-
GF0040457	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, RING/FYVE/PHD-type [IPR013083] (1); Zinc finger, RING-type [IPR001841] (1); Zinc finger, RING-type, conserved site [IPR017907] (1)	-	C_unshiu_01241_mRNA_2.1	-
GF0040456	0	1	0	SPX domain gene 1, putative (1)	cellular response to phosphate starvation [GO:0016036 biological_process] (1)	SPX domain-containing protein [IPR031142] (1); SPX domain [IPR004331] (1)	-	C_unshiu_01240_mRNA_9.1	-
GF0040455	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_01240_mRNA_5.1	-
GF0040454	0	1	0	Hypothetical protein (1)			-	C_unshiu_01240_mRNA_3.1	-
GF0040453	0	1	0	Hypothetical protein (1)			-	C_unshiu_01240_mRNA_1.1	-
GF0040452	0	1	0	Hypothetical protein (1)			-	C_unshiu_01238_mRNA_3.1	-
GF0040451	0	1	0	Hypothetical protein (1)			-	C_unshiu_01237_mRNA_4.1	-
GF0040450	0	1	0	Hypothetical protein (1)			-	C_unshiu_01237_mRNA_11.1	-
GF0040449	0	1	0	Hypothetical protein (1)			-	C_unshiu_01236_mRNA_6.1	-
GF0040448	0	1	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	NB-ARC [IPR002182] (1); Leucine-rich repeat [IPR001611] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01236_mRNA_4.1	-
GF0040447	0	1	0	Hypothetical protein (1)	phosphoric ester hydrolase activity [GO:0042578 molecular_function] (1)	SAC domain [IPR002013] (1)	-	C_unshiu_01236_mRNA_3.1	-
GF0040446	0	1	0	Hypothetical protein (1)			-	C_unshiu_01236_mRNA_1.1	-
GF0040445	0	1	0	Hypothetical protein (1)			-	C_unshiu_01235_mRNA_1.1	-
GF0040444	0	1	0	Hypothetical protein (1)			-	C_unshiu_01234_mRNA_4.1	-
GF0040443	0	1	0	Hypothetical protein (1)			-	C_unshiu_01234_mRNA_3.1	-
GF0040442	0	1	0	Hypothetical protein (1)			-	C_unshiu_01234_mRNA_2.1	-
GF0040441	0	1	0	Hypothetical protein (1)			-	C_unshiu_01233_mRNA_7.1	-
GF0040440	0	1	0	Hypothetical protein (1)	signal transduction [GO:0007165 biological_process] (1); protein binding [GO:0005515 molecular_function] (1)	Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1)	-	C_unshiu_01233_mRNA_6.1	-
GF0040439	0	1	0	Hypothetical protein (1)			-	C_unshiu_01233_mRNA_5.1	-
GF0040438	0	1	0	Putative WRKY transcription factor 19-like protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01233_mRNA_1.1	-
GF0040437	0	1	0	Hypothetical protein (1)			-	C_unshiu_01231_mRNA_8.1	-
GF0040436	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_01231_mRNA_7.1	-
GF0040435	0	1	0	Hypothetical protein (1)			-	C_unshiu_01231_mRNA_6.1	-
GF0040434	0	1	0	Hypothetical protein (1)	iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1)	Cytochrome P450 [IPR001128] (1)	-	C_unshiu_01231_mRNA_5.1	-
GF0040433	0	1	0	Cytochrome P450 (1)	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1)	Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450, conserved site [IPR017972] (1); Cytochrome P450 [IPR001128] (1)	-	C_unshiu_01231_mRNA_3.1	-
GF0040432	0	1	0	Hypothetical protein (1)			-	C_unshiu_01231_mRNA_13.1	-
GF0040431	0	1	0	Hypothetical protein (1)			-	C_unshiu_01231_mRNA_10.1	-
GF0040430	0	1	0	Hypothetical protein (1)			-	C_unshiu_01230_mRNA_7.1	-
GF0040429	0	1	0	Hypothetical protein (1)			-	C_unshiu_01230_mRNA_6.1	-
GF0040428	0	1	0	Two-component response regulator ARR22 (1)	phosphorelay signal transduction system [GO:0000160 biological_process] (1)	Signal transduction response regulator, receiver domain [IPR001789] (1); CheY-like superfamily [IPR011006] (1)	-	C_unshiu_01228_mRNA_2.1	-
GF0040427	0	1	0	Glutathione S-transferase tau 7, putative (1)		Glutathione S-transferase, C-terminal-like [IPR010987] (1); Glutathione S-transferase, C-terminal [IPR004046] (1)	-	C_unshiu_01228_mRNA_11.1	-
GF0040426	0	1	0	Phytochrome interacting factor 1 (1)			-	C_unshiu_01228_mRNA_1.1	-
GF0040425	0	1	0	Microtubule associated protein, MAP65/ASE1 family protein (1)	cytokinesis [GO:0000910 biological_process] (1); microtubule binding [GO:0008017 molecular_function] (1); microtubule cytoskeleton organization [GO:0000226 biological_process] (1)	Microtubule-associated protein, MAP65/Ase1/PRC1 [IPR007145] (1)	-	C_unshiu_01227_mRNA_9.1	-
GF0040424	0	1	0	Tetratricopeptide repeat (TPR)-like superfamily protein, putative isoform 3 (1)	nucleus [GO:0005634 cellular_component] (1); cell cycle [GO:0007049 biological_process] (1); protein binding [GO:0005515 molecular_function] (1)	Pentatricopeptide repeat [IPR002885] (1); Tetratricopeptide-like helical domain [IPR011990] (1); Cdk-activating kinase assembly factor MAT1/Tfb3 [IPR004575] (1)	-	C_unshiu_01226_mRNA_6.1	-
GF0040423	0	1	0	DNA-directed RNA polymerase (1)	transcription, DNA-templated [GO:0006351 biological_process] (1); DNA-directed RNA polymerase activity [GO:0003899 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	DNA-directed RNA polymerase, helix hairpin domain [IPR024075] (1); DNA-directed RNA polymerase, phage-type [IPR002092] (1)	-	C_unshiu_01226_mRNA_4.1	-
GF0040422	0	1	0	Hypothetical protein (1)	integral component of membrane [GO:0016021 cellular_component] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Nonaspanin (TM9SF) [IPR004240] (1); DYW domain [IPR032867] (1)	-	C_unshiu_01226_mRNA_3.1	-
GF0040421	0	1	0	Hypothetical protein (1)		LysM domain [IPR018392] (1)	-	C_unshiu_01225_mRNA_1.1	-
GF0040420	0	1	0	Integrase (1)		GAG-pre-integrase domain [IPR025724] (1)	-	C_unshiu_01224_mRNA_6.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0040419	0	1	0	Hypothetical protein (1)		Sucrose-phosphate synthase [IPR006380] (1); HAD-like domain [IPR023214] (1)	-	C_unshiu_01224_mRNA_3.1	-
GF0040418	0	1	0	Hypothetical protein (1)			-	C_unshiu_01223_mRNA_5.1	-
GF0040417	0	1	0	Hypothetical protein (1)			-	C_unshiu_01223_mRNA_2.1	-
GF0040416	0	1	0	Hypothetical protein (1)			-	C_unshiu_01222_mRNA_8.1	-
GF0040415	0	1	0	Hypothetical protein (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Short-chain dehydrogenase/reductase SDR [IPR002198] (1); Glucose/ribitol dehydrogenase [IPR002347] (1); NAD(P)-binding domain [IPR016040] (1)	-	C_unshiu_01221_mRNA_8.1	-
GF0040414	0	1	0	Hypothetical protein (1)			-	C_unshiu_01221_mRNA_1.1	-
GF0040413	0	1	0	Hypothetical protein (1)			-	C_unshiu_01220_mRNA_2.1	-
GF0040412	0	1	0	Hypothetical protein (1)			-	C_unshiu_01219_mRNA_5.1	-
GF0040411	0	1	0	Hypothetical protein (1)			-	C_unshiu_01219_mRNA_4.1	-
GF0040410	0	1	0	Hypothetical protein (1)			-	C_unshiu_01219_mRNA_2.1	-
GF0040409	0	1	0	Hypothetical protein (1)			-	C_unshiu_01219_mRNA_11.1	-
GF0040408	0	1	0	Hypothetical protein (1)			-	C_unshiu_01218_mRNA_9.1	-
GF0040407	0	1	0	Hypothetical protein (1)		Plant organelle RNA recognition domain [IPR021099] (1)	-	C_unshiu_01218_mRNA_7.1	-
GF0040406	0	1	0	ATP-dependent zinc metalloprotease FTSH 2, chloroplastic (1)	heme binding [GO:0020037 molecular_function] (1); response to oxidative stress [GO:0006979 biological_process] (1); metalloendopeptidase activity [GO:0004222 molecular_function] (1); peroxidase activity [GO:0004601 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1); oxidation-reduction process [GO:0055114 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1)	ATPase, AAA-type, conserved site [IPR003960] (1); Haem peroxidase [IPR010255] (1); Peptidase M41 [IPR000642] (1); AAA+ ATPase domain [IPR003593] (1); Plant peroxidase [IPR000823] (1); Haem peroxidase, plant/fungal/bacterial [IPR002016] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); ATPase, AAA-type, core [IPR003959] (1)	-	C_unshiu_01218_mRNA_4.1	-
GF0040405	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_01218_mRNA_12.1	-
GF0040404	0	1	0	Hypothetical protein (1)			-	C_unshiu_01218_mRNA_1.1	-
GF0040403	0	1	0	Hypothetical protein (1)			-	C_unshiu_01217_mRNA_9.1	-
GF0040402	0	1	0	Hypothetical protein (1)			-	C_unshiu_01217_mRNA_4.1	-
GF0040401	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_01217_mRNA_2.1	-
GF0040400	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	C_unshiu_01216_mRNA_8.1	-
GF0040399	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_01216_mRNA_6.1	-
GF0040398	0	1	0	Hypothetical protein (1)			-	C_unshiu_01216_mRNA_2.1	-
GF0040397	0	1	0	Hypothetical protein (1)			-	C_unshiu_01216_mRNA_11.1	-
GF0040396	0	1	0	Hypothetical protein (1)			-	C_unshiu_01216_mRNA_10.1	-
GF0040395	0	1	0	Hypothetical protein (1)			-	C_unshiu_01215_mRNA_9.1	-
GF0040394	0	1	0	Hypothetical protein (1)			-	C_unshiu_01215_mRNA_5.1	-
GF0040393	0	1	0	Hypothetical protein (1)			-	C_unshiu_01215_mRNA_4.1	-
GF0040392	0	1	0	Hypothetical protein (1)			-	C_unshiu_01215_mRNA_3.1	-
GF0040391	0	1	0	Hypothetical protein (1)			-	C_unshiu_01215_mRNA_2.1	-
GF0040390	0	1	0	Hypothetical protein (1)			-	C_unshiu_01215_mRNA_10.1	-
GF0040389	0	1	0	Hypothetical protein (1)		Chloramphenicol acetyltransferase-like domain [IPR023213] (1)	-	C_unshiu_01214_mRNA_6.1	-
GF0040388	0	1	0	Hypothetical protein (1)	cysteine biosynthetic process from serine [GO:0006535 biological_process] (1); serine O-acetyltransferase activity [GO:0009001 molecular_function] (1); cytoplasm [GO:0005737 cellular_component] (1)	Serine acetyltransferase, N-terminal [IPR010493] (1)	-	C_unshiu_01214_mRNA_5.1	-
GF0040387	0	1	0	Hypothetical protein (1)			-	C_unshiu_01214_mRNA_4.1	-
GF0040386	0	1	0	Hypothetical protein (1)			-	C_unshiu_01214_mRNA_1.1	-
GF0040385	0	1	0	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family, putative isoform 1 (1)			-	C_unshiu_01213_mRNA_8.1	-
GF0040384	0	1	0	Hypothetical protein (1)			-	C_unshiu_01213_mRNA_4.1	-
GF0040383	0	1	0	Hypothetical protein (1)			-	C_unshiu_01213_mRNA_3.1	-
GF0040382	0	1	0	Hypothetical protein (1)			-	C_unshiu_01212_mRNA_8.1	-
GF0040381	0	1	0	Hypothetical protein (1)			-	C_unshiu_01212_mRNA_13.1	-
GF0040380	0	1	0	Peroxisomal membrane carrier protein (1)		Mitochondrial substrate/solute carrier [IPR018108] (1); Mitochondrial carrier domain [IPR023395] (1)	-	C_unshiu_01212_mRNA_10.1	-
GF0040379	0	1	0	Hypothetical protein (1)			-	C_unshiu_01212_mRNA_1.1	-
GF0040378	0	1	0	Hypothetical protein (1)	binding [GO:0005488 molecular_function] (1)	Mo25-like [IPR013878] (1); Armadillo-like helical [IPR011989] (1); Armadillo-type fold [IPR016024] (1)	-	C_unshiu_01211_mRNA_7.1	-
GF0040377	0	1	0	Hypothetical protein (1)	diacylglycerol O-acyltransferase activity [GO:0004144 molecular_function] (1)	O-acyltransferase WSD1, C-terminal [IPR009721] (1)	-	C_unshiu_01211_mRNA_6.1	-
GF0040376	0	1	0	Hypothetical protein (1)	structural constituent of ribosome [GO:0003735 molecular_function] (1); intracellular [GO:0005622 cellular_component] (1); translation [GO:0006412 biological_process] (1); ribosome [GO:0005840 cellular_component] (1)	Ribosomal protein L14 [IPR002784] (1)	-	C_unshiu_01210_mRNA_7.1	-
GF0040375	0	1	0	Hypothetical protein (1)		Translation protein SH3-like domain [IPR008991] (1); Ribosomal protein L2 domain 2 [IPR014722] (1)	-	C_unshiu_01210_mRNA_6.1	-
GF0040374	0	1	0	Hypothetical protein (1)			-	C_unshiu_01210_mRNA_5.1	-
GF0040373	0	1	0	Hypothetical protein (1)			-	C_unshiu_01209_mRNA_7.1	-
GF0040372	0	1	0	Cytochrome P450 family protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1)	Cytochrome P450 [IPR001128] (1); Cytochrome P450, E-class, group I [IPR002401] (1)	-	C_unshiu_01209_mRNA_6.1	-
GF0040371	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	-	C_unshiu_01209_mRNA_10.1	-
GF0040370	0	1	0	Hypothetical protein (1)			-	C_unshiu_01208_mRNA_7.1	-
GF0040369	0	1	0	Lectin (1)	carbohydrate binding [GO:0030246 molecular_function] (1)	Legume lectin domain [IPR001220] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Lectin [IPR016363] (1); Legume lectin, alpha chain, conserved site [IPR000985] (1)	-	C_unshiu_01208_mRNA_2.1	-
GF0040368	0	1	0	Hypothetical protein (1)	small GTPase mediated signal transduction [GO:0007264 biological_process] (1); GTP binding [GO:0005525 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Small GTPase superfamily [IPR001806] (1)	-	C_unshiu_01207_mRNA_6.1	-
GF0040367	0	1	0	Hypothetical protein (1)	small GTPase mediated signal transduction [GO:0007264 biological_process] (1); GTP binding [GO:0005525 molecular_function] (1)	Small GTPase superfamily [IPR001806] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_01207_mRNA_4.1	-
GF0040366	0	1	0	Hypothetical protein (1)			-	C_unshiu_01206_mRNA_3.1	-
GF0040365	0	1	0	Hypothetical protein (1)	methyltransferase activity [GO:0008168 molecular_function] (1)	S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); SAM dependent carboxyl methyltransferase [IPR005299] (1)	-	C_unshiu_01205_mRNA_5.1	-
GF0040364	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01205_mRNA_1.1	-
GF0040363	0	1	0	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	C_unshiu_01204_mRNA_2.1	-
GF0040362	0	1	0	Hypothetical protein (1)	DNA-directed RNA polymerase activity [GO:0003899 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1); polysaccharide binding [GO:0030247 molecular_function] (1); transcription, DNA-templated [GO:0006351 biological_process] (1)	RNA polymerase Rpb1, domain 5 [IPR007081] (1); Protein kinase-like domain [IPR011009] (1); Wall-associated receptor kinase, galacturonan-binding domain [IPR025287] (1)	-	C_unshiu_01203_mRNA_9.1	-
GF0040361	0	1	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	hAT-like transposase, RNase-H fold [IPR025525] (1)	-	C_unshiu_01203_mRNA_8.1	-
GF0040360	0	1	0	Hypothetical protein (1)			-	C_unshiu_01203_mRNA_7.1	-
GF0040359	0	1	0	LRR receptor-like kinase family protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01203_mRNA_5.1	-
GF0040358	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); DNA integration [GO:0015074 biological_process] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Ribonuclease H-like domain [IPR012337] (1); Integrase, catalytic core [IPR001584] (1)	-	C_unshiu_01203_mRNA_2.1	-
GF0040357	0	1	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1); Probable transposase, Ptta/En/Spm, plant [IPR004252] (1)	-	C_unshiu_01201_mRNA_3.1	-
GF0040356	0	1	0	Hypothetical protein (1)	pectinesterase activity [GO:0030599 molecular_function] (1); cell wall modification [GO:0042545 biological_process] (1); cell wall [GO:0005618 cellular_component] (1)	Pectinesterase, catalytic [IPR000070] (1); Pectin lyase fold [IPR012334] (1)	-	C_unshiu_01201_mRNA_1.1	-
GF0040355	0	1	0	Hypothetical protein (1)		Myotubularin family [IPR030564] (1); Myotubularin-like phosphatase domain [IPR010569] (1); Protein-tyrosine phosphatase-like [IPR029021] (1)	-	C_unshiu_01199_mRNA_5.1	-
GF0040354	0	1	0	Hypothetical protein (1)			-	C_unshiu_01199_mRNA_4.1	-
GF0040353	0	1	0	Hypothetical protein (1)			-	C_unshiu_01199_mRNA_2.1	-
GF0040352	0	1	0	Hypothetical protein (1)			-	C_unshiu_01199_mRNA_12.1	-
GF0040351	0	1	0	Hypothetical protein (1)			-	C_unshiu_01198_mRNA_9.1	-
GF0040350	0	1	0	Hypothetical protein (1)			-	C_unshiu_01198_mRNA_6.1	-
GF0040349	0	1	0	Hypothetical protein (1)			-	C_unshiu_01198_mRNA_4.1	-
GF0040348	0	1	0	Hypothetical protein (1)			-	C_unshiu_01198_mRNA_3.1	-
GF0040347	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	TRAF-like [IPR008974] (1); MATH/TRAF domain [IPR002083] (1)	-	C_unshiu_01197_mRNA_9.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0040346	0	1	0	Ubiquitin carboxyl-terminal hydrolase 12 (1)	protein binding [GO:0005515 molecular_function] (1)	MATH/TRAF domain [IPR002083] (1); TRAF-like [IPR008974] (1)	-	C_unshiu_01197_mRNA_8.1	-
GF0040345	0	1	0	Hypothetical protein (1)			-	C_unshiu_01197_mRNA_6.1	-
GF0040344	0	1	0	Ubiquitin carboxyl-terminal hydrolase 13 (1)	protein binding [GO:0005515 molecular_function] (1)	MATH/TRAF domain [IPR002083] (1); TRAF-like [IPR008974] (1)	-	C_unshiu_01197_mRNA_10.1	-
GF0040343	0	1	0	Hypothetical protein (1)			-	C_unshiu_01196_mRNA_14.1	-
GF0040342	0	1	0	Hypothetical protein (1)			-	C_unshiu_01196_mRNA_12.1	-
GF0040341	0	1	0	Hypothetical protein (1)			-	C_unshiu_01195_mRNA_9.1	-
GF0040340	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, U1-type [IPR003604] (1)	-	C_unshiu_01195_mRNA_2.1	-
GF0040339	0	1	0	Translation initiation factor IF-3 (1)	translation initiation factor activity [GO:0003743 molecular_function] (1); translational initiation [GO:0006413 biological_process] (1)	Translation initiation factor 3 [IPR001288] (1); Translation initiation factor 3, C-terminal [IPR019815] (1)	-	C_unshiu_01195_mRNA_14.1	-
GF0040338	0	1	0	Translation initiation factor IF-3 (1)	translation initiation factor activity [GO:0003743 molecular_function] (1); translational initiation [GO:0006413 biological_process] (1)	Translation initiation factor 3 [IPR001288] (1); Translation initiation factor 3, N-terminal [IPR019814] (1)	-	C_unshiu_01195_mRNA_13.1	-
GF0040337	0	1	0	Hypothetical protein (1)			-	C_unshiu_01195_mRNA_12.1	-
GF0040336	0	1	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	-	C_unshiu_01194_mRNA_9.1	-
GF0040335	0	1	0	Hypothetical protein (1)			-	C_unshiu_01194_mRNA_6.1	-
GF0040334	0	1	0	Retrotransposon protein, putative, Ty1-copia subclass (1)			-	C_unshiu_01194_mRNA_5.1	-
GF0040333	0	1	0	Hypothetical protein (1)			-	C_unshiu_01194_mRNA_3.1	-
GF0040332	0	1	0	Hypothetical protein (1)			-	C_unshiu_01194_mRNA_1.1	-
GF0040331	0	1	0	Hypothetical protein (1)			-	C_unshiu_01193_mRNA_5.1	-
GF0040330	0	1	0	Naringenin-chalcone synthase (1)	metabolic process [GO:0008152 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1); biosynthetic process [GO:0009058 biological_process] (1); transferase activity, transferring acyl groups [GO:0016746 molecular_function] (1)	Chalcone/stilbene synthase, N-terminal [IPR001099] (1); Chalcone/stilbene synthase, C-terminal [IPR012328] (1); Thiolase-like [IPR016039] (1); Chalcone/stilbene synthase, active site [IPR018088] (1)	-	C_unshiu_01193_mRNA_1.1	-
GF0040329	0	1	0	Hypothetical protein (1)			-	C_unshiu_01192_mRNA_5.1	-
GF0040328	0	1	0	Hypothetical protein (1)			-	C_unshiu_01191_mRNA_9.1	-
GF0040327	0	1	0	Lysosomal beta glucosidase (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1); hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (1)	Glycoside hydrolase, family 3, N-terminal [IPR001764] (1); Glycoside hydrolase family 3 C-terminal domain [IPR002772] (1); Glycoside hydrolase family 3 [IPR026892] (1); Glycoside hydrolase superfamily [IPR017853] (1)	-	C_unshiu_01191_mRNA_10.1	-
GF0040326	0	1	0	Hypothetical protein (1)			-	C_unshiu_01189_mRNA_9.1	-
GF0040325	0	1	0	Hypothetical protein (1)			-	C_unshiu_01189_mRNA_8.1	-
GF0040324	0	1	0	Hypothetical protein (1)			-	C_unshiu_01189_mRNA_11.1	-
GF0040323	0	1	0	Hypothetical protein (1)			-	C_unshiu_01189_mRNA_10.1	-
GF0040322	0	1	0	Hypothetical protein (1)			-	C_unshiu_01188_mRNA_7.1	-
GF0040321	0	1	0	Hypothetical protein (1)			-	C_unshiu_01187_mRNA_8.1	-
GF0040320	0	1	0	TPR and ankyrin repeat-containing 1 (1)	hydrolase activity [GO:0016787 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	UvrD-like DNA helicase, C-terminal [IPR014017] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_01187_mRNA_7.1	-
GF0040319	0	1	0	Hypothetical protein (1)			-	C_unshiu_01187_mRNA_6.1	-
GF0040318	0	1	0	Hypothetical protein (1)			-	C_unshiu_01187_mRNA_5.1	-
GF0040317	0	1	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	-	C_unshiu_01187_mRNA_4.1	-
GF0040316	0	1	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); UvrD-like Helicase, ATP-binding domain [IPR014016] (1)	-	C_unshiu_01187_mRNA_2.1	-
GF0040315	0	1	0	Hypothetical protein (1)			-	C_unshiu_01186_mRNA_9.1	-
GF0040314	0	1	0	Transposon-like element Lyt2.0 DNA (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); FHY3/FAR1 family [IPR031052] (1); Zinc finger, SWIM-type [IPR007527] (1); Zinc finger, PMZ-type [IPR006564] (1)	-	C_unshiu_01186_mRNA_2.1	-
GF0040313	0	1	0	Hypothetical protein (1)			-	C_unshiu_01185_mRNA_8.1	-
GF0040312	0	1	0	Verticillium wilt resistance-like protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_01185_mRNA_4.1	-
GF0040311	0	1	0	Hypothetical protein (1)			-	C_unshiu_01185_mRNA_3.1	-
GF0040310	0	1	0	Hypothetical protein (1)			-	C_unshiu_01184_mRNA_6.1	-
GF0040309	0	1	0	Hypothetical protein (1)			-	C_unshiu_01183_mRNA_9.1	-
GF0040308	0	1	0	Hypothetical protein (1)			-	C_unshiu_01183_mRNA_6.1	-
GF0040307	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_01182_mRNA_8.1	-
GF0040306	0	1	0	Hypothetical protein (1)			-	C_unshiu_01182_mRNA_5.1	-
GF0040305	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Peptidase A2A, retrovirus, catalytic [IPR001995] (1); Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_01182_mRNA_10.1	-
GF0040304	0	1	0	Hypothetical protein (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1); polysaccharide binding [GO:0030247 molecular_function] (1)	Wall-associated receptor kinase, galacturonan-binding domain [IPR025287] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	-	C_unshiu_01180_mRNA_8.1	-
GF0040303	0	1	0	Hypothetical protein (1)			-	C_unshiu_01180_mRNA_6.1	-
GF0040302	0	1	0	Monosacharide transport protein (1)			-	C_unshiu_01180_mRNA_4.1	-
GF0040301	0	1	0	Hypothetical protein (1)	polysaccharide binding [GO:0030247 molecular_function] (1)	Wall-associated receptor kinase, galacturonan-binding domain [IPR025287] (1)	-	C_unshiu_01180_mRNA_1.1	-
GF0040300	0	1	0	Hypothetical protein (1)		NAD(P)-binding domain [IPR016040] (1)	-	C_unshiu_01179_mRNA_8.1	-
GF0040299	0	1	0	Hypothetical protein (1)			-	C_unshiu_01179_mRNA_5.1	-
GF0040298	0	1	0	Hypothetical protein (1)		Zinc knuckle CX2CX4HX4C [IPR025836] (1)	-	C_unshiu_01179_mRNA_2.1	-
GF0040297	0	1	0	Hypothetical protein (1)			-	C_unshiu_01178_mRNA_7.1	-
GF0040296	0	1	0	Disease resistance family protein / LRR family protein, putative (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_01178_mRNA_5.1	-
GF0040295	0	1	0	Hypothetical protein (1)			-	C_unshiu_01178_mRNA_2.1	-
GF0040294	0	1	0	Hypothetical protein (1)			-	C_unshiu_01178_mRNA_1.1	-
GF0040293	0	1	0	Hypothetical protein (1)			-	C_unshiu_01177_mRNA_9.1	-
GF0040292	0	1	0	Hypothetical protein (1)		GDP-fucose protein O-fucosyltransferase [IPR019378] (1)	-	C_unshiu_01177_mRNA_4.1	-
GF0040291	0	1	0	Hypothetical protein (1)			-	C_unshiu_01177_mRNA_3.1	-
GF0040290	0	1	0	Cyclic nucleotide-gated ion channel 1 (1)		Cyclic nucleotide-binding-like [IPR018490] (1); RmlC-like jelly roll fold [IPR014710] (1); Cyclic nucleotide-binding domain [IPR000595] (1)	-	C_unshiu_01177_mRNA_2.1	-
GF0040289	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	WD40 repeat [IPR001680] (1); WD40-repeat-containing domain [IPR017986] (1); WD40/YVTN repeat-like-containing domain [IPR015943] (1)	-	C_unshiu_01175_mRNA_2.1	-
GF0040288	0	1	0	Hypothetical protein (1)	G-protein coupled receptor signaling pathway [GO:0007186 biological_process] (1); G-protein beta/gamma-subunit complex binding [GO:0031683 molecular_function] (1); GTPase activity [GO:0003924 molecular_function] (1); guanyl nucleotide binding [GO:0019001 molecular_function] (1); signal transducer activity [GO:0004871 molecular_function] (1)	Guanine nucleotide binding protein (G-protein), alpha subunit [IPR001019] (1); Zinc finger, FYVE/PHD-type [IPR011011] (1)	-	C_unshiu_01175_mRNA_1.1	-
GF0040287	0	1	0	Ras-related protein RABD1 (1)	intracellular [GO:0005622 cellular_component] (1); GTP binding [GO:0005525 molecular_function] (1); intracellular protein transport [GO:0006886 biological_process] (1); signal transduction [GO:0007165 biological_process] (1); membrane [GO:0016020 cellular_component] (1); small GTPase mediated signal transduction [GO:0007264 biological_process] (1); nucleocytoplasmic transport [GO:0006913 biological_process] (1); protein transport [GO:0015031 biological_process] (1); GTPase activity [GO:0003924 molecular_function] (1)	Small GTPase superfamily, Ras type [IPR020849] (1); Ran GTPase [IPR002041] (1); Small GTPase superfamily, Rab type [IPR003579] (1); Small GTP-binding protein domain [IPR005225] (1); Small GTPase superfamily, Rho type [IPR003578] (1); Small GTPase superfamily [IPR001806] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_01174_mRNA_8.1	-
GF0040286	0	1	0	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_01174_mRNA_5.1	-
GF0040285	0	1	0	Hypothetical protein (1)			-	C_unshiu_01174_mRNA_2.1	-
GF0040284	0	1	0	Hypothetical protein (1)			-	C_unshiu_01174_mRNA_1.1	-
GF0040283	0	1	0	Putative alcohol dehydrogenase (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); zinc ion binding [GO:0008270 molecular_function] (1)	NAD(P)-binding domain [IPR016040] (1); GroES-like [IPR011032] (1); Alcohol dehydrogenase, C-terminal [IPR013149] (1); Alcohol dehydrogenase superfamily, zinc-type [IPR002085] (1)	-	C_unshiu_01173_mRNA_6.1	-
GF0040282	0	1	0	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	NAD(P)-binding domain [IPR016040] (1); Alcohol dehydrogenase superfamily, zinc-type [IPR002085] (1)	-	C_unshiu_01173_mRNA_4.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0040281	0	1	0	Hypothetical protein (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase, ATP binding site [IPR017441] (1)	-	C_unshiu_01173_mRNA_1.1	-
GF0040280	0	1	0	C2H2 type zinc finger protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); metal ion binding [GO:0046872 molecular_function] (1)	Zinc finger, C2H2-like [IPR015880] (1); Zinc finger C2H2-type/integrase DNA-binding domain [IPR013087] (1); Zinc finger, C2H2 [IPR007087] (1); NYN domain, limkain-b1-type [IPR021139] (1)	-	C_unshiu_01172_mRNA_5.1	-
GF0040279	0	1	0	Hypothetical protein (1)			-	C_unshiu_01172_mRNA_4.1	-
GF0040278	0	1	0	Disease resistance RPS2-like protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01172_mRNA_3.1	-
GF0040277	0	1	0	Hypothetical protein (1)	ribosome [GO:0005840 cellular_component] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1); translation [GO:0006412 biological_process] (1)	Ribosomal protein L14 domain [IPR023571] (1); Ribosomal protein L14b/L23e [IPR000218] (1)	-	C_unshiu_01172_mRNA_2.1	-
GF0040276	0	1	0	Hypothetical protein (1)			-	C_unshiu_01172_mRNA_11.1	-
GF0040275	0	1	0	C2H2 type zinc finger protein (1)			-	C_unshiu_01172_mRNA_10.1	-
GF0040274	0	1	0	Hypothetical protein (1)	pectinesterase activity [GO:0030599 molecular_function] (1); cell wall modification [GO:0042545 biological_process] (1); cell wall [GO:0005618 cellular_component] (1)	Pectinesterase, catalytic [IPR000070] (1); Pectin lyase fold [IPR012334] (1); HotDog domain [IPR029069] (1); Gag-polypeptide of LTR copia-type [IPR029472] (1); Pectin lyase fold/virulence factor [IPR011050] (1)	-	C_unshiu_01171_mRNA_6.1	-
GF0040273	0	1	0	Hypothetical protein (1)			-	C_unshiu_01171_mRNA_3.1	-
GF0040272	0	1	0	Hypothetical protein (1)			-	C_unshiu_01171_mRNA_2.1	-
GF0040271	0	1	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1)	-	C_unshiu_01171_mRNA_1.1	-
GF0040270	0	1	0	Cytochrome P450 93A3 (1)	heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1)	Cytochrome P450 [IPR001128] (1); Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450, conserved site [IPR017972] (1)	-	C_unshiu_01170_mRNA_5.1	-
GF0040269	0	1	0	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1); Leucine-rich repeat 3 [IPR011713] (1)	-	C_unshiu_01170_mRNA_4.1	-
GF0040268	0	1	0	Hypothetical protein (1)			-	C_unshiu_01169_mRNA_7.1	-
GF0040267	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Thioredoxin-like fold [IPR012336] (1); Glutathione S-transferase, N-terminal [IPR004045] (1)	-	C_unshiu_01169_mRNA_5.1	-
GF0040266	0	1	0	Hypothetical protein (1)			-	C_unshiu_01169_mRNA_1.1	-
GF0040265	0	1	0	Hypothetical protein (1)			-	C_unshiu_01168_mRNA_9.1	-
GF0040264	0	1	0	Hypothetical protein (1)			-	C_unshiu_01168_mRNA_8.1	-
GF0040263	0	1	0	Hypothetical protein (1)			-	C_unshiu_01168_mRNA_7.1	-
GF0040262	0	1	0	Hypothetical protein (1)			-	C_unshiu_01168_mRNA_6.1	-
GF0040261	0	1	0	Hypothetical protein (1)			-	C_unshiu_01168_mRNA_5.1	-
GF0040260	0	1	0	Hypothetical protein (1)			-	C_unshiu_01168_mRNA_3.1	-
GF0040259	0	1	0	Hypothetical protein (1)			-	C_unshiu_01168_mRNA_2.1	-
GF0040258	0	1	0	Probable pectinesterase 56 (1)	pectinesterase activity [GO:0030599 molecular_function] (1); cell wall [GO:0005618 cellular_component] (1); cell wall modification [GO:0042545 biological_process] (1)	Pectinesterase, Asp active site [IPR033131] (1); Pectinesterase, catalytic [IPR000070] (1); Pectin lyase fold [IPR012334] (1); Pectin lyase fold/virulence factor [IPR011050] (1)	-	C_unshiu_01168_mRNA_14.1	-
GF0040257	0	1	0	Hypothetical protein (1)			-	C_unshiu_01168_mRNA_13.1	-
GF0040256	0	1	0	Hypothetical protein (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Serine/threonine-protein kinase, active site [IPR008271] (1); Retrotransposon gag domain [IPR005162] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_01168_mRNA_10.1	-
GF0040255	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_01168_mRNA_1.1	-
GF0040254	0	1	0	Hypothetical protein (1)			-	C_unshiu_01167_mRNA_8.1	-
GF0040253	0	1	0	Hypothetical protein (1)			-	C_unshiu_01167_mRNA_2.1	-
GF0040252	0	1	0	Hypothetical protein (1)			-	C_unshiu_01167_mRNA_12.1	-
GF0040251	0	1	0	Hypothetical protein (1)		PUA-like domain [IPR015947] (1)	-	C_unshiu_01167_mRNA_1.1	-
GF0040250	0	1	0	Hypothetical protein (1)		Transposon, En/Spm-like [IPR004242] (1)	-	C_unshiu_01166_mRNA_6.1	-
GF0040249	0	1	0	Putative muDR family transposase-like (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Transposase, MuDR, plant [IPR004332] (1); MULE transposase domain [IPR018289] (1); Zinc finger, PMZ-type [IPR006564] (1); Zinc finger, SWIM-type [IPR007527] (1)	-	C_unshiu_01166_mRNA_2.1	-
GF0040248	0	1	0	Hypothetical protein (1)			-	C_unshiu_01166_mRNA_1.1	-
GF0040247	0	1	0	Hypothetical protein (1)			-	C_unshiu_01165_mRNA_3.1	-
GF0040246	0	1	0	Hypothetical protein (1)	nucleus [GO:0005634 cellular_component] (1); nucleotide binding [GO:0000166 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (1)	Nucleotide-binding alpha-beta plait domain [IPR012677] (1); Transcription factor, K-box [IPR002487] (1)	-	C_unshiu_01164_mRNA_9.1	-
GF0040245	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_01164_mRNA_7.1	-
GF0040244	0	1	0	Hypothetical protein (1)			-	C_unshiu_01164_mRNA_6.1	-
GF0040243	0	1	0	Hypothetical protein (1)			-	C_unshiu_01164_mRNA_5.1	-
GF0040242	0	1	0	Hypothetical protein (1)			-	C_unshiu_01164_mRNA_15.1	-
GF0040241	0	1	0	Hypothetical protein (1)			-	C_unshiu_01164_mRNA_14.1	-
GF0040240	0	1	0	Protein AIG1 (1)	GTP binding [GO:0005525 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); AIG1-type guanine nucleotide-binding (G) domain [IPR006703] (1)	-	C_unshiu_01164_mRNA_13.1	-
GF0040239	0	1	0	AIG1 domain-containing protein (1)	GTP binding [GO:0005525 molecular_function] (1)	AIG1-type guanine nucleotide-binding (G) domain [IPR006703] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_01164_mRNA_11.1	-
GF0040238	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01163_mRNA_9.1	-
GF0040237	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_01163_mRNA_6.1	-
GF0040236	0	1	0	Hypothetical protein (1)	NADP binding [GO:0050661 molecular_function] (1); glucose-6-phosphate dehydrogenase activity [GO:0004345 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); glucose metabolic process [GO:0006006 biological_process] (1)	Glucose-6-phosphate dehydrogenase, NAD-binding [IPR022674] (1); Glucose-6-phosphate dehydrogenase [IPR001282] (1); NAD(P)-binding domain [IPR016040] (1); Glucose-6-phosphate dehydrogenase, C-terminal [IPR022675] (1)	-	C_unshiu_01163_mRNA_4.1	-
GF0040235	0	1	0	Receptor like protein 33 (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_01163_mRNA_3.1	-
GF0040234	0	1	0	Hypothetical protein (1)	glucose metabolic process [GO:0006006 biological_process] (1); oxidation-reduction process [GO:0055114 biological_process] (1); glucose-6-phosphate dehydrogenase activity [GO:0004345 molecular_function] (1); NADP binding [GO:0050661 molecular_function] (1)	Glucose-6-phosphate dehydrogenase, active site [IPR019796] (1); Glucose-6-phosphate dehydrogenase, NAD-binding [IPR022674] (1); Glucose-6-phosphate dehydrogenase [IPR001282] (1); Glucose-6-phosphate dehydrogenase, C-terminal [IPR022675] (1); NAD(P)-binding domain [IPR016040] (1)	-	C_unshiu_01163_mRNA_2.1	-
GF0040233	0	1	0	Leucine-rich repeat, plant specific (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01163_mRNA_10.1	-
GF0040232	0	1	0	Hypothetical protein (1)		Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	-	C_unshiu_01163_mRNA_1.1	-
GF0040231	0	1	0	40S ribosomal protein S2-2 (1)	translation [GO:0006412 biological_process] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1); ribosome [GO:0005840 cellular_component] (1)	Ribosomal protein S5 [IPR000851] (1); Ribosomal protein S5 domain 2-type fold [IPR020568] (1); Ribosomal protein S5, C-terminal [IPR005324] (1); Ribosomal protein S5 domain 2-type fold, subgroup [IPR014721] (1)	-	C_unshiu_01162_mRNA_9.1	-
GF0040230	0	1	0	Hypothetical protein (1)		Peptidase S8, subtilisin-related [IPR015500] (1)	-	C_unshiu_01162_mRNA_5.1	-
GF0040229	0	1	0	Hypothetical protein (1)			-	C_unshiu_01162_mRNA_3.1	-
GF0040228	0	1	0	Hypothetical protein (1)			-	C_unshiu_01162_mRNA_14.1	-
GF0040227	0	1	0	Hypothetical protein (1)			-	C_unshiu_01162_mRNA_13.1	-
GF0040226	0	1	0	Hypothetical protein (1)			-	C_unshiu_01162_mRNA_12.1	-
GF0040225	0	1	0	Hypothetical protein (1)			-	C_unshiu_01162_mRNA_10.1	-
GF0040224	0	1	0	Maturase R (1)	mRNA processing [GO:0006397 biological_process] (1)	Domain X [IPR024937] (1)	-	C_unshiu_01161_mRNA_4.1	-
GF0040223	0	1	0	Hypothetical protein (1)			-	C_unshiu_01161_mRNA_3.1	-
GF0040222	0	1	0	Hypothetical protein (1)			-	C_unshiu_01161_mRNA_1.1	-
GF0040221	0	1	0	Hypothetical protein (1)			-	C_unshiu_01160_mRNA_14.1	-
GF0040220	0	1	0	SCO1 protein (1)		Thioredoxin-like fold [IPR012336] (1); Copper chaperone SCO1/SenC [IPR003782] (1)	-	C_unshiu_01159_mRNA_9.1	-
GF0040219	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, GRF-type [IPR010666] (1)	-	C_unshiu_01159_mRNA_4.1	-
GF0040218	0	1	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_01159_mRNA_3.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0040217	0	1	0	Hypothetical protein (1)	transmembrane transport [GO:0055085 biological_process] (1); integral component of membrane [GO:0016021 cellular_component] (1)	Major facilitator superfamily [IPR011701] (1); Major facilitator superfamily domain [IPR020846] (1)	-	C_unshiu_01159_mRNA_15.1	-
GF0040216	0	1	0	Monosacharide transport protein (1)			-	C_unshiu_01159_mRNA_14.1	-
GF0040215	0	1	0	Hypothetical protein (1)			-	C_unshiu_01159_mRNA_13.1	-
GF0040214	0	1	0	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); 2 iron, 2 sulfur cluster binding [GO:0051537 molecular_function] (1); electron carrier activity [GO:0009055 molecular_function] (1); tricarboxylic acid cycle [GO:0006099 biological_process] (1); iron-sulfur cluster binding [GO:0051536 molecular_function] (1)	4Fe-4S ferredoxin-type, iron-sulphur binding domain [IPR017896] (1); Succinate dehydogenase/fumarate reductase N-terminal [IPR025192] (1); 2Fe-2S ferredoxin, iron-sulphur binding site [IPR006058] (1); Beta-grasp domain [IPR012675] (1); 4Fe-4S ferredoxin, iron-sulphur binding, conserved site [IPR017900] (1); 2Fe-2S ferredoxin-type iron-sulfur binding domain [IPR001041] (1); Alpha-helical ferredoxin [IPR009051] (1); Succinate dehydrogenase/fumarate reductase iron-sulphur protein [IPR004489] (1)	-	C_unshiu_01159_mRNA_10.1	-
GF0040213	0	1	0	Hypothetical protein (1)			-	C_unshiu_01159_mRNA_1.1	-
GF0040212	0	1	0	Hypothetical protein (1)			-	C_unshiu_01158_mRNA_9.1	-
GF0040211	0	1	0	Hypothetical protein (1)			-	C_unshiu_01158_mRNA_8.1	-
GF0040210	0	1	0	Hypothetical protein (1)	RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Aspartic peptidase domain [IPR021109] (1); Ribonuclease H domain [IPR002156] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_01158_mRNA_7.1	-
GF0040209	0	1	0	Hypothetical protein (1)			-	C_unshiu_01158_mRNA_6.1	-
GF0040208	0	1	0	Hypothetical protein (1)			-	C_unshiu_01158_mRNA_5.1	-
GF0040207	0	1	0	Hypothetical protein (1)			-	C_unshiu_01158_mRNA_14.1	-
GF0040206	0	1	0	Hypothetical protein (1)			-	C_unshiu_01158_mRNA_12.1	-
GF0040205	0	1	0	Hypothetical protein (1)		DnaJ domain [IPR001623] (1)	-	C_unshiu_01158_mRNA_10.1	-
GF0040204	0	1	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	Transcription factor, MADS-box [IPR002100] (1)	-	C_unshiu_01156_mRNA_9.1	-
GF0040203	0	1	0	MADS-box transcription factor family protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	Transcription factor, MADS-box [IPR002100] (1)	-	C_unshiu_01156_mRNA_8.1	-
GF0040202	0	1	0	Hypothetical protein (1)			-	C_unshiu_01156_mRNA_7.1	-
GF0040201	0	1	0	Hypothetical protein (1)			-	C_unshiu_01156_mRNA_6.1	-
GF0040200	0	1	0	Hypothetical protein (1)			-	C_unshiu_01156_mRNA_5.1	-
GF0040199	0	1	0	Hypothetical protein (1)	calcium ion binding [GO:0005509 molecular_function] (1)	EF-hand domain [IPR002048] (1)	-	C_unshiu_01156_mRNA_2.1	-
GF0040198	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H domain [IPR002156] (1)	-	C_unshiu_01156_mRNA_11.1	-
GF0040197	0	1	0	Hypothetical protein (1)			-	C_unshiu_01156_mRNA_1.1	-
GF0040196	0	1	0	Hypothetical protein (1)		Wall-associated receptor kinase, C-terminal [IPR032872] (1)	-	C_unshiu_01155_mRNA_8.1	-
GF0040195	0	1	0	Hypothetical protein (1)	calmodulin binding [GO:0005516 molecular_function] (1); response to stress [GO:0006950 biological_process] (1)	CALMODULIN-BINDING PROTEIN60 [IPR012416] (1)	-	C_unshiu_01155_mRNA_7.1	-
GF0040194	0	1	0	Hypothetical protein (1)			-	C_unshiu_01155_mRNA_1.1	-
GF0040193	0	1	0	Hypothetical protein (1)			-	C_unshiu_01154_mRNA_8.1	-
GF0040192	0	1	0	Hypothetical protein (1)			-	C_unshiu_01154_mRNA_7.1	-
GF0040191	0	1	0	Hypothetical protein (1)			-	C_unshiu_01154_mRNA_5.1	-
GF0040190	0	1	0	Hypothetical protein (1)			-	C_unshiu_01154_mRNA_2.1	-
GF0040189	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	C_unshiu_01154_mRNA_12.1	-
GF0040188	0	1	0	Hypothetical protein (1)			-	C_unshiu_01153_mRNA_6.1	-
GF0040187	0	1	0	Hypothetical protein (1)			-	C_unshiu_01153_mRNA_2.1	-
GF0040186	0	1	0	Hypothetical protein (1)			-	C_unshiu_01153_mRNA_12.1	-
GF0040185	0	1	0	LRR receptor-like kinase family protein (1)	protein binding [GO:0005515 molecular_function] (1)	Protein kinase-like domain [IPR011009] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_01153_mRNA_10.1	-
GF0040184	0	1	0	Hypothetical protein (1)			-	C_unshiu_01153_mRNA_1.1	-
GF0040183	0	1	0	Hypothetical protein (1)	protein folding [GO:0006457 biological_process] (1)	FKBP-type peptidyl-prolyl cis-trans isomerase domain [IPR001179] (1); Peptidyl-prolyl cis-trans isomerase, FKBP-type [IPR023566] (1)	-	C_unshiu_01152_mRNA_8.1	-
GF0040182	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Bromodomain [IPR001487] (1); Ubiquitin domain [IPR000626] (1); Transcription initiation factor TFIID subunit 1, domain of unknown function [IPR022591] (1); Ubiquitin-related domain [IPR029071] (1)	-	C_unshiu_01152_mRNA_4.1	-
GF0040181	0	1	0	Hypothetical protein (1)		TAFII-230 TBP-binding [IPR009067] (1)	-	C_unshiu_01152_mRNA_3.1	-
GF0040180	0	1	0	Hypothetical protein (1)			-	C_unshiu_01152_mRNA_1.1	-
GF0040179	0	1	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1)	-	C_unshiu_01151_mRNA_8.1	-
GF0040178	0	1	0	Hypothetical protein (1)			-	C_unshiu_01151_mRNA_4.1	-
GF0040177	0	1	0	Hypothetical protein (1)			-	C_unshiu_01150_mRNA_9.1	-
GF0040176	0	1	0	Hypothetical protein (1)			-	C_unshiu_01150_mRNA_7.1	-
GF0040175	0	1	0	Phosphoprotein phosphatase (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01150_mRNA_3.1	-
GF0040174	0	1	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_01150_mRNA_11.1	-
GF0040173	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_01150_mRNA_10.1	-
GF0040172	0	1	0	Hypothetical protein (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1); polygalacturonase activity [GO:0004650 molecular_function] (1)	Glycoside hydrolase, family 28 [IPR000743] (1); Pectin lyase fold/virulence factor [IPR011050] (1); Pectin lyase fold [IPR012334] (1)	-	C_unshiu_01149_mRNA_8.1	-
GF0040171	0	1	0	Hypothetical protein (1)	metabolic process [GO:0008152 biological_process] (1); transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1)	GINS complex [IPR021151] (1); UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	-	C_unshiu_01149_mRNA_7.1	-
GF0040170	0	1	0	Hypothetical protein (1)			-	C_unshiu_01148_mRNA_8.1	-
GF0040169	0	1	0	Hypothetical protein (1)			-	C_unshiu_01147_mRNA_9.1	-
GF0040168	0	1	0	Monosacharide transport protein (1)			-	C_unshiu_01147_mRNA_5.1	-
GF0040167	0	1	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1)	Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_01147_mRNA_4.1	-
GF0040166	0	1	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1)	Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	-	C_unshiu_01147_mRNA_3.1	-
GF0040165	0	1	0	Hypothetical protein (1)			-	C_unshiu_01147_mRNA_12.1	-
GF0040164	0	1	0	Flavoprotein wrbA (1)	negative regulation of transcription, DNA-templated [GO:0045892 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); FMN binding [GO:0010181 molecular_function] (1)	Flavodoxin/nitric oxide synthase [IPR008254] (1); Flavoprotein WrbA [IPR010089] (1); Flavoprotein-like domain [IPR029039] (1); NADPH-dependent FMN reductase-like [IPR005025] (1)	-	C_unshiu_01146_mRNA_8.1	-
GF0040163	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	WD40/YVTN repeat-like-containing domain [IPR015943] (1); WD40 repeat, conserved site [IPR019775] (1); WD40-repeat-containing domain [IPR017986] (1); WD40 repeat [IPR001680] (1)	-	C_unshiu_01146_mRNA_15.1	-
GF0040162	0	1	0	Mutator-like transposase (1)		Transposase, MuDR, plant [IPR004332] (1); MULE transposase domain [IPR018289] (1)	-	C_unshiu_01146_mRNA_1.1	-
GF0040161	0	1	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1)	Aspartic peptidase domain [IPR021109] (1); Peptidase A2A, retrovirus, catalytic [IPR001995] (1); Reverse transcriptase domain [IPR000477] (1); Retropepsins [IPR018061] (1)	-	C_unshiu_01145_mRNA_8.1	-
GF0040160	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_01145_mRNA_5.1	-
GF0040159	0	1	0	Hypothetical protein (1)			-	C_unshiu_01145_mRNA_4.1	-
GF0040158	0	1	0	Hypothetical protein (1)			-	C_unshiu_01145_mRNA_3.1	-
GF0040157	0	1	0	Hypothetical protein (1)			-	C_unshiu_01145_mRNA_2.1	-
GF0040156	0	1	0	Hypothetical protein (1)			-	C_unshiu_01145_mRNA_12.1	-
GF0040155	0	1	0	Hypothetical protein (1)			-	C_unshiu_01145_mRNA_10.1	-
GF0040154	0	1	0	Heavy metal P-type ATPase (1)	integral component of membrane [GO:0016021 cellular_component] (1); cation transport [GO:0006812 biological_process] (1); metal ion binding [GO:0046872 molecular_function] (1); metal ion transport [GO:0030001 biological_process] (1); nucleotide binding [GO:0000166 molecular_function] (1); cation-transporting ATPase activity [GO:0019829 molecular_function] (1); copper ion binding [GO:0005507 molecular_function] (1)	Heavy-metal-associated, conserved site [IPR017969] (1); Heavy metal-associated domain, HMA [IPR006121] (1); Heavy metal-associated domain, copper ion-binding [IPR006122] (1); HAD-like domain [IPR023214] (1); P-type ATPase, A domain [IPR008250] (1); P-type ATPase, cytoplasmic domain N [IPR023299] (1); P-type ATPase [IPR001757] (1); P-type ATPase, subfamily IB [IPR027256] (1); P-type ATPase, phosphorylation site [IPR018303] (1)	-	C_unshiu_01144_mRNA_6.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0040153	0	1	0	Glutathione peroxidase (1)	oxidation-reduction process [GO:0055114 biological_process] (1); glutathione peroxidase activity [GO:0004602 molecular_function] (1); response to oxidative stress [GO:0006979 biological_process] (1)	Glutathione peroxidase [IPR000889] (1); Thioredoxin-like fold [IPR012336] (1); Glutathione peroxidase conserved site [IPR029760] (1); Glutathione peroxidase active site [IPR029759] (1)	-	C_unshiu_01144_mRNA_2.1	-
GF0040152	0	1	0	Hypothetical protein (1)		PPC domain [IPR005175] (1)	-	C_unshiu_01144_mRNA_1.1	-
GF0040151	0	1	0	Pentatricopeptide (PPR) repeat protein (1)	protein binding [GO:0005515 molecular_function] (1)	Pentatricopeptide repeat [IPR002885] (1); Tetratricopeptide-like helical domain [IPR011990] (1)	-	C_unshiu_01143_mRNA_9.1	-
GF0040150	0	1	0	Pentatricopeptide (PPR) repeat protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	C_unshiu_01143_mRNA_6.1	-
GF0040149	0	1	0	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	C_unshiu_01143_mRNA_5.1	-
GF0040148	0	1	0	Fertility restorer (1)		Pentatricopeptide repeat [IPR002885] (1)	-	C_unshiu_01143_mRNA_4.1	-
GF0040147	0	1	0	Hypothetical protein (1)			-	C_unshiu_01142_mRNA_9.1	-
GF0040146	0	1	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Aspartic peptidase domain [IPR021109] (1); WD40-repeat-containing domain [IPR017986] (1); WD40/YVTN repeat-like-containing domain [IPR015943] (1); Peptidase family A1 domain [IPR033121] (1); Xylanase inhibitor, C-terminal [IPR032799] (1); Xylanase inhibitor, N-terminal [IPR032861] (1); Aspartic peptidase A1 family [IPR001461] (1)	-	C_unshiu_01142_mRNA_7.1	-
GF0040145	0	1	0	Hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyl transferase (1)	transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (1)	Chloramphenicol acetyltransferase-like domain [IPR023213] (1); Transferase [IPR003480] (1)	-	C_unshiu_01142_mRNA_3.1	-
GF0040144	0	1	0	NF-kappa-B inhibitor-like protein 2 isoform 1 (1)			-	C_unshiu_01141_mRNA_7.1	-
GF0040143	0	1	0	Hypothetical protein (1)			-	C_unshiu_01141_mRNA_6.1	-
GF0040142	0	1	0	Hypothetical protein (1)			-	C_unshiu_01141_mRNA_10.1	-
GF0040141	0	1	0	Hypothetical protein (1)			-	C_unshiu_01140_mRNA_8.1	-
GF0040140	0	1	0	Hypothetical protein (1)			-	C_unshiu_01140_mRNA_6.1	-
GF0040139	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_01140_mRNA_5.1	-
GF0040138	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01140_mRNA_21.1	-
GF0040137	0	1	0	Cellular nucleic acid-binding protein (1)	proteolysis [GO:0006508 biological_process] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1)	Aspartic peptidase, active site [IPR001969] (1); Aspartic peptidase domain [IPR021109] (1)	-	C_unshiu_01140_mRNA_19.1	-
GF0040136	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_01140_mRNA_17.1	-
GF0040135	0	1	0	Hypothetical protein (1)			-	C_unshiu_01140_mRNA_16.1	-
GF0040134	0	1	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	-	C_unshiu_01140_mRNA_13.1	-
GF0040133	0	1	0	Putative disease resistance protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01140_mRNA_11.1	-
GF0040132	0	1	0	Glucose-6-phosphate dehydrogenase 4 (1)	glucose-6-phosphate dehydrogenase activity [GO:0004345 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); glucose metabolic process [GO:0006006 biological_process] (1); NADP binding [GO:0050661 molecular_function] (1)	NAD(P)-binding domain [IPR016040] (1); Glucose-6-phosphate dehydrogenase, C-terminal [IPR022675] (1); Glucose-6-phosphate dehydrogenase [IPR001282] (1); Glucose-6-phosphate dehydrogenase, NAD-binding [IPR022674] (1)	-	C_unshiu_01140_mRNA_10.1	-
GF0040131	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Transposon, En/Spm-like [IPR004242] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Transposase-associated domain [IPR029480] (1)	-	C_unshiu_01139_mRNA_7.1	-
GF0040130	0	1	0	Hypothetical protein (1)		S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	C_unshiu_01139_mRNA_4.1	-
GF0040129	0	1	0	Hypothetical protein (1)		GAG-pre-integrase domain [IPR025724] (1)	-	C_unshiu_01139_mRNA_3.1	-
GF0040128	0	1	0	Hypothetical protein (1)	rRNA processing [GO:0006364 biological_process] (1); nucleobase-containing compound metabolic process [GO:0006139 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	YqgF/RNase H-like domain [IPR006641] (1); Putative pre-16S rRNA nuclease [IPR005227] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_01138_mRNA_9.1	-
GF0040127	0	1	0	Hypothetical protein (1)			-	C_unshiu_01138_mRNA_8.1	-
GF0040126	0	1	0	Hypothetical protein (1)		Transposase, MuDR, plant [IPR004332] (1)	-	C_unshiu_01138_mRNA_6.1	-
GF0040125	0	1	0	Hypothetical protein (1)			-	C_unshiu_01138_mRNA_4.1	-
GF0040124	0	1	0	Hypothetical protein (1)		Myb/SANT-like domain [IPR024752] (1)	-	C_unshiu_01138_mRNA_2.1	-
GF0040123	0	1	0	Hypothetical protein (1)			-	C_unshiu_01137_mRNA_3.1	-
GF0040122	0	1	0	LRR receptor-like kinase (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_01136_mRNA_5.1	-
GF0040121	0	1	0	Hypothetical protein (1)			-	C_unshiu_01136_mRNA_1.1	-
GF0040120	0	1	0	Hypothetical protein (1)			-	C_unshiu_01135_mRNA_5.1	-
GF0040119	0	1	0	Hypothetical protein (1)			-	C_unshiu_01135_mRNA_1.1	-
GF0040118	0	1	0	Hypothetical protein (1)			-	C_unshiu_01134_mRNA_5.1	-
GF0040117	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat [IPR002110] (1); Ankyrin repeat-containing domain [IPR020683] (1); Tetratricopeptide-like helical domain [IPR011990] (1)	-	C_unshiu_01133_mRNA_4.1	-
GF0040116	0	1	0	Hypothetical protein (1)			-	C_unshiu_01133_mRNA_3.1	-
GF0040115	0	1	0	Hypothetical protein (1)		Iron hydrogenase, large subunit, C-terminal [IPR004108] (1); Iron hydrogenase [IPR009016] (1)	-	C_unshiu_01133_mRNA_1.1	-
GF0040114	0	1	0	Hypothetical protein (1)			-	C_unshiu_01132_mRNA_9.1	-
GF0040113	0	1	0	Putative integrase core domain protein (1)	DNA integration [GO:0015074 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Integrase, catalytic core [IPR001584] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_01132_mRNA_8.1	-
GF0040112	0	1	0	Hypothetical protein (1)			-	C_unshiu_01132_mRNA_7.1	-
GF0040111	0	1	0	Hypothetical protein (1)			-	C_unshiu_01132_mRNA_2.1	-
GF0040110	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	hAT-like transposase, RNase-H fold [IPR025525] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_01132_mRNA_15.1	-
GF0040109	0	1	0	Hypothetical protein (1)			-	C_unshiu_01131_mRNA_7.1	-
GF0040108	0	1	0	Mads box protein, putative (1)	protein dimerization activity [GO:0046983 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	Transcription factor, MADS-box [IPR002100] (1)	-	C_unshiu_01131_mRNA_1.1	-
GF0040107	0	1	0	Hypothetical protein (1)	ribulose-bisphosphate carboxylase activity [GO:0016984 molecular_function] (1); carbon fixation [GO:0015977 biological_process] (1)	Ribulose bisphosphate carboxylase, large subunit, ferrodoxin-like N-terminal [IPR017443] (1)	-	C_unshiu_01130_mRNA_3.1	-
GF0040106	0	1	0	Hypothetical protein (1)			-	C_unshiu_01129_mRNA_9.1	-
GF0040105	0	1	0	Hypothetical protein (1)			-	C_unshiu_01129_mRNA_6.1	-
GF0040104	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_01129_mRNA_16.1	-
GF0040103	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_01129_mRNA_15.1	-
GF0040102	0	1	0	Hypothetical protein (1)			-	C_unshiu_01128_mRNA_13.1	-
GF0040101	0	1	0	TVP38/TMEM64 family membrane protein (1)		Prolamin-like domain [IPR008502] (1); SNARE associated Golgi protein [IPR032816] (1)	-	C_unshiu_01128_mRNA_12.1	-
GF0040100	0	1	0	NB-ARC domain disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_01127_mRNA_5.1	-
GF0040099	0	1	0	Egg cell-secreted protein 1.2 (1)		Prolamin-like domain [IPR008502] (1)	-	C_unshiu_01127_mRNA_4.1	-
GF0040098	0	1	0	Pentatricopeptide repeat-containing protein, chloroplastic (1)	protein binding [GO:0005515 molecular_function] (1)	Pentatricopeptide repeat [IPR002885] (1); Tetratricopeptide-like helical domain [IPR011990] (1)	-	C_unshiu_01126_mRNA_9.1	-
GF0040097	0	1	0	Hypothetical protein (1)			-	C_unshiu_01126_mRNA_4.1	-
GF0040096	0	1	0	Hypothetical protein (1)		P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_01126_mRNA_3.1	-
GF0040095	0	1	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1)	UvrD-like Helicase, ATP-binding domain [IPR014016] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_01126_mRNA_2.1	-
GF0040094	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	C_unshiu_01126_mRNA_13.1	-
GF0040093	0	1	0	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	C_unshiu_01126_mRNA_10.1	-
GF0040092	0	1	0	Hypothetical protein (1)			-	C_unshiu_01126_mRNA_1.1	-
GF0040091	0	1	0	Hypothetical protein (1)	RNA binding [GO:0003723 molecular_function] (1); exosome (RNase complex) [GO:0000178 cellular_component] (1)	Nucleic acid-binding, OB-fold [IPR012340] (1); Exosome complex RNA-binding protein 1/RRP40/RRP4 [IPR026699] (1)	-	C_unshiu_01125_mRNA_6.1	-
GF0040090	0	1	0	Hypothetical protein (1)			-	C_unshiu_01125_mRNA_5.1	-
GF0040089	0	1	0	Hypothetical protein (1)			-	C_unshiu_01125_mRNA_2.1	-
GF0040088	0	1	0	Hypothetical protein (1)			-	C_unshiu_01124_mRNA_9.1	-
GF0040087	0	1	0	Hypothetical protein (1)			-	C_unshiu_01124_mRNA_8.1	-
GF0040086	0	1	0	Hypothetical protein (1)			-	C_unshiu_01124_mRNA_6.1	-
GF0040085	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	-	C_unshiu_01124_mRNA_14.1	-
GF0040084	0	1	0	Hypothetical protein (1)			-	C_unshiu_01124_mRNA_11.1	-
GF0040083	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1); zinc ion binding [GO:0008270 molecular_function] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Reverse transcriptase domain [IPR000477] (1); Peptidase A2A, retrovirus, catalytic [IPR001995] (1)	-	C_unshiu_01124_mRNA_10.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0040082	0	1	0	L-ascorbate peroxidase 1, cytosolic (1)	peroxidase activity [GO:0004601 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); response to oxidative stress [GO:0006979 biological_process] (1); heme binding [GO:0020037 molecular_function] (1)	Haem peroxidase, plant/fungal/bacterial [IPR002016] (1); Peroxidases heam-ligand binding site [IPR019793] (1); Plant ascorbate peroxidase [IPR002207] (1); Haem peroxidase [IPR010255] (1)	-	C_unshiu_01124_mRNA_1.1	-
GF0040081	0	1	0	Hypothetical protein (1)			-	C_unshiu_01123_mRNA_9.1	-
GF0040080	0	1	0	Hypothetical protein (1)			-	C_unshiu_01123_mRNA_6.1	-
GF0040079	0	1	0	Hypothetical protein (1)		Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_01123_mRNA_5.1	-
GF0040078	0	1	0	Hypothetical protein (1)			-	C_unshiu_01123_mRNA_3.1	-
GF0040077	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_01123_mRNA_2.1	-
GF0040076	0	1	0	Hypothetical protein (1)	magnesium ion binding [GO:0000287 molecular_function] (1); terpene synthase activity [GO:0010333 molecular_function] (1); lyase activity [GO:0016829 molecular_function] (1)	Isoprenoid synthase domain [IPR008949] (1); Terpene synthase, metal-binding domain [IPR005630] (1)	-	C_unshiu_01122_mRNA_9.1	-
GF0040075	0	1	0	Hypothetical protein (1)			-	C_unshiu_01122_mRNA_4.1	-
GF0040074	0	1	0	Hypothetical protein (1)			-	C_unshiu_01122_mRNA_3.1	-
GF0040073	0	1	0	Hypothetical protein (1)	ATP-dependent DNA helicase activity [GO:0004003 molecular_function] (1); nucleus [GO:0005634 cellular_component] (1); nucleotide-excision repair [GO:0006289 biological_process] (1); core TFIIH complex [GO:0000439 cellular_component] (1)	Transcription factor TFIIH subunit p52/Tfb2 [IPR004598] (1)	-	C_unshiu_01122_mRNA_12.1	-
GF0040072	0	1	0	Hypothetical protein (1)			-	C_unshiu_01122_mRNA_1.1	-
GF0040071	0	1	0	Hypothetical protein (1)			-	C_unshiu_01121_mRNA_6.1	-
GF0040070	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF1985 [IPR015410] (1)	-	C_unshiu_01121_mRNA_4.1	-
GF0040069	0	1	0	Hypothetical protein (1)	ferrous iron binding [GO:0008198 molecular_function] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); cellular aromatic compound metabolic process [GO:0006725 biological_process] (1)	Ribosomal RNA-processing protein 14/surfeit locus protein 6, C-terminal domain [IPR029190] (1); Extradiol ring-cleavage dioxygenase, class III enzyme, subunit B [IPR004183] (1)	-	C_unshiu_01120_mRNA_4.1	-
GF0040068	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	-	C_unshiu_01119_mRNA_9.1	-
GF0040067	0	1	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	-	C_unshiu_01119_mRNA_8.1	-
GF0040066	0	1	0	Hypothetical protein (1)			-	C_unshiu_01119_mRNA_6.1	-
GF0040065	0	1	0	Phosphoprotein phosphatase (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01119_mRNA_2.1	-
GF0040064	0	1	0	Hypothetical protein (1)			-	C_unshiu_01118_mRNA_9.1	-
GF0040063	0	1	0	Hypothetical protein (1)			-	C_unshiu_01118_mRNA_4.1	-
GF0040062	0	1	0	Hypothetical protein (1)			-	C_unshiu_01117_mRNA_4.1	-
GF0040061	0	1	0	Hypothetical protein (1)			-	C_unshiu_01116_mRNA_1.1	-
GF0040060	0	1	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	-	C_unshiu_01115_mRNA_5.1	-
GF0040059	0	1	0	Hypothetical protein (1)			-	C_unshiu_01114_mRNA_9.1	-
GF0040058	0	1	0	Hypothetical protein (1)			-	C_unshiu_01114_mRNA_8.1	-
GF0040057	0	1	0	Hypothetical protein (1)			-	C_unshiu_01114_mRNA_5.1	-
GF0040056	0	1	0	Hypothetical protein (1)			-	C_unshiu_01114_mRNA_3.1	-
GF0040055	0	1	0	Hypothetical protein (1)			-	C_unshiu_01114_mRNA_13.1	-
GF0040054	0	1	0	Hypothetical protein (1)			-	C_unshiu_01114_mRNA_12.1	-
GF0040053	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_01113_mRNA_7.1	-
GF0040052	0	1	0	Hypothetical protein (1)			-	C_unshiu_01113_mRNA_2.1	-
GF0040051	0	1	0	Hypothetical protein (1)			-	C_unshiu_01113_mRNA_17.1	-
GF0040050	0	1	0	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); FAD binding [GO:0071949 molecular_function] (1)	FAD/NAD(P)-binding domain [IPR023753] (1); FAD-binding domain [IPR002938] (1)	-	C_unshiu_01113_mRNA_15.1	-
GF0040049	0	1	0	Monooxygenase family protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1)	FAD/NAD(P)-binding domain [IPR023753] (1)	-	C_unshiu_01113_mRNA_14.1	-
GF0040048	0	1	0	FscO (1)	FAD binding [GO:0071949 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1)	FAD-binding domain [IPR002938] (1); FAD/NAD(P)-binding domain [IPR023753] (1)	-	C_unshiu_01113_mRNA_13.1	-
GF0040047	0	1	0	Hypothetical protein (1)	carbohydrate binding [GO:0030246 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1); hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (1)	Glycoside hydrolase family 31, N-terminal domain [IPR025887] (1); Glycoside hydrolase superfamily [IPR017853] (1); Galactose mutarotase-like domain [IPR011013] (1); Glycosyl hydrolases family 31, active site [IPR030458] (1); Glycoside hydrolase family 31 [IPR000322] (1)	-	C_unshiu_01112_mRNA_9.1	-
GF0040046	0	1	0	Pentatricopeptide repeat-containing family protein (1)	protein binding [GO:0005515 molecular_function] (1)	Pentatricopeptide repeat [IPR002885] (1); Tetratricopeptide-like helical domain [IPR011990] (1)	-	C_unshiu_01112_mRNA_8.1	-
GF0040045	0	1	0	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1)	Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450 [IPR001128] (1)	-	C_unshiu_01111_mRNA_3.1	-
GF0040044	0	1	0	Hypothetical protein (1)			-	C_unshiu_01111_mRNA_14.1	-
GF0040043	0	1	0	Hypothetical protein (1)	exocytosis [GO:0006887 biological_process] (1); exocyst [GO:0000145 cellular_component] (1)	Cullin repeat-like-containing domain [IPR016159] (1); Exocyst complex protein Exo70 [IPR004140] (1)	-	C_unshiu_01111_mRNA_12.1	-
GF0040042	0	1	0	Hypothetical protein (1)	transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (1)	Transferase [IPR003480] (1); Chloramphenicol acetyltransferase-like domain [IPR023213] (1)	-	C_unshiu_01110_mRNA_9.1	-
GF0040041	0	1	0	Hypothetical protein (1)			-	C_unshiu_01109_mRNA_9.1	-
GF0040040	0	1	0	Hypothetical protein (1)			-	C_unshiu_01109_mRNA_6.1	-
GF0040039	0	1	0	Hypothetical protein (1)			-	C_unshiu_01109_mRNA_10.1	-
GF0040038	0	1	0	Hypothetical protein (1)			-	C_unshiu_01108_mRNA_8.1	-
GF0040037	0	1	0	Hypothetical protein (1)			-	C_unshiu_01108_mRNA_7.1	-
GF0040036	0	1	0	Hypothetical protein (1)			-	C_unshiu_01108_mRNA_3.1	-
GF0040035	0	1	0	Hypothetical protein (1)			-	C_unshiu_01108_mRNA_2.1	-
GF0040034	0	1	0	Epoxide hydrolase 3 (1)		Alpha/Beta hydrolase fold [IPR029058] (1)	-	C_unshiu_01107_mRNA_9.1	-
GF0040033	0	1	0	Epoxide hydrolase 2 (1)	catalytic activity [GO:0003824 molecular_function] (1)	Gag-polypeptide of LTR copia-type [IPR029472] (1); Epoxide hydrolase-like [IPR000639] (1); Alpha/beta hydrolase fold-1 [IPR000073] (1); Alpha/Beta hydrolase fold [IPR029058] (1)	-	C_unshiu_01107_mRNA_8.1	-
GF0040032	0	1	0	Hypothetical protein (1)			-	C_unshiu_01107_mRNA_7.1	-
GF0040031	0	1	0	Hypothetical protein (1)			-	C_unshiu_01107_mRNA_17.1	-
GF0040030	0	1	0	Epoxide hydrolase 2 (1)	catalytic activity [GO:0003824 molecular_function] (1)	Alpha/Beta hydrolase fold [IPR029058] (1); Alpha/beta hydrolase fold-1 [IPR000073] (1); Epoxide hydrolase-like [IPR000639] (1)	-	C_unshiu_01107_mRNA_12.1	-
GF0040029	0	1	0	Hypothetical protein (1)		Isopenicillin N synthase-like [IPR027443] (1)	-	C_unshiu_01106_mRNA_9.1	-
GF0040028	0	1	0	Hypothetical protein (1)			-	C_unshiu_01106_mRNA_6.1	-
GF0040027	0	1	0	Hypothetical protein (1)			-	C_unshiu_01106_mRNA_5.1	-
GF0040026	0	1	0	Hypothetical protein (1)			-	C_unshiu_01106_mRNA_3.1	-
GF0040025	0	1	0	Hypothetical protein (1)			-	C_unshiu_01106_mRNA_2.1	-
GF0040024	0	1	0	Protein kinase protein with tetratricopeptide repeat domain (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Tetratricopeptide-like helical domain [IPR011990] (1)	-	C_unshiu_01105_mRNA_4.1	-
GF0040023	0	1	0	Glutathione peroxidase (1)	glutathione peroxidase activity [GO:0004602 molecular_function] (1); response to oxidative stress [GO:0006979 biological_process] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Glutathione peroxidase [IPR000889] (1); Thioredoxin-like fold [IPR012336] (1)	-	C_unshiu_01105_mRNA_1.1	-
GF0040022	0	1	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_01104_mRNA_5.1	-
GF0040021	0	1	0	Hypothetical protein (1)			-	C_unshiu_01104_mRNA_4.1	-
GF0040020	0	1	0	Hypothetical protein (1)			-	C_unshiu_01104_mRNA_1.1	-
GF0040019	0	1	0	Hypothetical protein (1)			-	C_unshiu_01103_mRNA_10.1	-
GF0040018	0	1	0	Hypothetical protein (1)			-	C_unshiu_01103_mRNA_1.1	-
GF0040017	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_01102_mRNA_8.1	-
GF0040016	0	1	0	LRR receptor-like kinase family protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	-	C_unshiu_01102_mRNA_6.1	-
GF0040015	0	1	0	Hypothetical protein (1)			-	C_unshiu_01102_mRNA_3.1	-
GF0040014	0	1	0	Hypothetical protein (1)			-	C_unshiu_01102_mRNA_1.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0040013	0	1	0	Hypothetical protein (1)	FMN binding [GO:0010181 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); catalytic activity [GO:0003824 molecular_function] (1)	Aldolase-type TIM barrel [IPR013785] (1); NADH:flavin oxidoreductase/NADH oxidase, N-terminal [IPR001155] (1)	-	C_unshiu_01101_mRNA_5.1	-
GF0040012	0	1	0	Hypothetical protein (1)			-	C_unshiu_01100_mRNA_9.1	-
GF0040011	0	1	0	Hypothetical protein (1)			-	C_unshiu_01100_mRNA_8.1	-
GF0040010	0	1	0	Hypothetical protein (1)			-	C_unshiu_01100_mRNA_7.1	-
GF0040009	0	1	0	Hypothetical protein (1)			-	C_unshiu_01100_mRNA_5.1	-
GF0040008	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1); zinc ion binding [GO:0008270 molecular_function] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1)	Aspartic peptidase domain [IPR021109] (1); Zinc finger, CCHC-type [IPR001878] (1); Retropepsins [IPR018061] (1); Peptidase A2A, retrovirus, catalytic [IPR001995] (1)	-	C_unshiu_01100_mRNA_4.1	-
GF0040007	0	1	0	Hypothetical protein (1)			-	C_unshiu_01100_mRNA_26.1	-
GF0040006	0	1	0	Hypothetical protein (1)			-	C_unshiu_01100_mRNA_24.1	-
GF0040005	0	1	0	NAD-dependent dihydropyrimidine dehydrogenase subunit PreA (1)	oxidation-reduction process [GO:0055114 biological_process] (1); cytoplasm [GO:0005737 cellular_component] (1); catalytic activity [GO:0003824 molecular_function] (1); oxidoreductase activity, acting on the CH-CH group of donors [GO:0016627 molecular_function] (1)	Dihydroorotate dehydrogenase domain [IPR005720] (1); Aldolase-type TIM barrel [IPR013785] (1)	-	C_unshiu_01100_mRNA_23.1	-
GF0040004	0	1	0	Hypothetical protein (1)			-	C_unshiu_01100_mRNA_20.1	-
GF0040003	0	1	0	Hypothetical protein (1)			-	C_unshiu_01100_mRNA_19.1	-
GF0040002	0	1	0	Hypothetical protein (1)			-	C_unshiu_01100_mRNA_1.1	-
GF0040001	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, SWIM-type [IPR007527] (1); Zinc finger, PMZ-type [IPR006564] (1)	-	C_unshiu_01099_mRNA_9.1	-
GF0040000	0	1	0	Hypothetical protein (1)			-	C_unshiu_01099_mRNA_3.1	-
GF0039999	0	1	0	Hypothetical protein (1)			-	C_unshiu_01098_mRNA_7.1	-
GF0039998	0	1	0	Hypothetical protein (1)			-	C_unshiu_01098_mRNA_6.1	-
GF0039997	0	1	0	Phytosulfokine receptor (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	-	C_unshiu_01097_mRNA_9.1	-
GF0039996	0	1	0	COBW domain-containing protein 1 (1)		P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); CobW/HypB/UreG domain [IPR003495] (1); Cobalamin (vitamin B12) biosynthesis CobW-like, C-terminal [IPR011629] (1)	-	C_unshiu_01097_mRNA_5.1	-
GF0039995	0	1	0	Hypothetical protein (1)			-	C_unshiu_01097_mRNA_2.1	-
GF0039994	0	1	0	Hypothetical protein (1)			-	C_unshiu_01097_mRNA_12.1	-
GF0039993	0	1	0	S locus F-box protein with the low allelic sequence polymorphism 1-S2 (1)	protein binding [GO:0005515 molecular_function] (1)	F-box associated domain, type 1 [IPR006527] (1); F-box domain [IPR001810] (1); F-box associated interaction domain [IPR017451] (1); Galactose oxidase/kelch, beta-propeller [IPR011043] (1)	-	C_unshiu_01097_mRNA_11.1	-
GF0039992	0	1	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1); High mobility group box domain [IPR009071] (1)	-	C_unshiu_01097_mRNA_1.1	-
GF0039991	0	1	0	Hypothetical protein (1)			-	C_unshiu_01096_mRNA_9.1	-
GF0039990	0	1	0	Hypothetical protein (1)			-	C_unshiu_01096_mRNA_4.1	-
GF0039989	0	1	0	Hypothetical protein (1)			-	C_unshiu_01096_mRNA_3.1	-
GF0039988	0	1	0	Hypothetical protein (1)			-	C_unshiu_01096_mRNA_2.1	-
GF0039987	0	1	0	Limonene synthase (1)	metabolic process [GO:0008152 biological_process] (1); lyase activity [GO:0016829 molecular_function] (1); terpene synthase activity [GO:0010333 molecular_function] (1)	Isoprenoid synthase domain [IPR008949] (1); Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (1); Terpene synthase, N-terminal domain [IPR001906] (1)	-	C_unshiu_01095_mRNA_9.1	-
GF0039986	0	1	0	Hypothetical protein (1)			-	C_unshiu_01095_mRNA_5.1	-
GF0039985	0	1	0	MADS9 protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	Retrotransposon gag domain [IPR005162] (1); Transcription factor, MADS-box [IPR002100] (1)	-	C_unshiu_01095_mRNA_4.1	-
GF0039984	0	1	0	Hypothetical protein (1)			-	C_unshiu_01095_mRNA_1.1	-
GF0039983	0	1	0	Hypothetical protein (1)			-	C_unshiu_01094_mRNA_5.1	-
GF0039982	0	1	0	Hypothetical protein (1)			-	C_unshiu_01094_mRNA_4.1	-
GF0039981	0	1	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	-	C_unshiu_01094_mRNA_2.1	-
GF0039980	0	1	0	Hypothetical protein (1)			-	C_unshiu_01094_mRNA_12.1	-
GF0039979	0	1	0	Hypothetical protein (1)			-	C_unshiu_01093_mRNA_7.1	-
GF0039978	0	1	0	Putative methyltransferase PMT20 (1)	methyltransferase activity [GO:0008168 molecular_function] (1)	S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); Putative S-adenosyl-L-methionine-dependent methyltransferase [IPR004159] (1)	-	C_unshiu_01093_mRNA_5.1	-
GF0039977	0	1	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01093_mRNA_2.1	-
GF0039976	0	1	0	Hypothetical protein (1)			-	C_unshiu_01092_mRNA_9.1	-
GF0039975	0	1	0	Hypothetical protein (1)			-	C_unshiu_01092_mRNA_8.1	-
GF0039974	0	1	0	Hypothetical protein (1)			-	C_unshiu_01091_mRNA_6.1	-
GF0039973	0	1	0	Hypothetical protein (1)			-	C_unshiu_01091_mRNA_1.1	-
GF0039972	0	1	0	Hypothetical protein (1)	magnesium ion binding [GO:0000287 molecular_function] (1); lyase activity [GO:0016829 molecular_function] (1); terpene synthase activity [GO:0010333 molecular_function] (1)	Terpene synthase, metal-binding domain [IPR005630] (1); Isoprenoid synthase domain [IPR008949] (1)	-	C_unshiu_01090_mRNA_4.1	-
GF0039971	0	1	0	Hypothetical protein (1)			-	C_unshiu_01089_mRNA_8.1	-
GF0039970	0	1	0	Hypothetical protein (1)	transporter activity [GO:0005215 molecular_function] (1); transport [GO:0006810 biological_process] (1); membrane [GO:0016020 cellular_component] (1)	Proton-dependent oligopeptide transporter family [IPR000109] (1)	-	C_unshiu_01089_mRNA_7.1	-
GF0039969	0	1	0	Non-LTR retroelement reverse transcriptase-like (1)		Domain of unknown function DUF4283 [IPR025558] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_01088_mRNA_11.1	-
GF0039968	0	1	0	Hypothetical protein (1)			-	C_unshiu_01087_mRNA_6.1	-
GF0039967	0	1	0	Clp protease ATP binding subunit (1)	ATP binding [GO:0005524 molecular_function] (1)	ClpA/B family [IPR001270] (1); Clp ATPase, C-terminal [IPR019489] (1); ATPase, AAA-type, core [IPR003959] (1); ClpA/B, conserved site 1 [IPR018368] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); AAA+ ATPase domain [IPR003593] (1)	-	C_unshiu_01086_mRNA_4.1	-
GF0039966	0	1	0	Hypothetical protein (1)			-	C_unshiu_01086_mRNA_3.1	-
GF0039965	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_01086_mRNA_11.1	-
GF0039964	0	1	0	Hypothetical protein (1)			-	C_unshiu_01085_mRNA_11.1	-
GF0039963	0	1	0	Hypothetical protein (1)			-	C_unshiu_01085_mRNA_1.1	-
GF0039962	0	1	0	Hypothetical protein (1)			-	C_unshiu_01084_mRNA_9.1	-
GF0039961	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01084_mRNA_12.1	-
GF0039960	0	1	0	LRR and NB-ARC domain disease resistance protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01084_mRNA_11.1	-
GF0039959	0	1	0	Hypothetical protein (1)		Winged helix-turn-helix DNA-binding domain [IPR011991] (1); RNA-binding protein Lupus La [IPR006630] (1)	-	C_unshiu_01084_mRNA_1.1	-
GF0039958	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4218 [IPR025452] (1)	-	C_unshiu_01083_mRNA_8.1	-
GF0039957	0	1	0	Hypothetical protein (1)			-	C_unshiu_01083_mRNA_7.1	-
GF0039956	0	1	0	Terpene synthase 21, putative isoform 3 (1)	lyase activity [GO:0016829 molecular_function] (1); terpene synthase activity [GO:0010333 molecular_function] (1); magnesium ion binding [GO:0000287 molecular_function] (1)	Terpene synthase, metal-binding domain [IPR005630] (1); Isoprenoid synthase domain [IPR008949] (1)	-	C_unshiu_01083_mRNA_1.1	-
GF0039955	0	1	0	Hypothetical protein (1)			-	C_unshiu_01082_mRNA_8.1	-
GF0039954	0	1	0	Hypothetical protein (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1)	Glycoside hydrolase, catalytic domain [IPR013781] (1)	-	C_unshiu_01082_mRNA_2.1	-
GF0039953	0	1	0	Hypothetical protein (1)			-	C_unshiu_01082_mRNA_1.1	-
GF0039952	0	1	0	Hypothetical protein (1)		MULE transposase domain [IPR018289] (1)	-	C_unshiu_01081_mRNA_4.1	-
GF0039951	0	1	0	Geraniol 10-hydroxylase-like protein (1)	heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1)	Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450, conserved site [IPR017972] (1); Cytochrome P450 [IPR001128] (1)	-	C_unshiu_01081_mRNA_3.1	-
GF0039950	0	1	0	Hypothetical protein (1)			-	C_unshiu_01081_mRNA_2.1	-
GF0039949	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			-	C_unshiu_01081_mRNA_10.1	-
GF0039948	0	1	0	Hypothetical protein (1)	phosphorelay signal transduction system [GO:0000160 biological_process] (1)	CheY-like superfamily [IPR011006] (1); Signal transduction response regulator, receiver domain [IPR001789] (1)	-	C_unshiu_01080_mRNA_9.1	-
GF0039947	0	1	0	Vesicle transport v-SNARE 13 (1)	vesicle-mediated transport [GO:0016192 biological_process] (1); intracellular protein transport [GO:0006886 biological_process] (1); membrane [GO:0016020 cellular_component] (1)	t-SNARE [IPR010989] (1); Vesicle transport v-SNARE, N-terminal [IPR007705] (1)	-	C_unshiu_01080_mRNA_7.2	-
GF0039946	0	1	0	Hypothetical protein (1)			-	C_unshiu_01079_mRNA_10.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0039945	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Tetratricopeptide-like helical domain [IPR011990] (1); EF-hand domain pair [IPR011992] (1); Tetratricopeptide repeat-containing domain [IPR013026] (1)	-	C_unshiu_01079_mRNA_1.1	-
GF0039944	0	1	0	Curculin-like (Mannose-binding) lectin family protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Bulb-type lectin domain [IPR001480] (1); PAN/Apple domain [IPR003609] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	-	C_unshiu_01078_mRNA_7.1	-
GF0039943	0	1	0	Hypothetical protein (1)	protein transport [GO:0015031 biological_process] (1)	Vacuolar protein sorting-associated protein Ist1 [IPR005061] (1)	-	C_unshiu_01078_mRNA_12.1	-
GF0039942	0	1	0	Hypothetical protein (1)		Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_01078_mRNA_10.1	-
GF0039941	0	1	0	Hypothetical protein (1)			-	C_unshiu_01077_mRNA_8.1	-
GF0039940	0	1	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); microtubule motor activity [GO:0003777 molecular_function] (1); microtubule-based movement [GO:0007018 biological_process] (1); protein binding [GO:0005515 molecular_function] (1); microtubule binding [GO:0008017 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Calponin homology domain [IPR001715] (1); Kinesin-like protein [IPR027640] (1); Mitochondrial carrier domain [IPR023395] (1); Kinesin motor domain [IPR001752] (1); Kinesin motor domain, conserved site [IPR019821] (1); Mitochondrial substrate/solute carrier [IPR018108] (1)	-	C_unshiu_01077_mRNA_5.1	-
GF0039939	0	1	0	Hypothetical protein (1)	ligase activity [GO:0016874 molecular_function] (1); biosynthetic process [GO:0009058 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1)	Mur ligase, central [IPR013221] (1); Mur ligase, C-terminal [IPR004101] (1)	-	C_unshiu_01077_mRNA_12.1	-
GF0039938	0	1	0	Hypothetical protein (1)			-	C_unshiu_01077_mRNA_1.1	-
GF0039937	0	1	0	Hypothetical protein (1)			-	C_unshiu_01076_mRNA_3.1	-
GF0039936	0	1	0	Hypothetical protein (1)	apoplast [GO:0048046 cellular_component] (1); cellular glucan metabolic process [GO:0006073 biological_process] (1); xyloglucan:xyloglucosyl transferase activity [GO:0016762 molecular_function] (1); hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (1); cell wall [GO:0005618 cellular_component] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1)	Xyloglucan endo-transglycosylase, C-terminal [IPR010713] (1); Nucleotide-diphospho-sugar transferase [IPR005069] (1); Glycoside hydrolase family 16 [IPR000757] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Glycoside hydrolase, family 16, active site [IPR008263] (1)	-	C_unshiu_01075_mRNA_7.1	-
GF0039935	0	1	0	Putative AMP-dependent synthetase and ligase superfamily protein (1)	metabolic process [GO:0008152 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1)	AMP-binding enzyme C-terminal domain [IPR025110] (1); AMP-dependent synthetase/ligase [IPR000873] (1)	-	C_unshiu_01075_mRNA_16.1	-
GF0039934	0	1	0	Nicotianamine synthase (1)	nicotianamine synthase activity [GO:0030410 molecular_function] (1); nicotianamine biosynthetic process [GO:0030418 biological_process] (1)	Nicotianamine synthase [IPR004298] (1)	-	C_unshiu_01075_mRNA_13.1	-
GF0039933	0	1	0	Putative xyloglucan endotransglucosylase/hydrolase protein 23 (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1); hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (1)	Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Glycoside hydrolase, family 16, active site [IPR008263] (1); Glycoside hydrolase family 16 [IPR000757] (1)	-	C_unshiu_01075_mRNA_1.1	-
GF0039932	0	1	0	Gibberellin 2-oxidase 2 (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1)	Non-haem dioxygenase N-terminal domain [IPR026992] (1); Isopenicillin N synthase-like [IPR027443] (1); Oxoglutarate/iron-dependent dioxygenase [IPR005123] (1)	-	C_unshiu_01074_mRNA_8.1	-
GF0039931	0	1	0	CWC16 protein (1)		CWC16 protein [IPR007590] (1)	-	C_unshiu_01074_mRNA_4.1	-
GF0039930	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_01073_mRNA_4.1	-
GF0039929	0	1	0	Hypothetical protein (1)		MULE transposase domain [IPR018289] (1)	-	C_unshiu_01073_mRNA_3.1	-
GF0039928	0	1	0	Hypothetical protein (1)			-	C_unshiu_01072_mRNA_7.1	-
GF0039927	0	1	0	Hypothetical protein (1)			-	C_unshiu_01072_mRNA_6.1	-
GF0039926	0	1	0	Hypothetical protein (1)			-	C_unshiu_01072_mRNA_3.1	-
GF0039925	0	1	0	Hypothetical protein (1)			-	C_unshiu_01072_mRNA_10.1	-
GF0039924	0	1	0	Cytochrome P450 71B20 (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1)	Cytochrome P450, conserved site [IPR017972] (1); Cytochrome P450 [IPR001128] (1)	-	C_unshiu_01071_mRNA_8.1	-
GF0039923	0	1	0	Hypothetical protein (1)	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1)	Cytochrome P450 [IPR001128] (1)	-	C_unshiu_01071_mRNA_6.1	-
GF0039922	0	1	0	Hypothetical protein (1)		Gag-polypeptide of LTR copia-type [IPR029472] (1)	-	C_unshiu_01071_mRNA_5.1	-
GF0039921	0	1	0	Hypothetical protein (1)			-	C_unshiu_01071_mRNA_4.1	-
GF0039920	0	1	0	Hypothetical protein (1)			-	C_unshiu_01071_mRNA_2.1	-
GF0039919	0	1	0	Hypothetical protein (1)			-	C_unshiu_01071_mRNA_1.1	-
GF0039918	0	1	0	Putative AMP-dependent synthetase and ligase superfamily protein (1)	catalytic activity [GO:0003824 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	AMP-dependent synthetase/ligase [IPR000873] (1)	-	C_unshiu_01070_mRNA_3.1	-
GF0039917	0	1	0	Hypothetical protein (1)	GTPase activity [GO:0003924 molecular_function] (1); GTP binding [GO:0005525 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Dynamin-type guanine nucleotide-binding (G) domain [IPR030381] (1); Dynamin, GTPase region, conserved site [IPR019762] (1); Dynamin superfamily [IPR022812] (1); Dynamin, GTPase domain [IPR001401] (1)	-	C_unshiu_01070_mRNA_12.1	-
GF0039916	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01070_mRNA_1.1	-
GF0039915	0	1	0	Hypothetical protein (1)			-	C_unshiu_01069_mRNA_1.1	-
GF0039914	0	1	0	Histone demethylase UTY (1)			-	C_unshiu_01067_mRNA_9.1	-
GF0039913	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1)	NAD(P)-binding domain [IPR016040] (1); Alcohol dehydrogenase superfamily, zinc-type [IPR002085] (1)	-	C_unshiu_01067_mRNA_3.1	-
GF0039912	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Alcohol dehydrogenase, zinc-type, conserved site [IPR002328] (1); Alcohol dehydrogenase, N-terminal [IPR013154] (1); Alcohol dehydrogenase superfamily, zinc-type [IPR002085] (1); GroES-like [IPR011032] (1)	-	C_unshiu_01067_mRNA_2.1	-
GF0039911	0	1	0	NAC domain-containing protein 42 (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); DNA binding [GO:0003677 molecular_function] (1)	NAC domain [IPR003441] (1)	-	C_unshiu_01067_mRNA_12.1	-
GF0039910	0	1	0	Hypothetical protein (1)			-	C_unshiu_01067_mRNA_11.1	-
GF0039909	0	1	0	Hypothetical protein (1)			-	C_unshiu_01067_mRNA_10.1	-
GF0039908	0	1	0	Two-component response regulator ARR14 (1)	DNA binding [GO:0003677 molecular_function] (1)	Myb domain [IPR017930] (1); Homeodomain-like [IPR009057] (1); SANT/Myb domain [IPR001005] (1); Myb domain, plants [IPR006447] (1)	-	C_unshiu_01066_mRNA_15.1	-
GF0039907	0	1	0	Hypothetical protein (1)		Autophagy-related protein 1010 [IPR012445] (1)	-	C_unshiu_01066_mRNA_1.1	-
GF0039906	0	1	0	Hypothetical protein (1)	metabolic process [GO:0008152 biological_process] (1); transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	-	C_unshiu_01065_mRNA_9.1	-
GF0039905	0	1	0	Hypothetical protein (1)			-	C_unshiu_01065_mRNA_2.1	-
GF0039904	0	1	0	UDP-glycosyltransferase 83A1 (1)	transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	-	C_unshiu_01065_mRNA_11.1	-
GF0039903	0	1	0	Hypothetical protein (1)			-	C_unshiu_01064_mRNA_1.1	-
GF0039902	0	1	0	Hypothetical protein (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1)	Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_01063_mRNA_4.1	-
GF0039901	0	1	0	Hypothetical protein (1)			-	C_unshiu_01063_mRNA_3.1	-
GF0039900	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01062_mRNA_3.1	-
GF0039899	0	1	0	Hypothetical protein (1)			-	C_unshiu_01062_mRNA_2.1	-
GF0039898	0	1	0	Hypothetical protein (1)			-	C_unshiu_01061_mRNA_9.1	-
GF0039897	0	1	0	Hypothetical protein (1)			-	C_unshiu_01061_mRNA_8.1	-
GF0039896	0	1	0	Disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01061_mRNA_5.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0039895	0	1	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); nucleotide binding [GO:0000166 molecular_function] (1); cytoplasm [GO:0005737 cellular_component] (1); serine-tRNA ligase activity [GO:0004828 molecular_function] (1); seryl-tRNA aminoacylation [GO:0006434 biological_process] (1)	Serine-tRNA ligase, type1 [IPR002317] (1)	-	C_unshiu_01061_mRNA_2.1	-
GF0039894	0	1	0	Hexosyltransferase (1)	transferase activity, transferring glycosyl groups [GO:0016757 molecular_function] (1)	Nucleotide-diphospho-sugar transferases [IPR029044] (1); Glycosyl transferase, family 8 [IPR002495] (1)	-	C_unshiu_01061_mRNA_16.1	-
GF0039893	0	1	0	Hypothetical protein (1)			-	C_unshiu_01061_mRNA_13.1	-
GF0039892	0	1	0	Hypothetical protein (1)			-	C_unshiu_01061_mRNA_12.1	-
GF0039891	0	1	0	Hypothetical protein (1)			-	C_unshiu_01061_mRNA_11.1	-
GF0039890	0	1	0	Hypothetical protein (1)			-	C_unshiu_01061_mRNA_1.1	-
GF0039889	0	1	0	LRR receptor-like serine/threonine-protein kinase EFR (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1)	-	C_unshiu_01060_mRNA_6.1	-
GF0039888	0	1	0	Hypothetical protein (1)			-	C_unshiu_01060_mRNA_3.1	-
GF0039887	0	1	0	Hypothetical protein (1)			-	C_unshiu_01060_mRNA_2.1	-
GF0039886	0	1	0	Hypothetical protein (1)		Gcp-like domain [IPR000905] (1)	-	C_unshiu_01059_mRNA_4.1	-
GF0039885	0	1	0	Putative ribonuclease H protein At1g65750 (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_01058_mRNA_9.1	-
GF0039884	0	1	0	Hypothetical protein (1)			-	C_unshiu_01058_mRNA_7.1	-
GF0039883	0	1	0	LRR receptor-like kinase family protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	-	C_unshiu_01057_mRNA_7.1	-
GF0039882	0	1	0	Hypothetical protein (1)			-	C_unshiu_01057_mRNA_5.1	-
GF0039881	0	1	0	Hypothetical protein (1)			-	C_unshiu_01057_mRNA_4.1	-
GF0039880	0	1	0	LRR receptor-like kinase (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	-	C_unshiu_01057_mRNA_3.1	-
GF0039879	0	1	0	Hypothetical protein (1)			-	C_unshiu_01057_mRNA_2.1	-
GF0039878	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01057_mRNA_1.1	-
GF0039877	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01056_mRNA_11.1	-
GF0039876	0	1	0	Hypothetical protein (1)			-	C_unshiu_01055_mRNA_2.1	-
GF0039875	0	1	0	Hypothetical protein (1)		Transposon, En/Spm-like [IPR004242] (1); Domain of unknown function DUF4218 [IPR025452] (1)	-	C_unshiu_01055_mRNA_1.1	-
GF0039874	0	1	0	Hypothetical protein (1)			-	C_unshiu_01054_mRNA_6.1	-
GF0039873	0	1	0	Hypothetical protein (1)		Elongation factor G, III-V domain [IPR009022] (1); Ribosomal protein S5 domain 2-type fold, subgroup [IPR014721] (1); Translation elongation factor EFG, V domain [IPR000640] (1)	-	C_unshiu_01054_mRNA_5.1	-
GF0039872	0	1	0	Hypothetical protein (1)			-	C_unshiu_01054_mRNA_4.1	-
GF0039871	0	1	0	Hypothetical protein (1)			-	C_unshiu_01054_mRNA_2.1	-
GF0039870	0	1	0	Hypothetical protein (1)			-	C_unshiu_01054_mRNA_1.1	-
GF0039869	0	1	0	Hypothetical protein (1)			-	C_unshiu_01053_mRNA_7.1	-
GF0039868	0	1	0	Hypothetical protein (1)		Leucine-rich repeat 2 [IPR013101] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01053_mRNA_5.1	-
GF0039867	0	1	0	Hypothetical protein (1)			-	C_unshiu_01053_mRNA_4.1	-
GF0039866	0	1	0	Hypothetical protein (1)			-	C_unshiu_01053_mRNA_13.1	-
GF0039865	0	1	0	Hypothetical protein (1)			-	C_unshiu_01052_mRNA_9.1	-
GF0039864	0	1	0	Hypothetical protein (1)			-	C_unshiu_01052_mRNA_8.1	-
GF0039863	0	1	0	Hypothetical protein (1)		Protein of unknown function wound-induced [IPR022251] (1)	-	C_unshiu_01052_mRNA_3.1	-
GF0039862	0	1	0	Hypothetical protein (1)			-	C_unshiu_01052_mRNA_10.1	-
GF0039861	0	1	0	Hypothetical protein (1)			-	C_unshiu_01052_mRNA_1.1	-
GF0039860	0	1	0	Tryptophan synthase alpha chain (1)	metabolic process [GO:0008152 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1); tryptophan synthase activity [GO:0004834 molecular_function] (1); tryptophan metabolic process [GO:0006568 biological_process] (1)	Tryptophan synthase, alpha chain [IPR002028] (1); Aldolase-type TIM barrel [IPR013785] (1); Ribulose-phosphate binding barrel [IPR011060] (1)	-	C_unshiu_01051_mRNA_6.1	-
GF0039859	0	1	0	Hexosyltransferase (1)	transferase activity, transferring glycosyl groups [GO:0016757 molecular_function] (1)	Glycosyl transferase, family 8 [IPR002495] (1); Nucleotide-diphospho-sugar transferases [IPR029044] (1)	-	C_unshiu_01050_mRNA_7.1	-
GF0039858	0	1	0	Hypothetical protein (1)			-	C_unshiu_01048_mRNA_4.1	-
GF0039857	0	1	0	Phosphoribosylformylglycinamidine cyclo-ligase (1)		AIR synthase-related protein, C-terminal domain [IPR010918] (1)	-	C_unshiu_01048_mRNA_13.1	-
GF0039856	0	1	0	Hypothetical protein (1)			-	C_unshiu_01047_mRNA_7.1	-
GF0039855	0	1	0	Flavonoid 3',5'-hydroxylase (1)	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1)	Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450, conserved site [IPR017972] (1); Cytochrome P450 [IPR001128] (1)	-	C_unshiu_01047_mRNA_4.1	-
GF0039854	0	1	0	Hypothetical protein (1)			-	C_unshiu_01047_mRNA_1.1	-
GF0039853	0	1	0	Hypothetical protein (1)			-	C_unshiu_01046_mRNA_7.1	-
GF0039852	0	1	0	Hypothetical protein (1)			-	C_unshiu_01046_mRNA_1.1	-
GF0039851	0	1	0	Hypothetical protein (1)			-	C_unshiu_01045_mRNA_9.1	-
GF0039850	0	1	0	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_01045_mRNA_8.1	-
GF0039849	0	1	0	Hypothetical protein (1)			-	C_unshiu_01045_mRNA_4.1	-
GF0039848	0	1	0	Hypothetical protein (1)			-	C_unshiu_01045_mRNA_3.1	-
GF0039847	0	1	0	Epidermis-specific secreted glycoprotein EP1, putative (1)		Bulb-type lectin domain [IPR001480] (1)	-	C_unshiu_01045_mRNA_15.1	-
GF0039846	0	1	0	Epidermis-specific secreted EP1-like glycoprotein (1)	recognition of pollen [GO:0048544 biological_process] (1)	PAN/Apple domain [IPR003609] (1); S-locus glycoprotein domain [IPR000858] (1)	-	C_unshiu_01045_mRNA_14.1	-
GF0039845	0	1	0	Hypothetical protein (1)			-	C_unshiu_01045_mRNA_1.1	-
GF0039844	0	1	0	Hypothetical protein (1)			-	C_unshiu_01044_mRNA_13.1	-
GF0039843	0	1	0	Hypothetical protein (1)			-	C_unshiu_01044_mRNA_12.1	-
GF0039842	0	1	0	Putative disease resistance protein Cf-2.1 (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1)	-	C_unshiu_01043_mRNA_2.1	-
GF0039841	0	1	0	LRR receptor-like kinase (1)	protein binding [GO:0005515 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Protein kinase-like domain [IPR011009] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1)	-	C_unshiu_01043_mRNA_1.1	-
GF0039840	0	1	0	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01042_mRNA_4.1	-
GF0039839	0	1	0	Hypothetical protein (1)			-	C_unshiu_01042_mRNA_2.1	-
GF0039838	0	1	0	Hypothetical protein (1)		Cytochrome b5-like heme/steroid binding domain [IPR001199] (1)	-	C_unshiu_01042_mRNA_1.1	-
GF0039837	0	1	0	Hypothetical protein (1)			-	C_unshiu_01041_mRNA_6.1	-
GF0039836	0	1	0	Hypothetical protein (1)			-	C_unshiu_01041_mRNA_14.1	-
GF0039835	0	1	0	Hypothetical protein (1)			-	C_unshiu_01041_mRNA_13.1	-
GF0039834	0	1	0	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); copper ion binding [GO:0005507 molecular_function] (1)	Multicopper oxidase, copper-binding site [IPR002355] (1); Multicopper oxidases, conserved site [IPR033138] (1); Multicopper oxidase, type 2 [IPR011706] (1); Cupredoxin [IPR008972] (1)	-	C_unshiu_01041_mRNA_12.1	-
GF0039833	0	1	0	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1)	Multicopper oxidase, type 1 [IPR001117] (1); Cupredoxin [IPR008972] (1)	-	C_unshiu_01041_mRNA_11.1	-
GF0039832	0	1	0	Hypothetical protein (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Aspartic peptidase, active site [IPR001969] (1)	-	C_unshiu_01040_mRNA_9.1	-
GF0039831	0	1	0	Hypothetical protein (1)			-	C_unshiu_01040_mRNA_7.1	-
GF0039830	0	1	0	Early nodulin-like protein 3 (1)	electron carrier activity [GO:0009055 molecular_function] (1)	Cupredoxin [IPR008972] (1); Phytocyanin domain [IPR003245] (1)	-	C_unshiu_01040_mRNA_5.1	-
GF0039829	0	1	0	Hypothetical protein (1)			-	C_unshiu_01040_mRNA_4.1	-
GF0039828	0	1	0	Hypothetical protein (1)			-	C_unshiu_01040_mRNA_3.1	-
GF0039827	0	1	0	Hypothetical protein (1)			-	C_unshiu_01040_mRNA_2.1	-
GF0039826	0	1	0	Hypothetical protein (1)			-	C_unshiu_01040_mRNA_1.1	-
GF0039825	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4219 [IPR025314] (1)	-	C_unshiu_01039_mRNA_5.1	-
GF0039824	0	1	0	Hypothetical protein (1)			-	C_unshiu_01039_mRNA_4.1	-
GF0039823	0	1	0	Hypothetical protein (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1)	Glycoside hydrolase, catalytic domain [IPR013781] (1)	-	C_unshiu_01039_mRNA_3.1	-
GF0039822	0	1	0	Hypothetical protein (1)			-	C_unshiu_01038_mRNA_2.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0039821	0	1	0	Putative ATP-dependent RNA helicase DHX36 (1)	helicase activity [GO:0004386 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Domain of unknown function DUF1605 [IPR011709] (1); Helicase-associated domain [IPR007502] (1); Double-stranded RNA-binding domain [IPR014720] (1)	-	C_unshiu_01038_mRNA_1.1	-
GF0039820	0	1	0	NBS-LRR type disease resistance protein (1)			-	C_unshiu_01037_mRNA_7.1	-
GF0039819	0	1	0	DUF247 domain protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	C_unshiu_01037_mRNA_6.1	-
GF0039818	0	1	0	Hypothetical protein (1)			-	C_unshiu_01037_mRNA_3.1	-
GF0039817	0	1	0	CC-NBS-LRR disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_01037_mRNA_1.1	-
GF0039816	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_01036_mRNA_2.1	-
GF0039815	0	1	0	Hypothetical protein (1)			-	C_unshiu_01036_mRNA_12.1	-
GF0039814	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_01035_mRNA_3.1	-
GF0039813	0	1	0	Hypothetical protein (1)			-	C_unshiu_01035_mRNA_2.1	-
GF0039812	0	1	0	Caffeic acid 3-O-methyltransferase (1)	methyltransferase activity [GO:0008168 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1); O-methyltransferase activity [GO:0008171 molecular_function] (1)	S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); Plant methyltransferase dimerisation [IPR012967] (1); O-methyltransferase COMT-type [IPR016461] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); O-methyltransferase, family 2 [IPR001077] (1)	-	C_unshiu_01034_mRNA_9.1	-
GF0039811	0	1	0	Cytochrome P450 83B1 (1)	heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450, conserved site [IPR017972] (1); Cytochrome P450 [IPR001128] (1)	-	C_unshiu_01034_mRNA_7.1	-
GF0039810	0	1	0	Hypothetical protein (1)	O-methyltransferase activity [GO:0008171 molecular_function] (1)	O-methyltransferase, family 2 [IPR001077] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	C_unshiu_01034_mRNA_3.1	-
GF0039809	0	1	0	Hypothetical protein (1)			-	C_unshiu_01034_mRNA_15.1	-
GF0039808	0	1	0	CAI-1 autoinducer sensor kinase/phosphatase cqsS isoform 1 (1)		Harbinger transposase-derived nuclease domain [IPR027806] (1); Myb/SANT-like domain [IPR024752] (1)	-	C_unshiu_01034_mRNA_13.1	-
GF0039807	0	1	0	Cytochrome P450 83B1 (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1)	Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450 [IPR001128] (1)	-	C_unshiu_01034_mRNA_12.1	-
GF0039806	0	1	0	Caffeic acid 3-O-methyltransferase (1)	protein dimerization activity [GO:0046983 molecular_function] (1)	Plant methyltransferase dimerisation [IPR012967] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1)	-	C_unshiu_01034_mRNA_11.1	-
GF0039805	0	1	0	Hypothetical protein (1)			-	C_unshiu_01033_mRNA_3.1	-
GF0039804	0	1	0	Hypothetical protein (1)			-	C_unshiu_01033_mRNA_2.1	-
GF0039803	0	1	0	Hypothetical protein (1)			-	C_unshiu_01032_mRNA_9.1	-
GF0039802	0	1	0	Hypothetical protein (1)	response to oxidative stress [GO:0006979 biological_process] (1); heme binding [GO:0020037 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); peroxidase activity [GO:0004601 molecular_function] (1)	Haem peroxidase [IPR010255] (1); Haem peroxidase, plant/fungal/bacterial [IPR002016] (1); Peroxidase, active site [IPR019794] (1); Plant peroxidase [IPR000823] (1)	-	C_unshiu_01032_mRNA_2.1	-
GF0039801	0	1	0	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); peroxidase activity [GO:0004601 molecular_function] (1); response to oxidative stress [GO:0006979 biological_process] (1); heme binding [GO:0020037 molecular_function] (1)	Haem peroxidase, plant/fungal/bacterial [IPR002016] (1); Plant peroxidase [IPR000823] (1); Peroxidases heam-ligand binding site [IPR019793] (1); Haem peroxidase [IPR010255] (1)	-	C_unshiu_01032_mRNA_1.1	-
GF0039800	0	1	0	Hypothetical protein (1)			-	C_unshiu_01031_mRNA_5.1	-
GF0039799	0	1	0	Hypothetical protein (1)			-	C_unshiu_01030_mRNA_7.1	-
GF0039798	0	1	0	Hypothetical protein (1)			-	C_unshiu_01030_mRNA_13.1	-
GF0039797	0	1	0	Hypothetical protein (1)			-	C_unshiu_01030_mRNA_11.1	-
GF0039796	0	1	0	Hypothetical protein (1)			-	C_unshiu_01029_mRNA_9.1	-
GF0039795	0	1	0	Hypothetical protein (1)			-	C_unshiu_01029_mRNA_6.1	-
GF0039794	0	1	0	Hypothetical protein (1)			-	C_unshiu_01029_mRNA_5.1	-
GF0039793	0	1	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1)	Peptidase A2A, retrovirus, catalytic [IPR001995] (1)	-	C_unshiu_01029_mRNA_3.1	-
GF0039792	0	1	0	Hypothetical protein (1)			-	C_unshiu_01029_mRNA_2.1	-
GF0039791	0	1	0	Hypothetical protein (1)			-	C_unshiu_01029_mRNA_15.1	-
GF0039790	0	1	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_01029_mRNA_12.1	-
GF0039789	0	1	0	Hypothetical protein (1)			-	C_unshiu_01029_mRNA_11.1	-
GF0039788	0	1	0	Hypothetical protein (1)			-	C_unshiu_01029_mRNA_10.1	-
GF0039787	0	1	0	Hypothetical protein (1)			-	C_unshiu_01028_mRNA_9.1	-
GF0039786	0	1	0	Hypothetical protein (1)			-	C_unshiu_01028_mRNA_11.1	-
GF0039785	0	1	0	Hypothetical protein (1)			-	C_unshiu_01028_mRNA_10.1	-
GF0039784	0	1	0	Hypothetical protein (1)			-	C_unshiu_01027_mRNA_10.1	-
GF0039783	0	1	0	Hypothetical protein (1)			-	C_unshiu_01026_mRNA_7.1	-
GF0039782	0	1	0	UDP-glycosyltransferase 73C7 (1)	metabolic process [GO:0008152 biological_process] (1); transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	-	C_unshiu_01026_mRNA_3.1	-
GF0039781	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_01026_mRNA_2.1	-
GF0039780	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	C_unshiu_01026_mRNA_1.1	-
GF0039779	0	1	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	-	C_unshiu_01025_mRNA_6.1	-
GF0039778	0	1	0	HAT family dimerisation domain containing protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	Zinc finger, BED-type [IPR003656] (1); hAT-like transposase, RNase-H fold [IPR025525] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_01025_mRNA_5.1	-
GF0039777	0	1	0	Hypothetical protein (1)			-	C_unshiu_01025_mRNA_3.1	-
GF0039776	0	1	0	Hypothetical protein (1)			-	C_unshiu_01025_mRNA_2.1	-
GF0039775	0	1	0	AP2-like ethylene-responsive transcription factor BBM2 (1)	DNA binding [GO:0003677 molecular_function] (1); multicellular organismal development [GO:0007275 biological_process] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (1)	AP2-like ethylene-responsive transcription factor [IPR031112] (1); AP2/ERF domain [IPR001471] (1); DNA-binding domain [IPR016177] (1)	-	C_unshiu_01025_mRNA_14.1	-
GF0039774	0	1	0	Hypothetical protein (1)			-	C_unshiu_01024_mRNA_9.1	-
GF0039773	0	1	0	Hypothetical protein (1)			-	C_unshiu_01024_mRNA_8.1	-
GF0039772	0	1	0	Hypothetical protein (1)			-	C_unshiu_01024_mRNA_7.1	-
GF0039771	0	1	0	Hypothetical protein (1)			-	C_unshiu_01024_mRNA_5.1	-
GF0039770	0	1	0	Hypothetical protein (1)			-	C_unshiu_01024_mRNA_3.1	-
GF0039769	0	1	0	Hypothetical protein (1)			-	C_unshiu_01024_mRNA_2.1	-
GF0039768	0	1	0	Hypothetical protein (1)			-	C_unshiu_01024_mRNA_18.1	-
GF0039767	0	1	0	Hypothetical protein (1)			-	C_unshiu_01024_mRNA_17.1	-
GF0039766	0	1	0	Hypothetical protein (1)			-	C_unshiu_01024_mRNA_1.1	-
GF0039765	0	1	0	Hypothetical protein (1)			-	C_unshiu_01023_mRNA_8.1	-
GF0039764	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4218 [IPR025452] (1); Transposon, En/Spm-like [IPR004242] (1)	-	C_unshiu_01022_mRNA_14.1	-
GF0039763	0	1	0	Hypothetical protein (1)			-	C_unshiu_01022_mRNA_13.1	-
GF0039762	0	1	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	-	C_unshiu_01022_mRNA_12.1	-
GF0039761	0	1	0	Hypothetical protein (1)			-	C_unshiu_01021_mRNA_5.1	-
GF0039760	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			-	C_unshiu_01021_mRNA_4.1	-
GF0039759	0	1	0	Hypothetical protein (1)			-	C_unshiu_01020_mRNA_7.1	-
GF0039758	0	1	0	Hypothetical protein (1)			-	C_unshiu_01020_mRNA_4.1	-
GF0039757	0	1	0	Hypothetical protein (1)			-	C_unshiu_01019_mRNA_6.1	-
GF0039756	0	1	0	Hypothetical protein (1)			-	C_unshiu_01019_mRNA_5.1	-
GF0039755	0	1	0	Hypothetical protein (1)			-	C_unshiu_01019_mRNA_2.1	-
GF0039754	0	1	0	Hypothetical protein (1)			-	C_unshiu_01019_mRNA_14.1	-
GF0039753	0	1	0	Hypothetical protein (1)			-	C_unshiu_01019_mRNA_13.1	-
GF0039752	0	1	0	Hypothetical protein (1)			-	C_unshiu_01019_mRNA_12.1	-
GF0039751	0	1	0	Hypothetical protein (1)		Chromo domain-like [IPR016197] (1); Chromo domain [IPR023780] (1)	-	C_unshiu_01019_mRNA_11.1	-
GF0039750	0	1	0	Hypothetical protein (1)			-	C_unshiu_01019_mRNA_1.1	-
GF0039749	0	1	0	Hypothetical protein (1)			-	C_unshiu_01018_mRNA_9.1	-
GF0039748	0	1	0	Hypothetical protein (1)			-	C_unshiu_01018_mRNA_10.1	-
GF0039747	0	1	0	Polynucleotidyl transferase, Ribonuclease H fold (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_01018_mRNA_1.1	-
GF0039746	0	1	0	Hypothetical protein (1)			-	C_unshiu_01017_mRNA_7.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0039745	0	1	0	Hypothetical protein (1)	DNA integration [GO:0015074 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Integrase, catalytic core [IPR001584] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_01017_mRNA_2.1	-
GF0039744	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_01017_mRNA_13.1	-
GF0039743	0	1	0	Hypothetical protein (1)			-	C_unshiu_01017_mRNA_12.1	-
GF0039742	0	1	0	Hypothetical protein (1)			-	C_unshiu_01017_mRNA_11.1	-
GF0039741	0	1	0	Hypothetical protein (1)			-	C_unshiu_01017_mRNA_10.1	-
GF0039740	0	1	0	Hypothetical protein (1)			-	C_unshiu_01017_mRNA_1.1	-
GF0039739	0	1	0	Hypothetical protein (1)	transcription, DNA-templated [GO:0006351 biological_process] (1); DNA-directed RNA polymerase activity [GO:0003899 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	RNA polymerase, alpha subunit, C-terminal [IPR011260] (1)	-	C_unshiu_01016_mRNA_7.1	-
GF0039738	0	1	0	DNA-directed RNA polymerase, alpha subunit (1)	transcription, DNA-templated [GO:0006351 biological_process] (1); DNA-directed RNA polymerase activity [GO:0003899 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	DNA-directed RNA polymerase, RBP11-like dimerisation domain [IPR009025] (1); DNA-directed RNA polymerase, insert domain [IPR011262] (1); DNA-directed RNA polymerase, RpoA/D/Rpb3-type [IPR011263] (1)	-	C_unshiu_01016_mRNA_4.1	-
GF0039737	0	1	0	30S ribosomal protein S11, chloroplastic (1)	ribosome [GO:0005840 cellular_component] (1); translation [GO:0006412 biological_process] (1); intracellular [GO:0005622 cellular_component] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1)	Ribosomal S11, conserved site [IPR018102] (1); Ribosomal protein S11 [IPR001971] (1); Ribosomal protein S11, bacterial-type [IPR019981] (1)	-	C_unshiu_01016_mRNA_3.1	-
GF0039736	0	1	0	DNA-directed RNA polymerase, alpha subunit (1)	transcription, DNA-templated [GO:0006351 biological_process] (1); protein dimerization activity [GO:0046983 molecular_function] (1); DNA-directed RNA polymerase activity [GO:0003899 molecular_function] (1)	DNA-directed RNA polymerase, RBP11-like dimerisation domain [IPR009025] (1); DNA-directed RNA polymerase, RpoA/D/Rpb3-type [IPR011263] (1); DNA-directed RNA polymerase, insert domain [IPR011262] (1)	-	C_unshiu_01016_mRNA_2.1	-
GF0039735	0	1	0	Hypothetical protein (1)			-	C_unshiu_01015_mRNA_9.1	-
GF0039734	0	1	0	Heat shock protein 70 (1)		Heat shock protein 70kD, peptide-binding domain [IPR029047] (1); Heat shock protein 70 family [IPR013126] (1); Heat shock protein 70, conserved site [IPR018181] (1); Heat shock protein 70kD, C-terminal domain [IPR029048] (1)	-	C_unshiu_01015_mRNA_8.1	-
GF0039733	0	1	0	Hypothetical protein (1)			-	C_unshiu_01015_mRNA_7.1	-
GF0039732	0	1	0	Probable retroelement pol polyprotein-, putative (1)			-	C_unshiu_01015_mRNA_6.1	-
GF0039731	0	1	0	Hypothetical protein (1)	iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1)	Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450 [IPR001128] (1)	-	C_unshiu_01015_mRNA_5.1	-
GF0039730	0	1	0	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	C_unshiu_01015_mRNA_2.1	-
GF0039729	0	1	0	Hypothetical protein (1)		Arabidopsis retrotransposon Orf1 [IPR004312] (1)	-	C_unshiu_01015_mRNA_10.1	-
GF0039728	0	1	0	LRR receptor-like kinase family protein (1)	protein binding [GO:0005515 molecular_function] (1)	Retrotransposon gag domain [IPR005162] (1); Leucine-rich repeat [IPR001611] (1); Protein kinase-like domain [IPR011009] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1)	-	C_unshiu_01015_mRNA_1.1	-
GF0039727	0	1	0	Hypothetical protein (1)		Thioredoxin-like fold [IPR012336] (1)	-	C_unshiu_01014_mRNA_8.1	-
GF0039726	0	1	0	Hypothetical protein (1)			-	C_unshiu_01014_mRNA_2.1	-
GF0039725	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Domain of unknown function DUF1985 [IPR015410] (1)	-	C_unshiu_01014_mRNA_14.1	-
GF0039724	0	1	0	Hypothetical protein (1)			-	C_unshiu_01014_mRNA_1.1	-
GF0039723	0	1	0	Hypothetical protein (1)			-	C_unshiu_01013_mRNA_8.1	-
GF0039722	0	1	0	Hypothetical protein (1)		NAD(P)-binding domain [IPR016040] (1); NmrA-like domain [IPR008030] (1)	-	C_unshiu_01013_mRNA_4.1	-
GF0039721	0	1	0	60S ribosomal protein L14 (1)	ribosome [GO:0005840 cellular_component] (1); translation [GO:0006412 biological_process] (1); intracellular [GO:0005622 cellular_component] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1)	Ribosomal protein L2 domain 2 [IPR014722] (1); Ribosomal protein L14 [IPR002784] (1); Translation protein SH3-like domain [IPR008991] (1)	-	C_unshiu_01013_mRNA_3.1	-
GF0039720	0	1	0	Hypothetical protein (1)			-	C_unshiu_01013_mRNA_11.1	-
GF0039719	0	1	0	Hypothetical protein (1)			-	C_unshiu_01010_mRNA_9.1	-
GF0039718	0	1	0	Hypothetical protein (1)			-	C_unshiu_01010_mRNA_8.1	-
GF0039717	0	1	0	Hypothetical protein (1)			-	C_unshiu_01010_mRNA_7.1	-
GF0039716	0	1	0	Hypothetical protein (1)			-	C_unshiu_01010_mRNA_6.1	-
GF0039715	0	1	0	Hypothetical protein (1)			-	C_unshiu_01010_mRNA_5.1	-
GF0039714	0	1	0	Hypothetical protein (1)			-	C_unshiu_01010_mRNA_4.1	-
GF0039713	0	1	0	Hypothetical protein (1)			-	C_unshiu_01010_mRNA_3.1	-
GF0039712	0	1	0	Hypothetical protein (1)			-	C_unshiu_01010_mRNA_2.1	-
GF0039711	0	1	0	Hypothetical protein (1)	secondary active sulfate transmembrane transporter activity [GO:0008271 molecular_function] (1); sulfate transport [GO:0008272 biological_process] (1); integral component of membrane [GO:0016021 cellular_component] (1); membrane [GO:0016020 cellular_component] (1); sulfate transmembrane transporter activity [GO:0015116 molecular_function] (1); transmembrane transport [GO:0055085 biological_process] (1); chloroplast [GO:0009507 cellular_component] (1)	STAS domain [IPR002645] (1); Sulphate anion transporter, conserved site [IPR018045] (1); SLC26A/SulP transporter domain [IPR011547] (1); Harbinger transposase-derived nuclease domain [IPR027806] (1); Sulfate transporter 3.1/3.2 [IPR030311] (1); SLC26A/SulP transporter [IPR001902] (1)	-	C_unshiu_01010_mRNA_11.1	-
GF0039710	0	1	0	Hypothetical protein (1)			-	C_unshiu_01010_mRNA_10.1	-
GF0039709	0	1	0	Nematode resistance-like protein (1)	signal transduction [GO:0007165 biological_process] (1); ADP binding [GO:0043531 molecular_function] (1); GTP binding [GO:0005525 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1); GTPase activity [GO:0003924 molecular_function] (1)	Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1); Dynamin GTPase effector [IPR003130] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); PH domain-like [IPR011993] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); GTPase effector domain [IPR020850] (1); Leucine-rich repeat [IPR001611] (1); Pleckstrin homology domain [IPR001849] (1); Dynamin central domain [IPR000375] (1); NB-ARC [IPR002182] (1)	-	C_unshiu_01010_mRNA_1.1	-
GF0039708	0	1	0	Orotate phosphoribosyltransferase, putative (1)	nucleoside metabolic process [GO:0009116 biological_process] (1); orotate phosphoribosyltransferase activity [GO:0004588 molecular_function] (1); pyrimidine nucleotide biosynthetic process [GO:0006221 biological_process] (1)	Orotate phosphoribosyltransferase [IPR023031] (1); Orotate phosphoribosyl transferase domain [IPR004467] (1); Phosphoribosyltransferase domain [IPR000836] (1); Phosphoribosyltransferase-like [IPR029057] (1)	-	C_unshiu_01009_mRNA_8.1	-
GF0039707	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_01009_mRNA_5.1	-
GF0039706	0	1	0	Hypothetical protein (1)			-	C_unshiu_01009_mRNA_10.1	-
GF0039705	0	1	0	Hypothetical protein (1)			-	C_unshiu_01007_mRNA_9.1	-
GF0039704	0	1	0	Hypothetical protein (1)			-	C_unshiu_01007_mRNA_8.1	-
GF0039703	0	1	0	BURP domain-containing protein (1)		BURP domain [IPR004873] (1)	-	C_unshiu_01007_mRNA_6.1	-
GF0039702	0	1	0	BURP domain-containing protein (1)		BURP domain [IPR004873] (1)	-	C_unshiu_01007_mRNA_2.1	-
GF0039701	0	1	0	Hypothetical protein (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); zinc ion binding [GO:0008270 molecular_function] (1)	NAD(P)-binding domain [IPR016040] (1); GroES-like [IPR011032] (1); Protein of unknown function DUF677 [IPR007749] (1); Alcohol dehydrogenase, N-terminal [IPR013154] (1); Alcohol dehydrogenase, zinc-type, conserved site [IPR002328] (1)	-	C_unshiu_01006_mRNA_6.1	-
GF0039700	0	1	0	Hypothetical protein (1)			-	C_unshiu_01006_mRNA_1.1	-
GF0039699	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Zinc knuckle CX2CX4HX4C [IPR025836] (1)	-	C_unshiu_01005_mRNA_9.1	-
GF0039698	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_01005_mRNA_5.1	-
GF0039697	0	1	0	Hemopexin (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	C_unshiu_01005_mRNA_4.1	-
GF0039696	0	1	0	Hypothetical protein (1)			-	C_unshiu_01005_mRNA_2.1	-
GF0039695	0	1	0	Hypothetical protein (1)			-	C_unshiu_01005_mRNA_12.1	-
GF0039694	0	1	0	Hypothetical protein (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_01004_mRNA_8.1	-
GF0039693	0	1	0	Dephospho-CoA kinase family isoform 1 (1)	ATP binding [GO:0005524 molecular_function] (1); coenzyme A biosynthetic process [GO:0015937 biological_process] (1); dephospho-CoA kinase activity [GO:0004140 molecular_function] (1)	Dephospho-CoA kinase [IPR001977] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_01004_mRNA_2.1	-
GF0039692	0	1	0	Hypothetical protein (1)			-	C_unshiu_01004_mRNA_1.1	-
GF0039691	0	1	0	Hypothetical protein (1)			-	C_unshiu_01003_mRNA_13.1	-
GF0039690	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	-	C_unshiu_01003_mRNA_11.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0039689	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_01003_mRNA_1.1	-
GF0039688	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4219 [IPR025314] (1)	-	C_unshiu_01002_mRNA_6.1	-
GF0039687	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			-	C_unshiu_01002_mRNA_3.1	-
GF0039686	0	1	0	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); pentose-phosphate shunt [GO:0006098 biological_process] (1); phosphogluconate dehydrogenase (decarboxylating) activity [GO:0004616 molecular_function] (1)	6-phosphogluconate dehydrogenase, C-terminal [IPR006114] (1); 6-phosphogluconate dehydrogenase, domain 3 [IPR012284] (1); 6-phosphogluconate dehydrogenase C-terminal domain-like [IPR008927] (1)	-	C_unshiu_01001_mRNA_5.1	-
GF0039685	0	1	0	Hypothetical protein (1)	signal transduction [GO:0007165 biological_process] (1); protein binding [GO:0005515 molecular_function] (1)	Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1)	-	C_unshiu_01001_mRNA_4.1	-
GF0039684	0	1	0	Hypothetical protein (1)		Alpha/Beta hydrolase fold [IPR029058] (1)	-	C_unshiu_01001_mRNA_11.1	-
GF0039683	0	1	0	Protein AIG1 (1)	GTP binding [GO:0005525 molecular_function] (1)	AIG1-type guanine nucleotide-binding (G) domain [IPR006703] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_01001_mRNA_1.1	-
GF0039682	0	1	0	Hypothetical protein (1)			-	C_unshiu_01000_mRNA_9.1	-
GF0039681	0	1	0	Hypothetical protein (1)			-	C_unshiu_01000_mRNA_8.1	-
GF0039680	0	1	0	Hypothetical protein (1)			-	C_unshiu_01000_mRNA_7.1	-
GF0039679	0	1	0	Hypothetical protein (1)			-	C_unshiu_01000_mRNA_6.1	-
GF0039678	0	1	0	Hypothetical protein (1)			-	C_unshiu_01000_mRNA_5.1	-
GF0039677	0	1	0	Hypothetical protein (1)			-	C_unshiu_01000_mRNA_2.1	-
GF0039676	0	1	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	Zinc finger, BED-type [IPR003656] (1)	-	C_unshiu_01000_mRNA_17.1	-
GF0039675	0	1	0	Hypothetical protein (1)			-	C_unshiu_01000_mRNA_15.1	-
GF0039674	0	1	0	Hypothetical protein (1)			-	C_unshiu_01000_mRNA_13.1	-
GF0039673	0	1	0	Hypothetical protein (1)			-	C_unshiu_01000_mRNA_11.1	-
GF0039672	0	1	0	Hypothetical protein (1)			-	C_unshiu_01000_mRNA_10.1	-
GF0039671	0	1	0	Trehalose-phosphatase (1)	trehalose biosynthetic process [GO:0005992 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1)	Trehalose-phosphatase [IPR003337] (1); HAD-like domain [IPR023214] (1)	-	C_unshiu_01000_mRNA_1.1	-
GF0039670	0	1	0	Eukaryotic peptide chain release factor subunit 1-3 (1)	translation release factor activity, codon specific [GO:0016149 molecular_function] (1); cytoplasm [GO:0005737 cellular_component] (1); translational termination [GO:0006415 biological_process] (1)	eRF1 domain 2 [IPR005141] (1); Peptide chain release factor eRF1/aRF1 [IPR004403] (1); eRF1 domain 3 [IPR005142] (1); 50S ribosomal protein L30e-like [IPR029064] (1)	-	C_unshiu_00999_mRNA_6.1	-
GF0039669	0	1	0	Hypothetical protein (1)			-	C_unshiu_00999_mRNA_12.1	-
GF0039668	0	1	0	Hypothetical protein (1)		Prolamin-like domain [IPR008502] (1)	-	C_unshiu_00999_mRNA_1.1	-
GF0039667	0	1	0	Hypothetical protein (1)			-	C_unshiu_00998_mRNA_12.1	-
GF0039666	0	1	0	Monosacharide transport protein (1)			-	C_unshiu_00998_mRNA_10.1	-
GF0039665	0	1	0	Hypothetical protein (1)	beta-fructofuranosidase activity [GO:0004564 molecular_function] (1); sucrose alpha-glucosidase activity [GO:0004575 molecular_function] (1)	Beta-fructofuranosidase [IPR021792] (1)	-	C_unshiu_00997_mRNA_8.1	-
GF0039664	0	1	0	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); copper ion binding [GO:0005507 molecular_function] (1); hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1)	Glycosyl hydrolase family 32, C-terminal [IPR013189] (1); Glycosyl hydrolase family 32, N-terminal [IPR013148] (1); Glycosyl hydrolase, five-bladed beta-propellor domain [IPR023296] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Multicopper oxidase, type 1 [IPR001117] (1); Multicopper oxidase, type 2 [IPR011706] (1); Cupredoxin [IPR008972] (1); Glycoside hydrolase, family 32 [IPR001362] (1)	-	C_unshiu_00997_mRNA_7.1	-
GF0039663	0	1	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	NAC domain [IPR003441] (1)	-	C_unshiu_00997_mRNA_3.1	-
GF0039662	0	1	0	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	-	C_unshiu_00996_mRNA_12.1	-
GF0039661	0	1	0	Hypothetical protein (1)			-	C_unshiu_00996_mRNA_11.1	-
GF0039660	0	1	0	Putative ubiquitin carboxyl-terminal hydrolase superfamily protein (1)	protein deubiquitination [GO:0016579 biological_process] (1); thiol-dependent ubiquitinyl hydrolase activity [GO:0036459 molecular_function] (1)	Peptidase C19, ubiquitin carboxyl-terminal hydrolase [IPR001394] (1); Ubiquitin specific protease domain [IPR028889] (1)	-	C_unshiu_00996_mRNA_1.1	-
GF0039659	0	1	0	Exonuclease family protein, expressed (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Exonuclease, RNase T/DNA polymerase III [IPR013520] (1)	-	C_unshiu_00995_mRNA_9.1	-
GF0039658	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_00995_mRNA_8.1	-
GF0039657	0	1	0	Hypothetical protein (1)			-	C_unshiu_00995_mRNA_7.1	-
GF0039656	0	1	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	Zinc finger, BED-type [IPR003656] (1)	-	C_unshiu_00995_mRNA_14.1	-
GF0039655	0	1	0	Hypothetical protein (1)			-	C_unshiu_00995_mRNA_12.1	-
GF0039654	0	1	0	Hypothetical protein (1)			-	C_unshiu_00994_mRNA_6.1	-
GF0039653	0	1	0	Hypothetical protein (1)	mRNA splicing, via spliceosome [GO:0000398 biological_process] (1); nucleus [GO:0005634 cellular_component] (1)	PRP1 splicing factor, N-terminal [IPR010491] (1)	-	C_unshiu_00994_mRNA_3.1	-
GF0039652	0	1	0	Hypothetical protein (1)			-	C_unshiu_00994_mRNA_2.1	-
GF0039651	0	1	0	Hypothetical protein (1)			-	C_unshiu_00994_mRNA_14.1	-
GF0039650	0	1	0	Hypothetical protein (1)			-	C_unshiu_00994_mRNA_13.1	-
GF0039649	0	1	0	Hypothetical protein (1)			-	C_unshiu_00994_mRNA_12.1	-
GF0039648	0	1	0	Hypothetical protein (1)			-	C_unshiu_00994_mRNA_11.1	-
GF0039647	0	1	0	Putative non-LTR retroelement reverse transcriptase (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Domain of unknown function DUF4283 [IPR025558] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00993_mRNA_7.1	-
GF0039646	0	1	0	Hypothetical protein (1)			-	C_unshiu_00992_mRNA_14.1	-
GF0039645	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_00991_mRNA_6.1	-
GF0039644	0	1	0	Hypothetical protein (1)			-	C_unshiu_00991_mRNA_4.1	-
GF0039643	0	1	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); Arabidopsis retrotransposon Orf1 [IPR004312] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00991_mRNA_10.1	-
GF0039642	0	1	0	26S proteasome non-ATPase regulatory subunit 4 (1)	ubiquitin-dependent protein catabolic process [GO:0006511 biological_process] (1); proteasome regulatory particle, base subcomplex [GO:0008540 cellular_component] (1)	von Willebrand factor, type A [IPR002035] (1); Proteasome subunit Rpn10 [IPR027040] (1); Ubiquitin interacting motif [IPR003903] (1)	-	C_unshiu_00990_mRNA_4.1	-
GF0039641	0	1	0	Hypothetical protein (1)			-	C_unshiu_00990_mRNA_3.1	-
GF0039640	0	1	0	Hypothetical protein (1)			-	C_unshiu_00990_mRNA_11.1	-
GF0039639	0	1	0	Hypothetical protein (1)			-	C_unshiu_00989_mRNA_17.1	-
GF0039638	0	1	0	Hypothetical protein (1)			-	C_unshiu_00989_mRNA_12.1	-
GF0039637	0	1	0	Hypothetical protein (1)			-	C_unshiu_00988_mRNA_9.1	-
GF0039636	0	1	0	Hypothetical protein (1)			-	C_unshiu_00988_mRNA_4.1	-
GF0039635	0	1	0	Hypothetical protein (1)			-	C_unshiu_00988_mRNA_3.1	-
GF0039634	0	1	0	Putative disease resistance gene NBS-LRR family protein (1)	ADP binding [GO:0043531 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); AAA+ ATPase domain [IPR003593] (1); NB-ARC [IPR002182] (1)	-	C_unshiu_00988_mRNA_17.1	-
GF0039633	0	1	0	Phosphoprotein phosphatase (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00988_mRNA_16.1	-
GF0039632	0	1	0	Hypothetical protein (1)			-	C_unshiu_00988_mRNA_14.1	-
GF0039631	0	1	0	Hypothetical protein (1)			-	C_unshiu_00988_mRNA_12.1	-
GF0039630	0	1	0	Hypothetical protein (1)			-	C_unshiu_00988_mRNA_10.1	-
GF0039629	0	1	0	Hypothetical protein (1)			-	C_unshiu_00986_mRNA_7.1	-
GF0039628	0	1	0	Hypothetical protein (1)			-	C_unshiu_00986_mRNA_6.1	-
GF0039627	0	1	0	START domain-containing protein (1)	lipid binding [GO:0008289 molecular_function] (1)	START-like domain [IPR023393] (1); START domain [IPR002913] (1); Pleckstrin homology domain [IPR001849] (1); Domain of unknown function DUF1336 [IPR009769] (1); PH domain-like [IPR011993] (1)	-	C_unshiu_00986_mRNA_10.1	-
GF0039626	0	1	0	Hypothetical protein (1)			-	C_unshiu_00986_mRNA_1.1	-
GF0039625	0	1	0	Transferase family protein (1)	transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (1)	Chloramphenicol acetyltransferase-like domain [IPR023213] (1); Transferase [IPR003480] (1)	-	C_unshiu_00983_mRNA_9.1	-
GF0039624	0	1	0	Acylsugar acyltransferase 3 (1)	transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (1)	Chloramphenicol acetyltransferase-like domain [IPR023213] (1); Transferase [IPR003480] (1)	-	C_unshiu_00983_mRNA_8.1	-
GF0039623	0	1	0	Hypothetical protein (1)			-	C_unshiu_00983_mRNA_6.1	-
GF0039622	0	1	0	Hypothetical protein (1)			-	C_unshiu_00983_mRNA_5.1	-
GF0039621	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00983_mRNA_2.1	-
GF0039620	0	1	0	Hypothetical protein (1)			-	C_unshiu_00983_mRNA_1.1	-
GF0039619	0	1	0	Hypothetical protein (1)			-	C_unshiu_00982_mRNA_9.1	-
GF0039618	0	1	0	Hypothetical protein (1)			-	C_unshiu_00982_mRNA_4.1	-
GF0039617	0	1	0	Hypothetical protein (1)			-	C_unshiu_00982_mRNA_12.1	-
GF0039616	0	1	0	Hypothetical protein (1)			-	C_unshiu_00982_mRNA_11.1	-
GF0039615	0	1	0	LRR receptor-like kinase family protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	-	C_unshiu_00982_mRNA_10.1	-
