Supplemental Table 5. *P. trifoliata* 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*
GF0000418	0	0	10	Hypothetical protein (10)			-	-	P_trifoliata_00022_mRNA_144.1,P_trifoliata_00047_mRNA_92.1,P_trifoliata_00047_mRNA_93.1,P_trifoliata_00047_mRNA_94.1,P_trifoliata_00047_mRNA_95.1,P_trifoliata_00047_mRNA_96.1,P_trifoliata_00047_mRNA_97.1,P_trifoliata_00257_mRNA_2.1,P_trifoliata_00257_mRNA_3.1,P_trifoliata_00257_mRNA_4.1
GF0001731	0	0	6	Hypothetical protein (4); Protein FAR1-RELATED SEQUENCE 9 (1); Transposon-like element Lyt2.0 DNA (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (6); zinc ion binding [GO:0008270 molecular_function] (5); nucleic acid binding [GO:0003676 molecular_function] (4)	FHY3/FAR1 family [IPR031052] (6); Zinc finger, PMZ-type [IPR006564] (4); Zinc finger, SWIM-type [IPR007527] (4); Zinc finger, CCHC-type [IPR001878] (4); FAR1 DNA binding domain [IPR004330] (3); MULE transposase domain [IPR018289] (2)	-	-	P_trifoliata_00090_mRNA_1.1,P_trifoliata_00297_mRNA_10.1,P_trifoliata_00297_mRNA_9.1,P_trifoliata_00858_mRNA_2.1,P_trifoliata_01143_mRNA_1.1,P_trifoliata_01252_mRNA_3.1
GF0002682	0	0	5	Hypothetical protein (5)			-	-	P_trifoliata_00046_mRNA_3.1,P_trifoliata_00046_mRNA_5.1,P_trifoliata_00107_mRNA_48.1,P_trifoliata_00339_mRNA_24.1,P_trifoliata_00609_mRNA_2.1
GF0019481	0	0	3	Hypothetical protein (1); Retrotransposon protein, putative, Ty1-copia subclass (1); FOG: Transposon-encoded proteins with TYA, reverse transcriptase, integrase domains in various combinations (1)	nucleic acid binding [GO:0003676 molecular_function] (2); zinc ion binding [GO:0008270 molecular_function] (2)	Zinc finger, CCHC-type [IPR001878] (2)	-	-	P_trifoliata_00023_mRNA_117.1,P_trifoliata_00377_mRNA_22.1,P_trifoliata_00600_mRNA_7.1
GF0026133	0	0	2	Hypothetical protein (1); Early auxin response 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 transferase [IPR015424] (1); Pyridoxal phosphate-dependent decarboxylase [IPR002129] (1); Pyridoxal phosphate-dependent transferase, major region, subdomain 1 [IPR015421] (1)	-	-	P_trifoliata_00205_mRNA_44.1,P_trifoliata_01108_mRNA_2.1
GF0026132	0	0	2	Hypothetical protein (2)			-	-	P_trifoliata_00129_mRNA_69.1,P_trifoliata_00892_mRNA_4.1
GF0051614	0	0	1	F-box protein SKIP22 (1)	protein binding [GO:0005515 molecular_function] (1)	F-box domain [IPR001810] (1)	-	-	P_trifoliata_01311_mRNA_1.1
GF0051613	0	0	1	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	B3 DNA binding domain [IPR003340] (1); DNA-binding pseudobarrel domain [IPR015300] (1)	-	-	P_trifoliata_01306_mRNA_1.1
GF0051612	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01305_mRNA_1.1
GF0051611	0	0	1	Receptor like protein 9 (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine rich repeat 4 [IPR025875] (1); Leucine-rich repeat [IPR001611] (1)	-	-	P_trifoliata_01304_mRNA_1.1
GF0051610	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01303_mRNA_1.1
GF0051609	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01302_mRNA_1.1
GF0051608	0	0	1	Acetolactate synthase small subunit (1)	branched-chain amino acid biosynthetic process [GO:0009082 biological_process] (1); acetolactate synthase activity [GO:0003984 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1); amino acid binding [GO:0016597 molecular_function] (1)	Acetolactate synthase, small subunit [IPR004789] (1); Acetolactate synthase, small subunit, C-terminal [IPR019455] (1); ACT domain [IPR002912] (1)	-	-	P_trifoliata_01301_mRNA_1.1
GF0051607	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01300_mRNA_2.1
GF0051606	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01300_mRNA_1.1
GF0051605	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01298_mRNA_1.1
GF0051604	0	0	1	Hypothetical protein (1)		Glutathione S-transferase, C-terminal-like [IPR010987] (1)	-	-	P_trifoliata_01296_mRNA_2.1
GF0051603	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01296_mRNA_1.1
GF0051602	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01294_mRNA_1.1
GF0051601	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01291_mRNA_2.1
GF0051600	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01291_mRNA_1.1
GF0051599	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01289_mRNA_2.1
GF0051598	0	0	1	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	-	P_trifoliata_01289_mRNA_1.1
GF0051597	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	SET domain [IPR001214] (1)	-	-	P_trifoliata_01286_mRNA_1.1
GF0051596	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01285_mRNA_2.1
GF0051595	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01281_mRNA_1.1
GF0051594	0	0	1	Hypothetical protein (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)	-	-	P_trifoliata_01279_mRNA_2.1
GF0051593	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01274_mRNA_2.1
GF0051592	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01271_mRNA_1.1
GF0051591	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01270_mRNA_2.1
GF0051590	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01265_mRNA_1.1
GF0051589	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01264_mRNA_3.1
GF0051588	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01264_mRNA_2.1
GF0051587	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01261_mRNA_1.1
GF0051586	0	0	1	Hypothetical protein (1)	enzyme inhibitor activity [GO:0004857 molecular_function] (1)	Pectinesterase inhibitor domain [IPR006501] (1)	-	-	P_trifoliata_01257_mRNA_3.1
GF0051585	0	0	1	Putative disease resistance protein RGA1 (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_01257_mRNA_2.1
GF0051584	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01257_mRNA_1.1
GF0051583	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01254_mRNA_1.1
GF0051582	0	0	1	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); High mobility group box domain [IPR009071] (1)	-	-	P_trifoliata_01252_mRNA_2.1
GF0051581	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01251_mRNA_3.1
GF0051580	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01251_mRNA_2.1
GF0051579	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01251_mRNA_1.1
GF0051578	0	0	1	Cytochrome c oxidase subunit 1 (1)	oxidation-reduction process [GO:0055114 biological_process] (1); aerobic respiration [GO:0009060 biological_process] (1); cytochrome-c oxidase activity [GO:0004129 molecular_function] (1); electron carrier activity [GO:0009055 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1); heme binding [GO:0020037 molecular_function] (1)	Cytochrome c oxidase subunit I [IPR000883] (1); Cytochrome c oxidase, subunit I domain [IPR023616] (1)	-	-	P_trifoliata_01249_mRNA_1.1
GF0051577	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01243_mRNA_4.1
GF0051576	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01241_mRNA_1.1
GF0051575	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01237_mRNA_6.1
GF0051574	0	0	1	Cytochrome P450 86A1 (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, E-class, group I [IPR002401] (1); Cytochrome P450 [IPR001128] (1)	-	-	P_trifoliata_01237_mRNA_5.1
GF0051573	0	0	1	Cytochrome P450 (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)	-	-	P_trifoliata_01237_mRNA_4.1
GF0051572	0	0	1	Cytochrome P450 86A1 (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)	-	-	P_trifoliata_01237_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*
GF0051571	0	0	1	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, E-class, group I [IPR002401] (1); Cytochrome P450, conserved site [IPR017972] (1); Cytochrome P450 [IPR001128] (1)	-	-	P_trifoliata_01237_mRNA_2.1
GF0051570	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01236_mRNA_1.1
GF0051569	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01234_mRNA_2.1
GF0051568	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01233_mRNA_1.1
GF0051567	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1)	-	-	P_trifoliata_01231_mRNA_1.1
GF0051566	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01227_mRNA_3.1
GF0051565	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01227_mRNA_1.1
GF0051564	0	0	1	Hypothetical protein (1)	endoplasmic reticulum [GO:0005783 cellular_component] (1); integral component of membrane [GO:0016021 cellular_component] (1)	Translocon-associated protein subunit beta [IPR008856] (1)	-	-	P_trifoliata_01225_mRNA_2.1
GF0051563	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01225_mRNA_1.1
GF0051562	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01223_mRNA_1.1
GF0051561	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01222_mRNA_2.1
GF0051560	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01222_mRNA_1.1
GF0051559	0	0	1	Hypothetical protein (1)	unfolded protein binding [GO:0051082 molecular_function] (1); protein folding [GO:0006457 biological_process] (1)	Chaperone DnaJ, C-terminal [IPR002939] (1); HSP40/DnaJ peptide-binding [IPR008971] (1)	-	-	P_trifoliata_01220_mRNA_1.1
GF0051558	0	0	1	Coiled-coil domain-containing protein 97 isoform 1 (1)		Protein of unknown function DUF2052, coiled-coil [IPR018613] (1)	-	-	P_trifoliata_01219_mRNA_2.1
GF0051557	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01218_mRNA_2.1
GF0051556	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01216_mRNA_3.1
GF0051555	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01216_mRNA_2.1
GF0051554	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01215_mRNA_2.1
GF0051553	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01214_mRNA_2.1
GF0051552	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01213_mRNA_2.1
GF0051551	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01207_mRNA_2.1
GF0051550	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01206_mRNA_3.1
GF0051549	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01203_mRNA_4.1
GF0051548	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01203_mRNA_3.1
GF0051547	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01203_mRNA_2.1
GF0051546	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01203_mRNA_1.1
GF0051545	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01202_mRNA_1.1
GF0051544	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01201_mRNA_2.1
GF0051543	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01201_mRNA_1.1
GF0051542	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01200_mRNA_2.1
GF0051541	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01200_mRNA_1.1
GF0051540	0	0	1	Hypothetical protein (1)		Plant self-incompatibility S1 [IPR010264] (1)	-	-	P_trifoliata_01199_mRNA_2.1
GF0051539	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01197_mRNA_1.1
GF0051538	0	0	1	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)	-	-	P_trifoliata_01196_mRNA_2.1
GF0051537	0	0	1	Hypothetical protein (1)	condensin complex [GO:0000796 cellular_component] (1); mitotic chromosome condensation [GO:0007076 biological_process] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Structural maintenance of chromosomes Smc2 [IPR027120] (1); RecF/RecN/SMC, N-terminal [IPR003395] (1)	-	-	P_trifoliata_01196_mRNA_1.1
GF0051536	0	0	1	Hypothetical protein (1)		Double-stranded RNA-binding domain [IPR014720] (1)	-	-	P_trifoliata_01195_mRNA_4.1
GF0051535	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01192_mRNA_2.1
GF0051534	0	0	1	Hypothetical protein (1)		Acylneuraminate cytidylyltransferase [IPR003329] (1); Nucleotide-diphospho-sugar transferases [IPR029044] (1)	-	-	P_trifoliata_01192_mRNA_1.1
GF0051533	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01191_mRNA_6.1
GF0051532	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01191_mRNA_5.1
GF0051531	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01190_mRNA_3.1
GF0051530	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01190_mRNA_2.1
GF0051529	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01190_mRNA_1.1
GF0051528	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01189_mRNA_5.1
GF0051527	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01189_mRNA_3.1
GF0051526	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01189_mRNA_1.1
GF0051525	0	0	1	Hypothetical protein (1)		Cysteine-rich flanking region, C-terminal [IPR000483] (1)	-	-	P_trifoliata_01186_mRNA_2.1
GF0051524	0	0	1	WD repeat-containing protein 82 (1)	protein binding [GO:0005515 molecular_function] (1)	WD40/YVTN repeat-like-containing domain [IPR015943] (1); WD40 repeat [IPR001680] (1); WD40-repeat-containing domain [IPR017986] (1)	-	-	P_trifoliata_01186_mRNA_1.1
GF0051523	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01183_mRNA_3.1
GF0051522	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01183_mRNA_1.1
GF0051521	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01182_mRNA_6.1
GF0051520	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01182_mRNA_5.1
GF0051519	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01182_mRNA_4.1
GF0051518	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01182_mRNA_3.1
GF0051517	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01182_mRNA_2.1
GF0051516	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01180_mRNA_2.1
GF0051515	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01180_mRNA_1.1
GF0051514	0	0	1	Hypothetical protein (1)		DNA-binding pseudobarrel domain [IPR015300] (1)	-	-	P_trifoliata_01179_mRNA_2.1
GF0051513	0	0	1	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	DNA-binding pseudobarrel domain [IPR015300] (1); B3 DNA binding domain [IPR003340] (1)	-	-	P_trifoliata_01179_mRNA_1.1
GF0051512	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01178_mRNA_3.1
GF0051511	0	0	1	COP9 signalosome complex subunit 7 (1)	protein binding [GO:0005515 molecular_function] (1)	Proteasome component (PCI) domain [IPR000717] (1)	-	-	P_trifoliata_01178_mRNA_1.1
GF0051510	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01177_mRNA_2.1
GF0051509	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01172_mRNA_4.1
GF0051508	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01172_mRNA_3.1
GF0051507	0	0	1	RnaseH 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)	-	-	P_trifoliata_01172_mRNA_2.1
GF0051506	0	0	1	Alpha/beta hydrolase fold superfamily (1)		DnaJ domain [IPR001623] (1); Alpha/beta hydrolase fold-1 [IPR000073] (1); Alpha/Beta hydrolase fold [IPR029058] (1)	-	-	P_trifoliata_01171_mRNA_4.1
GF0051505	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01171_mRNA_3.1
GF0051504	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01171_mRNA_2.1
GF0051503	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01170_mRNA_4.1
GF0051502	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01170_mRNA_2.1
GF0051501	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01169_mRNA_2.1
GF0051500	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01168_mRNA_1.1
GF0051499	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01166_mRNA_2.1
GF0051498	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01166_mRNA_1.1
GF0051497	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01164_mRNA_5.1
GF0051496	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01164_mRNA_2.1
GF0051495	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01164_mRNA_1.1
GF0051494	0	0	1	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)	-	-	P_trifoliata_01163_mRNA_3.1
GF0051493	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01162_mRNA_1.1
GF0051492	0	0	1	Xylosyltransferase 1 (1)	membrane [GO:0016020 cellular_component] (1); acetylglucosaminyltransferase activity [GO:0008375 molecular_function] (1)	Glycosyl transferase, family 14 [IPR003406] (1)	-	-	P_trifoliata_01160_mRNA_1.1
GF0051491	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01158_mRNA_5.1
GF0051490	0	0	1	Carboxyesterase 18 (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)	-	-	P_trifoliata_01157_mRNA_1.1
GF0051489	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01154_mRNA_1.1
GF0051488	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_01153_mRNA_2.1
GF0051487	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01152_mRNA_2.1
GF0051486	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01151_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*
GF0051485	0	0	1	Small nuclear ribonucleoprotein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); DEAD/DEAH box helicase domain [IPR011545] (1); Helicase superfamily 1/2, ATP-binding domain [IPR014001] (1)	-	-	P_trifoliata_01151_mRNA_1.1
GF0051484	0	0	1	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)	-	-	P_trifoliata_01150_mRNA_3.1
GF0051483	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01149_mRNA_7.1
GF0051482	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01149_mRNA_6.1
GF0051481	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01149_mRNA_5.1
GF0051480	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01149_mRNA_2.1
GF0051479	0	0	1	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)	-	-	P_trifoliata_01147_mRNA_5.1
GF0051478	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01146_mRNA_2.1
GF0051477	0	0	1	Translation initiation factor IF-2, putative (1)		Protein of unknown function DUF674 [IPR007750] (1)	-	-	P_trifoliata_01141_mRNA_6.1
GF0051476	0	0	1	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); phosphorelay signal transduction system [GO:0000160 biological_process] (1)	Homeodomain-like [IPR009057] (1); Signal transduction response regulator, receiver domain [IPR001789] (1); CheY-like superfamily [IPR011006] (1)	-	-	P_trifoliata_01141_mRNA_5.1
GF0051475	0	0	1	Hypothetical protein (1)		CheY-like superfamily [IPR011006] (1)	-	-	P_trifoliata_01141_mRNA_4.1
GF0051474	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01141_mRNA_1.1
GF0051473	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01139_mRNA_1.1
GF0051472	0	0	1	Hypothetical protein (1)	defense response [GO:0006952 biological_process] (1)	Knottin, scorpion toxin-like [IPR003614] (1)	-	-	P_trifoliata_01138_mRNA_2.1
GF0051471	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01138_mRNA_1.1
GF0051470	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01136_mRNA_1.1
GF0051469	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01135_mRNA_2.1
GF0051468	0	0	1	SAM domain family protein (1)	protein binding [GO:0005515 molecular_function] (1)	Sterile alpha motif/pointed domain [IPR013761] (1); Sterile alpha motif domain [IPR001660] (1)	-	-	P_trifoliata_01135_mRNA_1.1
GF0051467	0	0	1	Hypothetical protein (1)	mRNA processing [GO:0006397 biological_process] (1); 7-methylguanosine mRNA capping [GO:0006370 biological_process] (1); mRNA guanylyltransferase activity [GO:0004484 molecular_function] (1)	mRNA capping enzyme, catalytic domain [IPR001339] (1)	-	-	P_trifoliata_01133_mRNA_5.1
GF0051466	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01131_mRNA_3.1
GF0051465	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01131_mRNA_1.1
GF0051464	0	0	1	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)	-	-	P_trifoliata_01128_mRNA_1.1
GF0051463	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01126_mRNA_1.1
GF0051462	0	0	1	Far-red impaired responsive (FAR1) family protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FAR1 DNA binding domain [IPR004330] (1); FHY3/FAR1 family [IPR031052] (1)	-	-	P_trifoliata_01124_mRNA_2.1
GF0051461	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01122_mRNA_1.1
GF0051460	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01121_mRNA_1.1
GF0051459	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01120_mRNA_3.1
GF0051458	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01120_mRNA_2.1
GF0051457	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01119_mRNA_1.1
GF0051456	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01118_mRNA_4.1
GF0051455	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01118_mRNA_3.1
GF0051454	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01118_mRNA_1.1
GF0051453	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01117_mRNA_3.1
GF0051452	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01117_mRNA_1.1
GF0051451	0	0	1	Hypothetical protein (1)		EF-Hand 1, calcium-binding site [IPR018247] (1); Thioredoxin-like fold [IPR012336] (1)	-	-	P_trifoliata_01116_mRNA_4.1
GF0051450	0	0	1	Hypothetical protein (1)	carbohydrate binding [GO:0030246 molecular_function] (1)	Legume lectin domain [IPR001220] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1)	-	-	P_trifoliata_01115_mRNA_5.1
GF0051449	0	0	1	Hypothetical protein (1)	carbohydrate binding [GO:0030246 molecular_function] (1)	Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Legume lectin domain [IPR001220] (1)	-	-	P_trifoliata_01115_mRNA_4.1
GF0051448	0	0	1	Disease resistance RPS5-like 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 [IPR001611] (1); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	-	P_trifoliata_01115_mRNA_1.1
GF0051447	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01114_mRNA_3.1
GF0051446	0	0	1	Hypothetical protein (1)	voltage-gated chloride channel activity [GO:0005247 molecular_function] (1); transmembrane transport [GO:0055085 biological_process] (1); chloride transport [GO:0006821 biological_process] (1); membrane [GO:0016020 cellular_component] (1); ion channel activity [GO:0005216 molecular_function] (1)	Chloride channel, core [IPR014743] (1); Chloride channel, voltage gated [IPR001807] (1)	-	-	P_trifoliata_01113_mRNA_2.1
GF0051445	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01113_mRNA_1.1
GF0051444	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01112_mRNA_4.1
GF0051443	0	0	1	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); DNA binding [GO:0003677 molecular_function] (1)	AP2/ERF domain [IPR001471] (1); DNA-binding domain [IPR016177] (1)	-	-	P_trifoliata_01112_mRNA_3.1
GF0051442	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01111_mRNA_1.1
GF0051441	0	0	1	Malate synthase (1)	glyoxylate cycle [GO:0006097 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1); malate synthase activity [GO:0004474 molecular_function] (1)	Malate synthase-like [IPR011076] (1); Malate synthase [IPR001465] (1)	-	-	P_trifoliata_01110_mRNA_2.1
GF0051440	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01110_mRNA_1.1
GF0051439	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01109_mRNA_3.1
GF0051438	0	0	1	Cysteine desulfurase, putative, expressed (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)	-	-	P_trifoliata_01103_mRNA_4.1
GF0051437	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01103_mRNA_3.1
GF0051436	0	0	1	SufS subfamily cysteine desulfurase (1)	catalytic activity [GO:0003824 molecular_function] (1)	Pyridoxal phosphate-dependent transferase [IPR015424] (1); Aminotransferase class V domain [IPR000192] (1); Trimeric LpxA-like [IPR011004] (1); Nucleotide-diphospho-sugar transferases [IPR029044] (1); Pyridoxal phosphate-dependent transferase, major region, subdomain 1 [IPR015421] (1)	-	-	P_trifoliata_01103_mRNA_1.1
GF0051435	0	0	1	Tetratricopeptide repeat (TPR)-like superfamily protein, putative isoform 3 (1)	protein binding [GO:0005515 molecular_function] (1)	Tetratricopeptide repeat [IPR019734] (1); Tetratricopeptide repeat-containing domain [IPR013026] (1); Clustered mitochondria protein, N-terminal [IPR028275] (1); Tetratricopeptide-like helical domain [IPR011990] (1)	-	-	P_trifoliata_01102_mRNA_2.1
GF0051434	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01101_mRNA_8.1
GF0051433	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01101_mRNA_7.1
GF0051432	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01101_mRNA_6.1
GF0051431	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01101_mRNA_5.1
GF0051430	0	0	1	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, PMZ-type [IPR006564] (1); Zinc finger, SWIM-type [IPR007527] (1)	-	-	P_trifoliata_01100_mRNA_3.1
GF0051429	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_01099_mRNA_4.1
GF0051428	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	SH3 domain [IPR001452] (1)	-	-	P_trifoliata_01099_mRNA_3.1
GF0051427	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01098_mRNA_1.1
GF0051426	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01097_mRNA_1.1
GF0051425	0	0	1	Lectin (1)	carbohydrate binding [GO:0030246 molecular_function] (1)	Legume lectin, beta chain, Mn/Ca-binding site [IPR019825] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Legume lectin domain [IPR001220] (1)	-	-	P_trifoliata_01095_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*
GF0051424	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01094_mRNA_2.1
GF0051423	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01094_mRNA_1.1
GF0051422	0	0	1	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)	-	-	P_trifoliata_01093_mRNA_2.1
GF0051421	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01092_mRNA_4.1
GF0051420	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01092_mRNA_3.1
GF0051419	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01091_mRNA_7.1
GF0051418	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01091_mRNA_5.1
GF0051417	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01091_mRNA_3.1
GF0051416	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01090_mRNA_4.1
GF0051415	0	0	1	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, E-class, group I [IPR002401] (1); Cytochrome P450 [IPR001128] (1)	-	-	P_trifoliata_01089_mRNA_1.1
GF0051414	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01088_mRNA_2.1
GF0051413	0	0	1	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	-	-	P_trifoliata_01088_mRNA_1.1
GF0051412	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01085_mRNA_2.1
GF0051411	0	0	1	Hypothetical protein (1)	polysaccharide binding [GO:0030247 molecular_function] (1)	Wall-associated receptor kinase, galacturonan-binding domain [IPR025287] (1)	-	-	P_trifoliata_01084_mRNA_2.1
GF0051410	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01084_mRNA_1.1
GF0051409	0	0	1	Hypothetical protein (1)	response to stress [GO:0006950 biological_process] (1)	Late embryogenesis abundant protein, LEA5-type [IPR004926] (1)	-	-	P_trifoliata_01083_mRNA_8.1
GF0051408	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01083_mRNA_6.1
GF0051407	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01083_mRNA_5.1
GF0051406	0	0	1	Hypothetical protein (1)		Formin, FH2 domain [IPR015425] (1)	-	-	P_trifoliata_01082_mRNA_2.1
GF0051405	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01082_mRNA_1.1
GF0051404	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01081_mRNA_6.1
GF0051403	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01081_mRNA_4.1
GF0051402	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01080_mRNA_1.1
GF0051401	0	0	1	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)	-	-	P_trifoliata_01079_mRNA_5.1
GF0051400	0	0	1	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	-	-	P_trifoliata_01079_mRNA_4.1
GF0051399	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01078_mRNA_2.1
GF0051398	0	0	1	Hypothetical protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	-	P_trifoliata_01078_mRNA_1.1
GF0051397	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01077_mRNA_6.1
GF0051396	0	0	1	Hypothetical protein (1)		Isopenicillin N synthase-like [IPR027443] (1)	-	-	P_trifoliata_01077_mRNA_3.1
GF0051395	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01077_mRNA_1.1
GF0051394	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01076_mRNA_5.1
GF0051393	0	0	1	Hypothetical protein (1)	nuclear chromosome [GO:0000228 cellular_component] (1)	Rad21/Rec8-like protein, C-terminal [IPR023093] (1); Rad21/Rec8-like protein, C-terminal, eukaryotic [IPR006909] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1)	-	-	P_trifoliata_01076_mRNA_1.1
GF0051392	0	0	1	Transposon protein, putative, Mutator sub-class (1)		Transposase, MuDR, plant [IPR004332] (1); MULE transposase domain [IPR018289] (1)	-	-	P_trifoliata_01075_mRNA_3.1
GF0051391	0	0	1	Hypothetical protein (1)	integral component of membrane [GO:0016021 cellular_component] (1)	Nonaspanin (TM9SF) [IPR004240] (1)	-	-	P_trifoliata_01074_mRNA_2.1
GF0051390	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01072_mRNA_6.1
GF0051389	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01072_mRNA_5.1
GF0051388	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01072_mRNA_4.1
GF0051387	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01072_mRNA_3.1
GF0051386	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01071_mRNA_4.1
GF0051385	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01071_mRNA_1.1
GF0051384	0	0	1	Hypothetical protein (1)	polysaccharide binding [GO:0030247 molecular_function] (1)	Wall-associated receptor kinase, galacturonan-binding domain [IPR025287] (1)	-	-	P_trifoliata_01070_mRNA_4.1
GF0051383	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01070_mRNA_1.1
GF0051382	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01068_mRNA_5.1
GF0051381	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01068_mRNA_3.1
GF0051380	0	0	1	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)	AP2/ERF domain [IPR001471] (1)	-	-	P_trifoliata_01067_mRNA_1.1
GF0051379	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01066_mRNA_2.1
GF0051378	0	0	1	Disease resistance protein RPS5 (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); Protein of unknown function DUF2921 [IPR021319] (1)	-	-	P_trifoliata_01066_mRNA_1.1
GF0051377	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01065_mRNA_3.1
GF0051376	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01065_mRNA_1.1
GF0051375	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01063_mRNA_8.1
GF0051374	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01063_mRNA_7.1
GF0051373	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01063_mRNA_5.1
GF0051372	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01063_mRNA_4.1
GF0051371	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01063_mRNA_3.1
GF0051370	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01063_mRNA_2.1
GF0051369	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01063_mRNA_10.1
GF0051368	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01063_mRNA_1.1
GF0051367	0	0	1	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	-	P_trifoliata_01062_mRNA_5.1
GF0051366	0	0	1	TMV resistance protein N (1)		P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1)	-	-	P_trifoliata_01062_mRNA_4.1
GF0051365	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01062_mRNA_2.1
GF0051364	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01062_mRNA_1.1
GF0051363	0	0	1	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)	-	-	P_trifoliata_01061_mRNA_1.1
GF0051362	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01060_mRNA_2.1
GF0051361	0	0	1	Hypothetical protein (1)		Protein of unknown function DUF3522 [IPR021910] (1)	-	-	P_trifoliata_01059_mRNA_6.1
GF0051360	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01059_mRNA_1.1
GF0051359	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01057_mRNA_7.1
GF0051358	0	0	1	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)	-	-	P_trifoliata_01057_mRNA_4.1
GF0051357	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01057_mRNA_1.1
GF0051356	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	Carlavirus nucleic acid-binding protein [IPR002568] (1)	-	-	P_trifoliata_01056_mRNA_4.1
GF0051355	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01055_mRNA_4.1
GF0051354	0	0	1	Sex determination protein tasselseed-2 (1)	metabolic process [GO:0008152 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1)	Glucose/ribitol dehydrogenase [IPR002347] (1); Short-chain dehydrogenase/reductase SDR [IPR002198] (1); NAD(P)-binding domain [IPR016040] (1)	-	-	P_trifoliata_01054_mRNA_1.1
GF0051353	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01052_mRNA_7.1
GF0051352	0	0	1	CW14 protein isoform 1 (1)		Domain of unknown function DUF1336 [IPR009769] (1)	-	-	P_trifoliata_01052_mRNA_6.1
GF0051351	0	0	1	Ripening related protein family (1)		RlpA-like double-psi beta-barrel domain [IPR009009] (1)	-	-	P_trifoliata_01052_mRNA_5.1
GF0051350	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01052_mRNA_4.1
GF0051349	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01052_mRNA_2.1
GF0051348	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01051_mRNA_3.1
GF0051347	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01050_mRNA_4.1
GF0051346	0	0	1	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)	-	-	P_trifoliata_01050_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*
GF0051345	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01050_mRNA_1.1
GF0051344	0	0	1	Metacaspase 1 isoform 2 (1)		Caspase-like domain [IPR029030] (1)	-	-	P_trifoliata_01049_mRNA_5.1
GF0051343	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01049_mRNA_3.1
GF0051342	0	0	1	Hypothetical protein (1)		Caspase-like domain [IPR029030] (1)	-	-	P_trifoliata_01049_mRNA_2.1
GF0051341	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01049_mRNA_1.1
GF0051340	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01048_mRNA_2.1
GF0051339	0	0	1	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)	-	-	P_trifoliata_01046_mRNA_3.1
GF0051338	0	0	1	Cytochrome P450 (1)	heme binding [GO:0020037 molecular_function] (1); catalytic activity [GO:0003824 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)	Histidine triad, conserved site [IPR019808] (1); HIT-like domain [IPR011146] (1); Cytochrome P450 [IPR001128] (1); Histidine triad (HIT) protein [IPR001310] (1)	-	-	P_trifoliata_01046_mRNA_1.1
GF0051337	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01045_mRNA_2.1
GF0051336	0	0	1	Putative disease resistance RPP13-like protein 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)	-	-	P_trifoliata_01043_mRNA_2.1
GF0051335	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01043_mRNA_1.1
GF0051334	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01042_mRNA_4.1
GF0051333	0	0	1	Disease resistance protein RPS5 (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	-	P_trifoliata_01042_mRNA_2.1
GF0051332	0	0	1	Hypothetical protein (1)		Transposase-associated domain [IPR029480] (1)	-	-	P_trifoliata_01040_mRNA_3.1
GF0051331	0	0	1	DNA-(apurinic or apyrimidinic site) lyase (1)	endonuclease activity [GO:0004519 molecular_function] (1); DNA repair [GO:0006281 biological_process] (1); DNA binding [GO:0003677 molecular_function] (1); intracellular [GO:0005622 cellular_component] (1); nuclease activity [GO:0004518 molecular_function] (1)	Endonuclease/exonuclease/phosphatase [IPR005135] (1); AP endonuclease 1, conserved site [IPR020848] (1); AP endonuclease 1 [IPR004808] (1)	-	-	P_trifoliata_01040_mRNA_1.1
GF0051330	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01038_mRNA_7.1
GF0051329	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01038_mRNA_5.1
GF0051328	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01038_mRNA_2.1
GF0051327	0	0	1	Hypothetical protein (1)		Transposon, En/Spm-like [IPR004242] (1)	-	-	P_trifoliata_01038_mRNA_10.1
GF0051326	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01036_mRNA_2.1
GF0051325	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01035_mRNA_5.1
GF0051324	0	0	1	Hypothetical protein (1)	phospholipid binding [GO:0005543 molecular_function] (1)	AP180 N-terminal homology (ANTH) domain [IPR011417] (1); ENTH/VHS [IPR008942] (1); ENTH domain [IPR013809] (1)	-	-	P_trifoliata_01035_mRNA_1.1
GF0051323	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1); Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	-	P_trifoliata_01034_mRNA_4.1
GF0051322	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01034_mRNA_3.1
GF0051321	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01034_mRNA_1.1
GF0051320	0	0	1	Hydroxyproline-rich glycoprotein family protein (1)			-	-	P_trifoliata_01033_mRNA_5.1
GF0051319	0	0	1	Putative xaa-pro aminopeptidase p (1)		IGR protein motif [IPR019083] (1)	-	-	P_trifoliata_01033_mRNA_3.1
GF0051318	0	0	1	Hypothetical protein (1)	calcium ion binding [GO:0005509 molecular_function] (1)	EF-hand domain [IPR002048] (1)	-	-	P_trifoliata_01032_mRNA_1.1
GF0051317	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01031_mRNA_4.1
GF0051316	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01031_mRNA_1.1
GF0051315	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01030_mRNA_1.1
GF0051314	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01029_mRNA_7.1
GF0051313	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01029_mRNA_2.1
GF0051312	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4216 [IPR025312] (1)	-	-	P_trifoliata_01027_mRNA_8.1
GF0051311	0	0	1	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)	-	-	P_trifoliata_01027_mRNA_6.1
GF0051310	0	0	1	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1)	FAD/NAD(P)-binding domain [IPR023753] (1)	-	-	P_trifoliata_01027_mRNA_4.1
GF0051309	0	0	1	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1)	FAD/NAD(P)-binding domain [IPR023753] (1)	-	-	P_trifoliata_01027_mRNA_3.1
GF0051308	0	0	1	Salicylate 1-monooxygenase (1)	FAD binding [GO:0071949 molecular_function] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	FAD-binding domain [IPR002938] (1); FAD/NAD(P)-binding domain [IPR023753] (1)	-	-	P_trifoliata_01027_mRNA_2.1
GF0051307	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01025_mRNA_2.1
GF0051306	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01025_mRNA_1.1
GF0051305	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01024_mRNA_7.1
GF0051304	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01024_mRNA_6.1
GF0051303	0	0	1	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 H2A/H2B/H3 [IPR007125] (1); Histone H3/CENP-A [IPR000164] (1); Histone-fold [IPR009072] (1)	-	-	P_trifoliata_01024_mRNA_4.1
GF0051302	0	0	1	CDNA clone:002-110-H12, full insert sequence (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)	-	-	P_trifoliata_01024_mRNA_3.1
GF0051301	0	0	1	Hypothetical protein (1)		GAG-pre-integrase domain [IPR025724] (1)	-	-	P_trifoliata_01023_mRNA_3.1
GF0051300	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01023_mRNA_1.1
GF0051299	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01021_mRNA_9.1
GF0051298	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01021_mRNA_6.1
GF0051297	0	0	1	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); ATPase activity [GO:0016887 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); ABC transporter-like [IPR003439] (1)	-	-	P_trifoliata_01019_mRNA_1.1
GF0051296	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01018_mRNA_4.1
GF0051295	0	0	1	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)	-	-	P_trifoliata_01018_mRNA_2.1
GF0051294	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01017_mRNA_6.1
GF0051293	0	0	1	Putative ribonuclease H protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	-	P_trifoliata_01017_mRNA_3.1
GF0051292	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01017_mRNA_2.1
GF0051291	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01016_mRNA_9.1
GF0051290	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01016_mRNA_8.1
GF0051289	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01016_mRNA_7.1
GF0051288	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01016_mRNA_4.1
GF0051287	0	0	1	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	-	-	P_trifoliata_01016_mRNA_2.1
GF0051286	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01013_mRNA_7.1
GF0051285	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01013_mRNA_4.1
GF0051284	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	-	P_trifoliata_01013_mRNA_3.1
GF0051283	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01011_mRNA_4.1
GF0051282	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01011_mRNA_3.1
GF0051281	0	0	1	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)	NAD(P)-binding domain [IPR016040] (1); Alcohol dehydrogenase superfamily, zinc-type [IPR002085] (1)	-	-	P_trifoliata_01011_mRNA_2.1
GF0051280	0	0	1	Probably inactive leucine-rich repeat receptor-like protein 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)	-	-	P_trifoliata_01011_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*
GF0051279	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01010_mRNA_2.1
GF0051278	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01009_mRNA_1.1
GF0051277	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01008_mRNA_6.1
GF0051276	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01008_mRNA_4.1
GF0051275	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01008_mRNA_3.1
GF0051274	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01008_mRNA_2.1
GF0051273	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01008_mRNA_1.1
GF0051272	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01007_mRNA_5.1
GF0051271	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01007_mRNA_3.1
GF0051270	0	0	1	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	-	P_trifoliata_01006_mRNA_5.1
GF0051269	0	0	1	Pentatricopeptide repeat-containing protein, chloroplastic (1)		Pentatricopeptide repeat [IPR002885] (1)	-	-	P_trifoliata_01006_mRNA_4.1
GF0051268	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01006_mRNA_2.1
GF0051267	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01006_mRNA_1.1
GF0051266	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01005_mRNA_5.1
GF0051265	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01005_mRNA_4.1
GF0051264	0	0	1	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); O-methyltransferase, family 2 [IPR001077] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); O-methyltransferase COMT-type [IPR016461] (1); Plant methyltransferase dimerisation [IPR012967] (1)	-	-	P_trifoliata_01005_mRNA_1.1
GF0051263	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01004_mRNA_3.1
GF0051262	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01004_mRNA_2.1
GF0051261	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01004_mRNA_1.1
GF0051260	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01003_mRNA_4.1
GF0051259	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01003_mRNA_3.1
GF0051258	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01003_mRNA_2.1
GF0051257	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_01000_mRNA_4.1
GF0051256	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00999_mRNA_7.1
GF0051255	0	0	1	Hypothetical protein (1)		PGG domain [IPR026961] (1)	-	-	P_trifoliata_00999_mRNA_6.1
GF0051254	0	0	1	Hypothetical protein (1)		Ankyrin repeat-containing domain [IPR020683] (1); PGG domain [IPR026961] (1)	-	-	P_trifoliata_00999_mRNA_5.1
GF0051253	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00999_mRNA_4.1
GF0051252	0	0	1	Ankyrin repeat plant-like protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat [IPR002110] (1); PGG domain [IPR026961] (1); Ankyrin repeat-containing domain [IPR020683] (1)	-	-	P_trifoliata_00999_mRNA_3.1
GF0051251	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00999_mRNA_2.1
GF0051250	0	0	1	Neurofilament heavy protein, putative (1)			-	-	P_trifoliata_00999_mRNA_1.1
GF0051249	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00998_mRNA_4.1
GF0051248	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00998_mRNA_1.1
GF0051247	0	0	1	RING/FYVE/PHD zinc finger superfamily protein isoform 1 (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, RING/FYVE/PHD-type [IPR013083] (1); Zinc finger, RING-CH-type [IPR011016] (1)	-	-	P_trifoliata_00997_mRNA_4.1
GF0051246	0	0	1	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)	-	-	P_trifoliata_00996_mRNA_2.1
GF0051245	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00995_mRNA_4.1
GF0051244	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4219 [IPR025314] (1)	-	-	P_trifoliata_00995_mRNA_3.1
GF0051243	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	-	P_trifoliata_00994_mRNA_1.1
GF0051242	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00992_mRNA_8.1
GF0051241	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00992_mRNA_6.1
GF0051240	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00992_mRNA_5.1
GF0051239	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00992_mRNA_4.1
GF0051238	0	0	1	Polyamine oxidase 1-like protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1)	FAD/NAD(P)-binding domain [IPR023753] (1); Amine oxidase [IPR002937] (1)	-	-	P_trifoliata_00991_mRNA_7.1
GF0051237	0	0	1	Hypothetical protein (1)		NAD(P)-binding domain [IPR016040] (1)	-	-	P_trifoliata_00991_mRNA_5.1
GF0051236	0	0	1	Structural constituent of ribosome, putative (1)		Uncharacterised protein family UPF0114 [IPR005134] (1)	-	-	P_trifoliata_00991_mRNA_2.1
GF0051235	0	0	1	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); DNA-templated transcription, initiation [GO:0006352 biological_process] (1); sigma factor activity [GO:0016987 molecular_function] (1); transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (1)	Winged helix-turn-helix DNA-binding domain [IPR011991] (1); RNA polymerase sigma-70 region 3 [IPR007624] (1); RNA polymerase sigma factor, region 3/4 [IPR013324] (1); RNA polymerase sigma factor, region 2 [IPR013325] (1); RNA polymerase sigma-70 region 2 [IPR007627] (1)	-	-	P_trifoliata_00991_mRNA_1.1
GF0051234	0	0	1	DNA-(apurinic or apyrimidinic site) lyase (1)	nuclease activity [GO:0004518 molecular_function] (1); DNA repair [GO:0006281 biological_process] (1)	AP endonuclease 1 [IPR004808] (1); Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	-	P_trifoliata_00990_mRNA_6.1
GF0051233	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00990_mRNA_5.1
GF0051232	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00990_mRNA_1.1
GF0051231	0	0	1	Short-chain dehydrogenase TIC 32, chloroplastic (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)	-	-	P_trifoliata_00989_mRNA_7.1
GF0051230	0	0	1	Transcription factor (1)		DNA-binding pseudobarrel domain [IPR015300] (1)	-	-	P_trifoliata_00989_mRNA_6.1
GF0051229	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00989_mRNA_4.1
GF0051228	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00988_mRNA_3.1
GF0051227	0	0	1	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)	-	-	P_trifoliata_00988_mRNA_2.1
GF0051226	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00986_mRNA_3.1
GF0051225	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00986_mRNA_2.1
GF0051224	0	0	1	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)	-	-	P_trifoliata_00986_mRNA_1.1
GF0051223	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00984_mRNA_4.1
GF0051222	0	0	1	Putative cyclic nucleotide-gated ion channel 17 (1)		RmlC-like jelly roll fold [IPR014710] (1); Cyclic nucleotide-binding-like [IPR018490] (1); Cyclic nucleotide-binding domain [IPR000595] (1)	-	-	P_trifoliata_00984_mRNA_2.1
GF0051221	0	0	1	Cyclic nucleotide-gated calmodulin-binding ion channel-like (1)		Cyclic nucleotide-binding domain [IPR000595] (1); RmlC-like jelly roll fold [IPR014710] (1); Cyclic nucleotide-binding-like [IPR018490] (1)	-	-	P_trifoliata_00984_mRNA_1.1
GF0051220	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00983_mRNA_5.1
GF0051219	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00983_mRNA_4.1
GF0051218	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00983_mRNA_1.1
GF0051217	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00981_mRNA_2.1
GF0051216	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00980_mRNA_3.1
GF0051215	0	0	1	Mechanosensitive ion channel 10-like protein (1)	membrane [GO:0016020 cellular_component] (1); transmembrane transport [GO:0055085 biological_process] (1)	Mechanosensitive ion channel MscS [IPR006685] (1)	-	-	P_trifoliata_00979_mRNA_7.1
GF0051214	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00979_mRNA_5.1
GF0051213	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00979_mRNA_4.1
GF0051212	0	0	1	Mechanosensitive ion channel domain-containing protein-like (1)			-	-	P_trifoliata_00979_mRNA_3.1
GF0051211	0	0	1	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)	-	-	P_trifoliata_00979_mRNA_2.1
GF0051210	0	0	1	Hypothetical protein (1)	response to stress [GO:0006950 biological_process] (1)	Late embryogenesis abundant protein, LEA5-type [IPR004926] (1)	-	-	P_trifoliata_00978_mRNA_5.1
GF0051209	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00978_mRNA_3.1
GF0051208	0	0	1	RPS2 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); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1); Leucine-rich repeat [IPR001611] (1)	-	-	P_trifoliata_00978_mRNA_2.1
GF0051207	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00976_mRNA_5.1
GF0051206	0	0	1	Integrase (1)		Aspartic peptidase domain [IPR021109] (1)	-	-	P_trifoliata_00976_mRNA_4.1
GF0051205	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00976_mRNA_2.1
GF0051204	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00976_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*
GF0051203	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00975_mRNA_1.1
GF0051202	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00974_mRNA_7.1
GF0051201	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00974_mRNA_6.1
GF0051200	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00973_mRNA_6.1
GF0051199	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00973_mRNA_5.1
GF0051198	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00973_mRNA_3.1
GF0051197	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00973_mRNA_2.1
GF0051196	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00972_mRNA_3.1
GF0051195	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00972_mRNA_2.1
GF0051194	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00971_mRNA_3.1
GF0051193	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00971_mRNA_2.1
GF0051192	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00971_mRNA_1.1
GF0051191	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00970_mRNA_1.1
GF0051190	0	0	1	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, conserved site [IPR017972] (1); Cytochrome P450 [IPR001128] (1)	-	-	P_trifoliata_00969_mRNA_6.1
GF0051189	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00969_mRNA_4.1
GF0051188	0	0	1	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 S26e [IPR000892] (1)	-	-	P_trifoliata_00969_mRNA_2.1
GF0051187	0	0	1	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)	-	-	P_trifoliata_00969_mRNA_1.1
GF0051186	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00968_mRNA_5.1
GF0051185	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00968_mRNA_1.1
GF0051184	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00967_mRNA_4.1
GF0051183	0	0	1	Hypothetical protein (1)		HSP20-like chaperone [IPR008978] (1)	-	-	P_trifoliata_00967_mRNA_3.1
GF0051182	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00966_mRNA_3.1
GF0051181	0	0	1	Hypothetical protein (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)	-	-	P_trifoliata_00965_mRNA_3.1
GF0051180	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00964_mRNA_3.1
GF0051179	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00964_mRNA_2.1
GF0051178	0	0	1	Terpene synthase 21, putative isoform 3 (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)	-	-	P_trifoliata_00963_mRNA_5.1
GF0051177	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00963_mRNA_1.1
GF0051176	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00962_mRNA_2.1
GF0051175	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00961_mRNA_4.1
GF0051174	0	0	1	Caffeic acid O-methyltransferase (1)	methyltransferase activity [GO:0008168 molecular_function] (1); O-methyltransferase activity [GO:0008171 molecular_function] (1)	O-methyltransferase, family 2 [IPR001077] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); O-methyltransferase COMT-type [IPR016461] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	-	P_trifoliata_00961_mRNA_3.1
GF0051173	0	0	1	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 [IPR001128] (1); Cytochrome P450, E-class, group I [IPR002401] (1)	-	-	P_trifoliata_00961_mRNA_2.1
GF0051172	0	0	1	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)	-	-	P_trifoliata_00961_mRNA_1.1
GF0051171	0	0	1	Hypothetical protein (1)		Brf1, TBP-binding domain [IPR011665] (1)	-	-	P_trifoliata_00960_mRNA_3.1
GF0051170	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00960_mRNA_1.1
GF0051169	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00959_mRNA_8.1
GF0051168	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00959_mRNA_7.1
GF0051167	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00959_mRNA_4.1
GF0051166	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00959_mRNA_3.1
GF0051165	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00959_mRNA_2.1
GF0051164	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00959_mRNA_1.1
GF0051163	0	0	1	NAC domain-containing protein 72 (1)	DNA binding [GO:0003677 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	NAC domain [IPR003441] (1)	-	-	P_trifoliata_00958_mRNA_3.1
GF0051162	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00958_mRNA_1.1
GF0051161	0	0	1	Hypothetical protein (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)	-	-	P_trifoliata_00957_mRNA_5.1
GF0051160	0	0	1	Disease resistance protein RGA2 (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	-	P_trifoliata_00957_mRNA_3.1
GF0051159	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00957_mRNA_2.1
GF0051158	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00957_mRNA_1.1
GF0051157	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00956_mRNA_9.1
GF0051156	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00956_mRNA_8.1
GF0051155	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00956_mRNA_7.1
GF0051154	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00956_mRNA_5.1
GF0051153	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00956_mRNA_4.1
GF0051152	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00956_mRNA_3.1
GF0051151	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00956_mRNA_2.1
GF0051150	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00956_mRNA_15.1
GF0051149	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00956_mRNA_13.1
GF0051148	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00956_mRNA_10.1
GF0051147	0	0	1	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	-	-	P_trifoliata_00955_mRNA_9.1
GF0051146	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00955_mRNA_2.1
GF0051145	0	0	1	Lectin receptor kinase (1)		Bulb-type lectin domain [IPR001480] (1)	-	-	P_trifoliata_00955_mRNA_12.1
GF0051144	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00955_mRNA_1.1
GF0051143	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00953_mRNA_3.1
GF0051142	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00953_mRNA_2.1
GF0051141	0	0	1	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); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	-	-	P_trifoliata_00953_mRNA_1.1
GF0051140	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00952_mRNA_2.1
GF0051139	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00952_mRNA_1.1
GF0051138	0	0	1	Hypothetical protein (1)		EAL domain [IPR001633] (1)	-	-	P_trifoliata_00951_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*
GF0051137	0	0	1	Probable protein phosphatase 2C 11 (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)	-	-	P_trifoliata_00950_mRNA_6.1
GF0051136	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00949_mRNA_6.1
GF0051135	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00949_mRNA_5.1
GF0051134	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00948_mRNA_9.1
GF0051133	0	0	1	Hypothetical protein (1)	viral process [GO:0016032 biological_process] (1)	Retrotransposon gag domain [IPR005162] (1); Retroviral nucleocapsid protein Gag [IPR000721] (1); Retrovirus capsid, C-terminal [IPR008916] (1)	-	-	P_trifoliata_00948_mRNA_8.1
GF0051132	0	0	1	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, ZPR1-type [IPR004457] (1)	-	-	P_trifoliata_00948_mRNA_2.1
GF0051131	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00948_mRNA_1.1
GF0051130	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00947_mRNA_7.1
GF0051129	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00947_mRNA_4.1
GF0051128	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00947_mRNA_3.1
GF0051127	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00947_mRNA_1.1
GF0051126	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00946_mRNA_2.1
GF0051125	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00946_mRNA_1.1
GF0051124	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00945_mRNA_6.1
GF0051123	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00945_mRNA_4.1
GF0051122	0	0	1	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)	-	-	P_trifoliata_00945_mRNA_2.1
GF0051121	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00945_mRNA_12.1
GF0051120	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00945_mRNA_11.1
GF0051119	0	0	1	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)	-	-	P_trifoliata_00945_mRNA_10.1
GF0051118	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00945_mRNA_1.1
GF0051117	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00944_mRNA_5.1
GF0051116	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00944_mRNA_4.1
GF0051115	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00944_mRNA_2.1
GF0051114	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00942_mRNA_9.1
GF0051113	0	0	1	Hypothetical protein (1)		Protein of unknown function DUF2921 [IPR021319] (1)	-	-	P_trifoliata_00942_mRNA_5.1
GF0051112	0	0	1	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 [IPR001128] (1)	-	-	P_trifoliata_00942_mRNA_3.1
GF0051111	0	0	1	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, E-class, group I [IPR002401] (1); Cytochrome P450, conserved site [IPR017972] (1); Cytochrome P450 [IPR001128] (1)	-	-	P_trifoliata_00942_mRNA_2.1
GF0051110	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00940_mRNA_6.1
GF0051109	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00940_mRNA_5.1
GF0051108	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00940_mRNA_4.1
GF0051107	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00940_mRNA_2.1
GF0051106	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00940_mRNA_1.1
GF0051105	0	0	1	Hypothetical protein (1)		Zinc knuckle CX2CX4HX4C [IPR025836] (1)	-	-	P_trifoliata_00939_mRNA_8.1
GF0051104	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00939_mRNA_5.1
GF0051103	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00939_mRNA_16.1
GF0051102	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00939_mRNA_15.1
GF0051101	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00939_mRNA_14.1
GF0051100	0	0	1	Ribonuclease H (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00939_mRNA_13.1
GF0051099	0	0	1	Hypothetical protein (1)		Zinc knuckle CX2CX4HX4C [IPR025836] (1); Domain of unknown function DUF4283 [IPR025558] (1)	-	-	P_trifoliata_00939_mRNA_11.1
GF0051098	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00939_mRNA_10.1
GF0051097	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00939_mRNA_1.1
GF0051096	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00938_mRNA_1.1
GF0051095	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00936_mRNA_1.1
GF0051094	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00934_mRNA_5.1
GF0051093	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00934_mRNA_3.1
GF0051092	0	0	1	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); Aspartic peptidase domain [IPR021109] (1)	-	-	P_trifoliata_00933_mRNA_5.1
GF0051091	0	0	1	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Peptidase C1A [IPR013128] (1); Cysteine peptidase, cysteine active site [IPR000169] (1); Peptidase C1A, papain C-terminal [IPR000668] (1); Cathepsin propeptide inhibitor domain (I29) [IPR013201] (1)	-	-	P_trifoliata_00933_mRNA_1.1
GF0051090	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00932_mRNA_8.1
GF0051089	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00932_mRNA_7.1
GF0051088	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00932_mRNA_5.1
GF0051087	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00931_mRNA_5.1
GF0051086	0	0	1	O-methyltransferase ZRP4 (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)	-	-	P_trifoliata_00931_mRNA_4.1
GF0051085	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4371 [IPR025398] (1)	-	-	P_trifoliata_00931_mRNA_2.1
GF0051084	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00931_mRNA_1.1
GF0051083	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00930_mRNA_6.1
GF0051082	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00930_mRNA_5.1
GF0051081	0	0	1	Hypothetical protein (1)		Concanavalin A-like lectin/glucanase domain [IPR013320] (1)	-	-	P_trifoliata_00930_mRNA_3.1
GF0051080	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00930_mRNA_1.1
GF0051079	0	0	1	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)	-	-	P_trifoliata_00928_mRNA_6.1
GF0051078	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00928_mRNA_5.1
GF0051077	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00928_mRNA_4.1
GF0051076	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00928_mRNA_3.1
GF0051075	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00928_mRNA_2.1
GF0051074	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00927_mRNA_3.1
GF0051073	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00927_mRNA_2.1
GF0051072	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00927_mRNA_1.1
GF0051071	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00926_mRNA_5.1
GF0051070	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00926_mRNA_3.1
GF0051069	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00926_mRNA_2.1
GF0051068	0	0	1	Hypothetical protein (1)	microtubule [GO:0005874 cellular_component] (1); spindle [GO:0005819 cellular_component] (1); regulation of mitotic spindle organization [GO:0060236 biological_process] (1); activation of protein kinase activity [GO:0032147 biological_process] (1)	TPX2 central domain [IPR027330] (1); TPX2 [IPR009675] (1)	-	-	P_trifoliata_00926_mRNA_1.1
GF0051067	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00925_mRNA_4.1
GF0051066	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00925_mRNA_3.1
GF0051065	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00924_mRNA_4.1
GF0051064	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00924_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*
GF0051063	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00923_mRNA_2.1
GF0051062	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00922_mRNA_4.1
GF0051061	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00922_mRNA_3.1
GF0051060	0	0	1	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)	-	-	P_trifoliata_00922_mRNA_1.1
GF0051059	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00921_mRNA_2.1
GF0051058	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00920_mRNA_1.1
GF0051057	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00919_mRNA_1.1
GF0051056	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00918_mRNA_4.1
GF0051055	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00917_mRNA_4.1
GF0051054	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00916_mRNA_6.1
GF0051053	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00916_mRNA_5.1
GF0051052	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00916_mRNA_2.1
GF0051051	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00916_mRNA_1.1
GF0051050	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00915_mRNA_7.1
GF0051049	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00915_mRNA_6.1
GF0051048	0	0	1	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 [IPR001611] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	-	-	P_trifoliata_00915_mRNA_3.1
GF0051047	0	0	1	Hypothetical protein (1)		PAN/Apple domain [IPR003609] (1)	-	-	P_trifoliata_00914_mRNA_1.1
GF0051046	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00913_mRNA_8.1
GF0051045	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00913_mRNA_7.1
GF0051044	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00913_mRNA_5.1
GF0051043	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00913_mRNA_4.1
GF0051042	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00913_mRNA_3.1
GF0051041	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00913_mRNA_13.1
GF0051040	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00913_mRNA_1.1
GF0051039	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00912_mRNA_1.1
GF0051038	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00911_mRNA_2.1
GF0051037	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00910_mRNA_2.1
GF0051036	0	0	1	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)	-	-	P_trifoliata_00909_mRNA_8.1
GF0051035	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00909_mRNA_5.1
GF0051034	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00908_mRNA_9.1
GF0051033	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00908_mRNA_7.1
GF0051032	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00908_mRNA_6.1
GF0051031	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00908_mRNA_3.1
GF0051030	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00908_mRNA_2.1
GF0051029	0	0	1	TMV resistance protein N, putative (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1)	-	-	P_trifoliata_00908_mRNA_1.1
GF0051028	0	0	1	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)	-	-	P_trifoliata_00907_mRNA_3.1
GF0051027	0	0	1	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)	-	-	P_trifoliata_00906_mRNA_3.1
GF0051026	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00905_mRNA_7.1
GF0051025	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00905_mRNA_6.1
GF0051024	0	0	1	Hypothetical protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	-	P_trifoliata_00905_mRNA_2.1
GF0051023	0	0	1	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	-	P_trifoliata_00904_mRNA_9.1
GF0051022	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00904_mRNA_12.1
GF0051021	0	0	1	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-protein kinase, active site [IPR008271] (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)	-	-	P_trifoliata_00903_mRNA_7.1
GF0051020	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00903_mRNA_6.1
GF0051019	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00903_mRNA_4.1
GF0051018	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00903_mRNA_3.1
GF0051017	0	0	1	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	B3 DNA binding domain [IPR003340] (1); DNA-binding pseudobarrel domain [IPR015300] (1)	-	-	P_trifoliata_00903_mRNA_2.1
GF0051016	0	0	1	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)	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); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00903_mRNA_10.1
GF0051015	0	0	1	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-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)	-	-	P_trifoliata_00903_mRNA_1.1
GF0051014	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00901_mRNA_6.1
GF0051013	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00901_mRNA_4.1
GF0051012	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00900_mRNA_5.1
GF0051011	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00899_mRNA_2.1
GF0051010	0	0	1	Hypothetical protein (1)	GTP binding [GO:0005525 molecular_function] (1); GTPase activity [GO:0003924 molecular_function] (1)	Dynamin GTPase effector [IPR003130] (1); Dynamin superfamily [IPR022812] (1); GTPase effector domain [IPR020850] (1)	-	-	P_trifoliata_00898_mRNA_7.1
GF0051009	0	0	1	DYNAMIN-like 1E isoform 3 (1)	GTP binding [GO:0005525 molecular_function] (1)	PH domain-like [IPR011993] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Pleckstrin homology domain [IPR001849] (1); Dynamin superfamily [IPR022812] (1); Dynamin-type guanine nucleotide-binding (G) domain [IPR030381] (1)	-	-	P_trifoliata_00898_mRNA_6.1
GF0051008	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00898_mRNA_4.1
GF0051007	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00898_mRNA_3.1
GF0051006	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00898_mRNA_1.1
GF0051005	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00897_mRNA_6.1
GF0051004	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00897_mRNA_5.1
GF0051003	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00897_mRNA_4.1
GF0051002	0	0	1	Hypothetical protein (1)		Plant AUGMIN subunit 7 [IPR010604] (1); HAUS augmin-like complex subunit 7-like [IPR029711] (1)	-	-	P_trifoliata_00897_mRNA_1.1
GF0051001	0	0	1	Hypothetical protein (1)	electron carrier activity [GO:0009055 molecular_function] (1); protein complex scaffold [GO:0032947 molecular_function] (1); proteasome assembly [GO:0043248 biological_process] (1)	Proteasome component Ecm29/Translational activator Gcn1 [IPR026827] (1); Phytocyanin domain [IPR003245] (1); Cupredoxin [IPR008972] (1); Proteasome component Ecm29 [IPR024372] (1)	-	-	P_trifoliata_00896_mRNA_5.1
GF0051000	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00896_mRNA_3.1
GF0050999	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00895_mRNA_7.1
GF0050998	0	0	1	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 knuckle CX2CX4HX4C [IPR025836] (1); Zinc finger, CCHC-type [IPR001878] (1)	-	-	P_trifoliata_00895_mRNA_4.1
GF0050997	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00895_mRNA_2.1
GF0050996	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00895_mRNA_1.1
GF0050995	0	0	1	4-hydroxy-3-methylbut-2-enyl diphosphatereductase (1)	metal ion binding [GO:0046872 molecular_function] (1); isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway [GO:0019288 biological_process] (1); 4-hydroxy-3-methylbut-2-en-1-yl diphosphate reductase activity [GO:0051745 molecular_function] (1); dimethylallyl diphosphate biosynthetic process [GO:0050992 biological_process] (1)	4-hydroxy-3-methylbut-2-enyl diphosphate reductase [IPR003451] (1)	-	-	P_trifoliata_00894_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*
GF0050994	0	0	1	Hypothetical protein (1)		PUL domain [IPR013535] (1)	-	-	P_trifoliata_00894_mRNA_8.1
GF0050993	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00894_mRNA_7.1
GF0050992	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00894_mRNA_3.1
GF0050991	0	0	1	Hypothetical protein (1)		TLDc domain [IPR006571] (1)	-	-	P_trifoliata_00893_mRNA_3.1
GF0050990	0	0	1	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)	-	-	P_trifoliata_00893_mRNA_1.1
GF0050989	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00892_mRNA_6.1
GF0050988	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	NPR1/NIM1-like, C-terminal [IPR021094] (1); BTB/POZ domain [IPR000210] (1); Ankyrin repeat-containing domain [IPR020683] (1); Regulatory protein NPR, central domain [IPR024228] (1); SKP1/BTB/POZ domain [IPR011333] (1); Ankyrin repeat [IPR002110] (1)	-	-	P_trifoliata_00892_mRNA_3.1
GF0050987	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00891_mRNA_8.1
GF0050986	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00891_mRNA_7.1
GF0050985	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00891_mRNA_6.1
GF0050984	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00891_mRNA_5.1
GF0050983	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00891_mRNA_3.1
GF0050982	0	0	1	Hypothetical protein (1)	outer membrane [GO:0019867 cellular_component] (1)	Bacterial surface antigen (D15) [IPR000184] (1)	-	-	P_trifoliata_00891_mRNA_2.1
GF0050981	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00891_mRNA_15.1
GF0050980	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00891_mRNA_14.1
GF0050979	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00891_mRNA_13.1
GF0050978	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00891_mRNA_1.1
GF0050977	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00890_mRNA_1.1
GF0050976	0	0	1	NAC domain-containing protein 2 (1)	DNA binding [GO:0003677 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	NAC domain [IPR003441] (1)	-	-	P_trifoliata_00889_mRNA_8.1
GF0050975	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00889_mRNA_5.1
GF0050974	0	0	1	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	-	-	P_trifoliata_00889_mRNA_2.1
GF0050973	0	0	1	Hypothetical protein (1)		Squalene cyclase, N-terminal [IPR032697] (1); Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (1)	-	-	P_trifoliata_00889_mRNA_1.1
GF0050972	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00887_mRNA_7.1
GF0050971	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00887_mRNA_3.1
GF0050970	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00886_mRNA_4.1
GF0050969	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00885_mRNA_6.1
GF0050968	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00885_mRNA_1.1
GF0050967	0	0	1	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 3 [IPR011713] (1); Leucine-rich repeat [IPR001611] (1)	-	-	P_trifoliata_00884_mRNA_2.1
GF0050966	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00883_mRNA_3.1
GF0050965	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00881_mRNA_9.1
GF0050964	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	-	P_trifoliata_00881_mRNA_8.1
GF0050963	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00881_mRNA_6.1
GF0050962	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00879_mRNA_6.1
GF0050961	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00879_mRNA_5.1
GF0050960	0	0	1	Hypothetical 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)	-	-	P_trifoliata_00878_mRNA_1.1
GF0050959	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	-	P_trifoliata_00877_mRNA_8.1
GF0050958	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00877_mRNA_7.1
GF0050957	0	0	1	Zinc finger containing preotein, putative (1)			-	-	P_trifoliata_00877_mRNA_6.1
GF0050956	0	0	1	Peptide transporter PTR2 (1)	transport [GO:0006810 biological_process] (1); membrane [GO:0016020 cellular_component] (1); oligopeptide transport [GO:0006857 biological_process] (1); transporter activity [GO:0005215 molecular_function] (1)	Major facilitator superfamily domain [IPR020846] (1); Proton-dependent oligopeptide transporter family [IPR000109] (1); PTR2 family proton/oligopeptide symporter, conserved site [IPR018456] (1)	-	-	P_trifoliata_00877_mRNA_1.1
GF0050955	0	0	1	Cytochrome P450 family 88 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)	-	-	P_trifoliata_00876_mRNA_4.2
GF0050954	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00876_mRNA_1.1
GF0050953	0	0	1	Caffeic acid 3-O-methyltransferase 1 isoform 2 (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); Winged helix-turn-helix DNA-binding domain [IPR011991] (1)	-	-	P_trifoliata_00875_mRNA_6.1
GF0050952	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00875_mRNA_4.1
GF0050951	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00875_mRNA_2.1
GF0050950	0	0	1	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)	-	-	P_trifoliata_00874_mRNA_4.1
GF0050949	0	0	1	Hypothetical protein (1)		Histidine kinase-like ATPase, C-terminal domain [IPR003594] (1)	-	-	P_trifoliata_00873_mRNA_8.1
GF0050948	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00873_mRNA_6.1
GF0050947	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00873_mRNA_3.1
GF0050946	0	0	1	Hypothetical protein (1)	binding [GO:0005488 molecular_function] (1)	Armadillo-type fold [IPR016024] (1)	-	-	P_trifoliata_00873_mRNA_1.1
GF0050945	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00872_mRNA_8.1
GF0050944	0	0	1	Hypothetical protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	-	P_trifoliata_00872_mRNA_4.1
GF0050943	0	0	1	Hypothetical protein (1)		GroEL-like apical domain [IPR027409] (1)	-	-	P_trifoliata_00871_mRNA_8.1
GF0050942	0	0	1	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	-	P_trifoliata_00871_mRNA_6.1
GF0050941	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00871_mRNA_4.1
GF0050940	0	0	1	En Spm-like transposon protein (1)			-	-	P_trifoliata_00871_mRNA_3.1
GF0050939	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00870_mRNA_6.1
GF0050938	0	0	1	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); NADP binding [GO:0050661 molecular_function] (1); N,N-dimethylaniline monooxygenase activity [GO:0004499 molecular_function] (1)	Flavin monooxygenase-like [IPR020946] (1); FAD/NAD(P)-binding domain [IPR023753] (1)	-	-	P_trifoliata_00869_mRNA_8.1
GF0050937	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00869_mRNA_7.1
GF0050936	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00869_mRNA_4.1
GF0050935	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00868_mRNA_7.1
GF0050934	0	0	1	Glutathione S-transferase tau 7, putative (1)		Glutathione S-transferase, C-terminal-like [IPR010987] (1); Glutathione S-transferase, C-terminal [IPR004046] (1)	-	-	P_trifoliata_00868_mRNA_6.1
GF0050933	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00868_mRNA_1.1
GF0050932	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00867_mRNA_4.1
GF0050931	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00867_mRNA_3.1
GF0050930	0	0	1	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	-	P_trifoliata_00866_mRNA_7.1
GF0050929	0	0	1	Pentatricopeptide (PPR) repeat protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	-	P_trifoliata_00866_mRNA_5.1
GF0050928	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00865_mRNA_1.1
GF0050927	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00864_mRNA_7.1
GF0050926	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00864_mRNA_6.1
GF0050925	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00864_mRNA_5.1
GF0050924	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00864_mRNA_4.1
GF0050923	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00864_mRNA_3.1
GF0050922	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00863_mRNA_1.1
GF0050921	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00862_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*
GF0050920	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00862_mRNA_4.1
GF0050919	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00862_mRNA_15.1
GF0050918	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00862_mRNA_14.1
GF0050917	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00862_mRNA_12.1
GF0050916	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00862_mRNA_11.1
GF0050915	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00862_mRNA_10.1
GF0050914	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00861_mRNA_7.1
GF0050913	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00861_mRNA_6.1
GF0050912	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00861_mRNA_19.1
GF0050911	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00861_mRNA_17.1
GF0050910	0	0	1	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1); MULE transposase domain [IPR018289] (1)	-	-	P_trifoliata_00861_mRNA_16.1
GF0050909	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00861_mRNA_14.1
GF0050908	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00861_mRNA_12.1
GF0050907	0	0	1	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	-	P_trifoliata_00861_mRNA_1.1
GF0050906	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00860_mRNA_5.1
GF0050905	0	0	1	Chaperonin ATPase (1)	ATP binding [GO:0005524 molecular_function] (1)	Chaperonin Cpn60/TCP-1 family [IPR002423] (1); TCP-1-like chaperonin intermediate domain [IPR027410] (1); GroEL-like apical domain [IPR027409] (1); GroEL-like equatorial domain [IPR027413] (1)	-	-	P_trifoliata_00860_mRNA_4.1
GF0050904	0	0	1	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)	-	-	P_trifoliata_00859_mRNA_6.1
GF0050903	0	0	1	NBS type disease resistance 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); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	-	P_trifoliata_00859_mRNA_5.1
GF0050902	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00859_mRNA_4.1
GF0050901	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00859_mRNA_3.1
GF0050900	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00859_mRNA_2.1
GF0050899	0	0	1	Hypothetical protein (1)	NADP binding [GO:0050661 molecular_function] (1); glucose metabolic process [GO:0006006 biological_process] (1); glucose-6-phosphate dehydrogenase activity [GO:0004345 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Glucose-6-phosphate dehydrogenase, NAD-binding [IPR022674] (1); Glucose-6-phosphate dehydrogenase [IPR001282] (1); NAD(P)-binding domain [IPR016040] (1)	-	-	P_trifoliata_00859_mRNA_1.1
GF0050898	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00858_mRNA_8.1
GF0050897	0	0	1	MuDR family transposase isoform 1 (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Transposase, MuDR, plant [IPR004332] (1); Zinc finger, SWIM-type [IPR007527] (1)	-	-	P_trifoliata_00858_mRNA_6.1
GF0050896	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00858_mRNA_4.1
GF0050895	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00858_mRNA_3.1
GF0050894	0	0	1	Hypothetical protein (1)	sucrose metabolic process [GO:0005985 biological_process] (1); sucrose synthase activity [GO:0016157 molecular_function] (1)	Sucrose synthase [IPR000368] (1)	-	-	P_trifoliata_00858_mRNA_12.1
GF0050893	0	0	1	Pectinesterase 1 (1)	pectinesterase activity [GO:0030599 molecular_function] (1); cell wall modification [GO:0042545 biological_process] (1); cell wall [GO:0005618 cellular_component] (1)	Pectin lyase fold [IPR012334] (1); Pectinesterase, catalytic [IPR000070] (1); Pectin lyase fold/virulence factor [IPR011050] (1)	-	-	P_trifoliata_00858_mRNA_11.1
GF0050892	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00857_mRNA_2.1
GF0050891	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	MATH/TRAF domain [IPR002083] (1); TRAF-like [IPR008974] (1)	-	-	P_trifoliata_00857_mRNA_1.1
GF0050890	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	-	P_trifoliata_00856_mRNA_5.1
GF0050889	0	0	1	D-mannose binding lectin family protein, expressed (1)	protein binding [GO:0005515 molecular_function] (1); recognition of pollen [GO:0048544 biological_process] (1)	Bulb-type lectin domain [IPR001480] (1); S-locus glycoprotein domain [IPR000858] (1); EGF-like domain [IPR000742] (1)	-	-	P_trifoliata_00856_mRNA_4.1
GF0050888	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00856_mRNA_3.1
GF0050887	0	0	1	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)	-	-	P_trifoliata_00855_mRNA_8.1
GF0050886	0	0	1	Adenylate dimethylallyltransferase (1)	prenyltransferase activity [GO:0004659 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1)	UbiA prenyltransferase family [IPR000537] (1)	-	-	P_trifoliata_00855_mRNA_4.1
GF0050885	0	0	1	Zinc finger containing preotein, putative (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, SWIM-type [IPR007527] (1); Zinc finger, PMZ-type [IPR006564] (1)	-	-	P_trifoliata_00854_mRNA_9.1
GF0050884	0	0	1	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)	-	-	P_trifoliata_00854_mRNA_7.1
GF0050883	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00854_mRNA_3.1
GF0050882	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00854_mRNA_11.1
GF0050881	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00853_mRNA_9.1
GF0050880	0	0	1	Hypothetical protein (1)		Transposon, En/Spm-like [IPR004242] (1)	-	-	P_trifoliata_00853_mRNA_7.1
GF0050879	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4371 [IPR025398] (1)	-	-	P_trifoliata_00853_mRNA_3.1
GF0050878	0	0	1	Hypothetical protein (1)		Galactose oxidase, beta-propeller [IPR015916] (1); Glyoxal oxidase, N-terminal [IPR009880] (1); Galactose oxidase/kelch, beta-propeller [IPR011043] (1)	-	-	P_trifoliata_00853_mRNA_1.1
GF0050877	0	0	1	LRR receptor-like kinase family 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); protein binding [GO:0005515 molecular_function] (1); photosynthesis, light reaction [GO:0019684 biological_process] (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); Photosynthetic reaction centre, L/M [IPR000484] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (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); Protein kinase, ATP binding site [IPR017441] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Leucine-rich repeat [IPR001611] (1)	-	-	P_trifoliata_00852_mRNA_6.1
GF0050876	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00852_mRNA_5.1
GF0050875	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00852_mRNA_4.1
GF0050874	0	0	1	Hypothetical protein (1)		Zinc knuckle CX2CX4HX4C [IPR025836] (1)	-	-	P_trifoliata_00851_mRNA_6.1
GF0050873	0	0	1	Truncated non-smoky glycosyltransferase 1 (1)	metabolic process [GO:0008152 biological_process] (1); transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	-	-	P_trifoliata_00851_mRNA_4.1
GF0050872	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00851_mRNA_3.1
GF0050871	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00851_mRNA_2.1
GF0050870	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00851_mRNA_1.1
GF0050869	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00850_mRNA_5.1
GF0050868	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00849_mRNA_9.1
GF0050867	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00849_mRNA_8.1
GF0050866	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00849_mRNA_7.1
GF0050865	0	0	1	Retrotransposable element tf2 kDa protein type 1 (1)			-	-	P_trifoliata_00849_mRNA_5.1
GF0050864	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00849_mRNA_1.1
GF0050863	0	0	1	Pyruvate kinase (1)	glycolytic process [GO:0006096 biological_process] (1); pyruvate kinase activity [GO:0004743 molecular_function] (1); potassium ion binding [GO:0030955 molecular_function] (1); catalytic activity [GO:0003824 molecular_function] (1); magnesium ion binding [GO:0000287 molecular_function] (1)	Pyruvate/Phosphoenolpyruvate kinase-like domain [IPR015813] (1); Pyruvate kinase-like, insert domain [IPR011037] (1); Pyruvate kinase [IPR001697] (1); Pyruvate kinase, beta-barrel insert domain [IPR015806] (1); Pyruvate kinase, barrel [IPR015793] (1)	-	-	P_trifoliata_00848_mRNA_5.1
GF0050862	0	0	1	Hypothetical protein (1)		Cyclic nucleotide-binding domain [IPR000595] (1); RmlC-like jelly roll fold [IPR014710] (1); Cyclic nucleotide-binding-like [IPR018490] (1)	-	-	P_trifoliata_00848_mRNA_3.1
GF0050861	0	0	1	Hypothetical protein (1)		Cyclic nucleotide-binding-like [IPR018490] (1); RmlC-like jelly roll fold [IPR014710] (1); Cyclic nucleotide-binding domain [IPR000595] (1)	-	-	P_trifoliata_00848_mRNA_2.1
GF0050860	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00848_mRNA_1.1
GF0050859	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00847_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*
GF0050858	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00847_mRNA_1.1
GF0050857	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00846_mRNA_9.1
GF0050856	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00846_mRNA_8.1
GF0050855	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00846_mRNA_5.1
GF0050854	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00846_mRNA_4.1
GF0050853	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00846_mRNA_3.1
GF0050852	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00845_mRNA_9.1
GF0050851	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00845_mRNA_7.1
GF0050850	0	0	1	Hypothetical protein (1)	catalytic activity [GO:0003824 molecular_function] (1)	Aromatic amino acid lyase [IPR001106] (1); Fumarase/histidase, N-terminal [IPR024083] (1); L-Aspartase-like [IPR008948] (1)	-	-	P_trifoliata_00845_mRNA_6.1
GF0050849	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00845_mRNA_5.1
GF0050848	0	0	1	Hypothetical protein (1)		Mitochondrial inner membrane protein Mitofilin [IPR019133] (1)	-	-	P_trifoliata_00845_mRNA_4.1
GF0050847	0	0	1	Hypothetical protein (1)	binding [GO:0005488 molecular_function] (1)	Armadillo-type fold [IPR016024] (1)	-	-	P_trifoliata_00845_mRNA_3.1
GF0050846	0	0	1	Hypothetical protein (1)	binding [GO:0005488 molecular_function] (1)	Armadillo-type fold [IPR016024] (1); Armadillo-like helical [IPR011989] (1)	-	-	P_trifoliata_00845_mRNA_2.1
GF0050845	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00845_mRNA_12.1
GF0050844	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00845_mRNA_10.1
GF0050843	0	0	1	Hypothetical protein (1)	binding [GO:0005488 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Armadillo-type fold [IPR016024] (1); C2 domain [IPR000008] (1); Armadillo [IPR000225] (1); Armadillo-like helical [IPR011989] (1)	-	-	P_trifoliata_00845_mRNA_1.1
GF0050842	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00844_mRNA_5.1
GF0050841	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00844_mRNA_3.1
GF0050840	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00844_mRNA_1.1
GF0050839	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (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); Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00843_mRNA_5.1
GF0050838	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00842_mRNA_2.1
GF0050837	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	F-box domain [IPR001810] (1)	-	-	P_trifoliata_00842_mRNA_13.1
GF0050836	0	0	1	3'(2'),5'-bisphosphate nucleotidase (1)	phosphatidylinositol phosphorylation [GO:0046854 biological_process] (1); sulfur compound metabolic process [GO:0006790 biological_process] (1); 3'(2'),5'-bisphosphate nucleotidase activity [GO:0008441 molecular_function] (1)	Inositol monophosphatase, metal-binding site [IPR020583] (1); 3(2),5 -bisphosphate nucleotidase HAL2 [IPR006239] (1); Inositol monophosphatase [IPR000760] (1)	-	-	P_trifoliata_00842_mRNA_1.1
GF0050835	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00841_mRNA_8.1
GF0050834	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00841_mRNA_7.1
GF0050833	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00841_mRNA_5.1
GF0050832	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00841_mRNA_3.1
GF0050831	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00840_mRNA_4.1
GF0050830	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00840_mRNA_10.1
GF0050829	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00840_mRNA_1.1
GF0050828	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00839_mRNA_9.1
GF0050827	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00839_mRNA_7.1
GF0050826	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00839_mRNA_6.1
GF0050825	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00839_mRNA_5.1
GF0050824	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00839_mRNA_11.1
GF0050823	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00838_mRNA_9.1
GF0050822	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00838_mRNA_8.1
GF0050821	0	0	1	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FAR1 DNA binding domain [IPR004330] (1); FHY3/FAR1 family [IPR031052] (1)	-	-	P_trifoliata_00838_mRNA_7.1
GF0050820	0	0	1	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)	-	-	P_trifoliata_00838_mRNA_6.1
GF0050819	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00838_mRNA_4.1
GF0050818	0	0	1	Cytochrome P450 76AD1-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); Transposase, MuDR, plant [IPR004332] (1); Cytochrome P450, E-class, group I [IPR002401] (1)	-	-	P_trifoliata_00838_mRNA_3.1
GF0050817	0	0	1	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	-	P_trifoliata_00838_mRNA_12.1
GF0050816	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00838_mRNA_10.1
GF0050815	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00837_mRNA_9.1
GF0050814	0	0	1	NAC domain-containing protein 7 (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); DNA binding [GO:0003677 molecular_function] (1)	NAC domain [IPR003441] (1)	-	-	P_trifoliata_00837_mRNA_7.1
GF0050813	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00837_mRNA_4.1
GF0050812	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00837_mRNA_3.1
GF0050811	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00837_mRNA_2.1
GF0050810	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00837_mRNA_1.1
GF0050809	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00835_mRNA_4.1
GF0050808	0	0	1	Putative Athila retroelement ORF1 protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	-	P_trifoliata_00835_mRNA_2.1
GF0050807	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00835_mRNA_14.1
GF0050806	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00835_mRNA_13.1
GF0050805	0	0	1	Hypothetical protein (1)	membrane [GO:0016020 cellular_component] (1); transport [GO:0006810 biological_process] (1); transporter activity [GO:0005215 molecular_function] (1); oligopeptide transport [GO:0006857 biological_process] (1)	PTR2 family proton/oligopeptide symporter, conserved site [IPR018456] (1); Proton-dependent oligopeptide transporter family [IPR000109] (1); Major facilitator superfamily domain [IPR020846] (1)	-	-	P_trifoliata_00834_mRNA_8.1
GF0050804	0	0	1	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1); MULE transposase domain [IPR018289] (1)	-	-	P_trifoliata_00834_mRNA_6.1
GF0050803	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00833_mRNA_2.1
GF0050802	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	-	P_trifoliata_00832_mRNA_9.1
GF0050801	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00832_mRNA_4.1
GF0050800	0	0	1	Hypothetical protein (1)		Transposase, MuDR, plant [IPR004332] (1)	-	-	P_trifoliata_00831_mRNA_7.1
GF0050799	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00831_mRNA_6.1
GF0050798	0	0	1	Ubiquitin carboxyl-terminal hydrolase 12 (1)	protein binding [GO:0005515 molecular_function] (1)	MATH/TRAF domain [IPR002083] (1); TRAF-like [IPR008974] (1)	-	-	P_trifoliata_00831_mRNA_3.1
GF0050797	0	0	1	Ubiquitin carboxyl-terminal hydrolase 12 (1)	protein binding [GO:0005515 molecular_function] (1)	TRAF-like [IPR008974] (1); MATH/TRAF domain [IPR002083] (1)	-	-	P_trifoliata_00831_mRNA_2.1
GF0050796	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00830_mRNA_9.1
GF0050795	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00830_mRNA_7.1
GF0050794	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00830_mRNA_6.1
GF0050793	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00830_mRNA_4.1
GF0050792	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00830_mRNA_3.1
GF0050791	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00830_mRNA_12.1
GF0050790	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00830_mRNA_11.1
GF0050789	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00830_mRNA_1.1
GF0050788	0	0	1	Isoaspartyl peptidase/L-asparaginase (1)	hydrolase activity [GO:0016787 molecular_function] (1)	Peptidase T2, asparaginase 2 [IPR000246] (1); Nucleophile aminohydrolases, N-terminal [IPR029055] (1)	-	-	P_trifoliata_00829_mRNA_4.1
GF0050787	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00829_mRNA_3.1
GF0050786	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00829_mRNA_2.1
GF0050785	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00829_mRNA_1.1
GF0050784	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00828_mRNA_2.1
GF0050783	0	0	1	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)	-	-	P_trifoliata_00827_mRNA_1.1
GF0050782	0	0	1	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)	-	-	P_trifoliata_00826_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*
GF0050781	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00825_mRNA_9.1
GF0050780	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00825_mRNA_8.1
GF0050779	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00825_mRNA_6.1
GF0050778	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00825_mRNA_5.1
GF0050777	0	0	1	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	-	P_trifoliata_00825_mRNA_2.1
GF0050776	0	0	1	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); Peroxidase, active site [IPR019794] (1); Haem peroxidase [IPR010255] (1)	-	-	P_trifoliata_00825_mRNA_11.1
GF0050775	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00824_mRNA_8.1
GF0050774	0	0	1	CDNA clone:J023147E12, full insert sequence (1)			-	-	P_trifoliata_00824_mRNA_7.1
GF0050773	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00824_mRNA_3.1
GF0050772	0	0	1	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, PMZ-type [IPR006564] (1); Zinc finger, SWIM-type [IPR007527] (1)	-	-	P_trifoliata_00824_mRNA_2.1
GF0050771	0	0	1	Hypothetical protein (1)		MULE transposase domain [IPR018289] (1)	-	-	P_trifoliata_00824_mRNA_1.1
GF0050770	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00823_mRNA_8.1
GF0050769	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00823_mRNA_7.1
GF0050768	0	0	1	Zinc knuckle family protein (1)		Domain of unknown function DUF4219 [IPR025314] (1)	-	-	P_trifoliata_00823_mRNA_3.1
GF0050767	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00823_mRNA_1.1
GF0050766	0	0	1	Cyclic nucleotide-gated ion channel 1 (1)		Cyclic nucleotide-binding domain [IPR000595] (1); RmlC-like jelly roll fold [IPR014710] (1); Cyclic nucleotide-binding-like [IPR018490] (1)	-	-	P_trifoliata_00821_mRNA_8.1
GF0050765	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	F-box domain [IPR001810] (1)	-	-	P_trifoliata_00821_mRNA_7.1
GF0050764	0	0	1	Retrotransposon protein, putative, Ty1-copia subclass (1)			-	-	P_trifoliata_00821_mRNA_6.1
GF0050763	0	0	1	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	-	-	P_trifoliata_00821_mRNA_5.1
GF0050762	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00821_mRNA_3.1
GF0050761	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00821_mRNA_1.1
GF0050760	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00820_mRNA_9.1
GF0050759	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00820_mRNA_8.1
GF0050758	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00820_mRNA_7.1
GF0050757	0	0	1	Cysteine-rich receptor-like protein kinase 10 (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)	-	-	P_trifoliata_00820_mRNA_2.1
GF0050756	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00820_mRNA_10.1
GF0050755	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00819_mRNA_6.1
GF0050754	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat [IPR002110] (1); Ankyrin repeat-containing domain [IPR020683] (1)	-	-	P_trifoliata_00819_mRNA_4.1
GF0050753	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00819_mRNA_3.1
GF0050752	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00818_mRNA_6.1
GF0050751	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00818_mRNA_3.1
GF0050750	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00818_mRNA_2.1
GF0050749	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00818_mRNA_1.1
GF0050748	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00817_mRNA_9.1
GF0050747	0	0	1	Disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	-	P_trifoliata_00817_mRNA_4.1
GF0050746	0	0	1	Ligatin (1)	translation initiation factor activity [GO:0003743 molecular_function] (1); translational initiation [GO:0006413 biological_process] (1); protein binding [GO:0005515 molecular_function] (1)	SWIB/MDM2 domain [IPR003121] (1); Translation initiation factor SUI1 [IPR001950] (1)	-	-	P_trifoliata_00817_mRNA_2.1
GF0050745	0	0	1	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)	-	-	P_trifoliata_00817_mRNA_10.1
GF0050744	0	0	1	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)	-	-	P_trifoliata_00817_mRNA_1.1
GF0050743	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00816_mRNA_9.1
GF0050742	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00816_mRNA_13.1
GF0050741	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00815_mRNA_8.1
GF0050740	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00815_mRNA_7.1
GF0050739	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00815_mRNA_6.1
GF0050738	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00815_mRNA_5.1
GF0050737	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00815_mRNA_4.1
GF0050736	0	0	1	PHD finger plant-like protein (1)			-	-	P_trifoliata_00815_mRNA_2.1
GF0050735	0	0	1	Hypothetical protein (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (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, C-terminal [IPR007867] (1)	-	-	P_trifoliata_00815_mRNA_14.1
GF0050734	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00815_mRNA_13.1
GF0050733	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00815_mRNA_11.1
GF0050732	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00815_mRNA_10.1
GF0050731	0	0	1	Ankyrin repeat protein-like (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat [IPR002110] (1); Ankyrin repeat-containing domain [IPR020683] (1)	-	-	P_trifoliata_00814_mRNA_8.1
GF0050730	0	0	1	Hypothetical protein (1)		Zinc finger, RING/FYVE/PHD-type [IPR013083] (1)	-	-	P_trifoliata_00814_mRNA_3.1
GF0050729	0	0	1	TRNA dimethylallyltransferase (1)	tRNA processing [GO:0008033 biological_process] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); tRNA dimethylallyltransferase [IPR018022] (1)	-	-	P_trifoliata_00813_mRNA_7.1
GF0050728	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00813_mRNA_1.1
GF0050727	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00812_mRNA_5.1
GF0050726	0	0	1	Cytochrome P450 monooxygenase CYP83A1 (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)	-	-	P_trifoliata_00812_mRNA_3.1
GF0050725	0	0	1	Hypothetical protein (1)	nutrient reservoir activity [GO:0045735 molecular_function] (1)	Cupin 1 [IPR006045] (1); RmlC-like jelly roll fold [IPR014710] (1); RmlC-like cupin domain [IPR011051] (1)	-	-	P_trifoliata_00812_mRNA_13.1
GF0050724	0	0	1	Hypothetical protein (1)	protein N-linked glycosylation [GO:0006487 biological_process] (1); membrane [GO:0016020 cellular_component] (1); beta-1,4-mannosylglycoprotein 4-beta-N-acetylglucosaminyltransferase activity [GO:0003830 molecular_function] (1)	Glycosyl transferase, family 17 [IPR006813] (1)	-	-	P_trifoliata_00812_mRNA_1.1
GF0050723	0	0	1	Hypothetical protein (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)	-	-	P_trifoliata_00811_mRNA_5.1
GF0050722	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00811_mRNA_4.1
GF0050721	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00810_mRNA_9.1
GF0050720	0	0	1	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, family 2 [IPR001077] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); O-methyltransferase COMT-type [IPR016461] (1)	-	-	P_trifoliata_00810_mRNA_8.1
GF0050719	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00810_mRNA_6.1
GF0050718	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00810_mRNA_11.1
GF0050717	0	0	1	Hypothetical protein (1)		Myb/SANT-like domain [IPR024752] (1)	-	-	P_trifoliata_00810_mRNA_1.1
GF0050716	0	0	1	Caffeic acid 3-O-methyltransferase (1)	O-methyltransferase activity [GO:0008171 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1); methyltransferase activity [GO:0008168 molecular_function] (1)	O-methyltransferase COMT-type [IPR016461] (1); O-methyltransferase, family 2 [IPR001077] (1); Zinc finger, SWIM-type [IPR007527] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	-	P_trifoliata_00809_mRNA_3.1
GF0050715	0	0	1	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, SWIM-type [IPR007527] (1)	-	-	P_trifoliata_00809_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*
GF0050714	0	0	1	Hypothetical protein (1)	metal ion binding [GO:0046872 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)	Lipoxygenase, C-terminal [IPR013819] (1); Lipoxygenase [IPR000907] (1)	-	-	P_trifoliata_00808_mRNA_2.1
GF0050713	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00808_mRNA_13.1
GF0050712	0	0	1	Hypothetical protein (1)		Bulb-type lectin domain [IPR001480] (1)	-	-	P_trifoliata_00808_mRNA_11.1
GF0050711	0	0	1	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)	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); Protein kinase, ATP binding site [IPR017441] (1); Serine/threonine-protein kinase, active site [IPR008271] (1)	-	-	P_trifoliata_00808_mRNA_10.1
GF0050710	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00808_mRNA_1.1
GF0050709	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00807_mRNA_8.1
GF0050708	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00807_mRNA_7.1
GF0050707	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	-	P_trifoliata_00807_mRNA_6.1
GF0050706	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00807_mRNA_4.1
GF0050705	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00807_mRNA_2.1
GF0050704	0	0	1	Hypothetical protein (1)		Transposon, En/Spm-like [IPR004242] (1)	-	-	P_trifoliata_00806_mRNA_8.1
GF0050703	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00806_mRNA_16.1
GF0050702	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00806_mRNA_15.1
GF0050701	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00806_mRNA_12.1
GF0050700	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00806_mRNA_11.1
GF0050699	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00806_mRNA_10.1
GF0050698	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00806_mRNA_1.1
GF0050697	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00805_mRNA_7.1
GF0050696	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00805_mRNA_5.1
GF0050695	0	0	1	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)	-	-	P_trifoliata_00805_mRNA_4.1
GF0050694	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00805_mRNA_1.1
GF0050693	0	0	1	Transposable element Ac (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-like transposase, RNase-H fold [IPR025525] (1); Ribonuclease H-like domain [IPR012337] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	-	-	P_trifoliata_00804_mRNA_7.1
GF0050692	0	0	1	Hypothetical protein (1)	methyltransferase activity [GO:0008168 molecular_function] (1)	S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); SAM dependent carboxyl methyltransferase [IPR005299] (1)	-	-	P_trifoliata_00804_mRNA_5.1
GF0050691	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00804_mRNA_3.1
GF0050690	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00804_mRNA_2.1
GF0050689	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00804_mRNA_1.1
GF0050688	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00803_mRNA_5.1
GF0050687	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00803_mRNA_4.1
GF0050686	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00803_mRNA_3.1
GF0050685	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00803_mRNA_2.1
GF0050684	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00803_mRNA_1.1
GF0050683	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00802_mRNA_6.1
GF0050682	0	0	1	Hemopexin (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	-	P_trifoliata_00802_mRNA_5.1
GF0050681	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00801_mRNA_5.1
GF0050680	0	0	1	Putative WRKY transcription factor 28 (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)	-	-	P_trifoliata_00801_mRNA_4.1
GF0050679	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00800_mRNA_4.1
GF0050678	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00800_mRNA_2.1
GF0050677	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	-	P_trifoliata_00800_mRNA_1.1
GF0050676	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00799_mRNA_1.1
GF0050675	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00798_mRNA_15.1
GF0050674	0	0	1	Ac-like transposase THELMA13 (1)	DNA binding [GO:0003677 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)	-	-	P_trifoliata_00798_mRNA_14.1
GF0050673	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00798_mRNA_13.1
GF0050672	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00798_mRNA_10.1
GF0050671	0	0	1	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	-	P_trifoliata_00798_mRNA_1.1
GF0050670	0	0	1	Hypothetical protein (1)		Leucine-rich repeat 2 [IPR013101] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00797_mRNA_4.1
GF0050669	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00797_mRNA_2.1
GF0050668	0	0	1	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)	-	-	P_trifoliata_00797_mRNA_1.1
GF0050667	0	0	1	Ankyrin repeat family protein (1)		PGG domain [IPR026961] (1)	-	-	P_trifoliata_00796_mRNA_2.1
GF0050666	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00795_mRNA_7.1
GF0050665	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00795_mRNA_6.1
GF0050664	0	0	1	Hypothetical protein (1)		Alpha crystallin/Hsp20 domain [IPR002068] (1); HSP20-like chaperone [IPR008978] (1); Small heat shock protein HSP20 [IPR031107] (1)	-	-	P_trifoliata_00795_mRNA_5.1
GF0050663	0	0	1	Hypothetical protein (1)		Gamma interferon inducible lysosomal thiol reductase GILT [IPR004911] (1)	-	-	P_trifoliata_00795_mRNA_3.1
GF0050662	0	0	1	Heavy metal transport/detoxification superfamily 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)	-	-	P_trifoliata_00794_mRNA_7.1
GF0050661	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00794_mRNA_1.1
GF0050660	0	0	1	Hypothetical protein (1)		SGNH hydrolase-type esterase domain [IPR013830] (1)	-	-	P_trifoliata_00793_mRNA_4.1
GF0050659	0	0	1	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); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	-	-	P_trifoliata_00793_mRNA_2.1
GF0050658	0	0	1	Hypothetical 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-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)	-	-	P_trifoliata_00793_mRNA_1.1
GF0050657	0	0	1	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	-	P_trifoliata_00792_mRNA_7.1
GF0050656	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00792_mRNA_6.1
GF0050655	0	0	1	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)	-	-	P_trifoliata_00792_mRNA_1.1
GF0050654	0	0	1	Myosin heavy chain IB (1)	protein binding [GO:0005515 molecular_function] (1)	SH3 domain [IPR001452] (1)	-	-	P_trifoliata_00791_mRNA_6.1
GF0050653	0	0	1	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)	-	-	P_trifoliata_00791_mRNA_4.1
GF0050652	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	SH3 domain [IPR001452] (1)	-	-	P_trifoliata_00791_mRNA_3.1
GF0050651	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00790_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*
GF0050650	0	0	1	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); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00790_mRNA_7.1
GF0050649	0	0	1	Monosacharide transport protein (1)			-	-	P_trifoliata_00790_mRNA_11.1
GF0050648	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00789_mRNA_6.1
GF0050647	0	0	1	Phenylcoumaran benzylic ether reductase-like protein (1)		NmrA-like domain [IPR008030] (1); NAD(P)-binding domain [IPR016040] (1)	-	-	P_trifoliata_00789_mRNA_4.1
GF0050646	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00789_mRNA_2.1
GF0050645	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00789_mRNA_1.1
GF0050644	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00788_mRNA_9.1
GF0050643	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00788_mRNA_2.1
GF0050642	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00788_mRNA_11.1
GF0050641	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00788_mRNA_1.1
GF0050640	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00787_mRNA_9.1
GF0050639	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00787_mRNA_7.1
GF0050638	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	GYF domain [IPR003169] (1)	-	-	P_trifoliata_00787_mRNA_6.1
GF0050637	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00787_mRNA_4.1
GF0050636	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00787_mRNA_10.1
GF0050635	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00787_mRNA_1.1
GF0050634	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00786_mRNA_2.1
GF0050633	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00785_mRNA_9.1
GF0050632	0	0	1	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	-	P_trifoliata_00785_mRNA_8.1
GF0050631	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00785_mRNA_7.1
GF0050630	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00785_mRNA_5.1
GF0050629	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00785_mRNA_4.1
GF0050628	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00785_mRNA_2.1
GF0050627	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00785_mRNA_18.1
GF0050626	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00785_mRNA_16.1
GF0050625	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00785_mRNA_15.1
GF0050624	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00785_mRNA_13.1
GF0050623	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00785_mRNA_11.1
GF0050622	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00785_mRNA_1.1
GF0050621	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	-	P_trifoliata_00783_mRNA_9.1
GF0050620	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00783_mRNA_8.1
GF0050619	0	0	1	Hypothetical protein (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); phospholipid-translocating ATPase activity [GO:0004012 molecular_function] (1); metal ion binding [GO:0046872 molecular_function] (1); nucleotide binding [GO:0000166 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	P-type ATPase, N-terminal [IPR032631] (1); HAD-like domain [IPR023214] (1); P-type ATPase, A domain [IPR008250] (1); P-type ATPase, subfamily IV [IPR006539] (1); P-type ATPase, C-terminal [IPR032630] (1); P-type ATPase [IPR001757] (1)	-	-	P_trifoliata_00782_mRNA_1.1
GF0050618	0	0	1	Transcription factor MYB86 (1)	DNA binding [GO:0003677 molecular_function] (1)	Myb domain [IPR017930] (1); SANT/Myb domain [IPR001005] (1); Homeodomain-like [IPR009057] (1)	-	-	P_trifoliata_00781_mRNA_5.1
GF0050617	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00781_mRNA_3.1
GF0050616	0	0	1	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Domain of unknown function DUF4218 [IPR025452] (1)	-	-	P_trifoliata_00781_mRNA_2.1
GF0050615	0	0	1	Hypothetical protein (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1); hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 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)	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); Glycoside hydrolase family 18, catalytic domain [IPR001223] (1); Glycoside hydrolase, catalytic domain [IPR013781] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	-	-	P_trifoliata_00780_mRNA_8.1
GF0050614	0	0	1	Glycosyl hydrolase family protein with chitinase insertion domain (1)	chitin catabolic process [GO:0006032 biological_process] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1); chitinase activity [GO:0004568 molecular_function] (1); hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (1)	Chitinase II [IPR011583] (1); Glycoside hydrolase, catalytic domain [IPR013781] (1); Glycoside hydrolase superfamily [IPR017853] (1); Glycoside hydrolase family 18, catalytic domain [IPR001223] (1)	-	-	P_trifoliata_00780_mRNA_7.1
GF0050613	0	0	1	Hypothetical protein (1)		Protein kinase-like domain [IPR011009] (1)	-	-	P_trifoliata_00780_mRNA_1.1
GF0050612	0	0	1	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)	-	-	P_trifoliata_00779_mRNA_9.1
GF0050611	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4219 [IPR025314] (1)	-	-	P_trifoliata_00779_mRNA_8.1
GF0050610	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00779_mRNA_13.1
GF0050609	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00779_mRNA_12.1
GF0050608	0	0	1	Hypothetical protein (1)	polygalacturonate 4-alpha-galacturonosyltransferase activity [GO:0047262 molecular_function] (1)	Plant galacturonosyltransferase GAUT [IPR029993] (1)	-	-	P_trifoliata_00779_mRNA_11.1
GF0050607	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00779_mRNA_1.1
GF0050606	0	0	1	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)	-	-	P_trifoliata_00778_mRNA_5.1
GF0050605	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00778_mRNA_3.1
GF0050604	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00777_mRNA_9.1
GF0050603	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00777_mRNA_8.1
GF0050602	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00777_mRNA_7.1
GF0050601	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00777_mRNA_6.1
GF0050600	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00777_mRNA_10.1
GF0050599	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00777_mRNA_1.1
GF0050598	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00776_mRNA_9.1
GF0050597	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00776_mRNA_5.1
GF0050596	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00776_mRNA_4.1
GF0050595	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00776_mRNA_2.1
GF0050594	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00776_mRNA_19.1
GF0050593	0	0	1	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)	-	-	P_trifoliata_00776_mRNA_17.1
GF0050592	0	0	1	Hypothetical protein (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Aspartic peptidase, active site [IPR001969] (1)	-	-	P_trifoliata_00776_mRNA_16.1
GF0050591	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00776_mRNA_14.1
GF0050590	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00776_mRNA_13.1
GF0050589	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00776_mRNA_11.1
GF0050588	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00776_mRNA_10.1
GF0050587	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00776_mRNA_1.1
GF0050586	0	0	1	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); recognition of pollen [GO:0048544 biological_process] (1); protein serine/threonine kinase activity [GO:0004674 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); S-receptor-like serine/threonine-protein kinase [IPR024171] (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/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)	-	-	P_trifoliata_00775_mRNA_7.1
GF0050585	0	0	1	S locus glycoprotein (1)	recognition of pollen [GO:0048544 biological_process] (1)	S-locus glycoprotein domain [IPR000858] (1); Bulb-type lectin domain [IPR001480] (1)	-	-	P_trifoliata_00775_mRNA_4.1
GF0050584	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00774_mRNA_8.1
GF0050583	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00774_mRNA_5.1
GF0050582	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00774_mRNA_3.1
GF0050581	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00774_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*
GF0050580	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00773_mRNA_6.1
GF0050579	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00772_mRNA_7.1
GF0050578	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00772_mRNA_6.1
GF0050577	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00772_mRNA_15.1
GF0050576	0	0	1	Hypothetical protein (1)	proton-transporting ATP synthase complex, coupling factor F(o) [GO:0045263 cellular_component] (1); proton-transporting two-sector ATPase complex, proton-transporting domain [GO:0033177 cellular_component] (1); hydrogen ion transmembrane transporter activity [GO:0015078 molecular_function] (1); ATP hydrolysis coupled proton transport [GO:0015991 biological_process] (1); ATP synthesis coupled proton transport [GO:0015986 biological_process] (1)	ATPase, F0 complex, subunit C, DCCD-binding site [IPR020537] (1); NADH:quinone oxidoreductase/Mrp antiporter, membrane subunit [IPR001750] (1); ATPase, F0 complex, subunit C [IPR000454] (1); V-ATPase proteolipid subunit C-like domain [IPR002379] (1)	-	-	P_trifoliata_00772_mRNA_12.1
GF0050575	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00772_mRNA_10.1
GF0050574	0	0	1	Exocyst complex component sec3A isoform 2 (1)		Exocyst complex component Sec3, C-terminal [IPR019160] (1); Exocyst complex component Sec3, PIP2-binding N-terminal domain [IPR028258] (1)	-	-	P_trifoliata_00772_mRNA_1.1
GF0050573	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00771_mRNA_8.1
GF0050572	0	0	1	Hypothetical protein (1)	RNA binding [GO:0003723 molecular_function] (1); ribonuclease T2 activity [GO:0033897 molecular_function] (1)	Ribonuclease T2-like [IPR001568] (1)	-	-	P_trifoliata_00771_mRNA_6.1
GF0050571	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4219 [IPR025314] (1)	-	-	P_trifoliata_00771_mRNA_5.1
GF0050570	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00771_mRNA_4.1
GF0050569	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00771_mRNA_3.1
GF0050568	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00770_mRNA_6.1
GF0050567	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00770_mRNA_5.1
GF0050566	0	0	1	Putative muDR family transposase-like (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, SWIM-type [IPR007527] (1); Transposase, MuDR, plant [IPR004332] (1)	-	-	P_trifoliata_00770_mRNA_1.1
GF0050565	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00769_mRNA_7.1
GF0050564	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00769_mRNA_1.1
GF0050563	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1); ADP binding [GO:0043531 molecular_function] (1)	Ankyrin repeat [IPR002110] (1); PGG domain [IPR026961] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Ankyrin repeat-containing domain [IPR020683] (1); NB-ARC [IPR002182] (1)	-	-	P_trifoliata_00768_mRNA_9.1
GF0050562	0	0	1	Hypothetical protein (1)	enzyme inhibitor activity [GO:0004857 molecular_function] (1)	Pectinesterase inhibitor domain [IPR006501] (1)	-	-	P_trifoliata_00768_mRNA_10.1
GF0050561	0	0	1	Gag protease polyprotein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	-	P_trifoliata_00767_mRNA_6.1
GF0050560	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00767_mRNA_5.1
GF0050559	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00767_mRNA_4.1
GF0050558	0	0	1	Gag protease polyprotein (1)		Retrotransposon gag domain [IPR005162] (1)	-	-	P_trifoliata_00767_mRNA_1.1
GF0050557	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00766_mRNA_6.1
GF0050556	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00766_mRNA_5.1
GF0050555	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00766_mRNA_4.1
GF0050554	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00766_mRNA_3.1
GF0050553	0	0	1	Essential protein Yae1, putative isoform 3 (1)			-	-	P_trifoliata_00766_mRNA_2.1
GF0050552	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00765_mRNA_2.1
GF0050551	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00764_mRNA_7.1
GF0050550	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00764_mRNA_6.1
GF0050549	0	0	1	Nuclear pore complex Nup98-Nup96 (1)			-	-	P_trifoliata_00764_mRNA_5.1
GF0050548	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00764_mRNA_3.1
GF0050547	0	0	1	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); DNA binding [GO:0003677 molecular_function] (1)	Probable transposase, Ptta/En/Spm, plant [IPR004252] (1); NAC domain [IPR003441] (1)	-	-	P_trifoliata_00764_mRNA_2.1
GF0050546	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00764_mRNA_12.1
GF0050545	0	0	1	Caffeic acid O-methyltransferase (1)	methyltransferase activity [GO:0008168 molecular_function] (1); O-methyltransferase activity [GO:0008171 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)	-	-	P_trifoliata_00764_mRNA_11.1
GF0050544	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00764_mRNA_10.1
GF0050543	0	0	1	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)	Nitrilase/cyanide hydratase, conserved site [IPR000132] (1); Carbon-nitrogen hydrolase [IPR003010] (1)	-	-	P_trifoliata_00764_mRNA_1.1
GF0050542	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00763_mRNA_7.1
GF0050541	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00763_mRNA_2.1
GF0050540	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00763_mRNA_1.1
GF0050539	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00762_mRNA_6.1
GF0050538	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00761_mRNA_8.1
GF0050537	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00761_mRNA_7.1
GF0050536	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00761_mRNA_6.1
GF0050535	0	0	1	Hypothetical protein (1)		Arabidopsis retrotransposon Orf1 [IPR004312] (1)	-	-	P_trifoliata_00761_mRNA_5.1
GF0050534	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00761_mRNA_4.1
GF0050533	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Histidine kinase-like ATPase, C-terminal domain [IPR003594] (1); Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00761_mRNA_3.1
GF0050532	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00761_mRNA_2.1
GF0050531	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00761_mRNA_1.1
GF0050530	0	0	1	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Viral movement protein [IPR028919] (1); Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	-	P_trifoliata_00760_mRNA_9.1
GF0050529	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00760_mRNA_7.1
GF0050528	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00760_mRNA_5.1
GF0050527	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00760_mRNA_4.1
GF0050526	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00760_mRNA_3.1
GF0050525	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00760_mRNA_2.1
GF0050524	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00760_mRNA_16.1
GF0050523	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4218 [IPR025452] (1)	-	-	P_trifoliata_00760_mRNA_15.1
GF0050522	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00760_mRNA_14.1
GF0050521	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00760_mRNA_11.1
GF0050520	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00758_mRNA_4.1
GF0050519	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00758_mRNA_2.1
GF0050518	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00758_mRNA_1.1
GF0050517	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00757_mRNA_8.1
GF0050516	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00757_mRNA_6.1
GF0050515	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00757_mRNA_2.1
GF0050514	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00757_mRNA_10.1
GF0050513	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00756_mRNA_8.1
GF0050512	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00756_mRNA_6.1
GF0050511	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00756_mRNA_5.1
GF0050510	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00756_mRNA_4.1
GF0050509	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00756_mRNA_3.1
GF0050508	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00755_mRNA_8.1
GF0050507	0	0	1	Hypothetical protein (1)		Probable transposase, Ptta/En/Spm, plant [IPR004252] (1)	-	-	P_trifoliata_00755_mRNA_6.1
GF0050506	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00755_mRNA_2.1
GF0050505	0	0	1	(-)-germacrene D 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); metabolic process [GO:0008152 biological_process] (1)	Isoprenoid synthase domain [IPR008949] (1); Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (1); Terpene synthase, metal-binding domain [IPR005630] (1); Terpene synthase, N-terminal domain [IPR001906] (1)	-	-	P_trifoliata_00755_mRNA_1.1
GF0050504	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00754_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*
GF0050503	0	0	1	RNA-directed DNA polymerase (Reverse transcriptase), Polynucleotidyl transferase, Ribonuclease H fold-like protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1); Chromo domain [IPR023780] (1); Chromo domain-like [IPR016197] (1)	-	-	P_trifoliata_00753_mRNA_7.1
GF0050502	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00753_mRNA_6.1
GF0050501	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00753_mRNA_5.1
GF0050500	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00753_mRNA_3.1
GF0050499	0	0	1	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	-	P_trifoliata_00753_mRNA_2.1
GF0050498	0	0	1	Hypothetical protein (1)	exocytosis [GO:0006887 biological_process] (1); exocyst [GO:0000145 cellular_component] (1)	Exocyst complex component Sec6 [IPR010326] (1)	-	-	P_trifoliata_00752_mRNA_17.1
GF0050497	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00752_mRNA_16.1
GF0050496	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00752_mRNA_15.1
GF0050495	0	0	1	Disease resistance protein RPS5, putative (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)	-	-	P_trifoliata_00752_mRNA_1.1
GF0050494	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00751_mRNA_9.1
GF0050493	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00751_mRNA_6.1
GF0050492	0	0	1	Mo25 family protein (1)	binding [GO:0005488 molecular_function] (1)	Armadillo-type fold [IPR016024] (1); Mo25-like [IPR013878] (1); Armadillo-like helical [IPR011989] (1)	-	-	P_trifoliata_00751_mRNA_5.1
GF0050491	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00751_mRNA_12.1
GF0050490	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00750_mRNA_11.1
GF0050489	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00750_mRNA_1.1
GF0050488	0	0	1	Hypothetical protein (1)	mitochondrion [GO:0005739 cellular_component] (1); mitochondrial respiratory chain complex I [GO:0005747 cellular_component] (1); electron transport chain [GO:0022900 biological_process] (1)	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3 [IPR012576] (1)	-	-	P_trifoliata_00749_mRNA_4.1
GF0050487	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00749_mRNA_3.1
GF0050486	0	0	1	Putative transmembrane 9 superfamily member 3-like (1)	integral component of membrane [GO:0016021 cellular_component] (1)	Nonaspanin (TM9SF) [IPR004240] (1); Major facilitator superfamily domain [IPR020846] (1)	-	-	P_trifoliata_00749_mRNA_2.1
GF0050485	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00749_mRNA_12.1
GF0050484	0	0	1	Transmembrane 9 superfamily member 3-like protein (1)	integral component of membrane [GO:0016021 cellular_component] (1)	Nonaspanin (TM9SF) [IPR004240] (1)	-	-	P_trifoliata_00749_mRNA_1.1
GF0050483	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00748_mRNA_8.1
GF0050482	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00748_mRNA_7.1
GF0050481	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00748_mRNA_5.1
GF0050480	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00748_mRNA_2.1
GF0050479	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00747_mRNA_9.1
GF0050478	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00746_mRNA_9.1
GF0050477	0	0	1	Hypothetical protein (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on CH-OH group of donors [GO:0016614 molecular_function] (1)	Glucose-methanol-choline oxidoreductase, C-terminal [IPR007867] (1); FAD/NAD(P)-binding domain [IPR023753] (1)	-	-	P_trifoliata_00746_mRNA_8.1
GF0050476	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00746_mRNA_7.1
GF0050475	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00746_mRNA_5.1
GF0050474	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00746_mRNA_3.1
GF0050473	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00746_mRNA_23.1
GF0050472	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00746_mRNA_22.1
GF0050471	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00746_mRNA_21.1
GF0050470	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00746_mRNA_20.1
GF0050469	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00746_mRNA_2.1
GF0050468	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00746_mRNA_17.1
GF0050467	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00746_mRNA_16.1
GF0050466	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00746_mRNA_15.1
GF0050465	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00746_mRNA_13.1
GF0050464	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00746_mRNA_12.1
GF0050463	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00746_mRNA_11.1
GF0050462	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00746_mRNA_10.1
GF0050461	0	0	1	CcmC (1)	heme transporter activity [GO:0015232 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); heme transport [GO:0015886 biological_process] (1); membrane [GO:0016020 cellular_component] (1); cytochrome complex assembly [GO:0017004 biological_process] (1)	Cytochrome c-type biogenesis protein CcmC [IPR003557] (1); Cytochrome c assembly protein [IPR002541] (1)	-	-	P_trifoliata_00746_mRNA_1.1
GF0050460	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00745_mRNA_9.1
GF0050459	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00745_mRNA_7.1
GF0050458	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00745_mRNA_5.1
GF0050457	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00745_mRNA_4.1
GF0050456	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00745_mRNA_15.1
GF0050455	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00745_mRNA_12.1
GF0050454	0	0	1	Hypothetical protein (1)		Gibberellin regulated protein [IPR003854] (1)	-	-	P_trifoliata_00744_mRNA_8.1
GF0050453	0	0	1	Progesterone 5-beta-reductase (1)		NAD(P)-binding domain [IPR016040] (1)	-	-	P_trifoliata_00744_mRNA_5.1
GF0050452	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00744_mRNA_4.1
GF0050451	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00744_mRNA_3.1
GF0050450	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00744_mRNA_1.1
GF0050449	0	0	1	Hypothetical protein (1)		Trichome birefringence-like family [IPR029962] (1); PC-Esterase [IPR026057] (1)	-	-	P_trifoliata_00743_mRNA_9.1
GF0050448	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00743_mRNA_8.1
GF0050447	0	0	1	Triacylglycerol lipase (1)	lipid metabolic process [GO:0006629 biological_process] (1)	Alpha/Beta hydrolase fold [IPR029058] (1); Fungal lipase-like domain [IPR002921] (1)	-	-	P_trifoliata_00743_mRNA_5.1
GF0050446	0	0	1	Hypothetical protein (1)		Concanavalin A-like lectin/glucanase domain [IPR013320] (1)	-	-	P_trifoliata_00742_mRNA_10.1
GF0050445	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00740_mRNA_4.1
GF0050444	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00739_mRNA_7.1
GF0050443	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00738_mRNA_8.1
GF0050442	0	0	1	Leucine-rich repeat receptor protein kinase 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)	-	-	P_trifoliata_00738_mRNA_7.1
GF0050441	0	0	1	Retrotransposon protein, putative, unclassified (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1); Reverse transcriptase domain [IPR000477] (1)	-	-	P_trifoliata_00738_mRNA_3.1
GF0050440	0	0	1	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/tyrosine-protein kinase catalytic domain [IPR001245] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	-	-	P_trifoliata_00738_mRNA_10.1
GF0050439	0	0	1	Disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	-	P_trifoliata_00738_mRNA_1.1
GF0050438	0	0	1	Hypothetical protein (1)		MULE transposase domain [IPR018289] (1)	-	-	P_trifoliata_00736_mRNA_6.1
GF0050437	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00736_mRNA_5.1
GF0050436	0	0	1	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, SWIM-type [IPR007527] (1)	-	-	P_trifoliata_00736_mRNA_4.1
GF0050435	0	0	1	Putative mitochondrial chaperone bcs1 (1)	ATP binding [GO:0005524 molecular_function] (1)	ATPase, AAA-type, core [IPR003959] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); AAA+ ATPase domain [IPR003593] (1); ATPase, AAA-type, conserved site [IPR003960] (1)	-	-	P_trifoliata_00736_mRNA_2.1
GF0050434	0	0	1	Transcription factor TFIIIB component B (1)	transcription factor TFIIIB complex [GO:0000126 cellular_component] (1); regulation of transcription from RNA polymerase III promoter [GO:0006359 biological_process] (1); DNA binding [GO:0003677 molecular_function] (1); TFIIIB-type transcription factor activity [GO:0001026 molecular_function] (1)	Homeodomain-like [IPR009057] (1); SANT/Myb domain [IPR001005] (1); Transcription factor TFIIIB component B'' [IPR030701] (1); SANT domain [IPR017884] (1)	-	-	P_trifoliata_00736_mRNA_16.1
GF0050433	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00736_mRNA_1.1
GF0050432	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00735_mRNA_9.1
GF0050431	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00735_mRNA_6.1
GF0050430	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00735_mRNA_5.1
GF0050429	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00735_mRNA_20.1

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*
GF0050428	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00735_mRNA_18.1
GF0050427	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00735_mRNA_14.1
GF0050426	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00735_mRNA_13.1
GF0050425	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00734_mRNA_6.1
GF0050424	0	0	1	Germin-like protein subfamily 1 member 7 (1)	manganese ion binding [GO:0030145 molecular_function] (1); nutrient reservoir activity [GO:0045735 molecular_function] (1)	RmlC-like cupin domain [IPR011051] (1); Cupin 1 [IPR006045] (1); Germin, manganese binding site [IPR019780] (1); Germin [IPR001929] (1); RmlC-like jelly roll fold [IPR014710] (1)	-	-	P_trifoliata_00734_mRNA_4.1
GF0050423	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00733_mRNA_1.1
GF0050422	0	0	1	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	-	P_trifoliata_00732_mRNA_7.1
GF0050421	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00732_mRNA_6.1
GF0050420	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00732_mRNA_5.1
GF0050419	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00732_mRNA_15.1
GF0050418	0	0	1	Disease resistance family protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00732_mRNA_14.1
GF0050417	0	0	1	Mechanosensitive channel of small conductance-like 10, putative isoform 2 (1)	calcium ion binding [GO:0005509 molecular_function] (1)	EF-hand domain [IPR002048] (1)	-	-	P_trifoliata_00732_mRNA_13.1
GF0050416	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00731_mRNA_8.1
GF0050415	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00731_mRNA_5.1
GF0050414	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00731_mRNA_4.1
GF0050413	0	0	1	Hypothetical protein (1)	integral component of membrane [GO:0016021 cellular_component] (1); transmembrane transport [GO:0055085 biological_process] (1)	Sodium/calcium exchanger membrane region [IPR004837] (1)	-	-	P_trifoliata_00731_mRNA_1.1
GF0050412	0	0	1	Hypothetical protein (1)	RNA binding [GO:0003723 molecular_function] (1); ribonuclease T2 activity [GO:0033897 molecular_function] (1)	Ribonuclease T2-like [IPR001568] (1)	-	-	P_trifoliata_00730_mRNA_9.1
GF0050411	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00730_mRNA_7.1
GF0050410	0	0	1	Hypothetical protein (1)	calmodulin binding [GO:0005516 molecular_function] (1)	Calcium-transporting P-type ATPase, N-terminal autoinhibitory domain [IPR024750] (1)	-	-	P_trifoliata_00730_mRNA_6.1
GF0050409	0	0	1	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); calmodulin binding [GO:0005516 molecular_function] (1)	Protein kinase-like domain [IPR011009] (1); Calcium-transporting P-type ATPase, N-terminal autoinhibitory domain [IPR024750] (1); Protein kinase domain [IPR000719] (1)	-	-	P_trifoliata_00730_mRNA_5.1
GF0050408	0	0	1	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)	Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Protein kinase-like domain [IPR011009] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); LysM domain [IPR018392] (1); Protein kinase domain [IPR000719] (1)	-	-	P_trifoliata_00729_mRNA_4.1
GF0050407	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00728_mRNA_9.1
GF0050406	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00728_mRNA_8.1
GF0050405	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00728_mRNA_7.1
GF0050404	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00728_mRNA_5.1
GF0050403	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00728_mRNA_3.1
GF0050402	0	0	1	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	-	P_trifoliata_00728_mRNA_15.1
GF0050401	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00728_mRNA_14.1
GF0050400	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00728_mRNA_10.1
GF0050399	0	0	1	Folic acid binding / transferase (1)	transferase activity [GO:0016740 molecular_function] (1); folic acid binding [GO:0005542 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Formiminotransferase, C-terminal subdomain [IPR013802] (1); Formiminotransferase subdomain [IPR022384] (1); Formiminotransferase, N-terminal subdomain [IPR012886] (1)	-	-	P_trifoliata_00726_mRNA_4.1
GF0050398	0	0	1	Hypothetical protein (1)		P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00726_mRNA_12.1
GF0050397	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00726_mRNA_10.1
GF0050396	0	0	1	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	-	P_trifoliata_00725_mRNA_3.1
GF0050395	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00725_mRNA_2.1
GF0050394	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00725_mRNA_12.1
GF0050393	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00725_mRNA_10.1
GF0050392	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00724_mRNA_9.1
GF0050391	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00724_mRNA_7.1
GF0050390	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00724_mRNA_5.1
GF0050389	0	0	1	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	Transcription factor, MADS-box [IPR002100] (1)	-	-	P_trifoliata_00724_mRNA_4.1
GF0050388	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00724_mRNA_2.1
GF0050387	0	0	1	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)	-	-	P_trifoliata_00724_mRNA_11.1
GF0050386	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00723_mRNA_9.1
GF0050385	0	0	1	Complex I subunit (1)		NADH:ubiquinone oxidoreductase, ESSS subunit [IPR019329] (1)	-	-	P_trifoliata_00723_mRNA_1.1
GF0050384	0	0	1	Hypothetical protein (1)	hydrolase activity [GO:0016787 molecular_function] (1)	Calcineurin-like phosphoesterase domain, apaH type [IPR004843] (1); Metallo-dependent phosphatase-like [IPR029052] (1)	-	-	P_trifoliata_00722_mRNA_8.1
GF0050383	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00722_mRNA_6.1
GF0050382	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00721_mRNA_10.1
GF0050381	0	0	1	Hypothetical protein (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); NAD(P)-binding domain [IPR016040] (1); Glyceraldehyde/Erythrose phosphate dehydrogenase family [IPR020831] (1); Glyceraldehyde 3-phosphate dehydrogenase, active site [IPR020830] (1)	-	-	P_trifoliata_00721_mRNA_1.1
GF0050380	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00719_mRNA_9.1
GF0050379	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1); Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00719_mRNA_8.1
GF0050378	0	0	1	Monosacharide transport protein (1)			-	-	P_trifoliata_00719_mRNA_5.1
GF0050377	0	0	1	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	-	-	P_trifoliata_00719_mRNA_3.1
GF0050376	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00719_mRNA_2.1
GF0050375	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00719_mRNA_13.1
GF0050374	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00718_mRNA_8.1
GF0050373	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00718_mRNA_7.1
GF0050372	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00718_mRNA_6.1
GF0050371	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00718_mRNA_5.1
GF0050370	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00718_mRNA_19.1
GF0050369	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00718_mRNA_14.1
GF0050368	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00718_mRNA_13.1
GF0050367	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00718_mRNA_12.1
GF0050366	0	0	1	Cytochrome P450 71D8 (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)	-	-	P_trifoliata_00717_mRNA_7.1
GF0050365	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00717_mRNA_2.1
GF0050364	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00716_mRNA_5.1
GF0050363	0	0	1	Glucan endo-1,3-beta-glucosidase 11 isoform 4 (1)	hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1)	Glycoside hydrolase family 17 [IPR000490] (1); Glycoside hydrolase superfamily [IPR017853] (1); Glycoside hydrolase, catalytic domain [IPR013781] (1)	-	-	P_trifoliata_00716_mRNA_3.1
GF0050362	0	0	1	Glucan endo-1,3-beta-glucosidase 7 (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); Glycoside hydrolase family 17 [IPR000490] (1); X8 domain [IPR012946] (1)	-	-	P_trifoliata_00716_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*
GF0050361	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00716_mRNA_1.1
GF0050360	0	0	1	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	-	-	P_trifoliata_00715_mRNA_8.1
GF0050359	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00715_mRNA_7.1
GF0050358	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00715_mRNA_1.1
GF0050357	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00714_mRNA_8.1
GF0050356	0	0	1	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)	-	-	P_trifoliata_00714_mRNA_4.1
GF0050355	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00714_mRNA_3.1
GF0050354	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00714_mRNA_2.1
GF0050353	0	0	1	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); NmrA-like domain [IPR008030] (1); Ribosomal protein L2 domain 2 [IPR014722] (1); Translation protein SH3-like domain [IPR008991] (1); NAD(P)-binding domain [IPR016040] (1)	-	-	P_trifoliata_00713_mRNA_9.1
GF0050352	0	0	1	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	-	P_trifoliata_00713_mRNA_7.1
GF0050351	0	0	1	Germin-like protein subfamily 1 member 7 (1)	ATP binding [GO:0005524 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); nutrient reservoir activity [GO:0045735 molecular_function] (1); manganese ion binding [GO:0030145 molecular_function] (1)	Serine/threonine-protein kinase, active site [IPR008271] (1); RmlC-like cupin domain [IPR011051] (1); RmlC-like jelly roll fold [IPR014710] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1); Cupin 1 [IPR006045] (1); Germin, manganese binding site [IPR019780] (1)	-	-	P_trifoliata_00713_mRNA_6.1
GF0050350	0	0	1	PPR containing plant-like protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	-	P_trifoliata_00713_mRNA_4.1
GF0050349	0	0	1	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	-	P_trifoliata_00713_mRNA_3.1
GF0050348	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00713_mRNA_13.1
GF0050347	0	0	1	Disease resistance protein RPS5 (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	-	P_trifoliata_00712_mRNA_9.1
GF0050346	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00712_mRNA_7.1
GF0050345	0	0	1	Disease resistance RPS5-like 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)	-	-	P_trifoliata_00712_mRNA_5.1
GF0050344	0	0	1	Resistance protein RGC2 (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00712_mRNA_4.1
GF0050343	0	0	1	O-methyltransferase ZRP4 (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)	-	-	P_trifoliata_00712_mRNA_2.1
GF0050342	0	0	1	Disease resistance protein RPS5 (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	-	P_trifoliata_00712_mRNA_10.1
GF0050341	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00712_mRNA_1.1
GF0050340	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00710_mRNA_9.1
GF0050339	0	0	1	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); calmodulin binding [GO:0005516 molecular_function] (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); Calcium-transporting P-type ATPase, N-terminal autoinhibitory domain [IPR024750] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	-	-	P_trifoliata_00710_mRNA_7.1
GF0050338	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00710_mRNA_6.1
GF0050337	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00709_mRNA_7.1
GF0050336	0	0	1	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1)	-	-	P_trifoliata_00709_mRNA_5.1
GF0050335	0	0	1	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1); Protein kinase-like domain [IPR011009] (1)	-	-	P_trifoliata_00709_mRNA_11.1
GF0050334	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00709_mRNA_10.1
GF0050333	0	0	1	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)	-	-	P_trifoliata_00709_mRNA_1.1
GF0050332	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00708_mRNA_9.1
GF0050331	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00708_mRNA_8.1
GF0050330	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00708_mRNA_7.1
GF0050329	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00708_mRNA_6.1
GF0050328	0	0	1	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-like domain [IPR012337] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H domain [IPR002156] (1)	-	-	P_trifoliata_00708_mRNA_4.1
GF0050327	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00708_mRNA_3.1
GF0050326	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00708_mRNA_2.1
GF0050325	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00708_mRNA_15.1
GF0050324	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00708_mRNA_1.1
GF0050323	0	0	1	Hypothetical protein (1)	protein serine/threonine kinase activity [GO:0004674 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	WD40-repeat-containing domain [IPR017986] (1); S-locus receptor kinase, C-terminal [IPR021820] (1); WD40/YVTN repeat-like-containing domain [IPR015943] (1); Protein kinase-like domain [IPR011009] (1)	-	-	P_trifoliata_00707_mRNA_9.1
GF0050322	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	-	P_trifoliata_00707_mRNA_8.1
GF0050321	0	0	1	Male germ cell-associated 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-protein kinase, active site [IPR008271] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1)	-	-	P_trifoliata_00707_mRNA_5.1
GF0050320	0	0	1	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	-	P_trifoliata_00707_mRNA_3.1
GF0050319	0	0	1	UPF0481 protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	-	P_trifoliata_00707_mRNA_2.1
GF0050318	0	0	1	UPF0481 protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	-	P_trifoliata_00707_mRNA_1.1
GF0050317	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00706_mRNA_15.1
GF0050316	0	0	1	Hypothetical protein (1)		Transposase, MuDR, plant [IPR004332] (1)	-	-	P_trifoliata_00706_mRNA_11.1
GF0050315	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00706_mRNA_10.1
GF0050314	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00706_mRNA_1.1
GF0050313	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00705_mRNA_7.1
GF0050312	0	0	1	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)	-	-	P_trifoliata_00705_mRNA_6.1
GF0050311	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00705_mRNA_4.1
GF0050310	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00705_mRNA_1.1
GF0050309	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00704_mRNA_4.1
GF0050308	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00704_mRNA_1.1
GF0050307	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00703_mRNA_16.1
GF0050306	0	0	1	Alpha N-terminal protein methyltransferase 1 (1)	methyltransferase activity [GO:0008168 molecular_function] (1); N-terminal protein amino acid methylation [GO:0006480 biological_process] (1)	Alpha-N-methyltransferase NTM1 [IPR008576] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	-	P_trifoliata_00703_mRNA_15.1
GF0050305	0	0	1	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)	-	-	P_trifoliata_00703_mRNA_14.1
GF0050304	0	0	1	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1)	Myc-type, basic helix-loop-helix (bHLH) domain [IPR011598] (1)	-	-	P_trifoliata_00703_mRNA_13.1
GF0050303	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00702_mRNA_9.1
GF0050302	0	0	1	Pathogenesis-related family protein isoform 1 (1)		NTF2-like domain [IPR032710] (1)	-	-	P_trifoliata_00702_mRNA_8.1
GF0050301	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00702_mRNA_5.1
GF0050300	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00702_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*
GF0050299	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00702_mRNA_14.1
GF0050298	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00701_mRNA_6.1
GF0050297	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00701_mRNA_2.1
GF0050296	0	0	1	SUN domain-containing protein 1 (1)		SUN domain [IPR012919] (1)	-	-	P_trifoliata_00700_mRNA_9.1
GF0050295	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00700_mRNA_3.1
GF0050294	0	0	1	Hypothetical protein (1)	membrane [GO:0016020 cellular_component] (1)	Calcium-dependent channel, 7TM region, putative phosphate [IPR003864] (1)	-	-	P_trifoliata_00700_mRNA_2.1
GF0050293	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00699_mRNA_12.1
GF0050292	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00699_mRNA_11.1
GF0050291	0	0	1	GluA (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, family 3, N-terminal [IPR001764] (1); Glycoside hydrolase family 3 [IPR026892] (1)	-	-	P_trifoliata_00699_mRNA_1.1
GF0050290	0	0	1	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	-	P_trifoliata_00698_mRNA_9.1
GF0050289	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00698_mRNA_8.1
GF0050288	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00698_mRNA_7.1
GF0050287	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00698_mRNA_5.1
GF0050286	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00698_mRNA_1.1
GF0050285	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00697_mRNA_8.1
GF0050284	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00697_mRNA_7.1
GF0050283	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00697_mRNA_6.1
GF0050282	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00697_mRNA_5.1
GF0050281	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00697_mRNA_2.1
GF0050280	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00697_mRNA_15.1
GF0050279	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00697_mRNA_12.1
GF0050278	0	0	1	Hypothetical protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	-	P_trifoliata_00697_mRNA_10.1
GF0050277	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00696_mRNA_8.1
GF0050276	0	0	1	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	NAC domain [IPR003441] (1)	-	-	P_trifoliata_00696_mRNA_7.1
GF0050275	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00696_mRNA_4.1
GF0050274	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00696_mRNA_2.1
GF0050273	0	0	1	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); DNA binding [GO:0003677 molecular_function] (1)	NAC domain [IPR003441] (1)	-	-	P_trifoliata_00696_mRNA_13.1
GF0050272	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00696_mRNA_10.1
GF0050271	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00696_mRNA_1.1
GF0050270	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00695_mRNA_9.1
GF0050269	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	PGG domain [IPR026961] (1); Ankyrin repeat-containing domain [IPR020683] (1); Ankyrin repeat [IPR002110] (1)	-	-	P_trifoliata_00695_mRNA_8.1
GF0050268	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00695_mRNA_7.1
GF0050267	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00695_mRNA_6.1
GF0050266	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00695_mRNA_5.1
GF0050265	0	0	1	AT4g02470 protein (1)	ATP binding [GO:0005524 molecular_function] (1)	AAA+ ATPase domain [IPR003593] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); ATPase, AAA-type, core [IPR003959] (1); ATPase, AAA-type, conserved site [IPR003960] (1)	-	-	P_trifoliata_00695_mRNA_4.1
GF0050264	0	0	1	Ankyrin repeat family protein (1)		PGG domain [IPR026961] (1)	-	-	P_trifoliata_00695_mRNA_12.1
GF0050263	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat-containing domain [IPR020683] (1); Ankyrin repeat [IPR002110] (1)	-	-	P_trifoliata_00695_mRNA_11.1
GF0050262	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00695_mRNA_10.1
GF0050261	0	0	1	ATPase family AAA domain-containing protein 1-A (1)	ATP binding [GO:0005524 molecular_function] (1)	ATPase, AAA-type, conserved site [IPR003960] (1); ATPase, AAA-type, core [IPR003959] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); AAA+ ATPase domain [IPR003593] (1)	-	-	P_trifoliata_00695_mRNA_1.1
GF0050260	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00694_mRNA_3.1
GF0050259	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00694_mRNA_2.1
GF0050258	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00694_mRNA_1.1
GF0050257	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00693_mRNA_8.1
GF0050256	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00693_mRNA_6.1
GF0050255	0	0	1	Receptor-like cytosolic serine/threonine-protein kinase RBK2 (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); Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1)	-	-	P_trifoliata_00693_mRNA_5.1
GF0050254	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00693_mRNA_4.1
GF0050253	0	0	1	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			-	-	P_trifoliata_00692_mRNA_9.1
GF0050252	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00692_mRNA_8.1
GF0050251	0	0	1	Hypothetical protein (1)	methyltransferase activity [GO:0008168 molecular_function] (1); O-methyltransferase activity [GO:0008171 molecular_function] (1)	O-methyltransferase, family 2 [IPR001077] (1); Transposase, MuDR, plant [IPR004332] (1); O-methyltransferase COMT-type [IPR016461] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	-	P_trifoliata_00692_mRNA_7.1
GF0050250	0	0	1	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)	-	-	P_trifoliata_00692_mRNA_5.1
GF0050249	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00692_mRNA_15.1
GF0050248	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00692_mRNA_14.1
GF0050247	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00692_mRNA_13.1
GF0050246	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00692_mRNA_10.1
GF0050245	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00692_mRNA_1.1
GF0050244	0	0	1	Hypothetical protein (1)		Gag-polypeptide of LTR copia-type [IPR029472] (1)	-	-	P_trifoliata_00691_mRNA_7.1
GF0050243	0	0	1	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 [IPR001128] (1); Cytochrome P450, conserved site [IPR017972] (1); Cytochrome P450, E-class, group I [IPR002401] (1)	-	-	P_trifoliata_00691_mRNA_6.1
GF0050242	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00691_mRNA_4.1
GF0050241	0	0	1	Zinc finger protein-like protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Haemerythrin-like [IPR012312] (1); Zinc finger, CHY-type [IPR008913] (1); Zinc finger, RING-type [IPR001841] (1); Zinc finger, RING/FYVE/PHD-type [IPR013083] (1); Rubredoxin-type fold [IPR004039] (1); Zinc finger, CTCHY-type [IPR017921] (1)	-	-	P_trifoliata_00691_mRNA_2.1
GF0050240	0	0	1	Ribosomal protein S7e (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)	Bifunctional inhibitor/plant lipid transfer protein/seed storage helical domain [IPR016140] (1); Ribosomal protein S7e [IPR000554] (1); Hydrophobic seed protein [IPR027923] (1)	-	-	P_trifoliata_00690_mRNA_7.1
GF0050239	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00690_mRNA_3.1
GF0050238	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00690_mRNA_2.1
GF0050237	0	0	1	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	NAC domain [IPR003441] (1)	-	-	P_trifoliata_00690_mRNA_14.1
GF0050236	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00690_mRNA_11.1
GF0050235	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00690_mRNA_1.1
GF0050234	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00689_mRNA_8.1
GF0050233	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00689_mRNA_7.1
GF0050232	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00689_mRNA_6.1
GF0050231	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00689_mRNA_2.1
GF0050230	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00689_mRNA_15.1
GF0050229	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00689_mRNA_13.1
GF0050228	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00689_mRNA_12.1
GF0050227	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00689_mRNA_11.1
GF0050226	0	0	1	Hypothetical protein (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Retropepsins [IPR018061] (1); Peptidase A2A, retrovirus, catalytic [IPR001995] (1); Aspartic peptidase domain [IPR021109] (1)	-	-	P_trifoliata_00689_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*
GF0050225	0	0	1	CDNA clone:002-112-E03, full insert sequence (1)			-	-	P_trifoliata_00688_mRNA_7.1
GF0050224	0	0	1	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)	-	-	P_trifoliata_00688_mRNA_6.1
GF0050223	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00688_mRNA_20.1
GF0050222	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00688_mRNA_18.1
GF0050221	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00688_mRNA_12.1
GF0050220	0	0	1	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	-	P_trifoliata_00688_mRNA_11.1
GF0050219	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00688_mRNA_1.1
GF0050218	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00687_mRNA_11.1
GF0050217	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00686_mRNA_21.1
GF0050216	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00686_mRNA_20.1
GF0050215	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00686_mRNA_2.1
GF0050214	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00686_mRNA_19.1
GF0050213	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00686_mRNA_18.1
GF0050212	0	0	1	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	-	P_trifoliata_00686_mRNA_17.1
GF0050211	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00686_mRNA_16.1
GF0050210	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00686_mRNA_14.1
GF0050209	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00686_mRNA_12.1
GF0050208	0	0	1	Hypothetical protein (1)		Pentapeptide repeat [IPR001646] (1)	-	-	P_trifoliata_00686_mRNA_1.1
GF0050207	0	0	1	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1)	-	-	P_trifoliata_00685_mRNA_9.1
GF0050206	0	0	1	Disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	-	P_trifoliata_00685_mRNA_8.1
GF0050205	0	0	1	Hypothetical protein (1)	vesicle docking involved in exocytosis [GO:0006904 biological_process] (1); exocyst [GO:0000145 cellular_component] (1)	Exocyst complex subunit Sec15-like [IPR007225] (1)	-	-	P_trifoliata_00685_mRNA_5.1
GF0050204	0	0	1	RNA-directed DNA polymerase , related (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00685_mRNA_4.1
GF0050203	0	0	1	LRR and NB-ARC domains-containing disease resistance-like protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	-	P_trifoliata_00685_mRNA_11.1
GF0050202	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00684_mRNA_6.1
GF0050201	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00684_mRNA_5.1
GF0050200	0	0	1	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	-	-	P_trifoliata_00684_mRNA_3.1
GF0050199	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00684_mRNA_13.1
GF0050198	0	0	1	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	-	P_trifoliata_00684_mRNA_12.1
GF0050197	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00684_mRNA_11.1
GF0050196	0	0	1	Transposable element protein, putative, (1)		Retrotransposon gag domain [IPR005162] (1)	-	-	P_trifoliata_00684_mRNA_10.1
GF0050195	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00684_mRNA_1.1
GF0050194	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00683_mRNA_9.1
GF0050193	0	0	1	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); DNA binding [GO:0003677 molecular_function] (1)	NAC domain [IPR003441] (1)	-	-	P_trifoliata_00683_mRNA_7.1
GF0050192	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00683_mRNA_3.1
GF0050191	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00683_mRNA_2.1
GF0050190	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00683_mRNA_10.1
GF0050189	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00683_mRNA_1.1
GF0050188	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00682_mRNA_5.1
GF0050187	0	0	1	Hypothetical protein (1)		DNA-binding pseudobarrel domain [IPR015300] (1)	-	-	P_trifoliata_00682_mRNA_12.1
GF0050186	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00682_mRNA_11.1
GF0050185	0	0	1	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	B3 DNA binding domain [IPR003340] (1); DNA-binding pseudobarrel domain [IPR015300] (1)	-	-	P_trifoliata_00682_mRNA_10.1
GF0050184	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00682_mRNA_1.1
GF0050183	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00681_mRNA_9.1
GF0050182	0	0	1	Hypothetical protein (1)	oligosaccharyltransferase complex [GO:0008250 cellular_component] (1); integral component of membrane [GO:0016021 cellular_component] (1); dolichyl-diphosphooligosaccharide-protein glycotransferase activity [GO:0004579 molecular_function] (1)	DAD/Ost2 [IPR003038] (1)	-	-	P_trifoliata_00681_mRNA_6.1
GF0050181	0	0	1	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)	-	-	P_trifoliata_00681_mRNA_5.1
GF0050180	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00681_mRNA_4.1
GF0050179	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00681_mRNA_3.1
GF0050178	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00681_mRNA_11.1
GF0050177	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00681_mRNA_10.1
GF0050176	0	0	1	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)	Translation protein SH3-like domain [IPR008991] (1); Ribosomal protein L2, domain 3 [IPR014726] (1); Ribosomal protein L2 [IPR002171] (1)	-	-	P_trifoliata_00680_mRNA_8.1
GF0050175	0	0	1	Hypothetical protein (1)	polysaccharide binding [GO:0030247 molecular_function] (1)	Wall-associated receptor kinase, galacturonan-binding domain [IPR025287] (1)	-	-	P_trifoliata_00680_mRNA_3.1
GF0050174	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00680_mRNA_12.1
GF0050173	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00680_mRNA_11.1
GF0050172	0	0	1	Calcium-transporting ATPase 8, plasma membrane-type (1)	integral component of membrane [GO:0016021 cellular_component] (1); calcium ion transmembrane transport [GO:0070588 biological_process] (1); membrane [GO:0016020 cellular_component] (1); metal ion binding [GO:0046872 molecular_function] (1); calcium-transporting ATPase activity [GO:0005388 molecular_function] (1); nucleotide binding [GO:0000166 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	P-type ATPase, cytoplasmic domain N [IPR023299] (1); Cation-transporting P-type ATPase, C-terminal [IPR006068] (1); P-type ATPase, subfamily IIB [IPR006408] (1); P-type ATPase, transmembrane domain [IPR023298] (1); P-type ATPase [IPR001757] (1); HAD-like domain [IPR023214] (1); P-type ATPase, A domain [IPR008250] (1)	-	-	P_trifoliata_00680_mRNA_10.1
GF0050171	0	0	1	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)	Translation protein SH3-like domain [IPR008991] (1); Ribosomal protein L2, domain 3 [IPR014726] (1); Ribosomal protein L2 [IPR002171] (1); Ribosomal protein L2, C-terminal [IPR022669] (1)	-	-	P_trifoliata_00680_mRNA_1.1
GF0050170	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00679_mRNA_7.1
GF0050169	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00679_mRNA_3.1
GF0050168	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00679_mRNA_2.1
GF0050167	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00679_mRNA_18.1
GF0050166	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00679_mRNA_17.1
GF0050165	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00679_mRNA_13.1
GF0050164	0	0	1	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)	Tyrosine-protein kinase, active site [IPR008266] (1); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1)	-	-	P_trifoliata_00679_mRNA_12.1
GF0050163	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00679_mRNA_11.1
GF0050162	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00679_mRNA_10.1
GF0050161	0	0	1	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	-	P_trifoliata_00678_mRNA_8.1
GF0050160	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00678_mRNA_6.1
GF0050159	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00678_mRNA_5.1
GF0050158	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00678_mRNA_3.1
GF0050157	0	0	1	Retrotransposon protein, putative, Ty1-copia subclass (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	-	-	P_trifoliata_00678_mRNA_21.1
GF0050156	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00678_mRNA_19.1
GF0050155	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00678_mRNA_15.1
GF0050154	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00678_mRNA_13.1
GF0050153	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00678_mRNA_10.1
GF0050152	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00677_mRNA_9.1
GF0050151	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00677_mRNA_7.1
GF0050150	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00677_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*
GF0050149	0	0	1	Truncated RB (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	-	P_trifoliata_00677_mRNA_11.1
GF0050148	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00677_mRNA_1.1
GF0050147	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00676_mRNA_4.1
GF0050146	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00676_mRNA_18.1
GF0050145	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00675_mRNA_9.1
GF0050144	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00675_mRNA_8.1
GF0050143	0	0	1	Hypothetical 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)	-	-	P_trifoliata_00675_mRNA_5.1
GF0050142	0	0	1	Hypothetical protein (1)	translational initiation [GO:0006413 biological_process] (1); translation initiation factor activity [GO:0003743 molecular_function] (1)	Translation initiation factor IF2/IF5, N-terminal [IPR016189] (1)	-	-	P_trifoliata_00675_mRNA_13.1
GF0050141	0	0	1	Hypothetical protein (1)	serine-type peptidase activity [GO:0008236 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Peptidase S28 [IPR008758] (1)	-	-	P_trifoliata_00675_mRNA_11.1
GF0050140	0	0	1	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1); FAR1 DNA binding domain [IPR004330] (1)	-	-	P_trifoliata_00675_mRNA_10.1
GF0050139	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00674_mRNA_8.1
GF0050138	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00674_mRNA_6.1
GF0050137	0	0	1	Hypothetical protein (1)		Transposase, MuDR, plant [IPR004332] (1)	-	-	P_trifoliata_00674_mRNA_2.1
GF0050136	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00673_mRNA_9.1
GF0050135	0	0	1	NB-ARC domain-containing disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	-	P_trifoliata_00673_mRNA_7.1
GF0050134	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00673_mRNA_6.1
GF0050133	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00673_mRNA_5.1
GF0050132	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00673_mRNA_3.1
GF0050131	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00673_mRNA_2.1
GF0050130	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00673_mRNA_12.1
GF0050129	0	0	1	Hypothetical protein (1)		LOG family [IPR031100] (1)	-	-	P_trifoliata_00672_mRNA_9.1
GF0050128	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00672_mRNA_8.1
GF0050127	0	0	1	Hypothetical protein (1)	RNA binding [GO:0003723 molecular_function] (1); ribonuclease T2 activity [GO:0033897 molecular_function] (1)	Ribonuclease T2-like [IPR001568] (1)	-	-	P_trifoliata_00672_mRNA_5.1
GF0050126	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00672_mRNA_2.1
GF0050125	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00672_mRNA_13.1
GF0050124	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00672_mRNA_11.1
GF0050123	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00672_mRNA_1.1
GF0050122	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00671_mRNA_6.1
GF0050121	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00671_mRNA_5.1
GF0050120	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00671_mRNA_4.1
GF0050119	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00671_mRNA_3.1
GF0050118	0	0	1	L-type lectin-domain containing receptor kinase IV.2 (1)	carbohydrate binding [GO:0030246 molecular_function] (1)	Legume lectin domain [IPR001220] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1)	-	-	P_trifoliata_00671_mRNA_11.1
GF0050117	0	0	1	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	-	P_trifoliata_00670_mRNA_11.1
GF0050116	0	0	1	Hypothetical protein (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1)	Glycoside hydrolase, catalytic domain [IPR013781] (1)	-	-	P_trifoliata_00669_mRNA_1.1
GF0050115	0	0	1	5-pentadecatrienyl resorcinol O-methyltransferase (1)			-	-	P_trifoliata_00668_mRNA_8.1
GF0050114	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00668_mRNA_7.1
GF0050113	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00668_mRNA_6.1
GF0050112	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00668_mRNA_4.1
GF0050111	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00668_mRNA_3.1
GF0050110	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00668_mRNA_2.1
GF0050109	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00668_mRNA_1.1
GF0050108	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00667_mRNA_8.1
GF0050107	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00667_mRNA_7.1
GF0050106	0	0	1	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	-	P_trifoliata_00667_mRNA_6.1
GF0050105	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00667_mRNA_2.1
GF0050104	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00667_mRNA_15.1
GF0050103	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00667_mRNA_13.1
GF0050102	0	0	1	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	-	P_trifoliata_00667_mRNA_11.1
GF0050101	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00667_mRNA_1.1
GF0050100	0	0	1	Hypothetical protein (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Retropepsins [IPR018061] (1); Peptidase A2A, retrovirus, catalytic [IPR001995] (1); Aspartic peptidase domain [IPR021109] (1)	-	-	P_trifoliata_00666_mRNA_9.1
GF0050099	0	0	1	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	-	P_trifoliata_00666_mRNA_8.1
GF0050098	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00666_mRNA_7.1
GF0050097	0	0	1	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)	-	-	P_trifoliata_00666_mRNA_4.1
GF0050096	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00666_mRNA_3.1
GF0050095	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00666_mRNA_13.1
GF0050094	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00666_mRNA_12.1
GF0050093	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00666_mRNA_11.1
GF0050092	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00666_mRNA_10.1
GF0050091	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00665_mRNA_5.1
GF0050090	0	0	1	Disease resistance protein (NBS-LRR class) family protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00665_mRNA_3.1
GF0050089	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00665_mRNA_2.1
GF0050088	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00665_mRNA_11.1
GF0050087	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00664_mRNA_9.1
GF0050086	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00664_mRNA_7.1
GF0050085	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00664_mRNA_2.1
GF0050084	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00664_mRNA_11.1
GF0050083	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00663_mRNA_7.1
GF0050082	0	0	1	Retrotransposon protein, putative, Ty1-copia subclass (1)		Gag-polypeptide of LTR copia-type [IPR029472] (1)	-	-	P_trifoliata_00663_mRNA_3.1
GF0050081	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00663_mRNA_14.1
GF0050080	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00663_mRNA_12.1
GF0050079	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00663_mRNA_10.1
GF0050078	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00663_mRNA_1.1
GF0050077	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00662_mRNA_6.1
GF0050076	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00662_mRNA_3.1
GF0050075	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	-	P_trifoliata_00662_mRNA_2.1
GF0050074	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00661_mRNA_5.1
GF0050073	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00661_mRNA_1.1
GF0050072	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00660_mRNA_6.1
GF0050071	0	0	1	Polynucleotidyl transferase, Ribonuclease H fold (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00660_mRNA_12.1
GF0050070	0	0	1	Hypothetical 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)	-	-	P_trifoliata_00660_mRNA_11.1
GF0050069	0	0	1	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	-	P_trifoliata_00660_mRNA_10.1
GF0050068	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00660_mRNA_1.1
GF0050067	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00659_mRNA_9.1
GF0050066	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00659_mRNA_8.1
GF0050065	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00659_mRNA_4.1
GF0050064	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00658_mRNA_11.1
GF0050063	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00658_mRNA_1.1
GF0050062	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00657_mRNA_9.1
GF0050061	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00657_mRNA_8.1
GF0050060	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00657_mRNA_5.1
GF0050059	0	0	1	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)	Tyrosine-protein kinase, active site [IPR008266] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1)	-	-	P_trifoliata_00657_mRNA_4.1
GF0050058	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00657_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*
GF0050057	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00657_mRNA_14.1
GF0050056	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00657_mRNA_12.1
GF0050055	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00657_mRNA_10.1
GF0050054	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00656_mRNA_7.1
GF0050053	0	0	1	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)	-	-	P_trifoliata_00656_mRNA_6.1
GF0050052	0	0	1	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	-	-	P_trifoliata_00656_mRNA_3.1
GF0050051	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00655_mRNA_9.1
GF0050050	0	0	1	Homogentisate phytyltransferase 1, chloroplastic (1)	prenyltransferase activity [GO:0004659 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1)	UbiA prenyltransferase family [IPR000537] (1)	-	-	P_trifoliata_00655_mRNA_3.1
GF0050049	0	0	1	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	-	P_trifoliata_00655_mRNA_1.1
GF0050048	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00654_mRNA_21.1
GF0050047	0	0	1	NADH dehydrogenase subunit 9 (1)	oxidoreductase activity, acting on NAD(P)H [GO:0016651 molecular_function] (1); NADH dehydrogenase (ubiquinone) activity [GO:0008137 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	NADH dehydrogenase, subunit C [IPR010218] (1); NADH:ubiquinone oxidoreductase, 30kDa subunit, conserved site [IPR020396] (1); NADH:ubiquinone oxidoreductase, 30kDa subunit [IPR001268] (1)	-	-	P_trifoliata_00654_mRNA_20.1
GF0050046	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00654_mRNA_18.1
GF0050045	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00654_mRNA_16.1
GF0050044	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00654_mRNA_15.1
GF0050043	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00654_mRNA_13.1
GF0050042	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00654_mRNA_10.1
GF0050041	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00653_mRNA_8.1
GF0050040	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00653_mRNA_7.1
GF0050039	0	0	1	Hypothetical protein (1)		Periplasmic binding protein-like I [IPR028082] (1)	-	-	P_trifoliata_00653_mRNA_6.1
GF0050038	0	0	1	Hypothetical protein (1)		Periplasmic binding protein-like I [IPR028082] (1); Receptor, ligand binding region [IPR001828] (1)	-	-	P_trifoliata_00653_mRNA_4.1
GF0050037	0	0	1	General transcription factor 2-related zinc finger protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Domain of unknown function DUF4371 [IPR025398] (1)	-	-	P_trifoliata_00653_mRNA_2.1
GF0050036	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00653_mRNA_11.1
GF0050035	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00653_mRNA_10.1
GF0050034	0	0	1	Hypothetical protein (1)		Probable transposase, Ptta/En/Spm, plant [IPR004252] (1)	-	-	P_trifoliata_00652_mRNA_4.1
GF0050033	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00651_mRNA_9.1
GF0050032	0	0	1	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	-	P_trifoliata_00651_mRNA_4.1
GF0050031	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00651_mRNA_3.1
GF0050030	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1); cytoplasm [GO:0005737 cellular_component] (1); translation initiation factor activity [GO:0003743 molecular_function] (1); eukaryotic translation initiation factor 3 complex [GO:0005852 cellular_component] (1)	Proteasome component (PCI) domain [IPR000717] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Eukaryotic translation initiation factor 3 subunit E [IPR016650] (1)	-	-	P_trifoliata_00651_mRNA_14.1
GF0050029	0	0	1	Ubiquitin-conjugating enzyme E2 (1)		Ubiquitin-conjugating enzyme/RWD-like [IPR016135] (1); Ubiquitin-conjugating enzyme, active site [IPR023313] (1); Ubiquitin-conjugating enzyme E2 [IPR000608] (1)	-	-	P_trifoliata_00650_mRNA_2.1
GF0050028	0	0	1	General transcription factor (1)	nucleotide-excision repair [GO:0006289 biological_process] (1); core TFIIH complex [GO:0000439 cellular_component] (1); transcription, DNA-templated [GO:0006351 biological_process] (1)	TFIIH subunit Tfb1/p62 [IPR027079] (1)	-	-	P_trifoliata_00650_mRNA_15.2
GF0050027	0	0	1	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 S3, C-terminal [IPR001351] (1)	-	-	P_trifoliata_00649_mRNA_9.1
GF0050026	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00649_mRNA_8.1
GF0050025	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00649_mRNA_7.1
GF0050024	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00649_mRNA_26.1
GF0050023	0	0	1	NADH dehydrogenase subunit 9 (1)	oxidation-reduction process [GO:0055114 biological_process] (1); NADH dehydrogenase (ubiquinone) activity [GO:0008137 molecular_function] (1)	NADH:ubiquinone oxidoreductase, 30kDa subunit [IPR001268] (1)	-	-	P_trifoliata_00649_mRNA_24.1
GF0050022	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00649_mRNA_22.1
GF0050021	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00649_mRNA_2.1
GF0050020	0	0	1	Hypothetical protein (1)	membrane [GO:0016020 cellular_component] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	NADH:ubiquinone oxidoreductase, subunit 1, conserved site [IPR018086] (1); NADH:ubiquinone oxidoreductase, subunit 1/F420H2 oxidoreductase subunit H [IPR001694] (1)	-	-	P_trifoliata_00649_mRNA_17.1
GF0050019	0	0	1	Ribosomal protein L5 (1)		Ribosomal protein L5 domain [IPR022803] (1)	-	-	P_trifoliata_00649_mRNA_16.1
GF0050018	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00649_mRNA_14.1
GF0050017	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00649_mRNA_13.1
GF0050016	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00649_mRNA_12.1
GF0050015	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00649_mRNA_11.1
GF0050014	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00649_mRNA_10.1
GF0050013	0	0	1	Anthocyanin 5-aromatic acyltransferase (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)	-	-	P_trifoliata_00648_mRNA_9.1
GF0050012	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00648_mRNA_4.1
GF0050011	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00648_mRNA_15.1
GF0050010	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00648_mRNA_14.1
GF0050009	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00648_mRNA_13.1
GF0050008	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00648_mRNA_10.1
GF0050007	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00648_mRNA_1.1
GF0050006	0	0	1	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	-	P_trifoliata_00647_mRNA_5.1
GF0050005	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00647_mRNA_4.1
GF0050004	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00647_mRNA_3.1
GF0050003	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00647_mRNA_2.1
GF0050002	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00647_mRNA_13.1
GF0050001	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00647_mRNA_10.1
GF0050000	0	0	1	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)	-	-	P_trifoliata_00646_mRNA_8.1
GF0049999	0	0	1	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)	-	-	P_trifoliata_00646_mRNA_4.1
GF0049998	0	0	1	Hypothetical protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	-	P_trifoliata_00646_mRNA_2.1
GF0049997	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00646_mRNA_17.1
GF0049996	0	0	1	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			-	-	P_trifoliata_00646_mRNA_15.1
GF0049995	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00646_mRNA_14.1
GF0049994	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00646_mRNA_12.1
GF0049993	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00646_mRNA_11.1
GF0049992	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00646_mRNA_10.1
GF0049991	0	0	1	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); Histone deacetylase domain [IPR023801] (1); Ribonuclease H domain [IPR002156] (1)	-	-	P_trifoliata_00645_mRNA_5.1
GF0049990	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00645_mRNA_4.1
GF0049989	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00645_mRNA_2.1
GF0049988	0	0	1	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)	-	-	P_trifoliata_00645_mRNA_11.1
GF0049987	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00645_mRNA_1.1
GF0049986	0	0	1	Hypothetical protein (1)		Dymeclin [IPR019142] (1)	-	-	P_trifoliata_00644_mRNA_9.1
GF0049985	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00644_mRNA_8.1
GF0049984	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00644_mRNA_20.1
GF0049983	0	0	1	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	-	P_trifoliata_00644_mRNA_19.1
GF0049982	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00644_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*
GF0049981	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00644_mRNA_16.1
GF0049980	0	0	1	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	-	P_trifoliata_00644_mRNA_14.1
GF0049979	0	0	1	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 domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1)	-	-	P_trifoliata_00644_mRNA_1.1
GF0049978	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00643_mRNA_9.1
GF0049977	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00643_mRNA_6.1
GF0049976	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00643_mRNA_4.1
GF0049975	0	0	1	Hypothetical protein (1)	transmembrane transport [GO:0055085 biological_process] (1)	Oligopeptide transporter, OPT superfamily [IPR004813] (1)	-	-	P_trifoliata_00643_mRNA_3.1
GF0049974	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00643_mRNA_1.1
GF0049973	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Transposase, MuDR, plant [IPR004332] (1); F-box domain [IPR001810] (1)	-	-	P_trifoliata_00641_mRNA_8.1
GF0049972	0	0	1	Hypothetical protein (1)		Bifunctional inhibitor/plant lipid transfer protein/seed storage helical domain [IPR016140] (1)	-	-	P_trifoliata_00641_mRNA_4.1
GF0049971	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	-	P_trifoliata_00641_mRNA_2.1
GF0049970	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00641_mRNA_14.1
GF0049969	0	0	1	Hypothetical protein (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)	-	-	P_trifoliata_00641_mRNA_10.1
GF0049968	0	0	1	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)	-	-	P_trifoliata_00641_mRNA_1.1
GF0049967	0	0	1	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	-	P_trifoliata_00640_mRNA_9.1
GF0049966	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00640_mRNA_8.1
GF0049965	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00640_mRNA_7.1
GF0049964	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00640_mRNA_6.1
GF0049963	0	0	1	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	-	P_trifoliata_00640_mRNA_5.1
GF0049962	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00640_mRNA_3.1
GF0049961	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00640_mRNA_2.1
GF0049960	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00640_mRNA_18.1
GF0049959	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00640_mRNA_16.1
GF0049958	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00640_mRNA_15.1
GF0049957	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00640_mRNA_14.1
GF0049956	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00640_mRNA_1.1
GF0049955	0	0	1	Fatty acyl-CoA reductase 1 (1)	fatty-acyl-CoA reductase (alcohol-forming) activity [GO:0080019 molecular_function] (1)	Fatty acyl-CoA reductase [IPR026055] (1); Male sterility, NAD-binding [IPR013120] (1); NAD(P)-binding domain [IPR016040] (1)	-	-	P_trifoliata_00639_mRNA_5.1
GF0049954	0	0	1	Antiporter/ drug transporter (1)		Protein-only RNase P, C-terminal [IPR031595] (1)	-	-	P_trifoliata_00639_mRNA_3.1
GF0049953	0	0	1	Putative wall-associated receptor kinase-like 16 (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)	-	-	P_trifoliata_00638_mRNA_9.1
GF0049952	0	0	1	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	Transcription factor, MADS-box [IPR002100] (1)	-	-	P_trifoliata_00638_mRNA_6.1
GF0049951	0	0	1	Putative RNA-directed DNA polymerase (Reverse transcriptase) (1)		Reverse transcriptase domain [IPR000477] (1)	-	-	P_trifoliata_00637_mRNA_5.1
GF0049950	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00637_mRNA_3.1
GF0049949	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00637_mRNA_1.1
GF0049948	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00636_mRNA_8.1
GF0049947	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00635_mRNA_6.1
GF0049946	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00635_mRNA_5.1
GF0049945	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00635_mRNA_3.1
GF0049944	0	0	1	Inositol monophosphatase (1)	phosphatidylinositol phosphorylation [GO:0046854 biological_process] (1)	Inositol monophosphatase [IPR000760] (1); Inositol monophosphatase, metal-binding site [IPR020583] (1)	-	-	P_trifoliata_00635_mRNA_13.1
GF0049943	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00635_mRNA_11.1
GF0049942	0	0	1	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); peptidase activity [GO:0008233 molecular_function] (1); attachment of GPI anchor to protein [GO:0016255 biological_process] (1); GPI-anchor transamidase activity [GO:0003923 molecular_function] (1); GPI-anchor transamidase complex [GO:0042765 cellular_component] (1)	GPI-anchor transamidase [IPR028361] (1); Peptidase C13, legumain [IPR001096] (1)	-	-	P_trifoliata_00635_mRNA_1.1
GF0049941	0	0	1	Aldehyde dehydrogenase (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); oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Aldehyde dehydrogenase, glutamic acid active site [IPR029510] (1); Aldehyde dehydrogenase domain [IPR015590] (1); Aldehyde dehydrogenase, C-terminal [IPR016163] (1); Aldehyde/histidinol dehydrogenase [IPR016161] (1); Aldehyde dehydrogenase N-terminal domain [IPR016162] (1)	-	-	P_trifoliata_00634_mRNA_1.1
GF0049940	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00633_mRNA_7.1
GF0049939	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00633_mRNA_4.1
GF0049938	0	0	1	(+)-delta-cadinene synthase isozyme C2 (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)	Terpene synthase, metal-binding domain [IPR005630] (1); Terpene synthase, N-terminal domain [IPR001906] (1); Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (1); Isoprenoid synthase domain [IPR008949] (1)	-	-	P_trifoliata_00633_mRNA_3.1
GF0049937	0	0	1	(-)-germacrene D 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)	Terpene synthase, metal-binding domain [IPR005630] (1); Isoprenoid synthase domain [IPR008949] (1)	-	-	P_trifoliata_00633_mRNA_2.1
GF0049936	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00633_mRNA_15.1
GF0049935	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00633_mRNA_14.1
GF0049934	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00633_mRNA_12.1
GF0049933	0	0	1	Hypothetical protein (1)	nucleotide binding [GO:0000166 molecular_function] (1)	Nucleotide-binding alpha-beta plait domain [IPR012677] (1); Regulator of nonsense-mediated decay, UPF3 [IPR005120] (1)	-	-	P_trifoliata_00633_mRNA_10.1
GF0049932	0	0	1	Hypothetical protein (1)		LOG family [IPR031100] (1)	-	-	P_trifoliata_00633_mRNA_1.1
GF0049931	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00632_mRNA_1.1
GF0049930	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00631_mRNA_9.1
GF0049929	0	0	1	Putative disease resistance protein RGA3 (1)	ADP binding [GO:0043531 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); NB-ARC [IPR002182] (1)	-	-	P_trifoliata_00631_mRNA_4.1
GF0049928	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00631_mRNA_14.1
GF0049927	0	0	1	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	-	P_trifoliata_00630_mRNA_3.1
GF0049926	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00630_mRNA_1.1
GF0049925	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Tetratricopeptide-like helical domain [IPR011990] (1)	-	-	P_trifoliata_00629_mRNA_15.1
GF0049924	0	0	1	Plasma membrane ATPase (1)	integral component of membrane [GO:0016021 cellular_component] (1); metal ion binding [GO:0046872 molecular_function] (1); nucleotide binding [GO:0000166 molecular_function] (1)	P-type ATPase, cytoplasmic domain N [IPR023299] (1); P-type ATPase, transmembrane domain [IPR023298] (1); P-type ATPase [IPR001757] (1); HAD-like domain [IPR023214] (1); P-type ATPase, A domain [IPR008250] (1)	-	-	P_trifoliata_00628_mRNA_3.1
GF0049923	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00628_mRNA_2.1
GF0049922	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00628_mRNA_1.1
GF0049921	0	0	1	UDP-glycosyltransferase 76F1 (1)	transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	-	-	P_trifoliata_00627_mRNA_9.1
GF0049920	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00627_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***
GF0049919	0	0	1	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)	-	-	P_trifoliata_00627_mRNA_4.1
GF0049918	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00627_mRNA_2.1
GF0049917	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00627_mRNA_1.1
GF0049916	0	0	1	Putative disease resistance protein RGA4 (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00626_mRNA_5.1
GF0049915	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00626_mRNA_4.1
GF0049914	0	0	1	Pectinesterase inhibitor (1)	enzyme inhibitor activity [GO:0004857 molecular_function] (1)	Pectinesterase inhibitor domain [IPR006501] (1)	-	-	P_trifoliata_00626_mRNA_3.1
GF0049913	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00625_mRNA_8.1
GF0049912	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00625_mRNA_6.1
GF0049911	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00625_mRNA_4.1
GF0049910	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00625_mRNA_3.1
GF0049909	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00625_mRNA_2.1
GF0049908	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00625_mRNA_15.1
GF0049907	0	0	1	Hypothetical protein (1)		Ribosomal protein L18e/L15P [IPR021131] (1)	-	-	P_trifoliata_00625_mRNA_12.1
GF0049906	0	0	1	Hypothetical protein (1)		Transposase-associated domain [IPR029480] (1)	-	-	P_trifoliata_00625_mRNA_11.1
GF0049905	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00624_mRNA_9.1
GF0049904	0	0	1	Hypothetical protein (1)	polysaccharide binding [GO:0030247 molecular_function] (1)	Wall-associated receptor kinase, galacturonan-binding domain [IPR025287] (1)	-	-	P_trifoliata_00624_mRNA_8.1
GF0049903	0	0	1	Calmodulin binding protein, putative (1)	calmodulin binding [GO:0005516 molecular_function] (1); response to stress [GO:0006950 biological_process] (1)	CALMODULIN-BINDING PROTEIN60 [IPR012416] (1)	-	-	P_trifoliata_00624_mRNA_7.1
GF0049902	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00624_mRNA_15.1
GF0049901	0	0	1	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); Terpene synthase, metal-binding domain [IPR005630] (1); Terpene synthase, N-terminal domain [IPR001906] (1); Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (1)	-	-	P_trifoliata_00624_mRNA_14.1
GF0049900	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00623_mRNA_7.1
GF0049899	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00623_mRNA_6.1
GF0049898	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00623_mRNA_5.1
GF0049897	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00623_mRNA_4.1
GF0049896	0	0	1	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, conserved site [IPR017972] (1); Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450 [IPR001128] (1)	-	-	P_trifoliata_00623_mRNA_21.1
GF0049895	0	0	1	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)	-	-	P_trifoliata_00623_mRNA_20.1
GF0049894	0	0	1	Cytochrome P450, family 706, subfamily A, polypeptide 6, putative (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); Cytochrome P450, conserved site [IPR017972] (1)	-	-	P_trifoliata_00623_mRNA_18.1
GF0049893	0	0	1	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); iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1)	Cytochrome P450 [IPR001128] (1)	-	-	P_trifoliata_00623_mRNA_17.1
GF0049892	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00623_mRNA_13.1
GF0049891	0	0	1	Cytochrome P450 (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)	-	-	P_trifoliata_00622_mRNA_15.1
GF0049890	0	0	1	Hypothetical protein (1)		Gag-polypeptide of LTR copia-type [IPR029472] (1)	-	-	P_trifoliata_00622_mRNA_12.1
GF0049889	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00622_mRNA_11.1
GF0049888	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	UBX domain [IPR001012] (1); Ubiquitin-related domain [IPR029071] (1)	-	-	P_trifoliata_00622_mRNA_1.1
GF0049887	0	0	1	Hypothetical protein (1)	membrane [GO:0016020 cellular_component] (1)	Bile acid:sodium symporter/arsenical resistance protein Acr3 [IPR002657] (1); Isopenicillin N synthase-like [IPR027443] (1)	-	-	P_trifoliata_00620_mRNA_6.1
GF0049886	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00620_mRNA_2.1
GF0049885	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00620_mRNA_10.1
GF0049884	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00620_mRNA_1.1
GF0049883	0	0	1	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)	-	-	P_trifoliata_00619_mRNA_9.1
GF0049882	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00619_mRNA_19.1
GF0049881	0	0	1	Hypothetical protein (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 domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); S-locus receptor kinase, C-terminal [IPR021820] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Bulb-type lectin domain [IPR001480] (1)	-	-	P_trifoliata_00619_mRNA_15.1
GF0049880	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00619_mRNA_12.1
GF0049879	0	0	1	Glutathione S-transferase tau 7, putative (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)	-	-	P_trifoliata_00618_mRNA_9.1
GF0049878	0	0	1	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); Glutathione S-transferase, C-terminal [IPR004046] (1); Thioredoxin-like fold [IPR012336] (1)	-	-	P_trifoliata_00618_mRNA_6.1
GF0049877	0	0	1	Tau 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, C-terminal-like [IPR010987] (1); Glutathione S-transferase, N-terminal [IPR004045] (1)	-	-	P_trifoliata_00618_mRNA_5.1
GF0049876	0	0	1	Hypothetical protein (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Aspartic peptidase A1 family [IPR001461] (1); Peptidase family A1 domain [IPR033121] (1); Aspartic peptidase domain [IPR021109] (1)	-	-	P_trifoliata_00618_mRNA_3.1
GF0049875	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00618_mRNA_17.1
GF0049874	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00618_mRNA_16.1
GF0049873	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00618_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*
GF0049872	0	0	1	Hypothetical protein (1)	metallocarboxypeptidase activity [GO:0004181 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Peptidase M14, carboxypeptidase A [IPR000834] (1)	-	-	P_trifoliata_00617_mRNA_7.1
GF0049871	0	0	1	Hypothetical protein (1)		DNA-binding pseudobarrel domain [IPR015300] (1)	-	-	P_trifoliata_00617_mRNA_5.1
GF0049870	0	0	1	Hypothetical protein (1)	mitochondrial respiratory chain complex III assembly [GO:0034551 biological_process] (1)	Mitochondrial chaperone BCS1/plant AAA ATPases [IPR027243] (1); AAA-type ATPase, N-terminal domain [IPR025753] (1)	-	-	P_trifoliata_00617_mRNA_1.1
GF0049869	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00616_mRNA_5.1
GF0049868	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00616_mRNA_2.1
GF0049867	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00616_mRNA_10.1
GF0049866	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00616_mRNA_1.1
GF0049865	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00615_mRNA_9.1
GF0049864	0	0	1	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	-	P_trifoliata_00615_mRNA_2.1
GF0049863	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00615_mRNA_18.1
GF0049862	0	0	1	Hypothetical protein (1)		Retroviral aspartyl protease [IPR013242] (1)	-	-	P_trifoliata_00615_mRNA_15.1
GF0049861	0	0	1	Cytochrome P450 82A4 (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, conserved site [IPR017972] (1); Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450 [IPR001128] (1)	-	-	P_trifoliata_00615_mRNA_11.1
GF0049860	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00615_mRNA_10.1
GF0049859	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00614_mRNA_9.1
GF0049858	0	0	1	Disease resistance RPM1-like protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00614_mRNA_3.1
GF0049857	0	0	1	H/ACA ribonucleoprotein complex subunit 2-like protein (1)	nucleolus [GO:0005730 cellular_component] (1); RNA binding [GO:0003723 molecular_function] (1)	H/ACA ribonucleoprotein complex, subunit Nhp2, eukaryote [IPR002415] (1); Ribosomal protein L7Ae/L30e/S12e/Gadd45 [IPR004038] (1); 50S ribosomal protein L30e-like [IPR029064] (1)	-	-	P_trifoliata_00614_mRNA_26.1
GF0049856	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00614_mRNA_17.1
GF0049855	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00614_mRNA_13.1
GF0049854	0	0	1	Hypothetical protein (1)	cellulose biosynthetic process [GO:0030244 biological_process] (1); cellulose synthase (UDP-forming) activity [GO:0016760 molecular_function] (1); membrane [GO:0016020 cellular_component] (1)	Cellulose synthase [IPR005150] (1)	-	-	P_trifoliata_00614_mRNA_11.1
GF0049853	0	0	1	Cellulose synthase-like CSLG, family GT2 (1)	membrane [GO:0016020 cellular_component] (1); cellulose synthase (UDP-forming) activity [GO:0016760 molecular_function] (1); cellulose biosynthetic process [GO:0030244 biological_process] (1)	Nucleotide-diphospho-sugar transferases [IPR029044] (1); Cellulose synthase [IPR005150] (1)	-	-	P_trifoliata_00614_mRNA_10.1
GF0049852	0	0	1	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	-	P_trifoliata_00614_mRNA_1.1
GF0049851	0	0	1	Transcription factor bHLH35 (1)	protein dimerization activity [GO:0046983 molecular_function] (1)	Myc-type, basic helix-loop-helix (bHLH) domain [IPR011598] (1); Isoprenoid synthase domain [IPR008949] (1)	-	-	P_trifoliata_00613_mRNA_4.1
GF0049850	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00613_mRNA_3.1
GF0049849	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00613_mRNA_21.1
GF0049848	0	0	1	Hypothetical protein (1)	metal ion binding [GO:0046872 molecular_function] (1)	Zinc finger, C2H2 [IPR007087] (1)	-	-	P_trifoliata_00613_mRNA_20.1
GF0049847	0	0	1	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)	-	-	P_trifoliata_00613_mRNA_2.1
GF0049846	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00612_mRNA_21.1
GF0049845	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00612_mRNA_20.1
GF0049844	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00612_mRNA_19.1
GF0049843	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00612_mRNA_18.1
GF0049842	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00612_mRNA_16.1
GF0049841	0	0	1	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)	-	-	P_trifoliata_00612_mRNA_13.1
GF0049840	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00612_mRNA_11.1
GF0049839	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00612_mRNA_1.1
GF0049838	0	0	1	Hypothetical protein (1)	microtubule [GO:0005874 cellular_component] (1); structural constituent of cytoskeleton [GO:0005200 molecular_function] (1); GTP binding [GO:0005525 molecular_function] (1); microtubule-based process [GO:0007017 biological_process] (1)	Beta tubulin [IPR002453] (1); Glyoxal oxidase, N-terminal [IPR009880] (1); Tubulin [IPR000217] (1); Tubulin/FtsZ, C-terminal [IPR008280] (1); Tubulin, C-terminal [IPR023123] (1)	-	-	P_trifoliata_00611_mRNA_9.1
GF0049837	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00611_mRNA_3.1
GF0049836	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00611_mRNA_2.1
GF0049835	0	0	1	Strictosidine synthase family protein (1)	biosynthetic process [GO:0009058 biological_process] (1); strictosidine synthase activity [GO:0016844 molecular_function] (1)	Strictosidine synthase [IPR004141] (1); Strictosidine synthase, conserved region [IPR018119] (1); Six-bladed beta-propeller, TolB-like [IPR011042] (1)	-	-	P_trifoliata_00611_mRNA_13.1
GF0049834	0	0	1	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	-	P_trifoliata_00610_mRNA_2.1
GF0049833	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00609_mRNA_8.1
GF0049832	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00609_mRNA_13.1
GF0049831	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00609_mRNA_12.1
GF0049830	0	0	1	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)	-	-	P_trifoliata_00609_mRNA_11.1
GF0049829	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00609_mRNA_10.1
GF0049828	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00609_mRNA_1.1
GF0049827	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00608_mRNA_7.1
GF0049826	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00608_mRNA_15.1
GF0049825	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00608_mRNA_13.1
GF0049824	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00608_mRNA_11.1
GF0049823	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00608_mRNA_10.1
GF0049822	0	0	1	Limonene synthase (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); Terpene synthase, N-terminal domain [IPR001906] (1); Terpene synthase, metal-binding domain [IPR005630] (1); Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (1)	-	-	P_trifoliata_00607_mRNA_9.1
GF0049821	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00607_mRNA_7.1
GF0049820	0	0	1	C2 domain-containing protein / GRAM domain-containing protein isoform 4 (1)	protein binding [GO:0005515 molecular_function] (1)	C2 domain [IPR000008] (1)	-	-	P_trifoliata_00607_mRNA_6.1
GF0049819	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00607_mRNA_4.1
GF0049818	0	0	1	Hypothetical protein (1)	polyamine biosynthetic process [GO:0006596 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1)	PLP-binding barrel [IPR029066] (1); Ornithine decarboxylase [IPR002433] (1); Orn/DAP/Arg decarboxylase 2, N-terminal [IPR022644] (1)	-	-	P_trifoliata_00607_mRNA_2.1
GF0049817	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Kelch-type beta propeller [IPR015915] (1)	-	-	P_trifoliata_00607_mRNA_13.1
GF0049816	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00607_mRNA_1.1
GF0049815	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00606_mRNA_9.1
GF0049814	0	0	1	Hypothetical protein (1)		Chromo domain-like [IPR016197] (1); Chromo domain [IPR023780] (1); LOG family [IPR031100] (1)	-	-	P_trifoliata_00606_mRNA_2.1
GF0049813	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00606_mRNA_14.1
GF0049812	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00606_mRNA_1.1
GF0049811	0	0	1	Mitochondrial ribosomal protein S14 (1)	structural constituent of ribosome [GO:0003735 molecular_function] (1); translation [GO:0006412 biological_process] (1); intracellular [GO:0005622 cellular_component] (1); ribosome [GO:0005840 cellular_component] (1)	Ribosomal protein S14, conserved site [IPR018271] (1); Ribosomal protein S14 [IPR001209] (1)	-	-	P_trifoliata_00605_mRNA_21.1
GF0049810	0	0	1	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	SANT/Myb domain [IPR001005] (1); Homeodomain-like [IPR009057] (1); Myb-like domain [IPR017877] (1)	-	-	P_trifoliata_00605_mRNA_16.1
GF0049809	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00605_mRNA_11.1
GF0049808	0	0	1	Hypothetical protein (1)		Transposase, MuDR, plant [IPR004332] (1)	-	-	P_trifoliata_00604_mRNA_20.1
GF0049807	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00604_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*
GF0049806	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00604_mRNA_18.1
GF0049805	0	0	1	Putative peptidase C48 domain family 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)	-	-	P_trifoliata_00604_mRNA_16.1
GF0049804	0	0	1	Lipid transfer protein (1)		Bifunctional inhibitor/plant lipid transfer protein/seed storage helical domain [IPR016140] (1)	-	-	P_trifoliata_00604_mRNA_12.1
GF0049803	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00603_mRNA_3.1
GF0049802	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00603_mRNA_18.1
GF0049801	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00603_mRNA_16.1
GF0049800	0	0	1	Pumilio-family RNA-binding repeatprotein (1)	binding [GO:0005488 molecular_function] (1); RNA binding [GO:0003723 molecular_function] (1)	Pumilio homology domain [IPR033133] (1); Armadillo-type fold [IPR016024] (1); Armadillo-like helical [IPR011989] (1); Pumilio RNA-binding repeat [IPR001313] (1)	-	-	P_trifoliata_00602_mRNA_6.1
GF0049799	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00602_mRNA_20.1
GF0049798	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00601_mRNA_8.1
GF0049797	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00601_mRNA_6.1
GF0049796	0	0	1	Hypothetical protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	-	P_trifoliata_00601_mRNA_5.1
GF0049795	0	0	1	Serine/threonine-protein kinase fray2 (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)	-	-	P_trifoliata_00601_mRNA_4.1
GF0049794	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00601_mRNA_16.1
GF0049793	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00601_mRNA_14.1
GF0049792	0	0	1	Cellulose synthase-like protein E6 (1)	membrane [GO:0016020 cellular_component] (1); cellulose synthase (UDP-forming) activity [GO:0016760 molecular_function] (1); cellulose biosynthetic process [GO:0030244 biological_process] (1)	Cellulose synthase [IPR005150] (1)	-	-	P_trifoliata_00601_mRNA_13.1
GF0049791	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00601_mRNA_12.1
GF0049790	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00600_mRNA_8.1
GF0049789	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00600_mRNA_4.1
GF0049788	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00600_mRNA_3.1
GF0049787	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); UBX domain [IPR001012] (1); Ubiquitin-related domain [IPR029071] (1); LOG family [IPR031100] (1)	-	-	P_trifoliata_00600_mRNA_12.1
GF0049786	0	0	1	Defensin (1)	defense response [GO:0006952 biological_process] (1)	Knottin, scorpion toxin-like [IPR003614] (1); Gamma Purothionin [IPR008177] (1); Gamma-thionin [IPR008176] (1)	-	-	P_trifoliata_00600_mRNA_10.1
GF0049785	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00599_mRNA_9.1
GF0049784	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00599_mRNA_8.1
GF0049783	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00599_mRNA_7.1
GF0049782	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00599_mRNA_6.1
GF0049781	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00599_mRNA_17.1
GF0049780	0	0	1	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	-	-	P_trifoliata_00599_mRNA_14.1
GF0049779	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00599_mRNA_12.1
GF0049778	0	0	1	Hypothetical protein (1)		DJ-1/PfpI [IPR002818] (1); Class I glutamine amidotransferase-like [IPR029062] (1)	-	-	P_trifoliata_00599_mRNA_10.1
GF0049777	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00598_mRNA_2.1
GF0049776	0	0	1	Hypothetical protein (1)		Protein of unknown function DUF761, plant [IPR008480] (1); Domain of unknown function DUF4408 [IPR025520] (1)	-	-	P_trifoliata_00597_mRNA_8.1
GF0049775	0	0	1	Hypothetical 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)	-	-	P_trifoliata_00597_mRNA_6.1
GF0049774	0	0	1	Disease resistance protein family (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00597_mRNA_4.1
GF0049773	0	0	1	Disease resistance RPS5-like 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)	-	-	P_trifoliata_00597_mRNA_3.1
GF0049772	0	0	1	HUS1 checkpoint protein (1)	checkpoint clamp complex [GO:0030896 cellular_component] (1); DNA damage checkpoint [GO:0000077 biological_process] (1); DNA repair [GO:0006281 biological_process] (1)	Checkpoint protein Hus1/Mec3 [IPR007150] (1)	-	-	P_trifoliata_00597_mRNA_2.1
GF0049771	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00597_mRNA_15.1
GF0049770	0	0	1	Hypothetical protein (1)	DNA repair [GO:0006281 biological_process] (1); DNA damage checkpoint [GO:0000077 biological_process] (1); checkpoint clamp complex [GO:0030896 cellular_component] (1)	Checkpoint protein Hus1/Mec3 [IPR007150] (1)	-	-	P_trifoliata_00597_mRNA_13.1
GF0049769	0	0	1	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); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00597_mRNA_11.1
GF0049768	0	0	1	Disease resistance protein family (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00597_mRNA_1.1
GF0049767	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00596_mRNA_9.1
GF0049766	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00596_mRNA_7.1
GF0049765	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00596_mRNA_6.1
GF0049764	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00596_mRNA_4.1
GF0049763	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00596_mRNA_10.1
GF0049762	0	0	1	Putative aspartic protease (1)	proteolysis [GO:0006508 biological_process] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1)	Xylanase inhibitor, N-terminal [IPR032861] (1); Aspartic peptidase A1 family [IPR001461] (1); Aspartic peptidase domain [IPR021109] (1); Peptidase family A1 domain [IPR033121] (1)	-	-	P_trifoliata_00596_mRNA_1.1
GF0049761	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00595_mRNA_8.1
GF0049760	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00595_mRNA_7.1
GF0049759	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00595_mRNA_6.1
GF0049758	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00595_mRNA_4.1
GF0049757	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00595_mRNA_26.1
GF0049756	0	0	1	Hypothetical protein (1)	peptidyl-prolyl cis-trans isomerase activity [GO:0003755 molecular_function] (1); protein folding [GO:0006457 biological_process] (1)	Cyclophilin-type peptidyl-prolyl cis-trans isomerase [IPR024936] (1)	-	-	P_trifoliata_00595_mRNA_23.1
GF0049755	0	0	1	Hypothetical protein (1)	peptidyl-prolyl cis-trans isomerase activity [GO:0003755 molecular_function] (1); protein folding [GO:0006457 biological_process] (1)	Cyclophilin-like domain [IPR029000] (1); Cyclophilin-type peptidyl-prolyl cis-trans isomerase [IPR024936] (1)	-	-	P_trifoliata_00595_mRNA_22.1
GF0049754	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00595_mRNA_20.1
GF0049753	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00595_mRNA_18.1
GF0049752	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00595_mRNA_16.1
GF0049751	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00595_mRNA_15.1
GF0049750	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00595_mRNA_14.1
GF0049749	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00595_mRNA_13.1
GF0049748	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00595_mRNA_11.1
GF0049747	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00594_mRNA_9.1
GF0049746	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00594_mRNA_6.1
GF0049745	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00594_mRNA_5.1
GF0049744	0	0	1	Hypothetical protein (1)		Transposase, MuDR, plant [IPR004332] (1)	-	-	P_trifoliata_00594_mRNA_2.1
GF0049743	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00594_mRNA_16.1
GF0049742	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00594_mRNA_15.1
GF0049741	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00594_mRNA_13.1
GF0049740	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00594_mRNA_12.1
GF0049739	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00593_mRNA_6.1
GF0049738	0	0	1	Hypothetical protein (1)	magnesium ion binding [GO:0000287 molecular_function] (1)	Ribulose bisphosphate carboxylase, large subunit, C-terminal [IPR000685] (1)	-	-	P_trifoliata_00593_mRNA_22.1
GF0049737	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00593_mRNA_2.1
GF0049736	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00593_mRNA_14.1
GF0049735	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00593_mRNA_11.1
GF0049734	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00592_mRNA_17.1
GF0049733	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00592_mRNA_14.1
GF0049732	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00592_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*
GF0049731	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00592_mRNA_11.1
GF0049730	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00592_mRNA_10.1
GF0049729	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00592_mRNA_1.1
GF0049728	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00591_mRNA_9.1
GF0049727	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00591_mRNA_6.1
GF0049726	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00591_mRNA_4.1
GF0049725	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00591_mRNA_2.1
GF0049724	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00591_mRNA_13.1
GF0049723	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00590_mRNA_8.1
GF0049722	0	0	1	Hypothetical protein (1)		Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	-	-	P_trifoliata_00590_mRNA_6.1
GF0049721	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00590_mRNA_22.1
GF0049720	0	0	1	NAC domain protein (1)	DNA binding [GO:0003677 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	NAC domain [IPR003441] (1)	-	-	P_trifoliata_00590_mRNA_21.1
GF0049719	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00590_mRNA_19.1
GF0049718	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat-containing domain [IPR020683] (1); Ankyrin repeat [IPR002110] (1)	-	-	P_trifoliata_00590_mRNA_17.1
GF0049717	0	0	1	Hypothetical protein (1)		Transmembrane protein 135 [IPR026749] (1)	-	-	P_trifoliata_00590_mRNA_16.1
GF0049716	0	0	1	60S ribosomal protein L6 (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 L2 domain 2 [IPR014722] (1); 60S ribosomal protein L6E [IPR000915] (1); Ribosomal protein L6, N-terminal [IPR005568] (1); Translation protein SH3-like domain [IPR008991] (1)	-	-	P_trifoliata_00590_mRNA_11.1
GF0049715	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00590_mRNA_1.1
GF0049714	0	0	1	Cytochrome P450 (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)	-	-	P_trifoliata_00589_mRNA_7.1
GF0049713	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00589_mRNA_14.1
GF0049712	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00589_mRNA_10.1
GF0049711	0	0	1	Putative sodium-dependent transporter yocS (1)	membrane [GO:0016020 cellular_component] (1)	Bile acid:sodium symporter/arsenical resistance protein Acr3 [IPR002657] (1)	-	-	P_trifoliata_00588_mRNA_2.1
GF0049710	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF1117 [IPR010543] (1)	-	-	P_trifoliata_00588_mRNA_14.1
GF0049709	0	0	1	Chaperone DnaJ (1)	unfolded protein binding [GO:0051082 molecular_function] (1); heat shock protein binding [GO:0031072 molecular_function] (1)	Heat shock protein DnaJ, cysteine-rich domain [IPR001305] (1)	-	-	P_trifoliata_00588_mRNA_13.1
GF0049708	0	0	1	NAD(P)-binding Rossmann-fold superfamily protein isoform 2 (1)		NAD(P)-binding domain [IPR016040] (1)	-	-	P_trifoliata_00588_mRNA_1.1
GF0049707	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00587_mRNA_8.1
GF0049706	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00587_mRNA_3.1
GF0049705	0	0	1	Hypothetical protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	-	P_trifoliata_00587_mRNA_18.1
GF0049704	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00586_mRNA_9.1
GF0049703	0	0	1	Hypothetical protein (1)	catalytic activity [GO:0003824 molecular_function] (1)	Pyridoxal phosphate-dependent transferase, major region, subdomain 2 [IPR015422] (1)	-	-	P_trifoliata_00586_mRNA_8.1
GF0049702	0	0	1	Tyrosine transaminase (1)	cellular amino acid metabolic process [GO:0006520 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1); biosynthetic process [GO:0009058 biological_process] (1); transaminase activity [GO:0008483 molecular_function] (1); pyridoxal phosphate binding [GO:0030170 molecular_function] (1)	Pyridoxal phosphate-dependent transferase, major region, subdomain 1 [IPR015421] (1); Aminotransferase, class I/classII [IPR004839] (1); Pyridoxal phosphate-dependent transferase, major region, subdomain 2 [IPR015422] (1); Tyrosine/nicotianamine aminotransferase [IPR005958] (1); Pyridoxal phosphate-dependent transferase [IPR015424] (1)	-	-	P_trifoliata_00586_mRNA_7.1
GF0049701	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00586_mRNA_5.1
GF0049700	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00586_mRNA_3.1
GF0049699	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00586_mRNA_20.1
GF0049698	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00586_mRNA_2.1
GF0049697	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00586_mRNA_19.1
GF0049696	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00586_mRNA_18.1
GF0049695	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00586_mRNA_17.1
GF0049694	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00586_mRNA_16.1
GF0049693	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1); signal transduction [GO:0007165 biological_process] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1); Leucine-rich repeat 3 [IPR011713] (1)	-	-	P_trifoliata_00586_mRNA_15.1
GF0049692	0	0	1	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)	-	-	P_trifoliata_00586_mRNA_14.1
GF0049691	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00586_mRNA_13.1
GF0049690	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00585_mRNA_4.1
GF0049689	0	0	1	Hypothetical protein (1)		Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (1)	-	-	P_trifoliata_00585_mRNA_2.1
GF0049688	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00585_mRNA_13.1
GF0049687	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00585_mRNA_12.1
GF0049686	0	0	1	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	-	P_trifoliata_00585_mRNA_1.1
GF0049685	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00584_mRNA_4.1
GF0049684	0	0	1	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	-	P_trifoliata_00584_mRNA_2.1
GF0049683	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00583_mRNA_9.1
GF0049682	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00583_mRNA_8.1
GF0049681	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00583_mRNA_6.1
GF0049680	0	0	1	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)	-	-	P_trifoliata_00583_mRNA_16.1
GF0049679	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00583_mRNA_11.1
GF0049678	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00582_mRNA_8.1
GF0049677	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00582_mRNA_7.1
GF0049676	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00582_mRNA_10.1
GF0049675	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00582_mRNA_1.1
GF0049674	0	0	1	Voltage-gated potassium channel beta subunit (1)		NADP-dependent oxidoreductase domain [IPR023210] (1); Aldo/keto reductase/potassium channel subunit beta [IPR001395] (1)	-	-	P_trifoliata_00581_mRNA_8.1
GF0049673	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00581_mRNA_17.1
GF0049672	0	0	1	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	-	-	P_trifoliata_00581_mRNA_16.1
GF0049671	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00581_mRNA_14.1
GF0049670	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00580_mRNA_4.1
GF0049669	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00580_mRNA_20.1
GF0049668	0	0	1	Hypothetical protein (1)		MULE transposase domain [IPR018289] (1)	-	-	P_trifoliata_00580_mRNA_19.1
GF0049667	0	0	1	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	-	P_trifoliata_00580_mRNA_18.1
GF0049666	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00580_mRNA_17.1
GF0049665	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00580_mRNA_16.1
GF0049664	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00580_mRNA_13.1
GF0049663	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00580_mRNA_11.1
GF0049662	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00580_mRNA_10.1
GF0049661	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00579_mRNA_6.1
GF0049660	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00579_mRNA_5.1
GF0049659	0	0	1	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/dual specificity protein kinase, catalytic domain [IPR002290] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	-	-	P_trifoliata_00579_mRNA_3.1
GF0049658	0	0	1	Hypothetical protein (1)		Protein kinase-like domain [IPR011009] (1)	-	-	P_trifoliata_00579_mRNA_2.1
GF0049657	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00579_mRNA_11.1
GF0049656	0	0	1	UGT 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)	-	-	P_trifoliata_00579_mRNA_10.1
GF0049655	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00579_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*
GF0049654	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	-	P_trifoliata_00578_mRNA_8.1
GF0049653	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00578_mRNA_4.1
GF0049652	0	0	1	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	-	P_trifoliata_00578_mRNA_14.1
GF0049651	0	0	1	Hypothetical protein (1)		Alpha/Beta hydrolase fold [IPR029058] (1)	-	-	P_trifoliata_00578_mRNA_10.1
GF0049650	0	0	1	Probable pectinesterase 49 (1)	cell wall modification [GO:0042545 biological_process] (1); cell wall [GO:0005618 cellular_component] (1); pectinesterase activity [GO:0030599 molecular_function] (1)	Pectinesterase, catalytic [IPR000070] (1); Pectin lyase fold [IPR012334] (1); Pectin lyase fold/virulence factor [IPR011050] (1)	-	-	P_trifoliata_00578_mRNA_1.1
GF0049649	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00577_mRNA_26.1
GF0049648	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00577_mRNA_25.1
GF0049647	0	0	1	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	-	-	P_trifoliata_00577_mRNA_24.1
GF0049646	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00577_mRNA_23.1
GF0049645	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00577_mRNA_22.1
GF0049644	0	0	1	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	Homeodomain-like [IPR009057] (1)	-	-	P_trifoliata_00577_mRNA_12.1
GF0049643	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00577_mRNA_1.1
GF0049642	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00576_mRNA_7.1
GF0049641	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00576_mRNA_4.1
GF0049640	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00576_mRNA_14.1
GF0049639	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4219 [IPR025314] (1)	-	-	P_trifoliata_00576_mRNA_13.1
GF0049638	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00575_mRNA_8.1
GF0049637	0	0	1	Hypothetical protein (1)	integral component of membrane [GO:0016021 cellular_component] (1); heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1); electron carrier activity [GO:0009055 molecular_function] (1); cytochrome-c oxidase activity [GO:0004129 molecular_function] (1); aerobic respiration [GO:0009060 biological_process] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Cytochrome c oxidase subunit I [IPR000883] (1); Cytochrome c oxidase, subunit I domain [IPR023616] (1)	-	-	P_trifoliata_00575_mRNA_7.1
GF0049636	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00575_mRNA_6.1
GF0049635	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00575_mRNA_5.1
GF0049634	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00575_mRNA_20.1
GF0049633	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00575_mRNA_18.1
GF0049632	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00575_mRNA_15.1
GF0049631	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00575_mRNA_14.1
GF0049630	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00575_mRNA_1.1
GF0049629	0	0	1	50S ribosomal protein L18, chloroplastic (1)	structural constituent of ribosome [GO:0003735 molecular_function] (1); translation [GO:0006412 biological_process] (1); intracellular [GO:0005622 cellular_component] (1); ribosome [GO:0005840 cellular_component] (1)	Ribosomal protein L18, bacterial-type [IPR004389] (1); Ribosomal protein L18/L5 [IPR005484] (1)	-	-	P_trifoliata_00574_mRNA_8.1
GF0049628	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00574_mRNA_4.1
GF0049627	0	0	1	NAC domain-containing protein 7 (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); DNA binding [GO:0003677 molecular_function] (1)	NAC domain [IPR003441] (1)	-	-	P_trifoliata_00574_mRNA_13.1
GF0049626	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00574_mRNA_12.1
GF0049625	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00574_mRNA_11.1
GF0049624	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00573_mRNA_9.1
GF0049623	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00573_mRNA_2.1
GF0049622	0	0	1	Putative RNA-directed DNA polymerase (1)			-	-	P_trifoliata_00573_mRNA_16.1
GF0049621	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00573_mRNA_13.1
GF0049620	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00572_mRNA_9.1
GF0049619	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00572_mRNA_8.1
GF0049618	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00572_mRNA_6.1
GF0049617	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00572_mRNA_3.1
GF0049616	0	0	1	Hexaprenyldihydroxybenzoate methyltransferase, mitochondrial (1)	2-polyprenyl-6-methoxy-1,4-benzoquinone methyltransferase activity [GO:0008425 molecular_function] (1); ubiquinone biosynthetic process [GO:0006744 biological_process] (1)	Ubiquinone biosynthesis O-methyltransferase [IPR010233] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	-	P_trifoliata_00571_mRNA_6.1
GF0049615	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00570_mRNA_7.1
GF0049614	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00570_mRNA_5.1
GF0049613	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00570_mRNA_3.1
GF0049612	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00570_mRNA_17.1
GF0049611	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00570_mRNA_16.1
GF0049610	0	0	1	Hypothetical protein (1)		Transposase, MuDR, plant [IPR004332] (1)	-	-	P_trifoliata_00570_mRNA_1.1
GF0049609	0	0	1	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1)	-	-	P_trifoliata_00569_mRNA_5.1
GF0049608	0	0	1	Hypothetical protein (1)		Lysosomal cystine transporter [IPR005282] (1)	-	-	P_trifoliata_00569_mRNA_3.1
GF0049607	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00569_mRNA_18.1
GF0049606	0	0	1	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, PMZ-type [IPR006564] (1); Zinc finger, SWIM-type [IPR007527] (1)	-	-	P_trifoliata_00569_mRNA_14.1
GF0049605	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00568_mRNA_5.1
GF0049604	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00568_mRNA_16.1
GF0049603	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00568_mRNA_13.1
GF0049602	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00568_mRNA_11.1
GF0049601	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00567_mRNA_3.1
GF0049600	0	0	1	Hypothetical protein (1)	rRNA processing [GO:0006364 biological_process] (1); methyltransferase activity [GO:0008168 molecular_function] (1); RNA binding [GO:0003723 molecular_function] (1); tRNA processing [GO:0008033 biological_process] (1)	Fibrillarin [IPR000692] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	-	P_trifoliata_00567_mRNA_22.1
GF0049599	0	0	1	Hypothetical protein (1)		P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	-	P_trifoliata_00567_mRNA_2.1
GF0049598	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00567_mRNA_1.1
GF0049597	0	0	1	Ras-related protein RABE1c (1)	small GTPase mediated signal transduction [GO:0007264 biological_process] (1); membrane [GO:0016020 cellular_component] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1); signal transduction [GO:0007165 biological_process] (1); intracellular [GO:0005622 cellular_component] (1); translation [GO:0006412 biological_process] (1); GTP binding [GO:0005525 molecular_function] (1); ribosome [GO:0005840 cellular_component] (1); protein transport [GO:0015031 biological_process] (1)	Small GTPase superfamily, Rab type [IPR003579] (1); Ribosomal protein S8 [IPR000630] (1); Small GTPase superfamily, Rho type [IPR003578] (1); Small GTP-binding protein domain [IPR005225] (1); Small GTPase superfamily [IPR001806] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Small GTPase superfamily, Ras type [IPR020849] (1)	-	-	P_trifoliata_00566_mRNA_15.1
GF0049596	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00566_mRNA_13.1
GF0049595	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00565_mRNA_7.1
GF0049594	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00565_mRNA_6.1
GF0049593	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00565_mRNA_5.1
GF0049592	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00565_mRNA_4.1
GF0049591	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00565_mRNA_3.1
GF0049590	0	0	1	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); calcium ion binding [GO:0005509 molecular_function] (1)	Glycoside hydrolase superfamily [IPR017853] (1); Glycoside hydrolase, family 13 [IPR015902] (1); Glycosyl hydrolase, family 13, all-beta [IPR013780] (1); Glycoside hydrolase, catalytic domain [IPR013781] (1); Alpha-amylase, C-terminal beta-sheet [IPR012850] (1)	-	-	P_trifoliata_00564_mRNA_8.1
GF0049589	0	0	1	Hypothetical protein (1)		MULE transposase domain [IPR018289] (1); Transposase, MuDR, plant [IPR004332] (1)	-	-	P_trifoliata_00564_mRNA_3.1
GF0049588	0	0	1	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Cysteine peptidase, cysteine active site [IPR000169] (1); Peptidase C1A [IPR013128] (1); Cathepsin propeptide inhibitor domain (I29) [IPR013201] (1); Peptidase C1A, papain C-terminal [IPR000668] (1)	-	-	P_trifoliata_00564_mRNA_17.1
GF0049587	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00564_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*
GF0049586	0	0	1	Ferredoxin-dependent glutamate synthase 2 (1)	catalytic activity [GO:0003824 molecular_function] (1); nitrogen compound metabolic process [GO:0006807 biological_process] (1); oxidation-reduction process [GO:0055114 biological_process] (1); glutamate synthase activity [GO:0015930 molecular_function] (1)	Glutamine amidotransferase type 2 domain [IPR017932] (1); Glutamate synthase, central-N [IPR006982] (1); Nucleophile aminohydrolases, N-terminal [IPR029055] (1); Aldolase-type TIM barrel [IPR013785] (1)	-	-	P_trifoliata_00563_mRNA_8.1
GF0049585	0	0	1	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); glutamate synthase activity [GO:0015930 molecular_function] (1); glutamate biosynthetic process [GO:0006537 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1); oxidoreductase activity, acting on the CH-NH2 group of donors [GO:0016638 molecular_function] (1)	Glutamate synthase domain [IPR002932] (1); Aldolase-type TIM barrel [IPR013785] (1)	-	-	P_trifoliata_00563_mRNA_7.1
GF0049584	0	0	1	Hypothetical protein (1)		GAG-pre-integrase domain [IPR025724] (1)	-	-	P_trifoliata_00563_mRNA_4.1
GF0049583	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00563_mRNA_3.1
GF0049582	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00563_mRNA_16.1
GF0049581	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00563_mRNA_15.1
GF0049580	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00562_mRNA_27.1
GF0049579	0	0	1	Hypothetical protein (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Aspartic peptidase, active site [IPR001969] (1)	-	-	P_trifoliata_00562_mRNA_25.1
GF0049578	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00562_mRNA_24.1
GF0049577	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00562_mRNA_22.1
GF0049576	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00562_mRNA_21.1
GF0049575	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00562_mRNA_20.1
GF0049574	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00562_mRNA_19.1
GF0049573	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00562_mRNA_10.1
GF0049572	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00562_mRNA_1.1
GF0049571	0	0	1	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)	-	-	P_trifoliata_00561_mRNA_21.1
GF0049570	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00561_mRNA_20.1
GF0049569	0	0	1	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)	-	-	P_trifoliata_00561_mRNA_18.1
GF0049568	0	0	1	LRR receptor-like kinase 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)	-	-	P_trifoliata_00561_mRNA_16.1
GF0049567	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00561_mRNA_10.1
GF0049566	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00560_mRNA_6.1
GF0049565	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00560_mRNA_5.1
GF0049564	0	0	1	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)	-	-	P_trifoliata_00560_mRNA_4.1
GF0049563	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00560_mRNA_3.1
GF0049562	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00560_mRNA_2.1
GF0049561	0	0	1	Hypothetical protein (1)		Transposase, MuDR, plant [IPR004332] (1)	-	-	P_trifoliata_00559_mRNA_3.1
GF0049560	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00559_mRNA_2.1
GF0049559	0	0	1	Calcium-dependent protein kinase 16 (1)	calcium ion binding [GO:0005509 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-like domain [IPR011009] (1); EF-hand domain pair [IPR011992] (1); Protein kinase domain [IPR000719] (1); EF-Hand 1, calcium-binding site [IPR018247] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase, ATP binding site [IPR017441] (1); EF-hand domain [IPR002048] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1)	-	-	P_trifoliata_00559_mRNA_10.1
GF0049558	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00558_mRNA_6.1
GF0049557	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00558_mRNA_2.1
GF0049556	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00558_mRNA_14.1
GF0049555	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00558_mRNA_1.1
GF0049554	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00557_mRNA_5.1
GF0049553	0	0	1	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 family 17 [IPR000490] (1); Glycoside hydrolase, catalytic domain [IPR013781] (1)	-	-	P_trifoliata_00557_mRNA_4.1
GF0049552	0	0	1	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)	-	-	P_trifoliata_00557_mRNA_19.1
GF0049551	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00557_mRNA_18.1
GF0049550	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00557_mRNA_17.1
GF0049549	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00557_mRNA_16.1
GF0049548	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00557_mRNA_15.1
GF0049547	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00557_mRNA_14.1
GF0049546	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00557_mRNA_12.1
GF0049545	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00557_mRNA_10.1
GF0049544	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00557_mRNA_1.1
GF0049543	0	0	1	Hypothetical protein (1)	polygalacturonate 4-alpha-galacturonosyltransferase activity [GO:0047262 molecular_function] (1)	Plant galacturonosyltransferase GAUT [IPR029993] (1)	-	-	P_trifoliata_00556_mRNA_9.1
GF0049542	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00556_mRNA_7.1
GF0049541	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00556_mRNA_5.1
GF0049540	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00556_mRNA_2.1
GF0049539	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00556_mRNA_1.1
GF0049538	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00555_mRNA_2.1
GF0049537	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00555_mRNA_19.1
GF0049536	0	0	1	Hypothetical protein (1)		Alpha crystallin/Hsp20 domain [IPR002068] (1); HSP20-like chaperone [IPR008978] (1)	-	-	P_trifoliata_00555_mRNA_17.1
GF0049535	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00555_mRNA_1.1
GF0049534	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00554_mRNA_18.1
GF0049533	0	0	1	Hypothetical protein (1)		SGNH hydrolase-type esterase domain [IPR013830] (1)	-	-	P_trifoliata_00554_mRNA_13.1
GF0049532	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00553_mRNA_7.1
GF0049531	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00553_mRNA_5.1
GF0049530	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00553_mRNA_3.1
GF0049529	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00553_mRNA_2.1
GF0049528	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00553_mRNA_17.1
GF0049527	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00553_mRNA_1.1
GF0049526	0	0	1	Egg cell-secreted protein 1.3 (1)		Prolamin-like domain [IPR008502] (1)	-	-	P_trifoliata_00552_mRNA_7.1
GF0049525	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00552_mRNA_4.1
GF0049524	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00552_mRNA_16.1
GF0049523	0	0	1	Hypothetical protein (1)		NADH dehydrogenase [ubiquinone] (complex I), alpha subcomplex, subunit 2 [IPR016464] (1); Thioredoxin-like fold [IPR012336] (1)	-	-	P_trifoliata_00551_mRNA_9.1
GF0049522	0	0	1	Hypothetical protein (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)	50S ribosomal protein L30e-like [IPR029064] (1); Peptide chain release factor eRF1/aRF1 [IPR004403] (1); eRF1 domain 3 [IPR005142] (1)	-	-	P_trifoliata_00551_mRNA_8.1
GF0049521	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00551_mRNA_7.1
GF0049520	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00551_mRNA_2.1
GF0049519	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00551_mRNA_14.1
GF0049518	0	0	1	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, GRF-type [IPR010666] (1)	-	-	P_trifoliata_00551_mRNA_10.1
GF0049517	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00551_mRNA_1.1
GF0049516	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00550_mRNA_9.1
GF0049515	0	0	1	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)	-	-	P_trifoliata_00550_mRNA_7.1
GF0049514	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00550_mRNA_6.1
GF0049513	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00550_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*
GF0049512	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00550_mRNA_11.1
GF0049511	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00549_mRNA_9.1
GF0049510	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00549_mRNA_8.1
GF0049509	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00549_mRNA_11.1
GF0049508	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00549_mRNA_10.1
GF0049507	0	0	1	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); 3-Oxoacyl-[acyl-carrier-protein (ACP)] synthase III, C-terminal [IPR013747] (1); FAE1/Type III polyketide synthase-like protein [IPR013601] (1)	-	-	P_trifoliata_00548_mRNA_17.1
GF0049506	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00548_mRNA_16.1
GF0049505	0	0	1	37 kDa inner envelope membrane protein, chloroplastic (1)	metabolic process [GO:0008152 biological_process] (1); methyltransferase activity [GO:0008168 molecular_function] (1); methylation [GO:0032259 biological_process] (1)	Methyltransferase type 11 [IPR013216] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); SAM-binding methyltransferase MPBQ/MBSQ [IPR031164] (1)	-	-	P_trifoliata_00548_mRNA_1.1
GF0049504	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00547_mRNA_9.1
GF0049503	0	0	1	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)	-	-	P_trifoliata_00547_mRNA_7.1
GF0049502	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00547_mRNA_12.1
GF0049501	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00547_mRNA_1.1
GF0049500	0	0	1	Hypothetical protein (1)	phospholipid biosynthetic process [GO:0008654 biological_process] (1); phosphotransferase activity, for other substituted phosphate groups [GO:0016780 molecular_function] (1); membrane [GO:0016020 cellular_component] (1)	CDP-alcohol phosphatidyltransferase [IPR000462] (1)	-	-	P_trifoliata_00546_mRNA_7.1
GF0049499	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00546_mRNA_3.1
GF0049498	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00546_mRNA_2.1
GF0049497	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00546_mRNA_17.1
GF0049496	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00546_mRNA_10.1
GF0049495	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00546_mRNA_1.1
GF0049494	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00545_mRNA_8.1
GF0049493	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00545_mRNA_19.1
GF0049492	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00545_mRNA_13.1
GF0049491	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00545_mRNA_12.1
GF0049490	0	0	1	Hypothetical protein (1)		Protein of unknown function DUF707 [IPR007877] (1)	-	-	P_trifoliata_00545_mRNA_11.1
GF0049489	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00545_mRNA_10.1
GF0049488	0	0	1	Hypothetical protein (1)	metabolic process [GO:0008152 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1); triose-phosphate isomerase activity [GO:0004807 molecular_function] (1)	Triosephosphate isomerase [IPR000652] (1); Aldolase-type TIM barrel [IPR013785] (1)	-	-	P_trifoliata_00544_mRNA_9.1
GF0049487	0	0	1	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Transposon, En/Spm-like [IPR004242] (1); Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	-	P_trifoliata_00544_mRNA_8.1
GF0049486	0	0	1	Disease resistance protein (TIR-NBS-LRR class) (1)	protein binding [GO:0005515 molecular_function] (1); ADP binding [GO:0043531 molecular_function] (1); signal transduction [GO:0007165 biological_process] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	-	P_trifoliata_00544_mRNA_7.1
GF0049485	0	0	1	SH3 domain-containing protein 2 (1)	protein binding [GO:0005515 molecular_function] (1)	SH3 domain [IPR001452] (1)	-	-	P_trifoliata_00544_mRNA_4.1
GF0049484	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	-	P_trifoliata_00543_mRNA_21.1
GF0049483	0	0	1	Cyclin-dependent serine/threonine protein kinase 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)	Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1); Protein kinase, ATP binding site [IPR017441] (1)	-	-	P_trifoliata_00543_mRNA_14.1
GF0049482	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00542_mRNA_3.1
GF0049481	0	0	1	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-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1)	-	-	P_trifoliata_00542_mRNA_14.1
GF0049480	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00542_mRNA_10.1
GF0049479	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00542_mRNA_1.1
GF0049478	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00541_mRNA_9.1
GF0049477	0	0	1	Thioredoxin-dependent peroxidase 2 (1)	oxidoreductase activity [GO:0016491 molecular_function] (1)	Peptidase M20, dimerisation domain [IPR011650] (1); Thioredoxin-like fold [IPR012336] (1); Redoxin [IPR013740] (1)	-	-	P_trifoliata_00541_mRNA_7.1
GF0049476	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	DNA/RNA-binding protein Alba-like [IPR002775] (1)	-	-	P_trifoliata_00541_mRNA_6.1
GF0049475	0	0	1	Ankyrin repeat plant-like protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat-containing domain [IPR020683] (1); PGG domain [IPR026961] (1); Ankyrin repeat [IPR002110] (1)	-	-	P_trifoliata_00541_mRNA_4.1
GF0049474	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	PGG domain [IPR026961] (1); Ankyrin repeat-containing domain [IPR020683] (1); Domain of unknown function DUF1985 [IPR015410] (1); Ankyrin repeat [IPR002110] (1)	-	-	P_trifoliata_00541_mRNA_2.1
GF0049473	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat-containing domain [IPR020683] (1); Ankyrin repeat [IPR002110] (1)	-	-	P_trifoliata_00541_mRNA_11.1
GF0049472	0	0	1	Hypothetical protein (1)		Transposon, En/Spm-like [IPR004242] (1)	-	-	P_trifoliata_00540_mRNA_7.1
GF0049471	0	0	1	Shikimate kinase (1)		Shikimate kinase/gluconokinase [IPR031322] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	-	P_trifoliata_00540_mRNA_6.1
GF0049470	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00540_mRNA_3.1
GF0049469	0	0	1	Hypothetical protein (1)		Chromo domain-like [IPR016197] (1); Chromo domain [IPR023780] (1)	-	-	P_trifoliata_00540_mRNA_11.1
GF0049468	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00539_mRNA_9.1
GF0049467	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00539_mRNA_2.1
GF0049466	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00539_mRNA_12.1
GF0049465	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00539_mRNA_1.1
GF0049464	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00538_mRNA_7.1
GF0049463	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00538_mRNA_20.1
GF0049462	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00538_mRNA_2.1
GF0049461	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00538_mRNA_19.1
GF0049460	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00538_mRNA_18.1
GF0049459	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00538_mRNA_1.1
GF0049458	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00537_mRNA_8.1
GF0049457	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00537_mRNA_5.1
GF0049456	0	0	1	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)	-	-	P_trifoliata_00537_mRNA_3.1
GF0049455	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00537_mRNA_20.1
GF0049454	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00537_mRNA_14.1
GF0049453	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00537_mRNA_13.1
GF0049452	0	0	1	Hypothetical protein (1)		Transposon, En/Spm-like [IPR004242] (1)	-	-	P_trifoliata_00537_mRNA_12.1
GF0049451	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00537_mRNA_11.1
GF0049450	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00537_mRNA_10.1
GF0049449	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00536_mRNA_8.1
GF0049448	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00536_mRNA_6.1
GF0049447	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00536_mRNA_10.1
GF0049446	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00536_mRNA_1.1
GF0049445	0	0	1	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)	-	-	P_trifoliata_00535_mRNA_9.1
GF0049444	0	0	1	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)	-	-	P_trifoliata_00535_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*
GF0049443	0	0	1	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); Glutathione S-transferase, C-terminal [IPR004046] (1)	-	-	P_trifoliata_00535_mRNA_4.1
GF0049442	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00535_mRNA_23.1
GF0049441	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00534_mRNA_6.1
GF0049440	0	0	1	Transcription factor bHLH61 (1)	protein dimerization activity [GO:0046983 molecular_function] (1)	Myc-type, basic helix-loop-helix (bHLH) domain [IPR011598] (1)	-	-	P_trifoliata_00534_mRNA_29.1
GF0049439	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	-	P_trifoliata_00533_mRNA_2.1
GF0049438	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00533_mRNA_16.1
GF0049437	0	0	1	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	-	-	P_trifoliata_00533_mRNA_15.1
GF0049436	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00533_mRNA_14.1
GF0049435	0	0	1	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	DNA-binding pseudobarrel domain [IPR015300] (1); B3 DNA binding domain [IPR003340] (1)	-	-	P_trifoliata_00533_mRNA_10.1
GF0049434	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00532_mRNA_6.1
GF0049433	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00532_mRNA_5.1
GF0049432	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00532_mRNA_19.1
GF0049431	0	0	1	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)	-	-	P_trifoliata_00532_mRNA_15.1
GF0049430	0	0	1	Pentatricopeptide repeat-containing protein At2g37320 (1)		Pentatricopeptide repeat [IPR002885] (1)	-	-	P_trifoliata_00532_mRNA_1.1
GF0049429	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00531_mRNA_6.1
GF0049428	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00531_mRNA_4.1
GF0049427	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00531_mRNA_25.1
GF0049426	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00531_mRNA_21.1
GF0049425	0	0	1	Hypothetical protein (1)		Isopenicillin N synthase-like [IPR027443] (1); Non-haem dioxygenase N-terminal domain [IPR026992] (1)	-	-	P_trifoliata_00531_mRNA_20.1
GF0049424	0	0	1	SENESCENCE-RELATED GENE 1 family protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1)	Oxoglutarate/iron-dependent dioxygenase [IPR005123] (1); Non-haem dioxygenase N-terminal domain [IPR026992] (1); Isopenicillin N synthase-like [IPR027443] (1)	-	-	P_trifoliata_00531_mRNA_19.1
GF0049423	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00531_mRNA_17.1
GF0049422	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00531_mRNA_13.1
GF0049421	0	0	1	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	Transcription factor, MADS-box [IPR002100] (1)	-	-	P_trifoliata_00531_mRNA_11.1
GF0049420	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00531_mRNA_1.1
GF0049419	0	0	1	Phytoene desaturase (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); carotene 7,8-desaturase activity [GO:0016719 molecular_function] (1); carotenoid biosynthetic process [GO:0016117 biological_process] (1)	Zeta-carotene desaturase [IPR014103] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Amine oxidase [IPR002937] (1); FAD/NAD(P)-binding domain [IPR023753] (1)	-	-	P_trifoliata_00530_mRNA_6.1
GF0049418	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1); Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	-	P_trifoliata_00530_mRNA_17.1
GF0049417	0	0	1	DUF674 family protein (1)		Protein of unknown function DUF674 [IPR007750] (1)	-	-	P_trifoliata_00529_mRNA_16.1
GF0049416	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00528_mRNA_6.1
GF0049415	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00528_mRNA_2.1
GF0049414	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00528_mRNA_12.1
GF0049413	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00528_mRNA_11.1
GF0049412	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00528_mRNA_10.1
GF0049411	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00527_mRNA_7.1
GF0049410	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00527_mRNA_5.1
GF0049409	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00527_mRNA_3.1
GF0049408	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00527_mRNA_19.1
GF0049407	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00527_mRNA_18.1
GF0049406	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00527_mRNA_17.1
GF0049405	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00527_mRNA_15.1
GF0049404	0	0	1	Hypothetical protein (1)	diacylglycerol O-acyltransferase activity [GO:0004144 molecular_function] (1)	O-acyltransferase WSD1, C-terminal [IPR009721] (1)	-	-	P_trifoliata_00527_mRNA_12.1
GF0049403	0	0	1	Calmodulin (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)	-	-	P_trifoliata_00527_mRNA_1.1
GF0049402	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00526_mRNA_5.1
GF0049401	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00526_mRNA_4.1
GF0049400	0	0	1	Terpene cyclase/mutase family member (1)		Squalene cyclase, C-terminal [IPR032696] (1); Squalene cyclase, N-terminal [IPR032697] (1); Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (1)	-	-	P_trifoliata_00526_mRNA_2.1
GF0049399	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00526_mRNA_1.1
GF0049398	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00525_mRNA_7.1
GF0049397	0	0	1	MADS-box transcription factor 50 (1)	DNA binding [GO:0003677 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	Transcription factor, MADS-box [IPR002100] (1)	-	-	P_trifoliata_00525_mRNA_18.1
GF0049396	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00525_mRNA_13.1
GF0049395	0	0	1	Cc-nbs-lrr resistance protein, putative isoform 1 (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00525_mRNA_1.1
GF0049394	0	0	1	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); Reverse transcriptase domain [IPR000477] (1); Protein kinase-like domain [IPR011009] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1)	-	-	P_trifoliata_00524_mRNA_27.1
GF0049393	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00524_mRNA_24.1
GF0049392	0	0	1	Cytochrome P450 76C1 (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)	-	-	P_trifoliata_00524_mRNA_20.1
GF0049391	0	0	1	Hypothetical protein (1)	structural constituent of ribosome [GO:0003735 molecular_function] (1); translation [GO:0006412 biological_process] (1); intracellular [GO:0005622 cellular_component] (1); ribosome [GO:0005840 cellular_component] (1)	Ribosomal protein S8e [IPR001047] (1); Ribosomal protein S8e/ribosomal biogenesis NSA2 [IPR022309] (1)	-	-	P_trifoliata_00524_mRNA_1.1
GF0049390	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00523_mRNA_7.1
GF0049389	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00523_mRNA_4.1
GF0049388	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00523_mRNA_25.1
GF0049387	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00523_mRNA_24.1
GF0049386	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00523_mRNA_20.1
GF0049385	0	0	1	Disease resistance protein (1)			-	-	P_trifoliata_00523_mRNA_2.1
GF0049384	0	0	1	Hypothetical protein (1)	checkpoint clamp complex [GO:0030896 cellular_component] (1); DNA damage checkpoint [GO:0000077 biological_process] (1); DNA repair [GO:0006281 biological_process] (1)	Checkpoint protein Hus1/Mec3 [IPR007150] (1)	-	-	P_trifoliata_00523_mRNA_15.1
GF0049383	0	0	1	Hypothetical protein (1)	DNA repair [GO:0006281 biological_process] (1); checkpoint clamp complex [GO:0030896 cellular_component] (1); DNA damage checkpoint [GO:0000077 biological_process] (1)	Checkpoint protein Hus1/Mec3 [IPR007150] (1)	-	-	P_trifoliata_00523_mRNA_11.1
GF0049382	0	0	1	Hypothetical 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)	-	-	P_trifoliata_00523_mRNA_10.1
GF0049381	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00522_mRNA_9.1
GF0049380	0	0	1	Hypothetical protein (1)	transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1)	Glycosyl transferase, family 28, C-terminal [IPR007235] (1)	-	-	P_trifoliata_00522_mRNA_16.1
GF0049379	0	0	1	Alpha/beta fold hydrolase (1)		Alpha/Beta hydrolase fold [IPR029058] (1)	-	-	P_trifoliata_00522_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*
GF0049378	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00522_mRNA_14.1
GF0049377	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00522_mRNA_13.1
GF0049376	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00522_mRNA_11.1
GF0049375	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00522_mRNA_1.1
GF0049374	0	0	1	2-oxoacid dehydrogenases acyltransferase (1)	metabolic process [GO:0008152 biological_process] (1); transferase activity, transferring acyl groups [GO:0016746 molecular_function] (1)	2-oxoacid dehydrogenase acyltransferase, catalytic domain [IPR001078] (1); Chloramphenicol acetyltransferase-like domain [IPR023213] (1)	-	-	P_trifoliata_00521_mRNA_9.1
GF0049373	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00521_mRNA_8.1
GF0049372	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00521_mRNA_6.1
GF0049371	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00521_mRNA_5.1
GF0049370	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00521_mRNA_4.1
GF0049369	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00521_mRNA_3.1
GF0049368	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00521_mRNA_16.1
GF0049367	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00521_mRNA_14.1
GF0049366	0	0	1	Mavicyanin (1)	electron carrier activity [GO:0009055 molecular_function] (1)	Cupredoxin [IPR008972] (1); Phytocyanin domain [IPR003245] (1)	-	-	P_trifoliata_00521_mRNA_12.1
GF0049365	0	0	1	Hypothetical protein (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Aspartic peptidase A1 family [IPR001461] (1); Xylanase inhibitor, C-terminal [IPR032799] (1); Aspartic peptidase, active site [IPR001969] (1); Aspartic peptidase domain [IPR021109] (1)	-	-	P_trifoliata_00521_mRNA_11.1
GF0049364	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00519_mRNA_8.1
GF0049363	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00519_mRNA_5.1
GF0049362	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00519_mRNA_4.1
GF0049361	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00519_mRNA_3.1
GF0049360	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00519_mRNA_19.1
GF0049359	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00519_mRNA_18.1
GF0049358	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00519_mRNA_11.1
GF0049357	0	0	1	CDNA clone:J023027G01, full insert sequence (1)		Rossmann-like alpha/beta/alpha sandwich fold [IPR014729] (1); Transposase, MuDR, plant [IPR004332] (1); tRNA synthetases class I, catalytic domain [IPR032678] (1); Cysteinyl-tRNA synthetase/mycothiol ligase [IPR024909] (1)	-	-	P_trifoliata_00518_mRNA_3.1
GF0049356	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00518_mRNA_2.1
GF0049355	0	0	1	AtpA (1)			-	-	P_trifoliata_00518_mRNA_19.1
GF0049354	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00518_mRNA_15.1
GF0049353	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00516_mRNA_9.1
GF0049352	0	0	1	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); Frigida-like [IPR012474] (1)	-	-	P_trifoliata_00516_mRNA_19.1
GF0049351	0	0	1	DUF4283 domain protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	-	P_trifoliata_00516_mRNA_14.1
GF0049350	0	0	1	Ribonuclease H-like superfamily protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	-	P_trifoliata_00516_mRNA_13.1
GF0049349	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00515_mRNA_9.1
GF0049348	0	0	1	Ribonuclease H (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)	-	-	P_trifoliata_00515_mRNA_8.1
GF0049347	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00515_mRNA_7.1
GF0049346	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00515_mRNA_4.1
GF0049345	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00514_mRNA_3.1
GF0049344	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00514_mRNA_2.1
GF0049343	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00514_mRNA_1.1
GF0049342	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00513_mRNA_6.1
GF0049341	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00513_mRNA_22.1
GF0049340	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00513_mRNA_21.1
GF0049339	0	0	1	Transposon protein, putative, unclassified, expressed (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	MULE transposase domain [IPR018289] (1); FHY3/FAR1 family [IPR031052] (1)	-	-	P_trifoliata_00513_mRNA_20.1
GF0049338	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00513_mRNA_19.1
GF0049337	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00513_mRNA_1.1
GF0049336	0	0	1	Hypothetical protein (1)		Protein of unknown function DUF616 [IPR006852] (1)	-	-	P_trifoliata_00512_mRNA_8.1
GF0049335	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00512_mRNA_24.1
GF0049334	0	0	1	Hypothetical protein (1)		Glutathione S-transferase, C-terminal [IPR004046] (1); Glutathione S-transferase, C-terminal-like [IPR010987] (1)	-	-	P_trifoliata_00512_mRNA_22.1
GF0049333	0	0	1	Glutathione transferase (1)	protein binding [GO:0005515 molecular_function] (1)	Thioredoxin-like fold [IPR012336] (1); Glutathione S-transferase, N-terminal [IPR004045] (1); Glutathione S-transferase, C-terminal-like [IPR010987] (1)	-	-	P_trifoliata_00512_mRNA_21.1
GF0049332	0	0	1	Glutathione transferase (1)	protein binding [GO:0005515 molecular_function] (1)	Thioredoxin-like fold [IPR012336] (1); Glutathione S-transferase, N-terminal [IPR004045] (1); Glutathione S-transferase, C-terminal-like [IPR010987] (1)	-	-	P_trifoliata_00512_mRNA_20.1
GF0049331	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00511_mRNA_7.1
GF0049330	0	0	1	Hypothetical protein (1)	catalytic activity [GO:0003824 molecular_function] (1); transaminase activity [GO:0008483 molecular_function] (1); pyridoxal phosphate binding [GO:0030170 molecular_function] (1)	Pyridoxal phosphate-dependent transferase [IPR015424] (1); Aminotransferase class-III [IPR005814] (1); Pyridoxal phosphate-dependent transferase, major region, subdomain 2 [IPR015422] (1)	-	-	P_trifoliata_00511_mRNA_5.1
GF0049329	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00511_mRNA_4.1
GF0049328	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00511_mRNA_2.1
GF0049327	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00510_mRNA_8.1
GF0049326	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00509_mRNA_9.1
GF0049325	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00509_mRNA_7.1
GF0049324	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00509_mRNA_6.1
GF0049323	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00509_mRNA_5.1
GF0049322	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00509_mRNA_4.1
GF0049321	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	-	P_trifoliata_00509_mRNA_3.1
GF0049320	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00509_mRNA_2.1
GF0049319	0	0	1	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)	-	-	P_trifoliata_00509_mRNA_17.1
GF0049318	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00509_mRNA_11.1
GF0049317	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00508_mRNA_8.1
GF0049316	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00508_mRNA_5.1
GF0049315	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00508_mRNA_4.1
GF0049314	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00508_mRNA_14.1
GF0049313	0	0	1	Hypothetical protein (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Aspartic peptidase, active site [IPR001969] (1)	-	-	P_trifoliata_00508_mRNA_13.1
GF0049312	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00508_mRNA_12.1
GF0049311	0	0	1	Hypothetical protein (1)		Thaumatin [IPR001938] (1)	-	-	P_trifoliata_00507_mRNA_4.1
GF0049310	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00507_mRNA_3.1
GF0049309	0	0	1	Hypothetical protein (1)	RNA binding [GO:0003723 molecular_function] (1)	YTH domain [IPR007275] (1)	-	-	P_trifoliata_00507_mRNA_21.1
GF0049308	0	0	1	GATA transcription factor 9 (1)			-	-	P_trifoliata_00507_mRNA_14.1
GF0049307	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00507_mRNA_1.1
GF0049306	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00505_mRNA_13.1
GF0049305	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00505_mRNA_1.1
GF0049304	0	0	1	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	-	P_trifoliata_00504_mRNA_9.1
GF0049303	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00504_mRNA_8.1
GF0049302	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00504_mRNA_7.1
GF0049301	0	0	1	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)	-	-	P_trifoliata_00504_mRNA_6.1
GF0049300	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00504_mRNA_4.1
GF0049299	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00504_mRNA_3.1
GF0049298	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00504_mRNA_18.1
GF0049297	0	0	1	Hypothetical protein (1)		Probable transposase, Ptta/En/Spm, plant [IPR004252] (1)	-	-	P_trifoliata_00504_mRNA_17.1
GF0049296	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00504_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*
GF0049295	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00504_mRNA_10.1
GF0049294	0	0	1	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	-	P_trifoliata_00504_mRNA_1.1
GF0049293	0	0	1	Gag protease polyprotein (1)		Retroviral aspartyl protease [IPR013242] (1); Retrotransposon gag domain [IPR005162] (1)	-	-	P_trifoliata_00503_mRNA_9.1
GF0049292	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00503_mRNA_6.1
GF0049291	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00503_mRNA_5.1
GF0049290	0	0	1	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)	-	-	P_trifoliata_00503_mRNA_12.1
GF0049289	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00503_mRNA_11.1
GF0049288	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00503_mRNA_10.1
GF0049287	0	0	1	50S ribosomal protein L1 (1)	RNA binding [GO:0003723 molecular_function] (1)	Ribosomal protein L1-like [IPR023674] (1); Ribosomal protein L1, 3-layer alpha/beta-sandwich [IPR016095] (1); Ribosomal protein L1, 2-layer alpha/beta-sandwich [IPR016094] (1); Ribosomal protein L1/ribosomal biogenesis protein [IPR028364] (1)	-	-	P_trifoliata_00502_mRNA_33.1
GF0049286	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00502_mRNA_27.1
GF0049285	0	0	1	Selenoprotein K (1)		Selenoprotein SelK/SelG [IPR024491] (1)	-	-	P_trifoliata_00502_mRNA_13.1
GF0049284	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00501_mRNA_4.1
GF0049283	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00501_mRNA_27.1
GF0049282	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00501_mRNA_26.1
GF0049281	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00501_mRNA_1.1
GF0049280	0	0	1	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 L34Ae [IPR008195] (1); Protein of unknown function DUF1666 [IPR012870] (1)	-	-	P_trifoliata_00500_mRNA_4.1
GF0049279	0	0	1	Receptor-like kinase plant (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, ATP binding site [IPR017441] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	-	-	P_trifoliata_00500_mRNA_20.1
GF0049278	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00499_mRNA_9.1
GF0049277	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00499_mRNA_7.1
GF0049276	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00499_mRNA_5.1
GF0049275	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00499_mRNA_4.1
GF0049274	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00499_mRNA_3.1
GF0049273	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00499_mRNA_2.1
GF0049272	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00499_mRNA_11.1
GF0049271	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00499_mRNA_10.1
GF0049270	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00498_mRNA_7.1
GF0049269	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00498_mRNA_6.1
GF0049268	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00498_mRNA_5.1
GF0049267	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00498_mRNA_4.1
GF0049266	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00498_mRNA_18.1
GF0049265	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00498_mRNA_14.1
GF0049264	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00498_mRNA_11.1
GF0049263	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00498_mRNA_10.1
GF0049262	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00497_mRNA_9.1
GF0049261	0	0	1	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	-	-	P_trifoliata_00497_mRNA_3.1
GF0049260	0	0	1	Hypothetical protein (1)		Gag-polypeptide of LTR copia-type [IPR029472] (1)	-	-	P_trifoliata_00497_mRNA_2.1
GF0049259	0	0	1	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	-	P_trifoliata_00497_mRNA_16.1
GF0049258	0	0	1	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)	-	-	P_trifoliata_00497_mRNA_14.1
GF0049257	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00497_mRNA_1.1
GF0049256	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00496_mRNA_8.1
GF0049255	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00496_mRNA_5.1
GF0049254	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00496_mRNA_4.1
GF0049253	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00496_mRNA_18.1
GF0049252	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00496_mRNA_17.1
GF0049251	0	0	1	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	-	P_trifoliata_00496_mRNA_16.1
GF0049250	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00496_mRNA_15.1
GF0049249	0	0	1	Leucine-rich repeat, typical subtype (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00496_mRNA_13.1
GF0049248	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00496_mRNA_12.1
GF0049247	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00496_mRNA_10.1
GF0049246	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00495_mRNA_5.1
GF0049245	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	-	P_trifoliata_00495_mRNA_16.1
GF0049244	0	0	1	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); ATPase, AAA-type, core [IPR003959] (1); AAA+ ATPase domain [IPR003593] (1)	-	-	P_trifoliata_00494_mRNA_6.1
GF0049243	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00494_mRNA_5.1
GF0049242	0	0	1	Hypothetical protein (1)		Amino acid transporter, transmembrane domain [IPR013057] (1); FAR1 DNA binding domain [IPR004330] (1)	-	-	P_trifoliata_00494_mRNA_24.1
GF0049241	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Sec63 domain [IPR004179] (1); C2 domain [IPR000008] (1); Immunoglobulin E-set [IPR014756] (1)	-	-	P_trifoliata_00494_mRNA_2.1
GF0049240	0	0	1	Uridine diphosphate glycosyltransferase 74E2, putative isoform 1 (1)	metabolic process [GO:0008152 biological_process] (1); transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	-	-	P_trifoliata_00494_mRNA_15.1
GF0049239	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00494_mRNA_1.1
GF0049238	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00493_mRNA_9.1
GF0049237	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00493_mRNA_8.1
GF0049236	0	0	1	Hypothetical leucine rich repeat 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)	-	-	P_trifoliata_00493_mRNA_3.1
GF0049235	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00493_mRNA_2.1
GF0049234	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00493_mRNA_17.1
GF0049233	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00493_mRNA_16.1
GF0049232	0	0	1	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	Zinc finger, BED-type [IPR003656] (1)	-	-	P_trifoliata_00493_mRNA_12.1
GF0049231	0	0	1	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	-	P_trifoliata_00492_mRNA_4.1
GF0049230	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00492_mRNA_20.1
GF0049229	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00492_mRNA_18.1
GF0049228	0	0	1	Mutator-like transposase (1)		Transposase, MuDR, plant [IPR004332] (1); MULE transposase domain [IPR018289] (1)	-	-	P_trifoliata_00492_mRNA_17.1
GF0049227	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00492_mRNA_16.1
GF0049226	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00492_mRNA_1.1
GF0049225	0	0	1	Lipid phosphate phosphatase-like protein (1)		Lipid phosphate phosphatase, plant [IPR028681] (1); Phosphatidic acid phosphatase type 2/haloperoxidase [IPR000326] (1)	-	-	P_trifoliata_00491_mRNA_24.1
GF0049224	0	0	1	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1)	Myc-type, basic helix-loop-helix (bHLH) domain [IPR011598] (1)	-	-	P_trifoliata_00491_mRNA_15.1
GF0049223	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00491_mRNA_14.1
GF0049222	0	0	1	Retrotransposon protein, putative, Ty1-copia subclass (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	GAG-pre-integrase domain [IPR025724] (1); Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00490_mRNA_6.1
GF0049221	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00490_mRNA_4.1
GF0049220	0	0	1	General transcription factor-like zinc finger protein, putative (1)			-	-	P_trifoliata_00490_mRNA_3.1
GF0049219	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00490_mRNA_21.1
GF0049218	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00490_mRNA_20.1