GF0039614	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); nucleotide binding [GO:0000166 molecular_function] (1)	Nucleotide-binding alpha-beta plait domain [IPR012677] (1); RNA recognition motif 2 [IPR007201] (1); RNA recognition motif domain [IPR000504] (1)	-	C_unshiu_00981_mRNA_8.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0039613	0	1	0	Hypothetical protein (1)		MULE transposase domain [IPR018289] (1)	-	C_unshiu_00981_mRNA_5.1	-
GF0039612	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, PMZ-type [IPR006564] (1); Zinc finger, SWIM-type [IPR007527] (1)	-	C_unshiu_00981_mRNA_4.1	-
GF0039611	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	FAR1 DNA binding domain [IPR004330] (1); FHY3/FAR1 family [IPR031052] (1); Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00981_mRNA_10.1	-
GF0039610	0	1	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_00980_mRNA_8.1	-
GF0039609	0	1	0	Hypothetical protein (1)			-	C_unshiu_00980_mRNA_7.1	-
GF0039608	0	1	0	Hypothetical protein (1)			-	C_unshiu_00980_mRNA_4.1	-
GF0039607	0	1	0	Hypothetical protein (1)			-	C_unshiu_00978_mRNA_13.1	-
GF0039606	0	1	0	Calcium-transporting ATPase 4, endoplasmic reticulum-type (1)	metal ion binding [GO:0046872 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1); nucleotide binding [GO:0000166 molecular_function] (1)	P-type ATPase, phosphorylation site [IPR018303] (1); P-type ATPase [IPR001757] (1); P-type ATPase, transmembrane domain [IPR023298] (1); Cation-transporting P-type ATPase, C-terminal [IPR006068] (1); P-type ATPase, cytoplasmic domain N [IPR023299] (1); P-type ATPase, A domain [IPR008250] (1); Cation-transporting P-type ATPase, N-terminal [IPR004014] (1); HAD-like domain [IPR023214] (1)	-	C_unshiu_00978_mRNA_1.1	-
GF0039605	0	1	0	Hypothetical protein (1)			-	C_unshiu_00977_mRNA_8.1	-
GF0039604	0	1	0	Hypothetical protein (1)			-	C_unshiu_00977_mRNA_5.1	-
GF0039603	0	1	0	Hypothetical protein (1)			-	C_unshiu_00977_mRNA_3.1	-
GF0039602	0	1	0	Hypothetical protein (1)			-	C_unshiu_00977_mRNA_2.1	-
GF0039601	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4219 [IPR025314] (1)	-	C_unshiu_00977_mRNA_15.1	-
GF0039600	0	1	0	Hypothetical protein (1)			-	C_unshiu_00977_mRNA_14.1	-
GF0039599	0	1	0	Hypothetical protein (1)			-	C_unshiu_00977_mRNA_1.1	-
GF0039598	0	1	0	Hypothetical protein (1)		Nucleophile aminohydrolases, N-terminal [IPR029055] (1); Glutamine amidotransferase type 2 domain [IPR017932] (1)	-	C_unshiu_00976_mRNA_9.1	-
GF0039597	0	1	0	Hypothetical protein (1)		Peptidase S8, subtilisin-related [IPR015500] (1)	-	C_unshiu_00976_mRNA_7.1	-
GF0039596	0	1	0	Hypothetical protein (1)		Peptidase S8, subtilisin-related [IPR015500] (1)	-	C_unshiu_00976_mRNA_6.1	-
GF0039595	0	1	0	Hypothetical protein (1)			-	C_unshiu_00976_mRNA_2.1	-
GF0039594	0	1	0	LRR receptor-like kinase family protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1)	-	C_unshiu_00976_mRNA_1.1	-
GF0039593	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00975_mRNA_4.1	-
GF0039592	0	1	0	Hypothetical protein (1)			-	C_unshiu_00974_mRNA_9.1	-
GF0039591	0	1	0	Lysosomal Pro-Xaa carboxypeptidase (1)	serine-type peptidase activity [GO:0008236 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Peptidase S28 [IPR008758] (1); Alpha/Beta hydrolase fold [IPR029058] (1)	-	C_unshiu_00974_mRNA_5.1	-
GF0039590	0	1	0	Lysosomal Pro-Xaa carboxypeptidase (1)	proteolysis [GO:0006508 biological_process] (1); serine-type peptidase activity [GO:0008236 molecular_function] (1)	Alpha/Beta hydrolase fold [IPR029058] (1); Peptidase S28 [IPR008758] (1)	-	C_unshiu_00974_mRNA_2.1	-
GF0039589	0	1	0	LRR receptor-like kinase family protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	-	C_unshiu_00974_mRNA_11.1	-
GF0039588	0	1	0	Hypothetical protein (1)		Probable transposase, Ptta/En/Spm, plant [IPR004252] (1)	-	C_unshiu_00974_mRNA_1.1	-
GF0039587	0	1	0	Hypothetical protein (1)			-	C_unshiu_00973_mRNA_12.1	-
GF0039586	0	1	0	Hypothetical protein (1)			-	C_unshiu_00972_mRNA_9.1	-
GF0039585	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_00972_mRNA_8.1	-
GF0039584	0	1	0	Hypothetical protein (1)		Gag-polypeptide of LTR copia-type [IPR029472] (1)	-	C_unshiu_00972_mRNA_6.1	-
GF0039583	0	1	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1)	-	C_unshiu_00972_mRNA_5.1	-
GF0039582	0	1	0	Hypothetical protein (1)			-	C_unshiu_00972_mRNA_2.1	-
GF0039581	0	1	0	Hypothetical protein (1)			-	C_unshiu_00972_mRNA_11.1	-
GF0039580	0	1	0	Hypothetical protein (1)			-	C_unshiu_00972_mRNA_10.1	-
GF0039579	0	1	0	Hypothetical protein (1)			-	C_unshiu_00971_mRNA_18.1	-
GF0039578	0	1	0	Hypothetical protein (1)			-	C_unshiu_00971_mRNA_16.1	-
GF0039577	0	1	0	Hypothetical protein (1)			-	C_unshiu_00971_mRNA_15.1	-
GF0039576	0	1	0	Hypothetical protein (1)			-	C_unshiu_00970_mRNA_8.1	-
GF0039575	0	1	0	Hypothetical protein (1)			-	C_unshiu_00970_mRNA_7.1	-
GF0039574	0	1	0	Hypothetical protein (1)			-	C_unshiu_00970_mRNA_5.1	-
GF0039573	0	1	0	Hypothetical protein (1)			-	C_unshiu_00970_mRNA_4.1	-
GF0039572	0	1	0	Hypothetical protein (1)		Transposon, En/Spm-like [IPR004242] (1)	-	C_unshiu_00970_mRNA_3.1	-
GF0039571	0	1	0	Hypothetical protein (1)			-	C_unshiu_00970_mRNA_18.1	-
GF0039570	0	1	0	Hypothetical protein (1)			-	C_unshiu_00970_mRNA_17.1	-
GF0039569	0	1	0	Hypothetical protein (1)			-	C_unshiu_00970_mRNA_15.1	-
GF0039568	0	1	0	Hypothetical protein (1)			-	C_unshiu_00970_mRNA_14.1	-
GF0039567	0	1	0	Hypothetical protein (1)			-	C_unshiu_00970_mRNA_12.1	-
GF0039566	0	1	0	Hypothetical protein (1)			-	C_unshiu_00970_mRNA_10.1	-
GF0039565	0	1	0	Hypothetical protein (1)			-	C_unshiu_00970_mRNA_1.1	-
GF0039564	0	1	0	Hypothetical protein (1)			-	C_unshiu_00969_mRNA_4.1	-
GF0039563	0	1	0	Hypothetical protein (1)			-	C_unshiu_00969_mRNA_3.1	-
GF0039562	0	1	0	Hypothetical protein (1)			-	C_unshiu_00969_mRNA_1.1	-
GF0039561	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00968_mRNA_9.1	-
GF0039560	0	1	0	Hypothetical protein (1)		Cullin repeat-like-containing domain [IPR016159] (1)	-	C_unshiu_00968_mRNA_4.1	-
GF0039559	0	1	0	Hypothetical protein (1)		ATPase family AAA domain-containing protein 3, domain of unknown function DUF3523 [IPR021911] (1)	-	C_unshiu_00968_mRNA_11.1	-
GF0039558	0	1	0	Hypothetical protein (1)		MULE transposase domain [IPR018289] (1)	-	C_unshiu_00968_mRNA_10.1	-
GF0039557	0	1	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_00968_mRNA_1.1	-
GF0039556	0	1	0	Hypothetical protein (1)			-	C_unshiu_00967_mRNA_1.1	-
GF0039555	0	1	0	Hypothetical protein (1)			-	C_unshiu_00966_mRNA_9.1	-
GF0039554	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	C_unshiu_00964_mRNA_9.1	-
GF0039553	0	1	0	Hypothetical protein (1)			-	C_unshiu_00964_mRNA_3.1	-
GF0039552	0	1	0	Hypothetical protein (1)			-	C_unshiu_00964_mRNA_2.1	-
GF0039551	0	1	0	MADS-box protein MADS5 (1)	nucleotide binding [GO:0000166 molecular_function] (1)	Regulator of nonsense-mediated decay, UPF3 [IPR005120] (1); Nucleotide-binding alpha-beta plait domain [IPR012677] (1)	-	C_unshiu_00964_mRNA_11.1	-
GF0039550	0	1	0	Protein AIG1 (1)	GTP binding [GO:0005525 molecular_function] (1)	AIG1-type guanine nucleotide-binding (G) domain [IPR006703] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00964_mRNA_10.1	-
GF0039549	0	1	0	TPR and ankyrin repeat-containing protein 1 (1)	ATP binding [GO:0005524 molecular_function] (1)	UvrD-like Helicase, ATP-binding domain [IPR014016] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00963_mRNA_4.1	-
GF0039548	0	1	0	Hypothetical protein (1)			-	C_unshiu_00963_mRNA_3.1	-
GF0039547	0	1	0	Hypothetical protein (1)	inositol catabolic process [GO:0019310 biological_process] (1); iron ion binding [GO:0005506 molecular_function] (1); inositol oxygenase activity [GO:0050113 molecular_function] (1); cytoplasm [GO:0005737 cellular_component] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Inositol oxygenase [IPR007828] (1)	-	C_unshiu_00963_mRNA_14.1	-
GF0039546	0	1	0	Hypothetical protein (1)			-	C_unshiu_00963_mRNA_13.1	-
GF0039545	0	1	0	Hypothetical protein (1)			-	C_unshiu_00963_mRNA_11.1	-
GF0039544	0	1	0	Hypothetical protein (1)			-	C_unshiu_00963_mRNA_1.1	-
GF0039543	0	1	0	Hypothetical protein (1)		Malectin-like carbohydrate-binding domain [IPR024788] (1)	-	C_unshiu_00962_mRNA_4.1	-
GF0039542	0	1	0	Hypothetical protein (1)		Alpha crystallin/Hsp20 domain [IPR002068] (1); HSP20-like chaperone [IPR008978] (1)	-	C_unshiu_00962_mRNA_14.1	-
GF0039541	0	1	0	Hypothetical protein (1)			-	C_unshiu_00962_mRNA_13.1	-
GF0039540	0	1	0	SH3 domain-containing protein 2 (1)	protein binding [GO:0005515 molecular_function] (1)	SH3 domain [IPR001452] (1)	-	C_unshiu_00961_mRNA_8.1	-
GF0039539	0	1	0	Hypothetical protein (1)			-	C_unshiu_00961_mRNA_3.1	-
GF0039538	0	1	0	LRR receptor-like kinase family protein (1)	protein binding [GO:0005515 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Tyrosine-protein kinase, active site [IPR008266] (1); Protein kinase, ATP binding site [IPR017441] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_00960_mRNA_8.1	-
GF0039537	0	1	0	Monosacharide transport protein (1)			-	C_unshiu_00959_mRNA_7.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0039536	0	1	0	Sulfotransferase (1)		Transposase, MuDR, plant [IPR004332] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00959_mRNA_4.1	-
GF0039535	0	1	0	Hypothetical protein (1)			-	C_unshiu_00959_mRNA_10.1	-
GF0039534	0	1	0	Hypothetical protein (1)			-	C_unshiu_00958_mRNA_8.1	-
GF0039533	0	1	0	Hypothetical protein (1)			-	C_unshiu_00958_mRNA_3.1	-
GF0039532	0	1	0	Glyceraldehyde-3-phosphate dehydrogenase 3, cytosolic (1)	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor [GO:0016620 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Glyceraldehyde/Erythrose phosphate dehydrogenase family [IPR020831] (1); Glyceraldehyde 3-phosphate dehydrogenase, active site [IPR020830] (1); NAD(P)-binding domain [IPR016040] (1); Glyceraldehyde 3-phosphate dehydrogenase, catalytic domain [IPR020829] (1); Glyceraldehyde 3-phosphate dehydrogenase, NAD(P) binding domain [IPR020828] (1)	-	C_unshiu_00957_mRNA_9.1	-
GF0039531	0	1	0	Hypothetical protein (1)			-	C_unshiu_00957_mRNA_4.1	-
GF0039530	0	1	0	Hypothetical protein (1)			-	C_unshiu_00957_mRNA_13.1	-
GF0039529	0	1	0	Non-LTR reverse transcriptase (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Endonuclease/exonuclease/phosphatase [IPR005135] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00957_mRNA_12.1	-
GF0039528	0	1	0	UPF0481 protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	C_unshiu_00956_mRNA_13.1	-
GF0039527	0	1	0	Hypothetical protein (1)			-	C_unshiu_00956_mRNA_12.1	-
GF0039526	0	1	0	Hypothetical protein (1)			-	C_unshiu_00956_mRNA_1.1	-
GF0039525	0	1	0	Cell division cycle protein 48 (1)	ATP binding [GO:0005524 molecular_function] (1)	CDC48, N-terminal subdomain [IPR003338] (1); Aspartate decarboxylase-like domain [IPR009010] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); CDC48 domain 2-like [IPR029067] (1); CDC48, domain 2 [IPR004201] (1); ATPase, AAA-type, core [IPR003959] (1)	-	C_unshiu_00955_mRNA_8.1	-
GF0039524	0	1	0	Hypothetical protein (1)	transmembrane transport [GO:0055085 biological_process] (1); integral component of membrane [GO:0016021 cellular_component] (1)	Major facilitator superfamily [IPR011701] (1); Major facilitator superfamily domain [IPR020846] (1)	-	C_unshiu_00955_mRNA_6.1	-
GF0039523	0	1	0	High-affinity nitrate transporter (1)	transmembrane transport [GO:0055085 biological_process] (1); integral component of membrane [GO:0016021 cellular_component] (1)	Major facilitator superfamily [IPR011701] (1); Major facilitator superfamily domain [IPR020846] (1)	-	C_unshiu_00955_mRNA_5.1	-
GF0039522	0	1	0	High-affinity nitrate transporter (1)		Major facilitator superfamily domain [IPR020846] (1)	-	C_unshiu_00955_mRNA_3.1	-
GF0039521	0	1	0	Hypothetical protein (1)			-	C_unshiu_00955_mRNA_2.1	-
GF0039520	0	1	0	Hypothetical protein (1)		Polyprenol kinase family [IPR032974] (1)	-	C_unshiu_00955_mRNA_12.1	-
GF0039519	0	1	0	Hypothetical protein (1)			-	C_unshiu_00955_mRNA_11.1	-
GF0039518	0	1	0	Hypothetical protein (1)			-	C_unshiu_00955_mRNA_10.1	-
GF0039517	0	1	0	Hypothetical protein (1)			-	C_unshiu_00954_mRNA_9.1	-
GF0039516	0	1	0	Hypothetical protein (1)			-	C_unshiu_00954_mRNA_5.1	-
GF0039515	0	1	0	DAG protein, chloroplastic (1)			-	C_unshiu_00954_mRNA_2.1	-
GF0039514	0	1	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_00954_mRNA_1.1	-
GF0039513	0	1	0	Hypothetical protein (1)			-	C_unshiu_00953_mRNA_9.1	-
GF0039512	0	1	0	Hypothetical protein (1)			-	C_unshiu_00953_mRNA_6.1	-
GF0039511	0	1	0	Hypothetical protein (1)			-	C_unshiu_00953_mRNA_2.1	-
GF0039510	0	1	0	Hypothetical protein (1)			-	C_unshiu_00953_mRNA_11.1	-
GF0039509	0	1	0	Hypothetical protein (1)			-	C_unshiu_00953_mRNA_10.1	-
GF0039508	0	1	0	Hypothetical protein (1)			-	C_unshiu_00953_mRNA_1.1	-
GF0039507	0	1	0	Hypothetical protein (1)			-	C_unshiu_00952_mRNA_9.1	-
GF0039506	0	1	0	Hypothetical protein (1)			-	C_unshiu_00952_mRNA_8.1	-
GF0039505	0	1	0	Hypothetical protein (1)			-	C_unshiu_00952_mRNA_7.1	-
GF0039504	0	1	0	Hypothetical protein (1)			-	C_unshiu_00952_mRNA_6.1	-
GF0039503	0	1	0	Hypothetical protein (1)		Protein of unknown function DUF3223 [IPR021602] (1)	-	C_unshiu_00952_mRNA_2.1	-
GF0039502	0	1	0	TSA: Wollemia nobilis transcribed RNA sequence (1)		Lipin, N-terminal [IPR007651] (1)	-	C_unshiu_00951_mRNA_7.1	-
GF0039501	0	1	0	Hypothetical protein (1)			-	C_unshiu_00951_mRNA_17.1	-
GF0039500	0	1	0	Hypothetical protein (1)			-	C_unshiu_00951_mRNA_13.1	-
GF0039499	0	1	0	Inner membrane import protein Tic22, putative (1)		Tic22-like [IPR007378] (1)	-	C_unshiu_00951_mRNA_1.1	-
GF0039498	0	1	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	C_unshiu_00950_mRNA_7.1	-
GF0039497	0	1	0	Hypothetical protein (1)			-	C_unshiu_00950_mRNA_6.1	-
GF0039496	0	1	0	Cc-nbs-lrr resistance protein, putative isoform 4 (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00950_mRNA_5.1	-
GF0039495	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00950_mRNA_4.1	-
GF0039494	0	1	0	Hypothetical protein (1)			-	C_unshiu_00950_mRNA_2.1	-
GF0039493	0	1	0	Hypothetical protein (1)			-	C_unshiu_00950_mRNA_10.1	-
GF0039492	0	1	0	Hypothetical protein (1)			-	C_unshiu_00950_mRNA_1.1	-
GF0039491	0	1	0	Hypothetical protein (1)			-	C_unshiu_00949_mRNA_6.1	-
GF0039490	0	1	0	Hypothetical protein (1)			-	C_unshiu_00949_mRNA_2.1	-
GF0039489	0	1	0	Hypothetical protein (1)	malate transport [GO:0015743 biological_process] (1)	Aluminum-activated malate transporter [IPR020966] (1)	-	C_unshiu_00949_mRNA_11.1	-
GF0039488	0	1	0	NBS-LRR type disease resistance protein (1)			-	C_unshiu_00948_mRNA_6.1	-
GF0039487	0	1	0	Hypothetical protein (1)			-	C_unshiu_00948_mRNA_5.1	-
GF0039486	0	1	0	Hypothetical protein (1)			-	C_unshiu_00948_mRNA_3.1	-
GF0039485	0	1	0	Hypothetical protein (1)			-	C_unshiu_00948_mRNA_1.1	-
GF0039484	0	1	0	Hypothetical protein (1)			-	C_unshiu_00947_mRNA_9.1	-
GF0039483	0	1	0	Hypothetical protein (1)			-	C_unshiu_00946_mRNA_4.1	-
GF0039482	0	1	0	Hypothetical protein (1)	transmembrane transport [GO:0055085 biological_process] (1)	Oligopeptide transporter, OPT superfamily [IPR004813] (1)	-	C_unshiu_00946_mRNA_1.1	-
GF0039481	0	1	0	Protein transport protein Sec61 subunit alpha (1)	protein transport [GO:0015031 biological_process] (1); membrane [GO:0016020 cellular_component] (1)	SecY/SEC61-alpha family [IPR002208] (1); SecY subunit domain [IPR023201] (1)	-	C_unshiu_00945_mRNA_4.1	-
GF0039480	0	1	0	Putative DUF641 family protein-like (1)			-	C_unshiu_00945_mRNA_2.1	-
GF0039479	0	1	0	Hypothetical protein (1)			-	C_unshiu_00945_mRNA_13.1	-
GF0039478	0	1	0	Kunitz trypsin inhibitor (1)	endopeptidase inhibitor activity [GO:0004866 molecular_function] (1)	Kunitz inhibitor ST1-like [IPR011065] (1); Proteinase inhibitor I3, Kunitz legume [IPR002160] (1)	-	C_unshiu_00945_mRNA_12.1	-
GF0039477	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF641, plant [IPR006943] (1)	-	C_unshiu_00945_mRNA_1.1	-
GF0039476	0	1	0	Hypothetical protein (1)			-	C_unshiu_00944_mRNA_8.1	-
GF0039475	0	1	0	Hypothetical protein (1)			-	C_unshiu_00944_mRNA_21.1	-
GF0039474	0	1	0	Hypothetical protein (1)			-	C_unshiu_00944_mRNA_19.1	-
GF0039473	0	1	0	Hypothetical protein (1)			-	C_unshiu_00944_mRNA_14.1	-
GF0039472	0	1	0	Hypothetical protein (1)			-	C_unshiu_00944_mRNA_12.1	-
GF0039471	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_00943_mRNA_4.1	-
GF0039470	0	1	0	Hypothetical protein (1)			-	C_unshiu_00942_mRNA_1.1	-
GF0039469	0	1	0	Hypothetical protein (1)			-	C_unshiu_00941_mRNA_9.1	-
GF0039468	0	1	0	Hypothetical protein (1)			-	C_unshiu_00941_mRNA_8.1	-
GF0039467	0	1	0	Hypothetical protein (1)			-	C_unshiu_00941_mRNA_6.1	-
GF0039466	0	1	0	Hypothetical protein (1)			-	C_unshiu_00941_mRNA_5.1	-
GF0039465	0	1	0	Hypothetical protein (1)			-	C_unshiu_00941_mRNA_3.1	-
GF0039464	0	1	0	Hypothetical protein (1)			-	C_unshiu_00941_mRNA_15.1	-
GF0039463	0	1	0	Hypothetical protein (1)			-	C_unshiu_00941_mRNA_12.1	-
GF0039462	0	1	0	Hypothetical protein (1)			-	C_unshiu_00941_mRNA_10.1	-
GF0039461	0	1	0	Hypothetical protein (1)			-	C_unshiu_00941_mRNA_1.1	-
GF0039460	0	1	0	ARM-repeat/Tetratricopeptide repeat (TPR)-like protein isoform 2 (1)	protein binding [GO:0005515 molecular_function] (1); binding [GO:0005488 molecular_function] (1)	Armadillo-like helical [IPR011989] (1); Tetratricopeptide-like helical domain [IPR011990] (1); Armadillo-type fold [IPR016024] (1)	-	C_unshiu_00940_mRNA_9.1	-
GF0039459	0	1	0	Hypothetical protein (1)		MULE transposase domain [IPR018289] (1)	-	C_unshiu_00939_mRNA_4.1	-
GF0039458	0	1	0	Hypothetical protein (1)			-	C_unshiu_00939_mRNA_3.1	-
GF0039457	0	1	0	Hypothetical protein (1)			-	C_unshiu_00938_mRNA_7.1	-
GF0039456	0	1	0	Hypothetical protein (1)			-	C_unshiu_00938_mRNA_6.1	-
GF0039455	0	1	0	Monosacharide transport protein (1)			-	C_unshiu_00938_mRNA_3.1	-
GF0039454	0	1	0	Hypothetical protein (1)			-	C_unshiu_00938_mRNA_2.1	-
GF0039453	0	1	0	Hypothetical protein (1)		Rhodanese-like domain [IPR001763] (1)	-	C_unshiu_00937_mRNA_3.1	-
GF0039452	0	1	0	Hypothetical protein (1)			-	C_unshiu_00937_mRNA_2.1	-
GF0039451	0	1	0	LRR receptor-like kinase family protein (1)	protein binding [GO:0005515 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1); Leucine-rich repeat [IPR001611] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Protein kinase, ATP binding site [IPR017441] (1); Tyrosine-protein kinase, active site [IPR008266] (1)	-	C_unshiu_00936_mRNA_6.1	-
GF0039450	0	1	0	LRR receptor-like kinase family protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1); Pentatricopeptide repeat [IPR002885] (1); Tyrosine-protein kinase, active site [IPR008266] (1); Protein kinase, ATP binding site [IPR017441] (1)	-	C_unshiu_00936_mRNA_3.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0039449	0	1	0	Hypothetical protein (1)			-	C_unshiu_00936_mRNA_20.1	-
GF0039448	0	1	0	Hypothetical protein (1)			-	C_unshiu_00936_mRNA_11.1	-
GF0039447	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_00936_mRNA_10.1	-
GF0039446	0	1	0	Hypothetical protein (1)	fatty-acyl-CoA binding [GO:0000062 molecular_function] (1)	FERM/acyl-CoA-binding protein, 3-helical bundle [IPR014352] (1); Acyl-CoA-binding protein, ACBP [IPR000582] (1)	-	C_unshiu_00935_mRNA_9.1	-
GF0039445	0	1	0	Calcium-binding EF hand family protein (1)	calcium ion binding [GO:0005509 molecular_function] (1); fatty-acyl-CoA binding [GO:0000062 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	EF-hand domain [IPR002048] (1); Ankyrin repeat-containing domain [IPR020683] (1); EF-Hand 1, calcium-binding site [IPR018247] (1); EF-hand domain pair [IPR011992] (1); FERM/acyl-CoA-binding protein, 3-helical bundle [IPR014352] (1); Acyl-CoA-binding protein, ACBP [IPR000582] (1); Ankyrin repeat [IPR002110] (1)	-	C_unshiu_00935_mRNA_8.1	-
GF0039444	0	1	0	Hypothetical protein (1)			-	C_unshiu_00935_mRNA_7.1	-
GF0039443	0	1	0	Acyl-CoA binding protein 2 isoform 3 (1)	fatty-acyl-CoA binding [GO:0000062 molecular_function] (1)	FERM/acyl-CoA-binding protein, 3-helical bundle [IPR014352] (1); Acyl-CoA-binding protein, ACBP [IPR000582] (1)	-	C_unshiu_00935_mRNA_10.1	-
GF0039442	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF2431 [IPR019446] (1)	-	C_unshiu_00934_mRNA_8.1	-
GF0039441	0	1	0	Hypothetical protein (1)			-	C_unshiu_00934_mRNA_7.1	-
GF0039440	0	1	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00934_mRNA_4.1	-
GF0039439	0	1	0	Hypothetical protein (1)			-	C_unshiu_00934_mRNA_17.1	-
GF0039438	0	1	0	Hypothetical protein (1)	adenosylhomocysteinase activity [GO:0004013 molecular_function] (1); one-carbon metabolic process [GO:0006730 biological_process] (1)	Adenosylhomocysteinase [IPR000043] (1); S-adenosyl-L-homocysteine hydrolase, NAD binding domain [IPR015878] (1)	-	C_unshiu_00934_mRNA_16.1	-
GF0039437	0	1	0	Hypothetical protein (1)			-	C_unshiu_00934_mRNA_15.1	-
GF0039436	0	1	0	Ribonuclease H-like superfamily protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_00934_mRNA_14.1	-
GF0039435	0	1	0	Hypothetical protein (1)			-	C_unshiu_00932_mRNA_5.1	-
GF0039434	0	1	0	TMV resistance protein N (1)	protein binding [GO:0005515 molecular_function] (1); signal transduction [GO:0007165 biological_process] (1); ADP binding [GO:0043531 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat 3 [IPR011713] (1); Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1); NB-ARC [IPR002182] (1); Leucine-rich repeat [IPR001611] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00931_mRNA_9.1	-
GF0039433	0	1	0	Hypothetical protein (1)			-	C_unshiu_00931_mRNA_8.1	-
GF0039432	0	1	0	Hypothetical protein (1)			-	C_unshiu_00931_mRNA_3.1	-
GF0039431	0	1	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1); Transposon, En/Spm-like [IPR004242] (1)	-	C_unshiu_00930_mRNA_7.1	-
GF0039430	0	1	0	Hypothetical protein (1)			-	C_unshiu_00930_mRNA_2.1	-
GF0039429	0	1	0	Hypothetical protein (1)			-	C_unshiu_00929_mRNA_7.1	-
GF0039428	0	1	0	Hypothetical protein (1)			-	C_unshiu_00928_mRNA_8.1	-
GF0039427	0	1	0	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	C_unshiu_00928_mRNA_7.1	-
GF0039426	0	1	0	Hypothetical protein (1)			-	C_unshiu_00928_mRNA_4.1	-
GF0039425	0	1	0	CDNA clone:001-130-G10, full insert sequence (1)		Retroviral aspartyl protease [IPR013242] (1)	-	C_unshiu_00928_mRNA_3.1	-
GF0039424	0	1	0	Hypothetical protein (1)			-	C_unshiu_00928_mRNA_2.1	-
GF0039423	0	1	0	Hypothetical protein (1)			-	C_unshiu_00928_mRNA_12.1	-
GF0039422	0	1	0	Hypothetical protein (1)			-	C_unshiu_00928_mRNA_1.1	-
GF0039421	0	1	0	CC-NBS-LRR disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00927_mRNA_9.1	-
GF0039420	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_00927_mRNA_5.1	-
GF0039419	0	1	0	Xyloglucan endotransglucosylase/hydrolase protein 24 (1)	hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1)	Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Glycoside hydrolase family 16 [IPR000757] (1)	-	C_unshiu_00927_mRNA_2.1	-
GF0039418	0	1	0	Hypothetical protein (1)			-	C_unshiu_00927_mRNA_16.1	-
GF0039417	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00927_mRNA_13.1	-
GF0039416	0	1	0	Disease resistance RPS5-like protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00927_mRNA_12.1	-
GF0039415	0	1	0	Putative disease resistance gene NBS-LRR family protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00927_mRNA_11.1	-
GF0039414	0	1	0	Disease resistance protein RPS5 (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00927_mRNA_10.1	-
GF0039413	0	1	0	Hypothetical protein (1)			-	C_unshiu_00926_mRNA_6.1	-
GF0039412	0	1	0	Hypothetical protein (1)	chlorophyll binding [GO:0016168 molecular_function] (1); photosystem [GO:0009521 cellular_component] (1); photosynthesis, light reaction [GO:0019684 biological_process] (1); membrane [GO:0016020 cellular_component] (1); photosynthetic electron transport chain [GO:0009767 biological_process] (1)	Photosystem antenna protein-like [IPR000932] (1)	-	C_unshiu_00926_mRNA_2.1	-
GF0039411	0	1	0	Hypothetical protein (1)			-	C_unshiu_00924_mRNA_8.1	-
GF0039410	0	1	0	Disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	C_unshiu_00924_mRNA_18.1	-
GF0039409	0	1	0	Disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00924_mRNA_15.1	-
GF0039408	0	1	0	Hypothetical protein (1)			-	C_unshiu_00924_mRNA_14.1	-
GF0039407	0	1	0	Hypothetical protein (1)			-	C_unshiu_00924_mRNA_11.1	-
GF0039406	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_00924_mRNA_10.1	-
GF0039405	0	1	0	Exosome complex exonuclease rrp45, putative (1)	exosome (RNase complex) [GO:0000178 cellular_component] (1); RNA processing [GO:0006396 biological_process] (1)	Exosome complex component RRP45 [IPR033100] (1); PNPase/RNase PH domain [IPR027408] (1); Exoribonuclease, phosphorolytic domain 1 [IPR001247] (1); Ribosomal protein S5 domain 2-type fold [IPR020568] (1); Exoribonuclease, phosphorolytic domain 2 [IPR015847] (1)	-	C_unshiu_00923_mRNA_6.1	-
GF0039404	0	1	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1); Protein kinase, ATP binding site [IPR017441] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1)	-	C_unshiu_00923_mRNA_4.1	-
GF0039403	0	1	0	Subtilase family protein (1)	proteolysis [GO:0006508 biological_process] (1); serine-type endopeptidase activity [GO:0004252 molecular_function] (1)	Peptidase S8, subtilisin, Ser-active site [IPR023828] (1); Peptidase S8/S53 domain [IPR000209] (1); Peptidase S8, subtilisin-related [IPR015500] (1)	-	C_unshiu_00923_mRNA_15.1	-
GF0039402	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00922_mRNA_5.1	-
GF0039401	0	1	0	Hypothetical protein (1)			-	C_unshiu_00922_mRNA_11.1	-
GF0039400	0	1	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1); Ribonuclease H-like domain [IPR012337] (1); Zinc finger, BED-type [IPR003656] (1)	-	C_unshiu_00921_mRNA_7.1	-
GF0039399	0	1	0	Hypothetical protein (1)			-	C_unshiu_00920_mRNA_7.1	-
GF0039398	0	1	0	Hypothetical protein (1)			-	C_unshiu_00920_mRNA_5.1	-
GF0039397	0	1	0	Hypothetical protein (1)			-	C_unshiu_00919_mRNA_7.1	-
GF0039396	0	1	0	Hypothetical protein (1)			-	C_unshiu_00919_mRNA_6.1	-
GF0039395	0	1	0	Similarity to non-LTR retroelement reverse transcriptase (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00918_mRNA_4.1	-
GF0039394	0	1	0	Arginine 2-monooxygenase (1)	spermidine biosynthetic process [GO:0008295 biological_process] (1); arginine catabolic process [GO:0006527 biological_process] (1); arginine decarboxylase activity [GO:0008792 molecular_function] (1); catalytic activity [GO:0003824 molecular_function] (1)	PLP-binding barrel [IPR029066] (1); Orn/DAP/Arg decarboxylase 2, N-terminal [IPR022644] (1); Ornithine/DAP/Arg decarboxylase [IPR000183] (1); Arginine decarboxylase [IPR002985] (1); Orn/DAP/Arg decarboxylase 2, pyridoxal-phosphate binding site [IPR022653] (1)	-	C_unshiu_00918_mRNA_3.1	-
GF0039393	0	1	0	Arginine 2-monooxygenase (1)	arginine decarboxylase activity [GO:0008792 molecular_function] (1); arginine catabolic process [GO:0006527 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1); spermidine biosynthetic process [GO:0008295 biological_process] (1)	PLP-binding barrel [IPR029066] (1); Orn/DAP/Arg decarboxylase 2, C-terminal [IPR022643] (1); Orn/DAP/Arg decarboxylase 2, conserved site [IPR022657] (1); Alanine racemase/group IV decarboxylase, C-terminal [IPR009006] (1); Orn/DAP/Arg decarboxylase 2, N-terminal [IPR022644] (1); Ornithine/DAP/Arg decarboxylase [IPR000183] (1); Arginine decarboxylase [IPR002985] (1)	-	C_unshiu_00918_mRNA_2.1	-
GF0039392	0	1	0	Hypothetical protein (1)			-	C_unshiu_00918_mRNA_14.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0039391	0	1	0	LRR receptor-like kinase family protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Protein kinase-like domain [IPR011009] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00918_mRNA_13.1	-
GF0039390	0	1	0	Hypothetical protein (1)	transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	-	C_unshiu_00917_mRNA_7.1	-
GF0039389	0	1	0	Pre-mRNA-splicing factor ATP-dependent RNA helicase (1)	ATP binding [GO:0005524 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1); helicase activity [GO:0004386 molecular_function] (1); ATP-dependent helicase activity [GO:0008026 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Helicase superfamily 1/2, ATP-binding domain [IPR014001] (1); DNA/RNA helicase, ATP-dependent, DEAH-box type, conserved site [IPR002464] (1); Helicase-associated domain [IPR007502] (1); Domain of unknown function DUF1605 [IPR011709] (1); Helicase, C-terminal [IPR001650] (1)	-	C_unshiu_00917_mRNA_14.1	-
GF0039388	0	1	0	Hypothetical protein (1)	polysaccharide biosynthetic process [GO:0000271 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); NAD binding [GO:0051287 molecular_function] (1); oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor [GO:0016616 molecular_function] (1); UDP-glucose 6-dehydrogenase activity [GO:0003979 molecular_function] (1)	UDP-glucose/GDP-mannose dehydrogenase, dimerisation [IPR014026] (1); UDP-glucose/GDP-mannose dehydrogenase, N-terminal [IPR001732] (1); NAD(P)-binding domain [IPR016040] (1); UDP-glucose 6-dehydrogenase, bacterial type [IPR028357] (1); UDP-glucose/GDP-mannose dehydrogenase, C-terminal [IPR014027] (1); 6-phosphogluconate dehydrogenase C-terminal domain-like [IPR008927] (1); 6-phosphogluconate dehydrogenase, domain 2 [IPR013328] (1); UDP-glucose/GDP-mannose dehydrogenase [IPR017476] (1)	-	C_unshiu_00917_mRNA_13.1	-
GF0039387	0	1	0	Hypothetical protein (1)			-	C_unshiu_00916_mRNA_6.1	-
GF0039386	0	1	0	Hypothetical protein (1)			-	C_unshiu_00916_mRNA_5.1	-
GF0039385	0	1	0	Hypothetical protein (1)			-	C_unshiu_00916_mRNA_12.1	-
GF0039384	0	1	0	Hypothetical protein (1)			-	C_unshiu_00916_mRNA_11.1	-
GF0039383	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_00915_mRNA_9.1	-
GF0039382	0	1	0	Hypothetical protein (1)			-	C_unshiu_00915_mRNA_8.1	-
GF0039381	0	1	0	Hypothetical protein (1)			-	C_unshiu_00915_mRNA_7.1	-
GF0039380	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_00915_mRNA_6.1	-
GF0039379	0	1	0	Hypothetical protein (1)			-	C_unshiu_00915_mRNA_5.1	-
GF0039378	0	1	0	Hypothetical protein (1)			-	C_unshiu_00915_mRNA_4.1	-
GF0039377	0	1	0	Hypothetical protein (1)			-	C_unshiu_00915_mRNA_3.1	-
GF0039376	0	1	0	Hypothetical protein (1)			-	C_unshiu_00915_mRNA_2.1	-
GF0039375	0	1	0	Hypothetical protein (1)			-	C_unshiu_00915_mRNA_13.1	-
GF0039374	0	1	0	Hypothetical protein (1)			-	C_unshiu_00915_mRNA_12.1	-
GF0039373	0	1	0	Hypothetical protein (1)			-	C_unshiu_00915_mRNA_11.1	-
GF0039372	0	1	0	Hypothetical protein (1)			-	C_unshiu_00915_mRNA_10.1	-
GF0039371	0	1	0	Hypothetical protein (1)			-	C_unshiu_00914_mRNA_7.1	-
GF0039370	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_00914_mRNA_4.1	-
GF0039369	0	1	0	Hypothetical protein (1)			-	C_unshiu_00914_mRNA_13.1	-
GF0039368	0	1	0	Hypothetical protein (1)			-	C_unshiu_00914_mRNA_12.1	-
GF0039367	0	1	0	Hypothetical protein (1)		Chromo domain [IPR023780] (1); Chromo domain-like [IPR016197] (1)	-	C_unshiu_00914_mRNA_11.1	-
GF0039366	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF1985 [IPR015410] (1)	-	C_unshiu_00913_mRNA_7.1	-
GF0039365	0	1	0	Hypothetical protein (1)			-	C_unshiu_00913_mRNA_3.1	-
GF0039364	0	1	0	Hypothetical protein (1)			-	C_unshiu_00912_mRNA_7.1	-
GF0039363	0	1	0	Hypothetical protein (1)			-	C_unshiu_00912_mRNA_16.1	-
GF0039362	0	1	0	Hypothetical protein (1)			-	C_unshiu_00912_mRNA_14.1	-
GF0039361	0	1	0	Hypothetical protein (1)			-	C_unshiu_00912_mRNA_12.1	-
GF0039360	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_00912_mRNA_11.1	-
GF0039359	0	1	0	Hypothetical protein (1)			-	C_unshiu_00911_mRNA_9.1	-
GF0039358	0	1	0	Hypothetical protein (1)			-	C_unshiu_00911_mRNA_8.1	-
GF0039357	0	1	0	Disease resistance family protein / LRR family protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1)	-	C_unshiu_00911_mRNA_6.1	-
GF0039356	0	1	0	Leucine-rich repeat receptor-like protein kinase PXL1 (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	-	C_unshiu_00911_mRNA_5.1	-
GF0039355	0	1	0	Hypothetical protein (1)			-	C_unshiu_00911_mRNA_11.1	-
GF0039354	0	1	0	Hypothetical protein (1)			-	C_unshiu_00911_mRNA_10.1	-
GF0039353	0	1	0	Hypothetical protein (1)			-	C_unshiu_00910_mRNA_2.1	-
GF0039352	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00910_mRNA_13.1	-
GF0039351	0	1	0	Hypothetical protein (1)			-	C_unshiu_00910_mRNA_12.1	-
GF0039350	0	1	0	Hypothetical protein (1)			-	C_unshiu_00910_mRNA_11.1	-
GF0039349	0	1	0	Hypothetical protein (1)			-	C_unshiu_00909_mRNA_6.1	-
GF0039348	0	1	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_00909_mRNA_4.1	-
GF0039347	0	1	0	Hypothetical protein (1)			-	C_unshiu_00909_mRNA_1.1	-
GF0039346	0	1	0	Hypothetical protein (1)			-	C_unshiu_00908_mRNA_1.1	-
GF0039345	0	1	0	Hypothetical protein (1)			-	C_unshiu_00907_mRNA_2.1	-
GF0039344	0	1	0	Hypothetical protein (1)			-	C_unshiu_00907_mRNA_10.1	-
GF0039343	0	1	0	Hypothetical protein (1)	biosynthetic process [GO:0009058 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1); pyridoxal phosphate binding [GO:0030170 molecular_function] (1)	Pyridoxal phosphate-dependent transferase [IPR015424] (1); Pyridoxal phosphate-dependent transferase, major region, subdomain 2 [IPR015422] (1); Pyridoxal phosphate-dependent transferase, major region, subdomain 1 [IPR015421] (1); Aminotransferase, class I/classII [IPR004839] (1)	-	C_unshiu_00907_mRNA_1.1	-
GF0039342	0	1	0	Hypothetical protein (1)			-	C_unshiu_00906_mRNA_8.1	-
GF0039341	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4216 [IPR025312] (1)	-	C_unshiu_00906_mRNA_5.1	-
GF0039340	0	1	0	RNA polymerase II subunit 5-mediating protein like (1)		Prefoldin alpha-like [IPR004127] (1); Prefoldin [IPR009053] (1)	-	C_unshiu_00906_mRNA_4.1	-
GF0039339	0	1	0	Hypothetical protein (1)			-	C_unshiu_00906_mRNA_1.1	-
GF0039338	0	1	0	Hypothetical protein (1)			-	C_unshiu_00905_mRNA_8.1	-
GF0039337	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_00905_mRNA_7.1	-
GF0039336	0	1	0	Hypothetical protein (1)			-	C_unshiu_00905_mRNA_4.1	-
GF0039335	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_00905_mRNA_2.1	-
GF0039334	0	1	0	Hypothetical protein (1)			-	C_unshiu_00905_mRNA_14.1	-
GF0039333	0	1	0	Hypothetical protein (1)			-	C_unshiu_00905_mRNA_13.1	-
GF0039332	0	1	0	Hypothetical protein (1)			-	C_unshiu_00905_mRNA_12.1	-
GF0039331	0	1	0	Putative muDR family transposase-like (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, PMZ-type [IPR006564] (1); MULE transposase domain [IPR018289] (1); Zinc finger, SWIM-type [IPR007527] (1)	-	C_unshiu_00904_mRNA_7.1	-
GF0039330	0	1	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00904_mRNA_6.1	-
GF0039329	0	1	0	Hypothetical protein (1)			-	C_unshiu_00904_mRNA_3.1	-
GF0039328	0	1	0	Hydrolase, alpha/beta domain protein (1)		Alpha/beta hydrolase fold-1 [IPR000073] (1); Alpha/Beta hydrolase fold [IPR029058] (1)	-	C_unshiu_00904_mRNA_15.1	-
GF0039327	0	1	0	Hypothetical protein (1)			-	C_unshiu_00904_mRNA_1.1	-
GF0039326	0	1	0	Hypothetical protein (1)			-	C_unshiu_00903_mRNA_9.1	-
GF0039325	0	1	0	Hypothetical protein (1)			-	C_unshiu_00903_mRNA_8.1	-
GF0039324	0	1	0	Hypothetical protein (1)			-	C_unshiu_00903_mRNA_4.1	-
GF0039323	0	1	0	Hypothetical protein (1)			-	C_unshiu_00903_mRNA_3.1	-
GF0039322	0	1	0	Hypothetical protein (1)			-	C_unshiu_00903_mRNA_2.1	-
GF0039321	0	1	0	Hypothetical protein (1)			-	C_unshiu_00902_mRNA_8.1	-
GF0039320	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); transcription, DNA-templated [GO:0006351 biological_process] (1); nucleus [GO:0005634 cellular_component] (1)	Transcription elongation factor S-IIM [IPR017890] (1); Transcription elongation factor S-II, central domain [IPR003618] (1)	-	C_unshiu_00902_mRNA_7.1	-
GF0039319	0	1	0	Hypothetical protein (1)			-	C_unshiu_00902_mRNA_2.1	-
GF0039318	0	1	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	-	C_unshiu_00902_mRNA_12.1	-
GF0039317	0	1	0	Hypothetical protein (1)			-	C_unshiu_00901_mRNA_5.1	-
GF0039316	0	1	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1)	-	C_unshiu_00901_mRNA_4.1	-
GF0039315	0	1	0	Hypothetical protein (1)	ATPase activity [GO:0016887 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Anion-transporting ATPase-like domain [IPR025723] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Arsenical pump ATPase, ArsA/GET3 [IPR016300] (1)	-	C_unshiu_00900_mRNA_5.1	-
GF0039314	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, U1-type [IPR003604] (1)	-	C_unshiu_00900_mRNA_18.1	-
GF0039313	0	1	0	Hypothetical protein (1)			-	C_unshiu_00900_mRNA_14.1	-
GF0039312	0	1	0	Hypothetical protein (1)			-	C_unshiu_00900_mRNA_12.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0039311	0	1	0	Hypothetical protein (1)			-	C_unshiu_00900_mRNA_11.1	-
GF0039310	0	1	0	Hypothetical protein (1)			-	C_unshiu_00900_mRNA_10.1	-
GF0039309	0	1	0	Hypothetical protein (1)			-	C_unshiu_00899_mRNA_2.1	-
GF0039308	0	1	0	Hypothetical protein (1)			-	C_unshiu_00899_mRNA_16.1	-
GF0039307	0	1	0	Truncated cellulose synthase catalytic subunit (1)	cellulose biosynthetic process [GO:0030244 biological_process] (1); membrane [GO:0016020 cellular_component] (1); cellulose synthase (UDP-forming) activity [GO:0016760 molecular_function] (1)	Cellulose synthase [IPR005150] (1); Nucleotide-diphospho-sugar transferases [IPR029044] (1); Zinc finger, RING/FYVE/PHD-type [IPR013083] (1)	-	C_unshiu_00898_mRNA_6.1	-
GF0039306	0	1	0	Protein COBRA (1)	cell growth [GO:0016049 biological_process] (1); anchored component of membrane [GO:0031225 cellular_component] (1); cellulose microfibril organization [GO:0010215 biological_process] (1)	COBRA, plant [IPR006918] (1)	-	C_unshiu_00898_mRNA_5.1	-
GF0039305	0	1	0	Hypothetical protein (1)	vesicle-mediated transport [GO:0016192 biological_process] (1); membrane [GO:0016020 cellular_component] (1)	t-SNARE [IPR010989] (1)	-	C_unshiu_00898_mRNA_4.1	-
GF0039304	0	1	0	Hypothetical protein (1)		DnaJ domain, conserved site [IPR018253] (1); DnaJ domain [IPR001623] (1)	-	C_unshiu_00898_mRNA_1.1	-
GF0039303	0	1	0	Putative SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 3-like 3 (1)	ATP binding [GO:0005524 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	SNF2-related, N-terminal domain [IPR000330] (1); Zinc finger, RING/FYVE/PHD-type [IPR013083] (1); Helicase, C-terminal [IPR001650] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Zinc finger, RING-type, conserved site [IPR017907] (1); Protein of unknown function DUF3128 [IPR021475] (1); Helicase superfamily 1/2, ATP-binding domain [IPR014001] (1); Zinc finger, RING-type [IPR001841] (1)	-	C_unshiu_00897_mRNA_2.1	-
GF0039302	0	1	0	Hypothetical protein (1)			-	C_unshiu_00896_mRNA_7.1	-
GF0039301	0	1	0	Hypothetical protein (1)			-	C_unshiu_00896_mRNA_3.1	-
GF0039300	0	1	0	Ulp1 peptidase-like (1)		Domain of unknown function DUF1985 [IPR015410] (1)	-	C_unshiu_00895_mRNA_8.1	-
GF0039299	0	1	0	Hypothetical protein (1)			-	C_unshiu_00895_mRNA_6.1	-
GF0039298	0	1	0	Hypothetical protein (1)			-	C_unshiu_00894_mRNA_9.1	-
GF0039297	0	1	0	Hypothetical protein (1)			-	C_unshiu_00893_mRNA_7.1	-
GF0039296	0	1	0	Hypothetical protein (1)			-	C_unshiu_00893_mRNA_6.1	-
GF0039295	0	1	0	Putative muDR family transposase-like (1)		MULE transposase domain [IPR018289] (1)	-	C_unshiu_00893_mRNA_2.1	-
GF0039294	0	1	0	Hypothetical protein (1)		GroES-like [IPR011032] (1)	-	C_unshiu_00893_mRNA_14.1	-
GF0039293	0	1	0	Hypothetical protein (1)	metal ion binding [GO:0046872 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, C2H2 [IPR007087] (1); Zinc finger C2H2-type/integrase DNA-binding domain [IPR013087] (1); Zinc finger, C2H2-like [IPR015880] (1)	-	C_unshiu_00892_mRNA_9.1	-
GF0039292	0	1	0	Leucine-rich repeat transmembrane protein kinase (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_00892_mRNA_2.1	-
GF0039291	0	1	0	Hypothetical protein (1)			-	C_unshiu_00891_mRNA_7.1	-
GF0039290	0	1	0	E3 ubiquitin-protein ligase CHFR (1)	protein binding [GO:0005515 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, RING-type [IPR001841] (1); Zinc finger, RING/FYVE/PHD-type [IPR013083] (1)	-	C_unshiu_00891_mRNA_5.1	-
GF0039289	0	1	0	TMV resistance N (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00891_mRNA_13.1	-
GF0039288	0	1	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1)	Protein kinase, ATP binding site [IPR017441] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_00891_mRNA_1.1	-
GF0039287	0	1	0	Hypothetical protein (1)			-	C_unshiu_00890_mRNA_7.1	-
GF0039286	0	1	0	Hypothetical protein (1)			-	C_unshiu_00890_mRNA_3.1	-
GF0039285	0	1	0	Hypothetical protein (1)			-	C_unshiu_00890_mRNA_19.1	-
GF0039284	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4219 [IPR025314] (1)	-	C_unshiu_00890_mRNA_18.1	-
GF0039283	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_00890_mRNA_15.1	-
GF0039282	0	1	0	Hypothetical protein (1)			-	C_unshiu_00890_mRNA_14.1	-
GF0039281	0	1	0	Hypothetical protein (1)		Ribosomal protein L5 domain [IPR022803] (1); Ribosomal protein L5, N-terminal [IPR031310] (1)	-	C_unshiu_00889_mRNA_1.1	-
GF0039280	0	1	0	Hypothetical protein (1)	amino acid transmembrane transporter activity [GO:0015171 molecular_function] (1); amino acid transmembrane transport [GO:0003333 biological_process] (1); membrane [GO:0016020 cellular_component] (1)	Amino acid/polyamine transporter I [IPR002293] (1)	-	C_unshiu_00888_mRNA_7.1	-
GF0039279	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_00888_mRNA_5.1	-
GF0039278	0	1	0	Hypothetical protein (1)			-	C_unshiu_00888_mRNA_2.1	-
GF0039277	0	1	0	Hypothetical protein (1)			-	C_unshiu_00888_mRNA_11.1	-
GF0039276	0	1	0	Legumain (1)	peptidase activity [GO:0008233 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Peptidase C13, legumain [IPR001096] (1)	-	C_unshiu_00888_mRNA_1.1	-
GF0039275	0	1	0	Neutral invertase like protein (1)	catalytic activity [GO:0003824 molecular_function] (1); glycopeptide alpha-N-acetylgalactosaminidase activity [GO:0033926 molecular_function] (1)	Six-hairpin glycosidase-like [IPR008928] (1); Glycosyl hydrolase family 100 [IPR024746] (1)	-	C_unshiu_00887_mRNA_7.1	-
GF0039274	0	1	0	Hypothetical protein (1)	catalytic activity [GO:0003824 molecular_function] (1); glycopeptide alpha-N-acetylgalactosaminidase activity [GO:0033926 molecular_function] (1)	Six-hairpin glycosidase-like [IPR008928] (1); Glycosyl hydrolase family 100 [IPR024746] (1)	-	C_unshiu_00887_mRNA_6.1	-
GF0039273	0	1	0	Hypothetical protein (1)			-	C_unshiu_00887_mRNA_2.1	-
GF0039272	0	1	0	Hypothetical protein (1)			-	C_unshiu_00886_mRNA_2.1	-
GF0039271	0	1	0	Hypothetical protein (1)			-	C_unshiu_00886_mRNA_1.1	-
GF0039270	0	1	0	Monosacharide transport protein (1)			-	C_unshiu_00885_mRNA_3.1	-
GF0039269	0	1	0	RNA-directed DNA polymerase (Reverse transcriptase) (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Reverse transcriptase domain [IPR000477] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00885_mRNA_13.1	-
GF0039268	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_00885_mRNA_12.1	-
GF0039267	0	1	0	Hypothetical protein (1)			-	C_unshiu_00885_mRNA_11.1	-
GF0039266	0	1	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	C_unshiu_00884_mRNA_7.1	-
GF0039265	0	1	0	Hypothetical protein (1)			-	C_unshiu_00884_mRNA_6.1	-
GF0039264	0	1	0	Hypothetical protein (1)			-	C_unshiu_00884_mRNA_5.1	-
GF0039263	0	1	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); AAA+ ATPase domain [IPR003593] (1); NB-ARC [IPR002182] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00884_mRNA_3.1	-
GF0039262	0	1	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	AAA+ ATPase domain [IPR003593] (1); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00884_mRNA_1.1	-
GF0039261	0	1	0	Hypothetical protein (1)			-	C_unshiu_00883_mRNA_9.1	-
GF0039260	0	1	0	Hypothetical protein (1)			-	C_unshiu_00883_mRNA_8.1	-
GF0039259	0	1	0	Hypothetical protein (1)			-	C_unshiu_00883_mRNA_7.1	-
GF0039258	0	1	0	Hypothetical protein (1)			-	C_unshiu_00883_mRNA_6.1	-
GF0039257	0	1	0	Hypothetical protein (1)		Protein argonaute, N-terminal [IPR032474] (1)	-	C_unshiu_00883_mRNA_12.1	-
GF0039256	0	1	0	Hypothetical protein (1)			-	C_unshiu_00883_mRNA_11.1	-
GF0039255	0	1	0	Hypothetical protein (1)			-	C_unshiu_00883_mRNA_10.1	-
GF0039254	0	1	0	Hypothetical protein (1)			-	C_unshiu_00882_mRNA_8.1	-
GF0039253	0	1	0	Hypothetical protein (1)			-	C_unshiu_00882_mRNA_12.1	-
GF0039252	0	1	0	Hypothetical protein (1)			-	C_unshiu_00882_mRNA_1.1	-
GF0039251	0	1	0	Hypothetical protein (1)			-	C_unshiu_00881_mRNA_9.1	-
GF0039250	0	1	0	Hypothetical protein (1)			-	C_unshiu_00881_mRNA_8.1	-
GF0039249	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00881_mRNA_4.1	-
GF0039248	0	1	0	Hypothetical protein (1)			-	C_unshiu_00881_mRNA_2.1	-
GF0039247	0	1	0	Hypothetical protein (1)			-	C_unshiu_00880_mRNA_5.1	-
GF0039246	0	1	0	Hypothetical protein (1)			-	C_unshiu_00880_mRNA_11.1	-
GF0039245	0	1	0	Retrotransposon protein, putative, Ty3-gypsy subclass, expressed (1)		Aspartic peptidase domain [IPR021109] (1)	-	C_unshiu_00880_mRNA_10.1	-
GF0039244	0	1	0	Hypothetical protein (1)	GPI-anchor transamidase complex [GO:0042765 cellular_component] (1); GPI-anchor transamidase activity [GO:0003923 molecular_function] (1); attachment of GPI anchor to protein [GO:0016255 biological_process] (1); peptidase activity [GO:0008233 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Peptidase C13, legumain [IPR001096] (1); GPI-anchor transamidase [IPR028361] (1)	-	C_unshiu_00879_mRNA_9.1	-
GF0039243	0	1	0	Putative receptor-like protein kinase RLPK1 (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Malectin [IPR021720] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_00879_mRNA_8.1	-
GF0039242	0	1	0	Hypothetical protein (1)		Arabidopsis retrotransposon Orf1 [IPR004312] (1)	-	C_unshiu_00879_mRNA_7.1	-
GF0039241	0	1	0	Hypothetical protein (1)			-	C_unshiu_00879_mRNA_12.1	-
GF0039240	0	1	0	Hypothetical protein (1)			-	C_unshiu_00879_mRNA_1.1	-
GF0039239	0	1	0	Hypothetical protein (1)			-	C_unshiu_00878_mRNA_7.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0039238	0	1	0	Hypothetical protein (1)			-	C_unshiu_00878_mRNA_5.1	-
GF0039237	0	1	0	Hypothetical protein (1)			-	C_unshiu_00878_mRNA_4.1	-
GF0039236	0	1	0	Hypothetical protein (1)			-	C_unshiu_00878_mRNA_3.1	-
GF0039235	0	1	0	Hypothetical protein (1)	DNA integration [GO:0015074 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Aspartic peptidase domain [IPR021109] (1); Ribonuclease H-like domain [IPR012337] (1); Integrase, catalytic core [IPR001584] (1)	-	C_unshiu_00878_mRNA_12.1	-
GF0039234	0	1	0	Monosacharide transport protein (1)			-	C_unshiu_00878_mRNA_10.1	-
GF0039233	0	1	0	ABC transporter G family member 40 (1)	ATP binding [GO:0005524 molecular_function] (1); ATPase activity [GO:0016887 molecular_function] (1); membrane [GO:0016020 cellular_component] (1)	ABC-2 type transporter [IPR013525] (1); ABC transporter-like [IPR003439] (1); AAA+ ATPase domain [IPR003593] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00877_mRNA_8.1	-
GF0039232	0	1	0	Pleiotropic drug resistance 1 (1)	ATPase activity [GO:0016887 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); AAA+ ATPase domain [IPR003593] (1); ABC transporter-like [IPR003439] (1)	-	C_unshiu_00877_mRNA_6.1	-
GF0039231	0	1	0	Hypothetical protein (1)			-	C_unshiu_00877_mRNA_4.1	-
GF0039230	0	1	0	Hypothetical protein (1)			-	C_unshiu_00877_mRNA_18.1	-
GF0039229	0	1	0	Hypothetical protein (1)			-	C_unshiu_00877_mRNA_14.1	-
GF0039228	0	1	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00877_mRNA_12.1	-
GF0039227	0	1	0	Hypothetical protein (1)			-	C_unshiu_00877_mRNA_11.1	-
GF0039226	0	1	0	Hypothetical protein (1)			-	C_unshiu_00876_mRNA_8.1	-
GF0039225	0	1	0	Hypothetical protein (1)			-	C_unshiu_00876_mRNA_7.1	-
GF0039224	0	1	0	Hypothetical protein (1)			-	C_unshiu_00876_mRNA_5.1	-
GF0039223	0	1	0	ABC transporter G family member 16 (1)	membrane [GO:0016020 cellular_component] (1)	ABC-2 type transporter [IPR013525] (1)	-	C_unshiu_00876_mRNA_4.1	-
GF0039222	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, GRF-type [IPR010666] (1)	-	C_unshiu_00876_mRNA_3.1	-
GF0039221	0	1	0	Hypothetical protein (1)			-	C_unshiu_00876_mRNA_10.1	-
GF0039220	0	1	0	Hypothetical protein (1)			-	C_unshiu_00876_mRNA_1.1	-
GF0039219	0	1	0	Caffeic acid O-methyltransferase (1)	O-methyltransferase activity [GO:0008171 molecular_function] (1); methyltransferase activity [GO:0008168 molecular_function] (1)	S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); O-methyltransferase COMT-type [IPR016461] (1); MULE transposase domain [IPR018289] (1); O-methyltransferase, family 2 [IPR001077] (1)	-	C_unshiu_00875_mRNA_3.2	-
GF0039218	0	1	0	Hypothetical protein (1)			-	C_unshiu_00875_mRNA_10.1	-
GF0039217	0	1	0	Hypothetical protein (1)			-	C_unshiu_00875_mRNA_1.1	-
GF0039216	0	1	0	Hypothetical protein (1)			-	C_unshiu_00874_mRNA_1.1	-
GF0039215	0	1	0	Retrotransposon protein, putative, Ty1-copia subclass (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00873_mRNA_9.1	-
GF0039214	0	1	0	Disease resistance protein RPS2, putative (1)	ADP binding [GO:0043531 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00873_mRNA_7.1	-
GF0039213	0	1	0	Hypothetical protein (1)			-	C_unshiu_00873_mRNA_6.1	-
GF0039212	0	1	0	Disease resistance protein RPS2 (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00873_mRNA_4.1	-
GF0039211	0	1	0	Hypothetical protein (1)			-	C_unshiu_00873_mRNA_12.1	-
GF0039210	0	1	0	Hypothetical protein (1)			-	C_unshiu_00873_mRNA_11.1	-
GF0039209	0	1	0	Hypothetical protein (1)			-	C_unshiu_00873_mRNA_10.1	-
GF0039208	0	1	0	Hypothetical protein (1)		Phosphoribosyltransferase-like [IPR029057] (1)	-	C_unshiu_00873_mRNA_1.1	-
GF0039207	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	-	C_unshiu_00872_mRNA_9.1	-
GF0039206	0	1	0	Terpene cyclase/mutase family member (1)		Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (1); Squalene cyclase, N-terminal [IPR032697] (1)	-	C_unshiu_00872_mRNA_8.1	-
GF0039205	0	1	0	Terpene cyclase/mutase family member (1)	intramolecular transferase activity [GO:0016866 molecular_function] (1)	Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (1); Squalene cyclase, C-terminal [IPR032696] (1); Squalene cyclase, N-terminal [IPR032697] (1); Squalene cyclase [IPR018333] (1)	-	C_unshiu_00872_mRNA_6.1	-
GF0039204	0	1	0	Hypothetical protein (1)			-	C_unshiu_00871_mRNA_7.1	-
GF0039203	0	1	0	Hypothetical protein (1)			-	C_unshiu_00871_mRNA_6.1	-
GF0039202	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_00871_mRNA_35.1	-
GF0039201	0	1	0	Hypothetical protein (1)			-	C_unshiu_00871_mRNA_34.1	-
GF0039200	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_00871_mRNA_31.1	-
GF0039199	0	1	0	Hypothetical protein (1)			-	C_unshiu_00871_mRNA_30.1	-
GF0039198	0	1	0	Hypothetical protein (1)			-	C_unshiu_00871_mRNA_26.1	-
GF0039197	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_00871_mRNA_20.1	-
GF0039196	0	1	0	Hypothetical protein (1)			-	C_unshiu_00871_mRNA_2.1	-
GF0039195	0	1	0	Hypothetical protein (1)			-	C_unshiu_00871_mRNA_18.1	-
GF0039194	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_00871_mRNA_17.1	-
GF0039193	0	1	0	Hypothetical protein (1)			-	C_unshiu_00871_mRNA_16.1	-
GF0039192	0	1	0	Hypothetical protein (1)			-	C_unshiu_00871_mRNA_14.1	-
GF0039191	0	1	0	Hypothetical protein (1)			-	C_unshiu_00871_mRNA_12.1	-
GF0039190	0	1	0	Hypothetical protein (1)			-	C_unshiu_00871_mRNA_1.1	-
GF0039189	0	1	0	Germin-like protein subfamily 1 member 7 (1)	manganese ion binding [GO:0030145 molecular_function] (1); nutrient reservoir activity [GO:0045735 molecular_function] (1)	Cupin 1 [IPR006045] (1); Germin, manganese binding site [IPR019780] (1); Germin [IPR001929] (1); RmlC-like jelly roll fold [IPR014710] (1); RmlC-like cupin domain [IPR011051] (1)	-	C_unshiu_00870_mRNA_6.1	-
GF0039188	0	1	0	Hypothetical protein (1)			-	C_unshiu_00870_mRNA_5.1	-
GF0039187	0	1	0	Hypothetical protein (1)			-	C_unshiu_00870_mRNA_14.1	-
GF0039186	0	1	0	Hypothetical protein (1)			-	C_unshiu_00869_mRNA_8.1	-
GF0039185	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00869_mRNA_16.1	-
GF0039184	0	1	0	Putative ATP-dependent helicase HRQ1 (1)	ATP binding [GO:0005524 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	DEAD/DEAH-box helicase, putative [IPR018973] (1); Helicase, C-terminal [IPR001650] (1); Helicase superfamily 1/2, ATP-binding domain [IPR014001] (1); DEAD/DEAH box helicase domain [IPR011545] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00869_mRNA_15.1	-
GF0039183	0	1	0	Phospholipase A1-Igamma1, chloroplastic (1)	lipid metabolic process [GO:0006629 biological_process] (1)	Fungal lipase-like domain [IPR002921] (1); Alpha/Beta hydrolase fold [IPR029058] (1)	-	C_unshiu_00869_mRNA_1.1	-
GF0039182	0	1	0	Hypothetical protein (1)			-	C_unshiu_00868_mRNA_7.1	-
GF0039181	0	1	0	Miraculin (1)	endopeptidase inhibitor activity [GO:0004866 molecular_function] (1)	Proteinase inhibitor I3, Kunitz legume [IPR002160] (1); Kunitz inhibitor ST1-like [IPR011065] (1)	-	C_unshiu_00868_mRNA_5.1	-
GF0039180	0	1	0	Hypothetical protein (1)			-	C_unshiu_00867_mRNA_9.1	-
GF0039179	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); DNA integration [GO:0015074 biological_process] (1)	Integrase, catalytic core [IPR001584] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00867_mRNA_18.1	-
GF0039178	0	1	0	Hypothetical protein (1)			-	C_unshiu_00867_mRNA_10.1	-
GF0039177	0	1	0	Hypothetical protein (1)			-	C_unshiu_00866_mRNA_14.1	-
GF0039176	0	1	0	Hypothetical protein (1)			-	C_unshiu_00866_mRNA_13.1	-
GF0039175	0	1	0	UDP-glycosyltransferase 73C5 (1)	metabolic process [GO:0008152 biological_process] (1); transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	-	C_unshiu_00866_mRNA_12.1	-
GF0039174	0	1	0	Hypothetical protein (1)	transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	-	C_unshiu_00866_mRNA_11.1	-
GF0039173	0	1	0	Hypothetical protein (1)			-	C_unshiu_00865_mRNA_3.1	-
GF0039172	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00864_mRNA_5.1	-
GF0039171	0	1	0	Hypothetical protein (1)			-	C_unshiu_00864_mRNA_4.1	-
GF0039170	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_00864_mRNA_3.1	-
GF0039169	0	1	0	Hypothetical protein (1)			-	C_unshiu_00864_mRNA_2.1	-
GF0039168	0	1	0	SNF7 family protein isoform 1 (1)	vacuolar transport [GO:0007034 biological_process] (1)	Snf7 family [IPR005024] (1)	-	C_unshiu_00864_mRNA_16.1	-
GF0039167	0	1	0	Hypothetical protein (1)			-	C_unshiu_00864_mRNA_12.1	-
GF0039166	0	1	0	Hypothetical protein (1)			-	C_unshiu_00864_mRNA_1.1	-
GF0039165	0	1	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1)	Aspartic peptidase, active site [IPR001969] (1); Aspartic peptidase domain [IPR021109] (1)	-	C_unshiu_00863_mRNA_8.1	-
GF0039164	0	1	0	Putative leucine-rich repeat disease resistance protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_00863_mRNA_7.1	-
GF0039163	0	1	0	Hypothetical protein (1)			-	C_unshiu_00863_mRNA_6.1	-
GF0039162	0	1	0	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	C_unshiu_00863_mRNA_22.1	-
GF0039161	0	1	0	Hypothetical protein (1)			-	C_unshiu_00863_mRNA_21.1	-
GF0039160	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00863_mRNA_2.1	-
GF0039159	0	1	0	Maturase R (1)	mRNA processing [GO:0006397 biological_process] (1)	Domain X [IPR024937] (1)	-	C_unshiu_00863_mRNA_19.1	-
GF0039158	0	1	0	Hypothetical protein (1)			-	C_unshiu_00863_mRNA_18.1	-

ID	**Num. in *C. celementine***	**Num in *C. unshiu***	**Num in *P.trifoliata***	**Note**	**GO**	**InterPro**	**Members in *C.clementine***	**Members in *C.unshiu***	**Members in *P.trifoliata***
GF0039157	0	1	0	Hypothetical leucine rich repeat protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_00863_mRNA_10.1	-
GF0039156	0	1	0	Leucine-rich repeat disease resistance protein-like (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00863_mRNA_1.1	-
GF0039155	0	1	0	Hypothetical protein (1)			-	C_unshiu_00862_mRNA_7.1	-
GF0039154	0	1	0	Hypothetical protein (1)			-	C_unshiu_00862_mRNA_3.1	-
GF0039153	0	1	0	Hypothetical protein (1)			-	C_unshiu_00862_mRNA_2.1	-
GF0039152	0	1	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	-	C_unshiu_00862_mRNA_10.1	-
GF0039151	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Tetratricopeptide-like helical domain [IPR011990] (1)	-	C_unshiu_00861_mRNA_5.1	-
GF0039150	0	1	0	Hypothetical protein (1)			-	C_unshiu_00861_mRNA_11.1	-
GF0039149	0	1	0	Hypothetical protein (1)			-	C_unshiu_00861_mRNA_10.1	-
GF0039148	0	1	0	Hypothetical protein (1)			-	C_unshiu_00860_mRNA_3.1	-
GF0039147	0	1	0	Hypothetical protein (1)			-	C_unshiu_00859_mRNA_6.1	-
GF0039146	0	1	0	Hypothetical protein (1)			-	C_unshiu_00859_mRNA_5.1	-
GF0039145	0	1	0	Hypothetical protein (1)			-	C_unshiu_00859_mRNA_3.1	-
GF0039144	0	1	0	Monosacharide transport protein (1)			-	C_unshiu_00859_mRNA_15.1	-
GF0039143	0	1	0	Hypothetical protein (1)			-	C_unshiu_00859_mRNA_12.1	-
GF0039142	0	1	0	Hypothetical protein (1)			-	C_unshiu_00858_mRNA_9.1	-
GF0039141	0	1	0	Hypothetical protein (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_00858_mRNA_14.1	-
GF0039140	0	1	0	Hypothetical protein (1)			-	C_unshiu_00858_mRNA_12.1	-
GF0039139	0	1	0	Hypothetical protein (1)		Protein of unknown function DUF966 [IPR010369] (1)	-	C_unshiu_00858_mRNA_1.1	-
GF0039138	0	1	0	Hypothetical protein (1)	hydro-lyase activity [GO:0016836 molecular_function] (1)	Enoyl-CoA hydratase/isomerase, HIBYL-CoA-H type [IPR032259] (1); ClpP/crotonase-like domain [IPR029045] (1)	-	C_unshiu_00857_mRNA_3.1	-
GF0039137	0	1	0	Hypothetical protein (1)			-	C_unshiu_00857_mRNA_13.1	-
GF0039136	0	1	0	Hypothetical protein (1)			-	C_unshiu_00856_mRNA_7.1	-
GF0039135	0	1	0	Hypothetical protein (1)			-	C_unshiu_00856_mRNA_6.1	-
GF0039134	0	1	0	Hypothetical protein (1)			-	C_unshiu_00856_mRNA_5.1	-
GF0039133	0	1	0	Monoglyceride lipase (1)		Serine aminopeptidase, S33 [IPR022742] (1); Alpha/Beta hydrolase fold [IPR029058] (1)	-	C_unshiu_00856_mRNA_4.1	-
GF0039132	0	1	0	Hypothetical protein (1)			-	C_unshiu_00856_mRNA_13.1	-
GF0039131	0	1	0	Hypothetical protein (1)			-	C_unshiu_00856_mRNA_11.1	-
GF0039130	0	1	0	Hypothetical protein (1)			-	C_unshiu_00856_mRNA_1.1	-
GF0039129	0	1	0	Ribulose bisphosphate carboxylase small chain (1)		Ribulose bisphosphate carboxylase, small chain [IPR024681] (1); Ribulose bisphosphate carboxylase small chain, domain [IPR000894] (1)	-	C_unshiu_00855_mRNA_6.1	-
GF0039128	0	1	0	Hypothetical protein (1)			-	C_unshiu_00855_mRNA_4.1	-
GF0039127	0	1	0	Cytochrome P450 protein (1)	iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Cytochrome P450 [IPR001128] (1)	-	C_unshiu_00854_mRNA_4.1	-
GF0039126	0	1	0	E3 ubiquitin-protein ligase RHA2A (1)	protein binding [GO:0005515 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, RING/FYVE/PHD-type [IPR013083] (1); Zinc finger, RING-type [IPR001841] (1)	-	C_unshiu_00854_mRNA_17.1	-
GF0039125	0	1	0	Hypothetical protein (1)			-	C_unshiu_00854_mRNA_14.1	-
GF0039124	0	1	0	Hypothetical protein (1)	metalloendopeptidase activity [GO:0004222 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1); metallopeptidase activity [GO:0008237 molecular_function] (1)	Peptidase M3A/M3B [IPR001567] (1); Metallopeptidase, catalytic domain [IPR024079] (1)	-	C_unshiu_00853_mRNA_2.1	-
GF0039123	0	1	0	Hypothetical protein (1)			-	C_unshiu_00853_mRNA_12.1	-
GF0039122	0	1	0	Hypothetical protein (1)			-	C_unshiu_00852_mRNA_6.1	-
GF0039121	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_00852_mRNA_5.1	-
GF0039120	0	1	0	Putative retroelement pol polyprotein (1)			-	C_unshiu_00852_mRNA_4.1	-
GF0039119	0	1	0	Hypothetical protein (1)			-	C_unshiu_00852_mRNA_24.1	-
GF0039118	0	1	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00852_mRNA_20.1	-
GF0039117	0	1	0	Disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	C_unshiu_00852_mRNA_18.1	-
GF0039116	0	1	0	Hypothetical protein (1)			-	C_unshiu_00852_mRNA_16.1	-
GF0039115	0	1	0	Hypothetical protein (1)			-	C_unshiu_00852_mRNA_15.1	-
GF0039114	0	1	0	CDNA clone:002-110-H12, full insert sequence (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00851_mRNA_7.1	-
GF0039113	0	1	0	Hypothetical protein (1)			-	C_unshiu_00851_mRNA_6.1	-
GF0039112	0	1	0	Retrotransposon protein, putative, Ty1-copia subclass (1)			-	C_unshiu_00851_mRNA_4.1	-
GF0039111	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00851_mRNA_3.1	-
GF0039110	0	1	0	Alpha,alpha-trehalase (1)	catalytic activity [GO:0003824 molecular_function] (1); trehalose metabolic process [GO:0005991 biological_process] (1); alpha,alpha-trehalase activity [GO:0004555 molecular_function] (1)	Glycoside hydrolase, family 37, conserved site [IPR018232] (1); Six-hairpin glycosidase-like [IPR008928] (1); Glycoside hydrolase, family 37 [IPR001661] (1)	-	C_unshiu_00850_mRNA_3.1	-
GF0039109	0	1	0	MFS transporter (1)	molybdate ion transmembrane transporter activity [GO:0015098 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1); molybdate ion transport [GO:0015689 biological_process] (1)	Major facilitator superfamily domain [IPR020846] (1); Molybdate-anion transporter [IPR008509] (1)	-	C_unshiu_00850_mRNA_19.1	-
GF0039108	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ubiquitin-related domain [IPR029071] (1); UBX domain [IPR001012] (1)	-	C_unshiu_00850_mRNA_12.1	-
GF0039107	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF1605 [IPR011709] (1)	-	C_unshiu_00850_mRNA_1.1	-
GF0039106	0	1	0	Hypothetical protein (1)	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1)	Cytochrome P450 [IPR001128] (1)	-	C_unshiu_00849_mRNA_6.1	-
GF0039105	0	1	0	Hypothetical protein (1)			-	C_unshiu_00849_mRNA_20.1	-
GF0039104	0	1	0	Hypothetical protein (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_00849_mRNA_16.1	-
GF0039103	0	1	0	Hypothetical protein (1)	iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1)	Cytochrome P450 [IPR001128] (1)	-	C_unshiu_00849_mRNA_1.1	-
GF0039102	0	1	0	Hypothetical protein (1)	integral component of membrane [GO:0016021 cellular_component] (1); nucleotide binding [GO:0000166 molecular_function] (1)	P-type ATPase, transmembrane domain [IPR023298] (1); P-type ATPase, cytoplasmic domain N [IPR023299] (1); P-type ATPase [IPR001757] (1); HAD-like domain [IPR023214] (1)	-	C_unshiu_00848_mRNA_8.1	-
GF0039101	0	1	0	Hypothetical protein (1)			-	C_unshiu_00848_mRNA_2.1	-
GF0039100	0	1	0	UDP-glucose protein transglucosylase (1)	intramolecular transferase activity [GO:0016866 molecular_function] (1); cellulose biosynthetic process [GO:0030244 biological_process] (1)	Reversibly glycosylated polypeptide family [IPR004901] (1)	-	C_unshiu_00847_mRNA_12.1	-
GF0039099	0	1	0	Hypothetical protein (1)			-	C_unshiu_00847_mRNA_1.1	-
GF0039098	0	1	0	Hypothetical protein (1)	transmembrane transport [GO:0055085 biological_process] (1)	Oligopeptide transporter, OPT superfamily [IPR004813] (1)	-	C_unshiu_00846_mRNA_15.1	-
GF0039097	0	1	0	Endoglucanase (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1); hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (1)	Six-hairpin glycosidase [IPR012341] (1); Six-hairpin glycosidase-like [IPR008928] (1); Glycosyl hydrolases family 9, Asp/Glu active sites [IPR033126] (1); Glycoside hydrolase family 9 [IPR001701] (1)	-	C_unshiu_00845_mRNA_13.1	-
GF0039096	0	1	0	Hypothetical protein (1)	pyridoxal phosphate binding [GO:0030170 molecular_function] (1); catalytic activity [GO:0003824 molecular_function] (1); biosynthetic process [GO:0009058 biological_process] (1)	Pyridoxal phosphate-dependent transferase, major region, subdomain 1 [IPR015421] (1); Alpha crystallin/Hsp20 domain [IPR002068] (1); HSP20-like chaperone [IPR008978] (1); Aminotransferase, class I/classII [IPR004839] (1); Pyridoxal phosphate-dependent transferase [IPR015424] (1)	-	C_unshiu_00844_mRNA_9.1	-
GF0039095	0	1	0	Hypothetical protein (1)			-	C_unshiu_00844_mRNA_4.1	-
GF0039094	0	1	0	Hypothetical protein (1)			-	C_unshiu_00844_mRNA_3.1	-
GF0039093	0	1	0	Hypothetical protein (1)			-	C_unshiu_00844_mRNA_16.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0039092	0	1	0	Hypothetical protein (1)			-	C_unshiu_00844_mRNA_14.1	-
GF0039091	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	C_unshiu_00844_mRNA_13.1	-
GF0039090	0	1	0	Phosphopyruvate hydratase (1)	magnesium ion binding [GO:0000287 molecular_function] (1); phosphopyruvate hydratase activity [GO:0004634 molecular_function] (1); glycolytic process [GO:0006096 biological_process] (1); phosphopyruvate hydratase complex [GO:0000015 cellular_component] (1)	Enolase, conserved site [IPR020809] (1); Enolase [IPR000941] (1); Enolase C-terminal domain-like [IPR029065] (1); Enolase, C-terminal [IPR020810] (1)	-	C_unshiu_00843_mRNA_14.1	-
GF0039089	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	PAZ domain [IPR003100] (1); Argonaut, glycine-rich domain [IPR024357] (1); Protein argonaute, N-terminal [IPR032474] (1)	-	C_unshiu_00841_mRNA_6.1	-
GF0039088	0	1	0	Hypothetical protein (1)			-	C_unshiu_00841_mRNA_10.1	-
GF0039087	0	1	0	Hypothetical protein (1)			-	C_unshiu_00841_mRNA_1.1	-
GF0039086	0	1	0	Hypothetical protein (1)			-	C_unshiu_00840_mRNA_6.1	-
GF0039085	0	1	0	Hypothetical protein (1)			-	C_unshiu_00840_mRNA_5.1	-
GF0039084	0	1	0	Hypothetical protein (1)			-	C_unshiu_00840_mRNA_4.1	-
GF0039083	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00840_mRNA_2.1	-
GF0039082	0	1	0	Hypothetical protein (1)			-	C_unshiu_00839_mRNA_9.1	-
GF0039081	0	1	0	Hypothetical protein (1)			-	C_unshiu_00839_mRNA_7.1	-
GF0039080	0	1	0	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	C_unshiu_00839_mRNA_3.1	-
GF0039079	0	1	0	Hypothetical protein (1)		Rab-GTPase-TBC domain [IPR000195] (1)	-	C_unshiu_00839_mRNA_14.1	-
GF0039078	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_00839_mRNA_11.1	-
GF0039077	0	1	0	Hypothetical protein (1)			-	C_unshiu_00839_mRNA_10.1	-
GF0039076	0	1	0	Disease resistance protein (TIR-NBS-LRR class) (1)	signal transduction [GO:0007165 biological_process] (1); ADP binding [GO:0043531 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	C_unshiu_00839_mRNA_1.1	-
GF0039075	0	1	0	Cytochrome P450 78A3 (1)	iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450, conserved site [IPR017972] (1); Cytochrome P450 [IPR001128] (1)	-	C_unshiu_00838_mRNA_12.1	-
GF0039074	0	1	0	Hypothetical protein (1)			-	C_unshiu_00837_mRNA_5.1	-
GF0039073	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00836_mRNA_9.1	-
GF0039072	0	1	0	Hypothetical protein (1)			-	C_unshiu_00836_mRNA_4.1	-
GF0039071	0	1	0	LRR receptor-like serine/threonine-protein kinase GSO1 (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Peptidase M28 [IPR007484] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1)	-	C_unshiu_00836_mRNA_12.1	-
GF0039070	0	1	0	Gamma-glutamyl hydrolase 2 (1)	glutamine metabolic process [GO:0006541 biological_process] (1); omega peptidase activity [GO:0008242 molecular_function] (1); hydrolase activity [GO:0016787 molecular_function] (1); catalytic activity [GO:0003824 molecular_function] (1)	Class I glutamine amidotransferase-like [IPR029062] (1); Peptidase C26 [IPR011697] (1); Peptidase C26, gamma-glutamyl hydrolase [IPR015527] (1)	-	C_unshiu_00836_mRNA_1.1	-
GF0039069	0	1	0	MADS-box transcription factor family protein (1)	DNA binding [GO:0003677 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	Transcription factor, MADS-box [IPR002100] (1)	-	C_unshiu_00835_mRNA_3.1	-
GF0039068	0	1	0	Hypothetical protein (1)	racemase and epimerase activity, acting on carbohydrates and derivatives [GO:0016857 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1)	Aldolase-type TIM barrel [IPR013785] (1); Ribulose-phosphate binding barrel [IPR011060] (1); Ribulose-phosphate 3-epimerase-like [IPR000056] (1)	-	C_unshiu_00835_mRNA_10.1	-
GF0039067	0	1	0	Hypothetical protein (1)			-	C_unshiu_00834_mRNA_4.1	-
GF0039066	0	1	0	Pentatricopeptide repeat-containing protein, chloroplastic (1)		Pentatricopeptide repeat [IPR002885] (1)	-	C_unshiu_00834_mRNA_2.1	-
GF0039065	0	1	0	Hypothetical protein (1)			-	C_unshiu_00832_mRNA_4.1	-
GF0039064	0	1	0	Zinc finger protein ZAT11 (1)	metal ion binding [GO:0046872 molecular_function] (1)	Zinc finger, C2H2 [IPR007087] (1); Zinc finger, C2H2-like [IPR015880] (1)	-	C_unshiu_00832_mRNA_22.1	-
GF0039063	0	1	0	Hypothetical protein (1)			-	C_unshiu_00831_mRNA_7.1	-
GF0039062	0	1	0	Progesterone 5-beta-reductase (1)		NAD(P)-binding domain [IPR016040] (1)	-	C_unshiu_00831_mRNA_4.1	-
GF0039061	0	1	0	Hypothetical protein (1)			-	C_unshiu_00831_mRNA_14.1	-
GF0039060	0	1	0	BURP domain-containing protein (1)		BURP domain [IPR004873] (1)	-	C_unshiu_00831_mRNA_13.1	-
GF0039059	0	1	0	Putative leucine-rich repeat disease resistance protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_00830_mRNA_9.1	-
GF0039058	0	1	0	Transposase family tnp2, putative (1)		Transposon, En/Spm-like [IPR004242] (1)	-	C_unshiu_00830_mRNA_8.1	-
GF0039057	0	1	0	Hypothetical protein (1)			-	C_unshiu_00830_mRNA_6.1	-
GF0039056	0	1	0	Hypothetical protein (1)			-	C_unshiu_00830_mRNA_4.1	-
GF0039055	0	1	0	Hypothetical protein (1)			-	C_unshiu_00830_mRNA_20.1	-
GF0039054	0	1	0	Truncated verticillium wilt resistance-like protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00830_mRNA_2.1	-
GF0039053	0	1	0	Hypothetical protein (1)			-	C_unshiu_00830_mRNA_16.1	-
GF0039052	0	1	0	Nascent polypeptide-associated complex subunit alpha-like protein (1)		Nascent polypeptide-associated complex NAC domain [IPR002715] (1); Nascent polypeptide-associated complex subunit alpha [IPR016641] (1)	-	C_unshiu_00830_mRNA_13.1	-
GF0039051	0	1	0	Hypothetical protein (1)			-	C_unshiu_00830_mRNA_10.1	-
GF0039050	0	1	0	Hypothetical protein (1)			-	C_unshiu_00829_mRNA_8.1	-
GF0039049	0	1	0	Caffeic acid 3-O-methyltransferase (1)	O-methyltransferase activity [GO:0008171 molecular_function] (1); methyltransferase activity [GO:0008168 molecular_function] (1)	S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); O-methyltransferase COMT-type [IPR016461] (1); O-methyltransferase, family 2 [IPR001077] (1)	-	C_unshiu_00829_mRNA_7.1	-
GF0039048	0	1	0	Caffeic acid 3-O-methyltransferase (1)	protein dimerization activity [GO:0046983 molecular_function] (1); O-methyltransferase activity [GO:0008171 molecular_function] (1); methyltransferase activity [GO:0008168 molecular_function] (1)	S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); O-methyltransferase, family 2 [IPR001077] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Plant methyltransferase dimerisation [IPR012967] (1); O-methyltransferase COMT-type [IPR016461] (1)	-	C_unshiu_00829_mRNA_6.1	-
GF0039047	0	1	0	Tricetin 3',4',5'-O-trimethyltransferase (1)	O-methyltransferase activity [GO:0008171 molecular_function] (1); methyltransferase activity [GO:0008168 molecular_function] (1)	S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); O-methyltransferase, family 2 [IPR001077] (1); O-methyltransferase COMT-type [IPR016461] (1)	-	C_unshiu_00829_mRNA_4.1	-
GF0039046	0	1	0	Hypothetical protein (1)			-	C_unshiu_00829_mRNA_3.1	-
GF0039045	0	1	0	Hypothetical protein (1)			-	C_unshiu_00829_mRNA_10.1	-
GF0039044	0	1	0	Hypothetical protein (1)			-	C_unshiu_00828_mRNA_2.1	-
GF0039043	0	1	0	Hypothetical protein (1)			-	C_unshiu_00828_mRNA_14.1	-
GF0039042	0	1	0	Hypothetical protein (1)			-	C_unshiu_00827_mRNA_15.1	-
GF0039041	0	1	0	Hypothetical protein (1)			-	C_unshiu_00826_mRNA_7.1	-
GF0039040	0	1	0	Hypothetical protein (1)			-	C_unshiu_00826_mRNA_6.1	-
GF0039039	0	1	0	Hypothetical protein (1)	polysaccharide binding [GO:0030247 molecular_function] (1)	Wall-associated receptor kinase, galacturonan-binding domain [IPR025287] (1); EGF-like, conserved site [IPR013032] (1)	-	C_unshiu_00826_mRNA_5.1	-
GF0039038	0	1	0	Hypothetical protein (1)		Retroviral aspartyl protease [IPR013242] (1)	-	C_unshiu_00826_mRNA_2.1	-
GF0039037	0	1	0	Cysteine-rich RLK 34, putative isoform 3 (1)	chitin catabolic process [GO:0006032 biological_process] (1); hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1); chitinase activity [GO:0004568 molecular_function] (1)	Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Glycoside hydrolase, catalytic domain [IPR013781] (1); Glycoside hydrolase superfamily [IPR017853] (1); Chitinase II [IPR011583] (1); Glycoside hydrolase family 18, catalytic domain [IPR001223] (1)	-	C_unshiu_00826_mRNA_19.1	-
GF0039036	0	1	0	Hypothetical protein (1)			-	C_unshiu_00826_mRNA_18.1	-
GF0039035	0	1	0	Hypothetical protein (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1); hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (1)	Glycoside hydrolase superfamily [IPR017853] (1); Glycoside hydrolase, catalytic domain [IPR013781] (1); Glycoside hydrolase family 18, catalytic domain [IPR001223] (1)	-	C_unshiu_00826_mRNA_17.1	-
GF0039034	0	1	0	Hypothetical protein (1)		Receptor L-domain [IPR000494] (1)	-	C_unshiu_00826_mRNA_14.1	-
GF0039033	0	1	0	GDSL esterase/lipase APG (1)	lipid metabolic process [GO:0006629 biological_process] (1); hydrolase activity, acting on ester bonds [GO:0016788 molecular_function] (1); lipase activity [GO:0016298 molecular_function] (1)	SGNH hydrolase-type esterase domain [IPR013830] (1); GDSL lipase/esterase [IPR001087] (1); Lipase, GDSL, active site [IPR008265] (1)	-	C_unshiu_00826_mRNA_12.1	-
GF0039032	0	1	0	Hypothetical protein (1)			-	C_unshiu_00826_mRNA_1.1	-
GF0039031	0	1	0	Hypothetical protein (1)			-	C_unshiu_00825_mRNA_3.1	-
GF0039030	0	1	0	Hypothetical protein (1)			-	C_unshiu_00825_mRNA_2.1	-
GF0039029	0	1	0	Hypothetical protein (1)			-	C_unshiu_00825_mRNA_15.1	-
GF0039028	0	1	0	Hypothetical protein (1)	integral component of membrane [GO:0016021 cellular_component] (1); prenyltransferase activity [GO:0004659 molecular_function] (1)	UbiA prenyltransferase family [IPR000537] (1)	-	C_unshiu_00824_mRNA_8.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0039027	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF1985 [IPR015410] (1)	-	C_unshiu_00824_mRNA_1.1	-
GF0039026	0	1	0	Hypothetical protein (1)			-	C_unshiu_00823_mRNA_9.1	-
GF0039025	0	1	0	Hypothetical protein (1)			-	C_unshiu_00823_mRNA_8.1	-
GF0039024	0	1	0	Hypothetical protein (1)			-	C_unshiu_00823_mRNA_2.1	-
GF0039023	0	1	0	Hypothetical protein (1)			-	C_unshiu_00823_mRNA_13.1	-
GF0039022	0	1	0	Hypothetical protein (1)			-	C_unshiu_00823_mRNA_12.1	-
GF0039021	0	1	0	Systemin receptor SR160, putative (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_00822_mRNA_9.1	-
GF0039020	0	1	0	Monosacharide transport protein (1)			-	C_unshiu_00822_mRNA_14.1	-
GF0039019	0	1	0	Hypothetical protein (1)			-	C_unshiu_00821_mRNA_9.1	-
GF0039018	0	1	0	Hypothetical protein (1)			-	C_unshiu_00821_mRNA_7.1	-
GF0039017	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Tetratricopeptide-like helical domain [IPR011990] (1); Tetratricopeptide repeat [IPR019734] (1); Tetratricopeptide repeat-containing domain [IPR013026] (1)	-	C_unshiu_00821_mRNA_2.1	-
GF0039016	0	1	0	Hypothetical protein (1)			-	C_unshiu_00821_mRNA_16.1	-
GF0039015	0	1	0	Hypothetical protein (1)			-	C_unshiu_00821_mRNA_15.1	-
GF0039014	0	1	0	Hypothetical protein (1)			-	C_unshiu_00821_mRNA_14.1	-
GF0039013	0	1	0	Hypothetical protein (1)			-	C_unshiu_00821_mRNA_1.1	-
GF0039012	0	1	0	TBC1 domain family member 15 (1)		Rab-GTPase-TBC domain [IPR000195] (1)	-	C_unshiu_00820_mRNA_14.1	-
GF0039011	0	1	0	60S ribosomal protein L14 (1)	ribosome [GO:0005840 cellular_component] (1); translation [GO:0006412 biological_process] (1); intracellular [GO:0005622 cellular_component] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1)	Ribosomal protein L14 [IPR002784] (1)	-	C_unshiu_00820_mRNA_13.1	-
GF0039010	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00819_mRNA_5.1	-
GF0039009	0	1	0	Transposase tnp2 (1)		Transposon, En/Spm-like [IPR004242] (1)	-	C_unshiu_00819_mRNA_1.1	-
GF0039008	0	1	0	Disease resistance protein RPS2 (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00818_mRNA_9.1	-
GF0039007	0	1	0	Hypothetical protein (1)			-	C_unshiu_00818_mRNA_7.1	-
GF0039006	0	1	0	Hypothetical protein (1)			-	C_unshiu_00818_mRNA_5.1	-
GF0039005	0	1	0	Hypothetical protein (1)			-	C_unshiu_00818_mRNA_4.1	-
GF0039004	0	1	0	Hypothetical protein (1)	metabolic process [GO:0008152 biological_process] (1); hydrolase activity [GO:0016787 molecular_function] (1)	Alpha/Beta hydrolase fold [IPR029058] (1); Alpha/beta hydrolase fold-3 [IPR013094] (1)	-	C_unshiu_00818_mRNA_3.1	-
GF0039003	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00818_mRNA_10.1	-
GF0039002	0	1	0	Hypothetical protein (1)			-	C_unshiu_00818_mRNA_1.1	-
GF0039001	0	1	0	Flavin containing monooxygenase YUCCA10-like protein (1)	N,N-dimethylaniline monooxygenase activity [GO:0004499 molecular_function] (1); NADP binding [GO:0050661 molecular_function] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); flavin adenine dinucleotide binding [GO:0050660 molecular_function] (1)	Flavin monooxygenase FMO [IPR000960] (1); FAD/NAD(P)-binding domain [IPR023753] (1); Flavin monooxygenase-like [IPR020946] (1)	-	C_unshiu_00817_mRNA_6.1	-
GF0039000	0	1	0	Hypothetical protein (1)			-	C_unshiu_00817_mRNA_12.1	-
GF0038999	0	1	0	Hypothetical protein (1)			-	C_unshiu_00817_mRNA_1.1	-
GF0038998	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_00816_mRNA_9.1	-
GF0038997	0	1	0	Hypothetical protein (1)			-	C_unshiu_00816_mRNA_8.1	-
GF0038996	0	1	0	Hypothetical protein (1)			-	C_unshiu_00816_mRNA_7.1	-
GF0038995	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Viral movement protein [IPR028919] (1)	-	C_unshiu_00816_mRNA_6.1	-
GF0038994	0	1	0	Hypothetical protein (1)			-	C_unshiu_00816_mRNA_19.1	-
GF0038993	0	1	0	Transcription factor HEC3 (1)	protein dimerization activity [GO:0046983 molecular_function] (1)	Myc-type, basic helix-loop-helix (bHLH) domain [IPR011598] (1)	-	C_unshiu_00816_mRNA_17.1	-
GF0038992	0	1	0	Hypothetical protein (1)			-	C_unshiu_00816_mRNA_15.1	-
GF0038991	0	1	0	Hypothetical protein (1)			-	C_unshiu_00816_mRNA_11.1	-
GF0038990	0	1	0	Hypothetical protein (1)			-	C_unshiu_00816_mRNA_1.1	-
GF0038989	0	1	0	Monosacharide transport protein (1)			-	C_unshiu_00815_mRNA_2.1	-
GF0038988	0	1	0	Hypothetical protein (1)	hydrolase activity [GO:0016787 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Alpha/Beta hydrolase fold [IPR029058] (1); Alpha/beta hydrolase fold-3 [IPR013094] (1); Lipase, GDXG, putative serine active site [IPR033140] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00815_mRNA_13.1	-
GF0038987	0	1	0	Hypothetical protein (1)			-	C_unshiu_00815_mRNA_10.1	-
GF0038986	0	1	0	Hypothetical protein (1)			-	C_unshiu_00815_mRNA_1.1	-
GF0038985	0	1	0	Hypothetical protein (1)			-	C_unshiu_00814_mRNA_3.1	-
GF0038984	0	1	0	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family (1)		Late embryogenesis abundant protein, LEA-14 [IPR004864] (1)	-	C_unshiu_00814_mRNA_23.1	-
GF0038983	0	1	0	Hypothetical protein (1)			-	C_unshiu_00814_mRNA_19.1	-
GF0038982	0	1	0	Hypothetical protein (1)			-	C_unshiu_00814_mRNA_18.1	-
GF0038981	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00814_mRNA_17.1	-
GF0038980	0	1	0	Hypothetical protein (1)	heme binding [GO:0020037 molecular_function] (1); response to oxidative stress [GO:0006979 biological_process] (1); peroxidase activity [GO:0004601 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Haem peroxidase [IPR010255] (1); Haem peroxidase, plant/fungal/bacterial [IPR002016] (1); Plant peroxidase [IPR000823] (1)	-	C_unshiu_00814_mRNA_16.1	-
GF0038979	0	1	0	Germin-like protein subfamily 2 member 4 (1)	manganese ion binding [GO:0030145 molecular_function] (1); nutrient reservoir activity [GO:0045735 molecular_function] (1)	Germin [IPR001929] (1); RmlC-like jelly roll fold [IPR014710] (1); Cupin 1 [IPR006045] (1); RmlC-like cupin domain [IPR011051] (1)	-	C_unshiu_00814_mRNA_12.1	-
GF0038978	0	1	0	Cytochrome c biogenesis C (1)	heme transporter activity [GO:0015232 molecular_function] (1); heme transport [GO:0015886 biological_process] (1); heme binding [GO:0020037 molecular_function] (1); membrane [GO:0016020 cellular_component] (1); cytochrome complex assembly [GO:0017004 biological_process] (1)	Cytochrome c assembly protein [IPR002541] (1); Cytochrome c-type biogenesis protein CcmC [IPR003557] (1)	-	C_unshiu_00813_mRNA_9.1	-
GF0038977	0	1	0	Hypothetical protein (1)			-	C_unshiu_00813_mRNA_8.1	-
GF0038976	0	1	0	Hypothetical protein (1)			-	C_unshiu_00813_mRNA_7.1	-
GF0038975	0	1	0	Hypothetical protein (1)			-	C_unshiu_00813_mRNA_25.1	-
GF0038974	0	1	0	Hypothetical protein (1)			-	C_unshiu_00813_mRNA_23.1	-
GF0038973	0	1	0	Hypothetical protein (1)			-	C_unshiu_00813_mRNA_22.1	-
GF0038972	0	1	0	Hypothetical protein (1)			-	C_unshiu_00813_mRNA_17.1	-
GF0038971	0	1	0	Hypothetical protein (1)			-	C_unshiu_00813_mRNA_16.1	-
GF0038970	0	1	0	Cytochrome C biogenesis ccmF protein (1)		Cytochrome c-type biogenesis protein CcmF, C-terminal [IPR032523] (1)	-	C_unshiu_00813_mRNA_14.1	-
GF0038969	0	1	0	Hypothetical protein (1)			-	C_unshiu_00813_mRNA_13.1	-
GF0038968	0	1	0	Hypothetical protein (1)			-	C_unshiu_00813_mRNA_1.1	-
GF0038967	0	1	0	Hypothetical protein (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Aspartic peptidase, active site [IPR001969] (1); Retropepsins [IPR018061] (1)	-	C_unshiu_00812_mRNA_9.1	-
GF0038966	0	1	0	Hypothetical protein (1)			-	C_unshiu_00812_mRNA_7.1	-
GF0038965	0	1	0	Hypothetical protein (1)	binding [GO:0005488 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1); carotene 7,8-desaturase activity [GO:0016719 molecular_function] (1); carotenoid biosynthetic process [GO:0016117 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Zeta-carotene desaturase [IPR014103] (1); Armadillo [IPR000225] (1); Amine oxidase [IPR002937] (1); Armadillo-like helical [IPR011989] (1); FAD/NAD(P)-binding domain [IPR023753] (1); Armadillo-type fold [IPR016024] (1); NAD(P)-binding domain [IPR016040] (1)	-	C_unshiu_00812_mRNA_6.1	-
GF0038964	0	1	0	Putative disease resistance gene NBS-LRR family protein (1)	ADP binding [GO:0043531 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	C_unshiu_00812_mRNA_3.1	-
GF0038963	0	1	0	Hypothetical protein (1)			-	C_unshiu_00811_mRNA_8.1	-
GF0038962	0	1	0	Hypothetical protein (1)			-	C_unshiu_00811_mRNA_2.1	-
GF0038961	0	1	0	Hypothetical protein (1)	GTP binding [GO:0005525 molecular_function] (1)	AIG1-type guanine nucleotide-binding (G) domain [IPR006703] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00811_mRNA_1.1	-
GF0038960	0	1	0	Hypothetical protein (1)		Isoprenoid synthase domain [IPR008949] (1)	-	C_unshiu_00810_mRNA_7.1	-
GF0038959	0	1	0	Hypothetical protein (1)			-	C_unshiu_00810_mRNA_6.1	-
GF0038958	0	1	0	Hypothetical protein (1)			-	C_unshiu_00810_mRNA_5.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0038957	0	1	0	LRR receptor-like kinase family protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein binding [GO:0005515 molecular_function] (1)	Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Protein kinase, ATP binding site [IPR017441] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Leucine-rich repeat [IPR001611] (1); Protein kinase domain [IPR000719] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Leucine rich repeat 4 [IPR025875] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_00810_mRNA_3.1	-
GF0038956	0	1	0	Hypothetical protein (1)		Concanavalin A-like lectin/glucanase domain [IPR013320] (1)	-	C_unshiu_00810_mRNA_2.1	-
GF0038955	0	1	0	Hypothetical protein (1)			-	C_unshiu_00810_mRNA_1.1	-
GF0038954	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1); polyamine transport [GO:0015846 biological_process] (1); periplasmic space [GO:0042597 cellular_component] (1); polyamine binding [GO:0019808 molecular_function] (1)	Bacterial periplasmic spermidine/putrescine-binding protein [IPR001188] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_00809_mRNA_8.1	-
GF0038953	0	1	0	Hypothetical protein (1)		Aspartate/glutamate/uridylate kinase [IPR001048] (1)	-	C_unshiu_00809_mRNA_3.1	-
GF0038952	0	1	0	LRR receptor-like serine/threonine-protein kinase GSO1 (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	-	C_unshiu_00809_mRNA_11.1	-
GF0038951	0	1	0	Hypothetical protein (1)		Myb-like domain [IPR017877] (1)	-	C_unshiu_00808_mRNA_6.1	-
GF0038950	0	1	0	Hypothetical protein (1)	potassium ion transport [GO:0006813 biological_process] (1); sodium ion transport [GO:0006814 biological_process] (1); integral component of membrane [GO:0016021 cellular_component] (1); monovalent cation:proton antiporter activity [GO:0005451 molecular_function] (1)	Cation/H(+) exchanger CHX21/CHX23 [IPR030153] (1)	-	C_unshiu_00808_mRNA_3.1	-
GF0038949	0	1	0	Hypothetical protein (1)			-	C_unshiu_00808_mRNA_2.1	-
GF0038948	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	C_unshiu_00807_mRNA_5.1	-
GF0038947	0	1	0	Hypothetical protein (1)			-	C_unshiu_00807_mRNA_4.1	-
GF0038946	0	1	0	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase (1)	metabolic process [GO:0008152 biological_process] (1); intramolecular transferase activity, phosphotransferases [GO:0016868 molecular_function] (1); catalytic activity [GO:0003824 molecular_function] (1); phosphoglycerate mutase activity [GO:0004619 molecular_function] (1); glycolytic process [GO:0006096 biological_process] (1)	Histidine phosphatase superfamily, clade-1 [IPR013078] (1); Phosphoglycerate/bisphosphoglycerate mutase, active site [IPR001345] (1); Phosphoglycerate mutase 1 [IPR005952] (1); Histidine phosphatase superfamily [IPR029033] (1)	-	C_unshiu_00807_mRNA_13.1	-
GF0038945	0	1	0	Hypothetical protein (1)		Cactin, central domain [IPR018816] (1)	-	C_unshiu_00806_mRNA_3.1	-
GF0038944	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00805_mRNA_6.1	-
GF0038943	0	1	0	Hypothetical protein (1)			-	C_unshiu_00805_mRNA_15.1	-
GF0038942	0	1	0	Hypothetical protein (1)			-	C_unshiu_00805_mRNA_14.1	-
GF0038941	0	1	0	Hypothetical protein (1)	core TFIIH complex [GO:0000439 cellular_component] (1); nucleotide-excision repair [GO:0006289 biological_process] (1); ATP-dependent DNA helicase activity [GO:0004003 molecular_function] (1); nucleus [GO:0005634 cellular_component] (1)	Transcription factor TFIIH subunit p52/Tfb2 [IPR004598] (1)	-	C_unshiu_00805_mRNA_1.1	-
GF0038940	0	1	0	Hypothetical protein (1)			-	C_unshiu_00804_mRNA_14.1	-
GF0038939	0	1	0	Hypothetical protein (1)			-	C_unshiu_00804_mRNA_1.1	-
GF0038938	0	1	0	Hypothetical protein (1)			-	C_unshiu_00803_mRNA_8.1	-
GF0038937	0	1	0	NB-ARC domain disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00803_mRNA_7.1	-
GF0038936	0	1	0	Hypothetical protein (1)			-	C_unshiu_00803_mRNA_6.1	-
GF0038935	0	1	0	Hypothetical protein (1)			-	C_unshiu_00803_mRNA_15.1	-
GF0038934	0	1	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); response to oxidative stress [GO:0006979 biological_process] (1); peroxidase activity [GO:0004601 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Haem peroxidase, plant/fungal/bacterial [IPR002016] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1); Plant peroxidase [IPR000823] (1); Peroxidases heam-ligand binding site [IPR019793] (1); Peroxidase, active site [IPR019794] (1); Haem peroxidase [IPR010255] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00803_mRNA_14.1	-
GF0038933	0	1	0	Hypothetical protein (1)			-	C_unshiu_00803_mRNA_12.1	-
GF0038932	0	1	0	Hypothetical protein (1)			-	C_unshiu_00803_mRNA_11.1	-
GF0038931	0	1	0	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	-	C_unshiu_00803_mRNA_1.1	-
GF0038930	0	1	0	Hypothetical protein (1)	ATPase activity [GO:0016887 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	AAA+ ATPase domain [IPR003593] (1); ABC transporter-like [IPR003439] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00802_mRNA_1.1	-
GF0038929	0	1	0	Hypothetical protein (1)	fatty-acyl-CoA binding [GO:0000062 molecular_function] (1)	FERM/acyl-CoA-binding protein, 3-helical bundle [IPR014352] (1); Acyl-CoA-binding protein, ACBP [IPR000582] (1)	-	C_unshiu_00801_mRNA_14.1	-
GF0038928	0	1	0	Hypothetical protein (1)			-	C_unshiu_00800_mRNA_7.1	-
GF0038927	0	1	0	Hypothetical protein (1)			-	C_unshiu_00799_mRNA_11.1	-
GF0038926	0	1	0	Hypothetical protein (1)			-	C_unshiu_00798_mRNA_8.1	-
GF0038925	0	1	0	Hypothetical protein (1)			-	C_unshiu_00798_mRNA_6.1	-
GF0038924	0	1	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); DNA binding [GO:0003677 molecular_function] (1)	NAC domain [IPR003441] (1)	-	C_unshiu_00798_mRNA_4.1	-
GF0038923	0	1	0	Hypothetical protein (1)			-	C_unshiu_00798_mRNA_3.1	-
GF0038922	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4219 [IPR025314] (1)	-	C_unshiu_00797_mRNA_14.1	-
GF0038921	0	1	0	Hypothetical protein (1)			-	C_unshiu_00797_mRNA_10.1	-
GF0038920	0	1	0	Hypothetical protein (1)			-	C_unshiu_00796_mRNA_9.1	-
GF0038919	0	1	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); protein binding [GO:0005515 molecular_function] (1); histone modification [GO:0016570 biological_process] (1); Cdc73/Paf1 complex [GO:0016593 cellular_component] (1)	Tetratricopeptide-like helical domain [IPR011990] (1); RNA polymerase-associated protein Ctr9 [IPR031101] (1); Tetratricopeptide repeat-containing domain [IPR013026] (1)	-	C_unshiu_00796_mRNA_7.1	-
GF0038918	0	1	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	-	C_unshiu_00796_mRNA_2.1	-
GF0038917	0	1	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	MULE transposase domain [IPR018289] (1); FHY3/FAR1 family [IPR031052] (1)	-	C_unshiu_00796_mRNA_14.1	-
GF0038916	0	1	0	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	C_unshiu_00796_mRNA_13.1	-
GF0038915	0	1	0	Hypothetical protein (1)			-	C_unshiu_00796_mRNA_11.1	-
GF0038914	0	1	0	Hypothetical protein (1)			-	C_unshiu_00796_mRNA_10.1	-
GF0038913	0	1	0	G-type lectin S-receptor-like serine/threonine-protein kinase RLK1 (1)	ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1); Bulb-type lectin domain [IPR001480] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1)	-	C_unshiu_00795_mRNA_8.1	-
GF0038912	0	1	0	G-type lectin S-receptor-like serine/threonine-protein kinase RLK1 (1)	ATP binding [GO:0005524 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1)	Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	-	C_unshiu_00795_mRNA_7.1	-
GF0038911	0	1	0	Hypothetical protein (1)			-	C_unshiu_00795_mRNA_15.1	-
GF0038910	0	1	0	Hypothetical protein (1)			-	C_unshiu_00795_mRNA_13.1	-
GF0038909	0	1	0	Hypothetical protein (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_00795_mRNA_10.1	-
GF0038908	0	1	0	Hypothetical protein (1)			-	C_unshiu_00794_mRNA_9.1	-
GF0038907	0	1	0	Hypothetical protein (1)			-	C_unshiu_00794_mRNA_1.1	-
GF0038906	0	1	0	Hypothetical protein (1)			-	C_unshiu_00793_mRNA_15.1	-
GF0038905	0	1	0	Hypothetical protein (1)			-	C_unshiu_00793_mRNA_11.1	-
GF0038904	0	1	0	Ankyrin repeat family protein, putative (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat-containing domain [IPR020683] (1); Ankyrin repeat [IPR002110] (1)	-	C_unshiu_00792_mRNA_8.1	-
GF0038903	0	1	0	Hypothetical protein (1)			-	C_unshiu_00792_mRNA_7.1	-
GF0038902	0	1	0	Hypothetical protein (1)			-	C_unshiu_00792_mRNA_6.1	-
GF0038901	0	1	0	Hypothetical protein (1)			-	C_unshiu_00792_mRNA_4.1	-
GF0038900	0	1	0	RNA-directed DNA polymerase (Reverse transcriptase) (1)		Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_00792_mRNA_3.1	-
GF0038899	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	WD40/YVTN repeat-like-containing domain [IPR015943] (1); WD40-repeat-containing domain [IPR017986] (1); WD40 repeat [IPR001680] (1)	-	C_unshiu_00792_mRNA_13.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0038898	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	WD40 repeat [IPR001680] (1); WD40-repeat-containing domain [IPR017986] (1); WD40/YVTN repeat-like-containing domain [IPR015943] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00792_mRNA_12.1	-
GF0038897	0	1	0	Hypothetical protein (1)		P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); AAA-type ATPase, N-terminal domain [IPR025753] (1)	-	C_unshiu_00791_mRNA_8.1	-
GF0038896	0	1	0	Hypothetical protein (1)		P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00791_mRNA_2.1	-
GF0038895	0	1	0	Hypothetical protein (1)			-	C_unshiu_00791_mRNA_12.1	-
GF0038894	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00790_mRNA_16.1	-
GF0038893	0	1	0	Hypothetical protein (1)			-	C_unshiu_00790_mRNA_13.1	-
GF0038892	0	1	0	Hypothetical protein (1)			-	C_unshiu_00790_mRNA_11.1	-
GF0038891	0	1	0	Hypothetical protein (1)			-	C_unshiu_00790_mRNA_10.1	-
GF0038890	0	1	0	Hypothetical protein (1)			-	C_unshiu_00790_mRNA_1.1	-
GF0038889	0	1	0	Hypothetical protein (1)	metabolic process [GO:0008152 biological_process] (1); transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	-	C_unshiu_00789_mRNA_8.1	-
GF0038888	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00788_mRNA_8.1	-
GF0038887	0	1	0	S-locus lectin protein kinase family protein, putative (1)		Bulb-type lectin domain [IPR001480] (1)	-	C_unshiu_00788_mRNA_7.1	-
GF0038886	0	1	0	Hypothetical protein (1)			-	C_unshiu_00788_mRNA_5.1	-
GF0038885	0	1	0	Hypothetical protein (1)			-	C_unshiu_00788_mRNA_3.1	-
GF0038884	0	1	0	Hypothetical protein (1)			-	C_unshiu_00788_mRNA_2.1	-
GF0038883	0	1	0	DNA repair metallo-beta-lactamase family protein isoform 4 (1)		DNA repair metallo-beta-lactamase [IPR011084] (1)	-	C_unshiu_00788_mRNA_10.1	-
GF0038882	0	1	0	Hypothetical protein (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_00787_mRNA_8.1	-
GF0038881	0	1	0	Hypothetical protein (1)		Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_00787_mRNA_5.1	-
GF0038880	0	1	0	Hypothetical protein (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_00787_mRNA_4.1	-
GF0038879	0	1	0	Receptor protein kinase (1)	ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	-	C_unshiu_00787_mRNA_3.1	-
GF0038878	0	1	0	Hypothetical protein (1)			-	C_unshiu_00787_mRNA_21.1	-
GF0038877	0	1	0	Hypothetical protein (1)			-	C_unshiu_00787_mRNA_20.1	-
GF0038876	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00787_mRNA_14.1	-
GF0038875	0	1	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_00787_mRNA_13.1	-
GF0038874	0	1	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1)	Protein kinase, ATP binding site [IPR017441] (1); Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_00787_mRNA_12.1	-
GF0038873	0	1	0	BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1, putative (1)	ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase, ATP binding site [IPR017441] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1)	-	C_unshiu_00787_mRNA_10.1	-
GF0038872	0	1	0	Hypothetical protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	C_unshiu_00787_mRNA_1.1	-
GF0038871	0	1	0	Putative transposable element (1)		Transposase-associated domain [IPR029480] (1); Transposon, En/Spm-like [IPR004242] (1)	-	C_unshiu_00786_mRNA_6.1	-
GF0038870	0	1	0	Zinc knuckle family protein (1)			-	C_unshiu_00786_mRNA_5.1	-
GF0038869	0	1	0	Hypothetical protein (1)		Retroviral aspartyl protease [IPR013242] (1)	-	C_unshiu_00786_mRNA_4.1	-
GF0038868	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_00786_mRNA_3.1	-
GF0038867	0	1	0	Hypothetical protein (1)			-	C_unshiu_00786_mRNA_10.1	-
GF0038866	0	1	0	Hypothetical protein (1)		SGNH hydrolase-type esterase domain [IPR013830] (1)	-	C_unshiu_00785_mRNA_2.1	-
GF0038865	0	1	0	Hypothetical protein (1)			-	C_unshiu_00785_mRNA_19.1	-
GF0038864	0	1	0	Hypothetical protein (1)			-	C_unshiu_00784_mRNA_7.1	-
GF0038863	0	1	0	Hypothetical protein (1)	multicellular organismal development [GO:0007275 biological_process] (1)	YABBY protein [IPR006780] (1)	-	C_unshiu_00784_mRNA_5.1	-
GF0038862	0	1	0	Hypothetical protein (1)			-	C_unshiu_00784_mRNA_17.1	-
GF0038861	0	1	0	Hypothetical protein (1)			-	C_unshiu_00784_mRNA_12.1	-
GF0038860	0	1	0	Hypothetical protein (1)			-	C_unshiu_00783_mRNA_1.1	-
GF0038859	0	1	0	Disease resistance protein (CC-NBS-LRR class) family protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00782_mRNA_8.1	-
GF0038858	0	1	0	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	C_unshiu_00782_mRNA_7.1	-
GF0038857	0	1	0	Hypothetical protein (1)	metabolic process [GO:0008152 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1)	von Willebrand factor, type A [IPR002035] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Aminotransferase class IV [IPR001544] (1); Copine [IPR010734] (1)	-	C_unshiu_00782_mRNA_2.1	-
GF0038856	0	1	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00782_mRNA_10.1	-
GF0038855	0	1	0	Hypothetical protein (1)			-	C_unshiu_00781_mRNA_8.1	-
GF0038854	0	1	0	Hypothetical protein (1)			-	C_unshiu_00781_mRNA_6.1	-
GF0038853	0	1	0	Hypothetical protein (1)			-	C_unshiu_00781_mRNA_5.1	-
GF0038852	0	1	0	Hypothetical protein (1)			-	C_unshiu_00781_mRNA_18.1	-
GF0038851	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00781_mRNA_13.1	-
GF0038850	0	1	0	Hypothetical protein (1)			-	C_unshiu_00781_mRNA_1.1	-
GF0038849	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, SWIM-type [IPR007527] (1)	-	C_unshiu_00780_mRNA_9.1	-
GF0038848	0	1	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	C_unshiu_00780_mRNA_8.1	-
GF0038847	0	1	0	Hypothetical protein (1)			-	C_unshiu_00780_mRNA_3.1	-
GF0038846	0	1	0	Hypothetical protein (1)			-	C_unshiu_00780_mRNA_2.1	-
GF0038845	0	1	0	Hypothetical protein (1)			-	C_unshiu_00780_mRNA_13.1	-
GF0038844	0	1	0	Hypothetical protein (1)			-	C_unshiu_00780_mRNA_12.1	-
GF0038843	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Helicase superfamily 1/2, ATP-binding domain [IPR014001] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); DEAD/DEAH box helicase domain [IPR011545] (1)	-	C_unshiu_00780_mRNA_11.1	-
GF0038842	0	1	0	Hypothetical protein (1)			-	C_unshiu_00779_mRNA_7.1	-
GF0038841	0	1	0	Hypothetical protein (1)			-	C_unshiu_00779_mRNA_6.1	-
GF0038840	0	1	0	Hypothetical protein (1)	DNA repair [GO:0006281 biological_process] (1)	Fanconi anaemia protein FANCD2 [IPR029448] (1)	-	C_unshiu_00779_mRNA_13.1	-
GF0038839	0	1	0	Lactosylceramide 4-alpha-galactosyltransferase, putative (1)		Alpha 1,4-glycosyltransferase domain [IPR007652] (1); Glycosyltransferase, DXD sugar-binding motif [IPR007577] (1); Nucleotide-diphospho-sugar transferases [IPR029044] (1)	-	C_unshiu_00779_mRNA_10.1	-
GF0038838	0	1	0	Quinone oxidoreductase protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1)	GroES-like [IPR011032] (1); Alcohol dehydrogenase superfamily, zinc-type [IPR002085] (1); Polyketide synthase, enoylreductase domain [IPR020843] (1); Alcohol dehydrogenase, N-terminal [IPR013154] (1); NAD(P)-binding domain [IPR016040] (1)	-	C_unshiu_00778_mRNA_1.1	-
GF0038837	0	1	0	Hypothetical protein (1)			-	C_unshiu_00777_mRNA_1.1	-
GF0038836	0	1	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	-	C_unshiu_00776_mRNA_9.1	-
GF0038835	0	1	0	Hypothetical protein (1)			-	C_unshiu_00776_mRNA_6.1	-
GF0038834	0	1	0	Hypothetical protein (1)			-	C_unshiu_00776_mRNA_5.1	-
GF0038833	0	1	0	Hypothetical protein (1)			-	C_unshiu_00776_mRNA_3.1	-
GF0038832	0	1	0	Hypothetical protein (1)			-	C_unshiu_00776_mRNA_12.1	-
GF0038831	0	1	0	Hypothetical protein (1)			-	C_unshiu_00776_mRNA_10.1	-
GF0038830	0	1	0	Hypothetical protein (1)			-	C_unshiu_00775_mRNA_9.1	-
GF0038829	0	1	0	Hypothetical protein (1)			-	C_unshiu_00775_mRNA_8.1	-
GF0038828	0	1	0	Hypothetical protein (1)			-	C_unshiu_00775_mRNA_4.1	-
GF0038827	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); DnaJ domain [IPR001623] (1); DnaJ domain, conserved site [IPR018253] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_00775_mRNA_3.1	-
GF0038826	0	1	0	Hypothetical protein (1)			-	C_unshiu_00775_mRNA_12.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0038825	0	1	0	Hypothetical protein (1)			-	C_unshiu_00775_mRNA_11.1	-
GF0038824	0	1	0	Hypothetical protein (1)			-	C_unshiu_00775_mRNA_10.1	-
GF0038823	0	1	0	Hypothetical protein (1)	phosphoric ester hydrolase activity [GO:0042578 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	WW domain [IPR001202] (1); SAC domain [IPR002013] (1)	-	C_unshiu_00774_mRNA_9.1	-
GF0038822	0	1	0	Protein SUPPRESSOR OF npr1-1, CONSTITUTIVE 1 (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00774_mRNA_8.1	-
GF0038821	0	1	0	Putative receptor protein kinase ZmPK1 (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1)	Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	-	C_unshiu_00774_mRNA_4.1	-
GF0038820	0	1	0	Hypothetical protein (1)			-	C_unshiu_00772_mRNA_9.1	-
GF0038819	0	1	0	Hypothetical protein (1)			-	C_unshiu_00772_mRNA_8.1	-
GF0038818	0	1	0	Hypothetical protein (1)	metal ion binding [GO:0046872 molecular_function] (1)	Zinc finger, CCCH-type [IPR000571] (1)	-	C_unshiu_00772_mRNA_2.1	-
GF0038817	0	1	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00772_mRNA_10.1	-
GF0038816	0	1	0	Hypothetical protein (1)			-	C_unshiu_00772_mRNA_1.1	-
GF0038815	0	1	0	Hypothetical protein (1)			-	C_unshiu_00771_mRNA_9.1	-
GF0038814	0	1	0	Hypothetical protein (1)			-	C_unshiu_00771_mRNA_7.1	-
GF0038813	0	1	0	Hypothetical protein (1)			-	C_unshiu_00771_mRNA_3.1	-
GF0038812	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	-	C_unshiu_00770_mRNA_3.1	-
GF0038811	0	1	0	Hypothetical protein (1)			-	C_unshiu_00770_mRNA_10.1	-
GF0038810	0	1	0	Hypothetical protein (1)			-	C_unshiu_00770_mRNA_1.1	-
GF0038809	0	1	0	Hypothetical protein (1)			-	C_unshiu_00769_mRNA_9.1	-
GF0038808	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_00769_mRNA_8.1	-
GF0038807	0	1	0	Hypothetical protein (1)			-	C_unshiu_00769_mRNA_6.1	-
GF0038806	0	1	0	Hypothetical protein (1)		PGG domain [IPR026961] (1)	-	C_unshiu_00769_mRNA_5.1	-
GF0038805	0	1	0	EF1 protein (1)			-	C_unshiu_00769_mRNA_2.1	-
GF0038804	0	1	0	Hypothetical protein (1)			-	C_unshiu_00769_mRNA_18.1	-
GF0038803	0	1	0	Hypothetical protein (1)			-	C_unshiu_00769_mRNA_13.1	-
GF0038802	0	1	0	Expansin-like B1 (1)	extracellular region [GO:0005576 cellular_component] (1)	RlpA-like double-psi beta-barrel domain [IPR009009] (1); Expansin/pollen allergen, DPBB domain [IPR007112] (1); Expansin/Lol pI [IPR007118] (1); Expansin, cellulose-binding-like domain [IPR007117] (1)	-	C_unshiu_00768_mRNA_16.1	-
GF0038801	0	1	0	Hypothetical protein (1)			-	C_unshiu_00767_mRNA_3.1	-
GF0038800	0	1	0	Hypothetical protein (1)		USP8 dimerisation domain [IPR015063] (1)	-	C_unshiu_00767_mRNA_20.1	-
GF0038799	0	1	0	Hypothetical protein (1)			-	C_unshiu_00767_mRNA_19.1	-
GF0038798	0	1	0	Cytochrome P450 71A1 (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1)	Cytochrome P450 [IPR001128] (1); Cytochrome P450, E-class, group I [IPR002401] (1)	-	C_unshiu_00767_mRNA_18.1	-
GF0038797	0	1	0	Hypothetical protein (1)			-	C_unshiu_00767_mRNA_17.1	-
GF0038796	0	1	0	Hypothetical protein (1)			-	C_unshiu_00767_mRNA_16.1	-
GF0038795	0	1	0	Hypothetical protein (1)			-	C_unshiu_00767_mRNA_11.1	-
GF0038794	0	1	0	Hypothetical protein (1)			-	C_unshiu_00767_mRNA_1.1	-
GF0038793	0	1	0	SLG-Sc and SLA-Sc genes and Melmoth retrotransposon sequence (1)			-	C_unshiu_00766_mRNA_9.1	-
GF0038792	0	1	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_00766_mRNA_8.1	-
GF0038791	0	1	0	UDP-glycosyltransferase 73C5 (1)	transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	-	C_unshiu_00766_mRNA_5.1	-
GF0038790	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Domain of unknown function DUF4283 [IPR025558] (1); Zinc finger, CCHC-type [IPR001878] (1); Zinc knuckle CX2CX4HX4C [IPR025836] (1)	-	C_unshiu_00766_mRNA_11.1	-
GF0038789	0	1	0	Hypothetical protein (1)	transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (1)	Transferase [IPR003480] (1); Endonuclease/exonuclease/phosphatase [IPR005135] (1); Chloramphenicol acetyltransferase-like domain [IPR023213] (1)	-	C_unshiu_00766_mRNA_10.1	-
GF0038788	0	1	0	Hypothetical protein (1)			-	C_unshiu_00766_mRNA_1.1	-
GF0038787	0	1	0	Hypothetical protein (1)			-	C_unshiu_00765_mRNA_8.1	-
GF0038786	0	1	0	Hypothetical protein (1)	serine-type endopeptidase inhibitor activity [GO:0004867 molecular_function] (1); response to wounding [GO:0009611 biological_process] (1)	Proteinase inhibitor I13, potato inhibitor I [IPR000864] (1)	-	C_unshiu_00765_mRNA_7.1	-
GF0038785	0	1	0	Hypothetical protein (1)			-	C_unshiu_00765_mRNA_6.1	-
GF0038784	0	1	0	Hypothetical protein (1)			-	C_unshiu_00765_mRNA_2.1	-
GF0038783	0	1	0	Hypothetical protein (1)			-	C_unshiu_00765_mRNA_15.1	-
GF0038782	0	1	0	Hypothetical protein (1)			-	C_unshiu_00765_mRNA_14.1	-
GF0038781	0	1	0	Hypothetical protein (1)			-	C_unshiu_00765_mRNA_10.1	-
GF0038780	0	1	0	Hypothetical protein (1)			-	C_unshiu_00765_mRNA_1.1	-
GF0038779	0	1	0	Hypothetical protein (1)			-	C_unshiu_00764_mRNA_6.1	-
GF0038778	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, RING-type [IPR001841] (1); von Willebrand factor, type A [IPR002035] (1); Zinc finger, RING/FYVE/PHD-type [IPR013083] (1)	-	C_unshiu_00764_mRNA_5.1	-
GF0038777	0	1	0	Hypothetical protein (1)	transmembrane transport [GO:0055085 biological_process] (1); integral component of membrane [GO:0016021 cellular_component] (1)	Major facilitator superfamily [IPR011701] (1); Major facilitator superfamily domain [IPR020846] (1)	-	C_unshiu_00764_mRNA_13.1	-
GF0038776	0	1	0	Retrotransposon protein, putative, Ty1-copia subclass (1)			-	C_unshiu_00763_mRNA_9.1	-
GF0038775	0	1	0	Hypothetical protein (1)			-	C_unshiu_00763_mRNA_7.1	-
GF0038774	0	1	0	Hypothetical protein (1)			-	C_unshiu_00763_mRNA_5.1	-
GF0038773	0	1	0	Hypothetical protein (1)			-	C_unshiu_00763_mRNA_18.1	-
GF0038772	0	1	0	Hypothetical protein (1)			-	C_unshiu_00763_mRNA_16.1	-
GF0038771	0	1	0	Hypothetical protein (1)			-	C_unshiu_00763_mRNA_13.1	-
GF0038770	0	1	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_00762_mRNA_9.1	-
GF0038769	0	1	0	Hypothetical protein (1)			-	C_unshiu_00762_mRNA_5.1	-
GF0038768	0	1	0	Hypothetical protein (1)			-	C_unshiu_00762_mRNA_4.1	-
GF0038767	0	1	0	Hypothetical protein (1)			-	C_unshiu_00762_mRNA_3.1	-
GF0038766	0	1	0	Hypothetical protein (1)			-	C_unshiu_00762_mRNA_12.1	-
GF0038765	0	1	0	Chaperone protein DnaJ (1)	protein folding [GO:0006457 biological_process] (1); unfolded protein binding [GO:0051082 molecular_function] (1); response to heat [GO:0009408 biological_process] (1); heat shock protein binding [GO:0031072 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	HSP40/DnaJ peptide-binding [IPR008971] (1); DnaJ domain [IPR001623] (1); Chaperone DnaJ [IPR012724] (1); Heat shock protein DnaJ, cysteine-rich domain [IPR001305] (1); Chaperone DnaJ, C-terminal [IPR002939] (1)	-	C_unshiu_00761_mRNA_16.1	-
GF0038764	0	1	0	Lanthionine synthetase C-like protein, expressed (1)		LanC-like protein, eukaryotic [IPR020464] (1); Lanthionine synthetase C-like [IPR007822] (1)	-	C_unshiu_00761_mRNA_1.1	-
GF0038763	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00760_mRNA_7.1	-
GF0038762	0	1	0	Hypothetical protein (1)			-	C_unshiu_00760_mRNA_6.1	-
GF0038761	0	1	0	LRR and NB-ARC domain disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00760_mRNA_14.1	-
GF0038760	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Tetratricopeptide-like helical domain [IPR011990] (1)	-	C_unshiu_00760_mRNA_12.1	-
GF0038759	0	1	0	Disease resistance protein RPS2 (1)			-	C_unshiu_00760_mRNA_10.1	-
GF0038758	0	1	0	Hypothetical protein (1)			-	C_unshiu_00760_mRNA_1.1	-
GF0038757	0	1	0	Hypothetical protein (1)		MULE transposase domain [IPR018289] (1)	-	C_unshiu_00759_mRNA_8.1	-
GF0038756	0	1	0	Hypothetical protein (1)			-	C_unshiu_00759_mRNA_12.1	-
GF0038755	0	1	0	Hypothetical protein (1)			-	C_unshiu_00759_mRNA_10.1	-
GF0038754	0	1	0	Senescence-related gene 1 (1)		Non-haem dioxygenase N-terminal domain [IPR026992] (1); Isopenicillin N synthase-like [IPR027443] (1)	-	C_unshiu_00759_mRNA_1.1	-
GF0038753	0	1	0	Hypothetical protein (1)			-	C_unshiu_00758_mRNA_5.1	-
GF0038752	0	1	0	Amino acid permease family protein (1)	membrane [GO:0016020 cellular_component] (1); amino acid transmembrane transport [GO:0003333 biological_process] (1); amino acid transmembrane transporter activity [GO:0015171 molecular_function] (1)	Amino acid/polyamine transporter I [IPR002293] (1)	-	C_unshiu_00758_mRNA_4.1	-
GF0038751	0	1	0	Anthranilate N-benzoyltransferase protein 1 (1)	transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (1)	Chloramphenicol acetyltransferase-like domain [IPR023213] (1); Transferase [IPR003480] (1)	-	C_unshiu_00758_mRNA_18.1	-
GF0038750	0	1	0	Hypothetical protein (1)			-	C_unshiu_00758_mRNA_17.1	-
GF0038749	0	1	0	Hypothetical protein (1)			-	C_unshiu_00758_mRNA_16.1	-
GF0038748	0	1	0	Major facilitator protein (1)		Nodulin-like [IPR010658] (1); Major facilitator superfamily domain [IPR020846] (1)	-	C_unshiu_00758_mRNA_13.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0038747	0	1	0	Hypothetical protein (1)			-	C_unshiu_00757_mRNA_3.1	-
GF0038746	0	1	0	Hypothetical protein (1)			-	C_unshiu_00757_mRNA_2.1	-
GF0038745	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	-	C_unshiu_00757_mRNA_10.1	-
GF0038744	0	1	0	Hypothetical protein (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Aspartic peptidase domain [IPR021109] (1); Peptidase A2A, retrovirus, catalytic [IPR001995] (1); Retropepsins [IPR018061] (1)	-	C_unshiu_00756_mRNA_5.1	-
GF0038743	0	1	0	Hypothetical protein (1)			-	C_unshiu_00756_mRNA_4.1	-
GF0038742	0	1	0	Hypothetical protein (1)			-	C_unshiu_00756_mRNA_3.1	-
GF0038741	0	1	0	Hypothetical protein (1)			-	C_unshiu_00756_mRNA_20.1	-
GF0038740	0	1	0	Hypothetical protein (1)			-	C_unshiu_00756_mRNA_16.1	-
GF0038739	0	1	0	Hypothetical protein (1)			-	C_unshiu_00756_mRNA_10.1	-
GF0038738	0	1	0	Hypothetical protein (1)			-	C_unshiu_00756_mRNA_1.1	-
GF0038737	0	1	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1)	GroEL-like equatorial domain [IPR027413] (1); Chaperonin Cpn60/TCP-1 family [IPR002423] (1)	-	C_unshiu_00755_mRNA_8.1	-
GF0038736	0	1	0	Hypothetical protein (1)		Nucleotide-diphospho-sugar transferases [IPR029044] (1)	-	C_unshiu_00755_mRNA_6.1	-
GF0038735	0	1	0	Hypothetical protein (1)			-	C_unshiu_00755_mRNA_5.1	-
GF0038734	0	1	0	Disease resistance family protein / LRR family protein, putative (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_00755_mRNA_1.1	-
GF0038733	0	1	0	UPF0481 protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	C_unshiu_00754_mRNA_4.1	-
GF0038732	0	1	0	Hypothetical protein (1)			-	C_unshiu_00754_mRNA_2.1	-
GF0038731	0	1	0	Leucine-rich repeat receptor-like protein kinase family (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_00754_mRNA_18.1	-
GF0038730	0	1	0	Cytochrome P450 83B1 (1)	heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1)	Cytochrome P450 [IPR001128] (1); Cytochrome P450, conserved site [IPR017972] (1); Cytochrome P450, E-class, group I [IPR002401] (1)	-	C_unshiu_00754_mRNA_15.1	-
GF0038729	0	1	0	Plant viral-response family protein (1)		Protein of unknown function DUF716 (TMEM45) [IPR006904] (1)	-	C_unshiu_00754_mRNA_11.1	-
GF0038728	0	1	0	Hypothetical protein (1)			-	C_unshiu_00753_mRNA_6.1	-
GF0038727	0	1	0	Hypothetical protein (1)			-	C_unshiu_00753_mRNA_5.1	-
GF0038726	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_00753_mRNA_11.1	-
GF0038725	0	1	0	Hypothetical protein (1)		Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_00752_mRNA_9.1	-
GF0038724	0	1	0	Hypothetical protein (1)			-	C_unshiu_00752_mRNA_7.1	-
GF0038723	0	1	0	Hypothetical protein (1)		Transposase, MuDR, plant [IPR004332] (1)	-	C_unshiu_00752_mRNA_6.1	-
GF0038722	0	1	0	Hypothetical protein (1)			-	C_unshiu_00752_mRNA_1.1	-
GF0038721	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_00751_mRNA_9.1	-
GF0038720	0	1	0	Hypothetical protein (1)			-	C_unshiu_00751_mRNA_8.1	-
GF0038719	0	1	0	Hypothetical protein (1)			-	C_unshiu_00751_mRNA_7.1	-
GF0038718	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Ribonuclease H domain [IPR002156] (1)	-	C_unshiu_00751_mRNA_13.1	-
GF0038717	0	1	0	AT5G25460 protein (1)		Domain of unknown function DUF642 [IPR006946] (1); Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	C_unshiu_00751_mRNA_10.1	-
GF0038716	0	1	0	Metacaspase 2 (1)		Caspase-like domain [IPR029030] (1)	-	C_unshiu_00750_mRNA_8.1	-
GF0038715	0	1	0	Hypothetical protein (1)			-	C_unshiu_00750_mRNA_7.1	-
GF0038714	0	1	0	Hypothetical protein (1)			-	C_unshiu_00750_mRNA_6.1	-
GF0038713	0	1	0	Hypothetical protein (1)			-	C_unshiu_00750_mRNA_3.1	-
GF0038712	0	1	0	60S ribosomal protein L14-1 (1)	translation [GO:0006412 biological_process] (1); intracellular [GO:0005622 cellular_component] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1); ribosome [GO:0005840 cellular_component] (1)	Ribosomal protein L14 [IPR002784] (1); Ribosomal protein L2 domain 2 [IPR014722] (1); Translation protein SH3-like domain [IPR008991] (1)	-	C_unshiu_00750_mRNA_2.1	-
GF0038711	0	1	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	-	C_unshiu_00750_mRNA_14.1	-
GF0038710	0	1	0	Hypothetical protein (1)			-	C_unshiu_00750_mRNA_13.1	-
GF0038709	0	1	0	Hypothetical protein (1)			-	C_unshiu_00750_mRNA_12.1	-
GF0038708	0	1	0	Hypothetical protein (1)			-	C_unshiu_00750_mRNA_10.1	-
GF0038707	0	1	0	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	C_unshiu_00749_mRNA_6.1	-
GF0038706	0	1	0	Hypothetical protein (1)			-	C_unshiu_00749_mRNA_2.1	-
GF0038705	0	1	0	Hypothetical protein (1)			-	C_unshiu_00749_mRNA_18.1	-
GF0038704	0	1	0	Hypothetical protein (1)			-	C_unshiu_00749_mRNA_17.1	-
GF0038703	0	1	0	Transcription factor HY5 (1)	sequence-specific DNA binding [GO:0043565 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (1)	Basic-leucine zipper domain [IPR004827] (1)	-	C_unshiu_00749_mRNA_10.1	-
GF0038702	0	1	0	Hypothetical protein (1)			-	C_unshiu_00748_mRNA_15.1	-
GF0038701	0	1	0	Hypothetical protein (1)			-	C_unshiu_00748_mRNA_14.1	-
GF0038700	0	1	0	Hypothetical protein (1)			-	C_unshiu_00747_mRNA_5.1	-
GF0038699	0	1	0	Hypothetical protein (1)			-	C_unshiu_00747_mRNA_4.1	-
GF0038698	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00747_mRNA_3.1	-
GF0038697	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	C_unshiu_00747_mRNA_2.1	-
GF0038696	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00747_mRNA_11.1	-
GF0038695	0	1	0	Hypothetical protein (1)			-	C_unshiu_00747_mRNA_1.1	-
GF0038694	0	1	0	Hypothetical protein (1)			-	C_unshiu_00746_mRNA_8.1	-
GF0038693	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF1985 [IPR015410] (1)	-	C_unshiu_00746_mRNA_5.1	-
GF0038692	0	1	0	Hypothetical protein (1)			-	C_unshiu_00746_mRNA_1.1	-
GF0038691	0	1	0	Hypothetical protein (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1); hydrolase activity [GO:0016787 molecular_function] (1)	RNA pyrophosphohydrolase RppH [IPR022927] (1); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); NUDIX hydrolase [IPR020476] (1); NUDIX hydrolase domain [IPR000086] (1); NUDIX hydrolase, conserved site [IPR020084] (1); NUDIX hydrolase domain-like [IPR015797] (1)	-	C_unshiu_00745_mRNA_6.1	-
GF0038690	0	1	0	Hypothetical protein (1)			-	C_unshiu_00744_mRNA_9.1	-
GF0038689	0	1	0	Hypothetical protein (1)			-	C_unshiu_00744_mRNA_7.1	-
GF0038688	0	1	0	Hypothetical protein (1)			-	C_unshiu_00744_mRNA_6.1	-
GF0038687	0	1	0	Hypothetical protein (1)			-	C_unshiu_00744_mRNA_15.1	-
GF0038686	0	1	0	Hypothetical protein (1)			-	C_unshiu_00744_mRNA_10.1	-
GF0038685	0	1	0	Hypothetical protein (1)			-	C_unshiu_00743_mRNA_8.1	-
GF0038684	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_00743_mRNA_3.1	-
GF0038683	0	1	0	Hypothetical protein (1)			-	C_unshiu_00742_mRNA_9.1	-
GF0038682	0	1	0	Hypothetical protein (1)			-	C_unshiu_00742_mRNA_17.1	-
GF0038681	0	1	0	Hypothetical protein (1)			-	C_unshiu_00741_mRNA_7.1	-
GF0038680	0	1	0	Hypothetical protein (1)			-	C_unshiu_00741_mRNA_3.1	-
GF0038679	0	1	0	Receptor like protein 25 (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_00741_mRNA_14.1	-
GF0038678	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00741_mRNA_13.1	-
GF0038677	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_00741_mRNA_12.1	-
GF0038676	0	1	0	Hypothetical protein (1)			-	C_unshiu_00741_mRNA_11.1	-
GF0038675	0	1	0	Hypothetical protein (1)			-	C_unshiu_00741_mRNA_10.1	-
GF0038674	0	1	0	Hypothetical protein (1)			-	C_unshiu_00740_mRNA_7.1	-
GF0038673	0	1	0	Hypothetical protein (1)			-	C_unshiu_00740_mRNA_4.1	-
GF0038672	0	1	0	Hypothetical protein (1)		Cyclic nucleotide-binding domain [IPR000595] (1); Cyclic nucleotide-binding-like [IPR018490] (1); RmlC-like jelly roll fold [IPR014710] (1)	-	C_unshiu_00740_mRNA_2.1	-
GF0038671	0	1	0	Hypothetical protein (1)			-	C_unshiu_00740_mRNA_12.1	-