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*
GF0049217	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4371 [IPR025398] (1)	-	-	P_trifoliata_00490_mRNA_18.1
GF0049216	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00490_mRNA_17.1
GF0049215	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00490_mRNA_14.1
GF0049214	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00490_mRNA_11.1
GF0049213	0	0	1	WD repeat domain phosphoinositide-interacting 3 (1)	protein binding [GO:0005515 molecular_function] (1)	WD40-repeat-containing domain [IPR017986] (1); WD40/YVTN repeat-like-containing domain [IPR015943] (1)	-	-	P_trifoliata_00489_mRNA_20.1
GF0049212	0	0	1	60S ribosomal protein L10 (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 L10e/L16 [IPR016180] (1); Ribosomal protein L10e, conserved site [IPR018255] (1)	-	-	P_trifoliata_00489_mRNA_16.1
GF0049211	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00489_mRNA_13.1
GF0049210	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00489_mRNA_12.1
GF0049209	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00489_mRNA_1.1
GF0049208	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00488_mRNA_9.1
GF0049207	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00488_mRNA_8.1
GF0049206	0	0	1	Carbon catabolite repressor-like protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	-	P_trifoliata_00488_mRNA_4.1
GF0049205	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00488_mRNA_27.1
GF0049204	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00488_mRNA_26.1
GF0049203	0	0	1	LRR receptor-like serine/threonine-protein kinase GSO1 (1)	polyamine binding [GO:0019808 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1); periplasmic space [GO:0042597 cellular_component] (1); polyamine transport [GO:0015846 biological_process] (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); Bacterial periplasmic spermidine/putrescine-binding protein [IPR001188] (1)	-	-	P_trifoliata_00488_mRNA_24.1
GF0049202	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00488_mRNA_20.1
GF0049201	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00488_mRNA_2.1
GF0049200	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00487_mRNA_12.1
GF0049199	0	0	1	Hypothetical protein (1)		Iron hydrogenase, large subunit, C-terminal [IPR004108] (1); Iron hydrogenase [IPR009016] (1)	-	-	P_trifoliata_00487_mRNA_10.1
GF0049198	0	0	1	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)	-	-	P_trifoliata_00487_mRNA_1.1
GF0049197	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00486_mRNA_9.1
GF0049196	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF632 [IPR006867] (1)	-	-	P_trifoliata_00486_mRNA_8.1
GF0049195	0	0	1	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, PMZ-type [IPR006564] (1); Zinc finger, SWIM-type [IPR007527] (1)	-	-	P_trifoliata_00486_mRNA_7.1
GF0049194	0	0	1	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)	-	-	P_trifoliata_00486_mRNA_5.1
GF0049193	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00486_mRNA_3.1
GF0049192	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00486_mRNA_24.1
GF0049191	0	0	1	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)	-	-	P_trifoliata_00486_mRNA_19.1
GF0049190	0	0	1	Carboxypeptidase (1)	proteolysis [GO:0006508 biological_process] (1); serine-type carboxypeptidase activity [GO:0004185 molecular_function] (1)	Peptidase S10, serine carboxypeptidase [IPR001563] (1); Alpha/Beta hydrolase fold [IPR029058] (1)	-	-	P_trifoliata_00486_mRNA_16.1
GF0049189	0	0	1	Hypothetical protein (1)	metabolic process [GO:0008152 biological_process] (1); transport [GO:0006810 biological_process] (1); integral component of membrane [GO:0016021 cellular_component] (1); hydrolase activity [GO:0016787 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)	Alpha/Beta hydrolase fold [IPR029058] (1); ABC transporter type 1, transmembrane domain [IPR011527] (1); Alpha/beta hydrolase fold-3 [IPR013094] (1)	-	-	P_trifoliata_00486_mRNA_13.1
GF0049188	0	0	1	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)	-	-	P_trifoliata_00486_mRNA_10.1
GF0049187	0	0	1	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)	-	-	P_trifoliata_00486_mRNA_1.1
GF0049186	0	0	1	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	NAC domain [IPR003441] (1)	-	-	P_trifoliata_00485_mRNA_9.1
GF0049185	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00485_mRNA_8.1
GF0049184	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00485_mRNA_25.1
GF0049183	0	0	1	Non-LTR retroelement reverse transcriptase-like protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00485_mRNA_24.1
GF0049182	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00485_mRNA_23.1
GF0049181	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00485_mRNA_22.1
GF0049180	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00485_mRNA_12.1
GF0049179	0	0	1	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-like domain [IPR012337] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H domain [IPR002156] (1)	-	-	P_trifoliata_00485_mRNA_1.1
GF0049178	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00484_mRNA_8.1
GF0049177	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00483_mRNA_8.1
GF0049176	0	0	1	Ribonuclease H 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)	-	-	P_trifoliata_00483_mRNA_4.1
GF0049175	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00483_mRNA_3.1
GF0049174	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00483_mRNA_27.1
GF0049173	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00483_mRNA_25.1
GF0049172	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00483_mRNA_24.1
GF0049171	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00483_mRNA_23.1
GF0049170	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00483_mRNA_22.1
GF0049169	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00483_mRNA_20.1
GF0049168	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00483_mRNA_2.1
GF0049167	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00483_mRNA_18.1
GF0049166	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00483_mRNA_15.1
GF0049165	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00483_mRNA_1.1
GF0049164	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00482_mRNA_8.1
GF0049163	0	0	1	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)	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); Concanavalin A-like lectin/glucanase domain [IPR013320] (1)	-	-	P_trifoliata_00482_mRNA_22.1
GF0049162	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00482_mRNA_20.1
GF0049161	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00482_mRNA_19.1
GF0049160	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00482_mRNA_18.1
GF0049159	0	0	1	LRR receptor-like serine/threonine-protein kinase ERL2 (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)	-	-	P_trifoliata_00482_mRNA_17.1
GF0049158	0	0	1	Hypothetical protein (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1)	Glycoside hydrolase superfamily [IPR017853] (1); Glycoside hydrolase, catalytic domain [IPR013781] (1)	-	-	P_trifoliata_00482_mRNA_11.1
GF0049157	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00481_mRNA_9.1
GF0049156	0	0	1	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)	-	-	P_trifoliata_00481_mRNA_25.1

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*
GF0049155	0	0	1	G-type lectin S-receptor-like serine/threonine-protein kinase RLK1 (1)	protein phosphorylation [GO:0006468 biological_process] (1); recognition of pollen [GO:0048544 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); S-locus glycoprotein domain [IPR000858] (1); Bulb-type lectin domain [IPR001480] (1); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1)	-	-	P_trifoliata_00481_mRNA_23.1
GF0049154	0	0	1	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)	-	-	P_trifoliata_00481_mRNA_16.1
GF0049153	0	0	1	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); Reverse transcriptase zinc-binding domain [IPR026960] (1); Domain of unknown function DUF4283 [IPR025558] (1); Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00481_mRNA_15.1
GF0049152	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00481_mRNA_14.1
GF0049151	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00481_mRNA_13.1
GF0049150	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00481_mRNA_11.1
GF0049149	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00480_mRNA_9.1
GF0049148	0	0	1	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	-	P_trifoliata_00480_mRNA_7.1
GF0049147	0	0	1	Hypothetical protein (1)		Pre-mRNA 3'-end-processing endonuclease polyadenylation factor C-term [IPR021718] (1)	-	-	P_trifoliata_00480_mRNA_3.1
GF0049146	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00480_mRNA_22.1
GF0049145	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00480_mRNA_21.1
GF0049144	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00480_mRNA_20.1
GF0049143	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00480_mRNA_19.1
GF0049142	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00480_mRNA_18.1
GF0049141	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00480_mRNA_10.1
GF0049140	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00479_mRNA_9.1
GF0049139	0	0	1	Hypothetical protein (1)	recognition of pollen [GO:0048544 biological_process] (1)	S-locus glycoprotein domain [IPR000858] (1); Bulb-type lectin domain [IPR001480] (1)	-	-	P_trifoliata_00479_mRNA_3.1
GF0049138	0	0	1	Hypothetical protein (1)		Bulb-type lectin domain [IPR001480] (1)	-	-	P_trifoliata_00479_mRNA_2.1
GF0049137	0	0	1	Pentatricopeptide repeat-containing family protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	-	P_trifoliata_00479_mRNA_18.1
GF0049136	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00479_mRNA_12.1
GF0049135	0	0	1	S-type anion channel SLAH1 (1)	transmembrane transport [GO:0055085 biological_process] (1); integral component of membrane [GO:0016021 cellular_component] (1)	Voltage-dependent anion channel [IPR004695] (1)	-	-	P_trifoliata_00478_mRNA_8.1
GF0049134	0	0	1	BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1, putative, expressed (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00478_mRNA_5.1
GF0049133	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00478_mRNA_4.1
GF0049132	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00478_mRNA_27.1
GF0049131	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00478_mRNA_11.1
GF0049130	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00477_mRNA_6.1
GF0049129	0	0	1	Hypothetical protein (1)		NAD(P)-binding domain [IPR016040] (1)	-	-	P_trifoliata_00477_mRNA_5.1
GF0049128	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00477_mRNA_25.1
GF0049127	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00477_mRNA_23.1
GF0049126	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00477_mRNA_21.1
GF0049125	0	0	1	Hypothetical protein (1)		Zinc knuckle CX2CX4HX4C [IPR025836] (1)	-	-	P_trifoliata_00477_mRNA_20.1
GF0049124	0	0	1	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	-	-	P_trifoliata_00477_mRNA_19.1
GF0049123	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00477_mRNA_15.1
GF0049122	0	0	1	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			-	-	P_trifoliata_00477_mRNA_13.1
GF0049121	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00477_mRNA_12.1
GF0049120	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00476_mRNA_8.1
GF0049119	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00476_mRNA_7.1
GF0049118	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00476_mRNA_5.1
GF0049117	0	0	1	Hypothetical protein (1)	catalytic activity [GO:0003824 molecular_function] (1)	Pyridoxal phosphate-dependent transferase, major region, subdomain 1 [IPR015421] (1); Alpha crystallin/Hsp20 domain [IPR002068] (1); HSP20-like chaperone [IPR008978] (1); Pyridoxal phosphate-dependent transferase [IPR015424] (1)	-	-	P_trifoliata_00476_mRNA_4.1
GF0049116	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00476_mRNA_23.1
GF0049115	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00476_mRNA_15.1
GF0049114	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00476_mRNA_13.1
GF0049113	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00475_mRNA_8.1
GF0049112	0	0	1	Monosacharide transport protein (1)			-	-	P_trifoliata_00475_mRNA_7.1
GF0049111	0	0	1	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); Malectin-like carbohydrate-binding domain [IPR024788] (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/dual specificity protein kinase, catalytic domain [IPR002290] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1)	-	-	P_trifoliata_00475_mRNA_3.1
GF0049110	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00475_mRNA_19.1
GF0049109	0	0	1	Hypothetical protein (1)		FBD domain [IPR006566] (1)	-	-	P_trifoliata_00475_mRNA_15.1
GF0049108	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00475_mRNA_11.1
GF0049107	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00475_mRNA_1.1
GF0049106	0	0	1	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)	-	-	P_trifoliata_00474_mRNA_22.1
GF0049105	0	0	1	Hypothetical protein (1)	catalytic activity [GO:0003824 molecular_function] (1)	L-Aspartase-like [IPR008948] (1); Phenylalanine ammonia-lyase, shielding domain [IPR023144] (1)	-	-	P_trifoliata_00474_mRNA_15.1
GF0049104	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00474_mRNA_12.1
GF0049103	0	0	1	OTU domain-containing (1)		OTU domain [IPR003323] (1)	-	-	P_trifoliata_00474_mRNA_1.1
GF0049102	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00473_mRNA_4.1
GF0049101	0	0	1	Translationally-controlled tumor protein homolog (1)		Translationally controlled tumour protein, conserved site [IPR018103] (1); Mss4-like [IPR011057] (1); Translationally controlled tumour protein [IPR018105] (1); Mss4/translationally controlled tumour-associated TCTP [IPR011323] (1)	-	-	P_trifoliata_00473_mRNA_23.1
GF0049100	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00473_mRNA_10.1
GF0049099	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00472_mRNA_9.1
GF0049098	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00472_mRNA_8.1
GF0049097	0	0	1	Kinase domain protein (1)			-	-	P_trifoliata_00472_mRNA_7.1
GF0049096	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00472_mRNA_6.1
GF0049095	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00472_mRNA_4.1
GF0049094	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00472_mRNA_30.1
GF0049093	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00472_mRNA_29.1
GF0049092	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00472_mRNA_28.1
GF0049091	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00472_mRNA_26.1
GF0049090	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00472_mRNA_23.1
GF0049089	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00472_mRNA_22.1
GF0049088	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00472_mRNA_21.1
GF0049087	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00472_mRNA_20.1
GF0049086	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00472_mRNA_19.1
GF0049085	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00472_mRNA_17.1
GF0049084	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00472_mRNA_15.1
GF0049083	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00472_mRNA_10.1
GF0049082	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00472_mRNA_1.1
GF0049081	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00471_mRNA_2.1
GF0049080	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00471_mRNA_16.1
GF0049079	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00471_mRNA_12.1
GF0049078	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00471_mRNA_1.1
GF0049077	0	0	1	Maternal effect embryo arrest protein (1)			-	-	P_trifoliata_00470_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*
GF0049076	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00470_mRNA_26.1
GF0049075	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00470_mRNA_25.1
GF0049074	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00470_mRNA_16.1
GF0049073	0	0	1	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)	-	-	P_trifoliata_00470_mRNA_15.1
GF0049072	0	0	1	Hypothetical protein (1)		Gag-polypeptide of LTR copia-type [IPR029472] (1)	-	-	P_trifoliata_00469_mRNA_26.1
GF0049071	0	0	1	Mitochondrial import inner membrane translocase subunit TIM14 (1)		DnaJ domain [IPR001623] (1)	-	-	P_trifoliata_00469_mRNA_21.1
GF0049070	0	0	1	Hypothetical protein (1)		Winged helix-turn-helix DNA-binding domain [IPR011991] (1)	-	-	P_trifoliata_00469_mRNA_18.1
GF0049069	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	-	P_trifoliata_00469_mRNA_17.1
GF0049068	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00469_mRNA_11.1
GF0049067	0	0	1	Heat shock cognate 70 kDa protein 2 (1)		Heat shock protein 70 family [IPR013126] (1); Heat shock protein 70kD, C-terminal domain [IPR029048] (1)	-	-	P_trifoliata_00468_mRNA_9.1
GF0049066	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 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)	Ribonuclease H-like domain [IPR012337] (1); Domain of unknown function DUF4371 [IPR025398] (1); EamA domain [IPR000620] (1); WAT1-related protein [IPR030184] (1)	-	-	P_trifoliata_00468_mRNA_25.1
GF0049065	0	0	1	Egg cell-secreted protein 1.4 (1)		Prolamin-like domain [IPR008502] (1)	-	-	P_trifoliata_00468_mRNA_23.1
GF0049064	0	0	1	Oxoglutarate dehydrogenase (Succinyl-transferring), E1 component, variant 5 (1)	structural constituent of ribosome [GO:0003735 molecular_function] (1); signal transduction [GO:0007165 biological_process] (1); intracellular [GO:0005622 cellular_component] (1); intracellular protein transport [GO:0006886 biological_process] (1); translation [GO:0006412 biological_process] (1); GTP binding [GO:0005525 molecular_function] (1); nucleocytoplasmic transport [GO:0006913 biological_process] (1); small GTPase mediated signal transduction [GO:0007264 biological_process] (1); membrane [GO:0016020 cellular_component] (1); tricarboxylic acid cycle [GO:0006099 biological_process] (1); thiamine pyrophosphate binding [GO:0030976 molecular_function] (1); oxoglutarate dehydrogenase (succinyl-transferring) activity [GO:0004591 molecular_function] (1); protein transport [GO:0015031 biological_process] (1); oxidation-reduction process [GO:0055114 biological_process] (1); ribosome [GO:0005840 cellular component] (1);	Small GTPase superfamily [IPR001806] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Ribosomal protein S8 [IPR000630] (1); Small GTPase superfamily, Rho type [IPR003578] (1); Small GTP-binding protein domain [IPR005225] (1); Small GTPase superfamily, Rab type [IPR003579] (1); Small GTPase superfamily, ARF type [IPR024156] (1); Ran GTPase [IPR002041] (1); Transketolase-like, pyrimidine-binding domain [IPR005475] (1); Multifunctional 2-oxoglutarate metabolism enzyme, C-terminal [IPR031717] (1); Thiamin diphosphate-binding fold [IPR029061] (1); Small GTPase superfamily, Ras type [IPR020849] (1); 2-oxoglutarate dehydrogenase E1 component [IPR011603] (1)	-	-	P_trifoliata_00468_mRNA_22.1
GF0049063	0	0	1	Hypothetical protein (1)	DNA topoisomerase type II (ATP-hydrolyzing) activity [GO:0003918 molecular_function] (1); DNA metabolic process [GO:0006259 biological_process] (1); DNA binding [GO:0003677 molecular_function] (1); DNA topological change [GO:0006265 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1)	IKI3 [IPR006849] (1); DNA topoisomerase, type IIA-like domain [IPR013760] (1); DNA topoisomerase, type IIA, subunit A/C-terminal [IPR002205] (1); DNA topoisomerase, type IIA, subunit A/ C-terminal, alpha-beta [IPR013758] (1)	-	-	P_trifoliata_00468_mRNA_20.1
GF0049062	0	0	1	Hypothetical protein (1)		Frigida-like [IPR012474] (1)	-	-	P_trifoliata_00467_mRNA_24.1
GF0049061	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00467_mRNA_2.1
GF0049060	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00467_mRNA_19.1
GF0049059	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00466_mRNA_12.1
GF0049058	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00465_mRNA_8.1
GF0049057	0	0	1	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 knuckle CX2CX4HX4C [IPR025836] (1); Zinc finger, CCHC-type [IPR001878] (1)	-	-	P_trifoliata_00465_mRNA_7.1
GF0049056	0	0	1	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	-	P_trifoliata_00465_mRNA_6.1
GF0049055	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00465_mRNA_2.1
GF0049054	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00465_mRNA_14.1
GF0049053	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00465_mRNA_12.1
GF0049052	0	0	1	NADH dehydrogenase subunit 9 (1)	oxidation-reduction process [GO:0055114 biological_process] (1); NADH dehydrogenase (ubiquinone) activity [GO:0008137 molecular_function] (1); oxidoreductase activity, acting on NAD(P)H [GO:0016651 molecular_function] (1)	NADH:ubiquinone oxidoreductase, 30kDa subunit, conserved site [IPR020396] (1); NADH dehydrogenase, subunit C [IPR010218] (1); NADH:ubiquinone oxidoreductase, 30kDa subunit [IPR001268] (1)	-	-	P_trifoliata_00464_mRNA_9.1
GF0049051	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00464_mRNA_7.1
GF0049050	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00464_mRNA_5.1
GF0049049	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00464_mRNA_3.1
GF0049048	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00464_mRNA_28.1
GF0049047	0	0	1	Actin (1)		Actin family [IPR004000] (1)	-	-	P_trifoliata_00464_mRNA_23.1
GF0049046	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00464_mRNA_19.1
GF0049045	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00464_mRNA_15.1
GF0049044	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00464_mRNA_13.1
GF0049043	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00464_mRNA_12.1
GF0049042	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00464_mRNA_11.1
GF0049041	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00464_mRNA_10.1
GF0049040	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00463_mRNA_4.1
GF0049039	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00463_mRNA_3.1
GF0049038	0	0	1	Ankyrin repeat family protein (1)		Ankyrin repeat-containing domain [IPR020683] (1); PGG domain [IPR026961] (1)	-	-	P_trifoliata_00463_mRNA_29.1
GF0049037	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00463_mRNA_28.1
GF0049036	0	0	1	Hypothetical protein (1)		Nucleoporin, Nup133/Nup155-like, N-terminal [IPR014908] (1)	-	-	P_trifoliata_00463_mRNA_27.1
GF0049035	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00463_mRNA_2.1
GF0049034	0	0	1	Lipoxygenase (1)	metal ion binding [GO:0046872 molecular_function] (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 [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Lipoxygenase, plant [IPR001246] (1); Lipoxygenase [IPR000907] (1); Lipoxygenase, domain 3 [IPR027433] (1); Lipoxygenase, C-terminal [IPR013819] (1)	-	-	P_trifoliata_00463_mRNA_13.1
GF0049033	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1); Zinc knuckle CX2CX4HX4C [IPR025836] (1)	-	-	P_trifoliata_00462_mRNA_7.1
GF0049032	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00462_mRNA_6.1
GF0049031	0	0	1	Male germ cell-associated 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)	-	-	P_trifoliata_00462_mRNA_3.1
GF0049030	0	0	1	L-lactate dehydrogenase A (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); carboxylic acid metabolic process [GO:0019752 biological_process] (1); oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor [GO:0016616 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1)	L-lactate/malate dehydrogenase [IPR001557] (1); NAD(P)-binding domain [IPR016040] (1); Lactate dehydrogenase/glycoside hydrolase, family 4, C-terminal [IPR015955] (1); Lactate/malate dehydrogenase, N-terminal [IPR001236] (1)	-	-	P_trifoliata_00462_mRNA_25.1
GF0049029	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00462_mRNA_23.1
GF0049028	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00462_mRNA_14.1
GF0049027	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00462_mRNA_12.1
GF0049026	0	0	1	Cell division control protein 2 homolog (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/dual specificity protein kinase, catalytic domain [IPR002290] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase, ATP binding site [IPR017441] (1); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1)	-	-	P_trifoliata_00462_mRNA_10.1
GF0049025	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00461_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*
GF0049024	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00461_mRNA_8.1
GF0049023	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00461_mRNA_17.1
GF0049022	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00461_mRNA_15.1
GF0049021	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00461_mRNA_14.1
GF0049020	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00461_mRNA_13.1
GF0049019	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00461_mRNA_11.1
GF0049018	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00461_mRNA_1.1
GF0049017	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00460_mRNA_5.1
GF0049016	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00460_mRNA_4.1
GF0049015	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00460_mRNA_19.1
GF0049014	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00460_mRNA_13.1
GF0049013	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00460_mRNA_12.1
GF0049012	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00460_mRNA_10.1
GF0049011	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00460_mRNA_1.1
GF0049010	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00459_mRNA_9.1
GF0049009	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00459_mRNA_7.1
GF0049008	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00459_mRNA_12.1
GF0049007	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00458_mRNA_31.1
GF0049006	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00458_mRNA_27.1
GF0049005	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00458_mRNA_26.1
GF0049004	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	-	P_trifoliata_00458_mRNA_25.1
GF0049003	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00458_mRNA_24.1
GF0049002	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00458_mRNA_22.1
GF0049001	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00458_mRNA_21.1
GF0049000	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00458_mRNA_19.1
GF0048999	0	0	1	Hypothetical protein (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	NAD(P)-binding domain [IPR016040] (1); Glucose/ribitol dehydrogenase [IPR002347] (1); Short-chain dehydrogenase/reductase SDR [IPR002198] (1)	-	-	P_trifoliata_00458_mRNA_18.1
GF0048998	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00457_mRNA_7.1
GF0048997	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00457_mRNA_6.1
GF0048996	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00457_mRNA_5.1
GF0048995	0	0	1	Hypothetical protein (1)		P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	-	P_trifoliata_00457_mRNA_3.1
GF0048994	0	0	1	Hypothetical protein (1)	nucleus [GO:0005634 cellular_component] (1); ribosome biogenesis [GO:0042254 biological_process] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); AARP2CN [IPR012948] (1)	-	-	P_trifoliata_00457_mRNA_19.1
GF0048993	0	0	1	RNA-directed DNA polymerase (Reverse transcriptase) (1)		Reverse transcriptase domain [IPR000477] (1)	-	-	P_trifoliata_00457_mRNA_18.1
GF0048992	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00457_mRNA_16.1
GF0048991	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00457_mRNA_15.1
GF0048990	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00457_mRNA_14.1
GF0048989	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1); Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	-	P_trifoliata_00457_mRNA_12.1
GF0048988	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00457_mRNA_10.1
GF0048987	0	0	1	Hypothetical protein (1)		P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	-	P_trifoliata_00457_mRNA_1.1
GF0048986	0	0	1	GluA (1)	hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1)	Glycoside hydrolase, family 3, N-terminal [IPR001764] (1); Glycoside hydrolase family 3 [IPR026892] (1); Glycoside hydrolase superfamily [IPR017853] (1)	-	-	P_trifoliata_00456_mRNA_9.1
GF0048985	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00456_mRNA_8.1
GF0048984	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00456_mRNA_7.1
GF0048983	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00456_mRNA_6.1
GF0048982	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00456_mRNA_5.1
GF0048981	0	0	1	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 domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1)	-	-	P_trifoliata_00456_mRNA_22.1
GF0048980	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00456_mRNA_2.1
GF0048979	0	0	1	Glycosyl hydrolase 9B1 isoform 2 (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)	Glycoside hydrolase family 9 [IPR001701] (1); Six-hairpin glycosidase [IPR012341] (1); Six-hairpin glycosidase-like [IPR008928] (1)	-	-	P_trifoliata_00456_mRNA_19.1
GF0048978	0	0	1	Sucrose-6F-phosphate phosphohydrolase family protein isoform 3 (1)	sucrose biosynthetic process [GO:0005986 biological_process] (1); sucrose-phosphate phosphatase activity [GO:0050307 molecular_function] (1); magnesium ion binding [GO:0000287 molecular_function] (1)	HAD-superfamily hydrolase, subfamily IIB [IPR006379] (1); Sucrose-6-phosphate phosphohydrolase, C-terminal [IPR013679] (1); Sucrose-phosphate synthase [IPR006380] (1); Sucrose phosphatase, plant/cyanobacteria [IPR012847] (1); HAD-like domain [IPR023214] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00456_mRNA_18.1
GF0048977	0	0	1	Hypothetical protein (1)		MULE transposase domain [IPR018289] (1)	-	-	P_trifoliata_00456_mRNA_17.1
GF0048976	0	0	1	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	-	P_trifoliata_00456_mRNA_12.1
GF0048975	0	0	1	Glycosyl hydrolase family protein isoform 3 (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 [IPR026892] (1); Glycoside hydrolase family 3 C-terminal domain [IPR002772] (1); Glycoside hydrolase superfamily [IPR017853] (1)	-	-	P_trifoliata_00456_mRNA_10.1
GF0048974	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00455_mRNA_8.1
GF0048973	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00455_mRNA_5.1
GF0048972	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00455_mRNA_3.1
GF0048971	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00455_mRNA_22.1
GF0048970	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00455_mRNA_1.1
GF0048969	0	0	1	Hypothetical protein (1)		Transposon, En/Spm-like [IPR004242] (1); Transposase-associated domain [IPR029480] (1)	-	-	P_trifoliata_00454_mRNA_8.1
GF0048968	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00454_mRNA_4.1
GF0048967	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00454_mRNA_3.1
GF0048966	0	0	1	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	Zinc finger, BED-type [IPR003656] (1)	-	-	P_trifoliata_00454_mRNA_20.1
GF0048965	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00454_mRNA_14.1
GF0048964	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00454_mRNA_11.1
GF0048963	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00454_mRNA_10.1
GF0048962	0	0	1	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)	-	-	P_trifoliata_00453_mRNA_8.1
GF0048961	0	0	1	Hypothetical protein (1)		Nucleoporin, Nup133/Nup155-like, N-terminal [IPR014908] (1)	-	-	P_trifoliata_00453_mRNA_6.1
GF0048960	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00453_mRNA_4.1
GF0048959	0	0	1	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	-	P_trifoliata_00453_mRNA_21.1
GF0048958	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00453_mRNA_20.1
GF0048957	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00453_mRNA_19.1
GF0048956	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00453_mRNA_18.1
GF0048955	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00453_mRNA_17.1
GF0048954	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00453_mRNA_12.1
GF0048953	0	0	1	Nudix hydrolase 20, chloroplastic (1)	hydrolase activity [GO:0016787 molecular_function] (1)	NUDIX hydrolase domain-like [IPR015797] (1); NUDIX hydrolase domain [IPR000086] (1); Domain of unknown function DUF4743 [IPR031804] (1)	-	-	P_trifoliata_00452_mRNA_7.1
GF0048952	0	0	1	Hypothetical protein (1)	hydro-lyase activity [GO:0016836 molecular_function] (1)	ClpP/crotonase-like domain [IPR029045] (1); Enoyl-CoA hydratase/isomerase, HIBYL-CoA-H type [IPR032259] (1); Alpha/Beta hydrolase fold [IPR029058] (1); Alpha/beta hydrolase fold-1 [IPR000073] (1)	-	-	P_trifoliata_00452_mRNA_6.1
GF0048951	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00452_mRNA_22.1
GF0048950	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00452_mRNA_21.1
GF0048949	0	0	1	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	-	P_trifoliata_00452_mRNA_19.1
GF0048948	0	0	1	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			-	-	P_trifoliata_00452_mRNA_18.1
GF0048947	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00452_mRNA_14.1
GF0048946	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00451_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*
GF0048945	0	0	1	Amine oxidase (flavin-containing) (1)	primary amine oxidase activity [GO:0008131 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); copper ion binding [GO:0005507 molecular_function] (1); quinone binding [GO:0048038 molecular_function] (1); amine metabolic process [GO:0009308 biological_process] (1)	Copper amine oxidase, N2-terminal [IPR015800] (1); Copper amine oxidase [IPR000269] (1); Copper amine oxidase, N-terminal [IPR016182] (1); Copper amine oxidase, N3-terminal [IPR015802] (1)	-	-	P_trifoliata_00451_mRNA_6.1
GF0048944	0	0	1	Amine oxidase (flavin-containing) (1)	amine metabolic process [GO:0009308 biological_process] (1); quinone binding [GO:0048038 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); copper ion binding [GO:0005507 molecular_function] (1); primary amine oxidase activity [GO:0008131 molecular_function] (1)	Copper amine oxidase [IPR000269] (1); Copper amine oxidase, C-terminal [IPR015798] (1)	-	-	P_trifoliata_00451_mRNA_5.1
GF0048943	0	0	1	Amine oxidase (flavin-containing) (1)	amine metabolic process [GO:0009308 biological_process] (1); quinone binding [GO:0048038 molecular_function] (1); copper ion binding [GO:0005507 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); primary amine oxidase activity [GO:0008131 molecular_function] (1)	Copper amine oxidase, N2-terminal [IPR015800] (1); Copper amine oxidase [IPR000269] (1); Copper amine oxidase, N-terminal [IPR016182] (1); Copper amine oxidase, C-terminal [IPR015798] (1); Copper amine oxidase, N3-terminal [IPR015802] (1)	-	-	P_trifoliata_00451_mRNA_4.1
GF0048942	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00451_mRNA_22.1
GF0048941	0	0	1	Calreticulin (1)	endoplasmic reticulum [GO:0005783 cellular_component] (1); calcium ion binding [GO:0005509 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1); unfolded protein binding [GO:0051082 molecular_function] (1); protein folding [GO:0006457 biological_process] (1)	Calreticulin/calnexin, P domain [IPR009033] (1); Calreticulin/calnexin [IPR001580] (1); Calreticulin [IPR009169] (1); Calreticulin/calnexin, conserved site [IPR018124] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1)	-	-	P_trifoliata_00451_mRNA_19.1
GF0048940	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00451_mRNA_18.1
GF0048939	0	0	1	Amine oxidase (flavin-containing) (1)	amine metabolic process [GO:0009308 biological_process] (1); oxidation-reduction process [GO:0055114 biological_process] (1); copper ion binding [GO:0005507 molecular_function] (1); quinone binding [GO:0048038 molecular_function] (1); primary amine oxidase activity [GO:0008131 molecular_function] (1)	Copper amine oxidase [IPR000269] (1); Copper amine oxidase, C-terminal [IPR015798] (1)	-	-	P_trifoliata_00451_mRNA_1.1
GF0048938	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00450_mRNA_38.1
GF0048937	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00450_mRNA_35.1
GF0048936	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00450_mRNA_34.1
GF0048935	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00450_mRNA_33.1
GF0048934	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00450_mRNA_29.1
GF0048933	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00450_mRNA_27.1
GF0048932	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00450_mRNA_26.1
GF0048931	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00450_mRNA_21.1
GF0048930	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00450_mRNA_17.1
GF0048929	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00450_mRNA_15.1
GF0048928	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00450_mRNA_14.1
GF0048927	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00450_mRNA_13.1
GF0048926	0	0	1	Hypothetical protein (1)		LOG family [IPR031100] (1)	-	-	P_trifoliata_00450_mRNA_12.1
GF0048925	0	0	1	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/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)	-	-	P_trifoliata_00450_mRNA_10.1
GF0048924	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00449_mRNA_22.1
GF0048923	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00449_mRNA_18.1
GF0048922	0	0	1	Hypothetical protein (1)		Uncharacterised protein family, basic secretory protein [IPR007541] (1)	-	-	P_trifoliata_00449_mRNA_14.1
GF0048921	0	0	1	Hypothetical protein (1)		Uncharacterised protein family UPF0061 [IPR003846] (1)	-	-	P_trifoliata_00448_mRNA_8.1
GF0048920	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00448_mRNA_7.1
GF0048919	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00448_mRNA_6.1
GF0048918	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00448_mRNA_5.1
GF0048917	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00448_mRNA_4.1
GF0048916	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00448_mRNA_3.1
GF0048915	0	0	1	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	-	P_trifoliata_00448_mRNA_25.1
GF0048914	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00448_mRNA_24.1
GF0048913	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00448_mRNA_17.1
GF0048912	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00448_mRNA_1.1
GF0048911	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00447_mRNA_8.1
GF0048910	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00447_mRNA_7.1
GF0048909	0	0	1	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)	-	-	P_trifoliata_00447_mRNA_6.1
GF0048908	0	0	1	Hypothetical protein (1)		S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	-	P_trifoliata_00447_mRNA_5.1
GF0048907	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00447_mRNA_4.1
GF0048906	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00447_mRNA_20.1
GF0048905	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00446_mRNA_9.1
GF0048904	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00446_mRNA_7.1
GF0048903	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00446_mRNA_5.1
GF0048902	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00446_mRNA_31.1
GF0048901	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00446_mRNA_3.1
GF0048900	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00446_mRNA_2.1
GF0048899	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00446_mRNA_14.1
GF0048898	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00446_mRNA_13.1
GF0048897	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00446_mRNA_12.1
GF0048896	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00446_mRNA_10.1
GF0048895	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00446_mRNA_1.1
GF0048894	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat [IPR002110] (1); Ankyrin repeat-containing domain [IPR020683] (1)	-	-	P_trifoliata_00445_mRNA_9.1
GF0048893	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00445_mRNA_7.1
GF0048892	0	0	1	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	-	-	P_trifoliata_00445_mRNA_5.1
GF0048891	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00445_mRNA_27.1
GF0048890	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00445_mRNA_26.1
GF0048889	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00445_mRNA_25.1
GF0048888	0	0	1	Putative serine protease 45-like (1)		Protein of unknown function DUF538 [IPR007493] (1)	-	-	P_trifoliata_00445_mRNA_24.1
GF0048887	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00445_mRNA_18.1
GF0048886	0	0	1	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	-	P_trifoliata_00445_mRNA_16.1
GF0048885	0	0	1	NADP-dependent alkenal double bond reductase P2 (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); GroES-like [IPR011032] (1); Alcohol dehydrogenase superfamily, zinc-type [IPR002085] (1); Alcohol dehydrogenase, C-terminal [IPR013149] (1)	-	-	P_trifoliata_00445_mRNA_14.1
GF0048884	0	0	1	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	-	P_trifoliata_00445_mRNA_13.1
GF0048883	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00444_mRNA_21.1
GF0048882	0	0	1	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)	-	-	P_trifoliata_00444_mRNA_20.1

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*
GF0048881	0	0	1	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)	-	-	P_trifoliata_00444_mRNA_19.1
GF0048880	0	0	1	GAG1At protein (1)			-	-	P_trifoliata_00444_mRNA_14.1
GF0048879	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00444_mRNA_12.1
GF0048878	0	0	1	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)	-	-	P_trifoliata_00444_mRNA_1.1
GF0048877	0	0	1	Cytochrome P450 93A1 (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)	-	-	P_trifoliata_00443_mRNA_9.1
GF0048876	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00443_mRNA_8.1
GF0048875	0	0	1	Cytochrome P450 family 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); Cytochrome P450, E-class, group I [IPR002401] (1)	-	-	P_trifoliata_00443_mRNA_7.1
GF0048874	0	0	1	Hypothetical protein (1)	U2AF [GO:0089701 cellular_component] (1); metal ion binding [GO:0046872 molecular_function] (1); mRNA splicing, via spliceosome [GO:0000398 biological_process] (1); RNA binding [GO:0003723 molecular_function] (1); nucleotide binding [GO:0000166 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	RNA recognition motif domain, eukaryote [IPR003954] (1); U2 auxiliary factor small subunit [IPR009145] (1); RNA recognition motif domain [IPR000504] (1); Zinc finger, CCCH-type [IPR000571] (1); Nucleotide-binding alpha-beta plait domain [IPR012677] (1)	-	-	P_trifoliata_00443_mRNA_4.1
GF0048873	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00443_mRNA_3.1
GF0048872	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00443_mRNA_26.1
GF0048871	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00443_mRNA_25.1
GF0048870	0	0	1	AAA domain protein (1)		P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	-	P_trifoliata_00443_mRNA_24.1
GF0048869	0	0	1	Hypothetical protein (1)	calmodulin binding [GO:0005516 molecular_function] (1)	Calcium-transporting P-type ATPase, N-terminal autoinhibitory domain [IPR024750] (1)	-	-	P_trifoliata_00443_mRNA_2.1
GF0048868	0	0	1	Licodione synthase (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)	-	-	P_trifoliata_00443_mRNA_11.1
GF0048867	0	0	1	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); calmodulin binding [GO:0005516 molecular_function] (1)	Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Calcium-transporting P-type ATPase, N-terminal autoinhibitory domain [IPR024750] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	-	-	P_trifoliata_00443_mRNA_1.1
GF0048866	0	0	1	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	-	P_trifoliata_00442_mRNA_9.1
GF0048865	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00442_mRNA_7.1
GF0048864	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00442_mRNA_5.1
GF0048863	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00442_mRNA_2.1
GF0048862	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00442_mRNA_19.1
GF0048861	0	0	1	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	-	-	P_trifoliata_00442_mRNA_18.1
GF0048860	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00442_mRNA_17.1
GF0048859	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00442_mRNA_15.1
GF0048858	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00442_mRNA_11.1
GF0048857	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00441_mRNA_2.1
GF0048856	0	0	1	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); serine-type endopeptidase activity [GO:0004252 molecular_function] (1)	Peptidase S8/S53 domain [IPR000209] (1); Peptidase S8, subtilisin-related [IPR015500] (1)	-	-	P_trifoliata_00441_mRNA_18.1
GF0048855	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00441_mRNA_17.1
GF0048854	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00441_mRNA_1.1
GF0048853	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00440_mRNA_8.1
GF0048852	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00440_mRNA_6.1
GF0048851	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00440_mRNA_4.1
GF0048850	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00440_mRNA_31.1
GF0048849	0	0	1	Ubiquitin-protein ligase, PUB12 (1)	binding [GO:0005488 molecular_function] (1); protein ubiquitination [GO:0016567 biological_process] (1); ubiquitin-protein transferase activity [GO:0004842 molecular_function] (1)	Armadillo-like helical [IPR011989] (1); Zinc finger, RING/FYVE/PHD-type [IPR013083] (1); U box domain [IPR003613] (1); Armadillo-type fold [IPR016024] (1)	-	-	P_trifoliata_00440_mRNA_30.1
GF0048848	0	0	1	Ankyrin repeat family protein, putative (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat-containing domain [IPR020683] (1); Ankyrin repeat [IPR002110] (1)	-	-	P_trifoliata_00440_mRNA_2.1
GF0048847	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00440_mRNA_12.1
GF0048846	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat-containing domain [IPR020683] (1); Ankyrin repeat [IPR002110] (1)	-	-	P_trifoliata_00440_mRNA_11.1
GF0048845	0	0	1	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)	-	-	P_trifoliata_00440_mRNA_1.1
GF0048844	0	0	1	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); Viral movement protein [IPR028919] (1)	-	-	P_trifoliata_00439_mRNA_9.1
GF0048843	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00439_mRNA_5.1
GF0048842	0	0	1	Hypothetical protein (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Aspartic peptidase, active site [IPR001969] (1); Peptidase A2A, retrovirus, catalytic [IPR001995] (1)	-	-	P_trifoliata_00439_mRNA_36.1
GF0048841	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00439_mRNA_35.1
GF0048840	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00439_mRNA_32.1
GF0048839	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00439_mRNA_30.1
GF0048838	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00439_mRNA_29.1
GF0048837	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00439_mRNA_27.1
GF0048836	0	0	1	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)	-	-	P_trifoliata_00439_mRNA_26.1
GF0048835	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00439_mRNA_25.1
GF0048834	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00439_mRNA_24.1
GF0048833	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00439_mRNA_23.1
GF0048832	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00439_mRNA_15.1
GF0048831	0	0	1	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	-	P_trifoliata_00439_mRNA_14.1
GF0048830	0	0	1	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)	-	-	P_trifoliata_00438_mRNA_9.1
GF0048829	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00438_mRNA_6.1
GF0048828	0	0	1	Leucine-rich repeat (LRR) family protein (1)			-	-	P_trifoliata_00438_mRNA_5.1
GF0048827	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00438_mRNA_24.1
GF0048826	0	0	1	Acyl-CoA N-acyltransferases (NAT) superfamily protein (1)	N-acetyltransferase activity [GO:0008080 molecular_function] (1)	Acyl-CoA N-acyltransferase [IPR016181] (1); GNAT domain [IPR000182] (1)	-	-	P_trifoliata_00438_mRNA_21.1

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*
GF0048825	0	0	1	Translationally-controlled tumor protein homolog (1)		Mss4-like [IPR011057] (1); Translationally controlled tumour protein, conserved site [IPR018103] (1); Translationally controlled tumour protein [IPR018105] (1); Mss4/translationally controlled tumour-associated TCTP [IPR011323] (1)	-	-	P_trifoliata_00438_mRNA_2.1
GF0048824	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00438_mRNA_18.1
GF0048823	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00438_mRNA_17.1
GF0048822	0	0	1	Beta-hexosaminidase subunit B2 (1)	beta-N-acetylhexosaminidase activity [GO:0004563 molecular_function] (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); Chitobiase/beta-hexosaminidase domain 2-like [IPR029018] (1); Glycoside hydrolase superfamily [IPR017853] (1); Beta-hexosaminidase [IPR025705] (1); Glycoside hydrolase family 20, catalytic domain [IPR015883] (1); Beta-hexosaminidase, eukaryotic type, N-terminal [IPR029019] (1)	-	-	P_trifoliata_00438_mRNA_12.1
GF0048821	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00438_mRNA_11.1
GF0048820	0	0	1	Hypothetical protein (1)		Mss4-like [IPR011057] (1); Translationally controlled tumour protein, conserved site [IPR018103] (1); Mss4/translationally controlled tumour-associated TCTP [IPR011323] (1); Translationally controlled tumour protein [IPR018105] (1)	-	-	P_trifoliata_00438_mRNA_1.1
GF0048819	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00437_mRNA_9.1
GF0048818	0	0	1	Putative AC9 transposase (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)	-	-	P_trifoliata_00437_mRNA_8.1
GF0048817	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00437_mRNA_6.1
GF0048816	0	0	1	Hypothetical protein (1)	nucleotide binding [GO:0000166 molecular_function] (1)	P-type ATPase, cytoplasmic domain N [IPR023299] (1); HAD-like domain [IPR023214] (1)	-	-	P_trifoliata_00437_mRNA_3.1
GF0048815	0	0	1	Caffeic acid 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)	-	-	P_trifoliata_00437_mRNA_24.1
GF0048814	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00437_mRNA_20.1
GF0048813	0	0	1	Hypothetical protein (1)		P-type ATPase, transmembrane domain [IPR023298] (1); Cation-transporting P-type ATPase, C-terminal [IPR006068] (1)	-	-	P_trifoliata_00437_mRNA_2.1
GF0048812	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00437_mRNA_18.1
GF0048811	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00437_mRNA_16.1
GF0048810	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00437_mRNA_15.1
GF0048809	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00437_mRNA_14.1
GF0048808	0	0	1	DEAD-box ATP-dependent RNA helicase 20 (1)	nucleic acid binding [GO:0003676 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Helicase, C-terminal [IPR001650] (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); RNA helicase, DEAD-box type, Q motif [IPR014014] (1); Helicase superfamily 1/2, ATP-binding domain [IPR014001] (1)	-	-	P_trifoliata_00437_mRNA_1.1
GF0048807	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00436_mRNA_36.1
GF0048806	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00436_mRNA_33.1
GF0048805	0	0	1	UPF0481 protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	-	P_trifoliata_00436_mRNA_30.1
GF0048804	0	0	1	Hypothetical protein (1)	transcription factor TFIID complex [GO:0005669 cellular_component] (1); transcription initiation from RNA polymerase II promoter [GO:0006367 biological_process] (1)	TAFII55 protein, conserved region [IPR006751] (1)	-	-	P_trifoliata_00436_mRNA_3.1
GF0048803	0	0	1	Hypothetical protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	-	P_trifoliata_00436_mRNA_29.1
GF0048802	0	0	1	HAT dimerisation domain-containing protein, putative (1)			-	-	P_trifoliata_00436_mRNA_25.1
GF0048801	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00436_mRNA_22.1
GF0048800	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00436_mRNA_21.1
GF0048799	0	0	1	DUF247 domain protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	-	P_trifoliata_00436_mRNA_18.1
GF0048798	0	0	1	UPF0481 protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	-	P_trifoliata_00436_mRNA_17.1
GF0048797	0	0	1	Hypothetical protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	-	P_trifoliata_00436_mRNA_12.1
GF0048796	0	0	1	DUF247 domain protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	-	P_trifoliata_00436_mRNA_11.1
GF0048795	0	0	1	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, E-class, group I [IPR002401] (1); Cytochrome P450 [IPR001128] (1)	-	-	P_trifoliata_00435_mRNA_6.1
GF0048794	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00435_mRNA_4.1
GF0048793	0	0	1	Miraculin (1)	endopeptidase inhibitor activity [GO:0004866 molecular_function] (1)	Kunitz inhibitor ST1-like [IPR011065] (1); Proteinase inhibitor I3, Kunitz legume [IPR002160] (1)	-	-	P_trifoliata_00435_mRNA_3.1
GF0048792	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF676, lipase-like [IPR007751] (1); Alpha/Beta hydrolase fold [IPR029058] (1)	-	-	P_trifoliata_00435_mRNA_16.1
GF0048791	0	0	1	Hypothetical protein (1)	glycolytic process [GO:0006096 biological_process] (1); 6-phosphofructokinase activity [GO:0003872 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Phosphofructokinase domain [IPR000023] (1); Ankyrin repeat-containing domain [IPR020683] (1); Domain of unknown function DUF676, lipase-like [IPR007751] (1); Ankyrin repeat [IPR002110] (1); Alpha/Beta hydrolase fold [IPR029058] (1)	-	-	P_trifoliata_00435_mRNA_15.1
GF0048790	0	0	1	CDNA clone:J023022E20, full insert sequence (1)			-	-	P_trifoliata_00435_mRNA_14.1
GF0048789	0	0	1	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)	-	-	P_trifoliata_00435_mRNA_12.1
GF0048788	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00435_mRNA_11.1
GF0048787	0	0	1	Exocyst componenet sec8, putative (1)			-	-	P_trifoliata_00434_mRNA_8.1
GF0048786	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00434_mRNA_6.1
GF0048785	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00434_mRNA_31.1
GF0048784	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00434_mRNA_26.1
GF0048783	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00434_mRNA_25.1
GF0048782	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1); signal transduction [GO:0007165 biological_process] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1)	-	-	P_trifoliata_00434_mRNA_22.1
GF0048781	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00434_mRNA_21.1
GF0048780	0	0	1	TMV resistance protein N-like protein 5 (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)	-	-	P_trifoliata_00434_mRNA_19.1
GF0048779	0	0	1	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 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); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Protein kinase, ATP binding site [IPR017441] (1); Leucine-rich repeat [IPR001611] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1)	-	-	P_trifoliata_00434_mRNA_16.1
GF0048778	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00433_mRNA_8.1
GF0048777	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00433_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***
GF0048776	0	0	1	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)	-	-	P_trifoliata_00433_mRNA_2.1
GF0048775	0	0	1	Hypothetical protein (1)		Transposon, En/Spm-like [IPR004242] (1)	-	-	P_trifoliata_00433_mRNA_15.1
GF0048774	0	0	1	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)	-	-	P_trifoliata_00433_mRNA_13.1
GF0048773	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00432_mRNA_7.1
GF0048772	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00432_mRNA_5.1
GF0048771	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00432_mRNA_4.1
GF0048770	0	0	1	Hypothetical protein (1)		Plant disease resistance response protein [IPR004265] (1)	-	-	P_trifoliata_00432_mRNA_29.1
GF0048769	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00432_mRNA_24.1
GF0048768	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00432_mRNA_22.1
GF0048767	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00432_mRNA_21.1
GF0048766	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00432_mRNA_19.1
GF0048765	0	0	1	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	-	P_trifoliata_00432_mRNA_17.1
GF0048764	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00432_mRNA_16.1
GF0048763	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00432_mRNA_15.1
GF0048762	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00432_mRNA_13.1
GF0048761	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00432_mRNA_12.1
GF0048760	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00431_mRNA_9.1
GF0048759	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00431_mRNA_35.1
GF0048758	0	0	1	Hypothetical protein (1)		Aminotransferase-like, plant mobile domain [IPR019557] (1); Protein of unknown function DUF716 (TMEM45) [IPR006904] (1)	-	-	P_trifoliata_00431_mRNA_30.1
GF0048757	0	0	1	Cytochrome P450 716B1 (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)	-	-	P_trifoliata_00431_mRNA_23.1
GF0048756	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00431_mRNA_22.1
GF0048755	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00431_mRNA_14.1
GF0048754	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00431_mRNA_13.1
GF0048753	0	0	1	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			-	-	P_trifoliata_00431_mRNA_11.1
GF0048752	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00431_mRNA_1.1
GF0048751	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00430_mRNA_8.1
GF0048750	0	0	1	Hypothetical protein (1)	nucleoside diphosphate phosphorylation [GO:0006165 biological_process] (1); UTP biosynthetic process [GO:0006228 biological_process] (1); CTP biosynthetic process [GO:0006241 biological_process] (1); nucleoside diphosphate kinase activity [GO:0004550 molecular_function] (1); GTP biosynthetic process [GO:0006183 biological_process] (1)	Nucleoside diphosphate kinase [IPR001564] (1)	-	-	P_trifoliata_00430_mRNA_7.1
GF0048749	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00430_mRNA_6.1
GF0048748	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00430_mRNA_4.1
GF0048747	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00430_mRNA_21.1
GF0048746	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00430_mRNA_20.1
GF0048745	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00430_mRNA_17.1
GF0048744	0	0	1	Hypothetical protein (1)	L-ascorbic acid binding [GO:0031418 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (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)	Prolyl 4-hydroxylase, alpha subunit [IPR006620] (1); HAD-like domain [IPR023214] (1); ShKT domain [IPR003582] (1); Oxoglutarate/iron-dependent dioxygenase [IPR005123] (1)	-	-	P_trifoliata_00430_mRNA_1.1
GF0048743	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00429_mRNA_5.1
GF0048742	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00429_mRNA_4.1
GF0048741	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00429_mRNA_3.1
GF0048740	0	0	1	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Reverse transcriptase zinc-binding domain [IPR026960] (1); Zinc knuckle CX2CX4HX4C [IPR025836] (1); Zinc finger, CCHC-type [IPR001878] (1)	-	-	P_trifoliata_00429_mRNA_24.1
GF0048739	0	0	1	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 [IPR001128] (1); Cytochrome P450, E-class, group I [IPR002401] (1)	-	-	P_trifoliata_00429_mRNA_22.1
GF0048738	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00429_mRNA_21.1
GF0048737	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00429_mRNA_2.1
GF0048736	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00429_mRNA_18.1
GF0048735	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00428_mRNA_9.1
GF0048734	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00428_mRNA_32.1
GF0048733	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00428_mRNA_31.1
GF0048732	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00428_mRNA_3.1
GF0048731	0	0	1	Translation initiation factor IF-2, putative (1)		Protein of unknown function DUF674 [IPR007750] (1)	-	-	P_trifoliata_00428_mRNA_25.1
GF0048730	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00428_mRNA_13.1
GF0048729	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00427_mRNA_26.1
GF0048728	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00427_mRNA_2.1
GF0048727	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00427_mRNA_18.1
GF0048726	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00427_mRNA_15.1
GF0048725	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00427_mRNA_14.1
GF0048724	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00427_mRNA_12.1
GF0048723	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00426_mRNA_9.1
GF0048722	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Aspartic peptidase domain [IPR021109] (1); Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00426_mRNA_7.1
GF0048721	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00426_mRNA_5.1
GF0048720	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00426_mRNA_1.1
GF0048719	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00425_mRNA_9.1
GF0048718	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00425_mRNA_6.1
GF0048717	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00425_mRNA_5.1
GF0048716	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00425_mRNA_23.1
GF0048715	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00425_mRNA_22.1
GF0048714	0	0	1	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	-	P_trifoliata_00425_mRNA_21.1
GF0048713	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00425_mRNA_16.1
GF0048712	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00425_mRNA_10.1
GF0048711	0	0	1	Cytochrome P450 716B1 (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)	-	-	P_trifoliata_00425_mRNA_1.1
GF0048710	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00424_mRNA_21.1
GF0048709	0	0	1	GRAM domain protein/ABA-responsive-like protein (1)		GRAM domain [IPR004182] (1)	-	-	P_trifoliata_00424_mRNA_14.1
GF0048708	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00424_mRNA_1.1
GF0048707	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00423_mRNA_9.1
GF0048706	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00423_mRNA_8.1
GF0048705	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00423_mRNA_7.1
GF0048704	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00423_mRNA_6.1
GF0048703	0	0	1	Hypothetical protein (1)		SAP domain [IPR003034] (1)	-	-	P_trifoliata_00423_mRNA_33.1
GF0048702	0	0	1	CD2 antigen cytoplasmic tail-binding 2 (1)		EF-Hand 1, calcium-binding site [IPR018247] (1)	-	-	P_trifoliata_00423_mRNA_3.1
GF0048701	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00423_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***
GF0048700	0	0	1	Putative disease resistance protein RGA1 (1)			-	-	P_trifoliata_00423_mRNA_27.1
GF0048699	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00423_mRNA_26.1
GF0048698	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00423_mRNA_21.1
GF0048697	0	0	1	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)	-	-	P_trifoliata_00423_mRNA_14.1
GF0048696	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00423_mRNA_11.1
GF0048695	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00423_mRNA_10.1
GF0048694	0	0	1	Hypothetical protein (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)	-	-	P_trifoliata_00423_mRNA_1.1
GF0048693	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00422_mRNA_7.1
GF0048692	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00422_mRNA_33.1
GF0048691	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00422_mRNA_30.1
GF0048690	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00421_mRNA_9.1
GF0048689	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00421_mRNA_7.1
GF0048688	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00421_mRNA_5.1
GF0048687	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00421_mRNA_3.1
GF0048686	0	0	1	Hypothetical protein (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)	-	-	P_trifoliata_00421_mRNA_23.1
GF0048685	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00421_mRNA_22.1
GF0048684	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00421_mRNA_12.1
GF0048683	0	0	1	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	-	P_trifoliata_00420_mRNA_9.1
GF0048682	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00420_mRNA_7.1
GF0048681	0	0	1	Mitochondrial import inner membrane translocase subunit TIM14 (1)		DnaJ domain [IPR001623] (1)	-	-	P_trifoliata_00420_mRNA_5.1
GF0048680	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00420_mRNA_4.1
GF0048679	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00420_mRNA_25.1
GF0048678	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00420_mRNA_24.1
GF0048677	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00420_mRNA_22.1
GF0048676	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00420_mRNA_20.1
GF0048675	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00420_mRNA_2.1
GF0048674	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00420_mRNA_18.1
GF0048673	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00420_mRNA_17.1
GF0048672	0	0	1	Hypothetical protein (1)		Transposase, MuDR, plant [IPR004332] (1)	-	-	P_trifoliata_00420_mRNA_12.1
GF0048671	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00420_mRNA_10.1
GF0048670	0	0	1	Hypothetical 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)	Protein kinase-like domain [IPR011009] (1); EamA domain [IPR000620] (1); WAT1-related protein [IPR030184] (1)	-	-	P_trifoliata_00419_mRNA_9.1
GF0048669	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00419_mRNA_8.1
GF0048668	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00419_mRNA_7.1
GF0048667	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00419_mRNA_46.1
GF0048666	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00419_mRNA_45.1
GF0048665	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00419_mRNA_43.1
GF0048664	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00419_mRNA_42.1
GF0048663	0	0	1	DUF2921 family protein (1)		Protein of unknown function DUF2921 [IPR021319] (1); Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	-	-	P_trifoliata_00419_mRNA_40.1
GF0048662	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00419_mRNA_4.1
GF0048661	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00419_mRNA_39.1
GF0048660	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00419_mRNA_35.1
GF0048659	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00419_mRNA_31.1
GF0048658	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00419_mRNA_30.1
GF0048657	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00419_mRNA_3.1
GF0048656	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00419_mRNA_27.1
GF0048655	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00419_mRNA_26.1
GF0048654	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00419_mRNA_25.1
GF0048653	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00419_mRNA_24.1
GF0048652	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00419_mRNA_2.1
GF0048651	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00419_mRNA_19.1
GF0048650	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00419_mRNA_16.1
GF0048649	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00419_mRNA_15.1
GF0048648	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00419_mRNA_14.1
GF0048647	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00419_mRNA_12.1
GF0048646	0	0	1	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	-	P_trifoliata_00419_mRNA_11.1
GF0048645	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00418_mRNA_18.1
GF0048644	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00418_mRNA_13.1
GF0048643	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00418_mRNA_10.1
GF0048642	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00418_mRNA_1.1
GF0048641	0	0	1	Galactosyltransferase family protein (1)	galactosyltransferase activity [GO:0008378 molecular_function] (1); membrane [GO:0016020 cellular_component] (1); protein glycosylation [GO:0006486 biological_process] (1)	Domain of unknown function DUF4094 [IPR025298] (1); Glycosyl transferase, family 31 [IPR002659] (1)	-	-	P_trifoliata_00417_mRNA_18.1
GF0048640	0	0	1	Putative non-LTR retroelement reverse transcriptase (1)		Reverse transcriptase domain [IPR000477] (1)	-	-	P_trifoliata_00416_mRNA_9.1
GF0048639	0	0	1	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)	-	-	P_trifoliata_00416_mRNA_8.1
GF0048638	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00416_mRNA_7.1
GF0048637	0	0	1	Putative 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)	-	-	P_trifoliata_00416_mRNA_6.1
GF0048636	0	0	1	U3 small nucleolar RNA-associated protein 18 homolog (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)	-	-	P_trifoliata_00416_mRNA_25.1
GF0048635	0	0	1	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)	-	-	P_trifoliata_00416_mRNA_23.1
GF0048634	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00416_mRNA_21.1
GF0048633	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00416_mRNA_12.1
GF0048632	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00416_mRNA_1.1
GF0048631	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00415_mRNA_9.1
GF0048630	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00415_mRNA_4.1
GF0048629	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00415_mRNA_30.1
GF0048628	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00415_mRNA_29.1
GF0048627	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00415_mRNA_28.1
GF0048626	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00415_mRNA_25.1
GF0048625	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00415_mRNA_24.1
GF0048624	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00415_mRNA_19.1
GF0048623	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00415_mRNA_12.1
GF0048622	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00415_mRNA_11.1
GF0048621	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00415_mRNA_1.1
GF0048620	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00414_mRNA_4.1
GF0048619	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00414_mRNA_3.1
GF0048618	0	0	1	Oligopeptide transporter 4 (1)	nucleobase-containing compound metabolic process [GO:0006139 biological_process] (1); methyltransferase activity [GO:0008168 molecular_function] (1); transmembrane transport [GO:0055085 biological_process] (1)	Oligopeptide transporter, OPT superfamily [IPR004813] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); MT-A70-like [IPR007757] (1)	-	-	P_trifoliata_00414_mRNA_20.1
GF0048617	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00413_mRNA_8.1
GF0048616	0	0	1	Hypothetical protein (1)		Myo-inositol-1-phosphate synthase, GAPDH-like [IPR013021] (1)	-	-	P_trifoliata_00413_mRNA_3.1
GF0048615	0	0	1	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	-	P_trifoliata_00413_mRNA_19.1
GF0048614	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00413_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*
GF0048613	0	0	1	Hypothetical protein (1)		Transposase-associated domain [IPR029480] (1)	-	-	P_trifoliata_00413_mRNA_12.1
GF0048612	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00412_mRNA_6.1
GF0048611	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00412_mRNA_4.1
GF0048610	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00412_mRNA_3.1
GF0048609	0	0	1	Cell division control protein 2 homolog (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)	-	-	P_trifoliata_00412_mRNA_24.1
GF0048608	0	0	1	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	-	-	P_trifoliata_00412_mRNA_2.1
GF0048607	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00412_mRNA_19.1
GF0048606	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00412_mRNA_17.1
GF0048605	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat-containing domain [IPR020683] (1); Ankyrin repeat [IPR002110] (1)	-	-	P_trifoliata_00411_mRNA_8.1
GF0048604	0	0	1	Hypothetical protein (1)		PGG domain [IPR026961] (1)	-	-	P_trifoliata_00411_mRNA_5.1
GF0048603	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00411_mRNA_3.1
GF0048602	0	0	1	Hypothetical protein (1)	DNA repair [GO:0006281 biological_process] (1); endonuclease activity [GO:0004519 molecular_function] (1); nucleus [GO:0005634 cellular_component] (1); damaged DNA binding [GO:0003684 molecular_function] (1)	ERCC1/RAD10/SWI10 family [IPR004579] (1); Restriction endonuclease type II-like [IPR011335] (1)	-	-	P_trifoliata_00411_mRNA_25.1
GF0048601	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00411_mRNA_24.1
GF0048600	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00411_mRNA_23.1
GF0048599	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00411_mRNA_21.1
GF0048598	0	0	1	Ankyrin repeat protein-like (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat-containing domain [IPR020683] (1); Ankyrin repeat [IPR002110] (1)	-	-	P_trifoliata_00411_mRNA_2.1
GF0048597	0	0	1	SWIB complex BAF60b domain-containing protein (1)	DNA binding [GO:0003677 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	SWIB/MDM2 domain [IPR003121] (1); SWIB domain [IPR019835] (1); DEK, C-terminal [IPR014876] (1); Homeodomain-like [IPR009057] (1)	-	-	P_trifoliata_00411_mRNA_17.1
GF0048596	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00411_mRNA_12.1
GF0048595	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00410_mRNA_9.1
GF0048594	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00410_mRNA_7.1
GF0048593	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00410_mRNA_6.1
GF0048592	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00410_mRNA_40.1
GF0048591	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00410_mRNA_34.1
GF0048590	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00410_mRNA_32.1
GF0048589	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00410_mRNA_31.1
GF0048588	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00410_mRNA_30.1
GF0048587	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00410_mRNA_28.1
GF0048586	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00410_mRNA_25.1
GF0048585	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00410_mRNA_24.1
GF0048584	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00410_mRNA_19.1
GF0048583	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00410_mRNA_17.1
GF0048582	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00410_mRNA_16.1
GF0048581	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00410_mRNA_11.1
GF0048580	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00410_mRNA_10.1
GF0048579	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00410_mRNA_1.1
GF0048578	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4216 [IPR025312] (1)	-	-	P_trifoliata_00409_mRNA_9.1
GF0048577	0	0	1	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)	-	-	P_trifoliata_00409_mRNA_8.1
GF0048576	0	0	1	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	-	-	P_trifoliata_00409_mRNA_6.1
GF0048575	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00409_mRNA_5.1
GF0048574	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00409_mRNA_4.1
GF0048573	0	0	1	(-)-germacrene D synthase (1)	metabolic process [GO:0008152 biological_process] (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, 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)	-	-	P_trifoliata_00409_mRNA_20.1
GF0048572	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00409_mRNA_19.1
GF0048571	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00409_mRNA_16.1
GF0048570	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00409_mRNA_12.1
GF0048569	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00409_mRNA_11.1
GF0048568	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4219 [IPR025314] (1)	-	-	P_trifoliata_00408_mRNA_8.1
GF0048567	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00408_mRNA_7.1
GF0048566	0	0	1	LRR receptor-like serine/threonine-protein kinase EFR (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)	-	-	P_trifoliata_00408_mRNA_2.1
GF0048565	0	0	1	Hypothetical protein (1)	cytoplasm [GO:0005737 cellular_component] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 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); thioredoxin-disulfide reductase activity [GO:0004791 molecular_function] (1); removal of superoxide radicals [GO:0019430 biological_process] (1)	Pyridine nucleotide-disulphide oxidoreductase, class-II [IPR000103] (1); Pyridine nucleotide-disulphide oxidoreductase, class-II, active site [IPR008255] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1); FAD/NAD(P)-binding domain [IPR023753] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Thioredoxin reductase [IPR005982] (1); Serine/threonine-protein kinase, active site [IPR008271] (1)	-	-	P_trifoliata_00408_mRNA_15.1
GF0048564	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00407_mRNA_9.1
GF0048563	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00407_mRNA_6.1
GF0048562	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00407_mRNA_5.1
GF0048561	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00407_mRNA_4.1
GF0048560	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00407_mRNA_20.1
GF0048559	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00407_mRNA_2.1
GF0048558	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00407_mRNA_17.1
GF0048557	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00407_mRNA_14.1
GF0048556	0	0	1	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)	-	-	P_trifoliata_00406_mRNA_5.1
GF0048555	0	0	1	Hypothetical protein (1)		Chloramphenicol acetyltransferase-like domain [IPR023213] (1)	-	-	P_trifoliata_00406_mRNA_29.1
GF0048554	0	0	1	F-box protein At5g52880 (1)	protein binding [GO:0005515 molecular_function] (1)	F-box domain [IPR001810] (1)	-	-	P_trifoliata_00406_mRNA_22.1
GF0048553	0	0	1	LRR receptor-like kinase (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00406_mRNA_2.1
GF0048552	0	0	1	Anthocyanidin 5,3-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)	-	-	P_trifoliata_00406_mRNA_16.1
GF0048551	0	0	1	Anthocyanidin 5,3-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)	-	-	P_trifoliata_00406_mRNA_15.1
GF0048550	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00406_mRNA_1.1
GF0048549	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00405_mRNA_18.1
GF0048548	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00405_mRNA_17.1
GF0048547	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00403_mRNA_7.1
GF0048546	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00403_mRNA_6.1
GF0048545	0	0	1	NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial (1)		Zinc finger, CHCC-type [IPR019401] (1)	-	-	P_trifoliata_00403_mRNA_3.1
GF0048544	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00403_mRNA_25.1
GF0048543	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00403_mRNA_24.1
GF0048542	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00403_mRNA_23.1
GF0048541	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00403_mRNA_22.1
GF0048540	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00403_mRNA_21.1
GF0048539	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00403_mRNA_20.1

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*
GF0048538	0	0	1	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1)	ATPase, AAA-type, core [IPR003959] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	-	P_trifoliata_00403_mRNA_2.1
GF0048537	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00403_mRNA_19.1
GF0048536	0	0	1	Non-LTR retroelement reverse transcriptase (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	-	P_trifoliata_00403_mRNA_15.1
GF0048535	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00403_mRNA_14.1
GF0048534	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00403_mRNA_13.1
GF0048533	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00403_mRNA_12.1
GF0048532	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00403_mRNA_10.1
GF0048531	0	0	1	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)	-	-	P_trifoliata_00402_mRNA_9.1
GF0048530	0	0	1	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)	-	-	P_trifoliata_00402_mRNA_5.1
GF0048529	0	0	1	Hypothetical protein (1)		Protein of unknown function DUF594 [IPR007658] (1)	-	-	P_trifoliata_00402_mRNA_27.1
GF0048528	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00402_mRNA_25.1
GF0048527	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00402_mRNA_2.1
GF0048526	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00402_mRNA_10.1
GF0048525	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00402_mRNA_1.1
GF0048524	0	0	1	L-iditol 2-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 superfamily, zinc-type [IPR002085] (1); Alcohol dehydrogenase, N-terminal [IPR013154] (1); Alcohol dehydrogenase, zinc-type, conserved site [IPR002328] (1); Alcohol dehydrogenase, C-terminal [IPR013149] (1)	-	-	P_trifoliata_00401_mRNA_5.1
GF0048523	0	0	1	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)	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)	-	-	P_trifoliata_00401_mRNA_4.1
GF0048522	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00401_mRNA_22.1
GF0048521	0	0	1	Hypothetical protein (1)	catalytic activity [GO:0003824 molecular_function] (1)	L-Aspartase-like [IPR008948] (1); Phenylalanine ammonia-lyase, shielding domain [IPR023144] (1); Aromatic amino acid lyase [IPR001106] (1)	-	-	P_trifoliata_00401_mRNA_20.1
GF0048520	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00401_mRNA_2.1
GF0048519	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00401_mRNA_17.1
GF0048518	0	0	1	2-oxoglutarate and Fe(II)-dependent oxygenase superfamily protein isoform 1 (1)	iron ion binding [GO:0005506 molecular_function] (1); L-ascorbic acid binding [GO:0031418 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1)	Prolyl 4-hydroxylase, alpha subunit [IPR006620] (1); Oxoglutarate/iron-dependent dioxygenase [IPR005123] (1)	-	-	P_trifoliata_00401_mRNA_16.1
GF0048517	0	0	1	Hypothetical protein (1)	isoprenoid biosynthetic process [GO:0008299 biological_process] (1); metabolic process [GO:0008152 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1); hydroxymethylglutaryl-CoA synthase activity [GO:0004421 molecular_function] (1)	Hydroxymethylglutaryl-coenzyme A synthase, N-terminal [IPR013528] (1); Transcription factor, TCP [IPR005333] (1); Thiolase-like [IPR016039] (1); Transcription factor TCP subgroup [IPR017887] (1); Hydroxymethylglutaryl-coenzyme A synthase C-terminal domain [IPR013746] (1); Hydroxymethylglutaryl-coenzyme A synthase, active site [IPR000590] (1); Hydroxymethylglutaryl-CoA synthase, eukaryotic [IPR010122] (1)	-	-	P_trifoliata_00401_mRNA_14.1
GF0048516	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00401_mRNA_1.1
GF0048515	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00400_mRNA_8.1
GF0048514	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4219 [IPR025314] (1)	-	-	P_trifoliata_00400_mRNA_7.1
GF0048513	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00400_mRNA_3.1
GF0048512	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00400_mRNA_11.1
GF0048511	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00399_mRNA_9.1
GF0048510	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00399_mRNA_8.1
GF0048509	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00399_mRNA_6.1
GF0048508	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00399_mRNA_5.1
GF0048507	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00399_mRNA_4.1
GF0048506	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00399_mRNA_30.1
GF0048505	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00399_mRNA_3.1
GF0048504	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00399_mRNA_29.1
GF0048503	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00399_mRNA_28.1
GF0048502	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00399_mRNA_27.1
GF0048501	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00399_mRNA_24.1
GF0048500	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00399_mRNA_23.1
GF0048499	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00399_mRNA_22.1
GF0048498	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00399_mRNA_21.1
GF0048497	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00399_mRNA_20.1
GF0048496	0	0	1	Cysteine-rich RLK (Receptor-like kinase) protein (1)		Gnk2-homologous domain [IPR002902] (1)	-	-	P_trifoliata_00399_mRNA_2.1
GF0048495	0	0	1	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)	-	-	P_trifoliata_00399_mRNA_19.1
GF0048494	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00399_mRNA_17.1
GF0048493	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00399_mRNA_10.1
GF0048492	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00398_mRNA_8.1
GF0048491	0	0	1	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)	-	-	P_trifoliata_00398_mRNA_6.1
GF0048490	0	0	1	AT1G10290 protein (1)	GTP binding [GO:0005525 molecular_function] (1); GTPase activity [GO:0003924 molecular_function] (1)	Dynamin GTPase effector [IPR003130] (1); Dynamin superfamily [IPR022812] (1); PH domain-like [IPR011993] (1); GTPase effector domain [IPR020850] (1); Pleckstrin homology domain [IPR001849] (1)	-	-	P_trifoliata_00398_mRNA_5.1
GF0048489	0	0	1	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	-	P_trifoliata_00398_mRNA_19.1
GF0048488	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00398_mRNA_16.1
GF0048487	0	0	1	Small chain of ribonucleotide reductase (1)	deoxyribonucleoside diphosphate metabolic process [GO:0009186 biological_process] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1)	Ribonucleotide reductase small subunit [IPR000358] (1); Ferritin-like superfamily [IPR009078] (1); Ribonucleotide reductase-related [IPR012348] (1)	-	-	P_trifoliata_00398_mRNA_13.1
GF0048486	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00398_mRNA_10.1
GF0048485	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00398_mRNA_1.1
GF0048484	0	0	1	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)	-	-	P_trifoliata_00397_mRNA_7.1
GF0048483	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00397_mRNA_25.1
GF0048482	0	0	1	Hypothetical protein (1)		Cell division protein FtsZ, C-terminal [IPR024757] (1); Tubulin/FtsZ, 2-layer sandwich domain [IPR018316] (1); Tubulin/FtsZ, C-terminal [IPR008280] (1)	-	-	P_trifoliata_00397_mRNA_21.1
GF0048481	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00397_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*
GF0048480	0	0	1	NAC domain protein (1)	DNA binding [GO:0003677 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	NAC domain [IPR003441] (1)	-	-	P_trifoliata_00397_mRNA_18.1
GF0048479	0	0	1	Hypothetical protein (1)		Transposase, MuDR, plant [IPR004332] (1)	-	-	P_trifoliata_00397_mRNA_15.1
GF0048478	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00397_mRNA_1.1
GF0048477	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00396_mRNA_6.1
GF0048476	0	0	1	Hypothetical protein (1)	hydrolase activity [GO:0016787 molecular_function] (1)	Peptidase T2, asparaginase 2 [IPR000246] (1); Nucleophile aminohydrolases, N-terminal [IPR029055] (1)	-	-	P_trifoliata_00396_mRNA_3.1
GF0048475	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00396_mRNA_17.1
GF0048474	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00396_mRNA_16.1
GF0048473	0	0	1	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); catalytic activity [GO:0003824 molecular_function] (1)	ATP-grasp fold, ATP-dependent carboxylate-amine ligase-type [IPR003135] (1); ATP-grasp fold, subdomain 1 [IPR013815] (1)	-	-	P_trifoliata_00396_mRNA_15.1
GF0048472	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00396_mRNA_11.1
GF0048471	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00395_mRNA_9.1
GF0048470	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00395_mRNA_7.1
GF0048469	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00395_mRNA_5.1
GF0048468	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00395_mRNA_3.1
GF0048467	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00395_mRNA_29.1
GF0048466	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00395_mRNA_25.1
GF0048465	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00395_mRNA_23.1
GF0048464	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00395_mRNA_17.1
GF0048463	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00395_mRNA_16.1
GF0048462	0	0	1	Tyrosine-sulfated glycopeptide receptor 1 (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)	-	-	P_trifoliata_00393_mRNA_15.1
GF0048461	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00393_mRNA_13.1
GF0048460	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00393_mRNA_1.1
GF0048459	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00392_mRNA_6.1
GF0048458	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00392_mRNA_5.1
GF0048457	0	0	1	Hypothetical protein (1)	methyltransferase activity [GO:0008168 molecular_function] (1)	SAM dependent carboxyl methyltransferase [IPR005299] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	-	P_trifoliata_00392_mRNA_23.1
GF0048456	0	0	1	S-adenosyl-L-methionine:carboxyl methyltransferase family protein (1)	methyltransferase activity [GO:0008168 molecular_function] (1)	S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); SAM dependent carboxyl methyltransferase [IPR005299] (1)	-	-	P_trifoliata_00392_mRNA_21.1
GF0048455	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00392_mRNA_16.1
GF0048454	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00392_mRNA_15.1
GF0048453	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00392_mRNA_13.1
GF0048452	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00392_mRNA_10.1
GF0048451	0	0	1	UDP-glycosyltransferase 91C1 (1)	metabolic process [GO:0008152 biological_process] (1); transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	-	-	P_trifoliata_00392_mRNA_1.1
GF0048450	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00391_mRNA_28.1
GF0048449	0	0	1	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)	-	-	P_trifoliata_00391_mRNA_22.1
GF0048448	0	0	1	Cytochrome P450 81D1 (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 [IPR001128] (1)	-	-	P_trifoliata_00391_mRNA_17.1
GF0048447	0	0	1	Metal transporter (1)	transporter activity [GO:0005215 molecular_function] (1); transport [GO:0006810 biological_process] (1); membrane [GO:0016020 cellular_component] (1)	NRAMP family [IPR001046] (1)	-	-	P_trifoliata_00391_mRNA_10.1
GF0048446	0	0	1	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)	-	-	P_trifoliata_00391_mRNA_1.1
GF0048445	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00390_mRNA_8.1
GF0048444	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00390_mRNA_27.1
GF0048443	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00390_mRNA_26.1
GF0048442	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00390_mRNA_18.1
GF0048441	0	0	1	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	-	P_trifoliata_00390_mRNA_17.1
GF0048440	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00390_mRNA_15.1
GF0048439	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00390_mRNA_13.1
GF0048438	0	0	1	Hypothetical protein (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Peptidase A2A, retrovirus, catalytic [IPR001995] (1)	-	-	P_trifoliata_00390_mRNA_10.1
GF0048437	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00389_mRNA_5.1
GF0048436	0	0	1	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); GroES-like [IPR011032] (1); Alcohol dehydrogenase superfamily, zinc-type [IPR002085] (1)	-	-	P_trifoliata_00389_mRNA_27.1
GF0048435	0	0	1	Leucine-rich repeat receptor-like protein kinase PXL1 (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)	-	-	P_trifoliata_00389_mRNA_26.1
GF0048434	0	0	1	Glucan endo-1,3-beta-glucosidase 8 (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 family 17 [IPR000490] (1); Glycoside hydrolase, catalytic domain [IPR013781] (1); X8 domain [IPR012946] (1)	-	-	P_trifoliata_00389_mRNA_15.1
GF0048433	0	0	1	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)	-	-	P_trifoliata_00389_mRNA_1.1
GF0048432	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00388_mRNA_8.1
GF0048431	0	0	1	Flowering locus T (1)		Phosphatidylethanolamine-binding protein PEBP [IPR008914] (1); Phosphatidylethanolamine-binding, conserved site [IPR001858] (1)	-	-	P_trifoliata_00388_mRNA_30.1
GF0048430	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00388_mRNA_16.1
GF0048429	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00388_mRNA_12.1
GF0048428	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00387_mRNA_7.1
GF0048427	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00387_mRNA_6.1
GF0048426	0	0	1	Retrotransposon protein, putative, Ty1-copia subclass (1)	DNA integration [GO:0015074 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	GAG-pre-integrase domain [IPR025724] (1); Integrase, catalytic core [IPR001584] (1); Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00387_mRNA_22.1
GF0048425	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00387_mRNA_15.1
GF0048424	0	0	1	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)	-	-	P_trifoliata_00387_mRNA_1.1
GF0048423	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00386_mRNA_8.1
GF0048422	0	0	1	Hypothetical protein (1)		Transposase, MuDR, plant [IPR004332] (1)	-	-	P_trifoliata_00386_mRNA_6.1
GF0048421	0	0	1	Ribonucleoside-diphosphate reductase, beta subunit (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); deoxyribonucleoside diphosphate metabolic process [GO:0009186 biological_process] (1)	Ribonucleotide reductase small subunit, acitve site [IPR030475] (1); Ribonucleotide reductase small subunit [IPR000358] (1); Ferritin-like superfamily [IPR009078] (1); Ribonucleotide reductase-related [IPR012348] (1)	-	-	P_trifoliata_00386_mRNA_5.1
GF0048420	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00386_mRNA_3.1
GF0048419	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00386_mRNA_21.1
GF0048418	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00386_mRNA_12.1
GF0048417	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00386_mRNA_11.1
GF0048416	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00386_mRNA_1.1
GF0048415	0	0	1	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	-	P_trifoliata_00385_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*
GF0048414	0	0	1	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); oxidation-reduction process [GO:0055114 biological_process] (1); metal ion binding [GO:0046872 molecular_function] (1)	Lipoxygenase [IPR000907] (1); Lipoxygenase, C-terminal [IPR013819] (1)	-	-	P_trifoliata_00385_mRNA_5.1
GF0048413	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00385_mRNA_26.1
GF0048412	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00385_mRNA_22.1
GF0048411	0	0	1	Hypothetical protein (1)	metal ion binding [GO:0046872 molecular_function] (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)	Lipoxygenase, C-terminal [IPR013819] (1); Lipoxygenase [IPR000907] (1)	-	-	P_trifoliata_00385_mRNA_2.1
GF0048410	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00385_mRNA_19.1
GF0048409	0	0	1	Oxidoreductase family, NAD-binding rossmann fold protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Oxidoreductase, N-terminal [IPR000683] (1); Oxidoreductase, C-terminal [IPR004104] (1); NAD(P)-binding domain [IPR016040] (1)	-	-	P_trifoliata_00385_mRNA_14.1
GF0048408	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00385_mRNA_13.1
GF0048407	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00385_mRNA_11.1
GF0048406	0	0	1	Hypothetical protein (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 [IPR000907] (1)	-	-	P_trifoliata_00385_mRNA_10.1
GF0048405	0	0	1	Outer envelope protein of 80 kDa (1)	outer membrane [GO:0019867 cellular_component] (1)	Bacterial surface antigen (D15) [IPR000184] (1)	-	-	P_trifoliata_00384_mRNA_6.1
GF0048404	0	0	1	Hypothetical protein (1)		K homology domain-like, alpha/beta [IPR015946] (1); GTPase Der, C-terminal KH-domain-like [IPR032859] (1)	-	-	P_trifoliata_00384_mRNA_24.1
GF0048403	0	0	1	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Aldehyde dehydrogenase N-terminal domain [IPR016162] (1); Aldehyde/histidinol dehydrogenase [IPR016161] (1)	-	-	P_trifoliata_00384_mRNA_22.1
GF0048402	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00384_mRNA_2.1
GF0048401	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00384_mRNA_16.1
GF0048400	0	0	1	Extensin (1)			-	-	P_trifoliata_00384_mRNA_15.1
GF0048399	0	0	1	Hypothetical protein (1)		Ankyrin repeat-containing domain [IPR020683] (1)	-	-	P_trifoliata_00384_mRNA_13.1
GF0048398	0	0	1	Neurofilament heavy protein, putative (1)			-	-	P_trifoliata_00384_mRNA_12.1
GF0048397	0	0	1	Neurofilament heavy protein, putative (1)			-	-	P_trifoliata_00384_mRNA_11.1
GF0048396	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00383_mRNA_25.1
GF0048395	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00383_mRNA_10.1
GF0048394	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00382_mRNA_7.1
GF0048393	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00382_mRNA_6.1
GF0048392	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00382_mRNA_4.1
GF0048391	0	0	1	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	-	P_trifoliata_00382_mRNA_27.1
GF0048390	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00382_mRNA_24.1
GF0048389	0	0	1	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	-	-	P_trifoliata_00382_mRNA_23.1
GF0048388	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00382_mRNA_21.1
GF0048387	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00382_mRNA_20.1
GF0048386	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00382_mRNA_16.1
GF0048385	0	0	1	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	-	P_trifoliata_00382_mRNA_15.1
GF0048384	0	0	1	Glucan endo-1,3-beta-glucosidase 14 (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 family 17 [IPR000490] (1); Glycoside hydrolase, catalytic domain [IPR013781] (1)	-	-	P_trifoliata_00382_mRNA_13.1
GF0048383	0	0	1	Hypothetical protein (1)		X8 domain [IPR012946] (1)	-	-	P_trifoliata_00382_mRNA_12.1
GF0048382	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00382_mRNA_1.1
GF0048381	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00381_mRNA_27.1
GF0048380	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00381_mRNA_25.1
GF0048379	0	0	1	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	-	P_trifoliata_00381_mRNA_24.1
GF0048378	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00381_mRNA_21.1
GF0048377	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00381_mRNA_20.1
GF0048376	0	0	1	Crooked neck protein / cell cycle protein, putative (1)	protein binding [GO:0005515 molecular_function] (1); RNA processing [GO:0006396 biological_process] (1)	Tetratricopeptide-like helical domain [IPR011990] (1); HAT (Half-A-TPR) repeat [IPR003107] (1); Tetratricopeptide repeat-containing domain [IPR013026] (1)	-	-	P_trifoliata_00381_mRNA_16.1
GF0048375	0	0	1	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)	-	-	P_trifoliata_00380_mRNA_3.1
GF0048374	0	0	1	Hexose carrier protein HEX6 (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)	-	-	P_trifoliata_00380_mRNA_24.1
GF0048373	0	0	1	Hypothetical protein (1)		Chromo/chromo shadow domain [IPR000953] (1); Chromo domain-like [IPR016197] (1)	-	-	P_trifoliata_00380_mRNA_17.1
GF0048372	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00380_mRNA_15.1
GF0048371	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat-containing domain [IPR020683] (1); Ankyrin repeat [IPR002110] (1)	-	-	P_trifoliata_00380_mRNA_13.1
GF0048370	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00380_mRNA_10.1
GF0048369	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00380_mRNA_1.1
GF0048368	0	0	1	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)	-	-	P_trifoliata_00379_mRNA_4.1
GF0048367	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00379_mRNA_22.1
GF0048366	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00379_mRNA_17.1
GF0048365	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00379_mRNA_13.1
GF0048364	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00379_mRNA_12.1
GF0048363	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00378_mRNA_6.1
GF0048362	0	0	1	SOUL heme-binding family protein (1)		Regulatory factor, effector binding domain [IPR011256] (1); SOUL haem-binding protein [IPR006917] (1); NTF2-like domain [IPR032710] (1); Protein of unknown function DUF2358 [IPR018790] (1)	-	-	P_trifoliata_00378_mRNA_4.1
GF0048361	0	0	1	DEAD box RNA helicase (1)	ATP binding [GO:0005524 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (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)	-	-	P_trifoliata_00378_mRNA_34.1
GF0048360	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00378_mRNA_33.1
GF0048359	0	0	1	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	-	P_trifoliata_00378_mRNA_32.1
GF0048358	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00378_mRNA_30.1
GF0048357	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00378_mRNA_19.1
GF0048356	0	0	1	Hypothetical protein (1)		Protein of unknown function DUF2921 [IPR021319] (1)	-	-	P_trifoliata_00378_mRNA_18.1
GF0048355	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00378_mRNA_14.1
GF0048354	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00378_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*
GF0048353	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00378_mRNA_12.1
GF0048352	0	0	1	Transducin/WD40 repeat-like superfamily protein isoform 1 (1)	protein binding [GO:0005515 molecular_function] (1)	WD40/YVTN repeat-like-containing domain [IPR015943] (1); WD40 repeat [IPR001680] (1); WD40-repeat-containing domain [IPR017986] (1)	-	-	P_trifoliata_00378_mRNA_1.1
GF0048351	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00377_mRNA_9.1
GF0048350	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00377_mRNA_5.1
GF0048349	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00377_mRNA_3.1
GF0048348	0	0	1	Type I proteinase inhibitor-like protein (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)	-	-	P_trifoliata_00377_mRNA_24.1
GF0048347	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00377_mRNA_23.1
GF0048346	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00377_mRNA_2.1
GF0048345	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00377_mRNA_18.1
GF0048344	0	0	1	Leucine-rich repeat (LRR) family protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	-	P_trifoliata_00377_mRNA_17.1
GF0048343	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00377_mRNA_13.1
GF0048342	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00377_mRNA_12.1
GF0048341	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	MATH/TRAF domain [IPR002083] (1); TRAF-like [IPR008974] (1)	-	-	P_trifoliata_00376_mRNA_6.1
GF0048340	0	0	1	Translation elongation factor tu (1)		Translation elongation factor EFTu/EF1A, C-terminal [IPR004160] (1); Translation elongation factor EF1A/initiation factor IF2gamma, C-terminal [IPR009001] (1)	-	-	P_trifoliata_00376_mRNA_5.1
GF0048339	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00376_mRNA_46.1
GF0048338	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00376_mRNA_45.1
GF0048337	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00376_mRNA_44.1
GF0048336	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00376_mRNA_43.1
GF0048335	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00376_mRNA_40.1
GF0048334	0	0	1	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)	Major facilitator superfamily domain [IPR020846] (1); Major facilitator, sugar transporter-like [IPR005828] (1)	-	-	P_trifoliata_00376_mRNA_36.1
GF0048333	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00376_mRNA_35.1
GF0048332	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00376_mRNA_18.1
GF0048331	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00376_mRNA_12.1
GF0048330	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00375_mRNA_9.1
GF0048329	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00375_mRNA_6.1
GF0048328	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00375_mRNA_18.1
GF0048327	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00375_mRNA_14.1
GF0048326	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00375_mRNA_12.1
GF0048325	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00374_mRNA_8.1
GF0048324	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00374_mRNA_7.1
GF0048323	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00374_mRNA_4.1
GF0048322	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00374_mRNA_26.1
GF0048321	0	0	1	Reticuline oxidase (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); oxidoreductase activity, acting on CH-OH group of donors [GO:0016614 molecular_function] (1); catalytic activity [GO:0003824 molecular_function] (1)	FAD-binding, type 2 [IPR016166] (1); FAD linked oxidase, N-terminal [IPR006094] (1); CO dehydrogenase flavoprotein-like, FAD-binding, subdomain 2 [IPR016169] (1)	-	-	P_trifoliata_00374_mRNA_25.1
GF0048320	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00374_mRNA_24.1
GF0048319	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00374_mRNA_22.1
GF0048318	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00374_mRNA_17.1
GF0048317	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00374_mRNA_15.1
GF0048316	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00374_mRNA_14.1
GF0048315	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00374_mRNA_10.1
GF0048314	0	0	1	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	-	P_trifoliata_00373_mRNA_35.1
GF0048313	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00373_mRNA_1.1
GF0048312	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00372_mRNA_35.1
GF0048311	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00372_mRNA_34.1
GF0048310	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Tetratricopeptide-like helical domain [IPR011990] (1)	-	-	P_trifoliata_00372_mRNA_33.1
GF0048309	0	0	1	Hypothetical protein (1)		KHA domain [IPR021789] (1)	-	-	P_trifoliata_00372_mRNA_27.1
GF0048308	0	0	1	Hypothetical protein (1)	integral component of membrane [GO:0016021 cellular_component] (1); transporter activity [GO:0005215 molecular_function] (1)	Purine permease, plant [IPR030182] (1)	-	-	P_trifoliata_00372_mRNA_2.1
GF0048307	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00372_mRNA_17.1
GF0048306	0	0	1	Leucine-rich repeat, typical subtype (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	-	P_trifoliata_00371_mRNA_34.1
GF0048305	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00371_mRNA_29.1
GF0048304	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00371_mRNA_28.1
GF0048303	0	0	1	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)	Translation protein SH3-like domain [IPR008991] (1); Ribosomal protein L2 domain 2 [IPR014722] (1); Ribosomal protein L14 [IPR002784] (1)	-	-	P_trifoliata_00371_mRNA_26.1
GF0048302	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00371_mRNA_25.1
GF0048301	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00371_mRNA_22.1
GF0048300	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00371_mRNA_17.1
GF0048299	0	0	1	Hypothetical protein (1)		Jas TPL-binding domain [IPR032308] (1)	-	-	P_trifoliata_00371_mRNA_16.1
GF0048298	0	0	1	Hypothetical protein (1)		Acyl-CoA N-acyltransferase [IPR016181] (1)	-	-	P_trifoliata_00371_mRNA_15.1
GF0048297	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00371_mRNA_14.1
GF0048296	0	0	1	Pentatricopeptide repeat-containing protein, mitochondrial (1)	protein binding [GO:0005515 molecular_function] (1)	Pentatricopeptide repeat [IPR002885] (1); Tetratricopeptide-like helical domain [IPR011990] (1)	-	-	P_trifoliata_00371_mRNA_11.1
GF0048295	0	0	1	Hypothetical protein (1)		Glutathione S-transferase, C-terminal-like [IPR010987] (1)	-	-	P_trifoliata_00370_mRNA_9.1
GF0048294	0	0	1	Retrovirus-related Pol polyprotein from transposon TNT 1-94 (1)			-	-	P_trifoliata_00370_mRNA_8.1
GF0048293	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00370_mRNA_4.1
GF0048292	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00370_mRNA_25.1
GF0048291	0	0	1	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)	-	-	P_trifoliata_00370_mRNA_17.1
GF0048290	0	0	1	SLG-Sc and SLA-Sc genes and Melmoth retrotransposon sequence (1)			-	-	P_trifoliata_00370_mRNA_15.1
GF0048289	0	0	1	TMV resistance protein N (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	-	P_trifoliata_00370_mRNA_12.1
GF0048288	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00370_mRNA_1.1
GF0048287	0	0	1	Glutaredoxin (1)	cell redox homeostasis [GO:0045454 biological_process] (1); electron carrier activity [GO:0009055 molecular_function] (1); protein disulfide oxidoreductase activity [GO:0015035 molecular_function] (1)	Glutaredoxin, eukaryotic/virial [IPR011899] (1); Glutaredoxin [IPR002109] (1); Thioredoxin, conserved site [IPR017937] (1); Thioredoxin-like fold [IPR012336] (1); Glutaredoxin subgroup [IPR014025] (1)	-	-	P_trifoliata_00369_mRNA_7.1
GF0048286	0	0	1	Hypothetical 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 PHO80-like [IPR013922] (1)	-	-	P_trifoliata_00369_mRNA_6.1
GF0048285	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00369_mRNA_29.1
GF0048284	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00369_mRNA_27.1
GF0048283	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00369_mRNA_25.1
GF0048282	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00369_mRNA_23.1
GF0048281	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00369_mRNA_21.1
GF0048280	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00369_mRNA_20.1
GF0048279	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00369_mRNA_19.1
GF0048278	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00369_mRNA_18.1
GF0048277	0	0	1	Blue copper protein (1)	electron carrier activity [GO:0009055 molecular_function] (1)	Phytocyanin domain [IPR003245] (1); Cupredoxin [IPR008972] (1)	-	-	P_trifoliata_00369_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*
GF0048276	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00368_mRNA_46.1
GF0048275	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00368_mRNA_41.1
GF0048274	0	0	1	Hypothetical protein (1)	steroid biosynthetic process [GO:0006694 biological_process] (1); methyltransferase activity [GO:0008168 molecular_function] (1)	S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); SAM-dependent methyltransferase SMT-type [IPR030384] (1); Sterol methyltransferase C-terminal [IPR013705] (1)	-	-	P_trifoliata_00368_mRNA_3.1
GF0048273	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00368_mRNA_16.1
GF0048272	0	0	1	60S ribosomal protein L31 (1)	structural constituent of ribosome [GO:0003735 molecular_function] (1); translation [GO:0006412 biological_process] (1); intracellular [GO:0005622 cellular_component] (1); ribosome [GO:0005840 cellular_component] (1)	Ribosomal protein L31e, conserved site [IPR020052] (1); Ribosomal protein L31e [IPR000054] (1); Ribosomal protein L31e domain [IPR023621] (1)	-	-	P_trifoliata_00368_mRNA_10.1
GF0048271	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	-	P_trifoliata_00367_mRNA_5.1
GF0048270	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00367_mRNA_32.1
GF0048269	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00367_mRNA_29.1
GF0048268	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00367_mRNA_2.1
GF0048267	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00367_mRNA_1.1
GF0048266	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00366_mRNA_8.1
GF0048265	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00366_mRNA_7.1
GF0048264	0	0	1	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)	-	-	P_trifoliata_00366_mRNA_6.1
GF0048263	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00366_mRNA_5.1
GF0048262	0	0	1	Hypothetical protein (1)		FAR1 DNA binding domain [IPR004330] (1)	-	-	P_trifoliata_00366_mRNA_22.1
GF0048261	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00366_mRNA_2.1
GF0048260	0	0	1	Cytochrome P450 family protein (1)	heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1); DNA binding [GO:0003677 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)	Aspartate carbamoyltransferase regulatory subunit, C-terminal [IPR020542] (1); Cytochrome P450 [IPR001128] (1); Zinc finger, BED-type [IPR003656] (1)	-	-	P_trifoliata_00366_mRNA_12.1
GF0048259	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00366_mRNA_10.1
GF0048258	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00366_mRNA_1.1
GF0048257	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00365_mRNA_5.1
GF0048256	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00365_mRNA_45.1
GF0048255	0	0	1	Hypothetical protein (1)		Major facilitator superfamily domain [IPR020846] (1)	-	-	P_trifoliata_00365_mRNA_44.1
GF0048254	0	0	1	Hypothetical protein (1)		VQ [IPR008889] (1)	-	-	P_trifoliata_00365_mRNA_38.1
GF0048253	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00365_mRNA_27.1
GF0048252	0	0	1	Hypothetical protein (1)		Bulb-type lectin domain [IPR001480] (1)	-	-	P_trifoliata_00365_mRNA_26.1
GF0048251	0	0	1	Hypothetical protein (1)		Ankyrin repeat-containing domain [IPR020683] (1)	-	-	P_trifoliata_00364_mRNA_35.1
GF0048250	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00364_mRNA_29.1
GF0048249	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00364_mRNA_28.1
GF0048248	0	0	1	DNA repair and recombination protein RAD54-like (1)	ATP binding [GO:0005524 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Helicase superfamily 1/2, ATP-binding domain [IPR014001] (1); SNF2-related, N-terminal domain [IPR000330] (1); Helicase, C-terminal [IPR001650] (1)	-	-	P_trifoliata_00364_mRNA_27.1
GF0048247	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00364_mRNA_24.1
GF0048246	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00364_mRNA_23.1
GF0048245	0	0	1	DEAD-box ATP-dependent RNA helicase 18 (1)		Helicase, C-terminal [IPR001650] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	-	P_trifoliata_00364_mRNA_22.1
GF0048244	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00364_mRNA_2.1
GF0048243	0	0	1	Glutaredoxin (GRX) family protein (1)	electron carrier activity [GO:0009055 molecular_function] (1); cell redox homeostasis [GO:0045454 biological_process] (1); protein disulfide oxidoreductase activity [GO:0015035 molecular_function] (1)	Thioredoxin-like fold [IPR012336] (1); Glutaredoxin [IPR002109] (1)	-	-	P_trifoliata_00364_mRNA_15.1
GF0048242	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00363_mRNA_35.1
GF0048241	0	0	1	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)	Plant peroxidase [IPR000823] (1); Haem peroxidase, plant/fungal/bacterial [IPR002016] (1); Haem peroxidase [IPR010255] (1)	-	-	P_trifoliata_00363_mRNA_3.1
GF0048240	0	0	1	Hypothetical protein (1)	metallopeptidase activity [GO:0008237 molecular_function] (1)	Metallopeptidase, catalytic domain [IPR024079] (1)	-	-	P_trifoliata_00363_mRNA_13.1
GF0048239	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00363_mRNA_1.1
GF0048238	0	0	1	Hypothetical protein (1)		Zinc knuckle CX2CX4HX4C [IPR025836] (1)	-	-	P_trifoliata_00362_mRNA_34.1
GF0048237	0	0	1	Seed lectin (1)	carbohydrate binding [GO:0030246 molecular_function] (1)	Legume lectin, beta chain, Mn/Ca-binding site [IPR019825] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Legume lectin domain [IPR001220] (1)	-	-	P_trifoliata_00362_mRNA_29.1
GF0048236	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00362_mRNA_28.1
GF0048235	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00362_mRNA_14.1
GF0048234	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00361_mRNA_30.1
GF0048233	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00361_mRNA_28.1
GF0048232	0	0	1	Hypothetical protein (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1); polysaccharide catabolic process [GO:0000272 biological_process] (1); beta-amylase activity [GO:0016161 molecular_function] (1)	Glycoside hydrolase, family 14 [IPR001554] (1); Glycoside hydrolase, catalytic domain [IPR013781] (1); Glycoside hydrolase superfamily [IPR017853] (1)	-	-	P_trifoliata_00361_mRNA_24.1
GF0048231	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00361_mRNA_21.1
GF0048230	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00361_mRNA_2.1
GF0048229	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00361_mRNA_13.1
GF0048228	0	0	1	Monosacharide transport protein (1)			-	-	P_trifoliata_00360_mRNA_9.1
GF0048227	0	0	1	Putative disease resistance RPP8-like protein 2 (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00360_mRNA_4.1
GF0048226	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00360_mRNA_30.1
GF0048225	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00360_mRNA_23.1
GF0048224	0	0	1	DUF936 family protein (1)		Protein of unknown function DUF936, plant [IPR010341] (1)	-	-	P_trifoliata_00360_mRNA_17.1
GF0048223	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00360_mRNA_12.1
GF0048222	0	0	1	Hypothetical protein (1)	RNA binding [GO:0003723 molecular_function] (1)	RNA-binding, CRM domain [IPR001890] (1)	-	-	P_trifoliata_00359_mRNA_9.1
GF0048221	0	0	1	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	-	P_trifoliata_00359_mRNA_7.1
GF0048220	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00359_mRNA_6.1
GF0048219	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00359_mRNA_5.1
GF0048218	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00359_mRNA_37.1
GF0048217	0	0	1	Putative disease resistance gene NBS-LRR family protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00359_mRNA_36.1
GF0048216	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00359_mRNA_35.1
GF0048215	0	0	1	Putative disease resistance gene NBS-LRR family protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00359_mRNA_34.1
GF0048214	0	0	1	Phosphoprotein phosphatase (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00359_mRNA_32.1
GF0048213	0	0	1	NBS-LRR type disease resistance protein (1)		P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	-	P_trifoliata_00359_mRNA_30.1
GF0048212	0	0	1	Putative disease resistance gene NBS-LRR 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)	-	-	P_trifoliata_00359_mRNA_29.1
GF0048211	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00359_mRNA_26.1
GF0048210	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00359_mRNA_24.1
GF0048209	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00359_mRNA_23.1
GF0048208	0	0	1	Hypothetical protein (1)	membrane [GO:0016020 cellular_component] (1)	ABC-2 type transporter [IPR013525] (1)	-	-	P_trifoliata_00359_mRNA_21.1
GF0048207	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00359_mRNA_19.1
GF0048206	0	0	1	Putative transposable element (1)		Domain of unknown function DUF4216 [IPR025312] (1); Domain of unknown function DUF4218 [IPR025452] (1)	-	-	P_trifoliata_00359_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*
GF0048205	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00359_mRNA_17.1
GF0048204	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00359_mRNA_15.1
GF0048203	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00359_mRNA_14.1
GF0048202	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00359_mRNA_11.1
GF0048201	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00359_mRNA_1.1
GF0048200	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00358_mRNA_6.1
GF0048199	0	0	1	NBS-LRR class resistance protein Fy1-Ry1 (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	-	P_trifoliata_00358_mRNA_5.1
GF0048198	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00358_mRNA_4.1
GF0048197	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00358_mRNA_39.1
GF0048196	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00358_mRNA_36.1
GF0048195	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00358_mRNA_34.1
GF0048194	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00358_mRNA_33.1
GF0048193	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00358_mRNA_31.1
GF0048192	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00358_mRNA_30.1
GF0048191	0	0	1	Hypothetical protein (1)		Golgin subfamily A member 5 [IPR019177] (1)	-	-	P_trifoliata_00358_mRNA_3.1
GF0048190	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00358_mRNA_29.1
GF0048189	0	0	1	Hypothetical protein (1)		NADH:quinone oxidoreductase/Mrp antiporter, membrane subunit [IPR001750] (1)	-	-	P_trifoliata_00358_mRNA_27.1
GF0048188	0	0	1	Hypothetical protein (1)	proton-transporting ATP synthase complex, coupling factor F(o) [GO:0045263 cellular_component] (1); proton-transporting two-sector ATPase complex, proton-transporting domain [GO:0033177 cellular_component] (1); hydrogen ion transmembrane transporter activity [GO:0015078 molecular_function] (1); ATP hydrolysis coupled proton transport [GO:0015991 biological_process] (1); ATP synthesis coupled proton transport [GO:0015986 biological_process] (1)	NADH:quinone oxidoreductase/Mrp antiporter, membrane subunit [IPR001750] (1); ATPase, F0 complex, subunit C, DCCD-binding site [IPR020537] (1); ATPase, F0 complex, subunit C [IPR000454] (1); V-ATPase proteolipid subunit C-like domain [IPR002379] (1)	-	-	P_trifoliata_00358_mRNA_26.1
GF0048187	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00358_mRNA_17.1
GF0048186	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00358_mRNA_13.1
GF0048185	0	0	1	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)	-	-	P_trifoliata_00358_mRNA_12.1
GF0048184	0	0	1	Hypothetical protein (1)	malate dehydrogenase (decarboxylating) (NAD+) activity [GO:0004471 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Malic enzyme, N-terminal domain [IPR012301] (1)	-	-	P_trifoliata_00358_mRNA_1.1
GF0048183	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00357_mRNA_38.1
GF0048182	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00357_mRNA_37.1
GF0048181	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00357_mRNA_36.1
GF0048180	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00357_mRNA_27.1
GF0048179	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00357_mRNA_26.1
GF0048178	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00357_mRNA_23.1
GF0048177	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00357_mRNA_22.1
GF0048176	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00357_mRNA_2.1
GF0048175	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00357_mRNA_19.1
GF0048174	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00357_mRNA_18.1
GF0048173	0	0	1	Nucleoside diphosphate kinase (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); GTP biosynthetic process [GO:0006183 biological_process] (1)	Nucleoside diphosphate kinase [IPR001564] (1); Nucleoside diphosphate kinase, active site [IPR023005] (1)	-	-	P_trifoliata_00357_mRNA_14.1
GF0048172	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00356_mRNA_26.1
GF0048171	0	0	1	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	-	P_trifoliata_00356_mRNA_22.1
GF0048170	0	0	1	Non-LTR retroelement reverse transcriptase-like (1)	zinc ion binding [GO:0008270 molecular_function] (1); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1); methyltransferase activity [GO:0008168 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	SAM dependent carboxyl methyltransferase [IPR005299] (1); Zinc finger, CCHC-type [IPR001878] (1); Zinc knuckle CX2CX4HX4C [IPR025836] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); Ribonuclease H domain [IPR002156] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1); Domain of unknown function DUF4283 [IPR025558] (1); Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00356_mRNA_21.1
GF0048169	0	0	1	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)	-	-	P_trifoliata_00356_mRNA_20.1
GF0048168	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00356_mRNA_18.1
GF0048167	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00356_mRNA_17.1
GF0048166	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00356_mRNA_14.1
GF0048165	0	0	1	Hypothetical protein (1)	methyltransferase activity [GO:0008168 molecular_function] (1)	S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); O-methyltransferase COMT-type [IPR016461] (1)	-	-	P_trifoliata_00356_mRNA_13.1
GF0048164	0	0	1	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)	-	-	P_trifoliata_00356_mRNA_10.1
GF0048163	0	0	1	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			-	-	P_trifoliata_00356_mRNA_1.1
GF0048162	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00355_mRNA_9.1
GF0048161	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00355_mRNA_2.1
GF0048160	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00355_mRNA_19.1
GF0048159	0	0	1	Hypothetical protein (1)		Isopenicillin N synthase-like [IPR027443] (1); Non-haem dioxygenase N-terminal domain [IPR026992] (1)	-	-	P_trifoliata_00354_mRNA_9.1
GF0048158	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00354_mRNA_8.1
GF0048157	0	0	1	Hypothetical protein (1)	heme binding [GO:0020037 molecular_function] (1); response to oxidative stress [GO:0006979 biological_process] (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); Plant peroxidase [IPR000823] (1); Peroxidase, active site [IPR019794] (1)	-	-	P_trifoliata_00354_mRNA_6.1
GF0048156	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00354_mRNA_32.1
GF0048155	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00354_mRNA_28.1
GF0048154	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00354_mRNA_27.1
GF0048153	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00354_mRNA_24.1
GF0048152	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00354_mRNA_23.1
GF0048151	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00354_mRNA_14.1
GF0048150	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00354_mRNA_1.1
GF0048149	0	0	1	Calcium-dependent protein kinase 29 (1)	ATP binding [GO:0005524 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); calcium ion binding [GO:0005509 molecular_function] (1)	EF-hand domain pair [IPR011992] (1); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); EF-hand domain [IPR002048] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1)	-	-	P_trifoliata_00353_mRNA_7.1
GF0048148	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00353_mRNA_6.1
GF0048147	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00353_mRNA_3.1
GF0048146	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00353_mRNA_29.1
GF0048145	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00353_mRNA_28.1
GF0048144	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00353_mRNA_26.1
GF0048143	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00353_mRNA_25.1
GF0048142	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00353_mRNA_20.1