GF0038670	0	1	0	Hypothetical protein (1)	hydrolase activity [GO:0016787 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Alpha/Beta hydrolase fold [IPR029058] (1); Alpha/beta hydrolase fold-3 [IPR013094] (1)	-	C_unshiu_00739_mRNA_9.1	-
GF0038669	0	1	0	Hypothetical protein (1)			-	C_unshiu_00739_mRNA_8.1	-
GF0038668	0	1	0	Putative non-LTR retroelement reverse transcriptase (1)		Domain of unknown function DUF4283 [IPR025558] (1); Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_00739_mRNA_16.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0038667	0	1	0	Hypothetical protein (1)			-	C_unshiu_00739_mRNA_14.1	-
GF0038666	0	1	0	Dynamin-related protein 1E (1)	GTP binding [GO:0005525 molecular_function] (1); GTPase activity [GO:0003924 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Dynamin, GTPase domain [IPR001401] (1); Dynamin, GTPase region, conserved site [IPR019762] (1); Dynamin-type guanine nucleotide-binding (G) domain [IPR030381] (1); Dynamin superfamily [IPR022812] (1)	-	C_unshiu_00739_mRNA_1.1	-
GF0038665	0	1	0	Hypothetical protein (1)			-	C_unshiu_00738_mRNA_18.1	-
GF0038664	0	1	0	Hypothetical protein (1)			-	C_unshiu_00738_mRNA_15.1	-
GF0038663	0	1	0	Hypothetical protein (1)			-	C_unshiu_00737_mRNA_4.1	-
GF0038662	0	1	0	Hypothetical protein (1)			-	C_unshiu_00737_mRNA_3.1	-
GF0038661	0	1	0	Hypothetical protein (1)			-	C_unshiu_00737_mRNA_2.1	-
GF0038660	0	1	0	Hypothetical protein (1)			-	C_unshiu_00737_mRNA_11.1	-
GF0038659	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); SGNH hydrolase-type esterase domain [IPR013830] (1)	-	C_unshiu_00737_mRNA_10.1	-
GF0038658	0	1	0	Hypothetical protein (1)			-	C_unshiu_00737_mRNA_1.1	-
GF0038657	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00736_mRNA_9.1	-
GF0038656	0	1	0	Carboxylesterase 1 (1)	hydrolase activity [GO:0016787 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Alpha/Beta hydrolase fold [IPR029058] (1); Alpha/beta hydrolase fold-3 [IPR013094] (1)	-	C_unshiu_00736_mRNA_7.1	-
GF0038655	0	1	0	Putative carboxylesterase 2 (1)	hydrolase activity [GO:0016787 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Alpha/Beta hydrolase fold [IPR029058] (1); Alpha/beta hydrolase fold-3 [IPR013094] (1)	-	C_unshiu_00736_mRNA_5.1	-
GF0038654	0	1	0	Hypothetical protein (1)			-	C_unshiu_00736_mRNA_16.1	-
GF0038653	0	1	0	CXE carboxylesterase (1)	hydrolase activity [GO:0016787 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Alpha/Beta hydrolase fold [IPR029058] (1); Alpha/beta hydrolase fold-3 [IPR013094] (1)	-	C_unshiu_00736_mRNA_1.1	-
GF0038652	0	1	0	NAC transcription factor 29 (1)	DNA binding [GO:0003677 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	NAC domain [IPR003441] (1)	-	C_unshiu_00735_mRNA_9.1	-
GF0038651	0	1	0	Hypothetical protein (1)			-	C_unshiu_00735_mRNA_17.1	-
GF0038650	0	1	0	Hypothetical protein (1)			-	C_unshiu_00735_mRNA_16.1	-
GF0038649	0	1	0	Hypothetical protein (1)			-	C_unshiu_00734_mRNA_9.1	-
GF0038648	0	1	0	HAT family dimerisation domain containing protein (1)	DNA binding [GO:0003677 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	hAT-like transposase, RNase-H fold [IPR025525] (1); Ribonuclease H-like domain [IPR012337] (1); Aspartic peptidase domain [IPR021109] (1)	-	C_unshiu_00733_mRNA_9.1	-
GF0038647	0	1	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00733_mRNA_8.1	-
GF0038646	0	1	0	Hypothetical protein (1)			-	C_unshiu_00733_mRNA_6.1	-
GF0038645	0	1	0	Hypothetical protein (1)			-	C_unshiu_00733_mRNA_5.1	-
GF0038644	0	1	0	Hypothetical protein (1)			-	C_unshiu_00733_mRNA_4.1	-
GF0038643	0	1	0	Hypothetical protein (1)			-	C_unshiu_00733_mRNA_3.1	-
GF0038642	0	1	0	Hypothetical protein (1)			-	C_unshiu_00733_mRNA_12.1	-
GF0038641	0	1	0	Hypothetical protein (1)			-	C_unshiu_00732_mRNA_9.1	-
GF0038640	0	1	0	Hypothetical protein (1)			-	C_unshiu_00732_mRNA_7.1	-
GF0038639	0	1	0	LRR receptor-like kinase family protein (1)			-	C_unshiu_00732_mRNA_3.1	-
GF0038638	0	1	0	Hypothetical protein (1)			-	C_unshiu_00732_mRNA_2.1	-
GF0038637	0	1	0	Hypothetical protein (1)			-	C_unshiu_00731_mRNA_2.1	-
GF0038636	0	1	0	Hypothetical protein (1)		NADP-dependent oxidoreductase domain [IPR023210] (1); Aldo/keto reductase/potassium channel subunit beta [IPR001395] (1)	-	C_unshiu_00731_mRNA_15.1	-
GF0038635	0	1	0	Hypothetical protein (1)			-	C_unshiu_00731_mRNA_1.1	-
GF0038634	0	1	0	Probable F-box protein At1g60180 (1)	protein binding [GO:0005515 molecular_function] (1)	F-box domain [IPR001810] (1)	-	C_unshiu_00730_mRNA_13.1	-
GF0038633	0	1	0	Polygalacturonase (1)	polygalacturonase activity [GO:0004650 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1)	Parallel beta-helix repeat [IPR006626] (1); Glycoside hydrolase, family 28 [IPR000743] (1); Pectin lyase fold [IPR012334] (1); Pectin lyase fold/virulence factor [IPR011050] (1)	-	C_unshiu_00730_mRNA_11.1	-
GF0038632	0	1	0	Hypothetical protein (1)			-	C_unshiu_00729_mRNA_6.1	-
GF0038631	0	1	0	Transferase family (1)	transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (1)	Transferase [IPR003480] (1); Chloramphenicol acetyltransferase-like domain [IPR023213] (1)	-	C_unshiu_00729_mRNA_1.1	-
GF0038630	0	1	0	Hypothetical protein (1)			-	C_unshiu_00728_mRNA_21.1	-
GF0038629	0	1	0	Hypothetical protein (1)			-	C_unshiu_00728_mRNA_15.1	-
GF0038628	0	1	0	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_00728_mRNA_14.1	-
GF0038627	0	1	0	Putative amidase (1)	carbon-nitrogen ligase activity, with glutamine as amido-N-donor [GO:0016884 molecular_function] (1)	Amidase signature domain [IPR023631] (1); Amidase [IPR000120] (1)	-	C_unshiu_00728_mRNA_12.1	-
GF0038626	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00727_mRNA_17.1	-
GF0038625	0	1	0	Hypothetical protein (1)	nucleotide binding [GO:0000166 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Nucleotide-binding alpha-beta plait domain [IPR012677] (1); RNA recognition motif domain [IPR000504] (1)	-	C_unshiu_00727_mRNA_16.1	-
GF0038624	0	1	0	Putative muDR family transposase-like (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Zinc finger, SWIM-type [IPR007527] (1); Zinc finger, PMZ-type [IPR006564] (1); MULE transposase domain [IPR018289] (1)	-	C_unshiu_00727_mRNA_14.1	-
GF0038623	0	1	0	Hypothetical protein (1)			-	C_unshiu_00727_mRNA_11.1	-
GF0038622	0	1	0	Hypothetical protein (1)	transport [GO:0006810 biological_process] (1); integral component of membrane [GO:0016021 cellular_component] (1)	Solute carrier family 35 member SLC35F1/F2/F6 [IPR009262] (1)	-	C_unshiu_00727_mRNA_1.1	-
GF0038621	0	1	0	Seed dormancy control protein (1)	sequence-specific DNA binding [GO:0043565 molecular_function] (1); transcription, DNA-templated [GO:0006351 biological_process] (1)	Transcription factor TGA like domain [IPR025422] (1)	-	C_unshiu_00726_mRNA_6.1	-
GF0038620	0	1	0	Hypothetical protein (1)		Protein of unknown function DUF866, eukaryotic [IPR008584] (1)	-	C_unshiu_00726_mRNA_5.1	-
GF0038619	0	1	0	Putative F-box protein At1g49610 (1)	protein binding [GO:0005515 molecular_function] (1)	F-box domain [IPR001810] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00726_mRNA_4.1	-
GF0038618	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); F-box domain [IPR001810] (1)	-	C_unshiu_00726_mRNA_3.1	-
GF0038617	0	1	0	ABC transporter C family protein (1)	transmembrane transport [GO:0055085 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1); ATPase activity, coupled to transmembrane movement of substances [GO:0042626 molecular_function] (1); transport [GO:0006810 biological_process] (1); ATPase activity [GO:0016887 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); AAA+ ATPase domain [IPR003593] (1); ABC transporter-like [IPR003439] (1); ABC transporter type 1, transmembrane domain [IPR011527] (1)	-	C_unshiu_00726_mRNA_1.1	-
GF0038616	0	1	0	Hypothetical protein (1)			-	C_unshiu_00725_mRNA_12.1	-
GF0038615	0	1	0	Hypothetical protein (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Retropepsins [IPR018061] (1); Reverse transcriptase domain [IPR000477] (1); Aspartic peptidase, active site [IPR001969] (1)	-	C_unshiu_00725_mRNA_11.1	-
GF0038614	0	1	0	Hypothetical protein (1)			-	C_unshiu_00725_mRNA_1.1	-
GF0038613	0	1	0	Hypothetical protein (1)			-	C_unshiu_00724_mRNA_7.1	-
GF0038612	0	1	0	Hypothetical protein (1)			-	C_unshiu_00724_mRNA_23.1	-
GF0038611	0	1	0	Hypothetical protein (1)			-	C_unshiu_00724_mRNA_22.1	-
GF0038610	0	1	0	Hypothetical protein (1)			-	C_unshiu_00724_mRNA_21.1	-
GF0038609	0	1	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_00724_mRNA_20.1	-
GF0038608	0	1	0	Hypothetical protein (1)			-	C_unshiu_00724_mRNA_2.1	-
GF0038607	0	1	0	Hypothetical protein (1)			-	C_unshiu_00724_mRNA_18.1	-
GF0038606	0	1	0	Hypothetical protein (1)			-	C_unshiu_00724_mRNA_17.1	-
GF0038605	0	1	0	Hypothetical protein (1)			-	C_unshiu_00724_mRNA_13.1	-
GF0038604	0	1	0	Hypothetical protein (1)			-	C_unshiu_00724_mRNA_1.1	-
GF0038603	0	1	0	Hypothetical protein (1)			-	C_unshiu_00723_mRNA_7.1	-
GF0038602	0	1	0	Hypothetical protein (1)			-	C_unshiu_00723_mRNA_6.1	-
GF0038601	0	1	0	Hypothetical protein (1)			-	C_unshiu_00723_mRNA_5.1	-
GF0038600	0	1	0	Hypothetical protein (1)			-	C_unshiu_00723_mRNA_4.1	-
GF0038599	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00723_mRNA_14.1	-
GF0038598	0	1	0	Hypothetical protein (1)			-	C_unshiu_00723_mRNA_12.1	-
GF0038597	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	C_unshiu_00722_mRNA_6.1	-
GF0038596	0	1	0	Hypothetical protein (1)			-	C_unshiu_00722_mRNA_4.1	-
GF0038595	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			-	C_unshiu_00721_mRNA_10.1	-
GF0038594	0	1	0	N-carbamoylputrescine amidase (1)	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds [GO:0016810 molecular_function] (1); nitrogen compound metabolic process [GO:0006807 biological_process] (1)	Carbon-nitrogen hydrolase [IPR003010] (1)	-	C_unshiu_00720_mRNA_6.1	-
GF0038593	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00720_mRNA_5.1	-
GF0038592	0	1	0	Hypothetical protein (1)			-	C_unshiu_00720_mRNA_4.1	-
GF0038591	0	1	0	Hypothetical protein (1)			-	C_unshiu_00720_mRNA_3.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0038590	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_00720_mRNA_2.1	-
GF0038589	0	1	0	Hypothetical protein (1)	O-methyltransferase activity [GO:0008171 molecular_function] (1); methyltransferase activity [GO:0008168 molecular_function] (1)	O-methyltransferase, family 2 [IPR001077] (1); O-methyltransferase COMT-type [IPR016461] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	C_unshiu_00719_mRNA_9.1	-
GF0038588	0	1	0	Caffeic acid O-methyltransferase (1)	O-methyltransferase activity [GO:0008171 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1); methyltransferase activity [GO:0008168 molecular_function] (1)	S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); O-methyltransferase COMT-type [IPR016461] (1); Plant methyltransferase dimerisation [IPR012967] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); O-methyltransferase, family 2 [IPR001077] (1)	-	C_unshiu_00719_mRNA_8.1	-
GF0038587	0	1	0	ER lumen protein-retaining receptor (1)	protein retention in ER lumen [GO:0006621 biological_process] (1); integral component of membrane [GO:0016021 cellular_component] (1); ER retention sequence binding [GO:0046923 molecular_function] (1)	ER lumen protein retaining receptor [IPR000133] (1)	-	C_unshiu_00719_mRNA_2.1	-
GF0038586	0	1	0	Caffeic acid O-methyltransferase (1)	methyltransferase activity [GO:0008168 molecular_function] (1); O-methyltransferase activity [GO:0008171 molecular_function] (1)	O-methyltransferase COMT-type [IPR016461] (1); O-methyltransferase, family 2 [IPR001077] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	C_unshiu_00719_mRNA_10.1	-
GF0038585	0	1	0	Hypothetical protein (1)			-	C_unshiu_00718_mRNA_4.1	-
GF0038584	0	1	0	Dnajc14 protein, putative (1)			-	C_unshiu_00718_mRNA_2.1	-
GF0038583	0	1	0	HD domain class transcription factor (1)	protein binding [GO:0005515 molecular_function] (1); signal transduction [GO:0007165 biological_process] (1)	Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1)	-	C_unshiu_00717_mRNA_15.1	-
GF0038582	0	1	0	Hypothetical protein (1)			-	C_unshiu_00717_mRNA_1.1	-
GF0038581	0	1	0	Hypothetical protein (1)			-	C_unshiu_00716_mRNA_9.1	-
GF0038580	0	1	0	Hypothetical protein (1)			-	C_unshiu_00716_mRNA_8.1	-
GF0038579	0	1	0	Putative disease resistance protein At4g19050 (1)	ADP binding [GO:0043531 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Leucine-rich repeat [IPR001611] (1); NB-ARC [IPR002182] (1)	-	C_unshiu_00716_mRNA_4.1	-
GF0038578	0	1	0	Hypothetical protein (1)			-	C_unshiu_00716_mRNA_3.1	-
GF0038577	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_00716_mRNA_16.1	-
GF0038576	0	1	0	Hypothetical protein (1)			-	C_unshiu_00716_mRNA_15.1	-
GF0038575	0	1	0	Hypothetical protein (1)			-	C_unshiu_00716_mRNA_13.1	-
GF0038574	0	1	0	Hypothetical protein (1)			-	C_unshiu_00716_mRNA_10.1	-
GF0038573	0	1	0	Tobamovirus multiplication 1 isoform 4 (1)		Domain of unknown function DUF1084 [IPR009457] (1)	-	C_unshiu_00716_mRNA_1.1	-
GF0038572	0	1	0	P-loop containing nucleoside triphosphate hydrolases superfamily protein isoform 9 (1)	GTP binding [GO:0005525 molecular_function] (1)	GTP binding domain [IPR006073] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); EngB-type guanine nucleotide-binding (G) domain [IPR030393] (1)	-	C_unshiu_00715_mRNA_19.1	-
GF0038571	0	1	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_00715_mRNA_16.1	-
GF0038570	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00715_mRNA_1.1	-
GF0038569	0	1	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	Zinc finger, BED-type [IPR003656] (1)	-	C_unshiu_00714_mRNA_7.1	-
GF0038568	0	1	0	Hypothetical protein (1)			-	C_unshiu_00714_mRNA_6.1	-
GF0038567	0	1	0	Hypothetical protein (1)			-	C_unshiu_00714_mRNA_5.1	-
GF0038566	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00714_mRNA_2.1	-
GF0038565	0	1	0	Progesterone 5-beta-reductase (1)		NAD(P)-binding domain [IPR016040] (1)	-	C_unshiu_00714_mRNA_10.1	-
GF0038564	0	1	0	Pollen-specific protein C13 (1)			-	C_unshiu_00713_mRNA_7.1	-
GF0038563	0	1	0	Hypothetical protein (1)		HotDog domain [IPR029069] (1)	-	C_unshiu_00713_mRNA_3.1	-
GF0038562	0	1	0	Hypothetical protein (1)		Metallo-dependent phosphatase-like [IPR029052] (1)	-	C_unshiu_00712_mRNA_4.1	-
GF0038561	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1); signal transduction [GO:0007165 biological_process] (1); ADP binding [GO:0043531 molecular_function] (1)	Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	C_unshiu_00712_mRNA_17.1	-
GF0038560	0	1	0	Protein SUPPRESSOR OF npr1-1, CONSTITUTIVE 1 (1)	protein binding [GO:0005515 molecular_function] (1); signal transduction [GO:0007165 biological_process] (1)	Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_00712_mRNA_15.1	-
GF0038559	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, SWIM-type [IPR007527] (1); Zinc finger, PMZ-type [IPR006564] (1)	-	C_unshiu_00712_mRNA_14.1	-
GF0038558	0	1	0	Hypothetical protein (1)			-	C_unshiu_00712_mRNA_1.1	-
GF0038557	0	1	0	Hypothetical protein (1)			-	C_unshiu_00711_mRNA_7.1	-
GF0038556	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			-	C_unshiu_00711_mRNA_4.1	-
GF0038555	0	1	0	Hypothetical protein (1)			-	C_unshiu_00711_mRNA_2.1	-
GF0038554	0	1	0	Hypothetical protein (1)			-	C_unshiu_00710_mRNA_16.1	-
GF0038553	0	1	0	Hypothetical protein (1)			-	C_unshiu_00710_mRNA_13.1	-
GF0038552	0	1	0	Hypothetical protein (1)			-	C_unshiu_00710_mRNA_12.1	-
GF0038551	0	1	0	Putative disease resistance protein (1)	protein binding [GO:0005515 molecular_function] (1); ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Leucine-rich repeat [IPR001611] (1); NB-ARC [IPR002182] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00710_mRNA_11.1	-
GF0038550	0	1	0	Hypothetical protein (1)			-	C_unshiu_00709_mRNA_9.1	-
GF0038549	0	1	0	Hypothetical protein (1)			-	C_unshiu_00709_mRNA_8.1	-
GF0038548	0	1	0	Hypothetical protein (1)			-	C_unshiu_00709_mRNA_5.1	-
GF0038547	0	1	0	Hypothetical protein (1)			-	C_unshiu_00709_mRNA_2.1	-
GF0038546	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00709_mRNA_17.1	-
GF0038545	0	1	0	Hypothetical protein (1)			-	C_unshiu_00709_mRNA_16.1	-
GF0038544	0	1	0	Ribonuclease H protein (1)	RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Endonuclease/exonuclease/phosphatase [IPR005135] (1); Ribonuclease H domain [IPR002156] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00709_mRNA_15.1	-
GF0038543	0	1	0	Hypothetical protein (1)			-	C_unshiu_00709_mRNA_14.1	-
GF0038542	0	1	0	Hypothetical protein (1)			-	C_unshiu_00709_mRNA_13.1	-
GF0038541	0	1	0	Hypothetical protein (1)			-	C_unshiu_00709_mRNA_11.1	-
GF0038540	0	1	0	Hypothetical protein (1)			-	C_unshiu_00709_mRNA_10.1	-
GF0038539	0	1	0	Hypothetical protein (1)		Gag-polypeptide of LTR copia-type [IPR029472] (1)	-	C_unshiu_00708_mRNA_4.1	-
GF0038538	0	1	0	Hypothetical protein (1)			-	C_unshiu_00708_mRNA_12.1	-
GF0038537	0	1	0	Hypothetical protein (1)		SGNH hydrolase-type esterase domain [IPR013830] (1)	-	C_unshiu_00708_mRNA_1.1	-
GF0038536	0	1	0	Hypothetical protein (1)		Formin, FH2 domain [IPR015425] (1)	-	C_unshiu_00707_mRNA_9.1	-
GF0038535	0	1	0	Isoprene synthase (1)	metabolic process [GO:0008152 biological_process] (1); lyase activity [GO:0016829 molecular_function] (1); terpene synthase activity [GO:0010333 molecular_function] (1); magnesium ion binding [GO:0000287 molecular_function] (1)	Isoprenoid synthase domain [IPR008949] (1); Terpene synthase, metal-binding domain [IPR005630] (1); Terpene synthase, N-terminal domain [IPR001906] (1); Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (1)	-	C_unshiu_00707_mRNA_5.1	-
GF0038534	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Kelch-type beta propeller [IPR015915] (1)	-	C_unshiu_00707_mRNA_3.1	-
GF0038533	0	1	0	Hypothetical protein (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	-	C_unshiu_00707_mRNA_12.2	-
GF0038532	0	1	0	Hypothetical protein (1)		Alpha/gamma-adaptin-binding protein p34 [IPR019341] (1)	-	C_unshiu_00706_mRNA_2.1	-
GF0038531	0	1	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); serine-type endopeptidase activity [GO:0004252 molecular_function] (1)	Peptidase S8, subtilisin-related [IPR015500] (1); PA domain [IPR003137] (1); Peptidase S8/S53 domain [IPR000209] (1); Peptidase S8 propeptide/proteinase inhibitor I9 [IPR010259] (1)	-	C_unshiu_00706_mRNA_16.1	-
GF0038530	0	1	0	RNA recognition motif-containing protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); nucleotide binding [GO:0000166 molecular_function] (1)	RNA recognition motif domain [IPR000504] (1); Nucleotide-binding alpha-beta plait domain [IPR012677] (1)	-	C_unshiu_00706_mRNA_11.1	-
GF0038529	0	1	0	Hypothetical protein (1)			-	C_unshiu_00705_mRNA_6.1	-
GF0038528	0	1	0	Seipin (1)	lipid storage [GO:0019915 biological_process] (1)	Seipin family [IPR009617] (1)	-	C_unshiu_00705_mRNA_4.1	-
GF0038527	0	1	0	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_00705_mRNA_11.1	-
GF0038526	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00705_mRNA_10.1	-
GF0038525	0	1	0	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_00705_mRNA_1.1	-
GF0038524	0	1	0	Protein SUR2 , putative (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); iron ion binding [GO:0005506 molecular_function] (1); fatty acid biosynthetic process [GO:0006633 biological_process] (1)	Fatty acid hydroxylase [IPR006694] (1)	-	C_unshiu_00704_mRNA_6.1	-
GF0038523	0	1	0	Hypothetical protein (1)			-	C_unshiu_00704_mRNA_19.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0038522	0	1	0	DNA-directed RNA polymerase II non-catalytic subunit (1)	nucleic acid binding [GO:0003676 molecular_function] (1); DNA-directed RNA polymerase activity [GO:0003899 molecular_function] (1); transcription, DNA-templated [GO:0006351 biological_process] (1)	RNA polymerase Rpb7, N-terminal [IPR005576] (1); Nucleic acid-binding, OB-fold [IPR012340] (1); S1 domain [IPR003029] (1)	-	C_unshiu_00703_mRNA_7.1	-
GF0038521	0	1	0	Hypothetical protein (1)			-	C_unshiu_00703_mRNA_4.1	-
GF0038520	0	1	0	Hypothetical protein (1)			-	C_unshiu_00702_mRNA_16.1	-
GF0038519	0	1	0	Senescence-related gene 1 (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Non-haem dioxygenase N-terminal domain [IPR026992] (1); Isopenicillin N synthase-like [IPR027443] (1); Oxoglutarate/iron-dependent dioxygenase [IPR005123] (1)	-	C_unshiu_00702_mRNA_14.1	-
GF0038518	0	1	0	Hypothetical protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	C_unshiu_00701_mRNA_7.1	-
GF0038517	0	1	0	DNA-directed RNA polymerase, alpha subunit (1)	DNA binding [GO:0003677 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1); DNA-directed RNA polymerase activity [GO:0003899 molecular_function] (1); transcription, DNA-templated [GO:0006351 biological_process] (1)	RNA polymerase, alpha subunit, C-terminal [IPR011260] (1); DNA-directed RNA polymerase, alpha subunit [IPR011773] (1); DNA-directed RNA polymerase, RBP11-like dimerisation domain [IPR009025] (1); DNA-directed RNA polymerase, RpoA/D/Rpb3-type [IPR011263] (1); DNA-directed RNA polymerase, insert domain [IPR011262] (1)	-	C_unshiu_00701_mRNA_22.1	-
GF0038516	0	1	0	30S ribosomal protein S11, chloroplastic (1)	structural constituent of ribosome [GO:0003735 molecular_function] (1); translation [GO:0006412 biological_process] (1); ribosome [GO:0005840 cellular_component] (1)	Ribosomal S11, conserved site [IPR018102] (1); Ribosomal protein S11 [IPR001971] (1)	-	C_unshiu_00701_mRNA_21.1	-
GF0038515	0	1	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_00701_mRNA_20.1	-
GF0038514	0	1	0	Transposase (1)		Transposon, En/Spm-like [IPR004242] (1)	-	C_unshiu_00701_mRNA_2.1	-
GF0038513	0	1	0	Hypothetical protein (1)	catalytic activity [GO:0003824 molecular_function] (1)	Six-hairpin glycosidase [IPR012341] (1); MULE transposase domain [IPR018289] (1)	-	C_unshiu_00701_mRNA_18.1	-
GF0038512	0	1	0	Ribonuclease P/MRP protein subunit POP5 (1)	tRNA processing [GO:0008033 biological_process] (1); ribonuclease activity [GO:0004540 molecular_function] (1)	Ribonuclease P/MRP protein subunit [IPR002759] (1)	-	C_unshiu_00701_mRNA_16.1	-
GF0038511	0	1	0	Hypothetical protein (1)			-	C_unshiu_00701_mRNA_15.1	-
GF0038510	0	1	0	Hypothetical protein (1)			-	C_unshiu_00701_mRNA_13.1	-
GF0038509	0	1	0	Putative TNP2 like transposable element (1)			-	C_unshiu_00701_mRNA_1.1	-
GF0038508	0	1	0	Protein TRANSPARENT TESTA 12 (1)	antiporter activity [GO:0015297 molecular_function] (1); drug transmembrane transporter activity [GO:0015238 molecular_function] (1); membrane [GO:0016020 cellular_component] (1); drug transmembrane transport [GO:0006855 biological_process] (1); transmembrane transport [GO:0055085 biological_process] (1)	Multi antimicrobial extrusion protein [IPR002528] (1)	-	C_unshiu_00700_mRNA_6.1	-
GF0038507	0	1	0	Hypothetical protein (1)			-	C_unshiu_00700_mRNA_2.1	-
GF0038506	0	1	0	Hypothetical protein (1)			-	C_unshiu_00700_mRNA_16.1	-
GF0038505	0	1	0	Hypothetical protein (1)			-	C_unshiu_00699_mRNA_7.1	-
GF0038504	0	1	0	Hypothetical protein (1)	integral component of membrane [GO:0016021 cellular_component] (1)	EXS, C-terminal [IPR004342] (1)	-	C_unshiu_00699_mRNA_3.1	-
GF0038503	0	1	0	Far-red impaired response protein-like (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1)	-	C_unshiu_00698_mRNA_6.1	-
GF0038502	0	1	0	Hypothetical protein (1)			-	C_unshiu_00698_mRNA_5.1	-
GF0038501	0	1	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	-	C_unshiu_00697_mRNA_8.1	-
GF0038500	0	1	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1); MULE transposase domain [IPR018289] (1)	-	C_unshiu_00697_mRNA_5.1	-
GF0038499	0	1	0	Hypothetical protein (1)	transporter activity [GO:0005215 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1)	Purine permease, plant [IPR030182] (1); Myb-like domain [IPR017877] (1); Homeodomain-like [IPR009057] (1)	-	C_unshiu_00697_mRNA_4.1	-
GF0038498	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00696_mRNA_3.1	-
GF0038497	0	1	0	DDT domain-containing protein, putative isoform 5 (1)		DDT domain, subgroup [IPR018500] (1); DDT domain [IPR004022] (1); WSTF/Acf1/Cbp146 [IPR013136] (1); DDT domain superfamily [IPR018501] (1)	-	C_unshiu_00696_mRNA_16.1	-
GF0038496	0	1	0	Pre-mrna-splicing factor rse1 (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Domain of unknown function DUF239 [IPR004314] (1); Ribonuclease H-like domain [IPR012337] (1); Domain of unknown function DUF4409 [IPR025521] (1)	-	C_unshiu_00696_mRNA_1.1	-
GF0038495	0	1	0	Hypothetical protein (1)			-	C_unshiu_00694_mRNA_13.1	-
GF0038494	0	1	0	Putative non-LTR retroelement reverse transcriptase (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00694_mRNA_12.1	-
GF0038493	0	1	0	Hypothetical protein (1)			-	C_unshiu_00694_mRNA_1.1	-
GF0038492	0	1	0	Hypothetical protein (1)			-	C_unshiu_00693_mRNA_7.1	-
GF0038491	0	1	0	Hypothetical protein (1)			-	C_unshiu_00693_mRNA_6.1	-
GF0038490	0	1	0	RNA-directed DNA polymerase (Reverse transcriptase), Polynucleotidyl transferase, Ribonuclease H fold-like protein (1)	metabolic process [GO:0008152 biological_process] (1); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1); transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1); Ribonuclease H domain [IPR002156] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00693_mRNA_2.1	-
GF0038489	0	1	0	Hypothetical protein (1)			-	C_unshiu_00693_mRNA_16.1	-
GF0038488	0	1	0	Hypothetical protein (1)			-	C_unshiu_00693_mRNA_13.1	-
GF0038487	0	1	0	Hypothetical protein (1)			-	C_unshiu_00693_mRNA_1.1	-
GF0038486	0	1	0	Hypothetical protein (1)			-	C_unshiu_00692_mRNA_2.1	-
GF0038485	0	1	0	TMV resistance N (1)		Leucine-rich repeat 3 [IPR011713] (1)	-	C_unshiu_00692_mRNA_18.1	-
GF0038484	0	1	0	Hypothetical protein (1)			-	C_unshiu_00691_mRNA_8.1	-
GF0038483	0	1	0	Hypothetical protein (1)			-	C_unshiu_00691_mRNA_3.1	-
GF0038482	0	1	0	Hypothetical protein (1)			-	C_unshiu_00691_mRNA_15.1	-
GF0038481	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	C_unshiu_00691_mRNA_12.1	-
GF0038480	0	1	0	Hypothetical protein (1)			-	C_unshiu_00691_mRNA_10.1	-
GF0038479	0	1	0	C6HC-type zinc finger RING/U-box protein (1)	ubiquitin-protein transferase activity [GO:0004842 molecular_function] (1); protein ubiquitination [GO:0016567 biological_process] (1); zinc ion binding [GO:0008270 molecular_function] (1); metal ion binding [GO:0046872 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Zinc finger, C3HC4 RING-type [IPR018957] (1); Zinc finger, RING/FYVE/PHD-type [IPR013083] (1); IBR domain [IPR002867] (1); Zinc finger, RING-type [IPR001841] (1); Zinc finger, RING-type, conserved site [IPR017907] (1); E3 ubiquitin ligase RBR family [IPR031127] (1)	-	C_unshiu_00690_mRNA_4.1	-
GF0038478	0	1	0	RING zinc finger protein, putative (1)	ubiquitin-protein transferase activity [GO:0004842 molecular_function] (1); protein ubiquitination [GO:0016567 biological_process] (1); protein binding [GO:0005515 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, RING/FYVE/PHD-type [IPR013083] (1); Zinc finger, RING-type [IPR001841] (1); E3 ubiquitin ligase RBR family [IPR031127] (1); Zinc finger, RING-type, conserved site [IPR017907] (1)	-	C_unshiu_00690_mRNA_3.1	-
GF0038477	0	1	0	Hypothetical protein (1)	methyltransferase activity [GO:0008168 molecular_function] (1)	Putative S-adenosyl-L-methionine-dependent methyltransferase [IPR004159] (1)	-	C_unshiu_00689_mRNA_8.1	-
GF0038476	0	1	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1)	-	C_unshiu_00689_mRNA_4.1	-
GF0038475	0	1	0	Hypothetical protein (1)			-	C_unshiu_00689_mRNA_3.1	-
GF0038474	0	1	0	Hypothetical protein (1)			-	C_unshiu_00689_mRNA_2.1	-
GF0038473	0	1	0	Hypothetical protein (1)			-	C_unshiu_00689_mRNA_15.1	-
GF0038472	0	1	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_00689_mRNA_14.1	-
GF0038471	0	1	0	Hypothetical protein (1)			-	C_unshiu_00689_mRNA_12.1	-
GF0038470	0	1	0	Leucine-rich repeat protein kinase family protein, putative (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1)	-	C_unshiu_00689_mRNA_10.1	-
GF0038469	0	1	0	Hypothetical protein (1)			-	C_unshiu_00688_mRNA_9.1	-
GF0038468	0	1	0	Monosacharide transport protein (1)			-	C_unshiu_00688_mRNA_7.1	-
GF0038467	0	1	0	Hypothetical protein (1)			-	C_unshiu_00688_mRNA_4.1	-
GF0038466	0	1	0	Hypothetical protein (1)			-	C_unshiu_00688_mRNA_3.1	-
GF0038465	0	1	0	Hypothetical protein (1)			-	C_unshiu_00688_mRNA_2.1	-
GF0038464	0	1	0	Hypothetical protein (1)			-	C_unshiu_00688_mRNA_17.1	-
GF0038463	0	1	0	Hypothetical protein (1)			-	C_unshiu_00688_mRNA_12.1	-
GF0038462	0	1	0	Hypothetical protein (1)			-	C_unshiu_00688_mRNA_10.1	-
GF0038461	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00687_mRNA_8.1	-
GF0038460	0	1	0	Hypothetical protein (1)			-	C_unshiu_00686_mRNA_9.1	-
GF0038459	0	1	0	Hypothetical protein (1)		Protein of unknown function DUF3464 [IPR021855] (1)	-	C_unshiu_00686_mRNA_2.1	-
GF0038458	0	1	0	Hypothetical protein (1)			-	C_unshiu_00686_mRNA_11.1	-
GF0038457	0	1	0	Hypothetical protein (1)			-	C_unshiu_00686_mRNA_10.1	-
GF0038456	0	1	0	Retrovirus-related Pol polyprotein from transposon TNT 1-94 (1)			-	C_unshiu_00685_mRNA_7.1	-
GF0038455	0	1	0	Hypothetical protein (1)			-	C_unshiu_00685_mRNA_3.1	-
GF0038454	0	1	0	Hypothetical protein (1)			-	C_unshiu_00685_mRNA_12.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0038453	0	1	0	Receptor-like protein kinase FERONIA (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Malectin-like carbohydrate-binding domain [IPR024788] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase, ATP binding site [IPR017441] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1)	-	C_unshiu_00685_mRNA_11.1	-
GF0038452	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1); lipid metabolic process [GO:0006629 biological_process] (1)	Alpha/Beta hydrolase fold [IPR029058] (1); Zinc finger, CCHC-type [IPR001878] (1); Fungal lipase-like domain [IPR002921] (1)	-	C_unshiu_00685_mRNA_10.1	-
GF0038451	0	1	0	Hypothetical protein (1)			-	C_unshiu_00684_mRNA_9.1	-
GF0038450	0	1	0	Hypothetical protein (1)			-	C_unshiu_00684_mRNA_5.1	-
GF0038449	0	1	0	Hypothetical protein (1)			-	C_unshiu_00684_mRNA_4.1	-
GF0038448	0	1	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1)	-	C_unshiu_00684_mRNA_3.1	-
GF0038447	0	1	0	Hypothetical protein (1)			-	C_unshiu_00684_mRNA_15.1	-
GF0038446	0	1	0	Hypothetical protein (1)		Zinc knuckle CX2CX4HX4C [IPR025836] (1)	-	C_unshiu_00684_mRNA_12.1	-
GF0038445	0	1	0	Hypothetical protein (1)			-	C_unshiu_00684_mRNA_11.1	-
GF0038444	0	1	0	Hypothetical protein (1)			-	C_unshiu_00684_mRNA_1.1	-
GF0038443	0	1	0	Hypothetical protein (1)			-	C_unshiu_00683_mRNA_9.1	-
GF0038442	0	1	0	Hypothetical protein (1)			-	C_unshiu_00683_mRNA_5.1	-
GF0038441	0	1	0	Hypothetical protein (1)			-	C_unshiu_00683_mRNA_3.1	-
GF0038440	0	1	0	Hypothetical protein (1)			-	C_unshiu_00683_mRNA_11.1	-
GF0038439	0	1	0	Hypothetical protein (1)			-	C_unshiu_00682_mRNA_5.1	-
GF0038438	0	1	0	Hypothetical protein (1)			-	C_unshiu_00682_mRNA_2.1	-
GF0038437	0	1	0	Hypothetical protein (1)			-	C_unshiu_00682_mRNA_13.1	-
GF0038436	0	1	0	Hypothetical protein (1)		MULE transposase domain [IPR018289] (1)	-	C_unshiu_00682_mRNA_1.1	-
GF0038435	0	1	0	Hypothetical protein (1)	voltage-gated potassium channel activity [GO:0005249 molecular_function] (1); vacuolar membrane [GO:0005774 cellular_component] (1); cellular potassium ion homeostasis [GO:0030007 biological_process] (1); potassium ion transmembrane transport [GO:0071805 biological_process] (1)	Two pore domain potassium channel, plant [IPR031144] (1); Potassium channel domain [IPR013099] (1)	-	C_unshiu_00681_mRNA_7.1	-
GF0038434	0	1	0	Hypothetical protein (1)			-	C_unshiu_00681_mRNA_4.1	-
GF0038433	0	1	0	Hypothetical protein (1)			-	C_unshiu_00681_mRNA_3.1	-
GF0038432	0	1	0	Hypothetical protein (1)	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1)	Cytochrome P450 [IPR001128] (1)	-	C_unshiu_00681_mRNA_19.1	-
GF0038431	0	1	0	Hypothetical protein (1)			-	C_unshiu_00680_mRNA_5.1	-
GF0038430	0	1	0	Hypothetical protein (1)		Hydantoinaseoxoprolinase, N-terminal [IPR008040] (1)	-	C_unshiu_00680_mRNA_4.1	-
GF0038429	0	1	0	Progesterone 5-beta-reductase (1)		NAD(P)-binding domain [IPR016040] (1)	-	C_unshiu_00680_mRNA_3.1	-
GF0038428	0	1	0	Hypothetical protein (1)			-	C_unshiu_00680_mRNA_20.1	-
GF0038427	0	1	0	Truncated RB (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	C_unshiu_00680_mRNA_19.1	-
GF0038426	0	1	0	Hypothetical protein (1)			-	C_unshiu_00680_mRNA_16.1	-
GF0038425	0	1	0	Proteinase inhibitor (1)	response to wounding [GO:0009611 biological_process] (1); serine-type endopeptidase inhibitor activity [GO:0004867 molecular_function] (1)	Proteinase inhibitor I13, potato inhibitor I [IPR000864] (1)	-	C_unshiu_00679_mRNA_15.1	-
GF0038424	0	1	0	Hypothetical protein (1)			-	C_unshiu_00679_mRNA_14.1	-
GF0038423	0	1	0	CwfJ-like family protein, putative isoform 1 (1)		Cwf19-like protein, C-terminal domain-2 [IPR006767] (1); Cwf19-like, C-terminal domain-1 [IPR006768] (1)	-	C_unshiu_00679_mRNA_13.1	-
GF0038422	0	1	0	Hyccin protein (1)		Hyccin [IPR018619] (1)	-	C_unshiu_00678_mRNA_7.1	-
GF0038421	0	1	0	Hypothetical protein (1)		Probable transposase, Ptta/En/Spm, plant [IPR004252] (1)	-	C_unshiu_00678_mRNA_15.1	-
GF0038420	0	1	0	Hypothetical protein (1)			-	C_unshiu_00678_mRNA_14.1	-
GF0038419	0	1	0	Hypothetical protein (1)			-	C_unshiu_00678_mRNA_12.1	-
GF0038418	0	1	0	Hypothetical protein (1)			-	C_unshiu_00678_mRNA_11.1	-
GF0038417	0	1	0	Hypothetical protein (1)			-	C_unshiu_00678_mRNA_10.1	-
GF0038416	0	1	0	Hypothetical protein (1)			-	C_unshiu_00677_mRNA_9.1	-
GF0038415	0	1	0	Hypothetical protein (1)		Arabidopsis retrotransposon Orf1 [IPR004312] (1)	-	C_unshiu_00677_mRNA_6.1	-
GF0038414	0	1	0	Hypothetical protein (1)			-	C_unshiu_00677_mRNA_3.1	-
GF0038413	0	1	0	Hypothetical protein (1)			-	C_unshiu_00677_mRNA_11.1	-
GF0038412	0	1	0	CAI-1 autoinducer sensor kinase/phosphatase cqsS isoform 1 (1)		Harbinger transposase-derived nuclease domain [IPR027806] (1)	-	C_unshiu_00676_mRNA_3.1	-
GF0038411	0	1	0	Hypothetical protein (1)			-	C_unshiu_00676_mRNA_15.1	-
GF0038410	0	1	0	Amino acid transporter-like protein (1)		Amino acid transporter, transmembrane domain [IPR013057] (1)	-	C_unshiu_00676_mRNA_14.1	-
GF0038409	0	1	0	Hypothetical protein (1)			-	C_unshiu_00675_mRNA_8.1	-
GF0038408	0	1	0	Hypothetical protein (1)			-	C_unshiu_00675_mRNA_4.1	-
GF0038407	0	1	0	TRNA synthetase class I (C) family protein (1)	aminoacyl-tRNA ligase activity [GO:0004812 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1); nucleotide binding [GO:0000166 molecular_function] (1); tRNA aminoacylation for protein translation [GO:0006418 biological_process] (1)	Rossmann-like alpha/beta/alpha sandwich fold [IPR014729] (1); Aminoacyl-tRNA synthetase, class 1a, anticodon-binding [IPR009080] (1); Cysteinyl-tRNA synthetase/mycothiol ligase [IPR024909] (1); tRNA synthetases class I, catalytic domain [IPR032678] (1)	-	C_unshiu_00675_mRNA_14.1	-
GF0038406	0	1	0	Hypothetical protein (1)			-	C_unshiu_00675_mRNA_13.1	-
GF0038405	0	1	0	Hypothetical protein (1)		Cysteinyl-tRNA synthetase/mycothiol ligase [IPR024909] (1); tRNA synthetases class I, catalytic domain [IPR032678] (1); Rossmann-like alpha/beta/alpha sandwich fold [IPR014729] (1)	-	C_unshiu_00675_mRNA_12.1	-
GF0038404	0	1	0	Hypothetical protein (1)			-	C_unshiu_00675_mRNA_11.1	-
GF0038403	0	1	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	Transcription factor, MADS-box [IPR002100] (1)	-	C_unshiu_00675_mRNA_10.1	-
GF0038402	0	1	0	Hypothetical protein (1)			-	C_unshiu_00675_mRNA_1.1	-
GF0038401	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_00674_mRNA_6.1	-
GF0038400	0	1	0	Hypothetical protein (1)			-	C_unshiu_00674_mRNA_5.1	-
GF0038399	0	1	0	Hypothetical protein (1)			-	C_unshiu_00674_mRNA_4.1	-
GF0038398	0	1	0	Hypothetical protein (1)			-	C_unshiu_00674_mRNA_14.1	-
GF0038397	0	1	0	Hypothetical protein (1)			-	C_unshiu_00674_mRNA_12.1	-
GF0038396	0	1	0	Hypothetical protein (1)			-	C_unshiu_00674_mRNA_11.1	-
GF0038395	0	1	0	Hypothetical protein (1)			-	C_unshiu_00674_mRNA_10.1	-
GF0038394	0	1	0	Hypothetical protein (1)			-	C_unshiu_00674_mRNA_1.1	-
GF0038393	0	1	0	Envelope membrane protein, chloroplastic (1)	acetyl-CoA carboxylase complex [GO:0009317 cellular_component] (1); acetyl-CoA carboxylase activity [GO:0003989 molecular_function] (1); fatty acid biosynthetic process [GO:0006633 biological_process] (1); integral component of membrane [GO:0016021 cellular_component] (1)	Acetyl-coenzyme A carboxyltransferase, N-terminal [IPR011762] (1); Carboxyl transferase [IPR000022] (1); Chloroplast envelope membrane protein, CemA [IPR004282] (1); Acetyl-CoA carboxylase carboxyl transferase, beta subunit [IPR000438] (1); ClpP/crotonase-like domain [IPR029045] (1)	-	C_unshiu_00673_mRNA_9.1	-
GF0038392	0	1	0	RNA polymerase alpha subunit (1)	transcription, DNA-templated [GO:0006351 biological_process] (1); DNA-directed RNA polymerase activity [GO:0003899 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	DNA-directed RNA polymerase, insert domain [IPR011262] (1); DNA-directed RNA polymerase, RpoA/D/Rpb3-type [IPR011263] (1); DNA-directed RNA polymerase, RBP11-like dimerisation domain [IPR009025] (1)	-	C_unshiu_00673_mRNA_8.1	-
GF0038391	0	1	0	30S ribosomal protein S11, chloroplastic (1)	translation [GO:0006412 biological_process] (1); intracellular [GO:0005622 cellular_component] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1); ribosome [GO:0005840 cellular_component] (1)	Ribosomal protein S11 [IPR001971] (1); Ribosomal S11, conserved site [IPR018102] (1); Ribosomal protein S11, bacterial-type [IPR019981] (1)	-	C_unshiu_00673_mRNA_7.1	-
GF0038390	0	1	0	Translational activator gcn1 (1)			-	C_unshiu_00673_mRNA_3.1	-
GF0038389	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_00673_mRNA_19.1	-
GF0038388	0	1	0	Hypothetical protein (1)		High mobility group box domain [IPR009071] (1)	-	C_unshiu_00673_mRNA_16.1	-
GF0038387	0	1	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_00673_mRNA_15.1	-
GF0038386	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FAR1 DNA binding domain [IPR004330] (1); FHY3/FAR1 family [IPR031052] (1); Zinc finger, SWIM-type [IPR007527] (1)	-	C_unshiu_00673_mRNA_14.1	-
GF0038385	0	1	0	50S ribosomal protein L20 (1)	ribosome [GO:0005840 cellular_component] (1); rRNA binding [GO:0019843 molecular_function] (1); intracellular [GO:0005622 cellular_component] (1); translation [GO:0006412 biological_process] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1)	Ribosomal protein L20 [IPR005813] (1)	-	C_unshiu_00673_mRNA_13.1	-
GF0038384	0	1	0	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	-	C_unshiu_00672_mRNA_5.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0038383	0	1	0	Hypothetical protein (1)			-	C_unshiu_00672_mRNA_13.1	-
GF0038382	0	1	0	Hypothetical protein (1)			-	C_unshiu_00671_mRNA_9.1	-
GF0038381	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	TRAF-like [IPR008974] (1); MATH/TRAF domain [IPR002083] (1)	-	C_unshiu_00671_mRNA_4.1	-
GF0038380	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	TRAF-like [IPR008974] (1); MATH/TRAF domain [IPR002083] (1)	-	C_unshiu_00671_mRNA_2.1	-
GF0038379	0	1	0	Hypothetical protein (1)			-	C_unshiu_00670_mRNA_14.1	-
GF0038378	0	1	0	Retrotransposon protein, putative, unclassified (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_00670_mRNA_12.1	-
GF0038377	0	1	0	Hypothetical protein (1)			-	C_unshiu_00669_mRNA_6.1	-
GF0038376	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1); Zinc finger, CCHC-type [IPR001878] (1); Endonuclease/exonuclease/phosphatase [IPR005135] (1); Domain of unknown function DUF4283 [IPR025558] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Protein kinase-like domain [IPR011009] (1); Leucine-rich repeat, typical subtype [IPR003591] (1)	-	C_unshiu_00669_mRNA_4.1	-
GF0038375	0	1	0	Hypothetical protein (1)			-	C_unshiu_00669_mRNA_3.1	-
GF0038374	0	1	0	Hypothetical protein (1)			-	C_unshiu_00669_mRNA_20.1	-
GF0038373	0	1	0	Hypothetical protein (1)			-	C_unshiu_00669_mRNA_18.1	-
GF0038372	0	1	0	Pentatricopeptide repeat-containing family protein (1)	protein binding [GO:0005515 molecular_function] (1)	Tetratricopeptide-like helical domain [IPR011990] (1); Pentatricopeptide repeat [IPR002885] (1)	-	C_unshiu_00669_mRNA_10.1	-
GF0038371	0	1	0	Flavonoid 3',5'-hydroxylase (1)			-	C_unshiu_00668_mRNA_9.1	-
GF0038370	0	1	0	Hypothetical protein (1)			-	C_unshiu_00668_mRNA_5.1	-
GF0038369	0	1	0	Hypothetical protein (1)			-	C_unshiu_00668_mRNA_4.1	-
GF0038368	0	1	0	Hypothetical protein (1)			-	C_unshiu_00668_mRNA_2.1	-
GF0038367	0	1	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_00668_mRNA_18.1	-
GF0038366	0	1	0	Hypothetical protein (1)			-	C_unshiu_00668_mRNA_14.1	-
GF0038365	0	1	0	Hypothetical protein (1)			-	C_unshiu_00668_mRNA_11.1	-
GF0038364	0	1	0	Hypothetical protein (1)			-	C_unshiu_00668_mRNA_1.1	-
GF0038363	0	1	0	Hypothetical protein (1)			-	C_unshiu_00667_mRNA_4.1	-
GF0038362	0	1	0	Abscisic acid receptor PYL8 (1)		Polyketide cyclase/dehydrase [IPR019587] (1); START-like domain [IPR023393] (1)	-	C_unshiu_00667_mRNA_16.1	-
GF0038361	0	1	0	Hypothetical protein (1)		Transposon, En/Spm-like [IPR004242] (1)	-	C_unshiu_00667_mRNA_11.1	-
GF0038360	0	1	0	Hypothetical protein (1)			-	C_unshiu_00665_mRNA_9.1	-
GF0038359	0	1	0	Hypothetical protein (1)	RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Retrotransposon gag domain [IPR005162] (1); Ribonuclease H-like domain [IPR012337] (1); Ribonuclease H domain [IPR002156] (1)	-	C_unshiu_00665_mRNA_8.1	-
GF0038358	0	1	0	Hypothetical protein (1)			-	C_unshiu_00665_mRNA_13.1	-
GF0038357	0	1	0	Hypothetical protein (1)			-	C_unshiu_00665_mRNA_12.1	-
GF0038356	0	1	0	Phi class glutathione S-transferase (1)	protein binding [GO:0005515 molecular_function] (1)	Glutathione S-transferase, N-terminal [IPR004045] (1); Glutathione S-transferase, C-terminal-like [IPR010987] (1); Glutathione S-transferase, C-terminal [IPR004046] (1); Thioredoxin-like fold [IPR012336] (1)	-	C_unshiu_00665_mRNA_11.1	-
GF0038355	0	1	0	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); FMN binding [GO:0010181 molecular_function] (1); catalytic activity [GO:0003824 molecular_function] (1)	NADH:flavin oxidoreductase/NADH oxidase, N-terminal [IPR001155] (1); Aldolase-type TIM barrel [IPR013785] (1)	-	C_unshiu_00664_mRNA_12.1	-
GF0038354	0	1	0	Hypothetical protein (1)			-	C_unshiu_00663_mRNA_9.1	-
GF0038353	0	1	0	Hypothetical protein (1)			-	C_unshiu_00663_mRNA_6.1	-
GF0038352	0	1	0	Hypothetical protein (1)			-	C_unshiu_00663_mRNA_4.1	-
GF0038351	0	1	0	Hypothetical protein (1)			-	C_unshiu_00663_mRNA_3.1	-
GF0038350	0	1	0	Hypothetical protein (1)			-	C_unshiu_00663_mRNA_17.1	-
GF0038349	0	1	0	Hypothetical protein (1)			-	C_unshiu_00663_mRNA_14.1	-
GF0038348	0	1	0	Hypothetical protein (1)			-	C_unshiu_00663_mRNA_13.1	-
GF0038347	0	1	0	Hypothetical protein (1)			-	C_unshiu_00663_mRNA_10.1	-
GF0038346	0	1	0	Hypothetical protein (1)			-	C_unshiu_00663_mRNA_1.1	-
GF0038345	0	1	0	Monoglyceride lipase (1)		Alpha/Beta hydrolase fold [IPR029058] (1); Serine aminopeptidase, S33 [IPR022742] (1)	-	C_unshiu_00662_mRNA_25.1	-
GF0038344	0	1	0	Poly [ADP-ribose] polymerase (1)	protein ADP-ribosylation [GO:0006471 biological_process] (1); NAD+ ADP-ribosyltransferase activity [GO:0003950 molecular_function] (1)	Poly(ADP-ribose) polymerase, catalytic domain [IPR012317] (1); WGR domain [IPR008893] (1); SAP domain [IPR003034] (1); Poly(ADP-ribose) polymerase, regulatory domain [IPR004102] (1)	-	C_unshiu_00662_mRNA_17.1	-
GF0038343	0	1	0	Hypothetical protein (1)			-	C_unshiu_00661_mRNA_8.1	-
GF0038342	0	1	0	Hypothetical protein (1)			-	C_unshiu_00661_mRNA_6.1	-
GF0038341	0	1	0	Hypothetical protein (1)		P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); ATP-dependent RNA helicase DEAD-box, conserved site [IPR000629] (1)	-	C_unshiu_00661_mRNA_3.1	-
GF0038340	0	1	0	Hypothetical protein (1)			-	C_unshiu_00661_mRNA_10.1	-
GF0038339	0	1	0	Hypothetical protein (1)			-	C_unshiu_00660_mRNA_19.1	-
GF0038338	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1); binding [GO:0005488 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	Armadillo-like helical [IPR011989] (1); Homeodomain-like [IPR009057] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Atypical Arm repeat [IPR032413] (1); Myb domain [IPR017930] (1); Armadillo [IPR000225] (1); Armadillo-type fold [IPR016024] (1)	-	C_unshiu_00660_mRNA_17.1	-
GF0038337	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Zinc knuckle CX2CX4HX4C [IPR025836] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1); Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_00660_mRNA_15.1	-
GF0038336	0	1	0	UPF0481 protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	C_unshiu_00660_mRNA_1.1	-
GF0038335	0	1	0	Glutathione gamma-glutamylcysteinyltransferase (1)	response to metal ion [GO:0010038 biological_process] (1); phytochelatin biosynthetic process [GO:0046938 biological_process] (1); glutathione gamma-glutamylcysteinyltransferase activity [GO:0016756 molecular_function] (1); metal ion binding [GO:0046872 molecular_function] (1)	Phytochelatin synthase, C-terminal [IPR015407] (1); Phytochelatin synthase [IPR007719] (1)	-	C_unshiu_00659_mRNA_4.1	-
GF0038334	0	1	0	Hypothetical protein (1)			-	C_unshiu_00659_mRNA_25.1	-
GF0038333	0	1	0	Peptide transporter PTR5 (1)	transporter activity [GO:0005215 molecular_function] (1); transport [GO:0006810 biological_process] (1); membrane [GO:0016020 cellular_component] (1)	Major facilitator superfamily domain [IPR020846] (1); Proton-dependent oligopeptide transporter family [IPR000109] (1)	-	C_unshiu_00659_mRNA_22.1	-
GF0038332	0	1	0	Hypothetical protein (1)			-	C_unshiu_00659_mRNA_16.1	-
GF0038331	0	1	0	Hypothetical protein (1)			-	C_unshiu_00659_mRNA_10.1	-
GF0038330	0	1	0	Hypothetical protein (1)			-	C_unshiu_00656_mRNA_5.1	-
GF0038329	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_00655_mRNA_7.1	-
GF0038328	0	1	0	Hypothetical protein (1)			-	C_unshiu_00655_mRNA_36.1	-
GF0038327	0	1	0	Hypothetical protein (1)			-	C_unshiu_00655_mRNA_33.1	-
GF0038326	0	1	0	Hypothetical protein (1)			-	C_unshiu_00655_mRNA_32.1	-
GF0038325	0	1	0	Hypothetical protein (1)			-	C_unshiu_00655_mRNA_31.1	-
GF0038324	0	1	0	Hypothetical protein (1)			-	C_unshiu_00655_mRNA_30.1	-
GF0038323	0	1	0	Hypothetical protein (1)			-	C_unshiu_00655_mRNA_3.1	-
GF0038322	0	1	0	Hypothetical protein (1)			-	C_unshiu_00655_mRNA_25.1	-
GF0038321	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00655_mRNA_24.1	-
GF0038320	0	1	0	Hypothetical protein (1)			-	C_unshiu_00655_mRNA_23.1	-
GF0038319	0	1	0	Hypothetical protein (1)			-	C_unshiu_00655_mRNA_22.1	-
GF0038318	0	1	0	Hypothetical protein (1)			-	C_unshiu_00655_mRNA_20.1	-
GF0038317	0	1	0	Hypothetical protein (1)			-	C_unshiu_00655_mRNA_17.1	-
GF0038316	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_00654_mRNA_7.1	-
GF0038315	0	1	0	Hypothetical protein (1)			-	C_unshiu_00654_mRNA_4.1	-
GF0038314	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_00654_mRNA_12.1	-
GF0038313	0	1	0	Hypothetical protein (1)			-	C_unshiu_00653_mRNA_6.1	-
GF0038312	0	1	0	Hypothetical protein (1)		DNA repair metallo-beta-lactamase [IPR011084] (1); Metallo-beta-lactamase [IPR001279] (1)	-	C_unshiu_00653_mRNA_4.1	-
GF0038311	0	1	0	Hypothetical protein (1)			-	C_unshiu_00653_mRNA_2.1	-
GF0038310	0	1	0	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	C_unshiu_00653_mRNA_1.1	-
GF0038309	0	1	0	Hypothetical protein (1)			-	C_unshiu_00652_mRNA_15.1	-
GF0038308	0	1	0	Hypothetical protein (1)			-	C_unshiu_00651_mRNA_9.1	-
GF0038307	0	1	0	Hypothetical protein (1)		Transposase, MuDR, plant [IPR004332] (1)	-	C_unshiu_00651_mRNA_8.1	-
GF0038306	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_00651_mRNA_5.1	-
GF0038305	0	1	0	Hypothetical protein (1)			-	C_unshiu_00651_mRNA_4.1	-
GF0038304	0	1	0	Hypothetical protein (1)			-	C_unshiu_00651_mRNA_3.1	-
GF0038303	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00651_mRNA_2.1	-

ID	**Num. in *C. celementine***	**Num in *C. unshiu***	**Num in *P.trifoliata***	**Note**	**GO**	**InterPro**	**Members in *C.clementine***	**Members in *C.unshiu***	**Members in *P.trifoliata***
GF0038302	0	1	0	Hypothetical protein (1)			-	C_unshiu_00651_mRNA_12.1	-
GF0038301	0	1	0	Hypothetical protein (1)			-	C_unshiu_00651_mRNA_11.1	-
GF0038300	0	1	0	Hypothetical protein (1)			-	C_unshiu_00651_mRNA_10.1	-
GF0038299	0	1	0	Hypothetical protein (1)			-	C_unshiu_00651_mRNA_1.1	-
GF0038298	0	1	0	Hypothetical protein (1)			-	C_unshiu_00650_mRNA_2.1	-
GF0038297	0	1	0	Pathogenesis-related maize seed protein (1)	extracellular region [GO:0005576 cellular_component] (1)	Ves allergen [IPR002413] (1); Allergen V5/Tpx-1-related, conserved site [IPR018244] (1); CAP domain [IPR014044] (1); Cysteine-rich secretory protein, allergen V5/Tpx-1-related [IPR001283] (1)	-	C_unshiu_00650_mRNA_14.1	-
GF0038296	0	1	0	Hypothetical protein (1)		Trichome birefringence-like family [IPR029962] (1); PC-Esterase [IPR026057] (1); Protein trichome birefringence-like 13 [IPR029968] (1)	-	C_unshiu_00650_mRNA_13.1	-
GF0038295	0	1	0	Branched-chain-amino-acid transaminase (1)	metabolic process [GO:0008152 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1); branched-chain amino acid metabolic process [GO:0009081 biological_process] (1); branched-chain-amino-acid transaminase activity [GO:0004084 molecular_function] (1)	Branched-chain amino acid aminotransferase II [IPR005786] (1); Aminotransferase class IV [IPR001544] (1)	-	C_unshiu_00650_mRNA_12.1	-
GF0038294	0	1	0	Hypothetical protein (1)			-	C_unshiu_00650_mRNA_10.1	-
GF0038293	0	1	0	Hypothetical protein (1)			-	C_unshiu_00649_mRNA_7.1	-
GF0038292	0	1	0	Hypothetical protein (1)			-	C_unshiu_00649_mRNA_6.1	-
GF0038291	0	1	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	-	C_unshiu_00649_mRNA_3.1	-
GF0038290	0	1	0	Hypothetical protein (1)			-	C_unshiu_00649_mRNA_2.1	-
GF0038289	0	1	0	Hypothetical protein (1)	response to auxin [GO:0009733 biological_process] (1)	Small auxin-up RNA [IPR003676] (1)	-	C_unshiu_00649_mRNA_11.1	-
GF0038288	0	1	0	Hypothetical protein (1)			-	C_unshiu_00648_mRNA_8.1	-
GF0038287	0	1	0	Hypothetical protein (1)			-	C_unshiu_00648_mRNA_7.1	-
GF0038286	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1); Reverse transcriptase domain [IPR000477] (1); Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	C_unshiu_00648_mRNA_5.1	-
GF0038285	0	1	0	Leucine-rich repeat protein kinase family protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_00648_mRNA_4.1	-
GF0038284	0	1	0	Hypothetical protein (1)		ATPase family AAA domain-containing protein 3, domain of unknown function DUF3523 [IPR021911] (1)	-	C_unshiu_00648_mRNA_3.1	-
GF0038283	0	1	0	Hypothetical protein (1)			-	C_unshiu_00648_mRNA_2.1	-
GF0038282	0	1	0	Hypothetical protein (1)		Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00648_mRNA_19.1	-
GF0038281	0	1	0	HAT family dimerisation domain containing protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00648_mRNA_18.1	-
GF0038280	0	1	0	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	C_unshiu_00648_mRNA_14.1	-
GF0038279	0	1	0	Hypothetical protein (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1)	-	C_unshiu_00648_mRNA_12.1	-
GF0038278	0	1	0	Hypothetical protein (1)			-	C_unshiu_00648_mRNA_10.1	-
GF0038277	0	1	0	LRR receptor-like kinase family protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00648_mRNA_1.1	-
GF0038276	0	1	0	Hypothetical protein (1)		Quinoprotein alcohol dehydrogenase-like superfamily [IPR011047] (1)	-	C_unshiu_00646_mRNA_5.1	-
GF0038275	0	1	0	Hypothetical protein (1)			-	C_unshiu_00646_mRNA_4.1	-
GF0038274	0	1	0	Similar to ATP-binding domain 1 family member B (1)		P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); GPN-loop GTPase [IPR004130] (1); GPN-loop GTPase 2 [IPR030231] (1)	-	C_unshiu_00646_mRNA_21.1	-
GF0038273	0	1	0	Hypothetical protein (1)		P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); GPN-loop GTPase [IPR004130] (1); GPN-loop GTPase 2 [IPR030231] (1)	-	C_unshiu_00646_mRNA_20.1	-
GF0038272	0	1	0	Hypothetical protein (1)			-	C_unshiu_00646_mRNA_17.1	-
GF0038271	0	1	0	Hypothetical protein (1)			-	C_unshiu_00646_mRNA_13.1	-
GF0038270	0	1	0	Hypothetical protein (1)			-	C_unshiu_00646_mRNA_12.1	-
GF0038269	0	1	0	Hypothetical protein (1)			-	C_unshiu_00646_mRNA_11.1	-
GF0038268	0	1	0	Hypothetical protein (1)			-	C_unshiu_00645_mRNA_9.1	-
GF0038267	0	1	0	Hypothetical protein (1)			-	C_unshiu_00645_mRNA_7.1	-
GF0038266	0	1	0	Hypothetical protein (1)			-	C_unshiu_00645_mRNA_3.1	-
GF0038265	0	1	0	Hypothetical protein (1)			-	C_unshiu_00645_mRNA_16.1	-
GF0038264	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	GAG-pre-integrase domain [IPR025724] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00645_mRNA_11.1	-
GF0038263	0	1	0	PQ loop repeat family protein (1)		PQ-loop repeat [IPR006603] (1)	-	C_unshiu_00644_mRNA_5.1	-
GF0038262	0	1	0	Plant cadmium resistance 2 (1)		PLAC8 motif-containing protein [IPR006461] (1)	-	C_unshiu_00644_mRNA_4.1	-
GF0038261	0	1	0	Defective in meristem silencing protein (1)			-	C_unshiu_00644_mRNA_3.1	-
GF0038260	0	1	0	Hypothetical protein (1)			-	C_unshiu_00644_mRNA_26.1	-
GF0038259	0	1	0	Hypothetical protein (1)	DNA repair [GO:0006281 biological_process] (1)	Fanconi anaemia protein FANCD2 [IPR029448] (1)	-	C_unshiu_00644_mRNA_25.1	-
GF0038258	0	1	0	Hypothetical protein (1)			-	C_unshiu_00644_mRNA_24.1	-
GF0038257	0	1	0	Transcription elongation factor A protein 2 (1)	zinc ion binding [GO:0008270 molecular_function] (1); transcription, DNA-templated [GO:0006351 biological_process] (1); DNA binding [GO:0003677 molecular_function] (1); nucleus [GO:0005634 cellular_component] (1); regulation of DNA-templated transcription, elongation [GO:0032784 biological_process] (1); regulation of transcription from RNA polymerase II promoter [GO:0006357 biological_process] (1)	Transcription elongation factor S-IIM [IPR017890] (1); Transcription factor IIS, N-terminal [IPR017923] (1); Transcription elongation factor, TFIIS/CRSP70, N-terminal, sub-type [IPR003617] (1); Transcription elongation factor, TFIIS-related [IPR016492] (1); Transcription elongation factor S-II, central domain [IPR003618] (1)	-	C_unshiu_00644_mRNA_1.1	-
GF0038256	0	1	0	Hypothetical protein (1)			-	C_unshiu_00643_mRNA_8.1	-
GF0038255	0	1	0	Hypothetical protein (1)			-	C_unshiu_00643_mRNA_5.1	-
GF0038254	0	1	0	Hypothetical protein (1)			-	C_unshiu_00643_mRNA_4.1	-
GF0038253	0	1	0	Hypothetical protein (1)			-	C_unshiu_00643_mRNA_3.1	-
GF0038252	0	1	0	Hypothetical protein (1)			-	C_unshiu_00643_mRNA_11.1	-
GF0038251	0	1	0	Hypothetical protein (1)			-	C_unshiu_00642_mRNA_15.1	-
GF0038250	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_00641_mRNA_8.1	-
GF0038249	0	1	0	Hypothetical protein (1)			-	C_unshiu_00641_mRNA_5.1	-
GF0038248	0	1	0	Hypothetical protein (1)			-	C_unshiu_00640_mRNA_9.1	-
GF0038247	0	1	0	Hypothetical protein (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Aspartic peptidase, active site [IPR001969] (1)	-	C_unshiu_00640_mRNA_6.1	-
GF0038246	0	1	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_00640_mRNA_4.1	-
GF0038245	0	1	0	Hypothetical protein (1)			-	C_unshiu_00640_mRNA_2.1	-
GF0038244	0	1	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	-	C_unshiu_00640_mRNA_14.1	-
GF0038243	0	1	0	Hypothetical protein (1)			-	C_unshiu_00639_mRNA_18.1	-
GF0038242	0	1	0	Hypothetical protein (1)			-	C_unshiu_00639_mRNA_17.1	-
GF0038241	0	1	0	Seven transmembrane MLO family protein (1)	defense response [GO:0006952 biological_process] (1); integral component of membrane [GO:0016021 cellular_component] (1)	Mlo-related protein [IPR004326] (1)	-	C_unshiu_00639_mRNA_1.1	-
GF0038240	0	1	0	Hypothetical protein (1)			-	C_unshiu_00637_mRNA_8.1	-
GF0038239	0	1	0	Hypothetical protein (1)			-	C_unshiu_00637_mRNA_6.1	-
GF0038238	0	1	0	Hypothetical protein (1)			-	C_unshiu_00637_mRNA_15.1	-
GF0038237	0	1	0	Hypothetical protein (1)			-	C_unshiu_00637_mRNA_11.1	-
GF0038236	0	1	0	Hypothetical protein (1)			-	C_unshiu_00636_mRNA_8.1	-
GF0038235	0	1	0	Hypothetical protein (1)		Arabidopsis retrotransposon Orf1 [IPR004312] (1)	-	C_unshiu_00636_mRNA_7.1	-
GF0038234	0	1	0	Hypothetical protein (1)			-	C_unshiu_00636_mRNA_5.1	-
GF0038233	0	1	0	Hypothetical protein (1)	metal ion binding [GO:0046872 molecular_function] (1)	Peptidase M16 domain [IPR011237] (1)	-	C_unshiu_00636_mRNA_4.1	-
GF0038232	0	1	0	NAC domain protein NAC74 (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); DNA binding [GO:0003677 molecular_function] (1)	NAC domain [IPR003441] (1)	-	C_unshiu_00636_mRNA_3.1	-
GF0038231	0	1	0	Hypothetical protein (1)			-	C_unshiu_00636_mRNA_2.1	-
GF0038230	0	1	0	Hypothetical protein (1)			-	C_unshiu_00636_mRNA_17.1	-
GF0038229	0	1	0	Hypothetical protein (1)			-	C_unshiu_00636_mRNA_15.1	-
GF0038228	0	1	0	Hypothetical protein (1)			-	C_unshiu_00636_mRNA_12.1	-
GF0038227	0	1	0	Hypothetical protein (1)			-	C_unshiu_00635_mRNA_9.1	-
GF0038226	0	1	0	Hypothetical protein (1)			-	C_unshiu_00635_mRNA_7.1	-
GF0038225	0	1	0	Hypothetical protein (1)			-	C_unshiu_00635_mRNA_6.1	-
GF0038224	0	1	0	Hypothetical protein (1)			-	C_unshiu_00635_mRNA_5.1	-
GF0038223	0	1	0	Hypothetical protein (1)			-	C_unshiu_00635_mRNA_18.1	-
GF0038222	0	1	0	Hypothetical protein (1)			-	C_unshiu_00635_mRNA_17.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0038221	0	1	0	Hypothetical protein (1)	heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Cytochrome P450 [IPR001128] (1)	-	C_unshiu_00634_mRNA_3.1	-
GF0038220	0	1	0	Hypothetical protein (1)	heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1)	Cytochrome P450 [IPR001128] (1); Cytochrome P450, conserved site [IPR017972] (1)	-	C_unshiu_00634_mRNA_2.1	-
GF0038219	0	1	0	Hypothetical protein (1)			-	C_unshiu_00634_mRNA_15.1	-
GF0038218	0	1	0	Hypothetical protein (1)	O-methyltransferase activity [GO:0008171 molecular_function] (1)	S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); O-methyltransferase, family 3 [IPR002935] (1)	-	C_unshiu_00634_mRNA_14.1	-
GF0038217	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00634_mRNA_12.1	-
GF0038216	0	1	0	LRR receptor-like kinase (1)		Protein kinase-like domain [IPR011009] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	-	C_unshiu_00634_mRNA_10.1	-
GF0038215	0	1	0	Reticuline oxidase-like protein (1)	flavin adenine dinucleotide binding [GO:0050660 molecular_function] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Berberine/berberine-like [IPR012951] (1)	-	C_unshiu_00634_mRNA_1.1	-
GF0038214	0	1	0	Hypothetical protein (1)	RNA processing [GO:0006396 biological_process] (1); protein binding [GO:0005515 molecular_function] (1)	Tetratricopeptide-like helical domain [IPR011990] (1); HAT (Half-A-TPR) repeat [IPR003107] (1)	-	C_unshiu_00633_mRNA_7.1	-
GF0038213	0	1	0	LRR and NB-ARC domain disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00633_mRNA_6.1	-
GF0038212	0	1	0	Hypothetical protein (1)		Alpha crystallin/Hsp20 domain [IPR002068] (1); HSP20-like chaperone [IPR008978] (1); Small heat shock protein HSP20 [IPR031107] (1)	-	C_unshiu_00633_mRNA_5.1	-
GF0038211	0	1	0	DNA (Cytosine-5)-methyltransferase 1 (1)	chromatin binding [GO:0003682 molecular_function] (1); methyltransferase activity [GO:0008168 molecular_function] (1)	S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); Chromo/chromo shadow domain [IPR000953] (1); C-5 cytosine methyltransferase [IPR001525] (1); Bromo adjacent homology (BAH) domain [IPR001025] (1); Chromo domain-like [IPR016197] (1); Chromo domain [IPR023780] (1)	-	C_unshiu_00633_mRNA_3.1	-
GF0038210	0	1	0	LRR and NB-ARC domain disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	C_unshiu_00633_mRNA_12.1	-
GF0038209	0	1	0	Hypothetical protein (1)			-	C_unshiu_00633_mRNA_1.1	-
GF0038208	0	1	0	Hypothetical protein (1)			-	C_unshiu_00632_mRNA_6.1	-
GF0038207	0	1	0	Hypothetical protein (1)			-	C_unshiu_00632_mRNA_3.1	-
GF0038206	0	1	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00632_mRNA_25.1	-
GF0038205	0	1	0	Hypothetical protein (1)			-	C_unshiu_00632_mRNA_21.1	-
GF0038204	0	1	0	Hypothetical protein (1)			-	C_unshiu_00632_mRNA_20.1	-
GF0038203	0	1	0	Hypothetical protein (1)			-	C_unshiu_00632_mRNA_19.1	-
GF0038202	0	1	0	Hypothetical protein (1)			-	C_unshiu_00632_mRNA_18.1	-
GF0038201	0	1	0	Hypothetical protein (1)			-	C_unshiu_00632_mRNA_17.1	-
GF0038200	0	1	0	Hypothetical protein (1)			-	C_unshiu_00632_mRNA_16.1	-
GF0038199	0	1	0	Hypothetical protein (1)			-	C_unshiu_00632_mRNA_15.1	-
GF0038198	0	1	0	Hypothetical protein (1)			-	C_unshiu_00632_mRNA_14.1	-
GF0038197	0	1	0	Hypothetical protein (1)			-	C_unshiu_00632_mRNA_13.1	-
GF0038196	0	1	0	Hypothetical protein (1)			-	C_unshiu_00632_mRNA_12.1	-
GF0038195	0	1	0	Hypothetical protein (1)			-	C_unshiu_00632_mRNA_1.1	-
GF0038194	0	1	0	Putative RNA-directed DNA polymerase (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1); Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_00631_mRNA_5.1	-
GF0038193	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1); Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	C_unshiu_00631_mRNA_4.1	-
GF0038192	0	1	0	TMV resistance protein N (1)	signal transduction [GO:0007165 biological_process] (1); protein binding [GO:0005515 molecular_function] (1)	Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1)	-	C_unshiu_00631_mRNA_3.1	-
GF0038191	0	1	0	Hypothetical protein (1)			-	C_unshiu_00631_mRNA_11.1	-
GF0038190	0	1	0	Hypothetical protein (1)	phosphatidylinositol binding [GO:0035091 molecular_function] (1)	Sorting nexin, C-terminal [IPR013937] (1); Phox homologous domain [IPR001683] (1); Phox-associated domain [IPR003114] (1); PX-associated, sorting nexin 13 [IPR013996] (1)	-	C_unshiu_00630_mRNA_22.1	-
GF0038189	0	1	0	Hypothetical protein (1)			-	C_unshiu_00630_mRNA_21.1	-
GF0038188	0	1	0	Hypothetical protein (1)			-	C_unshiu_00630_mRNA_19.1	-
GF0038187	0	1	0	Hypothetical protein (1)	structural constituent of cell wall [GO:0005199 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Pistil-specific extensin-like protein [IPR003882] (1)	-	C_unshiu_00630_mRNA_17.1	-
GF0038186	0	1	0	RING/FYVE/PHD zinc finger protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Zinc finger, PHD-type, conserved site [IPR019786] (1); Zinc finger, RING/FYVE/PHD-type [IPR013083] (1); Zinc finger, PHD-type [IPR001965] (1); Acyl-CoA N-acyltransferase [IPR016181] (1); Zinc finger, PHD-finger [IPR019787] (1); Zinc finger, FYVE/PHD-type [IPR011011] (1)	-	C_unshiu_00628_mRNA_22.1	-
GF0038185	0	1	0	Hypothetical protein (1)			-	C_unshiu_00628_mRNA_21.1	-
GF0038184	0	1	0	Hypothetical protein (1)			-	C_unshiu_00628_mRNA_19.1	-
GF0038183	0	1	0	Hypothetical protein (1)		Polycomb protein, VEFS-Box [IPR019135] (1)	-	C_unshiu_00628_mRNA_18.1	-
GF0038182	0	1	0	Hypothetical protein (1)			-	C_unshiu_00628_mRNA_17.1	-
GF0038181	0	1	0	Phospholipase A1 (1)	lipid metabolic process [GO:0006629 biological_process] (1)	Fungal lipase-like domain [IPR002921] (1); Alpha/Beta hydrolase fold [IPR029058] (1)	-	C_unshiu_00628_mRNA_16.1	-
GF0038180	0	1	0	Ras-like GTP-binding protein YPT1 (1)	membrane [GO:0016020 cellular_component] (1); small GTPase mediated signal transduction [GO:0007264 biological_process] (1); intracellular [GO:0005622 cellular_component] (1); GTP binding [GO:0005525 molecular_function] (1); signal transduction [GO:0007165 biological_process] (1); protein transport [GO:0015031 biological_process] (1)	Small GTPase superfamily, Rab type [IPR003579] (1); Small GTP-binding protein domain [IPR005225] (1); Small GTPase superfamily, Rho type [IPR003578] (1); Small GTPase superfamily [IPR001806] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Small GTPase superfamily, Ras type [IPR020849] (1)	-	C_unshiu_00628_mRNA_14.1	-
GF0038179	0	1	0	Expansin-like B1 (1)		RlpA-like double-psi beta-barrel domain [IPR009009] (1); Expansin, cellulose-binding-like domain [IPR007117] (1)	-	C_unshiu_00628_mRNA_1.1	-
GF0038178	0	1	0	Hypothetical protein (1)		Calcium/calmodulin-dependent/calcium-dependent protein kinase [IPR020636] (1)	-	C_unshiu_00627_mRNA_21.1	-
GF0038177	0	1	0	Hypothetical protein (1)			-	C_unshiu_00627_mRNA_18.1	-
GF0038176	0	1	0	Hypothetical protein (1)			-	C_unshiu_00627_mRNA_17.1	-
GF0038175	0	1	0	Hypothetical protein (1)			-	C_unshiu_00627_mRNA_11.1	-
GF0038174	0	1	0	Hypothetical protein (1)		P-type ATPase, transmembrane domain [IPR023298] (1)	-	C_unshiu_00626_mRNA_8.1	-
GF0038173	0	1	0	Hypothetical protein (1)			-	C_unshiu_00626_mRNA_6.1	-
GF0038172	0	1	0	Hypothetical protein (1)			-	C_unshiu_00626_mRNA_5.1	-
GF0038171	0	1	0	Hypothetical protein (1)			-	C_unshiu_00626_mRNA_3.1	-
GF0038170	0	1	0	Hypothetical protein (1)	magnesium ion binding [GO:0000287 molecular_function] (1); terpene synthase activity [GO:0010333 molecular_function] (1); lyase activity [GO:0016829 molecular_function] (1)	Isoprenoid synthase domain [IPR008949] (1); Terpene synthase, metal-binding domain [IPR005630] (1)	-	C_unshiu_00626_mRNA_16.1	-
GF0038169	0	1	0	(+)-delta-cadinene synthase isozyme A (1)	metabolic process [GO:0008152 biological_process] (1); magnesium ion binding [GO:0000287 molecular_function] (1); terpene synthase activity [GO:0010333 molecular_function] (1); lyase activity [GO:0016829 molecular_function] (1)	Terpene synthase, N-terminal domain [IPR001906] (1); Terpene synthase, metal-binding domain [IPR005630] (1); Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (1); Isoprenoid synthase domain [IPR008949] (1)	-	C_unshiu_00626_mRNA_14.1	-
GF0038168	0	1	0	Hypothetical protein (1)			-	C_unshiu_00626_mRNA_12.1	-
GF0038167	0	1	0	Hypothetical protein (1)	magnesium ion binding [GO:0000287 molecular_function] (1); lyase activity [GO:0016829 molecular_function] (1); terpene synthase activity [GO:0010333 molecular_function] (1)	Terpene synthase, metal-binding domain [IPR005630] (1); Isoprenoid synthase domain [IPR008949] (1)	-	C_unshiu_00626_mRNA_10.1	-
GF0038166	0	1	0	Hypothetical protein (1)			-	C_unshiu_00625_mRNA_5.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0038165	0	1	0	Pre-mRNA-processing factor 17 (1)	protein binding [GO:0005515 molecular_function] (1); catalytic step 2 spliceosome [GO:0071013 cellular_component] (1); mRNA splicing, via spliceosome [GO:0000398 biological_process] (1)	WD40/YVTN repeat-like-containing domain [IPR015943] (1); WD40 repeat, conserved site [IPR019775] (1); WD40-repeat-containing domain [IPR017986] (1); WD40 repeat [IPR001680] (1); Pre-mRNA-processing factor 17 [IPR032847] (1); G-protein beta WD-40 repeat [IPR020472] (1)	-	C_unshiu_00625_mRNA_4.1	-
GF0038164	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00625_mRNA_18.1	-
GF0038163	0	1	0	Hypothetical protein (1)	metal ion binding [GO:0046872 molecular_function] (1)	Zinc finger, CCCH-type [IPR000571] (1)	-	C_unshiu_00624_mRNA_9.1	-
GF0038162	0	1	0	Hypothetical protein (1)			-	C_unshiu_00624_mRNA_7.1	-
GF0038161	0	1	0	Hypothetical protein (1)			-	C_unshiu_00624_mRNA_4.1	-
GF0038160	0	1	0	BED zinc finger,hAT family dimerization domain (1)	nucleic acid binding [GO:0003676 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	Zinc finger, BED-type [IPR003656] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00624_mRNA_3.1	-
GF0038159	0	1	0	Hypothetical protein (1)	membrane [GO:0016020 cellular_component] (1)	ABC-2 type transporter [IPR013525] (1)	-	C_unshiu_00624_mRNA_2.1	-
GF0038158	0	1	0	Cytochrome P450 family ferulate hydroxylase (1)	iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Cytochrome P450 [IPR001128] (1)	-	C_unshiu_00624_mRNA_15.1	-
GF0038157	0	1	0	Hypothetical protein (1)			-	C_unshiu_00624_mRNA_1.1	-
GF0038156	0	1	0	Hypothetical protein (1)			-	C_unshiu_00623_mRNA_25.1	-
GF0038155	0	1	0	Hypothetical protein (1)			-	C_unshiu_00623_mRNA_24.1	-
GF0038154	0	1	0	Hypothetical protein (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1); asparagine synthase (glutamine-hydrolyzing) activity [GO:0004066 molecular_function] (1); asparagine biosynthetic process [GO:0006529 biological_process] (1)	Glycoside hydrolase, catalytic domain [IPR013781] (1); Rossmann-like alpha/beta/alpha sandwich fold [IPR014729] (1); Asparagine synthase [IPR001962] (1)	-	C_unshiu_00622_mRNA_13.1	-
GF0038153	0	1	0	Hypothetical protein (1)			-	C_unshiu_00621_mRNA_6.1	-
GF0038152	0	1	0	Hypothetical protein (1)			-	C_unshiu_00620_mRNA_9.1	-
GF0038151	0	1	0	TMV resistance N (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00620_mRNA_5.1	-
GF0038150	0	1	0	Aspartate kinase (1)	aspartate kinase activity [GO:0004072 molecular_function] (1); cellular amino acid metabolic process [GO:0006520 biological_process] (1); NADP binding [GO:0050661 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1); cellular amino acid biosynthetic process [GO:0008652 biological_process] (1); amino acid binding [GO:0016597 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1)	Homoserine dehydrogenase, catalytic [IPR001342] (1); Aspartate/glutamate/uridylate kinase [IPR001048] (1); Aspartate kinase, conserved site [IPR018042] (1); GATS-like ACT domain [IPR027795] (1); ACT domain [IPR002912] (1); Aspartate/homoserine dehydrogenase, NAD-binding [IPR005106] (1); Aspartate kinase domain [IPR001341] (1); Homoserine dehydrogenase, conserved site [IPR019811] (1); NAD(P)-binding domain [IPR016040] (1)	-	C_unshiu_00620_mRNA_4.1	-
GF0038149	0	1	0	Hypothetical protein (1)		Phosphate-induced protein 1 [IPR006766] (1)	-	C_unshiu_00619_mRNA_9.1	-
GF0038148	0	1	0	Hypothetical protein (1)	transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	-	C_unshiu_00619_mRNA_13.1	-
GF0038147	0	1	0	Hypothetical protein (1)			-	C_unshiu_00618_mRNA_9.1	-
GF0038146	0	1	0	Hypothetical protein (1)			-	C_unshiu_00618_mRNA_7.1	-
GF0038145	0	1	0	Hypothetical protein (1)			-	C_unshiu_00618_mRNA_26.1	-
GF0038144	0	1	0	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_00618_mRNA_17.1	-
GF0038143	0	1	0	Monosacharide transport protein (1)			-	C_unshiu_00618_mRNA_13.1	-
GF0038142	0	1	0	Hypothetical protein (1)			-	C_unshiu_00618_mRNA_12.1	-
GF0038141	0	1	0	Hypothetical protein (1)			-	C_unshiu_00617_mRNA_7.1	-
GF0038140	0	1	0	Hypothetical protein (1)		S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	C_unshiu_00617_mRNA_4.1	-
GF0038139	0	1	0	Hypothetical protein (1)			-	C_unshiu_00617_mRNA_25.1	-
GF0038138	0	1	0	Hypothetical protein (1)			-	C_unshiu_00617_mRNA_24.1	-
GF0038137	0	1	0	Hypothetical protein (1)			-	C_unshiu_00617_mRNA_23.1	-
GF0038136	0	1	0	Hypothetical protein (1)			-	C_unshiu_00617_mRNA_22.1	-
GF0038135	0	1	0	Hypothetical protein (1)			-	C_unshiu_00617_mRNA_21.1	-
GF0038134	0	1	0	Hypothetical protein (1)		Plant disease resistance response protein [IPR004265] (1)	-	C_unshiu_00617_mRNA_19.1	-
GF0038133	0	1	0	Hypothetical protein (1)		Plant disease resistance response protein [IPR004265] (1)	-	C_unshiu_00617_mRNA_18.1	-
GF0038132	0	1	0	Hypothetical protein (1)	iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Cytochrome P450 [IPR001128] (1)	-	C_unshiu_00617_mRNA_17.1	-
GF0038131	0	1	0	Hypothetical protein (1)			-	C_unshiu_00617_mRNA_13.1	-
GF0038130	0	1	0	TTF-type zinc finger protein with HAT dimerisation domain (1)		Zinc finger, TTF-type [IPR006580] (1); Domain of unknown function DUF4371 [IPR025398] (1)	-	C_unshiu_00617_mRNA_12.1	-
GF0038129	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_00617_mRNA_10.1	-
GF0038128	0	1	0	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 5 (1)		S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	C_unshiu_00617_mRNA_1.1	-
GF0038127	0	1	0	Hypothetical protein (1)			-	C_unshiu_00616_mRNA_8.1	-
GF0038126	0	1	0	Hypothetical protein (1)			-	C_unshiu_00616_mRNA_7.1	-
GF0038125	0	1	0	Disease resistance protein (CC-NBS-LRR class) family protein (1)	ADP binding [GO:0043531 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); AAA+ ATPase domain [IPR003593] (1); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00616_mRNA_6.1	-
GF0038124	0	1	0	Hypothetical protein (1)			-	C_unshiu_00616_mRNA_20.1	-
GF0038123	0	1	0	Hypothetical protein (1)			-	C_unshiu_00616_mRNA_17.1	-
GF0038122	0	1	0	Hypothetical protein (1)			-	C_unshiu_00616_mRNA_11.1	-
GF0038121	0	1	0	Hypothetical protein (1)			-	C_unshiu_00616_mRNA_10.1	-
GF0038120	0	1	0	Hypothetical protein (1)			-	C_unshiu_00615_mRNA_12.1	-
GF0038119	0	1	0	Hypothetical protein (1)			-	C_unshiu_00615_mRNA_10.1	-
GF0038118	0	1	0	Hypothetical protein (1)			-	C_unshiu_00615_mRNA_1.1	-
GF0038117	0	1	0	Hypothetical protein (1)			-	C_unshiu_00613_mRNA_9.1	-
GF0038116	0	1	0	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1); Reverse transcriptase domain [IPR000477] (1); Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_00613_mRNA_14.1	-
GF0038115	0	1	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_00613_mRNA_12.1	-
GF0038114	0	1	0	Hypothetical protein (1)			-	C_unshiu_00612_mRNA_9.1	-
GF0038113	0	1	0	Hypothetical protein (1)			-	C_unshiu_00612_mRNA_8.1	-
GF0038112	0	1	0	Hypothetical protein (1)			-	C_unshiu_00612_mRNA_7.1	-
GF0038111	0	1	0	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1)	Oxoglutarate/iron-dependent dioxygenase [IPR005123] (1); Isopenicillin N synthase-like [IPR027443] (1); Non-haem dioxygenase N-terminal domain [IPR026992] (1)	-	C_unshiu_00612_mRNA_5.1	-
GF0038110	0	1	0	Retrovirus-related Pol polyprotein from transposon TNT 1-94 (1)			-	C_unshiu_00612_mRNA_24.1	-
GF0038109	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00612_mRNA_21.1	-
GF0038108	0	1	0	Hypothetical protein (1)			-	C_unshiu_00612_mRNA_20.1	-
GF0038107	0	1	0	Hypothetical protein (1)			-	C_unshiu_00612_mRNA_2.1	-
GF0038106	0	1	0	Hypothetical protein (1)		Arabidopsis retrotransposon Orf1 [IPR004312] (1)	-	C_unshiu_00612_mRNA_17.1	-
GF0038105	0	1	0	Hypothetical protein (1)			-	C_unshiu_00612_mRNA_16.1	-
GF0038104	0	1	0	Hypothetical protein (1)			-	C_unshiu_00612_mRNA_13.1	-
GF0038103	0	1	0	G-type lectin S-receptor-like serine/threonine-protein kinase RLK1 (1)	recognition of pollen [GO:0048544 biological_process] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Protein kinase-like domain [IPR011009] (1); S-locus glycoprotein domain [IPR000858] (1); Protein kinase, ATP binding site [IPR017441] (1); PAN/Apple domain [IPR003609] (1); Bulb-type lectin domain [IPR001480] (1)	-	C_unshiu_00611_mRNA_19.1	-
GF0038102	0	1	0	Hypothetical protein (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1)	-	C_unshiu_00611_mRNA_17.1	-
GF0038101	0	1	0	Hypothetical protein (1)		Bulb-type lectin domain [IPR001480] (1)	-	C_unshiu_00611_mRNA_15.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0038100	0	1	0	G-type lectin S-receptor-like serine/threonine-protein kinase RLK1 (1)	ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase, ATP binding site [IPR017441] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1)	-	C_unshiu_00611_mRNA_14.1	-
GF0038099	0	1	0	Hypothetical protein (1)	recognition of pollen [GO:0048544 biological_process] (1)	S-locus glycoprotein domain [IPR000858] (1)	-	C_unshiu_00611_mRNA_12.1	-
GF0038098	0	1	0	Hypothetical protein (1)		Bulb-type lectin domain [IPR001480] (1)	-	C_unshiu_00611_mRNA_10.1	-
GF0038097	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Retropepsins [IPR018061] (1); Aspartic peptidase domain [IPR021109] (1); Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00610_mRNA_6.1	-
GF0038096	0	1	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1)	Aspartic peptidase, active site [IPR001969] (1); Peptidase A2A, retrovirus, catalytic [IPR001995] (1)	-	C_unshiu_00610_mRNA_5.1	-
GF0038095	0	1	0	Hypothetical protein (1)		Retroviral aspartyl protease [IPR013242] (1)	-	C_unshiu_00610_mRNA_2.1	-
GF0038094	0	1	0	Hypothetical protein (1)			-	C_unshiu_00610_mRNA_10.1	-
GF0038093	0	1	0	Hypothetical protein (1)			-	C_unshiu_00610_mRNA_1.1	-
GF0038092	0	1	0	Hypothetical protein (1)			-	C_unshiu_00609_mRNA_9.1	-
GF0038091	0	1	0	Hypothetical protein (1)			-	C_unshiu_00609_mRNA_3.1	-
GF0038090	0	1	0	Trichome birefringence-like protein (1)		PC-Esterase [IPR026057] (1); Trichome birefringence-like family [IPR029962] (1)	-	C_unshiu_00609_mRNA_12.1	-
GF0038089	0	1	0	B3 DNA-binding domain protein (1)	DNA binding [GO:0003677 molecular_function] (1)	B3 DNA binding domain [IPR003340] (1); DNA-binding pseudobarrel domain [IPR015300] (1)	-	C_unshiu_00609_mRNA_1.1	-
GF0038088	0	1	0	Hypothetical protein (1)			-	C_unshiu_00608_mRNA_4.1	-
GF0038087	0	1	0	Hypothetical protein (1)			-	C_unshiu_00608_mRNA_3.1	-
GF0038086	0	1	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	Zinc finger, BED-type [IPR003656] (1)	-	C_unshiu_00608_mRNA_2.1	-
GF0038085	0	1	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); O-methyltransferase activity [GO:0008171 molecular_function] (1); methyltransferase activity [GO:0008168 molecular_function] (1)	S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); O-methyltransferase, family 2 [IPR001077] (1); Plant methyltransferase dimerisation [IPR012967] (1); O-methyltransferase COMT-type [IPR016461] (1)	-	C_unshiu_00607_mRNA_6.1	-
GF0038084	0	1	0	Caffeic acid 3-O-methyltransferase (1)	O-methyltransferase activity [GO:0008171 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	O-methyltransferase, family 2 [IPR001077] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Plant methyltransferase dimerisation [IPR012967] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	C_unshiu_00607_mRNA_5.1	-
GF0038083	0	1	0	Hypothetical protein (1)			-	C_unshiu_00607_mRNA_4.1	-
GF0038082	0	1	0	Hypothetical protein (1)			-	C_unshiu_00607_mRNA_24.1	-
GF0038081	0	1	0	Hypothetical protein (1)			-	C_unshiu_00607_mRNA_21.1	-
GF0038080	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	C_unshiu_00607_mRNA_16.1	-
GF0038079	0	1	0	Hypothetical protein (1)		Thioredoxin-like fold [IPR012336] (1)	-	C_unshiu_00607_mRNA_12.1	-
GF0038078	0	1	0	Hypothetical protein (1)			-	C_unshiu_00607_mRNA_10.1	-
GF0038077	0	1	0	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); flavin adenine dinucleotide binding [GO:0050660 molecular_function] (1)	Berberine/berberine-like [IPR012951] (1)	-	C_unshiu_00606_mRNA_9.1	-
GF0038076	0	1	0	FAD-binding Berberine family protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); flavin adenine dinucleotide binding [GO:0050660 molecular_function] (1); oxidoreductase activity, acting on CH-OH group of donors [GO:0016614 molecular_function] (1); catalytic activity [GO:0003824 molecular_function] (1)	CO dehydrogenase flavoprotein-like, FAD-binding, subdomain 2 [IPR016169] (1); FAD-binding, type 2, subdomain 1 [IPR016167] (1); FAD-binding, type 2 [IPR016166] (1); FAD linked oxidase, N-terminal [IPR006094] (1)	-	C_unshiu_00606_mRNA_8.1	-
GF0038075	0	1	0	Hypothetical protein (1)		P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00605_mRNA_9.1	-
GF0038074	0	1	0	Hypothetical protein (1)			-	C_unshiu_00605_mRNA_8.1	-
GF0038073	0	1	0	Hypothetical protein (1)			-	C_unshiu_00605_mRNA_7.1	-
GF0038072	0	1	0	Hypothetical protein (1)			-	C_unshiu_00605_mRNA_6.1	-
GF0038071	0	1	0	Hypothetical protein (1)		Neurochondrin [IPR008709] (1)	-	C_unshiu_00605_mRNA_3.1	-
GF0038070	0	1	0	Hypothetical protein (1)			-	C_unshiu_00605_mRNA_2.1	-
GF0038069	0	1	0	Hypothetical protein (1)			-	C_unshiu_00605_mRNA_19.1	-
GF0038068	0	1	0	Hypothetical protein (1)			-	C_unshiu_00605_mRNA_14.1	-
GF0038067	0	1	0	Hypothetical protein (1)			-	C_unshiu_00605_mRNA_13.1	-
GF0038066	0	1	0	Hypothetical protein (1)			-	C_unshiu_00605_mRNA_12.1	-
GF0038065	0	1	0	Hypothetical protein (1)			-	C_unshiu_00605_mRNA_10.1	-
GF0038064	0	1	0	Hypothetical protein (1)			-	C_unshiu_00604_mRNA_3.1	-
GF0038063	0	1	0	Hypothetical protein (1)			-	C_unshiu_00604_mRNA_12.1	-
GF0038062	0	1	0	Hypothetical protein (1)			-	C_unshiu_00604_mRNA_1.1	-
GF0038061	0	1	0	Hypothetical protein (1)		Transcription factor BREVIS RADIX, N-terminal domain [IPR027988] (1); PH domain-like [IPR011993] (1); Pleckstrin homology domain [IPR001849] (1); Brevis radix (BRX) domain [IPR013591] (1)	-	C_unshiu_00603_mRNA_2.1	-
GF0038060	0	1	0	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	C_unshiu_00602_mRNA_6.1	-
GF0038059	0	1	0	Hypothetical protein (1)			-	C_unshiu_00602_mRNA_5.1	-
GF0038058	0	1	0	Hypothetical protein (1)			-	C_unshiu_00602_mRNA_16.1	-
GF0038057	0	1	0	Hypothetical protein (1)			-	C_unshiu_00602_mRNA_14.1	-
GF0038056	0	1	0	Pentatricopeptide repeat-containing protein, chloroplastic (1)		Pentatricopeptide repeat [IPR002885] (1)	-	C_unshiu_00602_mRNA_12.1	-
GF0038055	0	1	0	Hypothetical protein (1)	integral component of membrane [GO:0016021 cellular_component] (1)	P-type ATPase [IPR001757] (1); P-type ATPase, transmembrane domain [IPR023298] (1); HAD-like domain [IPR023214] (1)	-	C_unshiu_00601_mRNA_3.1	-
GF0038054	0	1	0	Hypothetical protein (1)			-	C_unshiu_00601_mRNA_2.1	-
GF0038053	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	WD40-repeat-containing domain [IPR017986] (1); WD40/YVTN repeat-like-containing domain [IPR015943] (1)	-	C_unshiu_00601_mRNA_19.1	-
GF0038052	0	1	0	Hypothetical protein (1)			-	C_unshiu_00601_mRNA_16.1	-
GF0038051	0	1	0	Heavy metal ATPase transporter (1)	metal ion binding [GO:0046872 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1); nucleotide binding [GO:0000166 molecular_function] (1); metal ion transport [GO:0030001 biological_process] (1)	HAD-like domain [IPR023214] (1); P-type ATPase, A domain [IPR008250] (1); Heavy metal-associated domain, HMA [IPR006121] (1); P-type ATPase, phosphorylation site [IPR018303] (1); P-type ATPase, cytoplasmic domain N [IPR023299] (1); P-type ATPase, transmembrane domain [IPR023298] (1); P-type ATPase [IPR001757] (1)	-	C_unshiu_00601_mRNA_12.1	-
GF0038050	0	1	0	Flavonoid 3',5'-hydroxylase (1)	iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1)	Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450, conserved site [IPR017972] (1); Cytochrome P450 [IPR001128] (1)	-	C_unshiu_00601_mRNA_11.1	-
GF0038049	0	1	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	-	C_unshiu_00601_mRNA_1.1	-
GF0038048	0	1	0	Hypothetical protein (1)			-	C_unshiu_00600_mRNA_9.1	-
GF0038047	0	1	0	Hypothetical protein (1)			-	C_unshiu_00600_mRNA_24.1	-
GF0038046	0	1	0	Hypothetical protein (1)			-	C_unshiu_00600_mRNA_22.1	-
GF0038045	0	1	0	Hypothetical protein (1)			-	C_unshiu_00600_mRNA_2.1	-
GF0038044	0	1	0	Hypothetical protein (1)			-	C_unshiu_00600_mRNA_12.1	-
GF0038043	0	1	0	Hypothetical protein (1)			-	C_unshiu_00600_mRNA_11.1	-
GF0038042	0	1	0	Hypothetical protein (1)			-	C_unshiu_00600_mRNA_10.1	-
GF0038041	0	1	0	Hypothetical protein (1)			-	C_unshiu_00600_mRNA_1.1	-
GF0038040	0	1	0	Hypothetical protein (1)	microtubule [GO:0005874 cellular_component] (1); microtubule-based process [GO:0007017 biological_process] (1)	Tubulin [IPR000217] (1); Tubulin/FtsZ, 2-layer sandwich domain [IPR018316] (1); Tubulin/FtsZ, C-terminal [IPR008280] (1)	-	C_unshiu_00599_mRNA_8.1	-
GF0038039	0	1	0	Hypothetical protein (1)			-	C_unshiu_00599_mRNA_25.1	-
GF0038038	0	1	0	Hypothetical protein (1)			-	C_unshiu_00599_mRNA_23.1	-
GF0038037	0	1	0	Hypothetical protein (1)	transmembrane transporter activity [GO:0022857 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1); transmembrane transport [GO:0055085 biological_process] (1); transporter activity [GO:0005215 molecular_function] (1)	Major facilitator superfamily domain [IPR020846] (1); Sugar transporter, conserved site [IPR005829] (1); Major facilitator, sugar transporter-like [IPR005828] (1)	-	C_unshiu_00599_mRNA_22.1	-
GF0038036	0	1	0	Hypothetical protein (1)			-	C_unshiu_00599_mRNA_2.1	-
GF0038035	0	1	0	Hypothetical protein (1)			-	C_unshiu_00599_mRNA_1.1	-
GF0038034	0	1	0	Hypothetical protein (1)			-	C_unshiu_00598_mRNA_3.1	-
GF0038033	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	C_unshiu_00598_mRNA_2.1	-
GF0038032	0	1	0	Hypothetical protein (1)			-	C_unshiu_00598_mRNA_14.1	-
GF0038031	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00598_mRNA_10.1	-
GF0038030	0	1	0	Hypothetical protein (1)			-	C_unshiu_00598_mRNA_1.1	-
GF0038029	0	1	0	Hypothetical protein (1)			-	C_unshiu_00597_mRNA_8.1	-
GF0038028	0	1	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1)	-	C_unshiu_00597_mRNA_5.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0038027	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00597_mRNA_2.1	-
GF0038026	0	1	0	Hypothetical protein (1)			-	C_unshiu_00597_mRNA_12.1	-
GF0038025	0	1	0	Hypothetical protein (1)			-	C_unshiu_00597_mRNA_10.1	-
GF0038024	0	1	0	Hypothetical protein (1)		Histone-binding protein RBBP4, N-terminal [IPR022052] (1)	-	C_unshiu_00596_mRNA_7.1	-
GF0038023	0	1	0	Hypothetical protein (1)			-	C_unshiu_00596_mRNA_17.1	-
GF0038022	0	1	0	Caffeic acid O-methyltransferase (1)	protein dimerization activity [GO:0046983 molecular_function] (1); O-methyltransferase activity [GO:0008171 molecular_function] (1); methyltransferase activity [GO:0008168 molecular_function] (1)	Winged helix-turn-helix DNA-binding domain [IPR011991] (1); O-methyltransferase, family 2 [IPR001077] (1); O-methyltransferase COMT-type [IPR016461] (1); Plant methyltransferase dimerisation [IPR012967] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); SH2 domain [IPR000980] (1)	-	C_unshiu_00596_mRNA_15.1	-
GF0038021	0	1	0	Hypothetical protein (1)			-	C_unshiu_00595_mRNA_25.1	-
GF0038020	0	1	0	Hypothetical protein (1)			-	C_unshiu_00595_mRNA_23.1	-
GF0038019	0	1	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	C_unshiu_00595_mRNA_21.1	-
GF0038018	0	1	0	Hypothetical protein (1)			-	C_unshiu_00595_mRNA_17.1	-
GF0038017	0	1	0	Transmembrane proteins 14C (1)	membrane [GO:0016020 cellular_component] (1)	TMEM14 family [IPR005349] (1)	-	C_unshiu_00595_mRNA_12.1	-
GF0038016	0	1	0	Hypothetical protein (1)			-	C_unshiu_00594_mRNA_3.1	-
GF0038015	0	1	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1)	-	C_unshiu_00594_mRNA_11.1	-
GF0038014	0	1	0	Hypothetical protein (1)			-	C_unshiu_00593_mRNA_4.1	-
GF0038013	0	1	0	Hypothetical protein (1)	proton-transporting ATP synthase complex, coupling factor F(o) [GO:0045263 cellular_component] (1); hydrogen ion transmembrane transporter activity [GO:0015078 molecular_function] (1); ATP synthesis coupled proton transport [GO:0015986 biological_process] (1)	ATPase, F0 complex, subunit C [IPR000454] (1)	-	C_unshiu_00593_mRNA_2.1	-
GF0038012	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00593_mRNA_11.1	-
GF0038011	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1); Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_00593_mRNA_1.1	-
GF0038010	0	1	0	Hypothetical protein (1)			-	C_unshiu_00592_mRNA_5.1	-
GF0038009	0	1	0	Hypothetical protein (1)			-	C_unshiu_00591_mRNA_9.1	-
GF0038008	0	1	0	Hypothetical protein (1)			-	C_unshiu_00591_mRNA_7.1	-
GF0038007	0	1	0	Hypothetical protein (1)			-	C_unshiu_00591_mRNA_3.1	-
GF0038006	0	1	0	Elongation factor EF-2 (1)	GTP binding [GO:0005525 molecular_function] (1)	Ribosomal protein S5 domain 2-type fold [IPR020568] (1); Elongation factor G, III-V domain [IPR009022] (1); Translation elongation factor EFTu/EF1A, domain 2 [IPR004161] (1); Ribosomal protein S5 domain 2-type fold, subgroup [IPR014721] (1); Translation elongation factor EFG/EF2, domain IV [IPR005517] (1); Translation protein, beta-barrel domain [IPR009000] (1); Translation elongation factor EFG, V domain [IPR000640] (1)	-	C_unshiu_00591_mRNA_15.2	-
GF0038005	0	1	0	Hypothetical protein (1)			-	C_unshiu_00591_mRNA_10.1	-
GF0038004	0	1	0	Calcineurin-like metallo-phosphoesterase superfamily protein isoform 1 (1)	hydrolase activity [GO:0016787 molecular_function] (1)	Calcineurin-like phosphoesterase domain, apaH type [IPR004843] (1); Metallo-dependent phosphatase-like [IPR029052] (1); Conserved hypothetical protein CHP04168 [IPR027629] (1)	-	C_unshiu_00590_mRNA_8.1	-
GF0038003	0	1	0	Type B response regulator (1)	signal transduction [GO:0007165 biological_process] (1); transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (1); phosphorelay signal transduction system [GO:0000160 biological_process] (1); DNA binding [GO:0003677 molecular_function] (1)	Myb domain [IPR017930] (1); Myb domain, plants [IPR006447] (1); SANT/Myb domain [IPR001005] (1); Homeodomain-like [IPR009057] (1); Signal transduction response regulator, receiver domain [IPR001789] (1); CheY-like superfamily [IPR011006] (1); Response regulator B-type, plant [IPR017053] (1)	-	C_unshiu_00590_mRNA_6.1	-
GF0038002	0	1	0	Temperature-induced lipocalin (1)		Calycin [IPR012674] (1); Lipocalin/cytosolic fatty-acid binding domain [IPR000566] (1); Calycin-like [IPR011038] (1); Lipocalin family conserved site [IPR022272] (1)	-	C_unshiu_00590_mRNA_3.1	-
GF0038001	0	1	0	VAMP-like protein YKT61 (1)	transport [GO:0006810 biological_process] (1); integral component of membrane [GO:0016021 cellular_component] (1); vesicle-mediated transport [GO:0016192 biological_process] (1)	Longin domain [IPR010908] (1); Longin-like domain [IPR011012] (1); Synaptobrevin [IPR001388] (1)	-	C_unshiu_00590_mRNA_2.1	-
GF0038000	0	1	0	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	C_unshiu_00590_mRNA_18.1	-
GF0037999	0	1	0	Eukaryotic translation initiation factor 5A (1)	RNA binding [GO:0003723 molecular_function] (1); translational frameshifting [GO:0006452 biological_process] (1); ribosome binding [GO:0043022 molecular_function] (1); translation elongation factor activity [GO:0003746 molecular_function] (1); positive regulation of translational termination [GO:0045905 biological_process] (1); positive regulation of translational elongation [GO:0045901 biological_process] (1)	Translation protein SH3-like domain [IPR008991] (1); Translation elongation factor, IF5A, hypusine site [IPR019769] (1); Nucleic acid-binding, OB-fold [IPR012340] (1); Ribosomal protein L2 domain 2 [IPR014722] (1); Translation elongation factor IF5A [IPR001884] (1); Translation elongation factor, IF5A C-terminal [IPR020189] (1)	-	C_unshiu_00590_mRNA_13.1	-
GF0037998	0	1	0	Hypothetical protein (1)	phosphoric diester hydrolase activity [GO:0008081 molecular_function] (1); lipid metabolic process [GO:0006629 biological_process] (1)	Glycerophosphodiester phosphodiesterase domain [IPR030395] (1); PLC-like phosphodiesterase, TIM beta/alpha-barrel domain [IPR017946] (1)	-	C_unshiu_00590_mRNA_1.1	-
GF0037997	0	1	0	Polygalacturonase inhibitor (PGIP) (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00589_mRNA_8.1	-
GF0037996	0	1	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Protein kinase-like domain [IPR011009] (1); Alpha/beta hydrolase fold-1 [IPR000073] (1); Alpha/Beta hydrolase fold [IPR029058] (1); Protein kinase domain [IPR000719] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Protein kinase, ATP binding site [IPR017441] (1); Serine/threonine-protein kinase, active site [IPR008271] (1)	-	C_unshiu_00589_mRNA_6.1	-
GF0037995	0	1	0	Hypothetical protein (1)			-	C_unshiu_00589_mRNA_5.1	-
GF0037994	0	1	0	PPR containing plant-like protein (1)	protein binding [GO:0005515 molecular_function] (1); endonuclease activity [GO:0004519 molecular_function] (1)	Homing endonuclease, LAGLIDADG [IPR004860] (1); Pentatricopeptide repeat [IPR002885] (1); SWIB/MDM2 domain [IPR003121] (1); SWIB domain [IPR019835] (1); Homing endonuclease [IPR027434] (1); Tetratricopeptide-like helical domain [IPR011990] (1)	-	C_unshiu_00589_mRNA_3.1	-
GF0037993	0	1	0	Sorting nexin carboxy-terminal protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); phosphatidylinositol binding [GO:0035091 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Zinc finger, SWIM-type [IPR007527] (1); Sorting nexin, C-terminal [IPR013937] (1); Phox homologous domain [IPR001683] (1); Zinc finger, PMZ-type [IPR006564] (1)	-	C_unshiu_00589_mRNA_13.1	-
GF0037992	0	1	0	Hypothetical protein (1)			-	C_unshiu_00588_mRNA_9.1	-
GF0037991	0	1	0	Hypothetical protein (1)			-	C_unshiu_00588_mRNA_17.1	-
GF0037990	0	1	0	Putative RNA-directed DNA polymerase (1)			-	C_unshiu_00588_mRNA_14.1	-
GF0037989	0	1	0	Hypothetical protein (1)			-	C_unshiu_00587_mRNA_8.1	-
GF0037988	0	1	0	Hypothetical protein (1)			-	C_unshiu_00587_mRNA_5.1	-
GF0037987	0	1	0	Hypothetical protein (1)			-	C_unshiu_00587_mRNA_18.1	-
GF0037986	0	1	0	Hypothetical protein (1)			-	C_unshiu_00587_mRNA_11.1	-
GF0037985	0	1	0	Hypothetical protein (1)			-	C_unshiu_00586_mRNA_19.1	-
GF0037984	0	1	0	Hypothetical protein (1)			-	C_unshiu_00586_mRNA_18.1	-
GF0037983	0	1	0	Hypothetical protein (1)			-	C_unshiu_00586_mRNA_17.1	-
GF0037982	0	1	0	Hypothetical protein (1)		Glutamine amidotransferase type 2 domain [IPR017932] (1); Nucleophile aminohydrolases, N-terminal [IPR029055] (1)	-	C_unshiu_00586_mRNA_15.1	-
GF0037981	0	1	0	Hypothetical protein (1)			-	C_unshiu_00586_mRNA_12.1	-
GF0037980	0	1	0	Hypothetical protein (1)			-	C_unshiu_00586_mRNA_1.1	-
GF0037979	0	1	0	Hypothetical protein (1)			-	C_unshiu_00585_mRNA_31.1	-
GF0037978	0	1	0	Putative WRKY transcription factor 19 (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00585_mRNA_29.1	-
GF0037977	0	1	0	NBS type disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	Leucine-rich repeat 3 [IPR011713] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	C_unshiu_00585_mRNA_26.1	-
GF0037976	0	1	0	Hypothetical protein (1)			-	C_unshiu_00585_mRNA_24.1	-
GF0037975	0	1	0	Hypothetical protein (1)			-	C_unshiu_00585_mRNA_23.1	-
GF0037974	0	1	0	Hypothetical protein (1)			-	C_unshiu_00585_mRNA_22.1	-
GF0037973	0	1	0	Hypothetical protein (1)			-	C_unshiu_00585_mRNA_2.1	-
GF0037972	0	1	0	Hypothetical protein (1)			-	C_unshiu_00585_mRNA_19.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0037971	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat [IPR002110] (1); Gag-polypeptide of LTR copia-type [IPR029472] (1); Ankyrin repeat-containing domain [IPR020683] (1)	-	C_unshiu_00585_mRNA_18.1	-
GF0037970	0	1	0	Hypothetical protein (1)			-	C_unshiu_00585_mRNA_16.1	-
GF0037969	0	1	0	Putative calcium-binding protein CML30 (1)	calcium ion binding [GO:0005509 molecular_function] (1)	EF-Hand 1, calcium-binding site [IPR018247] (1); EF-hand domain [IPR002048] (1); EF-hand domain pair [IPR011992] (1)	-	C_unshiu_00585_mRNA_14.1	-
GF0037968	0	1	0	Putative WRKY transcription factor 19-like protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat 3 [IPR011713] (1)	-	C_unshiu_00585_mRNA_11.1	-
GF0037967	0	1	0	Hypothetical protein (1)			-	C_unshiu_00584_mRNA_5.1	-
GF0037966	0	1	0	Hypothetical protein (1)			-	C_unshiu_00584_mRNA_4.1	-
GF0037965	0	1	0	Hypothetical protein (1)			-	C_unshiu_00584_mRNA_30.1	-
GF0037964	0	1	0	Hypothetical protein (1)			-	C_unshiu_00584_mRNA_29.1	-
GF0037963	0	1	0	Hypothetical protein (1)			-	C_unshiu_00584_mRNA_28.1	-
GF0037962	0	1	0	Hypothetical protein (1)			-	C_unshiu_00584_mRNA_27.1	-
GF0037961	0	1	0	Hypothetical protein (1)			-	C_unshiu_00584_mRNA_25.1	-
GF0037960	0	1	0	Hypothetical protein (1)			-	C_unshiu_00584_mRNA_23.1	-
GF0037959	0	1	0	Hypothetical protein (1)			-	C_unshiu_00584_mRNA_21.1	-
GF0037958	0	1	0	Hypothetical protein (1)	translation [GO:0006412 biological_process] (1); intracellular [GO:0005622 cellular_component] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1); ribosome [GO:0005840 cellular_component] (1)	Ribosomal protein S30 [IPR006846] (1)	-	C_unshiu_00584_mRNA_17.1	-
GF0037957	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	F-box domain [IPR001810] (1)	-	C_unshiu_00584_mRNA_11.1	-
GF0037956	0	1	0	Hypothetical protein (1)	structural constituent of ribosome [GO:0003735 molecular_function] (1); intracellular [GO:0005622 cellular_component] (1); translation [GO:0006412 biological_process] (1); ribosome [GO:0005840 cellular_component] (1)	Ribosomal protein L2 domain 2 [IPR014722] (1); Ribosomal protein L14 [IPR002784] (1)	-	C_unshiu_00583_mRNA_4.1	-
GF0037955	0	1	0	Hypothetical protein (1)			-	C_unshiu_00583_mRNA_1.1	-
GF0037954	0	1	0	Hypothetical protein (1)			-	C_unshiu_00582_mRNA_9.1	-
GF0037953	0	1	0	Hypothetical protein (1)			-	C_unshiu_00582_mRNA_8.1	-
GF0037952	0	1	0	Hypothetical protein (1)			-	C_unshiu_00582_mRNA_34.1	-
GF0037951	0	1	0	Hypothetical protein (1)			-	C_unshiu_00582_mRNA_32.1	-
GF0037950	0	1	0	Hypothetical protein (1)			-	C_unshiu_00582_mRNA_29.1	-
GF0037949	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF861, cupin-3 [IPR008579] (1); RmlC-like cupin domain [IPR011051] (1); RmlC-like jelly roll fold [IPR014710] (1)	-	C_unshiu_00582_mRNA_22.1	-
GF0037948	0	1	0	Hypothetical protein (1)			-	C_unshiu_00582_mRNA_12.1	-
GF0037947	0	1	0	Hypothetical protein (1)			-	C_unshiu_00582_mRNA_10.1	-
GF0037946	0	1	0	Hypothetical protein (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Isopenicillin N synthase-like [IPR027443] (1); Oxoglutarate/iron-dependent dioxygenase [IPR005123] (1)	-	C_unshiu_00582_mRNA_1.1	-
GF0037945	0	1	0	Leucine-rich repeat, plant specific (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_00581_mRNA_7.1	-
GF0037944	0	1	0	Hypothetical protein (1)			-	C_unshiu_00581_mRNA_25.1	-
GF0037943	0	1	0	Hypothetical protein (1)			-	C_unshiu_00581_mRNA_21.1	-
GF0037942	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			-	C_unshiu_00581_mRNA_20.1	-
GF0037941	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00581_mRNA_2.1	-
GF0037940	0	1	0	Hypothetical protein (1)			-	C_unshiu_00581_mRNA_19.1	-
GF0037939	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00581_mRNA_13.1	-
GF0037938	0	1	0	BSD domain-containing protein, putative isoform 2 (1)			-	C_unshiu_00580_mRNA_7.1	-
GF0037937	0	1	0	Hypothetical protein (1)			-	C_unshiu_00580_mRNA_22.1	-
GF0037936	0	1	0	Hypothetical protein (1)			-	C_unshiu_00580_mRNA_20.1	-
GF0037935	0	1	0	Hypothetical protein (1)		mRNA splicing factor SYF2 [IPR013260] (1)	-	C_unshiu_00580_mRNA_13.1	-
GF0037934	0	1	0	Hypothetical protein (1)			-	C_unshiu_00579_mRNA_5.1	-
GF0037933	0	1	0	Hypothetical protein (1)			-	C_unshiu_00579_mRNA_15.1	-
GF0037932	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	-	C_unshiu_00579_mRNA_14.1	-
GF0037931	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00578_mRNA_5.1	-
GF0037930	0	1	0	Hypothetical protein (1)			-	C_unshiu_00578_mRNA_3.1	-
GF0037929	0	1	0	Hypothetical protein (1)			-	C_unshiu_00578_mRNA_11.1	-
GF0037928	0	1	0	Short chain alcohol dehydrogenase, putative (1)	metabolic process [GO:0008152 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1)	NAD(P)-binding domain [IPR016040] (1); Glucose/ribitol dehydrogenase [IPR002347] (1); Short-chain dehydrogenase/reductase SDR [IPR002198] (1)	-	C_unshiu_00578_mRNA_10.1	-
GF0037927	0	1	0	Ankyrin repeat plant-like protein (1)	protein binding [GO:0005515 molecular_function] (1)	PGG domain [IPR026961] (1); Ankyrin repeat-containing domain [IPR020683] (1); Ankyrin repeat [IPR002110] (1)	-	C_unshiu_00577_mRNA_4.1	-
GF0037926	0	1	0	Serine esterase family protein (1)	glycolytic process [GO:0006096 biological_process] (1); 6-phosphofructokinase activity [GO:0003872 molecular_function] (1)	Domain of unknown function DUF676, lipase-like [IPR007751] (1); Phosphofructokinase domain [IPR000023] (1); Alpha/Beta hydrolase fold [IPR029058] (1)	-	C_unshiu_00577_mRNA_3.1	-
GF0037925	0	1	0	Hypothetical protein (1)			-	C_unshiu_00577_mRNA_13.1	-
GF0037924	0	1	0	F-box protein At5g07610 (1)			-	C_unshiu_00577_mRNA_10.1	-
GF0037923	0	1	0	Hypothetical protein (1)			-	C_unshiu_00576_mRNA_26.1	-
GF0037922	0	1	0	Hypothetical protein (1)			-	C_unshiu_00576_mRNA_22.1	-
GF0037921	0	1	0	Ankyrin repeat protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat-containing domain [IPR020683] (1); Ankyrin repeat [IPR002110] (1)	-	C_unshiu_00576_mRNA_21.1	-
GF0037920	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00576_mRNA_19.1	-
GF0037919	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	PGG domain [IPR026961] (1); Ankyrin repeat-containing domain [IPR020683] (1); Ankyrin repeat [IPR002110] (1)	-	C_unshiu_00576_mRNA_14.1	-
GF0037918	0	1	0	Hypothetical protein (1)			-	C_unshiu_00576_mRNA_13.1	-
GF0037917	0	1	0	Hypothetical protein (1)			-	C_unshiu_00576_mRNA_12.1	-
GF0037916	0	1	0	Hypothetical protein (1)			-	C_unshiu_00575_mRNA_4.1	-
GF0037915	0	1	0	Terpene synthase 21, putative isoform 3 (1)	lyase activity [GO:0016829 molecular_function] (1); terpene synthase activity [GO:0010333 molecular_function] (1); magnesium ion binding [GO:0000287 molecular_function] (1)	Terpene synthase, metal-binding domain [IPR005630] (1); Isoprenoid synthase domain [IPR008949] (1)	-	C_unshiu_00575_mRNA_19.1	-
GF0037914	0	1	0	Sesquiterpene synthase (1)	metabolic process [GO:0008152 biological_process] (1); magnesium ion binding [GO:0000287 molecular_function] (1); terpene synthase activity [GO:0010333 molecular_function] (1); lyase activity [GO:0016829 molecular_function] (1)	Isoprenoid synthase domain [IPR008949] (1); Terpene synthase, N-terminal domain [IPR001906] (1); Terpene synthase, metal-binding domain [IPR005630] (1); Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (1)	-	C_unshiu_00575_mRNA_18.1	-
GF0037913	0	1	0	Hypothetical protein (1)			-	C_unshiu_00574_mRNA_9.1	-
GF0037912	0	1	0	No apical meristem family protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); DNA binding [GO:0003677 molecular_function] (1)	NAC domain [IPR003441] (1)	-	C_unshiu_00574_mRNA_8.1	-
GF0037911	0	1	0	Hypothetical protein (1)			-	C_unshiu_00574_mRNA_6.1	-
GF0037910	0	1	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	NAC domain [IPR003441] (1)	-	C_unshiu_00574_mRNA_4.1	-
GF0037909	0	1	0	Hypothetical protein (1)			-	C_unshiu_00574_mRNA_23.1	-
GF0037908	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00574_mRNA_22.1	-
GF0037907	0	1	0	Hypothetical protein (1)			-	C_unshiu_00574_mRNA_21.1	-
GF0037906	0	1	0	Hypothetical protein (1)			-	C_unshiu_00574_mRNA_2.1	-
GF0037905	0	1	0	Hypothetical protein (1)			-	C_unshiu_00574_mRNA_17.1	-
GF0037904	0	1	0	LRR receptor-like serine/threonine-protein kinase ERECTA (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_00574_mRNA_11.1	-
GF0037903	0	1	0	NAC domain-containing protein 29 (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); DNA binding [GO:0003677 molecular_function] (1)	NAC domain [IPR003441] (1)	-	C_unshiu_00574_mRNA_1.1	-
GF0037902	0	1	0	Hypothetical protein (1)			-	C_unshiu_00573_mRNA_9.1	-
GF0037901	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, PMZ-type [IPR006564] (1); Zinc finger, SWIM-type [IPR007527] (1)	-	C_unshiu_00573_mRNA_7.1	-
GF0037900	0	1	0	Hypothetical protein (1)			-	C_unshiu_00573_mRNA_6.1	-
GF0037899	0	1	0	Hypothetical protein (1)			-	C_unshiu_00573_mRNA_5.1	-
GF0037898	0	1	0	Hypothetical protein (1)			-	C_unshiu_00573_mRNA_3.1	-
GF0037897	0	1	0	Hypothetical protein (1)	NADP binding [GO:0050661 molecular_function] (1); glucose-6-phosphate dehydrogenase activity [GO:0004345 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); glucose metabolic process [GO:0006006 biological_process] (1)	Glucose-6-phosphate dehydrogenase, C-terminal [IPR022675] (1); Glucose-6-phosphate dehydrogenase [IPR001282] (1)	-	C_unshiu_00573_mRNA_2.1	-
GF0037896	0	1	0	Hypothetical protein (1)			-	C_unshiu_00573_mRNA_15.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0037895	0	1	0	Hypothetical protein (1)			-	C_unshiu_00573_mRNA_11.1	-
GF0037894	0	1	0	Putative disease resistance protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00573_mRNA_1.1	-
GF0037893	0	1	0	Hypothetical protein (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1)	-	C_unshiu_00571_mRNA_24.2	-
GF0037892	0	1	0	Heat shock protein 70 (1)		Heat shock protein 70kD, C-terminal domain [IPR029048] (1); Heat shock protein 70 family [IPR013126] (1); Heat shock protein 70, conserved site [IPR018181] (1); Heat shock protein 70kD, peptide-binding domain [IPR029047] (1)	-	C_unshiu_00571_mRNA_21.1	-
GF0037891	0	1	0	Hypothetical protein (1)			-	C_unshiu_00571_mRNA_2.1	-
GF0037890	0	1	0	Heat shock protein 70 (1)		Heat shock protein 70 family [IPR013126] (1); Heat shock protein 70, conserved site [IPR018181] (1); Heat shock protein 70kD, C-terminal domain [IPR029048] (1); Heat shock protein 70kD, peptide-binding domain [IPR029047] (1)	-	C_unshiu_00571_mRNA_19.1	-
GF0037889	0	1	0	Hypothetical protein (1)			-	C_unshiu_00571_mRNA_18.1	-
GF0037888	0	1	0	Hypothetical protein (1)			-	C_unshiu_00571_mRNA_17.1	-
GF0037887	0	1	0	U-box domain-containing protein kinase family protein isoform 1 (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Protein kinase, ATP binding site [IPR017441] (1); Serine/threonine-protein kinase, active site [IPR008271] (1)	-	C_unshiu_00571_mRNA_1.1	-
GF0037886	0	1	0	Hypothetical protein (1)			-	C_unshiu_00570_mRNA_6.1	-
GF0037885	0	1	0	Cysteine/Histidine-rich C1 domain family protein (1)	protein-disulfide reductase activity [GO:0047134 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Zinc finger, RING/FYVE/PHD-type [IPR013083] (1); C1-like [IPR011424] (1)	-	C_unshiu_00570_mRNA_5.1	-
GF0037884	0	1	0	Transcription regulation protein, putative (1)	protein binding [GO:0005515 molecular_function] (1)	F-box domain [IPR001810] (1)	-	C_unshiu_00570_mRNA_11.1	-
GF0037883	0	1	0	Hypothetical protein (1)			-	C_unshiu_00570_mRNA_1.1	-
GF0037882	0	1	0	Hypothetical protein (1)			-	C_unshiu_00569_mRNA_8.1	-
GF0037881	0	1	0	Hypothetical protein (1)		Bifunctional inhibitor/plant lipid transfer protein/seed storage helical domain [IPR016140] (1)	-	C_unshiu_00569_mRNA_18.1	-
GF0037880	0	1	0	Cytochrome P450 716B1 (1)	iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); monooxygenase activity [GO:0004497 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1)	Cytochrome P450 [IPR001128] (1); Cytochrome P450, B-class [IPR002397] (1); Cytochrome P450, conserved site [IPR017972] (1)	-	C_unshiu_00568_mRNA_8.1	-
GF0037879	0	1	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00568_mRNA_6.1	-
GF0037878	0	1	0	Hypothetical protein (1)			-	C_unshiu_00568_mRNA_5.1	-
GF0037877	0	1	0	Hypothetical protein (1)		Glycoside hydrolase superfamily [IPR017853] (1)	-	C_unshiu_00568_mRNA_3.1	-
GF0037876	0	1	0	Hypothetical protein (1)		Myo-inositol-1-phosphate synthase, GAPDH-like [IPR013021] (1)	-	C_unshiu_00568_mRNA_25.1	-
GF0037875	0	1	0	Truncated RB (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00568_mRNA_24.1	-
GF0037874	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00568_mRNA_2.1	-
GF0037873	0	1	0	Hypothetical protein (1)			-	C_unshiu_00568_mRNA_13.1	-
GF0037872	0	1	0	Hypothetical protein (1)			-	C_unshiu_00568_mRNA_1.1	-
GF0037871	0	1	0	Hypothetical protein (1)			-	C_unshiu_00567_mRNA_14.1	-
GF0037870	0	1	0	Hypothetical protein (1)			-	C_unshiu_00567_mRNA_10.1	-
GF0037869	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00566_mRNA_4.1	-
GF0037868	0	1	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	-	C_unshiu_00566_mRNA_15.1	-
GF0037867	0	1	0	Hypothetical protein (1)			-	C_unshiu_00566_mRNA_12.1	-
GF0037866	0	1	0	Polygalacturonase, family GH28 (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1); polygalacturonase activity [GO:0004650 molecular_function] (1)	Pectin lyase fold/virulence factor [IPR011050] (1); Pectin lyase fold [IPR012334] (1); Glycoside hydrolase, family 28 [IPR000743] (1); Parallel beta-helix repeat [IPR006626] (1)	-	C_unshiu_00565_mRNA_35.1	-
GF0037865	0	1	0	Hypothetical protein (1)			-	C_unshiu_00565_mRNA_32.1	-
GF0037864	0	1	0	Hypothetical protein (1)			-	C_unshiu_00565_mRNA_30.1	-
GF0037863	0	1	0	Hypothetical protein (1)			-	C_unshiu_00565_mRNA_28.1	-
GF0037862	0	1	0	Hypothetical protein (1)			-	C_unshiu_00565_mRNA_26.1	-
GF0037861	0	1	0	Hypothetical protein (1)			-	C_unshiu_00565_mRNA_25.1	-
GF0037860	0	1	0	Hypothetical protein (1)			-	C_unshiu_00565_mRNA_13.1	-
GF0037859	0	1	0	Hypothetical protein (1)			-	C_unshiu_00565_mRNA_10.1	-
GF0037858	0	1	0	Hypothetical protein (1)			-	C_unshiu_00564_mRNA_8.1	-
GF0037857	0	1	0	Hypothetical protein (1)			-	C_unshiu_00564_mRNA_7.1	-
GF0037856	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4218 [IPR025452] (1)	-	C_unshiu_00564_mRNA_6.1	-
GF0037855	0	1	0	Hypothetical protein (1)			-	C_unshiu_00564_mRNA_23.1	-
GF0037854	0	1	0	Hypothetical protein (1)			-	C_unshiu_00564_mRNA_2.1	-
GF0037853	0	1	0	Hypothetical protein (1)			-	C_unshiu_00563_mRNA_9.1	-
GF0037852	0	1	0	Hypothetical protein (1)			-	C_unshiu_00563_mRNA_22.1	-
GF0037851	0	1	0	Hypothetical protein (1)		Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_00563_mRNA_2.1	-
GF0037850	0	1	0	Hypothetical protein (1)			-	C_unshiu_00563_mRNA_17.1	-
GF0037849	0	1	0	Hypothetical protein (1)			-	C_unshiu_00563_mRNA_12.1	-
GF0037848	0	1	0	Hypothetical protein (1)			-	C_unshiu_00563_mRNA_10.1	-
GF0037847	0	1	0	Hypothetical protein (1)	phospholipid binding [GO:0005543 molecular_function] (1)	ENTH/VHS [IPR008942] (1); AP180 N-terminal homology (ANTH) domain [IPR011417] (1); ENTH domain [IPR013809] (1)	-	C_unshiu_00562_mRNA_24.1	-
GF0037846	0	1	0	Oxidoreductase electron carrier (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1)	FAD/NAD(P)-binding domain [IPR023753] (1)	-	C_unshiu_00562_mRNA_1.1	-
GF0037845	0	1	0	Hypothetical protein (1)			-	C_unshiu_00561_mRNA_9.1	-
GF0037844	0	1	0	Hypothetical protein (1)			-	C_unshiu_00561_mRNA_7.1	-
GF0037843	0	1	0	Hypothetical protein (1)			-	C_unshiu_00561_mRNA_5.1	-
GF0037842	0	1	0	Hypothetical protein (1)			-	C_unshiu_00561_mRNA_4.1	-
GF0037841	0	1	0	Putative invertase inhibitor (1)	enzyme inhibitor activity [GO:0004857 molecular_function] (1)	Pectinesterase inhibitor domain [IPR006501] (1)	-	C_unshiu_00561_mRNA_3.1	-
GF0037840	0	1	0	Hypothetical protein (1)			-	C_unshiu_00561_mRNA_2.1	-
GF0037839	0	1	0	Hypothetical protein (1)			-	C_unshiu_00561_mRNA_1.1	-
GF0037838	0	1	0	Transmembrane protein 45B (1)		Protein of unknown function DUF716 (TMEM45) [IPR006904] (1)	-	C_unshiu_00560_mRNA_8.1	-
GF0037837	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Tetratricopeptide-like helical domain [IPR011990] (1); Pentatricopeptide repeat [IPR002885] (1)	-	C_unshiu_00560_mRNA_7.1	-
GF0037836	0	1	0	Hypothetical protein (1)	binding [GO:0005488 molecular_function] (1); phosphorylation [GO:0016310 biological_process] (1); nuclear-transcribed mRNA catabolic process, nonsense-mediated decay [GO:0000184 biological_process] (1); protein serine/threonine kinase activity [GO:0004674 molecular_function] (1)	Armadillo-like helical [IPR011989] (1); Serine/threonine-protein kinase SMG1 [IPR031559] (1); Armadillo-type fold [IPR016024] (1)	-	C_unshiu_00560_mRNA_4.1	-
GF0037835	0	1	0	Hypothetical protein (1)			-	C_unshiu_00560_mRNA_32.1	-
GF0037834	0	1	0	Transcriptional factor B3 (1)	DNA binding [GO:0003677 molecular_function] (1)	DNA-binding pseudobarrel domain [IPR015300] (1); B3 DNA binding domain [IPR003340] (1)	-	C_unshiu_00560_mRNA_14.1	-
GF0037833	0	1	0	Hypothetical protein (1)			-	C_unshiu_00559_mRNA_6.1	-
GF0037832	0	1	0	Hypothetical protein (1)		PGG domain [IPR026961] (1); Ankyrin repeat-containing domain [IPR020683] (1)	-	C_unshiu_00559_mRNA_12.1	-
GF0037831	0	1	0	Hypothetical protein (1)			-	C_unshiu_00558_mRNA_8.1	-
GF0037830	0	1	0	Hypothetical protein (1)		Transposase, MuDR, plant [IPR004332] (1)	-	C_unshiu_00558_mRNA_7.1	-
GF0037829	0	1	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); peptidase activity [GO:0008233 molecular_function] (1)	Peptidase C13, legumain [IPR001096] (1)	-	C_unshiu_00558_mRNA_6.1	-
GF0037828	0	1	0	Hypothetical protein (1)			-	C_unshiu_00558_mRNA_4.1	-
GF0037827	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			-	C_unshiu_00558_mRNA_2.1	-
GF0037826	0	1	0	Hypothetical protein (1)			-	C_unshiu_00558_mRNA_17.1	-
GF0037825	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	-	C_unshiu_00558_mRNA_16.1	-
GF0037824	0	1	0	Hypothetical protein (1)			-	C_unshiu_00558_mRNA_15.1	-
GF0037823	0	1	0	Hypothetical protein (1)			-	C_unshiu_00557_mRNA_8.1	-
GF0037822	0	1	0	Hypothetical protein (1)		Transposase-associated domain [IPR029480] (1)	-	C_unshiu_00557_mRNA_7.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0037821	0	1	0	Hypothetical protein (1)			-	C_unshiu_00557_mRNA_6.1	-
GF0037820	0	1	0	Hypothetical protein (1)			-	C_unshiu_00557_mRNA_10.1	-
GF0037819	0	1	0	MuDR family transposase isoform 1 (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, SWIM-type [IPR007527] (1); MULE transposase domain [IPR018289] (1); Zinc finger, PMZ-type [IPR006564] (1)	-	C_unshiu_00557_mRNA_1.1	-
GF0037818	0	1	0	Hypothetical protein (1)			-	C_unshiu_00556_mRNA_21.1	-
GF0037817	0	1	0	Hypothetical protein (1)			-	C_unshiu_00556_mRNA_20.1	-
GF0037816	0	1	0	Hypothetical protein (1)			-	C_unshiu_00556_mRNA_2.1	-
GF0037815	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00556_mRNA_17.1	-
GF0037814	0	1	0	Hypothetical protein (1)		MULE transposase domain [IPR018289] (1)	-	C_unshiu_00556_mRNA_11.1	-
GF0037813	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_00555_mRNA_8.1	-
GF0037812	0	1	0	Hypothetical protein (1)			-	C_unshiu_00555_mRNA_7.1	-
GF0037811	0	1	0	Hypothetical protein (1)			-	C_unshiu_00555_mRNA_6.1	-
GF0037810	0	1	0	RNA-directed DNA polymerase (Reverse transcriptase) (1)		Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_00555_mRNA_3.1	-
GF0037809	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Domain of unknown function DUF4283 [IPR025558] (1); Zinc finger, CCHC-type [IPR001878] (1); Zinc knuckle CX2CX4HX4C [IPR025836] (1)	-	C_unshiu_00555_mRNA_2.1	-
GF0037808	0	1	0	Hypothetical protein (1)			-	C_unshiu_00555_mRNA_11.1	-
GF0037807	0	1	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	Zinc finger, BED-type [IPR003656] (1); Ribonuclease H-like domain [IPR012337] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	-	C_unshiu_00555_mRNA_1.1	-
GF0037806	0	1	0	Hypothetical protein (1)			-	C_unshiu_00554_mRNA_7.1	-
GF0037805	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_00554_mRNA_6.1	-
GF0037804	0	1	0	Cytochrome P450 (1)	iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1)	Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450 [IPR001128] (1)	-	C_unshiu_00554_mRNA_19.1	-
GF0037803	0	1	0	Hypothetical protein (1)	fatty acid biosynthetic process [GO:0006633 biological_process] (1); acetyl-CoA carboxylase activity [GO:0003989 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1); biotin carboxylase activity [GO:0004075 molecular_function] (1)	Single hybrid motif [IPR011053] (1); Biotin/lipoyl attachment [IPR000089] (1); ATP-grasp fold, subdomain 2 [IPR013816] (1); Biotin carboxylation domain [IPR011764] (1); Acetyl-CoA carboxylase, central domain [IPR013537] (1); Rudiment single hybrid motif [IPR011054] (1); Biotin-binding site [IPR001882] (1); Biotin carboxylase, C-terminal [IPR005482] (1)	-	C_unshiu_00553_mRNA_20.1	-
GF0037802	0	1	0	Hypothetical protein (1)			-	C_unshiu_00552_mRNA_8.1	-
GF0037801	0	1	0	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); 2 iron, 2 sulfur cluster binding [GO:0051537 molecular_function] (1)	Rieske [2Fe-2S] iron-sulphur domain [IPR017941] (1)	-	C_unshiu_00552_mRNA_20.1	-
GF0037800	0	1	0	Far-red impaired responsive family protein isoform 2 (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1); FAR1 DNA binding domain [IPR004330] (1)	-	C_unshiu_00552_mRNA_2.1	-
GF0037799	0	1	0	Hypothetical protein (1)			-	C_unshiu_00552_mRNA_16.1	-
GF0037798	0	1	0	Hypothetical protein (1)	metal ion binding [GO:0046872 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	WD40/YVTN repeat-like-containing domain [IPR015943] (1); WD40-repeat-containing domain [IPR017986] (1); Zinc finger, CCCH-type [IPR000571] (1)	-	C_unshiu_00552_mRNA_14.1	-
GF0037797	0	1	0	Hypothetical protein (1)	phosphotransferase activity, alcohol group as acceptor [GO:0016773 molecular_function] (1)	Carbohydrate kinase PfkB [IPR011611] (1); Carbohydrate/puine kinase, PfkB, conserved site [IPR002173] (1); Ribokinase-like [IPR029056] (1)	-	C_unshiu_00552_mRNA_11.1	-
GF0037796	0	1	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1); FAR1 DNA binding domain [IPR004330] (1)	-	C_unshiu_00552_mRNA_1.1	-
GF0037795	0	1	0	Hypothetical protein (1)			-	C_unshiu_00551_mRNA_4.1	-
GF0037794	0	1	0	Hypothetical protein (1)			-	C_unshiu_00551_mRNA_24.1	-
GF0037793	0	1	0	Hypothetical protein (1)		Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_00551_mRNA_12.1	-
GF0037792	0	1	0	Hypothetical protein (1)			-	C_unshiu_00551_mRNA_10.1	-
GF0037791	0	1	0	Hypothetical protein (1)		Protein of unknown function DUF594 [IPR007658] (1); Domain of unknown function DUF4220 [IPR025315] (1)	-	C_unshiu_00550_mRNA_3.1	-
GF0037790	0	1	0	Hypothetical protein (1)			-	C_unshiu_00550_mRNA_2.1	-