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*
GF0048141	0	0	1	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 serine/threonine kinase activity [GO:0004674 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1)	Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); S-locus receptor kinase, C-terminal [IPR021820] (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)	-	-	P_trifoliata_00353_mRNA_19.1
GF0048140	0	0	1	Hypothetical protein (1)		GAG-pre-integrase domain [IPR025724] (1)	-	-	P_trifoliata_00353_mRNA_17.1
GF0048139	0	0	1	Hypothetical protein (1)	calcium ion binding [GO:0005509 molecular_function] (1)	EF-hand domain [IPR002048] (1)	-	-	P_trifoliata_00353_mRNA_11.1
GF0048138	0	0	1	Hypothetical protein (1)		Protein of unknown function DUF594 [IPR007658] (1)	-	-	P_trifoliata_00352_mRNA_9.1
GF0048137	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4220 [IPR025315] (1)	-	-	P_trifoliata_00352_mRNA_8.1
GF0048136	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	-	-	P_trifoliata_00352_mRNA_6.1
GF0048135	0	0	1	Hypothetical protein (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)	-	-	P_trifoliata_00352_mRNA_4.1
GF0048134	0	0	1	Hypothetical protein (1)		Harbinger transposase-derived nuclease domain [IPR027806] (1)	-	-	P_trifoliata_00352_mRNA_27.1
GF0048133	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00352_mRNA_26.1
GF0048132	0	0	1	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)	-	-	P_trifoliata_00352_mRNA_25.1
GF0048131	0	0	1	Limonene synthase (1)	metabolic process [GO:0008152 biological_process] (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, 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)	-	-	P_trifoliata_00352_mRNA_22.1
GF0048130	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4220 [IPR025315] (1)	-	-	P_trifoliata_00352_mRNA_2.1
GF0048129	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00352_mRNA_11.1
GF0048128	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00351_mRNA_25.1
GF0048127	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00351_mRNA_24.1
GF0048126	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00351_mRNA_21.1
GF0048125	0	0	1	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, type 2 [IPR011706] (1); Cupredoxin [IPR008972] (1)	-	-	P_trifoliata_00351_mRNA_19.1
GF0048124	0	0	1	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)	-	-	P_trifoliata_00351_mRNA_12.1
GF0048123	0	0	1	Putative disease resistance protein (1)	inositol-3-phosphate synthase activity [GO:0004512 molecular_function] (1); inositol biosynthetic process [GO:0006021 biological_process] (1); phospholipid biosynthetic process [GO:0008654 biological_process] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Myo-inositol-1-phosphate synthase [IPR002587] (1); NAD(P)-binding domain [IPR016040] (1)	-	-	P_trifoliata_00351_mRNA_11.1
GF0048122	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00351_mRNA_10.1
GF0048121	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00350_mRNA_8.1
GF0048120	0	0	1	Carboxyesterase 18, putative (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)	-	-	P_trifoliata_00350_mRNA_7.1
GF0048119	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1); ADP binding [GO:0043531 molecular_function] (1); signal transduction [GO:0007165 biological_process] (1)	Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1); Leucine-rich repeat 3 [IPR011713] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	-	P_trifoliata_00350_mRNA_4.1
GF0048118	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00350_mRNA_25.1
GF0048117	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00350_mRNA_24.1
GF0048116	0	0	1	Hypothetical protein (1)		PH domain-like [IPR011993] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Pleckstrin homology domain [IPR001849] (1); Dynamin superfamily [IPR022812] (1)	-	-	P_trifoliata_00350_mRNA_2.1
GF0048115	0	0	1	Serine acetyltransferase 4 (1)	transferase activity [GO:0016740 molecular_function] (1)	Hexapeptide repeat [IPR001451] (1); Trimeric LpxA-like [IPR011004] (1); Hexapeptide transferase, conserved site [IPR018357] (1)	-	-	P_trifoliata_00350_mRNA_18.1
GF0048114	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00350_mRNA_17.1
GF0048113	0	0	1	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	-	-	P_trifoliata_00350_mRNA_15.1
GF0048112	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00350_mRNA_14.1
GF0048111	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00350_mRNA_13.1
GF0048110	0	0	1	Hypothetical protein (1)	GTP binding [GO:0005525 molecular_function] (1); GTPase activity [GO:0003924 molecular_function] (1)	GTPase effector domain [IPR020850] (1); Dynamin GTPase effector [IPR003130] (1); Dynamin superfamily [IPR022812] (1)	-	-	P_trifoliata_00350_mRNA_1.1
GF0048109	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00349_mRNA_9.1
GF0048108	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00349_mRNA_6.1
GF0048107	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00349_mRNA_4.1
GF0048106	0	0	1	Hypothetical protein (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 [GO:0003677 molecular_function] (1)	AP2/ERF domain [IPR001471] (1); DNA-binding domain [IPR016177] (1)	-	-	P_trifoliata_00349_mRNA_38.1
GF0048105	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00349_mRNA_37.1
GF0048104	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00349_mRNA_36.1
GF0048103	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00349_mRNA_34.1
GF0048102	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00349_mRNA_3.1
GF0048101	0	0	1	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)	-	-	P_trifoliata_00349_mRNA_26.1
GF0048100	0	0	1	Hypothetical protein (1)		MULE transposase domain [IPR018289] (1); Transposase, MuDR, plant [IPR004332] (1)	-	-	P_trifoliata_00349_mRNA_24.1
GF0048099	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00349_mRNA_23.1
GF0048098	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00349_mRNA_21.1
GF0048097	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00349_mRNA_2.1
GF0048096	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00349_mRNA_18.1
GF0048095	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00349_mRNA_17.1
GF0048094	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00349_mRNA_16.1
GF0048093	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00349_mRNA_15.1
GF0048092	0	0	1	Hypothetical protein (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Aspartic peptidase, active site [IPR001969] (1)	-	-	P_trifoliata_00349_mRNA_13.1
GF0048091	0	0	1	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)	-	-	P_trifoliata_00349_mRNA_11.1
GF0048090	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00349_mRNA_10.1
GF0048089	0	0	1	Regulator of chromosome condensation (RCC1) family protein isoform 2 (1)		Regulator of chromosome condensation 1/beta-lactamase-inhibitor protein II [IPR009091] (1); Regulator of chromosome condensation, RCC1 [IPR000408] (1)	-	-	P_trifoliata_00349_mRNA_1.1
GF0048088	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00348_mRNA_5.1
GF0048087	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00348_mRNA_3.1
GF0048086	0	0	1	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	-	P_trifoliata_00348_mRNA_18.1
GF0048085	0	0	1	Hypothetical protein (1)		Vps4 oligomerisation, C-terminal [IPR015415] (1)	-	-	P_trifoliata_00348_mRNA_12.1
GF0048084	0	0	1	Early nodulin-like protein 18 (1)	electron carrier activity [GO:0009055 molecular_function] (1)	Phytocyanin domain [IPR003245] (1); Cupredoxin [IPR008972] (1)	-	-	P_trifoliata_00347_mRNA_37.1
GF0048083	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00347_mRNA_29.1
GF0048082	0	0	1	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	-	P_trifoliata_00347_mRNA_28.1
GF0048081	0	0	1	Hypothetical protein (1)		PPC domain [IPR005175] (1)	-	-	P_trifoliata_00347_mRNA_12.1
GF0048080	0	0	1	Hypothetical protein (1)	sequence-specific DNA binding [GO:0043565 molecular_function] (1)	Translin [IPR002848] (1); Translin, C-terminal [IPR016069] (1)	-	-	P_trifoliata_00346_mRNA_9.1
GF0048079	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00346_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*
GF0048078	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00346_mRNA_31.1
GF0048077	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00346_mRNA_3.1
GF0048076	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00346_mRNA_27.1
GF0048075	0	0	1	Hypothetical protein (1)		Transposon, En/Spm-like [IPR004242] (1)	-	-	P_trifoliata_00346_mRNA_26.1
GF0048074	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00346_mRNA_23.1
GF0048073	0	0	1	Protein LTV1 like (1)		Low temperature viability protein [IPR007307] (1)	-	-	P_trifoliata_00346_mRNA_22.1
GF0048072	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00346_mRNA_20.1
GF0048071	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00346_mRNA_19.1
GF0048070	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00346_mRNA_18.1
GF0048069	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00346_mRNA_17.1
GF0048068	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00346_mRNA_12.1
GF0048067	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00345_mRNA_6.1
GF0048066	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00345_mRNA_5.1
GF0048065	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00345_mRNA_26.1
GF0048064	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00345_mRNA_24.1
GF0048063	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00345_mRNA_2.1
GF0048062	0	0	1	Hypothetical protein (1)		Chromo/chromo shadow domain [IPR000953] (1); Chromo domain [IPR023780] (1); Chromo domain-like [IPR016197] (1)	-	-	P_trifoliata_00345_mRNA_19.1
GF0048061	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00345_mRNA_17.1
GF0048060	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00345_mRNA_13.1
GF0048059	0	0	1	Stearoyl-acyl carrier protein desaturase (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 biosynthetic process [GO:0006633 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); Stearoyl-ACP desaturase, conserved site [IPR005803] (1)	-	-	P_trifoliata_00345_mRNA_11.1
GF0048058	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00344_mRNA_7.1
GF0048057	0	0	1	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	-	P_trifoliata_00344_mRNA_30.1
GF0048056	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00344_mRNA_29.1
GF0048055	0	0	1	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	-	P_trifoliata_00344_mRNA_28.1
GF0048054	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00344_mRNA_2.1
GF0048053	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1); acid phosphatase activity [GO:0003993 molecular_function] (1); hydrolase activity [GO:0016787 molecular_function] (1); metal ion binding [GO:0046872 molecular_function] (1)	Purple acid phosphatase-like, N-terminal [IPR008963] (1); Calcineurin-like phosphoesterase domain, apaH type [IPR004843] (1); HAT, C-terminal dimerisation domain [IPR008906] (1); Metallo-dependent phosphatase-like [IPR029052] (1); Purple acid phosphatase, N-terminal [IPR015914] (1); Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00344_mRNA_16.1
GF0048052	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00344_mRNA_13.1
GF0048051	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00344_mRNA_1.1
GF0048050	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00343_mRNA_5.1
GF0048049	0	0	1	Hypothetical protein (1)	hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1)	Glycoside hydrolase family 1 [IPR001360] (1); Glycoside hydrolase, catalytic domain [IPR013781] (1); Glycoside hydrolase superfamily [IPR017853] (1)	-	-	P_trifoliata_00343_mRNA_3.1
GF0048048	0	0	1	Ferredoxin (1)	electron transport chain [GO:0022900 biological_process] (1); iron-sulfur cluster binding [GO:0051536 molecular_function] (1); electron carrier activity [GO:0009055 molecular_function] (1); 2 iron, 2 sulfur cluster binding [GO:0051537 molecular_function] (1)	Ferredoxin [2Fe-2S] (1); 2Fe-2S ferredoxin, iron-sulphur binding site [IPR006058] (1); 2Fe-2S ferredoxin-type iron-sulfur binding domain [IPR001041] (1); Beta-grasp domain [IPR012675] (1); plant [IPR010241] (1)	-	-	P_trifoliata_00343_mRNA_29.1
GF0048047	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00343_mRNA_22.1
GF0048046	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00343_mRNA_2.1
GF0048045	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00343_mRNA_13.1
GF0048044	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00343_mRNA_12.1
GF0048043	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00343_mRNA_11.1
GF0048042	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00343_mRNA_10.1
GF0048041	0	0	1	Peroxisomal biogenesis factor 11 family protein (1)	peroxisome fission [GO:0016559 biological_process] (1); integral component of peroxisomal membrane [GO:0005779 cellular_component] (1)	Peroxisomal biogenesis factor 11 [IPR008733] (1)	-	-	P_trifoliata_00343_mRNA_1.1
GF0048040	0	0	1	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)	Sugar transporter, conserved site [IPR005829] (1); Major facilitator superfamily domain [IPR020846] (1); Major facilitator, sugar transporter-like [IPR005828] (1)	-	-	P_trifoliata_00342_mRNA_1.1
GF0048039	0	0	1	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)	-	-	P_trifoliata_00341_mRNA_7.1
GF0048038	0	0	1	GPI-anchor transamidase (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); proteolysis [GO:0006508 biological_process] (1); peptidase activity [GO:0008233 molecular_function] (1)	GPI-anchor transamidase [IPR028361] (1); Peptidase C13, legumain [IPR001096] (1)	-	-	P_trifoliata_00341_mRNA_3.1
GF0048037	0	0	1	Hypothetical protein (1)	RNA binding [GO:0003723 molecular_function] (1); ribonuclease T2 activity [GO:0033897 molecular_function] (1)	Ribonuclease T2-like [IPR001568] (1)	-	-	P_trifoliata_00341_mRNA_28.1
GF0048036	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00341_mRNA_27.1
GF0048035	0	0	1	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	-	-	P_trifoliata_00341_mRNA_24.1
GF0048034	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00341_mRNA_23.1
GF0048033	0	0	1	Putative disease resistance gene NBS-LRR 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)	-	-	P_trifoliata_00341_mRNA_22.1
GF0048032	0	0	1	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	-	P_trifoliata_00341_mRNA_21.1
GF0048031	0	0	1	Putative disease resistance 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)	-	-	P_trifoliata_00341_mRNA_20.1
GF0048030	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00341_mRNA_19.1
GF0048029	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00341_mRNA_18.1
GF0048028	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00341_mRNA_15.1
GF0048027	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00341_mRNA_14.1
GF0048026	0	0	1	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, GRF-type [IPR010666] (1)	-	-	P_trifoliata_00340_mRNA_4.1
GF0048025	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00340_mRNA_12.1
GF0048024	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00340_mRNA_1.1
GF0048023	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00339_mRNA_4.1
GF0048022	0	0	1	Hypothetical protein (1)		Pyridoxal phosphate-dependent transferase [IPR015424] (1)	-	-	P_trifoliata_00339_mRNA_36.1
GF0048021	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00339_mRNA_35.1
GF0048020	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00339_mRNA_33.1
GF0048019	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00339_mRNA_32.1
GF0048018	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00339_mRNA_30.1
GF0048017	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00339_mRNA_23.1
GF0048016	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00339_mRNA_22.1
GF0048015	0	0	1	Hypothetical protein (1)		Isy1-like splicing [IPR009360] (1)	-	-	P_trifoliata_00339_mRNA_20.1
GF0048014	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00339_mRNA_18.1
GF0048013	0	0	1	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-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1)	-	-	P_trifoliata_00339_mRNA_17.1
GF0048012	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00339_mRNA_15.1
GF0048011	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00339_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***
GF0048010	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00338_mRNA_6.1
GF0048009	0	0	1	Hypothetical protein (1)		Timeless protein [IPR006906] (1)	-	-	P_trifoliata_00338_mRNA_39.1
GF0048008	0	0	1	Pyruvate kinase (1)	magnesium ion binding [GO:0000287 molecular_function] (1); catalytic activity [GO:0003824 molecular_function] (1); potassium ion binding [GO:0030955 molecular_function] (1); pyruvate kinase activity [GO:0004743 molecular_function] (1); glycolytic process [GO:0006096 biological_process] (1)	Pyruvate kinase, barrel [IPR015793] (1); Pyruvate kinase, beta-barrel insert domain [IPR015806] (1); Pyruvate kinase [IPR001697] (1); Pyruvate kinase-like, insert domain [IPR011037] (1); Pyruvate/Phosphoenolpyruvate kinase-like domain [IPR015813] (1)	-	-	P_trifoliata_00338_mRNA_38.1
GF0048007	0	0	1	Salt tolerance protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); intracellular [GO:0005622 cellular_component] (1)	B-box-type zinc finger [IPR000315] (1)	-	-	P_trifoliata_00338_mRNA_35.1
GF0048006	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00338_mRNA_23.1
GF0048005	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00338_mRNA_19.1
GF0048004	0	0	1	Amino acid carrier 2 (1)	amino acid transmembrane transport [GO:0003333 biological_process] (1); membrane [GO:0016020 cellular_component] (1); amino acid transmembrane transporter activity [GO:0015171 molecular_function] (1)	Amino acid/polyamine transporter I [IPR002293] (1)	-	-	P_trifoliata_00338_mRNA_12.1
GF0048003	0	0	1	Hypothetical protein (1)		Isopenicillin N synthase-like [IPR027443] (1)	-	-	P_trifoliata_00338_mRNA_1.1
GF0048002	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00337_mRNA_29.1
GF0048001	0	0	1	Ent-kaurene oxidase family 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)	-	-	P_trifoliata_00337_mRNA_23.1
GF0048000	0	0	1	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); Cytochrome P450, conserved site [IPR017972] (1)	-	-	P_trifoliata_00337_mRNA_22.1
GF0047999	0	0	1	Hypothetical protein (1)		ClpP/crotonase-like domain [IPR029045] (1)	-	-	P_trifoliata_00336_mRNA_8.1
GF0047998	0	0	1	Ammonium transporter (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/urea transporter [IPR029020] (1); Ammonium transporter AmtB-like domain [IPR024041] (1); Ammonium transporter [IPR001905] (1)	-	-	P_trifoliata_00336_mRNA_7.1
GF0047997	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00336_mRNA_31.1
GF0047996	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00336_mRNA_3.1
GF0047995	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00336_mRNA_29.1
GF0047994	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00336_mRNA_27.1
GF0047993	0	0	1	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)	-	-	P_trifoliata_00336_mRNA_26.1
GF0047992	0	0	1	LDLR chaperone MESD (1)			-	-	P_trifoliata_00336_mRNA_20.1
GF0047991	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00336_mRNA_2.1
GF0047990	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00336_mRNA_19.1
GF0047989	0	0	1	Hypothetical protein (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1)	Glycoside hydrolase, catalytic domain [IPR013781] (1); Glycoside hydrolase superfamily [IPR017853] (1)	-	-	P_trifoliata_00336_mRNA_16.1
GF0047988	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00336_mRNA_15.1
GF0047987	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00336_mRNA_13.1
GF0047986	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00336_mRNA_12.1
GF0047985	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00336_mRNA_10.1
GF0047984	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00335_mRNA_9.1
GF0047983	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00335_mRNA_22.1
GF0047982	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00335_mRNA_2.1
GF0047981	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00335_mRNA_15.1
GF0047980	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00334_mRNA_9.1
GF0047979	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00334_mRNA_26.1
GF0047978	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00334_mRNA_20.1
GF0047977	0	0	1	Elongator complex protein 4 isoform 2 (1)	Elongator holoenzyme complex [GO:0033588 cellular_component] (1)	Elongator complex protein 4 [IPR008728] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	-	P_trifoliata_00334_mRNA_2.1
GF0047976	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00334_mRNA_17.1
GF0047975	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00334_mRNA_16.1
GF0047974	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00334_mRNA_10.1
GF0047973	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00334_mRNA_1.1
GF0047972	0	0	1	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)	-	-	P_trifoliata_00333_mRNA_8.1
GF0047971	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00333_mRNA_5.1
GF0047970	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00333_mRNA_32.1
GF0047969	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00333_mRNA_30.1
GF0047968	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00333_mRNA_1.1
GF0047967	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00332_mRNA_9.1
GF0047966	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00332_mRNA_7.1
GF0047965	0	0	1	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	-	P_trifoliata_00332_mRNA_5.1
GF0047964	0	0	1	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	-	P_trifoliata_00332_mRNA_4.1
GF0047963	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00332_mRNA_2.1
GF0047962	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00332_mRNA_17.1
GF0047961	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00332_mRNA_15.1
GF0047960	0	0	1	Hypothetical protein (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	-	-	P_trifoliata_00332_mRNA_14.1
GF0047959	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00332_mRNA_13.1
GF0047958	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00332_mRNA_11.1
GF0047957	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00331_mRNA_9.1
GF0047956	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00331_mRNA_8.1
GF0047955	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00331_mRNA_34.1
GF0047954	0	0	1	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)	-	-	P_trifoliata_00331_mRNA_31.1
GF0047953	0	0	1	Acylsugar acyltransferase 2 (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)	-	-	P_trifoliata_00331_mRNA_30.1
GF0047952	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat-containing domain [IPR020683] (1); Ankyrin repeat [IPR002110] (1)	-	-	P_trifoliata_00331_mRNA_23.1
GF0047951	0	0	1	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	-	-	P_trifoliata_00331_mRNA_13.1
GF0047950	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00331_mRNA_12.1
GF0047949	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00330_mRNA_4.1
GF0047948	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00330_mRNA_3.1
GF0047947	0	0	1	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)	-	-	P_trifoliata_00330_mRNA_23.1
GF0047946	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00330_mRNA_2.1
GF0047945	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00330_mRNA_14.1
GF0047944	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00330_mRNA_13.1
GF0047943	0	0	1	Plu (1)		Phloem protein 2-like [IPR025886] (1)	-	-	P_trifoliata_00330_mRNA_12.1
GF0047942	0	0	1	Protein YIPF (1)	membrane [GO:0016020 cellular_component] (1)	Yip1 domain [IPR006977] (1)	-	-	P_trifoliata_00330_mRNA_10.1
GF0047941	0	0	1	Hypothetical protein (1)		Iron hydrogenase, large subunit, C-terminal [IPR004108] (1); Iron hydrogenase [IPR009016] (1); Iron hydrogenase, small subunit [IPR003149] (1)	-	-	P_trifoliata_00329_mRNA_24.1
GF0047940	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00329_mRNA_22.1
GF0047939	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00329_mRNA_21.1
GF0047938	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00329_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*
GF0047937	0	0	1	Aspartate kinase (1)	aspartate kinase activity [GO:0004072 molecular_function] (1); cellular amino acid biosynthetic process [GO:0008652 biological_process] (1)	Aspartate/glutamate/uridylate kinase [IPR001048] (1); Aspartate kinase, conserved site [IPR018042] (1)	-	-	P_trifoliata_00329_mRNA_17.1
GF0047936	0	0	1	Aspartate kinase (1)	amino acid binding [GO:0016597 molecular_function] (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); metabolic process [GO:0008152 biological_process] (1); NADP binding [GO:0050661 molecular_function] (1)	Aspartate/homoserine dehydrogenase, NAD-binding [IPR005106] (1); ACT domain [IPR002912] (1); NAD(P)-binding domain [IPR016040] (1); Homoserine dehydrogenase, catalytic [IPR001342] (1); GATS-like ACT domain [IPR027795] (1)	-	-	P_trifoliata_00329_mRNA_16.1
GF0047935	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00329_mRNA_15.1
GF0047934	0	0	1	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)	-	-	P_trifoliata_00329_mRNA_14.1
GF0047933	0	0	1	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)	NAD(P)-binding domain [IPR016040] (1); GroES-like [IPR011032] (1); Alcohol dehydrogenase, C-terminal [IPR013149] (1); Alcohol dehydrogenase superfamily, zinc-type [IPR002085] (1)	-	-	P_trifoliata_00328_mRNA_6.1
GF0047932	0	0	1	Hypothetical protein (1)	transferase activity [GO:0016740 molecular_function] (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); RNA binding [GO:0003723 molecular_function] (1)	Translation protein SH3-like domain [IPR008991] (1); Ribosomal protein L2, domain 3 [IPR014726] (1); Ribosomal protein L2 [IPR002171] (1); Ribosomal protein L2, C-terminal [IPR022669] (1); Ribosomal protein L2, bacterial/organellar-type [IPR005880] (1)	-	-	P_trifoliata_00328_mRNA_4.1
GF0047931	0	0	1	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	-	P_trifoliata_00328_mRNA_34.1
GF0047930	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00328_mRNA_33.1
GF0047929	0	0	1	Polygalacturonase (1)	polygalacturonase activity [GO:0004650 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1)	Glycoside hydrolase, family 28 [IPR000743] (1); Parallel beta-helix repeat [IPR006626] (1); Pectin lyase fold/virulence factor [IPR011050] (1); Pectin lyase fold [IPR012334] (1)	-	-	P_trifoliata_00328_mRNA_30.1
GF0047928	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00328_mRNA_3.1
GF0047927	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00328_mRNA_29.1
GF0047926	0	0	1	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	-	-	P_trifoliata_00328_mRNA_27.1
GF0047925	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00328_mRNA_26.1
GF0047924	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00328_mRNA_25.1
GF0047923	0	0	1	Polygalacturonase, family GH28 (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)	-	-	P_trifoliata_00328_mRNA_22.1
GF0047922	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00328_mRNA_21.1
GF0047921	0	0	1	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); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Gnk2-homologous domain [IPR002902] (1)	-	-	P_trifoliata_00328_mRNA_18.1
GF0047920	0	0	1	Aminoacyl peptidase-like (1)	protein binding [GO:0005515 molecular_function] (1)	WD40/YVTN repeat-like-containing domain [IPR015943] (1)	-	-	P_trifoliata_00328_mRNA_14.1
GF0047919	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	-	P_trifoliata_00328_mRNA_12.1
GF0047918	0	0	1	RNA-directed DNA polymerase ; Ribonuclease H, putative (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	-	P_trifoliata_00328_mRNA_11.1
GF0047917	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00328_mRNA_1.1
GF0047916	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00327_mRNA_8.1
GF0047915	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00327_mRNA_6.1
GF0047914	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00327_mRNA_5.1
GF0047913	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00327_mRNA_22.1
GF0047912	0	0	1	Polyubiquitin (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 S30 [IPR006846] (1)	-	-	P_trifoliata_00327_mRNA_20.1
GF0047911	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00327_mRNA_2.1
GF0047910	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00327_mRNA_16.1
GF0047909	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00327_mRNA_13.1
GF0047908	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00327_mRNA_1.1
GF0047907	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00326_mRNA_44.1
GF0047906	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00326_mRNA_36.1
GF0047905	0	0	1	Hypothetical protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	-	P_trifoliata_00326_mRNA_35.1
GF0047904	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00326_mRNA_10.1
GF0047903	0	0	1	Hypothetical protein (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)	-	-	P_trifoliata_00326_mRNA_1.1
GF0047902	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00325_mRNA_8.1
GF0047901	0	0	1	Hypothetical protein (1)		50S ribosomal protein L30e-like [IPR029064] (1)	-	-	P_trifoliata_00325_mRNA_47.1
GF0047900	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00325_mRNA_45.1
GF0047899	0	0	1	Hypothetical protein (1)		50S ribosomal protein L30e-like [IPR029064] (1); Ribosomal protein L7Ae/L30e/S12e/Gadd45 [IPR004038] (1)	-	-	P_trifoliata_00325_mRNA_43.1
GF0047898	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00325_mRNA_40.1
GF0047897	0	0	1	Protein SEC13 like (1)	protein binding [GO:0005515 molecular_function] (1)	G-protein beta WD-40 repeat [IPR020472] (1); WD40/YVTN repeat-like-containing domain [IPR015943] (1); WD40 repeat [IPR001680] (1); WD40-repeat-containing domain [IPR017986] (1)	-	-	P_trifoliata_00325_mRNA_35.1
GF0047896	0	0	1	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)	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); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (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)	-	-	P_trifoliata_00325_mRNA_33.1
GF0047895	0	0	1	Peroxidase 5 (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)	Plant peroxidase [IPR000823] (1); Peroxidases heam-ligand binding site [IPR019793] (1); Peroxidase, active site [IPR019794] (1); Haem peroxidase, plant/fungal/bacterial [IPR002016] (1); Haem peroxidase [IPR010255] (1)	-	-	P_trifoliata_00325_mRNA_32.1
GF0047894	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00325_mRNA_28.1
GF0047893	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00325_mRNA_27.1
GF0047892	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00325_mRNA_22.1
GF0047891	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Bulb-type lectin domain [IPR001480] (1)	-	-	P_trifoliata_00325_mRNA_20.1
GF0047890	0	0	1	Secreted glycoprotein 1 (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)	-	-	P_trifoliata_00325_mRNA_19.1
GF0047889	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00325_mRNA_14.1
GF0047888	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00325_mRNA_11.1
GF0047887	0	0	1	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)	-	-	P_trifoliata_00325_mRNA_10.1
GF0047886	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00324_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*
GF0047885	0	0	1	Mavicyanin (1)	electron carrier activity [GO:0009055 molecular_function] (1)	Cupredoxin [IPR008972] (1); Blue (type 1) copper protein, binding site [IPR028871] (1); Phytocyanin domain [IPR003245] (1)	-	-	P_trifoliata_00324_mRNA_4.1
GF0047884	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00324_mRNA_37.1
GF0047883	0	0	1	28 kDa heat-and acid-stable phosphoprotein (1)		Casein kinase substrate, phosphoprotein PP28 [IPR019380] (1)	-	-	P_trifoliata_00324_mRNA_29.2
GF0047882	0	0	1	Ras-related protein RABA1f (1)	signal transduction [GO:0007165 biological_process] (1); intracellular protein transport [GO:0006886 biological_process] (1); GTP binding [GO:0005525 molecular_function] (1); intracellular [GO:0005622 cellular_component] (1); nucleocytoplasmic transport [GO:0006913 biological_process] (1); small GTPase mediated signal transduction [GO:0007264 biological_process] (1); membrane [GO:0016020 cellular_component] (1); protein transport [GO:0015031 biological_process] (1); GTPase activity [GO:0003924 molecular_function] (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)	-	-	P_trifoliata_00324_mRNA_26.1
GF0047881	0	0	1	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)	-	-	P_trifoliata_00324_mRNA_24.1
GF0047880	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00324_mRNA_23.1
GF0047879	0	0	1	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	-	P_trifoliata_00324_mRNA_19.1
GF0047878	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00324_mRNA_17.1
GF0047877	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00324_mRNA_16.1
GF0047876	0	0	1	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, GRF-type [IPR010666] (1)	-	-	P_trifoliata_00324_mRNA_15.1
GF0047875	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00324_mRNA_14.1
GF0047874	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00324_mRNA_13.1
GF0047873	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00324_mRNA_1.1
GF0047872	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00323_mRNA_8.1
GF0047871	0	0	1	Hypothetical protein (1)		Gag-polypeptide of LTR copia-type [IPR029472] (1)	-	-	P_trifoliata_00323_mRNA_6.1
GF0047870	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00323_mRNA_5.1
GF0047869	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00323_mRNA_4.1
GF0047868	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00323_mRNA_3.1
GF0047867	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00323_mRNA_29.1
GF0047866	0	0	1	Hypothetical protein (1)		SGNH hydrolase-type esterase domain [IPR013830] (1)	-	-	P_trifoliata_00323_mRNA_28.1
GF0047865	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00323_mRNA_22.1
GF0047864	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00323_mRNA_20.1
GF0047863	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00323_mRNA_15.1
GF0047862	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00323_mRNA_14.1
GF0047861	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00323_mRNA_10.1
GF0047860	0	0	1	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)	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)	-	-	P_trifoliata_00323_mRNA_1.1
GF0047859	0	0	1	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase (1)	ATP-dependent helicase activity [GO:0008026 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Helicase, C-terminal [IPR001650] (1); Helicase superfamily 1/2, ATP-binding domain [IPR014001] (1); DNA/RNA helicase, ATP-dependent, DEAH-box type, conserved site [IPR002464] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	-	P_trifoliata_00322_mRNA_43.1
GF0047858	0	0	1	Hypothetical protein (1)		Receptor, ligand binding region [IPR001828] (1); Periplasmic binding protein-like I [IPR028082] (1)	-	-	P_trifoliata_00322_mRNA_42.1
GF0047857	0	0	1	Glutamate receptor (1)	ionotropic glutamate receptor activity [GO:0004970 molecular_function] (1); membrane [GO:0016020 cellular_component] (1)	Ionotropic glutamate receptor [IPR001320] (1); Solute-binding protein family 3/N-terminal domain of MltF [IPR001638] (1)	-	-	P_trifoliata_00322_mRNA_41.1
GF0047856	0	0	1	Hypothetical protein (1)		Concanavalin A-like lectin/glucanase domain [IPR013320] (1)	-	-	P_trifoliata_00322_mRNA_22.1
GF0047855	0	0	1	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	-	P_trifoliata_00322_mRNA_12.1
GF0047854	0	0	1	Hypothetical protein (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)	Major facilitator superfamily domain [IPR020846] (1); Sugar transporter, conserved site [IPR005829] (1); Sugar/inositol transporter [IPR003663] (1); Major facilitator, sugar transporter-like [IPR005828] (1)	-	-	P_trifoliata_00321_mRNA_5.1
GF0047853	0	0	1	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)	Major facilitator, sugar transporter-like [IPR005828] (1); Major facilitator superfamily domain [IPR020846] (1); RNA-dependent RNA polymerase, mitoviral [IPR008686] (1)	-	-	P_trifoliata_00321_mRNA_4.1
GF0047852	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00321_mRNA_33.1
GF0047851	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00321_mRNA_31.1
GF0047850	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00321_mRNA_26.1
GF0047849	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00321_mRNA_22.1
GF0047848	0	0	1	Hypothetical protein (1)	extracellular region [GO:0005576 cellular_component] (1); sexual reproduction [GO:0019953 biological_process] (1)	Expansin, cellulose-binding-like domain [IPR007117] (1); GroES-like [IPR011032] (1); Major pollen allergen Lol pI [IPR005795] (1)	-	-	P_trifoliata_00321_mRNA_17.1
GF0047847	0	0	1	Hypothetical protein (1)	extracellular region [GO:0005576 cellular_component] (1); sexual reproduction [GO:0019953 biological_process] (1)	Expansin/Lol pI [IPR007118] (1); Expansin, cellulose-binding-like domain [IPR007117] (1); Isopenicillin N synthase-like [IPR027443] (1); RlpA-like double-psi beta-barrel domain [IPR009009] (1); Expansin/pollen allergen, DPBB domain [IPR007112] (1); Non-haem dioxygenase N-terminal domain [IPR026992] (1); Major pollen allergen Lol pI [IPR005795] (1)	-	-	P_trifoliata_00321_mRNA_16.1
GF0047846	0	0	1	Hypothetical protein (1)	transmembrane transport [GO:0055085 biological_process] (1); integral component of membrane [GO:0016021 cellular_component] (1); transmembrane transporter activity [GO:0022857 molecular_function] (1)	Major facilitator, sugar transporter-like [IPR005828] (1); Major facilitator superfamily domain [IPR020846] (1)	-	-	P_trifoliata_00321_mRNA_12.1
GF0047845	0	0	1	Hypothetical protein (1)		RmlC-like jelly roll fold [IPR014710] (1); RmlC-like cupin domain [IPR011051] (1)	-	-	P_trifoliata_00320_mRNA_8.1
GF0047844	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00320_mRNA_5.1
GF0047843	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00320_mRNA_35.1
GF0047842	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00320_mRNA_34.1
GF0047841	0	0	1	LRR and NB-ARC domains-containing disease resistance-like protein (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)	-	-	P_trifoliata_00320_mRNA_20.1
GF0047840	0	0	1	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	NAC domain [IPR003441] (1)	-	-	P_trifoliata_00320_mRNA_2.1
GF0047839	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00320_mRNA_19.1
GF0047838	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00320_mRNA_16.1
GF0047837	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	-	P_trifoliata_00320_mRNA_13.1
GF0047836	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00320_mRNA_12.1
GF0047835	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00320_mRNA_1.1
GF0047834	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00319_mRNA_7.1
GF0047833	0	0	1	Hypothetical protein (1)	enzyme inhibitor activity [GO:0004857 molecular_function] (1)	Pectinesterase inhibitor domain [IPR006501] (1)	-	-	P_trifoliata_00319_mRNA_24.1
GF0047832	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00319_mRNA_22.1
GF0047831	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00319_mRNA_2.1
GF0047830	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00319_mRNA_19.1
GF0047829	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00319_mRNA_14.1
GF0047828	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00319_mRNA_10.1
GF0047827	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00319_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*
GF0047826	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	-	P_trifoliata_00318_mRNA_5.1
GF0047825	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00318_mRNA_4.1
GF0047824	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00318_mRNA_24.1
GF0047823	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00318_mRNA_23.1
GF0047822	0	0	1	Hypothetical protein (1)		Gag-polypeptide of LTR copia-type [IPR029472] (1)	-	-	P_trifoliata_00318_mRNA_19.1
GF0047821	0	0	1	TTF-type zinc finger protein with HAT dimerisation domain (1)		Zinc finger, TTF-type [IPR006580] (1); Domain of unknown function DUF4371 [IPR025398] (1)	-	-	P_trifoliata_00318_mRNA_17.1
GF0047820	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00318_mRNA_13.1
GF0047819	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00318_mRNA_1.1
GF0047818	0	0	1	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	-	P_trifoliata_00317_mRNA_7.1
GF0047817	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00317_mRNA_3.1
GF0047816	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00317_mRNA_23.1
GF0047815	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00317_mRNA_22.1
GF0047814	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00317_mRNA_19.1
GF0047813	0	0	1	ABC transporter B family member 22 (1)	integral component of membrane [GO:0016021 cellular_component] (1); transport [GO:0006810 biological_process] (1); ATPase activity, coupled to transmembrane movement of substances [GO:0042626 molecular_function] (1); transmembrane transport [GO:0055085 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1)	ABC transporter type 1, transmembrane domain [IPR011527] (1)	-	-	P_trifoliata_00317_mRNA_18.1
GF0047812	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00317_mRNA_12.1
GF0047811	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00317_mRNA_10.1
GF0047810	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00316_mRNA_5.1
GF0047809	0	0	1	Dual specificity phosphatase domain protein (1)	dephosphorylation [GO:0016311 biological_process] (1); protein dephosphorylation [GO:0006470 biological_process] (1); phosphatase activity [GO:0016791 molecular_function] (1); protein tyrosine/serine/threonine phosphatase activity [GO:0008138 molecular_function] (1)	Protein-tyrosine phosphatase-like [IPR029021] (1); Tyrosine specific protein phosphatases domain [IPR000387] (1); Dual specificity phosphatase [IPR024950] (1); Dual specificity phosphatase, catalytic domain [IPR000340] (1)	-	-	P_trifoliata_00316_mRNA_2.1
GF0047808	0	0	1	4'-phosphopantetheinyl transferase family protein (1)	holo-[acyl-carrier-protein] synthase activity [GO:0008897 molecular_function] (1); magnesium ion binding [GO:0000287 molecular_function] (1)	4'-phosphopantetheinyl transferase superfamily [IPR008278] (1)	-	-	P_trifoliata_00316_mRNA_1.3
GF0047807	0	0	1	Hypothetical protein (1)	transferase activity, transferring glycosyl groups [GO:0016757 molecular_function] (1)	Glycosyltransferase AER61, uncharacterised [IPR007657] (1)	-	-	P_trifoliata_00315_mRNA_9.1
GF0047806	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00315_mRNA_33.1
GF0047805	0	0	1	Leucine-rich repeat receptor protein kinase EXS (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine rich repeat 4 [IPR025875] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	-	P_trifoliata_00315_mRNA_31.1
GF0047804	0	0	1	LRR receptor-like serine/threonine-protein kinase HSL2 (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00315_mRNA_26.1
GF0047803	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00315_mRNA_12.1
GF0047802	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00315_mRNA_1.1
GF0047801	0	0	1	Cytochrome P450 82A4 (1)	tRNA processing [GO:0008033 biological_process] (1); RNA binding [GO:0003723 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); tRNA (guanine-N2-)-methyltransferase activity [GO:0004809 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1)	S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450 [IPR001128] (1); tRNA methyltransferase, Trm1 [IPR002905] (1)	-	-	P_trifoliata_00314_mRNA_7.1
GF0047800	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00314_mRNA_5.1
GF0047799	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00314_mRNA_42.1
GF0047798	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00314_mRNA_35.1
GF0047797	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00314_mRNA_3.1
GF0047796	0	0	1	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-like [IPR008928] (1); Six-hairpin glycosidase [IPR012341] (1); Glycoside hydrolase family 9 [IPR001701] (1)	-	-	P_trifoliata_00314_mRNA_28.1
GF0047795	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00314_mRNA_24.1
GF0047794	0	0	1	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	-	-	P_trifoliata_00314_mRNA_22.1
GF0047793	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1); Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	-	P_trifoliata_00314_mRNA_20.1
GF0047792	0	0	1	Hypothetical protein (1)	catalytic activity [GO:0003824 molecular_function] (1)	PLP-binding barrel [IPR029066] (1); Orn/DAP/Arg decarboxylase 2, N-terminal [IPR022644] (1)	-	-	P_trifoliata_00314_mRNA_19.1
GF0047791	0	0	1	Cytochrome p450 79a2, putative (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)	-	-	P_trifoliata_00314_mRNA_18.1
GF0047790	0	0	1	Hypothetical protein (1)	catalytic activity [GO:0003824 molecular_function] (1); polyamine biosynthetic process [GO:0006596 biological_process] (1)	PLP-binding barrel [IPR029066] (1); Orn/DAP/Arg decarboxylase 2, N-terminal [IPR022644] (1); Ornithine decarboxylase [IPR002433] (1)	-	-	P_trifoliata_00314_mRNA_17.1
GF0047789	0	0	1	Hypothetical protein (1)	plant-type cell wall organization [GO:0009664 biological_process] (1); extracellular region [GO:0005576 cellular_component] (1)	Expansin/Lol pI [IPR007118] (1); Expansin [IPR002963] (1); Expansin, cellulose-binding-like domain [IPR007117] (1); RlpA-like double-psi beta-barrel domain [IPR009009] (1); Macro domain [IPR002589] (1); Expansin/pollen allergen, DPBB domain [IPR007112] (1)	-	-	P_trifoliata_00314_mRNA_13.1
GF0047788	0	0	1	Hypothetical protein (1)		Histone acetyltransferases subunit 3 [IPR019340] (1)	-	-	P_trifoliata_00314_mRNA_1.1
GF0047787	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00313_mRNA_22.1
GF0047786	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00313_mRNA_19.1
GF0047785	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00313_mRNA_11.1
GF0047784	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00313_mRNA_1.1
GF0047783	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00312_mRNA_9.1
GF0047782	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00312_mRNA_8.1
GF0047781	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00312_mRNA_7.1
GF0047780	0	0	1	FAD-binding Berberine family protein (1)	oxidoreductase activity, acting on CH-OH group of donors [GO:0016614 molecular_function] (1); catalytic activity [GO:0003824 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)	FAD-binding, type 2 [IPR016166] (1); FAD linked oxidase, N-terminal [IPR006094] (1); CO dehydrogenase flavoprotein-like, FAD-binding, subdomain 2 [IPR016169] (1); FAD-binding, type 2, subdomain 1 [IPR016167] (1); Oxygen oxidoreductase covalent FAD-binding site [IPR006093] (1)	-	-	P_trifoliata_00312_mRNA_4.1
GF0047779	0	0	1	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	-	P_trifoliata_00312_mRNA_3.1
GF0047778	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00312_mRNA_2.1
GF0047777	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00312_mRNA_17.1
GF0047776	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00312_mRNA_16.1
GF0047775	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00312_mRNA_15.1
GF0047774	0	0	1	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 DUF4218 [IPR025452] (1)	-	-	P_trifoliata_00312_mRNA_14.1
GF0047773	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00312_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*
GF0047772	0	0	1	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, family 2 [IPR001077] (1); O-methyltransferase COMT-type [IPR016461] (1)	-	-	P_trifoliata_00312_mRNA_1.1
GF0047771	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF642 [IPR006946] (1)	-	-	P_trifoliata_00311_mRNA_6.1
GF0047770	0	0	1	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	-	P_trifoliata_00311_mRNA_3.1
GF0047769	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00311_mRNA_27.1
GF0047768	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00311_mRNA_25.1
GF0047767	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00311_mRNA_13.1
GF0047766	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00310_mRNA_5.1
GF0047765	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00310_mRNA_36.1
GF0047764	0	0	1	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); Tyrosine-protein kinase, active site [IPR008266] (1)	-	-	P_trifoliata_00310_mRNA_30.1
GF0047763	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00310_mRNA_27.1
GF0047762	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	-	P_trifoliata_00310_mRNA_25.1
GF0047761	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00310_mRNA_24.1
GF0047760	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00310_mRNA_22.1
GF0047759	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00310_mRNA_19.1
GF0047758	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00310_mRNA_16.1
GF0047757	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00310_mRNA_15.1
GF0047756	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00310_mRNA_14.1
GF0047755	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00310_mRNA_13.1
GF0047754	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00310_mRNA_12.1
GF0047753	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00310_mRNA_11.1
GF0047752	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00310_mRNA_10.1
GF0047751	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00309_mRNA_9.1
GF0047750	0	0	1	Transcription factor bHLH36 (1)	DNA binding [GO:0003677 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	Achaete-scute transcription factor-related [IPR015660] (1); Myc-type, basic helix-loop-helix (bHLH) domain [IPR011598] (1)	-	-	P_trifoliata_00309_mRNA_8.1
GF0047749	0	0	1	Hypothetical protein (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); Achaete-scute transcription factor-related [IPR015660] (1)	-	-	P_trifoliata_00309_mRNA_7.1
GF0047748	0	0	1	Hypothetical protein (1)		Protein of unknown function DM15 [IPR006607] (1)	-	-	P_trifoliata_00309_mRNA_36.1
GF0047747	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00309_mRNA_35.1
GF0047746	0	0	1	Late embryogenesis abundant hydroxyproline-rich glycoprotein (1)		Late embryogenesis abundant protein, LEA-14 [IPR004864] (1)	-	-	P_trifoliata_00309_mRNA_28.1
GF0047745	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00309_mRNA_2.1
GF0047744	0	0	1	1-aminocyclopropane-1-carboxylate oxidase like 6 (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)	-	-	P_trifoliata_00309_mRNA_17.1
GF0047743	0	0	1	Molybdopterin synthase catalytic subunit (1)	molybdopterin synthase activity [GO:0030366 molecular_function] (1); Mo-molybdopterin cofactor biosynthetic process [GO:0006777 biological_process] (1); molybdopterin synthase complex [GO:0019008 cellular_component] (1); cytosol [GO:0005829 cellular_component] (1)	Molybdopterin synthase catalytic subunit, eukaryotes [IPR028888] (1); Molybdopterin biosynthesis MoaE [IPR003448] (1)	-	-	P_trifoliata_00309_mRNA_14.1
GF0047742	0	0	1	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1)	Myc-type, basic helix-loop-helix (bHLH) domain [IPR011598] (1)	-	-	P_trifoliata_00309_mRNA_10.1
GF0047741	0	0	1	Polygalacturonase (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1); polygalacturonase activity [GO:0004650 molecular_function] (1)	Glycoside hydrolase, family 28 [IPR000743] (1); Parallel beta-helix repeat [IPR006626] (1); Pectin lyase fold/virulence factor [IPR011050] (1); Pectin lyase fold [IPR012334] (1)	-	-	P_trifoliata_00309_mRNA_1.1
GF0047740	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00308_mRNA_9.1
GF0047739	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00308_mRNA_6.1
GF0047738	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00308_mRNA_31.1
GF0047737	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00308_mRNA_30.1
GF0047736	0	0	1	Hypothetical protein (1)	asparagine synthase (glutamine-hydrolyzing) activity [GO:0004066 molecular_function] (1); asparagine biosynthetic process [GO:0006529 biological_process] (1)	Reverse transcriptase zinc-binding domain [IPR026960] (1); Glutamine amidotransferase type 2 domain [IPR017932] (1); Rossmann-like alpha/beta/alpha sandwich fold [IPR014729] (1); Asparagine synthase [IPR001962] (1); Nucleophile aminohydrolases, N-terminal [IPR029055] (1)	-	-	P_trifoliata_00308_mRNA_25.1
GF0047735	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00308_mRNA_17.1
GF0047734	0	0	1	Hypothetical protein (1)		MULE transposase domain [IPR018289] (1)	-	-	P_trifoliata_00308_mRNA_11.1
GF0047733	0	0	1	Hypothetical protein (1)		PGG domain [IPR026961] (1)	-	-	P_trifoliata_00307_mRNA_36.1
GF0047732	0	0	1	Ankyrin repeat family protein, putative (1)		PGG domain [IPR026961] (1); Ankyrin repeat-containing domain [IPR020683] (1)	-	-	P_trifoliata_00307_mRNA_35.1
GF0047731	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00307_mRNA_31.1
GF0047730	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00307_mRNA_3.1
GF0047729	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00307_mRNA_27.1
GF0047728	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00307_mRNA_26.1
GF0047727	0	0	1	Pentatricopeptide repeat-containing family protein (1)	protein binding [GO:0005515 molecular_function] (1)	Pentatricopeptide repeat [IPR002885] (1); Tetratricopeptide-like helical domain [IPR011990] (1)	-	-	P_trifoliata_00307_mRNA_15.1
GF0047726	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00307_mRNA_12.1
GF0047725	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00307_mRNA_1.1
GF0047724	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00306_mRNA_9.1
GF0047723	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00306_mRNA_8.1
GF0047722	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00306_mRNA_7.1
GF0047721	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00306_mRNA_6.1
GF0047720	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00306_mRNA_5.1
GF0047719	0	0	1	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	-	-	P_trifoliata_00306_mRNA_4.1
GF0047718	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00306_mRNA_33.1
GF0047717	0	0	1	ADP-ribosylation factor A1F (1)	small GTPase mediated signal transduction [GO:0007264 biological_process] (1); intracellular [GO:0005622 cellular_component] (1); GTP binding [GO:0005525 molecular_function] (1)	Small GTP-binding protein domain [IPR005225] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Small GTPase superfamily, ARF type [IPR024156] (1); Small GTPase superfamily, ARF/SAR type [IPR006689] (1)	-	-	P_trifoliata_00306_mRNA_30.1
GF0047716	0	0	1	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)	-	-	P_trifoliata_00306_mRNA_3.1
GF0047715	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00306_mRNA_20.1
GF0047714	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00306_mRNA_14.1
GF0047713	0	0	1	Monosacharide transport protein (1)			-	-	P_trifoliata_00306_mRNA_12.1
GF0047712	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00305_mRNA_8.1
GF0047711	0	0	1	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)	-	-	P_trifoliata_00305_mRNA_7.1
GF0047710	0	0	1	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)	-	-	P_trifoliata_00305_mRNA_6.1
GF0047709	0	0	1	NBS-LRR type disease resistance protein (1)			-	-	P_trifoliata_00305_mRNA_3.1
GF0047708	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00305_mRNA_24.1
GF0047707	0	0	1	Hypothetical protein (1)	strictosidine synthase activity [GO:0016844 molecular_function] (1); biosynthetic process [GO:0009058 biological_process] (1)	Six-bladed beta-propeller, TolB-like [IPR011042] (1); Strictosidine synthase, conserved region [IPR018119] (1); Strictosidine synthase [IPR004141] (1)	-	-	P_trifoliata_00305_mRNA_22.1
GF0047706	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	-	P_trifoliata_00305_mRNA_2.1
GF0047705	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00305_mRNA_19.1
GF0047704	0	0	1	Hypothetical protein (1)	biosynthetic process [GO:0009058 biological_process] (1); strictosidine synthase activity [GO:0016844 molecular_function] (1)	Six-bladed beta-propeller, TolB-like [IPR011042] (1); Strictosidine synthase [IPR004141] (1)	-	-	P_trifoliata_00305_mRNA_16.1
GF0047703	0	0	1	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			-	-	P_trifoliata_00305_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*
GF0047702	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00305_mRNA_12.1
GF0047701	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00305_mRNA_1.1
GF0047700	0	0	1	Hypothetical protein (1)	DNA replication [GO:0006260 biological_process] (1); nucleus [GO:0005634 cellular_component] (1); origin recognition complex [GO:0000808 cellular_component] (1)	Origin recognition complex, subunit 5 [IPR020796] (1)	-	-	P_trifoliata_00304_mRNA_7.1
GF0047699	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00304_mRNA_3.1
GF0047698	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00304_mRNA_20.1
GF0047697	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00304_mRNA_18.1
GF0047696	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00304_mRNA_14.1
GF0047695	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00304_mRNA_13.1
GF0047694	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00304_mRNA_1.1
GF0047693	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00303_mRNA_7.1
GF0047692	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00303_mRNA_31.1
GF0047691	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00303_mRNA_28.1
GF0047690	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00303_mRNA_27.1
GF0047689	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00303_mRNA_26.1
GF0047688	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00303_mRNA_25.1
GF0047687	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00303_mRNA_24.1
GF0047686	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00303_mRNA_21.1
GF0047685	0	0	1	Hypothetical protein (1)		Transposase, MuDR, plant [IPR004332] (1)	-	-	P_trifoliata_00303_mRNA_19.1
GF0047684	0	0	1	Hypothetical protein (1)		LOG family [IPR031100] (1)	-	-	P_trifoliata_00303_mRNA_18.1
GF0047683	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00303_mRNA_16.1
GF0047682	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00303_mRNA_15.1
GF0047681	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00303_mRNA_13.1
GF0047680	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00303_mRNA_11.1
GF0047679	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00303_mRNA_1.1
GF0047678	0	0	1	Hypothetical protein (1)	lipase activity [GO:0016298 molecular_function] (1); lipid metabolic process [GO:0006629 biological_process] (1)	SGNH hydrolase-type esterase domain [IPR013830] (1); Lipase, GDSL, active site [IPR008265] (1)	-	-	P_trifoliata_00302_mRNA_27.1
GF0047677	0	0	1	Hypothetical protein (1)		SGNH hydrolase-type esterase domain [IPR013830] (1)	-	-	P_trifoliata_00302_mRNA_26.1
GF0047676	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00302_mRNA_22.1
GF0047675	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00302_mRNA_16.1
GF0047674	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00302_mRNA_1.1
GF0047673	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00301_mRNA_31.1
GF0047672	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00301_mRNA_26.1
GF0047671	0	0	1	Hypothetical protein (1)		NAD(P)-binding domain [IPR016040] (1); Gamma-secretase aspartyl protease complex, presenilin enhancer-2 subunit [IPR019379] (1)	-	-	P_trifoliata_00301_mRNA_21.1
GF0047670	0	0	1	Hypothetical protein (1)		Peroxisome membrane protein, Pex16 [IPR013919] (1)	-	-	P_trifoliata_00301_mRNA_2.1
GF0047669	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00301_mRNA_19.1
GF0047668	0	0	1	Putative RNA-directed DNA polymerase (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	-	P_trifoliata_00301_mRNA_15.1
GF0047667	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00300_mRNA_8.1
GF0047666	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00300_mRNA_7.1
GF0047665	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00300_mRNA_6.1
GF0047664	0	0	1	Hypothetical protein (1)	polysaccharide binding [GO:0030247 molecular_function] (1)	Wall-associated receptor kinase, galacturonan-binding domain [IPR025287] (1)	-	-	P_trifoliata_00300_mRNA_41.1
GF0047663	0	0	1	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); polysaccharide binding [GO:0030247 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); Wall-associated receptor kinase, galacturonan-binding domain [IPR025287] (1)	-	-	P_trifoliata_00300_mRNA_35.1
GF0047662	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Tetratricopeptide-like helical domain [IPR011990] (1)	-	-	P_trifoliata_00300_mRNA_26.1
GF0047661	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00300_mRNA_25.1
GF0047660	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00300_mRNA_2.1
GF0047659	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1); GDP-fucose protein O-fucosyltransferase [IPR019378] (1)	-	-	P_trifoliata_00299_mRNA_9.1
GF0047658	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00299_mRNA_45.1
GF0047657	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00299_mRNA_41.1
GF0047656	0	0	1	Hypothetical protein (1)		Ubiquitin-conjugating enzyme/RWD-like [IPR016135] (1); Ubiquitin-conjugating enzyme, active site [IPR023313] (1); Ubiquitin-conjugating enzyme E2 [IPR000608] (1)	-	-	P_trifoliata_00299_mRNA_40.1
GF0047655	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00299_mRNA_38.1
GF0047654	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00299_mRNA_33.1
GF0047653	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00299_mRNA_30.1
GF0047652	0	0	1	Hypothetical protein (1)		Thaumatin [IPR001938] (1)	-	-	P_trifoliata_00299_mRNA_3.1
GF0047651	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00299_mRNA_28.1
GF0047650	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00299_mRNA_26.1
GF0047649	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00299_mRNA_25.1
GF0047648	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00299_mRNA_24.1
GF0047647	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00299_mRNA_22.1
GF0047646	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00299_mRNA_2.1
GF0047645	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00299_mRNA_19.1
GF0047644	0	0	1	Hypothetical protein (1)		Receptor, ligand binding region [IPR001828] (1); Periplasmic binding protein-like I [IPR028082] (1)	-	-	P_trifoliata_00299_mRNA_18.1
GF0047643	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00299_mRNA_17.1
GF0047642	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00299_mRNA_14.1
GF0047641	0	0	1	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	-	P_trifoliata_00299_mRNA_13.1
GF0047640	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00299_mRNA_10.1
GF0047639	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00298_mRNA_32.1
GF0047638	0	0	1	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1)	Retropepsins [IPR018061] (1); Peptidase A2A, retrovirus, catalytic [IPR001995] (1)	-	-	P_trifoliata_00298_mRNA_31.1
GF0047637	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00298_mRNA_30.1
GF0047636	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00298_mRNA_18.1
GF0047635	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00298_mRNA_17.1
GF0047634	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1); FBD domain [IPR006566] (1)	-	-	P_trifoliata_00298_mRNA_16.1
GF0047633	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00297_mRNA_8.1
GF0047632	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00297_mRNA_7.1
GF0047631	0	0	1	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); nucleus [GO:0005634 cellular_component] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (1)	Transcription factor, K-box [IPR002487] (1); Ribonuclease H-like domain [IPR012337] (1); Transcription factor, MADS-box [IPR002100] (1)	-	-	P_trifoliata_00297_mRNA_33.1
GF0047630	0	0	1	Hypothetical 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)	-	-	P_trifoliata_00297_mRNA_25.1
GF0047629	0	0	1	Disease resistance response protein 206 (1)		Plant disease resistance response protein [IPR004265] (1)	-	-	P_trifoliata_00296_mRNA_6.1
GF0047628	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00296_mRNA_51.1
GF0047627	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00296_mRNA_48.1
GF0047626	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00296_mRNA_44.1
GF0047625	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00296_mRNA_43.1
GF0047624	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00296_mRNA_42.1
GF0047623	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00296_mRNA_40.1
GF0047622	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00296_mRNA_39.1
GF0047621	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00296_mRNA_38.1
GF0047620	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00296_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*
GF0047619	0	0	1	Hypothetical protein (1)		Isoprenoid synthase domain [IPR008949] (1)	-	-	P_trifoliata_00296_mRNA_33.1
GF0047618	0	0	1	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 [IPR001128] (1); Cytochrome P450, E-class, group I [IPR002401] (1)	-	-	P_trifoliata_00296_mRNA_14.1
GF0047617	0	0	1	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)	-	-	P_trifoliata_00296_mRNA_13.1
GF0047616	0	0	1	UPF0481 protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	-	P_trifoliata_00296_mRNA_1.1
GF0047615	0	0	1	RNA-directed DNA polymerase (Reverse transcriptase) (1)		Reverse transcriptase domain [IPR000477] (1)	-	-	P_trifoliata_00295_mRNA_8.1
GF0047614	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00295_mRNA_30.1
GF0047613	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00295_mRNA_26.1
GF0047612	0	0	1	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); DNA binding [GO:0003677 molecular_function] (1)	NAC domain [IPR003441] (1)	-	-	P_trifoliata_00295_mRNA_25.1
GF0047611	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00295_mRNA_24.1
GF0047610	0	0	1	Putative ribonuclease H protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00295_mRNA_10.1
GF0047609	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	Carlavirus nucleic acid-binding protein [IPR002568] (1)	-	-	P_trifoliata_00294_mRNA_6.1
GF0047608	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00294_mRNA_48.1
GF0047607	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00294_mRNA_44.1
GF0047606	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00294_mRNA_43.1
GF0047605	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00294_mRNA_42.1
GF0047604	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00294_mRNA_41.1
GF0047603	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00294_mRNA_27.1
GF0047602	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00294_mRNA_22.1
GF0047601	0	0	1	Ethylene receptor homolog (1)		GAF domain-like [IPR029016] (1)	-	-	P_trifoliata_00294_mRNA_13.1
GF0047600	0	0	1	Argininosuccinate lyase (1)		Conserved hypothetical protein CHP01589, plant [IPR006476] (1)	-	-	P_trifoliata_00293_mRNA_5.1
GF0047599	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00293_mRNA_34.1
GF0047598	0	0	1	Putative 60S ribosomal protein L14 (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 L2 domain 2 [IPR014722] (1); Ribosomal protein L14 [IPR002784] (1); Translation protein SH3-like domain [IPR008991] (1)	-	-	P_trifoliata_00293_mRNA_33.1
GF0047597	0	0	1	Hypothetical protein (1)		Myb/SANT-like domain [IPR024752] (1)	-	-	P_trifoliata_00293_mRNA_32.1
GF0047596	0	0	1	Hypothetical protein (1)		Oligosaccaryltransferase [IPR018943] (1)	-	-	P_trifoliata_00293_mRNA_26.1
GF0047595	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00293_mRNA_24.1
GF0047594	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00293_mRNA_23.1
GF0047593	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00293_mRNA_12.1
GF0047592	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00293_mRNA_1.1
GF0047591	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00292_mRNA_8.1
GF0047590	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00292_mRNA_7.1
GF0047589	0	0	1	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)	-	-	P_trifoliata_00292_mRNA_33.1
GF0047588	0	0	1	DUF247 domain protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	-	P_trifoliata_00292_mRNA_24.1
GF0047587	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00292_mRNA_1.1
GF0047586	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00291_mRNA_8.1
GF0047585	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00291_mRNA_4.1
GF0047584	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00291_mRNA_3.1
GF0047583	0	0	1	Hypothetical protein (1)		Protein kinase-like domain [IPR011009] (1)	-	-	P_trifoliata_00291_mRNA_21.1
GF0047582	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00291_mRNA_20.1
GF0047581	0	0	1	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)	-	-	P_trifoliata_00291_mRNA_19.1
GF0047580	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00291_mRNA_14.1
GF0047579	0	0	1	Kinase superfamily protein, putative isoform 3 (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)	-	-	P_trifoliata_00291_mRNA_13.1
GF0047578	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00290_mRNA_7.1
GF0047577	0	0	1	Progesterone 5-beta-reductase (1)		NAD(P)-binding domain [IPR016040] (1)	-	-	P_trifoliata_00290_mRNA_6.1
GF0047576	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00290_mRNA_5.1
GF0047575	0	0	1	Receptor like protein 33 (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	-	P_trifoliata_00290_mRNA_31.1
GF0047574	0	0	1	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)	-	-	P_trifoliata_00290_mRNA_30.1
GF0047573	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00290_mRNA_27.1
GF0047572	0	0	1	60S ribosomal protein L7a (1)	ribosome biogenesis [GO:0042254 biological_process] (1); intracellular ribonucleoprotein complex [GO:0030529 cellular_component] (1)	Ribosomal protein L7Ae/L8/Nhp2 family [IPR018492] (1); 50S ribosomal protein L30e-like [IPR029064] (1); Ribosomal protein L7Ae/L30e/S12e/Gadd45 [IPR004038] (1); Ribosomal protein L7A/L8 [IPR001921] (1); Ribosomal protein L7Ae conserved site [IPR004037] (1)	-	-	P_trifoliata_00290_mRNA_24.1
GF0047571	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00290_mRNA_23.1
GF0047570	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00290_mRNA_20.1
GF0047569	0	0	1	Hypothetical protein (1)	integral component of membrane [GO:0016021 cellular_component] (1); endoplasmic reticulum [GO:0005783 cellular_component] (1); transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1)	Glycosyltransferase, ALG3 [IPR007873] (1)	-	-	P_trifoliata_00290_mRNA_2.1
GF0047568	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00290_mRNA_17.1
GF0047567	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00290_mRNA_12.1
GF0047566	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00290_mRNA_11.1
GF0047565	0	0	1	Progesterone 5-beta-reductase (1)		NAD(P)-binding domain [IPR016040] (1)	-	-	P_trifoliata_00290_mRNA_10.1
GF0047564	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00289_mRNA_9.1
GF0047563	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00289_mRNA_44.1
GF0047562	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00289_mRNA_43.1
GF0047561	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00289_mRNA_4.1
GF0047560	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00289_mRNA_36.1
GF0047559	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00289_mRNA_35.1
GF0047558	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00289_mRNA_33.1
GF0047557	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00289_mRNA_32.1
GF0047556	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00289_mRNA_28.1
GF0047555	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00289_mRNA_27.1
GF0047554	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00289_mRNA_25.1
GF0047553	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00289_mRNA_24.1
GF0047552	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00289_mRNA_16.1
GF0047551	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00289_mRNA_12.1
GF0047550	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00289_mRNA_11.1
GF0047549	0	0	1	Retrovirus-related Pol polyprotein from transposon TNT 1-94 (1)			-	-	P_trifoliata_00289_mRNA_1.1
GF0047548	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00288_mRNA_9.1
GF0047547	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00288_mRNA_7.1
GF0047546	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00288_mRNA_6.1
GF0047545	0	0	1	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); DNA binding [GO:0003677 molecular_function] (1)	NAC domain [IPR003441] (1); Transmembrane protein 135 [IPR026749] (1)	-	-	P_trifoliata_00288_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*
GF0047544	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00288_mRNA_45.1
GF0047543	0	0	1	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); DNA binding [GO:0003677 molecular_function] (1)	NAC domain [IPR003441] (1)	-	-	P_trifoliata_00288_mRNA_43.1
GF0047542	0	0	1	Hypothetical protein (1)	potassium ion transmembrane transporter activity [GO:0015079 molecular_function] (1); membrane [GO:0016020 cellular_component] (1); potassium ion transmembrane transport [GO:0071805 biological_process] (1)	Potassium transporter [IPR003855] (1)	-	-	P_trifoliata_00288_mRNA_41.1
GF0047541	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00288_mRNA_39.1
GF0047540	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00288_mRNA_28.1
GF0047539	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00288_mRNA_22.1
GF0047538	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00288_mRNA_1.1
GF0047537	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00287_mRNA_9.1
GF0047536	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00287_mRNA_7.1
GF0047535	0	0	1	Nascent polypeptide-associated complex alpha chain-like protein (1)		Nascent polypeptide-associated complex NAC domain [IPR002715] (1); Nascent polypeptide-associated complex subunit alpha [IPR016641] (1)	-	-	P_trifoliata_00287_mRNA_4.1
GF0047534	0	0	1	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)	-	-	P_trifoliata_00287_mRNA_24.1
GF0047533	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00287_mRNA_18.1
GF0047532	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00287_mRNA_1.1
GF0047531	0	0	1	Benzyl alcohol O-benzoyltransferase (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)	-	-	P_trifoliata_00286_mRNA_9.1
GF0047530	0	0	1	Hypothetical protein (1)		Chloramphenicol acetyltransferase-like domain [IPR023213] (1)	-	-	P_trifoliata_00286_mRNA_6.1
GF0047529	0	0	1	Hypothetical protein (1)		Bifunctional inhibitor/plant lipid transfer protein/seed storage helical domain [IPR016140] (1)	-	-	P_trifoliata_00286_mRNA_41.1
GF0047528	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ubiquitin-related domain [IPR029071] (1); Ubiquitin domain [IPR000626] (1)	-	-	P_trifoliata_00286_mRNA_39.1
GF0047527	0	0	1	Benzyl alcohol O-benzoyltransferase (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)	-	-	P_trifoliata_00286_mRNA_23.1
GF0047526	0	0	1	Benzyl alcohol O-benzoyltransferase (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)	-	-	P_trifoliata_00286_mRNA_22.1
GF0047525	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00286_mRNA_14.1
GF0047524	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00286_mRNA_10.1
GF0047523	0	0	1	Epoxide hydrolase (1)	catalytic activity [GO:0003824 molecular_function] (1)	Epoxide hydrolase-like [IPR000639] (1); Alpha/Beta hydrolase fold [IPR029058] (1); Alpha/beta hydrolase fold-1 [IPR000073] (1)	-	-	P_trifoliata_00285_mRNA_42.1
GF0047522	0	0	1	Hypothetical protein (1)	transaminase activity [GO:0008483 molecular_function] (1); catalytic activity [GO:0003824 molecular_function] (1); pyridoxal phosphate binding [GO:0030170 molecular_function] (1)	Pyridoxal phosphate-dependent transferase, major region, subdomain 2 [IPR015422] (1); Aminotransferase class-III [IPR005814] (1)	-	-	P_trifoliata_00285_mRNA_41.1
GF0047521	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00285_mRNA_37.1
GF0047520	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF1985 [IPR015410] (1)	-	-	P_trifoliata_00285_mRNA_25.1
GF0047519	0	0	1	Hypothetical protein (1)	biosynthetic process [GO:0009058 biological_process] (1)	Chorismate-utilising enzyme, C-terminal [IPR015890] (1); ADC synthase [IPR005801] (1); Anthranilate synthase component I-like [IPR019999] (1)	-	-	P_trifoliata_00285_mRNA_2.1
GF0047518	0	0	1	Pentatricopeptide repeat (PPR) superfamily protein, putative (1)	protein binding [GO:0005515 molecular_function] (1)	Tetratricopeptide-like helical domain [IPR011990] (1); Pentatricopeptide repeat [IPR002885] (1)	-	-	P_trifoliata_00285_mRNA_11.1
GF0047517	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00284_mRNA_4.1
GF0047516	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4217 [IPR025313] (1)	-	-	P_trifoliata_00284_mRNA_33.1
GF0047515	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00284_mRNA_32.1
GF0047514	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00284_mRNA_30.1
GF0047513	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00284_mRNA_2.1
GF0047512	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00283_mRNA_8.1
GF0047511	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00283_mRNA_41.1
GF0047510	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00283_mRNA_40.1
GF0047509	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00283_mRNA_4.1
GF0047508	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00283_mRNA_38.1
GF0047507	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00283_mRNA_35.1
GF0047506	0	0	1	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	-	P_trifoliata_00283_mRNA_33.1
GF0047505	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00283_mRNA_31.1
GF0047504	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00283_mRNA_30.1
GF0047503	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00283_mRNA_28.1
GF0047502	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00283_mRNA_27.1
GF0047501	0	0	1	Hypothetical protein (1)		Double-stranded RNA-binding domain [IPR014720] (1)	-	-	P_trifoliata_00283_mRNA_26.1
GF0047500	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00283_mRNA_22.1
GF0047499	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00283_mRNA_19.1
GF0047498	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00283_mRNA_16.1
GF0047497	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00283_mRNA_15.1
GF0047496	0	0	1	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	-	P_trifoliata_00283_mRNA_14.1
GF0047495	0	0	1	Progesterone 5-beta-reductase (1)		NAD(P)-binding domain [IPR016040] (1)	-	-	P_trifoliata_00283_mRNA_13.1
GF0047494	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00283_mRNA_10.1
GF0047493	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00282_mRNA_6.1
GF0047492	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00282_mRNA_4.1
GF0047491	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00282_mRNA_38.1
GF0047490	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00282_mRNA_3.1
GF0047489	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00282_mRNA_1.1
GF0047488	0	0	1	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)	-	-	P_trifoliata_00281_mRNA_9.1
GF0047487	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00281_mRNA_7.1
GF0047486	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00281_mRNA_4.1
GF0047485	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00281_mRNA_33.1
GF0047484	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00281_mRNA_31.1
GF0047483	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00281_mRNA_30.1
GF0047482	0	0	1	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/dual specificity protein kinase, catalytic domain [IPR002290] (1); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1)	-	-	P_trifoliata_00281_mRNA_3.1
GF0047481	0	0	1	Hypothetical protein (1)		Chromo domain-like [IPR016197] (1); Chromo domain [IPR023780] (1)	-	-	P_trifoliata_00281_mRNA_17.1
GF0047480	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00281_mRNA_14.1
GF0047479	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00281_mRNA_11.1
GF0047478	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00281_mRNA_10.1
GF0047477	0	0	1	Zinc knuckle family protein (1)			-	-	P_trifoliata_00280_mRNA_9.1
GF0047476	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00280_mRNA_7.1
GF0047475	0	0	1	Kunitz-type trypsin inhibitor (1)	endopeptidase inhibitor activity [GO:0004866 molecular_function] (1)	Proteinase inhibitor I3, Kunitz legume [IPR002160] (1); Domain of unknown function DUF1985 [IPR015410] (1); Kunitz inhibitor ST1-like [IPR011065] (1)	-	-	P_trifoliata_00280_mRNA_5.1
GF0047474	0	0	1	Hypothetical protein (1)		GHMP kinase, C-terminal domain [IPR013750] (1)	-	-	P_trifoliata_00280_mRNA_43.1
GF0047473	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00280_mRNA_42.1
GF0047472	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00280_mRNA_41.1
GF0047471	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00280_mRNA_40.1
GF0047470	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00280_mRNA_4.1
GF0047469	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00280_mRNA_39.1
GF0047468	0	0	1	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)	-	-	P_trifoliata_00280_mRNA_37.1
GF0047467	0	0	1	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)	-	-	P_trifoliata_00280_mRNA_34.1
GF0047466	0	0	1	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)	-	-	P_trifoliata_00280_mRNA_33.1

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*
GF0047465	0	0	1	Chitinase (1)	chitin catabolic process [GO:0006032 biological_process] (1); chitinase activity [GO:0004568 molecular_function] (1); cell wall macromolecule catabolic process [GO:0016998 biological_process] (1)	Retrotransposon gag domain [IPR005162] (1); Lysozyme-like domain [IPR023346] (1); Glycoside hydrolase, family 19, catalytic [IPR000726] (1)	-	-	P_trifoliata_00280_mRNA_32.1
GF0047464	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00280_mRNA_29.1
GF0047463	0	0	1	Ribonuclease H protein, putative (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	-	P_trifoliata_00280_mRNA_22.1
GF0047462	0	0	1	Chitinase (1)	chitin catabolic process [GO:0006032 biological_process] (1); chitinase activity [GO:0004568 molecular_function] (1); cell wall macromolecule catabolic process [GO:0016998 biological_process] (1)	Glycoside hydrolase, family 19, catalytic [IPR000726] (1); Lysozyme-like domain [IPR023346] (1)	-	-	P_trifoliata_00280_mRNA_15.1
GF0047461	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00280_mRNA_13.1
GF0047460	0	0	1	MADS-box transcription factor family protein (1)			-	-	P_trifoliata_00279_mRNA_7.1
GF0047459	0	0	1	Hypothetical protein (1)	malate transport [GO:0015743 biological_process] (1)	Aluminum-activated malate transporter [IPR020966] (1)	-	-	P_trifoliata_00279_mRNA_6.1
GF0047458	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00279_mRNA_5.1
GF0047457	0	0	1	Hypothetical protein (1)	serine-type carboxypeptidase activity [GO:0004185 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Alpha/Beta hydrolase fold [IPR029058] (1); Peptidase S10, serine carboxypeptidase [IPR001563] (1)	-	-	P_trifoliata_00279_mRNA_40.1
GF0047456	0	0	1	Serine carboxypeptidase-like 7 (1)	proteolysis [GO:0006508 biological_process] (1); serine-type carboxypeptidase activity [GO:0004185 molecular_function] (1)	Peptidase S10, serine carboxypeptidase [IPR001563] (1); Alpha/Beta hydrolase fold [IPR029058] (1)	-	-	P_trifoliata_00279_mRNA_35.1
GF0047455	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00279_mRNA_3.1
GF0047454	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00279_mRNA_24.1
GF0047453	0	0	1	Short hypocotyl in white light1 protein (1)			-	-	P_trifoliata_00279_mRNA_17.1
GF0047452	0	0	1	Amino acid permease 6 (1)		Amino acid transporter, transmembrane domain [IPR013057] (1)	-	-	P_trifoliata_00279_mRNA_14.1
GF0047451	0	0	1	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			-	-	P_trifoliata_00279_mRNA_1.1
GF0047450	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00278_mRNA_9.1
GF0047449	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00278_mRNA_8.1
GF0047448	0	0	1	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Domain of unknown function DUF4218 [IPR025452] (1); Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1); Domain of unknown function DUF4216 [IPR025312] (1)	-	-	P_trifoliata_00278_mRNA_6.1
GF0047447	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00278_mRNA_5.1
GF0047446	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4219 [IPR025314] (1)	-	-	P_trifoliata_00278_mRNA_15.1
GF0047445	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00278_mRNA_13.1
GF0047444	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00278_mRNA_12.1
GF0047443	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00278_mRNA_10.1
GF0047442	0	0	1	Mavicyanin (1)	electron carrier activity [GO:0009055 molecular_function] (1)	Phytocyanin domain [IPR003245] (1); Cupredoxin [IPR008972] (1)	-	-	P_trifoliata_00277_mRNA_4.1
GF0047441	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00277_mRNA_26.1
GF0047440	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00277_mRNA_25.1
GF0047439	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00277_mRNA_24.1
GF0047438	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00277_mRNA_18.1
GF0047437	0	0	1	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	-	-	P_trifoliata_00277_mRNA_17.1
GF0047436	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00277_mRNA_11.1
GF0047435	0	0	1	Non-symbiotic hemoglobin (1)	oxygen binding [GO:0019825 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1)	Globin/Protoglobin [IPR012292] (1); Globin-like [IPR009050] (1); Globin [IPR000971] (1); Leghaemoglobin, iron-binding site [IPR019824] (1); Leghaemoglobin [IPR001032] (1)	-	-	P_trifoliata_00277_mRNA_10.1
GF0047434	0	0	1	Hypothetical protein (1)	transferase activity, transferring acyl groups [GO:0016746 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	E3-binding domain [IPR004167] (1)	-	-	P_trifoliata_00277_mRNA_1.1
GF0047433	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00276_mRNA_33.1
GF0047432	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00276_mRNA_31.1
GF0047431	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00276_mRNA_27.1
GF0047430	0	0	1	Adenine nucleotide alpha hydrolases-like superfamily protein (1)	response to stress [GO:0006950 biological_process] (1)	UspA [IPR006016] (1); Rossmann-like alpha/beta/alpha sandwich fold [IPR014729] (1)	-	-	P_trifoliata_00276_mRNA_18.1
GF0047429	0	0	1	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); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1)	-	-	P_trifoliata_00276_mRNA_17.1
GF0047428	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00276_mRNA_1.1
GF0047427	0	0	1	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); response to auxin [GO:0009733 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1); Small auxin-up RNA [IPR003676] (1); MULE transposase domain [IPR018289] (1)	-	-	P_trifoliata_00275_mRNA_6.1
GF0047426	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00275_mRNA_33.1
GF0047425	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00275_mRNA_21.1
GF0047424	0	0	1	Linalool 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); 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)	-	-	P_trifoliata_00275_mRNA_15.1
GF0047423	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00275_mRNA_12.1
GF0047422	0	0	1	AtpA (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, PMZ-type [IPR006564] (1); Zinc finger, SWIM-type [IPR007527] (1)	-	-	P_trifoliata_00274_mRNA_7.1
GF0047421	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00274_mRNA_24.1
GF0047420	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00274_mRNA_2.1
GF0047419	0	0	1	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)	-	-	P_trifoliata_00274_mRNA_18.1
GF0047418	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00274_mRNA_17.1
GF0047417	0	0	1	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)	-	-	P_trifoliata_00274_mRNA_13.1
GF0047416	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00274_mRNA_12.1
GF0047415	0	0	1	Caffeic acid 3-O-methyltransferase (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)	-	-	P_trifoliata_00274_mRNA_11.1
GF0047414	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00274_mRNA_1.1
GF0047413	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00273_mRNA_7.1
GF0047412	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00273_mRNA_26.1
GF0047411	0	0	1	Miraculin (1)	endopeptidase inhibitor activity [GO:0004866 molecular_function] (1)	Proteinase inhibitor I3, Kunitz legume [IPR002160] (1); Kunitz inhibitor ST1-like [IPR011065] (1)	-	-	P_trifoliata_00273_mRNA_25.1
GF0047410	0	0	1	Kunitz-type protease inhibitor KPI-C1 (1)	endopeptidase inhibitor activity [GO:0004866 molecular_function] (1)	Kunitz inhibitor ST1-like [IPR011065] (1); Proteinase inhibitor I3, Kunitz legume [IPR002160] (1)	-	-	P_trifoliata_00273_mRNA_24.1
GF0047409	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00273_mRNA_23.1
GF0047408	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00273_mRNA_11.1
GF0047407	0	0	1	Leucine-rich repeat receptor-like serine/threonine-protein kinase BAM1 (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00273_mRNA_10.1
GF0047406	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00273_mRNA_1.1
GF0047405	0	0	1	Transposase (1)		Transposon, En/Spm-like [IPR004242] (1)	-	-	P_trifoliata_00272_mRNA_9.1
GF0047404	0	0	1	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1)	Isopenicillin N synthase-like [IPR027443] (1); Oxoglutarate/iron-dependent dioxygenase [IPR005123] (1)	-	-	P_trifoliata_00272_mRNA_39.1
GF0047403	0	0	1	Acetyl-coenzyme A synthetase (1)	catalytic activity [GO:0003824 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	AMP-dependent synthetase/ligase [IPR000873] (1); AMP-binding, conserved site [IPR020845] (1)	-	-	P_trifoliata_00272_mRNA_34.1
GF0047402	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00272_mRNA_27.1
GF0047401	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00272_mRNA_25.1