GF0037789	0	1	0	UPF0481 protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	C_unshiu_00550_mRNA_17.1	-
GF0037788	0	1	0	Hypothetical protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	C_unshiu_00550_mRNA_16.1	-
GF0037787	0	1	0	Hypothetical protein (1)			-	C_unshiu_00548_mRNA_18.1	-
GF0037786	0	1	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00548_mRNA_13.1	-
GF0037785	0	1	0	Hypothetical protein (1)			-	C_unshiu_00547_mRNA_4.1	-
GF0037784	0	1	0	Hypothetical protein (1)			-	C_unshiu_00547_mRNA_2.1	-
GF0037783	0	1	0	Hypothetical protein (1)			-	C_unshiu_00547_mRNA_1.1	-
GF0037782	0	1	0	Hypothetical protein (1)			-	C_unshiu_00545_mRNA_20.1	-
GF0037781	0	1	0	Hypothetical protein (1)	response to auxin [GO:0009733 biological_process] (1)	Small auxin-up RNA [IPR003676] (1)	-	C_unshiu_00545_mRNA_2.1	-
GF0037780	0	1	0	Hypothetical protein (1)			-	C_unshiu_00545_mRNA_18.1	-
GF0037779	0	1	0	Hypothetical protein (1)			-	C_unshiu_00544_mRNA_6.1	-
GF0037778	0	1	0	Hypothetical protein (1)			-	C_unshiu_00544_mRNA_4.1	-
GF0037777	0	1	0	SFBBbeta protein (1)	protein binding [GO:0005515 molecular_function] (1)	F-box associated interaction domain [IPR017451] (1); F-box domain [IPR001810] (1); F-box associated domain, type 1 [IPR006527] (1)	-	C_unshiu_00544_mRNA_3.1	-
GF0037776	0	1	0	Mutant protein of flavanone-3-hydroxylase (1)		Non-haem dioxygenase N-terminal domain [IPR026992] (1); Isopenicillin N synthase-like [IPR027443] (1)	-	C_unshiu_00544_mRNA_12.1	-
GF0037775	0	1	0	Chalcone-flavanone isomerase family protein (1)			-	C_unshiu_00544_mRNA_11.1	-
GF0037774	0	1	0	Hypothetical protein (1)			-	C_unshiu_00543_mRNA_8.1	-
GF0037773	0	1	0	Hypothetical protein (1)			-	C_unshiu_00543_mRNA_5.1	-
GF0037772	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			-	C_unshiu_00543_mRNA_3.1	-
GF0037771	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	-	C_unshiu_00543_mRNA_2.1	-
GF0037770	0	1	0	Hypothetical protein (1)			-	C_unshiu_00543_mRNA_18.1	-
GF0037769	0	1	0	Hypothetical protein (1)			-	C_unshiu_00543_mRNA_17.1	-
GF0037768	0	1	0	Hypothetical protein (1)			-	C_unshiu_00543_mRNA_16.1	-
GF0037767	0	1	0	Hypothetical protein (1)			-	C_unshiu_00543_mRNA_14.1	-
GF0037766	0	1	0	Hypothetical protein (1)			-	C_unshiu_00543_mRNA_13.1	-
GF0037765	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	C_unshiu_00543_mRNA_10.1	-
GF0037764	0	1	0	Hypothetical protein (1)			-	C_unshiu_00542_mRNA_11.1	-
GF0037763	0	1	0	Hypothetical protein (1)			-	C_unshiu_00542_mRNA_1.1	-
GF0037762	0	1	0	Hypothetical protein (1)			-	C_unshiu_00541_mRNA_3.1	-
GF0037761	0	1	0	Hypothetical protein (1)			-	C_unshiu_00541_mRNA_11.1	-
GF0037760	0	1	0	Hypothetical protein (1)			-	C_unshiu_00540_mRNA_9.1	-
GF0037759	0	1	0	Hypothetical protein (1)			-	C_unshiu_00540_mRNA_4.1	-
GF0037758	0	1	0	Hypothetical protein (1)			-	C_unshiu_00540_mRNA_1.1	-
GF0037757	0	1	0	Hypothetical protein (1)			-	C_unshiu_00539_mRNA_8.1	-
GF0037756	0	1	0	Hypothetical protein (1)			-	C_unshiu_00539_mRNA_7.1	-
GF0037755	0	1	0	F-box protein interaction domain protein (1)	transcription from RNA polymerase III promoter [GO:0006383 biological_process] (1); DNA-directed RNA polymerase activity [GO:0003899 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1); DNA-directed RNA polymerase III complex [GO:0005666 cellular_component] (1); protein binding [GO:0005515 molecular_function] (1)	F-box associated interaction domain [IPR017451] (1); DNA-directed RNA polymerase III subunit RPC4 [IPR007811] (1); F-box associated domain, type 1 [IPR006527] (1); F-box domain [IPR001810] (1)	-	C_unshiu_00539_mRNA_3.1	-
GF0037754	0	1	0	Hypothetical protein (1)			-	C_unshiu_00539_mRNA_12.1	-
GF0037753	0	1	0	Hypothetical protein (1)	serine-type peptidase activity [GO:0008236 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1); serine-type endopeptidase activity [GO:0004252 molecular_function] (1); serine-type exopeptidase activity [GO:0070008 molecular_function] (1)	Alpha/Beta hydrolase fold [IPR029058] (1); Peptidase S9A, prolyl oligopeptidase [IPR002470] (1); Peptidase S9, serine active site [IPR002471] (1); Peptidase S9A, N-terminal domain [IPR023302] (1); Peptidase S9, prolyl oligopeptidase, catalytic domain [IPR001375] (1)	-	C_unshiu_00539_mRNA_10.1	-
GF0037752	0	1	0	Hypothetical protein (1)			-	C_unshiu_00539_mRNA_1.1	-
GF0037751	0	1	0	Hypothetical protein (1)			-	C_unshiu_00538_mRNA_6.1	-
GF0037750	0	1	0	Hypothetical protein (1)			-	C_unshiu_00538_mRNA_3.1	-
GF0037749	0	1	0	Hypothetical protein (1)			-	C_unshiu_00538_mRNA_16.1	-
GF0037748	0	1	0	Hypothetical protein (1)			-	C_unshiu_00538_mRNA_15.1	-
GF0037747	0	1	0	Hypothetical protein (1)			-	C_unshiu_00538_mRNA_12.1	-
GF0037746	0	1	0	Hypothetical protein (1)			-	C_unshiu_00538_mRNA_1.1	-
GF0037745	0	1	0	Hypothetical protein (1)			-	C_unshiu_00537_mRNA_3.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0037744	0	1	0	Small subunit ribosomal protein S7e (1)	ribosome [GO:0005840 cellular_component] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1); intracellular [GO:0005622 cellular_component] (1); translation [GO:0006412 biological_process] (1)	Ribosomal protein S7e [IPR000554] (1)	-	C_unshiu_00537_mRNA_12.1	-
GF0037743	0	1	0	Hypothetical protein (1)			-	C_unshiu_00537_mRNA_1.1	-
GF0037742	0	1	0	Hypothetical protein (1)			-	C_unshiu_00536_mRNA_9.1	-
GF0037741	0	1	0	Hypothetical protein (1)			-	C_unshiu_00536_mRNA_8.1	-
GF0037740	0	1	0	Hypothetical protein (1)			-	C_unshiu_00536_mRNA_7.1	-
GF0037739	0	1	0	Ubiquitin system component Cue protein, putative (1)			-	C_unshiu_00536_mRNA_5.1	-
GF0037738	0	1	0	Hypothetical protein (1)			-	C_unshiu_00536_mRNA_3.1	-
GF0037737	0	1	0	Hypothetical protein (1)			-	C_unshiu_00536_mRNA_22.1	-
GF0037736	0	1	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	Zinc finger, BED-type [IPR003656] (1)	-	C_unshiu_00536_mRNA_21.1	-
GF0037735	0	1	0	Hypothetical protein (1)			-	C_unshiu_00536_mRNA_16.1	-
GF0037734	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00536_mRNA_14.1	-
GF0037733	0	1	0	Hypothetical protein (1)			-	C_unshiu_00536_mRNA_13.1	-
GF0037732	0	1	0	Hypothetical protein (1)			-	C_unshiu_00536_mRNA_11.1	-
GF0037731	0	1	0	Hypothetical protein (1)			-	C_unshiu_00536_mRNA_10.1	-
GF0037730	0	1	0	Hypothetical protein (1)			-	C_unshiu_00535_mRNA_1.1	-
GF0037729	0	1	0	Hypothetical protein (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Aspartic peptidase, active site [IPR001969] (1); Aspartic peptidase domain [IPR021109] (1)	-	C_unshiu_00534_mRNA_14.1	-
GF0037728	0	1	0	Diacylglycerol kinase (1)	protein kinase C-activating G-protein coupled receptor signaling pathway [GO:0007205 biological_process] (1); kinase activity [GO:0016301 molecular_function] (1); diacylglycerol kinase activity [GO:0004143 molecular_function] (1)	Diacylglycerol kinase, accessory domain [IPR000756] (1); Diacylglycerol kinase, catalytic domain [IPR001206] (1); NAD kinase/diacylglycerol kinase-like domain [IPR016064] (1)	-	C_unshiu_00533_mRNA_24.1	-
GF0037727	0	1	0	Hypothetical protein (1)			-	C_unshiu_00533_mRNA_23.1	-
GF0037726	0	1	0	Hypothetical protein (1)			-	C_unshiu_00533_mRNA_10.1	-
GF0037725	0	1	0	Hypothetical protein (1)			-	C_unshiu_00532_mRNA_17.1	-
GF0037724	0	1	0	Hypothetical protein (1)			-	C_unshiu_00532_mRNA_1.1	-
GF0037723	0	1	0	Hypothetical protein (1)			-	C_unshiu_00531_mRNA_9.1	-
GF0037722	0	1	0	Hypothetical protein (1)			-	C_unshiu_00531_mRNA_8.1	-
GF0037721	0	1	0	Hypothetical protein (1)		Glycoside hydrolase superfamily [IPR017853] (1)	-	C_unshiu_00531_mRNA_25.1	-
GF0037720	0	1	0	Hypothetical protein (1)			-	C_unshiu_00531_mRNA_14.1	-
GF0037719	0	1	0	Hypothetical protein (1)			-	C_unshiu_00531_mRNA_13.1	-
GF0037718	0	1	0	Hypothetical protein (1)			-	C_unshiu_00531_mRNA_10.1	-
GF0037717	0	1	0	Hypothetical protein (1)			-	C_unshiu_00530_mRNA_9.1	-
GF0037716	0	1	0	Hypothetical protein (1)			-	C_unshiu_00530_mRNA_8.1	-
GF0037715	0	1	0	DUF247 domain protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	C_unshiu_00530_mRNA_7.1	-
GF0037714	0	1	0	Hypothetical protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	C_unshiu_00530_mRNA_6.1	-
GF0037713	0	1	0	Hypothetical protein (1)			-	C_unshiu_00530_mRNA_5.1	-
GF0037712	0	1	0	Hypothetical protein (1)			-	C_unshiu_00530_mRNA_11.1	-
GF0037711	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_00530_mRNA_10.1	-
GF0037710	0	1	0	Hypothetical protein (1)			-	C_unshiu_00530_mRNA_1.1	-
GF0037709	0	1	0	Putative retroelement pol polyprotein (1)			-	C_unshiu_00529_mRNA_9.1	-
GF0037708	0	1	0	Class I glutamine amidotransferase-like superfamily protein isoform 2 (1)		DJ-1 [IPR006287] (1); Class I glutamine amidotransferase-like [IPR029062] (1); DJ-1/PfpI [IPR002818] (1)	-	C_unshiu_00529_mRNA_7.1	-
GF0037707	0	1	0	Hypothetical protein (1)			-	C_unshiu_00529_mRNA_6.1	-
GF0037706	0	1	0	Hypothetical protein (1)			-	C_unshiu_00529_mRNA_5.1	-
GF0037705	0	1	0	LRR receptor-like kinase (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1)	-	C_unshiu_00529_mRNA_3.1	-
GF0037704	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_00529_mRNA_25.1	-
GF0037703	0	1	0	Hypothetical protein (1)			-	C_unshiu_00529_mRNA_22.1	-
GF0037702	0	1	0	Hypothetical protein (1)			-	C_unshiu_00529_mRNA_19.1	-
GF0037701	0	1	0	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1); Class I glutamine amidotransferase-like [IPR029062] (1); DJ-1/PfpI [IPR002818] (1)	-	C_unshiu_00529_mRNA_18.1	-
GF0037700	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_00529_mRNA_17.1	-
GF0037699	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1); Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	C_unshiu_00529_mRNA_13.1	-
GF0037698	0	1	0	Putative transcriptional regulator DJ-1 (1)		DJ-1/PfpI [IPR002818] (1); Class I glutamine amidotransferase-like [IPR029062] (1)	-	C_unshiu_00529_mRNA_10.1	-
GF0037697	0	1	0	Cytochrome P450 83B1 (1)	heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Cytochrome P450, conserved site [IPR017972] (1); Cytochrome P450, E-class, group I [IPR002401] (1); DJ-1/PfpI [IPR002818] (1); Cytochrome P450 [IPR001128] (1); DJ-1 [IPR006287] (1); Class I glutamine amidotransferase-like [IPR029062] (1)	-	C_unshiu_00529_mRNA_1.1	-
GF0037696	0	1	0	Serine/threonine-protein kinase PBS1 (1)			-	C_unshiu_00528_mRNA_9.1	-
GF0037695	0	1	0	Transcription elongation factor S-II (1)	regulation of DNA-templated transcription, elongation [GO:0032784 biological_process] (1); nucleus [GO:0005634 cellular_component] (1); DNA binding [GO:0003677 molecular_function] (1); regulation of transcription from RNA polymerase II promoter [GO:0006357 biological_process] (1); transcription, DNA-templated [GO:0006351 biological_process] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Transcription elongation factor S-IIM [IPR017890] (1); Transcription factor IIS, N-terminal [IPR017923] (1); Transcription elongation factor, TFIIS/CRSP70, N-terminal, sub-type [IPR003617] (1); Transcription elongation factor S-II, central domain [IPR003618] (1); Transcription elongation factor, TFIIS-related [IPR016492] (1)	-	C_unshiu_00528_mRNA_3.1	-
GF0037694	0	1	0	Hypothetical protein (1)			-	C_unshiu_00528_mRNA_20.1	-
GF0037693	0	1	0	Hypothetical protein (1)			-	C_unshiu_00528_mRNA_17.1	-
GF0037692	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_00528_mRNA_15.1	-
GF0037691	0	1	0	Hypothetical protein (1)			-	C_unshiu_00528_mRNA_14.1	-
GF0037690	0	1	0	Hypothetical protein (1)			-	C_unshiu_00528_mRNA_1.1	-
GF0037689	0	1	0	Pentatricopeptide repeat (PPR) superfamily protein (1)	protein binding [GO:0005515 molecular_function] (1)	Pentatricopeptide repeat [IPR002885] (1); Tetratricopeptide-like helical domain [IPR011990] (1)	-	C_unshiu_00527_mRNA_9.1	-
GF0037688	0	1	0	Retrotransposon gag protein (1)			-	C_unshiu_00527_mRNA_30.1	-
GF0037687	0	1	0	Pol polyprotein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	-	C_unshiu_00527_mRNA_27.1	-
GF0037686	0	1	0	Phi class glutathione S-transferase (1)	protein binding [GO:0005515 molecular_function] (1)	Thioredoxin-like fold [IPR012336] (1); Glutathione S-transferase, C-terminal [IPR004046] (1); Glutathione S-transferase, N-terminal [IPR004045] (1); Glutathione S-transferase, C-terminal-like [IPR010987] (1)	-	C_unshiu_00527_mRNA_20.1	-
GF0037685	0	1	0	Tetracycline transporter, putative (1)	integral component of membrane [GO:0016021 cellular_component] (1); transmembrane transport [GO:0055085 biological_process] (1)	Major facilitator superfamily [IPR011701] (1); Major facilitator superfamily domain [IPR020846] (1)	-	C_unshiu_00527_mRNA_15.1	-
GF0037684	0	1	0	Hypothetical protein (1)			-	C_unshiu_00527_mRNA_14.1	-
GF0037683	0	1	0	Hypothetical protein (1)			-	C_unshiu_00526_mRNA_3.1	-
GF0037682	0	1	0	Rab8/RabE-family small GTPase (1)	GTPase activity [GO:0003924 molecular_function] (1); ribosome [GO:0005840 cellular_component] (1); protein transport [GO:0015031 biological_process] (1); small GTPase mediated signal transduction [GO:0007264 biological_process] (1); nucleocytoplasmic transport [GO:0006913 biological_process] (1); membrane [GO:0016020 cellular_component] (1); signal transduction [GO:0007165 biological_process] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1); GTP binding [GO:0005525 molecular_function] (1); intracellular protein transport [GO:0006886 biological_process] (1); translation [GO:0006412 biological_process] (1); intracellular [GO:0005622 cellular_component] (1)	Small GTP-binding protein domain [IPR005225] (1); Small GTPase superfamily, Rho type [IPR003578] (1); Ribosomal protein S8 [IPR000630] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Small GTPase superfamily [IPR001806] (1); Ran GTPase [IPR002041] (1); Small GTPase superfamily, ARF type [IPR024156] (1); Small GTPase superfamily, Rab type [IPR003579] (1); Small GTPase superfamily, Ras type [IPR020849] (1)	-	C_unshiu_00525_mRNA_9.1	-
GF0037681	0	1	0	Putative ubiquitin-conjugating enzyme family (1)		Ubiquitin-conjugating enzyme E2 [IPR000608] (1); Ubiquitin-conjugating enzyme/RWD-like [IPR016135] (1)	-	C_unshiu_00525_mRNA_26.1	-
GF0037680	0	1	0	UDP-glucuronic acid decarboxylase 3 (1)		NAD(P)-binding domain [IPR016040] (1)	-	C_unshiu_00525_mRNA_23.1	-
GF0037679	0	1	0	Hypothetical protein (1)			-	C_unshiu_00525_mRNA_18.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0037678	0	1	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00524_mRNA_5.1	-
GF0037677	0	1	0	Hypothetical protein (1)			-	C_unshiu_00524_mRNA_20.1	-
GF0037676	0	1	0	Hypothetical protein (1)			-	C_unshiu_00524_mRNA_2.1	-
GF0037675	0	1	0	Hypothetical protein (1)			-	C_unshiu_00524_mRNA_19.1	-
GF0037674	0	1	0	Hypothetical protein (1)			-	C_unshiu_00524_mRNA_17.1	-
GF0037673	0	1	0	LRR and NB-ARC domain disease resistance protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00524_mRNA_11.1	-
GF0037672	0	1	0	Isoprene synthase (1)	magnesium ion binding [GO:0000287 molecular_function] (1); lyase activity [GO:0016829 molecular_function] (1); terpene synthase activity [GO:0010333 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Isoprenoid synthase domain [IPR008949] (1); Terpene synthase, N-terminal domain [IPR001906] (1); Terpene synthase, metal-binding domain [IPR005630] (1); Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (1)	-	C_unshiu_00523_mRNA_9.1	-
GF0037671	0	1	0	Hypothetical protein (1)			-	C_unshiu_00523_mRNA_6.1	-
GF0037670	0	1	0	Hypothetical protein (1)			-	C_unshiu_00523_mRNA_20.1	-
GF0037669	0	1	0	Hypothetical protein (1)			-	C_unshiu_00522_mRNA_5.1	-
GF0037668	0	1	0	Hypothetical protein (1)			-	C_unshiu_00522_mRNA_3.1	-
GF0037667	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_00522_mRNA_2.1	-
GF0037666	0	1	0	Polynucleotidyl transferase, Ribonuclease H fold (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_00522_mRNA_11.1	-
GF0037665	0	1	0	Hypothetical protein (1)	catalytic activity [GO:0003824 molecular_function] (1); protein dephosphorylation [GO:0006470 biological_process] (1); protein serine/threonine phosphatase activity [GO:0004722 molecular_function] (1)	PPM-type phosphatase domain [IPR001932] (1); Protein phosphatase 2C family [IPR015655] (1)	-	C_unshiu_00522_mRNA_1.1	-
GF0037664	0	1	0	Protein TONSOKU (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Mo25-like [IPR013878] (1); Tetratricopeptide repeat [IPR019734] (1); Tetratricopeptide repeat-containing domain [IPR013026] (1); Armadillo-like helical [IPR011989] (1); Leucine-rich repeat, ribonuclease inhibitor subtype [IPR003590] (1); Tetratricopeptide repeat 1 [IPR001440] (1); Tetratricopeptide-like helical domain [IPR011990] (1)	-	C_unshiu_00521_mRNA_6.1	-
GF0037663	0	1	0	Hypothetical protein (1)			-	C_unshiu_00521_mRNA_3.1	-
GF0037662	0	1	0	Hypothetical protein (1)			-	C_unshiu_00521_mRNA_18.1	-
GF0037661	0	1	0	Hypothetical protein (1)			-	C_unshiu_00521_mRNA_16.1	-
GF0037660	0	1	0	Cytochrome P450 76C2 (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1)	Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450, conserved site [IPR017972] (1); Cytochrome P450 [IPR001128] (1)	-	C_unshiu_00521_mRNA_1.1	-
GF0037659	0	1	0	Hypothetical protein (1)			-	C_unshiu_00520_mRNA_6.1	-
GF0037658	0	1	0	Hypothetical protein (1)			-	C_unshiu_00520_mRNA_4.1	-
GF0037657	0	1	0	Hypothetical protein (1)			-	C_unshiu_00520_mRNA_3.1	-
GF0037656	0	1	0	Hypothetical protein (1)			-	C_unshiu_00520_mRNA_20.1	-
GF0037655	0	1	0	Hypothetical protein (1)			-	C_unshiu_00520_mRNA_19.1	-
GF0037654	0	1	0	Hypothetical protein (1)	protein domain specific binding [GO:0019904 molecular_function] (1)	14-3-3 protein [IPR000308] (1); 14-3-3 domain [IPR023410] (1)	-	C_unshiu_00520_mRNA_18.1	-
GF0037653	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); DNA integration [GO:0015074 biological_process] (1)	Integrase, catalytic core [IPR001584] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00520_mRNA_14.1	-
GF0037652	0	1	0	Hypothetical protein (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Peptidase A2A, retrovirus, catalytic [IPR001995] (1); Retropepsins [IPR018061] (1); Aspartic peptidase domain [IPR021109] (1)	-	C_unshiu_00520_mRNA_10.1	-
GF0037651	0	1	0	Hypothetical protein (1)			-	C_unshiu_00519_mRNA_7.1	-
GF0037650	0	1	0	Putative retroelement pol polyprotein (1)			-	C_unshiu_00519_mRNA_3.1	-
GF0037649	0	1	0	Probable ribosome biogenesis protein (1)		Ribosome biogenesis protein [IPR022968] (1); Ribosome biogenesis protein, C-terminal [IPR007177] (1)	-	C_unshiu_00519_mRNA_16.1	-
GF0037648	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF1985 [IPR015410] (1)	-	C_unshiu_00519_mRNA_12.1	-
GF0037647	0	1	0	Nitrate transporter 1.1 (1)	membrane [GO:0016020 cellular_component] (1); transport [GO:0006810 biological_process] (1); transporter activity [GO:0005215 molecular_function] (1)	Proton-dependent oligopeptide transporter family [IPR000109] (1); Major facilitator superfamily domain [IPR020846] (1)	-	C_unshiu_00518_mRNA_4.1	-
GF0037646	0	1	0	Major facilitator superfamily protein isoform 2 (1)	transporter activity [GO:0005215 molecular_function] (1); membrane [GO:0016020 cellular_component] (1); transport [GO:0006810 biological_process] (1)	Proton-dependent oligopeptide transporter family [IPR000109] (1); Major facilitator superfamily domain [IPR020846] (1)	-	C_unshiu_00518_mRNA_3.1	-
GF0037645	0	1	0	Hypothetical protein (1)			-	C_unshiu_00518_mRNA_11.1	-
GF0037644	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF676, lipase-like [IPR007751] (1)	-	C_unshiu_00517_mRNA_6.1	-
GF0037643	0	1	0	Hypothetical protein (1)	biosynthetic process [GO:0009058 biological_process] (1); nucleotidyltransferase activity [GO:0016779 molecular_function] (1)	Nucleotidyl transferase domain [IPR005835] (1); Trimeric LpxA-like [IPR011004] (1); Nucleotide-diphospho-sugar transferases [IPR029044] (1)	-	C_unshiu_00517_mRNA_3.1	-
GF0037642	0	1	0	Disease resistance protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00517_mRNA_18.1	-
GF0037641	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00517_mRNA_17.1	-
GF0037640	0	1	0	Hypothetical protein (1)			-	C_unshiu_00517_mRNA_15.1	-
GF0037639	0	1	0	DUF241 domain protein (1)		Protein of unknown function DUF241, plant [IPR004320] (1)	-	C_unshiu_00517_mRNA_13.1	-
GF0037638	0	1	0	Hypothetical protein (1)			-	C_unshiu_00516_mRNA_9.1	-
GF0037637	0	1	0	Hypothetical protein (1)			-	C_unshiu_00515_mRNA_6.1	-
GF0037636	0	1	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	-	C_unshiu_00515_mRNA_2.1	-
GF0037635	0	1	0	Hypothetical protein (1)			-	C_unshiu_00515_mRNA_14.1	-
GF0037634	0	1	0	Hypothetical protein (1)			-	C_unshiu_00514_mRNA_27.1	-
GF0037633	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			-	C_unshiu_00514_mRNA_26.1	-
GF0037632	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_00514_mRNA_24.1	-
GF0037631	0	1	0	LINE-type retrotransposon LIb DNA, Insertion at the S11 site-like protein (1)		Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_00514_mRNA_22.1	-
GF0037630	0	1	0	Hypothetical protein (1)			-	C_unshiu_00514_mRNA_12.1	-
GF0037629	0	1	0	Hypothetical protein (1)			-	C_unshiu_00513_mRNA_8.1	-
GF0037628	0	1	0	Hypothetical protein (1)	potassium ion binding [GO:0030955 molecular_function] (1); catalytic activity [GO:0003824 molecular_function] (1); magnesium ion binding [GO:0000287 molecular_function] (1); glycolytic process [GO:0006096 biological_process] (1); pyruvate kinase activity [GO:0004743 molecular_function] (1)	Pyruvate kinase, barrel [IPR015793] (1); Pyruvate kinase, C-terminal [IPR015795] (1); Pyruvate/Phosphoenolpyruvate kinase-like domain [IPR015813] (1); Pyruvate kinase, alpha/beta [IPR015794] (1); Pyruvate kinase [IPR001697] (1)	-	C_unshiu_00513_mRNA_2.2	-
GF0037627	0	1	0	Hypothetical protein (1)			-	C_unshiu_00512_mRNA_9.1	-
GF0037626	0	1	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	-	C_unshiu_00512_mRNA_6.1	-
GF0037625	0	1	0	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	-	C_unshiu_00512_mRNA_5.1	-
GF0037624	0	1	0	Hypothetical protein (1)			-	C_unshiu_00512_mRNA_4.1	-
GF0037623	0	1	0	Hypothetical protein (1)			-	C_unshiu_00512_mRNA_22.1	-
GF0037622	0	1	0	Hypothetical protein (1)			-	C_unshiu_00512_mRNA_16.1	-
GF0037621	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4371 [IPR025398] (1)	-	C_unshiu_00512_mRNA_15.1	-
GF0037620	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1)	Protein kinase-like domain [IPR011009] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_00512_mRNA_12.1	-
GF0037619	0	1	0	Histidine biosynthesis bifunctional protein hisIE (1)	phosphoribosyl-AMP cyclohydrolase activity [GO:0004635 molecular_function] (1); phosphoribosyl-ATP diphosphatase activity [GO:0004636 molecular_function] (1); histidine biosynthetic process [GO:0000105 biological_process] (1)	Phosphoribosyl-AMP cyclohydrolase domain [IPR002496] (1); Phosphoribosyl-ATP pyrophosphohydrolase [IPR008179] (1); Phosphoribosyl-ATP pyrophosphohydrolase-like [IPR021130] (1)	-	C_unshiu_00512_mRNA_1.1	-
GF0037618	0	1	0	UDP-glycosyltransferase 85A2 (1)	metabolic process [GO:0008152 biological_process] (1); transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	-	C_unshiu_00511_mRNA_8.1	-
GF0037617	0	1	0	Hypothetical protein (1)			-	C_unshiu_00511_mRNA_6.1	-
GF0037616	0	1	0	Hypothetical protein (1)			-	C_unshiu_00511_mRNA_3.1	-
GF0037615	0	1	0	Hypothetical protein (1)			-	C_unshiu_00511_mRNA_2.1	-
GF0037614	0	1	0	Hypothetical protein (1)	nucleus [GO:0005634 cellular_component] (1); rRNA methylation [GO:0031167 biological_process] (1); rRNA processing [GO:0006364 biological_process] (1); rRNA methyltransferase activity [GO:0008649 molecular_function] (1); methyltransferase activity [GO:0008168 molecular_function] (1); RNA methylation [GO:0001510 biological_process] (1)	AdoMet-dependent rRNA methyltransferase, Spb1 [IPR028589] (1); Ribosomal RNA methyltransferase, Spb1, C-terminal [IPR012920] (1); Ribosomal RNA large subunit methyltransferase E [IPR015507] (1)	-	C_unshiu_00511_mRNA_13.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0037613	0	1	0	Phenylcoumaran benzylic ether reductase (1)		NmrA-like domain [IPR008030] (1); NAD(P)-binding domain [IPR016040] (1)	-	C_unshiu_00511_mRNA_11.1	-
GF0037612	0	1	0	BTB/POZ and TAZ domain protein (1)	histone acetyltransferase activity [GO:0004402 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); zinc ion binding [GO:0008270 molecular_function] (1); nucleus [GO:0005634 cellular_component] (1); transcription cofactor activity [GO:0003712 molecular_function] (1)	SKP1/BTB/POZ domain [IPR011333] (1); Zinc finger, TAZ-type [IPR000197] (1)	-	C_unshiu_00510_mRNA_3.1	-
GF0037611	0	1	0	Hypothetical protein (1)			-	C_unshiu_00510_mRNA_26.1	-
GF0037610	0	1	0	Hypothetical protein (1)			-	C_unshiu_00510_mRNA_24.1	-
GF0037609	0	1	0	Hypothetical protein (1)			-	C_unshiu_00510_mRNA_11.1	-
GF0037608	0	1	0	Oxalate oxidase 2 (1)	nutrient reservoir activity [GO:0045735 molecular_function] (1)	RmlC-like jelly roll fold [IPR014710] (1); Cupin 1 [IPR006045] (1); RmlC-like cupin domain [IPR011051] (1)	-	C_unshiu_00509_mRNA_21.1	-
GF0037607	0	1	0	Hypothetical protein (1)			-	C_unshiu_00508_mRNA_9.1	-
GF0037606	0	1	0	Hemopexin (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	C_unshiu_00508_mRNA_5.1	-
GF0037605	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc knuckle CX2CX4HX4C [IPR025836] (1); Zinc finger, CCHC-type [IPR001878] (1); Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_00508_mRNA_13.1	-
GF0037604	0	1	0	Retrotransposon protein, putative, unclassified (1)	ferrous iron binding [GO:0008198 molecular_function] (1); cellular aromatic compound metabolic process [GO:0006725 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1)	Reverse transcriptase zinc-binding domain [IPR026960] (1); Extradiol ring-cleavage dioxygenase, class III enzyme, subunit B [IPR004183] (1); Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	C_unshiu_00508_mRNA_12.1	-
GF0037603	0	1	0	Eukaryotic rpb5 RNA polymerase subunit family protein (1)	transcription, DNA-templated [GO:0006351 biological_process] (1); DNA-directed RNA polymerase activity [GO:0003899 molecular_function] (1); nucleus [GO:0005634 cellular_component] (1); DNA binding [GO:0003677 molecular_function] (1)	RNA polymerase, Rpb5, N-terminal [IPR005571] (1); RNA polymerase, subunit H/Rpb5 C-terminal [IPR000783] (1)	-	C_unshiu_00508_mRNA_1.1	-
GF0037602	0	1	0	Hypothetical protein (1)			-	C_unshiu_00507_mRNA_9.1	-
GF0037601	0	1	0	Hypothetical protein (1)			-	C_unshiu_00507_mRNA_5.1	-
GF0037600	0	1	0	Hypothetical protein (1)			-	C_unshiu_00507_mRNA_4.1	-
GF0037599	0	1	0	Hypothetical protein (1)			-	C_unshiu_00507_mRNA_14.1	-
GF0037598	0	1	0	Hypothetical protein (1)			-	C_unshiu_00507_mRNA_1.1	-
GF0037597	0	1	0	Hypothetical protein (1)			-	C_unshiu_00506_mRNA_3.1	-
GF0037596	0	1	0	Hypothetical protein (1)			-	C_unshiu_00506_mRNA_22.1	-
GF0037595	0	1	0	Hypothetical protein (1)			-	C_unshiu_00506_mRNA_21.1	-
GF0037594	0	1	0	Hypothetical protein (1)			-	C_unshiu_00506_mRNA_2.1	-
GF0037593	0	1	0	Hypothetical protein (1)		Arabidopsis retrotransposon Orf1 [IPR004312] (1)	-	C_unshiu_00506_mRNA_19.1	-
GF0037592	0	1	0	Hypothetical protein (1)	membrane [GO:0016020 cellular_component] (1); potassium ion transmembrane transport [GO:0071805 biological_process] (1); potassium ion transmembrane transporter activity [GO:0015079 molecular_function] (1)	Potassium transporter [IPR003855] (1)	-	C_unshiu_00506_mRNA_16.1	-
GF0037591	0	1	0	Hypothetical protein (1)			-	C_unshiu_00506_mRNA_11.1	-
GF0037590	0	1	0	NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial (1)	oxidation-reduction process [GO:0055114 biological_process] (1); quinone binding [GO:0048038 molecular_function] (1); NADH dehydrogenase (ubiquinone) activity [GO:0008137 molecular_function] (1); 4 iron, 4 sulfur cluster binding [GO:0051539 molecular_function] (1); iron-sulfur cluster binding [GO:0051536 molecular_function] (1)	NADH-ubiquinone oxidoreductase, 20 Kd subunit [IPR006138] (1); NADH:ubiquinone oxidoreductase-like, 20kDa subunit [IPR006137] (1)	-	C_unshiu_00505_mRNA_5.1	-
GF0037589	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4409 [IPR025521] (1)	-	C_unshiu_00505_mRNA_31.1	-
GF0037588	0	1	0	Hypothetical protein (1)			-	C_unshiu_00505_mRNA_19.1	-
GF0037587	0	1	0	Hypothetical protein (1)		Anoctamin [IPR007632] (1)	-	C_unshiu_00505_mRNA_16.1	-
GF0037586	0	1	0	Hypothetical protein (1)			-	C_unshiu_00504_mRNA_8.1	-
GF0037585	0	1	0	Blue copper protein (1)	electron carrier activity [GO:0009055 molecular_function] (1)	Phytocyanin domain [IPR003245] (1); Blue (type 1) copper protein, binding site [IPR028871] (1); Cupredoxin [IPR008972] (1)	-	C_unshiu_00504_mRNA_21.1	-
GF0037584	0	1	0	Hypothetical protein (1)			-	C_unshiu_00504_mRNA_20.1	-
GF0037583	0	1	0	Hypothetical protein (1)			-	C_unshiu_00504_mRNA_10.1	-
GF0037582	0	1	0	Hypothetical protein (1)			-	C_unshiu_00503_mRNA_4.1	-
GF0037581	0	1	0	Lipase class 3 family protein (1)	lipid metabolic process [GO:0006629 biological_process] (1)	Fungal lipase-like domain [IPR002921] (1); Alpha/Beta hydrolase fold [IPR029058] (1)	-	C_unshiu_00503_mRNA_3.1	-
GF0037580	0	1	0	Hypothetical protein (1)	protein transporter activity [GO:0008565 molecular_function] (1); nucleocytoplasmic transport [GO:0006913 biological_process] (1)	Importin subunit beta-1, plants [IPR027140] (1)	-	C_unshiu_00503_mRNA_29.1	-
GF0037579	0	1	0	Hypothetical protein (1)			-	C_unshiu_00503_mRNA_27.1	-
GF0037578	0	1	0	Beta-ketoacyl-acyl-carrier-protein synthase II (1)	catalytic activity [GO:0003824 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Beta-ketoacyl synthase, N-terminal [IPR014030] (1); Beta-ketoacyl synthase, active site [IPR018201] (1); Beta-ketoacyl synthase, C-terminal [IPR014031] (1); Polyketide synthase, beta-ketoacyl synthase domain [IPR020841] (1); Thiolase-like [IPR016039] (1)	-	C_unshiu_00503_mRNA_16.1	-
GF0037577	0	1	0	Hypothetical protein (1)		Development/cell death domain [IPR013989] (1)	-	C_unshiu_00503_mRNA_15.1	-
GF0037576	0	1	0	UDP-glucose 4-epimerase GEPI48 (1)	UDP-glucose 4-epimerase activity [GO:0003978 molecular_function] (1); galactose metabolic process [GO:0006012 biological_process] (1)	UDP-glucose 4-epimerase GalE [IPR005886] (1); NAD(P)-binding domain [IPR016040] (1)	-	C_unshiu_00503_mRNA_1.1	-
GF0037575	0	1	0	Hypothetical protein (1)			-	C_unshiu_00502_mRNA_8.1	-
GF0037574	0	1	0	Hypothetical protein (1)			-	C_unshiu_00502_mRNA_5.1	-
GF0037573	0	1	0	Hypothetical protein (1)			-	C_unshiu_00502_mRNA_2.1	-
GF0037572	0	1	0	Hypothetical protein (1)			-	C_unshiu_00502_mRNA_19.1	-
GF0037571	0	1	0	Hypothetical protein (1)			-	C_unshiu_00502_mRNA_14.1	-
GF0037570	0	1	0	Hypothetical protein (1)			-	C_unshiu_00502_mRNA_12.1	-
GF0037569	0	1	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	NAC domain [IPR003441] (1); Zinc finger, BED-type [IPR003656] (1)	-	C_unshiu_00502_mRNA_11.1	-
GF0037568	0	1	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_00501_mRNA_9.1	-
GF0037567	0	1	0	Hypothetical protein (1)			-	C_unshiu_00501_mRNA_7.1	-
GF0037566	0	1	0	Hypothetical protein (1)			-	C_unshiu_00501_mRNA_20.1	-
GF0037565	0	1	0	Hypothetical protein (1)			-	C_unshiu_00501_mRNA_2.1	-
GF0037564	0	1	0	Non-LTR retroelement reverse transcriptase-like (1)	nucleic acid binding [GO:0003676 molecular_function] (1); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1)	Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H-like domain [IPR012337] (1); Ribonuclease H domain [IPR002156] (1)	-	C_unshiu_00501_mRNA_19.1	-
GF0037563	0	1	0	Hypothetical protein (1)			-	C_unshiu_00501_mRNA_12.1	-
GF0037562	0	1	0	Hypothetical protein (1)			-	C_unshiu_00501_mRNA_11.1	-
GF0037561	0	1	0	Hypothetical protein (1)			-	C_unshiu_00501_mRNA_10.1	-
GF0037560	0	1	0	Hypothetical protein (1)			-	C_unshiu_00500_mRNA_20.1	-
GF0037559	0	1	0	Hypothetical protein (1)			-	C_unshiu_00500_mRNA_17.1	-
GF0037558	0	1	0	Hypothetical protein (1)			-	C_unshiu_00499_mRNA_26.1	-
GF0037557	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	C_unshiu_00499_mRNA_25.1	-
GF0037556	0	1	0	Hypothetical protein (1)			-	C_unshiu_00499_mRNA_24.1	-
GF0037555	0	1	0	Hypothetical protein (1)	DNA-directed RNA polymerase II, core complex [GO:0005665 cellular_component] (1); DNA binding [GO:0003677 molecular_function] (1); transcription from RNA polymerase II promoter [GO:0006366 biological_process] (1)	RNA polymerase II, heptapeptide repeat, eukaryotic [IPR000684] (1)	-	C_unshiu_00499_mRNA_23.1	-
GF0037554	0	1	0	Hypothetical protein (1)	ammonium transport [GO:0015696 biological_process] (1); membrane [GO:0016020 cellular_component] (1); transcription, DNA-templated [GO:0006351 biological_process] (1); DNA-directed RNA polymerase activity [GO:0003899 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1); ammonium transmembrane transporter activity [GO:0008519 molecular_function] (1)	RNA polymerase Rpb1, domain 1 [IPR007080] (1); Ammonium/urea transporter [IPR029020] (1); Ammonium transporter AmtB-like domain [IPR024041] (1)	-	C_unshiu_00499_mRNA_22.1	-
GF0037553	0	1	0	Hypothetical protein (1)			-	C_unshiu_00499_mRNA_18.1	-
GF0037552	0	1	0	Perakine reductase (1)		NADP-dependent oxidoreductase domain [IPR023210] (1); Aldo/keto reductase/potassium channel subunit beta [IPR001395] (1)	-	C_unshiu_00499_mRNA_14.1	-
GF0037551	0	1	0	Hypothetical protein (1)		Aldo/keto reductase/potassium channel subunit beta [IPR001395] (1); NADP-dependent oxidoreductase domain [IPR023210] (1)	-	C_unshiu_00499_mRNA_13.1	-
GF0037550	0	1	0	Hypothetical protein (1)			-	C_unshiu_00499_mRNA_12.1	-
GF0037549	0	1	0	Hypothetical protein (1)			-	C_unshiu_00499_mRNA_10.1	-
GF0037548	0	1	0	Hypothetical protein (1)			-	C_unshiu_00498_mRNA_23.1	-
GF0037547	0	1	0	Hypothetical protein (1)			-	C_unshiu_00498_mRNA_2.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0037546	0	1	0	Thermospermine synthase ACAULIS protein (1)		S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); Polyamine biosynthesis domain [IPR030374] (1)	-	C_unshiu_00498_mRNA_14.1	-
GF0037545	0	1	0	Hypothetical protein (1)			-	C_unshiu_00498_mRNA_1.1	-
GF0037544	0	1	0	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	C_unshiu_00497_mRNA_7.1	-
GF0037543	0	1	0	Hypothetical protein (1)			-	C_unshiu_00497_mRNA_26.1	-
GF0037542	0	1	0	Hypothetical protein (1)	hydrolase activity [GO:0016787 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Alpha/beta hydrolase fold-3 [IPR013094] (1); Alpha/Beta hydrolase fold [IPR029058] (1)	-	C_unshiu_00497_mRNA_25.1	-
GF0037541	0	1	0	CXE carboxylesterase (1)	hydrolase activity [GO:0016787 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Alpha/Beta hydrolase fold [IPR029058] (1); Alpha/beta hydrolase fold-3 [IPR013094] (1); Lipase, GDXG, putative serine active site [IPR033140] (1)	-	C_unshiu_00497_mRNA_24.1	-
GF0037540	0	1	0	Hypothetical protein (1)			-	C_unshiu_00497_mRNA_21.1	-
GF0037539	0	1	0	Hypothetical protein (1)	kinetochore [GO:0000776 cellular_component] (1); kinetochore assembly [GO:0051382 biological_process] (1); centromeric DNA binding [GO:0019237 molecular_function] (1)	Centromere protein C/Mif2/cnp3 [IPR028386] (1)	-	C_unshiu_00496_mRNA_9.1	-
GF0037538	0	1	0	Hypothetical protein (1)			-	C_unshiu_00496_mRNA_21.1	-
GF0037537	0	1	0	Monosacharide transport protein (1)			-	C_unshiu_00496_mRNA_11.1	-
GF0037536	0	1	0	Wall-associated receptor kinase 2 (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); polysaccharide binding [GO:0030247 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Wall-associated receptor kinase, galacturonan-binding domain [IPR025287] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Serine/threonine-protein kinase, active site [IPR008271] (1)	-	C_unshiu_00496_mRNA_1.1	-
GF0037535	0	1	0	L18 ribosomal protein Heart Stopper (1)	translation [GO:0006412 biological_process] (1); intracellular [GO:0005622 cellular_component] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1); ribosome [GO:0005840 cellular_component] (1)	Ribosomal protein L18/L5 [IPR005484] (1)	-	C_unshiu_00495_mRNA_29.1	-
GF0037534	0	1	0	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1)	Cytochrome P450 [IPR001128] (1)	-	C_unshiu_00495_mRNA_26.1	-
GF0037533	0	1	0	Hypothetical protein (1)	pseudouridine synthase activity [GO:0009982 molecular_function] (1); RNA modification [GO:0009451 biological_process] (1); pseudouridine synthesis [GO:0001522 biological_process] (1); RNA binding [GO:0003723 molecular_function] (1)	Probable zinc-ribbon domain, plant [IPR021480] (1); Pseudouridine synthase I, TruA, C-terminal [IPR020095] (1); Pseudouridine synthase I, TruA, alpha/beta domain [IPR020097] (1); Pseudouridine synthase, catalytic domain [IPR020103] (1); Pseudouridine synthase I, TruA, N-terminal [IPR020094] (1); Pseudouridine synthase I, TruA [IPR001406] (1)	-	C_unshiu_00495_mRNA_16.1	-
GF0037532	0	1	0	BZIP transcription factor, putative; 74638-73126 (1)			-	C_unshiu_00495_mRNA_14.1	-
GF0037531	0	1	0	Hypothetical protein (1)			-	C_unshiu_00495_mRNA_13.1	-
GF0037530	0	1	0	Crooked neck protein / cell cycle protein, putative (1)	protein binding [GO:0005515 molecular_function] (1); RNA processing [GO:0006396 biological_process] (1)	HAT (Half-A-TPR) repeat [IPR003107] (1); Tetratricopeptide-like helical domain [IPR011990] (1)	-	C_unshiu_00495_mRNA_12.1	-
GF0037529	0	1	0	Crooked neck protein/cell cycle protein, putative (1)	protein binding [GO:0005515 molecular_function] (1); RNA processing [GO:0006396 biological_process] (1)	HAT (Half-A-TPR) repeat [IPR003107] (1); Tetratricopeptide-like helical domain [IPR011990] (1); Tetratricopeptide repeat-containing domain [IPR013026] (1)	-	C_unshiu_00495_mRNA_11.1	-
GF0037528	0	1	0	Putative inactive receptor kinase (1)	ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Protein kinase-like domain [IPR011009] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Protein kinase, ATP binding site [IPR017441] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_00495_mRNA_1.1	-
GF0037527	0	1	0	Hypothetical protein (1)			-	C_unshiu_00493_mRNA_6.1	-
GF0037526	0	1	0	ABC transporter G family member 40 (1)	ATPase activity [GO:0016887 molecular_function] (1); membrane [GO:0016020 cellular_component] (1); ATP binding [GO:0005524 molecular_function] (1)	ABC transporter-like [IPR003439] (1); ABC-2 type transporter [IPR013525] (1); ABC-transporter extracellular N-terminal domain [IPR029481] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00493_mRNA_3.1	-
GF0037525	0	1	0	TIR-NBS-LRR type disease resistance protein (1)	protein binding [GO:0005515 molecular_function] (1); signal transduction [GO:0007165 biological_process] (1)	Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1)	-	C_unshiu_00493_mRNA_13.1	-
GF0037524	0	1	0	Hypothetical protein (1)			-	C_unshiu_00493_mRNA_12.1	-
GF0037523	0	1	0	Hypothetical protein (1)			-	C_unshiu_00492_mRNA_6.1	-
GF0037522	0	1	0	Hypothetical protein (1)			-	C_unshiu_00492_mRNA_2.1	-
GF0037521	0	1	0	Hypothetical protein (1)			-	C_unshiu_00492_mRNA_13.1	-
GF0037520	0	1	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Carlavirus nucleic acid-binding protein [IPR002568] (1)	-	C_unshiu_00492_mRNA_12.1	-
GF0037519	0	1	0	Hypothetical protein (1)			-	C_unshiu_00492_mRNA_11.1	-
GF0037518	0	1	0	Hypothetical protein (1)			-	C_unshiu_00492_mRNA_1.1	-
GF0037517	0	1	0	Hypothetical protein (1)	heme binding [GO:0020037 molecular_function] (1); response to oxidative stress [GO:0006979 biological_process] (1); peroxidase activity [GO:0004601 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Haem peroxidase, plant/fungal/bacterial [IPR002016] (1); Plant peroxidase [IPR000823] (1); Peroxidases heam-ligand binding site [IPR019793] (1); Haem peroxidase [IPR010255] (1)	-	C_unshiu_00491_mRNA_8.1	-
GF0037516	0	1	0	Hypothetical protein (1)			-	C_unshiu_00491_mRNA_7.1	-
GF0037515	0	1	0	Hypothetical protein (1)	nucleotide binding [GO:0000166 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	RNA recognition motif domain [IPR000504] (1); Nucleotide-binding alpha-beta plait domain [IPR012677] (1)	-	C_unshiu_00491_mRNA_4.1	-
GF0037514	0	1	0	Hypothetical protein (1)			-	C_unshiu_00491_mRNA_3.1	-
GF0037513	0	1	0	Hypothetical protein (1)			-	C_unshiu_00491_mRNA_2.1	-
GF0037512	0	1	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	AP2/ERF domain [IPR001471] (1); DNA-binding domain [IPR016177] (1)	-	C_unshiu_00491_mRNA_19.1	-
GF0037511	0	1	0	Hypothetical protein (1)			-	C_unshiu_00491_mRNA_18.1	-
GF0037510	0	1	0	Hypothetical protein (1)			-	C_unshiu_00491_mRNA_16.1	-
GF0037509	0	1	0	Hypothetical protein (1)	heme binding [GO:0020037 molecular_function] (1); response to oxidative stress [GO:0006979 biological_process] (1); peroxidase activity [GO:0004601 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Haem peroxidase [IPR010255] (1); Haem peroxidase, plant/fungal/bacterial [IPR002016] (1); Plant peroxidase [IPR000823] (1)	-	C_unshiu_00491_mRNA_12.1	-
GF0037508	0	1	0	Hypothetical protein (1)			-	C_unshiu_00491_mRNA_10.1	-
GF0037507	0	1	0	Hypothetical protein (1)			-	C_unshiu_00490_mRNA_8.1	-
GF0037506	0	1	0	Nucleosome assembly protein (1)	nucleus [GO:0005634 cellular_component] (1); nucleosome assembly [GO:0006334 biological_process] (1)	Nucleosome assembly protein (NAP) [IPR002164] (1)	-	C_unshiu_00490_mRNA_23.1	-
GF0037505	0	1	0	Hypothetical protein (1)			-	C_unshiu_00490_mRNA_1.1	-
GF0037504	0	1	0	Hypothetical protein (1)			-	C_unshiu_00489_mRNA_8.1	-
GF0037503	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4216 [IPR025312] (1)	-	C_unshiu_00489_mRNA_7.1	-
GF0037502	0	1	0	Hypothetical protein (1)			-	C_unshiu_00489_mRNA_18.1	-
GF0037501	0	1	0	Hypothetical protein (1)			-	C_unshiu_00489_mRNA_13.1	-
GF0037500	0	1	0	CDNA clone:002-110-H12, full insert sequence (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00489_mRNA_1.1	-
GF0037499	0	1	0	Hypothetical protein (1)			-	C_unshiu_00488_mRNA_26.1	-
GF0037498	0	1	0	Hypothetical protein (1)		Zinc knuckle CX2CX4HX4C [IPR025836] (1); Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_00488_mRNA_25.1	-
GF0037497	0	1	0	Hypothetical protein (1)		Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_00487_mRNA_9.1	-
GF0037496	0	1	0	Hypothetical protein (1)			-	C_unshiu_00487_mRNA_8.1	-
GF0037495	0	1	0	Hypothetical protein (1)			-	C_unshiu_00487_mRNA_7.1	-
GF0037494	0	1	0	Hypothetical protein (1)		MULE transposase domain [IPR018289] (1)	-	C_unshiu_00487_mRNA_5.1	-
GF0037493	0	1	0	Pis v 1 allergen 2S albumin (1)		Bifunctional inhibitor/plant lipid transfer protein/seed storage helical domain [IPR016140] (1)	-	C_unshiu_00487_mRNA_3.1	-
GF0037492	0	1	0	Hypothetical protein (1)		GAG-pre-integrase domain [IPR025724] (1)	-	C_unshiu_00487_mRNA_22.1	-
GF0037491	0	1	0	Hypothetical protein (1)			-	C_unshiu_00486_mRNA_4.1	-
GF0037490	0	1	0	Hypothetical protein (1)			-	C_unshiu_00486_mRNA_15.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0037489	0	1	0	S-adenosyl-L-methionine:salicylic acid carboxyl methyltransferase (1)	methyltransferase activity [GO:0008168 molecular_function] (1)	S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); SAM dependent carboxyl methyltransferase [IPR005299] (1)	-	C_unshiu_00486_mRNA_13.1	-
GF0037488	0	1	0	Hypothetical protein (1)			-	C_unshiu_00485_mRNA_9.1	-
GF0037487	0	1	0	Hypothetical protein (1)			-	C_unshiu_00485_mRNA_5.1	-
GF0037486	0	1	0	Hypothetical protein (1)			-	C_unshiu_00485_mRNA_13.1	-
GF0037485	0	1	0	Hypothetical protein (1)			-	C_unshiu_00485_mRNA_12.1	-
GF0037484	0	1	0	Hypothetical protein (1)			-	C_unshiu_00484_mRNA_9.1	-
GF0037483	0	1	0	Hypothetical protein (1)			-	C_unshiu_00484_mRNA_8.1	-
GF0037482	0	1	0	Hypothetical protein (1)			-	C_unshiu_00484_mRNA_6.1	-
GF0037481	0	1	0	Hypothetical protein (1)			-	C_unshiu_00484_mRNA_27.1	-
GF0037480	0	1	0	Hypothetical protein (1)			-	C_unshiu_00484_mRNA_24.1	-
GF0037479	0	1	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); protein binding [GO:0005515 molecular_function] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1); Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_00484_mRNA_21.1	-
GF0037478	0	1	0	Rho guanine nucleotide exchange factor 6 (1)			-	C_unshiu_00484_mRNA_20.1	-
GF0037477	0	1	0	Hypothetical protein (1)			-	C_unshiu_00484_mRNA_16.1	-
GF0037476	0	1	0	SH3 domain-containing protein 2 (1)	protein binding [GO:0005515 molecular_function] (1)	SH3 domain [IPR001452] (1); Arfaptin homology (AH) domain/BAR domain [IPR027267] (1)	-	C_unshiu_00484_mRNA_12.1	-
GF0037475	0	1	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	-	C_unshiu_00483_mRNA_1.1	-
GF0037474	0	1	0	Hypothetical protein (1)			-	C_unshiu_00482_mRNA_22.1	-
GF0037473	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00482_mRNA_21.1	-
GF0037472	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	C_unshiu_00482_mRNA_20.1	-
GF0037471	0	1	0	Hypothetical protein (1)			-	C_unshiu_00482_mRNA_19.1	-
GF0037470	0	1	0	Hypothetical protein (1)			-	C_unshiu_00482_mRNA_18.1	-
GF0037469	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1); signal transduction [GO:0007165 biological_process] (1); ADP binding [GO:0043531 molecular_function] (1)	Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	C_unshiu_00482_mRNA_16.1	-
GF0037468	0	1	0	Hypothetical protein (1)			-	C_unshiu_00481_mRNA_7.1	-
GF0037467	0	1	0	Calcium-dependent phospholipid-binding copine family protein (1)	negative regulation of cell death [GO:0060548 biological_process] (1); protein binding [GO:0005515 molecular_function] (1); calcium-dependent phospholipid binding [GO:0005544 molecular_function] (1)	C2 domain [IPR000008] (1); Protein BONZAI [IPR031116] (1)	-	C_unshiu_00481_mRNA_6.1	-
GF0037466	0	1	0	Hypothetical protein (1)		Transposase, MuDR, plant [IPR004332] (1)	-	C_unshiu_00481_mRNA_4.1	-
GF0037465	0	1	0	Ulp1 peptidase-like (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1); Domain of unknown function DUF1985 [IPR015410] (1)	-	C_unshiu_00481_mRNA_3.1	-
GF0037464	0	1	0	Hypothetical protein (1)			-	C_unshiu_00480_mRNA_7.1	-
GF0037463	0	1	0	Hypothetical protein (1)			-	C_unshiu_00480_mRNA_3.1	-
GF0037462	0	1	0	Hypothetical protein (1)			-	C_unshiu_00480_mRNA_26.1	-
GF0037461	0	1	0	Pol polyprotein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	-	C_unshiu_00480_mRNA_21.1	-
GF0037460	0	1	0	Phloem protein 2-B5 (1)	protein binding [GO:0005515 molecular_function] (1)	F-box domain [IPR001810] (1); Phloem protein 2-like [IPR025886] (1)	-	C_unshiu_00480_mRNA_2.1	-
GF0037459	0	1	0	Hypothetical protein (1)			-	C_unshiu_00480_mRNA_15.1	-
GF0037458	0	1	0	Hypothetical protein (1)			-	C_unshiu_00480_mRNA_14.1	-
GF0037457	0	1	0	Hypothetical protein (1)			-	C_unshiu_00480_mRNA_12.1	-
GF0037456	0	1	0	Hypothetical protein (1)			-	C_unshiu_00480_mRNA_11.1	-
GF0037455	0	1	0	Hypothetical protein (1)			-	C_unshiu_00479_mRNA_9.1	-
GF0037454	0	1	0	Hypothetical protein (1)			-	C_unshiu_00479_mRNA_7.1	-
GF0037453	0	1	0	Hypothetical protein (1)			-	C_unshiu_00479_mRNA_6.1	-
GF0037452	0	1	0	RNA-directed DNA polymerase (1)		Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_00479_mRNA_2.1	-
GF0037451	0	1	0	Hypothetical protein (1)			-	C_unshiu_00479_mRNA_15.1	-
GF0037450	0	1	0	Hypothetical protein (1)	DNA integration [GO:0015074 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Integrase, catalytic core [IPR001584] (1)	-	C_unshiu_00479_mRNA_1.1	-
GF0037449	0	1	0	Hypothetical protein (1)			-	C_unshiu_00478_mRNA_16.1	-
GF0037448	0	1	0	Hypothetical protein (1)			-	C_unshiu_00478_mRNA_15.1	-
GF0037447	0	1	0	Hypothetical protein (1)			-	C_unshiu_00478_mRNA_10.1	-
GF0037446	0	1	0	Hypothetical protein (1)			-	C_unshiu_00478_mRNA_1.1	-
GF0037445	0	1	0	Hypothetical protein (1)			-	C_unshiu_00477_mRNA_5.1	-
GF0037444	0	1	0	Hypothetical protein (1)		ADF-H/Gelsolin-like domain [IPR029006] (1); Gelsolin-like domain [IPR007123] (1)	-	C_unshiu_00477_mRNA_22.1	-
GF0037443	0	1	0	Beta-hexosaminidase subunit B2 (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1); hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (1); beta-N-acetylhexosaminidase activity [GO:0004563 molecular_function] (1)	Glycoside hydrolase, catalytic domain [IPR013781] (1); Glycoside hydrolase family 20, catalytic domain [IPR015883] (1); Glycoside hydrolase superfamily [IPR017853] (1); Beta-hexosaminidase [IPR025705] (1); Chitobiase/beta-hexosaminidase domain 2-like [IPR029018] (1); Beta-hexosaminidase, eukaryotic type, N-terminal [IPR029019] (1)	-	C_unshiu_00476_mRNA_4.1	-
GF0037442	0	1	0	Hypothetical protein (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Serine/threonine-protein kinase, active site [IPR008271] (1)	-	C_unshiu_00476_mRNA_24.1	-
GF0037441	0	1	0	Putative retroelement pol polyprotein (1)			-	C_unshiu_00476_mRNA_23.1	-
GF0037440	0	1	0	Hypothetical protein (1)		Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_00476_mRNA_22.1	-
GF0037439	0	1	0	Mitogen-activated protein kinase kinase (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Serine/threonine-protein kinase, active site [IPR008271] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	-	C_unshiu_00476_mRNA_20.1	-
GF0037438	0	1	0	Hypothetical protein (1)			-	C_unshiu_00476_mRNA_18.1	-
GF0037437	0	1	0	Hypothetical protein (1)			-	C_unshiu_00476_mRNA_16.1	-
GF0037436	0	1	0	Hypothetical protein (1)			-	C_unshiu_00475_mRNA_2.1	-
GF0037435	0	1	0	Hypothetical protein (1)			-	C_unshiu_00475_mRNA_17.1	-
GF0037434	0	1	0	Hypothetical protein (1)			-	C_unshiu_00475_mRNA_15.1	-
GF0037433	0	1	0	Hypothetical protein (1)			-	C_unshiu_00475_mRNA_13.1	-
GF0037432	0	1	0	Hypothetical protein (1)			-	C_unshiu_00475_mRNA_12.1	-
GF0037431	0	1	0	Hypothetical protein (1)			-	C_unshiu_00474_mRNA_6.1	-
GF0037430	0	1	0	Hypothetical protein (1)			-	C_unshiu_00474_mRNA_5.1	-
GF0037429	0	1	0	Hypothetical protein (1)			-	C_unshiu_00474_mRNA_4.1	-
GF0037428	0	1	0	Hypothetical protein (1)			-	C_unshiu_00474_mRNA_26.1	-
GF0037427	0	1	0	Hypothetical protein (1)			-	C_unshiu_00474_mRNA_25.1	-
GF0037426	0	1	0	Hypothetical protein (1)			-	C_unshiu_00474_mRNA_24.1	-
GF0037425	0	1	0	Hypothetical protein (1)			-	C_unshiu_00474_mRNA_2.1	-
GF0037424	0	1	0	Hypothetical protein (1)			-	C_unshiu_00474_mRNA_16.1	-
GF0037423	0	1	0	Hypothetical protein (1)			-	C_unshiu_00474_mRNA_14.1	-
GF0037422	0	1	0	Hypothetical protein (1)			-	C_unshiu_00474_mRNA_11.1	-
GF0037421	0	1	0	Hypothetical protein (1)			-	C_unshiu_00473_mRNA_23.1	-
GF0037420	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1); Aspartic peptidase domain [IPR021109] (1); Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_00473_mRNA_14.1	-
GF0037419	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00473_mRNA_12.1	-
GF0037418	0	1	0	Hypothetical protein (1)			-	C_unshiu_00473_mRNA_11.1	-
GF0037417	0	1	0	Hypothetical protein (1)			-	C_unshiu_00473_mRNA_1.1	-
GF0037416	0	1	0	Hypothetical protein (1)			-	C_unshiu_00472_mRNA_5.1	-
GF0037415	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	C_unshiu_00472_mRNA_1.1	-
GF0037414	0	1	0	Hypothetical protein (1)			-	C_unshiu_00471_mRNA_27.1	-
GF0037413	0	1	0	Hypothetical protein (1)			-	C_unshiu_00471_mRNA_26.1	-
GF0037412	0	1	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); DNA binding [GO:0003677 molecular_function] (1)	NAC domain [IPR003441] (1)	-	C_unshiu_00471_mRNA_21.1	-
GF0037411	0	1	0	Germin-like protein subfamily 1 member 7 (1)	nutrient reservoir activity [GO:0045735 molecular_function] (1); manganese ion binding [GO:0030145 molecular_function] (1)	RmlC-like cupin domain [IPR011051] (1); RmlC-like jelly roll fold [IPR014710] (1); Cupin 1 [IPR006045] (1); Germin, manganese binding site [IPR019780] (1)	-	C_unshiu_00471_mRNA_2.1	-
GF0037410	0	1	0	Hypothetical protein (1)			-	C_unshiu_00471_mRNA_19.1	-
GF0037409	0	1	0	Hypothetical protein (1)		Ribosomal protein L20, mitochondrial [IPR024388] (1)	-	C_unshiu_00471_mRNA_16.1	-
GF0037408	0	1	0	Hypothetical protein (1)			-	C_unshiu_00471_mRNA_14.1	-
GF0037407	0	1	0	Hypothetical protein (1)			-	C_unshiu_00470_mRNA_8.1	-
GF0037406	0	1	0	Hypothetical protein (1)			-	C_unshiu_00470_mRNA_5.1	-
GF0037405	0	1	0	Hypothetical protein (1)			-	C_unshiu_00470_mRNA_4.1	-
GF0037404	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_00470_mRNA_35.1	-
GF0037403	0	1	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_00470_mRNA_34.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0037402	0	1	0	Hypothetical protein (1)			-	C_unshiu_00470_mRNA_33.1	-
GF0037401	0	1	0	Hypothetical protein (1)			-	C_unshiu_00470_mRNA_32.1	-
GF0037400	0	1	0	Hypothetical protein (1)			-	C_unshiu_00470_mRNA_3.1	-
GF0037399	0	1	0	Hypothetical protein (1)			-	C_unshiu_00470_mRNA_23.1	-
GF0037398	0	1	0	Hypothetical protein (1)			-	C_unshiu_00470_mRNA_2.1	-
GF0037397	0	1	0	Hypothetical protein (1)			-	C_unshiu_00470_mRNA_19.1	-
GF0037396	0	1	0	Hypothetical protein (1)			-	C_unshiu_00470_mRNA_18.1	-
GF0037395	0	1	0	Hypothetical protein (1)			-	C_unshiu_00470_mRNA_16.1	-
GF0037394	0	1	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1); Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_00470_mRNA_15.1	-
GF0037393	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_00470_mRNA_12.1	-
GF0037392	0	1	0	Hypothetical protein (1)		Transposon, En/Spm-like [IPR004242] (1)	-	C_unshiu_00469_mRNA_8.1	-
GF0037391	0	1	0	Pollen-specific C2 domain containing protein (1)	protein binding [GO:0005515 molecular_function] (1)	C2 domain [IPR000008] (1)	-	C_unshiu_00469_mRNA_7.1	-
GF0037390	0	1	0	Hypothetical protein (1)			-	C_unshiu_00469_mRNA_2.1	-
GF0037389	0	1	0	BED zinc finger,hAT family dimerization domain isoform 5 (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1); Zinc finger, BED-type [IPR003656] (1); C2 domain [IPR000008] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00469_mRNA_13.1	-
GF0037388	0	1	0	Hypothetical protein (1)			-	C_unshiu_00469_mRNA_1.1	-
GF0037387	0	1	0	Guanylate kinase (1)	purine nucleotide metabolic process [GO:0006163 biological_process] (1); guanylate kinase activity [GO:0004385 molecular_function] (1)	Guanylate kinase, conserved site [IPR020590] (1); Guanylate kinase [IPR017665] (1); Guanylate kinase/L-type calcium channel beta subunit [IPR008145] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Guanylate kinase-like domain [IPR008144] (1)	-	C_unshiu_00468_mRNA_29.1	-
GF0037386	0	1	0	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	C_unshiu_00468_mRNA_26.1	-
GF0037385	0	1	0	Hypothetical protein (1)			-	C_unshiu_00468_mRNA_23.1	-
GF0037384	0	1	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1)	-	C_unshiu_00468_mRNA_21.1	-
GF0037383	0	1	0	Hypothetical protein (1)			-	C_unshiu_00468_mRNA_12.1	-
GF0037382	0	1	0	Non-LTR retroelement reverse transcriptase-like (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00468_mRNA_10.1	-
GF0037381	0	1	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_00467_mRNA_6.1	-
GF0037380	0	1	0	Hypothetical protein (1)			-	C_unshiu_00467_mRNA_5.1	-
GF0037379	0	1	0	Hypothetical protein (1)	cation transport [GO:0006812 biological_process] (1); integral component of membrane [GO:0016021 cellular_component] (1); solute:proton antiporter activity [GO:0015299 molecular_function] (1)	Cation/H+ exchanger, CPA1 family [IPR018422] (1)	-	C_unshiu_00467_mRNA_31.1	-
GF0037378	0	1	0	Hypothetical protein (1)			-	C_unshiu_00467_mRNA_30.1	-
GF0037377	0	1	0	Hypothetical protein (1)		Gnk2-homologous domain [IPR002902] (1)	-	C_unshiu_00467_mRNA_3.1	-
GF0037376	0	1	0	Hypothetical protein (1)			-	C_unshiu_00467_mRNA_19.1	-
GF0037375	0	1	0	Hypothetical protein (1)			-	C_unshiu_00467_mRNA_18.1	-
GF0037374	0	1	0	Hypothetical protein (1)			-	C_unshiu_00467_mRNA_17.1	-
GF0037373	0	1	0	Hypothetical protein (1)			-	C_unshiu_00467_mRNA_16.1	-
GF0037372	0	1	0	Hypothetical protein (1)		Major facilitator superfamily domain [IPR020846] (1)	-	C_unshiu_00467_mRNA_13.1	-
GF0037371	0	1	0	Hypothetical protein (1)	protein serine/threonine kinase activity [GO:0004674 molecular_function] (1)	S-locus receptor kinase, C-terminal [IPR021820] (1)	-	C_unshiu_00467_mRNA_10.1	-
GF0037370	0	1	0	Hypothetical protein (1)			-	C_unshiu_00467_mRNA_1.1	-
GF0037369	0	1	0	Hypothetical protein (1)			-	C_unshiu_00466_mRNA_19.1	-
GF0037368	0	1	0	Hypothetical protein (1)			-	C_unshiu_00466_mRNA_18.1	-
GF0037367	0	1	0	Glyceraldehyde-3-phosphate dehydrogenase 1, cytosolic (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor [GO:0016620 molecular_function] (1)	Glyceraldehyde 3-phosphate dehydrogenase, catalytic domain [IPR020829] (1); Glyceraldehyde 3-phosphate dehydrogenase, NAD(P) binding domain [IPR020828] (1); Glyceraldehyde 3-phosphate dehydrogenase, active site [IPR020830] (1); Glyceraldehyde/Erythrose phosphate dehydrogenase family [IPR020831] (1); NAD(P)-binding domain [IPR016040] (1)	-	C_unshiu_00466_mRNA_15.1	-
GF0037366	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_00466_mRNA_11.1	-
GF0037365	0	1	0	Hypothetical protein (1)			-	C_unshiu_00464_mRNA_4.1	-
GF0037364	0	1	0	Hypothetical protein (1)			-	C_unshiu_00464_mRNA_20.1	-
GF0037363	0	1	0	Hypothetical protein (1)			-	C_unshiu_00464_mRNA_2.1	-
GF0037362	0	1	0	Hypothetical protein (1)			-	C_unshiu_00464_mRNA_17.1	-
GF0037361	0	1	0	Hypothetical protein (1)			-	C_unshiu_00464_mRNA_10.1	-
GF0037360	0	1	0	Hypothetical protein (1)		Transposase, Tnp1/En/Spm-like [IPR004264] (1)	-	C_unshiu_00464_mRNA_1.1	-
GF0037359	0	1	0	Hypothetical protein (1)			-	C_unshiu_00463_mRNA_8.1	-
GF0037358	0	1	0	Hypothetical protein (1)	transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (1)	Chloramphenicol acetyltransferase-like domain [IPR023213] (1); Bulb-type lectin domain [IPR001480] (1); Transferase [IPR003480] (1)	-	C_unshiu_00463_mRNA_3.1	-
GF0037357	0	1	0	Hypothetical protein (1)			-	C_unshiu_00463_mRNA_20.1	-
GF0037356	0	1	0	Hypothetical protein (1)			-	C_unshiu_00463_mRNA_14.1	-
GF0037355	0	1	0	Hypothetical protein (1)			-	C_unshiu_00462_mRNA_7.1	-
GF0037354	0	1	0	Hypothetical protein (1)			-	C_unshiu_00462_mRNA_3.1	-
GF0037353	0	1	0	Hypothetical protein (1)			-	C_unshiu_00460_mRNA_9.1	-
GF0037352	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase-like domain [IPR011009] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Thioredoxin-like fold [IPR012336] (1); Protein kinase domain [IPR000719] (1); Glutathione S-transferase, N-terminal [IPR004045] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Protein kinase, ATP binding site [IPR017441] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Glutathione S-transferase, C-terminal-like [IPR010987] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1)	-	C_unshiu_00460_mRNA_8.1	-
GF0037351	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Tetratricopeptide repeat [IPR019734] (1); Tetratricopeptide repeat-containing domain [IPR013026] (1); Tetratricopeptide-like helical domain [IPR011990] (1)	-	C_unshiu_00460_mRNA_7.1	-
GF0037350	0	1	0	LRR receptor-like kinase family protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	-	C_unshiu_00460_mRNA_6.1	-
GF0037349	0	1	0	Glutathione transferase (1)	protein binding [GO:0005515 molecular_function] (1)	Glutathione S-transferase, C-terminal-like [IPR010987] (1); Glutathione S-transferase, N-terminal [IPR004045] (1); Thioredoxin-like fold [IPR012336] (1); Glutathione S-transferase, C-terminal [IPR004046] (1)	-	C_unshiu_00460_mRNA_5.1	-
GF0037348	0	1	0	Hypothetical protein (1)			-	C_unshiu_00460_mRNA_4.1	-
GF0037347	0	1	0	Hypothetical protein (1)			-	C_unshiu_00460_mRNA_32.1	-
GF0037346	0	1	0	LRR receptor-like kinase family protein (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Protein kinase, ATP binding site [IPR017441] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Leucine-rich repeat [IPR001611] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Protein kinase-like domain [IPR011009] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00460_mRNA_23.1	-
GF0037345	0	1	0	Hypothetical protein (1)			-	C_unshiu_00460_mRNA_20.1	-
GF0037344	0	1	0	Tau class glutathione S-transferase (1)	protein binding [GO:0005515 molecular_function] (1)	Glutathione S-transferase, C-terminal-like [IPR010987] (1); Glutathione S-transferase, N-terminal [IPR004045] (1); Thioredoxin-like fold [IPR012336] (1)	-	C_unshiu_00460_mRNA_2.1	-
GF0037343	0	1	0	Tetratricopeptide repeat protein 27-like protein (1)			-	C_unshiu_00460_mRNA_17.1	-
GF0037342	0	1	0	Hypothetical protein (1)			-	C_unshiu_00460_mRNA_16.1	-
GF0037341	0	1	0	Hypothetical protein (1)			-	C_unshiu_00460_mRNA_14.1	-
GF0037340	0	1	0	RNA-binding protein pno1 (1)	nucleic acid binding [GO:0003676 molecular_function] (1); RNA binding [GO:0003723 molecular_function] (1)	K Homology domain [IPR004087] (1); K Homology domain, type 1 [IPR004088] (1)	-	C_unshiu_00459_mRNA_3.1	-
GF0037339	0	1	0	Hypothetical protein (1)			-	C_unshiu_00459_mRNA_22.1	-
GF0037338	0	1	0	Hypothetical protein (1)			-	C_unshiu_00459_mRNA_21.1	-
GF0037337	0	1	0	Hypothetical protein (1)			-	C_unshiu_00459_mRNA_16.1	-
GF0037336	0	1	0	Hypothetical protein (1)			-	C_unshiu_00458_mRNA_6.1	-
GF0037335	0	1	0	Monosacharide transport protein (1)			-	C_unshiu_00458_mRNA_5.1	-
GF0037334	0	1	0	AT3G21090 protein (1)	ATP binding [GO:0005524 molecular_function] (1); ATPase activity [GO:0016887 molecular_function] (1)	ABC transporter, conserved site [IPR017871] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); ABC transporter-like [IPR003439] (1); AAA+ ATPase domain [IPR003593] (1)	-	C_unshiu_00458_mRNA_13.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0037333	0	1	0	Hypothetical protein (1)	phosphatidylinositol phosphate kinase activity [GO:0016307 molecular_function] (1); phosphatidylinositol metabolic process [GO:0046488 biological_process] (1)	Phosphatidylinositol-4-phosphate 5-kinase, core [IPR002498] (1); Phosphatidylinositol-4-phosphate 5-kinase, core, subgroup [IPR016034] (1); Phosphatidylinositol-4-phosphate 5-kinase, C-terminal [IPR027483] (1)	-	C_unshiu_00457_mRNA_35.1	-
GF0037332	0	1	0	Hypothetical protein (1)		Bulb-type lectin domain [IPR001480] (1)	-	C_unshiu_00457_mRNA_28.1	-
GF0037331	0	1	0	Hypothetical protein (1)		Concanavalin A-like lectin/glucanase domain [IPR013320] (1)	-	C_unshiu_00457_mRNA_27.1	-
GF0037330	0	1	0	Hypothetical protein (1)		Biotin/lipoyl attachment [IPR000089] (1); Single hybrid motif [IPR011053] (1); 2-oxo acid dehydrogenase, lipoyl-binding site [IPR003016] (1)	-	C_unshiu_00457_mRNA_15.1	-
GF0037329	0	1	0	Hypothetical protein (1)			-	C_unshiu_00456_mRNA_7.1	-
GF0037328	0	1	0	Hypothetical protein (1)			-	C_unshiu_00456_mRNA_6.1	-
GF0037327	0	1	0	Hypothetical protein (1)			-	C_unshiu_00456_mRNA_5.1	-
GF0037326	0	1	0	Ribonuclease H-like superfamily protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00456_mRNA_3.1	-
GF0037325	0	1	0	50S ribosomal protein L14, chloroplastic (1)	structural constituent of ribosome [GO:0003735 molecular_function] (1); large ribosomal subunit [GO:0015934 cellular_component] (1); translation [GO:0006412 biological_process] (1); ribosome [GO:0005840 cellular_component] (1)	Ribosomal protein L14b/L23e [IPR000218] (1); Ribosomal protein L14, bacterial-type [IPR005745] (1); Ribosomal protein L14 conserved site [IPR019972] (1); Ribosomal protein L14 domain [IPR023571] (1)	-	C_unshiu_00456_mRNA_22.1	-
GF0037324	0	1	0	30S ribosomal protein S11, chloroplastic (1)	structural constituent of ribosome [GO:0003735 molecular_function] (1); intracellular [GO:0005622 cellular_component] (1); translation [GO:0006412 biological_process] (1); ribosome [GO:0005840 cellular_component] (1)	Ribosomal protein S11, bacterial-type [IPR019981] (1); Ribosomal S11, conserved site [IPR018102] (1); Ribosomal protein S11 [IPR001971] (1)	-	C_unshiu_00456_mRNA_21.1	-
GF0037323	0	1	0	Hypothetical protein (1)	ribosome [GO:0005840 cellular_component] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1); translation [GO:0006412 biological_process] (1)	Ribosomal protein S11 [IPR001971] (1); Ribosomal S11, conserved site [IPR018102] (1)	-	C_unshiu_00456_mRNA_20.1	-
GF0037322	0	1	0	Hypothetical protein (1)			-	C_unshiu_00456_mRNA_2.1	-
GF0037321	0	1	0	Hypothetical protein (1)			-	C_unshiu_00456_mRNA_19.1	-
GF0037320	0	1	0	Hypothetical protein (1)			-	C_unshiu_00456_mRNA_16.1	-
GF0037319	0	1	0	RNA-dependent RNA polymerase family protein (1)	RNA-directed RNA polymerase activity [GO:0003968 molecular_function] (1)	RNA-dependent RNA polymerase, eukaryotic-type [IPR007855] (1)	-	C_unshiu_00456_mRNA_1.1	-
GF0037318	0	1	0	Hypothetical protein (1)			-	C_unshiu_00455_mRNA_5.1	-
GF0037317	0	1	0	Hypothetical protein (1)			-	C_unshiu_00455_mRNA_24.1	-
GF0037316	0	1	0	Hypothetical protein (1)			-	C_unshiu_00455_mRNA_23.1	-
GF0037315	0	1	0	Hypothetical protein (1)			-	C_unshiu_00455_mRNA_19.1	-
GF0037314	0	1	0	Protein WALLS ARE THIN 1 (1)	integral component of membrane [GO:0016021 cellular_component] (1); membrane [GO:0016020 cellular_component] (1); transmembrane transporter activity [GO:0022857 molecular_function] (1)	WAT1-related protein [IPR030184] (1); EamA domain [IPR000620] (1)	-	C_unshiu_00455_mRNA_14.1	-
GF0037313	0	1	0	Hypothetical protein (1)			-	C_unshiu_00454_mRNA_7.1	-
GF0037312	0	1	0	Glucan endo-1,3-beta-glucosidase, basic isoform (1)	hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1)	Glycoside hydrolase, catalytic domain [IPR013781] (1); Glycoside hydrolase superfamily [IPR017853] (1); Glycoside hydrolase family 17 [IPR000490] (1)	-	C_unshiu_00454_mRNA_4.1	-
GF0037311	0	1	0	Hypothetical protein (1)			-	C_unshiu_00454_mRNA_2.1	-
GF0037310	0	1	0	Hypothetical protein (1)			-	C_unshiu_00454_mRNA_13.1	-
GF0037309	0	1	0	Hypothetical protein (1)			-	C_unshiu_00454_mRNA_11.1	-
GF0037308	0	1	0	Disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); AAA+ ATPase domain [IPR003593] (1); NB-ARC [IPR002182] (1)	-	C_unshiu_00453_mRNA_27.1	-
GF0037307	0	1	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	C_unshiu_00453_mRNA_26.1	-
GF0037306	0	1	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	-	C_unshiu_00453_mRNA_23.1	-
GF0037305	0	1	0	Hypothetical protein (1)			-	C_unshiu_00453_mRNA_20.1	-
GF0037304	0	1	0	Putative non-LTR retroelement reverse transcriptase (1)	RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H domain [IPR002156] (1)	-	C_unshiu_00453_mRNA_17.1	-
GF0037303	0	1	0	Disease resistance protein (CC-NBS-LRR class) family protein (1)	ADP binding [GO:0043531 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	C_unshiu_00453_mRNA_16.1	-
GF0037302	0	1	0	Hypothetical protein (1)			-	C_unshiu_00453_mRNA_14.1	-
GF0037301	0	1	0	Hypothetical protein (1)			-	C_unshiu_00453_mRNA_1.1	-
GF0037300	0	1	0	Hypothetical protein (1)			-	C_unshiu_00452_mRNA_7.1	-
GF0037299	0	1	0	Hypothetical protein (1)			-	C_unshiu_00452_mRNA_4.1	-
GF0037298	0	1	0	Hypothetical protein (1)			-	C_unshiu_00452_mRNA_37.1	-
GF0037297	0	1	0	Hypothetical protein (1)			-	C_unshiu_00452_mRNA_35.1	-
GF0037296	0	1	0	Hypothetical protein (1)			-	C_unshiu_00452_mRNA_32.1	-
GF0037295	0	1	0	Hypothetical protein (1)			-	C_unshiu_00452_mRNA_24.1	-
GF0037294	0	1	0	Hypothetical protein (1)			-	C_unshiu_00452_mRNA_2.1	-
GF0037293	0	1	0	Hypothetical protein (1)			-	C_unshiu_00452_mRNA_13.1	-
GF0037292	0	1	0	Hypothetical protein (1)			-	C_unshiu_00452_mRNA_11.1	-
GF0037291	0	1	0	Hypothetical protein (1)			-	C_unshiu_00451_mRNA_9.1	-
GF0037290	0	1	0	NBS-LRR type disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00451_mRNA_13.1	-
GF0037289	0	1	0	Monosacharide transport protein (1)			-	C_unshiu_00451_mRNA_10.1	-
GF0037288	0	1	0	Hypothetical protein (1)			-	C_unshiu_00450_mRNA_7.1	-
GF0037287	0	1	0	Hypothetical protein (1)			-	C_unshiu_00450_mRNA_18.1	-
GF0037286	0	1	0	Hypothetical protein (1)			-	C_unshiu_00450_mRNA_17.1	-
GF0037285	0	1	0	Hypothetical protein (1)			-	C_unshiu_00449_mRNA_7.1	-
GF0037284	0	1	0	Uncharacterized mitochondrial protein AtMg00810 (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	-	C_unshiu_00449_mRNA_5.1	-
GF0037283	0	1	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); serine-type peptidase activity [GO:0008236 molecular_function] (1)	Peptidase S9, prolyl oligopeptidase, catalytic domain [IPR001375] (1); Protein-tyrosine phosphatase-like [IPR029021] (1); Alpha/Beta hydrolase fold [IPR029058] (1)	-	C_unshiu_00449_mRNA_4.1	-
GF0037282	0	1	0	Hypothetical protein (1)			-	C_unshiu_00449_mRNA_2.1	-
GF0037281	0	1	0	Hypothetical protein (1)			-	C_unshiu_00448_mRNA_7.1	-
GF0037280	0	1	0	Hypothetical protein (1)			-	C_unshiu_00448_mRNA_20.1	-
GF0037279	0	1	0	G-type lectin S-receptor-like serine/threonine-protein kinase (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase, ATP binding site [IPR017441] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1)	-	C_unshiu_00448_mRNA_12.1	-
GF0037278	0	1	0	Golgin candidate 1 (1)			-	C_unshiu_00448_mRNA_1.1	-
GF0037277	0	1	0	Hypothetical protein (1)			-	C_unshiu_00447_mRNA_41.1	-
GF0037276	0	1	0	Hypothetical protein (1)			-	C_unshiu_00447_mRNA_37.1	-
GF0037275	0	1	0	Hypothetical protein (1)			-	C_unshiu_00447_mRNA_36.1	-
GF0037274	0	1	0	Hypothetical protein (1)			-	C_unshiu_00447_mRNA_35.1	-
GF0037273	0	1	0	Hypothetical protein (1)			-	C_unshiu_00447_mRNA_34.1	-
GF0037272	0	1	0	Hypothetical protein (1)			-	C_unshiu_00447_mRNA_33.1	-
GF0037271	0	1	0	Hypothetical protein (1)			-	C_unshiu_00447_mRNA_25.1	-
GF0037270	0	1	0	Hypothetical protein (1)		Munc13 homology 1 [IPR014770] (1); Protein of unknown function DUF810 [IPR008528] (1)	-	C_unshiu_00447_mRNA_2.1	-
GF0037269	0	1	0	Hypothetical protein (1)		Agenet domain, plant type [IPR014002] (1)	-	C_unshiu_00447_mRNA_10.1	-
GF0037268	0	1	0	Hypothetical protein (1)			-	C_unshiu_00447_mRNA_1.1	-
GF0037267	0	1	0	Cation/H(+) antiporter 20 (1)	integral component of membrane [GO:0016021 cellular_component] (1); cation transport [GO:0006812 biological_process] (1); solute:proton antiporter activity [GO:0015299 molecular_function] (1); transmembrane transport [GO:0055085 biological_process] (1)	Cation/H+ exchanger [IPR006153] (1)	-	C_unshiu_00446_mRNA_7.1	-
GF0037266	0	1	0	Hypothetical protein (1)			-	C_unshiu_00446_mRNA_6.1	-
GF0037265	0	1	0	Hypothetical protein (1)			-	C_unshiu_00446_mRNA_5.1	-
GF0037264	0	1	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_00446_mRNA_14.1	-
GF0037263	0	1	0	Serine/threonine-protein phosphatase PP1 isozyme 2 (1)	hydrolase activity [GO:0016787 molecular_function] (1)	Serine/threonine-specific protein phosphatase/bis(5-nucleosyl)-tetraphosphatase [IPR006186] (1); Metallo-dependent phosphatase-like [IPR029052] (1); Calcineurin-like phosphoesterase domain, apaH type [IPR004843] (1)	-	C_unshiu_00446_mRNA_1.1	-
GF0037262	0	1	0	Hypothetical protein (1)			-	C_unshiu_00445_mRNA_5.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0037261	0	1	0	Accelerated cell death 6 (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat-containing domain [IPR020683] (1); PGG domain [IPR026961] (1); Ankyrin repeat [IPR002110] (1)	-	C_unshiu_00445_mRNA_4.1	-
GF0037260	0	1	0	Hypothetical protein (1)			-	C_unshiu_00445_mRNA_3.1	-
GF0037259	0	1	0	Hypothetical protein (1)	catalytic activity [GO:0003824 molecular_function] (1)	HIT-like domain [IPR011146] (1); Cwf19-like, C-terminal domain-1 [IPR006768] (1); Cwf19-like protein, C-terminal domain-2 [IPR006767] (1)	-	C_unshiu_00445_mRNA_24.1	-
GF0037258	0	1	0	Hypothetical protein (1)			-	C_unshiu_00445_mRNA_23.1	-
GF0037257	0	1	0	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	C_unshiu_00445_mRNA_22.1	-
GF0037256	0	1	0	Hypothetical protein (1)		Cwf19-like protein, C-terminal domain-2 [IPR006767] (1)	-	C_unshiu_00445_mRNA_21.1	-
GF0037255	0	1	0	Ankyrin repeat family protein, putative (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat [IPR002110] (1); Ankyrin repeat-containing domain [IPR020683] (1); PGG domain [IPR026961] (1)	-	C_unshiu_00445_mRNA_2.1	-
GF0037254	0	1	0	Ribonuclease H-like superfamily protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_00445_mRNA_1.1	-
GF0037253	0	1	0	Hypothetical protein (1)			-	C_unshiu_00444_mRNA_5.1	-
GF0037252	0	1	0	Hypothetical protein (1)			-	C_unshiu_00444_mRNA_4.1	-
GF0037251	0	1	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_00444_mRNA_18.1	-
GF0037250	0	1	0	Hypothetical protein (1)			-	C_unshiu_00444_mRNA_17.1	-
GF0037249	0	1	0	Hypothetical protein (1)			-	C_unshiu_00444_mRNA_16.1	-
GF0037248	0	1	0	Hypothetical protein (1)			-	C_unshiu_00444_mRNA_15.1	-
GF0037247	0	1	0	Hypothetical protein (1)			-	C_unshiu_00444_mRNA_11.1	-
GF0037246	0	1	0	Hypothetical protein (1)			-	C_unshiu_00443_mRNA_3.1	-
GF0037245	0	1	0	Hypothetical protein (1)			-	C_unshiu_00443_mRNA_22.1	-
GF0037244	0	1	0	Hypothetical protein (1)			-	C_unshiu_00443_mRNA_21.1	-
GF0037243	0	1	0	NBS type disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1)	-	C_unshiu_00443_mRNA_18.1	-
GF0037242	0	1	0	Hypothetical protein (1)			-	C_unshiu_00443_mRNA_16.1	-
GF0037241	0	1	0	Putative non-LTR reverse transcriptase (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_00443_mRNA_15.1	-
GF0037240	0	1	0	Hypothetical protein (1)			-	C_unshiu_00443_mRNA_14.1	-
GF0037239	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00442_mRNA_5.1	-
GF0037238	0	1	0	Hypothetical protein (1)			-	C_unshiu_00441_mRNA_5.1	-
GF0037237	0	1	0	Cysteine/Histidine-rich C1 domain family protein, putative (1)	intracellular signal transduction [GO:0035556 biological_process] (1)	Protein kinase C-like, phorbol ester/diacylglycerol-binding domain [IPR002219] (1)	-	C_unshiu_00441_mRNA_3.1	-
GF0037236	0	1	0	Hypothetical protein (1)			-	C_unshiu_00441_mRNA_24.1	-
GF0037235	0	1	0	Hypothetical protein (1)			-	C_unshiu_00441_mRNA_23.1	-
GF0037234	0	1	0	Hypothetical protein (1)			-	C_unshiu_00441_mRNA_21.1	-
GF0037233	0	1	0	Hypothetical protein (1)			-	C_unshiu_00441_mRNA_20.1	-
GF0037232	0	1	0	Hypothetical protein (1)			-	C_unshiu_00441_mRNA_19.1	-
GF0037231	0	1	0	Hypothetical protein (1)			-	C_unshiu_00441_mRNA_18.1	-
GF0037230	0	1	0	Hypothetical protein (1)			-	C_unshiu_00441_mRNA_17.1	-
GF0037229	0	1	0	Hypothetical protein (1)			-	C_unshiu_00441_mRNA_14.1	-
GF0037228	0	1	0	LRR receptor-like kinase family protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	-	C_unshiu_00441_mRNA_10.1	-
GF0037227	0	1	0	Hypothetical protein (1)			-	C_unshiu_00440_mRNA_8.1	-
GF0037226	0	1	0	Hypothetical protein (1)			-	C_unshiu_00440_mRNA_6.1	-
GF0037225	0	1	0	Hypothetical protein (1)			-	C_unshiu_00440_mRNA_23.1	-
GF0037224	0	1	0	Hypothetical protein (1)			-	C_unshiu_00440_mRNA_21.1	-
GF0037223	0	1	0	Retrotransposon gag protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_00439_mRNA_9.1	-
GF0037222	0	1	0	Hypothetical protein (1)	lipid metabolic process [GO:0006629 biological_process] (1); cytoplasm [GO:0005737 cellular_component] (1); integral component of membrane [GO:0016021 cellular_component] (1); oxidoreductase activity, acting on the CH-CH group of donors [GO:0016627 molecular_function] (1)	3-oxo-5-alpha-steroid 4-dehydrogenase, C-terminal [IPR001104] (1); Actin family [IPR004000] (1); Actin/actin-like conserved site [IPR020902] (1); Actin, conserved site [IPR004001] (1)	-	C_unshiu_00439_mRNA_6.1	-
GF0037221	0	1	0	Hypothetical protein (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	-	C_unshiu_00439_mRNA_40.1	-
GF0037220	0	1	0	PK (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_00439_mRNA_36.1	-
GF0037219	0	1	0	Monosacharide transport protein (1)			-	C_unshiu_00439_mRNA_35.1	-
GF0037218	0	1	0	Hypothetical protein (1)			-	C_unshiu_00439_mRNA_34.1	-
GF0037217	0	1	0	Hypothetical protein (1)			-	C_unshiu_00439_mRNA_32.1	-
GF0037216	0	1	0	Hypothetical protein (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	-	C_unshiu_00439_mRNA_31.1	-
GF0037215	0	1	0	Hypothetical protein (1)			-	C_unshiu_00439_mRNA_29.1	-
GF0037214	0	1	0	Monosacharide transport protein (1)			-	C_unshiu_00439_mRNA_28.1	-
GF0037213	0	1	0	Hypothetical protein (1)		F-box associated interaction domain [IPR017451] (1)	-	C_unshiu_00439_mRNA_21.1	-
GF0037212	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	F-box domain [IPR001810] (1)	-	C_unshiu_00439_mRNA_20.1	-
GF0037211	0	1	0	Germin-like protein subfamily 1 member 7 (1)	nutrient reservoir activity [GO:0045735 molecular_function] (1); manganese ion binding [GO:0030145 molecular_function] (1)	Germin, manganese binding site [IPR019780] (1); Cupin 1 [IPR006045] (1); RmlC-like jelly roll fold [IPR014710] (1); Germin [IPR001929] (1); RmlC-like cupin domain [IPR011051] (1)	-	C_unshiu_00438_mRNA_7.1	-
GF0037210	0	1	0	Hypothetical protein (1)			-	C_unshiu_00438_mRNA_22.1	-
GF0037209	0	1	0	Hypothetical protein (1)		Organ specific protein [IPR024489] (1)	-	C_unshiu_00438_mRNA_2.1	-
GF0037208	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1); Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_00438_mRNA_13.1	-
GF0037207	0	1	0	Hypothetical protein (1)	nutrient reservoir activity [GO:0045735 molecular_function] (1); manganese ion binding [GO:0030145 molecular_function] (1)	Germin, manganese binding site [IPR019780] (1); Cupin 1 [IPR006045] (1); RmlC-like jelly roll fold [IPR014710] (1); Germin [IPR001929] (1); RmlC-like cupin domain [IPR011051] (1)	-	C_unshiu_00438_mRNA_12.1	-
GF0037206	0	1	0	Hypothetical protein (1)			-	C_unshiu_00438_mRNA_1.1	-
GF0037205	0	1	0	Hypothetical protein (1)			-	C_unshiu_00437_mRNA_23.1	-
GF0037204	0	1	0	Hypothetical protein (1)			-	C_unshiu_00437_mRNA_21.1	-
GF0037203	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Tetratricopeptide-like helical domain [IPR011990] (1)	-	C_unshiu_00437_mRNA_11.1	-
GF0037202	0	1	0	3-ketoacyl-CoA synthase 11 (1)	transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (1); fatty acid biosynthetic process [GO:0006633 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1); membrane [GO:0016020 cellular_component] (1); metabolic process [GO:0008152 biological_process] (1)	FAE1/Type III polyketide synthase-like protein [IPR013601] (1); Very-long-chain 3-ketoacyl-CoA synthase [IPR012392] (1); Thiolase-like [IPR016039] (1)	-	C_unshiu_00436_mRNA_4.1	-
GF0037201	0	1	0	Hypothetical protein (1)		Ankyrin repeat-containing domain [IPR020683] (1)	-	C_unshiu_00436_mRNA_32.1	-
GF0037200	0	1	0	Hypothetical protein (1)			-	C_unshiu_00436_mRNA_31.1	-
GF0037199	0	1	0	Hypothetical protein (1)			-	C_unshiu_00436_mRNA_29.1	-
GF0037198	0	1	0	Hypothetical protein (1)			-	C_unshiu_00436_mRNA_21.1	-
GF0037197	0	1	0	Hypothetical protein (1)	catalytic activity [GO:0003824 molecular_function] (1); fatty acid biosynthetic process [GO:0006633 biological_process] (1); transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (1); membrane [GO:0016020 cellular_component] (1); metabolic process [GO:0008152 biological_process] (1)	FAE1/Type III polyketide synthase-like protein [IPR013601] (1); Thiolase-like [IPR016039] (1); Very-long-chain 3-ketoacyl-CoA synthase [IPR012392] (1)	-	C_unshiu_00436_mRNA_2.1	-
GF0037196	0	1	0	Hypothetical protein (1)		Transposase, MuDR, plant [IPR004332] (1)	-	C_unshiu_00436_mRNA_19.1	-
GF0037195	0	1	0	Hypothetical protein (1)		Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_00436_mRNA_14.1	-
GF0037194	0	1	0	Amidophosphoribosyltransferase (1)	amidophosphoribosyltransferase activity [GO:0004044 molecular_function] (1); purine nucleobase biosynthetic process [GO:0009113 biological_process] (1)	Amidophosphoribosyltransferase [IPR005854] (1); Nucleophile aminohydrolases, N-terminal [IPR029055] (1); Phosphoribosyltransferase-like [IPR029057] (1); Glutamine amidotransferase type 2 domain [IPR017932] (1)	-	C_unshiu_00435_mRNA_9.1	-
GF0037193	0	1	0	Hypothetical protein (1)		Phosphoribosyltransferase-like [IPR029057] (1); Nucleophile aminohydrolases, N-terminal [IPR029055] (1)	-	C_unshiu_00435_mRNA_5.1	-
GF0037192	0	1	0	Hypothetical protein (1)		Glutamine amidotransferase type 2 domain [IPR017932] (1); Nucleophile aminohydrolases, N-terminal [IPR029055] (1)	-	C_unshiu_00435_mRNA_4.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0037191	0	1	0	Hypothetical protein (1)			-	C_unshiu_00435_mRNA_22.1	-
GF0037190	0	1	0	Hypothetical protein (1)			-	C_unshiu_00435_mRNA_20.1	-
GF0037189	0	1	0	Hypothetical protein (1)			-	C_unshiu_00435_mRNA_19.1	-
GF0037188	0	1	0	Hypothetical protein (1)		Glutamine amidotransferase type 2 domain [IPR017932] (1); Nucleophile aminohydrolases, N-terminal [IPR029055] (1)	-	C_unshiu_00435_mRNA_10.1	-
GF0037187	0	1	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	C_unshiu_00435_mRNA_1.1	-
GF0037186	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00434_mRNA_30.1	-
GF0037185	0	1	0	BED zinc finger,hAT family dimerization domain (1)	DNA binding [GO:0003677 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, BED-type [IPR003656] (1); Ribonuclease H-like domain [IPR012337] (1); hAT-like transposase, RNase-H fold [IPR025525] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	-	C_unshiu_00434_mRNA_3.1	-
GF0037184	0	1	0	Putative RNA-directed DNA polymerase (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_00434_mRNA_29.1	-
GF0037183	0	1	0	Hypothetical protein (1)			-	C_unshiu_00434_mRNA_27.1	-
GF0037182	0	1	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1)	Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	-	C_unshiu_00434_mRNA_22.1	-
GF0037181	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4220 [IPR025315] (1)	-	C_unshiu_00434_mRNA_18.1	-
GF0037180	0	1	0	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	C_unshiu_00434_mRNA_12.1	-
GF0037179	0	1	0	BZIP domain class transcription factor isoform 6 (1)	transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); sequence-specific DNA binding [GO:0043565 molecular_function] (1)	Basic-leucine zipper domain [IPR004827] (1)	-	C_unshiu_00434_mRNA_10.1	-
GF0037178	0	1	0	Cytochrome P450 81D1 (1)	heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Cytochrome P450 [IPR001128] (1); Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450, conserved site [IPR017972] (1)	-	C_unshiu_00434_mRNA_1.1	-
GF0037177	0	1	0	Hypothetical protein (1)	nucleotide-sugar transport [GO:0015780 biological_process] (1); Golgi apparatus [GO:0005794 cellular_component] (1)	GDP-mannose transporter GONST3, plant [IPR029665] (1)	-	C_unshiu_00433_mRNA_7.1	-
GF0037176	0	1	0	Hypothetical protein (1)			-	C_unshiu_00433_mRNA_25.1	-
GF0037175	0	1	0	Hypothetical protein (1)			-	C_unshiu_00433_mRNA_21.1	-
GF0037174	0	1	0	Small heat shock protein (1)		Small heat shock protein HSP20 [IPR031107] (1); Alpha crystallin/Hsp20 domain [IPR002068] (1); HSP20-like chaperone [IPR008978] (1)	-	C_unshiu_00433_mRNA_20.1	-
GF0037173	0	1	0	Hypothetical protein (1)			-	C_unshiu_00433_mRNA_1.1	-
GF0037172	0	1	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	C_unshiu_00432_mRNA_9.1	-
GF0037171	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00432_mRNA_8.1	-
GF0037170	0	1	0	Hypothetical protein (1)		Glutamine amidotransferase type 2 domain [IPR017932] (1); Nucleophile aminohydrolases, N-terminal [IPR029055] (1)	-	C_unshiu_00432_mRNA_7.1	-
GF0037169	0	1	0	Amidophosphoribosyltransferase (1)	nucleoside metabolic process [GO:0009116 biological_process] (1)	Phosphoribosyltransferase-like [IPR029057] (1); Phosphoribosyltransferase domain [IPR000836] (1)	-	C_unshiu_00432_mRNA_6.1	-
GF0037168	0	1	0	Hypothetical protein (1)		Ribosomal protein L2 domain 2 [IPR014722] (1); Domain of unknown function DUF4218 [IPR025452] (1); Translation protein SH3-like domain [IPR008991] (1)	-	C_unshiu_00432_mRNA_5.1	-
GF0037167	0	1	0	Hypothetical protein (1)		DNA-binding pseudobarrel domain [IPR015300] (1)	-	C_unshiu_00432_mRNA_18.1	-
GF0037166	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00432_mRNA_16.1	-
GF0037165	0	1	0	Hypothetical protein (1)			-	C_unshiu_00432_mRNA_15.1	-
GF0037164	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00432_mRNA_14.1	-
GF0037163	0	1	0	Hypothetical protein (1)			-	C_unshiu_00432_mRNA_13.1	-
GF0037162	0	1	0	Hypothetical protein (1)			-	C_unshiu_00432_mRNA_12.1	-
GF0037161	0	1	0	Disease resistance protein RPS2, putative (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00432_mRNA_11.1	-
GF0037160	0	1	0	Hypothetical protein (1)			-	C_unshiu_00432_mRNA_1.1	-
GF0037159	0	1	0	Hypothetical protein (1)			-	C_unshiu_00431_mRNA_5.1	-
GF0037158	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	C_unshiu_00431_mRNA_3.1	-
GF0037157	0	1	0	Hypothetical protein (1)			-	C_unshiu_00431_mRNA_24.1	-
GF0037156	0	1	0	Hypothetical protein (1)			-	C_unshiu_00431_mRNA_21.1	-
GF0037155	0	1	0	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	-	C_unshiu_00431_mRNA_2.1	-
GF0037154	0	1	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_00431_mRNA_15.1	-
GF0037153	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00431_mRNA_14.1	-
GF0037152	0	1	0	Hypothetical protein (1)			-	C_unshiu_00431_mRNA_12.1	-
GF0037151	0	1	0	Hypothetical protein (1)			-	C_unshiu_00430_mRNA_3.1	-
GF0037150	0	1	0	Hypothetical protein (1)			-	C_unshiu_00430_mRNA_2.1	-
GF0037149	0	1	0	Hypothetical protein (1)			-	C_unshiu_00430_mRNA_11.1	-
GF0037148	0	1	0	Hypothetical protein (1)			-	C_unshiu_00429_mRNA_9.1	-
GF0037147	0	1	0	Hypothetical protein (1)			-	C_unshiu_00429_mRNA_8.1	-
GF0037146	0	1	0	Hypothetical protein (1)			-	C_unshiu_00429_mRNA_24.1	-
GF0037145	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	WD40/YVTN repeat-like-containing domain [IPR015943] (1); WD40-repeat-containing domain [IPR017986] (1)	-	C_unshiu_00429_mRNA_2.1	-
GF0037144	0	1	0	Hypothetical protein (1)			-	C_unshiu_00428_mRNA_9.1	-
GF0037143	0	1	0	Hypothetical protein (1)			-	C_unshiu_00428_mRNA_30.1	-
GF0037142	0	1	0	BTB/POZ ankyrin repeat protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat [IPR002110] (1); SKP1/BTB/POZ domain [IPR011333] (1); Regulatory protein NPR, central domain [IPR024228] (1); Ankyrin repeat-containing domain [IPR020683] (1); BTB/POZ domain [IPR000210] (1)	-	C_unshiu_00428_mRNA_26.1	-
GF0037141	0	1	0	Hypothetical protein (1)			-	C_unshiu_00428_mRNA_23.1	-
GF0037140	0	1	0	BTB/POZ domain containing protein, expressed (1)	protein binding [GO:0005515 molecular_function] (1)	NPR1/NIM1-like, C-terminal [IPR021094] (1); Ankyrin repeat-containing domain [IPR020683] (1); Ankyrin repeat [IPR002110] (1)	-	C_unshiu_00428_mRNA_22.1	-
GF0037139	0	1	0	Hypothetical protein (1)		Regulatory protein NPR, central domain [IPR024228] (1)	-	C_unshiu_00428_mRNA_21.1	-
GF0037138	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat-containing domain [IPR020683] (1); NPR1/NIM1-like, C-terminal [IPR021094] (1); Transposase, MuDR, plant [IPR004332] (1); MULE transposase domain [IPR018289] (1); Zinc finger, PMZ-type [IPR006564] (1); Regulatory protein NPR, central domain [IPR024228] (1); Zinc finger, SWIM-type [IPR007527] (1); Ankyrin repeat [IPR002110] (1)	-	C_unshiu_00428_mRNA_19.1	-
GF0037137	0	1	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	-	C_unshiu_00428_mRNA_13.1	-
GF0037136	0	1	0	Hypothetical protein (1)			-	C_unshiu_00428_mRNA_11.1	-
GF0037135	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_00427_mRNA_6.1	-
GF0037134	0	1	0	Hypothetical protein (1)			-	C_unshiu_00427_mRNA_5.1	-
GF0037133	0	1	0	Hypothetical protein (1)			-	C_unshiu_00427_mRNA_4.1	-
GF0037132	0	1	0	Hypothetical protein (1)			-	C_unshiu_00427_mRNA_3.1	-
GF0037131	0	1	0	Hypothetical protein (1)			-	C_unshiu_00427_mRNA_24.1	-
GF0037130	0	1	0	Putative muDR family transposase-like (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, PMZ-type [IPR006564] (1); MULE transposase domain [IPR018289] (1)	-	C_unshiu_00427_mRNA_23.1	-
GF0037129	0	1	0	Alba DNA/RNA-binding protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	DNA/RNA-binding protein Alba-like [IPR002775] (1); Uncharacterised conserved protein UCP030333, DNA/RNA-binding Alba-related [IPR014560] (1)	-	C_unshiu_00427_mRNA_22.1	-
GF0037128	0	1	0	Hypothetical protein (1)			-	C_unshiu_00427_mRNA_2.1	-
GF0037127	0	1	0	Hypothetical protein (1)		HSP20-like chaperone [IPR008978] (1); Alpha crystallin/Hsp20 domain [IPR002068] (1)	-	C_unshiu_00427_mRNA_18.1	-
GF0037126	0	1	0	Hypothetical protein (1)			-	C_unshiu_00427_mRNA_14.1	-
GF0037125	0	1	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); metabolic process [GO:0008152 biological_process] (1)	NAC domain [IPR003441] (1); NAD(P)-binding domain [IPR016040] (1); Glucose/ribitol dehydrogenase [IPR002347] (1); Short-chain dehydrogenase/reductase, conserved site [IPR020904] (1); Short-chain dehydrogenase/reductase SDR [IPR002198] (1)	-	C_unshiu_00426_mRNA_9.1	-
GF0037124	0	1	0	Hypothetical protein (1)			-	C_unshiu_00426_mRNA_3.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0037123	0	1	0	Elongator complex protein 4 (1)	Elongator holoenzyme complex [GO:0033588 cellular_component] (1)	NPR1/NIM1-like, C-terminal [IPR021094] (1); Elongator complex protein 4 [IPR008728] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00426_mRNA_24.1	-
GF0037122	0	1	0	Hypothetical protein (1)			-	C_unshiu_00426_mRNA_15.1	-
GF0037121	0	1	0	Hypothetical protein (1)			-	C_unshiu_00426_mRNA_14.1	-
GF0037120	0	1	0	Hypothetical protein (1)			-	C_unshiu_00426_mRNA_10.1	-
GF0037119	0	1	0	Hypothetical protein (1)			-	C_unshiu_00426_mRNA_1.1	-
GF0037118	0	1	0	Hypothetical protein (1)			-	C_unshiu_00425_mRNA_26.1	-
GF0037117	0	1	0	Hypothetical protein (1)			-	C_unshiu_00425_mRNA_24.1	-
GF0037116	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	F-box domain [IPR001810] (1)	-	C_unshiu_00425_mRNA_23.1	-
GF0037115	0	1	0	Hypothetical protein (1)	integral component of membrane [GO:0016021 cellular_component] (1); serine-type endopeptidase activity [GO:0004252 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Peptidase S54, rhomboid domain [IPR022764] (1); Peptidase S54, rhomboid [IPR002610] (1)	-	C_unshiu_00425_mRNA_14.1	-
GF0037114	0	1	0	Hypothetical protein (1)			-	C_unshiu_00425_mRNA_13.1	-
GF0037113	0	1	0	Polynucleotidyl transferase, Ribonuclease H fold (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00424_mRNA_3.1	-
GF0037112	0	1	0	Hypothetical protein (1)			-	C_unshiu_00424_mRNA_23.1	-
GF0037111	0	1	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_00424_mRNA_22.1	-
GF0037110	0	1	0	Hypothetical protein (1)			-	C_unshiu_00424_mRNA_21.1	-
GF0037109	0	1	0	BED zinc finger,hAT family dimerization domain isoform 1 (1)	DNA binding [GO:0003677 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1); Ribonuclease H-like domain [IPR012337] (1); hAT-like transposase, RNase-H fold [IPR025525] (1)	-	C_unshiu_00424_mRNA_19.1	-
GF0037108	0	1	0	Hypothetical protein (1)			-	C_unshiu_00424_mRNA_14.1	-
GF0037107	0	1	0	Hypothetical protein (1)			-	C_unshiu_00424_mRNA_11.1	-
GF0037106	0	1	0	Hypothetical protein (1)			-	C_unshiu_00423_mRNA_9.1	-
GF0037105	0	1	0	Hypothetical protein (1)			-	C_unshiu_00423_mRNA_8.1	-
GF0037104	0	1	0	Hypothetical protein (1)			-	C_unshiu_00423_mRNA_3.1	-
GF0037103	0	1	0	Hypothetical protein (1)			-	C_unshiu_00423_mRNA_16.1	-
GF0037102	0	1	0	Hypothetical protein (1)			-	C_unshiu_00423_mRNA_15.1	-
GF0037101	0	1	0	NBS-LRR type disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1); GPN-loop GTPase [IPR004130] (1); AAA+ ATPase domain [IPR003593] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00423_mRNA_14.1	-
GF0037100	0	1	0	Monosacharide transport protein (1)			-	C_unshiu_00422_mRNA_6.1	-
GF0037099	0	1	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1); Xylanase inhibitor, C-terminal [IPR032799] (1)	-	C_unshiu_00422_mRNA_21.1	-
GF0037098	0	1	0	Hypothetical protein (1)			-	C_unshiu_00422_mRNA_2.1	-
GF0037097	0	1	0	Hypothetical protein (1)			-	C_unshiu_00422_mRNA_18.1	-
GF0037096	0	1	0	Hypothetical protein (1)			-	C_unshiu_00421_mRNA_9.1	-
GF0037095	0	1	0	Hypothetical protein (1)			-	C_unshiu_00421_mRNA_4.1	-
GF0037094	0	1	0	Hypothetical protein (1)			-	C_unshiu_00421_mRNA_2.1	-
GF0037093	0	1	0	Monooxygenase (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); FAD binding [GO:0071949 molecular_function] (1)	FAD-binding domain [IPR002938] (1); FAD/NAD(P)-binding domain [IPR023753] (1)	-	C_unshiu_00421_mRNA_10.1	-
GF0037092	0	1	0	Suppressor of npr1-1, constitutive 1-like protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_00421_mRNA_1.1	-
GF0037091	0	1	0	BCS1 AAA-type ATPase (1)	ATP binding [GO:0005524 molecular_function] (1)	ATPase, AAA-type, core [IPR003959] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); AAA-type ATPase, N-terminal domain [IPR025753] (1)	-	C_unshiu_00420_mRNA_8.1	-
GF0037090	0	1	0	Hypothetical protein (1)			-	C_unshiu_00420_mRNA_2.1	-
GF0037089	0	1	0	Hypothetical protein (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	FAD/NAD(P)-binding domain [IPR023753] (1)	-	C_unshiu_00420_mRNA_19.1	-
GF0037088	0	1	0	Hypothetical protein (1)	quinone binding [GO:0048038 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1); oxidoreductase activity, acting on the CH-OH group of donors, quinone or similar compound as acceptor [GO:0016901 molecular_function] (1)	Glucose/Sorbosone dehydrogenase [IPR012938] (1); Soluble quinoprotein glucose/sorbosone dehydrogenase [IPR011041] (1); Six-bladed beta-propeller, TolB-like [IPR011042] (1)	-	C_unshiu_00420_mRNA_16.1	-
GF0037087	0	1	0	LRR receptor-like kinase family protein (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Protein kinase-like domain [IPR011009] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1)	-	C_unshiu_00419_mRNA_9.1	-
GF0037086	0	1	0	Sterile alpha motif domain-containing protein 9-like protein (1)			-	C_unshiu_00419_mRNA_7.1	-
GF0037085	0	1	0	Hypothetical protein (1)			-	C_unshiu_00419_mRNA_4.1	-
GF0037084	0	1	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1); FAR1 DNA binding domain [IPR004330] (1); Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_00419_mRNA_21.1	-
GF0037083	0	1	0	Hypothetical protein (1)	serine-type endopeptidase activity [GO:0004252 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Peptidase S8, subtilisin-related [IPR015500] (1); Peptidase S8/S53 domain [IPR000209] (1)	-	C_unshiu_00419_mRNA_17.1	-
GF0037082	0	1	0	Hypothetical protein (1)			-	C_unshiu_00419_mRNA_15.1	-
GF0037081	0	1	0	Hypothetical protein (1)			-	C_unshiu_00419_mRNA_14.1	-
GF0037080	0	1	0	Hypothetical protein (1)			-	C_unshiu_00419_mRNA_13.1	-
GF0037079	0	1	0	Wall-associated receptor kinase-like 20 (1)			-	C_unshiu_00419_mRNA_12.1	-
GF0037078	0	1	0	Cytochrome P450 83B1 (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1)	Cytochrome P450 [IPR001128] (1); Cytochrome P450, E-class, group I [IPR002401] (1)	-	C_unshiu_00419_mRNA_1.1	-
GF0037077	0	1	0	Hypothetical protein (1)			-	C_unshiu_00418_mRNA_9.1	-
GF0037076	0	1	0	Hypothetical protein (1)			-	C_unshiu_00418_mRNA_4.1	-
GF0037075	0	1	0	Hypothetical protein (1)			-	C_unshiu_00418_mRNA_21.1	-
GF0037074	0	1	0	Hypothetical protein (1)			-	C_unshiu_00418_mRNA_12.1	-
GF0037073	0	1	0	Hypothetical protein (1)			-	C_unshiu_00418_mRNA_10.1	-
GF0037072	0	1	0	Hypothetical protein (1)		Nucleotide-diphospho-sugar transferases [IPR029044] (1)	-	C_unshiu_00418_mRNA_1.1	-
GF0037071	0	1	0	Hypothetical protein (1)			-	C_unshiu_00417_mRNA_25.1	-
GF0037070	0	1	0	Hypothetical protein (1)			-	C_unshiu_00417_mRNA_21.1	-
GF0037069	0	1	0	Hypothetical protein (1)			-	C_unshiu_00417_mRNA_13.1	-
GF0037068	0	1	0	Hypothetical protein (1)			-	C_unshiu_00417_mRNA_12.1	-
GF0037067	0	1	0	Hypothetical protein (1)			-	C_unshiu_00417_mRNA_1.1	-
GF0037066	0	1	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); DNA binding [GO:0003677 molecular_function] (1)	NAC domain [IPR003441] (1)	-	C_unshiu_00416_mRNA_8.1	-
GF0037065	0	1	0	Hypothetical protein (1)			-	C_unshiu_00416_mRNA_6.1	-
GF0037064	0	1	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00416_mRNA_4.1	-
GF0037063	0	1	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); DNA-templated transcription, initiation [GO:0006352 biological_process] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Transcription factor TFIIB [IPR000812] (1)	-	C_unshiu_00416_mRNA_37.1	-
GF0037062	0	1	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); zinc ion binding [GO:0008270 molecular_function] (1); DNA-templated transcription, initiation [GO:0006352 biological_process] (1)	Transcription factor TFIIB [IPR000812] (1)	-	C_unshiu_00416_mRNA_36.1	-
GF0037061	0	1	0	Protein FAR1-RELATED SEQUENCE 9 (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, PMZ-type [IPR006564] (1); MULE transposase domain [IPR018289] (1); Zinc finger, SWIM-type [IPR007527] (1); FHY3/FAR1 family [IPR031052] (1)	-	C_unshiu_00416_mRNA_28.1	-
GF0037060	0	1	0	Hypothetical protein (1)			-	C_unshiu_00416_mRNA_12.1	-
GF0037059	0	1	0	Hypothetical protein (1)			-	C_unshiu_00416_mRNA_10.1	-
GF0037058	0	1	0	Hypothetical protein (1)			-	C_unshiu_00415_mRNA_9.1	-
GF0037057	0	1	0	Hypothetical protein (1)			-	C_unshiu_00415_mRNA_6.1	-
GF0037056	0	1	0	Hypothetical protein (1)			-	C_unshiu_00415_mRNA_4.1	-
GF0037055	0	1	0	Ankyrin repeat protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat [IPR002110] (1); Ankyrin repeat-containing domain [IPR020683] (1)	-	C_unshiu_00415_mRNA_3.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0037054	0	1	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	Winged helix-turn-helix DNA-binding domain [IPR011991] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	C_unshiu_00415_mRNA_14.1	-
GF0037053	0	1	0	Hypothetical protein (1)			-	C_unshiu_00415_mRNA_12.1	-
GF0037052	0	1	0	Hypothetical protein (1)			-	C_unshiu_00415_mRNA_1.1	-
GF0037051	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00414_mRNA_9.1	-
GF0037050	0	1	0	Serine/threonine-protein kinase ULK3 (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1)	-	C_unshiu_00414_mRNA_8.1	-
GF0037049	0	1	0	Hypothetical protein (1)			-	C_unshiu_00414_mRNA_29.1	-
GF0037048	0	1	0	RING-H2 finger protein ATL78 (1)	zinc ion binding [GO:0008270 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Zinc finger, RING/FYVE/PHD-type [IPR013083] (1); Zinc finger, RING-type [IPR001841] (1)	-	C_unshiu_00414_mRNA_24.1	-
GF0037047	0	1	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	-	C_unshiu_00414_mRNA_20.1	-
GF0037046	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	-	C_unshiu_00414_mRNA_19.1	-
GF0037045	0	1	0	Hypothetical protein (1)			-	C_unshiu_00414_mRNA_17.1	-
GF0037044	0	1	0	Hypothetical protein (1)			-	C_unshiu_00414_mRNA_1.1	-
GF0037043	0	1	0	Hypothetical protein (1)			-	C_unshiu_00413_mRNA_9.1	-
GF0037042	0	1	0	Hypothetical protein (1)		Probable transposase, Ptta/En/Spm, plant [IPR004252] (1)	-	C_unshiu_00413_mRNA_6.1	-
GF0037041	0	1	0	Hypothetical protein (1)			-	C_unshiu_00413_mRNA_3.1	-
GF0037040	0	1	0	Hypothetical protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	C_unshiu_00413_mRNA_25.1	-
GF0037039	0	1	0	Hypothetical protein (1)			-	C_unshiu_00413_mRNA_17.1	-
GF0037038	0	1	0	Hypothetical protein (1)			-	C_unshiu_00413_mRNA_16.1	-
GF0037037	0	1	0	Hypothetical protein (1)			-	C_unshiu_00413_mRNA_13.1	-
GF0037036	0	1	0	Hypothetical protein (1)			-	C_unshiu_00413_mRNA_12.1	-
GF0037035	0	1	0	Protein FAM63A (1)		Protein of unknown function DUF544 [IPR007518] (1)	-	C_unshiu_00412_mRNA_7.1	-
GF0037034	0	1	0	Hypothetical protein (1)			-	C_unshiu_00412_mRNA_4.1	-
GF0037033	0	1	0	Hypothetical protein (1)			-	C_unshiu_00412_mRNA_3.1	-
GF0037032	0	1	0	Hypothetical protein (1)	nucleus [GO:0005634 cellular_component] (1); developmental process [GO:0032502 biological_process] (1); transcription, DNA-templated [GO:0006351 biological_process] (1)	WRC domain [IPR014977] (1); Growth-regulating factor [IPR031137] (1)	-	C_unshiu_00412_mRNA_28.1	-
GF0037031	0	1	0	Hypothetical protein (1)	nucleus [GO:0005634 cellular_component] (1); ATP binding [GO:0005524 molecular_function] (1); developmental process [GO:0032502 biological_process] (1); transcription, DNA-templated [GO:0006351 biological_process] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	Glutamine-Leucine-Glutamine, QLQ [IPR014978] (1); Growth-regulating factor [IPR031137] (1)	-	C_unshiu_00412_mRNA_27.1	-
GF0037030	0	1	0	Hypothetical protein (1)			-	C_unshiu_00412_mRNA_18.1	-
GF0037029	0	1	0	Hypothetical protein (1)			-	C_unshiu_00411_mRNA_25.1	-
GF0037028	0	1	0	Hypothetical protein (1)			-	C_unshiu_00411_mRNA_21.1	-
GF0037027	0	1	0	Phosphate transporter (1)	transmembrane transport [GO:0055085 biological_process] (1); transmembrane transporter activity [GO:0022857 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1)	Major facilitator, sugar transporter-like [IPR005828] (1); Major facilitator superfamily domain [IPR020846] (1)	-	C_unshiu_00411_mRNA_16.1	-
GF0037026	0	1	0	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	C_unshiu_00410_mRNA_9.1	-
GF0037025	0	1	0	Hypothetical protein (1)			-	C_unshiu_00410_mRNA_3.1	-
GF0037024	0	1	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	Zinc finger, BED-type [IPR003656] (1)	-	C_unshiu_00410_mRNA_21.1	-
GF0037023	0	1	0	Hypothetical protein (1)			-	C_unshiu_00410_mRNA_20.1	-
GF0037022	0	1	0	Hypothetical protein (1)			-	C_unshiu_00410_mRNA_17.1	-
GF0037021	0	1	0	Hypothetical protein (1)			-	C_unshiu_00410_mRNA_16.1	-
GF0037020	0	1	0	Hypothetical protein (1)		Peptidase M20, dimerisation domain [IPR011650] (1)	-	C_unshiu_00410_mRNA_15.1	-
GF0037019	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	DNA/RNA-binding protein Alba-like [IPR002775] (1)	-	C_unshiu_00410_mRNA_14.1	-
GF0037018	0	1	0	Hypothetical protein (1)			-	C_unshiu_00410_mRNA_12.1	-
GF0037017	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat-containing domain [IPR020683] (1); PGG domain [IPR026961] (1); Ankyrin repeat [IPR002110] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_00410_mRNA_11.1	-
GF0037016	0	1	0	DNAse I-like superfamily protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1); Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_00410_mRNA_10.1	-
GF0037015	0	1	0	Flavone synthase II (1)	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1)	Cytochrome P450 [IPR001128] (1); Cytochrome P450, conserved site [IPR017972] (1); Cytochrome P450, E-class, group I [IPR002401] (1)	-	C_unshiu_00410_mRNA_1.1	-
GF0037014	0	1	0	Hypothetical protein (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Aspartic peptidase, active site [IPR001969] (1)	-	C_unshiu_00409_mRNA_26.1	-
GF0037013	0	1	0	Cell division protease ftsH-like protein, chloroplasti (1)	ATP binding [GO:0005524 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1); metalloendopeptidase activity [GO:0004222 molecular_function] (1)	Peptidase M41 [IPR000642] (1)	-	C_unshiu_00409_mRNA_21.1	-
GF0037012	0	1	0	Hypothetical protein (1)			-	C_unshiu_00409_mRNA_16.1	-
GF0037011	0	1	0	Hypothetical protein (1)			-	C_unshiu_00409_mRNA_13.1	-
GF0037010	0	1	0	Hypothetical protein (1)			-	C_unshiu_00408_mRNA_8.1	-
GF0037009	0	1	0	Hypothetical protein (1)			-	C_unshiu_00408_mRNA_7.1	-
GF0037008	0	1	0	Hypothetical protein (1)			-	C_unshiu_00408_mRNA_29.1	-
GF0037007	0	1	0	Hypothetical protein (1)		Nodulin-like [IPR010658] (1)	-	C_unshiu_00408_mRNA_27.1	-
GF0037006	0	1	0	Hypothetical protein (1)			-	C_unshiu_00408_mRNA_25.1	-
GF0037005	0	1	0	Hypothetical protein (1)			-	C_unshiu_00408_mRNA_24.1	-
GF0037004	0	1	0	Hypothetical protein (1)			-	C_unshiu_00408_mRNA_22.1	-
GF0037003	0	1	0	Hypothetical protein (1)			-	C_unshiu_00408_mRNA_21.1	-
GF0037002	0	1	0	Hypothetical protein (1)	multicellular organismal development [GO:0007275 biological_process] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (1)	AP2-like ethylene-responsive transcription factor [IPR031112] (1)	-	C_unshiu_00408_mRNA_20.1	-
GF0037001	0	1	0	Hypothetical protein (1)			-	C_unshiu_00408_mRNA_2.1	-
GF0037000	0	1	0	Hypothetical protein (1)			-	C_unshiu_00408_mRNA_18.1	-
GF0036999	0	1	0	Hypothetical protein (1)			-	C_unshiu_00408_mRNA_15.1	-
GF0036998	0	1	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_00408_mRNA_14.1	-
GF0036997	0	1	0	Hypothetical protein (1)			-	C_unshiu_00408_mRNA_13.1	-
GF0036996	0	1	0	Hypothetical protein (1)			-	C_unshiu_00407_mRNA_23.1	-
GF0036995	0	1	0	Hypothetical protein (1)	transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (1)	Chloramphenicol acetyltransferase-like domain [IPR023213] (1); Transferase [IPR003480] (1)	-	C_unshiu_00406_mRNA_6.1	-
GF0036994	0	1	0	Hypothetical protein (1)			-	C_unshiu_00406_mRNA_4.1	-
GF0036993	0	1	0	Hypothetical protein (1)		Chloramphenicol acetyltransferase-like domain [IPR023213] (1)	-	C_unshiu_00406_mRNA_3.1	-
GF0036992	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	-	C_unshiu_00406_mRNA_29.1	-
GF0036991	0	1	0	Hypothetical protein (1)			-	C_unshiu_00406_mRNA_27.1	-
GF0036990	0	1	0	Hypothetical protein (1)			-	C_unshiu_00406_mRNA_26.1	-
GF0036989	0	1	0	Hypothetical protein (1)			-	C_unshiu_00406_mRNA_11.1	-
GF0036988	0	1	0	Hypothetical protein (1)			-	C_unshiu_00406_mRNA_10.1	-
GF0036987	0	1	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_00406_mRNA_1.1	-
GF0036986	0	1	0	Hypothetical protein (1)			-	C_unshiu_00405_mRNA_25.1	-
GF0036985	0	1	0	Hypothetical protein (1)	binding [GO:0005488 molecular_function] (1)	Armadillo-like helical [IPR011989] (1); Armadillo-type fold [IPR016024] (1)	-	C_unshiu_00405_mRNA_23.1	-
GF0036984	0	1	0	Hypothetical protein (1)			-	C_unshiu_00405_mRNA_22.1	-
GF0036983	0	1	0	Hypothetical protein (1)			-	C_unshiu_00405_mRNA_21.1	-
GF0036982	0	1	0	Putative E3 ubiquitin-protein ligase LIN-1 (1)	binding [GO:0005488 molecular_function] (1)	Armadillo-type fold [IPR016024] (1); Armadillo-like helical [IPR011989] (1)	-	C_unshiu_00405_mRNA_20.1	-
GF0036981	0	1	0	Eukaryotic translation initiation factor 2c, putative (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Piwi domain [IPR003165] (1)	-	C_unshiu_00405_mRNA_19.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0036980	0	1	0	Eukaryotic translation initiation factor 2c, putative (1)	protein binding [GO:0005515 molecular_function] (1)	Protein argonaute, N-terminal [IPR032474] (1); PAZ domain [IPR003100] (1); Argonaute, linker 1 domain [IPR014811] (1)	-	C_unshiu_00405_mRNA_18.1	-
GF0036979	0	1	0	Hypothetical protein (1)			-	C_unshiu_00405_mRNA_17.1	-
GF0036978	0	1	0	Hypothetical protein (1)			-	C_unshiu_00405_mRNA_14.1	-
GF0036977	0	1	0	Hypothetical protein (1)		Gag-polypeptide of LTR copia-type [IPR029472] (1)	-	C_unshiu_00405_mRNA_10.1	-
GF0036976	0	1	0	Hypothetical protein (1)			-	C_unshiu_00404_mRNA_4.1	-
GF0036975	0	1	0	26.5 kDa heat shock protein, mitochondrial (1)		Small heat shock protein HSP20 [IPR031107] (1); Alpha crystallin/Hsp20 domain [IPR002068] (1); HSP20-like chaperone [IPR008978] (1)	-	C_unshiu_00404_mRNA_26.1	-
GF0036974	0	1	0	Hypothetical protein (1)			-	C_unshiu_00404_mRNA_25.1	-
GF0036973	0	1	0	Hypothetical protein (1)			-	C_unshiu_00404_mRNA_11.1	-
GF0036972	0	1	0	Hypothetical protein (1)			-	C_unshiu_00403_mRNA_7.1	-
GF0036971	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00403_mRNA_26.1	-
GF0036970	0	1	0	Hypothetical protein (1)	lipid metabolic process [GO:0006629 biological_process] (1)	Alpha/Beta hydrolase fold [IPR029058] (1); Fungal lipase-like domain [IPR002921] (1)	-	C_unshiu_00402_mRNA_18.1	-
GF0036969	0	1	0	Hypothetical protein (1)	transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Domain of unknown function DUF4216 [IPR025312] (1); Probable transposase, Ptta/En/Spm, plant [IPR004252] (1); UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	-	C_unshiu_00402_mRNA_16.1	-
GF0036968	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4371 [IPR025398] (1)	-	C_unshiu_00402_mRNA_14.1	-
GF0036967	0	1	0	Hypothetical protein (1)			-	C_unshiu_00402_mRNA_1.1	-
GF0036966	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	C_unshiu_00401_mRNA_6.1	-
GF0036965	0	1	0	Hypothetical protein (1)			-	C_unshiu_00401_mRNA_28.1	-
GF0036964	0	1	0	Hypothetical protein (1)			-	C_unshiu_00401_mRNA_20.1	-
GF0036963	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00401_mRNA_10.1	-
GF0036962	0	1	0	Hypothetical protein (1)		Plant self-incompatibility S1 [IPR010264] (1)	-	C_unshiu_00400_mRNA_5.1	-
GF0036961	0	1	0	PANC (1)	pantoate-beta-alanine ligase activity [GO:0004592 molecular_function] (1); pantothenate biosynthetic process [GO:0015940 biological_process] (1)	Pantoate-beta-alanine ligase [IPR003721] (1); Rossmann-like alpha/beta/alpha sandwich fold [IPR014729] (1)	-	C_unshiu_00400_mRNA_28.1	-
GF0036960	0	1	0	Hypothetical protein (1)			-	C_unshiu_00400_mRNA_23.1	-
GF0036959	0	1	0	Putative methyltransferase PMT2 (1)	methyltransferase activity [GO:0008168 molecular_function] (1)	Putative S-adenosyl-L-methionine-dependent methyltransferase [IPR004159] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	C_unshiu_00399_mRNA_19.1	-
GF0036958	0	1	0	Hypothetical protein (1)			-	C_unshiu_00399_mRNA_17.1	-
GF0036957	0	1	0	Hypothetical protein (1)			-	C_unshiu_00398_mRNA_27.1	-
GF0036956	0	1	0	Hypothetical protein (1)			-	C_unshiu_00398_mRNA_23.1	-
GF0036955	0	1	0	Hypothetical protein (1)			-	C_unshiu_00398_mRNA_2.1	-
GF0036954	0	1	0	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	C_unshiu_00398_mRNA_10.1	-
GF0036953	0	1	0	Hypothetical protein (1)			-	C_unshiu_00398_mRNA_1.1	-
GF0036952	0	1	0	Hypothetical protein (1)			-	C_unshiu_00397_mRNA_7.1	-
GF0036951	0	1	0	Hypothetical protein (1)		Ankyrin repeat-containing domain [IPR020683] (1)	-	C_unshiu_00397_mRNA_20.1	-
GF0036950	0	1	0	Hypothetical protein (1)			-	C_unshiu_00397_mRNA_18.1	-
GF0036949	0	1	0	Hypothetical protein (1)			-	C_unshiu_00397_mRNA_17.1	-
GF0036948	0	1	0	Hypothetical protein (1)		Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_00396_mRNA_25.1	-
GF0036947	0	1	0	Hypothetical protein (1)			-	C_unshiu_00396_mRNA_20.1	-
GF0036946	0	1	0	CASP-like protein 1F1 (1)		Domain of unknown function DUF588 [IPR006702] (1); Casparian strip membrane protein [IPR006459] (1)	-	C_unshiu_00395_mRNA_21.1	-
GF0036945	0	1	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	-	C_unshiu_00395_mRNA_16.1	-
GF0036944	0	1	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FAR1 DNA binding domain [IPR004330] (1); FHY3/FAR1 family [IPR031052] (1)	-	C_unshiu_00395_mRNA_11.1	-
GF0036943	0	1	0	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); peroxidase activity [GO:0004601 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); response to oxidative stress [GO:0006979 biological_process] (1)	Haem peroxidase [IPR010255] (1); Haem peroxidase, plant/fungal/bacterial [IPR002016] (1); Plant peroxidase [IPR000823] (1)	-	C_unshiu_00394_mRNA_8.1	-
GF0036942	0	1	0	Hypothetical protein (1)	spermine biosynthetic process [GO:0006597 biological_process] (1); spermidine biosynthetic process [GO:0008295 biological_process] (1); adenosylmethionine decarboxylase activity [GO:0004014 molecular_function] (1)	S-adenosylmethionine decarboxylase [IPR001985] (1); S-adenosylmethionine decarboxylase, conserved site [IPR018166] (1); S-adenosylmethionine decarboxylase, core [IPR016067] (1)	-	C_unshiu_00394_mRNA_34.1	-
GF0036941	0	1	0	Hypothetical protein (1)	spermidine biosynthetic process [GO:0008295 biological_process] (1); spermine biosynthetic process [GO:0006597 biological_process] (1); adenosylmethionine decarboxylase activity [GO:0004014 molecular_function] (1)	S-adenosylmethionine decarboxylase [IPR001985] (1); S-adenosylmethionine decarboxylase, core [IPR016067] (1)	-	C_unshiu_00394_mRNA_33.1	-
GF0036940	0	1	0	Hypothetical protein (1)		BRCT domain [IPR001357] (1)	-	C_unshiu_00394_mRNA_3.1	-
GF0036939	0	1	0	Hypothetical protein (1)			-	C_unshiu_00393_mRNA_5.1	-
GF0036938	0	1	0	Hypothetical protein (1)			-	C_unshiu_00393_mRNA_17.1	-
GF0036937	0	1	0	Hypothetical protein (1)			-	C_unshiu_00393_mRNA_12.1	-
GF0036936	0	1	0	Protein STAR1 (1)	ATP binding [GO:0005524 molecular_function] (1); ATPase activity [GO:0016887 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); AAA+ ATPase domain [IPR003593] (1); ABC transporter-like [IPR003439] (1); ABC transporter, conserved site [IPR017871] (1)	-	C_unshiu_00393_mRNA_11.1	-
GF0036935	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00393_mRNA_1.1	-
GF0036934	0	1	0	Hypothetical protein (1)			-	C_unshiu_00392_mRNA_9.1	-
GF0036933	0	1	0	Hypothetical protein (1)		Zinc knuckle CX2CX4HX4C [IPR025836] (1)	-	C_unshiu_00392_mRNA_7.1	-
GF0036932	0	1	0	Hypothetical protein (1)			-	C_unshiu_00392_mRNA_6.1	-
GF0036931	0	1	0	Hypothetical protein (1)			-	C_unshiu_00392_mRNA_40.1	-
GF0036930	0	1	0	Hypothetical protein (1)			-	C_unshiu_00392_mRNA_38.1	-
GF0036929	0	1	0	Hypothetical protein (1)			-	C_unshiu_00392_mRNA_36.1	-
GF0036928	0	1	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	-	C_unshiu_00392_mRNA_33.1	-
GF0036927	0	1	0	Hypothetical protein (1)			-	C_unshiu_00392_mRNA_31.1	-
GF0036926	0	1	0	Hypothetical protein (1)			-	C_unshiu_00392_mRNA_26.1	-
GF0036925	0	1	0	Cell division cycle 5-like protein (1)	DNA binding [GO:0003677 molecular_function] (1)	Myb domain [IPR017930] (1); Homeodomain-like [IPR009057] (1); SANT/Myb domain [IPR001005] (1)	-	C_unshiu_00392_mRNA_2.1	-
GF0036924	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00392_mRNA_15.1	-
GF0036923	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00392_mRNA_13.1	-
GF0036922	0	1	0	Hypothetical protein (1)		Pre-mRNA splicing factor component Cdc5p/Cef1 [IPR021786] (1)	-	C_unshiu_00392_mRNA_1.1	-
GF0036921	0	1	0	Xyloglucan galactosyltransferase (1)		Exostosin-like [IPR004263] (1)	-	C_unshiu_00391_mRNA_8.1	-
GF0036920	0	1	0	Hypothetical protein (1)			-	C_unshiu_00391_mRNA_6.1	-
GF0036919	0	1	0	Hypothetical protein (1)	endopeptidase inhibitor activity [GO:0004866 molecular_function] (1)	Proteinase inhibitor I3, Kunitz legume [IPR002160] (1); Kunitz inhibitor ST1-like [IPR011065] (1)	-	C_unshiu_00391_mRNA_23.1	-
GF0036918	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	-	C_unshiu_00391_mRNA_22.1	-
GF0036917	0	1	0	Hypothetical protein (1)			-	C_unshiu_00390_mRNA_5.1	-
GF0036916	0	1	0	Hypothetical protein (1)		Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00390_mRNA_25.1	-
GF0036915	0	1	0	Hypothetical protein (1)			-	C_unshiu_00390_mRNA_14.1	-
GF0036914	0	1	0	Hypothetical protein (1)			-	C_unshiu_00390_mRNA_12.1	-
GF0036913	0	1	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_00389_mRNA_8.1	-
GF0036912	0	1	0	Hypothetical protein (1)	integral component of membrane [GO:0016021 cellular_component] (1); nucleotide binding [GO:0000166 molecular_function] (1)	HAD-like domain [IPR023214] (1); P-type ATPase [IPR001757] (1); P-type ATPase, cytoplasmic domain N [IPR023299] (1); P-type ATPase, transmembrane domain [IPR023298] (1)	-	C_unshiu_00389_mRNA_7.1	-
GF0036911	0	1	0	Hypothetical protein (1)			-	C_unshiu_00389_mRNA_4.1	-
GF0036910	0	1	0	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_00389_mRNA_3.1	-
GF0036909	0	1	0	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_00389_mRNA_16.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0036908	0	1	0	Dicer-like protein isoform 5 (1)	ATP binding [GO:0005524 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1); RNA binding [GO:0003723 molecular_function] (1); RNA processing [GO:0006396 biological_process] (1); protein binding [GO:0005515 molecular_function] (1); ribonuclease III activity [GO:0004525 molecular_function] (1); endoribonuclease activity, producing 5'-phosphomonoesters [GO:0016891 molecular_function] (1)	PAZ domain [IPR003100] (1); Helicase, C-terminal [IPR001650] (1); Dicer dimerisation domain [IPR005034] (1); Helicase superfamily 1/2, ATP-binding domain [IPR014001] (1); Ribonuclease III domain [IPR000999] (1); DEAD/DEAH box helicase domain [IPR011545] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00389_mRNA_1.1	-
GF0036907	0	1	0	Hypothetical protein (1)			-	C_unshiu_00388_mRNA_9.1	-
GF0036906	0	1	0	DUF4283 domain protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Domain of unknown function DUF4283 [IPR025558] (1); Zinc knuckle CX2CX4HX4C [IPR025836] (1); Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00388_mRNA_31.1	-
GF0036905	0	1	0	Hypothetical protein (1)			-	C_unshiu_00388_mRNA_30.1	-
GF0036904	0	1	0	Hypothetical protein (1)			-	C_unshiu_00388_mRNA_22.1	-
GF0036903	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc knuckle CX2CX4HX4C [IPR025836] (1); Ribonuclease H-like domain [IPR012337] (1); Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_00388_mRNA_2.1	-
GF0036902	0	1	0	Hypothetical protein (1)		Clustered mitochondria protein, N-terminal [IPR028275] (1)	-	C_unshiu_00387_mRNA_9.1	-
GF0036901	0	1	0	Hypothetical protein (1)			-	C_unshiu_00387_mRNA_6.1	-
GF0036900	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Tetratricopeptide repeat-containing domain [IPR013026] (1); Tetratricopeptide repeat [IPR019734] (1); Tetratricopeptide-like helical domain [IPR011990] (1)	-	C_unshiu_00387_mRNA_4.1	-
GF0036899	0	1	0	Hypothetical protein (1)			-	C_unshiu_00387_mRNA_21.1	-
GF0036898	0	1	0	Hypothetical protein (1)			-	C_unshiu_00387_mRNA_20.1	-
GF0036897	0	1	0	Hypothetical protein (1)			-	C_unshiu_00387_mRNA_19.1	-