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*
GF0047400	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00272_mRNA_24.1
GF0047399	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00272_mRNA_23.1
GF0047398	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00272_mRNA_22.1
GF0047397	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00272_mRNA_21.1
GF0047396	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00272_mRNA_20.1
GF0047395	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00272_mRNA_19.1
GF0047394	0	0	1	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)	-	-	P_trifoliata_00272_mRNA_18.1
GF0047393	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00272_mRNA_16.1
GF0047392	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00272_mRNA_15.1
GF0047391	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00272_mRNA_13.1
GF0047390	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00272_mRNA_11.1
GF0047389	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00271_mRNA_26.1
GF0047388	0	0	1	Retrotransposon protein, putative, unclassified (1)			-	-	P_trifoliata_00271_mRNA_25.1
GF0047387	0	0	1	Ribose-phosphate diphosphokinase (1)	cellular biosynthetic process [GO:0044249 biological_process] (1); nucleotide biosynthetic process [GO:0009165 biological_process] (1); ribonucleoside monophosphate biosynthetic process [GO:0009156 biological_process] (1); ribose phosphate diphosphokinase activity [GO:0004749 molecular_function] (1); magnesium ion binding [GO:0000287 molecular_function] (1)	Phosphoribosyl pyrophosphate synthetase, conserved site [IPR000842] (1); Ribose-phosphate diphosphokinase [IPR005946] (1); Ribose-phosphate pyrophosphokinase, N-terminal domain [IPR029099] (1); Phosphoribosyltransferase-like [IPR029057] (1)	-	-	P_trifoliata_00271_mRNA_19.1
GF0047386	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00270_mRNA_45.1
GF0047385	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00270_mRNA_4.1
GF0047384	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00270_mRNA_33.1
GF0047383	0	0	1	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)	-	-	P_trifoliata_00270_mRNA_29.1
GF0047382	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00270_mRNA_23.1
GF0047381	0	0	1	Endomembrane protein 70 protein family isoform 1 (1)	integral component of membrane [GO:0016021 cellular_component] (1)	Nonaspanin (TM9SF) [IPR004240] (1)	-	-	P_trifoliata_00270_mRNA_2.1
GF0047380	0	0	1	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)	-	-	P_trifoliata_00270_mRNA_15.1
GF0047379	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4219 [IPR025314] (1)	-	-	P_trifoliata_00270_mRNA_13.1
GF0047378	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00269_mRNA_44.1
GF0047377	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00269_mRNA_43.1
GF0047376	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00269_mRNA_41.1
GF0047375	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00269_mRNA_36.1
GF0047374	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00269_mRNA_35.1
GF0047373	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00269_mRNA_33.1
GF0047372	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00269_mRNA_32.1
GF0047371	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00269_mRNA_30.1
GF0047370	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00269_mRNA_25.1
GF0047369	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00269_mRNA_22.1
GF0047368	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00269_mRNA_11.1
GF0047367	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00269_mRNA_1.1
GF0047366	0	0	1	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 [IPR001282] (1); Glucose-6-phosphate dehydrogenase, C-terminal [IPR022675] (1)	-	-	P_trifoliata_00268_mRNA_31.1
GF0047365	0	0	1	Hypothetical protein (1)	glucose metabolic process [GO:0006006 biological_process] (1); glucose-6-phosphate dehydrogenase activity [GO:0004345 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); NADP binding [GO:0050661 molecular_function] (1)	Glucose-6-phosphate dehydrogenase, C-terminal [IPR022675] (1); Glucose-6-phosphate dehydrogenase [IPR001282] (1)	-	-	P_trifoliata_00268_mRNA_27.1
GF0047364	0	0	1	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)	-	-	P_trifoliata_00268_mRNA_22.1
GF0047363	0	0	1	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)	-	-	P_trifoliata_00268_mRNA_2.1
GF0047362	0	0	1	FACT complex subunit SPT16 (1)		Peptidase M24, structural domain [IPR000994] (1); Creatinase/Aminopeptidase P/Spt16, N-terminal [IPR029149] (1); FACT complex subunit Spt16, N-terminal lobe domain [IPR029148] (1)	-	-	P_trifoliata_00268_mRNA_13.1
GF0047361	0	0	1	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FAR1 DNA binding domain [IPR004330] (1); FHY3/FAR1 family [IPR031052] (1)	-	-	P_trifoliata_00268_mRNA_11.1
GF0047360	0	0	1	Hypothetical protein (1)		Transposase-associated domain [IPR029480] (1)	-	-	P_trifoliata_00267_mRNA_7.1
GF0047359	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Domain of unknown function DUF1985 [IPR015410] (1); Zinc finger, CCHC-type [IPR001878] (1)	-	-	P_trifoliata_00267_mRNA_29.1
GF0047358	0	0	1	Hypothetical protein (1)		Domain unknown function DUF295 [IPR005174] (1)	-	-	P_trifoliata_00267_mRNA_28.1
GF0047357	0	0	1	Hypothetical protein (1)		LysM domain [IPR018392] (1)	-	-	P_trifoliata_00267_mRNA_27.1
GF0047356	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00267_mRNA_23.1
GF0047355	0	0	1	Ribonuclease H protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00267_mRNA_2.1
GF0047354	0	0	1	RNA-directed DNA polymerase , related (1)		Reverse transcriptase domain [IPR000477] (1)	-	-	P_trifoliata_00267_mRNA_18.1
GF0047353	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00267_mRNA_11.1
GF0047352	0	0	1	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1); Achaete-scute transcription factor-related [IPR015660] (1); Myc-type, basic helix-loop-helix (bHLH) domain [IPR011598] (1)	-	-	P_trifoliata_00266_mRNA_6.1
GF0047351	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00266_mRNA_4.1
GF0047350	0	0	1	AtpA (1)			-	-	P_trifoliata_00266_mRNA_33.1
GF0047349	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00266_mRNA_19.1
GF0047348	0	0	1	Hypothetical protein (1)	transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (1)	Transferase [IPR003480] (1); Domain of unknown function DUF4283 [IPR025558] (1); Chloramphenicol acetyltransferase-like domain [IPR023213] (1)	-	-	P_trifoliata_00266_mRNA_13.1
GF0047347	0	0	1	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)	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); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1)	-	-	P_trifoliata_00266_mRNA_10.1
GF0047346	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00266_mRNA_1.1
GF0047345	0	0	1	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	-	P_trifoliata_00265_mRNA_8.1
GF0047344	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00265_mRNA_5.1
GF0047343	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00265_mRNA_35.1
GF0047342	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00265_mRNA_33.1
GF0047341	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00265_mRNA_32.1
GF0047340	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00265_mRNA_30.1
GF0047339	0	0	1	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	-	P_trifoliata_00265_mRNA_29.1
GF0047338	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00265_mRNA_25.1
GF0047337	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00265_mRNA_24.1
GF0047336	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00265_mRNA_20.1
GF0047335	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00265_mRNA_2.1
GF0047334	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00265_mRNA_19.1
GF0047333	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00265_mRNA_16.1
GF0047332	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00265_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*
GF0047331	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00264_mRNA_9.1
GF0047330	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00264_mRNA_7.1
GF0047329	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00264_mRNA_6.1
GF0047328	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00264_mRNA_30.1
GF0047327	0	0	1	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); double-stranded DNA binding [GO:0003690 molecular_function] (1); mitochondrion [GO:0005739 cellular_component] (1)	Mitochodrial transcription termination factor [IPR003690] (1)	-	-	P_trifoliata_00264_mRNA_29.1
GF0047326	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF632 [IPR006867] (1)	-	-	P_trifoliata_00264_mRNA_26.1
GF0047325	0	0	1	Phenylcoumaran benzylic ether reductase-like protein (1)		NmrA-like domain [IPR008030] (1); NAD(P)-binding domain [IPR016040] (1)	-	-	P_trifoliata_00264_mRNA_24.1
GF0047324	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00264_mRNA_23.1
GF0047323	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00264_mRNA_17.1
GF0047322	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00264_mRNA_14.1
GF0047321	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00264_mRNA_12.1
GF0047320	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00264_mRNA_10.1
GF0047319	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00263_mRNA_50.1
GF0047318	0	0	1	Hypothetical protein (1)		Uncharacterised protein family, basic secretory protein [IPR007541] (1); Cullin repeat-like-containing domain [IPR016159] (1)	-	-	P_trifoliata_00263_mRNA_49.1
GF0047317	0	0	1	Plant basic secretory family protein (1)		Uncharacterised protein family, basic secretory protein [IPR007541] (1)	-	-	P_trifoliata_00263_mRNA_44.1
GF0047316	0	0	1	UPF0631 protein (1)		Complex 1 LYR protein [IPR008011] (1)	-	-	P_trifoliata_00263_mRNA_34.1
GF0047315	0	0	1	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)	-	-	P_trifoliata_00263_mRNA_3.1
GF0047314	0	0	1	Hypothetical protein (1)	nucleus [GO:0005634 cellular_component] (1)	Cyclin, C-terminal domain [IPR004367] (1); Cyclin A, plant [IPR029507] (1); Cyclin-like [IPR013763] (1)	-	-	P_trifoliata_00263_mRNA_24.1
GF0047313	0	0	1	Hypothetical protein (1)		GH3 family [IPR004993] (1)	-	-	P_trifoliata_00263_mRNA_18.1
GF0047312	0	0	1	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	-	P_trifoliata_00263_mRNA_13.1
GF0047311	0	0	1	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); thiol oxidase activity [GO:0016972 molecular_function] (1)	ERV/ALR sulfhydryl oxidase domain [IPR017905] (1)	-	-	P_trifoliata_00263_mRNA_1.1
GF0047310	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00262_mRNA_5.1
GF0047309	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00262_mRNA_36.1
GF0047308	0	0	1	Reticuline oxidase-like 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); catalytic activity [GO:0003824 molecular_function] (1); oxidoreductase activity, acting on CH-OH group of donors [GO:0016614 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)	-	-	P_trifoliata_00262_mRNA_34.1
GF0047307	0	0	1	Hypothetical protein (1)		Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	-	-	P_trifoliata_00262_mRNA_32.1
GF0047306	0	0	1	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)	-	-	P_trifoliata_00262_mRNA_30.1
GF0047305	0	0	1	Hypothetical protein (1)	iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); monooxygenase activity [GO:0004497 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 IV [IPR002403] (1); Cytochrome P450 [IPR001128] (1)	-	-	P_trifoliata_00262_mRNA_28.1
GF0047304	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00262_mRNA_27.1
GF0047303	0	0	1	Hypothetical protein (1)		Alpha crystallin/Hsp20 domain [IPR002068] (1); HSP20-like chaperone [IPR008978] (1); Small heat shock protein HSP20 [IPR031107] (1)	-	-	P_trifoliata_00262_mRNA_26.1
GF0047302	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00262_mRNA_24.1
GF0047301	0	0	1	Putative disease resistance RPP13-like protein 1 (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00262_mRNA_23.1
GF0047300	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00262_mRNA_17.1
GF0047299	0	0	1	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1)	ATP-grasp fold, subdomain 2 [IPR013816] (1); Phosphoribosylglycinamide synthetase, ATP-grasp (A) domain [IPR020561] (1)	-	-	P_trifoliata_00262_mRNA_16.1
GF0047298	0	0	1	Hypothetical protein (1)		Alpha crystallin/Hsp20 domain [IPR002068] (1); HSP20-like chaperone [IPR008978] (1); Small heat shock protein HSP20 [IPR031107] (1)	-	-	P_trifoliata_00262_mRNA_13.1
GF0047297	0	0	1	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	-	P_trifoliata_00262_mRNA_12.1
GF0047296	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00262_mRNA_11.1
GF0047295	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00262_mRNA_1.1
GF0047294	0	0	1	Mechanosensitive ion channel family protein (1)			-	-	P_trifoliata_00261_mRNA_5.1
GF0047293	0	0	1	Hypothetical protein (1)		Expansin, cellulose-binding-like domain [IPR007117] (1); RlpA-like double-psi beta-barrel domain [IPR009009] (1); Expansin/pollen allergen, DPBB domain [IPR007112] (1)	-	-	P_trifoliata_00261_mRNA_41.1
GF0047292	0	0	1	Receptor-like cytosolic serine/threonine-protein kinase RBK2 (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); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	-	-	P_trifoliata_00261_mRNA_35.1
GF0047291	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00261_mRNA_3.1
GF0047290	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00261_mRNA_21.1
GF0047289	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00261_mRNA_12.1
GF0047288	0	0	1	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)	-	-	P_trifoliata_00261_mRNA_11.1
GF0047287	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00261_mRNA_1.1
GF0047286	0	0	1	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)	-	-	P_trifoliata_00260_mRNA_32.1
GF0047285	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00260_mRNA_30.1
GF0047284	0	0	1	Protein trichome birefringence-like 31 (1)		PC-Esterase [IPR026057] (1); Trichome birefringence-like family [IPR029962] (1)	-	-	P_trifoliata_00260_mRNA_24.1
GF0047283	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00260_mRNA_20.1
GF0047282	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00260_mRNA_2.1
GF0047281	0	0	1	Hypothetical protein (1)		Transposase, MuDR, plant [IPR004332] (1)	-	-	P_trifoliata_00260_mRNA_19.1
GF0047280	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00260_mRNA_17.1
GF0047279	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00260_mRNA_15.1
GF0047278	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00260_mRNA_13.1
GF0047277	0	0	1	Hypothetical protein (1)	lipid binding [GO:0008289 molecular_function] (1); lipid transport [GO:0006869 biological_process] (1)	Bifunctional inhibitor/plant lipid transfer protein/seed storage helical domain [IPR016140] (1); Plant lipid transfer protein/Par allergen [IPR000528] (1)	-	-	P_trifoliata_00260_mRNA_12.1
GF0047276	0	0	1	Putative wound induced protein-like (1)		Protein of unknown function wound-induced [IPR022251] (1)	-	-	P_trifoliata_00259_mRNA_9.1
GF0047275	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00259_mRNA_8.1
GF0047274	0	0	1	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)	-	-	P_trifoliata_00259_mRNA_44.1
GF0047273	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF1985 [IPR015410] (1)	-	-	P_trifoliata_00259_mRNA_43.1
GF0047272	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00259_mRNA_39.1
GF0047271	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00259_mRNA_33.1
GF0047270	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00259_mRNA_30.1
GF0047269	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00259_mRNA_24.1
GF0047268	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00259_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*
GF0047267	0	0	1	Putative wound induced protein-like (1)		Protein of unknown function wound-induced [IPR022251] (1)	-	-	P_trifoliata_00259_mRNA_12.1
GF0047266	0	0	1	Putative wound induced protein-like (1)		Protein of unknown function wound-induced [IPR022251] (1)	-	-	P_trifoliata_00259_mRNA_11.1
GF0047265	0	0	1	Orf105b protein (1)			-	-	P_trifoliata_00258_mRNA_9.1
GF0047264	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00258_mRNA_6.1
GF0047263	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00258_mRNA_46.1
GF0047262	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00258_mRNA_45.1
GF0047261	0	0	1	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	-	P_trifoliata_00258_mRNA_44.1
GF0047260	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1); Zinc knuckle CX2CX4HX4C [IPR025836] (1)	-	-	P_trifoliata_00258_mRNA_41.1
GF0047259	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00258_mRNA_40.1
GF0047258	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00258_mRNA_39.1
GF0047257	0	0	1	Dynamin-like protein 6 isoform 2 (1)	GTP binding [GO:0005525 molecular_function] (1)	Pleckstrin homology domain [IPR001849] (1); Dynamin central domain [IPR000375] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); PH domain-like [IPR011993] (1); Dynamin superfamily [IPR022812] (1); Dynamin-type guanine nucleotide-binding (G) domain [IPR030381] (1)	-	-	P_trifoliata_00258_mRNA_34.1
GF0047256	0	0	1	Hypothetical protein (1)	GTPase activity [GO:0003924 molecular_function] (1); GTP binding [GO:0005525 molecular_function] (1)	GTPase effector domain [IPR020850] (1); Dynamin GTPase effector [IPR003130] (1); Dynamin superfamily [IPR022812] (1)	-	-	P_trifoliata_00258_mRNA_33.1
GF0047255	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4219 [IPR025314] (1)	-	-	P_trifoliata_00258_mRNA_30.1
GF0047254	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00258_mRNA_3.1
GF0047253	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00258_mRNA_29.1
GF0047252	0	0	1	Putative WRKY transcription factor 19 (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00258_mRNA_24.1
GF0047251	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00258_mRNA_23.1
GF0047250	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00258_mRNA_20.1
GF0047249	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00258_mRNA_2.1
GF0047248	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00258_mRNA_19.1
GF0047247	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00258_mRNA_17.1
GF0047246	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00258_mRNA_16.1
GF0047245	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00258_mRNA_15.1
GF0047244	0	0	1	Cytochrome c oxidase subunit 3 (1)	aerobic electron transport chain [GO:0019646 biological_process] (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); Cytochrome c oxidase subunit III [IPR024791] (1)	-	-	P_trifoliata_00258_mRNA_14.1
GF0047243	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00258_mRNA_13.1
GF0047242	0	0	1	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	-	-	P_trifoliata_00257_mRNA_9.1
GF0047241	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00257_mRNA_7.1
GF0047240	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00257_mRNA_6.1
GF0047239	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00257_mRNA_27.1
GF0047238	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00257_mRNA_26.1
GF0047237	0	0	1	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)	-	-	P_trifoliata_00257_mRNA_19.1
GF0047236	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00257_mRNA_17.1
GF0047235	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00257_mRNA_14.1
GF0047234	0	0	1	Hypothetical protein (1)		DnaJ domain [IPR001623] (1)	-	-	P_trifoliata_00257_mRNA_11.1
GF0047233	0	0	1	Hypothetical protein (1)	O-methyltransferase activity [GO:0008171 molecular_function] (1)	O-methyltransferase, family 3 [IPR002935] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	-	P_trifoliata_00256_mRNA_9.1
GF0047232	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00256_mRNA_6.1
GF0047231	0	0	1	Hypothetical protein (1)	protein methylation [GO:0006479 biological_process] (1); methyltransferase activity [GO:0008168 molecular_function] (1)	Protein arginine N-methyltransferase [IPR025799] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	-	P_trifoliata_00256_mRNA_22.1
GF0047230	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00256_mRNA_20.1
GF0047229	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00256_mRNA_19.1
GF0047228	0	0	1	Phospholipase A2 (1)	phospholipase A2 activity [GO:0004623 molecular_function] (1); calcium ion binding [GO:0005509 molecular_function] (1); lipid catabolic process [GO:0016042 biological_process] (1)	Phospholipase A2 domain [IPR016090] (1); Phospholipase A2, histidine active site [IPR033113] (1); Phospholipase A2 [IPR001211] (1)	-	-	P_trifoliata_00256_mRNA_16.1
GF0047227	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00256_mRNA_12.1
GF0047226	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00256_mRNA_10.1
GF0047225	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00255_mRNA_48.1
GF0047224	0	0	1	Expansin-like B1 (1)	serine-type endopeptidase activity [GO:0004252 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	RlpA-like double-psi beta-barrel domain [IPR009009] (1); Expansin/pollen allergen, DPBB domain [IPR007112] (1); ATP-dependent Clp protease proteolytic subunit [IPR001907] (1); ClpP/crotonase-like domain [IPR029045] (1); Expansin, cellulose-binding-like domain [IPR007117] (1); Clp protease proteolytic subunit /Translocation-enhancing protein TepA [IPR023562] (1)	-	-	P_trifoliata_00255_mRNA_47.1
GF0047223	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00255_mRNA_46.1
GF0047222	0	0	1	Hypothetical protein (1)	nucleus [GO:0005634 cellular_component] (1); histone lysine methylation [GO:0034968 biological_process] (1); histone-lysine N-methyltransferase activity [GO:0018024 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Pre-SET zinc-binding sub-group [IPR003606] (1); Pre-SET domain [IPR007728] (1)	-	-	P_trifoliata_00255_mRNA_44.1
GF0047221	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00255_mRNA_34.1
GF0047220	0	0	1	Similarity to non-LTR retroelement reverse transcriptase (1)			-	-	P_trifoliata_00255_mRNA_30.1
GF0047219	0	0	1	Cytochrome P450 82G1 (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, E-class, group I [IPR002401] (1)	-	-	P_trifoliata_00255_mRNA_28.1
GF0047218	0	0	1	Cytochrome P450 82C4 (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)	-	-	P_trifoliata_00255_mRNA_27.1
GF0047217	0	0	1	CBL-interacting serine/threonine-protein kinase 20 (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1); signal transduction [GO:0007165 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-like domain [IPR011009] (1); NAF/FISL domain [IPR018451] (1); Calcium/calmodulin-dependent/calcium-dependent protein kinase [IPR020636] (1); NAF domain [IPR004041] (1); Protein kinase domain [IPR000719] (1)	-	-	P_trifoliata_00255_mRNA_13.1
GF0047216	0	0	1	High mobility group B protein 7 (1)		High mobility group box domain [IPR009071] (1)	-	-	P_trifoliata_00255_mRNA_10.2
GF0047215	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00254_mRNA_7.1
GF0047214	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00254_mRNA_37.1
GF0047213	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00254_mRNA_23.1
GF0047212	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00254_mRNA_22.1
GF0047211	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00254_mRNA_17.1
GF0047210	0	0	1	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, SWIM-type [IPR007527] (1); Zinc finger, PMZ-type [IPR006564] (1)	-	-	P_trifoliata_00254_mRNA_13.1
GF0047209	0	0	1	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)	-	-	P_trifoliata_00254_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*
GF0047208	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00253_mRNA_28.1
GF0047207	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00253_mRNA_26.1
GF0047206	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00253_mRNA_25.1
GF0047205	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00253_mRNA_24.1
GF0047204	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00253_mRNA_20.1
GF0047203	0	0	1	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	-	P_trifoliata_00253_mRNA_19.1
GF0047202	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00253_mRNA_18.1
GF0047201	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00253_mRNA_11.1
GF0047200	0	0	1	(+)-delta-cadinene synthase isozyme A (1)	magnesium ion binding [GO:0000287 molecular_function] (1); lyase activity [GO:0016829 molecular_function] (1); terpene synthase activity [GO:0010333 molecular_function] (1)	Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (1); Terpene synthase, metal-binding domain [IPR005630] (1); Isoprenoid synthase domain [IPR008949] (1)	-	-	P_trifoliata_00252_mRNA_9.1
GF0047199	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00252_mRNA_7.1
GF0047198	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00252_mRNA_50.1
GF0047197	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00252_mRNA_5.1
GF0047196	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00252_mRNA_48.1
GF0047195	0	0	1	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)	-	-	P_trifoliata_00252_mRNA_38.1
GF0047194	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00252_mRNA_36.1
GF0047193	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00252_mRNA_33.1
GF0047192	0	0	1	Hypothetical protein (1)		Winged helix-turn-helix DNA-binding domain [IPR011991] (1)	-	-	P_trifoliata_00252_mRNA_31.1
GF0047191	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00252_mRNA_3.1
GF0047190	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00252_mRNA_29.1
GF0047189	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00252_mRNA_28.1
GF0047188	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00252_mRNA_26.1
GF0047187	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00252_mRNA_25.1
GF0047186	0	0	1	Transcription factor ILR3 (1)			-	-	P_trifoliata_00252_mRNA_16.1
GF0047185	0	0	1	(+)-delta-cadinene synthase isozyme A (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)	-	-	P_trifoliata_00252_mRNA_12.1
GF0047184	0	0	1	Sulfotransferase (1)		P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	-	P_trifoliata_00251_mRNA_39.1
GF0047183	0	0	1	Phospholipase, patatin family (1)	lipid metabolic process [GO:0006629 biological_process] (1); metabolic process [GO:0008152 biological_process] (1)	Acyl transferase/acyl hydrolase/lysophospholipase [IPR016035] (1); Patatin/Phospholipase A2-related [IPR002641] (1)	-	-	P_trifoliata_00251_mRNA_36.1
GF0047182	0	0	1	Hypothetical protein (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)	-	-	P_trifoliata_00251_mRNA_34.1
GF0047181	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00251_mRNA_33.1
GF0047180	0	0	1	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, RING-H2-type [IPR024766] (1); Zinc finger, RING/FYVE/PHD-type [IPR013083] (1)	-	-	P_trifoliata_00251_mRNA_30.1
GF0047179	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00251_mRNA_29.1
GF0047178	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00251_mRNA_28.1
GF0047177	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00251_mRNA_26.1
GF0047176	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00251_mRNA_24.1
GF0047175	0	0	1	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)	-	-	P_trifoliata_00251_mRNA_1.1
GF0047174	0	0	1	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, C-terminal [IPR013149] (1); Alcohol dehydrogenase superfamily, zinc-type [IPR002085] (1); NAD(P)-binding domain [IPR016040] (1)	-	-	P_trifoliata_00250_mRNA_4.1
GF0047173	0	0	1	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)	-	-	P_trifoliata_00250_mRNA_34.1
GF0047172	0	0	1	Hypothetical protein (1)	catalytic activity [GO:0003824 molecular_function] (1)	Cytidine deaminase-like [IPR016193] (1)	-	-	P_trifoliata_00250_mRNA_33.1
GF0047171	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00250_mRNA_32.1
GF0047170	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00250_mRNA_29.1
GF0047169	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00250_mRNA_27.1
GF0047168	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00249_mRNA_9.1
GF0047167	0	0	1	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)	-	-	P_trifoliata_00249_mRNA_8.1
GF0047166	0	0	1	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); Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1); Isoprenoid synthase domain [IPR008949] (1)	-	-	P_trifoliata_00249_mRNA_6.1
GF0047165	0	0	1	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 [IPR020471] (1); Aldo/keto reductase/potassium channel subunit beta [IPR001395] (1)	-	-	P_trifoliata_00249_mRNA_41.1
GF0047164	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00249_mRNA_40.1
GF0047163	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00249_mRNA_4.1
GF0047162	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00249_mRNA_37.1
GF0047161	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00249_mRNA_35.1
GF0047160	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00249_mRNA_28.1
GF0047159	0	0	1	General transcription factor IIH subunit 4 (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); Helicase XPB/Ssl2, N-terminal domain [IPR032830] (1)	-	-	P_trifoliata_00249_mRNA_2.1
GF0047158	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00249_mRNA_13.1
GF0047157	0	0	1	Hypothetical protein (1)		NAD(P)-binding domain [IPR016040] (1)	-	-	P_trifoliata_00248_mRNA_9.1
GF0047156	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00248_mRNA_8.1
GF0047155	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00248_mRNA_42.1
GF0047154	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00248_mRNA_4.1
GF0047153	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00248_mRNA_36.1
GF0047152	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00248_mRNA_35.1
GF0047151	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00248_mRNA_31.1
GF0047150	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00248_mRNA_28.1
GF0047149	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00248_mRNA_25.1
GF0047148	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00248_mRNA_24.1
GF0047147	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00248_mRNA_21.1
GF0047146	0	0	1	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 L36e [IPR000509] (1)	-	-	P_trifoliata_00248_mRNA_19.1
GF0047145	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00248_mRNA_16.1
GF0047144	0	0	1	Putative MATE efflux family protein 5-like (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)	-	-	P_trifoliata_00248_mRNA_15.1
GF0047143	0	0	1	Ribonuclease H (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00248_mRNA_11.1
GF0047142	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00248_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*
GF0047141	0	0	1	Potassium transporter (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)	-	-	P_trifoliata_00248_mRNA_1.1
GF0047140	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00247_mRNA_8.1
GF0047139	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00247_mRNA_42.1
GF0047138	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00247_mRNA_41.1
GF0047137	0	0	1	Geranylgeranyl diphosphate synthase (1)	isoprenoid biosynthetic process [GO:0008299 biological_process] (1)	Polyprenyl synthetase-related [IPR017446] (1); Polyprenyl synthetase [IPR000092] (1); Isoprenoid synthase domain [IPR008949] (1)	-	-	P_trifoliata_00247_mRNA_40.1
GF0047136	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00247_mRNA_38.1
GF0047135	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00247_mRNA_35.1
GF0047134	0	0	1	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); microtubule-based movement [GO:0007018 biological_process] (1); microtubule motor activity [GO:0003777 molecular_function] (1); microtubule binding [GO:0008017 molecular_function] (1)	Kinesin-like protein [IPR027640] (1); Kinesin motor domain [IPR001752] (1)	-	-	P_trifoliata_00247_mRNA_34.1
GF0047133	0	0	1	Calpain clp-1 (1)		PC-Esterase [IPR026057] (1); Trichome birefringence-like family [IPR029962] (1); PMR5 N-terminal domain [IPR025846] (1)	-	-	P_trifoliata_00247_mRNA_3.1
GF0047132	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00247_mRNA_23.1
GF0047131	0	0	1	Retrotransposon protein, putative, Ty1-copia subclass (1)		GAG-pre-integrase domain [IPR025724] (1)	-	-	P_trifoliata_00247_mRNA_20.1
GF0047130	0	0	1	AT1G08750 protein (1)	attachment of GPI anchor to protein [GO:0016255 biological_process] (1); proteolysis [GO:0006508 biological_process] (1); peptidase activity [GO:0008233 molecular_function] (1); GPI-anchor transamidase complex [GO:0042765 cellular_component] (1); GPI-anchor transamidase activity [GO:0003923 molecular_function] (1)	GPI-anchor transamidase [IPR028361] (1); Peptidase C13, legumain [IPR001096] (1)	-	-	P_trifoliata_00247_mRNA_18.1
GF0047129	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00247_mRNA_16.1
GF0047128	0	0	1	Hypothetical protein (1)		Malectin [IPR021720] (1)	-	-	P_trifoliata_00247_mRNA_11.1
GF0047127	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00247_mRNA_10.1
GF0047126	0	0	1	Leucine-rich repeat family protein /protein kinase family protein-like (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Malectin [IPR021720] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); PC-Esterase [IPR026057] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00247_mRNA_1.1
GF0047125	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00246_mRNA_9.1
GF0047124	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00246_mRNA_8.1
GF0047123	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00246_mRNA_7.1
GF0047122	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00246_mRNA_5.1
GF0047121	0	0	1	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	-	-	P_trifoliata_00246_mRNA_4.1
GF0047120	0	0	1	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)	-	-	P_trifoliata_00246_mRNA_34.1
GF0047119	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00246_mRNA_33.1
GF0047118	0	0	1	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)	-	-	P_trifoliata_00246_mRNA_30.1
GF0047117	0	0	1	12-oxophytodienoate reductase 2 (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (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)	-	-	P_trifoliata_00246_mRNA_26.1
GF0047116	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1); signal transduction [GO:0007165 biological_process] (1)	Leucine-rich repeat [IPR001611] (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); Domain of unknown function DUF1985 [IPR015410] (1)	-	-	P_trifoliata_00246_mRNA_24.1
GF0047115	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00246_mRNA_22.1
GF0047114	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00246_mRNA_20.1
GF0047113	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00246_mRNA_19.1
GF0047112	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00246_mRNA_18.1
GF0047111	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00246_mRNA_17.1
GF0047110	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00246_mRNA_15.1
GF0047109	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00246_mRNA_13.1
GF0047108	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF1985 [IPR015410] (1)	-	-	P_trifoliata_00246_mRNA_12.1
GF0047107	0	0	1	Peroxidase 4 (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)	Plant peroxidase [IPR000823] (1); Peroxidases heam-ligand binding site [IPR019793] (1); Haem peroxidase, plant/fungal/bacterial [IPR002016] (1); Haem peroxidase [IPR010255] (1)	-	-	P_trifoliata_00246_mRNA_11.1
GF0047106	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00245_mRNA_5.1
GF0047105	0	0	1	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	-	P_trifoliata_00245_mRNA_40.1
GF0047104	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00245_mRNA_37.1
GF0047103	0	0	1	Hypothetical protein (1)	FAD binding [GO:0071949 molecular_function] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	FAD-binding domain [IPR002938] (1); FAD/NAD(P)-binding domain [IPR023753] (1)	-	-	P_trifoliata_00245_mRNA_34.1
GF0047102	0	0	1	Hypothetical protein (1)		Gag-polypeptide of LTR copia-type [IPR029472] (1)	-	-	P_trifoliata_00245_mRNA_32.1
GF0047101	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00245_mRNA_28.1
GF0047100	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00245_mRNA_24.1
GF0047099	0	0	1	Hypothetical protein (1)		S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	-	P_trifoliata_00245_mRNA_23.1
GF0047098	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00245_mRNA_22.1
GF0047097	0	0	1	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)	-	-	P_trifoliata_00245_mRNA_21.1
GF0047096	0	0	1	Salutaridinol 7-O-acetyltransferase (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)	-	-	P_trifoliata_00245_mRNA_20.1
GF0047095	0	0	1	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)	Pectinesterase, catalytic [IPR000070] (1); Pectin lyase fold [IPR012334] (1); Pectin lyase fold/virulence factor [IPR011050] (1)	-	-	P_trifoliata_00245_mRNA_10.1
GF0047094	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00244_mRNA_9.1
GF0047093	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00244_mRNA_7.1
GF0047092	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00244_mRNA_6.1
GF0047091	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00244_mRNA_50.1
GF0047090	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00244_mRNA_49.1
GF0047089	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00244_mRNA_45.1
GF0047088	0	0	1	Hypothetical protein (1)		Plant disease resistance response protein [IPR004265] (1)	-	-	P_trifoliata_00244_mRNA_44.1
GF0047087	0	0	1	Disease resistance-responsive family protein (1)		Plant disease resistance response protein [IPR004265] (1)	-	-	P_trifoliata_00244_mRNA_42.1
GF0047086	0	0	1	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)	-	-	P_trifoliata_00244_mRNA_38.1
GF0047085	0	0	1	Reverse transcriptase, related (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	-	P_trifoliata_00244_mRNA_37.1
GF0047084	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00244_mRNA_36.1
GF0047083	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00244_mRNA_28.1
GF0047082	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00244_mRNA_24.1
GF0047081	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00244_mRNA_19.1
GF0047080	0	0	1	Disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	-	P_trifoliata_00244_mRNA_16.1
GF0047079	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00244_mRNA_15.1
GF0047078	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00243_mRNA_31.1
GF0047077	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00243_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***
GF0047076	0	0	1	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1)	-	-	P_trifoliata_00243_mRNA_25.1
GF0047075	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00243_mRNA_15.1
GF0047074	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00243_mRNA_11.1
GF0047073	0	0	1	Hypothetical protein (1)		Protein of unknown function DUF1191 [IPR010605] (1)	-	-	P_trifoliata_00242_mRNA_8.1
GF0047072	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00242_mRNA_58.1
GF0047071	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00242_mRNA_57.1
GF0047070	0	0	1	Hypothetical protein (1)	microtubule-based process [GO:0007017 biological_process] (1); microtubule [GO:0005874 cellular_component] (1)	Tubulin [IPR000217] (1); Tubulin/FtsZ, C-terminal [IPR008280] (1); Tubulin, C-terminal [IPR023123] (1)	-	-	P_trifoliata_00242_mRNA_31.1
GF0047069	0	0	1	Hypothetical protein (1)		Protein of unknown function DUF594 [IPR007658] (1)	-	-	P_trifoliata_00241_mRNA_6.1
GF0047068	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00241_mRNA_41.1
GF0047067	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00241_mRNA_40.1
GF0047066	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4220 [IPR025315] (1)	-	-	P_trifoliata_00241_mRNA_4.1
GF0047065	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00241_mRNA_37.1
GF0047064	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00241_mRNA_36.1
GF0047063	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00241_mRNA_34.1
GF0047062	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00241_mRNA_33.1
GF0047061	0	0	1	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)	Thiolase-like [IPR016039] (1); Very-long-chain 3-ketoacyl-CoA synthase [IPR012392] (1); FAE1/Type III polyketide synthase-like protein [IPR013601] (1)	-	-	P_trifoliata_00241_mRNA_32.1
GF0047060	0	0	1	Putative non-LTR retroelement reverse transcriptase (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Gag-polypeptide of LTR copia-type [IPR029472] (1)	-	-	P_trifoliata_00241_mRNA_31.1
GF0047059	0	0	1	Metal tolerance protein 9 (1)	integral component of membrane [GO:0016021 cellular_component] (1); cation transmembrane transporter activity [GO:0008324 molecular_function] (1); cation transport [GO:0006812 biological_process] (1); transmembrane transport [GO:0055085 biological_process] (1)	Cation efflux protein, cytoplasmic domain [IPR027470] (1); Cation efflux protein [IPR002524] (1); Cation efflux protein transmembrane domain [IPR027469] (1)	-	-	P_trifoliata_00241_mRNA_23.1
GF0047058	0	0	1	Hypothetical protein (1)	cell redox homeostasis [GO:0045454 biological_process] (1); glycerol ether metabolic process [GO:0006662 biological_process] (1); protein disulfide oxidoreductase activity [GO:0015035 molecular_function] (1)	Thioredoxin domain [IPR013766] (1); Thioredoxin [IPR005746] (1); Thioredoxin-like fold [IPR012336] (1)	-	-	P_trifoliata_00241_mRNA_15.1
GF0047057	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00241_mRNA_12.1
GF0047056	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00241_mRNA_1.1
GF0047055	0	0	1	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)	-	-	P_trifoliata_00240_mRNA_8.1
GF0047054	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00240_mRNA_7.1
GF0047053	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00240_mRNA_6.1
GF0047052	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00240_mRNA_32.1
GF0047051	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00240_mRNA_30.1
GF0047050	0	0	1	Toll-interleukin-resistance (TIR) domain protein (1)	protein binding [GO:0005515 molecular_function] (1); ADP binding [GO:0043531 molecular_function] (1); signal transduction [GO:0007165 biological_process] (1)	Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	-	P_trifoliata_00240_mRNA_3.1
GF0047049	0	0	1	1-acyl-sn-glycerol-3-phosphate acyltransferase 2 (1)	transferase activity, transferring acyl groups [GO:0016746 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Phospholipid/glycerol acyltransferase [IPR002123] (1); Acyltransferase, C-terminal domain [IPR032098] (1)	-	-	P_trifoliata_00240_mRNA_26.1
GF0047048	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00240_mRNA_21.1
GF0047047	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00240_mRNA_2.1
GF0047046	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00240_mRNA_15.1
GF0047045	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00240_mRNA_14.1
GF0047044	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00240_mRNA_11.1
GF0047043	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00240_mRNA_10.1
GF0047042	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00239_mRNA_26.1
GF0047041	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00239_mRNA_24.1
GF0047040	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00239_mRNA_23.1
GF0047039	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00239_mRNA_20.1
GF0047038	0	0	1	CASP-like protein 5A1 (1)		Domain of unknown function DUF588 [IPR006702] (1)	-	-	P_trifoliata_00239_mRNA_19.1
GF0047037	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00239_mRNA_13.1
GF0047036	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00238_mRNA_8.1
GF0047035	0	0	1	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)	-	-	P_trifoliata_00238_mRNA_6.1
GF0047034	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00238_mRNA_39.1
GF0047033	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00238_mRNA_38.1
GF0047032	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00238_mRNA_37.1
GF0047031	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00238_mRNA_36.1
GF0047030	0	0	1	Hypothetical protein (1)	phosphogluconate dehydrogenase (decarboxylating) activity [GO:0004616 molecular_function] (1); NAD binding [GO:0051287 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1)	NAD(P)-binding domain [IPR016040] (1); 6-phosphogluconate dehydrogenase, domain 2 [IPR013328] (1); 6-phosphogluconate dehydrogenase, NADP-binding [IPR006115] (1); 3-hydroxyisobutyrate dehydrogenase, NAD-binding domain [IPR029154] (1); 6-phosphogluconate dehydrogenase C-terminal domain-like [IPR008927] (1)	-	-	P_trifoliata_00238_mRNA_3.1
GF0047029	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00238_mRNA_27.1
GF0047028	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00238_mRNA_22.1
GF0047027	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00238_mRNA_17.1
GF0047026	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00238_mRNA_13.1
GF0047025	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00238_mRNA_11.1
GF0047024	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00238_mRNA_1.1
GF0047023	0	0	1	Hypothetical protein (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); GroEL-like equatorial domain [IPR027413] (1); Glycosyl transferase, family 8 [IPR002495] (1)	-	-	P_trifoliata_00237_mRNA_53.1
GF0047022	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00237_mRNA_24.1
GF0047021	0	0	1	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	B3 DNA binding domain [IPR003340] (1); DNA-binding pseudobarrel domain [IPR015300] (1)	-	-	P_trifoliata_00237_mRNA_22.1
GF0047020	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00237_mRNA_10.1
GF0047019	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00237_mRNA_1.1
GF0047018	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00236_mRNA_39.1
GF0047017	0	0	1	Lactosylceramide 4-alpha-galactosyltransferase (1)		Glycosyltransferase, DXD sugar-binding motif [IPR007577] (1); Alpha 1,4-glycosyltransferase domain [IPR007652] (1); Nucleotide-diphospho-sugar transferases [IPR029044] (1)	-	-	P_trifoliata_00236_mRNA_31.1
GF0047016	0	0	1	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); Multicopper oxidase, type 2 [IPR011706] (1); Cupredoxin [IPR008972] (1)	-	-	P_trifoliata_00236_mRNA_17.1
GF0047015	0	0	1	Peptide transporter (1)	membrane [GO:0016020 cellular_component] (1); transport [GO:0006810 biological_process] (1); transporter activity [GO:0005215 molecular_function] (1); oligopeptide transport [GO:0006857 biological_process] (1)	Major facilitator superfamily domain [IPR020846] (1); Proton-dependent oligopeptide transporter family [IPR000109] (1); PTR2 family proton/oligopeptide symporter, conserved site [IPR018456] (1)	-	-	P_trifoliata_00236_mRNA_16.1
GF0047014	0	0	1	Retrotransposon gag protein (1)			-	-	P_trifoliata_00235_mRNA_4.1
GF0047013	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00235_mRNA_36.1
GF0047012	0	0	1	Putative phosphomethylpyrimidine synthase-like (1)	protein disulfide oxidoreductase activity [GO:0015035 molecular_function] (1); cell redox homeostasis [GO:0045454 biological_process] (1); electron carrier activity [GO:0009055 molecular_function] (1)	Glutaredoxin [IPR002109] (1); Thioredoxin-like fold [IPR012336] (1); Glutaredoxin subgroup [IPR014025] (1)	-	-	P_trifoliata_00235_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*
GF0047011	0	0	1	Fiber protein Fb15 (1)			-	-	P_trifoliata_00235_mRNA_26.1
GF0047010	0	0	1	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1); DNA repair [GO:0006281 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); DNA recombination [GO:0006310 biological_process] (1); DNA ligase (ATP) activity [GO:0003910 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); DNA ligase, ATP-dependent, N-terminal [IPR012308] (1); Serine/threonine-protein kinase, active site [IPR008271] (1)	-	-	P_trifoliata_00235_mRNA_17.1
GF0047009	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00235_mRNA_13.1
GF0047008	0	0	1	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)	-	-	P_trifoliata_00234_mRNA_48.1
GF0047007	0	0	1	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)	-	-	P_trifoliata_00234_mRNA_46.1
GF0047006	0	0	1	Truncated verticillium wilt resistance-like protein (1)		Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00234_mRNA_44.1
GF0047005	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00234_mRNA_33.1
GF0047004	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00234_mRNA_1.1
GF0047003	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00233_mRNA_47.1
GF0047002	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00233_mRNA_41.1
GF0047001	0	0	1	Vignain (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (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)	-	-	P_trifoliata_00233_mRNA_36.1
GF0047000	0	0	1	Hypothetical protein (1)	branched-chain amino acid biosynthetic process [GO:0009082 biological_process] (1); ketol-acid reductoisomerase activity [GO:0004455 molecular_function] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Ketol-acid reductoisomerase [IPR013023] (1); Acetohydroxy acid isomeroreductase C-terminal [IPR000506] (1); 6-phosphogluconate dehydrogenase C-terminal domain-like [IPR008927] (1)	-	-	P_trifoliata_00233_mRNA_30.1
GF0046999	0	0	1	Nicotianamine synthase 9 (1)		Agenet-like domain [IPR008395] (1); Agenet domain, plant type [IPR014002] (1)	-	-	P_trifoliata_00233_mRNA_24.1
GF0046998	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00233_mRNA_11.1
GF0046997	0	0	1	Hypothetical protein (1)	DNA-templated transcription, termination [GO:0006353 biological_process] (1)	Rho termination factor, N-terminal [IPR011112] (1)	-	-	P_trifoliata_00233_mRNA_1.1
GF0046996	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00232_mRNA_40.1
GF0046995	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00232_mRNA_39.1
GF0046994	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00232_mRNA_38.1
GF0046993	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00232_mRNA_34.1
GF0046992	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00232_mRNA_33.1
GF0046991	0	0	1	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)	-	-	P_trifoliata_00232_mRNA_26.1
GF0046990	0	0	1	MADS-box transcription factor family protein (1)			-	-	P_trifoliata_00231_mRNA_9.1
GF0046989	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00231_mRNA_8.1
GF0046988	0	0	1	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)	-	-	P_trifoliata_00231_mRNA_36.1
GF0046987	0	0	1	Agamous-like MADS-box protein AGL80 (1)	protein dimerization activity [GO:0046983 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	Transcription factor, MADS-box [IPR002100] (1)	-	-	P_trifoliata_00231_mRNA_3.1
GF0046986	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00231_mRNA_29.1
GF0046985	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00231_mRNA_24.1
GF0046984	0	0	1	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)	-	-	P_trifoliata_00231_mRNA_1.1
GF0046983	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00230_mRNA_31.1
GF0046982	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00230_mRNA_28.1
GF0046981	0	0	1	40S ribosomal protein S23 (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); small ribosomal subunit [GO:0015935 cellular_component] (1)	Nucleic acid-binding, OB-fold [IPR012340] (1); Ribosomal protein S12/S23 [IPR006032] (1); Ribosomal protein S23, eukaryotic/archaeal [IPR005680] (1)	-	-	P_trifoliata_00230_mRNA_14.1
GF0046980	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00230_mRNA_10.1
GF0046979	0	0	1	Hypothetical protein (1)	aminoacyl-tRNA ligase activity [GO:0004812 molecular_function] (1); tRNA aminoacylation for protein translation [GO:0006418 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1); nucleotide binding [GO:0000166 molecular_function] (1)	Aminoacyl-tRNA synthetase, class 1a, anticodon-binding [IPR009080] (1); Aminoacyl-tRNA synthetase, class Ia [IPR002300] (1); Rossmann-like alpha/beta/alpha sandwich fold [IPR014729] (1)	-	-	P_trifoliata_00229_mRNA_41.1
GF0046978	0	0	1	Hypothetical protein (1)	tRNA aminoacylation for protein translation [GO:0006418 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1); nucleotide binding [GO:0000166 molecular_function] (1); aminoacyl-tRNA ligase activity [GO:0004812 molecular_function] (1)	Methionyl/Valyl/Leucyl/Isoleucyl-tRNA synthetase, anticodon-binding [IPR013155] (1); Aminoacyl-tRNA synthetase, class 1a, anticodon-binding [IPR009080] (1)	-	-	P_trifoliata_00229_mRNA_40.1
GF0046977	0	0	1	TMV resistance N (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	-	P_trifoliata_00229_mRNA_36.1
GF0046976	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00229_mRNA_23.1
GF0046975	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00229_mRNA_13.1
GF0046974	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00229_mRNA_12.1
GF0046973	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00229_mRNA_11.1
GF0046972	0	0	1	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)	-	-	P_trifoliata_00228_mRNA_8.1
GF0046971	0	0	1	Salicylate 1-monooxygenase (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1)	FAD/NAD(P)-binding domain [IPR023753] (1)	-	-	P_trifoliata_00228_mRNA_7.1
GF0046970	0	0	1	Hypothetical protein (1)		Acyl-CoA N-acyltransferase [IPR016181] (1)	-	-	P_trifoliata_00228_mRNA_6.1
GF0046969	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00228_mRNA_42.1
GF0046968	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00228_mRNA_41.1
GF0046967	0	0	1	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1)	FAD/NAD(P)-binding domain [IPR023753] (1)	-	-	P_trifoliata_00228_mRNA_4.1
GF0046966	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00228_mRNA_35.1
GF0046965	0	0	1	Extra-large guanine nucleotide-binding protein 3 (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); G-protein coupled receptor signaling pathway [GO:0007186 biological_process] (1); signal transduction [GO:0007165 biological_process] (1)	Guanine nucleotide binding protein (G-protein), alpha subunit [IPR001019] (1); G protein alpha subunit, helical insertion [IPR011025] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	-	P_trifoliata_00228_mRNA_20.1
GF0046964	0	0	1	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)	-	-	P_trifoliata_00228_mRNA_2.1
GF0046963	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00228_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*
GF0046962	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00228_mRNA_10.1
GF0046961	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00228_mRNA_1.1
GF0046960	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00227_mRNA_9.1
GF0046959	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00227_mRNA_8.1
GF0046958	0	0	1	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 domain [IPR002156] (1); Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00227_mRNA_40.1
GF0046957	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00227_mRNA_39.1
GF0046956	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00227_mRNA_25.1
GF0046955	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00227_mRNA_23.1
GF0046954	0	0	1	Hypothetical protein (1)	nucleobase-containing compound metabolic process [GO:0006139 biological_process] (1); nucleobase-containing compound kinase activity [GO:0019205 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	ATPase, AAA-type, core [IPR003959] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Adenylate kinase/UMP-CMP kinase [IPR000850] (1); ATPase, AAA-type, conserved site [IPR003960] (1)	-	-	P_trifoliata_00227_mRNA_18.1
GF0046953	0	0	1	Hypothetical protein (1)	nickel cation binding [GO:0016151 molecular_function] (1); urea catabolic process [GO:0043419 biological_process] (1)	Urease, gamma/gamma-beta subunit [IPR002026] (1); Urease, beta subunit [IPR002019] (1); Urease, gamma-beta subunit [IPR008223] (1)	-	-	P_trifoliata_00227_mRNA_17.1
GF0046952	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00227_mRNA_12.1
GF0046951	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00226_mRNA_9.1
GF0046950	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00226_mRNA_42.1
GF0046949	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00226_mRNA_41.1
GF0046948	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00226_mRNA_40.1
GF0046947	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00226_mRNA_38.1
GF0046946	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00226_mRNA_37.1
GF0046945	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00226_mRNA_3.1
GF0046944	0	0	1	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)	-	-	P_trifoliata_00226_mRNA_20.1
GF0046943	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00226_mRNA_2.1
GF0046942	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00226_mRNA_12.1
GF0046941	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00226_mRNA_10.1
GF0046940	0	0	1	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	-	-	P_trifoliata_00225_mRNA_27.1
GF0046939	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00225_mRNA_13.1
GF0046938	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00224_mRNA_7.1
GF0046937	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00224_mRNA_6.1
GF0046936	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00224_mRNA_35.1
GF0046935	0	0	1	Embryonic abundant protein-like (1)			-	-	P_trifoliata_00224_mRNA_32.1
GF0046934	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00224_mRNA_27.1
GF0046933	0	0	1	Putative far-red impaired response protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	MULE transposase domain [IPR018289] (1); FAR1 DNA binding domain [IPR004330] (1); FHY3/FAR1 family [IPR031052] (1)	-	-	P_trifoliata_00224_mRNA_16.1
GF0046932	0	0	1	Ras-related protein RABC2a (1)	signal transduction [GO:0007165 biological_process] (1); intracellular [GO:0005622 cellular_component] (1); GTP binding [GO:0005525 molecular_function] (1); intracellular protein transport [GO:0006886 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); protein transport [GO:0015031 biological_process] (1); GTPase activity [GO:0003924 molecular_function] (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); Sigma-54 interaction domain, ATP-binding site 1 [IPR025662] (1); Small GTPase superfamily, Rab type [IPR003579] (1); Small GTPase superfamily, Ras type [IPR020849] (1)	-	-	P_trifoliata_00224_mRNA_11.1
GF0046931	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00223_mRNA_6.1
GF0046930	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00223_mRNA_35.1
GF0046929	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00223_mRNA_32.1
GF0046928	0	0	1	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); GPN-loop GTPase [IPR004130] (1); NB-ARC [IPR002182] (1)	-	-	P_trifoliata_00223_mRNA_27.1
GF0046927	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00223_mRNA_25.1
GF0046926	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00223_mRNA_21.1
GF0046925	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00223_mRNA_20.1
GF0046924	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00223_mRNA_19.1
GF0046923	0	0	1	Hypothetical protein (1)	translational elongation [GO:0006414 biological_process] (1); translation elongation factor activity [GO:0003746 molecular_function] (1)	Translation elongation factor EF1B, gamma chain, conserved [IPR001662] (1)	-	-	P_trifoliata_00223_mRNA_17.1
GF0046922	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00223_mRNA_12.1
GF0046921	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00223_mRNA_11.1
GF0046920	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00223_mRNA_10.1
GF0046919	0	0	1	Putative non-LTR retrolelement reverse transcriptase (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	-	P_trifoliata_00222_mRNA_6.1
GF0046918	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00222_mRNA_43.1
GF0046917	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00222_mRNA_41.1
GF0046916	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00222_mRNA_40.1
GF0046915	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00222_mRNA_38.1
GF0046914	0	0	1	Hypothetical protein (1)	peptidyl-prolyl cis-trans isomerase activity [GO:0003755 molecular_function] (1); protein folding [GO:0006457 biological_process] (1)	Cyclophilin-type peptidyl-prolyl cis-trans isomerase [IPR024936] (1); Cyclophilin-like domain [IPR029000] (1)	-	-	P_trifoliata_00222_mRNA_33.1
GF0046913	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00222_mRNA_31.1
GF0046912	0	0	1	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)	-	-	P_trifoliata_00222_mRNA_30.1
GF0046911	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00222_mRNA_26.1
GF0046910	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00222_mRNA_25.1
GF0046909	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00222_mRNA_21.1
GF0046908	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00222_mRNA_20.1
GF0046907	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00222_mRNA_19.1
GF0046906	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00222_mRNA_12.1
GF0046905	0	0	1	Somatic embryogenesis receptor kinase 1 (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	-	-	P_trifoliata_00221_mRNA_5.1
GF0046904	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00221_mRNA_41.1
GF0046903	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00221_mRNA_40.1
GF0046902	0	0	1	Hypothetical protein (1)		MULE transposase domain [IPR018289] (1)	-	-	P_trifoliata_00221_mRNA_38.1
GF0046901	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00221_mRNA_37.1
GF0046900	0	0	1	Transcription factor (E2F) (1)	transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); transcription factor complex [GO:0005667 cellular_component] (1)	E2F/DP family, winged-helix DNA-binding domain [IPR003316] (1); E2F transcription factor, CC-MB domain [IPR032198] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); E2F Family [IPR015633] (1)	-	-	P_trifoliata_00221_mRNA_17.1
GF0046899	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00220_mRNA_8.1
GF0046898	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00220_mRNA_6.1
GF0046897	0	0	1	Hypothetical protein (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); 10TM putative phosphate transporter, cytosolic domain [IPR027815] (1)	-	-	P_trifoliata_00220_mRNA_40.1
GF0046896	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00220_mRNA_4.1
GF0046895	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00220_mRNA_3.1
GF0046894	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00220_mRNA_25.1
GF0046893	0	0	1	Cyclic nucleotide-gated ion channel 2 (1)		Cyclic nucleotide-binding domain [IPR000595] (1); Cyclic nucleotide-binding-like [IPR018490] (1); RmlC-like jelly roll fold [IPR014710] (1)	-	-	P_trifoliata_00220_mRNA_21.1
GF0046892	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00220_mRNA_20.2
GF0046891	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00220_mRNA_19.1
GF0046890	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00220_mRNA_18.1
GF0046889	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00220_mRNA_16.1
GF0046888	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00220_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*
GF0046887	0	0	1	Ulp1 protease family, carboxy-terminal domain 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)	-	-	P_trifoliata_00220_mRNA_12.1
GF0046886	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00220_mRNA_10.1
GF0046885	0	0	1	Hypothetical protein (1)	chitin catabolic process [GO:0006032 biological_process] (1); chitinase activity [GO:0004568 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1); hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 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)	Serine/threonine-protein kinase, active site [IPR008271] (1); Chitinase insertion domain [IPR029070] (1); Glycoside hydrolase family 18, catalytic domain [IPR001223] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Chitinase II [IPR011583] (1); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); Glycoside hydrolase superfamily [IPR017853] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Glycoside hydrolase, catalytic domain [IPR013781] (1)	-	-	P_trifoliata_00220_mRNA_1.1
GF0046884	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1); Peptidase M28 [IPR007484] (1)	-	-	P_trifoliata_00219_mRNA_7.1
GF0046883	0	0	1	LRR receptor-like serine/threonine-protein kinase ERL2 (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)	-	-	P_trifoliata_00219_mRNA_6.1
GF0046882	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00219_mRNA_31.1
GF0046881	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00219_mRNA_29.1
GF0046880	0	0	1	Hypothetical protein (1)		Protein kinase-like domain [IPR011009] (1)	-	-	P_trifoliata_00219_mRNA_28.1
GF0046879	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00219_mRNA_25.1
GF0046878	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00219_mRNA_23.1
GF0046877	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00219_mRNA_20.1
GF0046876	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00219_mRNA_18.1
GF0046875	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00219_mRNA_17.1
GF0046874	0	0	1	Gamma-glutamyl hydrolase 2 (1)	catalytic activity [GO:0003824 molecular_function] (1); omega peptidase activity [GO:0008242 molecular_function] (1); glutamine metabolic process [GO:0006541 biological_process] (1)	Peptidase C26, gamma-glutamyl hydrolase [IPR015527] (1); Class I glutamine amidotransferase-like [IPR029062] (1); Glutamine amidotransferase [IPR017926] (1)	-	-	P_trifoliata_00219_mRNA_10.1
GF0046873	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00219_mRNA_1.1
GF0046872	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00218_mRNA_60.1
GF0046871	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00218_mRNA_59.1
GF0046870	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00218_mRNA_57.1
GF0046869	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00218_mRNA_52.1
GF0046868	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00218_mRNA_50.1
GF0046867	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00218_mRNA_49.1
GF0046866	0	0	1	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)	WRKY domain [IPR003657] (1)	-	-	P_trifoliata_00218_mRNA_43.1
GF0046865	0	0	1	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); DNA binding [GO:0003677 molecular_function] (1)	AP2/ERF domain [IPR001471] (1); DNA-binding domain [IPR016177] (1)	-	-	P_trifoliata_00218_mRNA_40.1
GF0046864	0	0	1	Ethylene-responsive transcription factor 2 (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 [GO:0003677 molecular_function] (1)	DNA-binding domain [IPR016177] (1); AP2/ERF domain [IPR001471] (1)	-	-	P_trifoliata_00218_mRNA_39.1
GF0046863	0	0	1	Hypothetical protein (1)	ubiquitin-protein transferase activity [GO:0004842 molecular_function] (1); protein ubiquitination [GO:0016567 biological_process] (1)	E3 ubiquitin ligase RBR family [IPR031127] (1); Zinc finger, RING/FYVE/PHD-type [IPR013083] (1)	-	-	P_trifoliata_00218_mRNA_36.1
GF0046862	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00218_mRNA_30.1
GF0046861	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00218_mRNA_29.1
GF0046860	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00218_mRNA_26.1
GF0046859	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00218_mRNA_24.1
GF0046858	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00218_mRNA_20.1
GF0046857	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00218_mRNA_19.1
GF0046856	0	0	1	Putative DNA-directed RNA polymerase III subunit RPC7-like (1)	regulation of transcription from RNA polymerase III promoter [GO:0006359 biological_process] (1)	DNA-directed RNA polymerase III, subunit Rpc31 [IPR024661] (1)	-	-	P_trifoliata_00218_mRNA_10.1
GF0046855	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00217_mRNA_8.1
GF0046854	0	0	1	Hypothetical protein (1)	integral component of membrane [GO:0016021 cellular_component] (1)	Integral membrane protein TerC [IPR005496] (1); Integral membrane protein TerC, riboswitch-linked [IPR022369] (1)	-	-	P_trifoliata_00217_mRNA_37.1
GF0046853	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00217_mRNA_36.1
GF0046852	0	0	1	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	-	-	P_trifoliata_00217_mRNA_31.1
GF0046851	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00217_mRNA_30.1
GF0046850	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00217_mRNA_2.1
GF0046849	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00217_mRNA_19.1
GF0046848	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00217_mRNA_17.1
GF0046847	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00217_mRNA_16.1
GF0046846	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00217_mRNA_15.1
GF0046845	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00217_mRNA_14.1
GF0046844	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00217_mRNA_1.1
GF0046843	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00216_mRNA_9.1
GF0046842	0	0	1	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)	Thiolase-like [IPR016039] (1); Very-long-chain 3-ketoacyl-CoA synthase [IPR012392] (1); FAE1/Type III polyketide synthase-like protein [IPR013601] (1)	-	-	P_trifoliata_00216_mRNA_5.1
GF0046841	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00216_mRNA_3.1
GF0046840	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00216_mRNA_26.1
GF0046839	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00216_mRNA_24.1
GF0046838	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00216_mRNA_23.1
GF0046837	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00216_mRNA_18.1
GF0046836	0	0	1	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); ATPase activity [GO:0016887 molecular_function] (1)	Arsenical pump ATPase, ArsA/GET3 [IPR016300] (1)	-	-	P_trifoliata_00216_mRNA_14.1
GF0046835	0	0	1	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)	-	-	P_trifoliata_00216_mRNA_10.1
GF0046834	0	0	1	IQ calmodulin-binding motif protein (1)	protein binding [GO:0005515 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); IQ motif, EF-hand binding site [IPR000048] (1)	-	-	P_trifoliata_00215_mRNA_43.1
GF0046833	0	0	1	Hypothetical protein (1)		RmlC-like jelly roll fold [IPR014710] (1); RmlC-like cupin domain [IPR011051] (1)	-	-	P_trifoliata_00215_mRNA_3.1
GF0046832	0	0	1	Pto kinase interactor (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)	-	-	P_trifoliata_00215_mRNA_1.1
GF0046831	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00214_mRNA_9.1
GF0046830	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00214_mRNA_8.1
GF0046829	0	0	1	Hypothetical protein (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Peptidase family A1 domain [IPR033121] (1); Aspartic peptidase domain [IPR021109] (1); Aspartic peptidase, active site [IPR001969] (1); Aspartic peptidase A1 family [IPR001461] (1)	-	-	P_trifoliata_00214_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*
GF0046828	0	0	1	Hypothetical protein (1)	protein folding [GO:0006457 biological_process] (1); copper ion binding [GO:0005507 molecular_function] (1)	Multicopper oxidase, type 3 [IPR011707] (1); FKBP-type peptidyl-prolyl cis-trans isomerase domain [IPR001179] (1); Peptidyl-prolyl cis-trans isomerase, FKBP-type [IPR023566] (1)	-	-	P_trifoliata_00214_mRNA_5.1
GF0046827	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00214_mRNA_4.1
GF0046826	0	0	1	Wall-associated receptor kinase 2 (1)	integral component of membrane [GO:0016021 cellular_component] (1); protein serine/threonine kinase activity [GO:0004674 molecular_function] (1); polysaccharide binding [GO:0030247 molecular_function] (1)	Wall-associated receptor kinase, galacturonan-binding domain [IPR025287] (1); Wall-associated receptor kinase [IPR013695] (1)	-	-	P_trifoliata_00214_mRNA_38.1
GF0046825	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00214_mRNA_37.1
GF0046824	0	0	1	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1)	-	-	P_trifoliata_00214_mRNA_36.1
GF0046823	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00214_mRNA_3.1
GF0046822	0	0	1	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)	-	-	P_trifoliata_00214_mRNA_28.1
GF0046821	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00214_mRNA_24.1
GF0046820	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00214_mRNA_23.1
GF0046819	0	0	1	Truncated RB (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	-	P_trifoliata_00214_mRNA_21.1
GF0046818	0	0	1	Formation of crista junctions protein 1 (1)		Mitochondrial inner membrane protein Mitofilin [IPR019133] (1)	-	-	P_trifoliata_00214_mRNA_2.1
GF0046817	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00214_mRNA_17.1
GF0046816	0	0	1	Chaperonin CPN60-2, mitochondrial (1)	cytoplasm [GO:0005737 cellular_component] (1); ATP binding [GO:0005524 molecular_function] (1); protein refolding [GO:0042026 biological_process] (1)	Chaperonin Cpn60 [IPR001844] (1); GroEL-like equatorial domain [IPR027413] (1); GroEL-like apical domain [IPR027409] (1); Chaperonin Cpn60/TCP-1 family [IPR002423] (1)	-	-	P_trifoliata_00214_mRNA_16.1
GF0046815	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00214_mRNA_15.1
GF0046814	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00214_mRNA_13.1
GF0046813	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00214_mRNA_12.1
GF0046812	0	0	1	Polynucleotidyl transferase, ribonuclease H-like superfamily protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00214_mRNA_10.1
GF0046811	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00213_mRNA_55.1
GF0046810	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00213_mRNA_52.1
GF0046809	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00213_mRNA_50.1
GF0046808	0	0	1	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)	-	-	P_trifoliata_00213_mRNA_49.1
GF0046807	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00213_mRNA_48.1
GF0046806	0	0	1	F-box only 46 (1)			-	-	P_trifoliata_00213_mRNA_45.1
GF0046805	0	0	1	Disease resistance RPS5-like protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00213_mRNA_44.1
GF0046804	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00213_mRNA_38.1
GF0046803	0	0	1	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	-	P_trifoliata_00213_mRNA_34.1
GF0046802	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00213_mRNA_32.1
GF0046801	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00213_mRNA_30.1
GF0046800	0	0	1	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	-	P_trifoliata_00213_mRNA_3.1
GF0046799	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00213_mRNA_29.1
GF0046798	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00213_mRNA_27.1
GF0046797	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00213_mRNA_26.1
GF0046796	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00213_mRNA_22.1
GF0046795	0	0	1	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	-	-	P_trifoliata_00213_mRNA_20.1
GF0046794	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00213_mRNA_19.1
GF0046793	0	0	1	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	-	-	P_trifoliata_00213_mRNA_18.1
GF0046792	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00213_mRNA_14.1
GF0046791	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00213_mRNA_13.1
GF0046790	0	0	1	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	-	P_trifoliata_00213_mRNA_11.1
GF0046789	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00213_mRNA_1.1
GF0046788	0	0	1	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); Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00212_mRNA_9.1
GF0046787	0	0	1	Hypothetical protein (1)		Gnk2-homologous domain [IPR002902] (1)	-	-	P_trifoliata_00212_mRNA_6.1
GF0046786	0	0	1	Cytochrome P450 716B1 (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)	-	-	P_trifoliata_00212_mRNA_58.1
GF0046785	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00212_mRNA_57.1
GF0046784	0	0	1	TOBAMOVIRUS MULTIPLICATION 1 family protein (1)		Domain of unknown function DUF1084 [IPR009457] (1)	-	-	P_trifoliata_00212_mRNA_54.1
GF0046783	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00212_mRNA_52.1
GF0046782	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00212_mRNA_48.1
GF0046781	0	0	1	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)	-	-	P_trifoliata_00212_mRNA_30.1
GF0046780	0	0	1	Thiamine thiazole synthase 2, chloroplastic (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)	-	-	P_trifoliata_00212_mRNA_29.1
GF0046779	0	0	1	Putative cysteine-rich repeat secretory protein 24 (1)		Gnk2-homologous domain [IPR002902] (1)	-	-	P_trifoliata_00212_mRNA_11.1
GF0046778	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00211_mRNA_74.1
GF0046777	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00211_mRNA_67.1
GF0046776	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00211_mRNA_66.1
GF0046775	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00211_mRNA_65.1
GF0046774	0	0	1	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); Double-stranded RNA-binding domain [IPR014720] (1); Alpha/Beta hydrolase fold [IPR029058] (1)	-	-	P_trifoliata_00211_mRNA_61.1
GF0046773	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00211_mRNA_60.1
GF0046772	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00211_mRNA_57.1
GF0046771	0	0	1	Organic cation/carnitine transporter 3 (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)	Major facilitator superfamily domain [IPR020846] (1); Major facilitator, sugar transporter-like [IPR005828] (1)	-	-	P_trifoliata_00211_mRNA_40.1
GF0046770	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00211_mRNA_37.1
GF0046769	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00211_mRNA_27.1
GF0046768	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00211_mRNA_21.1
GF0046767	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00211_mRNA_10.1
GF0046766	0	0	1	MATE efflux family protein 9 (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); transmembrane transport [GO:0055085 biological_process] (1)	Multi antimicrobial extrusion protein [IPR002528] (1)	-	-	P_trifoliata_00210_mRNA_4.1
GF0046765	0	0	1	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)	-	-	P_trifoliata_00210_mRNA_30.1
GF0046764	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00210_mRNA_10.1
GF0046763	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00209_mRNA_52.1
GF0046762	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00209_mRNA_51.1
GF0046761	0	0	1	Pollen Ole e 1 allergen and extensin family protein (1)			-	-	P_trifoliata_00209_mRNA_5.1
GF0046760	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00209_mRNA_49.1

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*
GF0046759	0	0	1	UDP-glucose flavonoid 3-O-glucosyltransferase 7 (1)	metabolic process [GO:0008152 biological_process] (1); transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	-	-	P_trifoliata_00209_mRNA_42.1
GF0046758	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00209_mRNA_35.1
GF0046757	0	0	1	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	-	P_trifoliata_00209_mRNA_33.1
GF0046756	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00209_mRNA_32.1
GF0046755	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00209_mRNA_31.1
GF0046754	0	0	1	Calmodulin binding protein (1)		Protein of unknown function DUF1645, plant [IPR012442] (1)	-	-	P_trifoliata_00209_mRNA_30.1
GF0046753	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00209_mRNA_17.1
GF0046752	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00209_mRNA_1.1
GF0046751	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00208_mRNA_7.1
GF0046750	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00208_mRNA_4.1
GF0046749	0	0	1	Leucine-rich repeat receptor-like serine/threonine-protein kinase BAM1 (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 domain [IPR000719] (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/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 [IPR001611] (1)	-	-	P_trifoliata_00208_mRNA_33.1
GF0046748	0	0	1	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)	-	-	P_trifoliata_00208_mRNA_30.1
GF0046747	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00208_mRNA_3.1
GF0046746	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00208_mRNA_26.1
GF0046745	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00208_mRNA_24.1
GF0046744	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00208_mRNA_18.1
GF0046743	0	0	1	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)	-	-	P_trifoliata_00208_mRNA_14.1
GF0046742	0	0	1	Hypothetical protein (1)	heme binding [GO:0020037 molecular_function] (1)	Cytochrome b5, heme-binding site [IPR018506] (1); Cytochrome b5-like heme/steroid binding domain [IPR001199] (1)	-	-	P_trifoliata_00208_mRNA_13.1
GF0046741	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00208_mRNA_12.1
GF0046740	0	0	1	Phytosulfokine receptor (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	-	-	P_trifoliata_00207_mRNA_9.1
GF0046739	0	0	1	Hypothetical protein (1)		Cobalamin (vitamin B12) biosynthesis CobW-like, C-terminal [IPR011629] (1)	-	-	P_trifoliata_00207_mRNA_8.1
GF0046738	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00207_mRNA_5.1
GF0046737	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00207_mRNA_44.1
GF0046736	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00207_mRNA_41.1
GF0046735	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00207_mRNA_40.1
GF0046734	0	0	1	Hypothetical protein (1)		CobW/HypB/UreG domain [IPR003495] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	-	P_trifoliata_00207_mRNA_4.1
GF0046733	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00207_mRNA_38.1
GF0046732	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00207_mRNA_36.1
GF0046731	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00207_mRNA_27.1
GF0046730	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00207_mRNA_14.1
GF0046729	0	0	1	COBW domain-containing protein 1 (1)		CobW/HypB/UreG domain [IPR003495] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	-	P_trifoliata_00207_mRNA_1.1
GF0046728	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00206_mRNA_7.1
GF0046727	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00206_mRNA_4.1
GF0046726	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00206_mRNA_3.1
GF0046725	0	0	1	Exostosin family protein (1)		Exostosin-like [IPR004263] (1)	-	-	P_trifoliata_00206_mRNA_11.1
GF0046724	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00205_mRNA_59.1
GF0046723	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00205_mRNA_58.1
GF0046722	0	0	1	Trichome birefringence-like 14 (1)		PMR5 N-terminal domain [IPR025846] (1); PC-Esterase [IPR026057] (1)	-	-	P_trifoliata_00205_mRNA_41.1
GF0046721	0	0	1	Hypothetical protein (1)	biosynthetic process [GO:0009058 biological_process] (1); strictosidine synthase activity [GO:0016844 molecular_function] (1)	Six-bladed beta-propeller, TolB-like [IPR011042] (1); Strictosidine synthase [IPR004141] (1)	-	-	P_trifoliata_00205_mRNA_35.1
GF0046720	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00205_mRNA_34.1
GF0046719	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00205_mRNA_33.1
GF0046718	0	0	1	Hypothetical protein (1)		Peptidase S8 propeptide/proteinase inhibitor I9 [IPR010259] (1); Proteinase inhibitor, propeptide [IPR009020] (1); Peptidase S8, subtilisin-related [IPR015500] (1)	-	-	P_trifoliata_00205_mRNA_28.1
GF0046717	0	0	1	Phosphatidylinositol transfer-like protein II (1)		CRAL-TRIO lipid binding domain [IPR001251] (1)	-	-	P_trifoliata_00205_mRNA_1.1
GF0046716	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00204_mRNA_5.1
GF0046715	0	0	1	Glutamate [NMDA] receptor subunit epsilon-1 (1)		Calycin [IPR012674] (1); Calycin-like [IPR011038] (1); Domain of unknown function DUF3598 [IPR022017] (1)	-	-	P_trifoliata_00204_mRNA_49.1
GF0046714	0	0	1	Hypothetical protein (1)		RST domain of plant C-terminal [IPR022003] (1)	-	-	P_trifoliata_00204_mRNA_3.1
GF0046713	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00203_mRNA_8.1
GF0046712	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00203_mRNA_7.1
GF0046711	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00203_mRNA_62.1
GF0046710	0	0	1	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	-	-	P_trifoliata_00203_mRNA_58.1
GF0046709	0	0	1	Hypothetical protein (1)		Conserved hypothetical protein CHP01589, plant [IPR006476] (1)	-	-	P_trifoliata_00203_mRNA_46.1
GF0046708	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00203_mRNA_45.1
GF0046707	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00203_mRNA_4.1
GF0046706	0	0	1	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 L29 [IPR001854] (1)	-	-	P_trifoliata_00203_mRNA_34.1
GF0046705	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00203_mRNA_30.1
GF0046704	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00203_mRNA_29.1
GF0046703	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00203_mRNA_27.1
GF0046702	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00203_mRNA_20.1
GF0046701	0	0	1	Hypothetical protein (1)		Zinc knuckle CX2CX4HX4C [IPR025836] (1); SAC3/GANP/THP3 [IPR005062] (1)	-	-	P_trifoliata_00203_mRNA_18.1
GF0046700	0	0	1	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)	-	-	P_trifoliata_00203_mRNA_15.1
GF0046699	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00203_mRNA_11.1
GF0046698	0	0	1	Putative 26S protease regulatory subunit 6A like protein (1)	ATP binding [GO:0005524 molecular_function] (1)	ATPase, AAA-type, conserved site [IPR003960] (1); ATPase, AAA-type, core [IPR003959] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	-	P_trifoliata_00202_mRNA_73.1
GF0046697	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00202_mRNA_65.1
GF0046696	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00202_mRNA_28.1
GF0046695	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00202_mRNA_27.1
GF0046694	0	0	1	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)	-	-	P_trifoliata_00202_mRNA_26.1
GF0046693	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00202_mRNA_24.1
GF0046692	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00202_mRNA_19.1
GF0046691	0	0	1	Hypothetical protein (1)	enzyme inhibitor activity [GO:0004857 molecular_function] (1)	Pectinesterase inhibitor domain [IPR006501] (1)	-	-	P_trifoliata_00202_mRNA_18.1
GF0046690	0	0	1	Pectinesterase inhibitor (1)	enzyme inhibitor activity [GO:0004857 molecular_function] (1)	Pectinesterase inhibitor domain [IPR006501] (1)	-	-	P_trifoliata_00202_mRNA_17.1
GF0046689	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00202_mRNA_16.1
GF0046688	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00202_mRNA_15.1
GF0046687	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00202_mRNA_14.1
GF0046686	0	0	1	Hypothetical protein (1)		Alpha/Beta hydrolase fold [IPR029058] (1)	-	-	P_trifoliata_00202_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*
GF0046685	0	0	1	Class I peptide chain release factor (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)	-	-	P_trifoliata_00202_mRNA_11.1
GF0046684	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00202_mRNA_10.1
GF0046683	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00201_mRNA_9.1
GF0046682	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00201_mRNA_58.1
GF0046681	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00201_mRNA_34.1
GF0046680	0	0	1	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	-	P_trifoliata_00200_mRNA_9.1
GF0046679	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00200_mRNA_8.1
GF0046678	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00200_mRNA_7.1
GF0046677	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00200_mRNA_6.1
GF0046676	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00200_mRNA_30.1
GF0046675	0	0	1	Hypothetical protein (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1); hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (1)	Peptidase family A1 domain [IPR033121] (1); Glycoside hydrolase 35, catalytic domain [IPR031330] (1); Galactose-binding domain-like [IPR008979] (1); Aspartic peptidase domain [IPR021109] (1); Glycoside hydrolase superfamily [IPR017853] (1); Beta-galactosidase jelly roll domain [IPR025300] (1); Glycoside hydrolase, catalytic domain [IPR013781] (1); Glycoside hydrolase, family 35 [IPR001944] (1); Xylanase inhibitor, N-terminal [IPR032861] (1); Xylanase inhibitor, C-terminal [IPR032799] (1); Glycoside hydrolase, family 35, conserved site [IPR019801] (1)	-	-	P_trifoliata_00200_mRNA_26.1
GF0046674	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00200_mRNA_21.1
GF0046673	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00200_mRNA_19.1
GF0046672	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00200_mRNA_1.1
GF0046671	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00199_mRNA_9.1
GF0046670	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00199_mRNA_8.1
GF0046669	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00199_mRNA_7.1
GF0046668	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00199_mRNA_55.1
GF0046667	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00199_mRNA_54.1
GF0046666	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00199_mRNA_38.1
GF0046665	0	0	1	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 kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1)	-	-	P_trifoliata_00199_mRNA_37.1
GF0046664	0	0	1	Hypothetical protein (1)		Transposase, Tnp1/En/Spm-like [IPR004264] (1)	-	-	P_trifoliata_00199_mRNA_3.1
GF0046663	0	0	1	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)	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)	-	-	P_trifoliata_00199_mRNA_2.1
GF0046662	0	0	1	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); protein binding [GO:0005515 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1)	F-box domain [IPR001810] (1); Cytochrome P450 [IPR001128] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Cytochrome P450, E-class, group I [IPR002401] (1)	-	-	P_trifoliata_00199_mRNA_19.1
GF0046661	0	0	1	Cytochrome P450 93A2 (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, conserved site [IPR017972] (1); Cytochrome P450, E-class, group I [IPR002401] (1)	-	-	P_trifoliata_00199_mRNA_18.1
GF0046660	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	F-box domain [IPR001810] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00199_mRNA_14.1
GF0046659	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00199_mRNA_13.1
GF0046658	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00198_mRNA_9.1
GF0046657	0	0	1	Hypothetical protein (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)	Carotenoid oxygenase [IPR004294] (1)	-	-	P_trifoliata_00198_mRNA_8.1
GF0046656	0	0	1	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)	-	-	P_trifoliata_00198_mRNA_6.1
GF0046655	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00198_mRNA_30.1
GF0046654	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00198_mRNA_28.1
GF0046653	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00198_mRNA_21.1
GF0046652	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00198_mRNA_20.1
GF0046651	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00198_mRNA_2.1
GF0046650	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00198_mRNA_18.1
GF0046649	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00198_mRNA_16.1
GF0046648	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00198_mRNA_15.1
GF0046647	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00198_mRNA_14.1
GF0046646	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00198_mRNA_11.1
GF0046645	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00197_mRNA_4.1
GF0046644	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00197_mRNA_34.1
GF0046643	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00197_mRNA_33.1
GF0046642	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00197_mRNA_28.1
GF0046641	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00197_mRNA_22.1
GF0046640	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00197_mRNA_1.1
GF0046639	0	0	1	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)	-	-	P_trifoliata_00196_mRNA_61.1
GF0046638	0	0	1	Hypothetical protein (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)	-	-	P_trifoliata_00196_mRNA_59.1
GF0046637	0	0	1	Uridine kinase (1)	fructose-bisphosphate aldolase activity [GO:0004332 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1); kinase activity [GO:0016301 molecular_function] (1); catalytic activity [GO:0003824 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1); glycolytic process [GO:0006096 biological_process] (1)	Phosphoribosyltransferase-like [IPR029057] (1); Fructose-bisphosphate aldolase, class-I [IPR000741] (1); Fructose-bisphosphate aldolase class-I active site [IPR029768] (1); Aldolase-type TIM barrel [IPR013785] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Phosphoribulokinase/uridine kinase [IPR006083] (1); Uridine kinase-like [IPR000764] (1)	-	-	P_trifoliata_00196_mRNA_37.1
GF0046636	0	0	1	Protein transport protein SFT2 (1)	transport [GO:0006810 biological_process] (1); integral component of membrane [GO:0016021 cellular_component] (1); vesicle-mediated transport [GO:0016192 biological_process] (1)	Vesicle transport protein, SFT2-like [IPR011691] (1); Vesicle transport protein, Got1/SFT2-like [IPR007305] (1)	-	-	P_trifoliata_00196_mRNA_33.1
GF0046635	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00196_mRNA_31.1
GF0046634	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00196_mRNA_3.1
GF0046633	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00196_mRNA_26.1
GF0046632	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00196_mRNA_24.1
GF0046631	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00196_mRNA_1.1
GF0046630	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00195_mRNA_8.1
GF0046629	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00195_mRNA_70.1
GF0046628	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00195_mRNA_7.1
GF0046627	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00195_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*
GF0046626	0	0	1	LRR receptor-like serine/threonine-protein kinase RPK2 (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); 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 [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); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	-	-	P_trifoliata_00195_mRNA_59.1
GF0046625	0	0	1	Hypothetical protein (1)	molybdate ion transmembrane transporter activity [GO:0015098 molecular_function] (1); molybdate ion transport [GO:0015689 biological_process] (1)	Molybdate transporter 1/2 [IPR031563] (1)	-	-	P_trifoliata_00195_mRNA_55.1
GF0046624	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00195_mRNA_54.1
GF0046623	0	0	1	S-locus lectin protein kinase family protein isoform 2 (1)	protein phosphorylation [GO:0006468 biological_process] (1); recognition of pollen [GO:0048544 biological_process] (1); protein serine/threonine kinase activity [GO:0004674 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	S-locus glycoprotein domain [IPR000858] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); S-locus receptor kinase, C-terminal [IPR021820] (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); Protein kinase-like domain [IPR011009] (1)	-	-	P_trifoliata_00195_mRNA_5.1
GF0046622	0	0	1	Disease resistance protein RPS2 (1)	protein binding [GO:0005515 molecular_function] (1); ADP binding [GO:0043531 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)	-	-	P_trifoliata_00195_mRNA_47.1
GF0046621	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00195_mRNA_37.1
GF0046620	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00195_mRNA_35.1
GF0046619	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00195_mRNA_31.1
GF0046618	0	0	1	Disease resistance RPS5-like protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00195_mRNA_30.1
GF0046617	0	0	1	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1)	-	-	P_trifoliata_00195_mRNA_29.1
GF0046616	0	0	1	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	-	P_trifoliata_00195_mRNA_24.1
GF0046615	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00195_mRNA_23.1
GF0046614	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00195_mRNA_19.1
GF0046613	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00195_mRNA_17.1
GF0046612	0	0	1	Hypothetical protein (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Protein kinase-like domain [IPR011009] (1); Bulb-type lectin domain [IPR001480] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1)	-	-	P_trifoliata_00195_mRNA_13.1
GF0046611	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00195_mRNA_11.1
GF0046610	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00195_mRNA_1.1
GF0046609	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00194_mRNA_9.1
GF0046608	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00194_mRNA_8.1
GF0046607	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00194_mRNA_63.1
GF0046606	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00194_mRNA_59.1
GF0046605	0	0	1	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	-	P_trifoliata_00194_mRNA_57.1
GF0046604	0	0	1	Hypothetical protein (1)		Gag-polypeptide of LTR copia-type [IPR029472] (1)	-	-	P_trifoliata_00194_mRNA_55.1
GF0046603	0	0	1	Hypothetical protein (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); protein binding [GO:0005515 molecular_function] (1); metal ion binding [GO:0046872 molecular_function] (1)	PLAT/LH2 domain [IPR001024] (1); Lipoxygenase [IPR000907] (1)	-	-	P_trifoliata_00194_mRNA_53.1
GF0046602	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00194_mRNA_49.1
GF0046601	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00194_mRNA_48.1
GF0046600	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00194_mRNA_47.1
GF0046599	0	0	1	Pentatricopeptide repeat-containing protein, chloroplastic (1)		Pentatricopeptide repeat [IPR002885] (1)	-	-	P_trifoliata_00194_mRNA_46.1
GF0046598	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00194_mRNA_45.1
GF0046597	0	0	1	Peroxidase 4 (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)	-	-	P_trifoliata_00194_mRNA_44.1
GF0046596	0	0	1	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	-	P_trifoliata_00194_mRNA_41.1
GF0046595	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00194_mRNA_40.1
GF0046594	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00194_mRNA_38.1
GF0046593	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00194_mRNA_35.1
GF0046592	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00194_mRNA_3.1
GF0046591	0	0	1	Hypothetical protein (1)	structural constituent of ribosome [GO:0003735 molecular_function] (1); translation [GO:0006412 biological_process] (1); large ribosomal subunit [GO:0015934 cellular_component] (1)	Ribosomal protein L26/L24P, eukaryotic/archaeal [IPR005756] (1); Ribosomal protein L2 domain 2 [IPR014722] (1); Translation protein SH3-like domain [IPR008991] (1)	-	-	P_trifoliata_00194_mRNA_28.1
GF0046590	0	0	1	Putative carboxylesterase 18 (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)	-	-	P_trifoliata_00194_mRNA_26.1
GF0046589	0	0	1	Carboxyesterase 18, putative (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)	-	-	P_trifoliata_00194_mRNA_25.1
GF0046588	0	0	1	Receptor like protein 21 (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	-	-	P_trifoliata_00194_mRNA_23.1
GF0046587	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00194_mRNA_2.1
GF0046586	0	0	1	Otubain (1)		Transcription factor AFT [IPR014842] (1)	-	-	P_trifoliata_00194_mRNA_11.1
GF0046585	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00194_mRNA_1.1
GF0046584	0	0	1	Hypothetical protein (1)		Plant disease resistance response protein [IPR004265] (1)	-	-	P_trifoliata_00193_mRNA_9.1
GF0046583	0	0	1	Hypothetical protein (1)		START-like domain [IPR023393] (1)	-	-	P_trifoliata_00193_mRNA_72.1
GF0046582	0	0	1	Hypothetical protein (1)		GAG-pre-integrase domain [IPR025724] (1)	-	-	P_trifoliata_00193_mRNA_69.1
GF0046581	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00193_mRNA_4.1
GF0046580	0	0	1	60S ribosomal protein L29-1 (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 L29e [IPR002673] (1)	-	-	P_trifoliata_00193_mRNA_36.1
GF0046579	0	0	1	Hypothetical protein (1)		Glycosyl hydrolases 36 [IPR008811] (1)	-	-	P_trifoliata_00193_mRNA_26.1
GF0046578	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00193_mRNA_16.1
GF0046577	0	0	1	17.9 kDa class II heat shock protein (1)		HSP20-like chaperone [IPR008978] (1); Alpha crystallin/Hsp20 domain [IPR002068] (1); Small heat shock protein HSP20 [IPR031107] (1)	-	-	P_trifoliata_00192_mRNA_6.1
GF0046576	0	0	1	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, E-class, group I [IPR002401] (1); Cytochrome P450 [IPR001128] (1)	-	-	P_trifoliata_00192_mRNA_29.1

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*
GF0046575	0	0	1	Cytochrome P450 89A2 (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, conserved site [IPR017972] (1); Cytochrome P450 [IPR001128] (1); Cytochrome P450, E-class, group IV [IPR002403] (1)	-	-	P_trifoliata_00192_mRNA_28.1
GF0046574	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00192_mRNA_26.1
GF0046573	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00192_mRNA_25.1
GF0046572	0	0	1	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)	-	-	P_trifoliata_00192_mRNA_24.1
GF0046571	0	0	1	Hypothetical protein (1)		Zinc knuckle CX2CX4HX4C [IPR025836] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	-	P_trifoliata_00192_mRNA_23.1
GF0046570	0	0	1	Cytochrome P450, family 87, subfamily A, polypeptide 6 (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, E-class, group I [IPR002401] (1); Cytochrome P450 [IPR001128] (1)	-	-	P_trifoliata_00192_mRNA_20.1
GF0046569	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00192_mRNA_2.1
GF0046568	0	0	1	Hypothetical protein (1)		Transposase, MuDR, plant [IPR004332] (1)	-	-	P_trifoliata_00192_mRNA_14.1
GF0046567	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00192_mRNA_12.1
GF0046566	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00191_mRNA_47.1
GF0046565	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00191_mRNA_46.1
GF0046564	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00191_mRNA_35.1
GF0046563	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00191_mRNA_34.1
GF0046562	0	0	1	Hypothetical protein (1)		Transposase, MuDR, plant [IPR004332] (1)	-	-	P_trifoliata_00191_mRNA_32.1
GF0046561	0	0	1	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)	-	-	P_trifoliata_00191_mRNA_30.1
GF0046560	0	0	1	Hypothetical protein (1)	ionotropic glutamate receptor activity [GO:0004970 molecular_function] (1); membrane [GO:0016020 cellular_component] (1)	Periplasmic binding protein-like I [IPR028082] (1); Receptor, ligand binding region [IPR001828] (1); Ionotropic glutamate receptor [IPR001320] (1); Solute-binding protein family 3/N-terminal domain of MltF [IPR001638] (1)	-	-	P_trifoliata_00191_mRNA_3.1
GF0046559	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00191_mRNA_29.1
GF0046558	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00191_mRNA_24.1
GF0046557	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00191_mRNA_20.1
GF0046556	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00191_mRNA_2.1
GF0046555	0	0	1	UDP-glycosyltransferase 74B1 (1)	metabolic process [GO:0008152 biological_process] (1); transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	-	-	P_trifoliata_00191_mRNA_18.1
GF0046554	0	0	1	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)	-	-	P_trifoliata_00191_mRNA_16.1
GF0046553	0	0	1	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)	-	-	P_trifoliata_00191_mRNA_15.1
GF0046552	0	0	1	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)	-	-	P_trifoliata_00191_mRNA_14.1
GF0046551	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00191_mRNA_1.1
GF0046550	0	0	1	B3 domain-containing protein At1g49475 (1)	DNA binding [GO:0003677 molecular_function] (1)	DNA-binding pseudobarrel domain [IPR015300] (1); B3 DNA binding domain [IPR003340] (1)	-	-	P_trifoliata_00190_mRNA_6.1
GF0046549	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00190_mRNA_52.1
GF0046548	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00190_mRNA_50.1
GF0046547	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00190_mRNA_5.1
GF0046546	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00190_mRNA_42.1
GF0046545	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00190_mRNA_39.1
GF0046544	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00190_mRNA_38.1
GF0046543	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00190_mRNA_32.1
GF0046542	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00190_mRNA_31.1
GF0046541	0	0	1	B3 domain-containing transcription factor VRN1 (1)	DNA binding [GO:0003677 molecular_function] (1)	DNA-binding pseudobarrel domain [IPR015300] (1); B3 DNA binding domain [IPR003340] (1)	-	-	P_trifoliata_00190_mRNA_3.1
GF0046540	0	0	1	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1); MULE transposase domain [IPR018289] (1)	-	-	P_trifoliata_00190_mRNA_25.1
GF0046539	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00190_mRNA_20.1
GF0046538	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	-	P_trifoliata_00190_mRNA_17.1
GF0046537	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00190_mRNA_10.1
GF0046536	0	0	1	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	B3 DNA binding domain [IPR003340] (1); DNA-binding pseudobarrel domain [IPR015300] (1)	-	-	P_trifoliata_00190_mRNA_1.1
GF0046535	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00189_mRNA_40.1
GF0046534	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00189_mRNA_35.1
GF0046533	0	0	1	50S ribosomal protein L12, chloroplastic (1)	structural constituent of ribosome [GO:0003735 molecular_function] (1); translation [GO:0006412 biological_process] (1)	Ribosomal protein L7/L12, C-terminal [IPR013823] (1); Ribosomal protein L7/L12, C-terminal/adaptor protein ClpS-like [IPR014719] (1)	-	-	P_trifoliata_00189_mRNA_12.1
GF0046532	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00188_mRNA_7.1
GF0046531	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00188_mRNA_6.1
GF0046530	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00188_mRNA_5.1
GF0046529	0	0	1	Glycoside hydrolase family 2 protein (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1); hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (1)	Galactose-binding domain-like [IPR008979] (1); Glycosyl hydrolases family 2, sugar binding domain [IPR006104] (1)	-	-	P_trifoliata_00188_mRNA_43.1
GF0046528	0	0	1	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)	-	-	P_trifoliata_00188_mRNA_42.1
GF0046527	0	0	1	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	Zinc finger, BED-type [IPR003656] (1)	-	-	P_trifoliata_00188_mRNA_40.1
GF0046526	0	0	1	Hypothetical protein (1)		S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	-	P_trifoliata_00188_mRNA_4.1
GF0046525	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00188_mRNA_38.1
GF0046524	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00188_mRNA_36.1
GF0046523	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00188_mRNA_35.1
GF0046522	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00188_mRNA_33.1
GF0046521	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00188_mRNA_31.1
GF0046520	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00188_mRNA_3.1
GF0046519	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00188_mRNA_29.1
GF0046518	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00188_mRNA_26.1
GF0046517	0	0	1	Hypothetical protein (1)		Transposon, En/Spm-like [IPR004242] (1)	-	-	P_trifoliata_00188_mRNA_13.1
GF0046516	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4218 [IPR025452] (1); Transposase-associated domain [IPR029480] (1)	-	-	P_trifoliata_00188_mRNA_10.1
GF0046515	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00187_mRNA_6.1
GF0046514	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00187_mRNA_42.1
GF0046513	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00187_mRNA_38.1
GF0046512	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00187_mRNA_37.1
GF0046511	0	0	1	Hypothetical protein (1)	lipid binding [GO:0008289 molecular_function] (1); lipid transport [GO:0006869 biological_process] (1)	Bifunctional inhibitor/plant lipid transfer protein/seed storage helical domain [IPR016140] (1); Plant lipid transfer protein/Par allergen [IPR000528] (1)	-	-	P_trifoliata_00187_mRNA_33.1
GF0046510	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00187_mRNA_3.1
GF0046509	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00187_mRNA_29.1