GF0036896	0	1	0	Hypothetical protein (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1); phosphotransferase activity, alcohol group as acceptor [GO:0016773 molecular_function] (1)	Carbohydrate kinase, FGGY, conserved site [IPR018483] (1)	-	C_unshiu_00387_mRNA_18.1	-
GF0036895	0	1	0	LRR receptor-like serine/threonine-protein kinase GSO1 (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_00387_mRNA_17.1	-
GF0036894	0	1	0	Hypothetical protein (1)			-	C_unshiu_00387_mRNA_13.1	-
GF0036893	0	1	0	Hypothetical protein (1)	ubiquitin-protein transferase activity [GO:0004842 molecular_function] (1); glycopeptide alpha-N-acetylgalactosaminidase activity [GO:0033926 molecular_function] (1); protein ubiquitination [GO:0016567 biological_process] (1)	Glycosyl hydrolase family 100 [IPR024746] (1); U box domain [IPR003613] (1); Zinc finger, RING/FYVE/PHD-type [IPR013083] (1)	-	C_unshiu_00386_mRNA_25.1	-
GF0036892	0	1	0	Hypothetical protein (1)		ENTH/VHS [IPR008942] (1)	-	C_unshiu_00386_mRNA_24.1	-
GF0036891	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	WD40/YVTN repeat-like-containing domain [IPR015943] (1); WD40-repeat-containing domain [IPR017986] (1)	-	C_unshiu_00386_mRNA_18.1	-
GF0036890	0	1	0	Carnitine racemase like protein (1)	catalytic activity [GO:0003824 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	ClpP/crotonase-like domain [IPR029045] (1); Crotonase superfamily [IPR001753] (1)	-	C_unshiu_00386_mRNA_11.1	-
GF0036889	0	1	0	Enoyl-CoA delta isomerase 2, peroxisomal (1)	catalytic activity [GO:0003824 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	ClpP/crotonase-like domain [IPR029045] (1); Crotonase superfamily [IPR001753] (1)	-	C_unshiu_00386_mRNA_10.1	-
GF0036888	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Reverse transcriptase domain [IPR000477] (1); Zinc finger, CCHC-type [IPR001878] (1); Zinc knuckle CX2CX4HX4C [IPR025836] (1)	-	C_unshiu_00385_mRNA_25.1	-
GF0036887	0	1	0	Hypothetical protein (1)			-	C_unshiu_00385_mRNA_22.1	-
GF0036886	0	1	0	Hypothetical protein (1)			-	C_unshiu_00385_mRNA_21.1	-
GF0036885	0	1	0	Hypothetical protein (1)			-	C_unshiu_00385_mRNA_19.1	-
GF0036884	0	1	0	Hypothetical protein (1)			-	C_unshiu_00385_mRNA_17.1	-
GF0036883	0	1	0	Hypothetical protein (1)			-	C_unshiu_00385_mRNA_13.1	-
GF0036882	0	1	0	Hypothetical protein (1)	signal transduction [GO:0007165 biological_process] (1); protein binding [GO:0005515 molecular_function] (1)	Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1)	-	C_unshiu_00384_mRNA_5.1	-
GF0036881	0	1	0	Gibberellin 20 oxidase (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Non-haem dioxygenase N-terminal domain [IPR026992] (1); Isopenicillin N synthase-like [IPR027443] (1); Oxoglutarate/iron-dependent dioxygenase [IPR005123] (1)	-	C_unshiu_00384_mRNA_12.1	-
GF0036880	0	1	0	Hypothetical protein (1)			-	C_unshiu_00383_mRNA_7.1	-
GF0036879	0	1	0	Hypothetical protein (1)			-	C_unshiu_00383_mRNA_6.1	-
GF0036878	0	1	0	Hypothetical protein (1)			-	C_unshiu_00383_mRNA_3.1	-
GF0036877	0	1	0	Pectin acetylesterase (1)	hydrolase activity [GO:0016787 molecular_function] (1)	Pectinacetylesterase/NOTUM [IPR004963] (1)	-	C_unshiu_00383_mRNA_28.1	-
GF0036876	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00383_mRNA_22.1	-
GF0036875	0	1	0	Hypothetical protein (1)	calmodulin binding [GO:0005516 molecular_function] (1)	Calcium-transporting P-type ATPase, N-terminal autoinhibitory domain [IPR024750] (1)	-	C_unshiu_00383_mRNA_2.1	-
GF0036874	0	1	0	Hypothetical protein (1)	calmodulin binding [GO:0005516 molecular_function] (1)	Calcium-transporting P-type ATPase, N-terminal autoinhibitory domain [IPR024750] (1)	-	C_unshiu_00383_mRNA_12.1	-
GF0036873	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00383_mRNA_11.1	-
GF0036872	0	1	0	G-type lectin S-receptor-like serine/threonine-protein kinase (1)	recognition of pollen [GO:0048544 biological_process] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein serine/threonine kinase activity [GO:0004674 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); S-receptor-like serine/threonine-protein kinase [IPR024171] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); S-locus glycoprotein domain [IPR000858] (1); PAN/Apple domain [IPR003609] (1); Bulb-type lectin domain [IPR001480] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1)	-	C_unshiu_00382_mRNA_8.1	-
GF0036871	0	1	0	Hypothetical protein (1)		Chloramphenicol acetyltransferase-like domain [IPR023213] (1)	-	C_unshiu_00382_mRNA_19.1	-
GF0036870	0	1	0	Acylsugar acyltransferase 3 (1)	transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (1)	Transferase [IPR003480] (1); Chloramphenicol acetyltransferase-like domain [IPR023213] (1)	-	C_unshiu_00382_mRNA_18.1	-
GF0036869	0	1	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase, ATP binding site [IPR017441] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1)	-	C_unshiu_00382_mRNA_11.1	-
GF0036868	0	1	0	Hypothetical protein (1)	fatty-acyl-CoA reductase (alcohol-forming) activity [GO:0080019 molecular_function] (1)	Fatty acyl-CoA reductase [IPR026055] (1)	-	C_unshiu_00381_mRNA_4.1	-
GF0036867	0	1	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_00381_mRNA_1.1	-
GF0036866	0	1	0	Hypothetical protein (1)			-	C_unshiu_00380_mRNA_4.1	-
GF0036865	0	1	0	Hypothetical protein (1)			-	C_unshiu_00380_mRNA_22.1	-
GF0036864	0	1	0	Hypothetical protein (1)			-	C_unshiu_00380_mRNA_19.1	-
GF0036863	0	1	0	Retrotransposon protein, putative, unclassified (1)			-	C_unshiu_00380_mRNA_17.1	-
GF0036862	0	1	0	Hypothetical protein (1)			-	C_unshiu_00379_mRNA_8.1	-
GF0036861	0	1	0	Hypothetical protein (1)	metal ion binding [GO:0046872 molecular_function] (1); metal ion transport [GO:0030001 biological_process] (1)	Heavy metal-associated domain, HMA [IPR006121] (1)	-	C_unshiu_00379_mRNA_3.1	-
GF0036860	0	1	0	Hypothetical protein (1)			-	C_unshiu_00379_mRNA_25.1	-
GF0036859	0	1	0	Hypothetical protein (1)			-	C_unshiu_00379_mRNA_2.1	-
GF0036858	0	1	0	Hypothetical protein (1)			-	C_unshiu_00379_mRNA_19.1	-
GF0036857	0	1	0	Hypothetical protein (1)			-	C_unshiu_00379_mRNA_18.1	-
GF0036856	0	1	0	Hypothetical protein (1)			-	C_unshiu_00379_mRNA_17.1	-
GF0036855	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF1985 [IPR015410] (1)	-	C_unshiu_00379_mRNA_16.1	-
GF0036854	0	1	0	Hypothetical protein (1)			-	C_unshiu_00379_mRNA_11.1	-
GF0036853	0	1	0	Retrotransposon protein, putative, Ty3-gypsy subclass (1)	RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Ribonuclease H domain [IPR002156] (1)	-	C_unshiu_00379_mRNA_10.1	-
GF0036852	0	1	0	Monosacharide transport protein (1)			-	C_unshiu_00378_mRNA_8.1	-
GF0036851	0	1	0	Hypothetical protein (1)			-	C_unshiu_00378_mRNA_7.1	-
GF0036850	0	1	0	Hypothetical protein (1)			-	C_unshiu_00378_mRNA_4.1	-
GF0036849	0	1	0	Hypothetical protein (1)			-	C_unshiu_00378_mRNA_35.1	-
GF0036848	0	1	0	Hypothetical protein (1)			-	C_unshiu_00378_mRNA_31.1	-
GF0036847	0	1	0	RNA-directed DNA polymerase (Reverse transcriptase), Ribonuclease H, putative (1)	DNA integration [GO:0015074 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Integrase, catalytic core [IPR001584] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00378_mRNA_29.1	-
GF0036846	0	1	0	Hypothetical protein (1)			-	C_unshiu_00378_mRNA_25.1	-
GF0036845	0	1	0	Ankyrin repeat family protein (1)		PGG domain [IPR026961] (1); Ankyrin repeat-containing domain [IPR020683] (1)	-	C_unshiu_00378_mRNA_23.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0036844	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4371 [IPR025398] (1); Zinc finger, TTF-type [IPR006580] (1)	-	C_unshiu_00378_mRNA_22.1	-
GF0036843	0	1	0	Hypothetical protein (1)			-	C_unshiu_00378_mRNA_2.1	-
GF0036842	0	1	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	-	C_unshiu_00378_mRNA_19.1	-
GF0036841	0	1	0	Hypothetical protein (1)			-	C_unshiu_00378_mRNA_15.1	-
GF0036840	0	1	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Protein kinase-like domain [IPR011009] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Protein kinase, ATP binding site [IPR017441] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1)	-	C_unshiu_00378_mRNA_14.1	-
GF0036839	0	1	0	Ribonuclease H-like superfamily protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_00378_mRNA_13.1	-
GF0036838	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Transposon, En/Spm-like [IPR004242] (1)	-	C_unshiu_00378_mRNA_12.1	-
GF0036837	0	1	0	Hypothetical protein (1)			-	C_unshiu_00377_mRNA_9.1	-
GF0036836	0	1	0	Hypothetical protein (1)			-	C_unshiu_00377_mRNA_8.1	-
GF0036835	0	1	0	Hypothetical protein (1)			-	C_unshiu_00377_mRNA_43.1	-
GF0036834	0	1	0	Putative RNA-directed DNA polymerase (1)		Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_00377_mRNA_36.1	-
GF0036833	0	1	0	Hypothetical protein (1)			-	C_unshiu_00377_mRNA_31.1	-
GF0036832	0	1	0	Hypothetical protein (1)			-	C_unshiu_00377_mRNA_28.1	-
GF0036831	0	1	0	Hypothetical protein (1)			-	C_unshiu_00377_mRNA_27.1	-
GF0036830	0	1	0	Hypothetical protein (1)			-	C_unshiu_00377_mRNA_25.1	-
GF0036829	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00377_mRNA_24.1	-
GF0036828	0	1	0	Hypothetical protein (1)			-	C_unshiu_00377_mRNA_23.1	-
GF0036827	0	1	0	Hypothetical protein (1)			-	C_unshiu_00377_mRNA_21.1	-
GF0036826	0	1	0	Hypothetical protein (1)			-	C_unshiu_00377_mRNA_18.1	-
GF0036825	0	1	0	Hypothetical protein (1)			-	C_unshiu_00377_mRNA_13.1	-
GF0036824	0	1	0	Hypothetical protein (1)			-	C_unshiu_00376_mRNA_17.1	-
GF0036823	0	1	0	Hypothetical protein (1)			-	C_unshiu_00375_mRNA_30.1	-
GF0036822	0	1	0	Hypothetical protein (1)			-	C_unshiu_00375_mRNA_28.1	-
GF0036821	0	1	0	Hypothetical protein (1)		Zinc knuckle CX2CX4HX4C [IPR025836] (1)	-	C_unshiu_00375_mRNA_27.1	-
GF0036820	0	1	0	Hypothetical protein (1)	pyridoxal phosphate binding [GO:0030170 molecular_function] (1); catalytic activity [GO:0003824 molecular_function] (1)	Cys/Met metabolism, pyridoxal phosphate-dependent enzyme [IPR000277] (1); Pyridoxal phosphate-dependent transferase, major region, subdomain 1 [IPR015421] (1)	-	C_unshiu_00375_mRNA_25.1	-
GF0036819	0	1	0	Hypothetical protein (1)			-	C_unshiu_00375_mRNA_24.1	-
GF0036818	0	1	0	Hypothetical protein (1)			-	C_unshiu_00375_mRNA_23.1	-
GF0036817	0	1	0	Hypothetical protein (1)			-	C_unshiu_00375_mRNA_2.1	-
GF0036816	0	1	0	Hypothetical protein (1)			-	C_unshiu_00375_mRNA_13.1	-
GF0036815	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Reverse transcriptase domain [IPR000477] (1); Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00374_mRNA_7.1	-
GF0036814	0	1	0	Hypothetical protein (1)			-	C_unshiu_00374_mRNA_6.1	-
GF0036813	0	1	0	Diphthamide biosynthesis protein 2 (1)		Diphthamide synthesis DPH1/DPH2 [IPR016435] (1)	-	C_unshiu_00374_mRNA_48.1	-
GF0036812	0	1	0	Hypothetical protein (1)			-	C_unshiu_00374_mRNA_40.1	-
GF0036811	0	1	0	Hypothetical protein (1)			-	C_unshiu_00374_mRNA_39.1	-
GF0036810	0	1	0	Hypothetical protein (1)			-	C_unshiu_00374_mRNA_38.1	-
GF0036809	0	1	0	Hypothetical protein (1)			-	C_unshiu_00374_mRNA_30.1	-
GF0036808	0	1	0	Hypothetical protein (1)			-	C_unshiu_00374_mRNA_3.1	-
GF0036807	0	1	0	Hypothetical protein (1)			-	C_unshiu_00374_mRNA_2.1	-
GF0036806	0	1	0	Hypothetical protein (1)			-	C_unshiu_00374_mRNA_17.1	-
GF0036805	0	1	0	Hypothetical protein (1)			-	C_unshiu_00374_mRNA_14.1	-
GF0036804	0	1	0	Hypothetical protein (1)			-	C_unshiu_00374_mRNA_13.1	-
GF0036803	0	1	0	Hypothetical protein (1)			-	C_unshiu_00374_mRNA_11.1	-
GF0036802	0	1	0	Hypothetical protein (1)	GTP binding [GO:0005525 molecular_function] (1)	AIG1-type guanine nucleotide-binding (G) domain [IPR006703] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00373_mRNA_5.1	-
GF0036801	0	1	0	Hypothetical protein (1)			-	C_unshiu_00373_mRNA_34.1	-
GF0036800	0	1	0	Hypothetical protein (1)			-	C_unshiu_00373_mRNA_33.1	-
GF0036799	0	1	0	Hypothetical protein (1)			-	C_unshiu_00373_mRNA_31.1	-
GF0036798	0	1	0	Hypothetical protein (1)			-	C_unshiu_00373_mRNA_27.1	-
GF0036797	0	1	0	Hypothetical protein (1)			-	C_unshiu_00373_mRNA_26.1	-
GF0036796	0	1	0	Hypothetical protein (1)			-	C_unshiu_00373_mRNA_24.1	-
GF0036795	0	1	0	GTP binding protein (1)	GTP binding [GO:0005525 molecular_function] (1)	AIG1-type guanine nucleotide-binding (G) domain [IPR006703] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00373_mRNA_18.1	-
GF0036794	0	1	0	Protein AIG1 (1)	GTP binding [GO:0005525 molecular_function] (1)	AIG1-type guanine nucleotide-binding (G) domain [IPR006703] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00373_mRNA_15.1	-
GF0036793	0	1	0	Hypothetical protein (1)			-	C_unshiu_00372_mRNA_4.1	-
GF0036792	0	1	0	Hypothetical protein (1)			-	C_unshiu_00372_mRNA_23.1	-
GF0036791	0	1	0	Hypothetical protein (1)			-	C_unshiu_00372_mRNA_20.1	-
GF0036790	0	1	0	Hypothetical protein (1)			-	C_unshiu_00372_mRNA_2.1	-
GF0036789	0	1	0	Hypothetical protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	C_unshiu_00372_mRNA_18.1	-
GF0036788	0	1	0	Hypothetical protein (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1)	-	C_unshiu_00372_mRNA_16.1	-
GF0036787	0	1	0	LRR receptor-like kinase family protein (1)	protein binding [GO:0005515 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase, ATP binding site [IPR017441] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Protein kinase-like domain [IPR011009] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Protein kinase domain [IPR000719] (1)	-	C_unshiu_00372_mRNA_1.1	-
GF0036786	0	1	0	Hypothetical protein (1)	acetylglucosaminyltransferase activity [GO:0008375 molecular_function] (1); membrane [GO:0016020 cellular_component] (1)	Glycosyl transferase, family 14 [IPR003406] (1)	-	C_unshiu_00371_mRNA_5.1	-
GF0036785	0	1	0	Hypothetical protein (1)			-	C_unshiu_00371_mRNA_18.1	-
GF0036784	0	1	0	Hypothetical protein (1)			-	C_unshiu_00371_mRNA_11.1	-
GF0036783	0	1	0	Ubiquitin-specific protease family C19 protein (1)			-	C_unshiu_00371_mRNA_1.1	-
GF0036782	0	1	0	BZIP transcription factor 60-like protein (1)			-	C_unshiu_00370_mRNA_40.1	-
GF0036781	0	1	0	Hypothetical protein (1)			-	C_unshiu_00370_mRNA_31.1	-
GF0036780	0	1	0	Hypothetical protein (1)	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor [GO:0016616 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); 3-beta-hydroxy-delta5-steroid dehydrogenase activity [GO:0003854 molecular_function] (1); steroid biosynthetic process [GO:0006694 biological_process] (1)	3-beta hydroxysteroid dehydrogenase/isomerase [IPR002225] (1); NAD(P)-binding domain [IPR016040] (1)	-	C_unshiu_00370_mRNA_30.1	-
GF0036779	0	1	0	Kelch repeat-containing F-box family protein (1)	protein binding [GO:0005515 molecular_function] (1)	Kelch repeat type 1 [IPR006652] (1); Galactose oxidase/kelch, beta-propeller [IPR011043] (1); Galactose oxidase, beta-propeller [IPR015916] (1)	-	C_unshiu_00370_mRNA_2.1	-
GF0036778	0	1	0	Hypothetical protein (1)	integral component of membrane [GO:0016021 cellular_component] (1); defense response [GO:0006952 biological_process] (1)	Mlo-related protein [IPR004326] (1)	-	C_unshiu_00370_mRNA_10.1	-
GF0036777	0	1	0	Hypothetical protein (1)	binding [GO:0005488 molecular_function] (1)	Armadillo-like helical [IPR011989] (1); Armadillo-type fold [IPR016024] (1)	-	C_unshiu_00370_mRNA_1.1	-
GF0036776	0	1	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	-	C_unshiu_00369_mRNA_45.1	-
GF0036775	0	1	0	G-type lectin S-receptor-like serine/threonine-protein kinase (1)	ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	PAN/Apple domain [IPR003609] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	-	C_unshiu_00369_mRNA_43.1	-
GF0036774	0	1	0	Hypothetical protein (1)			-	C_unshiu_00369_mRNA_38.1	-
GF0036773	0	1	0	Hypothetical protein (1)			-	C_unshiu_00369_mRNA_37.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0036772	0	1	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1)	Peptidase A3A, cauliflower mosaic virus-type [IPR000588] (1); Aspartic peptidase domain [IPR021109] (1)	-	C_unshiu_00369_mRNA_35.1	-
GF0036771	0	1	0	Hypothetical protein (1)			-	C_unshiu_00369_mRNA_34.1	-
GF0036770	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_00369_mRNA_28.1	-
GF0036769	0	1	0	Hypothetical protein (1)			-	C_unshiu_00369_mRNA_27.1	-
GF0036768	0	1	0	Hypothetical protein (1)			-	C_unshiu_00369_mRNA_26.1	-
GF0036767	0	1	0	Hypothetical protein (1)			-	C_unshiu_00369_mRNA_25.1	-
GF0036766	0	1	0	Hypothetical protein (1)			-	C_unshiu_00369_mRNA_23.1	-
GF0036765	0	1	0	Hypothetical protein (1)		P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00369_mRNA_2.1	-
GF0036764	0	1	0	Hypothetical protein (1)		Helicase, C-terminal [IPR001650] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00369_mRNA_1.1	-
GF0036763	0	1	0	Hypothetical protein (1)			-	C_unshiu_00368_mRNA_22.1	-
GF0036762	0	1	0	Hypothetical protein (1)			-	C_unshiu_00368_mRNA_21.1	-
GF0036761	0	1	0	Hypothetical protein (1)			-	C_unshiu_00368_mRNA_18.1	-
GF0036760	0	1	0	Hypothetical protein (1)		Heat shock protein 70kD, peptide-binding domain [IPR029047] (1); Heat shock protein 70 family [IPR013126] (1); Heat shock protein 70, conserved site [IPR018181] (1); Heat shock protein 70kD, C-terminal domain [IPR029048] (1)	-	C_unshiu_00368_mRNA_1.1	-
GF0036759	0	1	0	Peter Pan-like protein (1)			-	C_unshiu_00367_mRNA_2.1	-
GF0036758	0	1	0	LRR receptor-like kinase family protein, putative (1)		Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00367_mRNA_19.1	-
GF0036757	0	1	0	Hypothetical protein (1)	transport [GO:0006810 biological_process] (1)	Longin domain [IPR010908] (1); Longin-like domain [IPR011012] (1)	-	C_unshiu_00367_mRNA_12.1	-
GF0036756	0	1	0	S-adenosylmethionine decarboxylase proenzyme (1)	spermidine biosynthetic process [GO:0008295 biological_process] (1); spermine biosynthetic process [GO:0006597 biological_process] (1); adenosylmethionine decarboxylase activity [GO:0004014 molecular_function] (1)	S-adenosylmethionine decarboxylase, core [IPR016067] (1); S-adenosylmethionine decarboxylase subgroup [IPR018167] (1); S-adenosylmethionine decarboxylase, conserved site [IPR018166] (1); S-adenosylmethionine decarboxylase [IPR001985] (1)	-	C_unshiu_00366_mRNA_33.1	-
GF0036755	0	1	0	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	-	C_unshiu_00366_mRNA_22.1	-
GF0036754	0	1	0	Hypothetical protein (1)			-	C_unshiu_00366_mRNA_16.1	-
GF0036753	0	1	0	Hypothetical protein (1)			-	C_unshiu_00366_mRNA_12.1	-
GF0036752	0	1	0	Hypothetical protein (1)			-	C_unshiu_00366_mRNA_1.1	-
GF0036751	0	1	0	Hypothetical protein (1)			-	C_unshiu_00365_mRNA_5.1	-
GF0036750	0	1	0	Retrotransposon protein, putative, Ty1-copia subclass (1)			-	C_unshiu_00365_mRNA_29.1	-
GF0036749	0	1	0	Disease resistance protein (NBS-LRR class) family protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00365_mRNA_28.1	-
GF0036748	0	1	0	Transposable element Ac (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00365_mRNA_12.1	-
GF0036747	0	1	0	Hypothetical protein (1)			-	C_unshiu_00364_mRNA_3.1	-
GF0036746	0	1	0	Hypothetical protein (1)			-	C_unshiu_00364_mRNA_23.1	-
GF0036745	0	1	0	Hypothetical protein (1)			-	C_unshiu_00364_mRNA_16.1	-
GF0036744	0	1	0	Hypothetical protein (1)			-	C_unshiu_00364_mRNA_10.1	-
GF0036743	0	1	0	Hypothetical protein (1)			-	C_unshiu_00364_mRNA_1.1	-
GF0036742	0	1	0	Hypothetical protein (1)			-	C_unshiu_00363_mRNA_7.1	-
GF0036741	0	1	0	S-methyl-5-thioribose kinase (1)		Protein kinase-like domain [IPR011009] (1); Aminoglycoside phosphotransferase [IPR002575] (1)	-	C_unshiu_00363_mRNA_6.1	-
GF0036740	0	1	0	Hypothetical protein (1)			-	C_unshiu_00363_mRNA_25.1	-
GF0036739	0	1	0	Hypothetical protein (1)	transcription elongation from RNA polymerase II promoter [GO:0006368 biological_process] (1); histone modification [GO:0016570 biological_process] (1); Cdc73/Paf1 complex [GO:0016593 cellular_component] (1)	RNA polymerase-associated protein Rtf1 [IPR031102] (1)	-	C_unshiu_00363_mRNA_17.1	-
GF0036738	0	1	0	Hypothetical protein (1)			-	C_unshiu_00363_mRNA_11.1	-
GF0036737	0	1	0	Hypothetical protein (1)		Gag-polypeptide of LTR copia-type [IPR029472] (1)	-	C_unshiu_00362_mRNA_8.1	-
GF0036736	0	1	0	Hypothetical protein (1)			-	C_unshiu_00362_mRNA_7.1	-
GF0036735	0	1	0	Hypothetical protein (1)			-	C_unshiu_00362_mRNA_6.1	-
GF0036734	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00362_mRNA_5.1	-
GF0036733	0	1	0	Hypothetical protein (1)			-	C_unshiu_00362_mRNA_2.1	-
GF0036732	0	1	0	Hypothetical protein (1)			-	C_unshiu_00362_mRNA_18.1	-
GF0036731	0	1	0	Hypothetical protein (1)			-	C_unshiu_00362_mRNA_16.1	-
GF0036730	0	1	0	Hypothetical protein (1)	membrane [GO:0016020 cellular_component] (1); transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (1); fatty acid biosynthetic process [GO:0006633 biological_process] (1)	Very-long-chain 3-ketoacyl-CoA synthase [IPR012392] (1)	-	C_unshiu_00362_mRNA_14.1	-
GF0036729	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00361_mRNA_7.1	-
GF0036728	0	1	0	Hypothetical protein (1)			-	C_unshiu_00361_mRNA_6.1	-
GF0036727	0	1	0	Hypothetical protein (1)			-	C_unshiu_00361_mRNA_19.1	-
GF0036726	0	1	0	Hypothetical protein (1)			-	C_unshiu_00361_mRNA_17.1	-
GF0036725	0	1	0	Hypothetical protein (1)			-	C_unshiu_00361_mRNA_11.1	-
GF0036724	0	1	0	Hypothetical protein (1)	hydrolase activity [GO:0016787 molecular_function] (1)	Pectinacetylesterase/NOTUM [IPR004963] (1)	-	C_unshiu_00361_mRNA_1.1	-
GF0036723	0	1	0	Hypothetical protein (1)			-	C_unshiu_00360_mRNA_6.1	-
GF0036722	0	1	0	Hypothetical protein (1)			-	C_unshiu_00360_mRNA_3.1	-
GF0036721	0	1	0	Hypothetical protein (1)			-	C_unshiu_00360_mRNA_27.1	-
GF0036720	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00360_mRNA_24.1	-
GF0036719	0	1	0	Hypothetical protein (1)			-	C_unshiu_00360_mRNA_19.1	-
GF0036718	0	1	0	Hypothetical protein (1)			-	C_unshiu_00360_mRNA_17.1	-
GF0036717	0	1	0	Hypothetical protein (1)			-	C_unshiu_00359_mRNA_9.1	-
GF0036716	0	1	0	Hypothetical protein (1)			-	C_unshiu_00359_mRNA_14.1	-
GF0036715	0	1	0	Hypothetical protein (1)			-	C_unshiu_00359_mRNA_12.1	-
GF0036714	0	1	0	Hypothetical protein (1)			-	C_unshiu_00359_mRNA_11.1	-
GF0036713	0	1	0	Hypothetical protein (1)			-	C_unshiu_00359_mRNA_10.1	-
GF0036712	0	1	0	Hypothetical protein (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1)	Glycoside hydrolase, catalytic domain [IPR013781] (1)	-	C_unshiu_00359_mRNA_1.1	-
GF0036711	0	1	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_00358_mRNA_8.1	-
GF0036710	0	1	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_00358_mRNA_5.1	-
GF0036709	0	1	0	Hypothetical protein (1)			-	C_unshiu_00358_mRNA_3.1	-
GF0036708	0	1	0	Hypothetical protein (1)			-	C_unshiu_00358_mRNA_2.1	-
GF0036707	0	1	0	Hypothetical protein (1)			-	C_unshiu_00358_mRNA_18.1	-
GF0036706	0	1	0	Hypothetical protein (1)			-	C_unshiu_00358_mRNA_16.1	-
GF0036705	0	1	0	3-ketoacyl-CoA synthase 11 (1)	fatty acid biosynthetic process [GO:0006633 biological_process] (1); transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (1); catalytic activity [GO:0003824 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1); membrane [GO:0016020 cellular_component] (1)	FAE1/Type III polyketide synthase-like protein [IPR013601] (1); 3-Oxoacyl-[acyl-carrier-protein (ACP)] synthase III, C-terminal [IPR013747] (1); Thiolase-like [IPR016039] (1); Very-long-chain 3-ketoacyl-CoA synthase [IPR012392] (1)	-	C_unshiu_00358_mRNA_15.1	-
GF0036704	0	1	0	Hypothetical protein (1)			-	C_unshiu_00358_mRNA_14.1	-
GF0036703	0	1	0	Hypothetical protein (1)			-	C_unshiu_00358_mRNA_12.1	-
GF0036702	0	1	0	Hypothetical protein (1)			-	C_unshiu_00358_mRNA_11.1	-
GF0036701	0	1	0	Hypothetical protein (1)			-	C_unshiu_00357_mRNA_8.1	-
GF0036700	0	1	0	Hypothetical protein (1)			-	C_unshiu_00357_mRNA_4.1	-
GF0036699	0	1	0	Hypothetical protein (1)			-	C_unshiu_00357_mRNA_26.1	-
GF0036698	0	1	0	Hypothetical protein (1)			-	C_unshiu_00357_mRNA_25.1	-
GF0036697	0	1	0	Hypothetical protein (1)			-	C_unshiu_00357_mRNA_23.1	-
GF0036696	0	1	0	Polynucleotidyl transferase, ribonuclease H-like superfamily protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00357_mRNA_16.1	-
GF0036695	0	1	0	Hypothetical protein (1)			-	C_unshiu_00357_mRNA_13.1	-
GF0036694	0	1	0	Hypothetical protein (1)			-	C_unshiu_00356_mRNA_9.1	-
GF0036693	0	1	0	Hypothetical protein (1)			-	C_unshiu_00356_mRNA_8.1	-
GF0036692	0	1	0	Hypothetical protein (1)			-	C_unshiu_00356_mRNA_6.1	-
GF0036691	0	1	0	Hypothetical protein (1)			-	C_unshiu_00356_mRNA_5.1	-
GF0036690	0	1	0	Hypothetical protein (1)			-	C_unshiu_00356_mRNA_3.1	-
GF0036689	0	1	0	Hypothetical protein (1)			-	C_unshiu_00356_mRNA_10.1	-
GF0036688	0	1	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1)	-	C_unshiu_00356_mRNA_1.1	-
GF0036687	0	1	0	Hypothetical protein (1)		Gag-polypeptide of LTR copia-type [IPR029472] (1)	-	C_unshiu_00354_mRNA_3.1	-
GF0036686	0	1	0	Hypothetical protein (1)			-	C_unshiu_00354_mRNA_19.1	-
GF0036685	0	1	0	Hypothetical protein (1)			-	C_unshiu_00354_mRNA_18.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0036684	0	1	0	Hypothetical protein (1)	transporter activity [GO:0005215 molecular_function] (1); transport [GO:0006810 biological_process] (1); membrane [GO:0016020 cellular_component] (1)	Reverse transcriptase zinc-binding domain [IPR026960] (1); Proton-dependent oligopeptide transporter family [IPR000109] (1)	-	C_unshiu_00354_mRNA_17.1	-
GF0036683	0	1	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_00354_mRNA_14.1	-
GF0036682	0	1	0	Hypothetical protein (1)		Tubby C-terminal-like domain [IPR025659] (1); LURP1-related protein domain [IPR007612] (1)	-	C_unshiu_00354_mRNA_13.1	-
GF0036681	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00354_mRNA_10.1	-
GF0036680	0	1	0	Hypothetical protein (1)		Senescence/spartin-associated [IPR009686] (1)	-	C_unshiu_00353_mRNA_9.1	-
GF0036679	0	1	0	Hypothetical protein (1)			-	C_unshiu_00353_mRNA_34.1	-
GF0036678	0	1	0	Hypothetical protein (1)			-	C_unshiu_00353_mRNA_28.1	-
GF0036677	0	1	0	Small GTPase RacB (1)	small GTPase mediated signal transduction [GO:0007264 biological_process] (1); membrane [GO:0016020 cellular_component] (1); signal transduction [GO:0007165 biological_process] (1); GTP binding [GO:0005525 molecular_function] (1); intracellular [GO:0005622 cellular_component] (1); protein transport [GO:0015031 biological_process] (1)	Ubiquitin-conjugating enzyme E2 [IPR000608] (1); Small GTPase superfamily, Ras type [IPR020849] (1); Small GTP-binding protein domain [IPR005225] (1); Small GTPase superfamily, Rho type [IPR003578] (1); Small GTPase superfamily [IPR001806] (1); Ubiquitin-conjugating enzyme/RWD-like [IPR016135] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Small GTPase superfamily, Rab type [IPR003579] (1)	-	C_unshiu_00353_mRNA_24.1	-
GF0036676	0	1	0	Hypothetical protein (1)			-	C_unshiu_00353_mRNA_15.1	-
GF0036675	0	1	0	Hypothetical protein (1)			-	C_unshiu_00353_mRNA_1.1	-
GF0036674	0	1	0	Hypothetical protein (1)			-	C_unshiu_00352_mRNA_7.1	-
GF0036673	0	1	0	Disease resistance protein RPS2 (1)	ADP binding [GO:0043531 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	C_unshiu_00352_mRNA_6.1	-
GF0036672	0	1	0	Putative calcium-binding protein CML15 (1)	calcium ion binding [GO:0005509 molecular_function] (1)	EF-hand domain pair [IPR011992] (1); EF-hand domain [IPR002048] (1); EF-Hand 1, calcium-binding site [IPR018247] (1)	-	C_unshiu_00352_mRNA_5.1	-
GF0036671	0	1	0	Disease resistance protein RPS2 (1)	ADP binding [GO:0043531 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00352_mRNA_4.1	-
GF0036670	0	1	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, SWIM-type [IPR007527] (1); Zinc finger, PMZ-type [IPR006564] (1); FHY3/FAR1 family [IPR031052] (1)	-	C_unshiu_00352_mRNA_34.1	-
GF0036669	0	1	0	Hypothetical protein (1)			-	C_unshiu_00352_mRNA_28.1	-
GF0036668	0	1	0	Hypothetical protein (1)			-	C_unshiu_00352_mRNA_26.1	-
GF0036667	0	1	0	Hypothetical protein (1)			-	C_unshiu_00352_mRNA_25.1	-
GF0036666	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_00352_mRNA_24.1	-
GF0036665	0	1	0	Hypothetical protein (1)			-	C_unshiu_00352_mRNA_17.1	-
GF0036664	0	1	0	Hypothetical protein (1)			-	C_unshiu_00352_mRNA_14.1	-
GF0036663	0	1	0	Hypothetical protein (1)			-	C_unshiu_00352_mRNA_1.1	-
GF0036662	0	1	0	Hypothetical protein (1)			-	C_unshiu_00351_mRNA_6.1	-
GF0036661	0	1	0	Hypothetical protein (1)			-	C_unshiu_00351_mRNA_5.1	-
GF0036660	0	1	0	Hypothetical protein (1)			-	C_unshiu_00351_mRNA_22.1	-
GF0036659	0	1	0	Hypothetical protein (1)			-	C_unshiu_00351_mRNA_21.1	-
GF0036658	0	1	0	Phloem protein 2-B5 (1)		Phloem protein 2-like [IPR025886] (1)	-	C_unshiu_00351_mRNA_15.1	-
GF0036657	0	1	0	Hypothetical protein (1)			-	C_unshiu_00350_mRNA_9.1	-
GF0036656	0	1	0	RNA-directed DNA polymerase (Reverse transcriptase) (1)		Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_00350_mRNA_5.1	-
GF0036655	0	1	0	CDNA clone:002-110-H12, full insert sequence (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00350_mRNA_37.1	-
GF0036654	0	1	0	Hypothetical protein (1)			-	C_unshiu_00350_mRNA_36.1	-
GF0036653	0	1	0	Hypothetical protein (1)	DNA integration [GO:0015074 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Integrase, catalytic core [IPR001584] (1)	-	C_unshiu_00350_mRNA_35.1	-
GF0036652	0	1	0	Hypothetical protein (1)			-	C_unshiu_00350_mRNA_31.1	-
GF0036651	0	1	0	Hypothetical protein (1)			-	C_unshiu_00350_mRNA_30.1	-
GF0036650	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1); zinc ion binding [GO:0008270 molecular_function] (1); transmembrane transporter activity [GO:0022857 molecular_function] (1); membrane [GO:0016020 cellular_component] (1)	EamA domain [IPR000620] (1); WAT1-related protein [IPR030184] (1); Zinc finger, CCHC-type [IPR001878] (1); Viral movement protein [IPR028919] (1)	-	C_unshiu_00350_mRNA_29.1	-
GF0036649	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_00350_mRNA_26.1	-
GF0036648	0	1	0	Hypothetical protein (1)	immune response [GO:0006955 biological_process] (1)	MHC class I-like antigen recognition-like [IPR011161] (1)	-	C_unshiu_00350_mRNA_25.1	-
GF0036647	0	1	0	Hypothetical protein (1)			-	C_unshiu_00350_mRNA_24.1	-
GF0036646	0	1	0	Hypothetical protein (1)			-	C_unshiu_00350_mRNA_23.1	-
GF0036645	0	1	0	Hypothetical protein (1)			-	C_unshiu_00350_mRNA_21.1	-
GF0036644	0	1	0	Hypothetical protein (1)			-	C_unshiu_00350_mRNA_19.1	-
GF0036643	0	1	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_00350_mRNA_17.1	-
GF0036642	0	1	0	Hypothetical protein (1)			-	C_unshiu_00350_mRNA_16.1	-
GF0036641	0	1	0	Hypothetical protein (1)			-	C_unshiu_00350_mRNA_13.1	-
GF0036640	0	1	0	Hypothetical protein (1)			-	C_unshiu_00350_mRNA_12.1	-
GF0036639	0	1	0	Hypothetical protein (1)			-	C_unshiu_00350_mRNA_10.1	-
GF0036638	0	1	0	Hypothetical protein (1)			-	C_unshiu_00350_mRNA_1.1	-
GF0036637	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Tetratricopeptide-like helical domain [IPR011990] (1); Tetratricopeptide repeat [IPR019734] (1); Tetratricopeptide repeat-containing domain [IPR013026] (1)	-	C_unshiu_00349_mRNA_8.1	-
GF0036636	0	1	0	Retrotransposon protein, putative, Ty1-copia subclass (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1); Gag-polypeptide of LTR copia-type [IPR029472] (1)	-	C_unshiu_00349_mRNA_7.1	-
GF0036635	0	1	0	Hypothetical protein (1)			-	C_unshiu_00349_mRNA_29.1	-
GF0036634	0	1	0	Hypothetical protein (1)			-	C_unshiu_00349_mRNA_28.1	-
GF0036633	0	1	0	Hypothetical protein (1)			-	C_unshiu_00349_mRNA_15.1	-
GF0036632	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H-like domain [IPR012337] (1); Tetratricopeptide repeat [IPR019734] (1); Tetratricopeptide repeat-containing domain [IPR013026] (1); Tetratricopeptide-like helical domain [IPR011990] (1); Zinc knuckle CX2CX4HX4C [IPR025836] (1); Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00349_mRNA_12.1	-
GF0036631	0	1	0	Hypothetical protein (1)			-	C_unshiu_00349_mRNA_1.1	-
GF0036630	0	1	0	Hypothetical protein (1)	transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (1)	Chloramphenicol acetyltransferase-like domain [IPR023213] (1); Transferase [IPR003480] (1)	-	C_unshiu_00348_mRNA_6.1	-
GF0036629	0	1	0	Hypothetical protein (1)			-	C_unshiu_00348_mRNA_3.1	-
GF0036628	0	1	0	Hypothetical protein (1)			-	C_unshiu_00348_mRNA_2.1	-
GF0036627	0	1	0	Transmembrane amino acid transporter family protein (1)		Amino acid transporter, transmembrane domain [IPR013057] (1)	-	C_unshiu_00348_mRNA_18.1	-
GF0036626	0	1	0	Cytochrome c oxidase subunit 6b (1)	cytochrome-c oxidase activity [GO:0004129 molecular_function] (1); mitochondrion [GO:0005739 cellular_component] (1)	Cytochrome c oxidase, subunit VIb [IPR003213] (1)	-	C_unshiu_00348_mRNA_16.1	-
GF0036625	0	1	0	Hypothetical protein (1)			-	C_unshiu_00348_mRNA_11.1	-
GF0036624	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_00346_mRNA_34.1	-
GF0036623	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	C_unshiu_00346_mRNA_31.1	-
GF0036622	0	1	0	Hypothetical protein (1)			-	C_unshiu_00346_mRNA_3.1	-
GF0036621	0	1	0	Hypothetical protein (1)			-	C_unshiu_00346_mRNA_22.1	-
GF0036620	0	1	0	Hypothetical protein (1)			-	C_unshiu_00346_mRNA_21.1	-
GF0036619	0	1	0	Hypothetical protein (1)			-	C_unshiu_00346_mRNA_20.1	-
GF0036618	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Peptidase A2A, retrovirus, catalytic [IPR001995] (1); Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00346_mRNA_19.1	-
GF0036617	0	1	0	Hypothetical protein (1)			-	C_unshiu_00346_mRNA_17.1	-
GF0036616	0	1	0	Hypothetical protein (1)			-	C_unshiu_00346_mRNA_13.1	-
GF0036615	0	1	0	Hypothetical protein (1)			-	C_unshiu_00346_mRNA_12.1	-
GF0036614	0	1	0	Hypothetical protein (1)			-	C_unshiu_00345_mRNA_7.1	-
GF0036613	0	1	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); DNA binding [GO:0003677 molecular_function] (1)	NAC domain [IPR003441] (1)	-	C_unshiu_00345_mRNA_5.1	-
GF0036612	0	1	0	Hypothetical protein (1)			-	C_unshiu_00345_mRNA_28.1	-
GF0036611	0	1	0	Hypothetical protein (1)			-	C_unshiu_00345_mRNA_26.1	-
GF0036610	0	1	0	Hypothetical protein (1)			-	C_unshiu_00345_mRNA_25.1	-
GF0036609	0	1	0	Hypothetical protein (1)			-	C_unshiu_00345_mRNA_24.1	-
GF0036608	0	1	0	Hypothetical protein (1)			-	C_unshiu_00345_mRNA_22.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0036607	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1); Myc-type, basic helix-loop-helix (bHLH) domain [IPR011598] (1)	-	C_unshiu_00345_mRNA_10.1	-
GF0036606	0	1	0	Hypothetical protein (1)			-	C_unshiu_00344_mRNA_9.1	-
GF0036605	0	1	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	-	C_unshiu_00344_mRNA_6.1	-
GF0036604	0	1	0	Hypothetical protein (1)			-	C_unshiu_00344_mRNA_5.1	-
GF0036603	0	1	0	Hypothetical protein (1)			-	C_unshiu_00344_mRNA_42.1	-
GF0036602	0	1	0	UPF0481 protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	C_unshiu_00344_mRNA_40.1	-
GF0036601	0	1	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	-	C_unshiu_00344_mRNA_39.1	-
GF0036600	0	1	0	Cyclin family protein (1)	regulation of cyclin-dependent protein serine/threonine kinase activity [GO:0000079 biological_process] (1); protein kinase binding [GO:0019901 molecular_function] (1)	Cyclin-like [IPR013763] (1); Cyclin PHO80-like [IPR013922] (1); Cyclin P/U [IPR012389] (1)	-	C_unshiu_00344_mRNA_3.1	-
GF0036599	0	1	0	Hypothetical protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	C_unshiu_00344_mRNA_27.1	-
GF0036598	0	1	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_00344_mRNA_26.1	-
GF0036597	0	1	0	Hypothetical protein (1)		P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00344_mRNA_2.1	-
GF0036596	0	1	0	Hypothetical protein (1)			-	C_unshiu_00344_mRNA_19.1	-
GF0036595	0	1	0	Hypothetical protein (1)			-	C_unshiu_00344_mRNA_12.1	-
GF0036594	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_00344_mRNA_11.1	-
GF0036593	0	1	0	Putative zinc finger BED domain-containing protein DAYSLEEPER-like (1)	DNA binding [GO:0003677 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	hAT-like transposase, RNase-H fold [IPR025525] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00343_mRNA_5.1	-
GF0036592	0	1	0	RNA-directed DNA polymerase (Reverse transcriptase), Ribonuclease H (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Beta tubulin, autoregulation binding site [IPR013838] (1)	-	C_unshiu_00343_mRNA_4.1	-
GF0036591	0	1	0	Hypothetical protein (1)			-	C_unshiu_00343_mRNA_3.1	-
GF0036590	0	1	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_00342_mRNA_21.1	-
GF0036589	0	1	0	Hypothetical protein (1)	pectinesterase activity [GO:0030599 molecular_function] (1); cell wall [GO:0005618 cellular_component] (1); cell wall modification [GO:0042545 biological_process] (1)	Pectin lyase fold/virulence factor [IPR011050] (1); Pectin lyase fold [IPR012334] (1); Pectinesterase, catalytic [IPR000070] (1)	-	C_unshiu_00341_mRNA_31.1	-
GF0036588	0	1	0	Hypothetical protein (1)	cell wall [GO:0005618 cellular_component] (1); cell wall modification [GO:0042545 biological_process] (1); pectinesterase activity [GO:0030599 molecular_function] (1)	Pectin lyase fold/virulence factor [IPR011050] (1); Pectin lyase fold [IPR012334] (1); Pectinesterase, catalytic [IPR000070] (1)	-	C_unshiu_00341_mRNA_29.1	-
GF0036587	0	1	0	Hypothetical protein (1)			-	C_unshiu_00341_mRNA_25.1	-
GF0036586	0	1	0	Hypothetical protein (1)			-	C_unshiu_00340_mRNA_3.1	-
GF0036585	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00340_mRNA_26.1	-
GF0036584	0	1	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00340_mRNA_25.1	-
GF0036583	0	1	0	Hypothetical protein (1)			-	C_unshiu_00340_mRNA_22.1	-
GF0036582	0	1	0	Hypothetical protein (1)			-	C_unshiu_00340_mRNA_20.1	-
GF0036581	0	1	0	Hypothetical protein (1)			-	C_unshiu_00340_mRNA_19.1	-
GF0036580	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00340_mRNA_16.1	-
GF0036579	0	1	0	Hypothetical protein (1)			-	C_unshiu_00340_mRNA_15.1	-
GF0036578	0	1	0	Hypothetical protein (1)		Gag-polypeptide of LTR copia-type [IPR029472] (1)	-	C_unshiu_00340_mRNA_13.1	-
GF0036577	0	1	0	Hypothetical protein (1)			-	C_unshiu_00340_mRNA_12.1	-
GF0036576	0	1	0	Cysteine proteinase inhibitor (1)			-	C_unshiu_00340_mRNA_1.1	-
GF0036575	0	1	0	Hypothetical protein (1)			-	C_unshiu_00339_mRNA_8.1	-
GF0036574	0	1	0	Hypothetical protein (1)			-	C_unshiu_00339_mRNA_6.1	-
GF0036573	0	1	0	Hypothetical protein (1)			-	C_unshiu_00339_mRNA_29.1	-
GF0036572	0	1	0	Hypothetical protein (1)	ribosome [GO:0005840 cellular_component] (1); translation [GO:0006412 biological_process] (1); intracellular [GO:0005622 cellular_component] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1)	Ribosomal protein L18/L5 [IPR005484] (1); Development/cell death domain [IPR013989] (1)	-	C_unshiu_00339_mRNA_25.1	-
GF0036571	0	1	0	Hypothetical protein (1)			-	C_unshiu_00339_mRNA_19.1	-
GF0036570	0	1	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	Frigida-like [IPR012474] (1); DNA-binding domain [IPR016177] (1); AP2/ERF domain [IPR001471] (1)	-	C_unshiu_00339_mRNA_18.1	-
GF0036569	0	1	0	Hypothetical protein (1)			-	C_unshiu_00339_mRNA_17.1	-
GF0036568	0	1	0	Hypothetical protein (1)			-	C_unshiu_00339_mRNA_16.1	-
GF0036567	0	1	0	Cellulose synthase-like protein E6 (1)	cellulose biosynthetic process [GO:0030244 biological_process] (1); membrane [GO:0016020 cellular_component] (1); cellulose synthase (UDP-forming) activity [GO:0016760 molecular_function] (1)	Nucleotide-diphospho-sugar transferases [IPR029044] (1); Cellulose synthase [IPR005150] (1)	-	C_unshiu_00338_mRNA_9.1	-
GF0036566	0	1	0	Hypothetical protein (1)			-	C_unshiu_00338_mRNA_4.1	-
GF0036565	0	1	0	Hypothetical protein (1)	enzyme inhibitor activity [GO:0004857 molecular_function] (1)	Pectinesterase inhibitor domain [IPR006501] (1)	-	C_unshiu_00338_mRNA_37.1	-
GF0036564	0	1	0	Monosacharide transport protein (1)			-	C_unshiu_00338_mRNA_34.1	-
GF0036563	0	1	0	Hypothetical protein (1)			-	C_unshiu_00338_mRNA_3.1	-
GF0036562	0	1	0	Hypothetical protein (1)			-	C_unshiu_00338_mRNA_2.1	-
GF0036561	0	1	0	Hypothetical protein (1)			-	C_unshiu_00338_mRNA_18.1	-
GF0036560	0	1	0	Monosacharide transport protein (1)			-	C_unshiu_00338_mRNA_1.1	-
GF0036559	0	1	0	DUF246 domain-containing protein (1)		GDP-fucose protein O-fucosyltransferase [IPR019378] (1)	-	C_unshiu_00337_mRNA_1.1	-
GF0036558	0	1	0	Hypothetical protein (1)			-	C_unshiu_00336_mRNA_7.1	-
GF0036557	0	1	0	Hypothetical protein (1)			-	C_unshiu_00336_mRNA_17.1	-
GF0036556	0	1	0	Hypothetical protein (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	-	C_unshiu_00336_mRNA_16.1	-
GF0036555	0	1	0	Hypothetical protein (1)			-	C_unshiu_00336_mRNA_13.1	-
GF0036554	0	1	0	Hypothetical protein (1)			-	C_unshiu_00336_mRNA_12.1	-
GF0036553	0	1	0	Endoribonuclease Dicer (1)	ammonium transport [GO:0015696 biological_process] (1); membrane [GO:0016020 cellular_component] (1); ammonium transmembrane transport [GO:0072488 biological_process] (1); ammonium transmembrane transporter activity [GO:0008519 molecular_function] (1)	Ammonium transporter AmtB-like domain [IPR024041] (1); Ammonium/urea transporter [IPR029020] (1); Ammonium transporter, conserved site [IPR018047] (1); Ammonium transporter [IPR001905] (1)	-	C_unshiu_00335_mRNA_36.1	-
GF0036552	0	1	0	Hypothetical protein (1)			-	C_unshiu_00335_mRNA_30.1	-
GF0036551	0	1	0	Putative inositol polyphosphate kinase-like (1)	inositol tetrakisphosphate 1-kinase activity [GO:0047325 molecular_function] (1); magnesium ion binding [GO:0000287 molecular_function] (1); inositol-1,3,4-trisphosphate 6-kinase activity [GO:0052725 molecular_function] (1); intracellular [GO:0005622 cellular_component] (1); ATP binding [GO:0005524 molecular_function] (1); inositol trisphosphate metabolic process [GO:0032957 biological_process] (1); inositol-1,3,4-trisphosphate 5-kinase activity [GO:0052726 molecular_function] (1)	Inositol-tetrakisphosphate 1-kinase [IPR008656] (1)	-	C_unshiu_00335_mRNA_23.1	-
GF0036550	0	1	0	Hypothetical protein (1)	intracellular [GO:0005622 cellular_component] (1); magnesium ion binding [GO:0000287 molecular_function] (1); inositol-1,3,4-trisphosphate 6-kinase activity [GO:0052725 molecular_function] (1); inositol tetrakisphosphate 1-kinase activity [GO:0047325 molecular_function] (1); inositol-1,3,4-trisphosphate 5-kinase activity [GO:0052726 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1); inositol trisphosphate metabolic process [GO:0032957 biological_process] (1)	Inositol-tetrakisphosphate 1-kinase [IPR008656] (1)	-	C_unshiu_00335_mRNA_22.1	-
GF0036549	0	1	0	Hypothetical protein (1)		NAD(P)-binding domain [IPR016040] (1)	-	C_unshiu_00335_mRNA_16.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0036548	0	1	0	Syntaxin (1)	vesicle-mediated transport [GO:0016192 biological_process] (1); SNAP receptor activity [GO:0005484 molecular_function] (1); intracellular protein transport [GO:0006886 biological_process] (1); protein binding [GO:0005515 molecular_function] (1); membrane [GO:0016020 cellular_component] (1)	t-SNARE [IPR010989] (1); Syntaxin/epimorphin, conserved site [IPR006012] (1); Target SNARE coiled-coil homology domain [IPR000727] (1); Syntaxin, N-terminal domain [IPR006011] (1)	-	C_unshiu_00335_mRNA_14.1	-
GF0036547	0	1	0	Hypothetical protein (1)			-	C_unshiu_00335_mRNA_12.1	-
GF0036546	0	1	0	Mutator-like transposase (1)	zinc ion binding [GO:0008270 molecular_function] (1)	MULE transposase domain [IPR018289] (1); Zinc finger, PMZ-type [IPR006564] (1); Transposase, MuDR, plant [IPR004332] (1); Zinc finger, SWIM-type [IPR007527] (1)	-	C_unshiu_00334_mRNA_5.1	-
GF0036545	0	1	0	Hypothetical protein (1)			-	C_unshiu_00334_mRNA_4.1	-
GF0036544	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat-containing domain [IPR020683] (1); Ankyrin repeat [IPR002110] (1)	-	C_unshiu_00334_mRNA_33.1	-
GF0036543	0	1	0	Hypothetical protein (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Isopenicillin N synthase-like [IPR027443] (1); Oxoglutarate/iron-dependent dioxygenase [IPR005123] (1)	-	C_unshiu_00334_mRNA_15.1	-
GF0036542	0	1	0	Retrotransposon protein, putative, Ty1-copia subclass (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	-	C_unshiu_00334_mRNA_11.1	-
GF0036541	0	1	0	Hypothetical protein (1)			-	C_unshiu_00334_mRNA_1.1	-
GF0036540	0	1	0	Hypothetical protein (1)	transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); nucleus [GO:0005634 cellular_component] (1); nucleotide binding [GO:0000166 molecular_function] (1)	Regulator of nonsense-mediated decay, UPF3 [IPR005120] (1); Nucleotide-binding alpha-beta plait domain [IPR012677] (1); Transcription factor, K-box [IPR002487] (1)	-	C_unshiu_00333_mRNA_6.1	-
GF0036539	0	1	0	Hypothetical protein (1)	GTP binding [GO:0005525 molecular_function] (1)	AIG1-type guanine nucleotide-binding (G) domain [IPR006703] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00333_mRNA_5.1	-
GF0036538	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	C_unshiu_00333_mRNA_4.1	-
GF0036537	0	1	0	Hypothetical protein (1)		Powdery mildew resistance protein, RPW8 domain [IPR008808] (1)	-	C_unshiu_00333_mRNA_30.1	-
GF0036536	0	1	0	Hypothetical protein (1)			-	C_unshiu_00333_mRNA_28.1	-
GF0036535	0	1	0	Hypothetical protein (1)			-	C_unshiu_00333_mRNA_26.1	-
GF0036534	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4216 [IPR025312] (1)	-	C_unshiu_00333_mRNA_25.1	-
GF0036533	0	1	0	AT-hook motif nuclear-localized protein 28 (1)		PPC domain [IPR005175] (1)	-	C_unshiu_00333_mRNA_22.1	-
GF0036532	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_00333_mRNA_20.1	-
GF0036531	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_00333_mRNA_2.1	-
GF0036530	0	1	0	Hypothetical protein (1)			-	C_unshiu_00333_mRNA_19.1	-
GF0036529	0	1	0	Hypothetical protein (1)		Alpha crystallin/Hsp20 domain [IPR002068] (1); HSP20-like chaperone [IPR008978] (1)	-	C_unshiu_00333_mRNA_18.1	-
GF0036528	0	1	0	Hypothetical protein (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	FAD/NAD(P)-binding domain [IPR023753] (1)	-	C_unshiu_00333_mRNA_17.1	-
GF0036527	0	1	0	Hypothetical protein (1)			-	C_unshiu_00333_mRNA_11.1	-
GF0036526	0	1	0	Hypothetical protein (1)			-	C_unshiu_00332_mRNA_3.1	-
GF0036525	0	1	0	Hypothetical protein (1)			-	C_unshiu_00332_mRNA_27.1	-
GF0036524	0	1	0	Hypothetical protein (1)			-	C_unshiu_00332_mRNA_26.1	-
GF0036523	0	1	0	Hypothetical protein (1)			-	C_unshiu_00332_mRNA_25.1	-
GF0036522	0	1	0	Hypothetical protein (1)	photosystem I reaction center [GO:0009538 cellular_component] (1); photosystem I [GO:0009522 cellular_component] (1); photosynthesis [GO:0015979 biological_process] (1); protein binding [GO:0005515 molecular_function] (1)	Photosystem I PsaD [IPR003685] (1); F-box domain [IPR001810] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00330_mRNA_8.1	-
GF0036521	0	1	0	Hypothetical protein (1)			-	C_unshiu_00330_mRNA_4.1	-
GF0036520	0	1	0	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	C_unshiu_00330_mRNA_27.1	-
GF0036519	0	1	0	Hypothetical protein (1)			-	C_unshiu_00330_mRNA_18.1	-
GF0036518	0	1	0	LRR receptor-like kinase family protein (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase-like domain [IPR011009] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Protein kinase domain [IPR000719] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1)	-	C_unshiu_00329_mRNA_8.1	-
GF0036517	0	1	0	Hypothetical protein (1)			-	C_unshiu_00329_mRNA_7.1	-
GF0036516	0	1	0	Hypothetical protein (1)			-	C_unshiu_00329_mRNA_6.1	-
GF0036515	0	1	0	Putative retroelement pol polyprotein (1)			-	C_unshiu_00329_mRNA_28.1	-
GF0036514	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00329_mRNA_21.1	-
GF0036513	0	1	0	Hypothetical protein (1)			-	C_unshiu_00329_mRNA_18.1	-
GF0036512	0	1	0	Hypothetical protein (1)			-	C_unshiu_00329_mRNA_13.1	-
GF0036511	0	1	0	Hypothetical protein (1)			-	C_unshiu_00329_mRNA_12.1	-
GF0036510	0	1	0	Hypothetical protein (1)			-	C_unshiu_00329_mRNA_11.1	-
GF0036509	0	1	0	LRR receptor-like kinase family protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Serine/threonine-protein kinase, active site [IPR008271] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Protein kinase domain [IPR000719] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_00329_mRNA_10.1	-
GF0036508	0	1	0	Hypothetical protein (1)			-	C_unshiu_00329_mRNA_1.1	-
GF0036507	0	1	0	Hypothetical protein (1)			-	C_unshiu_00328_mRNA_14.1	-
GF0036506	0	1	0	Laccase (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); copper ion binding [GO:0005507 molecular_function] (1)	Multicopper oxidase, type 2 [IPR011706] (1); Multicopper oxidase, type 1 [IPR001117] (1); Cupredoxin [IPR008972] (1)	-	C_unshiu_00328_mRNA_1.1	-
GF0036505	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF1985 [IPR015410] (1)	-	C_unshiu_00327_mRNA_8.1	-
GF0036504	0	1	0	Tetratricopeptide repeat (TPR)-containing protein (1)	protein binding [GO:0005515 molecular_function] (1)	Protein of unknown function DUF3493 [IPR021883] (1); Tetratricopeptide-like helical domain [IPR011990] (1)	-	C_unshiu_00326_mRNA_9.1	-
GF0036503	0	1	0	Hypothetical protein (1)			-	C_unshiu_00326_mRNA_7.1	-
GF0036502	0	1	0	Hypothetical protein (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1); hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (1)	Glycoside hydrolase, catalytic domain [IPR013781] (1); Glycoside hydrolase superfamily [IPR017853] (1); Glycosyl hydrolases family 1, N-terminal conserved site [IPR033132] (1); Glycoside hydrolase family 1 [IPR001360] (1)	-	C_unshiu_00326_mRNA_29.1	-
GF0036501	0	1	0	Dephospho-CoA kinase family isoform 1 (1)	coenzyme A biosynthetic process [GO:0015937 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1); dephospho-CoA kinase activity [GO:0004140 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Dephospho-CoA kinase [IPR001977] (1)	-	C_unshiu_00326_mRNA_2.1	-
GF0036500	0	1	0	Mismatch repair endonuclease PMS2 (1)	mismatch repair [GO:0006298 biological_process] (1); mismatched DNA binding [GO:0030983 molecular_function] (1); thiamine metabolic process [GO:0006772 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1); mismatch repair complex [GO:0032300 cellular_component] (1); thiamine diphosphokinase activity [GO:0004788 molecular_function] (1); thiamine binding [GO:0030975 molecular_function] (1); thiamine diphosphate biosynthetic process [GO:0009229 biological_process] (1)	DNA mismatch repair protein Pms1/Pms2 [IPR028831] (1); MutL, C-terminal, dimerisation [IPR014790] (1); Thiamin pyrophosphokinase, catalytic domain [IPR007371] (1); DNA mismatch repair, conserved site [IPR014762] (1); DNA mismatch repair protein, C-terminal [IPR013507] (1); Ribosomal protein S5 domain 2-type fold [IPR020568] (1); Thiamin pyrophosphokinase [IPR006282] (1); DNA mismatch repair protein family [IPR002099] (1); Thiamin pyrophosphokinase, vitamin B1-binding domain [IPR007373] (1); Histidine kinase-like ATPase, C-terminal domain [IPR003594] (1); Ribosomal protein S5 domain 2-type fold, subgroup [IPR014721] (1)	-	C_unshiu_00326_mRNA_19.1	-
GF0036499	0	1	0	Hypothetical protein (1)			-	C_unshiu_00326_mRNA_17.1	-
GF0036498	0	1	0	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	C_unshiu_00326_mRNA_1.1	-
GF0036497	0	1	0	Hypothetical protein (1)			-	C_unshiu_00325_mRNA_3.1	-
GF0036496	0	1	0	Hypothetical protein (1)		GAG-pre-integrase domain [IPR025724] (1)	-	C_unshiu_00325_mRNA_22.1	-
GF0036495	0	1	0	Hypothetical protein (1)			-	C_unshiu_00325_mRNA_2.1	-
GF0036494	0	1	0	Hypothetical protein (1)			-	C_unshiu_00325_mRNA_19.1	-
GF0036493	0	1	0	Hypothetical protein (1)	DNA replication [GO:0006260 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	MCM domain [IPR001208] (1)	-	C_unshiu_00325_mRNA_18.1	-
GF0036492	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00325_mRNA_17.1	-
GF0036491	0	1	0	Hypothetical protein (1)			-	C_unshiu_00325_mRNA_14.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0036490	0	1	0	Retrotransposon gag protein (1)		Eukaryotic translation initiation factor 3 subunit G, N-terminal [IPR024675] (1)	-	C_unshiu_00324_mRNA_9.1	-
GF0036489	0	1	0	Hypothetical protein (1)			-	C_unshiu_00324_mRNA_7.1	-
GF0036488	0	1	0	Hypothetical protein (1)			-	C_unshiu_00324_mRNA_5.1	-
GF0036487	0	1	0	Hypothetical protein (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1); polygalacturonase activity [GO:0004650 molecular_function] (1)	Glycoside hydrolase, family 28 [IPR000743] (1); Pectin lyase fold [IPR012334] (1); Pectin lyase fold/virulence factor [IPR011050] (1)	-	C_unshiu_00324_mRNA_3.1	-
GF0036486	0	1	0	Hypothetical protein (1)			-	C_unshiu_00324_mRNA_24.1	-
GF0036485	0	1	0	Hypothetical protein (1)		Pectin lyase fold/virulence factor [IPR011050] (1); Pectin lyase fold [IPR012334] (1)	-	C_unshiu_00324_mRNA_2.1	-
GF0036484	0	1	0	Hypothetical protein (1)			-	C_unshiu_00324_mRNA_12.1	-
GF0036483	0	1	0	Hypothetical protein (1)			-	C_unshiu_00324_mRNA_1.1	-
GF0036482	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00323_mRNA_9.1	-
GF0036481	0	1	0	Hypothetical protein (1)			-	C_unshiu_00323_mRNA_8.1	-
GF0036480	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	-	C_unshiu_00323_mRNA_24.1	-
GF0036479	0	1	0	Hypothetical protein (1)			-	C_unshiu_00323_mRNA_16.1	-
GF0036478	0	1	0	Hypothetical protein (1)			-	C_unshiu_00323_mRNA_15.1	-
GF0036477	0	1	0	Hypothetical protein (1)			-	C_unshiu_00323_mRNA_14.1	-
GF0036476	0	1	0	Polynucleotidyl transferase, Ribonuclease H fold (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_00323_mRNA_13.1	-
GF0036475	0	1	0	Hypothetical protein (1)			-	C_unshiu_00323_mRNA_10.1	-
GF0036474	0	1	0	Hypothetical protein (1)			-	C_unshiu_00322_mRNA_42.1	-
GF0036473	0	1	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	NAC domain [IPR003441] (1)	-	C_unshiu_00322_mRNA_38.1	-
GF0036472	0	1	0	60S ribosomal protein L13a (1)	ribosome [GO:0005840 cellular_component] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1); large ribosomal subunit [GO:0015934 cellular_component] (1); translation [GO:0006412 biological_process] (1)	Ribosomal protein L13, eukaryotic/archaeal [IPR005755] (1); Ribosomal protein L13 domain [IPR023564] (1); Ribosomal protein L13, conserved site [IPR023563] (1); Ribosomal protein L13 [IPR005822] (1)	-	C_unshiu_00322_mRNA_32.1	-
GF0036471	0	1	0	Pentatricopeptide repeat-containing protein, chloroplastic (1)	protein binding [GO:0005515 molecular_function] (1)	Pentatricopeptide repeat [IPR002885] (1); Tetratricopeptide-like helical domain [IPR011990] (1)	-	C_unshiu_00322_mRNA_26.1	-
GF0036470	0	1	0	Hypothetical protein (1)			-	C_unshiu_00322_mRNA_13.1	-
GF0036469	0	1	0	Hypothetical protein (1)	DNA replication initiation [GO:0006270 biological_process] (1)	CDC45 family [IPR003874] (1)	-	C_unshiu_00322_mRNA_10.1	-
GF0036468	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	MULE transposase domain [IPR018289] (1); Zinc finger, PMZ-type [IPR006564] (1); Zinc finger, SWIM-type [IPR007527] (1)	-	C_unshiu_00321_mRNA_6.1	-
GF0036467	0	1	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_00321_mRNA_5.1	-
GF0036466	0	1	0	Aspartic proteinase-like protein 2 (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); binding [GO:0005488 molecular_function] (1); RNA binding [GO:0003723 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Peptidase family A1 domain [IPR033121] (1); Armadillo-type fold [IPR016024] (1); Pumilio homology domain [IPR033133] (1); Aspartic peptidase domain [IPR021109] (1); Pumilio RNA-binding repeat [IPR001313] (1); Aspartic peptidase A1 family [IPR001461] (1); Xylanase inhibitor, N-terminal [IPR032861] (1); Xylanase inhibitor, C-terminal [IPR032799] (1); Armadillo-like helical [IPR011989] (1)	-	C_unshiu_00321_mRNA_20.1	-
GF0036465	0	1	0	Hypothetical protein (1)			-	C_unshiu_00321_mRNA_13.1	-
GF0036464	0	1	0	Hypothetical protein (1)			-	C_unshiu_00320_mRNA_3.1	-
GF0036463	0	1	0	Hypothetical protein (1)	metabolic process [GO:0008152 biological_process] (1); transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	-	C_unshiu_00320_mRNA_23.1	-
GF0036462	0	1	0	Hypothetical protein (1)			-	C_unshiu_00320_mRNA_21.1	-
GF0036461	0	1	0	Hypothetical protein (1)			-	C_unshiu_00320_mRNA_14.1	-
GF0036460	0	1	0	Hypothetical protein (1)			-	C_unshiu_00320_mRNA_10.1	-
GF0036459	0	1	0	Hypothetical protein (1)			-	C_unshiu_00319_mRNA_3.1	-
GF0036458	0	1	0	Basic blue protein (1)	electron carrier activity [GO:0009055 molecular_function] (1)	Cupredoxin [IPR008972] (1); Phytocyanin domain [IPR003245] (1)	-	C_unshiu_00319_mRNA_29.1	-
GF0036457	0	1	0	Hypothetical protein (1)			-	C_unshiu_00319_mRNA_21.1	-
GF0036456	0	1	0	Hypothetical protein (1)			-	C_unshiu_00319_mRNA_19.1	-
GF0036455	0	1	0	Putative pentatricopeptide repeat domain containing protein (1)	protein binding [GO:0005515 molecular_function] (1)	Tetratricopeptide-like helical domain [IPR011990] (1); Pentatricopeptide repeat [IPR002885] (1)	-	C_unshiu_00319_mRNA_15.1	-
GF0036454	0	1	0	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	C_unshiu_00319_mRNA_14.1	-
GF0036453	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Pentatricopeptide repeat [IPR002885] (1); Tetratricopeptide-like helical domain [IPR011990] (1)	-	C_unshiu_00319_mRNA_12.1	-
GF0036452	0	1	0	Lysine histidine transporter 1 (1)	amino acid transmembrane transport [GO:0003333 biological_process] (1)	Amino acid transporter, transmembrane domain [IPR013057] (1); Tryptophan/tyrosine permease [IPR018227] (1)	-	C_unshiu_00318_mRNA_2.1	-
GF0036451	0	1	0	Nucleic acid-binding, OB-fold-like protein isoform 2 (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	S1 domain [IPR003029] (1); Nucleic acid-binding, OB-fold [IPR012340] (1)	-	C_unshiu_00318_mRNA_1.1	-
GF0036450	0	1	0	Disease resistance protein (CC-NBS-LRR class) family protein (1)	ADP binding [GO:0043531 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	C_unshiu_00317_mRNA_7.1	-
GF0036449	0	1	0	Hypothetical protein (1)			-	C_unshiu_00317_mRNA_27.1	-
GF0036448	0	1	0	Hypothetical protein (1)	methyltransferase activity [GO:0008168 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); Methyltransferase type 11 [IPR013216] (1)	-	C_unshiu_00317_mRNA_21.1	-
GF0036447	0	1	0	Hypothetical protein (1)			-	C_unshiu_00317_mRNA_2.1	-
GF0036446	0	1	0	Hypothetical protein (1)			-	C_unshiu_00317_mRNA_19.1	-
GF0036445	0	1	0	Hypothetical protein (1)			-	C_unshiu_00317_mRNA_18.1	-
GF0036444	0	1	0	Hypothetical protein (1)			-	C_unshiu_00317_mRNA_16.1	-
GF0036443	0	1	0	Hypothetical protein (1)		Transposase-associated domain [IPR029480] (1)	-	C_unshiu_00317_mRNA_15.1	-
GF0036442	0	1	0	Hypothetical protein (1)			-	C_unshiu_00317_mRNA_14.1	-
GF0036441	0	1	0	Hypothetical protein (1)			-	C_unshiu_00317_mRNA_13.1	-
GF0036440	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF1336 [IPR009769] (1)	-	C_unshiu_00317_mRNA_12.1	-
GF0036439	0	1	0	Hypothetical protein (1)			-	C_unshiu_00317_mRNA_11.1	-
GF0036438	0	1	0	Disease resistance protein RPS2, putative (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00317_mRNA_10.1	-
GF0036437	0	1	0	Hypothetical protein (1)			-	C_unshiu_00316_mRNA_8.1	-
GF0036436	0	1	0	Hypothetical protein (1)			-	C_unshiu_00316_mRNA_7.1	-
GF0036435	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00316_mRNA_3.1	-
GF0036434	0	1	0	Hypothetical protein (1)			-	C_unshiu_00316_mRNA_23.1	-
GF0036433	0	1	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	B3 DNA binding domain [IPR003340] (1); DNA-binding pseudobarrel domain [IPR015300] (1)	-	C_unshiu_00316_mRNA_22.1	-
GF0036432	0	1	0	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1)	Non-haem dioxygenase N-terminal domain [IPR026992] (1); Isopenicillin N synthase-like [IPR027443] (1); Isopenicillin N synthase [IPR002283] (1); Oxoglutarate/iron-dependent dioxygenase [IPR005123] (1)	-	C_unshiu_00316_mRNA_21.1	-
GF0036431	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	C_unshiu_00316_mRNA_2.1	-
GF0036430	0	1	0	Hypothetical protein (1)		Gag-polypeptide of LTR copia-type [IPR029472] (1)	-	C_unshiu_00316_mRNA_19.1	-
GF0036429	0	1	0	NADPH-dependent codeinone reductase-like protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1)	NADP-dependent oxidoreductase domain [IPR023210] (1); Aldo/keto reductase, conserved site [IPR018170] (1); Aldo/keto reductase [IPR020471] (1); Aldo/keto reductase/potassium channel subunit beta [IPR001395] (1)	-	C_unshiu_00316_mRNA_17.1	-
GF0036428	0	1	0	Hypothetical protein (1)			-	C_unshiu_00316_mRNA_16.1	-
GF0036427	0	1	0	Terpene cyclase/mutase family member (1)	catalytic activity [GO:0003824 molecular_function] (1); intramolecular transferase activity [GO:0016866 molecular_function] (1)	Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (1); PFTB repeat [IPR001330] (1); Squalene cyclase [IPR018333] (1); Squalene cyclase, N-terminal [IPR032697] (1)	-	C_unshiu_00316_mRNA_14.1	-
GF0036426	0	1	0	P-loop nucleoside triphosphate hydrolase superfamily protein (1)		P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00316_mRNA_12.1	-
GF0036425	0	1	0	Hypothetical protein (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase, ATP binding site [IPR017441] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1)	-	C_unshiu_00315_mRNA_31.1	-
GF0036424	0	1	0	Hypothetical protein (1)	transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (1)	Chloramphenicol acetyltransferase-like domain [IPR023213] (1); Transferase [IPR003480] (1)	-	C_unshiu_00315_mRNA_29.1	-
GF0036423	0	1	0	Hydroxycinnamoyl-Coenzyme A shikimate/quinate hydroxycinnamoyltransferase (1)	transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (1)	Chloramphenicol acetyltransferase-like domain [IPR023213] (1); Transferase [IPR003480] (1)	-	C_unshiu_00315_mRNA_28.1	-
GF0036422	0	1	0	Hypothetical protein (1)			-	C_unshiu_00315_mRNA_22.1	-
GF0036421	0	1	0	Hypothetical protein (1)			-	C_unshiu_00315_mRNA_10.1	-
GF0036420	0	1	0	Hypothetical protein (1)			-	C_unshiu_00315_mRNA_1.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0036419	0	1	0	Importin subunit alpha (1)	cytoplasm [GO:0005737 cellular_component] (1); nucleus [GO:0005634 cellular_component] (1); protein transporter activity [GO:0008565 molecular_function] (1); protein import into nucleus [GO:0006606 biological_process] (1); protein binding [GO:0005515 molecular_function] (1); binding [GO:0005488 molecular_function] (1)	Armadillo [IPR000225] (1); Armadillo-like helical [IPR011989] (1); Armadillo-type fold [IPR016024] (1); Importin-alpha, importin-beta-binding domain [IPR002652] (1)	-	C_unshiu_00314_mRNA_22.1	-
GF0036418	0	1	0	Wall-associated receptor kinase-like 20 (1)	polysaccharide binding [GO:0030247 molecular_function] (1)	Wall-associated receptor kinase, galacturonan-binding domain [IPR025287] (1)	-	C_unshiu_00314_mRNA_15.1	-
GF0036417	0	1	0	Hypothetical protein (1)			-	C_unshiu_00314_mRNA_10.1	-
GF0036416	0	1	0	Hypothetical protein (1)			-	C_unshiu_00314_mRNA_1.1	-
GF0036415	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1); GTP binding [GO:0005525 molecular_function] (1)	Dynamin-type guanine nucleotide-binding (G) domain [IPR030381] (1); Dynamin superfamily [IPR022812] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat 3 [IPR011713] (1); Leucine-rich repeat [IPR001611] (1); Pleckstrin homology domain [IPR001849] (1); PH domain-like [IPR011993] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00313_mRNA_8.2	-
GF0036414	0	1	0	Hypothetical protein (1)			-	C_unshiu_00313_mRNA_26.1	-
GF0036413	0	1	0	Hypothetical protein (1)			-	C_unshiu_00313_mRNA_20.1	-
GF0036412	0	1	0	Hypothetical protein (1)			-	C_unshiu_00313_mRNA_19.1	-
GF0036411	0	1	0	Hypothetical protein (1)			-	C_unshiu_00313_mRNA_13.1	-
GF0036410	0	1	0	Caffeic acid 3-O-methyltransferase (1)	methyltransferase activity [GO:0008168 molecular_function] (1); O-methyltransferase activity [GO:0008171 molecular_function] (1)	O-methyltransferase COMT-type [IPR016461] (1); O-methyltransferase, family 2 [IPR001077] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	C_unshiu_00313_mRNA_11.1	-
GF0036409	0	1	0	Hypothetical protein (1)			-	C_unshiu_00313_mRNA_10.1	-
GF0036408	0	1	0	Hypothetical protein (1)			-	C_unshiu_00313_mRNA_1.1	-
GF0036407	0	1	0	Hypothetical protein (1)	drug transmembrane transport [GO:0006855 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1); antiporter activity [GO:0015297 molecular_function] (1); drug transmembrane transporter activity [GO:0015238 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1); membrane [GO:0016020 cellular_component] (1); transmembrane transport [GO:0055085 biological_process] (1)	AMP-dependent synthetase/ligase [IPR000873] (1); Multi antimicrobial extrusion protein [IPR002528] (1); AMP-binding enzyme C-terminal domain [IPR025110] (1); AMP-binding, conserved site [IPR020845] (1)	-	C_unshiu_00312_mRNA_36.1	-
GF0036406	0	1	0	Putative serine/threonine-protein kinase Cx32 (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase, ATP binding site [IPR017441] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1)	-	C_unshiu_00312_mRNA_24.1	-
GF0036405	0	1	0	Hypothetical protein (1)			-	C_unshiu_00312_mRNA_21.1	-
GF0036404	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1); calcium ion binding [GO:0005509 molecular_function] (1)	EF-hand domain pair [IPR011992] (1); EH domain [IPR000261] (1); EF-hand domain [IPR002048] (1); EF-Hand 1, calcium-binding site [IPR018247] (1)	-	C_unshiu_00312_mRNA_13.1	-
GF0036403	0	1	0	Hypothetical protein (1)	integral component of membrane [GO:0016021 cellular_component] (1); defense response [GO:0006952 biological_process] (1)	Mlo-related protein [IPR004326] (1)	-	C_unshiu_00312_mRNA_1.1	-
GF0036402	0	1	0	Protein ARABIDILLO 1-like protein (1)	protein binding [GO:0005515 molecular_function] (1)	F-box domain [IPR001810] (1)	-	C_unshiu_00311_mRNA_6.1	-
GF0036401	0	1	0	Hypothetical protein (1)	RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Zinc knuckle CX2CX4HX4C [IPR025836] (1); Ribonuclease H domain [IPR002156] (1); Ribonuclease H-like domain [IPR012337] (1); Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_00311_mRNA_27.1	-
GF0036400	0	1	0	Hypothetical protein (1)			-	C_unshiu_00311_mRNA_21.1	-
GF0036399	0	1	0	Hypothetical protein (1)			-	C_unshiu_00311_mRNA_16.1	-
GF0036398	0	1	0	Hypothetical protein (1)			-	C_unshiu_00310_mRNA_5.1	-
GF0036397	0	1	0	Hypothetical protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	C_unshiu_00310_mRNA_29.1	-
GF0036396	0	1	0	UPF0481 protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	C_unshiu_00310_mRNA_27.1	-
GF0036395	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_00310_mRNA_25.1	-
GF0036394	0	1	0	Hypothetical protein (1)			-	C_unshiu_00310_mRNA_24.1	-
GF0036393	0	1	0	Hypothetical protein (1)			-	C_unshiu_00309_mRNA_30.1	-
GF0036392	0	1	0	Putative RNA-directed DNA polymerase (1)	nucleic acid binding [GO:0003676 molecular_function] (1); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1)	Endonuclease/exonuclease/phosphatase [IPR005135] (1); Ribonuclease H-like domain [IPR012337] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H domain [IPR002156] (1)	-	C_unshiu_00309_mRNA_27.1	-
GF0036391	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Domain of unknown function DUF4219 [IPR025314] (1)	-	C_unshiu_00309_mRNA_21.1	-
GF0036390	0	1	0	Hypothetical protein (1)			-	C_unshiu_00309_mRNA_19.1	-
GF0036389	0	1	0	Hypothetical protein (1)			-	C_unshiu_00309_mRNA_1.1	-
GF0036388	0	1	0	Hypothetical protein (1)			-	C_unshiu_00308_mRNA_9.1	-
GF0036387	0	1	0	Hypothetical protein (1)	RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Endonuclease/exonuclease/phosphatase [IPR005135] (1); Ribonuclease H-like domain [IPR012337] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H domain [IPR002156] (1)	-	C_unshiu_00308_mRNA_8.1	-
GF0036386	0	1	0	Hypothetical protein (1)			-	C_unshiu_00308_mRNA_7.1	-
GF0036385	0	1	0	Hypothetical protein (1)			-	C_unshiu_00308_mRNA_5.1	-
GF0036384	0	1	0	Hypothetical protein (1)			-	C_unshiu_00308_mRNA_4.1	-
GF0036383	0	1	0	Hypothetical protein (1)			-	C_unshiu_00308_mRNA_31.1	-
GF0036382	0	1	0	Hypothetical protein (1)			-	C_unshiu_00308_mRNA_23.1	-
GF0036381	0	1	0	Hypothetical protein (1)	phosphatase activity [GO:0016791 molecular_function] (1); protein tyrosine phosphatase activity [GO:0004725 molecular_function] (1); dephosphorylation [GO:0016311 biological_process] (1)	Protein-tyrosine phosphatase, active site [IPR016130] (1); Myotubularin-like phosphatase domain [IPR010569] (1); Myotubularin family [IPR030564] (1); Protein-tyrosine phosphatase-like [IPR029021] (1)	-	C_unshiu_00308_mRNA_18.1	-
GF0036380	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1); Aspartate/glutamate/uridylate kinase [IPR001048] (1)	-	C_unshiu_00308_mRNA_16.1	-
GF0036379	0	1	0	Hypothetical protein (1)			-	C_unshiu_00308_mRNA_15.1	-
GF0036378	0	1	0	Hypothetical protein (1)			-	C_unshiu_00308_mRNA_11.1	-
GF0036377	0	1	0	Hypothetical protein (1)			-	C_unshiu_00307_mRNA_33.1	-
GF0036376	0	1	0	Peptide transporter (1)	transporter activity [GO:0005215 molecular_function] (1); membrane [GO:0016020 cellular_component] (1); transport [GO:0006810 biological_process] (1)	Proton-dependent oligopeptide transporter family [IPR000109] (1); Major facilitator superfamily domain [IPR020846] (1)	-	C_unshiu_00307_mRNA_32.1	-
GF0036375	0	1	0	Hypothetical protein (1)			-	C_unshiu_00307_mRNA_2.1	-
GF0036374	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	DYW domain [IPR032867] (1); Pentatricopeptide repeat [IPR002885] (1)	-	C_unshiu_00307_mRNA_17.1	-
GF0036373	0	1	0	Hypothetical protein (1)			-	C_unshiu_00307_mRNA_1.1	-
GF0036372	0	1	0	Hypothetical protein (1)	cell redox homeostasis [GO:0045454 biological_process] (1)	Thioredoxin domain [IPR013766] (1); Thioredoxin-like fold [IPR012336] (1)	-	C_unshiu_00306_mRNA_7.1	-
GF0036371	0	1	0	Cellular nucleic acid-binding protein (1)		Aspartic peptidase domain [IPR021109] (1)	-	C_unshiu_00306_mRNA_3.1	-
GF0036370	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_00306_mRNA_2.1	-
GF0036369	0	1	0	Hypothetical protein (1)			-	C_unshiu_00306_mRNA_1.1	-
GF0036368	0	1	0	Hypothetical protein (1)			-	C_unshiu_00305_mRNA_30.1	-
GF0036367	0	1	0	Transcription factor Pur-alpha 1 (1)		Purine-rich element binding protein family [IPR006628] (1)	-	C_unshiu_00305_mRNA_29.1	-
GF0036366	0	1	0	Hypothetical protein (1)	adenylate kinase activity [GO:0004017 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1); nucleobase-containing compound metabolic process [GO:0006139 biological_process] (1); nucleobase-containing compound kinase activity [GO:0019205 molecular_function] (1); phosphotransferase activity, phosphate group as acceptor [GO:0016776 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Adenylate kinase subfamily [IPR006259] (1); Nonaspanin (TM9SF) [IPR004240] (1); Domain of unknown function DUF1995 [IPR018962] (1); Adenylate kinase, active site lid domain [IPR007862] (1); Adenylate kinase/UMP-CMP kinase [IPR000850] (1)	-	C_unshiu_00305_mRNA_25.1	-
GF0036365	0	1	0	Hypothetical protein (1)			-	C_unshiu_00305_mRNA_17.1	-
GF0036364	0	1	0	Disease resistance protein (CC-NBS-LRR class) family protein (1)	ADP binding [GO:0043531 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Leucine-rich repeat [IPR001611] (1); NB-ARC [IPR002182] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00304_mRNA_9.1	-
GF0036363	0	1	0	Hypothetical protein (1)			-	C_unshiu_00304_mRNA_8.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0036362	0	1	0	Hypothetical protein (1)	binding [GO:0005488 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Armadillo-type fold [IPR016024] (1); Armadillo [IPR000225] (1); Atypical Arm repeat [IPR032413] (1); Armadillo-like helical [IPR011989] (1)	-	C_unshiu_00304_mRNA_6.1	-
GF0036361	0	1	0	Hypothetical protein (1)	binding [GO:0005488 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Armadillo-like helical [IPR011989] (1); Armadillo [IPR000225] (1); Armadillo-type fold [IPR016024] (1)	-	C_unshiu_00304_mRNA_30.1	-
GF0036360	0	1	0	Hypothetical protein (1)			-	C_unshiu_00304_mRNA_29.1	-
GF0036359	0	1	0	Importin subunit alpha (1)	binding [GO:0005488 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Armadillo-type fold [IPR016024] (1); Armadillo [IPR000225] (1); Armadillo-like helical [IPR011989] (1)	-	C_unshiu_00304_mRNA_28.1	-
GF0036358	0	1	0	Disease resistance protein RPS2 (1)	protein binding [GO:0005515 molecular_function] (1); ADP binding [GO:0043531 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Leucine-rich repeat [IPR001611] (1); NB-ARC [IPR002182] (1)	-	C_unshiu_00304_mRNA_27.1	-
GF0036357	0	1	0	Potato DNA for copia-like transposable element (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	-	C_unshiu_00304_mRNA_25.1	-
GF0036356	0	1	0	Hypothetical protein (1)			-	C_unshiu_00304_mRNA_24.1	-
GF0036355	0	1	0	Hypothetical protein (1)			-	C_unshiu_00304_mRNA_22.1	-
GF0036354	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00304_mRNA_21.1	-
GF0036353	0	1	0	Hypothetical protein (1)			-	C_unshiu_00304_mRNA_17.1	-
GF0036352	0	1	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	C_unshiu_00304_mRNA_16.1	-
GF0036351	0	1	0	Hypothetical protein (1)			-	C_unshiu_00304_mRNA_14.1	-
GF0036350	0	1	0	Importin subunit alpha (1)	binding [GO:0005488 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Armadillo-like helical [IPR011989] (1); Armadillo [IPR000225] (1); Atypical Arm repeat [IPR032413] (1); Armadillo-type fold [IPR016024] (1)	-	C_unshiu_00304_mRNA_11.1	-
GF0036349	0	1	0	Hypothetical protein (1)			-	C_unshiu_00304_mRNA_10.1	-
GF0036348	0	1	0	Hypothetical protein (1)			-	C_unshiu_00304_mRNA_1.1	-
GF0036347	0	1	0	Calcium-transporting ATPase 8, plasma membrane-type-like protein (1)	magnesium ion transport [GO:0015693 biological_process] (1); integral component of membrane [GO:0016021 cellular_component] (1); magnesium-importing ATPase activity [GO:0015444 molecular_function] (1)	HAD-like domain [IPR023214] (1); P-type ATPase, transmembrane domain [IPR023298] (1); P-type ATPase [IPR001757] (1); P-type ATPase, subfamily IIIB [IPR006415] (1)	-	C_unshiu_00303_mRNA_15.1	-
GF0036346	0	1	0	Protein DETOXIFICATION 27 (1)	transmembrane transport [GO:0055085 biological_process] (1); antiporter activity [GO:0015297 molecular_function] (1); drug transmembrane transporter activity [GO:0015238 molecular_function] (1); membrane [GO:0016020 cellular_component] (1); drug transmembrane transport [GO:0006855 biological_process] (1)	Multi antimicrobial extrusion protein [IPR002528] (1)	-	C_unshiu_00303_mRNA_11.1	-
GF0036345	0	1	0	Retrotransposon protein, putative, Ty1-copia subclass (1)			-	C_unshiu_00302_mRNA_33.1	-
GF0036344	0	1	0	Hypothetical protein (1)			-	C_unshiu_00302_mRNA_28.1	-
GF0036343	0	1	0	Hypothetical protein (1)			-	C_unshiu_00302_mRNA_23.1	-
GF0036342	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)	ATP binding [GO:0005524 molecular_function] (1); dTDP biosynthetic process [GO:0006233 biological_process] (1); thymidylate kinase activity [GO:0004798 molecular_function] (1)	Thymidylate kinase, conserved site [IPR018095] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00302_mRNA_2.1	-
GF0036341	0	1	0	Hypothetical protein (1)	lipid metabolic process [GO:0006629 biological_process] (1)	Fungal lipase-like domain [IPR002921] (1); Alpha/Beta hydrolase fold [IPR029058] (1)	-	C_unshiu_00302_mRNA_18.1	-
GF0036340	0	1	0	Hypothetical protein (1)			-	C_unshiu_00302_mRNA_14.1	-
GF0036339	0	1	0	Hypothetical protein (1)			-	C_unshiu_00302_mRNA_12.1	-
GF0036338	0	1	0	Hypothetical protein (1)			-	C_unshiu_00302_mRNA_10.1	-
GF0036337	0	1	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Peptidase C1A [IPR013128] (1); Cathepsin propeptide inhibitor domain (I29) [IPR013201] (1)	-	C_unshiu_00301_mRNA_8.1	-
GF0036336	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00301_mRNA_3.1	-
GF0036335	0	1	0	Zeaxanthin epoxidase, chloroplastic (1)	FAD binding [GO:0071949 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	FAD/NAD(P)-binding domain [IPR023753] (1); Forkhead-associated (FHA) domain [IPR000253] (1); SMAD/FHA domain [IPR008984] (1); FAD-binding domain [IPR002938] (1)	-	C_unshiu_00301_mRNA_27.2	-
GF0036334	0	1	0	Putative P-loop containing nucleoside triphosphate hydrolases superfamily protein-like (1)	ATP binding [GO:0005524 molecular_function] (1); microtubule binding [GO:0008017 molecular_function] (1); microtubule motor activity [GO:0003777 molecular_function] (1); microtubule-based movement [GO:0007018 biological_process] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Kinesin motor domain [IPR001752] (1); Kinesin-like protein [IPR027640] (1)	-	C_unshiu_00301_mRNA_17.1	-
GF0036333	0	1	0	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	C_unshiu_00300_mRNA_7.1	-
GF0036332	0	1	0	Hypothetical protein (1)			-	C_unshiu_00300_mRNA_6.1	-
GF0036331	0	1	0	Hypothetical protein (1)			-	C_unshiu_00300_mRNA_5.1	-
GF0036330	0	1	0	Hypothetical protein (1)			-	C_unshiu_00300_mRNA_4.1	-
GF0036329	0	1	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_00300_mRNA_30.1	-
GF0036328	0	1	0	Hypothetical protein (1)			-	C_unshiu_00300_mRNA_24.1	-
GF0036327	0	1	0	Hypothetical protein (1)			-	C_unshiu_00300_mRNA_2.1	-
GF0036326	0	1	0	Hypothetical protein (1)			-	C_unshiu_00300_mRNA_13.1	-
GF0036325	0	1	0	Hypothetical protein (1)			-	C_unshiu_00300_mRNA_1.1	-
GF0036324	0	1	0	Hypothetical protein (1)			-	C_unshiu_00299_mRNA_46.1	-
GF0036323	0	1	0	Hypothetical protein (1)	adenosylhomocysteinase activity [GO:0004013 molecular_function] (1); one-carbon metabolic process [GO:0006730 biological_process] (1)	S-adenosyl-L-homocysteine hydrolase, NAD binding domain [IPR015878] (1); NAD(P)-binding domain [IPR016040] (1); Adenosylhomocysteinase [IPR000043] (1)	-	C_unshiu_00299_mRNA_20.1	-
GF0036322	0	1	0	Hypothetical protein (1)			-	C_unshiu_00299_mRNA_1.1	-
GF0036321	0	1	0	Hypothetical protein (1)			-	C_unshiu_00298_mRNA_5.1	-
GF0036320	0	1	0	Hypothetical protein (1)			-	C_unshiu_00298_mRNA_29.1	-
GF0036319	0	1	0	Hypothetical protein (1)			-	C_unshiu_00298_mRNA_28.1	-
GF0036318	0	1	0	Hypothetical protein (1)			-	C_unshiu_00298_mRNA_25.1	-
GF0036317	0	1	0	Hypothetical protein (1)		Zinc knuckle CX2CX4HX4C [IPR025836] (1); Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_00298_mRNA_2.1	-
GF0036316	0	1	0	ATP sulfurylase (1)	sulfate adenylyltransferase (ATP) activity [GO:0004781 molecular_function] (1)	Rossmann-like alpha/beta/alpha sandwich fold [IPR014729] (1); Sulphate adenylyltransferase catalytic domain [IPR024951] (1); PUA-like domain [IPR015947] (1); ATP-sulfurylase PUA-like domain [IPR025980] (1)	-	C_unshiu_00298_mRNA_17.1	-
GF0036315	0	1	0	Iron-sulfur cluster assembly enzyme ISCU, mitochondrial (1)	iron-sulfur cluster binding [GO:0051536 molecular_function] (1); iron-sulfur cluster assembly [GO:0016226 biological_process] (1); iron ion binding [GO:0005506 molecular_function] (1)	NIF system FeS cluster assembly, NifU, N-terminal [IPR002871] (1)	-	C_unshiu_00297_mRNA_8.1	-
GF0036314	0	1	0	Hypothetical protein (1)			-	C_unshiu_00297_mRNA_4.1	-
GF0036313	0	1	0	Hypothetical protein (1)			-	C_unshiu_00297_mRNA_22.1	-
GF0036312	0	1	0	Hypothetical protein (1)			-	C_unshiu_00297_mRNA_2.1	-
GF0036311	0	1	0	Hypothetical protein (1)			-	C_unshiu_00297_mRNA_19.1	-
GF0036310	0	1	0	Hypothetical protein (1)			-	C_unshiu_00297_mRNA_18.1	-
GF0036309	0	1	0	Hypothetical protein (1)			-	C_unshiu_00297_mRNA_16.1	-
GF0036308	0	1	0	Hypothetical protein (1)	transmembrane transporter activity [GO:0022857 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1)	WAT1-related protein [IPR030184] (1)	-	C_unshiu_00297_mRNA_12.1	-
GF0036307	0	1	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Domain of unknown function DUF1985 [IPR015410] (1); Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_00296_mRNA_7.1	-
GF0036306	0	1	0	Hypothetical protein (1)	hydrogen ion transmembrane transporter activity [GO:0015078 molecular_function] (1); mitochondrial proton-transporting ATP synthase complex, coupling factor F(o) [GO:0000276 cellular_component] (1); ATP synthesis coupled proton transport [GO:0015986 biological_process] (1)	Phospholipase A2, histidine active site [IPR033113] (1); Phospholipase A2 domain [IPR016090] (1); ATPase, F0 complex, subunit G, mitochondrial [IPR006808] (1)	-	C_unshiu_00296_mRNA_6.1	-
GF0036305	0	1	0	Hypothetical protein (1)			-	C_unshiu_00296_mRNA_21.1	-
GF0036304	0	1	0	Hypothetical protein (1)			-	C_unshiu_00296_mRNA_20.1	-
GF0036303	0	1	0	Chaperonin CPN60-2, mitochondrial (1)	cytoplasm [GO:0005737 cellular_component] (1); ATP binding [GO:0005524 molecular_function] (1); protein folding [GO:0006457 biological_process] (1)	Chaperonin Cpn60, conserved site [IPR018370] (1); GroEL-like apical domain [IPR027409] (1); TCP-1-like chaperonin intermediate domain [IPR027410] (1); Chaperonin Cpn60/TCP-1 family [IPR002423] (1); GroEL-like equatorial domain [IPR027413] (1)	-	C_unshiu_00296_mRNA_19.1	-
GF0036302	0	1	0	Hypothetical protein (1)			-	C_unshiu_00296_mRNA_18.1	-
GF0036301	0	1	0	Hypothetical protein (1)			-	C_unshiu_00296_mRNA_17.1	-
GF0036300	0	1	0	Hypothetical protein (1)			-	C_unshiu_00296_mRNA_13.1	-
GF0036299	0	1	0	Hypothetical protein (1)			-	C_unshiu_00295_mRNA_3.1	-
GF0036298	0	1	0	Hypothetical protein (1)			-	C_unshiu_00295_mRNA_21.1	-
GF0036297	0	1	0	Hypothetical protein (1)			-	C_unshiu_00294_mRNA_9.1	-
GF0036296	0	1	0	Hypothetical protein (1)			-	C_unshiu_00294_mRNA_4.1	-
GF0036295	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_00294_mRNA_3.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0036294	0	1	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Transposase-associated domain [IPR029480] (1); Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_00294_mRNA_19.1	-
GF0036293	0	1	0	DNA-directed RNA polymerase II (1)	transcription, DNA-templated [GO:0006351 biological_process] (1); DNA-directed RNA polymerase activity [GO:0003899 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1); nucleus [GO:0005634 cellular_component] (1)	RNA polymerase, Rpb5, N-terminal [IPR005571] (1); RNA polymerase, subunit H/Rpb5 C-terminal [IPR000783] (1)	-	C_unshiu_00294_mRNA_17.1	-
GF0036292	0	1	0	Cytochrome P450 82C4 (1)	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1)	Cytochrome P450 [IPR001128] (1)	-	C_unshiu_00293_mRNA_18.1	-
GF0036291	0	1	0	Cytochrome P450 82A4 (1)	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1)	Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450 [IPR001128] (1)	-	C_unshiu_00293_mRNA_17.1	-
GF0036290	0	1	0	Hypothetical protein (1)			-	C_unshiu_00293_mRNA_15.1	-
GF0036289	0	1	0	60 kDa chaperonin, chloroplastic (1)	ATP binding [GO:0005524 molecular_function] (1)	GroEL-like apical domain [IPR027409] (1); Chaperonin Cpn60/TCP-1 family [IPR002423] (1); GroEL-like equatorial domain [IPR027413] (1)	-	C_unshiu_00293_mRNA_11.1	-
GF0036288	0	1	0	Hypothetical protein (1)			-	C_unshiu_00293_mRNA_10.1	-
GF0036287	0	1	0	Retrotransposon protein, putative, Ty1-copia subclass (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00292_mRNA_32.1	-
GF0036286	0	1	0	Hypothetical protein (1)			-	C_unshiu_00292_mRNA_26.1	-
GF0036285	0	1	0	Hypothetical protein (1)			-	C_unshiu_00292_mRNA_18.1	-
GF0036284	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Bromodomain [IPR001487] (1)	-	C_unshiu_00291_mRNA_8.1	-
GF0036283	0	1	0	60S ribosomal protein L36 (1)	intracellular [GO:0005622 cellular_component] (1); translation [GO:0006412 biological_process] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1); ribosome [GO:0005840 cellular_component] (1)	Ribosomal protein L36e [IPR000509] (1)	-	C_unshiu_00291_mRNA_3.1	-
GF0036282	0	1	0	Hypothetical protein (1)			-	C_unshiu_00290_mRNA_32.1	-
GF0036281	0	1	0	Hypothetical protein (1)			-	C_unshiu_00290_mRNA_31.1	-
GF0036280	0	1	0	Hypothetical protein (1)			-	C_unshiu_00290_mRNA_18.1	-
GF0036279	0	1	0	Class III homeodomain leucine zipper protein (1)	DNA binding [GO:0003677 molecular_function] (1); lipid binding [GO:0008289 molecular_function] (1)	START-like domain [IPR023393] (1); START domain [IPR002913] (1); Homeodomain-like [IPR009057] (1); Homeobox domain [IPR001356] (1); MEKHLA [IPR013978] (1)	-	C_unshiu_00290_mRNA_16.1	-
GF0036278	0	1	0	Hypothetical protein (1)	ATPase activity [GO:0016887 molecular_function] (1); malic enzyme activity [GO:0004470 molecular_function] (1); membrane [GO:0016020 cellular_component] (1); ATP binding [GO:0005524 molecular_function] (1); malate dehydrogenase (decarboxylating) (NAD+) activity [GO:0004471 molecular_function] (1); NAD binding [GO:0051287 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); malate metabolic process [GO:0006108 biological_process] (1)	Plant PDR ABC transporter associated [IPR013581] (1); Malic enzyme, conserved site [IPR015884] (1); Malic oxidoreductase [IPR001891] (1); ABC-2 type transporter [IPR013525] (1); ABC transporter-like [IPR003439] (1); Malic enzyme, N-terminal domain [IPR012301] (1); Malic enzyme, NAD-binding [IPR012302] (1); ABC-transporter extracellular N-terminal domain [IPR029481] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NAD(P)-binding domain [IPR016040] (1)	-	C_unshiu_00290_mRNA_10.1	-
GF0036277	0	1	0	(1-4)-beta-mannan endohydrolase (1)	hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1)	Glycoside hydrolase, catalytic domain [IPR013781] (1); Glycoside hydrolase superfamily [IPR017853] (1); Glycoside hydrolase, family 5 [IPR001547] (1)	-	C_unshiu_00289_mRNA_8.1	-
GF0036276	0	1	0	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	C_unshiu_00289_mRNA_7.1	-
GF0036275	0	1	0	Putative random slug protein 5-like (1)		CRAL-TRIO lipid binding domain [IPR001251] (1)	-	C_unshiu_00289_mRNA_43.1	-
GF0036274	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF59 [IPR002744] (1)	-	C_unshiu_00289_mRNA_42.1	-
GF0036273	0	1	0	Laccase 11 (1)	copper ion binding [GO:0005507 molecular_function] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Multicopper oxidases, conserved site [IPR033138] (1); Multicopper oxidase, type 2 [IPR011706] (1); Cupredoxin [IPR008972] (1); Multicopper oxidase, copper-binding site [IPR002355] (1)	-	C_unshiu_00289_mRNA_21.1	-
GF0036272	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	DYW domain [IPR032867] (1); Pentatricopeptide repeat [IPR002885] (1); Tetratricopeptide-like helical domain [IPR011990] (1)	-	C_unshiu_00289_mRNA_19.1	-
GF0036271	0	1	0	Hypothetical protein (1)			-	C_unshiu_00289_mRNA_12.1	-
GF0036270	0	1	0	Hypothetical protein (1)		Uncharacterised protein family UPF0261 [IPR008322] (1)	-	C_unshiu_00289_mRNA_1.1	-
GF0036269	0	1	0	Hypothetical protein (1)	actin binding [GO:0003779 molecular_function] (1)	Protein Networked (NET), actin-binding (NAB) domain [IPR011684] (1)	-	C_unshiu_00288_mRNA_39.1	-
GF0036268	0	1	0	Kinase interacting (KIP1-like) family protein (1)			-	C_unshiu_00288_mRNA_38.1	-
GF0036267	0	1	0	Hypothetical protein (1)			-	C_unshiu_00288_mRNA_37.1	-
GF0036266	0	1	0	Hypothetical protein (1)			-	C_unshiu_00288_mRNA_24.1	-
GF0036265	0	1	0	Threonine endopeptidase (1)		Cyanobacterial aminoacyl-tRNA synthetase, CAAD domain [IPR025564] (1)	-	C_unshiu_00288_mRNA_17.1	-
GF0036264	0	1	0	Hypothetical protein (1)			-	C_unshiu_00288_mRNA_15.1	-
GF0036263	0	1	0	Hypothetical protein (1)			-	C_unshiu_00288_mRNA_11.1	-
GF0036262	0	1	0	Hypothetical protein (1)			-	C_unshiu_00287_mRNA_6.1	-
GF0036261	0	1	0	Hypothetical protein (1)	pectinesterase activity [GO:0030599 molecular_function] (1); cell wall [GO:0005618 cellular_component] (1); cell wall modification [GO:0042545 biological_process] (1)	Pectin lyase fold/virulence factor [IPR011050] (1); Pectin lyase fold [IPR012334] (1); Pectinesterase, catalytic [IPR000070] (1)	-	C_unshiu_00287_mRNA_22.1	-
GF0036260	0	1	0	Hypothetical protein (1)			-	C_unshiu_00287_mRNA_2.1	-
GF0036259	0	1	0	Hypothetical protein (1)			-	C_unshiu_00287_mRNA_16.1	-
GF0036258	0	1	0	Hypothetical protein (1)			-	C_unshiu_00287_mRNA_11.1	-
GF0036257	0	1	0	Hypothetical protein (1)			-	C_unshiu_00287_mRNA_1.1	-
GF0036256	0	1	0	60S ribosomal protein L9 (1)	ribosome [GO:0005840 cellular_component] (1); rRNA binding [GO:0019843 molecular_function] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1); translation [GO:0006412 biological_process] (1)	Ribosomal protein L6, alpha-beta domain [IPR020040] (1); Ribosomal protein L6 [IPR000702] (1)	-	C_unshiu_00286_mRNA_31.1	-
GF0036255	0	1	0	Hypothetical protein (1)			-	C_unshiu_00286_mRNA_30.1	-
GF0036254	0	1	0	Hypothetical protein (1)			-	C_unshiu_00286_mRNA_3.1	-
GF0036253	0	1	0	Hypothetical protein (1)			-	C_unshiu_00286_mRNA_2.1	-
GF0036252	0	1	0	Putative disease resistance protein RGA1 (1)	ADP binding [GO:0043531 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00286_mRNA_14.1	-
GF0036251	0	1	0	Hypothetical protein (1)			-	C_unshiu_00286_mRNA_12.1	-
GF0036250	0	1	0	NAC protein 3 (1)	DNA binding [GO:0003677 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	NAC domain [IPR003441] (1)	-	C_unshiu_00286_mRNA_11.1	-
GF0036249	0	1	0	Suppressor of npr1-1, constitutive 1-like protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00286_mRNA_1.1	-
GF0036248	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); GAG-pre-integrase domain [IPR025724] (1)	-	C_unshiu_00285_mRNA_9.1	-
GF0036247	0	1	0	Hypothetical protein (1)			-	C_unshiu_00285_mRNA_7.1	-
GF0036246	0	1	0	Hypothetical protein (1)			-	C_unshiu_00285_mRNA_34.1	-
GF0036245	0	1	0	Monosacharide transport protein (1)			-	C_unshiu_00285_mRNA_31.1	-
GF0036244	0	1	0	Hypothetical protein (1)			-	C_unshiu_00285_mRNA_30.1	-
GF0036243	0	1	0	Hypothetical protein (1)			-	C_unshiu_00285_mRNA_28.1	-
GF0036242	0	1	0	Polygalacturonase, family GH28 (1)	polygalacturonase activity [GO:0004650 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1)	Glycoside hydrolase, family 28 [IPR000743] (1); Pectin lyase fold/virulence factor [IPR011050] (1); Pectin lyase fold [IPR012334] (1)	-	C_unshiu_00285_mRNA_26.1	-
GF0036241	0	1	0	Hypothetical protein (1)			-	C_unshiu_00285_mRNA_21.1	-
GF0036240	0	1	0	Hypothetical protein (1)			-	C_unshiu_00285_mRNA_2.1	-
GF0036239	0	1	0	Hypothetical protein (1)			-	C_unshiu_00285_mRNA_19.1	-
GF0036238	0	1	0	MuDR family transposase (1)		MULE transposase domain [IPR018289] (1); Transposase, MuDR, plant [IPR004332] (1)	-	C_unshiu_00285_mRNA_18.1	-
GF0036237	0	1	0	Hypothetical protein (1)			-	C_unshiu_00285_mRNA_16.1	-
GF0036236	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Tetratricopeptide-like helical domain [IPR011990] (1); Pentatricopeptide repeat [IPR002885] (1)	-	C_unshiu_00285_mRNA_15.1	-
GF0036235	0	1	0	Hypothetical protein (1)			-	C_unshiu_00285_mRNA_13.1	-
GF0036234	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00285_mRNA_12.1	-
GF0036233	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_00285_mRNA_1.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0036232	0	1	0	Hypothetical protein (1)			-	C_unshiu_00284_mRNA_9.1	-
GF0036231	0	1	0	Hypothetical protein (1)			-	C_unshiu_00284_mRNA_8.1	-
GF0036230	0	1	0	Hypothetical protein (1)			-	C_unshiu_00284_mRNA_7.1	-
GF0036229	0	1	0	Flavonoid 3',5'-hydroxylase (1)	iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1)	Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450, conserved site [IPR017972] (1); Cytochrome P450 [IPR001128] (1)	-	C_unshiu_00284_mRNA_5.1	-
GF0036228	0	1	0	Flavonoid 3-monooxygenase (1)	iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Cytochrome P450 [IPR001128] (1); Cytochrome P450, E-class, group I [IPR002401] (1)	-	C_unshiu_00284_mRNA_4.1	-
GF0036227	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1); prenyltransferase activity [GO:0004659 molecular_function] (1)	UbiA prenyltransferase family [IPR000537] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00284_mRNA_3.1	-
GF0036226	0	1	0	Hypothetical protein (1)			-	C_unshiu_00284_mRNA_25.1	-
GF0036225	0	1	0	Integrase core domain containing protein, putative (1)			-	C_unshiu_00284_mRNA_1.1	-
GF0036224	0	1	0	Hypothetical protein (1)			-	C_unshiu_00283_mRNA_14.1	-
GF0036223	0	1	0	Hypothetical protein (1)			-	C_unshiu_00283_mRNA_12.1	-
GF0036222	0	1	0	Hypothetical protein (1)			-	C_unshiu_00282_mRNA_24.1	-
GF0036221	0	1	0	Pectate lyase (1)		AmbAllergen [IPR018082] (1); Pectin lyase fold [IPR012334] (1); Pectate lyase/Amb allergen [IPR002022] (1); Pectin lyase fold/virulence factor [IPR011050] (1)	-	C_unshiu_00282_mRNA_23.1	-
GF0036220	0	1	0	F-box and Leucine Rich Repeat domains containing protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); F-box domain [IPR001810] (1)	-	C_unshiu_00282_mRNA_22.1	-
GF0036219	0	1	0	Hypothetical protein (1)			-	C_unshiu_00282_mRNA_21.1	-
GF0036218	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00282_mRNA_14.1	-
GF0036217	0	1	0	Hypothetical protein (1)			-	C_unshiu_00282_mRNA_1.1	-
GF0036216	0	1	0	Hypothetical protein (1)			-	C_unshiu_00281_mRNA_8.1	-
GF0036215	0	1	0	Hypothetical protein (1)			-	C_unshiu_00281_mRNA_42.1	-
GF0036214	0	1	0	Hypothetical protein (1)	carbohydrate binding [GO:0030246 molecular_function] (1)	Legume lectin domain [IPR001220] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1)	-	C_unshiu_00281_mRNA_40.1	-
GF0036213	0	1	0	Hypothetical protein (1)			-	C_unshiu_00281_mRNA_23.1	-
GF0036212	0	1	0	Putative transcription factor X1 (1)	gene silencing by RNA [GO:0031047 biological_process] (1)	Uncharacterised domain XH [IPR005379] (1); XS domain [IPR005380] (1)	-	C_unshiu_00281_mRNA_11.1	-
GF0036211	0	1	0	Hypothetical protein (1)			-	C_unshiu_00280_mRNA_8.1	-
GF0036210	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	-	C_unshiu_00280_mRNA_7.1	-
GF0036209	0	1	0	Hypothetical protein (1)			-	C_unshiu_00280_mRNA_5.1	-
GF0036208	0	1	0	Hypothetical protein (1)			-	C_unshiu_00280_mRNA_4.1	-
GF0036207	0	1	0	Hypothetical protein (1)			-	C_unshiu_00280_mRNA_36.1	-
GF0036206	0	1	0	Hypothetical protein (1)			-	C_unshiu_00280_mRNA_3.1	-
GF0036205	0	1	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_00280_mRNA_29.1	-
GF0036204	0	1	0	Hypothetical protein (1)			-	C_unshiu_00280_mRNA_15.1	-
GF0036203	0	1	0	Hypothetical protein (1)			-	C_unshiu_00280_mRNA_13.1	-
GF0036202	0	1	0	Hypothetical protein (1)			-	C_unshiu_00280_mRNA_11.1	-
GF0036201	0	1	0	Hypothetical protein (1)		Transposase-associated domain [IPR029480] (1)	-	C_unshiu_00280_mRNA_1.1	-
GF0036200	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00279_mRNA_7.1	-
GF0036199	0	1	0	Hypothetical protein (1)			-	C_unshiu_00279_mRNA_3.1	-
GF0036198	0	1	0	Hypothetical protein (1)			-	C_unshiu_00279_mRNA_22.1	-
GF0036197	0	1	0	Hypothetical protein (1)	acetyl-CoA carboxylase activity [GO:0003989 molecular_function] (1); acetyl-CoA carboxylase complex [GO:0009317 cellular_component] (1); fatty acid biosynthetic process [GO:0006633 biological_process] (1)	Carboxyl transferase [IPR000022] (1); Acetyl-coenzyme A carboxyltransferase, N-terminal [IPR011762] (1); Acetyl-CoA carboxylase carboxyl transferase, beta subunit [IPR000438] (1); ClpP/crotonase-like domain [IPR029045] (1)	-	C_unshiu_00279_mRNA_2.1	-
GF0036196	0	1	0	Extended synaptotagmin-1 (1)	protein binding [GO:0005515 molecular_function] (1)	C2 domain [IPR000008] (1)	-	C_unshiu_00279_mRNA_14.1	-
GF0036195	0	1	0	Extended synaptotagmin-2-A (1)	lipid binding [GO:0008289 molecular_function] (1)	Synaptotagmin-like mitochondrial-lipid-binding domain [IPR031468] (1)	-	C_unshiu_00279_mRNA_13.1	-
GF0036194	0	1	0	Hypothetical protein (1)			-	C_unshiu_00279_mRNA_1.1	-
GF0036193	0	1	0	Hypothetical protein (1)			-	C_unshiu_00278_mRNA_4.1	-
GF0036192	0	1	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); zinc ion binding [GO:0008270 molecular_function] (1); metallocarboxypeptidase activity [GO:0004181 molecular_function] (1)	Peptidase M14, carboxypeptidase A [IPR000834] (1)	-	C_unshiu_00278_mRNA_39.1	-
GF0036191	0	1	0	Protein GIGANTEA (1)	regulation of photoperiodism, flowering [GO:2000028 biological_process] (1)	GIGANTEA [IPR026211] (1)	-	C_unshiu_00278_mRNA_37.1	-
GF0036190	0	1	0	Cell division protein kinase, putative (1)	ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase, ATP binding site [IPR017441] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1)	-	C_unshiu_00278_mRNA_32.1	-
GF0036189	0	1	0	Hypothetical protein (1)			-	C_unshiu_00278_mRNA_31.1	-
GF0036188	0	1	0	Hypothetical protein (1)		MULE transposase domain [IPR018289] (1)	-	C_unshiu_00278_mRNA_2.1	-
GF0036187	0	1	0	Hypothetical protein (1)			-	C_unshiu_00278_mRNA_15.1	-
GF0036186	0	1	0	Sesquiterpene synthase (1)	magnesium ion binding [GO:0000287 molecular_function] (1); lyase activity [GO:0016829 molecular_function] (1); terpene synthase activity [GO:0010333 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (1); Terpene synthase, N-terminal domain [IPR001906] (1); Terpene synthase, metal-binding domain [IPR005630] (1); Isoprenoid synthase domain [IPR008949] (1)	-	C_unshiu_00278_mRNA_13.1	-
GF0036185	0	1	0	Hypothetical protein (1)	lyase activity [GO:0016829 molecular_function] (1); terpene synthase activity [GO:0010333 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Terpene synthase, N-terminal domain [IPR001906] (1); Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (1)	-	C_unshiu_00278_mRNA_12.1	-
GF0036184	0	1	0	Hypothetical protein (1)			-	C_unshiu_00278_mRNA_1.1	-
GF0036183	0	1	0	Hypothetical protein (1)	integral component of membrane [GO:0016021 cellular_component] (1); cellular response to salicylic acid stimulus [GO:0071446 biological_process] (1); protein binding [GO:0005515 molecular_function] (1); regulation of defense response [GO:0031347 biological_process] (1); regulation of salicylic acid mediated signaling pathway [GO:2000031 biological_process] (1)	Protein accelerated cell death 6 [IPR032846] (1); Ankyrin repeat-containing domain [IPR020683] (1); Ankyrin repeat [IPR002110] (1)	-	C_unshiu_00277_mRNA_4.1	-
GF0036182	0	1	0	Hypothetical protein (1)			-	C_unshiu_00277_mRNA_24.1	-
GF0036181	0	1	0	Hypothetical protein (1)	DNA replication [GO:0006260 biological_process] (1); origin recognition complex [GO:0000808 cellular_component] (1); nucleus [GO:0005634 cellular_component] (1)	Origin recognition complex, subunit 2 [IPR007220] (1)	-	C_unshiu_00277_mRNA_21.1	-
GF0036180	0	1	0	Hypothetical protein (1)			-	C_unshiu_00277_mRNA_20.1	-
GF0036179	0	1	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1); EF-hand domain pair [IPR011992] (1); Domain of unknown function DUF1985 [IPR015410] (1)	-	C_unshiu_00277_mRNA_2.1	-
GF0036178	0	1	0	Putative muDR family transposase-like (1)	zinc ion binding [GO:0008270 molecular_function] (1)	MULE transposase domain [IPR018289] (1); Zinc finger, PMZ-type [IPR006564] (1); Zinc finger, SWIM-type [IPR007527] (1)	-	C_unshiu_00277_mRNA_19.1	-
GF0036177	0	1	0	Calcium-dependent protein kinase 21 isoform 3 (1)	ATP binding [GO:0005524 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Protein kinase, ATP binding site [IPR017441] (1); Serine/threonine-protein kinase, active site [IPR008271] (1)	-	C_unshiu_00277_mRNA_13.1	-
GF0036176	0	1	0	Hypothetical protein (1)	nucleosome [GO:0000786 cellular_component] (1); protein heterodimerization activity [GO:0046982 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	Histone H2B [IPR000558] (1); Histone-fold [IPR009072] (1)	-	C_unshiu_00275_mRNA_8.1	-
GF0036175	0	1	0	Shugoshin protein (1)	chromosome, centromeric region [GO:0000775 cellular_component] (1); meiotic chromosome segregation [GO:0045132 biological_process] (1); nucleus [GO:0005634 cellular_component] (1)	Shugoshin, C-terminal [IPR011515] (1)	-	C_unshiu_00275_mRNA_37.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0036174	0	1	0	Hypothetical protein (1)	hydrolase activity [GO:0016787 molecular_function] (1)	Pectinacetylesterase/NOTUM [IPR004963] (1)	-	C_unshiu_00275_mRNA_33.1	-
GF0036173	0	1	0	Hypothetical protein (1)			-	C_unshiu_00275_mRNA_32.1	-
GF0036172	0	1	0	Hypothetical protein (1)			-	C_unshiu_00275_mRNA_31.1	-
GF0036171	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_00275_mRNA_27.1	-
GF0036170	0	1	0	Hypothetical protein (1)			-	C_unshiu_00275_mRNA_18.1	-
GF0036169	0	1	0	Hypothetical protein (1)			-	C_unshiu_00275_mRNA_11.1	-
GF0036168	0	1	0	Hypothetical protein (1)			-	C_unshiu_00274_mRNA_7.1	-
GF0036167	0	1	0	Hypothetical protein (1)			-	C_unshiu_00274_mRNA_35.1	-
GF0036166	0	1	0	Hypothetical protein (1)			-	C_unshiu_00274_mRNA_34.1	-
GF0036165	0	1	0	Hypothetical protein (1)			-	C_unshiu_00274_mRNA_31.1	-
GF0036164	0	1	0	Hypothetical protein (1)			-	C_unshiu_00274_mRNA_23.1	-
GF0036163	0	1	0	Hypothetical protein (1)		Bulb-type lectin domain [IPR001480] (1)	-	C_unshiu_00274_mRNA_22.1	-
GF0036162	0	1	0	Hypothetical protein (1)			-	C_unshiu_00274_mRNA_20.1	-
GF0036161	0	1	0	Hypothetical protein (1)			-	C_unshiu_00274_mRNA_19.1	-
GF0036160	0	1	0	Hypothetical protein (1)			-	C_unshiu_00274_mRNA_16.1	-
GF0036159	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_00274_mRNA_12.1	-
GF0036158	0	1	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); recognition of pollen [GO:0048544 biological_process] (1)	PAN/Apple domain [IPR003609] (1); Bulb-type lectin domain [IPR001480] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); S-locus glycoprotein domain [IPR000858] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	-	C_unshiu_00274_mRNA_10.1	-
GF0036157	0	1	0	Hypothetical protein (1)			-	C_unshiu_00274_mRNA_1.1	-
GF0036156	0	1	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_00273_mRNA_32.1	-
GF0036155	0	1	0	Hypothetical protein (1)			-	C_unshiu_00273_mRNA_19.1	-
GF0036154	0	1	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1); FAR1 DNA binding domain [IPR004330] (1)	-	C_unshiu_00273_mRNA_16.1	-
GF0036153	0	1	0	N(6)-adenine-specific DNA methyltransferase 2 (1)	methyltransferase activity [GO:0008168 molecular_function] (1); methylation [GO:0032259 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Protein-lysine N-methyltransferase Efm5 [IPR019369] (1); DNA methylase, N-6 adenine-specific, conserved site [IPR002052] (1)	-	C_unshiu_00273_mRNA_14.1	-
GF0036152	0	1	0	Hypothetical protein (1)			-	C_unshiu_00273_mRNA_11.1	-
GF0036151	0	1	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	C_unshiu_00272_mRNA_9.1	-
GF0036150	0	1	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); ATPase activity [GO:0016887 molecular_function] (1); membrane [GO:0016020 cellular_component] (1)	ABC transporter-like [IPR003439] (1); ABC-2 type transporter [IPR013525] (1); AAA+ ATPase domain [IPR003593] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Plant PDR ABC transporter associated [IPR013581] (1)	-	C_unshiu_00272_mRNA_7.1	-
GF0036149	0	1	0	Pleiotropic drug resistance protein 3 (1)	membrane [GO:0016020 cellular_component] (1); ATPase activity [GO:0016887 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Plant PDR ABC transporter associated [IPR013581] (1); ABC transporter-like [IPR003439] (1); ABC-2 type transporter [IPR013525] (1); AAA+ ATPase domain [IPR003593] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00272_mRNA_4.1	-
GF0036148	0	1	0	Hypothetical protein (1)			-	C_unshiu_00272_mRNA_25.1	-
GF0036147	0	1	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	C_unshiu_00272_mRNA_23.1	-
GF0036146	0	1	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Helicase superfamily 1/2, ATP-binding domain [IPR014001] (1); DEAD/DEAH box helicase domain [IPR011545] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00272_mRNA_10.1	-
GF0036145	0	1	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1)	ATPase, F1/V1/A1 complex, alpha/beta subunit, nucleotide-binding domain [IPR000194] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00271_mRNA_5.1	-
GF0036144	0	1	0	Hypothetical protein (1)			-	C_unshiu_00271_mRNA_40.1	-
GF0036143	0	1	0	Hypothetical protein (1)			-	C_unshiu_00271_mRNA_33.1	-
GF0036142	0	1	0	Zinc finger HIT domain-containing protein 1 (1)		Zinc finger, HIT-type [IPR007529] (1)	-	C_unshiu_00271_mRNA_24.1	-
GF0036141	0	1	0	ATP synthase subunit beta, chloroplastic (1)	proton-transporting ATPase activity, rotational mechanism [GO:0046961 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1); proton-transporting ATP synthase activity, rotational mechanism [GO:0046933 molecular_function] (1); proton-transporting ATP synthase complex, catalytic core F(1) [GO:0045261 cellular_component] (1); ATP metabolic process [GO:0046034 biological_process] (1); ATP hydrolysis coupled proton transport [GO:0015991 biological_process] (1); proton-transporting two-sector ATPase complex, catalytic domain [GO:0033178 cellular_component] (1); hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances [GO:0016820 molecular_function] (1); proton transport [GO:0015992 biological_process] (1); ATP synthesis coupled proton transport [GO:0015986 biological_process] (1)	ATPase, F1 complex alpha/beta subunit, N-terminal domain [IPR004100] (1); ATPase, alpha/beta subunit, nucleotide-binding domain, active site [IPR020003] (1); ATPase, F1 complex beta subunit/V1 complex, C-terminal [IPR024034] (1); ATP synthase delta/epsilon subunit, C-terminal domain [IPR020547] (1); ATPase, F1/V1/A1 complex, alpha/beta subunit, C-terminal [IPR000793] (1); ATPase, F1 complex, beta subunit [IPR005722] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); ATPase, F1/V1/A1 complex, alpha/beta subunit, nucleotide-binding domain [IPR000194] (1); AAA+ ATPase domain [IPR003593] (1); ATPase, F1 complex, delta/epsilon subunit, N-terminal [IPR020546] (1); ATPase, F1 complex, delta/epsilon subunit [IPR001469] (1)	-	C_unshiu_00271_mRNA_2.1	-
GF0036140	0	1	0	Hypothetical protein (1)			-	C_unshiu_00271_mRNA_13.1	-
GF0036139	0	1	0	NAD(P)H-quinone oxidoreductase subunit K, chloroplastic (1)	NADH dehydrogenase (ubiquinone) activity [GO:0008137 molecular_function] (1); quinone binding [GO:0048038 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); 4 iron, 4 sulfur cluster binding [GO:0051539 molecular_function] (1); iron-sulfur cluster binding [GO:0051536 molecular_function] (1)	NADH-ubiquinone oxidoreductase, 20 Kd subunit [IPR006138] (1); NADH:ubiquinone oxidoreductase-like, 20kDa subunit [IPR006137] (1)	-	C_unshiu_00271_mRNA_1.1	-
GF0036138	0	1	0	Hypothetical protein (1)			-	C_unshiu_00270_mRNA_6.1	-
GF0036137	0	1	0	Hypothetical protein (1)			-	C_unshiu_00270_mRNA_5.1	-
GF0036136	0	1	0	Hypothetical protein (1)			-	C_unshiu_00270_mRNA_4.1	-
GF0036135	0	1	0	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	-	C_unshiu_00270_mRNA_3.1	-
GF0036134	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00270_mRNA_14.1	-
GF0036133	0	1	0	Hypothetical protein (1)			-	C_unshiu_00270_mRNA_1.1	-
GF0036132	0	1	0	Hypothetical protein (1)	methyltransferase activity [GO:0008168 molecular_function] (1)	S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); Putative S-adenosyl-L-methionine-dependent methyltransferase [IPR004159] (1)	-	C_unshiu_00269_mRNA_7.1	-
GF0036131	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00269_mRNA_6.1	-
GF0036130	0	1	0	Hypothetical protein (1)			-	C_unshiu_00269_mRNA_30.1	-
GF0036129	0	1	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	-	C_unshiu_00269_mRNA_29.1	-
GF0036128	0	1	0	Putative copia-type pol polyprotein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	-	C_unshiu_00269_mRNA_26.1	-
GF0036127	0	1	0	Hypothetical protein (1)			-	C_unshiu_00269_mRNA_23.1	-
GF0036126	0	1	0	Hypothetical protein (1)			-	C_unshiu_00269_mRNA_22.1	-
GF0036125	0	1	0	Hypothetical protein (1)	carbohydrate binding [GO:0030246 molecular_function] (1)	Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Legume lectin domain [IPR001220] (1)	-	C_unshiu_00269_mRNA_12.1	-
GF0036124	0	1	0	Hypothetical protein (1)			-	C_unshiu_00269_mRNA_1.1	-
GF0036123	0	1	0	Hypothetical protein (1)			-	C_unshiu_00268_mRNA_5.1	-
GF0036122	0	1	0	Hypothetical protein (1)			-	C_unshiu_00268_mRNA_4.1	-
GF0036121	0	1	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_00268_mRNA_3.1	-
GF0036120	0	1	0	Hypothetical protein (1)			-	C_unshiu_00268_mRNA_23.1	-
GF0036119	0	1	0	Glutathione S-transferase TAU 25 (1)		Glutathione S-transferase, C-terminal-like [IPR010987] (1)	-	C_unshiu_00267_mRNA_9.1	-
GF0036118	0	1	0	Exocyst subunit exo70 family protein (1)	exocytosis [GO:0006887 biological_process] (1); exocyst [GO:0000145 cellular_component] (1)	Cullin repeat-like-containing domain [IPR016159] (1); Exocyst complex protein Exo70 [IPR004140] (1)	-	C_unshiu_00267_mRNA_4.1	-
GF0036117	0	1	0	Hypothetical protein (1)			-	C_unshiu_00267_mRNA_3.1	-
GF0036116	0	1	0	Hypothetical protein (1)			-	C_unshiu_00267_mRNA_15.1	-
GF0036115	0	1	0	Glutathione S-transferase 3 (1)	protein binding [GO:0005515 molecular_function] (1)	Thioredoxin-like fold [IPR012336] (1); Glutathione S-transferase, C-terminal-like [IPR010987] (1); Glutathione S-transferase, N-terminal [IPR004045] (1)	-	C_unshiu_00267_mRNA_14.1	-
GF0036114	0	1	0	Glutathione S-transferase U19 (1)		Glutathione S-transferase, C-terminal-like [IPR010987] (1)	-	C_unshiu_00267_mRNA_13.1	-
GF0036113	0	1	0	Hypothetical protein (1)			-	C_unshiu_00267_mRNA_10.1	-
GF0036112	0	1	0	Hypothetical protein (1)			-	C_unshiu_00266_mRNA_6.1	-
GF0036111	0	1	0	Hypothetical protein (1)			-	C_unshiu_00266_mRNA_5.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0036110	0	1	0	NADP-dependent alkenal double bond reductase (1)	zinc ion binding [GO:0008270 molecular_function] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	NAD(P)-binding domain [IPR016040] (1); Alcohol dehydrogenase, C-terminal [IPR013149] (1); Polyketide synthase, enoylreductase domain [IPR020843] (1); Alcohol dehydrogenase superfamily, zinc-type [IPR002085] (1); GroES-like [IPR011032] (1)	-	C_unshiu_00266_mRNA_33.1	-
GF0036109	0	1	0	NADP-dependent alkenal double bond reductase P2 (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Alcohol dehydrogenase superfamily, zinc-type [IPR002085] (1); GroES-like [IPR011032] (1); NAD(P)-binding domain [IPR016040] (1)	-	C_unshiu_00266_mRNA_32.1	-
GF0036108	0	1	0	LETM1 and EF-hand domain-containing protein 1, mitochondrial (1)	ribosome binding [GO:0043022 molecular_function] (1)	LETM1-like [IPR011685] (1); Letm1 ribosome-binding domain [IPR033122] (1)	-	C_unshiu_00266_mRNA_28.1	-
GF0036107	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_00266_mRNA_23.1	-
GF0036106	0	1	0	Hypothetical protein (1)			-	C_unshiu_00266_mRNA_22.1	-
GF0036105	0	1	0	Hypothetical protein (1)			-	C_unshiu_00266_mRNA_21.1	-
GF0036104	0	1	0	Hypothetical protein (1)			-	C_unshiu_00266_mRNA_20.1	-
GF0036103	0	1	0	Putative RNA-directed DNA polymerase (1)	RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H domain [IPR002156] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00266_mRNA_14.1	-
GF0036102	0	1	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	Transcription factor, MADS-box [IPR002100] (1)	-	C_unshiu_00266_mRNA_13.1	-
GF0036101	0	1	0	Hypothetical protein (1)			-	C_unshiu_00266_mRNA_12.1	-
GF0036100	0	1	0	Hypothetical protein (1)			-	C_unshiu_00266_mRNA_11.1	-
GF0036099	0	1	0	Hypothetical protein (1)	DNA-directed RNA polymerase activity [GO:0003899 molecular_function] (1); ribonucleoside binding [GO:0032549 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1); transcription, DNA-templated [GO:0006351 biological_process] (1)	RNA polymerase Rpb2, domain 7 [IPR007641] (1); DNA-directed RNA polymerase, subunit 2, domain 6 [IPR007120] (1); RNA polymerase Rpb2, OB-fold [IPR014724] (1); RNA polymerase Rpb1, domain 3 [IPR007066] (1); RNA polymerase Rpb1, domain 1 [IPR007080] (1); RNA polymerase, beta subunit, conserved site [IPR007121] (1); DNA-directed RNA polymerase, subunit 2 [IPR015712] (1); RNA polymerase, alpha subunit [IPR000722] (1); RNA polymerase, N-terminal [IPR006592] (1)	-	C_unshiu_00265_mRNA_27.1	-
GF0036098	0	1	0	Hypothetical protein (1)			-	C_unshiu_00265_mRNA_26.1	-
GF0036097	0	1	0	Hypothetical protein (1)	transcription, DNA-templated [GO:0006351 biological_process] (1); DNA binding [GO:0003677 molecular_function] (1); DNA-directed RNA polymerase activity [GO:0003899 molecular_function] (1)	RNA polymerase Rpb1, domain 5 [IPR007081] (1)	-	C_unshiu_00265_mRNA_25.1	-
GF0036096	0	1	0	30S ribosomal protein S2, chloroplastic (1)	translation [GO:0006412 biological_process] (1); intracellular [GO:0005622 cellular_component] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1); small ribosomal subunit [GO:0015935 cellular_component] (1); ribosome [GO:0005840 cellular_component] (1)	Ribosomal protein S2, bacteria/mitochondria/plastid [IPR005706] (1); Ribosomal protein S2, flavodoxin-like domain [IPR023591] (1); Ribosomal protein S2 [IPR001865] (1)	-	C_unshiu_00265_mRNA_24.1	-
GF0036095	0	1	0	ATP synthase subunit a, chloroplastic (1)	hydrogen ion transmembrane transporter activity [GO:0015078 molecular_function] (1); ATP synthesis coupled proton transport [GO:0015986 biological_process] (1)	ATPase, F0 complex, subunit A, active site [IPR023011] (1); ATPase, F0 complex, subunit A [IPR000568] (1)	-	C_unshiu_00265_mRNA_23.1	-
GF0036094	0	1	0	Photosystem II protein D1 (1)	ribosome [GO:0005840 cellular_component] (1); photosynthesis, light reaction [GO:0019684 biological_process] (1); electron carrier activity [GO:0009055 molecular_function] (1); translation [GO:0006412 biological_process] (1); photosynthetic electron transport in photosystem II [GO:0009772 biological_process] (1); intracellular [GO:0005622 cellular_component] (1); electron transporter, transferring electrons within the cyclic electron transport pathway of photosynthesis activity [GO:0045156 molecular_function] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1)	Photosystem II protein D1 [IPR005867] (1); Photosynthetic reaction centre, L/M [IPR000484] (1); Ribosomal protein S16, conserved site [IPR020592] (1)	-	C_unshiu_00265_mRNA_22.1	-
GF0036093	0	1	0	Putative muDR family transposase-like (1)			-	C_unshiu_00265_mRNA_20.1	-
GF0036092	0	1	0	Hypothetical protein (1)	nucleus [GO:0005634 cellular_component] (1); regulation of cell cycle [GO:0051726 biological_process] (1)	Cyclin D, plant [IPR031093] (1); Cyclin-like [IPR013763] (1); Cyclin, N-terminal [IPR006671] (1)	-	C_unshiu_00265_mRNA_2.1	-
GF0036091	0	1	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_00265_mRNA_15.1	-
GF0036090	0	1	0	Hypothetical protein (1)			-	C_unshiu_00265_mRNA_10.1	-
GF0036089	0	1	0	Hypothetical protein (1)			-	C_unshiu_00264_mRNA_9.1	-
GF0036088	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_00264_mRNA_8.1	-
GF0036087	0	1	0	Hypothetical protein (1)			-	C_unshiu_00264_mRNA_7.1	-
GF0036086	0	1	0	Hypothetical protein (1)			-	C_unshiu_00264_mRNA_6.1	-
GF0036085	0	1	0	Hypothetical protein (1)			-	C_unshiu_00264_mRNA_5.1	-
GF0036084	0	1	0	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1)	Cytochrome P450 [IPR001128] (1)	-	C_unshiu_00264_mRNA_23.1	-
GF0036083	0	1	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	hAT-like transposase, RNase-H fold [IPR025525] (1)	-	C_unshiu_00264_mRNA_21.1	-
GF0036082	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase [IPR029068] (1)	-	C_unshiu_00264_mRNA_2.1	-
GF0036081	0	1	0	Hypothetical protein (1)			-	C_unshiu_00264_mRNA_18.1	-
GF0036080	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Domain of unknown function DUF4283 [IPR025558] (1); Ribonuclease H-like domain [IPR012337] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1); Reverse transcriptase domain [IPR000477] (1); Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	C_unshiu_00264_mRNA_16.1	-
GF0036079	0	1	0	Nodulin MtN21/EamA-like transporter family protein (1)	integral component of membrane [GO:0016021 cellular_component] (1); transmembrane transporter activity [GO:0022857 molecular_function] (1); membrane [GO:0016020 cellular_component] (1)	EamA domain [IPR000620] (1); WAT1-related protein [IPR030184] (1)	-	C_unshiu_00264_mRNA_1.1	-
GF0036078	0	1	0	Hypothetical protein (1)			-	C_unshiu_00263_mRNA_9.1	-
GF0036077	0	1	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_00263_mRNA_6.1	-
GF0036076	0	1	0	Hypothetical protein (1)			-	C_unshiu_00263_mRNA_28.1	-
GF0036075	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF1336 [IPR009769] (1)	-	C_unshiu_00263_mRNA_26.1	-
GF0036074	0	1	0	Hypothetical protein (1)			-	C_unshiu_00263_mRNA_24.1	-
GF0036073	0	1	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00263_mRNA_23.1	-
GF0036072	0	1	0	Hypothetical protein (1)			-	C_unshiu_00263_mRNA_21.1	-
GF0036071	0	1	0	Hypothetical protein (1)			-	C_unshiu_00263_mRNA_19.1	-
GF0036070	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	C_unshiu_00263_mRNA_18.1	-
GF0036069	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00263_mRNA_13.1	-
GF0036068	0	1	0	Hypothetical protein (1)			-	C_unshiu_00263_mRNA_10.1	-
GF0036067	0	1	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_00261_mRNA_5.1	-
GF0036066	0	1	0	Hypothetical protein (1)			-	C_unshiu_00261_mRNA_40.1	-
GF0036065	0	1	0	Hypothetical protein (1)			-	C_unshiu_00261_mRNA_38.1	-
GF0036064	0	1	0	Hypothetical protein (1)			-	C_unshiu_00261_mRNA_35.1	-
GF0036063	0	1	0	Hypothetical protein (1)			-	C_unshiu_00261_mRNA_34.1	-
GF0036062	0	1	0	Hypothetical protein (1)			-	C_unshiu_00261_mRNA_32.1	-
GF0036061	0	1	0	Hypothetical protein (1)			-	C_unshiu_00261_mRNA_27.1	-
GF0036060	0	1	0	Kinesin light chain, putative (1)	protein binding [GO:0005515 molecular_function] (1)	Tetratricopeptide repeat [IPR019734] (1); Tetratricopeptide repeat-containing domain [IPR013026] (1); Tetratricopeptide-like helical domain [IPR011990] (1); Tetratricopeptide repeat 2 [IPR013105] (1)	-	C_unshiu_00261_mRNA_16.1	-
GF0036059	0	1	0	Hypothetical protein (1)	metal ion binding [GO:0046872 molecular_function] (1); nucleotide binding [GO:0000166 molecular_function] (1)	P-type ATPase, A domain [IPR008250] (1); Cation-transporting P-type ATPase, N-terminal [IPR004014] (1)	-	C_unshiu_00261_mRNA_1.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0036058	0	1	0	UDP-glucose flavonoid 3-O-glucosyltransferase 7 (1)	transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	-	C_unshiu_00260_mRNA_3.1	-
GF0036057	0	1	0	Hypothetical protein (1)			-	C_unshiu_00260_mRNA_24.1	-
GF0036056	0	1	0	Flavonoid 3'-monooxygenase (1)	heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450, conserved site [IPR017972] (1); Cytochrome P450 [IPR001128] (1)	-	C_unshiu_00260_mRNA_21.1	-
GF0036055	0	1	0	Hypothetical protein (1)			-	C_unshiu_00259_mRNA_6.1	-
GF0036054	0	1	0	Hypothetical protein (1)			-	C_unshiu_00259_mRNA_26.1	-
GF0036053	0	1	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_00259_mRNA_23.1	-
GF0036052	0	1	0	Hypothetical protein (1)			-	C_unshiu_00259_mRNA_21.1	-
GF0036051	0	1	0	Hypothetical protein (1)		Aminotransferase-like, plant mobile domain [IPR019557] (1)	-	C_unshiu_00259_mRNA_19.1	-
GF0036050	0	1	0	Hypothetical protein (1)	HAUS complex [GO:0070652 cellular_component] (1); spindle assembly [GO:0051225 biological_process] (1)	HAUS augmin-like complex subunit 3 [IPR026206] (1); FAR1 DNA binding domain [IPR004330] (1)	-	C_unshiu_00259_mRNA_14.1	-
GF0036049	0	1	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_00258_mRNA_8.1	-
GF0036048	0	1	0	Hypothetical protein (1)			-	C_unshiu_00258_mRNA_7.1	-
GF0036047	0	1	0	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	C_unshiu_00258_mRNA_5.1	-
GF0036046	0	1	0	Hypothetical protein (1)			-	C_unshiu_00258_mRNA_42.1	-
GF0036045	0	1	0	Hypothetical protein (1)			-	C_unshiu_00258_mRNA_41.1	-
GF0036044	0	1	0	Hypothetical protein (1)			-	C_unshiu_00258_mRNA_4.1	-
GF0036043	0	1	0	Hypothetical protein (1)			-	C_unshiu_00258_mRNA_36.1	-
GF0036042	0	1	0	Polynucleotidyl transferase, Ribonuclease H fold (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00258_mRNA_2.1	-
GF0036041	0	1	0	Hypothetical protein (1)			-	C_unshiu_00258_mRNA_16.1	-
GF0036040	0	1	0	Hypothetical protein (1)			-	C_unshiu_00257_mRNA_8.1	-
GF0036039	0	1	0	Hypothetical protein (1)			-	C_unshiu_00257_mRNA_7.1	-
GF0036038	0	1	0	Hypothetical protein (1)			-	C_unshiu_00257_mRNA_5.1	-
GF0036037	0	1	0	Putative muDR family transposase-like (1)	zinc ion binding [GO:0008270 molecular_function] (1); transposition, DNA-mediated [GO:0006313 biological_process] (1); transposase activity [GO:0004803 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	Zinc finger, SWIM-type [IPR007527] (1); Transposase, MuDR, plant [IPR004332] (1); Transposase, mutator type [IPR001207] (1); MULE transposase domain [IPR018289] (1); Zinc finger, PMZ-type [IPR006564] (1)	-	C_unshiu_00257_mRNA_4.1	-
GF0036036	0	1	0	Sterile alpha motif domain-containing protein 9-like protein (1)			-	C_unshiu_00257_mRNA_3.1	-
GF0036035	0	1	0	Hypothetical protein (1)			-	C_unshiu_00257_mRNA_21.1	-
GF0036034	0	1	0	Hypothetical protein (1)			-	C_unshiu_00257_mRNA_18.1	-
GF0036033	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00257_mRNA_17.1	-
GF0036032	0	1	0	Hypothetical protein (1)			-	C_unshiu_00257_mRNA_13.1	-
GF0036031	0	1	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00257_mRNA_11.1	-
GF0036030	0	1	0	TIR domain protein (1)			-	C_unshiu_00256_mRNA_9.1	-
GF0036029	0	1	0	Hypothetical protein (1)			-	C_unshiu_00256_mRNA_30.1	-
GF0036028	0	1	0	Hypothetical protein (1)			-	C_unshiu_00256_mRNA_25.1	-
GF0036027	0	1	0	GDSL-like Lipase/Acylhydrolase superfamily protein, putative isoform 2 (1)		SGNH hydrolase-type esterase domain [IPR013830] (1)	-	C_unshiu_00256_mRNA_22.1	-
GF0036026	0	1	0	Hypothetical protein (1)	transport [GO:0006810 biological_process] (1)	Longin-like domain [IPR011012] (1)	-	C_unshiu_00256_mRNA_21.1	-
GF0036025	0	1	0	Hypothetical protein (1)			-	C_unshiu_00256_mRNA_17.1	-
GF0036024	0	1	0	Caffeic acid 3-O-methyltransferase (1)			-	C_unshiu_00256_mRNA_1.1	-
GF0036023	0	1	0	Leguminosin group485 secreted peptide (1)			-	C_unshiu_00255_mRNA_6.1	-
GF0036022	0	1	0	Putative MATE efflux family protein (1)	drug transmembrane transport [GO:0006855 biological_process] (1); membrane [GO:0016020 cellular_component] (1); antiporter activity [GO:0015297 molecular_function] (1); drug transmembrane transporter activity [GO:0015238 molecular_function] (1); transmembrane transport [GO:0055085 biological_process] (1)	Multi antimicrobial extrusion protein [IPR002528] (1)	-	C_unshiu_00255_mRNA_38.1	-
GF0036021	0	1	0	Hypothetical protein (1)			-	C_unshiu_00255_mRNA_30.1	-
GF0036020	0	1	0	14-3-3-like protein GF14 kappa (1)	protein domain specific binding [GO:0019904 molecular_function] (1)	14-3-3 protein [IPR000308] (1); 14-3-3 protein, conserved site [IPR023409] (1); 14-3-3 domain [IPR023410] (1)	-	C_unshiu_00255_mRNA_22.1	-
GF0036019	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF1985 [IPR015410] (1)	-	C_unshiu_00255_mRNA_21.1	-
GF0036018	0	1	0	Hypothetical protein (1)			-	C_unshiu_00255_mRNA_20.1	-
GF0036017	0	1	0	Ribonuclease H-like superfamily protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00254_mRNA_7.1	-
GF0036016	0	1	0	Hypothetical protein (1)	heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Cytochrome P450 [IPR001128] (1); Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450, conserved site [IPR017972] (1)	-	C_unshiu_00253_mRNA_40.2	-
GF0036015	0	1	0	Hypothetical protein (1)		P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00253_mRNA_30.1	-
GF0036014	0	1	0	Hypothetical protein (1)	binding [GO:0005488 molecular_function] (1)	E3 ubiquitin ligase, UBR4 [IPR025704] (1); Armadillo-type fold [IPR016024] (1)	-	C_unshiu_00253_mRNA_3.1	-
GF0036013	0	1	0	Hypothetical protein (1)			-	C_unshiu_00252_mRNA_9.1	-
GF0036012	0	1	0	Hypothetical protein (1)			-	C_unshiu_00252_mRNA_42.1	-
GF0036011	0	1	0	DNA/RNA polymerases superfamily protein (1)			-	C_unshiu_00252_mRNA_41.1	-
GF0036010	0	1	0	Wall-associated receptor kinase 2 (1)	polysaccharide binding [GO:0030247 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Serine/threonine-protein kinase, active site [IPR008271] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Wall-associated receptor kinase, galacturonan-binding domain [IPR025287] (1)	-	C_unshiu_00252_mRNA_39.1	-
GF0036009	0	1	0	Hypothetical protein (1)			-	C_unshiu_00252_mRNA_37.1	-
GF0036008	0	1	0	Hypothetical protein (1)			-	C_unshiu_00252_mRNA_35.1	-
GF0036007	0	1	0	Hypothetical protein (1)			-	C_unshiu_00252_mRNA_23.1	-
GF0036006	0	1	0	Hypothetical protein (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1); hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (1)	Glycoside hydrolase family 9 [IPR001701] (1); Six-hairpin glycosidase-like [IPR008928] (1); Six-hairpin glycosidase [IPR012341] (1); Glycoside hydrolase family 9, His active site [IPR018221] (1)	-	C_unshiu_00252_mRNA_21.1	-
GF0036005	0	1	0	Heat stress transcription factor B-2b (1)		Heat shock transcription factor family [IPR027725] (1)	-	C_unshiu_00252_mRNA_19.1	-
GF0036004	0	1	0	21 kDa protein (1)	enzyme inhibitor activity [GO:0004857 molecular_function] (1)	Pectinesterase inhibitor domain [IPR006501] (1)	-	C_unshiu_00252_mRNA_17.1	-
GF0036003	0	1	0	Hypothetical protein (1)			-	C_unshiu_00251_mRNA_30.1	-
GF0036002	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00251_mRNA_29.1	-
GF0036001	0	1	0	Polynucleotidyl transferase, ribonuclease H-like superfamily protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_00251_mRNA_20.1	-
GF0036000	0	1	0	Hypothetical protein (1)	protein serine/threonine phosphatase activity [GO:0004722 molecular_function] (1); protein dephosphorylation [GO:0006470 biological_process] (1)	Protein phosphatase 2C family [IPR015655] (1)	-	C_unshiu_00251_mRNA_18.1	-
GF0035999	0	1	0	MD-2-related lipid recognition domain-containing family protein (1)		Immunoglobulin E-set [IPR014756] (1); MD-2-related lipid-recognition domain [IPR003172] (1)	-	C_unshiu_00251_mRNA_16.1	-
GF0035998	0	1	0	MD-like lipid recognition domain protein/ML domain protein (1)		Immunoglobulin E-set [IPR014756] (1); MD-2-related lipid-recognition domain [IPR003172] (1)	-	C_unshiu_00251_mRNA_15.1	-
GF0035997	0	1	0	Hypothetical protein (1)			-	C_unshiu_00251_mRNA_11.1	-
GF0035996	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00251_mRNA_1.1	-
GF0035995	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1)	Ribonuclease H domain [IPR002156] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00250_mRNA_4.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0035994	0	1	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1); MULE transposase domain [IPR018289] (1)	-	C_unshiu_00250_mRNA_35.1	-
GF0035993	0	1	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_00250_mRNA_23.1	-
GF0035992	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00250_mRNA_20.1	-
GF0035991	0	1	0	Hypothetical protein (1)			-	C_unshiu_00250_mRNA_2.1	-
GF0035990	0	1	0	Hypothetical protein (1)			-	C_unshiu_00250_mRNA_17.1	-
GF0035989	0	1	0	Hypothetical protein (1)			-	C_unshiu_00250_mRNA_16.1	-
GF0035988	0	1	0	Hypothetical protein (1)			-	C_unshiu_00250_mRNA_11.1	-
GF0035987	0	1	0	Hypothetical protein (1)		10TM putative phosphate transporter, cytosolic domain [IPR027815] (1)	-	C_unshiu_00249_mRNA_45.1	-
GF0035986	0	1	0	ERD (Early-responsive to dehydration stress) family protein isoform 3 (1)	membrane [GO:0016020 cellular_component] (1)	10TM putative phosphate transporter, cytosolic domain [IPR027815] (1); Calcium-dependent channel, 7TM region, putative phosphate [IPR003864] (1); Calcium permeable stress-gated cation channel 1, N-terminal transmembrane domain [IPR032880] (1)	-	C_unshiu_00249_mRNA_44.1	-
GF0035985	0	1	0	Hypothetical protein (1)		10TM putative phosphate transporter, cytosolic domain [IPR027815] (1); Calcium permeable stress-gated cation channel 1, N-terminal transmembrane domain [IPR032880] (1)	-	C_unshiu_00249_mRNA_43.1	-
GF0035984	0	1	0	Hypothetical protein (1)			-	C_unshiu_00249_mRNA_39.1	-
GF0035983	0	1	0	Hypothetical protein (1)			-	C_unshiu_00249_mRNA_2.1	-
GF0035982	0	1	0	Hypothetical protein (1)			-	C_unshiu_00249_mRNA_14.1	-
GF0035981	0	1	0	Disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00249_mRNA_11.1	-
GF0035980	0	1	0	Non-LTR reverse transcriptase (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	C_unshiu_00249_mRNA_10.1	-
GF0035979	0	1	0	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein (1)		Hydrophobic seed protein [IPR027923] (1); Bifunctional inhibitor/plant lipid transfer protein/seed storage helical domain [IPR016140] (1)	-	C_unshiu_00248_mRNA_37.1	-
GF0035978	0	1	0	Bimodular protein (1)		Bifunctional inhibitor/plant lipid transfer protein/seed storage helical domain [IPR016140] (1); Hydrophobic seed protein [IPR027923] (1)	-	C_unshiu_00248_mRNA_36.1	-
GF0035977	0	1	0	Hypothetical protein (1)		Bifunctional inhibitor/plant lipid transfer protein/seed storage helical domain [IPR016140] (1); Hydrophobic seed protein [IPR027923] (1)	-	C_unshiu_00248_mRNA_34.1	-
GF0035976	0	1	0	Hypothetical protein (1)		Transposase, MuDR, plant [IPR004332] (1)	-	C_unshiu_00248_mRNA_31.1	-
GF0035975	0	1	0	Hypothetical protein (1)			-	C_unshiu_00248_mRNA_3.1	-
GF0035974	0	1	0	Zinc transporter 5 (1)	metal ion transmembrane transporter activity [GO:0046873 molecular_function] (1); metal ion transport [GO:0030001 biological_process] (1); transmembrane transport [GO:0055085 biological_process] (1); membrane [GO:0016020 cellular_component] (1)	Zinc/iron permease [IPR003689] (1)	-	C_unshiu_00248_mRNA_27.1	-
GF0035973	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00247_mRNA_36.1	-
GF0035972	0	1	0	Hypothetical protein (1)			-	C_unshiu_00247_mRNA_32.1	-
GF0035971	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat-containing domain [IPR020683] (1); Ankyrin repeat [IPR002110] (1)	-	C_unshiu_00247_mRNA_28.1	-
GF0035970	0	1	0	Hypothetical protein (1)			-	C_unshiu_00247_mRNA_27.1	-
GF0035969	0	1	0	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (1)	cellular amino acid biosynthetic process [GO:0008652 biological_process] (1); zinc ion binding [GO:0008270 molecular_function] (1); methionine biosynthetic process [GO:0009086 biological_process] (1); 5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase activity [GO:0003871 molecular_function] (1)	Cobalamin-independent methionine synthase MetE, C-terminal/archaeal [IPR002629] (1); Cobalamin-independent methionine synthase MetE, N-terminal [IPR013215] (1)	-	C_unshiu_00247_mRNA_26.1	-
GF0035968	0	1	0	Hypothetical protein (1)			-	C_unshiu_00246_mRNA_36.1	-
GF0035967	0	1	0	Hypothetical protein (1)			-	C_unshiu_00246_mRNA_34.1	-
GF0035966	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, SWIM-type [IPR007527] (1); Domain of unknown function DUF4219 [IPR025314] (1); Transposase, MuDR, plant [IPR004332] (1); Zinc finger, PMZ-type [IPR006564] (1)	-	C_unshiu_00246_mRNA_33.1	-
GF0035965	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, GRF-type [IPR010666] (1)	-	C_unshiu_00246_mRNA_32.1	-
GF0035964	0	1	0	Hypothetical protein (1)			-	C_unshiu_00246_mRNA_31.1	-
GF0035963	0	1	0	Hypothetical protein (1)			-	C_unshiu_00246_mRNA_1.1	-
GF0035962	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1); ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1)	-	C_unshiu_00245_mRNA_8.1	-
GF0035961	0	1	0	Sister chromatid cohesion protein PDS5 (1)	binding [GO:0005488 molecular_function] (1)	Armadillo-type fold [IPR016024] (1)	-	C_unshiu_00245_mRNA_6.1	-
GF0035960	0	1	0	Hypothetical protein (1)			-	C_unshiu_00245_mRNA_3.1	-
GF0035959	0	1	0	Putative muDR family transposase-like (1)	zinc ion binding [GO:0008270 molecular_function] (1)	MULE transposase domain [IPR018289] (1); Zinc finger, PMZ-type [IPR006564] (1); Zinc finger, SWIM-type [IPR007527] (1)	-	C_unshiu_00245_mRNA_28.1	-
GF0035958	0	1	0	Hypothetical protein (1)			-	C_unshiu_00245_mRNA_24.1	-
GF0035957	0	1	0	Hypothetical protein (1)			-	C_unshiu_00245_mRNA_20.1	-
GF0035956	0	1	0	Hypothetical protein (1)			-	C_unshiu_00245_mRNA_17.1	-
GF0035955	0	1	0	Cytochrome P450 71A1 (1)	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1)	Cytochrome P450 [IPR001128] (1); Cytochrome P450, E-class, group I [IPR002401] (1)	-	C_unshiu_00245_mRNA_15.1	-
GF0035954	0	1	0	Hypothetical protein (1)			-	C_unshiu_00245_mRNA_11.1	-
GF0035953	0	1	0	Cytochrome P450 76AD1-like protein (1)			-	C_unshiu_00244_mRNA_4.1	-
GF0035952	0	1	0	Hypothetical protein (1)			-	C_unshiu_00244_mRNA_32.1	-
GF0035951	0	1	0	Hypothetical protein (1)			-	C_unshiu_00244_mRNA_3.1	-
GF0035950	0	1	0	Hypothetical protein (1)			-	C_unshiu_00244_mRNA_28.1	-
GF0035949	0	1	0	Hypothetical protein (1)			-	C_unshiu_00244_mRNA_19.1	-
GF0035948	0	1	0	Hypothetical protein (1)			-	C_unshiu_00244_mRNA_18.1	-
GF0035947	0	1	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	C_unshiu_00244_mRNA_15.1	-
GF0035946	0	1	0	Hypothetical protein (1)			-	C_unshiu_00244_mRNA_14.1	-
GF0035945	0	1	0	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein, putative isoform 1 (1)		Lysine methyltransferase [IPR019410] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); FAM86 [IPR029426] (1)	-	C_unshiu_00244_mRNA_13.1	-
GF0035944	0	1	0	Hypothetical protein (1)			-	C_unshiu_00244_mRNA_12.1	-
GF0035943	0	1	0	Hypothetical protein (1)			-	C_unshiu_00243_mRNA_9.1	-
GF0035942	0	1	0	Truncated RB (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	C_unshiu_00243_mRNA_8.1	-
GF0035941	0	1	0	Hypothetical protein (1)			-	C_unshiu_00243_mRNA_40.1	-
GF0035940	0	1	0	Hypothetical protein (1)			-	C_unshiu_00243_mRNA_39.1	-
GF0035939	0	1	0	Hypothetical protein (1)			-	C_unshiu_00243_mRNA_37.1	-
GF0035938	0	1	0	Hypothetical protein (1)			-	C_unshiu_00243_mRNA_36.1	-
GF0035937	0	1	0	Hypothetical protein (1)			-	C_unshiu_00243_mRNA_32.1	-
GF0035936	0	1	0	Putative disease resistance protein RGA4 (1)			-	C_unshiu_00243_mRNA_3.1	-
GF0035935	0	1	0	Hypothetical protein (1)			-	C_unshiu_00243_mRNA_27.1	-
GF0035934	0	1	0	Hypothetical protein (1)			-	C_unshiu_00243_mRNA_23.1	-
GF0035933	0	1	0	Hypothetical protein (1)			-	C_unshiu_00243_mRNA_22.1	-
GF0035932	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00243_mRNA_2.1	-
GF0035931	0	1	0	Hypothetical protein (1)			-	C_unshiu_00243_mRNA_19.1	-
GF0035930	0	1	0	Hypothetical protein (1)			-	C_unshiu_00243_mRNA_16.1	-
GF0035929	0	1	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	C_unshiu_00243_mRNA_15.1	-
GF0035928	0	1	0	Anthocyanidin 3-O-glucosyltransferase (1)	transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	-	C_unshiu_00243_mRNA_14.1	-
GF0035927	0	1	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	C_unshiu_00243_mRNA_12.1	-
GF0035926	0	1	0	Hypothetical protein (1)		Transposase, MuDR, plant [IPR004332] (1)	-	C_unshiu_00242_mRNA_9.1	-
GF0035925	0	1	0	Hypothetical protein (1)			-	C_unshiu_00242_mRNA_5.1	-
GF0035924	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00242_mRNA_30.1	-
GF0035923	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	C_unshiu_00242_mRNA_28.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0035922	0	1	0	Hypothetical protein (1)			-	C_unshiu_00242_mRNA_27.1	-
GF0035921	0	1	0	Hypothetical protein (1)			-	C_unshiu_00242_mRNA_26.1	-
GF0035920	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_00242_mRNA_23.1	-
GF0035919	0	1	0	Hypothetical protein (1)			-	C_unshiu_00242_mRNA_2.1	-
GF0035918	0	1	0	Hypothetical protein (1)			-	C_unshiu_00242_mRNA_18.1	-
GF0035917	0	1	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	Zinc finger, BED-type [IPR003656] (1)	-	C_unshiu_00242_mRNA_14.1	-
GF0035916	0	1	0	Hypothetical protein (1)			-	C_unshiu_00242_mRNA_13.1	-
GF0035915	0	1	0	Synaptonemal complex protein 2 (1)			-	C_unshiu_00241_mRNA_4.1	-
GF0035914	0	1	0	Hypothetical protein (1)			-	C_unshiu_00241_mRNA_28.1	-
GF0035913	0	1	0	Hypothetical protein (1)			-	C_unshiu_00241_mRNA_27.1	-
GF0035912	0	1	0	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	C_unshiu_00241_mRNA_17.1	-
GF0035911	0	1	0	Hypothetical protein (1)			-	C_unshiu_00240_mRNA_6.1	-
GF0035910	0	1	0	Hypothetical protein (1)			-	C_unshiu_00240_mRNA_21.1	-
GF0035909	0	1	0	Hypothetical protein (1)			-	C_unshiu_00240_mRNA_2.1	-
GF0035908	0	1	0	Hypothetical protein (1)			-	C_unshiu_00240_mRNA_17.1	-
GF0035907	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1); Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	C_unshiu_00240_mRNA_14.1	-
GF0035906	0	1	0	Hypothetical protein (1)			-	C_unshiu_00239_mRNA_38.1	-
GF0035905	0	1	0	Hypothetical protein (1)			-	C_unshiu_00239_mRNA_37.1	-
GF0035904	0	1	0	Hypothetical protein (1)			-	C_unshiu_00239_mRNA_32.1	-
GF0035903	0	1	0	Lysosomal beta glucosidase (1)	hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1)	Glycoside hydrolase superfamily [IPR017853] (1); Glycoside hydrolase family 3 C-terminal domain [IPR002772] (1); Glycoside hydrolase family 3 [IPR026892] (1); Glycoside hydrolase, family 3, N-terminal [IPR001764] (1)	-	C_unshiu_00239_mRNA_2.1	-
GF0035902	0	1	0	Squamous cell carcinoma antigen recognized by T-cells 3 (1)	RNA processing [GO:0006396 biological_process] (1); protein binding [GO:0005515 molecular_function] (1)	HAT (Half-A-TPR) repeat [IPR003107] (1); Tetratricopeptide-like helical domain [IPR011990] (1)	-	C_unshiu_00239_mRNA_13.1	-
GF0035901	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	WD40/YVTN repeat-like-containing domain [IPR015943] (1); WD40-repeat-containing domain [IPR017986] (1)	-	C_unshiu_00239_mRNA_1.1	-
GF0035900	0	1	0	Hypothetical protein (1)			-	C_unshiu_00238_mRNA_34.1	-
GF0035899	0	1	0	Hypothetical protein (1)			-	C_unshiu_00237_mRNA_8.1	-
GF0035898	0	1	0	Hypothetical protein (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1); hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (1)	Glycoside hydrolase family 16 [IPR000757] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Glycoside hydrolase, family 16, active site [IPR008263] (1)	-	C_unshiu_00237_mRNA_43.1	-
GF0035897	0	1	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	NAC domain [IPR003441] (1)	-	C_unshiu_00237_mRNA_42.1	-
GF0035896	0	1	0	Hypothetical protein (1)			-	C_unshiu_00237_mRNA_36.1	-
GF0035895	0	1	0	Polynucleotidyl transferase, Ribonuclease H fold (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_00237_mRNA_3.1	-
GF0035894	0	1	0	Hypothetical protein (1)	terpenoid biosynthetic process [GO:0016114 biological_process] (1); GTP binding [GO:0005525 molecular_function] (1); intracellular [GO:0005622 cellular_component] (1); small GTPase mediated signal transduction [GO:0007264 biological_process] (1); 1-deoxy-D-xylulose-5-phosphate synthase activity [GO:0008661 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Small GTP-binding protein domain [IPR005225] (1); Small GTPase superfamily, ARF type [IPR024156] (1); Thiamin diphosphate-binding fold [IPR029061] (1); Deoxyxylulose-5-phosphate synthase [IPR005477] (1); Small GTPase superfamily, ARF/SAR type [IPR006689] (1)	-	C_unshiu_00237_mRNA_26.1	-
GF0035893	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Thiamin diphosphate-binding fold [IPR029061] (1); Transketolase binding site [IPR020826] (1); CCT domain [IPR010402] (1); Transketolase-like, pyrimidine-binding domain [IPR005475] (1)	-	C_unshiu_00237_mRNA_25.1	-
GF0035892	0	1	0	Hypothetical protein (1)			-	C_unshiu_00237_mRNA_2.1	-
GF0035891	0	1	0	Hypothetical protein (1)			-	C_unshiu_00237_mRNA_19.1	-
GF0035890	0	1	0	Hypothetical protein (1)		Receptor, ligand binding region [IPR001828] (1); Periplasmic binding protein-like I [IPR028082] (1)	-	C_unshiu_00237_mRNA_17.1	-
GF0035889	0	1	0	Hypothetical protein (1)	G-protein coupled receptor activity [GO:0004930 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1); G-protein coupled receptor signaling pathway [GO:0007186 biological_process] (1)	GPCR, family 3 [IPR000337] (1); Receptor, ligand binding region [IPR001828] (1); Periplasmic binding protein-like I [IPR028082] (1)	-	C_unshiu_00237_mRNA_14.1	-
GF0035888	0	1	0	Cysteine-rich receptor-like protein kinase 25 (1)		Gnk2-homologous domain [IPR002902] (1)	-	C_unshiu_00236_mRNA_9.1	-
GF0035887	0	1	0	NADP-dependent alkenal double bond reductase P2 (1)	zinc ion binding [GO:0008270 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1)	NAD(P)-binding domain [IPR016040] (1); Alcohol dehydrogenase superfamily, zinc-type [IPR002085] (1); Alcohol dehydrogenase, C-terminal [IPR013149] (1); GroES-like [IPR011032] (1)	-	C_unshiu_00236_mRNA_7.1	-
GF0035886	0	1	0	Hypothetical protein (1)			-	C_unshiu_00236_mRNA_5.1	-
GF0035885	0	1	0	Hypothetical protein (1)			-	C_unshiu_00236_mRNA_44.1	-
GF0035884	0	1	0	Hypothetical protein (1)	RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Ribonuclease H domain [IPR002156] (1)	-	C_unshiu_00236_mRNA_4.1	-
GF0035883	0	1	0	Hypothetical protein (1)		Transposase, MuDR, plant [IPR004332] (1)	-	C_unshiu_00236_mRNA_14.1	-
GF0035882	0	1	0	Hypothetical protein (1)			-	C_unshiu_00236_mRNA_13.1	-
GF0035881	0	1	0	Hypothetical protein (1)			-	C_unshiu_00236_mRNA_12.1	-
GF0035880	0	1	0	Polygalacturonase (1)	polygalacturonase activity [GO:0004650 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1)	Glycoside hydrolase, family 28 [IPR000743] (1); Pectin lyase fold [IPR012334] (1); Pectin lyase fold/virulence factor [IPR011050] (1)	-	C_unshiu_00236_mRNA_1.1	-
GF0035879	0	1	0	Hypothetical protein (1)			-	C_unshiu_00235_mRNA_35.1	-
GF0035878	0	1	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_00235_mRNA_34.1	-
GF0035877	0	1	0	Putative muDR family transposase-like (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Zinc finger, SWIM-type [IPR007527] (1); Zinc finger, PMZ-type [IPR006564] (1)	-	C_unshiu_00235_mRNA_33.1	-
GF0035876	0	1	0	Basic helix-loop-helix DNA-binding superfamily protein (1)	DNA binding [GO:0003677 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	Myc-type, basic helix-loop-helix (bHLH) domain [IPR011598] (1); Achaete-scute transcription factor-related [IPR015660] (1)	-	C_unshiu_00235_mRNA_31.1	-
GF0035875	0	1	0	Protein FAR1-RELATED SEQUENCE 3 (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FAR1 DNA binding domain [IPR004330] (1); FHY3/FAR1 family [IPR031052] (1)	-	C_unshiu_00235_mRNA_12.1	-
GF0035874	0	1	0	Hypothetical protein (1)			-	C_unshiu_00234_mRNA_34.1	-
GF0035873	0	1	0	Hypothetical protein (1)			-	C_unshiu_00234_mRNA_3.1	-
GF0035872	0	1	0	GNS1/SUR4 membrane family protein (1)	integral component of membrane [GO:0016021 cellular_component] (1)	ELO family [IPR002076] (1)	-	C_unshiu_00234_mRNA_26.1	-
GF0035871	0	1	0	Hypothetical protein (1)			-	C_unshiu_00234_mRNA_19.1	-
GF0035870	0	1	0	30S ribosomal protein S9, chloroplastic (1)	ribosome [GO:0005840 cellular_component] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1); translation [GO:0006412 biological_process] (1)	Ribosomal protein S9, bacterial/plastid [IPR023035] (1); Ribosomal protein S5 domain 2-type fold, subgroup [IPR014721] (1); Ribosomal protein S5 domain 2-type fold [IPR020568] (1); Ribosomal protein S9 [IPR000754] (1); Ribosomal protein S9, conserved site [IPR020574] (1)	-	C_unshiu_00234_mRNA_16.1	-
GF0035869	0	1	0	FAM32A protein (1)		Protein of unknown function DUF1754, eukaryotic [IPR013865] (1)	-	C_unshiu_00233_mRNA_9.1	-
GF0035868	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_00233_mRNA_5.1	-
GF0035867	0	1	0	Hypothetical protein (1)			-	C_unshiu_00233_mRNA_3.1	-
GF0035866	0	1	0	YELLOW STRIPE like 1 isoform 3 (1)	transmembrane transport [GO:0055085 biological_process] (1)	Oligopeptide transporter, OPT superfamily [IPR004813] (1)	-	C_unshiu_00233_mRNA_29.1	-
GF0035865	0	1	0	Hypothetical protein (1)			-	C_unshiu_00233_mRNA_24.1	-
GF0035864	0	1	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1)	ATPase, AAA-type, core [IPR003959] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00233_mRNA_11.1	-
GF0035863	0	1	0	Hypothetical protein (1)			-	C_unshiu_00232_mRNA_8.1	-
GF0035862	0	1	0	GDSL esterase/lipase EXL3 (1)	hydrolase activity, acting on ester bonds [GO:0016788 molecular_function] (1)	Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); GDSL lipase/esterase [IPR001087] (1); SGNH hydrolase-type esterase domain [IPR013830] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00232_mRNA_4.1	-
GF0035861	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	-	C_unshiu_00232_mRNA_32.1	-
GF0035860	0	1	0	Hypothetical protein (1)			-	C_unshiu_00232_mRNA_3.1	-
GF0035859	0	1	0	Hypothetical protein (1)			-	C_unshiu_00232_mRNA_23.1	-
GF0035858	0	1	0	Hypothetical protein (1)			-	C_unshiu_00232_mRNA_22.1	-
GF0035857	0	1	0	LRR receptor-like kinase (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_00232_mRNA_2.1	-
GF0035856	0	1	0	Hypothetical protein (1)			-	C_unshiu_00232_mRNA_18.1	-
GF0035855	0	1	0	Hypothetical protein (1)			-	C_unshiu_00232_mRNA_16.1	-
GF0035854	0	1	0	Hypothetical protein (1)			-	C_unshiu_00232_mRNA_15.1	-
GF0035853	0	1	0	Hypothetical protein (1)			-	C_unshiu_00232_mRNA_13.1	-
GF0035852	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4219 [IPR025314] (1)	-	C_unshiu_00232_mRNA_12.1	-
GF0035851	0	1	0	Metal-nicotianamine transporter YSL3 (1)	transmembrane transport [GO:0055085 biological_process] (1)	Oligopeptide transporter, OPT superfamily [IPR004813] (1)	-	C_unshiu_00231_mRNA_47.1	-
GF0035850	0	1	0	Hypothetical protein (1)			-	C_unshiu_00231_mRNA_42.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0035849	0	1	0	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1)	Aldehyde oxidase/xanthine dehydrogenase, molybdopterin binding [IPR008274] (1)	-	C_unshiu_00231_mRNA_35.1	-
GF0035848	0	1	0	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); electron carrier activity [GO:0009055 molecular_function] (1); iron-sulfur cluster binding [GO:0051536 molecular_function] (1); metal ion binding [GO:0046872 molecular_function] (1)	[2Fe-2S]-binding [IPR002888] (1); 2Fe-2S ferredoxin-type iron-sulfur binding domain [IPR001041] (1); Beta-grasp domain [IPR012675] (1)	-	C_unshiu_00231_mRNA_34.1	-
GF0035847	0	1	0	Hypothetical protein (1)			-	C_unshiu_00231_mRNA_29.1	-
GF0035846	0	1	0	Hypothetical protein (1)			-	C_unshiu_00231_mRNA_28.1	-
GF0035845	0	1	0	Hypothetical protein (1)			-	C_unshiu_00231_mRNA_27.1	-
GF0035844	0	1	0	Hypothetical protein (1)			-	C_unshiu_00231_mRNA_26.1	-
GF0035843	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat 3 [IPR011713] (1)	-	C_unshiu_00231_mRNA_24.1	-
GF0035842	0	1	0	Hypothetical protein (1)			-	C_unshiu_00231_mRNA_23.1	-
GF0035841	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1); Protein of unknown function DUF901 [IPR010298] (1)	-	C_unshiu_00231_mRNA_22.1	-
GF0035840	0	1	0	Hypothetical protein (1)			-	C_unshiu_00231_mRNA_19.1	-
GF0035839	0	1	0	Hypothetical protein (1)			-	C_unshiu_00230_mRNA_7.1	-
GF0035838	0	1	0	17.5 kDa class I heat shock protein (1)		Small heat shock protein HSP20 [IPR031107] (1); HSP20-like chaperone [IPR008978] (1); Alpha crystallin/Hsp20 domain [IPR002068] (1)	-	C_unshiu_00230_mRNA_62.1	-
GF0035837	0	1	0	Disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00230_mRNA_61.1	-
GF0035836	0	1	0	Disease resistance protein RPS2 (1)			-	C_unshiu_00230_mRNA_60.1	-
GF0035835	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00230_mRNA_59.1	-
GF0035834	0	1	0	Hypothetical protein (1)			-	C_unshiu_00230_mRNA_44.1	-
GF0035833	0	1	0	Mutator-like transposase (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, SWIM-type [IPR007527] (1); Transposase, MuDR, plant [IPR004332] (1); Zinc finger, PMZ-type [IPR006564] (1)	-	C_unshiu_00230_mRNA_43.1	-
GF0035832	0	1	0	Hypothetical protein (1)			-	C_unshiu_00230_mRNA_4.1	-
GF0035831	0	1	0	Hypothetical protein (1)			-	C_unshiu_00230_mRNA_35.1	-
GF0035830	0	1	0	Hypothetical protein (1)			-	C_unshiu_00230_mRNA_26.1	-
GF0035829	0	1	0	Hypothetical protein (1)			-	C_unshiu_00230_mRNA_25.1	-
GF0035828	0	1	0	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	C_unshiu_00230_mRNA_20.1	-
GF0035827	0	1	0	Hypothetical protein (1)			-	C_unshiu_00230_mRNA_2.1	-
GF0035826	0	1	0	Hypothetical protein (1)			-	C_unshiu_00230_mRNA_19.1	-
GF0035825	0	1	0	Maturase R (1)	mRNA processing [GO:0006397 biological_process] (1)	Domain X [IPR024937] (1)	-	C_unshiu_00230_mRNA_17.1	-
GF0035824	0	1	0	Hypothetical protein (1)			-	C_unshiu_00230_mRNA_14.1	-
GF0035823	0	1	0	Hypothetical protein (1)			-	C_unshiu_00230_mRNA_13.1	-
GF0035822	0	1	0	Hypothetical protein (1)			-	C_unshiu_00230_mRNA_12.1	-
GF0035821	0	1	0	Hypothetical protein (1)			-	C_unshiu_00230_mRNA_10.1	-
GF0035820	0	1	0	Hypothetical protein (1)			-	C_unshiu_00230_mRNA_1.1	-
GF0035819	0	1	0	Mitogen-activated protein kinase kinase kinase (1)	ATP binding [GO:0005524 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase, ATP binding site [IPR017441] (1)	-	C_unshiu_00229_mRNA_9.1	-
GF0035818	0	1	0	Hypothetical protein (1)			-	C_unshiu_00229_mRNA_42.1	-
GF0035817	0	1	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1)	Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	-	C_unshiu_00229_mRNA_41.1	-
GF0035816	0	1	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_00229_mRNA_40.1	-
GF0035815	0	1	0	Hypothetical protein (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_00229_mRNA_39.1	-
GF0035814	0	1	0	Kinase superfamily protein, putative isoform 2 (1)	ATP binding [GO:0005524 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_00229_mRNA_36.1	-
GF0035813	0	1	0	Hypothetical protein (1)		Alpha/Beta hydrolase fold [IPR029058] (1)	-	C_unshiu_00229_mRNA_22.1	-
GF0035812	0	1	0	Hypothetical protein (1)	microtubule binding [GO:0008017 molecular_function] (1); microtubule-based movement [GO:0007018 biological_process] (1); microtubule motor activity [GO:0003777 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Kinesin-like protein [IPR027640] (1); Kinesin motor domain [IPR001752] (1); Kinesin motor domain, conserved site [IPR019821] (1)	-	C_unshiu_00229_mRNA_10.1	-
GF0035811	0	1	0	Hypothetical protein (1)			-	C_unshiu_00228_mRNA_38.1	-
GF0035810	0	1	0	Hypothetical protein (1)		Zinc knuckle CX2CX4HX4C [IPR025836] (1)	-	C_unshiu_00228_mRNA_34.1	-
GF0035809	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF1985 [IPR015410] (1)	-	C_unshiu_00228_mRNA_26.1	-
GF0035808	0	1	0	Hypothetical protein (1)			-	C_unshiu_00227_mRNA_9.1	-
GF0035807	0	1	0	Hypothetical protein (1)			-	C_unshiu_00227_mRNA_3.1	-
GF0035806	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00227_mRNA_27.1	-
GF0035805	0	1	0	Hypothetical protein (1)			-	C_unshiu_00227_mRNA_24.1	-
GF0035804	0	1	0	Hypothetical protein (1)			-	C_unshiu_00227_mRNA_2.1	-
GF0035803	0	1	0	Hypothetical protein (1)			-	C_unshiu_00227_mRNA_18.1	-
GF0035802	0	1	0	Hypothetical protein (1)			-	C_unshiu_00227_mRNA_17.1	-
GF0035801	0	1	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Myb/SANT-like domain [IPR024752] (1); Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1); Domain of unknown function DUF1985 [IPR015410] (1)	-	C_unshiu_00227_mRNA_16.1	-
GF0035800	0	1	0	Hypothetical protein (1)			-	C_unshiu_00227_mRNA_12.1	-
GF0035799	0	1	0	Hypothetical protein (1)			-	C_unshiu_00227_mRNA_11.1	-
GF0035798	0	1	0	Hypothetical protein (1)			-	C_unshiu_00227_mRNA_10.1	-
GF0035797	0	1	0	Hypothetical protein (1)			-	C_unshiu_00227_mRNA_1.1	-
GF0035796	0	1	0	Hypothetical protein (1)			-	C_unshiu_00226_mRNA_9.1	-
GF0035795	0	1	0	Hypothetical protein (1)			-	C_unshiu_00226_mRNA_8.1	-
GF0035794	0	1	0	Hypothetical protein (1)			-	C_unshiu_00226_mRNA_7.1	-
GF0035793	0	1	0	Hypothetical protein (1)			-	C_unshiu_00226_mRNA_43.1	-
GF0035792	0	1	0	Hypothetical protein (1)			-	C_unshiu_00226_mRNA_42.1	-
GF0035791	0	1	0	Hypothetical protein (1)			-	C_unshiu_00226_mRNA_40.1	-
GF0035790	0	1	0	Hypothetical protein (1)			-	C_unshiu_00226_mRNA_34.1	-
GF0035789	0	1	0	Hypothetical protein (1)			-	C_unshiu_00226_mRNA_29.1	-
GF0035788	0	1	0	Hypothetical protein (1)			-	C_unshiu_00226_mRNA_27.1	-
GF0035787	0	1	0	Hypothetical protein (1)			-	C_unshiu_00226_mRNA_16.1	-
GF0035786	0	1	0	Hypothetical protein (1)			-	C_unshiu_00226_mRNA_14.1	-
GF0035785	0	1	0	Hypothetical protein (1)			-	C_unshiu_00226_mRNA_13.1	-
GF0035784	0	1	0	Hypothetical protein (1)			-	C_unshiu_00226_mRNA_12.1	-
GF0035783	0	1	0	No apical meristem family protein (1)	DNA binding [GO:0003677 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	NAC domain [IPR003441] (1)	-	C_unshiu_00225_mRNA_6.1	-
GF0035782	0	1	0	Hypothetical protein (1)		ELMO domain [IPR006816] (1)	-	C_unshiu_00225_mRNA_5.1	-
GF0035781	0	1	0	NAC transcription factor-like protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); DNA binding [GO:0003677 molecular_function] (1)	NAC domain [IPR003441] (1)	-	C_unshiu_00225_mRNA_4.1	-
GF0035780	0	1	0	Hypothetical protein (1)			-	C_unshiu_00225_mRNA_30.1	-
GF0035779	0	1	0	Hypothetical protein (1)			-	C_unshiu_00225_mRNA_3.1	-
GF0035778	0	1	0	Chlororespiratory reduction 42 (1)		Protein of unknown function DUF3148 [IPR021495] (1)	-	C_unshiu_00225_mRNA_28.1	-
GF0035777	0	1	0	Hypothetical protein (1)			-	C_unshiu_00225_mRNA_22.1	-
GF0035776	0	1	0	NAC protein 1 (1)	DNA binding [GO:0003677 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	NAC domain [IPR003441] (1)	-	C_unshiu_00225_mRNA_2.1	-
GF0035775	0	1	0	Hypothetical protein (1)			-	C_unshiu_00225_mRNA_17.1	-
GF0035774	0	1	0	Hypothetical protein (1)			-	C_unshiu_00225_mRNA_16.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0035773	0	1	0	Hypothetical protein (1)	acyl-[acyl-carrier-protein] desaturase activity [GO:0045300 molecular_function] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); fatty acid metabolic process [GO:0006631 biological_process] (1)	Ribonucleotide reductase-related [IPR012348] (1); Ferritin-like superfamily [IPR009078] (1); Fatty acid desaturase, type 2 [IPR005067] (1)	-	C_unshiu_00225_mRNA_14.1	-
GF0035772	0	1	0	Hypothetical protein (1)		ELMO domain [IPR006816] (1)	-	C_unshiu_00225_mRNA_1.1	-
GF0035771	0	1	0	Hypothetical protein (1)			-	C_unshiu_00224_mRNA_42.1	-
GF0035770	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00224_mRNA_41.1	-
GF0035769	0	1	0	Hypothetical protein (1)			-	C_unshiu_00224_mRNA_38.1	-
GF0035768	0	1	0	Hypothetical protein (1)			-	C_unshiu_00224_mRNA_36.1	-
GF0035767	0	1	0	Hypothetical protein (1)			-	C_unshiu_00224_mRNA_15.1	-
GF0035766	0	1	0	Hypothetical protein (1)			-	C_unshiu_00224_mRNA_10.1	-
GF0035765	0	1	0	50S ribosomal protein L25 (1)	translation [GO:0006412 biological_process] (1)	Ribosomal protein L25/Gln-tRNA synthetase, anti-codon-binding domain [IPR011035] (1); Ribosomal protein L25, beta domain [IPR020057] (1)	-	C_unshiu_00223_mRNA_35.1	-
GF0035764	0	1	0	Late embryogenesis abundant hydroxyproline-rich glycofamily protein, putative (1)		Immunoglobulin-like fold [IPR013783] (1); Late embryogenesis abundant protein, LEA-14 [IPR004864] (1)	-	C_unshiu_00223_mRNA_32.1	-
GF0035763	0	1	0	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	C_unshiu_00223_mRNA_3.1	-
GF0035762	0	1	0	Hypothetical protein (1)			-	C_unshiu_00223_mRNA_25.1	-
GF0035761	0	1	0	Hypothetical protein (1)			-	C_unshiu_00223_mRNA_12.1	-
GF0035760	0	1	0	BEL1-like homeodomain protein 7 (1)	DNA binding [GO:0003677 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	Homeobox KN domain [IPR008422] (1); Homeodomain-like [IPR009057] (1); POX domain [IPR006563] (1); Homeobox domain [IPR001356] (1)	-	C_unshiu_00223_mRNA_1.1	-
GF0035759	0	1	0	MADS-box transcription factor family protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	Transcription factor, MADS-box [IPR002100] (1)	-	C_unshiu_00222_mRNA_26.1	-
GF0035758	0	1	0	Hypothetical protein (1)			-	C_unshiu_00222_mRNA_24.1	-
GF0035757	0	1	0	Putative disease resistance RPP13-like protein 1 (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00222_mRNA_1.1	-
GF0035756	0	1	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1)	Chaperonin Cpn60/TCP-1 family [IPR002423] (1); GroEL-like equatorial domain [IPR027413] (1)	-	C_unshiu_00221_mRNA_49.1	-
GF0035755	0	1	0	Tonoplast intrinsic protein (1)	transport [GO:0006810 biological_process] (1); membrane [GO:0016020 cellular_component] (1); transporter activity [GO:0005215 molecular_function] (1)	Major intrinsic protein, conserved site [IPR022357] (1); Aquaporin-like [IPR023271] (1); Major intrinsic protein [IPR000425] (1)	-	C_unshiu_00221_mRNA_4.1	-
GF0035754	0	1	0	Hypothetical protein (1)			-	C_unshiu_00221_mRNA_30.1	-
GF0035753	0	1	0	Hypothetical protein (1)			-	C_unshiu_00221_mRNA_27.1	-
GF0035752	0	1	0	Hypothetical protein (1)			-	C_unshiu_00221_mRNA_22.1	-
GF0035751	0	1	0	Hypothetical protein (1)	metabolic process [GO:0008152 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1)	Isochorismatase-like [IPR000868] (1)	-	C_unshiu_00221_mRNA_16.1	-
GF0035750	0	1	0	Hypothetical protein (1)			-	C_unshiu_00220_mRNA_9.1	-
GF0035749	0	1	0	MATE efflux family protein 4, chloroplastic (1)	transmembrane transport [GO:0055085 biological_process] (1); membrane [GO:0016020 cellular_component] (1); drug transmembrane transporter activity [GO:0015238 molecular_function] (1); antiporter activity [GO:0015297 molecular_function] (1); drug transmembrane transport [GO:0006855 biological_process] (1)	Multi antimicrobial extrusion protein [IPR002528] (1)	-	C_unshiu_00220_mRNA_28.1	-
GF0035748	0	1	0	Hypothetical protein (1)			-	C_unshiu_00220_mRNA_21.1	-
GF0035747	0	1	0	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	C_unshiu_00220_mRNA_1.1	-
GF0035746	0	1	0	Hypothetical protein (1)			-	C_unshiu_00219_mRNA_7.1	-
GF0035745	0	1	0	Hypothetical protein (1)			-	C_unshiu_00219_mRNA_5.1	-
GF0035744	0	1	0	Hypothetical protein (1)			-	C_unshiu_00219_mRNA_19.1	-
GF0035743	0	1	0	Hypothetical protein (1)			-	C_unshiu_00219_mRNA_17.1	-
GF0035742	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_00219_mRNA_16.1	-
GF0035741	0	1	0	Hypothetical protein (1)			-	C_unshiu_00219_mRNA_15.1	-
GF0035740	0	1	0	Hypothetical protein (1)			-	C_unshiu_00219_mRNA_12.1	-
GF0035739	0	1	0	Hypothetical protein (1)			-	C_unshiu_00219_mRNA_11.1	-
GF0035738	0	1	0	Hypothetical protein (1)			-	C_unshiu_00219_mRNA_1.1	-
GF0035737	0	1	0	Hypothetical protein (1)			-	C_unshiu_00218_mRNA_48.1	-
GF0035736	0	1	0	Hypothetical protein (1)			-	C_unshiu_00218_mRNA_47.1	-
GF0035735	0	1	0	Hypothetical protein (1)			-	C_unshiu_00218_mRNA_45.1	-
GF0035734	0	1	0	Hypothetical protein (1)			-	C_unshiu_00218_mRNA_4.1	-
GF0035733	0	1	0	Hypothetical protein (1)		Pectin lyase fold/virulence factor [IPR011050] (1); Pectin lyase fold [IPR012334] (1)	-	C_unshiu_00218_mRNA_35.1	-
GF0035732	0	1	0	Hypothetical protein (1)			-	C_unshiu_00218_mRNA_30.1	-
GF0035731	0	1	0	Hypothetical protein (1)			-	C_unshiu_00218_mRNA_21.1	-
GF0035730	0	1	0	Hypothetical protein (1)	metal ion binding [GO:0046872 molecular_function] (1)	Zinc finger, CCCH-type [IPR000571] (1)	-	C_unshiu_00218_mRNA_16.1	-
GF0035729	0	1	0	Auxin-induced protein 15A (1)	response to auxin [GO:0009733 biological_process] (1)	Small auxin-up RNA [IPR003676] (1)	-	C_unshiu_00218_mRNA_10.1	-
GF0035728	0	1	0	Hypothetical protein (1)			-	C_unshiu_00217_mRNA_47.1	-
GF0035727	0	1	0	Hypothetical protein (1)			-	C_unshiu_00217_mRNA_46.1	-
GF0035726	0	1	0	Hypothetical protein (1)			-	C_unshiu_00217_mRNA_45.1	-
GF0035725	0	1	0	Hypothetical protein (1)			-	C_unshiu_00217_mRNA_44.1	-
GF0035724	0	1	0	Hypothetical protein (1)			-	C_unshiu_00217_mRNA_40.1	-
GF0035723	0	1	0	Hypothetical protein (1)			-	C_unshiu_00217_mRNA_37.1	-
GF0035722	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1); chlorophyllase activity [GO:0047746 molecular_function] (1); chlorophyll catabolic process [GO:0015996 biological_process] (1)	Ankyrin repeat [IPR002110] (1); Tify domain [IPR010399] (1); CO/COL/TOC1, conserved site [IPR018467] (1); Alpha/Beta hydrolase fold [IPR029058] (1); Chlorophyllase [IPR017395] (1); Ankyrin repeat-containing domain [IPR020683] (1)	-	C_unshiu_00217_mRNA_31.1	-
GF0035721	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	SKP1/BTB/POZ domain [IPR011333] (1); BTB/POZ domain [IPR000210] (1)	-	C_unshiu_00217_mRNA_30.1	-
GF0035720	0	1	0	CMGC protein kinase (1)	protein serine/threonine phosphatase activity [GO:0004722 molecular_function] (1); protein dephosphorylation [GO:0006470 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1)	Protein kinase-like domain [IPR011009] (1); PPM-type phosphatase domain [IPR001932] (1); Protein phosphatase 2C family [IPR015655] (1)	-	C_unshiu_00217_mRNA_28.1	-
GF0035719	0	1	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_00217_mRNA_27.1	-
GF0035718	0	1	0	Hypothetical protein (1)			-	C_unshiu_00217_mRNA_18.1	-
GF0035717	0	1	0	Hypothetical protein (1)	metal ion binding [GO:0046872 molecular_function] (1); nucleotide binding [GO:0000166 molecular_function] (1)	P-type ATPase, transmembrane domain [IPR023298] (1); Cation-transporting P-type ATPase, N-terminal [IPR004014] (1); P-type ATPase, A domain [IPR008250] (1)	-	C_unshiu_00217_mRNA_16.1	-
GF0035716	0	1	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	-	C_unshiu_00217_mRNA_15.1	-
GF0035715	0	1	0	Hypothetical protein (1)			-	C_unshiu_00216_mRNA_40.1	-
GF0035714	0	1	0	Hypothetical protein (1)	translation [GO:0006412 biological_process] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1); ribosome [GO:0005840 cellular_component] (1)	Ribosomal protein L14 conserved site [IPR019972] (1); Ribosomal protein L14 domain [IPR023571] (1); PGG domain [IPR026961] (1); Ribosomal protein L14b/L23e [IPR000218] (1)	-	C_unshiu_00216_mRNA_34.1	-
GF0035713	0	1	0	Hypothetical protein (1)	histone-lysine N-methyltransferase activity [GO:0018024 molecular_function] (1)	WIYLD domain [IPR018848] (1)	-	C_unshiu_00216_mRNA_31.1	-
GF0035712	0	1	0	Hypothetical protein (1)			-	C_unshiu_00216_mRNA_25.1	-
GF0035711	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00216_mRNA_23.1	-
GF0035710	0	1	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	Zinc finger, BED-type [IPR003656] (1)	-	C_unshiu_00216_mRNA_16.1	-
GF0035709	0	1	0	Myosin-J heavy chain (1)	myosin complex [GO:0016459 cellular_component] (1); ATP binding [GO:0005524 molecular_function] (1); motor activity [GO:0003774 molecular_function] (1)	Myosin head, motor domain [IPR001609] (1); Myosin, N-terminal, SH3-like [IPR004009] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00216_mRNA_1.1	-
GF0035708	0	1	0	Hypothetical protein (1)			-	C_unshiu_00215_mRNA_54.1	-
GF0035707	0	1	0	Heterogeneous nuclear ribonucleoprotein Q (1)	nucleotide binding [GO:0000166 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Nucleotide-binding alpha-beta plait domain [IPR012677] (1); RNA recognition motif domain, eukaryote [IPR003954] (1); RNA recognition motif domain [IPR000504] (1)	-	C_unshiu_00215_mRNA_50.1	-
GF0035706	0	1	0	Hypothetical protein (1)			-	C_unshiu_00215_mRNA_4.1	-
GF0035705	0	1	0	Hypothetical protein (1)			-	C_unshiu_00215_mRNA_33.1	-
GF0035704	0	1	0	Hypothetical protein (1)			-	C_unshiu_00215_mRNA_14.1	-
GF0035703	0	1	0	Hypothetical protein (1)			-	C_unshiu_00214_mRNA_55.1	-
GF0035702	0	1	0	Hypothetical protein (1)			-	C_unshiu_00214_mRNA_53.1	-
GF0035701	0	1	0	Hypothetical protein (1)			-	C_unshiu_00214_mRNA_52.1	-
GF0035700	0	1	0	Hypothetical protein (1)			-	C_unshiu_00214_mRNA_49.1	-
GF0035699	0	1	0	Hypothetical protein (1)			-	C_unshiu_00214_mRNA_42.1	-
GF0035698	0	1	0	Hypothetical protein (1)			-	C_unshiu_00214_mRNA_4.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0035697	0	1	0	Cytochrome P450 83B1 (1)	iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1)	Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450, conserved site [IPR017972] (1); Cytochrome P450 [IPR001128] (1)	-	C_unshiu_00213_mRNA_6.1	-
GF0035696	0	1	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1); Domain of unknown function DUF1985 [IPR015410] (1)	-	C_unshiu_00213_mRNA_59.1	-
GF0035695	0	1	0	Wall-associated receptor kinase 2 (1)	calcium ion binding [GO:0005509 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Serine/threonine-protein kinase, active site [IPR008271] (1); EGF-type aspartate/asparagine hydroxylation site [IPR000152] (1); EGF-like domain [IPR000742] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); EGF-like calcium-binding domain [IPR001881] (1); Intein C-terminal splicing region [IPR030934] (1); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); EGF-like calcium-binding, conserved site [IPR018097] (1); EGF-like, conserved site [IPR013032] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1)	-	C_unshiu_00213_mRNA_51.1	-
GF0035694	0	1	0	Hypothetical protein (1)			-	C_unshiu_00213_mRNA_48.1	-
GF0035693	0	1	0	Hypothetical protein (1)			-	C_unshiu_00213_mRNA_47.1	-
GF0035692	0	1	0	Hypothetical protein (1)			-	C_unshiu_00213_mRNA_46.1	-
GF0035691	0	1	0	1-aminocyclopropane-1-carboxylate oxidase like 5 (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Isopenicillin N synthase-like [IPR027443] (1); Oxoglutarate/iron-dependent dioxygenase [IPR005123] (1)	-	C_unshiu_00213_mRNA_43.1	-
GF0035690	0	1	0	Hypothetical protein (1)		MULE transposase domain [IPR018289] (1); Isopenicillin N synthase-like [IPR027443] (1); Non-haem dioxygenase N-terminal domain [IPR026992] (1); FAR1 DNA binding domain [IPR004330] (1)	-	C_unshiu_00213_mRNA_41.1	-
GF0035689	0	1	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	Myb domain [IPR017930] (1); Homeodomain-like [IPR009057] (1); SANT/Myb domain [IPR001005] (1)	-	C_unshiu_00213_mRNA_25.1	-
GF0035688	0	1	0	Hypothetical protein (1)		Zinc knuckle CX2CX4HX4C [IPR025836] (1); Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_00213_mRNA_2.1	-
GF0035687	0	1	0	Hypothetical protein (1)			-	C_unshiu_00212_mRNA_3.1	-
GF0035686	0	1	0	Hypothetical protein (1)			-	C_unshiu_00212_mRNA_29.1	-
GF0035685	0	1	0	Hypothetical protein (1)			-	C_unshiu_00212_mRNA_19.1	-
GF0035684	0	1	0	Hypothetical protein (1)			-	C_unshiu_00212_mRNA_17.1	-
GF0035683	0	1	0	Retrotransposon protein, putative, unclassified (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	-	C_unshiu_00212_mRNA_16.1	-
GF0035682	0	1	0	Hypothetical protein (1)		Chromo domain [IPR023780] (1); Chromo domain-like [IPR016197] (1)	-	C_unshiu_00211_mRNA_8.1	-
GF0035681	0	1	0	Hypothetical protein (1)			-	C_unshiu_00211_mRNA_30.1	-
GF0035680	0	1	0	Hypothetical protein (1)			-	C_unshiu_00211_mRNA_17.1	-
GF0035679	0	1	0	Hypothetical protein (1)	protein serine/threonine kinase activity [GO:0004674 molecular_function] (1)	Bulb-type lectin domain [IPR001480] (1); S-locus receptor kinase, C-terminal [IPR021820] (1)	-	C_unshiu_00210_mRNA_39.1	-
GF0035678	0	1	0	Hypothetical protein (1)			-	C_unshiu_00210_mRNA_33.1	-
GF0035677	0	1	0	Hypothetical protein (1)			-	C_unshiu_00210_mRNA_32.1	-
GF0035676	0	1	0	Hypothetical protein (1)			-	C_unshiu_00210_mRNA_27.1	-
GF0035675	0	1	0	Hypothetical protein (1)			-	C_unshiu_00210_mRNA_26.1	-
GF0035674	0	1	0	Hypothetical protein (1)			-	C_unshiu_00209_mRNA_39.1	-
GF0035673	0	1	0	Hypothetical protein (1)	binding [GO:0005488 molecular_function] (1); ATP hydrolysis coupled proton transport [GO:0015991 biological_process] (1); proton-transporting ATPase activity, rotational mechanism [GO:0046961 molecular_function] (1); vacuolar proton-transporting V-type ATPase, V1 domain [GO:0000221 cellular_component] (1)	Armadillo-type fold [IPR016024] (1); Armadillo-like helical [IPR011989] (1); ATPase, V1 complex, subunit H [IPR004908] (1)	-	C_unshiu_00209_mRNA_32.1	-
GF0035672	0	1	0	Pentatricopeptide repeat-containing family protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	DYW domain [IPR032867] (1); Pentatricopeptide repeat [IPR002885] (1); Tetratricopeptide-like helical domain [IPR011990] (1)	-	C_unshiu_00209_mRNA_28.1	-
GF0035671	0	1	0	40S ribosomal protein S14e (1)	ribosome [GO:0005840 cellular_component] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1); translation [GO:0006412 biological_process] (1)	Alpha/Beta hydrolase fold [IPR029058] (1); Ribosomal protein S11 [IPR001971] (1)	-	C_unshiu_00209_mRNA_23.1	-
GF0035670	0	1	0	TSA: Wollemia nobilis transcribed RNA sequence (1)	methyltransferase activity [GO:0008168 molecular_function] (1)	Putative S-adenosyl-L-methionine-dependent methyltransferase [IPR004159] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	C_unshiu_00209_mRNA_11.1	-
GF0035669	0	1	0	Hypothetical protein (1)			-	C_unshiu_00208_mRNA_6.1	-
GF0035668	0	1	0	To encode a PR protein, Belongs to the plant thionin family with the following members:, putative (1)			-	C_unshiu_00208_mRNA_5.1	-
GF0035667	0	1	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	hAT-like transposase, RNase-H fold [IPR025525] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00208_mRNA_39.1	-
GF0035666	0	1	0	Hypothetical protein (1)	metal ion binding [GO:0046872 molecular_function] (1)	Peptidase M16, C-terminal [IPR007863] (1); Peptidase M16 domain [IPR011237] (1)	-	C_unshiu_00208_mRNA_38.1	-
GF0035665	0	1	0	Hypothetical protein (1)			-	C_unshiu_00208_mRNA_32.1	-
GF0035664	0	1	0	Hypothetical protein (1)			-	C_unshiu_00208_mRNA_31.1	-
GF0035663	0	1	0	Hypothetical protein (1)			-	C_unshiu_00208_mRNA_30.1	-
GF0035662	0	1	0	Hydroxycinnamoyl-Coenzyme A shikimate/quinate hydroxycinnamoyltransferase (1)	transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (1)	Transferase [IPR003480] (1); Chloramphenicol acetyltransferase-like domain [IPR023213] (1)	-	C_unshiu_00208_mRNA_28.1	-
GF0035661	0	1	0	Hypothetical protein (1)			-	C_unshiu_00208_mRNA_17.1	-
GF0035660	0	1	0	F-box/LRR-repeat protein At3g58900 (1)			-	C_unshiu_00208_mRNA_16.1	-
GF0035659	0	1	0	Hypothetical protein (1)			-	C_unshiu_00208_mRNA_13.1	-
GF0035658	0	1	0	Hypothetical protein (1)			-	C_unshiu_00208_mRNA_12.1	-
GF0035657	0	1	0	Hypothetical protein (1)			-	C_unshiu_00207_mRNA_4.1	-
GF0035656	0	1	0	Hypothetical protein (1)			-	C_unshiu_00207_mRNA_30.1	-
GF0035655	0	1	0	Hypothetical protein (1)			-	C_unshiu_00207_mRNA_22.1	-
GF0035654	0	1	0	Hypothetical protein (1)			-	C_unshiu_00207_mRNA_20.1	-
GF0035653	0	1	0	Hypothetical protein (1)			-	C_unshiu_00207_mRNA_2.1	-
GF0035652	0	1	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	AP2/ERF domain [IPR001471] (1); DNA-binding domain [IPR016177] (1); Domain of unknown function DUF4371 [IPR025398] (1)	-	C_unshiu_00207_mRNA_18.1	-
GF0035651	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Zinc knuckle CX2CX4HX4C [IPR025836] (1)	-	C_unshiu_00207_mRNA_12.1	-
GF0035650	0	1	0	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	C_unshiu_00207_mRNA_11.1	-
GF0035649	0	1	0	Hypothetical protein (1)			-	C_unshiu_00207_mRNA_10.1	-
GF0035648	0	1	0	Hypothetical protein (1)			-	C_unshiu_00207_mRNA_1.1	-
GF0035647	0	1	0	Hypothetical protein (1)			-	C_unshiu_00206_mRNA_7.1	-
GF0035646	0	1	0	Endoglucanase (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1); hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (1)	Glycoside hydrolase family 9 [IPR001701] (1); Six-hairpin glycosidase [IPR012341] (1); Six-hairpin glycosidase-like [IPR008928] (1)	-	C_unshiu_00206_mRNA_45.1	-
GF0035645	0	1	0	Phantastica (1)	transcription, DNA-templated [GO:0006351 biological_process] (1); nucleus [GO:0005634 cellular_component] (1); leaf formation [GO:0010338 biological_process] (1)	Protein rough sheath 2/ASYMMETRIC LEAVES1 [IPR031055] (1)	-	C_unshiu_00206_mRNA_10.1	-
GF0035644	0	1	0	Hypothetical protein (1)			-	C_unshiu_00205_mRNA_5.1	-
GF0035643	0	1	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	-	C_unshiu_00205_mRNA_4.1	-
GF0035642	0	1	0	UPF0481 protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	C_unshiu_00205_mRNA_39.1	-
GF0035641	0	1	0	UPF0481 protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	C_unshiu_00205_mRNA_38.1	-
GF0035640	0	1	0	Hypothetical protein (1)			-	C_unshiu_00205_mRNA_37.1	-
GF0035639	0	1	0	Hypothetical protein (1)			-	C_unshiu_00205_mRNA_28.1	-
GF0035638	0	1	0	Hypothetical protein (1)			-	C_unshiu_00205_mRNA_2.1	-
GF0035637	0	1	0	Short chain alcohol dehydrogenase, putative (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Glucose/ribitol dehydrogenase [IPR002347] (1); Short-chain dehydrogenase/reductase SDR [IPR002198] (1); NAD(P)-binding domain [IPR016040] (1)	-	C_unshiu_00204_mRNA_7.1	-
GF0035636	0	1	0	Bystin (1)		Bystin [IPR007955] (1)	-	C_unshiu_00204_mRNA_4.2	-
GF0035635	0	1	0	Hypothetical protein (1)			-	C_unshiu_00204_mRNA_25.1	-
GF0035634	0	1	0	Hypothetical protein (1)			-	C_unshiu_00204_mRNA_15.1	-
GF0035633	0	1	0	Hypothetical protein (1)			-	C_unshiu_00204_mRNA_13.1	-
GF0035632	0	1	0	Hypothetical protein (1)			-	C_unshiu_00203_mRNA_7.1	-
GF0035631	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_00203_mRNA_6.1	-
GF0035630	0	1	0	Hypothetical protein (1)			-	C_unshiu_00203_mRNA_5.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0035629	0	1	0	Hypothetical protein (1)			-	C_unshiu_00203_mRNA_40.1	-
GF0035628	0	1	0	Hypothetical protein (1)			-	C_unshiu_00203_mRNA_38.1	-
GF0035627	0	1	0	Hypothetical protein (1)			-	C_unshiu_00203_mRNA_3.1	-
GF0035626	0	1	0	Hypothetical protein (1)			-	C_unshiu_00203_mRNA_28.1	-
GF0035625	0	1	0	Hypothetical protein (1)			-	C_unshiu_00203_mRNA_13.1	-
GF0035624	0	1	0	Non-LTR retroelement reverse transcriptase-like (1)	nucleic acid binding [GO:0003676 molecular_function] (1); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1)	Ribonuclease H domain [IPR002156] (1); Ribonuclease H-like domain [IPR012337] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_00202_mRNA_8.1	-
GF0035623	0	1	0	Hypothetical protein (1)			-	C_unshiu_00202_mRNA_6.1	-
GF0035622	0	1	0	Hypothetical protein (1)			-	C_unshiu_00202_mRNA_3.1	-
GF0035621	0	1	0	Hypothetical protein (1)			-	C_unshiu_00202_mRNA_23.1	-
GF0035620	0	1	0	Hypothetical protein (1)			-	C_unshiu_00202_mRNA_22.1	-
GF0035619	0	1	0	Thylakoid lumenal 15 kDa protein 1, chloroplastic (1)		Pentapeptide repeat [IPR001646] (1)	-	C_unshiu_00202_mRNA_11.1	-
GF0035618	0	1	0	Hypothetical protein (1)			-	C_unshiu_00202_mRNA_1.1	-
GF0035617	0	1	0	Hypothetical protein (1)			-	C_unshiu_00201_mRNA_5.1	-
GF0035616	0	1	0	Hypothetical protein (1)			-	C_unshiu_00201_mRNA_21.1	-
GF0035615	0	1	0	Hypothetical protein (1)			-	C_unshiu_00201_mRNA_20.1	-
GF0035614	0	1	0	Hypothetical protein (1)			-	C_unshiu_00201_mRNA_17.1	-
GF0035613	0	1	0	Hypothetical protein (1)			-	C_unshiu_00201_mRNA_16.1	-
GF0035612	0	1	0	Ribonuclease H protein, putative (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_00201_mRNA_13.1	-
GF0035611	0	1	0	Hypothetical protein (1)			-	C_unshiu_00201_mRNA_12.1	-
GF0035610	0	1	0	TMV resistance N (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00200_mRNA_35.1	-
GF0035609	0	1	0	Hypothetical protein (1)			-	C_unshiu_00200_mRNA_33.1	-
GF0035608	0	1	0	Leucine-rich repeat (LRR) family protein (1)			-	C_unshiu_00200_mRNA_31.1	-
GF0035607	0	1	0	Hypothetical protein (1)			-	C_unshiu_00200_mRNA_28.1	-
GF0035606	0	1	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	-	C_unshiu_00200_mRNA_27.1	-
GF0035605	0	1	0	Hypothetical protein (1)			-	C_unshiu_00200_mRNA_23.1	-
GF0035604	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc knuckle CX2CX4HX4C [IPR025836] (1); Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00200_mRNA_19.1	-
GF0035603	0	1	0	Mitochondrial import inner membrane translocase subunit TIM16 (1)	mitochondrial inner membrane presequence translocase complex [GO:0005744 cellular_component] (1); protein import into mitochondrial matrix [GO:0030150 biological_process] (1)	Mitochondrial import inner membrane translocase subunit Tim16 [IPR005341] (1)	-	C_unshiu_00200_mRNA_15.1	-
GF0035602	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00200_mRNA_14.1	-
GF0035601	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00199_mRNA_46.1	-
GF0035600	0	1	0	Hypothetical protein (1)			-	C_unshiu_00199_mRNA_44.1	-
GF0035599	0	1	0	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	C_unshiu_00199_mRNA_4.1	-
GF0035598	0	1	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FAR1 DNA binding domain [IPR004330] (1); FHY3/FAR1 family [IPR031052] (1)	-	C_unshiu_00199_mRNA_33.1	-
GF0035597	0	1	0	Protein GAST1 (1)		Gibberellin regulated protein [IPR003854] (1)	-	C_unshiu_00199_mRNA_32.1	-
GF0035596	0	1	0	Hypothetical protein (1)			-	C_unshiu_00199_mRNA_31.1	-
GF0035595	0	1	0	Hypothetical protein (1)			-	C_unshiu_00199_mRNA_21.1	-
GF0035594	0	1	0	Hypothetical protein (1)			-	C_unshiu_00198_mRNA_9.1	-
GF0035593	0	1	0	Hypothetical protein (1)			-	C_unshiu_00198_mRNA_8.1	-
GF0035592	0	1	0	Hypothetical protein (1)			-	C_unshiu_00198_mRNA_7.1	-
GF0035591	0	1	0	Hypothetical protein (1)			-	C_unshiu_00198_mRNA_5.1	-
GF0035590	0	1	0	Hypothetical protein (1)			-	C_unshiu_00198_mRNA_33.1	-
GF0035589	0	1	0	Hypothetical protein (1)			-	C_unshiu_00198_mRNA_32.1	-
GF0035588	0	1	0	Hypothetical protein (1)			-	C_unshiu_00198_mRNA_29.1	-
GF0035587	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00198_mRNA_26.1	-
GF0035586	0	1	0	Hypothetical protein (1)			-	C_unshiu_00198_mRNA_25.1	-
GF0035585	0	1	0	Hypothetical protein (1)			-	C_unshiu_00198_mRNA_24.1	-
GF0035584	0	1	0	Hypothetical protein (1)			-	C_unshiu_00198_mRNA_10.1	-
GF0035583	0	1	0	Hypothetical protein (1)			-	C_unshiu_00198_mRNA_1.1	-
GF0035582	0	1	0	Hypothetical protein (1)			-	C_unshiu_00197_mRNA_7.1	-
GF0035581	0	1	0	AtpA (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, PMZ-type [IPR006564] (1); Zinc finger, SWIM-type [IPR007527] (1)	-	C_unshiu_00197_mRNA_5.1	-
GF0035580	0	1	0	Hypothetical protein (1)			-	C_unshiu_00197_mRNA_4.1	-
GF0035579	0	1	0	Hypothetical protein (1)			-	C_unshiu_00197_mRNA_34.1	-
GF0035578	0	1	0	Hypothetical protein (1)			-	C_unshiu_00197_mRNA_33.1	-
GF0035577	0	1	0	Hypothetical protein (1)	RNA binding [GO:0003723 molecular_function] (1); O-methyltransferase activity [GO:0008171 molecular_function] (1); mRNA splicing, via spliceosome [GO:0000398 biological_process] (1); metal ion binding [GO:0046872 molecular_function] (1); U2AF [GO:0089701 cellular_component] (1)	S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); U2 auxiliary factor small subunit [IPR009145] (1); O-methyltransferase, family 2 [IPR001077] (1); Zinc finger, CCCH-type [IPR000571] (1)	-	C_unshiu_00197_mRNA_3.1	-
GF0035576	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	WD40/YVTN repeat-like-containing domain [IPR015943] (1); WD40-repeat-containing domain [IPR017986] (1)	-	C_unshiu_00197_mRNA_21.2	-
GF0035575	0	1	0	Hypothetical protein (1)			-	C_unshiu_00197_mRNA_19.1	-
GF0035574	0	1	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	-	C_unshiu_00197_mRNA_18.1	-
GF0035573	0	1	0	Hypothetical protein (1)		Gag-polypeptide of LTR copia-type [IPR029472] (1)	-	C_unshiu_00197_mRNA_14.1	-
GF0035572	0	1	0	Hypothetical protein (1)			-	C_unshiu_00197_mRNA_13.1	-
GF0035571	0	1	0	Hypothetical protein (1)			-	C_unshiu_00197_mRNA_12.1	-
GF0035570	0	1	0	Hypothetical protein (1)			-	C_unshiu_00197_mRNA_11.1	-
GF0035569	0	1	0	Ribosome-binding factor A (1)	rRNA processing [GO:0006364 biological_process] (1)	Ribosome-binding factor A [IPR000238] (1); Ribosome-binding factor A domain [IPR023799] (1); K homology domain-like, alpha/beta [IPR015946] (1); Ribosome-binding factor A, conserved site [IPR020053] (1)	-	C_unshiu_00197_mRNA_10.1	-
GF0035568	0	1	0	Hypothetical protein (1)			-	C_unshiu_00196_mRNA_39.1	-
GF0035567	0	1	0	Hypothetical protein (1)		Transposase, Tnp1/En/Spm-like [IPR004264] (1)	-	C_unshiu_00196_mRNA_35.1	-
GF0035566	0	1	0	Hypothetical protein (1)			-	C_unshiu_00196_mRNA_31.1	-
GF0035565	0	1	0	PPR containing plant-like protein (1)	protein binding [GO:0005515 molecular_function] (1)	Tetratricopeptide-like helical domain [IPR011990] (1); Pentatricopeptide repeat [IPR002885] (1)	-	C_unshiu_00196_mRNA_23.1	-
GF0035564	0	1	0	Hypothetical protein (1)			-	C_unshiu_00196_mRNA_14.1	-
GF0035563	0	1	0	Hypothetical protein (1)			-	C_unshiu_00195_mRNA_39.1	-
GF0035562	0	1	0	Hypothetical protein (1)			-	C_unshiu_00195_mRNA_31.1	-
GF0035561	0	1	0	Retrotransposon protein, putative, Ty1-copia subclass (1)			-	C_unshiu_00195_mRNA_24.1	-
GF0035560	0	1	0	Expansin (1)		Expansin, cellulose-binding-like domain [IPR007117] (1); RlpA-like double-psi beta-barrel domain [IPR009009] (1)	-	C_unshiu_00194_mRNA_48.1	-
GF0035559	0	1	0	Hypothetical protein (1)			-	C_unshiu_00194_mRNA_47.1	-
GF0035558	0	1	0	Hypothetical protein (1)			-	C_unshiu_00194_mRNA_40.1	-
GF0035557	0	1	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); nucleus [GO:0005634 cellular_component] (1)	CCR4-Not complex component, Not N-terminal domain [IPR007207] (1)	-	C_unshiu_00194_mRNA_39.1	-
GF0035556	0	1	0	Hypothetical protein (1)			-	C_unshiu_00194_mRNA_34.1	-
GF0035555	0	1	0	Hypothetical protein (1)			-	C_unshiu_00194_mRNA_25.1	-
GF0035554	0	1	0	Hypothetical protein (1)			-	C_unshiu_00194_mRNA_24.1	-
GF0035553	0	1	0	Hypothetical protein (1)	sulfate assimilation [GO:0000103 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1); adenylylsulfate kinase activity [GO:0004020 molecular_function] (1)	Adenylyl-sulfate kinase [IPR002891] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00194_mRNA_12.1	-
GF0035552	0	1	0	Hypothetical protein (1)			-	C_unshiu_00194_mRNA_11.1	-
GF0035551	0	1	0	Hypothetical protein (1)			-	C_unshiu_00193_mRNA_26.1	-
GF0035550	0	1	0	Hypothetical protein (1)			-	C_unshiu_00193_mRNA_23.1	-
GF0035549	0	1	0	Hypothetical protein (1)			-	C_unshiu_00193_mRNA_11.1	-
GF0035548	0	1	0	Hypothetical protein (1)			-	C_unshiu_00193_mRNA_1.1	-
GF0035547	0	1	0	Hypothetical protein (1)			-	C_unshiu_00192_mRNA_27.1	-
GF0035546	0	1	0	Hypothetical protein (1)			-	C_unshiu_00192_mRNA_21.1	-
GF0035545	0	1	0	Retrotransposon protein, putative, Ty1-copia subclass (1)		Gag-polypeptide of LTR copia-type [IPR029472] (1)	-	C_unshiu_00191_mRNA_9.1	-
GF0035544	0	1	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	-	C_unshiu_00191_mRNA_13.1	-
GF0035543	0	1	0	Hypothetical protein (1)			-	C_unshiu_00190_mRNA_51.1	-
GF0035542	0	1	0	Cytochrome b5 (1)	heme binding [GO:0020037 molecular_function] (1)	Cytochrome b5-like heme/steroid binding domain [IPR001199] (1); Cytochrome b5, heme-binding site [IPR018506] (1)	-	C_unshiu_00190_mRNA_50.1	-
GF0035541	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat [IPR002110] (1); Ankyrin repeat-containing domain [IPR020683] (1)	-	C_unshiu_00190_mRNA_48.1	-
GF0035540	0	1	0	Hypothetical protein (1)			-	C_unshiu_00190_mRNA_41.1	-
GF0035539	0	1	0	Exocyst complex component 7 (1)	exocyst [GO:0000145 cellular_component] (1); exocytosis [GO:0006887 biological_process] (1)	Exocyst complex protein Exo70 [IPR004140] (1); Cullin repeat-like-containing domain [IPR016159] (1)	-	C_unshiu_00190_mRNA_18.1	-
GF0035538	0	1	0	Hypothetical protein (1)			-	C_unshiu_00190_mRNA_12.1	-
GF0035537	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1)	Ribonuclease H domain [IPR002156] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00189_mRNA_6.1	-
GF0035536	0	1	0	Hypothetical protein (1)	potassium ion transmembrane transport [GO:0071805 biological_process] (1); membrane [GO:0016020 cellular_component] (1); potassium ion transmembrane transporter activity [GO:0015079 molecular_function] (1)	Potassium transporter [IPR003855] (1)	-	C_unshiu_00189_mRNA_56.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0035535	0	1	0	Nodulin MtN21/EamA-like transporter family protein (1)	membrane [GO:0016020 cellular_component] (1); transmembrane transporter activity [GO:0022857 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1)	WAT1-related protein [IPR030184] (1); EamA domain [IPR000620] (1)	-	C_unshiu_00189_mRNA_42.1	-
GF0035534	0	1	0	Hypothetical protein (1)			-	C_unshiu_00189_mRNA_4.1	-
GF0035533	0	1	0	Hypothetical protein (1)			-	C_unshiu_00189_mRNA_37.1	-
GF0035532	0	1	0	Hypothetical protein (1)			-	C_unshiu_00189_mRNA_3.1	-
GF0035531	0	1	0	Tyrosine kinase family protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Protein kinase-like domain [IPR011009] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1)	-	C_unshiu_00189_mRNA_24.1	-
GF0035530	0	1	0	Hypothetical protein (1)			-	C_unshiu_00189_mRNA_16.1	-
GF0035529	0	1	0	Hypothetical protein (1)			-	C_unshiu_00189_mRNA_15.1	-
GF0035528	0	1	0	Hypothetical protein (1)			-	C_unshiu_00189_mRNA_13.1	-
GF0035527	0	1	0	Hypothetical protein (1)			-	C_unshiu_00189_mRNA_12.1	-
GF0035526	0	1	0	Hypothetical protein (1)			-	C_unshiu_00189_mRNA_11.1	-
GF0035525	0	1	0	Hypothetical protein (1)			-	C_unshiu_00188_mRNA_9.1	-
GF0035524	0	1	0	Hypothetical protein (1)			-	C_unshiu_00188_mRNA_7.1	-
GF0035523	0	1	0	Vacuolarprocessing enzyme putative (1)	proteolysis [GO:0006508 biological_process] (1); peptidase activity [GO:0008233 molecular_function] (1)	Peptidase C13, legumain [IPR001096] (1)	-	C_unshiu_00188_mRNA_36.1	-
GF0035522	0	1	0	Legumain (1)	proteolysis [GO:0006508 biological_process] (1); peptidase activity [GO:0008233 molecular_function] (1)	Peptidase C13, legumain [IPR001096] (1)	-	C_unshiu_00188_mRNA_34.1	-
GF0035521	0	1	0	LRR receptor-like kinase family protein (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Protein kinase-like domain [IPR011009] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Protein kinase domain [IPR000719] (1); Leucine-rich repeat [IPR001611] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Protein kinase, ATP binding site [IPR017441] (1); Serine/threonine-protein kinase, active site [IPR008271] (1)	-	C_unshiu_00188_mRNA_32.1	-
GF0035520	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	-	C_unshiu_00188_mRNA_31.1	-
GF0035519	0	1	0	Hypothetical protein (1)			-	C_unshiu_00188_mRNA_23.1	-
GF0035518	0	1	0	Potato DNA for copia-like transposable element (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	-	C_unshiu_00188_mRNA_16.1	-
GF0035517	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_00188_mRNA_15.1	-
GF0035516	0	1	0	Hypothetical protein (1)			-	C_unshiu_00188_mRNA_14.1	-
GF0035515	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00188_mRNA_13.1	-
GF0035514	0	1	0	Hypothetical protein (1)			-	C_unshiu_00188_mRNA_10.1	-
GF0035513	0	1	0	Hypothetical protein (1)			-	C_unshiu_00187_mRNA_40.1	-
GF0035512	0	1	0	Hypothetical protein (1)			-	C_unshiu_00187_mRNA_3.1	-
GF0035511	0	1	0	Hypothetical protein (1)			-	C_unshiu_00187_mRNA_19.1	-
GF0035510	0	1	0	Hypothetical protein (1)			-	C_unshiu_00186_mRNA_31.1	-
GF0035509	0	1	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); nucleobase-containing compound metabolic process [GO:0006139 biological_process] (1); nucleobase-containing compound kinase activity [GO:0019205 molecular_function] (1)	Adenylate kinase/UMP-CMP kinase [IPR000850] (1)	-	C_unshiu_00186_mRNA_29.1	-
GF0035508	0	1	0	Hypothetical protein (1)			-	C_unshiu_00186_mRNA_25.1	-
GF0035507	0	1	0	F-box/RNI-like superfamily protein isoform 1 (1)	protein binding [GO:0005515 molecular_function] (1)	F-box domain [IPR001810] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00186_mRNA_2.1	-
GF0035506	0	1	0	Ribonucleoside-diphosphate reductase subunit beta (1)	protein serine/threonine kinase activity [GO:0004674 molecular_function] (1)	Serine/threonine-protein kinase Rio1 [IPR017407] (1)	-	C_unshiu_00186_mRNA_12.1	-
GF0035505	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Proteasome component (PCI) domain [IPR000717] (1)	-	C_unshiu_00186_mRNA_1.1	-
GF0035504	0	1	0	Hypothetical protein (1)			-	C_unshiu_00185_mRNA_7.1	-
GF0035503	0	1	0	Hypothetical protein (1)			-	C_unshiu_00185_mRNA_6.1	-
GF0035502	0	1	0	Hypothetical protein (1)			-	C_unshiu_00185_mRNA_5.1	-
GF0035501	0	1	0	Receptor like protein 27 (1)	protein binding [GO:0005515 molecular_function] (1)	Exostosin-like [IPR004263] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_00185_mRNA_41.1	-
GF0035500	0	1	0	Hypothetical protein (1)			-	C_unshiu_00185_mRNA_40.1	-
GF0035499	0	1	0	Hypothetical protein (1)			-	C_unshiu_00185_mRNA_37.1	-
GF0035498	0	1	0	Receptor like protein 33 (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00185_mRNA_33.1	-
GF0035497	0	1	0	Hypothetical protein (1)			-	C_unshiu_00185_mRNA_11.1	-
GF0035496	0	1	0	Hypothetical protein (1)			-	C_unshiu_00185_mRNA_10.1	-
GF0035495	0	1	0	Ras-related protein RABA1f (1)	protein transport [GO:0015031 biological_process] (1); GTPase activity [GO:0003924 molecular_function] (1); intracellular protein transport [GO:0006886 biological_process] (1); GTP binding [GO:0005525 molecular_function] (1); intracellular [GO:0005622 cellular_component] (1); signal transduction [GO:0007165 biological_process] (1); membrane [GO:0016020 cellular_component] (1); nucleocytoplasmic transport [GO:0006913 biological_process] (1); small GTPase mediated signal transduction [GO:0007264 biological_process] (1)	Small GTPase superfamily, Rho type [IPR003578] (1); Small GTP-binding protein domain [IPR005225] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Small GTPase superfamily [IPR001806] (1); Ran GTPase [IPR002041] (1); Small GTPase superfamily, Rab type [IPR003579] (1); Small GTPase superfamily, Ras type [IPR020849] (1)	-	C_unshiu_00184_mRNA_6.1	-
GF0035494	0	1	0	Hypothetical protein (1)		Bulb-type lectin domain [IPR001480] (1)	-	C_unshiu_00184_mRNA_5.1	-
GF0035493	0	1	0	Zinc knuckle family protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00184_mRNA_40.1	-
GF0035492	0	1	0	Hypothetical protein (1)			-	C_unshiu_00184_mRNA_28.1	-
GF0035491	0	1	0	Hypothetical protein (1)			-	C_unshiu_00184_mRNA_24.1	-
GF0035490	0	1	0	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	C_unshiu_00184_mRNA_2.1	-
GF0035489	0	1	0	Glycogen synthase kinase-3 MsK-3 family protein (1)	ATP binding [GO:0005524 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); peroxidase activity [GO:0004601 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); heme binding [GO:0020037 molecular_function] (1); response to oxidative stress [GO:0006979 biological_process] (1)	Haem peroxidase, plant/fungal/bacterial [IPR002016] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase, ATP binding site [IPR017441] (1); Peroxidase, active site [IPR019794] (1); Plant peroxidase [IPR000823] (1); Peroxidases heam-ligand binding site [IPR019793] (1); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); Haem peroxidase [IPR010255] (1)	-	C_unshiu_00184_mRNA_13.1	-
GF0035488	0	1	0	Hypothetical protein (1)		Ribosomal protein L5 domain [IPR022803] (1); Ribosomal protein L5, N-terminal [IPR031310] (1)	-	C_unshiu_00184_mRNA_10.1	-
GF0035487	0	1	0	Hypothetical protein (1)		Bulb-type lectin domain [IPR001480] (1)	-	C_unshiu_00184_mRNA_1.1	-
GF0035486	0	1	0	Alcohol dehydrogenase 1 (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); zinc ion binding [GO:0008270 molecular_function] (1)	NAD(P)-binding domain [IPR016040] (1); Alcohol dehydrogenase, C-terminal [IPR013149] (1); Alcohol dehydrogenase, N-terminal [IPR013154] (1); Alcohol dehydrogenase, zinc-type, conserved site [IPR002328] (1); Alcohol dehydrogenase superfamily, zinc-type [IPR002085] (1); GroES-like [IPR011032] (1)	-	C_unshiu_00183_mRNA_37.1	-
GF0035485	0	1	0	Alcohol dehydrogenase 1 (1)	zinc ion binding [GO:0008270 molecular_function] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Alcohol dehydrogenase superfamily, zinc-type [IPR002085] (1); GroES-like [IPR011032] (1)	-	C_unshiu_00183_mRNA_35.1	-
GF0035484	0	1	0	Hypothetical protein (1)	iron ion binding [GO:0005506 molecular_function] (1); fatty acid metabolic process [GO:0006631 biological_process] (1); heme binding [GO:0020037 molecular_function] (1); acyl-[acyl-carrier-protein] desaturase activity [GO:0045300 molecular_function] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Fatty acid desaturase, type 2 [IPR005067] (1); Ferritin-like superfamily [IPR009078] (1); Ribonucleotide reductase-related [IPR012348] (1); Cytochrome P450 [IPR001128] (1)	-	C_unshiu_00183_mRNA_32.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0035483	0	1	0	Hypothetical protein (1)			-	C_unshiu_00183_mRNA_16.1	-
GF0035482	0	1	0	Envelope glycoprotein (1)	protein binding [GO:0005515 molecular_function] (1)	PLAT/LH2 domain [IPR001024] (1); Embryo-specific 3 [IPR010417] (1)	-	C_unshiu_00182_mRNA_41.1	-
GF0035481	0	1	0	Hypothetical protein (1)			-	C_unshiu_00182_mRNA_4.1	-
GF0035480	0	1	0	Cysteine and histidine-rich domain-containing protein (1)		CHORD domain [IPR007051] (1)	-	C_unshiu_00182_mRNA_36.1	-
GF0035479	0	1	0	Putative rRNA-processing protein EBP2 (1)		Eukaryotic rRNA processing [IPR008610] (1)	-	C_unshiu_00182_mRNA_30.1	-
GF0035478	0	1	0	Hypothetical protein (1)			-	C_unshiu_00182_mRNA_18.1	-
GF0035477	0	1	0	Hypothetical protein (1)			-	C_unshiu_00182_mRNA_12.1	-
GF0035476	0	1	0	Hypothetical protein (1)			-	C_unshiu_00181_mRNA_32.1	-
GF0035475	0	1	0	Hexosyltransferase (1)	transferase activity, transferring glycosyl groups [GO:0016757 molecular_function] (1); polygalacturonate 4-alpha-galacturonosyltransferase activity [GO:0047262 molecular_function] (1)	Nucleotide-diphospho-sugar transferases [IPR029044] (1); Plant galacturonosyltransferase GAUT [IPR029993] (1); Glycosyl transferase, family 8 [IPR002495] (1)	-	C_unshiu_00181_mRNA_25.1	-
GF0035474	0	1	0	LRR receptor-like kinase (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_00181_mRNA_15.1	-
GF0035473	0	1	0	Hypothetical protein (1)			-	C_unshiu_00181_mRNA_14.1	-
GF0035472	0	1	0	Hypothetical protein (1)			-	C_unshiu_00180_mRNA_7.1	-
GF0035471	0	1	0	Hypothetical protein (1)			-	C_unshiu_00180_mRNA_4.1	-
GF0035470	0	1	0	Hypothetical protein (1)			-	C_unshiu_00180_mRNA_34.1	-
GF0035469	0	1	0	Putative calcium-transporting ATPase 13, plasma membrane-type (1)	metal ion binding [GO:0046872 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1); nucleotide binding [GO:0000166 molecular_function] (1)	P-type ATPase, A domain [IPR008250] (1); HAD-like domain [IPR023214] (1); Cation-transporting P-type ATPase, N-terminal [IPR004014] (1); P-type ATPase [IPR001757] (1); P-type ATPase, cytoplasmic domain N [IPR023299] (1); P-type ATPase, phosphorylation site [IPR018303] (1)	-	C_unshiu_00180_mRNA_32.1	-
GF0035468	0	1	0	Hypothetical protein (1)			-	C_unshiu_00180_mRNA_23.1	-
GF0035467	0	1	0	Hypothetical protein (1)			-	C_unshiu_00180_mRNA_17.1	-
GF0035466	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_00180_mRNA_12.1	-
GF0035465	0	1	0	Disease resistance protein RPS2, putative (1)			-	C_unshiu_00180_mRNA_11.1	-
GF0035464	0	1	0	Hypothetical protein (1)			-	C_unshiu_00180_mRNA_1.1	-
GF0035463	0	1	0	Polynucleotidyl transferase, Ribonuclease H fold (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00179_mRNA_27.1	-
GF0035462	0	1	0	Hypothetical protein (1)			-	C_unshiu_00179_mRNA_26.1	-
GF0035461	0	1	0	Protein arginine N-methyltransferase 7 (1)	protein methylation [GO:0006479 biological_process] (1); methyltransferase activity [GO:0008168 molecular_function] (1)	DnaJ-like protein C11, C-terminal [IPR024586] (1); Protein arginine N-methyltransferase [IPR025799] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	C_unshiu_00179_mRNA_11.1	-
GF0035460	0	1	0	Hypothetical protein (1)		Heat shock protein 70kD, C-terminal domain [IPR029048] (1); Heat shock protein 70 family [IPR013126] (1); Heat shock protein 70kD, peptide-binding domain [IPR029047] (1)	-	C_unshiu_00179_mRNA_1.1	-
GF0035459	0	1	0	Hypothetical protein (1)	membrane [GO:0016020 cellular_component] (1); transport [GO:0006810 biological_process] (1); transporter activity [GO:0005215 molecular_function] (1)	Major facilitator superfamily domain [IPR020846] (1); Proton-dependent oligopeptide transporter family [IPR000109] (1)	-	C_unshiu_00178_mRNA_7.1	-
GF0035458	0	1	0	Hypothetical protein (1)			-	C_unshiu_00178_mRNA_34.1	-
GF0035457	0	1	0	Hypothetical protein (1)			-	C_unshiu_00178_mRNA_31.1	-
GF0035456	0	1	0	Hypothetical protein (1)	GTP binding [GO:0005525 molecular_function] (1); microtubule [GO:0005874 cellular_component] (1); structural constituent of cytoskeleton [GO:0005200 molecular_function] (1); microtubule-based process [GO:0007017 biological_process] (1)	Reverse transcriptase zinc-binding domain [IPR026960] (1); Tubulin/FtsZ, C-terminal [IPR008280] (1); Tubulin [IPR000217] (1); Tubulin/FtsZ, 2-layer sandwich domain [IPR018316] (1); Tubulin, C-terminal [IPR023123] (1); Alpha tubulin [IPR002452] (1)	-	C_unshiu_00178_mRNA_30.1	-
GF0035455	0	1	0	Hypothetical protein (1)			-	C_unshiu_00178_mRNA_23.1	-
GF0035454	0	1	0	Hypothetical protein (1)			-	C_unshiu_00178_mRNA_22.1	-
GF0035453	0	1	0	Transposable element Ac (1)	DNA binding [GO:0003677 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1); Zinc finger, BED-type [IPR003656] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00178_mRNA_16.1	-
GF0035452	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00178_mRNA_1.1	-
GF0035451	0	1	0	Hypothetical protein (1)			-	C_unshiu_00177_mRNA_9.1	-
GF0035450	0	1	0	Hypothetical protein (1)			-	C_unshiu_00177_mRNA_8.1	-
GF0035449	0	1	0	Hypothetical protein (1)			-	C_unshiu_00177_mRNA_32.1	-
GF0035448	0	1	0	Hypothetical protein (1)			-	C_unshiu_00177_mRNA_31.1	-
GF0035447	0	1	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); zinc ion binding [GO:0008270 molecular_function] (1)	FAR1 DNA binding domain [IPR004330] (1); FHY3/FAR1 family [IPR031052] (1); Zinc finger, SWIM-type [IPR007527] (1); Zinc finger, PMZ-type [IPR006564] (1)	-	C_unshiu_00177_mRNA_30.1	-
GF0035446	0	1	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Sec63 domain [IPR004179] (1); DnaJ domain [IPR001623] (1); Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_00177_mRNA_29.1	-
GF0035445	0	1	0	Hypothetical protein (1)			-	C_unshiu_00177_mRNA_20.1	-
GF0035444	0	1	0	Hypothetical protein (1)			-	C_unshiu_00177_mRNA_16.1	-
GF0035443	0	1	0	Hypothetical protein (1)			-	C_unshiu_00177_mRNA_11.1	-
GF0035442	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_00176_mRNA_9.1	-
GF0035441	0	1	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_00176_mRNA_7.1	-
GF0035440	0	1	0	Hypothetical protein (1)			-	C_unshiu_00176_mRNA_6.1	-
GF0035439	0	1	0	Hypothetical protein (1)			-	C_unshiu_00176_mRNA_50.1	-
GF0035438	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_00176_mRNA_5.1	-
GF0035437	0	1	0	Hypothetical protein (1)			-	C_unshiu_00176_mRNA_39.1	-
GF0035436	0	1	0	Hypothetical protein (1)			-	C_unshiu_00176_mRNA_29.1	-
GF0035435	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00176_mRNA_18.1	-
GF0035434	0	1	0	Hypothetical protein (1)			-	C_unshiu_00176_mRNA_17.1	-
GF0035433	0	1	0	Hypothetical protein (1)			-	C_unshiu_00176_mRNA_14.1	-
GF0035432	0	1	0	Hypothetical protein (1)			-	C_unshiu_00175_mRNA_8.1	-
GF0035431	0	1	0	TIR-NBS-LRR type disease resistance protein (1)	signal transduction [GO:0007165 biological_process] (1); protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_00175_mRNA_7.1	-
GF0035430	0	1	0	Oligopeptide transporter 7 (1)	transmembrane transport [GO:0055085 biological_process] (1)	Oligopeptide transporter, OPT superfamily [IPR004813] (1)	-	C_unshiu_00175_mRNA_36.1	-
GF0035429	0	1	0	Hypothetical protein (1)			-	C_unshiu_00175_mRNA_27.1	-
GF0035428	0	1	0	Hypothetical protein (1)			-	C_unshiu_00175_mRNA_25.1	-
GF0035427	0	1	0	Ribonuclease H-like superfamily protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_00175_mRNA_24.1	-
GF0035426	0	1	0	Hypothetical protein (1)		FCP1 homology domain [IPR004274] (1); HAD-like domain [IPR023214] (1)	-	C_unshiu_00175_mRNA_23.1	-
GF0035425	0	1	0	Hypothetical protein (1)			-	C_unshiu_00175_mRNA_22.1	-
GF0035424	0	1	0	Hypothetical protein (1)			-	C_unshiu_00175_mRNA_2.1	-
GF0035423	0	1	0	Heat stress transcription factor B-4b, putative (1)			-	C_unshiu_00175_mRNA_18.1	-
GF0035422	0	1	0	60S ribosomal protein L18a-1 (1)			-	C_unshiu_00175_mRNA_11.1	-
GF0035421	0	1	0	Hypothetical protein (1)			-	C_unshiu_00174_mRNA_6.1	-
GF0035420	0	1	0	Hypothetical protein (1)			-	C_unshiu_00174_mRNA_59.1	-
GF0035419	0	1	0	Hypothetical protein (1)			-	C_unshiu_00174_mRNA_58.1	-
GF0035418	0	1	0	Hypothetical protein (1)			-	C_unshiu_00174_mRNA_55.1	-
GF0035417	0	1	0	Hypothetical protein (1)			-	C_unshiu_00174_mRNA_54.1	-
GF0035416	0	1	0	Hypothetical protein (1)			-	C_unshiu_00174_mRNA_53.1	-
GF0035415	0	1	0	Hypothetical protein (1)			-	C_unshiu_00174_mRNA_52.1	-
GF0035414	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_00174_mRNA_51.1	-
GF0035413	0	1	0	Hypothetical protein (1)			-	C_unshiu_00174_mRNA_49.1	-
GF0035412	0	1	0	Hypothetical protein (1)			-	C_unshiu_00174_mRNA_47.1	-
GF0035411	0	1	0	Hypothetical protein (1)			-	C_unshiu_00174_mRNA_44.1	-
GF0035410	0	1	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_00174_mRNA_42.1	-
GF0035409	0	1	0	Hypothetical protein (1)			-	C_unshiu_00174_mRNA_41.1	-
GF0035408	0	1	0	Hypothetical protein (1)			-	C_unshiu_00174_mRNA_38.1	-
GF0035407	0	1	0	Hypothetical protein (1)			-	C_unshiu_00174_mRNA_37.1	-
GF0035406	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00174_mRNA_33.1	-
GF0035405	0	1	0	Hypothetical protein (1)			-	C_unshiu_00174_mRNA_30.1	-
GF0035404	0	1	0	Hypothetical protein (1)			-	C_unshiu_00174_mRNA_29.1	-
GF0035403	0	1	0	Hypothetical protein (1)			-	C_unshiu_00174_mRNA_21.1	-
GF0035402	0	1	0	Hypothetical protein (1)			-	C_unshiu_00174_mRNA_2.1	-
GF0035401	0	1	0	Hypothetical protein (1)		Chloramphenicol acetyltransferase-like domain [IPR023213] (1)	-	C_unshiu_00173_mRNA_8.1	-
GF0035400	0	1	0	Hypothetical protein (1)			-	C_unshiu_00173_mRNA_41.1	-
GF0035399	0	1	0	Hypothetical protein (1)			-	C_unshiu_00173_mRNA_39.1	-
GF0035398	0	1	0	Hypothetical protein (1)			-	C_unshiu_00173_mRNA_35.1	-
GF0035397	0	1	0	Hypothetical protein (1)			-	C_unshiu_00173_mRNA_3.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0035396	0	1	0	Cysteine/Histidine-rich C1 domain family protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); protein-disulfide reductase activity [GO:0047134 molecular_function] (1)	C1-like [IPR011424] (1)	-	C_unshiu_00173_mRNA_29.1	-
GF0035395	0	1	0	Hypothetical protein (1)	transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (1)	Transferase [IPR003480] (1); Ribosomal protein L18e/L15P [IPR021131] (1); Chloramphenicol acetyltransferase-like domain [IPR023213] (1)	-	C_unshiu_00173_mRNA_2.1	-
GF0035394	0	1	0	Hypothetical protein (1)			-	C_unshiu_00173_mRNA_17.1	-
GF0035393	0	1	0	Hypothetical protein (1)			-	C_unshiu_00173_mRNA_16.1	-
GF0035392	0	1	0	Oxalate oxidase 2 (1)	manganese ion binding [GO:0030145 molecular_function] (1); nutrient reservoir activity [GO:0045735 molecular_function] (1)	Cupin 1 [IPR006045] (1); RmlC-like jelly roll fold [IPR014710] (1); Germin [IPR001929] (1); RmlC-like cupin domain [IPR011051] (1)	-	C_unshiu_00173_mRNA_1.1	-
GF0035391	0	1	0	Hypothetical protein (1)			-	C_unshiu_00172_mRNA_37.1	-
GF0035390	0	1	0	Hypothetical protein (1)			-	C_unshiu_00172_mRNA_34.1	-
GF0035389	0	1	0	Hypothetical protein (1)			-	C_unshiu_00172_mRNA_30.1	-
GF0035388	0	1	0	Ubiquitin-specific protease family C19-related protein isoform 1 (1)			-	C_unshiu_00172_mRNA_17.1	-
GF0035387	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00171_mRNA_40.1	-
GF0035386	0	1	0	Hypothetical protein (1)			-	C_unshiu_00171_mRNA_2.1	-
GF0035385	0	1	0	Hypothetical protein (1)			-	C_unshiu_00171_mRNA_13.1	-
GF0035384	0	1	0	Hypothetical protein (1)			-	C_unshiu_00171_mRNA_1.1	-
GF0035383	0	1	0	Hypothetical protein (1)			-	C_unshiu_00170_mRNA_4.1	-
GF0035382	0	1	0	Hypothetical protein (1)			-	C_unshiu_00170_mRNA_25.1	-
GF0035381	0	1	0	Hypothetical protein (1)			-	C_unshiu_00170_mRNA_23.1	-
GF0035380	0	1	0	NF-kappa-B inhibitor cactus (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat [IPR002110] (1); PGG domain [IPR026961] (1); Ankyrin repeat-containing domain [IPR020683] (1)	-	C_unshiu_00170_mRNA_20.1	-
GF0035379	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	-	C_unshiu_00169_mRNA_36.1	-
GF0035378	0	1	0	Hypothetical protein (1)			-	C_unshiu_00169_mRNA_33.1	-
GF0035377	0	1	0	Hypothetical protein (1)			-	C_unshiu_00169_mRNA_3.1	-
GF0035376	0	1	0	Hypothetical protein (1)			-	C_unshiu_00169_mRNA_24.1	-
GF0035375	0	1	0	Hypothetical protein (1)			-	C_unshiu_00169_mRNA_19.1	-
GF0035374	0	1	0	Myocardin (1)			-	C_unshiu_00169_mRNA_14.1	-
GF0035373	0	1	0	Hypothetical protein (1)		GAG-pre-integrase domain [IPR025724] (1)	-	C_unshiu_00169_mRNA_10.1	-
GF0035372	0	1	0	Hypothetical protein (1)			-	C_unshiu_00168_mRNA_4.1	-
GF0035371	0	1	0	Maternal effect embryo arrest protein (1)			-	C_unshiu_00168_mRNA_17.1	-
GF0035370	0	1	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	-	C_unshiu_00167_mRNA_25.1	-
GF0035369	0	1	0	Hypothetical protein (1)			-	C_unshiu_00167_mRNA_19.1	-
GF0035368	0	1	0	Retrotransposon gag protein (1)			-	C_unshiu_00167_mRNA_14.1	-
GF0035367	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc knuckle CX2CX4HX4C [IPR025836] (1); Ribonuclease H-like domain [IPR012337] (1); Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_00166_mRNA_50.1	-
GF0035366	0	1	0	Hypothetical protein (1)	phospholipid-translocating ATPase activity [GO:0004012 molecular_function] (1); metal ion binding [GO:0046872 molecular_function] (1); magnesium ion binding [GO:0000287 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1); phospholipid transport [GO:0015914 biological_process] (1); nucleotide binding [GO:0000166 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	P-type ATPase, C-terminal [IPR032630] (1); P-type ATPase [IPR001757] (1); P-type ATPase, subfamily IV [IPR006539] (1); HAD-like domain [IPR023214] (1); P-type ATPase, N-terminal [IPR032631] (1); P-type ATPase, A domain [IPR008250] (1)	-	C_unshiu_00166_mRNA_31.1	-
GF0035365	0	1	0	Eukaryotic initiation factor 4A-10 (1)	nucleic acid binding [GO:0003676 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	RNA helicase, DEAD-box type, Q motif [IPR014014] (1); Helicase superfamily 1/2, ATP-binding domain [IPR014001] (1); ATP-dependent RNA helicase DEAD-box, conserved site [IPR000629] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); DEAD/DEAH box helicase domain [IPR011545] (1)	-	C_unshiu_00166_mRNA_28.1	-
GF0035364	0	1	0	Putative telomere repeat-binding factor 4-like (1)	nucleosome [GO:0000786 cellular_component] (1); nucleus [GO:0005634 cellular_component] (1); DNA binding [GO:0003677 molecular_function] (1); nucleosome assembly [GO:0006334 biological_process] (1)	Linker histone H1/H5, domain H15 [IPR005818] (1); SANT/Myb domain [IPR001005] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Homeodomain-like [IPR009057] (1); Myb domain [IPR017930] (1)	-	C_unshiu_00166_mRNA_27.2	-
GF0035363	0	1	0	Hypothetical protein (1)	nucleus [GO:0005634 cellular_component] (1); ATPase activity [GO:0016887 molecular_function] (1); ribosomal large subunit assembly [GO:0000027 biological_process] (1)	von Willebrand factor, type A [IPR002035] (1); Midasin [IPR012099] (1)	-	C_unshiu_00166_mRNA_13.1	-
GF0035362	0	1	0	Hypothetical protein (1)		Mitochondrial carrier domain [IPR023395] (1); Mitochondrial substrate/solute carrier [IPR018108] (1)	-	C_unshiu_00166_mRNA_11.1	-
GF0035361	0	1	0	GDSL esterase/lipase 5 (1)	hydrolase activity, acting on ester bonds [GO:0016788 molecular_function] (1)	SGNH hydrolase-type esterase domain [IPR013830] (1); GDSL lipase/esterase [IPR001087] (1)	-	C_unshiu_00166_mRNA_1.1	-
GF0035360	0	1	0	Hypothetical protein (1)			-	C_unshiu_00165_mRNA_3.1	-
GF0035359	0	1	0	Hypothetical protein (1)		Gag-polypeptide of LTR copia-type [IPR029472] (1)	-	C_unshiu_00165_mRNA_25.1	-
GF0035358	0	1	0	Hypothetical protein (1)			-	C_unshiu_00165_mRNA_23.1	-
GF0035357	0	1	0	Hypothetical protein (1)			-	C_unshiu_00165_mRNA_2.1	-
GF0035356	0	1	0	Ankyrin repeat plant-like protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat-containing domain [IPR020683] (1); Ankyrin repeat [IPR002110] (1)	-	C_unshiu_00165_mRNA_19.1	-
GF0035355	0	1	0	Hypothetical protein (1)	polysaccharide binding [GO:0030247 molecular_function] (1)	Wall-associated receptor kinase, galacturonan-binding domain [IPR025287] (1)	-	C_unshiu_00165_mRNA_18.1	-
GF0035354	0	1	0	Hypothetical protein (1)			-	C_unshiu_00165_mRNA_14.1	-
GF0035353	0	1	0	Wall-associated receptor kinase 1 (1)	polysaccharide binding [GO:0030247 molecular_function] (1)	Wall-associated receptor kinase, galacturonan-binding domain [IPR025287] (1)	-	C_unshiu_00165_mRNA_13.1	-
GF0035352	0	1	0	Hypothetical protein (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); polysaccharide binding [GO:0030247 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Wall-associated receptor kinase, galacturonan-binding domain [IPR025287] (1); Protein kinase-like domain [IPR011009] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1)	-	C_unshiu_00165_mRNA_12.1	-
GF0035351	0	1	0	Hypothetical protein (1)		Gag-polypeptide of LTR copia-type [IPR029472] (1)	-	C_unshiu_00165_mRNA_11.1	-
GF0035350	0	1	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Protein kinase-like domain [IPR011009] (1); Serine/threonine-protein kinase, active site [IPR008271] (1)	-	C_unshiu_00164_mRNA_45.1	-
GF0035349	0	1	0	Mutator-like transposase (1)	zinc ion binding [GO:0008270 molecular_function] (1)	MULE transposase domain [IPR018289] (1); Zinc finger, PMZ-type [IPR006564] (1); Transposase, MuDR, plant [IPR004332] (1)	-	C_unshiu_00164_mRNA_44.1	-
GF0035348	0	1	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Domain of unknown function DUF1985 [IPR015410] (1); Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_00164_mRNA_43.1	-
GF0035347	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, PMZ-type [IPR006564] (1); Zinc finger, SWIM-type [IPR007527] (1)	-	C_unshiu_00164_mRNA_39.1	-
GF0035346	0	1	0	Hypothetical protein (1)			-	C_unshiu_00164_mRNA_36.1	-
GF0035345	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4219 [IPR025314] (1)	-	C_unshiu_00164_mRNA_30.1	-
GF0035344	0	1	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	-	C_unshiu_00164_mRNA_11.1	-
GF0035343	0	1	0	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_00163_mRNA_44.1	-
GF0035342	0	1	0	Oligopeptide transporter 4 (1)	transmembrane transport [GO:0055085 biological_process] (1)	Tetrapeptide transporter, OPT1/isp4 [IPR004648] (1); Oligopeptide transporter, OPT superfamily [IPR004813] (1)	-	C_unshiu_00163_mRNA_4.1	-
GF0035341	0	1	0	Hypothetical protein (1)			-	C_unshiu_00163_mRNA_2.1	-
GF0035340	0	1	0	Hypothetical protein (1)			-	C_unshiu_00163_mRNA_15.1	-
GF0035339	0	1	0	Hypothetical protein (1)			-	C_unshiu_00162_mRNA_7.1	-
GF0035338	0	1	0	Hypothetical protein (1)		Protein of unknown function DUF604 [IPR006740] (1)	-	C_unshiu_00162_mRNA_38.1	-
GF0035337	0	1	0	Hypothetical protein (1)			-	C_unshiu_00162_mRNA_26.1	-
GF0035336	0	1	0	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_00162_mRNA_15.1	-
GF0035335	0	1	0	Hypothetical protein (1)		Phosphatidylinositol N-acetylglucosaminyltransferase subunit Y [IPR029164] (1)	-	C_unshiu_00162_mRNA_12.1	-
GF0035334	0	1	0	Hypothetical protein (1)			-	C_unshiu_00161_mRNA_40.1	-
GF0035333	0	1	0	Hypothetical protein (1)			-	C_unshiu_00161_mRNA_32.1	-
GF0035332	0	1	0	Hypothetical protein (1)			-	C_unshiu_00161_mRNA_26.1	-
GF0035331	0	1	0	Hypothetical protein (1)			-	C_unshiu_00161_mRNA_23.1	-
GF0035330	0	1	0	Hypothetical protein (1)			-	C_unshiu_00161_mRNA_21.1	-
GF0035329	0	1	0	Hypothetical protein (1)			-	C_unshiu_00161_mRNA_15.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0035328	0	1	0	Hypothetical protein (1)			-	C_unshiu_00161_mRNA_1.1	-
GF0035327	0	1	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	-	C_unshiu_00160_mRNA_21.1	-
GF0035326	0	1	0	Hypothetical protein (1)			-	C_unshiu_00160_mRNA_2.1	-
GF0035325	0	1	0	Hypothetical protein (1)	DNA-templated transcription, termination [GO:0006353 biological_process] (1)	Rho termination factor, N-terminal [IPR011112] (1)	-	C_unshiu_00160_mRNA_16.1	-
GF0035324	0	1	0	Hypothetical protein (1)			-	C_unshiu_00160_mRNA_11.1	-
GF0035323	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Domain of unknown function DUF4371 [IPR025398] (1)	-	C_unshiu_00159_mRNA_9.1	-
GF0035322	0	1	0	Hypothetical protein (1)			-	C_unshiu_00159_mRNA_8.1	-
GF0035321	0	1	0	Hypothetical protein (1)			-	C_unshiu_00159_mRNA_39.1	-
GF0035320	0	1	0	Hypothetical protein (1)			-	C_unshiu_00159_mRNA_34.1	-
GF0035319	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00159_mRNA_31.1	-
GF0035318	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Zinc finger, BED-type [IPR003656] (1)	-	C_unshiu_00159_mRNA_30.1	-
GF0035317	0	1	0	Hypothetical protein (1)			-	C_unshiu_00159_mRNA_29.1	-
GF0035316	0	1	0	Hypothetical protein (1)			-	C_unshiu_00159_mRNA_28.1	-
GF0035315	0	1	0	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1); Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	C_unshiu_00159_mRNA_24.1	-
GF0035314	0	1	0	Hypothetical protein (1)			-	C_unshiu_00159_mRNA_2.1	-
GF0035313	0	1	0	Hypothetical protein (1)			-	C_unshiu_00159_mRNA_10.1	-
GF0035312	0	1	0	Hypothetical protein (1)			-	C_unshiu_00158_mRNA_7.1	-
GF0035311	0	1	0	Hypothetical protein (1)			-	C_unshiu_00158_mRNA_6.1	-
GF0035310	0	1	0	Disease resistance-responsive family protein (1)		Plant disease resistance response protein [IPR004265] (1)	-	C_unshiu_00158_mRNA_50.1	-
GF0035309	0	1	0	Hypothetical protein (1)	exocytosis [GO:0006887 biological_process] (1); exocyst [GO:0000145 cellular_component] (1)	Exocyst complex protein Exo70 [IPR004140] (1); Cullin repeat-like-containing domain [IPR016159] (1)	-	C_unshiu_00158_mRNA_45.1	-
GF0035308	0	1	0	Hypothetical protein (1)		Cation-transporting P-type ATPase, N-terminal [IPR004014] (1)	-	C_unshiu_00158_mRNA_36.1	-
GF0035307	0	1	0	Calcium-transporting atpase 4, endoplasmic reticulum-type, putative (1)	integral component of membrane [GO:0016021 cellular_component] (1)	P-type ATPase [IPR001757] (1); P-type ATPase, transmembrane domain [IPR023298] (1); Cation-transporting P-type ATPase, C-terminal [IPR006068] (1); HAD-like domain [IPR023214] (1)	-	C_unshiu_00158_mRNA_35.1	-
GF0035306	0	1	0	Laccase (1)	copper ion binding [GO:0005507 molecular_function] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Multicopper oxidase, type 1 [IPR001117] (1); Cupredoxin [IPR008972] (1); Multicopper oxidase, type 3 [IPR011707] (1)	-	C_unshiu_00158_mRNA_27.1	-
GF0035305	0	1	0	Reticulon-like protein B21 (1)		Reticulon [IPR003388] (1)	-	C_unshiu_00158_mRNA_2.1	-
GF0035304	0	1	0	Disease resistance family protein / LRR family protein, putative (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_00157_mRNA_9.1	-
GF0035303	0	1	0	Hypothetical protein (1)			-	C_unshiu_00157_mRNA_5.1	-
GF0035302	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_00157_mRNA_39.1	-
GF0035301	0	1	0	Hypothetical protein (1)			-	C_unshiu_00157_mRNA_31.1	-
GF0035300	0	1	0	Hypothetical protein (1)			-	C_unshiu_00157_mRNA_3.1	-
GF0035299	0	1	0	Hypothetical protein (1)			-	C_unshiu_00157_mRNA_24.1	-
GF0035298	0	1	0	Hypothetical protein (1)			-	C_unshiu_00157_mRNA_21.1	-
GF0035297	0	1	0	Hypothetical protein (1)			-	C_unshiu_00157_mRNA_19.1	-
GF0035296	0	1	0	Hypothetical protein (1)			-	C_unshiu_00157_mRNA_18.1	-
GF0035295	0	1	0	Disease resistance family protein / LRR family protein, putative (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_00157_mRNA_15.1	-
GF0035294	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_00157_mRNA_14.1	-
GF0035293	0	1	0	Hypothetical protein (1)			-	C_unshiu_00157_mRNA_13.1	-
GF0035292	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_00157_mRNA_12.1	-
GF0035291	0	1	0	Hypothetical protein (1)			-	C_unshiu_00157_mRNA_1.1	-
GF0035290	0	1	0	Hypothetical protein (1)			-	C_unshiu_00156_mRNA_38.1	-
GF0035289	0	1	0	Hypothetical protein (1)			-	C_unshiu_00156_mRNA_35.1	-
GF0035288	0	1	0	Hypothetical protein (1)			-	C_unshiu_00156_mRNA_34.1	-
GF0035287	0	1	0	Hypothetical protein (1)			-	C_unshiu_00156_mRNA_30.1	-
GF0035286	0	1	0	Hypothetical protein (1)			-	C_unshiu_00156_mRNA_29.1	-
GF0035285	0	1	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_00156_mRNA_28.1	-
GF0035284	0	1	0	Hypothetical protein (1)			-	C_unshiu_00156_mRNA_27.1	-
GF0035283	0	1	0	Hypothetical protein (1)			-	C_unshiu_00156_mRNA_25.1	-
GF0035282	0	1	0	Hypothetical protein (1)			-	C_unshiu_00156_mRNA_21.1	-
GF0035281	0	1	0	Hypothetical protein (1)		Retroviral aspartyl protease [IPR013242] (1)	-	C_unshiu_00156_mRNA_16.1	-
GF0035280	0	1	0	Hypothetical protein (1)			-	C_unshiu_00156_mRNA_14.1	-
GF0035279	0	1	0	Hypothetical protein (1)			-	C_unshiu_00156_mRNA_13.1	-
GF0035278	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	-	C_unshiu_00156_mRNA_12.1	-
GF0035277	0	1	0	Hypothetical protein (1)			-	C_unshiu_00155_mRNA_9.1	-
GF0035276	0	1	0	Protein phosphatase 2C 35 (1)	catalytic activity [GO:0003824 molecular_function] (1); protein dephosphorylation [GO:0006470 biological_process] (1); protein serine/threonine phosphatase activity [GO:0004722 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Protein phosphatase 2C family [IPR015655] (1); PPM-type phosphatase domain [IPR001932] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00155_mRNA_6.1	-
GF0035275	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF3741 [IPR022212] (1)	-	C_unshiu_00155_mRNA_5.1	-
GF0035274	0	1	0	Ubiquitin carboxyl-terminal hydrolase 12 (1)	protein binding [GO:0005515 molecular_function] (1)	MATH/TRAF domain [IPR002083] (1); TRAF-like [IPR008974] (1)	-	C_unshiu_00155_mRNA_40.1	-
GF0035273	0	1	0	Envelope glycoprotein (1)			-	C_unshiu_00155_mRNA_39.1	-
GF0035272	0	1	0	Hypothetical protein (1)			-	C_unshiu_00155_mRNA_32.1	-
GF0035271	0	1	0	Hypothetical protein (1)			-	C_unshiu_00155_mRNA_28.1	-
GF0035270	0	1	0	Hypothetical protein (1)			-	C_unshiu_00155_mRNA_19.1	-
GF0035269	0	1	0	Hypothetical protein (1)			-	C_unshiu_00155_mRNA_18.1	-
GF0035268	0	1	0	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	C_unshiu_00155_mRNA_14.1	-
GF0035267	0	1	0	Hypothetical protein (1)			-	C_unshiu_00154_mRNA_8.1	-
GF0035266	0	1	0	Hypothetical protein (1)	transporter activity [GO:0005215 molecular_function] (1); transmembrane transport [GO:0055085 biological_process] (1); mitochondrial inner membrane [GO:0005743 cellular_component] (1); transport [GO:0006810 biological_process] (1)	Endonuclease/exonuclease/phosphatase [IPR005135] (1); Mitochondrial carrier protein [IPR002067] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1); Adenine nucleotide translocator 1 [IPR002113] (1); Mitochondrial substrate/solute carrier [IPR018108] (1); Mitochondrial carrier domain [IPR023395] (1)	-	C_unshiu_00154_mRNA_5.1	-
GF0035265	0	1	0	Hypothetical protein (1)			-	C_unshiu_00154_mRNA_42.1	-
GF0035264	0	1	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	NAC domain [IPR003441] (1)	-	C_unshiu_00154_mRNA_41.1	-
GF0035263	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); nucleotide binding [GO:0000166 molecular_function] (1)	RNA recognition motif domain [IPR000504] (1); Nucleotide-binding alpha-beta plait domain [IPR012677] (1)	-	C_unshiu_00154_mRNA_38.1	-
GF0035262	0	1	0	Phytochelatin synthetase-like protein (1)	cell growth [GO:0016049 biological_process] (1); anchored component of membrane [GO:0031225 cellular_component] (1); cellulose microfibril organization [GO:0010215 biological_process] (1)	COBRA, plant [IPR006918] (1)	-	C_unshiu_00154_mRNA_13.1	-
GF0035261	0	1	0	Hypothetical protein (1)			-	C_unshiu_00153_mRNA_47.1	-
GF0035260	0	1	0	Hypothetical protein (1)	phosphoric diester hydrolase activity [GO:0008081 molecular_function] (1); lipid metabolic process [GO:0006629 biological_process] (1)	Phosphatidylinositol-specific phospholipase C, X domain [IPR000909] (1); Pentatricopeptide repeat [IPR002885] (1); PLC-like phosphodiesterase, TIM beta/alpha-barrel domain [IPR017946] (1)	-	C_unshiu_00152_mRNA_6.1	-
GF0035259	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_00152_mRNA_58.1	-
GF0035258	0	1	0	Putative non-LTR reverse transcriptase (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_00152_mRNA_45.1	-
GF0035257	0	1	0	Hypothetical protein (1)	transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	-	C_unshiu_00152_mRNA_31.1	-
GF0035256	0	1	0	Hypothetical protein (1)	vacuolar proton-transporting V-type ATPase complex assembly [GO:0070072 biological_process] (1)	Peptidase S8, subtilisin-related [IPR015500] (1); Peptidase S8 propeptide/proteinase inhibitor I9 [IPR010259] (1); Vacuolar ATPase assembly integral membrane protein Vma21 [IPR019013] (1)	-	C_unshiu_00152_mRNA_3.1	-
GF0035255	0	1	0	Subtilisin-like serine protease (1)	proteolysis [GO:0006508 biological_process] (1); serine-type endopeptidase activity [GO:0004252 molecular_function] (1)	Peptidase S8, subtilisin-related [IPR015500] (1); Peptidase S8/S53 domain [IPR000209] (1); Peptidase S8 propeptide/proteinase inhibitor I9 [IPR010259] (1)	-	C_unshiu_00152_mRNA_2.1	-
GF0035254	0	1	0	Hypothetical protein (1)		Filament-like plant protein [IPR008587] (1)	-	C_unshiu_00152_mRNA_17.1	-
GF0035253	0	1	0	Hypothetical protein (1)		Filament-like plant protein [IPR008587] (1)	-	C_unshiu_00152_mRNA_16.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0035252	0	1	0	Hypothetical protein (1)	nucleoside metabolic process [GO:0009116 biological_process] (1); metabolic process [GO:0008152 biological_process] (1); 'de novo' pyrimidine nucleobase biosynthetic process [GO:0006207 biological_process] (1); cellular metabolic process [GO:0044237 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1); orotate phosphoribosyltransferase activity [GO:0004588 molecular_function] (1); orotidine-5'-phosphate decarboxylase activity [GO:0004590 molecular_function] (1); 'de novo' UMP biosynthetic process [GO:0044205 biological_process] (1); pyrimidine nucleotide biosynthetic process [GO:0006221 biological_process] (1)	Orotate phosphoribosyltransferase [IPR023031] (1); Orotidine 5'-phosphate decarboxylase [IPR014732] (1); Ribulose-phosphate binding barrel [IPR011060] (1); Orotate phosphoribosyl transferase domain [IPR004467] (1); Aldolase-type TIM barrel [IPR013785] (1); Phosphoribosyltransferase domain [IPR000836] (1); Orotidine 5'-phosphate decarboxylase, active site [IPR018089] (1); Initiation factor 2B-related [IPR000649] (1); Phosphoribosyltransferase-like [IPR029057] (1); Orotidine 5'-phosphate decarboxylase domain [IPR001754] (1)	-	C_unshiu_00151_mRNA_3.1	-
GF0035251	0	1	0	Chloroplast terpenoid cyclase (1)	magnesium ion binding [GO:0000287 molecular_function] (1); terpene synthase activity [GO:0010333 molecular_function] (1); lyase activity [GO:0016829 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Isoprenoid synthase domain [IPR008949] (1); Terpene synthase, N-terminal domain [IPR001906] (1); Terpene synthase, metal-binding domain [IPR005630] (1); Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (1)	-	C_unshiu_00151_mRNA_29.1	-
GF0035250	0	1	0	Hypothetical protein (1)			-	C_unshiu_00151_mRNA_28.1	-
GF0035249	0	1	0	Hypothetical protein (1)	metabolic process [GO:0008152 biological_process] (1); terpene synthase activity [GO:0010333 molecular_function] (1); lyase activity [GO:0016829 molecular_function] (1)	Terpene synthase, N-terminal domain [IPR001906] (1); Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (1)	-	C_unshiu_00151_mRNA_26.1	-
GF0035248	0	1	0	Monosacharide transport protein (1)			-	C_unshiu_00151_mRNA_24.1	-
GF0035247	0	1	0	Leguminosin group485 secreted peptide (1)			-	C_unshiu_00151_mRNA_22.1	-
GF0035246	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc knuckle CX2CX4HX4C [IPR025836] (1); Zinc finger, CCHC-type [IPR001878] (1); Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_00151_mRNA_20.1	-
GF0035245	0	1	0	Hypothetical protein (1)			-	C_unshiu_00151_mRNA_17.1	-
GF0035244	0	1	0	Hypothetical protein (1)			-	C_unshiu_00151_mRNA_16.1	-
GF0035243	0	1	0	Hypothetical protein (1)			-	C_unshiu_00151_mRNA_14.1	-
GF0035242	0	1	0	Hypothetical protein (1)			-	C_unshiu_00151_mRNA_13.1	-
GF0035241	0	1	0	Hypothetical protein (1)			-	C_unshiu_00150_mRNA_52.1	-
GF0035240	0	1	0	Hypothetical protein (1)			-	C_unshiu_00150_mRNA_24.1	-
GF0035239	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	F-box domain [IPR001810] (1)	-	C_unshiu_00150_mRNA_14.1	-
GF0035238	0	1	0	40S ribosomal protein S23 (1)	small ribosomal subunit [GO:0015935 cellular_component] (1); ribosome [GO:0005840 cellular_component] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1); intracellular [GO:0005622 cellular_component] (1); translation [GO:0006412 biological_process] (1)	Ribosomal protein S23, eukaryotic/archaeal [IPR005680] (1); Ribosomal protein S12/S23 [IPR006032] (1); Nucleic acid-binding, OB-fold [IPR012340] (1)	-	C_unshiu_00149_mRNA_7.1	-
GF0035237	0	1	0	Cysteine-rich RLK 29 isoform 1 (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1)	Serine/threonine-protein kinase, active site [IPR008271] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_00149_mRNA_36.1	-
GF0035236	0	1	0	Hypothetical protein (1)			-	C_unshiu_00149_mRNA_35.1	-
GF0035235	0	1	0	Hypothetical protein (1)			-	C_unshiu_00149_mRNA_34.1	-
GF0035234	0	1	0	AT1G67060 protein (1)			-	C_unshiu_00149_mRNA_33.1	-
GF0035233	0	1	0	Hypothetical protein (1)	ribosome [GO:0005840 cellular_component] (1); intracellular [GO:0005622 cellular_component] (1); translation [GO:0006412 biological_process] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1)	Ribosomal protein S7e [IPR000554] (1); MULE transposase domain [IPR018289] (1)	-	C_unshiu_00149_mRNA_32.1	-
GF0035232	0	1	0	Hypothetical protein (1)	thiol-dependent ubiquitinyl hydrolase activity [GO:0036459 molecular_function] (1); protein deubiquitination [GO:0016579 biological_process] (1)	Peptidase C19, ubiquitin carboxyl-terminal hydrolase [IPR001394] (1); Ubiquitin specific protease domain [IPR028889] (1)	-	C_unshiu_00149_mRNA_27.1	-
GF0035231	0	1	0	Hypothetical protein (1)			-	C_unshiu_00149_mRNA_25.1	-
GF0035230	0	1	0	Hypothetical protein (1)			-	C_unshiu_00149_mRNA_23.1	-
GF0035229	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); HAT, C-terminal dimerisation domain [IPR008906] (1); Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00149_mRNA_12.1	-
GF0035228	0	1	0	Hypothetical protein (1)			-	C_unshiu_00149_mRNA_10.1	-
GF0035227	0	1	0	No apical meristem family protein (1)	DNA binding [GO:0003677 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	Domain of unknown function DUF1985 [IPR015410] (1); NAC domain [IPR003441] (1)	-	C_unshiu_00148_mRNA_8.1	-
GF0035226	0	1	0	Hypothetical protein (1)			-	C_unshiu_00148_mRNA_7.1	-
GF0035225	0	1	0	Hypothetical protein (1)			-	C_unshiu_00148_mRNA_5.1	-
GF0035224	0	1	0	Hypothetical protein (1)			-	C_unshiu_00148_mRNA_42.1	-
GF0035223	0	1	0	Hypothetical protein (1)			-	C_unshiu_00148_mRNA_33.1	-
GF0035222	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00148_mRNA_3.1	-
GF0035221	0	1	0	Aldehyde dehydrogenase family 2 member C4 (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor [GO:0016620 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Aldehyde dehydrogenase N-terminal domain [IPR016162] (1); Aldehyde dehydrogenase domain [IPR015590] (1); Aldehyde dehydrogenase, C-terminal [IPR016163] (1); Aldehyde/histidinol dehydrogenase [IPR016161] (1); Aldehyde dehydrogenase, glutamic acid active site [IPR029510] (1)	-	C_unshiu_00148_mRNA_28.1	-
GF0035220	0	1	0	Hypothetical protein (1)			-	C_unshiu_00148_mRNA_22.1	-
GF0035219	0	1	0	Calcium-transporting ATPase 2, plasma membrane-type (1)	calmodulin binding [GO:0005516 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1); metal ion binding [GO:0046872 molecular_function] (1); calcium ion transmembrane transport [GO:0070588 biological_process] (1); membrane [GO:0016020 cellular_component] (1); calcium-transporting ATPase activity [GO:0005388 molecular_function] (1); nucleotide binding [GO:0000166 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	HAD-like domain [IPR023214] (1); Cation-transporting P-type ATPase, N-terminal [IPR004014] (1); Calcium-transporting P-type ATPase, N-terminal autoinhibitory domain [IPR024750] (1); P-type ATPase, A domain [IPR008250] (1); P-type ATPase, phosphorylation site [IPR018303] (1); P-type ATPase, cytoplasmic domain N [IPR023299] (1); P-type ATPase, subfamily IIB [IPR006408] (1); P-type ATPase [IPR001757] (1)	-	C_unshiu_00148_mRNA_16.1	-
GF0035218	0	1	0	Hypothetical protein (1)		Cation-transporting P-type ATPase, C-terminal [IPR006068] (1); P-type ATPase, transmembrane domain [IPR023298] (1)	-	C_unshiu_00148_mRNA_13.1	-
GF0035217	0	1	0	Hypothetical protein (1)			-	C_unshiu_00148_mRNA_1.1	-
GF0035216	0	1	0	Hypothetical protein (1)	regulation of gene expression [GO:0010468 biological_process] (1); peroxisome [GO:0005777 cellular_component] (1)	OST-HTH associated domain [IPR025677] (1); OST-HTH/LOTUS domain [IPR025605] (1); Meiosis arrest female protein 1 [IPR024768] (1)	-	C_unshiu_00147_mRNA_35.1	-
GF0035215	0	1	0	Hypothetical protein (1)			-	C_unshiu_00147_mRNA_32.1	-
GF0035214	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	DNA/RNA-binding protein Alba-like [IPR002775] (1)	-	C_unshiu_00147_mRNA_30.1	-
GF0035213	0	1	0	Polynucleotidyl transferase, ribonuclease H-like superfamily protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_00147_mRNA_3.1	-
GF0035212	0	1	0	Ribonuclease H protein, putative (1)	transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (1); one-carbon metabolic process [GO:0006730 biological_process] (1); sequence-specific DNA binding [GO:0043565 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); zinc ion binding [GO:0008270 molecular_function] (1); adenosylhomocysteinase activity [GO:0004013 molecular_function] (1)	Reverse transcriptase zinc-binding domain [IPR026960] (1); Zinc finger, GATA-type [IPR000679] (1); S-adenosyl-L-homocysteine hydrolase, NAD binding domain [IPR015878] (1); NAD(P)-binding domain [IPR016040] (1); Adenosylhomocysteinase [IPR000043] (1)	-	C_unshiu_00147_mRNA_28.1	-
GF0035211	0	1	0	Hypothetical protein (1)			-	C_unshiu_00147_mRNA_25.1	-
GF0035210	0	1	0	Hypothetical protein (1)		High mobility group box domain [IPR009071] (1)	-	C_unshiu_00147_mRNA_21.1	-
GF0035209	0	1	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1)	-	C_unshiu_00147_mRNA_20.1	-
GF0035208	0	1	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1)	-	C_unshiu_00147_mRNA_19.1	-
GF0035207	0	1	0	F-box/LRR-repeat protein At4g14103 (1)	protein binding [GO:0005515 molecular_function] (1)	FBD domain [IPR006566] (1); F-box domain [IPR001810] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00147_mRNA_18.1	-
GF0035206	0	1	0	Hypothetical protein (1)			-	C_unshiu_00147_mRNA_15.1	-
GF0035205	0	1	0	Hypothetical protein (1)			-	C_unshiu_00147_mRNA_11.1	-
GF0035204	0	1	0	Hypothetical protein (1)	calcium ion binding [GO:0005509 molecular_function] (1)	EF-Hand 1, calcium-binding site [IPR018247] (1); EF-hand domain [IPR002048] (1); EF-hand domain pair [IPR011992] (1)	-	C_unshiu_00147_mRNA_1.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0035203	0	1	0	Hypothetical protein (1)			-	C_unshiu_00146_mRNA_39.1	-
GF0035202	0	1	0	Long-chain-alcohol oxidase FAO2 (1)	oxidoreductase activity, acting on CH-OH group of donors [GO:0016614 molecular_function] (1); flavin adenine dinucleotide binding [GO:0050660 molecular_function] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	FAD/NAD(P)-binding domain [IPR023753] (1); Glucose-methanol-choline oxidoreductase, C-terminal [IPR007867] (1); Glucose-methanol-choline oxidoreductase, N-terminal [IPR000172] (1)	-	C_unshiu_00146_mRNA_33.1	-
GF0035201	0	1	0	Hypothetical protein (1)			-	C_unshiu_00146_mRNA_31.1	-
GF0035200	0	1	0	Hypothetical protein (1)			-	C_unshiu_00146_mRNA_27.1	-
GF0035199	0	1	0	Plastid developmental protein DAG (1)			-	C_unshiu_00146_mRNA_20.1	-
GF0035198	0	1	0	Hypothetical protein (1)			-	C_unshiu_00146_mRNA_2.1	-
GF0035197	0	1	0	Hypothetical protein (1)		Transposase, Tnp1/En/Spm-like [IPR004264] (1); Probable transposase, Ptta/En/Spm, plant [IPR004252] (1)	-	C_unshiu_00146_mRNA_16.1	-
GF0035196	0	1	0	Hypothetical protein (1)	ATPase activity [GO:0016887 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); ABC transporter-like [IPR003439] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00146_mRNA_12.1	-
GF0035195	0	1	0	Hypothetical protein (1)			-	C_unshiu_00146_mRNA_10.1	-
GF0035194	0	1	0	Hypothetical protein (1)			-	C_unshiu_00145_mRNA_9.1	-
GF0035193	0	1	0	Hypothetical protein (1)			-	C_unshiu_00145_mRNA_74.1	-
GF0035192	0	1	0	Hypothetical protein (1)			-	C_unshiu_00145_mRNA_70.1	-
GF0035191	0	1	0	Hypothetical protein (1)			-	C_unshiu_00145_mRNA_7.1	-
GF0035190	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_00145_mRNA_60.1	-
GF0035189	0	1	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_00145_mRNA_54.1	-
GF0035188	0	1	0	Hypothetical protein (1)			-	C_unshiu_00145_mRNA_5.1	-
GF0035187	0	1	0	Hypothetical protein (1)			-	C_unshiu_00145_mRNA_49.1	-
GF0035186	0	1	0	Hypothetical protein (1)			-	C_unshiu_00145_mRNA_48.1	-
GF0035185	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_00145_mRNA_40.1	-
GF0035184	0	1	0	Hypothetical protein (1)			-	C_unshiu_00145_mRNA_38.1	-
GF0035183	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Reverse transcriptase domain [IPR000477] (1); Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00145_mRNA_37.1	-
GF0035182	0	1	0	Hypothetical protein (1)			-	C_unshiu_00145_mRNA_30.1	-
GF0035181	0	1	0	Hypothetical protein (1)			-	C_unshiu_00145_mRNA_23.1	-
GF0035180	0	1	0	Hypothetical protein (1)			-	C_unshiu_00145_mRNA_22.1	-
GF0035179	0	1	0	Hypothetical protein (1)			-	C_unshiu_00145_mRNA_21.1	-
GF0035178	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00145_mRNA_20.1	-
GF0035177	0	1	0	Hypothetical protein (1)			-	C_unshiu_00145_mRNA_2.1	-
GF0035176	0	1	0	Hypothetical protein (1)			-	C_unshiu_00145_mRNA_19.1	-
GF0035175	0	1	0	Hypothetical protein (1)			-	C_unshiu_00145_mRNA_16.1	-
GF0035174	0	1	0	Hypothetical protein (1)			-	C_unshiu_00145_mRNA_1.1	-
GF0035173	0	1	0	Hypothetical protein (1)			-	C_unshiu_00144_mRNA_9.1	-
GF0035172	0	1	0	Hypothetical protein (1)			-	C_unshiu_00144_mRNA_8.1	-
GF0035171	0	1	0	Hypothetical protein (1)			-	C_unshiu_00144_mRNA_6.1	-