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*
GF0046508	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00187_mRNA_28.1
GF0046507	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00187_mRNA_26.1
GF0046506	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00187_mRNA_21.1
GF0046505	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00187_mRNA_20.1
GF0046504	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00187_mRNA_15.1
GF0046503	0	0	1	Aspartyl protease family protein, putative (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)	-	-	P_trifoliata_00187_mRNA_14.1
GF0046502	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00187_mRNA_12.1
GF0046501	0	0	1	Nepenthesin II (1)	proteolysis [GO:0006508 biological_process] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1)	Xylanase inhibitor, C-terminal [IPR032799] (1); Xylanase inhibitor, N-terminal [IPR032861] (1); Aspartic peptidase A1 family [IPR001461] (1); Peptidase family A1 domain [IPR033121] (1); Aspartic peptidase domain [IPR021109] (1)	-	-	P_trifoliata_00187_mRNA_10.1
GF0046500	0	0	1	Class I chitinase (1)	chitinase activity [GO:0004568 molecular_function] (1); chitin catabolic process [GO:0006032 biological_process] (1); cell wall macromolecule catabolic process [GO:0016998 biological_process] (1)	Lysozyme-like domain [IPR023346] (1); Glycoside hydrolase, family 19, catalytic [IPR000726] (1)	-	-	P_trifoliata_00186_mRNA_64.1
GF0046499	0	0	1	Hypothetical protein (1)		Protein of unknown function DUF241, plant [IPR004320] (1)	-	-	P_trifoliata_00186_mRNA_62.1
GF0046498	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00186_mRNA_59.1
GF0046497	0	0	1	Protein spotted leaf 11 (1)	protein ubiquitination [GO:0016567 biological_process] (1); ubiquitin-protein transferase activity [GO:0004842 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1); binding [GO:0005488 molecular_function] (1)	U box domain [IPR003613] (1); Armadillo [IPR000225] (1); Zinc finger, RING/FYVE/PHD-type [IPR013083] (1); Armadillo-like helical [IPR011989] (1); Armadillo-type fold [IPR016024] (1)	-	-	P_trifoliata_00186_mRNA_41.1
GF0046496	0	0	1	Pantothenate kinase (1)		Domain of unknown function DUF89 [IPR002791] (1)	-	-	P_trifoliata_00186_mRNA_20.1
GF0046495	0	0	1	CBL-interacting serine/threonine-protein kinase 21 (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, ATP binding site [IPR017441] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1)	-	-	P_trifoliata_00186_mRNA_1.1
GF0046494	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00185_mRNA_64.1
GF0046493	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ubiquitin domain [IPR000626] (1); Ubiquitin-related domain [IPR029071] (1); Ubiquitin [IPR019956] (1)	-	-	P_trifoliata_00185_mRNA_53.1
GF0046492	0	0	1	Ankyrin repeat plant-like protein (1)		PGG domain [IPR026961] (1)	-	-	P_trifoliata_00185_mRNA_46.1
GF0046491	0	0	1	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	-	P_trifoliata_00185_mRNA_43.1
GF0046490	0	0	1	Disease resistance protein (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); NB-ARC [IPR002182] (1); Leucine-rich repeat [IPR001611] (1)	-	-	P_trifoliata_00185_mRNA_4.1
GF0046489	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00185_mRNA_30.1
GF0046488	0	0	1	Protein FAR1-RELATED SEQUENCE 6 (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)	-	-	P_trifoliata_00185_mRNA_3.1
GF0046487	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00185_mRNA_28.1
GF0046486	0	0	1	Hypothetical protein (1)	transmembrane transport [GO:0055085 biological_process] (1)	Mitochondrial carrier protein [IPR002067] (1); Mitochondrial carrier domain [IPR023395] (1); Mitochondrial substrate/solute carrier [IPR018108] (1)	-	-	P_trifoliata_00185_mRNA_21.1
GF0046485	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00185_mRNA_18.1
GF0046484	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00185_mRNA_17.1
GF0046483	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00185_mRNA_16.1
GF0046482	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00185_mRNA_14.1
GF0046481	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00185_mRNA_1.1
GF0046480	0	0	1	Nodulin MtN21 /EamA transporter family protein, putative (1)	integral component of membrane [GO:0016021 cellular_component] (1); transmembrane transporter activity [GO:0022857 molecular_function] (1)	WAT1-related protein [IPR030184] (1)	-	-	P_trifoliata_00184_mRNA_56.1
GF0046479	0	0	1	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)	-	-	P_trifoliata_00184_mRNA_55.1
GF0046478	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00184_mRNA_54.1
GF0046477	0	0	1	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)	-	-	P_trifoliata_00184_mRNA_53.1
GF0046476	0	0	1	Hypothetical protein (1)	serine-type endopeptidase activity [GO:0004252 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Peptidase S8/S53 domain [IPR000209] (1); Peptidase S8, subtilisin-related [IPR015500] (1)	-	-	P_trifoliata_00184_mRNA_50.1
GF0046475	0	0	1	Hypothetical protein (1)		Peptidase S8, subtilisin-related [IPR015500] (1)	-	-	P_trifoliata_00184_mRNA_49.1
GF0046474	0	0	1	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	-	P_trifoliata_00184_mRNA_44.1
GF0046473	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00184_mRNA_42.1
GF0046472	0	0	1	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	-	P_trifoliata_00184_mRNA_41.1
GF0046471	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00184_mRNA_38.1
GF0046470	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00184_mRNA_32.1
GF0046469	0	0	1	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FAR1 DNA binding domain [IPR004330] (1); FHY3/FAR1 family [IPR031052] (1)	-	-	P_trifoliata_00184_mRNA_27.1
GF0046468	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00184_mRNA_21.1
GF0046467	0	0	1	Glyoxal oxidase-related protein (1)		Galactose oxidase/kelch, beta-propeller [IPR011043] (1); Galactose oxidase, beta-propeller [IPR015916] (1); Glyoxal oxidase, N-terminal [IPR009880] (1)	-	-	P_trifoliata_00184_mRNA_17.1
GF0046466	0	0	1	Hypothetical protein (1)		Gag-polypeptide of LTR copia-type [IPR029472] (1)	-	-	P_trifoliata_00183_mRNA_9.1
GF0046465	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00183_mRNA_8.1
GF0046464	0	0	1	MADS-box transcription factor family protein (1)			-	-	P_trifoliata_00183_mRNA_4.1
GF0046463	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00183_mRNA_39.1
GF0046462	0	0	1	Hypothetical protein (1)		Gag-polypeptide of LTR copia-type [IPR029472] (1)	-	-	P_trifoliata_00183_mRNA_35.1
GF0046461	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00183_mRNA_33.1
GF0046460	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00183_mRNA_30.1
GF0046459	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00183_mRNA_29.1
GF0046458	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00183_mRNA_27.1
GF0046457	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00183_mRNA_26.1
GF0046456	0	0	1	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)	-	-	P_trifoliata_00183_mRNA_20.1
GF0046455	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00183_mRNA_18.1
GF0046454	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00183_mRNA_17.1
GF0046453	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00183_mRNA_15.1
GF0046452	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00183_mRNA_13.1
GF0046451	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00183_mRNA_11.1
GF0046450	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00183_mRNA_10.1
GF0046449	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00182_mRNA_6.1
GF0046448	0	0	1	Hypothetical protein (1)		CTAG/Pcc1 family [IPR015419] (1)	-	-	P_trifoliata_00182_mRNA_51.1
GF0046447	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00182_mRNA_50.1
GF0046446	0	0	1	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/dual specificity protein kinase, catalytic domain [IPR002290] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	-	-	P_trifoliata_00182_mRNA_49.1
GF0046445	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00182_mRNA_48.1
GF0046444	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00182_mRNA_47.1
GF0046443	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00182_mRNA_45.1
GF0046442	0	0	1	Hypothetical protein (1)		Peroxisome membrane protein, Pex16 [IPR013919] (1)	-	-	P_trifoliata_00182_mRNA_41.1
GF0046441	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00182_mRNA_40.1
GF0046440	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00182_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*
GF0046439	0	0	1	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1); FAR1 DNA binding domain [IPR004330] (1)	-	-	P_trifoliata_00182_mRNA_32.1
GF0046438	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00182_mRNA_23.1
GF0046437	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00182_mRNA_22.1
GF0046436	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00182_mRNA_21.1
GF0046435	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00182_mRNA_20.1
GF0046434	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00182_mRNA_19.1
GF0046433	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00182_mRNA_18.1
GF0046432	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00182_mRNA_15.1
GF0046431	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00182_mRNA_11.1
GF0046430	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00182_mRNA_1.1
GF0046429	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00181_mRNA_46.1
GF0046428	0	0	1	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, PMZ-type [IPR006564] (1)	-	-	P_trifoliata_00181_mRNA_39.1
GF0046427	0	0	1	Cytochrome P450 83B1 (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 [IPR001128] (1)	-	-	P_trifoliata_00181_mRNA_38.1
GF0046426	0	0	1	Cytochrome P450 family 71 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, conserved site [IPR017972] (1); Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450 [IPR001128] (1)	-	-	P_trifoliata_00181_mRNA_37.1
GF0046425	0	0	1	IPYR (1)	phosphate-containing compound metabolic process [GO:0006796 biological_process] (1); inorganic diphosphatase activity [GO:0004427 molecular_function] (1); cytoplasm [GO:0005737 cellular_component] (1); magnesium ion binding [GO:0000287 molecular_function] (1)	Inorganic pyrophosphatase [IPR008162] (1)	-	-	P_trifoliata_00181_mRNA_34.1
GF0046424	0	0	1	Hypothetical protein (1)	cytoplasm [GO:0005737 cellular_component] (1); phosphate-containing compound metabolic process [GO:0006796 biological_process] (1); inorganic diphosphatase activity [GO:0004427 molecular_function] (1); magnesium ion binding [GO:0000287 molecular_function] (1)	Inorganic pyrophosphatase [IPR008162] (1)	-	-	P_trifoliata_00181_mRNA_33.1
GF0046423	0	0	1	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)	-	-	P_trifoliata_00181_mRNA_19.1
GF0046422	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00180_mRNA_9.1
GF0046421	0	0	1	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)	-	-	P_trifoliata_00180_mRNA_8.1
GF0046420	0	0	1	LRR receptor-like serine/threonine-protein kinase GSO1 (1)	protein binding [GO:0005515 molecular_function] (1)	Reverse transcriptase domain [IPR000477] (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)	-	-	P_trifoliata_00180_mRNA_38.1
GF0046419	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00180_mRNA_36.1
GF0046418	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00180_mRNA_33.1
GF0046417	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00180_mRNA_32.1
GF0046416	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00180_mRNA_28.1
GF0046415	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00180_mRNA_27.1
GF0046414	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00180_mRNA_24.1
GF0046413	0	0	1	Hypothetical protein (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Peptidase A2A, retrovirus, catalytic [IPR001995] (1); Aspartic peptidase domain [IPR021109] (1); P-type ATPase, transmembrane domain [IPR023298] (1)	-	-	P_trifoliata_00180_mRNA_11.1
GF0046412	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00179_mRNA_58.1
GF0046411	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00179_mRNA_56.1
GF0046410	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00179_mRNA_52.1
GF0046409	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00179_mRNA_51.1
GF0046408	0	0	1	Salutaridine reductase (1)	metabolic process [GO:0008152 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1)	Short-chain dehydrogenase/reductase SDR [IPR002198] (1); Short-chain dehydrogenase/reductase, conserved site [IPR020904] (1); Glucose/ribitol dehydrogenase [IPR002347] (1); NAD(P)-binding domain [IPR016040] (1)	-	-	P_trifoliata_00179_mRNA_49.1
GF0046407	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00179_mRNA_47.1
GF0046406	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00179_mRNA_16.1
GF0046405	0	0	1	Hypothetical protein (1)	protein ubiquitination [GO:0016567 biological_process] (1); ubiquitin-protein transferase activity [GO:0004842 molecular_function] (1)	Zinc finger, RING/FYVE/PHD-type [IPR013083] (1); U box domain [IPR003613] (1)	-	-	P_trifoliata_00179_mRNA_10.1
GF0046404	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00178_mRNA_57.1
GF0046403	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00178_mRNA_56.1
GF0046402	0	0	1	Serine/threonine-protein kinase ULK3 (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); Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase, ATP binding site [IPR017441] (1)	-	-	P_trifoliata_00178_mRNA_53.1
GF0046401	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00178_mRNA_52.1
GF0046400	0	0	1	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1)	Aldo/keto reductase [IPR020471] (1); Aldo/keto reductase/potassium channel subunit beta [IPR001395] (1); NADP-dependent oxidoreductase domain [IPR023210] (1); Aldo/keto reductase, conserved site [IPR018170] (1)	-	-	P_trifoliata_00178_mRNA_42.1
GF0046399	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00178_mRNA_38.1
GF0046398	0	0	1	Aldo-keto reductase family 4 member C10 (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)	-	-	P_trifoliata_00178_mRNA_37.1
GF0046397	0	0	1	Hypothetical protein (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); Aldo/keto reductase, conserved site [IPR018170] (1); NADP-dependent oxidoreductase domain [IPR023210] (1)	-	-	P_trifoliata_00178_mRNA_35.1
GF0046396	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00178_mRNA_26.1
GF0046395	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00178_mRNA_24.1
GF0046394	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00178_mRNA_23.1
GF0046393	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00178_mRNA_20.1
GF0046392	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00177_mRNA_9.1
GF0046391	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00177_mRNA_42.1
GF0046390	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00177_mRNA_40.1
GF0046389	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00177_mRNA_4.1
GF0046388	0	0	1	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	-	P_trifoliata_00177_mRNA_39.1
GF0046387	0	0	1	Hypothetical protein (1)		Zinc knuckle CX2CX4HX4C [IPR025836] (1)	-	-	P_trifoliata_00177_mRNA_33.1
GF0046386	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00177_mRNA_3.1
GF0046385	0	0	1	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	-	P_trifoliata_00177_mRNA_25.1
GF0046384	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00177_mRNA_24.1
GF0046383	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00177_mRNA_22.1
GF0046382	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00177_mRNA_20.1
GF0046381	0	0	1	Ribonuclease H-like superfamily protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	-	P_trifoliata_00177_mRNA_2.1
GF0046380	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00177_mRNA_18.1
GF0046379	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00177_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*
GF0046378	0	0	1	Phospholipase A1 (1)	lipid metabolic process [GO:0006629 biological_process] (1)	Fungal lipase-like domain [IPR002921] (1); Alpha/Beta hydrolase fold [IPR029058] (1)	-	-	P_trifoliata_00176_mRNA_60.1
GF0046377	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00176_mRNA_55.1
GF0046376	0	0	1	Small GTPase RacB (1)	protein transport [GO:0015031 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); small GTPase mediated signal transduction [GO:0007264 biological_process] (1)	Small GTPase superfamily, Ras type [IPR020849] (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)	-	-	P_trifoliata_00176_mRNA_44.1
GF0046375	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00176_mRNA_36.1
GF0046374	0	0	1	Hypothetical protein (1)		Protein of unknown function DUF3769 [IPR022244] (1)	-	-	P_trifoliata_00176_mRNA_32.1
GF0046373	0	0	1	Ras-related protein RABH1b (1)	intracellular [GO:0005622 cellular_component] (1); intracellular protein transport [GO:0006886 biological_process] (1); GTP binding [GO:0005525 molecular_function] (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); protein transport [GO:0015031 biological_process] (1); GTPase activity [GO:0003924 molecular_function] (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); Small GTPase superfamily, Ras type [IPR020849] (1)	-	-	P_trifoliata_00176_mRNA_28.2
GF0046372	0	0	1	Gl1 protein (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); fatty acid biosynthetic process [GO:0006633 biological_process] (1); iron ion binding [GO:0005506 molecular_function] (1)	Fatty acid hydroxylase [IPR006694] (1); Uncharacterised domain Wax2, C-terminal [IPR021940] (1)	-	-	P_trifoliata_00176_mRNA_21.1
GF0046371	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00176_mRNA_18.1
GF0046370	0	0	1	ABC transporter C family protein, putative (1)			-	-	P_trifoliata_00176_mRNA_17.1
GF0046369	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00175_mRNA_68.1
GF0046368	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00175_mRNA_60.1
GF0046367	0	0	1	Putative hexose transporter (1)	transmembrane transport [GO:0055085 biological_process] (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)	Major facilitator superfamily domain [IPR020846] (1); Major facilitator, sugar transporter-like [IPR005828] (1); Sugar/inositol transporter [IPR003663] (1)	-	-	P_trifoliata_00175_mRNA_4.1
GF0046366	0	0	1	Hypothetical protein (1)	transferase activity, transferring alkyl or aryl (other than methyl) groups [GO:0016765 molecular_function] (1)	Decaprenyl diphosphate synthase-like [IPR001441] (1)	-	-	P_trifoliata_00175_mRNA_30.1
GF0046365	0	0	1	Flavoprotein wrbA (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); FMN binding [GO:0010181 molecular_function] (1); negative regulation of transcription, DNA-templated [GO:0045892 biological_process] (1)	NADPH-dependent FMN reductase-like [IPR005025] (1); Flavodoxin/nitric oxide synthase [IPR008254] (1); Flavoprotein-like domain [IPR029039] (1); Flavoprotein WrbA [IPR010089] (1)	-	-	P_trifoliata_00175_mRNA_21.1
GF0046364	0	0	1	GDP-mannose transporter GONST1 (1)		Sugar phosphate transporter domain [IPR004853] (1)	-	-	P_trifoliata_00175_mRNA_18.1
GF0046363	0	0	1	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, conserved site [IPR017972] (1); Cytochrome P450 [IPR001128] (1)	-	-	P_trifoliata_00175_mRNA_15.1
GF0046362	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00174_mRNA_65.1
GF0046361	0	0	1	RNA-directed DNA polymerase , related (1)			-	-	P_trifoliata_00174_mRNA_64.1
GF0046360	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00174_mRNA_63.1
GF0046359	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00174_mRNA_62.1
GF0046358	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00174_mRNA_58.1
GF0046357	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00174_mRNA_53.1
GF0046356	0	0	1	Hypothetical protein (1)		Winged helix-turn-helix DNA-binding domain [IPR011991] (1)	-	-	P_trifoliata_00174_mRNA_52.1
GF0046355	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00174_mRNA_50.1
GF0046354	0	0	1	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	-	P_trifoliata_00174_mRNA_45.1
GF0046353	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00174_mRNA_44.1
GF0046352	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00174_mRNA_42.1
GF0046351	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00174_mRNA_40.1
GF0046350	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00174_mRNA_4.1
GF0046349	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00174_mRNA_39.1
GF0046348	0	0	1	Polynucleotidyl transferase, ribonuclease H-like superfamily protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00174_mRNA_37.1
GF0046347	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00174_mRNA_36.1
GF0046346	0	0	1	Myb-related protein 308 (1)	DNA binding [GO:0003677 molecular_function] (1)	Homeodomain-like [IPR009057] (1)	-	-	P_trifoliata_00174_mRNA_27.1
GF0046345	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00174_mRNA_23.1
GF0046344	0	0	1	Hypothetical protein (1)	phosphorelay signal transduction system [GO:0000160 biological_process] (1)	Signal transduction response regulator, receiver domain [IPR001789] (1); CheY-like superfamily [IPR011006] (1)	-	-	P_trifoliata_00174_mRNA_22.1
GF0046343	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00174_mRNA_20.1
GF0046342	0	0	1	Senescence-associated protein DIN1 (1)		Rhodanese-like domain [IPR001763] (1)	-	-	P_trifoliata_00174_mRNA_15.1
GF0046341	0	0	1	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (1)		Lysine methyltransferase [IPR019410] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	-	P_trifoliata_00174_mRNA_10.1
GF0046340	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00173_mRNA_40.1
GF0046339	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00173_mRNA_37.1
GF0046338	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00173_mRNA_30.1
GF0046337	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00173_mRNA_3.1
GF0046336	0	0	1	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)	-	-	P_trifoliata_00173_mRNA_29.1
GF0046335	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00173_mRNA_28.1
GF0046334	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00172_mRNA_8.1
GF0046333	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00172_mRNA_64.1
GF0046332	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00172_mRNA_56.1
GF0046331	0	0	1	Hypothetical protein (1)		GroEL-like equatorial domain [IPR027413] (1)	-	-	P_trifoliata_00172_mRNA_2.1
GF0046330	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00172_mRNA_18.1
GF0046329	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00172_mRNA_10.1
GF0046328	0	0	1	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	-	P_trifoliata_00171_mRNA_7.1
GF0046327	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00171_mRNA_52.1
GF0046326	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00171_mRNA_50.1
GF0046325	0	0	1	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	-	P_trifoliata_00171_mRNA_49.1
GF0046324	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00171_mRNA_48.1
GF0046323	0	0	1	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); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); EGF-like, conserved site [IPR013032] (1)	-	-	P_trifoliata_00171_mRNA_38.1
GF0046322	0	0	1	Glycerol kinase (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); Carbohydrate kinase, FGGY, N-terminal [IPR018484] (1)	-	-	P_trifoliata_00171_mRNA_37.1
GF0046321	0	0	1	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)	-	-	P_trifoliata_00171_mRNA_35.1
GF0046320	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00171_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*
GF0046319	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00171_mRNA_25.1
GF0046318	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00171_mRNA_23.1
GF0046317	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00171_mRNA_17.1
GF0046316	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00171_mRNA_16.1
GF0046315	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00171_mRNA_15.1
GF0046314	0	0	1	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)	-	-	P_trifoliata_00171_mRNA_14.1
GF0046313	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00171_mRNA_13.1
GF0046312	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00171_mRNA_12.1
GF0046311	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00170_mRNA_9.1
GF0046310	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00170_mRNA_62.1
GF0046309	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00170_mRNA_59.1
GF0046308	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00170_mRNA_58.1
GF0046307	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00170_mRNA_57.1
GF0046306	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00170_mRNA_56.1
GF0046305	0	0	1	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	-	P_trifoliata_00170_mRNA_55.1
GF0046304	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00170_mRNA_54.1
GF0046303	0	0	1	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1)	Peptidase A2A, retrovirus, catalytic [IPR001995] (1)	-	-	P_trifoliata_00170_mRNA_52.1
GF0046302	0	0	1	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	-	P_trifoliata_00170_mRNA_48.1
GF0046301	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00170_mRNA_44.1
GF0046300	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00170_mRNA_43.1
GF0046299	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00170_mRNA_41.1
GF0046298	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00170_mRNA_40.1
GF0046297	0	0	1	Photosystem II CP47 chlorophyll apoprotein (1)	photosynthetic electron transport chain [GO:0009767 biological_process] (1); membrane [GO:0016020 cellular_component] (1); photosynthesis, light reaction [GO:0019684 biological_process] (1); photosystem [GO:0009521 cellular_component] (1); chlorophyll binding [GO:0016168 molecular_function] (1)	Photosystem antenna protein-like [IPR000932] (1)	-	-	P_trifoliata_00170_mRNA_38.1
GF0046296	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00170_mRNA_35.1
GF0046295	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00170_mRNA_33.1
GF0046294	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00170_mRNA_32.1
GF0046293	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00170_mRNA_31.1
GF0046292	0	0	1	Cornichon family protein (1)	intracellular signal transduction [GO:0035556 biological_process] (1); membrane [GO:0016020 cellular_component] (1)	Cornichon [IPR003377] (1)	-	-	P_trifoliata_00170_mRNA_28.1
GF0046291	0	0	1	PGRL1A transmembrane protein (1)			-	-	P_trifoliata_00170_mRNA_1.1
GF0046290	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); intracellular [GO:0005622 cellular_component] (1)	HRDC domain [IPR002121] (1)	-	-	P_trifoliata_00169_mRNA_44.1
GF0046289	0	0	1	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	-	P_trifoliata_00169_mRNA_37.1
GF0046288	0	0	1	Putative MYB DNA-binding domain superfamily protein (1)	DNA binding [GO:0003677 molecular_function] (1)	SANT/Myb domain [IPR001005] (1); Homeodomain-like [IPR009057] (1); Myb domain [IPR017930] (1)	-	-	P_trifoliata_00169_mRNA_27.1
GF0046287	0	0	1	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)	-	-	P_trifoliata_00169_mRNA_25.1
GF0046286	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4219 [IPR025314] (1)	-	-	P_trifoliata_00169_mRNA_22.1
GF0046285	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00169_mRNA_2.1
GF0046284	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	MATH/TRAF domain [IPR002083] (1); TRAF-like [IPR008974] (1)	-	-	P_trifoliata_00169_mRNA_18.1
GF0046283	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00169_mRNA_15.1
GF0046282	0	0	1	Ubiquitin carboxyl-terminal hydrolase 12 (1)	protein binding [GO:0005515 molecular_function] (1)	TRAF-like [IPR008974] (1); MATH/TRAF domain [IPR002083] (1)	-	-	P_trifoliata_00169_mRNA_13.1
GF0046281	0	0	1	Envelope glycoprotein (1)			-	-	P_trifoliata_00169_mRNA_12.1
GF0046280	0	0	1	Ubiquitin carboxyl-terminal hydrolase 13 (1)	protein binding [GO:0005515 molecular_function] (1)	MATH/TRAF domain [IPR002083] (1); TRAF-like [IPR008974] (1)	-	-	P_trifoliata_00169_mRNA_11.1
GF0046279	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00169_mRNA_1.1
GF0046278	0	0	1	Hypothetical protein (1)	RNA binding [GO:0003723 molecular_function] (1)	RNA-binding, CRM domain [IPR001890] (1)	-	-	P_trifoliata_00168_mRNA_7.1
GF0046277	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00168_mRNA_5.1
GF0046276	0	0	1	Hypothetical protein (1)		Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00168_mRNA_49.1
GF0046275	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00168_mRNA_47.1
GF0046274	0	0	1	Hypothetical protein (1)		Gag-polypeptide of LTR copia-type [IPR029472] (1)	-	-	P_trifoliata_00168_mRNA_4.1
GF0046273	0	0	1	Aspartic proteinase-like protein 1 (1)	proteolysis [GO:0006508 biological_process] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1)	Aspartic peptidase, active site [IPR001969] (1); Aspartic peptidase A1 family [IPR001461] (1); Aspartic peptidase domain [IPR021109] (1)	-	-	P_trifoliata_00168_mRNA_3.2
GF0046272	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00168_mRNA_29.1
GF0046271	0	0	1	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); Ribonuclease H-like domain [IPR012337] (1); Domain of unknown function DUF4283 [IPR025558] (1)	-	-	P_trifoliata_00168_mRNA_2.1
GF0046270	0	0	1	Hypothetical protein (1)		SGNH hydrolase-type esterase domain [IPR013830] (1)	-	-	P_trifoliata_00168_mRNA_19.1
GF0046269	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); nucleus [GO:0005634 cellular_component] (1)	Cleavage/polyadenylation specificity factor, A subunit, C-terminal [IPR004871] (1)	-	-	P_trifoliata_00168_mRNA_18.1
GF0046268	0	0	1	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 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); Protein kinase, ATP binding site [IPR017441] (1); Leucine-rich repeat [IPR001611] (1)	-	-	P_trifoliata_00168_mRNA_13.1
GF0046267	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00167_mRNA_8.1
GF0046266	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00167_mRNA_7.1
GF0046265	0	0	1	Hypothetical protein (1)		Ysc84 actin-binding domain [IPR007461] (1)	-	-	P_trifoliata_00167_mRNA_5.1
GF0046264	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00167_mRNA_32.1
GF0046263	0	0	1	Nodulation signaling pathway 2-like protein (1)		Transcription factor GRAS [IPR005202] (1)	-	-	P_trifoliata_00167_mRNA_29.1
GF0046262	0	0	1	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FAR1 DNA binding domain [IPR004330] (1); FHY3/FAR1 family [IPR031052] (1)	-	-	P_trifoliata_00167_mRNA_28.1
GF0046261	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00167_mRNA_19.1
GF0046260	0	0	1	Hypothetical protein (1)		Zinc knuckle CX2CX4HX4C [IPR025836] (1)	-	-	P_trifoliata_00167_mRNA_16.1
GF0046259	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00167_mRNA_14.1
GF0046258	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00167_mRNA_11.1
GF0046257	0	0	1	Verticillium wilt resistance-like 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)	-	-	P_trifoliata_00167_mRNA_10.1
GF0046256	0	0	1	Hypothetical protein (1)	integral component of membrane [GO:0016021 cellular_component] (1); transmembrane transporter activity [GO:0022857 molecular_function] (1); transmembrane transport [GO:0055085 biological_process] (1)	Major facilitator superfamily domain [IPR020846] (1); Major facilitator, sugar transporter-like [IPR005828] (1)	-	-	P_trifoliata_00166_mRNA_58.1
GF0046255	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00166_mRNA_48.1
GF0046254	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	F-box domain [IPR001810] (1)	-	-	P_trifoliata_00166_mRNA_43.1
GF0046253	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00166_mRNA_40.1
GF0046252	0	0	1	Hypothetical protein (1)	ion transport [GO:0006811 biological_process] (1); transmembrane transport [GO:0055085 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1); ion channel activity [GO:0005216 molecular_function] (1); trehalose biosynthetic process [GO:0005992 biological_process] (1); membrane [GO:0016020 cellular_component] (1)	Cyclic nucleotide-binding domain [IPR000595] (1); Trehalose-phosphatase [IPR003337] (1); Cyclic nucleotide-binding-like [IPR018490] (1); Ribosomal protein L2, domain 3 [IPR014726] (1); Ion transport domain [IPR005821] (1); RmlC-like jelly roll fold [IPR014710] (1); HAD-like domain [IPR023214] (1)	-	-	P_trifoliata_00166_mRNA_24.1

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*
GF0046251	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00166_mRNA_23.1
GF0046250	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00166_mRNA_21.1
GF0046249	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00166_mRNA_19.1
GF0046248	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00166_mRNA_15.1
GF0046247	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00165_mRNA_7.1
GF0046246	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00165_mRNA_6.1
GF0046245	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00165_mRNA_59.1
GF0046244	0	0	1	Hypothetical protein (1)	membrane [GO:0016020 cellular_component] (1); ionotropic glutamate receptor activity [GO:0004970 molecular_function] (1)	Ionotropic glutamate receptor [IPR001320] (1)	-	-	P_trifoliata_00165_mRNA_52.1
GF0046243	0	0	1	Hypothetical protein (1)		Periplasmic binding protein-like I [IPR028082] (1)	-	-	P_trifoliata_00165_mRNA_51.1
GF0046242	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00165_mRNA_34.1
GF0046241	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00165_mRNA_31.1
GF0046240	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00165_mRNA_27.1
GF0046239	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00165_mRNA_2.1
GF0046238	0	0	1	DnaJ like subfamily B member 13 (1)	unfolded protein binding [GO:0051082 molecular_function] (1); protein folding [GO:0006457 biological_process] (1)	HSP40/DnaJ peptide-binding [IPR008971] (1); Chaperone DnaJ, C-terminal [IPR002939] (1)	-	-	P_trifoliata_00165_mRNA_19.1
GF0046237	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00165_mRNA_15.1
GF0046236	0	0	1	Hypothetical protein (1)	binding [GO:0005488 molecular_function] (1)	Armadillo-type fold [IPR016024] (1)	-	-	P_trifoliata_00165_mRNA_1.1
GF0046235	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00164_mRNA_9.1
GF0046234	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00164_mRNA_40.1
GF0046233	0	0	1	Hypothetical protein (1)	serine-type carboxypeptidase activity [GO:0004185 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Serine carboxypeptidase, serine active site [IPR018202] (1); Alpha/Beta hydrolase fold [IPR029058] (1); Peptidase S10, serine carboxypeptidase [IPR001563] (1)	-	-	P_trifoliata_00164_mRNA_35.1
GF0046232	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00164_mRNA_29.1
GF0046231	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00164_mRNA_25.1
GF0046230	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00164_mRNA_24.1
GF0046229	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00164_mRNA_23.1
GF0046228	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00164_mRNA_21.1
GF0046227	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00164_mRNA_20.1
GF0046226	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00164_mRNA_19.1
GF0046225	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00164_mRNA_18.1
GF0046224	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00164_mRNA_17.1
GF0046223	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00164_mRNA_15.1
GF0046222	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00164_mRNA_14.1
GF0046221	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00164_mRNA_12.1
GF0046220	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00164_mRNA_1.1
GF0046219	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	F-box domain [IPR001810] (1)	-	-	P_trifoliata_00163_mRNA_68.1
GF0046218	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00163_mRNA_64.1
GF0046217	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00163_mRNA_63.1
GF0046216	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00163_mRNA_6.1
GF0046215	0	0	1	Putative WRKY transcription factor 70 (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)	-	-	P_trifoliata_00163_mRNA_56.1
GF0046214	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00163_mRNA_54.1
GF0046213	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00163_mRNA_47.1
GF0046212	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00163_mRNA_41.1
GF0046211	0	0	1	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, SWIM-type [IPR007527] (1); Zinc finger, PMZ-type [IPR006564] (1)	-	-	P_trifoliata_00163_mRNA_4.1
GF0046210	0	0	1	Polynucleotidyl transferase, ribonuclease H-like superfamily protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00163_mRNA_10.1
GF0046209	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4057 [IPR025131] (1)	-	-	P_trifoliata_00163_mRNA_1.1
GF0046208	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00162_mRNA_62.1
GF0046207	0	0	1	Peptide chain release factor 1 (1)		Leucine-rich repeat 3 [IPR011713] (1)	-	-	P_trifoliata_00162_mRNA_59.1
GF0046206	0	0	1	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)	-	-	P_trifoliata_00162_mRNA_58.1
GF0046205	0	0	1	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); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	-	P_trifoliata_00162_mRNA_56.1
GF0046204	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00162_mRNA_54.1
GF0046203	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00162_mRNA_50.1
GF0046202	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00162_mRNA_49.1
GF0046201	0	0	1	Hypothetical protein (1)	phosphorelay signal transduction system [GO:0000160 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1); signal transducer activity [GO:0004871 molecular_function] (1); coenzyme binding [GO:0050662 molecular_function] (1)	NAD(P)-binding domain [IPR016040] (1); Signal transduction histidine kinase, phosphotransfer (Hpt) domain [IPR008207] (1); NAD-dependent epimerase/dehydratase, N-terminal domain [IPR001509] (1)	-	-	P_trifoliata_00162_mRNA_45.1
GF0046200	0	0	1	Inosine-uridine preferring nucleoside hydrolase (1)		Inosine/uridine-preferring nucleoside hydrolase domain [IPR001910] (1); Inosine/uridine-preferring nucleoside hydrolase [IPR023186] (1); Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	-	P_trifoliata_00162_mRNA_44.1
GF0046199	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00162_mRNA_4.1
GF0046198	0	0	1	Cytochrome P450 family 88 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, conserved site [IPR017972] (1); Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450 [IPR001128] (1)	-	-	P_trifoliata_00162_mRNA_33.1
GF0046197	0	0	1	Phosphoprotein phosphatase (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00162_mRNA_31.1
GF0046196	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00162_mRNA_3.1
GF0046195	0	0	1	Phosphoprotein phosphatase (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00162_mRNA_27.1
GF0046194	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00162_mRNA_23.1
GF0046193	0	0	1	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	-	P_trifoliata_00162_mRNA_12.1
GF0046192	0	0	1	Putative disease resistance gene NBS-LRR family protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00162_mRNA_11.1
GF0046191	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00161_mRNA_8.1
GF0046190	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00161_mRNA_6.1
GF0046189	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00161_mRNA_40.1
GF0046188	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00161_mRNA_4.1
GF0046187	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00161_mRNA_38.1
GF0046186	0	0	1	Hypothetical protein (1)		LOG family [IPR031100] (1)	-	-	P_trifoliata_00161_mRNA_36.1
GF0046185	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00161_mRNA_35.1
GF0046184	0	0	1	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	-	P_trifoliata_00161_mRNA_33.1
GF0046183	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00161_mRNA_14.1
GF0046182	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00161_mRNA_1.1
GF0046181	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00160_mRNA_9.1
GF0046180	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00160_mRNA_4.1
GF0046179	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00160_mRNA_38.1
GF0046178	0	0	1	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	-	P_trifoliata_00160_mRNA_26.1
GF0046177	0	0	1	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	-	P_trifoliata_00160_mRNA_25.1
GF0046176	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	-	P_trifoliata_00160_mRNA_21.1
GF0046175	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00160_mRNA_2.1
GF0046174	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00160_mRNA_19.1
GF0046173	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00160_mRNA_16.1
GF0046172	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00160_mRNA_1.1
GF0046171	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00159_mRNA_62.1
GF0046170	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00159_mRNA_61.1

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*
GF0046169	0	0	1	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)	-	-	P_trifoliata_00159_mRNA_58.1
GF0046168	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00159_mRNA_52.1
GF0046167	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00159_mRNA_38.1
GF0046166	0	0	1	Hypothetical protein (1)		P-type ATPase, transmembrane domain [IPR023298] (1)	-	-	P_trifoliata_00159_mRNA_36.1
GF0046165	0	0	1	Hypothetical protein (1)		P-type ATPase, transmembrane domain [IPR023298] (1); Cation-transporting P-type ATPase, C-terminal [IPR006068] (1)	-	-	P_trifoliata_00159_mRNA_35.1
GF0046164	0	0	1	Hypothetical protein (1)		Mitochondrial inner membrane protein Mitofilin [IPR019133] (1)	-	-	P_trifoliata_00159_mRNA_33.1
GF0046163	0	0	1	ARM repeat superfamily protein, putative isoform 1 (1)			-	-	P_trifoliata_00159_mRNA_32.1
GF0046162	0	0	1	Hypothetical protein (1)	binding [GO:0005488 molecular_function] (1)	Armadillo-type fold [IPR016024] (1)	-	-	P_trifoliata_00159_mRNA_31.1
GF0046161	0	0	1	Hypothetical protein (1)	binding [GO:0005488 molecular_function] (1)	Armadillo-like helical [IPR011989] (1); Armadillo-type fold [IPR016024] (1)	-	-	P_trifoliata_00159_mRNA_28.1
GF0046160	0	0	1	Hypothetical protein (1)	binding [GO:0005488 molecular_function] (1)	Armadillo-type fold [IPR016024] (1); Armadillo-like helical [IPR011989] (1)	-	-	P_trifoliata_00159_mRNA_27.1
GF0046159	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00159_mRNA_26.1
GF0046158	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00159_mRNA_25.1
GF0046157	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00159_mRNA_23.1
GF0046156	0	0	1	Carbohydrate-binding protein of the ER protein (1)		Protein kinase-like domain [IPR011009] (1); Malectin-like carbohydrate-binding domain [IPR024788] (1)	-	-	P_trifoliata_00159_mRNA_21.1
GF0046155	0	0	1	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); 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)	-	-	P_trifoliata_00159_mRNA_18.1
GF0046154	0	0	1	Hypothetical protein (1)		Malectin-like carbohydrate-binding domain [IPR024788] (1)	-	-	P_trifoliata_00159_mRNA_17.1
GF0046153	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00159_mRNA_15.1
GF0046152	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00159_mRNA_1.1
GF0046151	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00158_mRNA_7.1
GF0046150	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00158_mRNA_6.1
GF0046149	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00158_mRNA_58.1
GF0046148	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00158_mRNA_54.1
GF0046147	0	0	1	Auroralike 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-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	-	-	P_trifoliata_00158_mRNA_52.1
GF0046146	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00158_mRNA_50.1
GF0046145	0	0	1	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); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	-	P_trifoliata_00158_mRNA_5.1
GF0046144	0	0	1	Hypothetical protein (1)		Bulb-type lectin domain [IPR001480] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1)	-	-	P_trifoliata_00158_mRNA_47.1
GF0046143	0	0	1	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); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1)	-	-	P_trifoliata_00158_mRNA_46.1
GF0046142	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00158_mRNA_45.1
GF0046141	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00158_mRNA_41.1
GF0046140	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00158_mRNA_40.1
GF0046139	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00158_mRNA_39.1
GF0046138	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00158_mRNA_38.1
GF0046137	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00158_mRNA_37.1
GF0046136	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00158_mRNA_35.1
GF0046135	0	0	1	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)	-	-	P_trifoliata_00158_mRNA_33.1
GF0046134	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00158_mRNA_32.1
GF0046133	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00158_mRNA_3.1
GF0046132	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00158_mRNA_28.1
GF0046131	0	0	1	Hypothetical protein (1)		Isopenicillin N synthase-like [IPR027443] (1)	-	-	P_trifoliata_00158_mRNA_27.1
GF0046130	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00158_mRNA_26.1
GF0046129	0	0	1	2OG-Fe(II) oxygenase family oxidoreductase (1)		Non-haem dioxygenase N-terminal domain [IPR026992] (1); Isopenicillin N synthase-like [IPR027443] (1)	-	-	P_trifoliata_00158_mRNA_25.1
GF0046128	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00158_mRNA_23.1
GF0046127	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00158_mRNA_22.1
GF0046126	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00158_mRNA_21.1
GF0046125	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00158_mRNA_20.1
GF0046124	0	0	1	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)	Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Serine/threonine-protein kinase, active site [IPR008271] (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)	-	-	P_trifoliata_00158_mRNA_2.1
GF0046123	0	0	1	Hypothetical protein (1)		Lateral organ boundaries, LOB [IPR004883] (1)	-	-	P_trifoliata_00157_mRNA_56.1
GF0046122	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00157_mRNA_48.1
GF0046121	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00157_mRNA_45.1
GF0046120	0	0	1	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	DNA-binding pseudobarrel domain [IPR015300] (1); B3 DNA binding domain [IPR003340] (1)	-	-	P_trifoliata_00157_mRNA_42.1
GF0046119	0	0	1	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	B3 DNA binding domain [IPR003340] (1); DNA-binding pseudobarrel domain [IPR015300] (1)	-	-	P_trifoliata_00157_mRNA_41.1
GF0046118	0	0	1	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); 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)	-	-	P_trifoliata_00157_mRNA_40.1
GF0046117	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00157_mRNA_4.1
GF0046116	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00157_mRNA_39.1
GF0046115	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00157_mRNA_37.1
GF0046114	0	0	1	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 [IPR001128] (1)	-	-	P_trifoliata_00157_mRNA_34.1
GF0046113	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00157_mRNA_33.1
GF0046112	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00157_mRNA_31.1
GF0046111	0	0	1	Ankyrin repeat family protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat [IPR002110] (1); PGG domain [IPR026961] (1); Ankyrin repeat-containing domain [IPR020683]	-	-	P_trifoliata_00157_mRNA_3.1
GF0046110	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00157_mRNA_27.1
GF0046109	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00157_mRNA_26.1
GF0046108	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00157_mRNA_25.1
GF0046107	0	0	1	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1); MULE transposase domain [IPR018289] (1)	-	-	P_trifoliata_00157_mRNA_24.1
GF0046106	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00157_mRNA_23.1
GF0046105	0	0	1	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			-	-	P_trifoliata_00157_mRNA_22.1
GF0046104	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00157_mRNA_19.1
GF0046103	0	0	1	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	-	P_trifoliata_00157_mRNA_18.1
GF0046102	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00156_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*
GF0046101	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00156_mRNA_4.1
GF0046100	0	0	1	Hypothetical protein (1)	transporter activity [GO:0005215 molecular_function] (1); transport [GO:0006810 biological_process] (1); membrane [GO:0016020 cellular_component] (1)	Endonuclease/exonuclease/phosphatase [IPR005135] (1); Proton-dependent oligopeptide transporter family [IPR000109] (1)	-	-	P_trifoliata_00156_mRNA_32.1
GF0046099	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00156_mRNA_30.1
GF0046098	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00156_mRNA_25.1
GF0046097	0	0	1	NBS-LRR class resistance protein Fy2-Ry2 (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); ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); Cytochrome P450, E-class, group I [IPR002401] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Cytochrome P450 [IPR001128] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00155_mRNA_8.1
GF0046096	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00155_mRNA_6.1
GF0046095	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00155_mRNA_50.1
GF0046094	0	0	1	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)	-	-	P_trifoliata_00155_mRNA_46.1
GF0046093	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00155_mRNA_45.1
GF0046092	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00155_mRNA_43.1
GF0046091	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00155_mRNA_41.1
GF0046090	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00155_mRNA_39.1
GF0046089	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00155_mRNA_36.1
GF0046088	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00155_mRNA_35.1
GF0046087	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00155_mRNA_32.1
GF0046086	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00155_mRNA_31.1
GF0046085	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00155_mRNA_28.1
GF0046084	0	0	1	Steroid 5-alpha-reductase DET2 (1)	cytoplasm [GO:0005737 cellular_component] (1); lipid metabolic process [GO:0006629 biological_process] (1); oxidoreductase activity, acting on the CH-CH group of donors [GO:0016627 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1)	3-oxo-5-alpha-steroid 4-dehydrogenase, C-terminal [IPR001104] (1)	-	-	P_trifoliata_00155_mRNA_27.1
GF0046083	0	0	1	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	-	P_trifoliata_00155_mRNA_26.1
GF0046082	0	0	1	Putative steroid reductase DET2 (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); lipid metabolic process [GO:0006629 biological_process] (1); cytoplasm [GO:0005737 cellular_component] (1)	3-oxo-5-alpha-steroid 4-dehydrogenase, C-terminal [IPR001104] (1)	-	-	P_trifoliata_00155_mRNA_25.1
GF0046081	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00155_mRNA_23.1
GF0046080	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00155_mRNA_20.1
GF0046079	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00155_mRNA_18.1
GF0046078	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00155_mRNA_16.1
GF0046077	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00155_mRNA_15.1
GF0046076	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00155_mRNA_12.1
GF0046075	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00155_mRNA_11.1
GF0046074	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00155_mRNA_1.1
GF0046073	0	0	1	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)	-	-	P_trifoliata_00154_mRNA_57.1
GF0046072	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00154_mRNA_56.1
GF0046071	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00154_mRNA_55.1
GF0046070	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00154_mRNA_54.1
GF0046069	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00154_mRNA_4.1
GF0046068	0	0	1	Transposable element protein, putative, (1)		Retrotransposon gag domain [IPR005162] (1)	-	-	P_trifoliata_00154_mRNA_35.1
GF0046067	0	0	1	P-loop nucleoside triphosphate hydrolase superfamily 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)	-	-	P_trifoliata_00154_mRNA_34.1
GF0046066	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00154_mRNA_33.1
GF0046065	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00154_mRNA_31.1
GF0046064	0	0	1	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); Haem peroxidase [IPR010255] (1)	-	-	P_trifoliata_00154_mRNA_30.1
GF0046063	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00154_mRNA_29.1
GF0046062	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00154_mRNA_27.1
GF0046061	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00154_mRNA_21.1
GF0046060	0	0	1	Hypothetical protein (1)		MULE transposase domain [IPR018289] (1)	-	-	P_trifoliata_00154_mRNA_2.1
GF0046059	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00154_mRNA_18.1
GF0046058	0	0	1	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)	-	-	P_trifoliata_00154_mRNA_17.1
GF0046057	0	0	1	Sulfotransferase (1)	sulfotransferase activity [GO:0008146 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Sulfotransferase domain [IPR000863] (1)	-	-	P_trifoliata_00154_mRNA_1.1
GF0046056	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00153_mRNA_9.1
GF0046055	0	0	1	UDP-glycosyltransferase 91C1 (1)	transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	-	-	P_trifoliata_00153_mRNA_56.1
GF0046054	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00153_mRNA_53.1
GF0046053	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00153_mRNA_48.1
GF0046052	0	0	1	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)	-	-	P_trifoliata_00153_mRNA_34.1
GF0046051	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	F-box domain [IPR001810] (1); Kelch-type beta propeller [IPR015915] (1)	-	-	P_trifoliata_00153_mRNA_28.1
GF0046050	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00153_mRNA_27.1
GF0046049	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00153_mRNA_24.1
GF0046048	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00153_mRNA_23.1
GF0046047	0	0	1	Hypothetical protein (1)		P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	-	P_trifoliata_00153_mRNA_13.1
GF0046046	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00153_mRNA_12.1
GF0046045	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00152_mRNA_6.1
GF0046044	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00152_mRNA_4.1
GF0046043	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00152_mRNA_35.1
GF0046042	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00152_mRNA_3.1
GF0046041	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00152_mRNA_28.1
GF0046040	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00152_mRNA_27.1
GF0046039	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00152_mRNA_26.1
GF0046038	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00152_mRNA_21.1
GF0046037	0	0	1	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	-	-	P_trifoliata_00152_mRNA_20.1
GF0046036	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00152_mRNA_2.1
GF0046035	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00152_mRNA_17.1
GF0046034	0	0	1	Hypothetical protein (1)	integral component of membrane [GO:0016021 cellular_component] (1)	Chloroplast envelope membrane protein, CemA [IPR004282] (1); NOSIC [IPR012976] (1); Nop domain [IPR002687] (1); NOP5, N-terminal [IPR012974] (1)	-	-	P_trifoliata_00152_mRNA_14.1
GF0046033	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00152_mRNA_12.1
GF0046032	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00152_mRNA_1.1
GF0046031	0	0	1	MRNA decapping enzyme 1A, putative (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); PH domain-like [IPR011993] (1)	-	-	P_trifoliata_00151_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*
GF0046030	0	0	1	Non-symbiotic hemoglobin 1 (1)	oxygen binding [GO:0019825 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1)	Globin/Protoglobin [IPR012292] (1); Globin-like [IPR009050] (1); Globin [IPR000971] (1); Leghaemoglobin [IPR001032] (1)	-	-	P_trifoliata_00151_mRNA_46.1
GF0046029	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00151_mRNA_45.1
GF0046028	0	0	1	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1)	-	-	P_trifoliata_00151_mRNA_40.1
GF0046027	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00151_mRNA_28.1
GF0046026	0	0	1	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	Zinc finger, BED-type [IPR003656] (1); hAT-like transposase, RNase-H fold [IPR025525] (1)	-	-	P_trifoliata_00151_mRNA_22.1
GF0046025	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00151_mRNA_21.1
GF0046024	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00151_mRNA_20.1
GF0046023	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00151_mRNA_17.1
GF0046022	0	0	1	Glycosyl hydrolase family protein with chitinase insertion domain (1)	chitin catabolic process [GO:0006032 biological_process] (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)	Chitinase II [IPR011583] (1); Glycoside hydrolase, catalytic domain [IPR013781] (1); Glycoside hydrolase superfamily [IPR017853] (1); Glycoside hydrolase family 18, catalytic domain [IPR001223] (1)	-	-	P_trifoliata_00151_mRNA_14.1
GF0046021	0	0	1	Sulfotransferase (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	-	P_trifoliata_00151_mRNA_13.1
GF0046020	0	0	1	MRNA decapping enzyme 1A, putative (1)	positive regulation of catalytic activity [GO:0043085 biological_process] (1); deadenylation-dependent decapping of nuclear-transcribed mRNA [GO:0000290 biological_process] (1); enzyme activator activity [GO:0008047 molecular_function] (1)	mRNA-decapping enzyme subunit 1 [IPR010334] (1); PH domain-like [IPR011993] (1)	-	-	P_trifoliata_00151_mRNA_12.1
GF0046019	0	0	1	LRR receptor-like serine/threonine-protein kinase GSO1 (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)	-	-	P_trifoliata_00151_mRNA_10.1
GF0046018	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	-	P_trifoliata_00151_mRNA_1.1
GF0046017	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00150_mRNA_54.1
GF0046016	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00150_mRNA_53.1
GF0046015	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00150_mRNA_47.1
GF0046014	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00150_mRNA_45.1
GF0046013	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00150_mRNA_34.1
GF0046012	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00150_mRNA_33.1
GF0046011	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00150_mRNA_31.1
GF0046010	0	0	1	PAP fibrillin (1)		Plastid lipid-associated protein/fibrillin conserved domain [IPR006843] (1)	-	-	P_trifoliata_00150_mRNA_28.1
GF0046009	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00150_mRNA_25.1
GF0046008	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00150_mRNA_21.1
GF0046007	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00150_mRNA_17.1
GF0046006	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00150_mRNA_15.1
GF0046005	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00150_mRNA_1.1
GF0046004	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00149_mRNA_8.1
GF0046003	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00149_mRNA_63.1
GF0046002	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00149_mRNA_60.1
GF0046001	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00149_mRNA_59.1
GF0046000	0	0	1	Type II peroxiredoxin (1)	oxidoreductase activity [GO:0016491 molecular_function] (1)	Redoxin [IPR013740] (1); Thioredoxin-like fold [IPR012336] (1)	-	-	P_trifoliata_00149_mRNA_35.1
GF0045999	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00149_mRNA_34.1
GF0045998	0	0	1	Hypothetical protein (1)	copper ion binding [GO:0005507 molecular_function] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Cupredoxin [IPR008972] (1); Multicopper oxidase, type 1 [IPR001117] (1); Multicopper oxidase, type 3 [IPR011707] (1)	-	-	P_trifoliata_00149_mRNA_25.1
GF0045997	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00149_mRNA_22.1
GF0045996	0	0	1	G10 family protein (1)	nucleus [GO:0005634 cellular_component] (1)	G10 protein [IPR001748] (1); BUD31/G10-related, conserved site [IPR018230] (1)	-	-	P_trifoliata_00148_mRNA_9.1
GF0045995	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00148_mRNA_74.1
GF0045994	0	0	1	CDNA clone:J023022E20, full insert sequence (1)			-	-	P_trifoliata_00148_mRNA_59.1
GF0045993	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00148_mRNA_57.1
GF0045992	0	0	1	ADP-ribosylation factor 2 (1)	small GTPase mediated signal transduction [GO:0007264 biological_process] (1); GTP binding [GO:0005525 molecular_function] (1); intracellular [GO:0005622 cellular_component] (1)	Small GTP-binding protein domain [IPR005225] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Small GTPase superfamily, ARF type [IPR024156] (1); Small GTPase superfamily, ARF/SAR type [IPR006689] (1)	-	-	P_trifoliata_00148_mRNA_46.1
GF0045991	0	0	1	Transferring glycosyl group transferase (1)			-	-	P_trifoliata_00148_mRNA_44.1
GF0045990	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00148_mRNA_42.1
GF0045989	0	0	1	Hypothetical protein (1)	hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1)	Glycoside hydrolase family 16 [IPR000757] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1)	-	-	P_trifoliata_00148_mRNA_30.1
GF0045988	0	0	1	Hypothetical protein (1)		Concanavalin A-like lectin/glucanase domain [IPR013320] (1)	-	-	P_trifoliata_00148_mRNA_29.1
GF0045987	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00148_mRNA_27.1
GF0045986	0	0	1	Xyloglucan endotransglucosylase/hydrolase protein 22 (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, active site [IPR008263] (1); Glycoside hydrolase family 16 [IPR000757] (1)	-	-	P_trifoliata_00148_mRNA_25.1
GF0045985	0	0	1	Hypothetical protein (1)	cellular glucan metabolic process [GO:0006073 biological_process] (1); apoplast [GO:0048046 cellular_component] (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); xyloglucan:xyloglucosyl transferase activity [GO:0016762 molecular_function] (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)	-	-	P_trifoliata_00148_mRNA_14.1
GF0045984	0	0	1	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)	-	-	P_trifoliata_00147_mRNA_7.1
GF0045983	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00147_mRNA_5.1
GF0045982	0	0	1	Hypothetical protein (1)		Viral movement protein [IPR028919] (1); Reverse transcriptase domain [IPR000477] (1)	-	-	P_trifoliata_00147_mRNA_35.1
GF0045981	0	0	1	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	hAT-like transposase, RNase-H fold [IPR025525] (1); Zinc finger, BED-type [IPR003656] (1)	-	-	P_trifoliata_00147_mRNA_32.1
GF0045980	0	0	1	CACTA transposable element (1)		Transposon, En/Spm-like [IPR004242] (1)	-	-	P_trifoliata_00147_mRNA_31.1
GF0045979	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00147_mRNA_29.1
GF0045978	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00147_mRNA_28.1
GF0045977	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00147_mRNA_27.1
GF0045976	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00147_mRNA_26.1
GF0045975	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00147_mRNA_23.1
GF0045974	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00147_mRNA_19.1
GF0045973	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00147_mRNA_18.1
GF0045972	0	0	1	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); ATPase, AAA-type, core [IPR003959] (1)	-	-	P_trifoliata_00147_mRNA_17.1
GF0045971	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00147_mRNA_15.1
GF0045970	0	0	1	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	-	P_trifoliata_00147_mRNA_11.1
GF0045969	0	0	1	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	-	P_trifoliata_00147_mRNA_1.1
GF0045968	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00146_mRNA_9.1
GF0045967	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00146_mRNA_62.1
GF0045966	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00146_mRNA_57.1
GF0045965	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00146_mRNA_55.1
GF0045964	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00146_mRNA_50.1
GF0045963	0	0	1	GTPase Der (1)		Domain of unknown function DUF642 [IPR006946] (1)	-	-	P_trifoliata_00146_mRNA_43.1

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*
GF0045962	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00146_mRNA_41.1
GF0045961	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00146_mRNA_26.1
GF0045960	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00146_mRNA_21.1
GF0045959	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00146_mRNA_19.1
GF0045958	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00146_mRNA_14.1
GF0045957	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00146_mRNA_11.1
GF0045956	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00145_mRNA_9.1
GF0045955	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00145_mRNA_69.1
GF0045954	0	0	1	Hypothetical protein (1)		GAG-pre-integrase domain [IPR025724] (1)	-	-	P_trifoliata_00145_mRNA_68.1
GF0045953	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00145_mRNA_67.1
GF0045952	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00145_mRNA_64.1
GF0045951	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00145_mRNA_61.1
GF0045950	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00145_mRNA_60.1
GF0045949	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00145_mRNA_59.1
GF0045948	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00145_mRNA_51.1
GF0045947	0	0	1	Receptor-like kinase plant (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); Serine/threonine-protein kinase, active site [IPR008271] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1)	-	-	P_trifoliata_00145_mRNA_35.1
GF0045946	0	0	1	Tubulin alpha chain (1)	GTPase activity [GO:0003924 molecular_function] (1); microtubule-based process [GO:0007017 biological_process] (1); structural constituent of cytoskeleton [GO:0005200 molecular_function] (1); microtubule [GO:0005874 cellular_component] (1); GTP binding [GO:0005525 molecular_function] (1)	Alpha tubulin [IPR002452] (1); Tubulin/FtsZ, 2-layer sandwich domain [IPR018316] (1); Tubulin [IPR000217] (1); Tubulin/FtsZ, C-terminal [IPR008280] (1); Beta tubulin, autoregulation binding site [IPR013838] (1); Tubulin, conserved site [IPR017975] (1); Tubulin/FtsZ, GTPase domain [IPR003008] (1)	-	-	P_trifoliata_00145_mRNA_15.1
GF0045945	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00145_mRNA_1.1
GF0045944	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00144_mRNA_8.1
GF0045943	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00144_mRNA_7.1
GF0045942	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00144_mRNA_59.1
GF0045941	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00144_mRNA_57.1
GF0045940	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00144_mRNA_56.1
GF0045939	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	-	P_trifoliata_00144_mRNA_5.1
GF0045938	0	0	1	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); serine-type peptidase activity [GO:0008236 molecular_function] (1)	Peptidase S28 [IPR008758] (1); Alpha/Beta hydrolase fold [IPR029058] (1)	-	-	P_trifoliata_00144_mRNA_49.1
GF0045937	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00144_mRNA_48.1
GF0045936	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00144_mRNA_42.1
GF0045935	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00144_mRNA_4.1
GF0045934	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00144_mRNA_37.1
GF0045933	0	0	1	Hypothetical protein (1)	transmembrane transport [GO:0055085 biological_process] (1)	Oligopeptide transporter, OPT superfamily [IPR004813] (1)	-	-	P_trifoliata_00144_mRNA_30.1
GF0045932	0	0	1	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	-	P_trifoliata_00144_mRNA_3.1
GF0045931	0	0	1	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	-	P_trifoliata_00144_mRNA_28.1
GF0045930	0	0	1	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1)	Protein kinase, ATP binding site [IPR017441] (1); Protein kinase-like domain [IPR011009] (1)	-	-	P_trifoliata_00144_mRNA_26.1
GF0045929	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00144_mRNA_22.1
GF0045928	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00144_mRNA_20.1
GF0045927	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00144_mRNA_2.1
GF0045926	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00144_mRNA_14.1
GF0045925	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00144_mRNA_12.1
GF0045924	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00143_mRNA_9.1
GF0045923	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00143_mRNA_58.1
GF0045922	0	0	1	Amino acid permease family protein (1)	binding [GO:0005488 molecular_function] (1); amino acid transmembrane transporter activity [GO:0015171 molecular_function] (1); signal transduction [GO:0007165 biological_process] (1); membrane [GO:0016020 cellular_component] (1); protein phosphatase type 2A regulator activity [GO:0008601 molecular_function] (1); protein phosphatase type 2A complex [GO:0000159 cellular_component] (1); amino acid transmembrane transport [GO:0003333 biological_process] (1)	Protein phosphatase 2A, regulatory B subunit, B56 [IPR002554] (1); Armadillo-type fold [IPR016024] (1); Amino acid/polyamine transporter I [IPR002293] (1)	-	-	P_trifoliata_00143_mRNA_54.1
GF0045921	0	0	1	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	-	-	P_trifoliata_00143_mRNA_5.1
GF0045920	0	0	1	Hypothetical protein (1)	microtubule cytoskeleton organization [GO:0000226 biological_process] (1); spindle pole [GO:0000922 cellular_component] (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)	-	-	P_trifoliata_00143_mRNA_48.1
GF0045919	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00143_mRNA_33.1
GF0045918	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00143_mRNA_25.1
GF0045917	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00143_mRNA_11.1
GF0045916	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00143_mRNA_1.1
GF0045915	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00142_mRNA_7.1
GF0045914	0	0	1	Phosphatase 2C family 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)	-	-	P_trifoliata_00142_mRNA_67.1
GF0045913	0	0	1	14-3-3-like protein GF14 omicron (1)	protein domain specific binding [GO:0019904 molecular_function] (1)	14-3-3 protein, conserved site [IPR023409] (1); 14-3-3 protein [IPR000308] (1); Alpha/Beta hydrolase fold [IPR029058] (1); Alpha/beta hydrolase fold-1 [IPR000073] (1); 14-3-3 domain [IPR023410] (1)	-	-	P_trifoliata_00142_mRNA_66.1
GF0045912	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00142_mRNA_54.1
GF0045911	0	0	1	Hypothetical protein (1)		Phosphate-induced protein 1 [IPR006766] (1)	-	-	P_trifoliata_00142_mRNA_53.1
GF0045910	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00142_mRNA_42.1
GF0045909	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00142_mRNA_41.1
GF0045908	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00142_mRNA_40.1
GF0045907	0	0	1	Hypothetical protein (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Oxoglutarate/iron-dependent dioxygenase [IPR005123] (1); Non-haem dioxygenase N-terminal domain [IPR026992] (1); Isopenicillin N synthase-like [IPR027443] (1)	-	-	P_trifoliata_00142_mRNA_23.1
GF0045906	0	0	1	Tau class glutathione S-transferase (1)	protein binding [GO:0005515 molecular_function] (1)	Glutathione S-transferase, C-terminal [IPR004046] (1); Thioredoxin-like fold [IPR012336] (1); Glutathione S-transferase, C-terminal-like [IPR010987] (1); Glutathione S-transferase, N-terminal [IPR004045] (1)	-	-	P_trifoliata_00142_mRNA_14.1
GF0045905	0	0	1	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)	-	-	P_trifoliata_00141_mRNA_5.1
GF0045904	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00141_mRNA_41.1
GF0045903	0	0	1	Putative RNA-directed DNA polymerase (1)	iron ion binding [GO:0005506 molecular_function] (1); L-ascorbic acid binding [GO:0031418 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Oxoglutarate/iron-dependent dioxygenase [IPR005123] (1); Prolyl 4-hydroxylase, alpha subunit [IPR006620] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00141_mRNA_39.1
GF0045902	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00141_mRNA_37.1
GF0045901	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	-	P_trifoliata_00141_mRNA_3.1
GF0045900	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00141_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*
GF0045899	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00141_mRNA_26.1
GF0045898	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00141_mRNA_24.1
GF0045897	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00141_mRNA_21.1
GF0045896	0	0	1	Sesquiterpene synthase (1)	metabolic process [GO:0008152 biological_process] (1); magnesium ion binding [GO:0000287 molecular_function] (1); lyase activity [GO:0016829 molecular_function] (1); terpene synthase activity [GO:0010333 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); Isoprenoid synthase domain [IPR008949] (1)	-	-	P_trifoliata_00141_mRNA_19.1
GF0045895	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00141_mRNA_14.1
GF0045894	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00140_mRNA_9.1
GF0045893	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00140_mRNA_8.1
GF0045892	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00140_mRNA_7.1
GF0045891	0	0	1	Hypothetical protein (1)	ATPase activity [GO:0016887 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); ABC transporter-like [IPR003439] (1)	-	-	P_trifoliata_00140_mRNA_55.1
GF0045890	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	F-box domain [IPR001810] (1); Phloem protein 2-like [IPR025886] (1)	-	-	P_trifoliata_00140_mRNA_5.1
GF0045889	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00140_mRNA_49.1
GF0045888	0	0	1	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 binding [GO:0005515 molecular_function] (1); protein tyrosine kinase activity [GO:0004713 molecular_function] (1)	Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Leucine-rich repeat [IPR001611] (1); Protein kinase, ATP binding site [IPR017441] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Protein kinase-like domain [IPR011009] (1); Tyrosine-protein kinase, catalytic domain [IPR020635] (1); Protein kinase domain [IPR000719] (1)	-	-	P_trifoliata_00140_mRNA_48.1
GF0045887	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00140_mRNA_44.1
GF0045886	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00140_mRNA_43.1
GF0045885	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00140_mRNA_41.1
GF0045884	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00140_mRNA_40.1
GF0045883	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	F-box domain [IPR001810] (1)	-	-	P_trifoliata_00140_mRNA_4.1
GF0045882	0	0	1	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)	-	-	P_trifoliata_00140_mRNA_38.1
GF0045881	0	0	1	Polynucleotidyl transferase, Ribonuclease H fold (1)			-	-	P_trifoliata_00140_mRNA_32.1
GF0045880	0	0	1	Phloem protein 2-B5 (1)	protein binding [GO:0005515 molecular_function] (1)	Phloem protein 2-like [IPR025886] (1); F-box domain [IPR001810] (1)	-	-	P_trifoliata_00140_mRNA_3.1
GF0045879	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00140_mRNA_28.1
GF0045878	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00140_mRNA_2.1
GF0045877	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00140_mRNA_18.1
GF0045876	0	0	1	Putative enone 5-beta-reductase (1)		NAD(P)-binding domain [IPR016040] (1)	-	-	P_trifoliata_00140_mRNA_13.1
GF0045875	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00139_mRNA_65.1
GF0045874	0	0	1	Hypothetical protein (1)		Nodulin-like [IPR010658] (1)	-	-	P_trifoliata_00139_mRNA_57.1
GF0045873	0	0	1	Germin-like protein subfamily 2 member 4 (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)	-	-	P_trifoliata_00139_mRNA_47.1
GF0045872	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00139_mRNA_38.1
GF0045871	0	0	1	Hypothetical protein (1)	manganese ion binding [GO:0030145 molecular_function] (1); nutrient reservoir activity [GO:0045735 molecular_function] (1)	RmlC-like cupin domain [IPR011051] (1); RmlC-like jelly roll fold [IPR014710] (1); Germin [IPR001929] (1); Cupin 1 [IPR006045] (1)	-	-	P_trifoliata_00139_mRNA_36.1
GF0045870	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00139_mRNA_2.1
GF0045869	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00138_mRNA_68.1
GF0045868	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00138_mRNA_61.1
GF0045867	0	0	1	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, conserved site [IPR017972] (1); Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450 [IPR001128] (1)	-	-	P_trifoliata_00137_mRNA_9.1
GF0045866	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00137_mRNA_77.1
GF0045865	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00137_mRNA_75.1
GF0045864	0	0	1	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)	-	-	P_trifoliata_00137_mRNA_74.1
GF0045863	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00137_mRNA_73.1
GF0045862	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00137_mRNA_71.1
GF0045861	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00137_mRNA_68.1
GF0045860	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00137_mRNA_67.1
GF0045859	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00137_mRNA_65.1
GF0045858	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00137_mRNA_62.1
GF0045857	0	0	1	Disease resistance protein RPS2 (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)	-	-	P_trifoliata_00137_mRNA_59.1
GF0045856	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00137_mRNA_56.1
GF0045855	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00137_mRNA_55.1
GF0045854	0	0	1	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	-	P_trifoliata_00137_mRNA_50.1
GF0045853	0	0	1	Hypothetical protein (1)		Protein of unknown function DUF4666 [IPR031421] (1)	-	-	P_trifoliata_00137_mRNA_46.1
GF0045852	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00137_mRNA_38.1
GF0045851	0	0	1	Hypothetical protein (1)	serine-type endopeptidase activity [GO:0004252 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1); integral component of membrane [GO:0016021 cellular_component] (1)	Peptidase S54, rhomboid [IPR002610] (1); Peptidase S54, rhomboid domain [IPR022764] (1)	-	-	P_trifoliata_00137_mRNA_34.1
GF0045850	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00137_mRNA_33.1
GF0045849	0	0	1	Hypothetical protein (1)	O-methyltransferase activity [GO:0008171 molecular_function] (1)	O-methyltransferase, family 3 [IPR002935] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	-	P_trifoliata_00137_mRNA_30.1
GF0045848	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00137_mRNA_28.1
GF0045847	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00137_mRNA_27.1
GF0045846	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00137_mRNA_21.1
GF0045845	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00137_mRNA_19.1
GF0045844	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00137_mRNA_16.1
GF0045843	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00137_mRNA_15.1
GF0045842	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00137_mRNA_13.1
GF0045841	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00137_mRNA_12.1
GF0045840	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00137_mRNA_11.1
GF0045839	0	0	1	Essential protein Yae1, putative isoform 3 (1)		Essential protein Yae1, N-terminal [IPR019191] (1)	-	-	P_trifoliata_00137_mRNA_10.1
GF0045838	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00137_mRNA_1.1
GF0045837	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00136_mRNA_6.1
GF0045836	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00136_mRNA_58.1
GF0045835	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00136_mRNA_47.1
GF0045834	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00136_mRNA_46.1
GF0045833	0	0	1	Eukaryotic translation initiation factor 1A (1)	translational initiation [GO:0006413 biological_process] (1); translation initiation factor activity [GO:0003743 molecular_function] (1)	Nucleic acid-binding, OB-fold [IPR012340] (1); Translation initiation factor 1A (eIF-1A) [IPR001253] (1)	-	-	P_trifoliata_00136_mRNA_20.1
GF0045832	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00136_mRNA_14.1
GF0045831	0	0	1	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)	-	-	P_trifoliata_00136_mRNA_1.1
GF0045830	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00135_mRNA_7.1
GF0045829	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00135_mRNA_5.1
GF0045828	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00135_mRNA_48.1
GF0045827	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00135_mRNA_46.1
GF0045826	0	0	1	Hypothetical protein (1)		RmlC-like jelly roll fold [IPR014710] (1)	-	-	P_trifoliata_00135_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*
GF0045825	0	0	1	Germin-like protein subfamily 1 member 18 (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); Germin [IPR001929] (1); Germin, manganese binding site [IPR019780] (1); Cupin 1 [IPR006045] (1)	-	-	P_trifoliata_00135_mRNA_41.1
GF0045824	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00135_mRNA_34.1
GF0045823	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00135_mRNA_32.1
GF0045822	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00135_mRNA_31.1
GF0045821	0	0	1	Hypothetical protein (1)		Prolamin-like domain [IPR008502] (1)	-	-	P_trifoliata_00135_mRNA_19.1
GF0045820	0	0	1	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, DHHC-type, palmitoyltransferase [IPR001594] (1)	-	-	P_trifoliata_00135_mRNA_18.1
GF0045819	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00135_mRNA_15.1
GF0045818	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00134_mRNA_9.1
GF0045817	0	0	1	Hypothetical protein (1)	O-methyltransferase activity [GO:0008171 molecular_function] (1)	Winged helix-turn-helix DNA-binding domain [IPR011991] (1); O-methyltransferase, family 2 [IPR001077] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	-	P_trifoliata_00134_mRNA_73.1
GF0045816	0	0	1	Naringenin-chalcone synthase (1)	catalytic activity [GO:0003824 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Chalcone/stilbene synthase, N-terminal [IPR001099] (1); Chalcone/stilbene synthase, C-terminal [IPR012328] (1); Thiolase-like [IPR016039] (1)	-	-	P_trifoliata_00134_mRNA_72.1
GF0045815	0	0	1	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, family 2 [IPR001077] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); O-methyltransferase COMT-type [IPR016461] (1)	-	-	P_trifoliata_00134_mRNA_71.1
GF0045814	0	0	1	Caffeic acid 3-O-methyltransferase (1)	protein dimerization activity [GO:0046983 molecular_function] (1)	Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Plant methyltransferase dimerisation [IPR012967] (1)	-	-	P_trifoliata_00134_mRNA_70.1
GF0045813	0	0	1	Carboxyvinyl-carboxyphosphonate phosphorylmutase (1)	catalytic activity [GO:0003824 molecular_function] (1)	Pyruvate/Phosphoenolpyruvate kinase-like domain [IPR015813] (1)	-	-	P_trifoliata_00134_mRNA_61.1
GF0045812	0	0	1	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (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)	-	-	P_trifoliata_00134_mRNA_55.1
GF0045811	0	0	1	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	-	P_trifoliata_00134_mRNA_49.1
GF0045810	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00134_mRNA_48.1
GF0045809	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00134_mRNA_43.1
GF0045808	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00134_mRNA_34.1
GF0045807	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00134_mRNA_27.1
GF0045806	0	0	1	Hypothetical protein (1)	catalytic activity [GO:0003824 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	AMP-dependent synthetase/ligase [IPR000873] (1)	-	-	P_trifoliata_00134_mRNA_26.1
GF0045805	0	0	1	Hypothetical protein (1)		Protein of unknown function DUF241, plant [IPR004320] (1)	-	-	P_trifoliata_00133_mRNA_8.1
GF0045804	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00133_mRNA_7.1
GF0045803	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00133_mRNA_6.1
GF0045802	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00133_mRNA_5.1
GF0045801	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00133_mRNA_47.1
GF0045800	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00133_mRNA_40.1
GF0045799	0	0	1	Hypothetical protein (1)		Alpha/Beta hydrolase fold [IPR029058] (1)	-	-	P_trifoliata_00133_mRNA_4.1
GF0045798	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00133_mRNA_39.1
GF0045797	0	0	1	Hypothetical protein (1)		Formin, FH2 domain [IPR015425] (1)	-	-	P_trifoliata_00133_mRNA_37.1
GF0045796	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00133_mRNA_30.1
GF0045795	0	0	1	LETM1 and EF-hand domain-containing protein 1, mitochondrial (1)	calcium ion binding [GO:0005509 molecular_function] (1); ribosome binding [GO:0043022 molecular_function] (1)	LETM1-like [IPR011685] (1); Letm1 ribosome-binding domain [IPR033122] (1); EF-Hand 1, calcium-binding site [IPR018247] (1); EF-hand domain [IPR002048] (1); EF-hand domain pair [IPR011992] (1)	-	-	P_trifoliata_00133_mRNA_26.1
GF0045794	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00133_mRNA_24.1
GF0045793	0	0	1	Hypothetical protein (1)	translation [GO:0006412 biological_process] (1); ADP binding [GO:0043531 molecular_function] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1); ribosome [GO:0005840 cellular_component] (1)	Ribosomal protein L2, C-terminal [IPR022669] (1); Ribosomal protein L2 domain 2 [IPR014722] (1); NB-ARC [IPR002182] (1); Translation protein SH3-like domain [IPR008991] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	-	P_trifoliata_00133_mRNA_23.1
GF0045792	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00133_mRNA_20.1
GF0045791	0	0	1	Cysteine-rich RLK (Receptor-like kinase) protein (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); protein serine/threonine kinase activity [GO:0004674 molecular_function] (1)	S-locus glycoprotein domain [IPR000858] (1); S-locus receptor kinase, C-terminal [IPR021820] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Tyrosine-protein kinase, catalytic domain [IPR020635] (1); Protein kinase-like domain [IPR011009] (1)	-	-	P_trifoliata_00133_mRNA_17.1
GF0045790	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00133_mRNA_16.1
GF0045789	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00133_mRNA_15.1
GF0045788	0	0	1	Hypothetical protein (1)		PAN/Apple domain [IPR003609] (1)	-	-	P_trifoliata_00133_mRNA_14.1
GF0045787	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00133_mRNA_13.1
GF0045786	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4218 [IPR025452] (1)	-	-	P_trifoliata_00132_mRNA_47.1
GF0045785	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00132_mRNA_45.1
GF0045784	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00132_mRNA_43.1
GF0045783	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00132_mRNA_39.1
GF0045782	0	0	1	Purple acid phosphatase (1)	metal ion binding [GO:0046872 molecular_function] (1); hydrolase activity [GO:0016787 molecular_function] (1); acid phosphatase activity [GO:0003993 molecular_function] (1)	Purple acid phosphatase-like, N-terminal [IPR008963] (1); Calcineurin-like phosphoesterase domain, apaH type [IPR004843] (1); Metallo-dependent phosphatase-like [IPR029052] (1); Purple acid phosphatase, N-terminal [IPR015914] (1); Iron/zinc purple acid phosphatase-like C-terminal domain [IPR025733] (1)	-	-	P_trifoliata_00132_mRNA_38.1
GF0045781	0	0	1	Hypothetical protein (1)		VQ [IPR008889] (1)	-	-	P_trifoliata_00132_mRNA_18.1
GF0045780	0	0	1	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)	-	-	P_trifoliata_00132_mRNA_15.1
GF0045779	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00132_mRNA_1.1
GF0045778	0	0	1	Pentatricopeptide repeat-containing protein, putative isoform 1 (1)	protein binding [GO:0005515 molecular_function] (1)	Pentatricopeptide repeat [IPR002885] (1); Tetratricopeptide-like helical domain [IPR011990] (1)	-	-	P_trifoliata_00131_mRNA_9.1
GF0045777	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00131_mRNA_64.1
GF0045776	0	0	1	Signal recognition particle subunit SRP68 (1)	endoplasmic reticulum signal peptide binding [GO:0030942 molecular_function] (1); SRP-dependent cotranslational protein targeting to membrane [GO:0006614 biological_process] (1); 7S RNA binding [GO:0008312 molecular_function] (1); signal recognition particle, endoplasmic reticulum targeting [GO:0005786 cellular_component] (1); signal recognition particle binding [GO:0005047 molecular_function] (1)	Signal recognition particle subunit SRP68 [IPR026258] (1)	-	-	P_trifoliata_00131_mRNA_6.1
GF0045775	0	0	1	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	-	P_trifoliata_00131_mRNA_48.1
GF0045774	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00131_mRNA_43.1
GF0045773	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00131_mRNA_17.1
GF0045772	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	-	P_trifoliata_00131_mRNA_1.1
GF0045771	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00130_mRNA_9.1
GF0045770	0	0	1	Putative metal tolerance protein 4-like (1)	cation transmembrane transporter activity [GO:0008324 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1); cation transport [GO:0006812 biological_process] (1); transmembrane transport [GO:0055085 biological_process] (1)	Cation efflux protein [IPR002524] (1); Cation efflux protein transmembrane domain [IPR027469] (1)	-	-	P_trifoliata_00130_mRNA_7.1
GF0045769	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00130_mRNA_5.1
GF0045768	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00130_mRNA_38.1

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*
GF0045767	0	0	1	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 L2 [IPR002171] (1); Ribosomal protein L2, C-terminal [IPR022669] (1); Ribosomal protein L2, domain 3 [IPR014726] (1); Ribosomal protein L2 domain 2 [IPR014722] (1); Translation protein SH3-like domain [IPR008991] (1); NAD(P)-binding domain [IPR016040] (1)	-	-	P_trifoliata_00130_mRNA_37.1
GF0045766	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00130_mRNA_34.1
GF0045765	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00130_mRNA_33.1
GF0045764	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00130_mRNA_30.1
GF0045763	0	0	1	Hypothetical protein (1)		PAN/Apple domain [IPR003609] (1)	-	-	P_trifoliata_00130_mRNA_29.1
GF0045762	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00130_mRNA_28.1
GF0045761	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00130_mRNA_25.1
GF0045760	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00130_mRNA_21.1
GF0045759	0	0	1	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	Zinc finger, BED-type [IPR003656] (1)	-	-	P_trifoliata_00130_mRNA_18.1
GF0045758	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00130_mRNA_17.1
GF0045757	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00130_mRNA_11.1
GF0045756	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00130_mRNA_10.1
GF0045755	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00130_mRNA_1.1
GF0045754	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00129_mRNA_63.1
GF0045753	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00129_mRNA_60.1
GF0045752	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00129_mRNA_58.1
GF0045751	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00129_mRNA_53.1
GF0045750	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00129_mRNA_46.1
GF0045749	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00129_mRNA_34.1
GF0045748	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00129_mRNA_30.1
GF0045747	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00129_mRNA_24.1
GF0045746	0	0	1	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1)	FAD/NAD(P)-binding domain [IPR023753] (1)	-	-	P_trifoliata_00129_mRNA_13.1
GF0045745	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00128_mRNA_75.1
GF0045744	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00128_mRNA_61.1
GF0045743	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00128_mRNA_55.1
GF0045742	0	0	1	SAM:benzoic acid/salicylic acid carboxyl methyltransferase (1)	methyltransferase activity [GO:0008168 molecular_function] (1)	SAM dependent carboxyl methyltransferase [IPR005299] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	-	P_trifoliata_00128_mRNA_2.1
GF0045741	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00128_mRNA_1.1
GF0045740	0	0	1	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)	-	-	P_trifoliata_00127_mRNA_7.1
GF0045739	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00127_mRNA_67.1
GF0045738	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00127_mRNA_62.1
GF0045737	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00127_mRNA_61.1
GF0045736	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00127_mRNA_60.1
GF0045735	0	0	1	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 [IPR001128] (1)	-	-	P_trifoliata_00127_mRNA_6.1
GF0045734	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00127_mRNA_59.1
GF0045733	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00127_mRNA_58.1
GF0045732	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00127_mRNA_53.1
GF0045731	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00127_mRNA_52.1
GF0045730	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00127_mRNA_51.1
GF0045729	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00127_mRNA_49.1
GF0045728	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00127_mRNA_45.1
GF0045727	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00127_mRNA_43.1
GF0045726	0	0	1	Codeine O-demethylase (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)	-	-	P_trifoliata_00127_mRNA_42.1
GF0045725	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00127_mRNA_40.1
GF0045724	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00127_mRNA_39.1
GF0045723	0	0	1	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1)	Oxoglutarate/iron-dependent dioxygenase [IPR005123] (1); Non-haem dioxygenase N-terminal domain [IPR026992] (1); Isopenicillin N synthase-like [IPR027443] (1)	-	-	P_trifoliata_00127_mRNA_36.1
GF0045722	0	0	1	2OG-Fe(II) oxygenase family oxidoreductase (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)	-	-	P_trifoliata_00127_mRNA_35.1
GF0045721	0	0	1	Senescence-related gene 1 (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)	-	-	P_trifoliata_00127_mRNA_34.1
GF0045720	0	0	1	Hypothetical protein (1)		Non-haem dioxygenase N-terminal domain [IPR026992] (1); Isopenicillin N synthase-like [IPR027443] (1)	-	-	P_trifoliata_00127_mRNA_32.1
GF0045719	0	0	1	Hypothetical protein (1)	mitochondrion [GO:0005739 cellular_component] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); double-stranded DNA binding [GO:0003690 molecular_function] (1)	Mitochodrial transcription termination factor [IPR003690] (1)	-	-	P_trifoliata_00127_mRNA_3.1
GF0045718	0	0	1	Phenylcoumaran benzylic ether reductase-like protein (1)		NmrA-like domain [IPR008030] (1)	-	-	P_trifoliata_00127_mRNA_2.1
GF0045717	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00126_mRNA_7.1
GF0045716	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00126_mRNA_58.1
GF0045715	0	0	1	Hypothetical protein (1)	nucleotide binding [GO:0000166 molecular_function] (1); calmodulin binding [GO:0005516 molecular_function] (1)	P-type ATPase, cytoplasmic domain N [IPR023299] (1); Cation-transporting P-type ATPase, N-terminal [IPR004014] (1); Calcium-transporting P-type ATPase, N-terminal autoinhibitory domain [IPR024750] (1)	-	-	P_trifoliata_00126_mRNA_57.1
GF0045714	0	0	1	Nodulin family protein (1)		Major facilitator superfamily domain [IPR020846] (1); Nodulin-like [IPR010658] (1)	-	-	P_trifoliata_00126_mRNA_38.1
GF0045713	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00126_mRNA_35.1
GF0045712	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00126_mRNA_3.1
GF0045711	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00126_mRNA_28.1
GF0045710	0	0	1	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)	-	-	P_trifoliata_00126_mRNA_11.1
GF0045709	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00125_mRNA_6.1
GF0045708	0	0	1	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	Homeodomain-like [IPR009057] (1); SANT/Myb domain [IPR001005] (1); Myb domain [IPR017930] (1)	-	-	P_trifoliata_00125_mRNA_54.1
GF0045707	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00125_mRNA_5.1
GF0045706	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00125_mRNA_39.1
GF0045705	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00125_mRNA_35.1
GF0045704	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00125_mRNA_32.1
GF0045703	0	0	1	Isoprene synthase (1)	metabolic process [GO:0008152 biological_process] (1); magnesium ion binding [GO:0000287 molecular_function] (1); lyase activity [GO:0016829 molecular_function] (1); terpene synthase activity [GO:0010333 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)	-	-	P_trifoliata_00125_mRNA_29.1
GF0045702	0	0	1	(3S)-linalool/(E)-nerolidol/(E,E)-geranyl linalool 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)	-	-	P_trifoliata_00125_mRNA_26.1
GF0045701	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00125_mRNA_20.1

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*
GF0045700	0	0	1	Hypothetical protein (1)		Protein of unknown function DUF538 [IPR007493] (1)	-	-	P_trifoliata_00125_mRNA_13.1
GF0045699	0	0	1	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)	Pectinesterase, catalytic [IPR000070] (1); Pectin lyase fold [IPR012334] (1); Pectin lyase fold/virulence factor [IPR011050] (1)	-	-	P_trifoliata_00124_mRNA_9.1
GF0045698	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00124_mRNA_6.1
GF0045697	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00124_mRNA_53.1
GF0045696	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00124_mRNA_52.1
GF0045695	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00124_mRNA_40.1
GF0045694	0	0	1	SNF1-related protein kinase regulatory subunit gamma 1, putative (1)		CBS domain [IPR000644] (1)	-	-	P_trifoliata_00124_mRNA_39.1
GF0045693	0	0	1	Pollen-specific protein SF3 (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, LIM-type [IPR001781] (1)	-	-	P_trifoliata_00124_mRNA_32.1
GF0045692	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00124_mRNA_31.1
GF0045691	0	0	1	Pectinesterase 31 (1)	cell wall modification [GO:0042545 biological_process] (1); cell wall [GO:0005618 cellular_component] (1); pectinesterase activity [GO:0030599 molecular_function] (1)	Pectin lyase fold [IPR012334] (1); Pectinesterase, catalytic [IPR000070] (1); Pectinesterase, Tyr active site [IPR018040] (1); Pectin lyase fold/virulence factor [IPR011050] (1)	-	-	P_trifoliata_00124_mRNA_21.1
GF0045690	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); IQ motif, EF-hand binding site [IPR000048] (1)	-	-	P_trifoliata_00124_mRNA_2.1
GF0045689	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00124_mRNA_17.1
GF0045688	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00124_mRNA_16.1
GF0045687	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00124_mRNA_13.1
GF0045686	0	0	1	Probable pectinesterase 67 (1)	cell wall [GO:0005618 cellular_component] (1); cell wall modification [GO:0042545 biological_process] (1); pectinesterase activity [GO:0030599 molecular_function] (1)	Pectinesterase, catalytic [IPR000070] (1); Pectin lyase fold [IPR012334] (1); Pectinesterase, Asp active site [IPR033131] (1); Pectin lyase fold/virulence factor [IPR011050] (1)	-	-	P_trifoliata_00124_mRNA_10.1
GF0045685	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00124_mRNA_1.1
GF0045684	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00123_mRNA_70.1
GF0045683	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00123_mRNA_65.1
GF0045682	0	0	1	Translation initiation factor 3 family protein, putative isoform 2 (1)	translational initiation [GO:0006413 biological_process] (1); translation initiation factor activity [GO:0003743 molecular_function] (1)	Translation initiation factor 3 [IPR001288] (1)	-	-	P_trifoliata_00123_mRNA_63.1
GF0045681	0	0	1	Hypothetical protein (1)		Glutathione S-transferase, C-terminal-like [IPR010987] (1)	-	-	P_trifoliata_00123_mRNA_52.1
GF0045680	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00123_mRNA_49.1
GF0045679	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00123_mRNA_48.1
GF0045678	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00123_mRNA_47.1
GF0045677	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00123_mRNA_46.1
GF0045676	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00123_mRNA_45.1
GF0045675	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00123_mRNA_44.1
GF0045674	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00123_mRNA_43.1
GF0045673	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00123_mRNA_42.1
GF0045672	0	0	1	Hypothetical protein (1)		Sieve element occlusion, N-terminal [IPR027942] (1)	-	-	P_trifoliata_00123_mRNA_38.1
GF0045671	0	0	1	Hypothetical protein (1)		Protein of unknown function DUF538 [IPR007493] (1)	-	-	P_trifoliata_00123_mRNA_36.1
GF0045670	0	0	1	Ac-like transposase THELMA13 (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1); hAT-like transposase, RNase-H fold [IPR025525] (1); Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00123_mRNA_34.1
GF0045669	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00123_mRNA_29.1
GF0045668	0	0	1	Vesicle transport v-SNARE 13 (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); Golgi apparatus [GO:0005794 cellular_component] (1); membrane [GO:0016020 cellular_component] (1); transport [GO:0006810 biological_process] (1)	t-SNARE [IPR010989] (1); GOSR2/Membrin/Bos1 [IPR027027] (1); Vesicle transport v-SNARE, N-terminal [IPR007705] (1)	-	-	P_trifoliata_00123_mRNA_27.1
GF0045667	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00123_mRNA_20.1
GF0045666	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00123_mRNA_2.1
GF0045665	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00122_mRNA_77.1
GF0045664	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00122_mRNA_74.1
GF0045663	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00122_mRNA_71.1
GF0045662	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00122_mRNA_60.1
GF0045661	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00122_mRNA_6.1
GF0045660	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00122_mRNA_59.1
GF0045659	0	0	1	Mo25 family protein (1)	binding [GO:0005488 molecular_function] (1)	Armadillo-like helical [IPR011989] (1); Mo25-like [IPR013878] (1); Armadillo-type fold [IPR016024] (1)	-	-	P_trifoliata_00122_mRNA_49.4
GF0045658	0	0	1	Hypothetical protein (1)	binding [GO:0005488 molecular_function] (1)	Armadillo-type fold [IPR016024] (1); Armadillo-like helical [IPR011989] (1); Mo25-like [IPR013878] (1)	-	-	P_trifoliata_00122_mRNA_48.1
GF0045657	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00122_mRNA_43.1
GF0045656	0	0	1	Xyloglucan endotransglucosylase/hydrolase protein A (1)	apoplast [GO:0048046 cellular_component] (1); cellular glucan metabolic process [GO:0006073 biological_process] (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:xyloglucosyl transferase activity [GO:0016762 molecular_function] (1)	Glycoside hydrolase family 16 [IPR000757] (1); Xyloglucan endo-transglycosylase, C-terminal [IPR010713] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1)	-	-	P_trifoliata_00122_mRNA_42.1
GF0045655	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00122_mRNA_3.1
GF0045654	0	0	1	Disease resistance protein RPP8 (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)	-	-	P_trifoliata_00122_mRNA_22.1
GF0045653	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00122_mRNA_20.1
GF0045652	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00122_mRNA_2.1
GF0045651	0	0	1	Hypothetical protein (1)		Nucleolar pre-ribosomal-associated protein 1, N-terminal [IPR021714] (1)	-	-	P_trifoliata_00122_mRNA_18.1
GF0045650	0	0	1	Polyadenylate-binding protein RBP47 (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)	-	-	P_trifoliata_00122_mRNA_17.1
GF0045649	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00121_mRNA_57.1
GF0045648	0	0	1	RNA polymerase I-specific transcription initiation factor RRN3 (1)		RNA polymerase I specific transcription initiation factor RRN3 [IPR007991] (1)	-	-	P_trifoliata_00121_mRNA_53.1
GF0045647	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00121_mRNA_4.1
GF0045646	0	0	1	Aspartic proteinase nepenthesin-2 (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Xylanase inhibitor, N-terminal [IPR032861] (1); Xylanase inhibitor, C-terminal [IPR032799] (1); Aspartic peptidase A1 family [IPR001461] (1); Peptidase family A1 domain [IPR033121] (1); Aspartic peptidase domain [IPR021109] (1)	-	-	P_trifoliata_00121_mRNA_15.1
GF0045645	0	0	1	Aspartic proteinase nepenthesin-2 (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Xylanase inhibitor, C-terminal [IPR032799] (1); Xylanase inhibitor, N-terminal [IPR032861] (1); Aspartic peptidase A1 family [IPR001461] (1); Peptidase family A1 domain [IPR033121] (1); Aspartic peptidase domain [IPR021109] (1)	-	-	P_trifoliata_00121_mRNA_13.1
GF0045644	0	0	1	Asparticase nepenthesin-2 (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Aspartic peptidase A1 family [IPR001461] (1); Xylanase inhibitor, C-terminal [IPR032799] (1); Xylanase inhibitor, N-terminal [IPR032861] (1); Peptidase family A1 domain [IPR033121] (1); Aspartic peptidase domain [IPR021109] (1)	-	-	P_trifoliata_00121_mRNA_12.1
GF0045643	0	0	1	Hypothetical protein (1)	membrane [GO:0016020 cellular_component] (1); DNA-templated transcription, initiation [GO:0006352 biological_process] (1); ionotropic glutamate receptor activity [GO:0004970 molecular_function] (1); nucleus [GO:0005634 cellular_component] (1)	Transcription initiation factor TFIID, 23-30kDa subunit [IPR003923] (1); Ionotropic glutamate receptor [IPR001320] (1); Solute-binding protein family 3/N-terminal domain of MltF [IPR001638] (1)	-	-	P_trifoliata_00121_mRNA_1.1
GF0045642	0	0	1	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	-	P_trifoliata_00120_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*
GF0045641	0	0	1	Hypothetical protein (1)	transport [GO:0006810 biological_process] (1); intracellular [GO:0005622 cellular_component] (1)	Nuclear transport factor 2 [IPR002075] (1); Nuclear transport factor 2, eukaryote [IPR018222] (1); NTF2-like domain [IPR032710] (1)	-	-	P_trifoliata_00120_mRNA_57.1
GF0045640	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00120_mRNA_56.1
GF0045639	0	0	1	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)	Protein kinase, ATP binding site [IPR017441] (1); Leucine-rich repeat [IPR001611] (1); Protein kinase domain [IPR000719] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Protein kinase-like domain [IPR011009] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00120_mRNA_53.1
GF0045638	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00120_mRNA_49.1
GF0045637	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00120_mRNA_47.1
GF0045636	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00120_mRNA_44.1
GF0045635	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Domain of unknown function DUF4283 [IPR025558] (1)	-	-	P_trifoliata_00120_mRNA_40.1
GF0045634	0	0	1	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 [IPR001611] (1)	-	-	P_trifoliata_00120_mRNA_4.1
GF0045633	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00120_mRNA_37.1
GF0045632	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00120_mRNA_30.1
GF0045631	0	0	1	BED zinc finger,hAT family dimerization domain (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)	-	-	P_trifoliata_00120_mRNA_25.1
GF0045630	0	0	1	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)	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)	-	-	P_trifoliata_00120_mRNA_23.1
GF0045629	0	0	1	Glycerol kinase (1)			-	-	P_trifoliata_00120_mRNA_17.1
GF0045628	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00120_mRNA_15.1
GF0045627	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00120_mRNA_14.1
GF0045626	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00120_mRNA_13.1
GF0045625	0	0	1	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 [IPR001611] (1)	-	-	P_trifoliata_00120_mRNA_1.1
GF0045624	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00119_mRNA_66.1
GF0045623	0	0	1	Hypothetical protein (1)		Gag-polypeptide of LTR copia-type [IPR029472] (1)	-	-	P_trifoliata_00119_mRNA_62.1
GF0045622	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00119_mRNA_61.1
GF0045621	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00119_mRNA_60.1
GF0045620	0	0	1	RNA-binding protein pno1 (1)	RNA binding [GO:0003723 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	K Homology domain [IPR004087] (1); K Homology domain, type 1 [IPR004088] (1)	-	-	P_trifoliata_00119_mRNA_54.1
GF0045619	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00119_mRNA_43.1
GF0045618	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00119_mRNA_32.1
GF0045617	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00119_mRNA_31.1
GF0045616	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00119_mRNA_29.1
GF0045615	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00119_mRNA_28.1
GF0045614	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00119_mRNA_27.1
GF0045613	0	0	1	Aluminum-activated malate transporter 1 (1)	malate transport [GO:0015743 biological_process] (1)	Aluminum-activated malate transporter [IPR020966] (1)	-	-	P_trifoliata_00119_mRNA_20.1
GF0045612	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00119_mRNA_2.1
GF0045611	0	0	1	Hypothetical protein (1)	malate transport [GO:0015743 biological_process] (1)	Aluminum-activated malate transporter [IPR020966] (1)	-	-	P_trifoliata_00119_mRNA_19.1
GF0045610	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00119_mRNA_18.1
GF0045609	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00119_mRNA_17.1
GF0045608	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00119_mRNA_16.1
GF0045607	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00119_mRNA_15.1
GF0045606	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00118_mRNA_59.1
GF0045605	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00118_mRNA_56.1
GF0045604	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00118_mRNA_55.1
GF0045603	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00118_mRNA_52.1
GF0045602	0	0	1	Hypothetical protein (1)	response to auxin [GO:0009733 biological_process] (1)	Small auxin-up RNA [IPR003676] (1)	-	-	P_trifoliata_00118_mRNA_51.1
GF0045601	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00118_mRNA_49.1
GF0045600	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00118_mRNA_47.1
GF0045599	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00118_mRNA_45.1
GF0045598	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00118_mRNA_43.1
GF0045597	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00118_mRNA_42.1
GF0045596	0	0	1	Auxin-induced protein 10A5 (1)	response to auxin [GO:0009733 biological_process] (1)	Small auxin-up RNA [IPR003676] (1)	-	-	P_trifoliata_00118_mRNA_39.1
GF0045595	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00118_mRNA_36.1
GF0045594	0	0	1	Hypothetical protein (1)		Prolamin-like domain [IPR008502] (1)	-	-	P_trifoliata_00118_mRNA_3.1
GF0045593	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00118_mRNA_28.1
GF0045592	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00118_mRNA_22.1
GF0045591	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00118_mRNA_21.1
GF0045590	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00118_mRNA_20.1
GF0045589	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00118_mRNA_18.1
GF0045588	0	0	1	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)	-	-	P_trifoliata_00118_mRNA_13.1
GF0045587	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00118_mRNA_10.1
GF0045586	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00117_mRNA_9.1
GF0045585	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00117_mRNA_8.1
GF0045584	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00117_mRNA_7.1
GF0045583	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00117_mRNA_54.1
GF0045582	0	0	1	Hypothetical protein (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Peptidase A2A, retrovirus, catalytic [IPR001995] (1); Aspartic peptidase domain [IPR021109] (1)	-	-	P_trifoliata_00117_mRNA_53.1
GF0045581	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00117_mRNA_48.1
GF0045580	0	0	1	Hypothetical protein (1)		Ribosomal protein L9/RNase H1, N-terminal [IPR009027] (1); Ribonuclease H1, N-terminal [IPR011320] (1)	-	-	P_trifoliata_00117_mRNA_30.1
GF0045579	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00117_mRNA_28.1
GF0045578	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00117_mRNA_24.1
GF0045577	0	0	1	Non-LTR reverse transcriptase (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	-	P_trifoliata_00117_mRNA_2.1
GF0045576	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00117_mRNA_18.1
GF0045575	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00117_mRNA_17.1
GF0045574	0	0	1	Monosacharide transport protein (1)			-	-	P_trifoliata_00117_mRNA_11.1
GF0045573	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00117_mRNA_10.1
GF0045572	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00117_mRNA_1.1
GF0045571	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00116_mRNA_7.1
GF0045570	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00116_mRNA_46.1
GF0045569	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00116_mRNA_42.1
GF0045568	0	0	1	Hypothetical protein (1)		Protein of unknown function wound-induced [IPR022251] (1)	-	-	P_trifoliata_00116_mRNA_41.1
GF0045567	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00116_mRNA_40.1
GF0045566	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00116_mRNA_33.1
GF0045565	0	0	1	Hypothetical protein (1)	fatty-acyl-CoA reductase (alcohol-forming) activity [GO:0080019 molecular_function] (1)	Fatty acyl-CoA reductase [IPR026055] (1); Retrotransposon gag domain [IPR005162] (1); Male sterility, NAD-binding [IPR013120] (1)	-	-	P_trifoliata_00116_mRNA_3.1
GF0045564	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00116_mRNA_28.1
GF0045563	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00116_mRNA_2.1
GF0045562	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00116_mRNA_12.1
GF0045561	0	0	1	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	-	P_trifoliata_00116_mRNA_1.1
GF0045560	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00115_mRNA_9.1
GF0045559	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00115_mRNA_57.1
GF0045558	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00115_mRNA_56.1
GF0045557	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00115_mRNA_53.1
GF0045556	0	0	1	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	-	P_trifoliata_00115_mRNA_37.1
GF0045555	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00115_mRNA_34.1
GF0045554	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00115_mRNA_33.1