GF0035170	0	1	0	Long chain acyl-CoA synthetase 8 (1)	metabolic process [GO:0008152 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1)	AMP-dependent synthetase/ligase [IPR000873] (1)	-	C_unshiu_00144_mRNA_5.1	-
GF0035169	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00144_mRNA_47.1	-
GF0035168	0	1	0	Hypothetical protein (1)			-	C_unshiu_00144_mRNA_42.1	-
GF0035167	0	1	0	Hypothetical protein (1)			-	C_unshiu_00144_mRNA_38.1	-
GF0035166	0	1	0	Hypothetical protein (1)			-	C_unshiu_00144_mRNA_37.1	-
GF0035165	0	1	0	Hypothetical protein (1)			-	C_unshiu_00144_mRNA_36.1	-
GF0035164	0	1	0	Trihydroxystilbene synthase (1)	catalytic activity [GO:0003824 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Chalcone/stilbene synthase, N-terminal [IPR001099] (1); Thiolase-like [IPR016039] (1); Chalcone/stilbene synthase, C-terminal [IPR012328] (1)	-	C_unshiu_00144_mRNA_33.1	-
GF0035163	0	1	0	Hypothetical protein (1)	transmembrane transporter activity [GO:0022857 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1)	WAT1-related protein [IPR030184] (1)	-	C_unshiu_00144_mRNA_21.1	-
GF0035162	0	1	0	Hypothetical protein (1)	cell cycle [GO:0007049 biological_process] (1); nucleus [GO:0005634 cellular_component] (1); DNA repair [GO:0006281 biological_process] (1)	Checkpoint protein Rad17/Rad24 [IPR004582] (1)	-	C_unshiu_00144_mRNA_15.1	-
GF0035161	0	1	0	Hypothetical protein (1)			-	C_unshiu_00143_mRNA_7.1	-
GF0035160	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00143_mRNA_52.1	-
GF0035159	0	1	0	Putative retroelement pol polyprotein (1)			-	C_unshiu_00143_mRNA_51.1	-
GF0035158	0	1	0	Hypothetical protein (1)			-	C_unshiu_00143_mRNA_48.1	-
GF0035157	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00143_mRNA_46.1	-
GF0035156	0	1	0	Hypothetical protein (1)			-	C_unshiu_00143_mRNA_33.1	-
GF0035155	0	1	0	Hypothetical protein (1)			-	C_unshiu_00143_mRNA_3.1	-
GF0035154	0	1	0	LSD1-type zinc finger protein (1)		Zinc finger, LSD1-type [IPR005735] (1)	-	C_unshiu_00143_mRNA_29.1	-
GF0035153	0	1	0	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	C_unshiu_00143_mRNA_16.1	-
GF0035152	0	1	0	Transposon protein, putative, unclassified (1)	zinc ion binding [GO:0008270 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1); Zinc finger, SWIM-type [IPR007527] (1); MULE transposase domain [IPR018289] (1); Zinc finger, PMZ-type [IPR006564] (1)	-	C_unshiu_00142_mRNA_41.1	-
GF0035151	0	1	0	MADS-box protein STMADS11 subfamily (1)	DNA binding [GO:0003677 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	Transcription factor, MADS-box [IPR002100] (1)	-	C_unshiu_00142_mRNA_30.1	-
GF0035150	0	1	0	Rab GDP dissociation inhibitor alpha (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	GDP dissociation inhibitor [IPR018203] (1); FAD/NAD(P)-binding domain [IPR023753] (1)	-	C_unshiu_00142_mRNA_28.1	-
GF0035149	0	1	0	Hypothetical protein (1)			-	C_unshiu_00142_mRNA_25.1	-
GF0035148	0	1	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1)	-	C_unshiu_00142_mRNA_23.1	-
GF0035147	0	1	0	Hypothetical protein (1)		Rab-GTPase-TBC domain [IPR000195] (1)	-	C_unshiu_00142_mRNA_20.1	-
GF0035146	0	1	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00142_mRNA_10.1	-
GF0035145	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4477 [IPR027951] (1)	-	C_unshiu_00142_mRNA_1.1	-
GF0035144	0	1	0	UDP-glycosyltransferase 74E2 (1)	metabolic process [GO:0008152 biological_process] (1); transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	-	C_unshiu_00141_mRNA_7.1	-
GF0035143	0	1	0	Hypothetical protein (1)			-	C_unshiu_00141_mRNA_64.1	-
GF0035142	0	1	0	Hypothetical protein (1)			-	C_unshiu_00141_mRNA_63.1	-
GF0035141	0	1	0	Hypothetical protein (1)			-	C_unshiu_00141_mRNA_46.1	-
GF0035140	0	1	0	Hypothetical protein (1)		Solute-binding protein family 3/N-terminal domain of MltF [IPR001638] (1)	-	C_unshiu_00141_mRNA_30.1	-
GF0035139	0	1	0	UDP-glycosyltransferase 74E2 (1)	transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	-	C_unshiu_00141_mRNA_2.1	-
GF0035138	0	1	0	Putative non-LTR retroelement reverse transcriptase (1)	RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H domain [IPR002156] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00141_mRNA_11.1	-
GF0035137	0	1	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1)	Aspartic peptidase, active site [IPR001969] (1)	-	C_unshiu_00141_mRNA_1.1	-
GF0035136	0	1	0	Hypothetical protein (1)			-	C_unshiu_00140_mRNA_39.1	-
GF0035135	0	1	0	Hypothetical protein (1)			-	C_unshiu_00140_mRNA_38.1	-
GF0035134	0	1	0	Hypothetical protein (1)			-	C_unshiu_00140_mRNA_36.1	-
GF0035133	0	1	0	Hypothetical protein (1)			-	C_unshiu_00140_mRNA_2.1	-
GF0035132	0	1	0	Hypothetical protein (1)			-	C_unshiu_00140_mRNA_11.1	-
GF0035131	0	1	0	Hypothetical protein (1)		Protein of unknown function DUF597 [IPR006734] (1)	-	C_unshiu_00140_mRNA_1.1	-
GF0035130	0	1	0	Hypothetical protein (1)			-	C_unshiu_00139_mRNA_52.1	-
GF0035129	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_00139_mRNA_40.1	-
GF0035128	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_00138_mRNA_7.1	-
GF0035127	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_00138_mRNA_68.1	-
GF0035126	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Viral movement protein [IPR028919] (1)	-	C_unshiu_00138_mRNA_66.1	-
GF0035125	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00138_mRNA_64.1	-
GF0035124	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00138_mRNA_63.1	-
GF0035123	0	1	0	Hypothetical protein (1)			-	C_unshiu_00138_mRNA_62.1	-
GF0035122	0	1	0	Hypothetical protein (1)			-	C_unshiu_00138_mRNA_61.1	-
GF0035121	0	1	0	Hypothetical protein (1)			-	C_unshiu_00138_mRNA_60.1	-
GF0035120	0	1	0	Hypothetical protein (1)			-	C_unshiu_00138_mRNA_6.1	-
GF0035119	0	1	0	Hypothetical protein (1)			-	C_unshiu_00138_mRNA_59.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0035118	0	1	0	Hypothetical protein (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Peptidase A2A, retrovirus, catalytic [IPR001995] (1)	-	C_unshiu_00138_mRNA_58.1	-
GF0035117	0	1	0	Hypothetical protein (1)			-	C_unshiu_00138_mRNA_57.1	-
GF0035116	0	1	0	Hypothetical protein (1)			-	C_unshiu_00138_mRNA_55.1	-
GF0035115	0	1	0	Hypothetical protein (1)			-	C_unshiu_00138_mRNA_54.1	-
GF0035114	0	1	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1)	Aspartic peptidase domain [IPR021109] (1); Peptidase A2A, retrovirus, catalytic [IPR001995] (1); Reverse transcriptase domain [IPR000477] (1); Retropepsins [IPR018061] (1)	-	C_unshiu_00138_mRNA_52.1	-
GF0035113	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_00138_mRNA_50.1	-
GF0035112	0	1	0	Hypothetical protein (1)			-	C_unshiu_00138_mRNA_48.1	-
GF0035111	0	1	0	Hypothetical protein (1)			-	C_unshiu_00138_mRNA_47.1	-
GF0035110	0	1	0	Hypothetical protein (1)			-	C_unshiu_00138_mRNA_46.1	-
GF0035109	0	1	0	Hypothetical protein (1)			-	C_unshiu_00138_mRNA_45.1	-
GF0035108	0	1	0	Hypothetical protein (1)			-	C_unshiu_00138_mRNA_44.1	-
GF0035107	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Reverse transcriptase domain [IPR000477] (1); Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00138_mRNA_39.1	-
GF0035106	0	1	0	Hypothetical protein (1)			-	C_unshiu_00138_mRNA_36.1	-
GF0035105	0	1	0	PHD finger protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Zinc finger, PHD-finger [IPR019787] (1); Zinc finger, PHD-type [IPR001965] (1); Zinc finger, RING/FYVE/PHD-type [IPR013083] (1); Zinc finger, PHD-type, conserved site [IPR019786] (1); Zinc finger, FYVE/PHD-type [IPR011011] (1)	-	C_unshiu_00138_mRNA_35.1	-
GF0035104	0	1	0	Hypothetical protein (1)			-	C_unshiu_00138_mRNA_32.1	-
GF0035103	0	1	0	Hypothetical protein (1)			-	C_unshiu_00138_mRNA_28.1	-
GF0035102	0	1	0	Hypothetical protein (1)			-	C_unshiu_00138_mRNA_23.1	-
GF0035101	0	1	0	Hypothetical protein (1)			-	C_unshiu_00138_mRNA_22.1	-
GF0035100	0	1	0	Hypothetical protein (1)			-	C_unshiu_00138_mRNA_21.1	-
GF0035099	0	1	0	Hypothetical protein (1)			-	C_unshiu_00138_mRNA_2.1	-
GF0035098	0	1	0	Hypothetical protein (1)			-	C_unshiu_00138_mRNA_15.1	-
GF0035097	0	1	0	Hypothetical protein (1)			-	C_unshiu_00138_mRNA_13.1	-
GF0035096	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_00138_mRNA_12.1	-
GF0035095	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	F-box domain [IPR001810] (1)	-	C_unshiu_00137_mRNA_9.1	-
GF0035094	0	1	0	TRNA (Guanine(37)-N1)-methyltransferase 2 (1)		S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); SAM-dependent methyltransferase TRM5/TYW2-type [IPR030382] (1)	-	C_unshiu_00137_mRNA_8.1	-
GF0035093	0	1	0	Hypothetical protein (1)			-	C_unshiu_00137_mRNA_7.1	-
GF0035092	0	1	0	Hypothetical protein (1)	nucleus [GO:0005634 cellular_component] (1)	Cyclin-like [IPR013763] (1); Cyclin, C-terminal domain [IPR004367] (1)	-	C_unshiu_00137_mRNA_6.1	-
GF0035091	0	1	0	Hypothetical protein (1)			-	C_unshiu_00137_mRNA_49.1	-
GF0035090	0	1	0	Hypothetical protein (1)			-	C_unshiu_00137_mRNA_47.1	-
GF0035089	0	1	0	Hypothetical protein (1)			-	C_unshiu_00137_mRNA_46.1	-
GF0035088	0	1	0	Hypothetical protein (1)			-	C_unshiu_00137_mRNA_31.1	-
GF0035087	0	1	0	Hypothetical protein (1)			-	C_unshiu_00137_mRNA_3.1	-
GF0035086	0	1	0	Hypothetical protein (1)		Protein of unknown function wound-induced [IPR022251] (1)	-	C_unshiu_00137_mRNA_24.1	-
GF0035085	0	1	0	Hypothetical protein (1)			-	C_unshiu_00136_mRNA_37.1	-
GF0035084	0	1	0	Transmembrane emp24 domain-containing protein A (1)	transport [GO:0006810 biological_process] (1); integral component of membrane [GO:0016021 cellular_component] (1)	TMP21-related [IPR015720] (1); GOLD domain [IPR009038] (1)	-	C_unshiu_00136_mRNA_15.1	-
GF0035083	0	1	0	Hypothetical protein (1)			-	C_unshiu_00135_mRNA_57.1	-
GF0035082	0	1	0	Hypothetical protein (1)			-	C_unshiu_00135_mRNA_56.1	-
GF0035081	0	1	0	Hypothetical protein (1)			-	C_unshiu_00135_mRNA_53.1	-
GF0035080	0	1	0	Hypothetical protein (1)			-	C_unshiu_00135_mRNA_52.1	-
GF0035079	0	1	0	Hypothetical protein (1)			-	C_unshiu_00135_mRNA_5.1	-
GF0035078	0	1	0	Hypothetical protein (1)			-	C_unshiu_00135_mRNA_43.1	-
GF0035077	0	1	0	Hypothetical protein (1)		Ubiquitin-conjugating enzyme/RWD-like [IPR016135] (1); Ubiquitin-conjugating enzyme E2 [IPR000608] (1)	-	C_unshiu_00135_mRNA_41.1	-
GF0035076	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00135_mRNA_35.1	-
GF0035075	0	1	0	Hypothetical protein (1)			-	C_unshiu_00135_mRNA_2.1	-
GF0035074	0	1	0	Hypothetical protein (1)			-	C_unshiu_00135_mRNA_18.1	-
GF0035073	0	1	0	Hypothetical protein (1)	metal ion binding [GO:0046872 molecular_function] (1)	ZF-HD homeobox protein, Cys/His-rich dimerisation domain [IPR006456] (1); Zinc finger, C2H2 [IPR007087] (1)	-	C_unshiu_00135_mRNA_10.1	-
GF0035072	0	1	0	LRR receptor-like kinase family protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00134_mRNA_53.1	-
GF0035071	0	1	0	Acidic endochitinase (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1); hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (1)	Glycoside hydrolase, chitinase active site [IPR001579] (1); Glycoside hydrolase superfamily [IPR017853] (1); Glycoside hydrolase, catalytic domain [IPR013781] (1); Glycoside hydrolase family 18, catalytic domain [IPR001223] (1)	-	C_unshiu_00134_mRNA_47.1	-
GF0035070	0	1	0	ABC transporter (1)	transport [GO:0006810 biological_process] (1); integral component of membrane [GO:0016021 cellular_component] (1); ATP binding [GO:0005524 molecular_function] (1); transmembrane transport [GO:0055085 biological_process] (1); ATPase activity, coupled to transmembrane movement of substances [GO:0042626 molecular_function] (1)	ABC transporter type 1, transmembrane domain [IPR011527] (1)	-	C_unshiu_00134_mRNA_40.1	-
GF0035069	0	1	0	Hypothetical protein (1)			-	C_unshiu_00134_mRNA_26.1	-
GF0035068	0	1	0	Hypothetical protein (1)	membrane [GO:0016020 cellular_component] (1); ion channel activity [GO:0005216 molecular_function] (1); transmembrane transport [GO:0055085 biological_process] (1); ion transport [GO:0006811 biological_process] (1)	Cyclic nucleotide-binding domain [IPR000595] (1); Ion transport domain [IPR005821] (1); Cyclic nucleotide-binding-like [IPR018490] (1); RmlC-like jelly roll fold [IPR014710] (1)	-	C_unshiu_00134_mRNA_11.1	-
GF0035067	0	1	0	Hypothetical protein (1)		SGNH hydrolase-type esterase domain [IPR013830] (1)	-	C_unshiu_00133_mRNA_9.1	-
GF0035066	0	1	0	Hypothetical protein (1)			-	C_unshiu_00133_mRNA_62.1	-
GF0035065	0	1	0	Hypothetical protein (1)			-	C_unshiu_00133_mRNA_60.1	-
GF0035064	0	1	0	Hypothetical protein (1)		Gag-polypeptide of LTR copia-type [IPR029472] (1)	-	C_unshiu_00133_mRNA_58.1	-
GF0035063	0	1	0	Hypothetical protein (1)	electron carrier activity [GO:0009055 molecular_function] (1); iron-sulfur cluster binding [GO:0051536 molecular_function] (1)	Beta-grasp domain [IPR012675] (1); 2Fe-2S ferredoxin-type iron-sulfur binding domain [IPR001041] (1)	-	C_unshiu_00133_mRNA_54.1	-
GF0035062	0	1	0	ABC transporter B family member 15 (1)	transport [GO:0006810 biological_process] (1); integral component of membrane [GO:0016021 cellular_component] (1); ATPase activity [GO:0016887 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1); transmembrane transport [GO:0055085 biological_process] (1); ATPase activity, coupled to transmembrane movement of substances [GO:0042626 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); ABC transporter type 1, transmembrane domain [IPR011527] (1); ABC transporter-like [IPR003439] (1)	-	C_unshiu_00133_mRNA_53.1	-
GF0035061	0	1	0	Hypothetical protein (1)			-	C_unshiu_00133_mRNA_52.1	-
GF0035060	0	1	0	Hypothetical protein (1)			-	C_unshiu_00133_mRNA_48.1	-
GF0035059	0	1	0	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1)	Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450 [IPR001128] (1)	-	C_unshiu_00133_mRNA_34.1	-
GF0035058	0	1	0	Hypothetical protein (1)			-	C_unshiu_00133_mRNA_32.1	-
GF0035057	0	1	0	Hypothetical protein (1)			-	C_unshiu_00133_mRNA_30.1	-
GF0035056	0	1	0	Hypothetical protein (1)	binding [GO:0005488 molecular_function] (1)	Armadillo-type fold [IPR016024] (1); Cell morphogenesis protein C-terminal [IPR025481] (1); Cell morphogenesis central region [IPR029473] (1)	-	C_unshiu_00133_mRNA_20.1	-
GF0035055	0	1	0	Hypothetical protein (1)			-	C_unshiu_00133_mRNA_17.1	-
GF0035054	0	1	0	Hypothetical protein (1)			-	C_unshiu_00132_mRNA_31.1	-
GF0035053	0	1	0	Hypothetical protein (1)			-	C_unshiu_00132_mRNA_24.1	-
GF0035052	0	1	0	Potassium channel AKT1 (1)	protein binding [GO:0005515 molecular_function] (1)	Cyclic nucleotide-binding-like [IPR018490] (1); Ankyrin repeat [IPR002110] (1); KHA domain [IPR021789] (1); RmlC-like jelly roll fold [IPR014710] (1); Cyclic nucleotide-binding domain [IPR000595] (1); Ankyrin repeat-containing domain [IPR020683] (1)	-	C_unshiu_00132_mRNA_21.1	-
GF0035051	0	1	0	Hypothetical protein (1)			-	C_unshiu_00132_mRNA_19.1	-
GF0035050	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00132_mRNA_18.1	-
GF0035049	0	1	0	Hypothetical protein (1)			-	C_unshiu_00132_mRNA_16.1	-
GF0035048	0	1	0	Hypothetical protein (1)			-	C_unshiu_00132_mRNA_12.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0035047	0	1	0	L-type lectin-domain containing receptor kinase IV.1 (1)	ATP binding [GO:0005524 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); carbohydrate binding [GO:0030246 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1)	Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase, ATP binding site [IPR017441] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Legume lectin domain [IPR001220] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	-	C_unshiu_00131_mRNA_6.1	-
GF0035046	0	1	0	Hypothetical protein (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); FAD binding [GO:0071949 molecular_function] (1)	FAD/NAD(P)-binding domain [IPR023753] (1); FAD-binding domain [IPR002938] (1)	-	C_unshiu_00131_mRNA_59.1	-
GF0035045	0	1	0	Hypothetical protein (1)			-	C_unshiu_00131_mRNA_5.1	-
GF0035044	0	1	0	DNA repair protein rhp7 (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, cysteine-containing subtype [IPR006553] (1)	-	C_unshiu_00131_mRNA_41.1	-
GF0035043	0	1	0	Putative transporter MCH1 (1)		Major facilitator superfamily domain [IPR020846] (1); Nodulin-like [IPR010658] (1)	-	C_unshiu_00131_mRNA_40.1	-
GF0035042	0	1	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_00131_mRNA_4.1	-
GF0035041	0	1	0	Hypothetical protein (1)			-	C_unshiu_00131_mRNA_2.1	-
GF0035040	0	1	0	Hypothetical protein (1)			-	C_unshiu_00131_mRNA_15.1	-
GF0035039	0	1	0	Hypothetical protein (1)			-	C_unshiu_00131_mRNA_12.1	-
GF0035038	0	1	0	Hypothetical protein (1)	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances [GO:0016820 molecular_function] (1); ATP hydrolysis coupled proton transport [GO:0015991 biological_process] (1); binding [GO:0005488 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); vacuolar proton-transporting V-type ATPase, V1 domain [GO:0000221 cellular_component] (1); proton-transporting ATPase activity, rotational mechanism [GO:0046961 molecular_function] (1)	ATPase, V1 complex, subunit H, C-terminal [IPR011987] (1); Cytochrome b5, heme-binding site [IPR018506] (1); Armadillo-type fold [IPR016024] (1); ATPase, V1 complex, subunit H [IPR004908] (1); Armadillo-like helical [IPR011989] (1)	-	C_unshiu_00130_mRNA_61.1	-
GF0035037	0	1	0	Hypothetical protein (1)			-	C_unshiu_00130_mRNA_6.1	-
GF0035036	0	1	0	Hypothetical protein (1)			-	C_unshiu_00130_mRNA_49.1	-
GF0035035	0	1	0	Hypothetical protein (1)			-	C_unshiu_00130_mRNA_46.1	-
GF0035034	0	1	0	Hypothetical protein (1)			-	C_unshiu_00130_mRNA_4.1	-
GF0035033	0	1	0	Pentatricopeptide repeat-containing protein At1g31790 (1)		Pentatricopeptide repeat [IPR002885] (1)	-	C_unshiu_00130_mRNA_25.1	-
GF0035032	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc knuckle CX2CX4HX4C [IPR025836] (1); Zinc finger, CCHC-type [IPR001878] (1); Endonuclease/exonuclease/phosphatase [IPR005135] (1); Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_00130_mRNA_21.1	-
GF0035031	0	1	0	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	C_unshiu_00130_mRNA_20.1	-
GF0035030	0	1	0	Hypothetical protein (1)			-	C_unshiu_00129_mRNA_6.1	-
GF0035029	0	1	0	Hypothetical protein (1)			-	C_unshiu_00129_mRNA_42.1	-
GF0035028	0	1	0	GDP-mannose transporter GONST3 (1)		Sugar phosphate transporter domain [IPR004853] (1)	-	C_unshiu_00129_mRNA_25.1	-
GF0035027	0	1	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1)	Aspartic peptidase domain [IPR021109] (1); Xylanase inhibitor, C-terminal [IPR032799] (1); Aspartic peptidase A1 family [IPR001461] (1)	-	C_unshiu_00129_mRNA_2.1	-
GF0035026	0	1	0	Hypothetical protein (1)			-	C_unshiu_00129_mRNA_15.1	-
GF0035025	0	1	0	Hypothetical protein (1)			-	C_unshiu_00128_mRNA_8.1	-
GF0035024	0	1	0	Hypothetical protein (1)			-	C_unshiu_00128_mRNA_6.1	-
GF0035023	0	1	0	Hypothetical protein (1)			-	C_unshiu_00128_mRNA_51.1	-
GF0035022	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Transposase-associated domain [IPR029480] (1); Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00128_mRNA_45.1	-
GF0035021	0	1	0	Hypothetical protein (1)			-	C_unshiu_00128_mRNA_42.1	-
GF0035020	0	1	0	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein, putative (1)	lipid binding [GO:0008289 molecular_function] (1); lipid transport [GO:0006869 biological_process] (1)	Plant lipid transfer protein/Par allergen [IPR000528] (1); Bifunctional inhibitor/plant lipid transfer protein/seed storage helical domain [IPR016140] (1)	-	C_unshiu_00128_mRNA_39.1	-
GF0035019	0	1	0	Hypothetical protein (1)			-	C_unshiu_00128_mRNA_38.1	-
GF0035018	0	1	0	Hypothetical protein (1)			-	C_unshiu_00128_mRNA_37.1	-
GF0035017	0	1	0	Hypothetical protein (1)			-	C_unshiu_00128_mRNA_36.1	-
GF0035016	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1); zinc ion binding [GO:0008270 molecular_function] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1)	Peptidase A2A, retrovirus, catalytic [IPR001995] (1); Retropepsins [IPR018061] (1); Zinc finger, CCHC-type [IPR001878] (1); Aspartic peptidase domain [IPR021109] (1)	-	C_unshiu_00128_mRNA_35.1	-
GF0035015	0	1	0	Hypothetical protein (1)			-	C_unshiu_00128_mRNA_32.1	-
GF0035014	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_00128_mRNA_23.1	-
GF0035013	0	1	0	Hypothetical protein (1)			-	C_unshiu_00128_mRNA_22.1	-
GF0035012	0	1	0	Hypothetical protein (1)			-	C_unshiu_00128_mRNA_21.1	-
GF0035011	0	1	0	Hypothetical protein (1)			-	C_unshiu_00128_mRNA_17.1	-
GF0035010	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_00128_mRNA_13.1	-
GF0035009	0	1	0	Hypothetical protein (1)			-	C_unshiu_00128_mRNA_1.1	-
GF0035008	0	1	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_00127_mRNA_7.1	-
GF0035007	0	1	0	Hypothetical protein (1)			-	C_unshiu_00127_mRNA_6.1	-
GF0035006	0	1	0	Phenylcoumaran benzylic ether reductase (1)		NAD(P)-binding domain [IPR016040] (1); NmrA-like domain [IPR008030] (1)	-	C_unshiu_00127_mRNA_51.1	-
GF0035005	0	1	0	Hypothetical protein (1)	metal ion transport [GO:0030001 biological_process] (1); metal ion binding [GO:0046872 molecular_function] (1)	Heavy metal-associated domain, HMA [IPR006121] (1)	-	C_unshiu_00127_mRNA_37.1	-
GF0035004	0	1	0	Hypothetical protein (1)			-	C_unshiu_00127_mRNA_20.1	-
GF0035003	0	1	0	Hypothetical protein (1)			-	C_unshiu_00127_mRNA_19.1	-
GF0035002	0	1	0	Hypothetical protein (1)			-	C_unshiu_00127_mRNA_18.1	-
GF0035001	0	1	0	Hypothetical protein (1)			-	C_unshiu_00127_mRNA_17.1	-
GF0035000	0	1	0	Hypothetical protein (1)			-	C_unshiu_00127_mRNA_16.1	-
GF0034999	0	1	0	Hypothetical protein (1)			-	C_unshiu_00127_mRNA_15.1	-
GF0034998	0	1	0	Hypothetical protein (1)			-	C_unshiu_00127_mRNA_12.1	-
GF0034997	0	1	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	Zinc finger, BED-type [IPR003656] (1)	-	C_unshiu_00126_mRNA_53.1	-
GF0034996	0	1	0	Hypothetical protein (1)	metabolic process [GO:0008152 biological_process] (1); oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor [GO:0016616 molecular_function] (1); NAD binding [GO:0051287 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	D-isomer specific 2-hydroxyacid dehydrogenase, catalytic domain [IPR006139] (1); Isopenicillin N synthase-like [IPR027443] (1); NAD(P)-binding domain [IPR016040] (1)	-	C_unshiu_00126_mRNA_29.1	-
GF0034995	0	1	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); serine-type endopeptidase activity [GO:0004252 molecular_function] (1)	Peptidase S8 propeptide/proteinase inhibitor I9 [IPR010259] (1); Peptidase S8, subtilisin, Ser-active site [IPR023828] (1); Peptidase S8, subtilisin-related [IPR015500] (1); Peptidase S8/S53 domain [IPR000209] (1)	-	C_unshiu_00126_mRNA_22.1	-
GF0034994	0	1	0	Adenosine 3'-phospho 5'-phosphosulfate transporter 2 (1)	ATP binding [GO:0005524 molecular_function] (1); transmembrane transport [GO:0055085 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1)	UAA transporter [IPR013657] (1); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1)	-	C_unshiu_00126_mRNA_16.1	-
GF0034993	0	1	0	Hypothetical protein (1)			-	C_unshiu_00125_mRNA_8.1	-
GF0034992	0	1	0	Hypothetical protein (1)			-	C_unshiu_00125_mRNA_7.1	-
GF0034991	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00125_mRNA_68.1	-
GF0034990	0	1	0	Hypothetical protein (1)			-	C_unshiu_00125_mRNA_6.1	-
GF0034989	0	1	0	Monosacharide transport protein (1)			-	C_unshiu_00125_mRNA_4.1	-
GF0034988	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_00125_mRNA_27.1	-
GF0034987	0	1	0	Hypothetical protein (1)			-	C_unshiu_00125_mRNA_11.1	-
GF0034986	0	1	0	Adenylyltransferase and sulfurtransferase (1)	small protein activating enzyme activity [GO:0008641 molecular_function] (1)	NAD(P)-binding domain [IPR016040] (1); THIF-type NAD/FAD binding fold [IPR000594] (1)	-	C_unshiu_00125_mRNA_1.1	-
GF0034985	0	1	0	Hypothetical protein (1)			-	C_unshiu_00124_mRNA_9.1	-
GF0034984	0	1	0	Hypothetical protein (1)			-	C_unshiu_00124_mRNA_6.1	-
GF0034983	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Cohesin loading factor [IPR019440] (1); Tetratricopeptide-like helical domain [IPR011990] (1)	-	C_unshiu_00124_mRNA_41.1	-
GF0034982	0	1	0	Hypothetical protein (1)			-	C_unshiu_00124_mRNA_4.1	-
GF0034981	0	1	0	Hypothetical protein (1)			-	C_unshiu_00124_mRNA_38.1	-
GF0034980	0	1	0	Retrotransposon protein, putative, Ty1-copia subclass (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); GAG-pre-integrase domain [IPR025724] (1)	-	C_unshiu_00124_mRNA_36.1	-
GF0034979	0	1	0	Hypothetical protein (1)			-	C_unshiu_00124_mRNA_34.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0034978	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	-	C_unshiu_00124_mRNA_32.1	-
GF0034977	0	1	0	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	C_unshiu_00124_mRNA_31.1	-
GF0034976	0	1	0	Hypothetical protein (1)			-	C_unshiu_00124_mRNA_24.1	-
GF0034975	0	1	0	Hypothetical protein (1)			-	C_unshiu_00124_mRNA_22.1	-
GF0034974	0	1	0	Hypothetical protein (1)		S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	C_unshiu_00124_mRNA_21.1	-
GF0034973	0	1	0	Hypothetical protein (1)			-	C_unshiu_00124_mRNA_18.1	-
GF0034972	0	1	0	Nucleolar GTP-binding protein 1 (1)	GTP binding [GO:0005525 molecular_function] (1)	NOG, C-terminal [IPR012973] (1); GTP binding domain [IPR006073] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00124_mRNA_17.1	-
GF0034971	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00123_mRNA_62.1	-
GF0034970	0	1	0	Hypothetical protein (1)	intracellular [GO:0005622 cellular_component] (1); translation [GO:0006412 biological_process] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1); ribosome [GO:0005840 cellular_component] (1)	Ribosomal protein L27 [IPR001684] (1)	-	C_unshiu_00123_mRNA_59.1	-
GF0034969	0	1	0	Hypothetical protein (1)			-	C_unshiu_00123_mRNA_57.1	-
GF0034968	0	1	0	Hypothetical protein (1)			-	C_unshiu_00123_mRNA_56.1	-
GF0034967	0	1	0	Flavodoxin family protein / radical SAM domain-containing protein isoform 1 (1)	iron-sulfur cluster binding [GO:0051536 molecular_function] (1); catalytic activity [GO:0003824 molecular_function] (1)	Aldolase-type TIM barrel [IPR013785] (1); tRNA wybutosine-synthesis [IPR013917] (1); Radical SAM [IPR007197] (1); Flavoprotein-like domain [IPR029039] (1)	-	C_unshiu_00123_mRNA_51.1	-
GF0034966	0	1	0	Hypothetical protein (1)			-	C_unshiu_00123_mRNA_47.1	-
GF0034965	0	1	0	Hypothetical protein (1)		Protein of unknown function DUF620 [IPR006873] (1)	-	C_unshiu_00123_mRNA_42.1	-
GF0034964	0	1	0	Hypothetical protein (1)			-	C_unshiu_00123_mRNA_33.1	-
GF0034963	0	1	0	Hypothetical protein (1)			-	C_unshiu_00123_mRNA_32.1	-
GF0034962	0	1	0	Hypothetical protein (1)			-	C_unshiu_00123_mRNA_29.1	-
GF0034961	0	1	0	Hypothetical protein (1)			-	C_unshiu_00123_mRNA_28.1	-
GF0034960	0	1	0	Hypothetical protein (1)			-	C_unshiu_00123_mRNA_27.1	-
GF0034959	0	1	0	Hypothetical protein (1)	nucleus [GO:0005634 cellular_component] (1)	YLP motif-containing protein 1 [IPR026314] (1)	-	C_unshiu_00123_mRNA_26.1	-
GF0034958	0	1	0	Hypothetical protein (1)			-	C_unshiu_00123_mRNA_19.1	-
GF0034957	0	1	0	Hypothetical protein (1)			-	C_unshiu_00123_mRNA_10.1	-
GF0034956	0	1	0	Hypothetical protein (1)			-	C_unshiu_00123_mRNA_1.1	-
GF0034955	0	1	0	Hypothetical protein (1)			-	C_unshiu_00122_mRNA_4.1	-
GF0034954	0	1	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); zinc ion binding [GO:0008270 molecular_function] (1)	FAR1 DNA binding domain [IPR004330] (1); FHY3/FAR1 family [IPR031052] (1); Zinc finger, SWIM-type [IPR007527] (1)	-	C_unshiu_00122_mRNA_38.1	-
GF0034953	0	1	0	Hypothetical protein (1)			-	C_unshiu_00122_mRNA_27.1	-
GF0034952	0	1	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_00122_mRNA_21.1	-
GF0034951	0	1	0	Hypothetical protein (1)			-	C_unshiu_00122_mRNA_17.1	-
GF0034950	0	1	0	Hypothetical protein (1)			-	C_unshiu_00122_mRNA_1.1	-
GF0034949	0	1	0	Hypothetical protein (1)			-	C_unshiu_00121_mRNA_8.1	-
GF0034948	0	1	0	Hypothetical protein (1)	metal ion binding [GO:0046872 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ubiquitin-conjugating enzyme E2 [IPR000608] (1); Zinc finger, C2H2 [IPR007087] (1); Ubiquitin-conjugating enzyme/RWD-like [IPR016135] (1); Zinc finger C2H2-type/integrase DNA-binding domain [IPR013087] (1)	-	C_unshiu_00121_mRNA_49.1	-
GF0034947	0	1	0	Phosphatidylinositol N-acetylglucosaminyltransferase subunit Q (1)	GPI anchor biosynthetic process [GO:0006506 biological_process] (1); phosphatidylinositol N-acetylglucosaminyltransferase activity [GO:0017176 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1)	N-acetylglucosaminyl transferase component [IPR007720] (1)	-	C_unshiu_00121_mRNA_48.1	-
GF0034946	0	1	0	Hypothetical protein (1)		Protein of unknown function DUF2343 [IPR018786] (1)	-	C_unshiu_00121_mRNA_42.1	-
GF0034945	0	1	0	Hypothetical protein (1)			-	C_unshiu_00121_mRNA_4.1	-
GF0034944	0	1	0	Hypothetical protein (1)			-	C_unshiu_00121_mRNA_38.1	-
GF0034943	0	1	0	Plasma membrane ATPase (1)	ATPase activity [GO:0016887 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1); metal ion binding [GO:0046872 molecular_function] (1); ATP biosynthetic process [GO:0006754 biological_process] (1); nucleotide binding [GO:0000166 molecular_function] (1)	P-type ATPase, transmembrane domain [IPR023298] (1); P-type ATPase, cytoplasmic domain N [IPR023299] (1); P-type ATPase [IPR001757] (1); P-type ATPase, phosphorylation site [IPR018303] (1); P-type ATPase, subfamily IIIA [IPR006534] (1); Cation-transporting P-type ATPase, N-terminal [IPR004014] (1); HAD-like domain [IPR023214] (1); P-type ATPase, A domain [IPR008250] (1)	-	C_unshiu_00121_mRNA_36.1	-
GF0034942	0	1	0	Hypothetical protein (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase, ATP binding site [IPR017441] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Protein kinase domain [IPR000719] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Malectin-like carbohydrate-binding domain [IPR024788] (1); Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_00121_mRNA_35.1	-
GF0034941	0	1	0	Hypothetical protein (1)			-	C_unshiu_00121_mRNA_3.1	-
GF0034940	0	1	0	Serine-threonine kinase STK15 (1)	ATP binding [GO:0005524 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Malectin-like carbohydrate-binding domain [IPR024788] (1); Protein kinase, ATP binding site [IPR017441] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1)	-	C_unshiu_00121_mRNA_29.1	-
GF0034939	0	1	0	Hypothetical protein (1)			-	C_unshiu_00121_mRNA_22.1	-
GF0034938	0	1	0	Hypothetical protein (1)			-	C_unshiu_00121_mRNA_21.1	-
GF0034937	0	1	0	Stem 28 kDa glycoprotein (1)		Acid phosphatase, class B-like [IPR005519] (1); HAD-like domain [IPR023214] (1)	-	C_unshiu_00121_mRNA_2.1	-
GF0034936	0	1	0	Hypothetical protein (1)	nucleotide binding [GO:0000166 molecular_function] (1)	Nucleotide-binding alpha-beta plait domain [IPR012677] (1)	-	C_unshiu_00121_mRNA_12.1	-
GF0034935	0	1	0	Hypothetical protein (1)			-	C_unshiu_00121_mRNA_10.1	-
GF0034934	0	1	0	Hypothetical protein (1)			-	C_unshiu_00121_mRNA_1.1	-
GF0034933	0	1	0	Hypothetical protein (1)			-	C_unshiu_00120_mRNA_7.1	-
GF0034932	0	1	0	Hypothetical protein (1)			-	C_unshiu_00120_mRNA_63.1	-
GF0034931	0	1	0	Hypothetical protein (1)			-	C_unshiu_00120_mRNA_6.1	-
GF0034930	0	1	0	Hypothetical protein (1)			-	C_unshiu_00120_mRNA_59.1	-
GF0034929	0	1	0	NADH-ubiquinone oxidoreductase chain 1 (1)	oxidation-reduction process [GO:0055114 biological_process] (1); membrane [GO:0016020 cellular_component] (1)	NADH:ubiquinone oxidoreductase, subunit 1/F420H2 oxidoreductase subunit H [IPR001694] (1)	-	C_unshiu_00120_mRNA_51.1	-
GF0034928	0	1	0	NADH-ubiquinone oxidoreductase chain 1 (1)	oxidation-reduction process [GO:0055114 biological_process] (1); membrane [GO:0016020 cellular_component] (1)	NADH:ubiquinone oxidoreductase, subunit 1/F420H2 oxidoreductase subunit H [IPR001694] (1)	-	C_unshiu_00120_mRNA_50.1	-
GF0034927	0	1	0	Hypothetical protein (1)			-	C_unshiu_00120_mRNA_5.1	-
GF0034926	0	1	0	Hypothetical protein (1)			-	C_unshiu_00120_mRNA_48.1	-
GF0034925	0	1	0	Hypothetical protein (1)	heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1)	Cytochrome P450 [IPR001128] (1); Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_00120_mRNA_46.1	-
GF0034924	0	1	0	Cytochrome P450 (1)	iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Cytochrome P450 [IPR001128] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1); Cytochrome P450, E-class, group I [IPR002401] (1)	-	C_unshiu_00120_mRNA_44.1	-
GF0034923	0	1	0	Hypothetical protein (1)			-	C_unshiu_00120_mRNA_3.1	-
GF0034922	0	1	0	Hypothetical protein (1)			-	C_unshiu_00120_mRNA_22.1	-
GF0034921	0	1	0	60S ribosomal protein L27a (1)	structural constituent of ribosome [GO:0003735 molecular_function] (1); large ribosomal subunit [GO:0015934 cellular_component] (1); translation [GO:0006412 biological_process] (1); intracellular [GO:0005622 cellular_component] (1); ribosome [GO:0005840 cellular_component] (1)	Ribosomal protein L18e/L15P [IPR021131] (1); Ribosomal protein L15, conserved site [IPR001196] (1); Ribosomal protein L15 [IPR030878] (1)	-	C_unshiu_00120_mRNA_16.1	-
GF0034920	0	1	0	Transcription factor MYB86 (1)	DNA binding [GO:0003677 molecular_function] (1)	SANT/Myb domain [IPR001005] (1); Homeodomain-like [IPR009057] (1); Myb domain [IPR017930] (1)	-	C_unshiu_00120_mRNA_12.1	-
GF0034919	0	1	0	Hypothetical protein (1)			-	C_unshiu_00119_mRNA_40.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0034918	0	1	0	BED zinc finger,hAT family dimerization domain (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00119_mRNA_37.1	-
GF0034917	0	1	0	Hypothetical protein (1)			-	C_unshiu_00119_mRNA_31.1	-
GF0034916	0	1	0	Wall-associated receptor kinase 2 (1)	polysaccharide binding [GO:0030247 molecular_function] (1)	Wall-associated receptor kinase, galacturonan-binding domain [IPR025287] (1)	-	C_unshiu_00119_mRNA_21.1	-
GF0034915	0	1	0	MATE efflux family protein 1 (1)	transmembrane transport [GO:0055085 biological_process] (1); drug transmembrane transport [GO:0006855 biological_process] (1); membrane [GO:0016020 cellular_component] (1); drug transmembrane transporter activity [GO:0015238 molecular_function] (1); antiporter activity [GO:0015297 molecular_function] (1)	Multi antimicrobial extrusion protein [IPR002528] (1)	-	C_unshiu_00119_mRNA_17.1	-
GF0034914	0	1	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); DNA binding [GO:0003677 molecular_function] (1)	NAC domain [IPR003441] (1)	-	C_unshiu_00119_mRNA_15.1	-
GF0034913	0	1	0	NAC domain-containing protein 67 (1)	DNA binding [GO:0003677 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	NAC domain [IPR003441] (1)	-	C_unshiu_00119_mRNA_14.1	-
GF0034912	0	1	0	Hypothetical protein (1)			-	C_unshiu_00119_mRNA_13.1	-
GF0034911	0	1	0	Hypothetical protein (1)			-	C_unshiu_00118_mRNA_9.1	-
GF0034910	0	1	0	Hypothetical protein (1)			-	C_unshiu_00118_mRNA_70.1	-
GF0034909	0	1	0	Hypothetical protein (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Peptidase A2A, retrovirus, catalytic [IPR001995] (1); Retropepsins [IPR018061] (1); Aspartic peptidase domain [IPR021109] (1)	-	C_unshiu_00118_mRNA_7.1	-
GF0034908	0	1	0	Hypothetical protein (1)			-	C_unshiu_00118_mRNA_6.1	-
GF0034907	0	1	0	Hypothetical protein (1)			-	C_unshiu_00118_mRNA_53.1	-
GF0034906	0	1	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_00118_mRNA_47.1	-
GF0034905	0	1	0	Hypothetical protein (1)			-	C_unshiu_00118_mRNA_36.1	-
GF0034904	0	1	0	Hypothetical protein (1)			-	C_unshiu_00118_mRNA_35.1	-
GF0034903	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1); zinc ion binding [GO:0008270 molecular_function] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Peptidase A2A, retrovirus, catalytic [IPR001995] (1)	-	C_unshiu_00118_mRNA_30.1	-
GF0034902	0	1	0	Hypothetical protein (1)			-	C_unshiu_00118_mRNA_14.1	-
GF0034901	0	1	0	Hypothetical protein (1)			-	C_unshiu_00118_mRNA_13.1	-
GF0034900	0	1	0	Hypothetical protein (1)			-	C_unshiu_00118_mRNA_10.1	-
GF0034899	0	1	0	Hypothetical protein (1)			-	C_unshiu_00117_mRNA_77.1	-
GF0034898	0	1	0	Hypothetical protein (1)			-	C_unshiu_00117_mRNA_76.1	-
GF0034897	0	1	0	MATE efflux family protein 4, chloroplastic (1)	transmembrane transport [GO:0055085 biological_process] (1); drug transmembrane transport [GO:0006855 biological_process] (1); drug transmembrane transporter activity [GO:0015238 molecular_function] (1); antiporter activity [GO:0015297 molecular_function] (1); membrane [GO:0016020 cellular_component] (1)	Multi antimicrobial extrusion protein [IPR002528] (1)	-	C_unshiu_00117_mRNA_74.1	-
GF0034896	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF1985 [IPR015410] (1)	-	C_unshiu_00117_mRNA_71.1	-
GF0034895	0	1	0	Hypothetical protein (1)			-	C_unshiu_00117_mRNA_47.1	-
GF0034894	0	1	0	Hypothetical protein (1)			-	C_unshiu_00117_mRNA_46.1	-
GF0034893	0	1	0	Hypothetical protein (1)	transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Reverse transcriptase zinc-binding domain [IPR026960] (1); UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	-	C_unshiu_00117_mRNA_41.1	-
GF0034892	0	1	0	Hypothetical protein (1)		Peptidase S8, subtilisin-related [IPR015500] (1)	-	C_unshiu_00117_mRNA_40.1	-
GF0034891	0	1	0	Hypothetical protein (1)			-	C_unshiu_00117_mRNA_23.1	-
GF0034890	0	1	0	Hypothetical protein (1)	integral component of membrane [GO:0016021 cellular_component] (1); copper ion transmembrane transport [GO:0035434 biological_process] (1); copper ion transmembrane transporter activity [GO:0005375 molecular_function] (1)	Ctr copper transporter [IPR007274] (1)	-	C_unshiu_00117_mRNA_21.1	-
GF0034889	0	1	0	Hypothetical protein (1)			-	C_unshiu_00117_mRNA_20.1	-
GF0034888	0	1	0	Pathogenesis-related maize seed protein (1)	extracellular region [GO:0005576 cellular_component] (1)	Ves allergen [IPR002413] (1); Allergen V5/Tpx-1-related, conserved site [IPR018244] (1); Cysteine-rich secretory protein, allergen V5/Tpx-1-related [IPR001283] (1); CAP domain [IPR014044] (1)	-	C_unshiu_00116_mRNA_7.1	-
GF0034887	0	1	0	Hypothetical protein (1)			-	C_unshiu_00116_mRNA_60.1	-
GF0034886	0	1	0	LOB domain-containing protein 1 (1)		Lateral organ boundaries, LOB [IPR004883] (1)	-	C_unshiu_00116_mRNA_3.1	-
GF0034885	0	1	0	Hypothetical protein (1)			-	C_unshiu_00116_mRNA_27.1	-
GF0034884	0	1	0	DNA-directed RNA polymerase (1)	DNA binding [GO:0003677 molecular_function] (1); nucleus [GO:0005634 cellular_component] (1); DNA-directed RNA polymerase activity [GO:0003899 molecular_function] (1); transcription, DNA-templated [GO:0006351 biological_process] (1); zinc ion binding [GO:0008270 molecular_function] (1)	RNA polymerase Rpb1, domain 5 [IPR007081] (1); DNA-directed RNA pol I, largest subunit [IPR015699] (1)	-	C_unshiu_00115_mRNA_55.1	-
GF0034883	0	1	0	Hypothetical protein (1)			-	C_unshiu_00115_mRNA_45.1	-
GF0034882	0	1	0	Chaperone protein dnaJ 6 (1)		DnaJ domain [IPR001623] (1)	-	C_unshiu_00115_mRNA_41.1	-
GF0034881	0	1	0	Hypothetical protein (1)			-	C_unshiu_00115_mRNA_34.1	-
GF0034880	0	1	0	Hypothetical protein (1)			-	C_unshiu_00115_mRNA_33.1	-
GF0034879	0	1	0	Hypothetical protein (1)			-	C_unshiu_00115_mRNA_27.1	-
GF0034878	0	1	0	Uroporphyrinogen decarboxylase (1)	uroporphyrinogen decarboxylase activity [GO:0004853 molecular_function] (1); porphyrin-containing compound biosynthetic process [GO:0006779 biological_process] (1)	Uroporphyrinogen decarboxylase (URO-D) [IPR000257] (1)	-	C_unshiu_00115_mRNA_1.1	-
GF0034877	0	1	0	Hypothetical protein (1)			-	C_unshiu_00114_mRNA_9.1	-
GF0034876	0	1	0	Hypothetical protein (1)			-	C_unshiu_00114_mRNA_7.1	-
GF0034875	0	1	0	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_00114_mRNA_45.1	-
GF0034874	0	1	0	Hypothetical protein (1)			-	C_unshiu_00114_mRNA_39.1	-
GF0034873	0	1	0	Hypothetical protein (1)			-	C_unshiu_00114_mRNA_35.1	-
GF0034872	0	1	0	Hypothetical protein (1)			-	C_unshiu_00114_mRNA_11.1	-
GF0034871	0	1	0	Hypothetical protein (1)			-	C_unshiu_00114_mRNA_1.1	-
GF0034870	0	1	0	Hypothetical protein (1)			-	C_unshiu_00113_mRNA_9.1	-
GF0034869	0	1	0	Hypothetical protein (1)			-	C_unshiu_00113_mRNA_7.1	-
GF0034868	0	1	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00113_mRNA_6.1	-
GF0034867	0	1	0	Glucan endo-1,3-beta-glucosidase 8 (1)	hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1)	X8 domain [IPR012946] (1); Glycoside hydrolase, catalytic domain [IPR013781] (1); Glycoside hydrolase superfamily [IPR017853] (1); Glycoside hydrolase family 17 [IPR000490] (1)	-	C_unshiu_00113_mRNA_52.1	-
GF0034866	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	C2 domain [IPR000008] (1)	-	C_unshiu_00113_mRNA_44.1	-
GF0034865	0	1	0	Ankyrin repeat family protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat-containing domain [IPR020683] (1); PGG domain [IPR026961] (1); Ankyrin repeat [IPR002110] (1)	-	C_unshiu_00113_mRNA_42.1	-
GF0034864	0	1	0	Ankyrin repeat family protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat-containing domain [IPR020683] (1); Ankyrin repeat [IPR002110] (1)	-	C_unshiu_00113_mRNA_36.1	-
GF0034863	0	1	0	Glutamate dehydrogenase (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); cellular amino acid metabolic process [GO:0006520 biological_process] (1)	Glutamate/phenylalanine/leucine/valine dehydrogenase, C-terminal [IPR006096] (1); NAD(P)-binding domain [IPR016040] (1); Glutamate/phenylalanine/leucine/valine dehydrogenase, dimerisation domain [IPR006097] (1); Glutamate/phenylalanine/leucine/valine dehydrogenase [IPR006095] (1)	-	C_unshiu_00113_mRNA_34.1	-
GF0034862	0	1	0	Hypothetical protein (1)			-	C_unshiu_00113_mRNA_21.1	-
GF0034861	0	1	0	Hypothetical protein (1)			-	C_unshiu_00113_mRNA_10.1	-
GF0034860	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, SWIM-type [IPR007527] (1); Zinc finger, PMZ-type [IPR006564] (1)	-	C_unshiu_00113_mRNA_1.1	-
GF0034859	0	1	0	Leguminosin group486 secreted peptide (1)		Plant self-incompatibility S1 [IPR010264] (1)	-	C_unshiu_00112_mRNA_52.1	-
GF0034858	0	1	0	Hypothetical protein (1)			-	C_unshiu_00112_mRNA_47.1	-
GF0034857	0	1	0	Disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); DDRGK domain containing protein [IPR019153] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1)	-	C_unshiu_00112_mRNA_46.1	-
GF0034856	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	F-box domain [IPR001810] (1)	-	C_unshiu_00112_mRNA_23.1	-
GF0034855	0	1	0	Hypothetical protein (1)			-	C_unshiu_00112_mRNA_22.1	-
GF0034854	0	1	0	Hemopexin (1)			-	C_unshiu_00112_mRNA_20.1	-
GF0034853	0	1	0	Ankyrin repeat family protein, putative (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat-containing domain [IPR020683] (1); PGG domain [IPR026961] (1); Ankyrin repeat [IPR002110] (1)	-	C_unshiu_00112_mRNA_19.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0034852	0	1	0	Ankyrin repeat family protein, putative (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat [IPR002110] (1); Ankyrin repeat-containing domain [IPR020683] (1)	-	C_unshiu_00112_mRNA_17.1	-
GF0034851	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	F-box domain [IPR001810] (1)	-	C_unshiu_00112_mRNA_14.1	-
GF0034850	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	F-box domain [IPR001810] (1)	-	C_unshiu_00112_mRNA_13.1	-
GF0034849	0	1	0	Hypothetical protein (1)		GAG-pre-integrase domain [IPR025724] (1); Gag-polypeptide of LTR copia-type [IPR029472] (1)	-	C_unshiu_00112_mRNA_12.1	-
GF0034848	0	1	0	Ankyrin repeat family protein, putative (1)	protein binding [GO:0005515 molecular_function] (1)	PGG domain [IPR026961] (1); Ankyrin repeat-containing domain [IPR020683] (1); Ankyrin repeat [IPR002110] (1)	-	C_unshiu_00112_mRNA_11.1	-
GF0034847	0	1	0	Hypothetical protein (1)		Ankyrin repeat-containing domain [IPR020683] (1)	-	C_unshiu_00112_mRNA_1.1	-
GF0034846	0	1	0	Hypothetical protein (1)		SGNH hydrolase-type esterase domain [IPR013830] (1)	-	C_unshiu_00111_mRNA_6.1	-
GF0034845	0	1	0	Hypothetical protein (1)			-	C_unshiu_00111_mRNA_4.1	-
GF0034844	0	1	0	Putative non-LTR retroelement reverse transcriptase (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1); Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_00111_mRNA_24.1	-
GF0034843	0	1	0	Hypothetical protein (1)			-	C_unshiu_00111_mRNA_16.1	-
GF0034842	0	1	0	Hypothetical protein (1)			-	C_unshiu_00110_mRNA_54.1	-
GF0034841	0	1	0	Peptide transporter PTR5 (1)	transporter activity [GO:0005215 molecular_function] (1); transport [GO:0006810 biological_process] (1); membrane [GO:0016020 cellular_component] (1)	Proton-dependent oligopeptide transporter family [IPR000109] (1); Major facilitator superfamily domain [IPR020846] (1)	-	C_unshiu_00110_mRNA_45.1	-
GF0034840	0	1	0	Hypothetical protein (1)			-	C_unshiu_00110_mRNA_40.1	-
GF0034839	0	1	0	Thioredoxin peroxidase 1 (1)	oxidoreductase activity [GO:0016491 molecular_function] (1)	Thioredoxin-like fold [IPR012336] (1); Redoxin [IPR013740] (1)	-	C_unshiu_00110_mRNA_39.1	-
GF0034838	0	1	0	Senescence-related gene 1 (1)		Isopenicillin N synthase-like [IPR027443] (1); Non-haem dioxygenase N-terminal domain [IPR026992] (1)	-	C_unshiu_00110_mRNA_37.1	-
GF0034837	0	1	0	Senescence-related gene 1 (1)		Isopenicillin N synthase-like [IPR027443] (1)	-	C_unshiu_00110_mRNA_35.1	-
GF0034836	0	1	0	Hypothetical protein (1)			-	C_unshiu_00110_mRNA_3.1	-
GF0034835	0	1	0	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	C_unshiu_00110_mRNA_17.1	-
GF0034834	0	1	0	Hypothetical protein (1)			-	C_unshiu_00110_mRNA_1.1	-
GF0034833	0	1	0	Hypothetical protein (1)			-	C_unshiu_00108_mRNA_38.1	-
GF0034832	0	1	0	CXE carboxylesterase (1)	hydrolase activity [GO:0016787 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Alpha/Beta hydrolase fold [IPR029058] (1); Alpha/beta hydrolase fold-3 [IPR013094] (1)	-	C_unshiu_00108_mRNA_29.1	-
GF0034831	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00108_mRNA_22.1	-
GF0034830	0	1	0	Hypothetical protein (1)			-	C_unshiu_00108_mRNA_21.1	-
GF0034829	0	1	0	Hypothetical protein (1)	polysaccharide binding [GO:0030247 molecular_function] (1); protein serine/threonine kinase activity [GO:0004674 molecular_function] (1); calcium ion binding [GO:0005509 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1)	EGF-like calcium-binding domain [IPR001881] (1); Protein kinase-like domain [IPR011009] (1); EGF-like calcium-binding, conserved site [IPR018097] (1); Wall-associated receptor kinase [IPR013695] (1); Wall-associated receptor kinase, galacturonan-binding domain [IPR025287] (1)	-	C_unshiu_00108_mRNA_2.1	-
GF0034828	0	1	0	Hypothetical protein (1)			-	C_unshiu_00107_mRNA_50.1	-
GF0034827	0	1	0	Hypothetical protein (1)			-	C_unshiu_00107_mRNA_42.1	-
GF0034826	0	1	0	Hypothetical protein (1)			-	C_unshiu_00107_mRNA_4.1	-
GF0034825	0	1	0	Peptidyl-prolyl cis-trans isomerase FKBP62 (1)	protein binding [GO:0005515 molecular_function] (1); protein folding [GO:0006457 biological_process] (1)	FKBP-type peptidyl-prolyl cis-trans isomerase domain [IPR001179] (1); Tetratricopeptide repeat [IPR019734] (1); Peptidyl-prolyl cis-trans isomerase, FKBP-type [IPR023566] (1); Elongated TPR repeat-containing domain [IPR023114] (1); Tetratricopeptide-like helical domain [IPR011990] (1)	-	C_unshiu_00107_mRNA_32.1	-
GF0034824	0	1	0	Hypothetical protein (1)			-	C_unshiu_00107_mRNA_31.1	-
GF0034823	0	1	0	Hypothetical protein (1)			-	C_unshiu_00107_mRNA_3.1	-
GF0034822	0	1	0	Hypothetical protein (1)	adenosylhomocysteinase activity [GO:0004013 molecular_function] (1); one-carbon metabolic process [GO:0006730 biological_process] (1)	Adenosylhomocysteinase [IPR000043] (1); NAD(P)-binding domain [IPR016040] (1); S-adenosyl-L-homocysteine hydrolase, NAD binding domain [IPR015878] (1)	-	C_unshiu_00107_mRNA_23.1	-
GF0034821	0	1	0	Eugenol O-methyltransferase (1)	methyltransferase activity [GO:0008168 molecular_function] (1); O-methyltransferase activity [GO:0008171 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); O-methyltransferase, family 2 [IPR001077] (1); O-methyltransferase COMT-type [IPR016461] (1); Plant methyltransferase dimerisation [IPR012967] (1)	-	C_unshiu_00107_mRNA_20.1	-
GF0034820	0	1	0	Ribosomal protein L6 (1)	structural constituent of ribosome [GO:0003735 molecular_function] (1); translation [GO:0006412 biological_process] (1); ribosome [GO:0005840 cellular_component] (1); rRNA binding [GO:0019843 molecular_function] (1)	Ribosomal protein L6 [IPR000702] (1); Ribosomal protein L6, alpha-beta domain [IPR020040] (1); Ribosomal protein L6, bacterial-type [IPR019906] (1)	-	C_unshiu_00107_mRNA_19.1	-
GF0034819	0	1	0	Hypothetical protein (1)			-	C_unshiu_00107_mRNA_14.1	-
GF0034818	0	1	0	Hypothetical protein (1)			-	C_unshiu_00107_mRNA_13.1	-
GF0034817	0	1	0	Hypothetical protein (1)	O-methyltransferase activity [GO:0008171 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1); methyltransferase activity [GO:0008168 molecular_function] (1)	Plant methyltransferase dimerisation [IPR012967] (1); O-methyltransferase COMT-type [IPR016461] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); O-methyltransferase, family 2 [IPR001077] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	C_unshiu_00107_mRNA_10.1	-
GF0034816	0	1	0	Hypothetical protein (1)			-	C_unshiu_00107_mRNA_1.1	-
GF0034815	0	1	0	Hypothetical protein (1)			-	C_unshiu_00106_mRNA_6.1	-
GF0034814	0	1	0	Hypothetical protein (1)			-	C_unshiu_00106_mRNA_39.1	-
GF0034813	0	1	0	Cellulose synthase (1)	zinc ion binding [GO:0008270 molecular_function] (1); cellulose synthase (UDP-forming) activity [GO:0016760 molecular_function] (1); membrane [GO:0016020 cellular_component] (1); protein binding [GO:0005515 molecular_function] (1); cellulose biosynthetic process [GO:0030244 biological_process] (1)	Zinc finger, RING/FYVE/PHD-type [IPR013083] (1); Cellulose synthase, RING-type zinc finger [IPR027934] (1); Cellulose synthase [IPR005150] (1); Zinc finger, RING-type [IPR001841] (1)	-	C_unshiu_00106_mRNA_38.1	-
GF0034812	0	1	0	LysM type receptor kinase (1)		LysM domain [IPR018392] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_00106_mRNA_31.1	-
GF0034811	0	1	0	Hypothetical protein (1)			-	C_unshiu_00106_mRNA_28.1	-
GF0034810	0	1	0	Hypothetical protein (1)			-	C_unshiu_00106_mRNA_26.1	-
GF0034809	0	1	0	Hypothetical protein (1)		Transposon, En/Spm-like [IPR004242] (1)	-	C_unshiu_00106_mRNA_23.1	-
GF0034808	0	1	0	Hypothetical protein (1)			-	C_unshiu_00106_mRNA_22.1	-
GF0034807	0	1	0	Hypothetical protein (1)			-	C_unshiu_00106_mRNA_18.1	-
GF0034806	0	1	0	Hypothetical protein (1)			-	C_unshiu_00106_mRNA_13.1	-
GF0034805	0	1	0	Hypothetical protein (1)			-	C_unshiu_00106_mRNA_11.1	-
GF0034804	0	1	0	Hypothetical protein (1)	peroxidase activity [GO:0004601 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); response to oxidative stress [GO:0006979 biological_process] (1); heme binding [GO:0020037 molecular_function] (1)	Haem peroxidase [IPR010255] (1); Ribonuclease H-like domain [IPR012337] (1); Peroxidases heam-ligand binding site [IPR019793] (1); Plant peroxidase [IPR000823] (1); Haem peroxidase, plant/fungal/bacterial [IPR002016] (1)	-	C_unshiu_00105_mRNA_5.1	-
GF0034803	0	1	0	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); peroxidase activity [GO:0004601 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); response to oxidative stress [GO:0006979 biological_process] (1)	Haem peroxidase [IPR010255] (1)	-	C_unshiu_00105_mRNA_4.1	-
GF0034802	0	1	0	Hypothetical protein (1)			-	C_unshiu_00105_mRNA_23.1	-
GF0034801	0	1	0	Hypothetical protein (1)			-	C_unshiu_00104_mRNA_9.1	-
GF0034800	0	1	0	Hypothetical protein (1)			-	C_unshiu_00104_mRNA_6.1	-
GF0034799	0	1	0	Hypothetical protein (1)			-	C_unshiu_00104_mRNA_52.1	-
GF0034798	0	1	0	Putative auxin efflux carrier component 6 (1)	integral component of membrane [GO:0016021 cellular_component] (1); transmembrane transport [GO:0055085 biological_process] (1)	Auxin efflux carrier [IPR004776] (1)	-	C_unshiu_00104_mRNA_50.1	-
GF0034797	0	1	0	Hypothetical protein (1)			-	C_unshiu_00104_mRNA_5.1	-
GF0034796	0	1	0	SET and MYND domain-containing (1)			-	C_unshiu_00104_mRNA_49.1	-
GF0034795	0	1	0	Hypothetical protein (1)		Gag-polypeptide of LTR copia-type [IPR029472] (1)	-	C_unshiu_00104_mRNA_48.1	-
GF0034794	0	1	0	Hypothetical protein (1)			-	C_unshiu_00104_mRNA_47.1	-
GF0034793	0	1	0	Hypothetical protein (1)			-	C_unshiu_00104_mRNA_45.1	-
GF0034792	0	1	0	Hypothetical protein (1)			-	C_unshiu_00104_mRNA_42.1	-
GF0034791	0	1	0	Hypothetical protein (1)			-	C_unshiu_00104_mRNA_40.1	-
GF0034790	0	1	0	Hypothetical protein (1)			-	C_unshiu_00104_mRNA_4.1	-
GF0034789	0	1	0	Hypothetical protein (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Aspartic peptidase domain [IPR021109] (1); Aspartic peptidase, active site [IPR001969] (1)	-	C_unshiu_00104_mRNA_32.1	-
GF0034788	0	1	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_00104_mRNA_29.1	-
GF0034787	0	1	0	Hypothetical protein (1)			-	C_unshiu_00104_mRNA_27.1	-
GF0034786	0	1	0	Hypothetical protein (1)			-	C_unshiu_00104_mRNA_26.1	-
GF0034785	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00104_mRNA_22.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0034784	0	1	0	Hypothetical protein (1)			-	C_unshiu_00104_mRNA_21.1	-
GF0034783	0	1	0	Hypothetical protein (1)			-	C_unshiu_00104_mRNA_20.1	-
GF0034782	0	1	0	Hypothetical protein (1)			-	C_unshiu_00104_mRNA_19.1	-
GF0034781	0	1	0	Hypothetical protein (1)			-	C_unshiu_00104_mRNA_18.1	-
GF0034780	0	1	0	Hypothetical protein (1)			-	C_unshiu_00104_mRNA_12.1	-
GF0034779	0	1	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	-	C_unshiu_00103_mRNA_8.1	-
GF0034778	0	1	0	RNA-binding Musashi (1)	nucleotide binding [GO:0000166 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Nucleotide-binding alpha-beta plait domain [IPR012677] (1); RNA recognition motif domain [IPR000504] (1)	-	C_unshiu_00103_mRNA_76.1	-
GF0034777	0	1	0	Hypothetical protein (1)			-	C_unshiu_00103_mRNA_5.1	-
GF0034776	0	1	0	Hypothetical protein (1)			-	C_unshiu_00103_mRNA_46.1	-
GF0034775	0	1	0	Hypothetical protein (1)			-	C_unshiu_00103_mRNA_43.1	-
GF0034774	0	1	0	Hypothetical protein (1)			-	C_unshiu_00103_mRNA_38.1	-
GF0034773	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_00103_mRNA_37.1	-
GF0034772	0	1	0	CDNA clone:J013021P22, full insert sequence (1)			-	C_unshiu_00103_mRNA_28.1	-
GF0034771	0	1	0	Hypothetical protein (1)			-	C_unshiu_00103_mRNA_25.1	-
GF0034770	0	1	0	Hypothetical protein (1)		Glucose/ribitol dehydrogenase [IPR002347] (1); NAD(P)-binding domain [IPR016040] (1)	-	C_unshiu_00102_mRNA_8.1	-
GF0034769	0	1	0	Hypothetical protein (1)			-	C_unshiu_00102_mRNA_61.1	-
GF0034768	0	1	0	Flavonoid 3'-monooxygenase (1)	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1)	Cytochrome P450 [IPR001128] (1); Cytochrome P450, conserved site [IPR017972] (1); Cytochrome P450, E-class, group I [IPR002401] (1)	-	C_unshiu_00102_mRNA_60.1	-
GF0034767	0	1	0	Hypothetical protein (1)			-	C_unshiu_00102_mRNA_58.1	-
GF0034766	0	1	0	Hypothetical protein (1)			-	C_unshiu_00102_mRNA_55.1	-
GF0034765	0	1	0	Hypothetical protein (1)			-	C_unshiu_00102_mRNA_53.1	-
GF0034764	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1); recognition of pollen [GO:0048544 biological_process] (1)	S-locus glycoprotein domain [IPR000858] (1); EGF-like domain [IPR000742] (1)	-	C_unshiu_00102_mRNA_52.1	-
GF0034763	0	1	0	Hypothetical protein (1)		Bulb-type lectin domain [IPR001480] (1)	-	C_unshiu_00102_mRNA_51.1	-
GF0034762	0	1	0	Hypothetical protein (1)			-	C_unshiu_00102_mRNA_45.1	-
GF0034761	0	1	0	Hypothetical protein (1)			-	C_unshiu_00102_mRNA_44.1	-
GF0034760	0	1	0	Hypothetical protein (1)			-	C_unshiu_00102_mRNA_39.1	-
GF0034759	0	1	0	Hypothetical protein (1)			-	C_unshiu_00102_mRNA_35.1	-
GF0034758	0	1	0	Hypothetical protein (1)			-	C_unshiu_00102_mRNA_34.1	-
GF0034757	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_00102_mRNA_32.1	-
GF0034756	0	1	0	Hypothetical protein (1)			-	C_unshiu_00102_mRNA_26.1	-
GF0034755	0	1	0	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1)	NADP-dependent oxidoreductase domain [IPR023210] (1); Aldo/keto reductase, conserved site [IPR018170] (1); Aldo/keto reductase [IPR020471] (1); Reverse transcriptase domain [IPR000477] (1); Aldo/keto reductase/potassium channel subunit beta [IPR001395] (1)	-	C_unshiu_00102_mRNA_24.1	-
GF0034754	0	1	0	Hypothetical protein (1)			-	C_unshiu_00102_mRNA_22.1	-
GF0034753	0	1	0	Aldo-keto reductase family 4 member C9 (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1)	NADP-dependent oxidoreductase domain [IPR023210] (1); Aldo/keto reductase, conserved site [IPR018170] (1); Aldo/keto reductase [IPR020471] (1); Aldo/keto reductase/potassium channel subunit beta [IPR001395] (1)	-	C_unshiu_00102_mRNA_20.1	-
GF0034752	0	1	0	Mannose-1-phosphate guanyltransferase alpha-like protein (1)		Trimeric LpxA-like [IPR011004] (1); Hexapeptide repeat [IPR001451] (1)	-	C_unshiu_00102_mRNA_17.1	-
GF0034751	0	1	0	Mannose-1-phosphate guanylyltransferase (1)	biosynthetic process [GO:0009058 biological_process] (1); nucleotidyltransferase activity [GO:0016779 molecular_function] (1)	Nucleotidyl transferase domain [IPR005835] (1); Nucleotide-diphospho-sugar transferases [IPR029044] (1)	-	C_unshiu_00102_mRNA_16.1	-
GF0034750	0	1	0	Hypothetical protein (1)			-	C_unshiu_00102_mRNA_1.1	-
GF0034749	0	1	0	Hypothetical protein (1)			-	C_unshiu_00101_mRNA_8.1	-
GF0034748	0	1	0	Transposable element protein, putative, (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_00101_mRNA_54.1	-
GF0034747	0	1	0	Putative non-LTR reverse transcriptase (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_00101_mRNA_52.1	-
GF0034746	0	1	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	-	C_unshiu_00101_mRNA_45.1	-
GF0034745	0	1	0	Hypothetical protein (1)			-	C_unshiu_00101_mRNA_4.1	-
GF0034744	0	1	0	Hypothetical protein (1)			-	C_unshiu_00101_mRNA_3.1	-
GF0034743	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF3700 [IPR024286] (1)	-	C_unshiu_00101_mRNA_19.1	-
GF0034742	0	1	0	Triosephosphate isomerase, cytosolic (1)	catalytic activity [GO:0003824 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1); triose-phosphate isomerase activity [GO:0004807 molecular_function] (1)	Triosephosphate isomerase [IPR000652] (1); Aldolase-type TIM barrel [IPR013785] (1)	-	C_unshiu_00101_mRNA_12.1	-
GF0034741	0	1	0	Hypothetical protein (1)			-	C_unshiu_00101_mRNA_1.1	-
GF0034740	0	1	0	Hypothetical protein (1)			-	C_unshiu_00100_mRNA_9.1	-
GF0034739	0	1	0	Hypothetical protein (1)			-	C_unshiu_00100_mRNA_57.1	-
GF0034738	0	1	0	Hypothetical protein (1)			-	C_unshiu_00100_mRNA_56.1	-
GF0034737	0	1	0	Hypothetical protein (1)			-	C_unshiu_00100_mRNA_55.1	-
GF0034736	0	1	0	Hypothetical protein (1)			-	C_unshiu_00100_mRNA_53.1	-
GF0034735	0	1	0	Hypothetical protein (1)			-	C_unshiu_00100_mRNA_49.1	-
GF0034734	0	1	0	Hypothetical protein (1)	serine-type endopeptidase activity [GO:0004252 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Peptidase S8/S53 domain [IPR000209] (1)	-	C_unshiu_00100_mRNA_29.1	-
GF0034733	0	1	0	Hypothetical protein (1)		Peptidase S8, subtilisin-related [IPR015500] (1)	-	C_unshiu_00100_mRNA_27.1	-
GF0034732	0	1	0	TLP domain class transcription factor (1)	protein binding [GO:0005515 molecular_function] (1)	Tubby, C-terminal, conserved site [IPR018066] (1); F-box domain [IPR001810] (1); Tubby C-terminal-like domain [IPR025659] (1); Tubby, C-terminal [IPR000007] (1)	-	C_unshiu_00100_mRNA_24.1	-
GF0034731	0	1	0	Hypothetical protein (1)			-	C_unshiu_00100_mRNA_18.1	-
GF0034730	0	1	0	Zinc finger protein 830 (1)			-	C_unshiu_00099_mRNA_53.1	-
GF0034729	0	1	0	Hypothetical protein (1)			-	C_unshiu_00099_mRNA_50.1	-
GF0034728	0	1	0	Hypothetical protein (1)			-	C_unshiu_00099_mRNA_47.1	-
GF0034727	0	1	0	Disease resistance protein RPS2 (1)	protein binding [GO:0005515 molecular_function] (1); ADP binding [GO:0043531 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat [IPR001611] (1); NB-ARC [IPR002182] (1)	-	C_unshiu_00099_mRNA_45.1	-
GF0034726	0	1	0	NBS-LRR type disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); AAA+ ATPase domain [IPR003593] (1); NB-ARC [IPR002182] (1)	-	C_unshiu_00099_mRNA_44.1	-
GF0034725	0	1	0	Hypothetical protein (1)	transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (1)	Chloramphenicol acetyltransferase-like domain [IPR023213] (1); Transferase [IPR003480] (1)	-	C_unshiu_00099_mRNA_40.1	-
GF0034724	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	-	C_unshiu_00099_mRNA_36.1	-
GF0034723	0	1	0	Hypothetical protein (1)			-	C_unshiu_00099_mRNA_34.1	-
GF0034722	0	1	0	Hypothetical protein (1)			-	C_unshiu_00099_mRNA_32.1	-
GF0034721	0	1	0	Aspartic proteinase nepenthesin-2 (1)	proteolysis [GO:0006508 biological_process] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1)	Aspartic peptidase A1 family [IPR001461] (1); Xylanase inhibitor, C-terminal [IPR032799] (1); Peptidase family A1 domain [IPR033121] (1); Aspartic peptidase domain [IPR021109] (1)	-	C_unshiu_00099_mRNA_31.1	-
GF0034720	0	1	0	Lysine histidine transporter 1 (1)		Amino acid transporter, transmembrane domain [IPR013057] (1)	-	C_unshiu_00099_mRNA_16.1	-
GF0034719	0	1	0	Hypothetical protein (1)			-	C_unshiu_00099_mRNA_12.1	-
GF0034718	0	1	0	Hypothetical protein (1)			-	C_unshiu_00098_mRNA_9.1	-
GF0034717	0	1	0	Hypothetical protein (1)			-	C_unshiu_00098_mRNA_8.1	-
GF0034716	0	1	0	Hypothetical protein (1)			-	C_unshiu_00098_mRNA_7.1	-
GF0034715	0	1	0	Hypothetical protein (1)		P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00098_mRNA_61.1	-
GF0034714	0	1	0	UMP-CMP kinase 3 (1)	ATP binding [GO:0005524 molecular_function] (1); nucleobase-containing compound metabolic process [GO:0006139 biological_process] (1); nucleobase-containing compound kinase activity [GO:0019205 molecular_function] (1)	Adenylate kinase/UMP-CMP kinase [IPR000850] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00098_mRNA_60.1	-
GF0034713	0	1	0	Hypothetical protein (1)			-	C_unshiu_00098_mRNA_6.1	-
GF0034712	0	1	0	Hypothetical protein (1)			-	C_unshiu_00098_mRNA_59.1	-
GF0034711	0	1	0	Hypothetical protein (1)			-	C_unshiu_00098_mRNA_5.1	-
GF0034710	0	1	0	Hypothetical protein (1)			-	C_unshiu_00098_mRNA_4.1	-
GF0034709	0	1	0	Hypothetical protein (1)		Lsm14 N-terminal [IPR025609] (1); LSM domain [IPR010920] (1)	-	C_unshiu_00098_mRNA_31.1	-
GF0034708	0	1	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	Zinc finger, BED-type [IPR003656] (1)	-	C_unshiu_00098_mRNA_3.1	-
GF0034707	0	1	0	Hypothetical protein (1)			-	C_unshiu_00098_mRNA_28.1	-
GF0034706	0	1	0	Hypothetical protein (1)			-	C_unshiu_00098_mRNA_17.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0034705	0	1	0	Hypothetical protein (1)			-	C_unshiu_00097_mRNA_8.1	-
GF0034704	0	1	0	Hypothetical protein (1)			-	C_unshiu_00097_mRNA_6.1	-
GF0034703	0	1	0	Hypothetical protein (1)			-	C_unshiu_00097_mRNA_5.1	-
GF0034702	0	1	0	Hypothetical protein (1)			-	C_unshiu_00097_mRNA_49.1	-
GF0034701	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_00097_mRNA_48.1	-
GF0034700	0	1	0	Hypothetical protein (1)			-	C_unshiu_00097_mRNA_40.1	-
GF0034699	0	1	0	Cytoplasmic membrane protein (1)		Domain of unknown function DUF2062 [IPR018639] (1)	-	C_unshiu_00097_mRNA_4.2	-
GF0034698	0	1	0	Calcium ion binding protein, putative (1)	calcium ion binding [GO:0005509 molecular_function] (1)	EF-hand domain pair [IPR011992] (1); EF-Hand 1, calcium-binding site [IPR018247] (1); EF-hand domain [IPR002048] (1)	-	C_unshiu_00097_mRNA_39.1	-
GF0034697	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00097_mRNA_35.1	-
GF0034696	0	1	0	Hypothetical protein (1)			-	C_unshiu_00097_mRNA_34.1	-
GF0034695	0	1	0	Calcium ion binding protein, putative (1)	calcium ion binding [GO:0005509 molecular_function] (1)	EF-hand domain pair [IPR011992] (1); EF-Hand 1, calcium-binding site [IPR018247] (1); EF-hand domain [IPR002048] (1)	-	C_unshiu_00097_mRNA_33.1	-
GF0034694	0	1	0	Putative Glycerophosphoryl diester phosphodiesterase (1)	phosphoric diester hydrolase activity [GO:0008081 molecular_function] (1); lipid metabolic process [GO:0006629 biological_process] (1); glycerophosphodiester phosphodiesterase activity [GO:0008889 molecular_function] (1)	Glycerophosphoryl diester phosphodiesterase [IPR004129] (1); Glycerophosphodiester phosphodiesterase domain [IPR030395] (1); PLC-like phosphodiesterase, TIM beta/alpha-barrel domain [IPR017946] (1)	-	C_unshiu_00097_mRNA_3.1	-
GF0034693	0	1	0	MUTE (1)	protein dimerization activity [GO:0046983 molecular_function] (1)	Myc-type, basic helix-loop-helix (bHLH) domain [IPR011598] (1)	-	C_unshiu_00097_mRNA_15.1	-
GF0034692	0	1	0	Basic 7S globulin (1)	proteolysis [GO:0006508 biological_process] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1)	Aspartic peptidase domain [IPR021109] (1); Peptidase family A1 domain [IPR033121] (1); Aspartic peptidase A1 family [IPR001461] (1); Xylanase inhibitor, N-terminal [IPR032861] (1); Xylanase inhibitor, C-terminal [IPR032799] (1)	-	C_unshiu_00097_mRNA_11.1	-
GF0034691	0	1	0	Phosphatidate phosphatase LPIN2 (1)		HAD-like domain [IPR023214] (1); Lipin/Ned1/Smp2 (LNS2) [IPR013209] (1); LNS2/PITP [IPR031315] (1)	-	C_unshiu_00096_mRNA_67.1	-
GF0034690	0	1	0	ABSCISIC ACID-INSENSITIVE 5-like protein 6 (1)	transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); sequence-specific DNA binding [GO:0043565 molecular_function] (1)	Basic-leucine zipper domain [IPR004827] (1)	-	C_unshiu_00096_mRNA_48.1	-
GF0034689	0	1	0	Hypothetical protein (1)			-	C_unshiu_00096_mRNA_45.1	-
GF0034688	0	1	0	Leucine-rich repeat protein kinase family protein isoform 3 (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00096_mRNA_23.1	-
GF0034687	0	1	0	Hypothetical protein (1)			-	C_unshiu_00096_mRNA_21.1	-
GF0034686	0	1	0	C2 domain protein (1)	protein binding [GO:0005515 molecular_function] (1)	C2 domain [IPR000008] (1)	-	C_unshiu_00096_mRNA_18.1	-
GF0034685	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	F-box domain [IPR001810] (1)	-	C_unshiu_00096_mRNA_15.1	-
GF0034684	0	1	0	Hypothetical protein (1)			-	C_unshiu_00096_mRNA_12.1	-
GF0034683	0	1	0	MiaB-like tRNA modifying enzyme, archaeal-type (1)	catalytic activity [GO:0003824 molecular_function] (1); 4 iron, 4 sulfur cluster binding [GO:0051539 molecular_function] (1); RNA modification [GO:0009451 biological_process] (1); transferase activity [GO:0016740 molecular_function] (1); iron-sulfur cluster binding [GO:0051536 molecular_function] (1); macromolecule modification [GO:0043412 biological_process] (1)	Methylthiotransferase, conserved site [IPR020612] (1); Methylthiotransferase [IPR005839] (1); MiaB-like tRNA modifying enzyme, archaeal-type [IPR006466] (1); Methylthiotransferase/radical SAM-type protein [IPR023970] (1); Radical SAM, alpha/beta horseshoe [IPR023404] (1); Elongator protein 3/MiaB/NifB [IPR006638] (1); Methylthiotransferase, N-terminal [IPR013848] (1); Radical SAM [IPR007197] (1)	-	C_unshiu_00096_mRNA_1.1	-
GF0034682	0	1	0	Hypothetical protein (1)			-	C_unshiu_00095_mRNA_53.1	-
GF0034681	0	1	0	Sugar carrier protein C (1)	substrate-specific transmembrane transporter activity [GO:0022891 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1); transmembrane transporter activity [GO:0022857 molecular_function] (1); membrane [GO:0016020 cellular_component] (1); transmembrane transport [GO:0055085 biological_process] (1)	Major facilitator, sugar transporter-like [IPR005828] (1); Sugar/inositol transporter [IPR003663] (1); Major facilitator superfamily domain [IPR020846] (1)	-	C_unshiu_00095_mRNA_49.1	-
GF0034680	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_00095_mRNA_46.1	-
GF0034679	0	1	0	Hypothetical protein (1)	transmembrane transport [GO:0055085 biological_process] (1); transporter activity [GO:0005215 molecular_function] (1); membrane [GO:0016020 cellular_component] (1); transmembrane transporter activity [GO:0022857 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1); substrate-specific transmembrane transporter activity [GO:0022891 molecular_function] (1)	Sugar transporter, conserved site [IPR005829] (1); Major facilitator superfamily domain [IPR020846] (1); Major facilitator, sugar transporter-like [IPR005828] (1); Sugar/inositol transporter [IPR003663] (1)	-	C_unshiu_00095_mRNA_42.1	-
GF0034678	0	1	0	Hypothetical protein (1)			-	C_unshiu_00095_mRNA_4.1	-
GF0034677	0	1	0	Hypothetical protein (1)			-	C_unshiu_00095_mRNA_3.1	-
GF0034676	0	1	0	Hypothetical protein (1)	serine-type endopeptidase inhibitor activity [GO:0004867 molecular_function] (1); response to wounding [GO:0009611 biological_process] (1)	Proteinase inhibitor I13, potato inhibitor I [IPR000864] (1)	-	C_unshiu_00095_mRNA_29.1	-
GF0034675	0	1	0	Hypothetical protein (1)			-	C_unshiu_00095_mRNA_21.1	-
GF0034674	0	1	0	LRR receptor-like kinase family protein (1)	protein binding [GO:0005515 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase, ATP binding site [IPR017441] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1); Protein kinase domain [IPR000719] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Protein kinase-like domain [IPR011009] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1)	-	C_unshiu_00095_mRNA_2.1	-
GF0034673	0	1	0	Agmatine N(4)-coumaroyltransferase (1)	transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (1)	Chloramphenicol acetyltransferase-like domain [IPR023213] (1); Transferase [IPR003480] (1)	-	C_unshiu_00095_mRNA_18.1	-
GF0034672	0	1	0	Hypothetical protein (1)			-	C_unshiu_00095_mRNA_14.1	-
GF0034671	0	1	0	Hypothetical protein (1)			-	C_unshiu_00094_mRNA_9.1	-
GF0034670	0	1	0	Hypothetical protein (1)			-	C_unshiu_00094_mRNA_46.1	-
GF0034669	0	1	0	6a-hydroxymaackiain methyltransferase family protein (1)	methyltransferase activity [GO:0008168 molecular_function] (1); O-methyltransferase activity [GO:0008171 molecular_function] (1)	S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); O-methyltransferase COMT-type [IPR016461] (1); O-methyltransferase, family 2 [IPR001077] (1)	-	C_unshiu_00094_mRNA_39.1	-
GF0034668	0	1	0	Hypothetical protein (1)			-	C_unshiu_00094_mRNA_3.1	-
GF0034667	0	1	0	Hypothetical protein (1)			-	C_unshiu_00094_mRNA_25.1	-
GF0034666	0	1	0	Hypothetical protein (1)			-	C_unshiu_00094_mRNA_10.1	-
GF0034665	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Major coat protein, L-A virus [IPR015302] (1); LOG family [IPR031100] (1)	-	C_unshiu_00093_mRNA_9.1	-
GF0034664	0	1	0	Hypothetical protein (1)			-	C_unshiu_00093_mRNA_7.1	-
GF0034663	0	1	0	Hypothetical protein (1)			-	C_unshiu_00093_mRNA_43.1	-
GF0034662	0	1	0	Hypothetical protein (1)			-	C_unshiu_00093_mRNA_38.1	-
GF0034661	0	1	0	Hypothetical protein (1)			-	C_unshiu_00093_mRNA_34.1	-
GF0034660	0	1	0	Hypothetical protein (1)		Transposase-associated domain [IPR029480] (1)	-	C_unshiu_00093_mRNA_27.1	-
GF0034659	0	1	0	U3 small nucleolar RNA-associated protein 18 (1)	protein binding [GO:0005515 molecular_function] (1)	WD40 repeat [IPR001680] (1); WD40-repeat-containing domain [IPR017986] (1); WD40/YVTN repeat-like-containing domain [IPR015943] (1)	-	C_unshiu_00093_mRNA_23.1	-
GF0034658	0	1	0	Peroxisomal membrane protein PEX14 (1)	protein binding [GO:0005515 molecular_function] (1); peroxisomal membrane [GO:0005778 cellular_component] (1); protein import into peroxisome matrix, docking [GO:0016560 biological_process] (1)	Peroxisomal membrane protein 14 [IPR025655] (1); Peroxisome membrane anchor protein Pex14p, N-terminal [IPR006785] (1)	-	C_unshiu_00092_mRNA_67.1	-
GF0034657	0	1	0	Hypothetical protein (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Protein kinase-like domain [IPR011009] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1)	-	C_unshiu_00092_mRNA_62.1	-
GF0034656	0	1	0	Hypothetical protein (1)	lipid metabolic process [GO:0006629 biological_process] (1)	Fungal lipase-like domain [IPR002921] (1); Alpha/Beta hydrolase fold [IPR029058] (1); Formin, FH2 domain [IPR015425] (1)	-	C_unshiu_00092_mRNA_13.1	-
GF0034655	0	1	0	Triacylglycerol lipase (1)			-	C_unshiu_00092_mRNA_12.1	-
GF0034654	0	1	0	Hypothetical protein (1)			-	C_unshiu_00091_mRNA_7.1	-
GF0034653	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00091_mRNA_50.1	-
GF0034652	0	1	0	Polynucleotidyl transferase, Ribonuclease H fold (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_00091_mRNA_5.1	-
GF0034651	0	1	0	Non-LTR reverse transcriptase (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	C_unshiu_00091_mRNA_4.1	-
GF0034650	0	1	0	Hypothetical protein (1)			-	C_unshiu_00091_mRNA_33.1	-
GF0034649	0	1	0	Hypothetical protein (1)			-	C_unshiu_00091_mRNA_30.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0034648	0	1	0	Obg-like ATPase 1 (1)	GTP binding [GO:0005525 molecular_function] (1)	Beta-grasp domain [IPR012675] (1); TGS-like domain [IPR023192] (1); TGS-like [IPR012676] (1); Domain of unknown function DUF933 [IPR013029] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); GTP binding domain [IPR006073] (1); Ribosome-binding ATPase YchF/Obg-like ATPase 1 [IPR004396] (1); OBG-type guanine nucleotide-binding (G) domain [IPR031167] (1)	-	C_unshiu_00091_mRNA_28.1	-
GF0034647	0	1	0	Hypothetical protein (1)		Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	-	C_unshiu_00091_mRNA_27.1	-
GF0034646	0	1	0	NADH-ubiquinone oxidoreductase 18 kDa subunit (1)	oxidoreductase activity, acting on NAD(P)H [GO:0016651 molecular_function] (1); electron transport chain [GO:0022900 biological_process] (1)	NADH dehydrogenase ubiquinone Fe-S protein 4, mitochondrial [IPR006885] (1)	-	C_unshiu_00091_mRNA_12.1	-
GF0034645	0	1	0	Hypothetical protein (1)			-	C_unshiu_00090_mRNA_66.1	-
GF0034644	0	1	0	Hypothetical protein (1)			-	C_unshiu_00090_mRNA_5.1	-
GF0034643	0	1	0	Hypothetical protein (1)		FBD domain [IPR006566] (1)	-	C_unshiu_00090_mRNA_46.1	-
GF0034642	0	1	0	Hypothetical protein (1)			-	C_unshiu_00090_mRNA_2.1	-
GF0034641	0	1	0	GPN-loop GTPase 2 (1)		GPN-loop GTPase [IPR004130] (1); GPN-loop GTPase 2 [IPR030231] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00090_mRNA_1.1	-
GF0034640	0	1	0	Fatty acyl-CoA reductase 1 (1)	fatty-acyl-CoA reductase (alcohol-forming) activity [GO:0080019 molecular_function] (1)	Fatty acyl-CoA reductase [IPR026055] (1)	-	C_unshiu_00089_mRNA_58.1	-
GF0034639	0	1	0	Basic 7S globulin (1)	proteolysis [GO:0006508 biological_process] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1)	Aspartic peptidase domain [IPR021109] (1); Xylanase inhibitor, C-terminal [IPR032799] (1); Xylanase inhibitor, N-terminal [IPR032861] (1); Aspartic peptidase A1 family [IPR001461] (1)	-	C_unshiu_00089_mRNA_55.1	-
GF0034638	0	1	0	Hypothetical protein (1)			-	C_unshiu_00089_mRNA_51.1	-
GF0034637	0	1	0	Hypothetical protein (1)			-	C_unshiu_00089_mRNA_39.1	-
GF0034636	0	1	0	Hypothetical protein (1)			-	C_unshiu_00089_mRNA_31.1	-
GF0034635	0	1	0	Hypothetical protein (1)			-	C_unshiu_00089_mRNA_14.1	-
GF0034634	0	1	0	Hypothetical protein (1)			-	C_unshiu_00088_mRNA_68.1	-
GF0034633	0	1	0	Hypothetical protein (1)			-	C_unshiu_00088_mRNA_66.1	-
GF0034632	0	1	0	Putative glucan 1,3-beta-glucosidase A (1)	actin filament binding [GO:0051015 molecular_function] (1); hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (1); actin filament organization [GO:0007015 biological_process] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1)	Glycoside hydrolase, catalytic domain [IPR013781] (1); Glycoside hydrolase superfamily [IPR017853] (1); Fascin [IPR010431] (1); Glycoside hydrolase, family 5 [IPR001547] (1)	-	C_unshiu_00088_mRNA_62.1	-
GF0034631	0	1	0	Hypothetical protein (1)	nucleotide binding [GO:0000166 molecular_function] (1)	Nucleotide-binding alpha-beta plait domain [IPR012677] (1); RNA recognition motif 2 [IPR007201] (1)	-	C_unshiu_00088_mRNA_6.1	-
GF0034630	0	1	0	Hypothetical protein (1)			-	C_unshiu_00088_mRNA_59.1	-
GF0034629	0	1	0	Hypothetical protein (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase, ATP binding site [IPR017441] (1)	-	C_unshiu_00088_mRNA_57.1	-
GF0034628	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Ubiquitin-fold modifier 1 [IPR005375] (1); Ubiquitin-related domain [IPR029071] (1)	-	C_unshiu_00088_mRNA_56.1	-
GF0034627	0	1	0	Probable glycerol-3-phosphate acyltransferase 3 (1)	metabolic process [GO:0008152 biological_process] (1); methyltransferase activity [GO:0008168 molecular_function] (1); transferase activity, transferring acyl groups [GO:0016746 molecular_function] (1)	Methyltransferase type 11 [IPR013216] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); Phospholipid/glycerol acyltransferase [IPR002123] (1)	-	C_unshiu_00088_mRNA_34.1	-
GF0034626	0	1	0	Hypothetical protein (1)		Phosphatidylinositol-4-phosphate 5-kinase [IPR023610] (1); MORN motif [IPR003409] (1)	-	C_unshiu_00088_mRNA_2.1	-
GF0034625	0	1	0	Hypothetical protein (1)			-	C_unshiu_00088_mRNA_14.1	-
GF0034624	0	1	0	Hypothetical protein (1)			-	C_unshiu_00087_mRNA_63.1	-
GF0034623	0	1	0	Hemolysin A (1)	methyltransferase activity [GO:0008168 molecular_function] (1); RNA binding [GO:0003723 molecular_function] (1); methylation [GO:0032259 biological_process] (1)	S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); RNA-binding S4 domain [IPR002942] (1); Ribosomal RNA methyltransferase FtsJ domain [IPR002877] (1)	-	C_unshiu_00087_mRNA_58.1	-
GF0034622	0	1	0	Hypothetical protein (1)			-	C_unshiu_00087_mRNA_45.1	-
GF0034621	0	1	0	Hypothetical protein (1)			-	C_unshiu_00087_mRNA_23.1	-
GF0034620	0	1	0	Retrotransposon gag protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_00087_mRNA_22.1	-
GF0034619	0	1	0	Gag protein (1)			-	C_unshiu_00087_mRNA_21.1	-
GF0034618	0	1	0	Hypothetical protein (1)			-	C_unshiu_00087_mRNA_20.1	-
GF0034617	0	1	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_00087_mRNA_13.1	-
GF0034616	0	1	0	Hypothetical protein (1)			-	C_unshiu_00086_mRNA_49.1	-
GF0034615	0	1	0	Hypothetical protein (1)			-	C_unshiu_00086_mRNA_48.1	-
GF0034614	0	1	0	TSA: Wollemia nobilis transcribed RNA sequence (1)	integral component of membrane [GO:0016021 cellular_component] (1)	Tetraspanin/Peripherin [IPR018499] (1)	-	C_unshiu_00086_mRNA_44.1	-
GF0034613	0	1	0	Hypothetical protein (1)			-	C_unshiu_00086_mRNA_38.1	-
GF0034612	0	1	0	Putative rhamnose biosynthetic enzyme 1 (1)		NAD(P)-binding domain [IPR016040] (1); RmlD-like substrate binding domain [IPR029903] (1)	-	C_unshiu_00086_mRNA_11.1	-
GF0034611	0	1	0	Hypothetical protein (1)			-	C_unshiu_00085_mRNA_71.1	-
GF0034610	0	1	0	Hypothetical protein (1)			-	C_unshiu_00085_mRNA_69.1	-
GF0034609	0	1	0	Hypothetical protein (1)			-	C_unshiu_00085_mRNA_68.1	-
GF0034608	0	1	0	Hypothetical protein (1)			-	C_unshiu_00085_mRNA_63.1	-
GF0034607	0	1	0	Hypothetical protein (1)	transferase activity, transferring glycosyl groups [GO:0016757 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1)	Glycosyltransferase 34 [IPR008630] (1)	-	C_unshiu_00085_mRNA_62.1	-
GF0034606	0	1	0	Receptor like protein 33 (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00085_mRNA_52.1	-
GF0034605	0	1	0	Hypothetical protein (1)			-	C_unshiu_00085_mRNA_34.1	-
GF0034604	0	1	0	Proline-rich receptor-like protein kinase PERK4 (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1)	-	C_unshiu_00085_mRNA_2.1	-
GF0034603	0	1	0	Hypothetical protein (1)			-	C_unshiu_00085_mRNA_10.1	-
GF0034602	0	1	0	Ribosomal RNA small subunit methyltransferase G (1)			-	C_unshiu_00084_mRNA_6.1	-
GF0034601	0	1	0	Hypothetical protein (1)			-	C_unshiu_00084_mRNA_5.1	-
GF0034600	0	1	0	Hypothetical protein (1)			-	C_unshiu_00084_mRNA_4.1	-
GF0034599	0	1	0	Hypothetical protein (1)			-	C_unshiu_00084_mRNA_36.1	-
GF0034598	0	1	0	Hypothetical protein (1)			-	C_unshiu_00084_mRNA_3.1	-
GF0034597	0	1	0	Red chlorophyll catabolite reductase (1)		Red chlorophyll catabolite reductase [IPR009439] (1)	-	C_unshiu_00084_mRNA_19.1	-
GF0034596	0	1	0	Triacylglycerol lipase (1)	lipid metabolic process [GO:0006629 biological_process] (1)	Fungal lipase-like domain [IPR002921] (1); Alpha/Beta hydrolase fold [IPR029058] (1)	-	C_unshiu_00084_mRNA_10.1	-
GF0034595	0	1	0	Hypothetical protein (1)			-	C_unshiu_00083_mRNA_39.1	-
GF0034594	0	1	0	Hypothetical protein (1)			-	C_unshiu_00083_mRNA_32.1	-
GF0034593	0	1	0	Retrotransposon protein, putative, unclassified (1)			-	C_unshiu_00083_mRNA_30.1	-
GF0034592	0	1	0	Homogentisate phytyltransferase (1)	prenyltransferase activity [GO:0004659 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1)	UbiA prenyltransferase family [IPR000537] (1)	-	C_unshiu_00083_mRNA_25.1	-
GF0034591	0	1	0	Hypothetical protein (1)		PMR5 N-terminal domain [IPR025846] (1)	-	C_unshiu_00083_mRNA_2.1	-
GF0034590	0	1	0	Hypothetical protein (1)			-	C_unshiu_00082_mRNA_66.1	-
GF0034589	0	1	0	Hypothetical protein (1)			-	C_unshiu_00082_mRNA_65.1	-
GF0034588	0	1	0	Hypothetical protein (1)			-	C_unshiu_00082_mRNA_63.1	-
GF0034587	0	1	0	Hypothetical protein (1)			-	C_unshiu_00082_mRNA_38.1	-
GF0034586	0	1	0	30S ribosomal protein S18, chloroplastic (1)	intracellular [GO:0005622 cellular_component] (1); translation [GO:0006412 biological_process] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1); electron carrier activity [GO:0009055 molecular_function] (1); cytochrome b6f complex [GO:0009512 cellular_component] (1); ribosome [GO:0005840 cellular_component] (1)	Ribosomal protein S18 [IPR001648] (1); Ribosomal protein S18, conserved site [IPR018275] (1); Cytochrome b6-f complex subunit 6 [IPR007802] (1)	-	C_unshiu_00082_mRNA_31.1	-
GF0034585	0	1	0	DNA-directed RNA polymerase, alpha subunit (1)	DNA-directed RNA polymerase activity [GO:0003899 molecular_function] (1); ribosome [GO:0005840 cellular_component] (1); protein dimerization activity [GO:0046983 molecular_function] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1); translation [GO:0006412 biological_process] (1); transcription, DNA-templated [GO:0006351 biological_process] (1)	DNA-directed RNA polymerase, RBP11-like dimerisation domain [IPR009025] (1); DNA-directed RNA polymerase, RpoA/D/Rpb3-type [IPR011263] (1); DNA-directed RNA polymerase, insert domain [IPR011262] (1); Ribosomal protein S11 [IPR001971] (1)	-	C_unshiu_00082_mRNA_29.1	-
GF0034584	0	1	0	Hypothetical protein (1)			-	C_unshiu_00082_mRNA_24.1	-
GF0034583	0	1	0	Hypothetical protein (1)			-	C_unshiu_00082_mRNA_23.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0034582	0	1	0	Ankyrin repeat protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat-containing domain [IPR020683] (1); PGG domain [IPR026961] (1); Ankyrin repeat [IPR002110] (1)	-	C_unshiu_00082_mRNA_20.1	-
GF0034581	0	1	0	Hypothetical protein (1)			-	C_unshiu_00082_mRNA_19.1	-
GF0034580	0	1	0	Hypothetical protein (1)			-	C_unshiu_00081_mRNA_77.1	-
GF0034579	0	1	0	Receptor like protein 27 (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00081_mRNA_76.1	-
GF0034578	0	1	0	Truncated verticillium wilt resistance-like protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00081_mRNA_75.1	-
GF0034577	0	1	0	Hypothetical protein (1)	glucose-6-phosphate dehydrogenase activity [GO:0004345 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); glucose metabolic process [GO:0006006 biological_process] (1); NADP binding [GO:0050661 molecular_function] (1)	Glucose-6-phosphate dehydrogenase [IPR001282] (1); NAD(P)-binding domain [IPR016040] (1); Glucose-6-phosphate dehydrogenase, C-terminal [IPR022675] (1); Glucose-6-phosphate dehydrogenase, NAD-binding [IPR022674] (1)	-	C_unshiu_00081_mRNA_73.1	-
GF0034576	0	1	0	Brassinosteroid insensitive 1, putative (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_00081_mRNA_70.1	-
GF0034575	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00081_mRNA_68.1	-
GF0034574	0	1	0	Transposon protein, putative, Mutator sub-class (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, PMZ-type [IPR006564] (1); Transposase, MuDR, plant [IPR004332] (1); Zinc finger, SWIM-type [IPR007527] (1)	-	C_unshiu_00081_mRNA_34.1	-
GF0034573	0	1	0	Hypothetical protein (1)			-	C_unshiu_00081_mRNA_33.1	-
GF0034572	0	1	0	Hypothetical protein (1)			-	C_unshiu_00081_mRNA_28.1	-
GF0034571	0	1	0	Hypothetical protein (1)			-	C_unshiu_00081_mRNA_22.1	-
GF0034570	0	1	0	Hypothetical protein (1)			-	C_unshiu_00081_mRNA_21.1	-
GF0034569	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF2431 [IPR019446] (1)	-	C_unshiu_00080_mRNA_44.1	-
GF0034568	0	1	0	Hypothetical protein (1)			-	C_unshiu_00080_mRNA_42.1	-
GF0034567	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF2431 [IPR019446] (1)	-	C_unshiu_00080_mRNA_39.1	-
GF0034566	0	1	0	Hypothetical protein (1)			-	C_unshiu_00080_mRNA_38.1	-
GF0034565	0	1	0	Hypothetical protein (1)			-	C_unshiu_00080_mRNA_36.1	-
GF0034564	0	1	0	Hypothetical protein (1)			-	C_unshiu_00080_mRNA_35.1	-
GF0034563	0	1	0	Hypothetical protein (1)			-	C_unshiu_00080_mRNA_32.1	-
GF0034562	0	1	0	NBS-LRR type disease resistance protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00080_mRNA_31.1	-
GF0034561	0	1	0	Importin subunit alpha (1)	protein binding [GO:0005515 molecular_function] (1); binding [GO:0005488 molecular_function] (1)	Armadillo-type fold [IPR016024] (1); Armadillo-like helical [IPR011989] (1); Atypical Arm repeat [IPR032413] (1); Armadillo [IPR000225] (1)	-	C_unshiu_00080_mRNA_29.1	-
GF0034560	0	1	0	Hypothetical protein (1)			-	C_unshiu_00080_mRNA_27.1	-
GF0034559	0	1	0	Hypothetical protein (1)	binding [GO:0005488 molecular_function] (1)	Armadillo-type fold [IPR016024] (1)	-	C_unshiu_00080_mRNA_25.1	-
GF0034558	0	1	0	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	C_unshiu_00080_mRNA_19.1	-
GF0034557	0	1	0	Hypothetical protein (1)	protein prenylation [GO:0018342 biological_process] (1); protein prenyltransferase activity [GO:0008318 molecular_function] (1)	Protein prenyltransferase, alpha subunit [IPR002088] (1)	-	C_unshiu_00080_mRNA_18.1	-
GF0034556	0	1	0	Hypothetical protein (1)			-	C_unshiu_00080_mRNA_17.1	-
GF0034555	0	1	0	Hypothetical protein (1)			-	C_unshiu_00080_mRNA_13.1	-
GF0034554	0	1	0	Hypothetical protein (1)			-	C_unshiu_00079_mRNA_8.1	-
GF0034553	0	1	0	Hypothetical protein (1)		Lysine-rich nucleolar protein 1 [IPR028125] (1); Small acidic protein-like domain [IPR028124] (1)	-	C_unshiu_00079_mRNA_67.1	-
GF0034552	0	1	0	Hypothetical protein (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Serine/threonine-protein kinase, active site [IPR008271] (1)	-	C_unshiu_00079_mRNA_5.1	-
GF0034551	0	1	0	Tubulin beta-1 chain (1)	GTPase activity [GO:0003924 molecular_function] (1); structural constituent of cytoskeleton [GO:0005200 molecular_function] (1); microtubule [GO:0005874 cellular_component] (1); GTP binding [GO:0005525 molecular_function] (1); microtubule-based process [GO:0007017 biological_process] (1)	Beta tubulin [IPR002453] (1); Tubulin, conserved site [IPR017975] (1); Tubulin/FtsZ, GTPase domain [IPR003008] (1); Tubulin, C-terminal [IPR023123] (1); Tubulin/FtsZ, C-terminal [IPR008280] (1); Tubulin [IPR000217] (1)	-	C_unshiu_00079_mRNA_49.1	-
GF0034550	0	1	0	Hypothetical protein (1)			-	C_unshiu_00079_mRNA_42.1	-
GF0034549	0	1	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	Zinc finger, BED-type [IPR003656] (1)	-	C_unshiu_00079_mRNA_33.1	-
GF0034548	0	1	0	Hypothetical protein (1)	integral component of membrane [GO:0016021 cellular_component] (1); membrane [GO:0016020 cellular_component] (1); transmembrane transporter activity [GO:0022857 molecular_function] (1)	WAT1-related protein [IPR030184] (1); EamA domain [IPR000620] (1)	-	C_unshiu_00079_mRNA_32.1	-
GF0034547	0	1	0	Auxin-induced 5NG4 (1)	integral component of membrane [GO:0016021 cellular_component] (1); transmembrane transporter activity [GO:0022857 molecular_function] (1); membrane [GO:0016020 cellular_component] (1)	EamA domain [IPR000620] (1); WAT1-related protein [IPR030184] (1)	-	C_unshiu_00079_mRNA_31.1	-
GF0034546	0	1	0	Hypothetical protein (1)			-	C_unshiu_00079_mRNA_29.1	-
GF0034545	0	1	0	Hypothetical protein (1)			-	C_unshiu_00079_mRNA_11.1	-
GF0034544	0	1	0	Hypothetical protein (1)			-	C_unshiu_00078_mRNA_9.1	-
GF0034543	0	1	0	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1)	Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450 [IPR001128] (1)	-	C_unshiu_00078_mRNA_7.1	-
GF0034542	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	TRAF-like [IPR008974] (1); MATH/TRAF domain [IPR002083] (1)	-	C_unshiu_00078_mRNA_39.1	-
GF0034541	0	1	0	Hypothetical protein (1)			-	C_unshiu_00078_mRNA_23.1	-
GF0034540	0	1	0	Hypothetical protein (1)			-	C_unshiu_00078_mRNA_22.1	-
GF0034539	0	1	0	Hypothetical protein (1)			-	C_unshiu_00078_mRNA_13.1	-
GF0034538	0	1	0	Hypothetical protein (1)			-	C_unshiu_00078_mRNA_12.1	-
GF0034537	0	1	0	Hypothetical protein (1)			-	C_unshiu_00077_mRNA_75.1	-
GF0034536	0	1	0	Hexosyltransferase (1)	transferase activity, transferring glycosyl groups [GO:0016757 molecular_function] (1); polygalacturonate 4-alpha-galacturonosyltransferase activity [GO:0047262 molecular_function] (1)	Plant galacturonosyltransferase GAUT [IPR029993] (1); Nucleotide-diphospho-sugar transferases [IPR029044] (1); Glycosyl transferase, family 8 [IPR002495] (1)	-	C_unshiu_00077_mRNA_64.1	-
GF0034535	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ubiquitin-related domain [IPR029071] (1); Ubiquitin [IPR019956] (1); Ubiquitin domain [IPR000626] (1)	-	C_unshiu_00077_mRNA_1.1	-
GF0034534	0	1	0	Hypothetical protein (1)			-	C_unshiu_00076_mRNA_59.1	-
GF0034533	0	1	0	Hypothetical protein (1)			-	C_unshiu_00076_mRNA_50.1	-
GF0034532	0	1	0	Lipoxygenase (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen [GO:0016702 molecular_function] (1); metal ion binding [GO:0046872 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	PLAT/LH2 domain [IPR001024] (1); Lipoxygenase, domain 3 [IPR027433] (1); Lipoxygenase [IPR000907] (1); Lipoxygenase, plant [IPR001246] (1); Lipoxygenase, C-terminal [IPR013819] (1)	-	C_unshiu_00076_mRNA_40.1	-
GF0034531	0	1	0	G-type lectin S-receptor-like serine/threonine-protein kinase RLK1 (1)	protein serine/threonine kinase activity [GO:0004674 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase-like domain [IPR011009] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); S-receptor-like serine/threonine-protein kinase [IPR024171] (1); Protein kinase domain [IPR000719] (1); Bulb-type lectin domain [IPR001480] (1); Protein kinase, ATP binding site [IPR017441] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1)	-	C_unshiu_00076_mRNA_30.1	-
GF0034530	0	1	0	Hypothetical protein (1)			-	C_unshiu_00076_mRNA_26.1	-
GF0034529	0	1	0	G-type lectin S-receptor-like serine/threonine-protein kinase RLK1 (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1)	Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Protein kinase, ATP binding site [IPR017441] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase domain [IPR000719] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_00076_mRNA_21.1	-
GF0034528	0	1	0	Hypothetical protein (1)		Bulb-type lectin domain [IPR001480] (1)	-	C_unshiu_00076_mRNA_19.1	-
GF0034527	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Ribonuclease H domain [IPR002156] (1)	-	C_unshiu_00076_mRNA_15.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0034526	0	1	0	Hypothetical protein (1)		NAD(P)-binding domain [IPR016040] (1)	-	C_unshiu_00075_mRNA_43.1	-
GF0034525	0	1	0	Hypothetical protein (1)			-	C_unshiu_00075_mRNA_42.1	-
GF0034524	0	1	0	Hypothetical protein (1)			-	C_unshiu_00075_mRNA_41.1	-
GF0034523	0	1	0	Hypothetical protein (1)		Gag-polypeptide of LTR copia-type [IPR029472] (1)	-	C_unshiu_00075_mRNA_40.1	-
GF0034522	0	1	0	Transcription factor (1)	ATP-dependent DNA helicase activity [GO:0004003 molecular_function] (1); nucleus [GO:0005634 cellular_component] (1); nucleotide-excision repair [GO:0006289 biological_process] (1); core TFIIH complex [GO:0000439 cellular_component] (1)	Transcription factor TFIIH subunit p52/Tfb2 [IPR004598] (1); Helicase XPB/Ssl2, N-terminal domain [IPR032830] (1)	-	C_unshiu_00075_mRNA_4.1	-
GF0034521	0	1	0	Hypothetical protein (1)			-	C_unshiu_00075_mRNA_39.1	-
GF0034520	0	1	0	Hypothetical protein (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Pentatricopeptide repeat [IPR002885] (1); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_00075_mRNA_37.1	-
GF0034519	0	1	0	Hypothetical protein (1)			-	C_unshiu_00075_mRNA_36.1	-
GF0034518	0	1	0	Hypothetical protein (1)			-	C_unshiu_00075_mRNA_32.1	-
GF0034517	0	1	0	Hypothetical protein (1)			-	C_unshiu_00075_mRNA_25.1	-
GF0034516	0	1	0	Hypothetical protein (1)	nucleotide-excision repair [GO:0006289 biological_process] (1); core TFIIH complex [GO:0000439 cellular_component] (1); ATP-dependent DNA helicase activity [GO:0004003 molecular_function] (1); nucleus [GO:0005634 cellular_component] (1)	Transcription factor TFIIH subunit p52/Tfb2 [IPR004598] (1)	-	C_unshiu_00075_mRNA_1.1	-
GF0034515	0	1	0	Hypothetical protein (1)			-	C_unshiu_00074_mRNA_69.1	-
GF0034514	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Viral movement protein [IPR028919] (1)	-	C_unshiu_00074_mRNA_67.1	-
GF0034513	0	1	0	Hypothetical protein (1)			-	C_unshiu_00074_mRNA_60.1	-
GF0034512	0	1	0	Hypothetical protein (1)			-	C_unshiu_00074_mRNA_58.1	-
GF0034511	0	1	0	Hypothetical protein (1)			-	C_unshiu_00074_mRNA_56.1	-
GF0034510	0	1	0	Hypothetical protein (1)			-	C_unshiu_00074_mRNA_55.1	-
GF0034509	0	1	0	Dual specificity phosphatase Cdc25 (1)		Rhodanese-like domain [IPR001763] (1)	-	C_unshiu_00074_mRNA_54.1	-
GF0034508	0	1	0	Hypothetical protein (1)		Rhodanese-like domain [IPR001763] (1)	-	C_unshiu_00074_mRNA_53.1	-
GF0034507	0	1	0	Hypothetical protein (1)			-	C_unshiu_00074_mRNA_51.1	-
GF0034506	0	1	0	Hypothetical protein (1)			-	C_unshiu_00074_mRNA_50.1	-
GF0034505	0	1	0	Hypothetical protein (1)			-	C_unshiu_00074_mRNA_49.1	-
GF0034504	0	1	0	Hypothetical protein (1)			-	C_unshiu_00074_mRNA_46.1	-
GF0034503	0	1	0	Hypothetical protein (1)			-	C_unshiu_00074_mRNA_45.1	-
GF0034502	0	1	0	Hypothetical protein (1)			-	C_unshiu_00074_mRNA_44.1	-
GF0034501	0	1	0	Hypothetical protein (1)			-	C_unshiu_00074_mRNA_39.1	-
GF0034500	0	1	0	Trichome birefringence-like protein (1)		Trichome birefringence-like family [IPR029962] (1); PMR5 N-terminal domain [IPR025846] (1); PC-Esterase [IPR026057] (1)	-	C_unshiu_00074_mRNA_15.1	-
GF0034499	0	1	0	Hypothetical protein (1)			-	C_unshiu_00072_mRNA_57.1	-
GF0034498	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00072_mRNA_55.1	-
GF0034497	0	1	0	Hypothetical protein (1)			-	C_unshiu_00072_mRNA_52.1	-
GF0034496	0	1	0	Hypothetical protein (1)		Cytochrome c oxidase assembly protein PET191 [IPR018793] (1)	-	C_unshiu_00072_mRNA_49.1	-
GF0034495	0	1	0	P-type ATPase superfamily (1)	integral component of membrane [GO:0016021 cellular_component] (1); nucleotide binding [GO:0000166 molecular_function] (1)	P-type ATPase, phosphorylation site [IPR018303] (1); P-type ATPase [IPR001757] (1); P-type ATPase, cytoplasmic domain N [IPR023299] (1); HAD-like domain [IPR023214] (1)	-	C_unshiu_00072_mRNA_48.1	-
GF0034494	0	1	0	Hypothetical protein (1)			-	C_unshiu_00072_mRNA_43.1	-
GF0034493	0	1	0	Extensin (1)			-	C_unshiu_00072_mRNA_42.1	-
GF0034492	0	1	0	Extensin (1)			-	C_unshiu_00072_mRNA_39.1	-
GF0034491	0	1	0	Hypothetical protein (1)			-	C_unshiu_00072_mRNA_37.1	-
GF0034490	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF2431 [IPR019446] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	C_unshiu_00072_mRNA_33.1	-
GF0034489	0	1	0	Hypothetical protein (1)		NAD(P)-binding domain [IPR016040] (1)	-	C_unshiu_00072_mRNA_3.1	-
GF0034488	0	1	0	Hypothetical protein (1)			-	C_unshiu_00072_mRNA_20.1	-
GF0034487	0	1	0	Hypothetical protein (1)			-	C_unshiu_00071_mRNA_48.1	-
GF0034486	0	1	0	Hypothetical protein (1)			-	C_unshiu_00071_mRNA_47.1	-
GF0034485	0	1	0	Hypothetical protein (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Serine/threonine-protein kinase, active site [IPR008271] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	-	C_unshiu_00071_mRNA_45.1	-
GF0034484	0	1	0	Hypothetical protein (1)			-	C_unshiu_00071_mRNA_44.1	-
GF0034483	0	1	0	Hypothetical protein (1)			-	C_unshiu_00071_mRNA_43.1	-
GF0034482	0	1	0	Hypothetical protein (1)			-	C_unshiu_00071_mRNA_40.1	-
GF0034481	0	1	0	Hypothetical protein (1)			-	C_unshiu_00071_mRNA_15.1	-
GF0034480	0	1	0	General transcription factor 2-related zinc finger protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Domain of unknown function DUF4371 [IPR025398] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00071_mRNA_11.1	-
GF0034479	0	1	0	Hypothetical protein (1)		Bulb-type lectin domain [IPR001480] (1)	-	C_unshiu_00070_mRNA_49.1	-
GF0034478	0	1	0	G-type lectin S-receptor-like serine/threonine-protein kinase (1)	protein binding [GO:0005515 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1); protein serine/threonine kinase activity [GO:0004674 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); recognition of pollen [GO:0048544 biological_process] (1)	S-locus glycoprotein domain [IPR000858] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); EGF-like domain [IPR000742] (1); Protein kinase, ATP binding site [IPR017441] (1); S-locus receptor kinase, C-terminal [IPR021820] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); S-locus, receptor kinase [IPR022126] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Bulb-type lectin domain [IPR001480] (1); PAN/Apple domain [IPR003609] (1); Protein kinase domain [IPR000719] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_00070_mRNA_47.1	-
GF0034477	0	1	0	Anthocyanidin reductase (1)	catalytic activity [GO:0003824 molecular_function] (1); coenzyme binding [GO:0050662 molecular_function] (1)	NAD(P)-binding domain [IPR016040] (1); NAD-dependent epimerase/dehydratase, N-terminal domain [IPR001509] (1)	-	C_unshiu_00070_mRNA_33.1	-
GF0034476	0	1	0	DNA-binding storekeeper protein-related transcriptional regulator, putative (1)		Protein of unknown function DUF573 [IPR007592] (1)	-	C_unshiu_00070_mRNA_30.1	-
GF0034475	0	1	0	Hypothetical protein (1)			-	C_unshiu_00070_mRNA_21.1	-
GF0034474	0	1	0	Cysteine-rich receptor-like protein kinase 25 (1)		Gnk2-homologous domain [IPR002902] (1)	-	C_unshiu_00070_mRNA_20.1	-
GF0034473	0	1	0	Cysteine-rich RLK 29 (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Protein kinase-like domain [IPR011009] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Gnk2-homologous domain [IPR002902] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1)	-	C_unshiu_00070_mRNA_18.1	-
GF0034472	0	1	0	Hypothetical protein (1)	membrane [GO:0016020 cellular_component] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1)	Calcium-dependent channel, 7TM region, putative phosphate [IPR003864] (1); 10TM putative phosphate transporter, cytosolic domain [IPR027815] (1); Glycoside hydrolase superfamily [IPR017853] (1); Glycoside hydrolase, catalytic domain [IPR013781] (1); Glycosyl hydrolase, family 13, all-beta [IPR013780] (1); Calcium permeable stress-gated cation channel 1, N-terminal transmembrane domain [IPR032880] (1)	-	C_unshiu_00069_mRNA_53.1	-
GF0034471	0	1	0	Hypothetical protein (1)	metal ion binding [GO:0046872 molecular_function] (1); metal ion transport [GO:0030001 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Heavy metal-associated domain, HMA [IPR006121] (1); Ribonuclease H-like domain [IPR012337] (1); Zinc finger C2H2-type/integrase DNA-binding domain [IPR013087] (1); Zinc finger, C2H2 [IPR007087] (1)	-	C_unshiu_00069_mRNA_51.1	-
GF0034470	0	1	0	Hypothetical protein (1)	peroxidase activity [GO:0004601 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); heme binding [GO:0020037 molecular_function] (1); response to oxidative stress [GO:0006979 biological_process] (1)	Haem peroxidase [IPR010255] (1); Haem peroxidase, plant/fungal/bacterial [IPR002016] (1)	-	C_unshiu_00069_mRNA_5.1	-
GF0034469	0	1	0	Hypothetical protein (1)			-	C_unshiu_00069_mRNA_41.1	-
GF0034468	0	1	0	Hypothetical protein (1)			-	C_unshiu_00069_mRNA_27.1	-
GF0034467	0	1	0	Hypothetical protein (1)		Major facilitator superfamily domain [IPR020846] (1)	-	C_unshiu_00069_mRNA_23.1	-
GF0034466	0	1	0	Histone H2A (1)	nucleosome [GO:0000786 cellular_component] (1); protein heterodimerization activity [GO:0046982 molecular_function] (1); nucleus [GO:0005634 cellular_component] (1); DNA binding [GO:0003677 molecular_function] (1)	Histone H2A/H2B/H3 [IPR007125] (1); Histone H2A, C-terminal domain [IPR032454] (1); Histone-fold [IPR009072] (1); Histone H2A [IPR002119] (1)	-	C_unshiu_00069_mRNA_11.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0034465	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00068_mRNA_45.1	-
GF0034464	0	1	0	Hypothetical protein (1)	methyltransferase activity [GO:0008168 molecular_function] (1)	Bin3-type S-adenosyl-L-methionine binding domain [IPR024160] (1); RNA methyltransferase bin3, C-terminal [IPR010675] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	C_unshiu_00068_mRNA_29.1	-
GF0034463	0	1	0	Hypothetical protein (1)			-	C_unshiu_00068_mRNA_16.1	-
GF0034462	0	1	0	Alpha-amylase type B isozyme (1)	catalytic activity [GO:0003824 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1); alpha-amylase activity [GO:0004556 molecular_function] (1); cation binding [GO:0043169 molecular_function] (1); calcium ion binding [GO:0005509 molecular_function] (1)	Glycosyl hydrolase, family 13, all-beta [IPR013780] (1); Glycoside hydrolase, catalytic domain [IPR013781] (1); Glycosyl hydrolase, family 13, catalytic domain [IPR006047] (1); Glycosyl hydrolase, family 13, subfamily, catalytic domain [IPR006589] (1); Glycoside hydrolase superfamily [IPR017853] (1); Glycoside hydrolase, family 13 [IPR015902] (1); Alpha-amylase, C-terminal beta-sheet [IPR012850] (1)	-	C_unshiu_00067_mRNA_6.1	-
GF0034461	0	1	0	Hypothetical protein (1)	transporter activity [GO:0005215 molecular_function] (1); transport [GO:0006810 biological_process] (1); membrane [GO:0016020 cellular_component] (1)	Proton-dependent oligopeptide transporter family [IPR000109] (1)	-	C_unshiu_00067_mRNA_58.1	-
GF0034460	0	1	0	Hypothetical protein (1)	membrane [GO:0016020 cellular_component] (1); transport [GO:0006810 biological_process] (1); potassium ion transmembrane transport [GO:0071805 biological_process] (1); potassium ion transmembrane transporter activity [GO:0015079 molecular_function] (1); transporter activity [GO:0005215 molecular_function] (1)	Proton-dependent oligopeptide transporter family [IPR000109] (1); Potassium transporter [IPR003855] (1)	-	C_unshiu_00067_mRNA_57.1	-
GF0034459	0	1	0	UDP-glucose flavonoid 3-O-glucosyltransferase 7 (1)	transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Tudor domain [IPR002999] (1); UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	-	C_unshiu_00067_mRNA_48.1	-
GF0034458	0	1	0	Hypothetical protein (1)			-	C_unshiu_00067_mRNA_30.1	-
GF0034457	0	1	0	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); peroxidase activity [GO:0004601 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); response to oxidative stress [GO:0006979 biological_process] (1)	Haem peroxidase [IPR010255] (1); Plant peroxidase [IPR000823] (1); Prolamin-like domain [IPR008502] (1); Haem peroxidase, plant/fungal/bacterial [IPR002016] (1)	-	C_unshiu_00067_mRNA_24.1	-
GF0034456	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat-containing domain [IPR020683] (1); Ankyrin repeat [IPR002110] (1)	-	C_unshiu_00066_mRNA_88.1	-
GF0034455	0	1	0	Hypothetical protein (1)			-	C_unshiu_00066_mRNA_87.1	-
GF0034454	0	1	0	Hypothetical protein (1)			-	C_unshiu_00066_mRNA_86.1	-
GF0034453	0	1	0	Hypothetical protein (1)			-	C_unshiu_00066_mRNA_85.1	-
GF0034452	0	1	0	Hypothetical protein (1)		Prolamin-like domain [IPR008502] (1)	-	C_unshiu_00066_mRNA_8.1	-
GF0034451	0	1	0	Hypothetical protein (1)			-	C_unshiu_00066_mRNA_72.1	-
GF0034450	0	1	0	Hypothetical protein (1)			-	C_unshiu_00066_mRNA_68.1	-
GF0034449	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Helicase, C-terminal [IPR001650] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); ATP-dependent RNA helicase DEAD-box, conserved site [IPR000629] (1); DEAD/DEAH box helicase domain [IPR011545] (1); Helicase superfamily 1/2, ATP-binding domain [IPR014001] (1); RNA helicase, DEAD-box type, Q motif [IPR014014] (1)	-	C_unshiu_00066_mRNA_57.1	-
GF0034448	0	1	0	Hypothetical protein (1)		Exostosin-like [IPR004263] (1)	-	C_unshiu_00066_mRNA_42.1	-
GF0034447	0	1	0	Hypothetical protein (1)	sucrose metabolic process [GO:0005985 biological_process] (1); sucrose synthase activity [GO:0016157 molecular_function] (1)	Sucrose-phosphate synthase [IPR006380] (1); Sucrose synthase [IPR000368] (1)	-	C_unshiu_00066_mRNA_39.1	-
GF0034446	0	1	0	Actin-related protein 2/3 complex subunit 3 (1)	Arp2/3 protein complex [GO:0005885 cellular_component] (1); Arp2/3 complex-mediated actin nucleation [GO:0034314 biological_process] (1); regulation of actin filament polymerization [GO:0030833 biological_process] (1); cytoskeleton [GO:0005856 cellular_component] (1)	Actin-related protein 2/3 complex subunit 3 [IPR007204] (1)	-	C_unshiu_00066_mRNA_29.1	-
GF0034445	0	1	0	Hypothetical protein (1)			-	C_unshiu_00066_mRNA_21.1	-
GF0034444	0	1	0	Hypothetical protein (1)			-	C_unshiu_00065_mRNA_75.1	-
GF0034443	0	1	0	Hypothetical protein (1)	catalytic activity [GO:0003824 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Thiolase-like [IPR016039] (1); Beta-ketoacyl synthase, N-terminal [IPR014030] (1)	-	C_unshiu_00065_mRNA_61.1	-
GF0034442	0	1	0	Hypothetical protein (1)			-	C_unshiu_00065_mRNA_59.1	-
GF0034441	0	1	0	Hypothetical protein (1)	catalytic activity [GO:0003824 molecular_function] (1); oxidoreductase activity [GO:0016491 molecular_function] (1)	Aldolase-type TIM barrel [IPR013785] (1); FMN-dependent dehydrogenase [IPR000262] (1)	-	C_unshiu_00065_mRNA_54.1	-
GF0034440	0	1	0	Hypothetical protein (1)	metabolic process [GO:0008152 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1)	Beta-ketoacyl synthase, N-terminal [IPR014030] (1); Beta-ketoacyl synthase, active site [IPR018201] (1); Thiolase-like [IPR016039] (1)	-	C_unshiu_00065_mRNA_51.1	-
GF0034439	0	1	0	Hypothetical protein (1)			-	C_unshiu_00065_mRNA_47.1	-
GF0034438	0	1	0	Hypothetical protein (1)		Protein of unknown function DUF594 [IPR007658] (1)	-	C_unshiu_00065_mRNA_46.1	-
GF0034437	0	1	0	Hypothetical protein (1)			-	C_unshiu_00065_mRNA_45.1	-
GF0034436	0	1	0	Hypothetical protein (1)			-	C_unshiu_00065_mRNA_43.1	-
GF0034435	0	1	0	Hypothetical protein (1)			-	C_unshiu_00065_mRNA_42.1	-
GF0034434	0	1	0	Hypothetical protein (1)			-	C_unshiu_00065_mRNA_41.1	-
GF0034433	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00065_mRNA_31.1	-
GF0034432	0	1	0	Hypothetical protein (1)	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen [GO:0016702 molecular_function] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1); metal ion binding [GO:0046872 molecular_function] (1)	Lipoxygenase, domain 3 [IPR027433] (1); Lipoxygenase [IPR000907] (1); Cytochrome P450 [IPR001128] (1); Lipoxygenase, C-terminal [IPR013819] (1)	-	C_unshiu_00065_mRNA_17.1	-
GF0034431	0	1	0	Kinase 1B (1)	ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase, ATP binding site [IPR017441] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1)	-	C_unshiu_00065_mRNA_10.1	-
GF0034430	0	1	0	Hypothetical protein (1)		Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_00064_mRNA_68.1	-
GF0034429	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00064_mRNA_65.1	-
GF0034428	0	1	0	Hypothetical protein (1)			-	C_unshiu_00064_mRNA_64.1	-
GF0034427	0	1	0	Hypothetical protein (1)			-	C_unshiu_00064_mRNA_63.1	-
GF0034426	0	1	0	Hypothetical protein (1)	polysaccharide binding [GO:0030247 molecular_function] (1)	Wall-associated receptor kinase, galacturonan-binding domain [IPR025287] (1)	-	C_unshiu_00064_mRNA_62.1	-
GF0034425	0	1	0	Hypothetical protein (1)	methyltransferase activity [GO:0008168 molecular_function] (1)	SAM dependent carboxyl methyltransferase [IPR005299] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	C_unshiu_00064_mRNA_42.1	-
GF0034424	0	1	0	Repressor of RNA polymerase III transcription (1)	negative regulation of transcription from RNA polymerase III promoter [GO:0016480 biological_process] (1)	Repressor of RNA polymerase III transcription Maf1 [IPR015257] (1)	-	C_unshiu_00064_mRNA_37.1	-
GF0034423	0	1	0	Hypothetical protein (1)			-	C_unshiu_00064_mRNA_36.1	-
GF0034422	0	1	0	Hypothetical protein (1)		5'-3' exoribonuclease [IPR027073] (1); Domain of unknown function DUF1985 [IPR015410] (1)	-	C_unshiu_00064_mRNA_34.1	-
GF0034421	0	1	0	Hypothetical protein (1)	sequence-specific DNA binding [GO:0043565 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (1)	Leucine zipper, homeobox-associated [IPR003106] (1)	-	C_unshiu_00064_mRNA_1.1	-
GF0034420	0	1	0	Hypothetical protein (1)			-	C_unshiu_00063_mRNA_50.1	-
GF0034419	0	1	0	Hypothetical protein (1)			-	C_unshiu_00063_mRNA_5.1	-
GF0034418	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00063_mRNA_48.1	-
GF0034417	0	1	0	Hypothetical protein (1)			-	C_unshiu_00063_mRNA_4.1	-
GF0034416	0	1	0	Hypothetical protein (1)			-	C_unshiu_00063_mRNA_27.1	-
GF0034415	0	1	0	Hypothetical protein (1)			-	C_unshiu_00063_mRNA_25.1	-
GF0034414	0	1	0	Hypothetical protein (1)			-	C_unshiu_00063_mRNA_23.1	-
GF0034413	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_00063_mRNA_21.1	-
GF0034412	0	1	0	Hypothetical protein (1)			-	C_unshiu_00063_mRNA_15.1	-
GF0034411	0	1	0	Hypothetical protein (1)		EEIG1/EHBP1 N-terminal domain [IPR019448] (1)	-	C_unshiu_00063_mRNA_1.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0034410	0	1	0	Hypothetical protein (1)			-	C_unshiu_00062_mRNA_52.1	-
GF0034409	0	1	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1)	-	C_unshiu_00062_mRNA_34.1	-
GF0034408	0	1	0	Hypothetical protein (1)			-	C_unshiu_00062_mRNA_18.1	-
GF0034407	0	1	0	Hypothetical protein (1)			-	C_unshiu_00062_mRNA_17.1	-
GF0034406	0	1	0	Hypothetical protein (1)			-	C_unshiu_00062_mRNA_12.1	-
GF0034405	0	1	0	Hypothetical protein (1)			-	C_unshiu_00062_mRNA_11.1	-
GF0034404	0	1	0	Hypothetical protein (1)			-	C_unshiu_00061_mRNA_67.1	-
GF0034403	0	1	0	Hypothetical protein (1)			-	C_unshiu_00061_mRNA_60.1	-
GF0034402	0	1	0	Hypothetical protein (1)			-	C_unshiu_00061_mRNA_57.1	-
GF0034401	0	1	0	Hypothetical protein (1)			-	C_unshiu_00061_mRNA_56.1	-
GF0034400	0	1	0	Hypothetical protein (1)			-	C_unshiu_00061_mRNA_53.1	-
GF0034399	0	1	0	Hypothetical protein (1)			-	C_unshiu_00061_mRNA_52.1	-
GF0034398	0	1	0	Neutral alpha-glucosidase (1)	hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (1); catalytic activity [GO:0003824 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1); carbohydrate binding [GO:0030246 molecular_function] (1)	Glycoside hydrolase family 31 [IPR000322] (1); Glycosyl hydrolases family 31, active site [IPR030458] (1); Aldolase-type TIM barrel [IPR013785] (1); Galactose mutarotase-like domain [IPR011013] (1); Glycoside hydrolase superfamily [IPR017853] (1); Glycoside hydrolase family 31, N-terminal domain [IPR025887] (1)	-	C_unshiu_00061_mRNA_44.1	-
GF0034397	0	1	0	Hypothetical protein (1)			-	C_unshiu_00061_mRNA_41.1	-
GF0034396	0	1	0	Hypothetical protein (1)			-	C_unshiu_00061_mRNA_38.1	-
GF0034395	0	1	0	Hypothetical protein (1)			-	C_unshiu_00061_mRNA_37.1	-
GF0034394	0	1	0	Hypothetical protein (1)			-	C_unshiu_00061_mRNA_29.1	-
GF0034393	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_00061_mRNA_23.1	-
GF0034392	0	1	0	RNA-directed DNA polymerase (Reverse transcriptase) (1)		Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_00061_mRNA_21.1	-
GF0034391	0	1	0	Hypothetical protein (1)			-	C_unshiu_00061_mRNA_10.1	-
GF0034390	0	1	0	Hypothetical protein (1)			-	C_unshiu_00060_mRNA_61.1	-
GF0034389	0	1	0	Hypothetical protein (1)			-	C_unshiu_00060_mRNA_58.1	-
GF0034388	0	1	0	Hypothetical protein (1)			-	C_unshiu_00060_mRNA_57.1	-
GF0034387	0	1	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1)	Aspartic peptidase, active site [IPR001969] (1)	-	C_unshiu_00060_mRNA_55.1	-
GF0034386	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00060_mRNA_47.1	-
GF0034385	0	1	0	Gag protease polyprotein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_00060_mRNA_46.1	-
GF0034384	0	1	0	Cc-nbs-lrr resistance protein, putative isoform 4 (1)		DNA (cytosine-5)-methyltransferase 1, replication foci domain [IPR022702] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00060_mRNA_34.1	-
GF0034383	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00060_mRNA_30.1	-
GF0034382	0	1	0	Hypothetical protein (1)			-	C_unshiu_00060_mRNA_29.1	-
GF0034381	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	F-box domain [IPR001810] (1)	-	C_unshiu_00060_mRNA_24.1	-
GF0034380	0	1	0	Hypothetical protein (1)			-	C_unshiu_00060_mRNA_18.1	-
GF0034379	0	1	0	Hypothetical protein (1)			-	C_unshiu_00060_mRNA_15.1	-
GF0034378	0	1	0	Hypothetical protein (1)			-	C_unshiu_00060_mRNA_1.1	-
GF0034377	0	1	0	Hypothetical protein (1)			-	C_unshiu_00059_mRNA_9.1	-
GF0034376	0	1	0	Hypothetical protein (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	-	C_unshiu_00059_mRNA_55.1	-
GF0034375	0	1	0	Hypothetical protein (1)			-	C_unshiu_00059_mRNA_46.1	-
GF0034374	0	1	0	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_00059_mRNA_44.1	-
GF0034373	0	1	0	Retrotransposon protein, putative, Ty3-gypsy subclass, expressed (1)		Aspartic peptidase domain [IPR021109] (1)	-	C_unshiu_00059_mRNA_32.1	-
GF0034372	0	1	0	Hypothetical protein (1)			-	C_unshiu_00058_mRNA_6.1	-
GF0034371	0	1	0	Hypothetical protein (1)			-	C_unshiu_00058_mRNA_59.1	-
GF0034370	0	1	0	Hypothetical protein (1)		Histone deacetylase domain [IPR023801] (1); Histone deacetylase superfamily [IPR000286] (1)	-	C_unshiu_00058_mRNA_35.1	-
GF0034369	0	1	0	Hypothetical protein (1)		Histone deacetylase domain [IPR023801] (1); Histone deacetylase superfamily [IPR000286] (1)	-	C_unshiu_00058_mRNA_34.1	-
GF0034368	0	1	0	Hypothetical protein (1)			-	C_unshiu_00058_mRNA_33.1	-
GF0034367	0	1	0	Hypothetical protein (1)	mismatch repair complex [GO:0032300 cellular_component] (1); DNA binding [GO:0003677 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1); mismatch repair [GO:0006298 biological_process] (1); mismatched DNA binding [GO:0030983 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); DNA mismatch repair protein Msh2 [IPR032642] (1); DNA mismatch repair protein MutS, C-terminal [IPR000432] (1)	-	C_unshiu_00058_mRNA_30.1	-
GF0034366	0	1	0	Hypothetical protein (1)			-	C_unshiu_00058_mRNA_16.1	-
GF0034365	0	1	0	Hypothetical protein (1)			-	C_unshiu_00058_mRNA_13.1	-
GF0034364	0	1	0	Hypothetical protein (1)			-	C_unshiu_00058_mRNA_12.1	-
GF0034363	0	1	0	Hypothetical protein (1)			-	C_unshiu_00058_mRNA_1.1	-
GF0034362	0	1	0	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1); Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_00057_mRNA_62.1	-
GF0034361	0	1	0	Hypothetical protein (1)			-	C_unshiu_00057_mRNA_61.1	-
GF0034360	0	1	0	Hypothetical protein (1)			-	C_unshiu_00057_mRNA_59.1	-
GF0034359	0	1	0	Hypothetical protein (1)			-	C_unshiu_00057_mRNA_58.1	-
GF0034358	0	1	0	Hypothetical protein (1)			-	C_unshiu_00057_mRNA_57.1	-
GF0034357	0	1	0	Putative methyltransferase PMT21 (1)	methyltransferase activity [GO:0008168 molecular_function] (1)	Putative S-adenosyl-L-methionine-dependent methyltransferase [IPR004159] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	C_unshiu_00057_mRNA_54.1	-
GF0034356	0	1	0	Hypothetical protein (1)		Glutathione S-transferase, C-terminal [IPR004046] (1); Glutathione S-transferase, C-terminal-like [IPR010987] (1)	-	C_unshiu_00057_mRNA_45.1	-
GF0034355	0	1	0	Hypothetical protein (1)			-	C_unshiu_00057_mRNA_44.1	-
GF0034354	0	1	0	Hypothetical protein (1)			-	C_unshiu_00057_mRNA_43.1	-
GF0034353	0	1	0	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	C_unshiu_00057_mRNA_42.1	-
GF0034352	0	1	0	Hypothetical protein (1)			-	C_unshiu_00057_mRNA_41.1	-
GF0034351	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4219 [IPR025314] (1)	-	C_unshiu_00057_mRNA_40.1	-
GF0034350	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00057_mRNA_39.1	-
GF0034349	0	1	0	Voltage-gated potassium channel subunit beta (1)		Aldo/keto reductase/potassium channel subunit beta [IPR001395] (1); Potassium channel, voltage-dependent, beta subunit, KCNAB-related [IPR005399] (1); NADP-dependent oxidoreductase domain [IPR023210] (1)	-	C_unshiu_00057_mRNA_29.1	-
GF0034348	0	1	0	Hypothetical protein (1)			-	C_unshiu_00057_mRNA_25.1	-
GF0034347	0	1	0	Hypothetical protein (1)			-	C_unshiu_00057_mRNA_24.1	-
GF0034346	0	1	0	Hypothetical protein (1)			-	C_unshiu_00057_mRNA_21.1	-
GF0034345	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, PMZ-type [IPR006564] (1)	-	C_unshiu_00057_mRNA_2.1	-
GF0034344	0	1	0	UPF0481 protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	C_unshiu_00057_mRNA_17.1	-
GF0034343	0	1	0	Hypothetical protein (1)			-	C_unshiu_00057_mRNA_15.1	-
GF0034342	0	1	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1); FAR1 DNA binding domain [IPR004330] (1)	-	C_unshiu_00057_mRNA_10.1	-
GF0034341	0	1	0	Hypothetical protein (1)		Transposon, En/Spm-like [IPR004242] (1)	-	C_unshiu_00056_mRNA_79.1	-
GF0034340	0	1	0	Hypothetical protein (1)			-	C_unshiu_00056_mRNA_76.1	-
GF0034339	0	1	0	Hypothetical protein (1)			-	C_unshiu_00056_mRNA_70.1	-
GF0034338	0	1	0	Hypothetical protein (1)			-	C_unshiu_00056_mRNA_67.1	-
GF0034337	0	1	0	Hypothetical protein (1)		Chromo/chromo shadow domain [IPR000953] (1); Chromo domain-like [IPR016197] (1); Chromo domain [IPR023780] (1)	-	C_unshiu_00056_mRNA_66.1	-
GF0034336	0	1	0	Hypothetical protein (1)			-	C_unshiu_00056_mRNA_64.1	-
GF0034335	0	1	0	FAD-binding Berberine family protein (1)	flavin adenine dinucleotide binding [GO:0050660 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); oxidoreductase activity, acting on CH-OH group of donors [GO:0016614 molecular_function] (1); catalytic activity [GO:0003824 molecular_function] (1)	Berberine/berberine-like [IPR012951] (1); FAD-binding, type 2, subdomain 1 [IPR016167] (1); CO dehydrogenase flavoprotein-like, FAD-binding, subdomain 2 [IPR016169] (1); FAD linked oxidase, N-terminal [IPR006094] (1); FAD-binding, type 2 [IPR016166] (1)	-	C_unshiu_00056_mRNA_44.1	-
GF0034334	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	F-box domain [IPR001810] (1)	-	C_unshiu_00056_mRNA_38.1	-
GF0034333	0	1	0	Hypothetical protein (1)		F-box associated domain, type 3 [IPR013187] (1)	-	C_unshiu_00056_mRNA_37.1	-
GF0034332	0	1	0	Ferric reduction oxidase 2 (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1)	FAD-binding 8 [IPR013112] (1); Ferric reductase, NAD binding domain [IPR013121] (1); Ferredoxin reductase-type FAD-binding domain [IPR017927] (1); Ferric reductase transmembrane component-like domain [IPR013130] (1)	-	C_unshiu_00056_mRNA_11.1	-
GF0034331	0	1	0	Hypothetical protein (1)			-	C_unshiu_00055_mRNA_7.1	-
GF0034330	0	1	0	Hypothetical protein (1)			-	C_unshiu_00055_mRNA_59.1	-
GF0034329	0	1	0	Hypothetical protein (1)		Transposase, MuDR, plant [IPR004332] (1)	-	C_unshiu_00055_mRNA_39.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0034328	0	1	0	Hypothetical protein (1)			-	C_unshiu_00055_mRNA_26.1	-
GF0034327	0	1	0	Hypothetical protein (1)			-	C_unshiu_00055_mRNA_25.1	-
GF0034326	0	1	0	Hypothetical protein (1)	glycine dehydrogenase (decarboxylating) activity [GO:0004375 molecular_function] (1); glycine catabolic process [GO:0006546 biological_process] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Glycine cleavage system P protein [IPR020581] (1); Glycine cleavage system P-protein, N-terminal [IPR020580] (1); Pyridoxal phosphate-dependent transferase [IPR015424] (1)	-	C_unshiu_00055_mRNA_2.1	-
GF0034325	0	1	0	K(+) efflux antiporter 4 (1)	cation transport [GO:0006812 biological_process] (1); integral component of membrane [GO:0016021 cellular_component] (1); transmembrane transport [GO:0055085 biological_process] (1); solute:proton antiporter activity [GO:0015299 molecular_function] (1)	Histone deacetylase domain [IPR023801] (1); Histone deacetylase superfamily [IPR000286] (1); Cation/H+ exchanger [IPR006153] (1)	-	C_unshiu_00055_mRNA_11.1	-
GF0034324	0	1	0	Hypothetical protein (1)			-	C_unshiu_00054_mRNA_8.1	-
GF0034323	0	1	0	Hypothetical protein (1)			-	C_unshiu_00054_mRNA_70.1	-
GF0034322	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF1985 [IPR015410] (1); Agenet domain, plant type [IPR014002] (1); EMSY N-terminal [IPR005491] (1)	-	C_unshiu_00054_mRNA_66.1	-
GF0034321	0	1	0	Mutator-like transposase (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Zinc finger, PMZ-type [IPR006564] (1); Transposase, MuDR, plant [IPR004332] (1); Zinc finger, SWIM-type [IPR007527] (1)	-	C_unshiu_00054_mRNA_65.1	-
GF0034320	0	1	0	Disease resistance protein family, putative (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00054_mRNA_63.1	-
GF0034319	0	1	0	Disease resistance RPS5-like protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_00054_mRNA_62.1	-
GF0034318	0	1	0	Disease resistance protein family, putative (1)			-	C_unshiu_00054_mRNA_60.1	-
GF0034317	0	1	0	Disease resistance RPS5-like protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00054_mRNA_57.1	-
GF0034316	0	1	0	Hypothetical protein (1)			-	C_unshiu_00054_mRNA_55.1	-
GF0034315	0	1	0	Hypothetical protein (1)			-	C_unshiu_00054_mRNA_49.1	-
GF0034314	0	1	0	Hypothetical protein (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1)	Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	-	C_unshiu_00054_mRNA_48.1	-
GF0034313	0	1	0	Hypothetical protein (1)		Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_00054_mRNA_45.1	-
GF0034312	0	1	0	Receptor protein kinase (1)	ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1)	-	C_unshiu_00054_mRNA_44.1	-
GF0034311	0	1	0	Hypothetical protein (1)			-	C_unshiu_00054_mRNA_42.1	-
GF0034310	0	1	0	60S ribosomal protein L51, mitochondrial (1)		Ribosomal protein/NADH dehydrogenase domain [IPR007741] (1); Thioredoxin-like fold [IPR012336] (1)	-	C_unshiu_00054_mRNA_34.1	-
GF0034309	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Domain of unknown function DUF4283 [IPR025558] (1); Zinc finger, CCHC-type [IPR001878] (1); Zinc knuckle CX2CX4HX4C [IPR025836] (1)	-	C_unshiu_00054_mRNA_3.1	-
GF0034308	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00054_mRNA_24.1	-
GF0034307	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00054_mRNA_21.1	-
GF0034306	0	1	0	Hypothetical protein (1)			-	C_unshiu_00053_mRNA_8.1	-
GF0034305	0	1	0	Hypothetical protein (1)			-	C_unshiu_00053_mRNA_72.1	-
GF0034304	0	1	0	Hypothetical protein (1)			-	C_unshiu_00053_mRNA_68.1	-
GF0034303	0	1	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_00053_mRNA_65.1	-
GF0034302	0	1	0	Hypothetical protein (1)			-	C_unshiu_00053_mRNA_6.1	-
GF0034301	0	1	0	Hypothetical protein (1)			-	C_unshiu_00053_mRNA_5.1	-
GF0034300	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00053_mRNA_4.1	-
GF0034299	0	1	0	Hypothetical protein (1)	RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H domain [IPR002156] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00053_mRNA_37.1	-
GF0034298	0	1	0	Hypothetical protein (1)	photosynthesis, light reaction [GO:0019684 biological_process] (1); photosynthetic electron transport in photosystem II [GO:0009772 biological_process] (1); electron transporter, transferring electrons within the cyclic electron transport pathway of photosynthesis activity [GO:0045156 molecular_function] (1)	Photosynthetic reaction centre, L/M [IPR000484] (1)	-	C_unshiu_00053_mRNA_2.1	-
GF0034297	0	1	0	Hypothetical protein (1)			-	C_unshiu_00053_mRNA_10.1	-
GF0034296	0	1	0	Hypothetical protein (1)	DNA-directed RNA polymerase activity [GO:0003899 molecular_function] (1); ribonucleoside binding [GO:0032549 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1); hydrogen ion transmembrane transporter activity [GO:0015078 molecular_function] (1); ATP synthesis coupled proton transport [GO:0015986 biological_process] (1); transcription, DNA-templated [GO:0006351 biological_process] (1)	RNA polymerase, beta subunit, conserved site [IPR007121] (1); DNA-directed RNA polymerase, subunit 2 [IPR015712] (1); ATPase, F0 complex, subunit A [IPR000568] (1); ATPase, F0 complex, subunit A, active site [IPR023011] (1); RNA polymerase, N-terminal [IPR006592] (1); RNA polymerase, alpha subunit [IPR000722] (1); RNA polymerase Rpb2, domain 7 [IPR007641] (1); RNA polymerase Rpb2, OB-fold [IPR014724] (1); DNA-directed RNA polymerase, subunit 2, domain 6 [IPR007120] (1); RNA polymerase Rpb1, domain 1 [IPR007080] (1); RNA polymerase Rpb1, domain 3 [IPR007066] (1)	-	C_unshiu_00053_mRNA_1.1	-
GF0034295	0	1	0	Hypothetical protein (1)			-	C_unshiu_00052_mRNA_72.1	-
GF0034294	0	1	0	Hypothetical protein (1)			-	C_unshiu_00052_mRNA_71.1	-
GF0034293	0	1	0	Hypothetical protein (1)			-	C_unshiu_00052_mRNA_70.1	-
GF0034292	0	1	0	Hypothetical protein (1)			-	C_unshiu_00052_mRNA_69.1	-
GF0034291	0	1	0	Hypothetical protein (1)			-	C_unshiu_00052_mRNA_59.1	-
GF0034290	0	1	0	ABC transporter G family member 41 (1)	membrane [GO:0016020 cellular_component] (1); ATPase activity [GO:0016887 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1); nucleus [GO:0005634 cellular_component] (1)	AAA+ ATPase domain [IPR003593] (1); ABC transporter-like [IPR003439] (1); ABC-2 type transporter [IPR013525] (1); G10 protein [IPR001748] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00052_mRNA_53.1	-
GF0034289	0	1	0	Acetylcholinesterase (1)	nucleic acid binding [GO:0003676 molecular_function] (1); nucleus [GO:0005634 cellular_component] (1); hydrolase activity, acting on ester bonds [GO:0016788 molecular_function] (1)	Cleavage/polyadenylation specificity factor, A subunit, C-terminal [IPR004871] (1); SGNH hydrolase-type esterase domain [IPR013830] (1); GDSL lipase/esterase [IPR001087] (1)	-	C_unshiu_00052_mRNA_5.1	-
GF0034288	0	1	0	Hypothetical protein (1)			-	C_unshiu_00052_mRNA_4.1	-
GF0034287	0	1	0	Hypothetical protein (1)			-	C_unshiu_00052_mRNA_3.1	-
GF0034286	0	1	0	Geraniol 10-hydroxylase-like protein (1)	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1)	Cytochrome P450 [IPR001128] (1); Cytochrome P450, conserved site [IPR017972] (1); Cytochrome P450, E-class, group I [IPR002401] (1)	-	C_unshiu_00052_mRNA_19.1	-
GF0034285	0	1	0	Hypothetical protein (1)			-	C_unshiu_00052_mRNA_15.1	-
GF0034284	0	1	0	Hypothetical protein (1)			-	C_unshiu_00052_mRNA_12.1	-
GF0034283	0	1	0	Amine oxidase (flavin-containing) (1)	quinone binding [GO:0048038 molecular_function] (1); copper ion binding [GO:0005507 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); amine metabolic process [GO:0009308 biological_process] (1); primary amine oxidase activity [GO:0008131 molecular_function] (1)	Copper amine oxidase [IPR000269] (1); Copper amine oxidase, C-terminal [IPR015798] (1)	-	C_unshiu_00051_mRNA_71.1	-
GF0034282	0	1	0	Hypothetical protein (1)	quinone binding [GO:0048038 molecular_function] (1); copper ion binding [GO:0005507 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); amine metabolic process [GO:0009308 biological_process] (1); primary amine oxidase activity [GO:0008131 molecular_function] (1)	Copper amine oxidase, C-terminal [IPR015798] (1); Copper amine oxidase [IPR000269] (1)	-	C_unshiu_00051_mRNA_70.1	-
GF0034281	0	1	0	Hypothetical protein (1)			-	C_unshiu_00051_mRNA_7.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0034280	0	1	0	Sugar transport protein 13 (1)	membrane [GO:0016020 cellular_component] (1); transmembrane transporter activity [GO:0022857 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1); substrate-specific transmembrane transporter activity [GO:0022891 molecular_function] (1); transmembrane transport [GO:0055085 biological_process] (1); transporter activity [GO:0005215 molecular_function] (1)	Sugar transporter, conserved site [IPR005829] (1); Major facilitator superfamily domain [IPR020846] (1); Major facilitator, sugar transporter-like [IPR005828] (1); Sugar/inositol transporter [IPR003663] (1)	-	C_unshiu_00051_mRNA_63.1	-
GF0034279	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_00051_mRNA_20.1	-
GF0034278	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00051_mRNA_19.1	-
GF0034277	0	1	0	Hypothetical protein (1)			-	C_unshiu_00051_mRNA_18.1	-
GF0034276	0	1	0	Hypothetical protein (1)			-	C_unshiu_00051_mRNA_17.1	-
GF0034275	0	1	0	Hypothetical protein (1)			-	C_unshiu_00051_mRNA_16.1	-
GF0034274	0	1	0	Hypothetical protein (1)			-	C_unshiu_00051_mRNA_13.1	-
GF0034273	0	1	0	Hypothetical protein (1)			-	C_unshiu_00051_mRNA_11.1	-
GF0034272	0	1	0	Hypothetical protein (1)			-	C_unshiu_00050_mRNA_7.1	-
GF0034271	0	1	0	Hypothetical protein (1)			-	C_unshiu_00050_mRNA_6.1	-
GF0034270	0	1	0	Phospholipase C 3 (1)	hydrolase activity, acting on ester bonds [GO:0016788 molecular_function] (1); catalytic activity [GO:0003824 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Phosphoesterase [IPR007312] (1); Alkaline-phosphatase-like, core domain [IPR017850] (1)	-	C_unshiu_00050_mRNA_50.1	-
GF0034269	0	1	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00050_mRNA_5.1	-
GF0034268	0	1	0	Phospholipase A22 (1)		Phospholipase A2 domain [IPR016090] (1)	-	C_unshiu_00050_mRNA_48.1	-
GF0034267	0	1	0	Rho GTPase-activating 35 (1)	signal transduction [GO:0007165 biological_process] (1)	Pleckstrin homology domain [IPR001849] (1); Rho GTPase activation protein [IPR008936] (1); Ternary complex factor MIP1, leucine-zipper [IPR025757] (1); PH domain-like [IPR011993] (1); Rho GTPase-activating protein domain [IPR000198] (1)	-	C_unshiu_00050_mRNA_47.1	-
GF0034266	0	1	0	Hypothetical protein (1)			-	C_unshiu_00050_mRNA_3.1	-
GF0034265	0	1	0	Hypothetical protein (1)			-	C_unshiu_00050_mRNA_22.1	-
GF0034264	0	1	0	Hypothetical protein (1)			-	C_unshiu_00050_mRNA_2.1	-
GF0034263	0	1	0	Hypothetical protein (1)			-	C_unshiu_00050_mRNA_19.1	-
GF0034262	0	1	0	Hypothetical protein (1)			-	C_unshiu_00049_mRNA_69.1	-
GF0034261	0	1	0	Hypothetical protein (1)			-	C_unshiu_00049_mRNA_58.1	-
GF0034260	0	1	0	Hypothetical protein (1)			-	C_unshiu_00049_mRNA_44.1	-
GF0034259	0	1	0	Hypothetical protein (1)			-	C_unshiu_00049_mRNA_40.1	-
GF0034258	0	1	0	F-box protein interaction domain protein (1)	protein binding [GO:0005515 molecular_function] (1)	F-box associated domain, type 1 [IPR006527] (1); F-box domain [IPR001810] (1); F-box associated interaction domain [IPR017451] (1)	-	C_unshiu_00049_mRNA_37.1	-
GF0034257	0	1	0	Hypothetical protein (1)			-	C_unshiu_00049_mRNA_24.1	-
GF0034256	0	1	0	DNA ligase (1)	DNA repair [GO:0006281 biological_process] (1); DNA binding [GO:0003677 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1); DNA recombination [GO:0006310 biological_process] (1); DNA ligase (ATP) activity [GO:0003910 molecular_function] (1); DNA biosynthetic process [GO:0071897 biological_process] (1); DNA ligase activity [GO:0003909 molecular_function] (1); DNA ligation involved in DNA repair [GO:0051103 biological_process] (1)	DNA ligase, ATP-dependent, N-terminal [IPR012308] (1); DNA ligase, ATP-dependent, central [IPR012310] (1); DNA ligase, ATP-dependent, conserved site [IPR016059] (1); DNA ligase, ATP-dependent [IPR000977] (1)	-	C_unshiu_00049_mRNA_1.1	-
GF0034255	0	1	0	Chlorophyll a/b binding protein (1)	membrane [GO:0016020 cellular_component] (1); photosynthesis, light harvesting [GO:0009765 biological_process] (1)	Chlorophyll A-B binding protein, plant [IPR001344] (1); Chlorophyll a/b binding protein domain [IPR023329] (1)	-	C_unshiu_00048_mRNA_94.1	-
GF0034254	0	1	0	Light-harvesting complex II chlorophyll a/b binding protein, n-terminal part (1)	membrane [GO:0016020 cellular_component] (1); photosynthesis, light harvesting [GO:0009765 biological_process] (1)	Chlorophyll A-B binding protein, plant [IPR001344] (1)	-	C_unshiu_00048_mRNA_93.1	-
GF0034253	0	1	0	Chlorophyll a-b binding protein, chloroplastic (1)	photosynthesis, light harvesting [GO:0009765 biological_process] (1); membrane [GO:0016020 cellular_component] (1)	Chlorophyll A-B binding protein, plant [IPR001344] (1); Chlorophyll a/b binding protein domain [IPR023329] (1); Chlorophyll A-B binding protein [IPR022796] (1)	-	C_unshiu_00048_mRNA_92.1	-
GF0034252	0	1	0	Hypothetical protein (1)			-	C_unshiu_00048_mRNA_89.1	-
GF0034251	0	1	0	Hypothetical protein (1)			-	C_unshiu_00048_mRNA_47.1	-
GF0034250	0	1	0	Hypothetical protein (1)		Ankyrin repeat domain-containing protein 13 [IPR021832] (1)	-	C_unshiu_00048_mRNA_27.1	-
GF0034249	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); nucleus [GO:0005634 cellular_component] (1)	AUX/IAA protein [IPR003311] (1); PB1 domain [IPR000270] (1)	-	C_unshiu_00047_mRNA_92.1	-
GF0034248	0	1	0	Hypothetical protein (1)			-	C_unshiu_00047_mRNA_88.1	-
GF0034247	0	1	0	Hypothetical protein (1)			-	C_unshiu_00047_mRNA_73.1	-
GF0034246	0	1	0	Hypothetical protein (1)			-	C_unshiu_00047_mRNA_70.1	-
GF0034245	0	1	0	Hypothetical protein (1)			-	C_unshiu_00047_mRNA_7.1	-
GF0034244	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_00047_mRNA_6.1	-
GF0034243	0	1	0	Hypothetical protein (1)			-	C_unshiu_00047_mRNA_5.1	-
GF0034242	0	1	0	Hypothetical protein (1)			-	C_unshiu_00047_mRNA_49.1	-
GF0034241	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1); signal transduction [GO:0007165 biological_process] (1)	Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1)	-	C_unshiu_00047_mRNA_37.1	-
GF0034240	0	1	0	Hypothetical protein (1)			-	C_unshiu_00047_mRNA_34.1	-
GF0034239	0	1	0	GPI-anchored protein LORELEI (1)			-	C_unshiu_00047_mRNA_31.3	-
GF0034238	0	1	0	Hypothetical protein (1)			-	C_unshiu_00047_mRNA_3.1	-
GF0034237	0	1	0	Hypothetical protein (1)			-	C_unshiu_00047_mRNA_26.1	-
GF0034236	0	1	0	Hypothetical protein (1)			-	C_unshiu_00047_mRNA_24.1	-
GF0034235	0	1	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); serine-type endopeptidase activity [GO:0004252 molecular_function] (1)	Peptidase S8, subtilisin-related [IPR015500] (1); Peptidase S8/S53 domain [IPR000209] (1)	-	C_unshiu_00047_mRNA_2.1	-
GF0034234	0	1	0	Hypothetical protein (1)			-	C_unshiu_00047_mRNA_17.1	-
GF0034233	0	1	0	Subtilase family protein, putative (1)	proteolysis [GO:0006508 biological_process] (1); serine-type endopeptidase activity [GO:0004252 molecular_function] (1)	Peptidase S8, subtilisin-related [IPR015500] (1); Peptidase S8/S53 domain [IPR000209] (1); PA domain [IPR003137] (1); Peptidase S8 propeptide/proteinase inhibitor I9 [IPR010259] (1); Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1); Peptidase S8, subtilisin, Ser-active site [IPR023828] (1)	-	C_unshiu_00047_mRNA_1.1	-
GF0034232	0	1	0	Hypothetical protein (1)			-	C_unshiu_00046_mRNA_9.1	-
GF0034231	0	1	0	Hypothetical protein (1)			-	C_unshiu_00046_mRNA_81.1	-
GF0034230	0	1	0	Hypothetical protein (1)			-	C_unshiu_00046_mRNA_8.1	-
GF0034229	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00046_mRNA_75.1	-
GF0034228	0	1	0	UPF0481 protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	C_unshiu_00046_mRNA_60.1	-
GF0034227	0	1	0	DNA repair DNA-dependent ATPase RecA (1)	DNA repair [GO:0006281 biological_process] (1); DNA binding [GO:0003677 molecular_function] (1); DNA-dependent ATPase activity [GO:0008094 molecular_function] (1); SOS response [GO:0009432 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1); single-stranded DNA binding [GO:0003697 molecular_function] (1)	DNA recombination and repair protein RecA [IPR013765] (1); DNA recombination and repair protein RecA-like, ATP-binding domain [IPR020588] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00046_mRNA_6.1	-
GF0034226	0	1	0	Hypothetical protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	C_unshiu_00046_mRNA_59.1	-
GF0034225	0	1	0	Hypothetical protein (1)			-	C_unshiu_00046_mRNA_58.1	-
GF0034224	0	1	0	Hypothetical protein (1)			-	C_unshiu_00046_mRNA_50.1	-
GF0034223	0	1	0	Hypothetical protein (1)			-	C_unshiu_00046_mRNA_5.1	-
GF0034222	0	1	0	Iron-sulfur cluster assembly protein, putative (1)	iron-sulfur cluster binding [GO:0051536 molecular_function] (1); iron-sulfur cluster assembly [GO:0016226 biological_process] (1); structural molecule activity [GO:0005198 molecular_function] (1)	FeS cluster biogenesis [IPR000361] (1); FeS cluster insertion protein [IPR016092] (1); FeS cluster insertion, C-terminal, conserved site [IPR017870] (1)	-	C_unshiu_00046_mRNA_49.1	-
GF0034221	0	1	0	Hypothetical protein (1)		Metallo-dependent phosphatase-like [IPR029052] (1); Iron/zinc purple acid phosphatase-like C-terminal domain [IPR025733] (1)	-	C_unshiu_00046_mRNA_40.1	-
GF0034220	0	1	0	Hypothetical protein (1)			-	C_unshiu_00046_mRNA_4.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0034219	0	1	0	NAD(P)H-quinone oxidoreductase subunit K, chloroplastic (1)	4 iron, 4 sulfur cluster binding [GO:0051539 molecular_function] (1); iron-sulfur cluster binding [GO:0051536 molecular_function] (1); NADH dehydrogenase (ubiquinone) activity [GO:0008137 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); quinone binding [GO:0048038 molecular_function] (1)	NADH-ubiquinone oxidoreductase, 20 Kd subunit [IPR006138] (1); NADH:ubiquinone oxidoreductase-like, 20kDa subunit [IPR006137] (1)	-	C_unshiu_00046_mRNA_30.1	-
GF0034218	0	1	0	Hypothetical protein (1)			-	C_unshiu_00046_mRNA_2.1	-
GF0034217	0	1	0	Hypothetical protein (1)			-	C_unshiu_00045_mRNA_92.1	-
GF0034216	0	1	0	Hypothetical protein (1)		Immunoglobulin E-set [IPR014756] (1); Helicase, C-terminal [IPR001650] (1); Sec63 domain [IPR004179] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00045_mRNA_84.1	-
GF0034215	0	1	0	Hypothetical protein (1)			-	C_unshiu_00045_mRNA_82.1	-
GF0034214	0	1	0	Hypothetical protein (1)			-	C_unshiu_00045_mRNA_69.1	-
GF0034213	0	1	0	Hypothetical protein (1)			-	C_unshiu_00045_mRNA_62.1	-
GF0034212	0	1	0	Hypothetical protein (1)			-	C_unshiu_00045_mRNA_19.1	-
GF0034211	0	1	0	Hypothetical protein (1)			-	C_unshiu_00045_mRNA_18.1	-
GF0034210	0	1	0	Hypothetical protein (1)	carbohydrate binding [GO:0030246 molecular_function] (1)	Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Legume lectin domain [IPR001220] (1)	-	C_unshiu_00044_mRNA_47.1	-
GF0034209	0	1	0	Hypothetical protein (1)		Protein of unknown function DUF2921 [IPR021319] (1)	-	C_unshiu_00044_mRNA_40.1	-
GF0034208	0	1	0	Hypothetical protein (1)	RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H domain [IPR002156] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00044_mRNA_4.1	-
GF0034207	0	1	0	Hypothetical protein (1)			-	C_unshiu_00044_mRNA_31.1	-
GF0034206	0	1	0	Monosacharide transport protein (1)			-	C_unshiu_00044_mRNA_29.1	-
GF0034205	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_00044_mRNA_19.1	-
GF0034204	0	1	0	Hypothetical protein (1)			-	C_unshiu_00044_mRNA_18.1	-
GF0034203	0	1	0	Pectate lyase (1)	pectate lyase activity [GO:0030570 molecular_function] (1)	AmbAllergen [IPR018082] (1); Pectin lyase fold [IPR012334] (1); Pectate lyase/Amb allergen [IPR002022] (1); Pectate lyase, N-terminal [IPR007524] (1); Pectin lyase fold/virulence factor [IPR011050] (1)	-	C_unshiu_00044_mRNA_11.1	-
GF0034202	0	1	0	Hypothetical protein (1)			-	C_unshiu_00044_mRNA_10.1	-
GF0034201	0	1	0	Hypothetical protein (1)	transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (1)	Chloramphenicol acetyltransferase-like domain [IPR023213] (1); Transferase [IPR003480] (1)	-	C_unshiu_00044_mRNA_1.1	-
GF0034200	0	1	0	Hypothetical protein (1)	nucleus [GO:0005634 cellular_component] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Ubiquitin-conjugating enzyme E2 [IPR000608] (1); Ubiquitin-conjugating enzyme/RWD-like [IPR016135] (1); Ribonuclease CAF1 [IPR006941] (1)	-	C_unshiu_00043_mRNA_79.1	-
GF0034199	0	1	0	Hypothetical protein (1)			-	C_unshiu_00043_mRNA_52.1	-
GF0034198	0	1	0	Hypothetical protein (1)			-	C_unshiu_00043_mRNA_51.1	-
GF0034197	0	1	0	Hypothetical protein (1)			-	C_unshiu_00043_mRNA_41.1	-
GF0034196	0	1	0	Hypothetical protein (1)			-	C_unshiu_00043_mRNA_35.1	-
GF0034195	0	1	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Domain of unknown function DUF1985 [IPR015410] (1); Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_00043_mRNA_19.1	-
GF0034194	0	1	0	Zinc finger containing preotein, putative (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, PMZ-type [IPR006564] (1)	-	C_unshiu_00043_mRNA_18.1	-
GF0034193	0	1	0	Hypothetical protein (1)		Transposase, MuDR, plant [IPR004332] (1)	-	C_unshiu_00043_mRNA_17.1	-
GF0034192	0	1	0	Hypothetical protein (1)			-	C_unshiu_00043_mRNA_16.1	-
GF0034191	0	1	0	Dihydrokaempferol 4-reductase (1)	catalytic activity [GO:0003824 molecular_function] (1); coenzyme binding [GO:0050662 molecular_function] (1)	NAD-dependent epimerase/dehydratase, N-terminal domain [IPR001509] (1); NAD(P)-binding domain [IPR016040] (1)	-	C_unshiu_00042_mRNA_9.1	-
GF0034190	0	1	0	Naringenin-chalcone synthase (1)	catalytic activity [GO:0003824 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Thiolase-like [IPR016039] (1); Chalcone/stilbene synthase, N-terminal [IPR001099] (1)	-	C_unshiu_00042_mRNA_8.1	-
GF0034189	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_00042_mRNA_78.1	-
GF0034188	0	1	0	Hypothetical protein (1)		Iron hydrogenase, small subunit [IPR003149] (1); Iron hydrogenase [IPR009016] (1); Iron hydrogenase, large subunit, C-terminal [IPR004108] (1)	-	C_unshiu_00042_mRNA_75.1	-
GF0034187	0	1	0	Hypothetical protein (1)	metabolic process [GO:0008152 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1)	Thiolase-like [IPR016039] (1); Chalcone/stilbene synthase, C-terminal [IPR012328] (1)	-	C_unshiu_00042_mRNA_7.1	-
GF0034186	0	1	0	Rhamnogalacturonate lyase (1)	carbohydrate binding [GO:0030246 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1)	Galactose-binding domain-like [IPR008979] (1); Galactose mutarotase-like domain [IPR011013] (1); Rhamnogalacturonan lyase, domain III [IPR029411] (1); Rhamnogalacturonate lyase [IPR010325] (1)	-	C_unshiu_00042_mRNA_64.1	-
GF0034185	0	1	0	Hypothetical protein (1)			-	C_unshiu_00042_mRNA_62.1	-
GF0034184	0	1	0	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	C_unshiu_00042_mRNA_53.1	-
GF0034183	0	1	0	Hypothetical protein (1)			-	C_unshiu_00042_mRNA_49.1	-
GF0034182	0	1	0	Phosphoglycerate mutase family protein (1)	catalytic activity [GO:0003824 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Histidine phosphatase superfamily [IPR029033] (1); Phosphoglycerate/bisphosphoglycerate mutase, active site [IPR001345] (1); Histidine phosphatase superfamily, clade-1 [IPR013078] (1)	-	C_unshiu_00042_mRNA_43.1	-
GF0034181	0	1	0	Auxin-responsive protein IAA16 (1)	nucleus [GO:0005634 cellular_component] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); protein binding [GO:0005515 molecular_function] (1)	PB1 domain [IPR000270] (1); AUX/IAA protein [IPR003311] (1)	-	C_unshiu_00042_mRNA_39.1	-
GF0034180	0	1	0	Hypothetical protein (1)		von Willebrand factor, type A [IPR002035] (1)	-	C_unshiu_00042_mRNA_37.1	-
GF0034179	0	1	0	Phosphoenolpyruvate carboxykinase (ATP) (1)	gluconeogenesis [GO:0006094 biological_process] (1); purine nucleotide binding [GO:0017076 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1); phosphoenolpyruvate carboxykinase activity [GO:0004611 molecular_function] (1); phosphoenolpyruvate carboxykinase (ATP) activity [GO:0004612 molecular_function] (1)	Phosphoenolpyruvate carboxykinase, N-terminal [IPR008210] (1); Phosphoenolpyruvate carboxykinase (ATP), conserved site [IPR015994] (1); Phosphoenolpyruvate carboxykinase, ATP-utilising [IPR001272] (1); Phosphoenolpyruvate carboxykinase, C-terminal [IPR013035] (1)	-	C_unshiu_00042_mRNA_35.1	-
GF0034178	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00042_mRNA_33.1	-
GF0034177	0	1	0	Hypothetical protein (1)			-	C_unshiu_00042_mRNA_3.1	-
GF0034176	0	1	0	Hypothetical protein (1)		Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00042_mRNA_27.1	-
GF0034175	0	1	0	Hypothetical protein (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase, ATP binding site [IPR017441] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1)	-	C_unshiu_00042_mRNA_26.1	-
GF0034174	0	1	0	Hypothetical protein (1)			-	C_unshiu_00042_mRNA_15.1	-
GF0034173	0	1	0	Hypothetical protein (1)			-	C_unshiu_00042_mRNA_14.1	-
GF0034172	0	1	0	Hypothetical protein (1)			-	C_unshiu_00042_mRNA_12.1	-
GF0034171	0	1	0	Hypothetical protein (1)	steroid biosynthetic process [GO:0006694 biological_process] (1); 3-beta-hydroxy-delta5-steroid dehydrogenase activity [GO:0003854 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor [GO:0016616 molecular_function] (1)	NAD(P)-binding domain [IPR016040] (1); Domain of unknown function DUF4371 [IPR025398] (1); 3-beta hydroxysteroid dehydrogenase/isomerase [IPR002225] (1)	-	C_unshiu_00042_mRNA_11.1	-
GF0034170	0	1	0	Hypothetical protein (1)			-	C_unshiu_00042_mRNA_1.1	-
GF0034169	0	1	0	Hypothetical protein (1)			-	C_unshiu_00041_mRNA_94.1	-
GF0034168	0	1	0	Hypothetical protein (1)	spindle pole [GO:0000922 cellular_component] (1); microtubule cytoskeleton organization [GO:0000226 biological_process] (1); microtubule organizing center [GO:0005815 cellular_component] (1); positive regulation of microtubule nucleation [GO:0090063 biological_process] (1)	Gamma-tubulin complex component protein [IPR007259] (1)	-	C_unshiu_00041_mRNA_76.1	-
GF0034167	0	1	0	Amino acid permease family protein (1)	membrane [GO:0016020 cellular_component] (1); amino acid transmembrane transport [GO:0003333 biological_process] (1); amino acid transmembrane transporter activity [GO:0015171 molecular_function] (1)	Amino acid/polyamine transporter I [IPR002293] (1)	-	C_unshiu_00041_mRNA_72.1	-
GF0034166	0	1	0	Hypothetical protein (1)			-	C_unshiu_00041_mRNA_55.1	-
GF0034165	0	1	0	Hypothetical protein (1)	metabolic process [GO:0008152 biological_process] (1); transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	-	C_unshiu_00041_mRNA_54.1	-
GF0034164	0	1	0	Hypothetical protein (1)			-	C_unshiu_00041_mRNA_5.1	-
GF0034163	0	1	0	Hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyltransferase (1)	transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (1)	Chloramphenicol acetyltransferase-like domain [IPR023213] (1); Transferase [IPR003480] (1)	-	C_unshiu_00041_mRNA_47.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0034162	0	1	0	Hypothetical protein (1)			-	C_unshiu_00041_mRNA_40.1	-
GF0034161	0	1	0	Hypothetical protein (1)			-	C_unshiu_00041_mRNA_4.1	-
GF0034160	0	1	0	Hypothetical protein (1)			-	C_unshiu_00041_mRNA_37.1	-
GF0034159	0	1	0	Auxin-responsive protein SAUR61 (1)	response to auxin [GO:0009733 biological_process] (1)	Small auxin-up RNA [IPR003676] (1)	-	C_unshiu_00041_mRNA_35.1	-
GF0034158	0	1	0	Lysine histidine transporter 1 (1)		Amino acid transporter, transmembrane domain [IPR013057] (1)	-	C_unshiu_00041_mRNA_31.1	-
GF0034157	0	1	0	Hypothetical protein (1)			-	C_unshiu_00041_mRNA_1.1	-
GF0034156	0	1	0	Hypothetical protein (1)			-	C_unshiu_00040_mRNA_9.1	-
GF0034155	0	1	0	Hypothetical protein (1)			-	C_unshiu_00040_mRNA_8.1	-
GF0034154	0	1	0	Ankyrin repeat protein (1)		PGG domain [IPR026961] (1); Ankyrin repeat-containing domain [IPR020683] (1)	-	C_unshiu_00040_mRNA_7.1	-
GF0034153	0	1	0	Hypothetical protein (1)			-	C_unshiu_00040_mRNA_68.1	-
GF0034152	0	1	0	Hypothetical protein (1)			-	C_unshiu_00040_mRNA_58.1	-
GF0034151	0	1	0	Hypothetical protein (1)			-	C_unshiu_00040_mRNA_54.1	-
GF0034150	0	1	0	Hypothetical protein (1)			-	C_unshiu_00040_mRNA_52.1	-
GF0034149	0	1	0	Hypothetical protein (1)			-	C_unshiu_00040_mRNA_47.1	-
GF0034148	0	1	0	Hypothetical protein (1)			-	C_unshiu_00040_mRNA_46.1	-
GF0034147	0	1	0	Hypothetical protein (1)			-	C_unshiu_00040_mRNA_45.1	-
GF0034146	0	1	0	Hypothetical protein (1)			-	C_unshiu_00040_mRNA_44.1	-
GF0034145	0	1	0	Hypothetical protein (1)			-	C_unshiu_00040_mRNA_42.1	-
GF0034144	0	1	0	Hypothetical protein (1)			-	C_unshiu_00040_mRNA_41.1	-
GF0034143	0	1	0	Hypothetical protein (1)			-	C_unshiu_00040_mRNA_4.1	-
GF0034142	0	1	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); ribonucleoside binding [GO:0032549 molecular_function] (1); DNA-directed RNA polymerase activity [GO:0003899 molecular_function] (1); transcription, DNA-templated [GO:0006351 biological_process] (1)	RNA polymerase, beta subunit, conserved site [IPR007121] (1); DNA-directed RNA polymerase, subunit 2 [IPR015712] (1); RNA polymerase, N-terminal [IPR006592] (1); RNA polymerase, alpha subunit [IPR000722] (1); RNA polymerase Rpb2, domain 7 [IPR007641] (1); DNA-directed RNA polymerase, subunit 2, domain 6 [IPR007120] (1); RNA polymerase Rpb2, OB-fold [IPR014724] (1); RNA polymerase Rpb1, domain 1 [IPR007080] (1); RNA polymerase Rpb1, domain 3 [IPR007066] (1)	-	C_unshiu_00040_mRNA_36.1	-
GF0034141	0	1	0	Hypothetical protein (1)			-	C_unshiu_00040_mRNA_33.1	-
GF0034140	0	1	0	Hypothetical protein (1)		Arabidopsis retrotransposon Orf1 [IPR004312] (1)	-	C_unshiu_00040_mRNA_31.1	-
GF0034139	0	1	0	Hypothetical protein (1)			-	C_unshiu_00040_mRNA_30.1	-
GF0034138	0	1	0	Hypothetical protein (1)			-	C_unshiu_00040_mRNA_27.1	-
GF0034137	0	1	0	Hypothetical protein (1)			-	C_unshiu_00040_mRNA_11.1	-
GF0034136	0	1	0	Hypothetical protein (1)			-	C_unshiu_00039_mRNA_62.1	-
GF0034135	0	1	0	Sugar transport protein 14 (1)	membrane [GO:0016020 cellular_component] (1); transmembrane transporter activity [GO:0022857 molecular_function] (1); substrate-specific transmembrane transporter activity [GO:0022891 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1); transmembrane transport [GO:0055085 biological_process] (1)	Major facilitator, sugar transporter-like [IPR005828] (1); Sugar/inositol transporter [IPR003663] (1); Major facilitator superfamily domain [IPR020846] (1)	-	C_unshiu_00039_mRNA_42.1	-
GF0034134	0	1	0	Protein FAR1-RELATED SEQUENCE 5 (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1); FAR1 DNA binding domain [IPR004330] (1)	-	C_unshiu_00039_mRNA_33.1	-
GF0034133	0	1	0	Hypothetical protein (1)		Bifunctional inhibitor/plant lipid transfer protein/seed storage helical domain [IPR016140] (1)	-	C_unshiu_00039_mRNA_21.1	-
GF0034132	0	1	0	Hypothetical protein (1)			-	C_unshiu_00038_mRNA_99.1	-
GF0034131	0	1	0	Hypothetical protein (1)			-	C_unshiu_00038_mRNA_91.1	-
GF0034130	0	1	0	Hypothetical protein (1)			-	C_unshiu_00038_mRNA_71.1	-
GF0034129	0	1	0	Hypothetical protein (1)	thiamine pyrophosphate binding [GO:0030976 molecular_function] (1); magnesium ion binding [GO:0000287 molecular_function] (1)	Thiamin diphosphate-binding fold [IPR029061] (1); DHS-like NAD/FAD-binding domain [IPR029035] (1); Thiamine pyrophosphate enzyme, central domain [IPR012000] (1)	-	C_unshiu_00038_mRNA_69.1	-
GF0034128	0	1	0	Hypothetical protein (1)			-	C_unshiu_00038_mRNA_68.1	-
GF0034127	0	1	0	Hypothetical protein (1)	magnesium ion binding [GO:0000287 molecular_function] (1); terpene synthase activity [GO:0010333 molecular_function] (1); lyase activity [GO:0016829 molecular_function] (1)	Terpene synthase, metal-binding domain [IPR005630] (1); Isoprenoid synthase domain [IPR008949] (1)	-	C_unshiu_00038_mRNA_63.1	-
GF0034126	0	1	0	Hypothetical protein (1)	methyltransferase activity [GO:0008168 molecular_function] (1)	SAM dependent carboxyl methyltransferase [IPR005299] (1)	-	C_unshiu_00038_mRNA_57.1	-
GF0034125	0	1	0	E3 ubiquitin-protein ligase (1)	zinc ion binding [GO:0008270 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1); protein ubiquitination [GO:0016567 biological_process] (1); nucleus [GO:0005634 cellular_component] (1); multicellular organismal development [GO:0007275 biological_process] (1); ubiquitin-dependent protein catabolic process [GO:0006511 biological_process] (1); ubiquitin-protein transferase activity [GO:0004842 molecular_function] (1)	E3 ubiquitin-protein ligase SIN-like [IPR004162] (1); Zinc finger, SIAH-type [IPR013010] (1); TRAF-like [IPR008974] (1); SIAH-type domain [IPR013323] (1); Seven-in-absentia protein, TRAF-like domain [IPR018121] (1); Zinc finger, RING/FYVE/PHD-type [IPR013083] (1)	-	C_unshiu_00038_mRNA_41.1	-
GF0034124	0	1	0	E3 ubiquitin-protein ligase (1)	protein binding [GO:0005515 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1); ubiquitin-protein transferase activity [GO:0004842 molecular_function] (1); ubiquitin-dependent protein catabolic process [GO:0006511 biological_process] (1); multicellular organismal development [GO:0007275 biological_process] (1); nucleus [GO:0005634 cellular_component] (1); protein ubiquitination [GO:0016567 biological_process] (1)	SIAH-type domain [IPR013323] (1); Zinc finger, RING/FYVE/PHD-type [IPR013083] (1); Zinc finger, RING-type [IPR001841] (1); E3 ubiquitin-protein ligase SIN-like [IPR004162] (1); TRAF-like [IPR008974] (1)	-	C_unshiu_00038_mRNA_40.1	-
GF0034123	0	1	0	Beta-glucosidase 44 (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1); hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (1)	Glycoside hydrolase family 1 [IPR001360] (1); Glycoside hydrolase, catalytic domain [IPR013781] (1); Glycoside hydrolase superfamily [IPR017853] (1)	-	C_unshiu_00038_mRNA_36.1	-
GF0034122	0	1	0	Hypothetical protein (1)			-	C_unshiu_00038_mRNA_24.1	-
GF0034121	0	1	0	Hypothetical protein (1)			-	C_unshiu_00038_mRNA_22.1	-
GF0034120	0	1	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1)	ATPase, F1/V1/A1 complex, alpha/beta subunit, nucleotide-binding domain [IPR000194] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00038_mRNA_113.1	-
GF0034119	0	1	0	ATP synthase subunit beta, chloroplastic (1)	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances [GO:0016820 molecular_function] (1); ATP synthesis coupled proton transport [GO:0015986 biological_process] (1); proton-transporting two-sector ATPase complex, catalytic domain [GO:0033178 cellular_component] (1); ATP hydrolysis coupled proton transport [GO:0015991 biological_process] (1); proton-transporting ATP synthase complex, catalytic core F(1) [GO:0045261 cellular_component] (1); proton-transporting ATP synthase activity, rotational mechanism [GO:0046933 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1); proton-transporting ATPase activity, rotational mechanism [GO:0046961 molecular_function] (1)	ATPase, F1 complex beta subunit/V1 complex, C-terminal [IPR024034] (1); ATPase, alpha/beta subunit, nucleotide-binding domain, active site [IPR020003] (1); ATPase, F1/V1/A1 complex, alpha/beta subunit, C-terminal [IPR000793] (1); ATP synthase delta/epsilon subunit, C-terminal domain [IPR020547] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); ATPase, F1 complex, delta/epsilon subunit, N-terminal [IPR020546] (1); ATPase, F1 complex, delta/epsilon subunit [IPR001469] (1); ATPase, F1/V1/A1 complex, alpha/beta subunit, nucleotide-binding domain [IPR000194] (1)	-	C_unshiu_00038_mRNA_112.1	-
GF0034118	0	1	0	NAD(P)H-quinone oxidoreductase subunit K, chloroplastic (1)	iron-sulfur cluster binding [GO:0051536 molecular_function] (1); 4 iron, 4 sulfur cluster binding [GO:0051539 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); quinone binding [GO:0048038 molecular_function] (1); NADH dehydrogenase (ubiquinone) activity [GO:0008137 molecular_function] (1)	NADH:ubiquinone oxidoreductase-like, 20kDa subunit [IPR006137] (1); NADH-ubiquinone oxidoreductase, 20 Kd subunit [IPR006138] (1)	-	C_unshiu_00038_mRNA_111.1	-
GF0034117	0	1	0	Hypothetical protein (1)	NADH dehydrogenase (ubiquinone) activity [GO:0008137 molecular_function] (1); quinone binding [GO:0048038 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); iron-sulfur cluster binding [GO:0051536 molecular_function] (1); oxidoreductase activity, acting on NAD(P)H [GO:0016651 molecular_function] (1); 4 iron, 4 sulfur cluster binding [GO:0051539 molecular_function] (1)	NADH:ubiquinone oxidoreductase-like, 20kDa subunit [IPR006137] (1); NADH:ubiquinone oxidoreductase, 30kDa subunit, conserved site [IPR020396] (1); NADH dehydrogenase, subunit C [IPR010218] (1); NADH:ubiquinone oxidoreductase, 30kDa subunit [IPR001268] (1); NADH-ubiquinone oxidoreductase, 20 Kd subunit [IPR006138] (1)	-	C_unshiu_00038_mRNA_110.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0034116	0	1	0	Hypothetical protein (1)	photosynthesis [GO:0015979 biological_process] (1); integral component of membrane [GO:0016021 cellular_component] (1); photosystem I [GO:0009522 cellular_component] (1); carbon fixation [GO:0015977 biological_process] (1); ribulose-bisphosphate carboxylase activity [GO:0016984 molecular_function] (1); thylakoid [GO:0009579 cellular_component] (1)	Ribulose bisphosphate carboxylase, large subunit, ferrodoxin-like N-terminal [IPR017443] (1); Photosystem I Ycf4, assembly [IPR003359] (1)	-	C_unshiu_00038_mRNA_108.1	-
GF0034115	0	1	0	Cytochrome f (1)	iron ion binding [GO:0005506 molecular_function] (1); photosynthesis [GO:0015979 biological_process] (1); electron carrier activity [GO:0009055 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); integral component of thylakoid membrane [GO:0031361 cellular_component] (1)	Cytochrome f [IPR002325] (1); Cytochrome f large domain [IPR024094] (1)	-	C_unshiu_00038_mRNA_107.1	-
GF0034114	0	1	0	Hypothetical protein (1)	photosystem I [GO:0009522 cellular_component] (1); carbon fixation [GO:0015977 biological_process] (1); ribulose-bisphosphate carboxylase activity [GO:0016984 molecular_function] (1); thylakoid [GO:0009579 cellular_component] (1); photosynthesis [GO:0015979 biological_process] (1); integral component of membrane [GO:0016021 cellular_component] (1)	Photosystem I Ycf4, assembly [IPR003359] (1); Ribulose bisphosphate carboxylase, large subunit, ferrodoxin-like N-terminal [IPR017443] (1)	-	C_unshiu_00038_mRNA_106.1	-
GF0034113	0	1	0	DNA-directed RNA polymerase, alpha subunit (1)	transcription, DNA-templated [GO:0006351 biological_process] (1); DNA-directed RNA polymerase activity [GO:0003899 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	DNA-directed RNA polymerase, alpha subunit [IPR011773] (1); RNA polymerase, alpha subunit, C-terminal [IPR011260] (1); DNA-directed RNA polymerase, RBP11-like dimerisation domain [IPR009025] (1); DNA-directed RNA polymerase, insert domain [IPR011262] (1); DNA-directed RNA polymerase, RpoA/D/Rpb3-type [IPR011263] (1)	-	C_unshiu_00038_mRNA_104.1	-
GF0034112	0	1	0	30S ribosomal protein S11, chloroplastic (1)	ribosome [GO:0005840 cellular_component] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1); intracellular [GO:0005622 cellular_component] (1); translation [GO:0006412 biological_process] (1)	Ribosomal protein S11, bacterial-type [IPR019981] (1); Ribosomal S11, conserved site [IPR018102] (1); Ribosomal protein S11 [IPR001971] (1)	-	C_unshiu_00038_mRNA_103.1	-
GF0034111	0	1	0	Hypothetical protein (1)			-	C_unshiu_00038_mRNA_102.1	-
GF0034110	0	1	0	50S ribosomal protein L22, chloroplastic (1)	ribosome [GO:0005840 cellular_component] (1); translation [GO:0006412 biological_process] (1); large ribosomal subunit [GO:0015934 cellular_component] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1)	Ribosomal protein L22, bacterial/chloroplast-type [IPR005727] (1); Ribosomal protein L22/L17 [IPR001063] (1)	-	C_unshiu_00038_mRNA_100.1	-
GF0034109	0	1	0	Hypothetical protein (1)			-	C_unshiu_00037_mRNA_95.1	-
GF0034108	0	1	0	Hypothetical protein (1)			-	C_unshiu_00037_mRNA_94.1	-
GF0034107	0	1	0	Hypothetical protein (1)	binding [GO:0005488 molecular_function] (1)	Armadillo-like helical [IPR011989] (1); Armadillo-type fold [IPR016024] (1)	-	C_unshiu_00037_mRNA_90.1	-
GF0034106	0	1	0	Hypothetical protein (1)			-	C_unshiu_00037_mRNA_87.1	-
GF0034105	0	1	0	Hypothetical protein (1)			-	C_unshiu_00037_mRNA_83.1	-
GF0034104	0	1	0	Hypothetical protein (1)			-	C_unshiu_00037_mRNA_77.1	-
GF0034103	0	1	0	Hypothetical protein (1)			-	C_unshiu_00037_mRNA_70.1	-
GF0034102	0	1	0	Hypothetical protein (1)			-	C_unshiu_00037_mRNA_54.1	-
GF0034101	0	1	0	Protein argonaute PNH1 (1)	protein binding [GO:0005515 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Argonaute, linker 1 domain [IPR014811] (1); Argonaute linker 2 domain [IPR032472] (1); PAZ domain [IPR003100] (1); Piwi domain [IPR003165] (1)	-	C_unshiu_00037_mRNA_19.1	-
GF0034100	0	1	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	NAC domain [IPR003441] (1)	-	C_unshiu_00037_mRNA_1.1	-
GF0034099	0	1	0	Hypothetical protein (1)			-	C_unshiu_00036_mRNA_85.1	-
GF0034098	0	1	0	Hypothetical protein (1)			-	C_unshiu_00036_mRNA_80.1	-
GF0034097	0	1	0	Hypothetical protein (1)			-	C_unshiu_00036_mRNA_76.1	-
GF0034096	0	1	0	Hypothetical protein (1)	GTP binding [GO:0005525 molecular_function] (1); small GTPase mediated signal transduction [GO:0007264 biological_process] (1)	Small GTPase superfamily [IPR001806] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00036_mRNA_74.1	-
GF0034095	0	1	0	Hypothetical protein (1)	GTP binding [GO:0005525 molecular_function] (1); small GTPase mediated signal transduction [GO:0007264 biological_process] (1); protein transport [GO:0015031 biological_process] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Small GTPase superfamily [IPR001806] (1); Small GTP-binding protein domain [IPR005225] (1); Small GTPase superfamily, Rab type [IPR003579] (1)	-	C_unshiu_00036_mRNA_69.1	-
GF0034094	0	1	0	Hypothetical protein (1)			-	C_unshiu_00036_mRNA_61.1	-
GF0034093	0	1	0	Hypothetical protein (1)		Zinc finger, FYVE/PHD-type [IPR011011] (1); Zinc finger, RING/FYVE/PHD-type [IPR013083] (1)	-	C_unshiu_00036_mRNA_59.1	-
GF0034092	0	1	0	Hypothetical protein (1)			-	C_unshiu_00036_mRNA_57.1	-
GF0034091	0	1	0	Hypothetical protein (1)			-	C_unshiu_00036_mRNA_56.1	-
GF0034090	0	1	0	Hypothetical protein (1)			-	C_unshiu_00036_mRNA_49.1	-
GF0034089	0	1	0	Disease resistance family protein / LRR family protein, putative (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00036_mRNA_48.1	-
GF0034088	0	1	0	DNA-directed RNA polymerase, beta subunit (1)	transcription, DNA-templated [GO:0006351 biological_process] (1); DNA-directed RNA polymerase activity [GO:0003899 molecular_function] (1); ribonucleoside binding [GO:0032549 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	DNA-directed RNA polymerase, subunit 2 [IPR015712] (1); RNA polymerase Rpb2, domain 7 [IPR007641] (1); DNA-directed RNA polymerase, subunit 2, domain 6 [IPR007120] (1)	-	C_unshiu_00036_mRNA_45.1	-
GF0034087	0	1	0	DNA-directed RNA polymerase (1)	transcription, DNA-templated [GO:0006351 biological_process] (1); DNA binding [GO:0003677 molecular_function] (1); DNA-directed RNA polymerase activity [GO:0003899 molecular_function] (1)	RNA polymerase Rpb1, domain 3 [IPR007066] (1); RNA polymerase, alpha subunit [IPR000722] (1); RNA polymerase, N-terminal [IPR006592] (1)	-	C_unshiu_00036_mRNA_44.1	-
GF0034086	0	1	0	DNA-directed RNA polymerase (1)	DNA binding [GO:0003677 molecular_function] (1); ribonucleoside binding [GO:0032549 molecular_function] (1); DNA-directed RNA polymerase activity [GO:0003899 molecular_function] (1); transcription, DNA-templated [GO:0006351 biological_process] (1)	RNA polymerase Rpb2, domain 7 [IPR007641] (1); RNA polymerase Rpb2, OB-fold [IPR014724] (1); DNA-directed RNA polymerase, subunit 2, domain 6 [IPR007120] (1); DNA-directed RNA polymerase, subunit 2 [IPR015712] (1); RNA polymerase, beta subunit, conserved site [IPR007121] (1)	-	C_unshiu_00036_mRNA_42.1	-
GF0034085	0	1	0	Hypothetical protein (1)	DNA-directed RNA polymerase activity [GO:0003899 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1); transcription, DNA-templated [GO:0006351 biological_process] (1)	RNA polymerase Rpb1, domain 5 [IPR007081] (1)	-	C_unshiu_00036_mRNA_41.1	-
GF0034084	0	1	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); DNA-directed RNA polymerase activity [GO:0003899 molecular_function] (1); transcription, DNA-templated [GO:0006351 biological_process] (1)	RNA polymerase Rpb1, domain 1 [IPR007080] (1); DNA-directed RNA polymerase, subunit beta" [IPR012756] (1); RNA polymerase Rpb1, domain 5 [IPR007081] (1); RNA polymerase Rpb1, domain 4 [IPR007083] (1)	-	C_unshiu_00036_mRNA_40.1	-
GF0034083	0	1	0	Hypothetical protein (1)	transcription, DNA-templated [GO:0006351 biological_process] (1); DNA-directed RNA polymerase activity [GO:0003899 molecular_function] (1); ribonucleoside binding [GO:0032549 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	DNA-directed RNA polymerase, subunit 2 [IPR015712] (1); RNA polymerase Rpb2, domain 7 [IPR007641] (1)	-	C_unshiu_00036_mRNA_39.1	-
GF0034082	0	1	0	Epoxide hydrolase (1)	catalytic activity [GO:0003824 molecular_function] (1)	Alpha/beta hydrolase fold-1 [IPR000073] (1); Alpha/Beta hydrolase fold [IPR029058] (1); Epoxide hydrolase-like [IPR000639] (1)	-	C_unshiu_00036_mRNA_38.1	-
GF0034081	0	1	0	Hypothetical protein (1)	metabolic process [GO:0008152 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1)	Fumarylacetoacetase, C-terminal-related [IPR011234] (1)	-	C_unshiu_00036_mRNA_37.1	-
GF0034080	0	1	0	Ribosomal L22e family protein (1)	intracellular [GO:0005622 cellular_component] (1); translation [GO:0006412 biological_process] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1); ribosome [GO:0005840 cellular_component] (1)	Ribosomal protein L22e [IPR002671] (1)	-	C_unshiu_00036_mRNA_22.1	-
GF0034079	0	1	0	Hypothetical protein (1)			-	C_unshiu_00036_mRNA_21.1	-
GF0034078	0	1	0	Hypothetical protein (1)			-	C_unshiu_00036_mRNA_2.1	-
GF0034077	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	F-box domain [IPR001810] (1)	-	C_unshiu_00036_mRNA_10.1	-
GF0034076	0	1	0	Hypothetical protein (1)			-	C_unshiu_00035_mRNA_99.1	-
GF0034075	0	1	0	Hypothetical protein (1)			-	C_unshiu_00035_mRNA_97.1	-
GF0034074	0	1	0	Hypothetical protein (1)			-	C_unshiu_00035_mRNA_85.1	-
GF0034073	0	1	0	Hypothetical protein (1)			-	C_unshiu_00035_mRNA_83.1	-
GF0034072	0	1	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00035_mRNA_81.1	-
GF0034071	0	1	0	Hypothetical protein (1)			-	C_unshiu_00035_mRNA_74.1	-
GF0034070	0	1	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	C_unshiu_00035_mRNA_68.1	-

ID	**Num. in *C. celementine***	**Num in *C. unshiu***	**Num in *P.trifoliata***	**Note**	**GO**	**InterPro**	**Members in *C.clementine***	**Members in *C.unshiu***	**Members in *P.trifoliata***
GF0034069	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00035_mRNA_59.1	-
GF0034068	0	1	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	C_unshiu_00035_mRNA_55.1	-
GF0034067	0	1	0	Hypothetical protein (1)			-	C_unshiu_00035_mRNA_53.1	-
GF0034066	0	1	0	Hypothetical protein (1)			-	C_unshiu_00035_mRNA_2.1	-
GF0034065	0	1	0	Hypothetical protein (1)			-	C_unshiu_00035_mRNA_101.1	-
GF0034064	0	1	0	Hypothetical protein (1)			-	C_unshiu_00035_mRNA_100.1	-
GF0034063	0	1	0	Hypothetical protein (1)			-	C_unshiu_00034_mRNA_68.1	-
GF0034062	0	1	0	Laccase (1)	hydroquinone:oxygen oxidoreductase activity [GO:0052716 molecular_function] (1); apoplast [GO:0048046 cellular_component] (1); copper ion binding [GO:0005507 molecular_function] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); lignin catabolic process [GO:0046274 biological_process] (1)	Multicopper oxidase, type 3 [IPR011707] (1); Cupredoxin [IPR008972] (1); Multicopper oxidase, type 1 [IPR001117] (1); Laccase [IPR017761] (1)	-	C_unshiu_00034_mRNA_61.1	-
GF0034061	0	1	0	Hypothetical protein (1)			-	C_unshiu_00034_mRNA_31.1	-
GF0034060	0	1	0	Hypothetical protein (1)			-	C_unshiu_00034_mRNA_29.1	-
GF0034059	0	1	0	Hypothetical protein (1)			-	C_unshiu_00034_mRNA_27.1	-
GF0034058	0	1	0	Hypothetical protein (1)		Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_00034_mRNA_24.1	-
GF0034057	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1); WD40/YVTN repeat-like-containing domain [IPR015943] (1); WD40 repeat [IPR001680] (1); WD40-repeat-containing domain [IPR017986] (1)	-	C_unshiu_00034_mRNA_23.1	-
GF0034056	0	1	0	Hypothetical protein (1)			-	C_unshiu_00033_mRNA_8.1	-
GF0034055	0	1	0	Hypothetical protein (1)			-	C_unshiu_00033_mRNA_7.1	-
GF0034054	0	1	0	Hypothetical protein (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase, ATP binding site [IPR017441] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	-	C_unshiu_00033_mRNA_59.1	-
GF0034053	0	1	0	Contains similarity to reverse trancriptase , related (1)			-	C_unshiu_00033_mRNA_58.1	-
GF0034052	0	1	0	Hypothetical protein (1)			-	C_unshiu_00033_mRNA_57.1	-
GF0034051	0	1	0	Hypothetical protein (1)			-	C_unshiu_00033_mRNA_51.1	-
GF0034050	0	1	0	Non-LTR retroelement reverse transcriptase-like (1)	RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H domain [IPR002156] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00033_mRNA_50.1	-
GF0034049	0	1	0	Hypothetical protein (1)			-	C_unshiu_00033_mRNA_35.1	-
GF0034048	0	1	0	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	C_unshiu_00033_mRNA_31.1	-
GF0034047	0	1	0	Hypothetical protein (1)			-	C_unshiu_00033_mRNA_28.1	-
GF0034046	0	1	0	Hypothetical protein (1)			-	C_unshiu_00033_mRNA_26.1	-
GF0034045	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00033_mRNA_24.1	-
GF0034044	0	1	0	Hypothetical protein (1)			-	C_unshiu_00033_mRNA_23.1	-
GF0034043	0	1	0	Hypothetical protein (1)			-	C_unshiu_00033_mRNA_21.1	-
GF0034042	0	1	0	Hypothetical protein (1)			-	C_unshiu_00033_mRNA_20.1	-
GF0034041	0	1	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	-	C_unshiu_00033_mRNA_16.1	-
GF0034040	0	1	0	Hypothetical protein (1)			-	C_unshiu_00033_mRNA_11.1	-
GF0034039	0	1	0	Hypothetical protein (1)			-	C_unshiu_00033_mRNA_10.1	-
GF0034038	0	1	0	Hypothetical protein (1)			-	C_unshiu_00033_mRNA_1.1	-
GF0034037	0	1	0	Hypothetical protein (1)			-	C_unshiu_00032_mRNA_78.1	-
GF0034036	0	1	0	Hypothetical protein (1)			-	C_unshiu_00032_mRNA_74.1	-
GF0034035	0	1	0	Hypothetical protein (1)			-	C_unshiu_00032_mRNA_59.1	-
GF0034034	0	1	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	Homeodomain-like [IPR009057] (1)	-	C_unshiu_00032_mRNA_46.1	-
GF0034033	0	1	0	Hypothetical protein (1)			-	C_unshiu_00032_mRNA_16.1	-
GF0034032	0	1	0	Putative WRKY transcription factor 49 (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); sequence-specific DNA binding [GO:0043565 molecular_function] (1); transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (1)	WRKY domain [IPR003657] (1)	-	C_unshiu_00032_mRNA_15.1	-
GF0034031	0	1	0	Hypothetical protein (1)			-	C_unshiu_00031_mRNA_60.1	-
GF0034030	0	1	0	Hypothetical protein (1)			-	C_unshiu_00031_mRNA_58.1	-
GF0034029	0	1	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	C_unshiu_00031_mRNA_54.1	-
GF0034028	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00031_mRNA_41.1	-
GF0034027	0	1	0	Hypothetical protein (1)			-	C_unshiu_00031_mRNA_40.1	-
GF0034026	0	1	0	Hypothetical protein (1)			-	C_unshiu_00031_mRNA_38.1	-
GF0034025	0	1	0	Leucine-rich repeat (LRR) family protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	-	C_unshiu_00031_mRNA_3.1	-
GF0034024	0	1	0	Hypothetical protein (1)			-	C_unshiu_00031_mRNA_24.1	-
GF0034023	0	1	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FAR1 DNA binding domain [IPR004330] (1); FHY3/FAR1 family [IPR031052] (1)	-	C_unshiu_00031_mRNA_18.1	-
GF0034022	0	1	0	Hypothetical protein (1)			-	C_unshiu_00031_mRNA_16.1	-
GF0034021	0	1	0	Hypothetical protein (1)			-	C_unshiu_00031_mRNA_15.1	-
GF0034020	0	1	0	LRR receptor-like serine/threonine-protein kinase ERL1 (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00031_mRNA_14.1	-
GF0034019	0	1	0	LRR amino-terminal domain protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00031_mRNA_13.1	-
GF0034018	0	1	0	Hypothetical protein (1)			-	C_unshiu_00031_mRNA_10.1	-
GF0034017	0	1	0	Hypothetical protein (1)			-	C_unshiu_00031_mRNA_1.1	-
GF0034016	0	1	0	Acid phosphatase 1 (1)		Sieve element occlusion, C-terminal [IPR027944] (1); Sieve element occlusion, N-terminal [IPR027942] (1)	-	C_unshiu_00030_mRNA_66.1	-
GF0034015	0	1	0	Cp protein (1)		Protein of unknown function DUF538 [IPR007493] (1)	-	C_unshiu_00030_mRNA_63.1	-
GF0034014	0	1	0	Integrase (1)		Aspartic peptidase domain [IPR021109] (1)	-	C_unshiu_00030_mRNA_59.1	-
GF0034013	0	1	0	Hypothetical protein (1)			-	C_unshiu_00030_mRNA_58.1	-
GF0034012	0	1	0	Hypothetical protein (1)			-	C_unshiu_00030_mRNA_57.1	-
GF0034011	0	1	0	Hypothetical protein (1)			-	C_unshiu_00030_mRNA_43.1	-
GF0034010	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc knuckle CX2CX4HX4C [IPR025836] (1); Zinc finger, CCHC-type [IPR001878] (1); Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_00030_mRNA_41.1	-
GF0034009	0	1	0	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_00030_mRNA_16.1	-
GF0034008	0	1	0	Hypothetical protein (1)			-	C_unshiu_00030_mRNA_13.1	-
GF0034007	0	1	0	Hypothetical protein (1)			-	C_unshiu_00030_mRNA_12.1	-
GF0034006	0	1	0	Hypothetical protein (1)			-	C_unshiu_00030_mRNA_10.1	-
GF0034005	0	1	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1); FAR1 DNA binding domain [IPR004330] (1)	-	C_unshiu_00030_mRNA_1.1	-
GF0034004	0	1	0	Hypothetical protein (1)			-	C_unshiu_00029_mRNA_99.1	-
GF0034003	0	1	0	Hypothetical protein (1)			-	C_unshiu_00029_mRNA_98.1	-
GF0034002	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	-	C_unshiu_00029_mRNA_95.1	-
GF0034001	0	1	0	Dcp1-like decapping family protein, expressed (1)	enzyme activator activity [GO:0008047 molecular_function] (1); positive regulation of catalytic activity [GO:0043085 biological_process] (1); deadenylation-dependent decapping of nuclear-transcribed mRNA [GO:0000290 biological_process] (1)	mRNA-decapping enzyme subunit 1 [IPR010334] (1)	-	C_unshiu_00029_mRNA_94.1	-
GF0034000	0	1	0	Hypothetical protein (1)			-	C_unshiu_00029_mRNA_93.1	-
GF0033999	0	1	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	-	C_unshiu_00029_mRNA_92.1	-
GF0033998	0	1	0	Hypothetical protein (1)			-	C_unshiu_00029_mRNA_89.1	-
GF0033997	0	1	0	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_00029_mRNA_88.1	-
GF0033996	0	1	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_00029_mRNA_75.1	-
GF0033995	0	1	0	Hypothetical protein (1)			-	C_unshiu_00029_mRNA_71.1	-
GF0033994	0	1	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	C_unshiu_00029_mRNA_70.1	-
GF0033993	0	1	0	Translation initiation factor SUI1 (1)	translation initiation factor activity [GO:0003743 molecular_function] (1); translational initiation [GO:0006413 biological_process] (1)	Translation initiation factor SUI1 [IPR001950] (1); Eukaryotic translation initiation factor SUI1 [IPR005874] (1)	-	C_unshiu_00029_mRNA_69.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0033992	0	1	0	Hypothetical protein (1)	peroxidase activity [GO:0004601 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); heme binding [GO:0020037 molecular_function] (1); response to oxidative stress [GO:0006979 biological_process] (1)	Haem peroxidase [IPR010255] (1); Peroxidase, active site [IPR019794] (1); Plant peroxidase [IPR000823] (1); Haem peroxidase, plant/fungal/bacterial [IPR002016] (1)	-	C_unshiu_00029_mRNA_63.1	-
GF0033991	0	1	0	DUF247 domain protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	C_unshiu_00029_mRNA_62.1	-
GF0033990	0	1	0	Hypothetical protein (1)		Protein kinase-like domain [IPR011009] (1)	-	C_unshiu_00029_mRNA_55.1	-
GF0033989	0	1	0	Hypothetical protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	C_unshiu_00029_mRNA_53.1	-
GF0033988	0	1	0	Hypothetical protein (1)		Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (1)	-	C_unshiu_00029_mRNA_48.1	-
GF0033987	0	1	0	Hypothetical protein (1)			-	C_unshiu_00029_mRNA_38.1	-
GF0033986	0	1	0	Hypothetical protein (1)			-	C_unshiu_00029_mRNA_32.1	-
GF0033985	0	1	0	Mitogen-activated protein kinase 7 (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1)	-	C_unshiu_00029_mRNA_31.1	-
GF0033984	0	1	0	Hypothetical protein (1)			-	C_unshiu_00029_mRNA_12.1	-
GF0033983	0	1	0	[Protein-PII] uridylyltransferase (1)	metabolic process [GO:0008152 biological_process] (1); amino acid binding [GO:0016597 molecular_function] (1)	ACT domain [IPR002912] (1)	-	C_unshiu_00028_mRNA_80.1	-
GF0033982	0	1	0	Hypothetical protein (1)	nucleotide binding [GO:0000166 molecular_function] (1)	Nucleotide-binding alpha-beta plait domain [IPR012677] (1)	-	C_unshiu_00028_mRNA_71.1	-
GF0033981	0	1	0	Hypothetical protein (1)			-	C_unshiu_00028_mRNA_7.1	-
GF0033980	0	1	0	Hypothetical protein (1)			-	C_unshiu_00028_mRNA_6.1	-
GF0033979	0	1	0	Hypothetical protein (1)			-	C_unshiu_00028_mRNA_48.1	-
GF0033978	0	1	0	Retrovirus-related Pol polyprotein from transposon TNT 1-94 (1)			-	C_unshiu_00028_mRNA_39.1	-
GF0033977	0	1	0	Hypothetical protein (1)		Arabidopsis retrotransposon Orf1 [IPR004312] (1)	-	C_unshiu_00028_mRNA_34.1	-
GF0033976	0	1	0	Hypothetical protein (1)			-	C_unshiu_00028_mRNA_32.1	-
GF0033975	0	1	0	Hypothetical protein (1)			-	C_unshiu_00028_mRNA_27.1	-
GF0033974	0	1	0	Importin subunit alpha (1)	protein import into nucleus [GO:0006606 biological_process] (1); cytoplasm [GO:0005737 cellular_component] (1); protein transporter activity [GO:0008565 molecular_function] (1); nucleus [GO:0005634 cellular_component] (1); binding [GO:0005488 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Armadillo [IPR000225] (1); Importin subunit alpha [IPR024931] (1); Armadillo-like helical [IPR011989] (1); Armadillo-type fold [IPR016024] (1)	-	C_unshiu_00028_mRNA_23.1	-
GF0033973	0	1	0	Hypothetical protein (1)			-	C_unshiu_00028_mRNA_17.1	-
GF0033972	0	1	0	Hypothetical protein (1)			-	C_unshiu_00028_mRNA_10.1	-
GF0033971	0	1	0	Hypothetical protein (1)			-	C_unshiu_00027_mRNA_83.1	-
GF0033970	0	1	0	Hypothetical protein (1)	ribosome [GO:0005840 cellular_component] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1); translation [GO:0006412 biological_process] (1); intracellular [GO:0005622 cellular_component] (1)	Ribosomal protein S8e/ribosomal biogenesis NSA2 [IPR022309] (1); Ribosomal protein S8e [IPR001047] (1)	-	C_unshiu_00027_mRNA_51.1	-
GF0033969	0	1	0	Hypothetical protein (1)			-	C_unshiu_00027_mRNA_49.1	-
GF0033968	0	1	0	Hypothetical protein (1)	nucleotide binding [GO:0000166 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Nucleotide-binding alpha-beta plait domain [IPR012677] (1); RNA recognition motif domain [IPR000504] (1)	-	C_unshiu_00027_mRNA_37.1	-
GF0033967	0	1	0	Serine/threonine-protein kinase PBS1 (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1); Serine/threonine-protein kinase, active site [IPR008271] (1)	-	C_unshiu_00027_mRNA_26.1	-
GF0033966	0	1	0	Hypothetical protein (1)			-	C_unshiu_00026_mRNA_85.1	-
GF0033965	0	1	0	Hypothetical protein (1)			-	C_unshiu_00026_mRNA_58.1	-
GF0033964	0	1	0	Hydroquinone glucosyltransferase (1)	metabolic process [GO:0008152 biological_process] (1); transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	-	C_unshiu_00026_mRNA_57.1	-
GF0033963	0	1	0	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	C_unshiu_00026_mRNA_5.1	-
GF0033962	0	1	0	Hypothetical protein (1)		Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00026_mRNA_26.1	-
GF0033961	0	1	0	Hypothetical protein (1)			-	C_unshiu_00026_mRNA_24.1	-
GF0033960	0	1	0	Hypothetical protein (1)			-	C_unshiu_00026_mRNA_23.1	-
GF0033959	0	1	0	Hypothetical protein (1)			-	C_unshiu_00026_mRNA_18.1	-
GF0033958	0	1	0	Hypothetical protein (1)			-	C_unshiu_00026_mRNA_17.1	-
GF0033957	0	1	0	Hypothetical protein (1)			-	C_unshiu_00026_mRNA_1.1	-
GF0033956	0	1	0	Hypothetical protein (1)			-	C_unshiu_00025_mRNA_95.1	-
GF0033955	0	1	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	NAC domain [IPR003441] (1)	-	C_unshiu_00025_mRNA_94.1	-
GF0033954	0	1	0	Hypothetical protein (1)			-	C_unshiu_00025_mRNA_90.1	-
GF0033953	0	1	0	Hypothetical protein (1)			-	C_unshiu_00025_mRNA_83.1	-
GF0033952	0	1	0	Hypothetical protein (1)			-	C_unshiu_00025_mRNA_78.1	-
GF0033951	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Elongated TPR repeat-containing domain [IPR023114] (1); Tetratricopeptide-like helical domain [IPR011990] (1)	-	C_unshiu_00025_mRNA_75.1	-
GF0033950	0	1	0	Hypothetical protein (1)			-	C_unshiu_00025_mRNA_73.1	-
GF0033949	0	1	0	Putative SET domain protein SDG117 (1)	histone lysine methylation [GO:0034968 biological_process] (1); nucleus [GO:0005634 cellular_component] (1); metal ion binding [GO:0046872 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1); histone-lysine N-methyltransferase activity [GO:0018024 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Post-SET domain [IPR003616] (1); Zinc finger, C2H2 [IPR007087] (1); Zinc finger, C2H2-like [IPR015880] (1); Pre-SET zinc-binding sub-group [IPR003606] (1); Pre-SET domain [IPR007728] (1); SET domain [IPR001214] (1)	-	C_unshiu_00025_mRNA_61.1	-
GF0033948	0	1	0	Hypothetical protein (1)	methyltransferase activity [GO:0008168 molecular_function] (1)	Zinc finger, CCCH-type, TRM13 [IPR021721] (1)	-	C_unshiu_00025_mRNA_60.1	-
GF0033947	0	1	0	Hypothetical protein (1)			-	C_unshiu_00025_mRNA_6.1	-
GF0033946	0	1	0	Hypothetical protein (1)			-	C_unshiu_00025_mRNA_58.1	-
GF0033945	0	1	0	Ribonuclease P protein subunit P38-related isoform 1 (1)	integral component of membrane [GO:0016021 cellular_component] (1)	Protein kinase-like domain [IPR011009] (1); Cold-regulated 413 protein [IPR008892] (1)	-	C_unshiu_00025_mRNA_54.1	-
GF0033944	0	1	0	Hypothetical protein (1)			-	C_unshiu_00025_mRNA_50.1	-
GF0033943	0	1	0	Pentatricopeptide repeat-containing protein At2g01360 (1)		Pentatricopeptide repeat [IPR002885] (1)	-	C_unshiu_00025_mRNA_45.1	-
GF0033942	0	1	0	Hydroquinone glucosyltransferase (1)	metabolic process [GO:0008152 biological_process] (1); transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	-	C_unshiu_00025_mRNA_36.1	-
GF0033941	0	1	0	Hypothetical protein (1)			-	C_unshiu_00025_mRNA_34.1	-
GF0033940	0	1	0	Hypothetical protein (1)			-	C_unshiu_00025_mRNA_27.1	-
GF0033939	0	1	0	Hypothetical protein (1)			-	C_unshiu_00025_mRNA_26.1	-
GF0033938	0	1	0	Hypothetical protein (1)			-	C_unshiu_00025_mRNA_22.1	-
GF0033937	0	1	0	Hypothetical protein (1)			-	C_unshiu_00025_mRNA_15.1	-
GF0033936	0	1	0	Transmembrane amino acid transporter family protein (1)		Amino acid transporter, transmembrane domain [IPR013057] (1)	-	C_unshiu_00024_mRNA_86.1	-
GF0033935	0	1	0	Amino acid permease 8 (1)		Amino acid transporter, transmembrane domain [IPR013057] (1)	-	C_unshiu_00024_mRNA_85.1	-
GF0033934	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	F-box domain [IPR001810] (1)	-	C_unshiu_00024_mRNA_83.1	-
GF0033933	0	1	0	Hypothetical protein (1)			-	C_unshiu_00024_mRNA_7.1	-
GF0033932	0	1	0	Serine carboxypeptidase-like 6 (1)	proteolysis [GO:0006508 biological_process] (1); serine-type carboxypeptidase activity [GO:0004185 molecular_function] (1)	Alpha/Beta hydrolase fold [IPR029058] (1); Peptidase S10, serine carboxypeptidase [IPR001563] (1)	-	C_unshiu_00024_mRNA_66.1	-
GF0033931	0	1	0	Hypothetical protein (1)			-	C_unshiu_00024_mRNA_61.1	-
GF0033930	0	1	0	Hypothetical protein (1)			-	C_unshiu_00024_mRNA_54.1	-
GF0033929	0	1	0	Hypothetical protein (1)			-	C_unshiu_00024_mRNA_53.1	-
GF0033928	0	1	0	Glycosyl hydrolase family 10 protein (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1); hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (1); hydrolase activity, acting on glycosyl bonds [GO:0016798 molecular_function] (1)	Galactose-binding domain-like [IPR008979] (1); Carbohydrate-binding, CenC-like [IPR003305] (1); Glycoside hydrolase family 10 domain [IPR001000] (1); Glycoside hydrolase superfamily [IPR017853] (1); Glycoside hydrolase, catalytic domain [IPR013781] (1)	-	C_unshiu_00024_mRNA_43.1	-
GF0033927	0	1	0	Hypothetical protein (1)			-	C_unshiu_00024_mRNA_42.1	-
GF0033926	0	1	0	Hypothetical protein (1)			-	C_unshiu_00024_mRNA_33.1	-
GF0033925	0	1	0	Thioredoxin domain-containing protein 9 like (1)			-	C_unshiu_00024_mRNA_3.1	-
GF0033924	0	1	0	Hypothetical protein (1)			-	C_unshiu_00024_mRNA_21.1	-
GF0033923	0	1	0	Hypothetical protein (1)		GH3 family [IPR004993] (1)	-	C_unshiu_00024_mRNA_2.1	-
GF0033922	0	1	0	Branched-chain-amino-acid aminotransferase isoform 2 (1)	metabolic process [GO:0008152 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1)	Aminotransferase class IV [IPR001544] (1)	-	C_unshiu_00024_mRNA_110.1	-
GF0033921	0	1	0	Branched-chain-amino-acid transaminase (1)	metabolic process [GO:0008152 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1)	Aminotransferase class IV [IPR001544] (1)	-	C_unshiu_00024_mRNA_109.1	-
GF0033920	0	1	0	Hypothetical protein (1)		Cysteine-rich secretory protein, allergen V5/Tpx-1-related [IPR001283] (1); CAP domain [IPR014044] (1)	-	C_unshiu_00024_mRNA_108.1	-
GF0033919	0	1	0	Hypothetical protein (1)			-	C_unshiu_00024_mRNA_1.1	-
GF0033918	0	1	0	Hypothetical protein (1)			-	C_unshiu_00023_mRNA_9.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0033917	0	1	0	Hypothetical protein (1)			-	C_unshiu_00023_mRNA_63.1	-
GF0033916	0	1	0	Hypothetical protein (1)			-	C_unshiu_00023_mRNA_28.1	-
GF0033915	0	1	0	Hypothetical protein (1)	catalytic activity [GO:0003824 molecular_function] (1)	Pyridoxal phosphate-dependent transferase, major region, subdomain 1 [IPR015421] (1); Pyridoxal phosphate-dependent transferase [IPR015424] (1)	-	C_unshiu_00023_mRNA_15.1	-
GF0033914	0	1	0	Hypothetical protein (1)			-	C_unshiu_00023_mRNA_1.1	-
GF0033913	0	1	0	Hypothetical protein (1)	nitrogen compound metabolic process [GO:0006807 biological_process] (1); hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds [GO:0016810 molecular_function] (1)	Carbon-nitrogen hydrolase [IPR003010] (1)	-	C_unshiu_00022_mRNA_85.1	-
GF0033912	0	1	0	Hypothetical protein (1)	pyruvate kinase activity [GO:0004743 molecular_function] (1); glycolytic process [GO:0006096 biological_process] (1); nitrogen compound metabolic process [GO:0006807 biological_process] (1); magnesium ion binding [GO:0000287 molecular_function] (1); catalytic activity [GO:0003824 molecular_function] (1); potassium ion binding [GO:0030955 molecular_function] (1); hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds [GO:0016810 molecular_function] (1)	Pyruvate kinase-like, insert domain [IPR011037] (1); Pyruvate kinase [IPR001697] (1); Pyruvate/Phosphoenolpyruvate kinase-like domain [IPR015813] (1); Pyruvate kinase, beta-barrel insert domain [IPR015806] (1); Carbon-nitrogen hydrolase [IPR003010] (1); Pyruvate kinase, barrel [IPR015793] (1)	-	C_unshiu_00022_mRNA_83.1	-
GF0033911	0	1	0	Hypothetical protein (1)			-	C_unshiu_00022_mRNA_24.1	-
GF0033910	0	1	0	Hypothetical protein (1)			-	C_unshiu_00022_mRNA_16.1	-
GF0033909	0	1	0	Hypothetical protein (1)			-	C_unshiu_00022_mRNA_14.1	-
GF0033908	0	1	0	Hypothetical protein (1)			-	C_unshiu_00021_mRNA_9.1	-
GF0033907	0	1	0	Hypothetical protein (1)	vitamin B6 biosynthetic process [GO:0042819 biological_process] (1); pyridoxal phosphate biosynthetic process [GO:0042823 biological_process] (1); metabolic process [GO:0008152 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1)	Ribulose-phosphate binding barrel [IPR011060] (1); Pyridoxal 5'-phosphate synthase subunit PdxS/SNZ [IPR001852] (1); Aldolase-type TIM barrel [IPR013785] (1)	-	C_unshiu_00021_mRNA_85.1	-
GF0033906	0	1	0	Hypothetical protein (1)	binding [GO:0005488 molecular_function] (1); transposase activity [GO:0004803 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1); transposition, DNA-mediated [GO:0006313 biological_process] (1); DNA binding [GO:0003677 molecular_function] (1)	Armadillo-type fold [IPR016024] (1); Transposase, MuDR, plant [IPR004332] (1); Transposase, mutator type [IPR001207] (1); Armadillo-like helical [IPR011989] (1); Zinc finger, PMZ-type [IPR006564] (1); MULE transposase domain [IPR018289] (1); Zinc finger, SWIM-type [IPR007527] (1); Armadillo [IPR000225] (1); Atypical Arm repeat [IPR032413] (1)	-	C_unshiu_00021_mRNA_8.1	-
GF0033905	0	1	0	Hypothetical protein (1)			-	C_unshiu_00021_mRNA_6.1	-
GF0033904	0	1	0	Laccase (1)	lignin catabolic process [GO:0046274 biological_process] (1); apoplast [GO:0048046 cellular_component] (1); copper ion binding [GO:0005507 molecular_function] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); hydroquinone:oxygen oxidoreductase activity [GO:0052716 molecular_function] (1)	Multicopper oxidase, type 1 [IPR001117] (1); Multicopper oxidases, conserved site [IPR033138] (1); Laccase [IPR017761] (1); Multicopper oxidase, type 2 [IPR011706] (1); Cupredoxin [IPR008972] (1); Multicopper oxidase, copper-binding site [IPR002355] (1)	-	C_unshiu_00021_mRNA_52.1	-
GF0033903	0	1	0	Hypothetical protein (1)			-	C_unshiu_00021_mRNA_45.1	-
GF0033902	0	1	0	Hypothetical protein (1)			-	C_unshiu_00021_mRNA_39.1	-
GF0033901	0	1	0	Cytochrome P450 82A3 (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1)	Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450 [IPR001128] (1)	-	C_unshiu_00021_mRNA_25.1	-
GF0033900	0	1	0	Importin subunit alpha (1)	binding [GO:0005488 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Armadillo-type fold [IPR016024] (1); Armadillo [IPR000225] (1); Atypical Arm repeat [IPR032413] (1); Armadillo-like helical [IPR011989] (1)	-	C_unshiu_00021_mRNA_18.1	-
GF0033899	0	1	0	Hypothetical protein (1)			-	C_unshiu_00021_mRNA_15.1	-
GF0033898	0	1	0	Hypothetical protein (1)			-	C_unshiu_00021_mRNA_103.1	-
GF0033897	0	1	0	Hypothetical protein (1)		Transposase-associated domain [IPR029480] (1)	-	C_unshiu_00020_mRNA_75.1	-
GF0033896	0	1	0	Hypothetical protein (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1)	Glycoside hydrolase, catalytic domain [IPR013781] (1)	-	C_unshiu_00020_mRNA_72.1	-
GF0033895	0	1	0	Hypothetical protein (1)			-	C_unshiu_00020_mRNA_70.1	-
GF0033894	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_00020_mRNA_68.1	-
GF0033893	0	1	0	Auxin-induced protein 10A5 (1)	response to auxin [GO:0009733 biological_process] (1)	Small auxin-up RNA [IPR003676] (1)	-	C_unshiu_00020_mRNA_64.1	-
GF0033892	0	1	0	Origin recognition complex subunit 3 (1)	DNA replication [GO:0006260 biological_process] (1); nuclear origin of replication recognition complex [GO:0005664 cellular_component] (1); DNA binding [GO:0003677 molecular_function] (1)	Origin recognition complex, subunit 3 [IPR020795] (1)	-	C_unshiu_00020_mRNA_57.1	-
GF0033891	0	1	0	Hypothetical protein (1)	RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Ribonuclease H domain [IPR002156] (1)	-	C_unshiu_00020_mRNA_52.1	-
GF0033890	0	1	0	Hypothetical protein (1)			-	C_unshiu_00020_mRNA_50.1	-
GF0033889	0	1	0	Hypothetical protein (1)		Harbinger transposase-derived nuclease domain [IPR027806] (1)	-	C_unshiu_00020_mRNA_47.1	-
GF0033888	0	1	0	Mechanosensitive ion channel protein 10 (1)	transmembrane transport [GO:0055085 biological_process] (1); membrane [GO:0016020 cellular_component] (1)	EF-hand domain pair [IPR011992] (1); LSM domain [IPR010920] (1); Mechanosensitive ion channel MscS-like, plants/fungi [IPR016688] (1); Mechanosensitive ion channel MscS [IPR006685] (1)	-	C_unshiu_00020_mRNA_3.1	-
GF0033887	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_00020_mRNA_28.1	-
GF0033886	0	1	0	Cytochrome P450 89A2 (1)	heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1)	Cytochrome P450, conserved site [IPR017972] (1); Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450 [IPR001128] (1)	-	C_unshiu_00020_mRNA_26.1	-
GF0033885	0	1	0	Ribonucleoside-diphosphate reductase large subunit (1)	oxidation-reduction process [GO:0055114 biological_process] (1); DNA replication [GO:0006260 biological_process] (1)	Ribonucleotide reductase large subunit, C-terminal [IPR000788] (1); Ribonucleotide reductase, class I , alpha subunit [IPR013346] (1); Ribonucleotide reductase R1 subunit, N-terminal [IPR008926] (1); ATP-cone domain [IPR005144] (1)	-	C_unshiu_00020_mRNA_23.1	-
GF0033884	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_00020_mRNA_2.1	-
GF0033883	0	1	0	Hypothetical protein (1)	translation [GO:0006412 biological_process] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1); ribosome [GO:0005840 cellular_component] (1)	Ribosomal protein L14b/L23e [IPR000218] (1); Ribosomal protein L14 domain [IPR023571] (1)	-	C_unshiu_00020_mRNA_16.1	-
GF0033882	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00019_mRNA_99.1	-
GF0033881	0	1	0	Alpha,alpha-trehalase (1)	catalytic activity [GO:0003824 molecular_function] (1); trehalose metabolic process [GO:0005991 biological_process] (1); alpha,alpha-trehalase activity [GO:0004555 molecular_function] (1)	Glycoside hydrolase, family 37 [IPR001661] (1); Six-hairpin glycosidase-like [IPR008928] (1)	-	C_unshiu_00019_mRNA_90.1	-
GF0033880	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Domain of unknown function DUF4283 [IPR025558] (1); Ribonuclease H-like domain [IPR012337] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1); Leucine-rich repeat [IPR001611] (1); Zinc knuckle CX2CX4HX4C [IPR025836] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	-	C_unshiu_00019_mRNA_75.1	-
GF0033879	0	1	0	Hypothetical protein (1)			-	C_unshiu_00019_mRNA_47.1	-
GF0033878	0	1	0	Disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00019_mRNA_104.1	-
GF0033877	0	1	0	Hypothetical protein (1)			-	C_unshiu_00019_mRNA_103.1	-
GF0033876	0	1	0	C2 calcium/lipid-binding plant phosphoribosyltransferase family protein (1)	protein binding [GO:0005515 molecular_function] (1)	C2 domain [IPR000008] (1); Phosphoribosyltransferase C-terminal [IPR013583] (1)	-	C_unshiu_00018_mRNA_95.1	-
GF0033875	0	1	0	Hypothetical protein (1)			-	C_unshiu_00018_mRNA_9.1	-
GF0033874	0	1	0	Ribosomal RNA small subunit methyltransferase G (1)		HAD-like domain [IPR023214] (1)	-	C_unshiu_00018_mRNA_65.1	-
GF0033873	0	1	0	Hypothetical protein (1)			-	C_unshiu_00018_mRNA_63.1	-
GF0033872	0	1	0	Hypothetical protein (1)		Mesoderm development candidate 2 [IPR019330] (1)	-	C_unshiu_00018_mRNA_62.1	-
GF0033871	0	1	0	ATP binding , related (1)		Malectin-like carbohydrate-binding domain [IPR024788] (1); Protein of unknown function DUF604 [IPR006740] (1)	-	C_unshiu_00018_mRNA_45.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0033870	0	1	0	Hypothetical protein (1)	protein phosphorylation [GO:0006468 biological_process] (1); MAP kinase activity [GO:0004707 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Mitogen-activated protein (MAP) kinase, conserved site [IPR003527] (1); Protein kinase-like domain [IPR011009] (1); Protein of unknown function DUF241, plant [IPR004320] (1); Protein kinase domain [IPR000719] (1)	-	C_unshiu_00018_mRNA_41.1	-
GF0033869	0	1	0	NADP-dependent alkenal double bond reductase P1 (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	NAD(P)-binding domain [IPR016040] (1); Alcohol dehydrogenase, C-terminal [IPR013149] (1); Alcohol dehydrogenase superfamily, zinc-type [IPR002085] (1)	-	C_unshiu_00018_mRNA_3.1	-
GF0033868	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00018_mRNA_115.1	-
GF0033867	0	1	0	Galactolipid galactosyltransferase (1)			-	C_unshiu_00018_mRNA_112.2	-
GF0033866	0	1	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1); Domain of unknown function DUF1985 [IPR015410] (1)	-	C_unshiu_00018_mRNA_11.1	-
GF0033865	0	1	0	Menthol dehydrogenase (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Glucose/ribitol dehydrogenase [IPR002347] (1); Short-chain dehydrogenase/reductase SDR [IPR002198] (1); NAD(P)-binding domain [IPR016040] (1)	-	C_unshiu_00018_mRNA_109.1	-
GF0033864	0	1	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_00018_mRNA_10.1	-
GF0033863	0	1	0	2OG-Fe(II) oxygenase family oxidoreductase (1)		Isopenicillin N synthase-like [IPR027443] (1)	-	C_unshiu_00017_mRNA_9.1	-
GF0033862	0	1	0	MATE efflux family protein 9 (1)	transmembrane transport [GO:0055085 biological_process] (1); membrane [GO:0016020 cellular_component] (1); antiporter activity [GO:0015297 molecular_function] (1); drug transmembrane transporter activity [GO:0015238 molecular_function] (1); drug transmembrane transport [GO:0006855 biological_process] (1)	Glutathione S-transferase, C-terminal [IPR004046] (1); Multi antimicrobial extrusion protein [IPR002528] (1); Glutathione S-transferase, C-terminal-like [IPR010987] (1)	-	C_unshiu_00017_mRNA_8.1	-
GF0033861	0	1	0	Major latex protein, putative (1)	response to biotic stimulus [GO:0009607 biological_process] (1); defense response [GO:0006952 biological_process] (1)	Major latex protein domain [IPR024948] (1); START-like domain [IPR023393] (1); Bet v I/Major latex protein [IPR000916] (1)	-	C_unshiu_00017_mRNA_74.1	-
GF0033860	0	1	0	Hypothetical protein (1)			-	C_unshiu_00017_mRNA_73.1	-
GF0033859	0	1	0	Hypothetical protein (1)			-	C_unshiu_00017_mRNA_63.1	-
GF0033858	0	1	0	Hypothetical protein (1)			-	C_unshiu_00017_mRNA_60.1	-
GF0033857	0	1	0	Hypothetical protein (1)	transmembrane transport [GO:0055085 biological_process] (1); membrane [GO:0016020 cellular_component] (1); drug transmembrane transporter activity [GO:0015238 molecular_function] (1); antiporter activity [GO:0015297 molecular_function] (1); drug transmembrane transport [GO:0006855 biological_process] (1)	Multi antimicrobial extrusion protein [IPR002528] (1)	-	C_unshiu_00017_mRNA_6.1	-
GF0033856	0	1	0	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	C_unshiu_00017_mRNA_4.1	-
GF0033855	0	1	0	Hypothetical protein (1)	cytoskeleton organization [GO:0007010 biological_process] (1); microtubule binding [GO:0008017 molecular_function] (1)	Microtubule-associated protein 70 [IPR009768] (1)	-	C_unshiu_00017_mRNA_32.1	-
GF0033854	0	1	0	LRR receptor-like kinase (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_00017_mRNA_21.1	-
GF0033853	0	1	0	LRR receptor-like serine/threonine-protein kinase FLS2 (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_00017_mRNA_20.1	-
GF0033852	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00017_mRNA_18.1	-
GF0033851	0	1	0	Glutathione S-transferase tau 7, putative (1)	protein binding [GO:0005515 molecular_function] (1)	Thioredoxin-like fold [IPR012336] (1); Glutathione S-transferase, C-terminal-like [IPR010987] (1); Glutathione S-transferase, N-terminal [IPR004045] (1)	-	C_unshiu_00017_mRNA_11.1	-
GF0033850	0	1	0	Hypothetical protein (1)	transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (1); fatty acid biosynthetic process [GO:0006633 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1); membrane [GO:0016020 cellular_component] (1); metabolic process [GO:0008152 biological_process] (1)	3-Oxoacyl-[acyl-carrier-protein (ACP)] synthase III, C-terminal [IPR013747] (1); FAE1/Type III polyketide synthase-like protein [IPR013601] (1); Very-long-chain 3-ketoacyl-CoA synthase [IPR012392] (1); Protein of unknown function DUF2358 [IPR018790] (1); SOUL haem-binding protein [IPR006917] (1); Regulatory factor, effector binding domain [IPR011256] (1); Thiolase-like [IPR016039] (1)	-	C_unshiu_00016_mRNA_94.1	-
GF0033849	0	1	0	Hypothetical protein (1)			-	C_unshiu_00016_mRNA_87.1	-
GF0033848	0	1	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	C_unshiu_00016_mRNA_69.1	-
GF0033847	0	1	0	Hypothetical protein (1)			-	C_unshiu_00016_mRNA_46.1	-
GF0033846	0	1	0	Hypothetical protein (1)			-	C_unshiu_00016_mRNA_44.1	-
GF0033845	0	1	0	Hypothetical protein (1)		Chromo domain-like [IPR016197] (1); Chromo domain [IPR023780] (1)	-	C_unshiu_00016_mRNA_42.1	-
GF0033844	0	1	0	Ribonucleoside-diphosphate reductase large subunit (1)	ATP binding [GO:0005524 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); ribonucleoside-diphosphate reductase activity, thioredoxin disulfide as acceptor [GO:0004748 molecular_function] (1); DNA replication [GO:0006260 biological_process] (1)	Ribonucleotide reductase, class I , alpha subunit [IPR013346] (1); Ribonucleotide reductase large subunit, C-terminal [IPR000788] (1); Ribonucleotide reductase large subunit, N-terminal [IPR013509] (1); Ribonucleotide reductase R1 subunit, N-terminal [IPR008926] (1)	-	C_unshiu_00016_mRNA_40.1	-
GF0033843	0	1	0	Hypothetical protein (1)			-	C_unshiu_00016_mRNA_4.1	-
GF0033842	0	1	0	Alba-like protein C9orf23 like (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	DNA/RNA-binding protein Alba-like [IPR002775] (1)	-	C_unshiu_00016_mRNA_37.1	-
GF0033841	0	1	0	Hypothetical protein (1)	mRNA splicing, via spliceosome [GO:0000398 biological_process] (1)	Pre-mRNA-processing factor 6/Prp1/STA1 [IPR027108] (1)	-	C_unshiu_00016_mRNA_31.1	-
GF0033840	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	WD40-repeat-containing domain [IPR017986] (1); WD40 repeat [IPR001680] (1); WD40/YVTN repeat-like-containing domain [IPR015943] (1)	-	C_unshiu_00016_mRNA_30.1	-
GF0033839	0	1	0	Hypothetical protein (1)			-	C_unshiu_00016_mRNA_29.1	-
GF0033838	0	1	0	Hypothetical protein (1)		Prolamin-like domain [IPR008502] (1)	-	C_unshiu_00016_mRNA_28.1	-
GF0033837	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	WD40 repeat [IPR001680] (1); WD40-repeat-containing domain [IPR017986] (1); WD40/YVTN repeat-like-containing domain [IPR015943] (1)	-	C_unshiu_00016_mRNA_27.1	-
GF0033836	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF1985 [IPR015410] (1)	-	C_unshiu_00016_mRNA_26.1	-
GF0033835	0	1	0	Hypothetical protein (1)		Prolamin-like domain [IPR008502] (1)	-	C_unshiu_00016_mRNA_25.1	-
GF0033834	0	1	0	Truncated tyrosine decarboxylase (1)	carboxy-lyase activity [GO:0016831 molecular_function] (1); carboxylic acid metabolic process [GO:0019752 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1); cellular amino acid metabolic process [GO:0006520 biological_process] (1); pyridoxal phosphate binding [GO:0030170 molecular_function] (1)	Aromatic-L-amino-acid decarboxylase [IPR010977] (1); Pyridoxal phosphate-dependent transferase [IPR015424] (1); Pyridoxal phosphate-dependent transferase, major region, subdomain 1 [IPR015421] (1); Pyridoxal phosphate-dependent decarboxylase [IPR002129] (1)	-	C_unshiu_00016_mRNA_23.1	-
GF0033833	0	1	0	Hypothetical protein (1)			-	C_unshiu_00016_mRNA_20.1	-
GF0033832	0	1	0	Hypothetical protein (1)		Intron-binding protein aquarius [IPR032464] (1)	-	C_unshiu_00016_mRNA_18.1	-
GF0033831	0	1	0	Hypothetical protein (1)		Intron-binding protein aquarius [IPR032464] (1)	-	C_unshiu_00016_mRNA_17.1	-
GF0033830	0	1	0	Hypothetical protein (1)			-	C_unshiu_00016_mRNA_101.1	-
GF0033829	0	1	0	General transcription factor 3C-like protein (1)		Transcription factor IIIC, subunit 5 [IPR019136] (1)	-	C_unshiu_00016_mRNA_10.1	-
GF0033828	0	1	0	Cell division cycle protein 48 (1)	ATP binding [GO:0005524 molecular_function] (1)	ATPase, AAA-type, conserved site [IPR003960] (1); AAA+ ATPase domain [IPR003593] (1); ATPase, AAA-type, core [IPR003959] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	C_unshiu_00015_mRNA_91.1	-
GF0033827	0	1	0	Hypothetical protein (1)			-	C_unshiu_00015_mRNA_9.1	-
GF0033826	0	1	0	Hypothetical protein (1)			-	C_unshiu_00015_mRNA_8.1	-
GF0033825	0	1	0	Hypothetical protein (1)			-	C_unshiu_00015_mRNA_57.1	-
GF0033824	0	1	0	Hypothetical protein (1)	RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H domain [IPR002156] (1); Ribonuclease H-like domain [IPR012337] (1); Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	C_unshiu_00015_mRNA_52.1	-
GF0033823	0	1	0	Hypothetical protein (1)	metabolic process [GO:0008152 biological_process] (1); protein binding [GO:0005515 molecular_function] (1); transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1)	WD40 repeat [IPR001680] (1); WD40-repeat-containing domain [IPR017986] (1); WD40/YVTN repeat-like-containing domain [IPR015943] (1); UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1); WD40 repeat, conserved site [IPR019775] (1)	-	C_unshiu_00015_mRNA_38.1	-
GF0033822	0	1	0	Hypothetical protein (1)			-	C_unshiu_00015_mRNA_26.1	-
GF0033821	0	1	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Peptidase C1A [IPR013128] (1); Cathepsin propeptide inhibitor domain (I29) [IPR013201] (1)	-	C_unshiu_00015_mRNA_18.1	-
GF0033820	0	1	0	Hypothetical protein (1)			-	C_unshiu_00015_mRNA_15.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0033819	0	1	0	Anaphase-promoting complex subunit 11 (1)	ubiquitin-protein transferase activity [GO:0004842 molecular_function] (1); anaphase-promoting complex [GO:0005680 cellular_component] (1); protein binding [GO:0005515 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Anaphase-promoting complex subunit 11 [IPR024991] (1); Zinc finger, RING/FYVE/PHD-type [IPR013083] (1); Zinc finger, RING-type [IPR001841] (1)	-	C_unshiu_00015_mRNA_13.1	-
GF0033818	0	1	0	Hypothetical protein (1)			-	C_unshiu_00014_mRNA_9.1	-
GF0033817	0	1	0	Hypothetical protein (1)			-	C_unshiu_00014_mRNA_8.1	-
GF0033816	0	1	0	Hypothetical protein (1)			-	C_unshiu_00014_mRNA_7.1	-
GF0033815	0	1	0	SPX domain-containing protein 2 (1)	cellular response to phosphate starvation [GO:0016036 biological_process] (1)	SPX domain [IPR004331] (1); SPX domain-containing protein [IPR031142] (1)	-	C_unshiu_00014_mRNA_59.1	-
GF0033814	0	1	0	Hypothetical protein (1)			-	C_unshiu_00014_mRNA_3.1	-
GF0033813	0	1	0	Hypothetical protein (1)			-	C_unshiu_00014_mRNA_119.1	-
GF0033812	0	1	0	Hypothetical protein (1)			-	C_unshiu_00014_mRNA_118.1	-
GF0033811	0	1	0	Hypothetical protein (1)			-	C_unshiu_00013_mRNA_97.1	-
GF0033810	0	1	0	Hypothetical protein (1)			-	C_unshiu_00013_mRNA_96.1	-
GF0033809	0	1	0	Hypothetical protein (1)			-	C_unshiu_00013_mRNA_93.1	-
GF0033808	0	1	0	Hypothetical protein (1)			-	C_unshiu_00013_mRNA_92.1	-
GF0033807	0	1	0	Hypothetical protein (1)			-	C_unshiu_00013_mRNA_91.1	-
GF0033806	0	1	0	Hypothetical protein (1)			-	C_unshiu_00013_mRNA_90.1	-
GF0033805	0	1	0	Hypothetical protein (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Tyrosine-protein kinase, active site [IPR008266] (1); Protein kinase, ATP binding site [IPR017441] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	-	C_unshiu_00013_mRNA_86.1	-
GF0033804	0	1	0	LRR receptor-like kinase family protein (1)	protein binding [GO:0005515 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1); Leucine-rich repeat [IPR001611] (1); Protein kinase, ATP binding site [IPR017441] (1); Tyrosine-protein kinase, active site [IPR008266] (1)	-	C_unshiu_00013_mRNA_85.1	-
GF0033803	0	1	0	Hypothetical protein (1)	serine-type peptidase activity [GO:0008236 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Alpha/Beta hydrolase fold [IPR029058] (1); Peptidase S28 [IPR008758] (1)	-	C_unshiu_00013_mRNA_84.1	-
GF0033802	0	1	0	Hypothetical protein (1)			-	C_unshiu_00013_mRNA_7.1	-
GF0033801	0	1	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	DNA-binding domain [IPR016177] (1); AP2/ERF domain [IPR001471] (1)	-	C_unshiu_00013_mRNA_68.1	-
GF0033800	0	1	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	DNA-binding domain [IPR016177] (1); AP2/ERF domain [IPR001471] (1)	-	C_unshiu_00013_mRNA_67.1	-
GF0033799	0	1	0	Hypothetical protein (1)			-	C_unshiu_00013_mRNA_65.1	-
GF0033798	0	1	0	Hypothetical protein (1)			-	C_unshiu_00013_mRNA_49.1	-
GF0033797	0	1	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	Zinc finger, BED-type [IPR003656] (1)	-	C_unshiu_00013_mRNA_25.1	-
GF0033796	0	1	0	Hypothetical protein (1)			-	C_unshiu_00013_mRNA_22.1	-
GF0033795	0	1	0	Hypothetical protein (1)			-	C_unshiu_00013_mRNA_21.1	-
GF0033794	0	1	0	Hypothetical protein (1)			-	C_unshiu_00013_mRNA_2.1	-
GF0033793	0	1	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Powdery mildew resistance protein, RPW8 domain [IPR008808] (1); NB-ARC [IPR002182] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00013_mRNA_115.1	-
GF0033792	0	1	0	CST complex subunit CTC1 (1)	telomere maintenance [GO:0000723 biological_process] (1)	CST complex subunit CTC1, plant [IPR028262] (1)	-	C_unshiu_00013_mRNA_112.1	-
GF0033791	0	1	0	Myb-like HTH transcriptional regulator-like protein (1)	DNA binding [GO:0003677 molecular_function] (1)	Myb domain [IPR017930] (1); Myb domain, plants [IPR006447] (1); SANT/Myb domain [IPR001005] (1); Homeodomain-like [IPR009057] (1)	-	C_unshiu_00012_mRNA_84.1	-
GF0033790	0	1	0	Fasciclin domain-containing protein, putative isoform 1 (1)		FAS1 domain [IPR000782] (1)	-	C_unshiu_00012_mRNA_7.1	-
GF0033789	0	1	0	Hypothetical protein (1)			-	C_unshiu_00012_mRNA_64.1	-
GF0033788	0	1	0	Hypothetical protein (1)		Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00012_mRNA_31.1	-
GF0033787	0	1	0	Hypothetical protein (1)			-	C_unshiu_00012_mRNA_123.1	-
GF0033786	0	1	0	Hypothetical protein (1)			-	C_unshiu_00012_mRNA_113.1	-
GF0033785	0	1	0	Hypothetical protein (1)			-	C_unshiu_00011_mRNA_98.1	-
GF0033784	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1); Gag-polypeptide of LTR copia-type [IPR029472] (1); Pleckstrin homology domain [IPR001849] (1)	-	C_unshiu_00011_mRNA_97.1	-
GF0033783	0	1	0	Hypothetical protein (1)			-	C_unshiu_00011_mRNA_95.1	-
GF0033782	0	1	0	Hypothetical protein (1)			-	C_unshiu_00011_mRNA_94.1	-
GF0033781	0	1	0	Hypothetical protein (1)			-	C_unshiu_00011_mRNA_89.1	-
GF0033780	0	1	0	Hypothetical protein (1)			-	C_unshiu_00011_mRNA_88.1	-
GF0033779	0	1	0	Hypothetical protein (1)			-	C_unshiu_00011_mRNA_87.1	-
GF0033778	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00011_mRNA_81.1	-
GF0033777	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	C_unshiu_00011_mRNA_79.1	-
GF0033776	0	1	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	C_unshiu_00011_mRNA_73.1	-
GF0033775	0	1	0	Hypothetical protein (1)			-	C_unshiu_00011_mRNA_70.1	-
GF0033774	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	C_unshiu_00011_mRNA_67.1	-
GF0033773	0	1	0	Hypothetical protein (1)			-	C_unshiu_00011_mRNA_65.1	-
GF0033772	0	1	0	Monosacharide transport protein (1)			-	C_unshiu_00011_mRNA_63.1	-
GF0033771	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00011_mRNA_61.1	-
GF0033770	0	1	0	Hypothetical protein (1)	GTP binding [GO:0005525 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1); GTPase activity [GO:0003924 molecular_function] (1)	Tubulin/FtsZ, GTPase domain [IPR003008] (1); Cell division protein FtsZ, C-terminal [IPR024757] (1); Tubulin/FtsZ, C-terminal [IPR008280] (1); Nonaspanin (TM9SF) [IPR004240] (1); Tubulin/FtsZ, 2-layer sandwich domain [IPR018316] (1); Cell division protein FtsZ [IPR000158] (1)	-	C_unshiu_00011_mRNA_5.1	-
GF0033769	0	1	0	Hypothetical protein (1)			-	C_unshiu_00011_mRNA_47.1	-
GF0033768	0	1	0	Hypothetical protein (1)			-	C_unshiu_00011_mRNA_46.1	-
GF0033767	0	1	0	Progesterone 5-beta-reductase (1)		NAD(P)-binding domain [IPR016040] (1)	-	C_unshiu_00011_mRNA_43.1	-
GF0033766	0	1	0	Hypothetical protein (1)			-	C_unshiu_00011_mRNA_41.1	-
GF0033765	0	1	0	Hypothetical protein (1)			-	C_unshiu_00011_mRNA_39.1	-
GF0033764	0	1	0	Hypothetical protein (1)			-	C_unshiu_00011_mRNA_38.1	-
GF0033763	0	1	0	Hypothetical protein (1)			-	C_unshiu_00011_mRNA_36.1	-
GF0033762	0	1	0	Hypothetical protein (1)			-	C_unshiu_00011_mRNA_35.1	-
GF0033761	0	1	0	Hypothetical protein (1)			-	C_unshiu_00011_mRNA_32.1	-
GF0033760	0	1	0	Hypothetical protein (1)			-	C_unshiu_00011_mRNA_2.1	-
GF0033759	0	1	0	Hypothetical protein (1)		Transposase, MuDR, plant [IPR004332] (1); MULE transposase domain [IPR018289] (1)	-	C_unshiu_00011_mRNA_18.1	-
GF0033758	0	1	0	Hypothetical protein (1)		S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	C_unshiu_00011_mRNA_13.1	-
GF0033757	0	1	0	Hypothetical protein (1)			-	C_unshiu_00010_mRNA_59.1	-
GF0033756	0	1	0	Hypothetical protein (1)	integral component of membrane [GO:0016021 cellular_component] (1); protein insertion into membrane [GO:0051205 biological_process] (1)	Membrane insertase OXA1/ALB3/YidC [IPR001708] (1)	-	C_unshiu_00010_mRNA_3.1	-
GF0033755	0	1	0	Hypothetical protein (1)			-	C_unshiu_00010_mRNA_133.1	-
GF0033754	0	1	0	Hypothetical protein (1)			-	C_unshiu_00010_mRNA_1.1	-
GF0033753	0	1	0	Hypothetical protein (1)			-	C_unshiu_00009_mRNA_97.1	-
GF0033752	0	1	0	Hypothetical protein (1)			-	C_unshiu_00009_mRNA_93.1	-
GF0033751	0	1	0	Hypothetical protein (1)			-	C_unshiu_00009_mRNA_64.1	-
GF0033750	0	1	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, SWIM-type [IPR007527] (1); MULE transposase domain [IPR018289] (1); Zinc finger, PMZ-type [IPR006564] (1)	-	C_unshiu_00009_mRNA_26.1	-
GF0033749	0	1	0	Hypothetical protein (1)			-	C_unshiu_00009_mRNA_24.1	-
GF0033748	0	1	0	Hypothetical protein (1)			-	C_unshiu_00009_mRNA_23.1	-
GF0033747	0	1	0	Pattern formation protein, putative (1)			-	C_unshiu_00009_mRNA_16.1	-
GF0033746	0	1	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); nucleus [GO:0005634 cellular_component] (1)	PB1 domain [IPR000270] (1); AUX/IAA protein [IPR003311] (1)	-	C_unshiu_00009_mRNA_146.1	-
GF0033745	0	1	0	Heavy metal transport/detoxification superfamily protein (1)	metal ion transport [GO:0030001 biological_process] (1); metal ion binding [GO:0046872 molecular_function] (1)	Heavy metal-associated domain, HMA [IPR006121] (1)	-	C_unshiu_00009_mRNA_144.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0033744	0	1	0	Cytochrome P450 83B1 (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1)	Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450, conserved site [IPR017972] (1); Cytochrome P450 [IPR001128] (1)	-	C_unshiu_00009_mRNA_140.1	-
GF0033743	0	1	0	Hypothetical protein (1)			-	C_unshiu_00009_mRNA_134.1	-
GF0033742	0	1	0	Hypothetical protein (1)			-	C_unshiu_00009_mRNA_132.1	-
GF0033741	0	1	0	Hypothetical protein (1)	microtubule-based movement [GO:0007018 biological_process] (1); microtubule motor activity [GO:0003777 molecular_function] (1)	Kinesin-like protein [IPR027640] (1); NPK1-activating kinesin-like protein, C-terminal [IPR021881] (1)	-	C_unshiu_00009_mRNA_127.1	-
GF0033740	0	1	0	Hypothetical protein (1)	transport [GO:0006810 biological_process] (1); membrane [GO:0016020 cellular_component] (1); transporter activity [GO:0005215 molecular_function] (1)	Proton-dependent oligopeptide transporter family [IPR000109] (1)	-	C_unshiu_00009_mRNA_112.1	-
GF0033739	0	1	0	Hypothetical protein (1)			-	C_unshiu_00009_mRNA_101.1	-
GF0033738	0	1	0	Hypothetical protein (1)	extracellular region [GO:0005576 cellular_component] (1)	Expansin/Lol pI [IPR007118] (1); Expansin/pollen allergen, DPBB domain [IPR007112] (1); RlpA-like double-psi beta-barrel domain [IPR009009] (1)	-	C_unshiu_00009_mRNA_1.1	-
GF0033737	0	1	0	Hypothetical protein (1)			-	C_unshiu_00008_mRNA_71.1	-
GF0033736	0	1	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1); Domain of unknown function DUF4371 [IPR025398] (1); Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00008_mRNA_58.1	-
GF0033735	0	1	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	Zinc finger, BED-type [IPR003656] (1)	-	C_unshiu_00008_mRNA_40.1	-
GF0033734	0	1	0	Verticillium wilt resistance-like protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1)	-	C_unshiu_00008_mRNA_37.1	-
GF0033733	0	1	0	Hypothetical protein (1)			-	C_unshiu_00008_mRNA_16.1	-
GF0033732	0	1	0	Receptor like protein 33 (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00008_mRNA_149.1	-
GF0033731	0	1	0	LRR receptor-like kinase (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1)	-	C_unshiu_00008_mRNA_148.1	-
GF0033730	0	1	0	Hypothetical protein (1)			-	C_unshiu_00008_mRNA_141.1	-
GF0033729	0	1	0	Hypothetical protein (1)	transporter activity [GO:0005215 molecular_function] (1); purine nucleobase transport [GO:0006863 biological_process] (1); transmembrane transport [GO:0055085 biological_process] (1); transport [GO:0006810 biological_process] (1); membrane [GO:0016020 cellular_component] (1); purine nucleobase transmembrane transporter activity [GO:0005345 molecular_function] (1)	Xanthine/uracil/vitamin C permease [IPR006043] (1); AzgA purine transporter [IPR029940] (1)	-	C_unshiu_00008_mRNA_125.1	-
GF0033728	0	1	0	Hypothetical protein (1)	transmembrane transport [GO:0055085 biological_process] (1); transporter activity [GO:0005215 molecular_function] (1); purine nucleobase transport [GO:0006863 biological_process] (1); transport [GO:0006810 biological_process] (1); membrane [GO:0016020 cellular_component] (1); purine nucleobase transmembrane transporter activity [GO:0005345 molecular_function] (1)	Xanthine/uracil/vitamin C permease [IPR006043] (1); AzgA purine transporter [IPR029940] (1)	-	C_unshiu_00008_mRNA_124.1	-
GF0033727	0	1	0	Hypothetical protein (1)	pyridoxal phosphate binding [GO:0030170 molecular_function] (1); transaminase activity [GO:0008483 molecular_function] (1); catalytic activity [GO:0003824 molecular_function] (1)	Pyridoxal phosphate-dependent transferase, major region, subdomain 1 [IPR015421] (1); Pyridoxal phosphate-dependent transferase [IPR015424] (1); Aminotransferase class-III [IPR005814] (1); Pyridoxal phosphate-dependent transferase, major region, subdomain 2 [IPR015422] (1)	-	C_unshiu_00008_mRNA_113.1	-
GF0033726	0	1	0	Putative non-LTR retroelement reverse transcriptase (1)	nucleic acid binding [GO:0003676 molecular_function] (1); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H domain [IPR002156] (1)	-	C_unshiu_00008_mRNA_108.1	-
GF0033725	0	1	0	Hypothetical protein (1)			-	C_unshiu_00007_mRNA_60.1	-
GF0033724	0	1	0	Hypothetical protein (1)			-	C_unshiu_00007_mRNA_23.1	-
GF0033723	0	1	0	Hypothetical protein (1)			-	C_unshiu_00007_mRNA_17.1	-
GF0033722	0	1	0	Hypothetical protein (1)			-	C_unshiu_00007_mRNA_169.1	-
GF0033721	0	1	0	Hypothetical protein (1)			-	C_unshiu_00007_mRNA_142.1	-
GF0033720	0	1	0	S-adenosylmethionine synthase 2 (1)	S-adenosylmethionine biosynthetic process [GO:0006556 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1); methionine adenosyltransferase activity [GO:0004478 molecular_function] (1)	S-adenosylmethionine synthetase, N-terminal [IPR022628] (1); S-adenosylmethionine synthetase, conserved site [IPR022631] (1); S-adenosylmethionine synthetase superfamily [IPR022636] (1); S-adenosylmethionine synthetase [IPR002133] (1); S-adenosylmethionine synthetase, C-terminal [IPR022630] (1); S-adenosylmethionine synthetase, central domain [IPR022629] (1)	-	C_unshiu_00007_mRNA_140.1	-
GF0033719	0	1	0	Bidirectional sugar transporter SWEET6b (1)	integral component of membrane [GO:0016021 cellular_component] (1)	Autophagy protein Atg8 ubiquitin-like [IPR004241] (1); Ubiquitin-related domain [IPR029071] (1); SWEET sugar transporter [IPR004316] (1); Major facilitator superfamily domain [IPR020846] (1)	-	C_unshiu_00007_mRNA_138.1	-
GF0033718	0	1	0	Hypothetical protein (1)			-	C_unshiu_00007_mRNA_137.1	-
GF0033717	0	1	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	C_unshiu_00007_mRNA_134.1	-
GF0033716	0	1	0	Hypothetical protein (1)			-	C_unshiu_00007_mRNA_124.1	-
GF0033715	0	1	0	Putative vacuolar sorting-associated protein 13A (1)		Vacuolar protein sorting-associated protein 13, N-terminal domain [IPR026854] (1); Vacuolar protein sorting-associated protein 13 [IPR026847] (1); Vacuolar protein sorting-associated protein 13, second N-terminal domain [IPR031646] (1)	-	C_unshiu_00007_mRNA_118.1	-
GF0033714	0	1	0	Hypothetical protein (1)			-	C_unshiu_00007_mRNA_1.1	-
GF0033713	0	1	0	Hypothetical protein (1)			-	C_unshiu_00006_mRNA_9.1	-
GF0033712	0	1	0	Hypothetical protein (1)		PGG domain [IPR026961] (1)	-	C_unshiu_00006_mRNA_85.1	-
GF0033711	0	1	0	Exosome complex exonuclease RRP46 like (1)		Ribosomal protein S5 domain 2-type fold [IPR020568] (1); Exoribonuclease, phosphorolytic domain 1 [IPR001247] (1)	-	C_unshiu_00006_mRNA_82.1	-
GF0033710	0	1	0	H+-transporting two-sector ATPase, alpha/beta subunit, central region (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	C_unshiu_00006_mRNA_76.1	-
GF0033709	0	1	0	Hypothetical protein (1)			-	C_unshiu_00006_mRNA_75.1	-
GF0033708	0	1	0	Hypothetical protein (1)			-	C_unshiu_00006_mRNA_6.1	-
GF0033707	0	1	0	Hypothetical protein (1)			-	C_unshiu_00006_mRNA_54.1	-
GF0033706	0	1	0	Hypothetical protein (1)		RNA-binding protein Lupus La [IPR006630] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1)	-	C_unshiu_00006_mRNA_43.1	-
GF0033705	0	1	0	Hypothetical protein (1)	DNA replication-independent nucleosome assembly [GO:0006336 biological_process] (1)	Histone transcription regulator 3/CABIN1 [IPR033053] (1)	-	C_unshiu_00006_mRNA_42.1	-
GF0033704	0	1	0	Monosacharide transport protein (1)			-	C_unshiu_00006_mRNA_31.1	-
GF0033703	0	1	0	Hypothetical protein (1)			-	C_unshiu_00006_mRNA_133.1	-
GF0033702	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4409 [IPR025521] (1); Domain of unknown function DUF239 [IPR004314] (1)	-	C_unshiu_00006_mRNA_13.1	-
GF0033701	0	1	0	Hypothetical protein (1)		Flotillin family [IPR027705] (1)	-	C_unshiu_00005_mRNA_93.1	-
GF0033700	0	1	0	Aspartate aminotransferase B (1)			-	C_unshiu_00005_mRNA_83.1	-
GF0033699	0	1	0	Hypothetical protein (1)			-	C_unshiu_00005_mRNA_79.1	-
GF0033698	0	1	0	Homogentisate phytyltransferase (1)	intracellular [GO:0005622 cellular_component] (1); integral component of membrane [GO:0016021 cellular_component] (1); translation [GO:0006412 biological_process] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1); prenyltransferase activity [GO:0004659 molecular_function] (1); ribosome [GO:0005840 cellular_component] (1)	Ribosomal protein L39e, conserved site [IPR020083] (1); Ribosomal protein L39e [IPR000077] (1); UbiA prenyltransferase family [IPR000537] (1); Ribosomal protein L39e domain [IPR023626] (1)	-	C_unshiu_00005_mRNA_70.1	-
GF0033697	0	1	0	Hypothetical protein (1)			-	C_unshiu_00005_mRNA_63.1	-
GF0033696	0	1	0	Hypothetical protein (1)			-	C_unshiu_00005_mRNA_61.1	-
GF0033695	0	1	0	Hypothetical protein (1)			-	C_unshiu_00005_mRNA_59.1	-
GF0033694	0	1	0	Integral membrane transporter family protein (1)	transport [GO:0006810 biological_process] (1); integral component of membrane [GO:0016021 cellular_component] (1); cell cycle [GO:0007049 biological_process] (1); pyrimidine nucleotide biosynthetic process [GO:0006221 biological_process] (1); positive regulation of Notch signaling pathway [GO:0045747 biological_process] (1)	Enhancer of rudimentary [IPR000781] (1); Major facilitator superfamily domain [IPR020846] (1); Folate-biopterin transporter [IPR004324] (1)	-	C_unshiu_00005_mRNA_23.1	-
GF0033693	0	1	0	NB-ARC domain disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	C_unshiu_00005_mRNA_142.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0033692	0	1	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	C_unshiu_00005_mRNA_140.1	-
GF0033691	0	1	0	Hypothetical protein (1)			-	C_unshiu_00005_mRNA_138.1	-
GF0033690	0	1	0	TMV resistance protein N (1)	protein binding [GO:0005515 molecular_function] (1); signal transduction [GO:0007165 biological_process] (1)	Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1)	-	C_unshiu_00005_mRNA_137.1	-
GF0033689	0	1	0	Hypothetical protein (1)			-	C_unshiu_00005_mRNA_136.1	-
GF0033688	0	1	0	Hypothetical protein (1)			-	C_unshiu_00005_mRNA_135.1	-
GF0033687	0	1	0	Hypothetical protein (1)			-	C_unshiu_00005_mRNA_133.1	-
GF0033686	0	1	0	F-box/RNI-like superfamily protein isoform 2 (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, cysteine-containing subtype [IPR006553] (1)	-	C_unshiu_00005_mRNA_132.1	-
GF0033685	0	1	0	Hypothetical protein (1)		Domain of unknown function DUF4050 [IPR025124] (1)	-	C_unshiu_00005_mRNA_128.1	-
GF0033684	0	1	0	Hypothetical protein (1)			-	C_unshiu_00005_mRNA_1.1	-
GF0033683	0	1	0	Nucleotide-diphospho-sugar transferase family protein (1)		Nucleotide-diphospho-sugar transferase [IPR005069] (1)	-	C_unshiu_00004_mRNA_98.1	-
GF0033682	0	1	0	Hypothetical protein (1)			-	C_unshiu_00004_mRNA_75.1	-
GF0033681	0	1	0	Hypothetical protein (1)		Conserved hypothetical protein CHP01589, plant [IPR006476] (1)	-	C_unshiu_00004_mRNA_73.1	-
GF0033680	0	1	0	Hypothetical protein (1)			-	C_unshiu_00004_mRNA_168.1	-
GF0033679	0	1	0	Hypothetical protein (1)			-	C_unshiu_00004_mRNA_164.1	-
GF0033678	0	1	0	Monosacharide transport protein (1)			-	C_unshiu_00004_mRNA_158.1	-
GF0033677	0	1	0	Hypothetical protein (1)			-	C_unshiu_00004_mRNA_103.1	-
GF0033676	0	1	0	Hypothetical protein (1)			-	C_unshiu_00004_mRNA_10.1	-
GF0033675	0	1	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	SANT/Myb domain [IPR001005] (1); Homeodomain-like [IPR009057] (1); Myb-like domain [IPR017877] (1)	-	C_unshiu_00003_mRNA_91.1	-
GF0033674	0	1	0	Hypothetical protein (1)			-	C_unshiu_00003_mRNA_86.1	-
GF0033673	0	1	0	Hypothetical protein (1)			-	C_unshiu_00003_mRNA_43.1	-
GF0033672	0	1	0	Hypothetical protein (1)			-	C_unshiu_00003_mRNA_25.1	-
GF0033671	0	1	0	Hypothetical protein (1)			-	C_unshiu_00003_mRNA_171.1	-
GF0033670	0	1	0	Hypothetical protein (1)			-	C_unshiu_00003_mRNA_168.1	-
GF0033669	0	1	0	Hypothetical protein (1)			-	C_unshiu_00003_mRNA_167.1	-
GF0033668	0	1	0	Hypothetical protein (1)			-	C_unshiu_00003_mRNA_165.1	-
GF0033667	0	1	0	Xyloglucan galactosyltransferase KATAMARI1 (1)		Exostosin-like [IPR004263] (1)	-	C_unshiu_00003_mRNA_14.1	-
GF0033666	0	1	0	Hypothetical protein (1)			-	C_unshiu_00003_mRNA_130.1	-
GF0033665	0	1	0	T-complex protein 1 subunit gamma (1)	ATP binding [GO:0005524 molecular_function] (1); protein folding [GO:0006457 biological_process] (1); unfolded protein binding [GO:0051082 molecular_function] (1)	Chaperone tailless complex polypeptide 1 (TCP-1) [IPR017998] (1); Chaperonin TCP-1, conserved site [IPR002194] (1); GroEL-like equatorial domain [IPR027413] (1); GroEL-like apical domain [IPR027409] (1); Chaperonin Cpn60/TCP-1 family [IPR002423] (1); TCP-1-like chaperonin intermediate domain [IPR027410] (1); T-complex protein 1, gamma subunit [IPR012719] (1)	-	C_unshiu_00003_mRNA_117.2	-
GF0033664	0	1	0	Hypothetical protein (1)			-	C_unshiu_00003_mRNA_103.1	-
GF0033663	0	1	0	Vignain (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Cysteine peptidase, asparagine active site [IPR025661] (1); Peptidase C1A, papain C-terminal [IPR000668] (1); Cathepsin propeptide inhibitor domain (I29) [IPR013201] (1); Peptidase C1A [IPR013128] (1); Cysteine peptidase, histidine active site [IPR025660] (1); Cysteine peptidase, cysteine active site [IPR000169] (1)	-	C_unshiu_00002_mRNA_85.1	-
GF0033662	0	1	0	Hypothetical protein (1)			-	C_unshiu_00002_mRNA_72.1	-
GF0033661	0	1	0	Hypothetical protein (1)			-	C_unshiu_00002_mRNA_51.1	-
GF0033660	0	1	0	Hypothetical protein (1)			-	C_unshiu_00002_mRNA_215.1	-
GF0033659	0	1	0	Hypothetical protein (1)			-	C_unshiu_00002_mRNA_2.1	-
GF0033658	0	1	0	L-type lectin-domain containing receptor kinase IV.2 (1)	ATP binding [GO:0005524 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1)	Protein kinase, ATP binding site [IPR017441] (1); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1)	-	C_unshiu_00002_mRNA_169.1	-
GF0033657	0	1	0	Putative retroelement pol polyprotein (1)			-	C_unshiu_00002_mRNA_164.1	-
GF0033656	0	1	0	FAR1 DNA-binding domain protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1); FAR1 DNA binding domain [IPR004330] (1)	-	C_unshiu_00002_mRNA_117.1	-
GF0033655	0	1	0	ERF2 transcription factor (1)	DNA binding [GO:0003677 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (1)	DNA-binding domain [IPR016177] (1); AP2/ERF domain [IPR001471] (1)	-	C_unshiu_00002_mRNA_115.1	-
GF0033654	0	1	0	Hypothetical protein (1)			-	C_unshiu_00001_mRNA_57.1	-
GF0033653	0	1	0	Hypothetical protein (1)	translation [GO:0006412 biological_process] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1); ribosome [GO:0005840 cellular_component] (1)	Ribosomal protein L10e/L16 [IPR016180] (1)	-	C_unshiu_00001_mRNA_395.1	-
GF0033652	0	1	0	Hypothetical protein (1)			-	C_unshiu_00001_mRNA_339.1	-
GF0033651	0	1	0	E3 ubiquitin ligase BIG BROTHER (1)	protein binding [GO:0005515 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, RING/FYVE/PHD-type [IPR013083] (1); Zinc finger, RING-type [IPR001841] (1)	-	C_unshiu_00001_mRNA_332.1	-
GF0033650	0	1	0	Hypothetical protein (1)		ATP-dependent RNA helicase Ski2, C-terminal [IPR012961] (1)	-	C_unshiu_00001_mRNA_33.1	-
GF0033649	0	1	0	Hypothetical protein (1)			-	C_unshiu_00001_mRNA_309.1	-
GF0033648	0	1	0	Hypothetical protein (1)			-	C_unshiu_00001_mRNA_3.1	-
GF0033647	0	1	0	Germin-like protein subfamily 1 member 8 (1)	nutrient reservoir activity [GO:0045735 molecular_function] (1); manganese ion binding [GO:0030145 molecular_function] (1)	Cupin 1 [IPR006045] (1); Germin, manganese binding site [IPR019780] (1); RmlC-like jelly roll fold [IPR014710] (1); RmlC-like cupin domain [IPR011051] (1)	-	C_unshiu_00001_mRNA_29.1	-
GF0033646	0	1	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); nucleotide binding [GO:0000166 molecular_function] (1); calcium-transporting ATPase activity [GO:0005388 molecular_function] (1); metal ion binding [GO:0046872 molecular_function] (1); membrane [GO:0016020 cellular_component] (1); calcium ion transmembrane transport [GO:0070588 biological_process] (1); calmodulin binding [GO:0005516 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1)	Calcium-transporting P-type ATPase, N-terminal autoinhibitory domain [IPR024750] (1); P-type ATPase, A domain [IPR008250] (1); HAD-like domain [IPR023214] (1); Cation-transporting P-type ATPase, N-terminal [IPR004014] (1); P-type ATPase [IPR001757] (1); Cation-transporting P-type ATPase, C-terminal [IPR006068] (1); P-type ATPase, subfamily IIB [IPR006408] (1); P-type ATPase, cytoplasmic domain N [IPR023299] (1); P-type ATPase, transmembrane domain [IPR023298] (1)	-	C_unshiu_00001_mRNA_283.1	-
GF0033645	0	1	0	Hypothetical protein (1)	cytokinin metabolic process [GO:0009690 biological_process] (1); oxidoreductase activity, acting on CH-OH group of donors [GO:0016614 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1); cytokinin dehydrogenase activity [GO:0019139 molecular_function] (1); glycerol-3-phosphate metabolic process [GO:0006072 biological_process] (1); glycerol-3-phosphate dehydrogenase complex [GO:0009331 cellular_component] (1); glycerol-3-phosphate dehydrogenase [NAD+] activity [GO:0004367 molecular_function] (1); glycerol-3-phosphate catabolic process [GO:0046168 biological_process] (1); flavin adenine dinucleotide binding [GO:0050660 molecular_function] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); NAD binding [GO:0051287 molecular_function] (1); oxidoreductase activity, acting on the CH-	FAD-binding, type 2 [IPR016166] (1); Glycerol-3-phosphate dehydrogenase, NAD-dependent, N-terminal [IPR011128] (1); FAD linked oxidase, N-terminal [IPR006094] (1); Glycerol-3-phosphate dehydrogenase, NAD-dependent [IPR006168] (1); Vanillyl-alcohol oxidase/Cytokinin dehydrogenase C-terminal domain [IPR016170] (1); NAD(P)-binding domain [IPR016040] (1); CO dehydrogenase flavoprotein-like, FAD-binding, subdomain 2 [IPR016169] (1); Glycerol-3-phosphate dehydrogenase, NAD-dependent, C-terminal [IPR006109] (1); FAD-binding, type 2, subdomain 1 [IPR016167] (1); Oxygen oxidoreductase covalent FAD-binding site [IPR006093] (1); 6-phosphogluconate dehydrogenase C-terminal domain-like [IPR008927] (1); FAD-linked oxidase-like, C-terminal [IPR016164] (1); Cytokinin dehydrogenase 1, FAD/cytokinin binding domain [IPR015345] (1); 6-phosphogluconate dehydrogenase, domain 2 [IPR013328] (1)	-	C_unshiu_00001_mRNA_282.1	-
GF0033644	0	1	0	Hypothetical protein (1)	actin binding [GO:0003779 molecular_function] (1)	Protein Networked (NET), actin-binding (NAB) domain [IPR011684] (1)	-	C_unshiu_00001_mRNA_250.1	-
GF0033643	0	1	0	Hypothetical protein (1)			-	C_unshiu_00001_mRNA_243.1	-
GF0033642	0	1	0	Hypothetical protein (1)		Peptidoglycan binding-like [IPR002477] (1)	-	C_unshiu_00001_mRNA_22.1	-
GF0033641	0	1	0	Hypothetical protein (1)	metal ion binding [GO:0046872 molecular_function] (1)	Zinc finger, C2H2 [IPR007087] (1)	-	C_unshiu_00001_mRNA_214.1	-
GF0033640	0	1	0	Hypothetical protein (1)			-	C_unshiu_00001_mRNA_18.1	-
GF0033639	0	1	0	Hypothetical protein (1)			-	C_unshiu_00001_mRNA_177.1	-
GF0033638	0	1	0	Hypothetical protein (1)		GDP-fucose protein O-fucosyltransferase [IPR019378] (1)	-	C_unshiu_00001_mRNA_171.1	-
GF0033637	0	1	0	Hypothetical protein (1)			-	C_unshiu_00001_mRNA_169.1	-
GF0033636	0	1	0	Hypothetical protein (1)			-	C_unshiu_00001_mRNA_150.1	-
GF0033635	0	1	0	Hypothetical protein (1)			-	C_unshiu_00001_mRNA_147.1	-
GF0033634	0	1	0	Hypothetical protein (1)		Protein of unknown function DUF679 [IPR007770] (1)	-	C_unshiu_00001_mRNA_139.1	-
GF0033633	0	1	0	Hypothetical protein (1)			-	C_unshiu_00001_mRNA_126.1	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0033632	0	1	0	Cullin 3B (1)	ubiquitin-dependent protein catabolic process [GO:0006511 biological_process] (1); ubiquitin protein ligase binding [GO:0031625 molecular_function] (1)	Cullin homology [IPR016158] (1); Cullin, N-terminal [IPR001373] (1); Cullin repeat-like-containing domain [IPR016159] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Cullin protein, neddylation domain [IPR019559] (1)	-	C_unshiu_00001_mRNA_117.1	-
GF0033631	0	1	0	TSA: Wollemia nobilis transcribed RNA sequence (1)	ubiquitin protein ligase binding [GO:0031625 molecular_function] (1); ubiquitin-dependent protein catabolic process [GO:0006511 biological_process] (1)	Cullin repeat-like-containing domain [IPR016159] (1); Cullin, N-terminal [IPR001373] (1)	-	C_unshiu_00001_mRNA_116.1	-
GF0033630	0	1	0	F-box/kelch-repeat protein SKIP11 (1)	protein binding [GO:0005515 molecular_function] (1)	Kelch repeat type 1 [IPR006652] (1); Galactose oxidase, beta-propeller [IPR015916] (1)	-	C_unshiu_00001_mRNA_109.1	-
GF0033629	0	1	0	Receptor-like protein kinase HSL1 (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1)	Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Serine/threonine-protein kinase, active site [IPR008271] (1)	-	C_unshiu_00001_mRNA_1.1	-