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*
GF0045553	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00115_mRNA_32.1
GF0045552	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00115_mRNA_31.1
GF0045551	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00115_mRNA_27.1
GF0045550	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00115_mRNA_22.1
GF0045549	0	0	1	Hypothetical protein (1)	polysaccharide binding [GO:0030247 molecular_function] (1)	Wall-associated receptor kinase, galacturonan-binding domain [IPR025287] (1)	-	-	P_trifoliata_00115_mRNA_21.1
GF0045548	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00115_mRNA_20.1
GF0045547	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00115_mRNA_10.1
GF0045546	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00114_mRNA_74.1
GF0045545	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00114_mRNA_7.1
GF0045544	0	0	1	G-type lectin S-receptor-like serine/threonine-protein kinase RLK1 (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)	-	-	P_trifoliata_00114_mRNA_68.1
GF0045543	0	0	1	G-type lectin S-receptor-like serine/threonine-protein kinase RLK1 (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/dual specificity protein kinase, catalytic domain [IPR002290] (1); Protein kinase, ATP binding site [IPR017441] (1); Serine/threonine-protein kinase, active site [IPR008271] (1)	-	-	P_trifoliata_00114_mRNA_66.1
GF0045542	0	0	1	Ribosomal protein L11 methyltransferase (1)		S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	-	P_trifoliata_00114_mRNA_6.1
GF0045541	0	0	1	Hypothetical protein (1)	metal ion binding [GO:0046872 molecular_function] (1)	Zinc finger, CCCH-type [IPR000571] (1)	-	-	P_trifoliata_00114_mRNA_58.1
GF0045540	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00114_mRNA_51.1
GF0045539	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00114_mRNA_50.1
GF0045538	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00114_mRNA_47.1
GF0045537	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00114_mRNA_46.1
GF0045536	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00114_mRNA_45.1
GF0045535	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00114_mRNA_44.1
GF0045534	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00114_mRNA_37.1
GF0045533	0	0	1	Putative muDR family transposase-like (1)		Transposase, MuDR, plant [IPR004332] (1); MULE transposase domain [IPR018289] (1)	-	-	P_trifoliata_00114_mRNA_33.1
GF0045532	0	0	1	Protein yippee-like At5g53940 (1)		Yippee/Mis18 [IPR004910] (1)	-	-	P_trifoliata_00114_mRNA_29.1
GF0045531	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00114_mRNA_25.1
GF0045530	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00114_mRNA_24.1
GF0045529	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00114_mRNA_2.1
GF0045528	0	0	1	Hypothetical protein (1)		HAD-like domain [IPR023214] (1); P-type ATPase, phosphorylation site [IPR018303] (1)	-	-	P_trifoliata_00114_mRNA_18.1
GF0045527	0	0	1	Ribosomal protein L11 methyltransferase (1)		S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	-	P_trifoliata_00114_mRNA_11.1
GF0045526	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00113_mRNA_8.1
GF0045525	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00113_mRNA_7.1
GF0045524	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00113_mRNA_58.1
GF0045523	0	0	1	Hypothetical protein (1)	integral component of membrane [GO:0016021 cellular_component] (1); transmembrane transporter activity [GO:0022857 molecular_function] (1)	WAT1-related protein [IPR030184] (1)	-	-	P_trifoliata_00113_mRNA_40.1
GF0045522	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00113_mRNA_34.1
GF0045521	0	0	1	Putative potassium transporter 8 (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)	-	-	P_trifoliata_00113_mRNA_26.1
GF0045520	0	0	1	Hypothetical protein (1)	catalytic step 2 spliceosome [GO:0071013 cellular_component] (1); mRNA splicing, via spliceosome [GO:0000398 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1); iron-sulfur cluster binding [GO:0051536 molecular_function] (1)	HD domain [IPR006674] (1); Pre-mRNA-processing factor 17 [IPR032847] (1); WD40-repeat-containing domain [IPR017986] (1); WD40 repeat [IPR001680] (1); HD/PDEase domain [IPR003607] (1); Radical SAM [IPR007197] (1); WD40 repeat, conserved site [IPR019775] (1); WD40/YVTN repeat-like-containing domain [IPR015943] (1)	-	-	P_trifoliata_00113_mRNA_13.1
GF0045519	0	0	1	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)	-	-	P_trifoliata_00113_mRNA_12.1
GF0045518	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00113_mRNA_1.1
GF0045517	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00112_mRNA_8.1
GF0045516	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00112_mRNA_60.1
GF0045515	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00112_mRNA_45.1
GF0045514	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00112_mRNA_42.1
GF0045513	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00112_mRNA_39.1
GF0045512	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00112_mRNA_38.1
GF0045511	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00112_mRNA_36.1
GF0045510	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00112_mRNA_27.1
GF0045509	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00112_mRNA_18.1
GF0045508	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00112_mRNA_17.1
GF0045507	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00112_mRNA_14.1
GF0045506	0	0	1	Phospholipase, patatin family (1)	metabolic process [GO:0008152 biological_process] (1); lipid metabolic process [GO:0006629 biological_process] (1)	Patatin/Phospholipase A2-related [IPR002641] (1); Acyl transferase/acyl hydrolase/lysophospholipase [IPR016035] (1)	-	-	P_trifoliata_00112_mRNA_1.1
GF0045505	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00111_mRNA_9.1
GF0045504	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00111_mRNA_8.1
GF0045503	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00111_mRNA_74.1
GF0045502	0	0	1	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)	-	-	P_trifoliata_00111_mRNA_7.1
GF0045501	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00111_mRNA_6.1
GF0045500	0	0	1	Hypothetical protein (1)	protein folding [GO:0006457 biological_process] (1); unfolded protein binding [GO:0051082 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Chaperonin TCP-1, conserved site [IPR002194] (1); Chaperone tailless complex polypeptide 1 (TCP-1) [IPR017998] (1); Chaperonin Cpn60/TCP-1 family [IPR002423] (1); GroEL-like equatorial domain [IPR027413] (1)	-	-	P_trifoliata_00111_mRNA_57.1
GF0045499	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00111_mRNA_55.1
GF0045498	0	0	1	Hypothetical protein (1)	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor [GO:0016616 molecular_function] (1); malate metabolic process [GO:0006108 biological_process] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); malate dehydrogenase activity [GO:0016615 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1)	Malate dehydrogenase, type 2 [IPR010945] (1); Lactate dehydrogenase/glycoside hydrolase, family 4, C-terminal [IPR015955] (1); NAD(P)-binding domain [IPR016040] (1); Lactate/malate dehydrogenase, N-terminal [IPR001236] (1)	-	-	P_trifoliata_00111_mRNA_50.1
GF0045497	0	0	1	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1)	Aspartic peptidase, active site [IPR001969] (1)	-	-	P_trifoliata_00111_mRNA_5.1
GF0045496	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00111_mRNA_31.1
GF0045495	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00111_mRNA_3.1
GF0045494	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00111_mRNA_2.1
GF0045493	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00110_mRNA_6.1
GF0045492	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00110_mRNA_52.1
GF0045491	0	0	1	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	-	P_trifoliata_00110_mRNA_50.1
GF0045490	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00110_mRNA_5.1
GF0045489	0	0	1	Putative alcohol dehydrogenase superfamily 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); Alcohol dehydrogenase, N-terminal [IPR013154] (1); Polyketide synthase, enoylreductase domain [IPR020843] (1); GroES-like [IPR011032] (1)	-	-	P_trifoliata_00110_mRNA_49.1
GF0045488	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00110_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*
GF0045487	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00110_mRNA_46.1
GF0045486	0	0	1	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)	-	-	P_trifoliata_00110_mRNA_44.1
GF0045485	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00110_mRNA_42.1
GF0045484	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00110_mRNA_41.1
GF0045483	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00110_mRNA_40.1
GF0045482	0	0	1	Gag protease polyprotein (1)		Retrotransposon gag domain [IPR005162] (1)	-	-	P_trifoliata_00110_mRNA_39.1
GF0045481	0	0	1	Hypothetical protein (1)		Prolamin-like domain [IPR008502] (1)	-	-	P_trifoliata_00110_mRNA_38.1
GF0045480	0	0	1	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	-	P_trifoliata_00110_mRNA_36.1
GF0045479	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00110_mRNA_35.1
GF0045478	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00110_mRNA_34.1
GF0045477	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00110_mRNA_32.1
GF0045476	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00110_mRNA_28.1
GF0045475	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00110_mRNA_25.1
GF0045474	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00110_mRNA_23.1
GF0045473	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00110_mRNA_2.1
GF0045472	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00110_mRNA_18.1
GF0045471	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00110_mRNA_17.1
GF0045470	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00110_mRNA_15.1
GF0045469	0	0	1	Hypothetical protein (1)		MULE transposase domain [IPR018289] (1)	-	-	P_trifoliata_00110_mRNA_14.1
GF0045468	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00109_mRNA_72.1
GF0045467	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00109_mRNA_69.1
GF0045466	0	0	1	Putative phorbol ester / diacylglycerol binding protein (1)	protein binding [GO:0005515 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, PHD-type [IPR001965] (1); Zinc finger, RING/FYVE/PHD-type [IPR013083] (1); Zinc finger, PHD-finger [IPR019787] (1); Zinc finger, FYVE/PHD-type [IPR011011] (1)	-	-	P_trifoliata_00109_mRNA_57.1
GF0045465	0	0	1	Galactosyltransferase family protein isoform 2 (1)	galactosyltransferase activity [GO:0008378 molecular_function] (1); membrane [GO:0016020 cellular_component] (1); protein glycosylation [GO:0006486 biological_process] (1)	Domain of unknown function DUF4094 [IPR025298] (1); Glycosyl transferase, family 31 [IPR002659] (1)	-	-	P_trifoliata_00109_mRNA_53.1
GF0045464	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00109_mRNA_31.1
GF0045463	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00109_mRNA_20.1
GF0045462	0	0	1	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase (1)	glycolytic process [GO:0006096 biological_process] (1); phosphoglycerate mutase activity [GO:0004619 molecular_function] (1); catalytic activity [GO:0003824 molecular_function] (1); intramolecular transferase activity, phosphotransferases [GO:0016868 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Phosphoglycerate mutase 1 [IPR005952] (1); Histidine phosphatase superfamily [IPR029033] (1); Histidine phosphatase superfamily, clade-1 [IPR013078] (1); Phosphoglycerate/bisphosphoglycerate mutase, active site [IPR001345] (1)	-	-	P_trifoliata_00109_mRNA_16.1
GF0045461	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00109_mRNA_14.1
GF0045460	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00109_mRNA_13.1
GF0045459	0	0	1	Hypothetical protein (1)	hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (1)	Fibronectin type III-like domain [IPR026891] (1); Glycoside hydrolase family 3 [IPR026892] (1)	-	-	P_trifoliata_00109_mRNA_11.1
GF0045458	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00108_mRNA_66.1
GF0045457	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00108_mRNA_65.1
GF0045456	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00108_mRNA_63.1
GF0045455	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00108_mRNA_62.1
GF0045454	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00108_mRNA_61.1
GF0045453	0	0	1	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)	-	-	P_trifoliata_00108_mRNA_58.1
GF0045452	0	0	1	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	-	P_trifoliata_00108_mRNA_57.1
GF0045451	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00108_mRNA_56.1
GF0045450	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00108_mRNA_54.1
GF0045449	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00108_mRNA_49.1
GF0045448	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00108_mRNA_48.1
GF0045447	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00108_mRNA_47.1
GF0045446	0	0	1	Hypothetical protein (1)		Dynamin superfamily [IPR022812] (1)	-	-	P_trifoliata_00108_mRNA_46.1
GF0045445	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00108_mRNA_42.1
GF0045444	0	0	1	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	-	-	P_trifoliata_00108_mRNA_40.1
GF0045443	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00108_mRNA_37.1
GF0045442	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00108_mRNA_36.1
GF0045441	0	0	1	Hypothetical protein (1)		LOG family [IPR031100] (1)	-	-	P_trifoliata_00108_mRNA_33.1
GF0045440	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00108_mRNA_32.1
GF0045439	0	0	1	O-acyltransferase WSD1 (1)	diacylglycerol O-acyltransferase activity [GO:0004144 molecular_function] (1)	O-acyltransferase WSD1, C-terminal [IPR009721] (1)	-	-	P_trifoliata_00108_mRNA_31.1
GF0045438	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00108_mRNA_30.1
GF0045437	0	0	1	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	-	P_trifoliata_00108_mRNA_27.1
GF0045436	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00108_mRNA_26.1
GF0045435	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00108_mRNA_23.1
GF0045434	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00108_mRNA_21.1
GF0045433	0	0	1	Hypothetical protein (1)	transport [GO:0006810 biological_process] (1); integral component of membrane [GO:0016021 cellular_component] (1); ATPase activity [GO:0016887 molecular_function] (1); hydrolase activity [GO:0016787 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1); cytoplasm [GO:0005737 cellular_component] (1); transmembrane transport [GO:0055085 biological_process] (1); protein catabolic process [GO:0030163 biological_process] (1); ATPase activity, coupled to transmembrane movement of substances [GO:0042626 molecular_function] (1)	ATPase, AAA-type, core [IPR003959] (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); ABC transporter, conserved site [IPR017871] (1); 26S proteasome subunit P45 [IPR005937] (1); ATPase, AAA-type, conserved site [IPR003960] (1)	-	-	P_trifoliata_00108_mRNA_18.1
GF0045432	0	0	1	Hypothetical protein (1)		Mitochondrial carrier domain [IPR023395] (1)	-	-	P_trifoliata_00108_mRNA_12.1
GF0045431	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00107_mRNA_9.1
GF0045430	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00107_mRNA_67.1
GF0045429	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00107_mRNA_65.1
GF0045428	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00107_mRNA_64.1
GF0045427	0	0	1	Cytochrome P450 76C1 (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)	-	-	P_trifoliata_00107_mRNA_62.1
GF0045426	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00107_mRNA_61.1
GF0045425	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00107_mRNA_60.1
GF0045424	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00107_mRNA_54.1
GF0045423	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00107_mRNA_52.1
GF0045422	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00107_mRNA_51.1
GF0045421	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00107_mRNA_49.1
GF0045420	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00107_mRNA_47.1
GF0045419	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00107_mRNA_46.1
GF0045418	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00107_mRNA_45.1
GF0045417	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00107_mRNA_44.1
GF0045416	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00107_mRNA_40.1
GF0045415	0	0	1	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1)	Pentatricopeptide repeat [IPR002885] (1); Aspartic peptidase, active site [IPR001969] (1)	-	-	P_trifoliata_00107_mRNA_4.1
GF0045414	0	0	1	60S ribosomal protein L14 (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 L2 domain 2 [IPR014722] (1); Ribosomal protein L14 [IPR002784] (1); Translation protein SH3-like domain [IPR008991] (1)	-	-	P_trifoliata_00107_mRNA_38.1

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*
GF0045413	0	0	1	Hypothetical protein (1)		Arabidopsis retrotransposon Orf1 [IPR004312] (1); B3 domain-containing protein [IPR005508] (1)	-	-	P_trifoliata_00107_mRNA_37.1
GF0045412	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00107_mRNA_35.1
GF0045411	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00107_mRNA_34.1
GF0045410	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00107_mRNA_33.1
GF0045409	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00107_mRNA_32.1
GF0045408	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00107_mRNA_31.1
GF0045407	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00107_mRNA_3.1
GF0045406	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00107_mRNA_2.1
GF0045405	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00107_mRNA_18.1
GF0045404	0	0	1	Somatic embryogenesis receptor kinase 1 (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)	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); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1)	-	-	P_trifoliata_00107_mRNA_13.1
GF0045403	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00106_mRNA_63.1
GF0045402	0	0	1	Hypothetical protein (1)		Transposase, MuDR, plant [IPR004332] (1); MULE transposase domain [IPR018289] (1)	-	-	P_trifoliata_00106_mRNA_60.1
GF0045401	0	0	1	Protein LIKE COV 2 (1)		Protein of unknown function DUF502 [IPR007462] (1)	-	-	P_trifoliata_00106_mRNA_56.1
GF0045400	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1); Reverse transcriptase domain [IPR000477] (1)	-	-	P_trifoliata_00106_mRNA_52.1
GF0045399	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00106_mRNA_50.1
GF0045398	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00106_mRNA_49.1
GF0045397	0	0	1	Hypothetical protein (1)	DNA replication [GO:0006260 biological_process] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Ribonucleotide reductase large subunit, C-terminal [IPR000788] (1)	-	-	P_trifoliata_00106_mRNA_47.1
GF0045396	0	0	1	Hypothetical protein (1)	DNA replication [GO:0006260 biological_process] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Ribonucleotide reductase large subunit, C-terminal [IPR000788] (1); Ribonucleotide reductase, class I , alpha subunit [IPR013346] (1)	-	-	P_trifoliata_00106_mRNA_46.1
GF0045395	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00106_mRNA_41.1
GF0045394	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00106_mRNA_40.1
GF0045393	0	0	1	Hypothetical protein (1)		Bulb-type lectin domain [IPR001480] (1)	-	-	P_trifoliata_00106_mRNA_36.1
GF0045392	0	0	1	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); Protein kinase, ATP binding site [IPR017441] (1); S-locus glycoprotein domain [IPR000858] (1); Protein kinase-like domain [IPR011009] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1)	-	-	P_trifoliata_00106_mRNA_34.1
GF0045391	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00106_mRNA_27.1
GF0045390	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00106_mRNA_24.1
GF0045389	0	0	1	UDP-glycosyltransferase 92A1 (1)	metabolic process [GO:0008152 biological_process] (1); transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	-	-	P_trifoliata_00106_mRNA_22.1
GF0045388	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00106_mRNA_21.1
GF0045387	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00105_mRNA_87.1
GF0045386	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	PB1 domain [IPR000270] (1)	-	-	P_trifoliata_00105_mRNA_82.1
GF0045385	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00105_mRNA_77.1
GF0045384	0	0	1	Hypothetical protein (1)	membrane [GO:0016020 cellular_component] (1)	Plant PDR ABC transporter associated [IPR013581] (1); ABC-transporter extracellular N-terminal domain [IPR029481] (1); ABC-2 type transporter [IPR013525] (1)	-	-	P_trifoliata_00105_mRNA_76.1
GF0045383	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00105_mRNA_66.1
GF0045382	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00105_mRNA_64.1
GF0045381	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00105_mRNA_37.1
GF0045380	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00105_mRNA_33.1
GF0045379	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00105_mRNA_32.1
GF0045378	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00105_mRNA_31.1
GF0045377	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00105_mRNA_30.1
GF0045376	0	0	1	Elongation factor 1-alpha (1)		Translation elongation factor EF1A/initiation factor IF2gamma, C-terminal [IPR009001] (1); Translation elongation factor EFTu/EF1A, C-terminal [IPR004160] (1)	-	-	P_trifoliata_00105_mRNA_26.1
GF0045375	0	0	1	Hypothetical protein (1)	GTP binding [GO:0005525 molecular_function] (1)	Translation elongation factor EFTu/EF1A, domain 2 [IPR004161] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Translation protein, beta-barrel domain [IPR009000] (1)	-	-	P_trifoliata_00105_mRNA_25.1
GF0045374	0	0	1	Elongation factor 1-alpha (1)	GTP binding [GO:0005525 molecular_function] (1); translational elongation [GO:0006414 biological_process] (1); cytoplasm [GO:0005737 cellular_component] (1); GTPase activity [GO:0003924 molecular_function] (1); translation elongation factor activity [GO:0003746 molecular_function] (1)	Translation elongation factor EFTu/EF1A, domain 2 [IPR004161] (1); Tr-type G domain, conserved site [IPR031157] (1); Translation elongation factor EF1A, eukaryotic/archaeal [IPR004539] (1); Translation elongation factor EF1A/initiation factor IF2gamma, C-terminal [IPR009001] (1); Transcription factor, GTP-binding domain [IPR000795] (1); Pentatricopeptide repeat [IPR002885] (1); Translation elongation factor EFTu/EF1A, C-terminal [IPR004160] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Translation protein, beta-barrel domain [IPR009000] (1)	-	-	P_trifoliata_00105_mRNA_24.1
GF0045373	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00105_mRNA_13.1
GF0045372	0	0	1	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	-	P_trifoliata_00104_mRNA_8.1
GF0045371	0	0	1	Hypothetical protein (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); Aspartic peptidase, active site [IPR001969] (1)	-	-	P_trifoliata_00104_mRNA_74.1
GF0045370	0	0	1	Cysteine-rich receptor-like protein kinase 25 (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)	Protein kinase-like domain [IPR011009] (1); S-locus receptor kinase, C-terminal [IPR021820] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Gnk2-homologous domain [IPR002902] (1)	-	-	P_trifoliata_00104_mRNA_71.1
GF0045369	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00104_mRNA_7.1
GF0045368	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00104_mRNA_6.1
GF0045367	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00104_mRNA_59.1
GF0045366	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00104_mRNA_58.1
GF0045365	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00104_mRNA_51.1
GF0045364	0	0	1	Hypothetical protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	-	P_trifoliata_00104_mRNA_5.1
GF0045363	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00104_mRNA_4.1
GF0045362	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00104_mRNA_39.1
GF0045361	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00104_mRNA_3.1
GF0045360	0	0	1	Phosphoprotein phosphatase (1)	protein binding [GO:0005515 molecular_function] (1); binding [GO:0005488 molecular_function] (1)	Armadillo-like helical [IPR011989] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Armadillo [IPR000225] (1); Armadillo-type fold [IPR016024] (1)	-	-	P_trifoliata_00104_mRNA_24.1
GF0045359	0	0	1	Hypothetical protein (1)	binding [GO:0005488 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Armadillo [IPR000225] (1); Armadillo-like helical [IPR011989] (1); Armadillo-type fold [IPR016024] (1)	-	-	P_trifoliata_00104_mRNA_21.1
GF0045358	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00104_mRNA_18.1
GF0045357	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00104_mRNA_15.1
GF0045356	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00104_mRNA_14.1
GF0045355	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00104_mRNA_13.1
GF0045354	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00103_mRNA_73.1
GF0045353	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00103_mRNA_71.1

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*
GF0045352	0	0	1	Putative non-LTR reverse transcriptase (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Phloem protein 2-like [IPR025886] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00103_mRNA_68.1
GF0045351	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00103_mRNA_63.1
GF0045350	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00103_mRNA_62.1
GF0045349	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1); Zinc knuckle CX2CX4HX4C [IPR025836] (1); Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	-	P_trifoliata_00103_mRNA_61.1
GF0045348	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00103_mRNA_6.1
GF0045347	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	-	P_trifoliata_00103_mRNA_57.1
GF0045346	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00103_mRNA_55.1
GF0045345	0	0	1	Calmodulin (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)	-	-	P_trifoliata_00103_mRNA_53.1
GF0045344	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00103_mRNA_50.1
GF0045343	0	0	1	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)	-	-	P_trifoliata_00103_mRNA_43.1
GF0045342	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00103_mRNA_37.1
GF0045341	0	0	1	Putative oligopeptide transporter (1)	transmembrane transport [GO:0055085 biological_process] (1)	Oligopeptide transporter, OPT superfamily [IPR004813] (1)	-	-	P_trifoliata_00103_mRNA_30.1
GF0045340	0	0	1	WD repeat-containing protein 82 (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)	-	-	P_trifoliata_00103_mRNA_28.1
GF0045339	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00103_mRNA_16.1
GF0045338	0	0	1	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	-	P_trifoliata_00102_mRNA_59.1
GF0045337	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00102_mRNA_54.1
GF0045336	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00102_mRNA_53.1
GF0045335	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00102_mRNA_50.1
GF0045334	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00102_mRNA_49.1
GF0045333	0	0	1	Disease resistance protein (TIR-NBS-LRR class) (1)	protein binding [GO:0005515 molecular_function] (1); ADP binding [GO:0043531 molecular_function] (1); signal transduction [GO:0007165 biological_process] (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); Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1)	-	-	P_trifoliata_00102_mRNA_46.1
GF0045332	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00102_mRNA_45.1
GF0045331	0	0	1	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Probable transposase, Ptta/En/Spm, plant [IPR004252] (1); Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	-	-	P_trifoliata_00102_mRNA_36.1
GF0045330	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00102_mRNA_35.1
GF0045329	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00102_mRNA_31.1
GF0045328	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00102_mRNA_3.1
GF0045327	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00102_mRNA_17.1
GF0045326	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00102_mRNA_1.1
GF0045325	0	0	1	LRR receptor-like serine/threonine-protein kinase GSO2 (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00101_mRNA_79.1
GF0045324	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00101_mRNA_78.1
GF0045323	0	0	1	Hypothetical protein (1)	protein domain specific binding [GO:0019904 molecular_function] (1)	14-3-3 domain [IPR023410] (1); 14-3-3 protein [IPR000308] (1)	-	-	P_trifoliata_00101_mRNA_77.1
GF0045322	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00101_mRNA_73.1
GF0045321	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00101_mRNA_7.1
GF0045320	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00101_mRNA_66.1
GF0045319	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00101_mRNA_60.1
GF0045318	0	0	1	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); iron ion binding [GO:0005506 molecular_function] (1)	Isopenicillin N synthase [IPR002283] (1); Isopenicillin N synthase-like [IPR027443] (1); Non-haem dioxygenase N-terminal domain [IPR026992] (1); Oxoglutarate/iron-dependent dioxygenase [IPR005123] (1)	-	-	P_trifoliata_00101_mRNA_58.1
GF0045317	0	0	1	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)	Oxoglutarate/iron-dependent dioxygenase [IPR005123] (1); Isopenicillin N synthase-like [IPR027443] (1)	-	-	P_trifoliata_00101_mRNA_57.1
GF0045316	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00101_mRNA_56.1
GF0045315	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00101_mRNA_52.1
GF0045314	0	0	1	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); Protein kinase-like domain [IPR011009] (1)	-	-	P_trifoliata_00101_mRNA_50.1
GF0045313	0	0	1	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1)	Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase, ATP binding site [IPR017441] (1)	-	-	P_trifoliata_00101_mRNA_49.1
GF0045312	0	0	1	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-protein kinase, active site [IPR008271] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	-	-	P_trifoliata_00101_mRNA_48.1
GF0045311	0	0	1	Hypothetical protein (1)		Probable transposase, Ptta/En/Spm, plant [IPR004252] (1)	-	-	P_trifoliata_00101_mRNA_41.1
GF0045310	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00101_mRNA_40.1
GF0045309	0	0	1	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	-	P_trifoliata_00101_mRNA_4.1
GF0045308	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00101_mRNA_37.1
GF0045307	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00101_mRNA_3.1
GF0045306	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00101_mRNA_28.1
GF0045305	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00101_mRNA_25.1
GF0045304	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00101_mRNA_20.1
GF0045303	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00101_mRNA_12.1
GF0045302	0	0	1	Hypothetical protein (1)	phospholipid biosynthetic process [GO:0008654 biological_process] (1); inositol biosynthetic process [GO:0006021 biological_process] (1); inositol-3-phosphate synthase activity [GO:0004512 molecular_function] (1)	Myo-inositol-1-phosphate synthase [IPR002587] (1); NAD(P)-binding domain [IPR016040] (1)	-	-	P_trifoliata_00100_mRNA_5.1
GF0045301	0	0	1	Hypothetical protein (1)		MULE transposase domain [IPR018289] (1)	-	-	P_trifoliata_00100_mRNA_44.1
GF0045300	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00100_mRNA_43.1
GF0045299	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00100_mRNA_39.1
GF0045298	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00100_mRNA_19.1
GF0045297	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00100_mRNA_16.1
GF0045296	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00100_mRNA_15.1
GF0045295	0	0	1	Hypothetical protein (1)		Myo-inositol-1-phosphate synthase, GAPDH-like [IPR013021] (1)	-	-	P_trifoliata_00100_mRNA_1.1
GF0045294	0	0	1	Hypothetical protein (1)	mRNA splicing, via spliceosome [GO:0000398 biological_process] (1); spliceosomal complex [GO:0005681 cellular_component] (1)	Dim1 family [IPR004123] (1); Thioredoxin-like fold [IPR012336] (1)	-	-	P_trifoliata_00099_mRNA_8.1
GF0045293	0	0	1	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	-	P_trifoliata_00099_mRNA_77.1
GF0045292	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00099_mRNA_7.1
GF0045291	0	0	1	Hypothetical protein (1)	binding [GO:0005488 molecular_function] (1)	Armadillo-like helical [IPR011989] (1); Domain of unknown function DUF3067 [IPR021420] (1); Armadillo-type fold [IPR016024] (1)	-	-	P_trifoliata_00099_mRNA_59.1
GF0045290	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00099_mRNA_46.1
GF0045289	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00099_mRNA_45.1
GF0045288	0	0	1	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); Protein kinase-like domain [IPR011009] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	-	-	P_trifoliata_00099_mRNA_42.1
GF0045287	0	0	1	Ribonuclease H protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	-	P_trifoliata_00099_mRNA_31.1
GF0045286	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00099_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*
GF0045285	0	0	1	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, 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)	-	-	P_trifoliata_00099_mRNA_20.1
GF0045284	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00099_mRNA_16.1
GF0045283	0	0	1	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)	-	-	P_trifoliata_00099_mRNA_13.1
GF0045282	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00098_mRNA_88.1
GF0045281	0	0	1	Epoxide hydrolase 2 (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)	-	-	P_trifoliata_00098_mRNA_84.1
GF0045280	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00098_mRNA_61.1
GF0045279	0	0	1	Hypothetical protein (1)		Malectin-like carbohydrate-binding domain [IPR024788] (1)	-	-	P_trifoliata_00098_mRNA_55.1
GF0045278	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00098_mRNA_54.1
GF0045277	0	0	1	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); double-stranded DNA binding [GO:0003690 molecular_function] (1); mitochondrion [GO:0005739 cellular_component] (1)	Mitochodrial transcription termination factor [IPR003690] (1)	-	-	P_trifoliata_00098_mRNA_10.1
GF0045276	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00097_mRNA_55.1
GF0045275	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00097_mRNA_54.1
GF0045274	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00097_mRNA_53.1
GF0045273	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00097_mRNA_46.1
GF0045272	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00097_mRNA_40.1
GF0045271	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00097_mRNA_35.1
GF0045270	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00097_mRNA_34.1
GF0045269	0	0	1	Hypothetical protein (1)		DnaJ domain, conserved site [IPR018253] (1); DnaJ domain [IPR001623] (1)	-	-	P_trifoliata_00097_mRNA_32.1
GF0045268	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00097_mRNA_3.1
GF0045267	0	0	1	Hypothetical protein (1)		Transposase, MuDR, plant [IPR004332] (1)	-	-	P_trifoliata_00097_mRNA_26.1
GF0045266	0	0	1	Hypothetical protein (1)	mitochondrial respiratory chain [GO:0005746 cellular_component] (1)	Cytochrome c oxidase subunit 5c [IPR008432] (1)	-	-	P_trifoliata_00097_mRNA_24.1
GF0045265	0	0	1	Hypothetical protein (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)	-	-	P_trifoliata_00097_mRNA_22.1
GF0045264	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00097_mRNA_20.1
GF0045263	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00097_mRNA_19.1
GF0045262	0	0	1	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	-	P_trifoliata_00096_mRNA_96.1
GF0045261	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00096_mRNA_94.1
GF0045260	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00096_mRNA_93.1
GF0045259	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00096_mRNA_92.1
GF0045258	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00096_mRNA_89.1
GF0045257	0	0	1	Hypothetical protein (1)	enzyme inhibitor activity [GO:0004857 molecular_function] (1)	Pectinesterase inhibitor domain [IPR006501] (1)	-	-	P_trifoliata_00096_mRNA_79.1
GF0045256	0	0	1	Myeloid leukemia factor 1 (1)		Myeloid leukemia factor [IPR019376] (1)	-	-	P_trifoliata_00096_mRNA_62.1
GF0045255	0	0	1	Hypothetical protein (1)		NAD(P)-binding domain [IPR016040] (1)	-	-	P_trifoliata_00096_mRNA_60.1
GF0045254	0	0	1	Hypothetical protein (1)		Glutathione S-transferase, C-terminal-like [IPR010987] (1)	-	-	P_trifoliata_00096_mRNA_58.1
GF0045253	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00096_mRNA_21.1
GF0045252	0	0	1	SOC1 MADS-box protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	Transcription factor, MADS-box [IPR002100] (1)	-	-	P_trifoliata_00096_mRNA_19.1
GF0045251	0	0	1	ATPase ASNA1 homolog (1)	ATPase activity [GO:0016887 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Arsenical pump ATPase, ArsA/GET3, eukaryotic [IPR027542] (1); Arsenical pump ATPase, ArsA/GET3 [IPR016300] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Anion-transporting ATPase-like domain [IPR025723] (1)	-	-	P_trifoliata_00096_mRNA_13.1
GF0045250	0	0	1	Peptidoglycan-binding LysM domain protein (1)		LysM domain [IPR018392] (1)	-	-	P_trifoliata_00096_mRNA_11.1
GF0045249	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00095_mRNA_9.1
GF0045248	0	0	1	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)	-	-	P_trifoliata_00095_mRNA_63.1
GF0045247	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00095_mRNA_6.1
GF0045246	0	0	1	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	-	P_trifoliata_00095_mRNA_51.1
GF0045245	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00095_mRNA_50.1
GF0045244	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00095_mRNA_49.1
GF0045243	0	0	1	Hypothetical protein (1)		Chromo domain-like [IPR016197] (1); Chromo domain [IPR023780] (1)	-	-	P_trifoliata_00095_mRNA_40.1
GF0045242	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00095_mRNA_39.1
GF0045241	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00095_mRNA_37.1
GF0045240	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00095_mRNA_28.1
GF0045239	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00095_mRNA_2.1
GF0045238	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00095_mRNA_10.1
GF0045237	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00095_mRNA_1.1
GF0045236	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00094_mRNA_81.1
GF0045235	0	0	1	Kunitz trypsin inhibitor (1)	endopeptidase inhibitor activity [GO:0004866 molecular_function] (1)	Proteinase inhibitor I3, Kunitz legume [IPR002160] (1); Kunitz inhibitor ST1-like [IPR011065] (1)	-	-	P_trifoliata_00094_mRNA_78.1
GF0045234	0	0	1	Hypothetical protein (1)		Protein of unknown function DUF597 [IPR006734] (1)	-	-	P_trifoliata_00094_mRNA_68.1
GF0045233	0	0	1	Cytochrome P450 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); monooxygenase activity [GO:0004497 molecular_function] (1)	Cytochrome P450 [IPR001128] (1); Red chlorophyll catabolite reductase [IPR009439] (1); Cytochrome P450, conserved site [IPR017972] (1); Cytochrome P450, B-class [IPR002397] (1)	-	-	P_trifoliata_00094_mRNA_6.1
GF0045232	0	0	1	Isoflavone 2'-hydroxylase (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 [IPR001128] (1)	-	-	P_trifoliata_00094_mRNA_55.1
GF0045231	0	0	1	Methyl esterase 1 (1)		Alpha/Beta hydrolase fold [IPR029058] (1)	-	-	P_trifoliata_00094_mRNA_46.1
GF0045230	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00094_mRNA_22.1
GF0045229	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00094_mRNA_21.1
GF0045228	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00094_mRNA_2.1
GF0045227	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00094_mRNA_11.1
GF0045226	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00093_mRNA_78.1
GF0045225	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00093_mRNA_76.1
GF0045224	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00093_mRNA_75.1
GF0045223	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00093_mRNA_71.1
GF0045222	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00093_mRNA_66.1
GF0045221	0	0	1	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	-	P_trifoliata_00093_mRNA_62.1
GF0045220	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00093_mRNA_56.1
GF0045219	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00093_mRNA_55.1
GF0045218	0	0	1	Hypothetical protein (1)	protein domain specific binding [GO:0019904 molecular_function] (1)	14-3-3 protein [IPR000308] (1); 14-3-3 domain [IPR023410] (1)	-	-	P_trifoliata_00093_mRNA_50.1
GF0045217	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00093_mRNA_44.1
GF0045216	0	0	1	Hypothetical protein (1)		MULE transposase domain [IPR018289] (1)	-	-	P_trifoliata_00093_mRNA_41.1
GF0045215	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00093_mRNA_29.1

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***
GF0045214	0	0	1	Seryl-tRNA synthetase / serine--tRNA ligase isoform 1 (1)	aminoacyl-tRNA ligase activity [GO:0004812 molecular_function] (1); seryl-tRNA aminoacylation [GO:0006434 biological_process] (1); serine-tRNA ligase activity [GO:0004828 molecular_function] (1); cytoplasm [GO:0005737 cellular_component] (1); tRNA aminoacylation for protein translation [GO:0006418 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1); nucleotide binding [GO:0000166 molecular_function] (1); protein kinase binding [GO:0019901 molecular_function] (1); regulation of cyclin-dependent protein serine/threonine kinase activity [GO:0000079 biological_process] (1)	Aminoacyl-tRNA synthetase, class II (G/ P/ S/T) [IPR002314] (1); Cyclin PHO80-like [IPR013922] (1); Cyclin-like [IPR013763] (1); Serine-tRNA ligase, type1 [IPR002317] (1); Aminoacyl-tRNA synthetase, class II [IPR006195] (1)	-	-	P_trifoliata_00093_mRNA_25.1
GF0045213	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00093_mRNA_24.1
GF0045212	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00093_mRNA_23.1
GF0045211	0	0	1	Truncated RB (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	-	P_trifoliata_00093_mRNA_22.1
GF0045210	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00093_mRNA_20.1
GF0045209	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00092_mRNA_99.1
GF0045208	0	0	1	Cytochrome P450 87A3 (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)	-	-	P_trifoliata_00092_mRNA_97.1
GF0045207	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00092_mRNA_96.1
GF0045206	0	0	1	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)	-	-	P_trifoliata_00092_mRNA_95.1
GF0045205	0	0	1	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 [IPR001128] (1)	-	-	P_trifoliata_00092_mRNA_94.1
GF0045204	0	0	1	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)	-	-	P_trifoliata_00092_mRNA_93.1
GF0045203	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00092_mRNA_90.1
GF0045202	0	0	1	Hypothetical protein (1)	trehalose metabolic process [GO:0005991 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1); alpha,alpha-trehalase activity [GO:0004555 molecular_function] (1)	Six-hairpin glycosidase-like [IPR008928] (1); Glycoside hydrolase, family 37 [IPR001661] (1)	-	-	P_trifoliata_00092_mRNA_9.1
GF0045201	0	0	1	Mitochondrial substrate carrier family protein B (1)	transmembrane transport [GO:0055085 biological_process] (1)	Mitochondrial carrier protein [IPR002067] (1); Mitochondrial carrier domain [IPR023395] (1); Mitochondrial substrate/solute carrier [IPR018108] (1)	-	-	P_trifoliata_00092_mRNA_88.1
GF0045200	0	0	1	Alpha,alpha-trehalase (1)	alpha,alpha-trehalase activity [GO:0004555 molecular_function] (1); catalytic activity [GO:0003824 molecular_function] (1); trehalose metabolic process [GO:0005991 biological_process] (1)	Six-hairpin glycosidase-like [IPR008928] (1); Glycoside hydrolase, family 37, conserved site [IPR018232] (1); Glycoside hydrolase, family 37 [IPR001661] (1)	-	-	P_trifoliata_00092_mRNA_8.1
GF0045199	0	0	1	Glycoside hydrolase family 28 protein (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/virulence factor [IPR011050] (1); Pectin lyase fold [IPR012334] (1); Pectate lyase superfamily protein [IPR024535] (1)	-	-	P_trifoliata_00092_mRNA_74.1
GF0045198	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00092_mRNA_73.1
GF0045197	0	0	1	Hypothetical protein (1)	trehalose metabolic process [GO:0005991 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1); alpha,alpha-trehalase activity [GO:0004555 molecular_function] (1)	Glycoside hydrolase, family 37 [IPR001661] (1); Six-hairpin glycosidase-like [IPR008928] (1)	-	-	P_trifoliata_00092_mRNA_7.1
GF0045196	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00092_mRNA_66.1
GF0045195	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00092_mRNA_62.1
GF0045194	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00092_mRNA_61.1
GF0045193	0	0	1	Hypothetical protein (1)		Bifunctional inhibitor/plant lipid transfer protein/seed storage helical domain [IPR016140] (1)	-	-	P_trifoliata_00092_mRNA_60.1
GF0045192	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00092_mRNA_6.1
GF0045191	0	0	1	Putative RING-H2 finger protein ATL21A (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/FYVE/PHD-type [IPR013083] (1)	-	-	P_trifoliata_00092_mRNA_59.1
GF0045190	0	0	1	Pleckstrin-like (PH) domain protein (1)		PH domain-like [IPR011993] (1); Pleckstrin homology domain [IPR001849] (1)	-	-	P_trifoliata_00092_mRNA_52.1
GF0045189	0	0	1	Nucleoside diphosphate kinase (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); GTP biosynthetic process [GO:0006183 biological_process] (1)	Nucleoside diphosphate kinase [IPR001564] (1); Nucleoside diphosphate kinase, active site [IPR023005] (1)	-	-	P_trifoliata_00092_mRNA_51.1
GF0045188	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00092_mRNA_5.1
GF0045187	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00092_mRNA_49.1
GF0045186	0	0	1	Hypothetical protein (1)		ElonginA binding-protein 1 [IPR031736] (1)	-	-	P_trifoliata_00092_mRNA_41.1
GF0045185	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00092_mRNA_3.1
GF0045184	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	PB1 domain [IPR000270] (1)	-	-	P_trifoliata_00092_mRNA_22.1
GF0045183	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00092_mRNA_17.1
GF0045182	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00092_mRNA_14.1
GF0045181	0	0	1	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	-	-	P_trifoliata_00092_mRNA_13.1
GF0045180	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00092_mRNA_113.1
GF0045179	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00092_mRNA_109.1
GF0045178	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00092_mRNA_108.1
GF0045177	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00092_mRNA_106.1
GF0045176	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00092_mRNA_103.1
GF0045175	0	0	1	Flavonoid 3'-monooxygenase (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)	-	-	P_trifoliata_00092_mRNA_100.1
GF0045174	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00092_mRNA_10.1
GF0045173	0	0	1	Homeobox prospero (1)			-	-	P_trifoliata_00091_mRNA_90.1
GF0045172	0	0	1	Transformer serine/arginine-rich ribonucleoprotein (1)	nucleotide binding [GO:0000166 molecular_function] (1)	Nucleotide-binding alpha-beta plait domain [IPR012677] (1)	-	-	P_trifoliata_00091_mRNA_86.1

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*
GF0045171	0	0	1	Tubulin beta-3 chain (1)	microtubule-based process [GO:0007017 biological_process] (1); structural constituent of cytoskeleton [GO:0005200 molecular_function] (1); microtubule [GO:0005874 cellular_component] (1); GTP binding [GO:0005525 molecular_function] (1)	Beta tubulin [IPR002453] (1); Tubulin/FtsZ, C-terminal [IPR008280] (1); Tubulin [IPR000217] (1); Tubulin/FtsZ, 2-layer sandwich domain [IPR018316] (1); Tubulin, C-terminal [IPR023123] (1)	-	-	P_trifoliata_00091_mRNA_76.1
GF0045170	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00091_mRNA_70.1
GF0045169	0	0	1	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)	-	-	P_trifoliata_00091_mRNA_69.1
GF0045168	0	0	1	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); Glutathione S-transferase, C-terminal [IPR004046] (1); Thioredoxin-like fold [IPR012336] (1)	-	-	P_trifoliata_00091_mRNA_56.1
GF0045167	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00091_mRNA_55.1
GF0045166	0	0	1	Glutathione S-transferase GST 18 (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)	-	-	P_trifoliata_00091_mRNA_54.1
GF0045165	0	0	1	Hypothetical protein (1)	multicellular organismal development [GO:0007275 biological_process] (1)	YABBY protein [IPR006780] (1)	-	-	P_trifoliata_00091_mRNA_4.1
GF0045164	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00091_mRNA_33.1
GF0045163	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00091_mRNA_30.1
GF0045162	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00091_mRNA_3.1
GF0045161	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00091_mRNA_24.1
GF0045160	0	0	1	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)	-	-	P_trifoliata_00090_mRNA_5.1
GF0045159	0	0	1	Hypothetical protein (1)	NADP binding [GO:0050661 molecular_function] (1); N,N-dimethylaniline monooxygenase activity [GO:0004499 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); Flavin monooxygenase-like [IPR020946] (1)	-	-	P_trifoliata_00090_mRNA_40.1
GF0045158	0	0	1	Sucrose synthase (1)	sucrose synthase activity [GO:0016157 molecular_function] (1); sucrose metabolic process [GO:0005985 biological_process] (1)	Sucrose synthase [IPR000368] (1); Glycosyl transferase, family 1 [IPR001296] (1)	-	-	P_trifoliata_00090_mRNA_4.1
GF0045157	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00090_mRNA_37.1
GF0045156	0	0	1	Hypothetical protein (1)		Modifier of rudimentary, Modr [IPR009851] (1)	-	-	P_trifoliata_00090_mRNA_3.1
GF0045155	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00090_mRNA_22.1
GF0045154	0	0	1	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); High mobility group box domain [IPR009071] (1)	-	-	P_trifoliata_00090_mRNA_2.1
GF0045153	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00090_mRNA_19.1
GF0045152	0	0	1	Hypothetical protein (1)		S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	-	P_trifoliata_00089_mRNA_9.1
GF0045151	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00089_mRNA_69.1
GF0045150	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00089_mRNA_63.1
GF0045149	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00089_mRNA_61.1
GF0045148	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00089_mRNA_57.1
GF0045147	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00089_mRNA_56.1
GF0045146	0	0	1	NAC domain transcription factor, putative, expressed (1)	DNA binding [GO:0003677 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	NAC domain [IPR003441] (1)	-	-	P_trifoliata_00089_mRNA_5.1
GF0045145	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00089_mRNA_48.1
GF0045144	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00089_mRNA_43.1
GF0045143	0	0	1	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	-	P_trifoliata_00089_mRNA_34.1
GF0045142	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00089_mRNA_33.1
GF0045141	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00089_mRNA_32.1
GF0045140	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00089_mRNA_28.1
GF0045139	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00089_mRNA_27.1
GF0045138	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00089_mRNA_22.1
GF0045137	0	0	1	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	Zinc finger, BED-type [IPR003656] (1)	-	-	P_trifoliata_00089_mRNA_21.1
GF0045136	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00089_mRNA_20.1
GF0045135	0	0	1	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)	-	-	P_trifoliata_00089_mRNA_19.1
GF0045134	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00089_mRNA_14.1
GF0045133	0	0	1	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)	Endonuclease/exonuclease/phosphatase [IPR005135] (1); Ribonuclease H-like domain [IPR012337] (1); Ribonuclease H domain [IPR002156] (1)	-	-	P_trifoliata_00089_mRNA_11.1
GF0045132	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00089_mRNA_10.1
GF0045131	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00089_mRNA_1.1
GF0045130	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00088_mRNA_8.1
GF0045129	0	0	1	Cytochrome P450 family 72 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); monooxygenase activity [GO:0004497 molecular_function] (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 IV [IPR002403] (1); Cytochrome P450 [IPR001128] (1)	-	-	P_trifoliata_00088_mRNA_74.1
GF0045128	0	0	1	RNA-dependent RNA polymerase 2 (1)	RNA-directed RNA polymerase activity [GO:0003968 molecular_function] (1)	RNA-dependent RNA polymerase, eukaryotic-type [IPR007855] (1)	-	-	P_trifoliata_00088_mRNA_73.1
GF0045127	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00088_mRNA_71.1
GF0045126	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00088_mRNA_7.1
GF0045125	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00088_mRNA_69.1
GF0045124	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00088_mRNA_68.1
GF0045123	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00088_mRNA_61.1
GF0045122	0	0	1	Chaperonin-like RbcX protein (1)		Chaperonin-like RbcX [IPR003435] (1)	-	-	P_trifoliata_00088_mRNA_56.1
GF0045121	0	0	1	Orf105b protein (1)			-	-	P_trifoliata_00088_mRNA_5.1
GF0045120	0	0	1	Bifunctional dihydroflavonol 4-reductase/flavanone 4-reductase (1)	3-beta-hydroxy-delta5-steroid dehydrogenase activity [GO:0003854 molecular_function] (1); steroid biosynthetic process [GO:0006694 biological_process] (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)	3-beta hydroxysteroid dehydrogenase/isomerase [IPR002225] (1); NAD(P)-binding domain [IPR016040] (1)	-	-	P_trifoliata_00088_mRNA_42.1
GF0045119	0	0	1	Beta-1,3-N-acetylglucosaminyltransferase lunatic fringe (1)		Protein of unknown function DUF604 [IPR006740] (1)	-	-	P_trifoliata_00088_mRNA_38.1
GF0045118	0	0	1	Hypothetical protein (1)	integral component of membrane [GO:0016021 cellular_component] (1); transport [GO:0006810 biological_process] (1); ATPase activity, coupled to transmembrane movement of substances [GO:0042626 molecular_function] (1); transmembrane transport [GO:0055085 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1)	ABC transporter type 1, transmembrane domain [IPR011527] (1)	-	-	P_trifoliata_00088_mRNA_36.1
GF0045117	0	0	1	Hypothetical protein (1)	ATPase activity [GO:0016887 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	ABC transporter-like [IPR003439] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	-	P_trifoliata_00088_mRNA_35.1
GF0045116	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00088_mRNA_3.1
GF0045115	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00088_mRNA_27.1
GF0045114	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00088_mRNA_26.1
GF0045113	0	0	1	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); O-methyltransferase, family 2 [IPR001077] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	-	P_trifoliata_00088_mRNA_25.1

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*
GF0045112	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00088_mRNA_22.1
GF0045111	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00088_mRNA_21.1
GF0045110	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00088_mRNA_2.1
GF0045109	0	0	1	RNA-binding protein 8A (1)	RNA processing [GO:0006396 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1); nucleotide binding [GO:0000166 molecular_function] (1); RNA binding [GO:0003723 molecular_function] (1); nucleus [GO:0005634 cellular_component] (1); cytoplasm [GO:0005737 cellular_component] (1)	RNA-binding motif protein 8 [IPR008111] (1); RNA recognition motif domain [IPR000504] (1); Nucleotide-binding alpha-beta plait domain [IPR012677] (1)	-	-	P_trifoliata_00088_mRNA_11.1
GF0045108	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00088_mRNA_1.1
GF0045107	0	0	1	Monosacharide transport protein (1)			-	-	P_trifoliata_00087_mRNA_70.1
GF0045106	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00087_mRNA_7.1
GF0045105	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00087_mRNA_69.1
GF0045104	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00087_mRNA_67.1
GF0045103	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00087_mRNA_59.1
GF0045102	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00087_mRNA_57.1
GF0045101	0	0	1	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)	-	-	P_trifoliata_00087_mRNA_55.1
GF0045100	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00087_mRNA_53.1
GF0045099	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00087_mRNA_42.1
GF0045098	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00087_mRNA_39.1
GF0045097	0	0	1	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); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1)	-	-	P_trifoliata_00087_mRNA_38.1
GF0045096	0	0	1	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	-	-	P_trifoliata_00087_mRNA_35.1
GF0045095	0	0	1	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)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1)	-	-	P_trifoliata_00087_mRNA_34.1
GF0045094	0	0	1	Hypothetical protein (1)		LOG family [IPR031100] (1)	-	-	P_trifoliata_00087_mRNA_33.1
GF0045093	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00087_mRNA_32.1
GF0045092	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00087_mRNA_31.1
GF0045091	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00087_mRNA_30.1
GF0045090	0	0	1	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	Zinc finger, BED-type [IPR003656] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00087_mRNA_28.1
GF0045089	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1); histone-lysine N-methyltransferase activity [GO:0018024 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1); nucleus [GO:0005634 cellular_component] (1); histone lysine methylation [GO:0034968 biological_process] (1); histone binding [GO:0042393 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); Pre-SET zinc-binding sub-group [IPR003606] (1); Pre-SET domain [IPR007728] (1); PUA-like domain [IPR015947] (1); SRA-YDG [IPR003105] (1)	-	-	P_trifoliata_00087_mRNA_27.1
GF0045088	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00087_mRNA_2.1
GF0045087	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00087_mRNA_19.1
GF0045086	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00087_mRNA_18.1
GF0045085	0	0	1	Hypothetical protein (1)	enzyme inhibitor activity [GO:0004857 molecular_function] (1)	Pectinesterase inhibitor domain [IPR006501] (1)	-	-	P_trifoliata_00087_mRNA_15.1
GF0045084	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00087_mRNA_11.1
GF0045083	0	0	1	Hypothetical protein (1)	N-acetyltransferase activity [GO:0008080 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); GNAT domain [IPR000182] (1); Acyl-CoA N-acyltransferase [IPR016181] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00087_mRNA_1.1
GF0045082	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00086_mRNA_9.1
GF0045081	0	0	1	Hypothetical protein (1)	hydroquinone:oxygen oxidoreductase activity [GO:0052716 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); copper ion binding [GO:0005507 molecular_function] (1); apoplast [GO:0048046 cellular_component] (1); lignin catabolic process [GO:0046274 biological_process] (1)	Multicopper oxidase, type 2 [IPR011706] (1); Laccase [IPR017761] (1); Multicopper oxidase, type 1 [IPR001117] (1); Cupredoxin [IPR008972] (1); Multicopper oxidase, type 3 [IPR011707] (1)	-	-	P_trifoliata_00086_mRNA_78.1
GF0045080	0	0	1	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	hAT-like transposase, RNase-H fold [IPR025525] (1)	-	-	P_trifoliata_00086_mRNA_63.1
GF0045079	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00086_mRNA_62.1
GF0045078	0	0	1	Hypothetical protein (1)		Gag-polypeptide of LTR copia-type [IPR029472] (1)	-	-	P_trifoliata_00086_mRNA_52.1
GF0045077	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00086_mRNA_50.1
GF0045076	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00086_mRNA_49.1
GF0045075	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00086_mRNA_48.1
GF0045074	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00086_mRNA_46.1
GF0045073	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00086_mRNA_40.1
GF0045072	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00086_mRNA_37.1
GF0045071	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00086_mRNA_36.1
GF0045070	0	0	1	Putative carboxylesterase 11 (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)	-	-	P_trifoliata_00086_mRNA_30.1
GF0045069	0	0	1	TSA: Wollemia nobilis transcribed RNA sequence (1)	ATPase activity [GO:0016887 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	ABC transporter-like [IPR003439] (1); AAA+ ATPase domain [IPR003593] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	-	P_trifoliata_00086_mRNA_17.1
GF0045068	0	0	1	Glyceraldehyde-3-phosphate dehydrogenase C2 isoform 3 (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/Erythrose phosphate dehydrogenase family [IPR020831] (1); Glyceraldehyde 3-phosphate dehydrogenase, active site [IPR020830] (1); NAD(P)-binding domain [IPR016040] (1); Glyceraldehyde 3-phosphate dehydrogenase, NAD(P) binding domain [IPR020828] (1); Glyceraldehyde 3-phosphate dehydrogenase, catalytic domain [IPR020829] (1)	-	-	P_trifoliata_00086_mRNA_15.1
GF0045067	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00085_mRNA_97.1
GF0045066	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00085_mRNA_96.1
GF0045065	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat-containing domain [IPR020683] (1); Ankyrin repeat [IPR002110] (1)	-	-	P_trifoliata_00085_mRNA_92.1
GF0045064	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00085_mRNA_9.1
GF0045063	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00085_mRNA_8.1
GF0045062	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00085_mRNA_79.1
GF0045061	0	0	1	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)	-	-	P_trifoliata_00085_mRNA_78.1
GF0045060	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00085_mRNA_74.1
GF0045059	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00085_mRNA_7.1
GF0045058	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00085_mRNA_69.1
GF0045057	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00085_mRNA_62.1
GF0045056	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00085_mRNA_6.1
GF0045055	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00085_mRNA_51.1
GF0045054	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00085_mRNA_50.1
GF0045053	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00085_mRNA_5.1
GF0045052	0	0	1	Heavy metal ATPase transporter (1)	integral component of membrane [GO:0016021 cellular_component] (1); metal ion binding [GO:0046872 molecular_function] (1); cation transport [GO:0006812 biological_process] (1); nucleotide binding [GO:0000166 molecular_function] (1); cation-transporting ATPase activity [GO:0019829 molecular_function] (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); HAD-like domain [IPR023214] (1); P-type ATPase, A domain [IPR008250] (1)	-	-	P_trifoliata_00085_mRNA_45.1
GF0045051	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00085_mRNA_43.1
GF0045050	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00085_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*
GF0045049	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00085_mRNA_41.1
GF0045048	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00085_mRNA_40.1
GF0045047	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00085_mRNA_39.1
GF0045046	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00085_mRNA_38.1
GF0045045	0	0	1	Monosacharide transport protein (1)			-	-	P_trifoliata_00085_mRNA_37.1
GF0045044	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00085_mRNA_32.1
GF0045043	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00085_mRNA_31.1
GF0045042	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00085_mRNA_29.1
GF0045041	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00085_mRNA_28.1
GF0045040	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00085_mRNA_20.1
GF0045039	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00085_mRNA_18.1
GF0045038	0	0	1	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1)	Peptidase A2A, retrovirus, catalytic [IPR001995] (1)	-	-	P_trifoliata_00085_mRNA_17.1
GF0045037	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00085_mRNA_15.1
GF0045036	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00085_mRNA_14.1
GF0045035	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00085_mRNA_13.1
GF0045034	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00085_mRNA_102.1
GF0045033	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00085_mRNA_101.1
GF0045032	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00085_mRNA_100.1
GF0045031	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00085_mRNA_10.1
GF0045030	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00085_mRNA_1.1
GF0045029	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Post-SET domain [IPR003616] (1); SET domain [IPR001214] (1)	-	-	P_trifoliata_00084_mRNA_9.1
GF0045028	0	0	1	Hypothetical protein (1)		Sieve element occlusion, N-terminal [IPR027942] (1)	-	-	P_trifoliata_00084_mRNA_83.1
GF0045027	0	0	1	Hypothetical protein (1)		MULE transposase domain [IPR018289] (1)	-	-	P_trifoliata_00084_mRNA_70.1
GF0045026	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00084_mRNA_7.1
GF0045025	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00084_mRNA_68.1
GF0045024	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00084_mRNA_64.1
GF0045023	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00084_mRNA_61.1
GF0045022	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00084_mRNA_60.1
GF0045021	0	0	1	Hypothetical protein (1)		Eukaryotic translation initiation factor 3 subunit G, N-terminal [IPR024675] (1)	-	-	P_trifoliata_00084_mRNA_6.1
GF0045020	0	0	1	Hypothetical protein (1)		TB2/DP1/HVA22-related protein [IPR004345] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00084_mRNA_59.1
GF0045019	0	0	1	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase 1 (1)	nucleoside metabolic process [GO:0009116 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1)	Nucleoside phosphorylase domain [IPR000845] (1); Nucleoside phosphorylase [IPR018017] (1)	-	-	P_trifoliata_00084_mRNA_52.1
GF0045018	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00084_mRNA_47.1
GF0045017	0	0	1	Hypothetical protein (1)		Nucleolar 27S pre-rRNA processing, Urb2/Npa2, C-terminal [IPR018849] (1)	-	-	P_trifoliata_00084_mRNA_45.1
GF0045016	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00084_mRNA_44.1
GF0045015	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00084_mRNA_42.1
GF0045014	0	0	1	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); AMP-dependent synthetase/ligase [IPR000873] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	-	-	P_trifoliata_00084_mRNA_4.1
GF0045013	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00084_mRNA_39.1
GF0045012	0	0	1	Hypothetical protein (1)		Gag-polypeptide of LTR copia-type [IPR029472] (1)	-	-	P_trifoliata_00084_mRNA_26.1
GF0045011	0	0	1	Hypothetical protein (1)		Arfaptin homology (AH) domain/BAR domain [IPR027267] (1)	-	-	P_trifoliata_00084_mRNA_24.1
GF0045010	0	0	1	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)	-	-	P_trifoliata_00084_mRNA_21.1
GF0045009	0	0	1	Phosphoprotein phosphatase (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00084_mRNA_18.1
GF0045008	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00084_mRNA_17.1
GF0045007	0	0	1	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)	-	-	P_trifoliata_00084_mRNA_16.1
GF0045006	0	0	1	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)	-	-	P_trifoliata_00084_mRNA_15.1
GF0045005	0	0	1	Expansin-like B1 (1)	sexual reproduction [GO:0019953 biological_process] (1); extracellular region [GO:0005576 cellular_component] (1)	Expansin/Lol pI [IPR007118] (1); Expansin, cellulose-binding-like domain [IPR007117] (1); RlpA-like double-psi beta-barrel domain [IPR009009] (1); Expansin/pollen allergen, DPBB domain [IPR007112] (1); Major pollen allergen Lol pI [IPR005795] (1)	-	-	P_trifoliata_00084_mRNA_13.1
GF0045004	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00084_mRNA_12.1
GF0045003	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00084_mRNA_11.1
GF0045002	0	0	1	Hypothetical protein (1)	nucleus [GO:0005634 cellular_component] (1); histone lysine methylation [GO:0034968 biological_process] (1); histone binding [GO:0042393 molecular_function] (1); histone-lysine N-methyltransferase activity [GO:0018024 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Pre-SET zinc-binding sub-group [IPR003606] (1); Pre-SET domain [IPR007728] (1); PUA-like domain [IPR015947] (1); SRA-YDG [IPR003105] (1)	-	-	P_trifoliata_00084_mRNA_10.1
GF0045001	0	0	1	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)	-	-	P_trifoliata_00083_mRNA_9.1
GF0045000	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4371 [IPR025398] (1)	-	-	P_trifoliata_00083_mRNA_80.1
GF0044999	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00083_mRNA_8.1
GF0044998	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00083_mRNA_74.1
GF0044997	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00083_mRNA_61.1
GF0044996	0	0	1	Hypothetical protein (1)	helicase activity [GO:0004386 molecular_function] (1)	Helicase-associated domain [IPR007502] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	-	P_trifoliata_00083_mRNA_51.1
GF0044995	0	0	1	Pre-mRNA-splicing factor ATP-dependent RNA helicase (1)	ATP binding [GO:0005524 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1); ATP-dependent helicase activity [GO:0008026 molecular_function] (1)	Helicase, C-terminal [IPR001650] (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)	-	-	P_trifoliata_00083_mRNA_50.1
GF0044994	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00083_mRNA_5.1
GF0044993	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00083_mRNA_42.1
GF0044992	0	0	1	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)	-	-	P_trifoliata_00083_mRNA_41.1
GF0044991	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00083_mRNA_39.1
GF0044990	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	-	P_trifoliata_00083_mRNA_32.1
GF0044989	0	0	1	Hypothetical protein (1)		MULE transposase domain [IPR018289] (1)	-	-	P_trifoliata_00083_mRNA_27.1
GF0044988	0	0	1	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)	-	-	P_trifoliata_00083_mRNA_25.1
GF0044987	0	0	1	Hypothetical protein (1)	response to stress [GO:0006950 biological_process] (1)	Late embryogenesis abundant protein, LEA5-type [IPR004926] (1)	-	-	P_trifoliata_00083_mRNA_21.1
GF0044986	0	0	1	Hypothetical protein (1)		TB2/DP1/HVA22-related protein [IPR004345] (1)	-	-	P_trifoliata_00083_mRNA_17.1
GF0044985	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00083_mRNA_14.1
GF0044984	0	0	1	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	-	-	P_trifoliata_00083_mRNA_10.1
GF0044983	0	0	1	Agamous-like MADS-box protein AGL11 (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (1); nucleus [GO:0005634 cellular_component] (1)	Transcription factor, K-box [IPR002487] (1)	-	-	P_trifoliata_00083_mRNA_1.1
GF0044982	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00082_mRNA_87.1
GF0044981	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00082_mRNA_85.1

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*
GF0044980	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00082_mRNA_77.1
GF0044979	0	0	1	Cytochrome P450 family 71 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 [IPR001128] (1)	-	-	P_trifoliata_00082_mRNA_76.1
GF0044978	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00082_mRNA_75.1
GF0044977	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00082_mRNA_72.1
GF0044976	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00082_mRNA_56.1
GF0044975	0	0	1	LRR receptor-like serine/threonine-protein kinase ERL1 (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)	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); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Leucine-rich repeat [IPR001611] (1); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00082_mRNA_51.1
GF0044974	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00082_mRNA_5.1
GF0044973	0	0	1	Metacaspase 1 isoform 2 (1)		Caspase-like domain [IPR029030] (1)	-	-	P_trifoliata_00082_mRNA_4.1
GF0044972	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00082_mRNA_23.1
GF0044971	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00082_mRNA_2.1
GF0044970	0	0	1	Hypothetical protein (1)		Caspase-like domain [IPR029030] (1)	-	-	P_trifoliata_00082_mRNA_1.1
GF0044969	0	0	1	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	-	P_trifoliata_00081_mRNA_86.1
GF0044968	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00081_mRNA_84.1
GF0044967	0	0	1	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 superfamily, zinc-type [IPR002085] (1); GroES-like [IPR011032] (1)	-	-	P_trifoliata_00081_mRNA_8.1
GF0044966	0	0	1	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); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Protein kinase-like domain [IPR011009] (1)	-	-	P_trifoliata_00081_mRNA_54.1
GF0044965	0	0	1	Bidirectional sugar transporter SWEET2a (1)	integral component of membrane [GO:0016021 cellular_component] (1)	SWEET sugar transporter [IPR004316] (1)	-	-	P_trifoliata_00081_mRNA_39.1
GF0044964	0	0	1	Meiosis protein mei2 (1)	nucleic acid binding [GO:0003676 molecular_function] (1); nucleotide binding [GO:0000166 molecular_function] (1)	RNA recognition motif domain [IPR000504] (1); RNA recognition motif 2 [IPR007201] (1); Nucleotide-binding alpha-beta plait domain [IPR012677] (1)	-	-	P_trifoliata_00081_mRNA_28.1
GF0044963	0	0	1	Hypothetical protein (1)		Probable transposase, Ptta/En/Spm, plant [IPR004252] (1)	-	-	P_trifoliata_00081_mRNA_22.1
GF0044962	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00081_mRNA_19.1
GF0044961	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00081_mRNA_18.1
GF0044960	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00081_mRNA_17.1
GF0044959	0	0	1	Hypothetical protein (1)		The fantastic four family [IPR021410] (1)	-	-	P_trifoliata_00081_mRNA_12.1
GF0044958	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00081_mRNA_1.1
GF0044957	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00080_mRNA_8.1
GF0044956	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00080_mRNA_69.1
GF0044955	0	0	1	Homogentisate phytyltransferase (1)	integral component of membrane [GO:0016021 cellular_component] (1); prenyltransferase activity [GO:0004659 molecular_function] (1)	UbiA prenyltransferase family [IPR000537] (1)	-	-	P_trifoliata_00080_mRNA_68.1
GF0044954	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00080_mRNA_62.1
GF0044953	0	0	1	Hypothetical protein (1)	(1->3)-beta-D-glucan biosynthetic process [GO:0006075 biological_process] (1); 1,3-beta-D-glucan synthase activity [GO:0003843 molecular_function] (1); 1,3-beta-D-glucan synthase complex [GO:0000148 cellular_component] (1); membrane [GO:0016020 cellular_component] (1)	Glycosyl transferase, family 48 [IPR003440] (1)	-	-	P_trifoliata_00080_mRNA_60.1
GF0044952	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00080_mRNA_58.1
GF0044951	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00080_mRNA_57.1
GF0044950	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00080_mRNA_53.1
GF0044949	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00080_mRNA_52.1
GF0044948	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00080_mRNA_49.1
GF0044947	0	0	1	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); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Protein kinase domain [IPR000719] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Protein kinase-like domain [IPR011009] (1)	-	-	P_trifoliata_00080_mRNA_47.1
GF0044946	0	0	1	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	-	-	P_trifoliata_00080_mRNA_37.1
GF0044945	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Protein of unknown function DUF247, plant [IPR004158] (1); Zinc finger, CCHC-type [IPR001878] (1); Domain of unknown function DUF4283 [IPR025558] (1)	-	-	P_trifoliata_00080_mRNA_36.1
GF0044944	0	0	1	UPF0481 protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	-	P_trifoliata_00080_mRNA_33.1
GF0044943	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00080_mRNA_3.1
GF0044942	0	0	1	Hypothetical protein (1)	photosystem I [GO:0009522 cellular_component] (1); chlorophyll binding [GO:0016168 molecular_function] (1); membrane [GO:0016020 cellular_component] (1); photosynthesis [GO:0015979 biological_process] (1)	Photosystem I PsaK, reaction centre, plant [IPR017493] (1); Photosystem I PsaG/PsaK domain [IPR023618] (1); Photosystem I PsaG/PsaK protein [IPR000549] (1); Protein of unknown function DUF247, plant [IPR004158] (1)	-	-	P_trifoliata_00080_mRNA_28.1
GF0044941	0	0	1	Hypothetical protein (1)		PGG domain [IPR026961] (1)	-	-	P_trifoliata_00080_mRNA_2.1
GF0044940	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00080_mRNA_14.1
GF0044939	0	0	1	Ankyrin repeat family protein, putative (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat-containing domain [IPR020683] (1); Ankyrin repeat [IPR002110] (1)	-	-	P_trifoliata_00080_mRNA_1.1
GF0044938	0	0	1	Hypothetical protein (1)	binding [GO:0005488 molecular_function] (1)	Armadillo-like helical [IPR011989] (1); Armadillo-type fold [IPR016024] (1)	-	-	P_trifoliata_00079_mRNA_91.1
GF0044937	0	0	1	Hypothetical protein (1)	integral component of membrane [GO:0016021 cellular_component] (1); ATPase activity [GO:0016887 molecular_function] (1); transport [GO:0006810 biological_process] (1); ATPase activity, coupled to transmembrane movement of substances [GO:0042626 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1); transmembrane transport [GO:0055085 biological_process] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); ABC transporter type 1, transmembrane domain [IPR011527] (1); ABC transporter-like [IPR003439] (1)	-	-	P_trifoliata_00079_mRNA_89.1
GF0044936	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00079_mRNA_82.1
GF0044935	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00079_mRNA_8.1
GF0044934	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00079_mRNA_76.1
GF0044933	0	0	1	Hypothetical protein (1)		Pyrrolo-quinoline quinone repeat [IPR002372] (1); Quinoprotein alcohol dehydrogenase-like superfamily [IPR011047] (1); Pyrrolo-quinoline quinone beta-propeller repeat [IPR018391] (1); Quinoprotein alcohol dehydrogenase-like domain [IPR027295] (1)	-	-	P_trifoliata_00079_mRNA_70.1
GF0044932	0	0	1	Hypothetical protein (1)		Pectin lyase fold [IPR012334] (1); Pectin lyase fold/virulence factor [IPR011050] (1); AmbAllergen [IPR018082] (1)	-	-	P_trifoliata_00079_mRNA_61.1
GF0044931	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00079_mRNA_6.1
GF0044930	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00079_mRNA_59.1
GF0044929	0	0	1	Putative mitochondrial chaperone BCS1-B (1)	ATP binding [GO:0005524 molecular_function] (1)	ATPase, AAA-type, conserved site [IPR003960] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); ATPase, AAA-type, core [IPR003959] (1); AAA+ ATPase domain [IPR003593] (1)	-	-	P_trifoliata_00079_mRNA_41.1
GF0044928	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00079_mRNA_4.1
GF0044927	0	0	1	Hypothetical protein (1)		AAA-type ATPase, N-terminal domain [IPR025753] (1)	-	-	P_trifoliata_00079_mRNA_38.1
GF0044926	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00079_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*
GF0044925	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1); hydrolase activity [GO:0016787 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); NUDIX hydrolase domain-like [IPR015797] (1); NUDIX hydrolase domain [IPR000086] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	-	-	P_trifoliata_00079_mRNA_2.1
GF0044924	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00079_mRNA_13.1
GF0044923	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00079_mRNA_1.1
GF0044922	0	0	1	Hypothetical protein (1)	membrane [GO:0016020 cellular_component] (1)	Calcium-dependent channel, 7TM region, putative phosphate [IPR003864] (1)	-	-	P_trifoliata_00078_mRNA_88.1
GF0044921	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00078_mRNA_78.1
GF0044920	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00078_mRNA_5.1
GF0044919	0	0	1	Hypothetical protein (1)		RNA polymerase I specific transcription initiation factor RRN3 [IPR007991] (1)	-	-	P_trifoliata_00078_mRNA_12.1
GF0044918	0	0	1	Hypothetical protein (1)	response to oxidative stress [GO:0006979 biological_process] (1); heme binding [GO:0020037 molecular_function] (1); peroxidase activity [GO:0004601 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Haem peroxidase [IPR010255] (1); Plant ascorbate peroxidase [IPR002207] (1); Peroxidase, active site [IPR019794] (1); Haem peroxidase, plant/fungal/bacterial [IPR002016] (1)	-	-	P_trifoliata_00078_mRNA_109.1
GF0044917	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00078_mRNA_107.1
GF0044916	0	0	1	Hypothetical protein (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); GTP binding [GO:0005525 molecular_function] (1); intracellular protein transport [GO:0006886 biological_process] (1); intracellular [GO:0005622 cellular_component] (1); GTPase activity [GO:0003924 molecular_function] (1); tRNA processing [GO:0008033 biological_process] (1); protein transport [GO:0015031 biological_process] (1)	Small GTPase superfamily, Ras type [IPR020849] (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); tRNA dimethylallyltransferase [IPR018022] (1); Ran GTPase [IPR002041] (1); Small GTPase superfamily, Rab type [IPR003579] (1)	-	-	P_trifoliata_00078_mRNA_103.1
GF0044915	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00077_mRNA_85.1
GF0044914	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00077_mRNA_83.1
GF0044913	0	0	1	Sulfotransferase (1)	sulfotransferase activity [GO:0008146 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Sulfotransferase domain [IPR000863] (1)	-	-	P_trifoliata_00077_mRNA_82.1
GF0044912	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00077_mRNA_78.1
GF0044911	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00077_mRNA_77.1
GF0044910	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00077_mRNA_75.1
GF0044909	0	0	1	50S ribosomal protein L12, chloroplastic (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 L7/L12, C-terminal/adaptor protein ClpS-like [IPR014719] (1); Ribosomal protein L7/L12, C-terminal [IPR013823] (1); Ribosomal protein L7/L12, oligomerisation [IPR008932] (1)	-	-	P_trifoliata_00077_mRNA_71.1
GF0044908	0	0	1	Hypothetical protein (1)		PWWP domain [IPR000313] (1)	-	-	P_trifoliata_00077_mRNA_70.1
GF0044907	0	0	1	Carbonate dehydratase (1)	carbonate dehydratase activity [GO:0004089 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1); carbon utilization [GO:0015976 biological_process] (1)	Carbonic anhydrase, prokaryotic-like, conserved site [IPR015892] (1); Carbonic anhydrase [IPR001765] (1)	-	-	P_trifoliata_00077_mRNA_57.1
GF0044906	0	0	1	Trypsin-like serine protease (1)	protein binding [GO:0005515 molecular_function] (1); serine-type endopeptidase activity [GO:0004252 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	PDZ domain [IPR001478] (1); Peptidase S1C [IPR001940] (1); Peptidase S1, PA clan [IPR009003] (1)	-	-	P_trifoliata_00077_mRNA_55.2
GF0044905	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00077_mRNA_48.1
GF0044904	0	0	1	Hypothetical protein (1)		Ribosomal protein L7Ae/L30e/S12e/Gadd45 [IPR004038] (1); 50S ribosomal protein L30e-like [IPR029064] (1)	-	-	P_trifoliata_00077_mRNA_4.1
GF0044903	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00077_mRNA_34.1
GF0044902	0	0	1	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)	-	-	P_trifoliata_00077_mRNA_27.1
GF0044901	0	0	1	Ubiquitin-conjugating enzyme E2-23 kDa (1)		Ubiquitin-conjugating enzyme/RWD-like [IPR016135] (1); Ubiquitin-conjugating enzyme E2 [IPR000608] (1)	-	-	P_trifoliata_00077_mRNA_17.1
GF0044900	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00077_mRNA_16.1
GF0044899	0	0	1	Hypothetical protein (1)	integral component of membrane [GO:0016021 cellular_component] (1); membrane [GO:0016020 cellular_component] (1); protein binding [GO:0005515 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1); serine-type endopeptidase activity [GO:0004252 molecular_function] (1)	Peptidase S1C [IPR001940] (1); PDZ domain [IPR001478] (1); EamA domain [IPR000620] (1); Peptidase S1, PA clan [IPR009003] (1)	-	-	P_trifoliata_00077_mRNA_10.1
GF0044898	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00076_mRNA_9.1
GF0044897	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00076_mRNA_74.1
GF0044896	0	0	1	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 L14 [IPR002784] (1); NmrA-like domain [IPR008030] (1); Ribosomal protein L2 domain 2 [IPR014722] (1); Translation protein SH3-like domain [IPR008991] (1); NAD(P)-binding domain [IPR016040] (1)	-	-	P_trifoliata_00076_mRNA_71.1
GF0044895	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00076_mRNA_69.1
GF0044894	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00076_mRNA_67.1
GF0044893	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00076_mRNA_61.1
GF0044892	0	0	1	Hypothetical protein (1)		Chloramphenicol acetyltransferase-like domain [IPR023213] (1)	-	-	P_trifoliata_00076_mRNA_6.1
GF0044891	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00076_mRNA_53.1
GF0044890	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00076_mRNA_52.1
GF0044889	0	0	1	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)	-	-	P_trifoliata_00076_mRNA_50.1
GF0044888	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00076_mRNA_5.1
GF0044887	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00076_mRNA_46.1
GF0044886	0	0	1	Similarity to non-LTR retroelement reverse transcriptase (1)		Reverse transcriptase domain [IPR000477] (1)	-	-	P_trifoliata_00076_mRNA_41.1
GF0044885	0	0	1	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)	-	-	P_trifoliata_00076_mRNA_4.1
GF0044884	0	0	1	Hypothetical protein (1)		Ankyrin repeat-containing domain [IPR020683] (1); PGG domain [IPR026961] (1)	-	-	P_trifoliata_00076_mRNA_39.1
GF0044883	0	0	1	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)	-	-	P_trifoliata_00076_mRNA_36.1
GF0044882	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00076_mRNA_33.1
GF0044881	0	0	1	Glutathione S-transferase tau 7, putative (1)		Glutathione S-transferase, C-terminal-like [IPR010987] (1); Glutathione S-transferase, C-terminal [IPR004046] (1)	-	-	P_trifoliata_00076_mRNA_32.1
GF0044880	0	0	1	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)	-	-	P_trifoliata_00076_mRNA_3.1
GF0044879	0	0	1	Hypothetical protein (1)		Transposase, MuDR, plant [IPR004332] (1)	-	-	P_trifoliata_00076_mRNA_23.1
GF0044878	0	0	1	Vinorine synthase (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)	-	-	P_trifoliata_00076_mRNA_17.1
GF0044877	0	0	1	Hypothetical protein (1)		Transposase, MuDR, plant [IPR004332] (1)	-	-	P_trifoliata_00076_mRNA_13.1
GF0044876	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00076_mRNA_12.1
GF0044875	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00075_mRNA_9.1
GF0044874	0	0	1	Basic 7S globulin (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Aspartic peptidase domain [IPR021109] (1); Xylanase inhibitor, N-terminal [IPR032861] (1); Xylanase inhibitor, C-terminal [IPR032799] (1); Aspartic peptidase A1 family [IPR001461] (1)	-	-	P_trifoliata_00075_mRNA_86.1

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*
GF0044873	0	0	1	Heterogeneous nuclear ribonucleoprotein A3 (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)	-	-	P_trifoliata_00075_mRNA_72.1
GF0044872	0	0	1	Rhodanese/cell cycle control phosphatase superfamily protein (1)		Rhodanese-like domain [IPR001763] (1)	-	-	P_trifoliata_00075_mRNA_63.1
GF0044871	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00075_mRNA_6.1
GF0044870	0	0	1	Hypothetical 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)	EamA domain [IPR000620] (1); WAT1-related protein [IPR030184] (1)	-	-	P_trifoliata_00075_mRNA_49.1
GF0044869	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00075_mRNA_48.1
GF0044868	0	0	1	Hypothetical protein (1)	integral component of membrane [GO:0016021 cellular_component] (1); transmembrane transporter activity [GO:0022857 molecular_function] (1)	WAT1-related protein [IPR030184] (1)	-	-	P_trifoliata_00075_mRNA_46.1
GF0044867	0	0	1	Hypothetical protein (1)		Bifunctional inhibitor/plant lipid transfer protein/seed storage helical domain [IPR016140] (1); Hydrophobic seed protein [IPR027923] (1)	-	-	P_trifoliata_00075_mRNA_38.1
GF0044866	0	0	1	Hypothetical protein (1)		Hydrophobic seed protein [IPR027923] (1); Bifunctional inhibitor/plant lipid transfer protein/seed storage helical domain [IPR016140] (1)	-	-	P_trifoliata_00075_mRNA_37.1
GF0044865	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00075_mRNA_2.1
GF0044864	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00075_mRNA_14.1
GF0044863	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00075_mRNA_13.1
GF0044862	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00075_mRNA_12.1
GF0044861	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00075_mRNA_11.1
GF0044860	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00074_mRNA_58.1
GF0044859	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00074_mRNA_45.1
GF0044858	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00074_mRNA_4.1
GF0044857	0	0	1	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	-	-	P_trifoliata_00074_mRNA_30.1
GF0044856	0	0	1	Hypothetical protein (1)		Cupredoxin [IPR008972] (1)	-	-	P_trifoliata_00074_mRNA_28.1
GF0044855	0	0	1	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)	-	-	P_trifoliata_00074_mRNA_2.1
GF0044854	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00074_mRNA_18.1
GF0044853	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00073_mRNA_92.1
GF0044852	0	0	1	Putative methyltransferase PMT18 (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)	-	-	P_trifoliata_00073_mRNA_90.1
GF0044851	0	0	1	Hypothetical protein (1)		Gag-polypeptide of LTR copia-type [IPR029472] (1)	-	-	P_trifoliata_00073_mRNA_9.1
GF0044850	0	0	1	ATP binding 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)	-	-	P_trifoliata_00073_mRNA_89.1
GF0044849	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00073_mRNA_8.1
GF0044848	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00073_mRNA_78.1
GF0044847	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00073_mRNA_62.1
GF0044846	0	0	1	UPF0481 protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	-	P_trifoliata_00073_mRNA_60.1
GF0044845	0	0	1	Glutamate receptor (1)		Periplasmic binding protein-like I [IPR028082] (1); Receptor, ligand binding region [IPR001828] (1); Solute-binding protein family 3/N-terminal domain of MltF [IPR001638] (1)	-	-	P_trifoliata_00073_mRNA_6.1
GF0044844	0	0	1	UPF0481 protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	-	P_trifoliata_00073_mRNA_56.1
GF0044843	0	0	1	Putative aarF domain-containing protein kinase, chloroplastic (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1)	UbiB domain [IPR004147] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	-	-	P_trifoliata_00073_mRNA_49.1
GF0044842	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00073_mRNA_43.1
GF0044841	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00073_mRNA_41.1
GF0044840	0	0	1	Glutamate receptor (1)	membrane [GO:0016020 cellular_component] (1); ionotropic glutamate receptor activity [GO:0004970 molecular_function] (1)	Solute-binding protein family 3/N-terminal domain of MltF [IPR001638] (1); Ionotropic glutamate receptor [IPR001320] (1); Receptor, ligand binding region [IPR001828] (1); Periplasmic binding protein-like I [IPR028082] (1)	-	-	P_trifoliata_00073_mRNA_4.1
GF0044839	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00073_mRNA_37.1
GF0044838	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00073_mRNA_3.1
GF0044837	0	0	1	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	-	P_trifoliata_00073_mRNA_29.1
GF0044836	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00073_mRNA_26.1
GF0044835	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00073_mRNA_13.1
GF0044834	0	0	1	Glutamate receptor (1)	membrane [GO:0016020 cellular_component] (1); ionotropic glutamate receptor activity [GO:0004970 molecular_function] (1)	Periplasmic binding protein-like I [IPR028082] (1); Receptor, ligand binding region [IPR001828] (1); Ionotropic glutamate receptor [IPR001320] (1); Solute-binding protein family 3/N-terminal domain of MltF [IPR001638] (1)	-	-	P_trifoliata_00073_mRNA_1.1
GF0044833	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00072_mRNA_93.1
GF0044832	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00072_mRNA_9.1
GF0044831	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00072_mRNA_88.1
GF0044830	0	0	1	Hypothetical protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	-	P_trifoliata_00072_mRNA_84.1
GF0044829	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00072_mRNA_8.1
GF0044828	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00072_mRNA_74.1
GF0044827	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00072_mRNA_73.1
GF0044826	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00072_mRNA_72.1
GF0044825	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00072_mRNA_71.1
GF0044824	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00072_mRNA_70.1
GF0044823	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00072_mRNA_69.1
GF0044822	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00072_mRNA_64.1
GF0044821	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00072_mRNA_51.1
GF0044820	0	0	1	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)	-	-	P_trifoliata_00072_mRNA_49.1
GF0044819	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00072_mRNA_47.1
GF0044818	0	0	1	Acyl-protein thioesterase 2 (1)	hydrolase activity [GO:0016787 molecular_function] (1)	Alpha/Beta hydrolase fold [IPR029058] (1); Phospholipase/carboxylesterase/thioesterase [IPR003140] (1)	-	-	P_trifoliata_00072_mRNA_27.1
GF0044817	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00072_mRNA_15.1
GF0044816	0	0	1	Disease resistance protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00071_mRNA_97.1
GF0044815	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00071_mRNA_8.1
GF0044814	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00071_mRNA_60.1
GF0044813	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00071_mRNA_5.1
GF0044812	0	0	1	Hypothetical protein (1)	thiamine pyrophosphate binding [GO:0030976 molecular_function] (1)	Thiamine pyrophosphate enzyme, N-terminal TPP-binding domain [IPR012001] (1); Thiamin diphosphate-binding fold [IPR029061] (1)	-	-	P_trifoliata_00071_mRNA_48.1
GF0044811	0	0	1	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); Multicopper oxidases, conserved site [IPR033138] (1); Multicopper oxidase, type 2 [IPR011706] (1); Cupredoxin [IPR008972] (1); Multicopper oxidase, type 3 [IPR011707] (1); Multicopper oxidase, copper-binding site [IPR002355] (1)	-	-	P_trifoliata_00071_mRNA_41.1
GF0044810	0	0	1	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)	-	-	P_trifoliata_00071_mRNA_32.1
GF0044809	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00071_mRNA_15.1
GF0044808	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00071_mRNA_13.1
GF0044807	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00071_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*
GF0044806	0	0	1	TRNA pseudouridine synthase A (1)	RNA modification [GO:0009451 biological_process] (1); pseudouridine synthase activity [GO:0009982 molecular_function] (1); RNA binding [GO:0003723 molecular_function] (1); pseudouridine synthesis [GO:0001522 biological_process] (1)	Pseudouridine synthase I, TruA, alpha/beta domain [IPR020097] (1); Pseudouridine synthase I, TruA [IPR001406] (1); Pseudouridine synthase I, TruA, N-terminal [IPR020094] (1); Pseudouridine synthase, catalytic domain [IPR020103] (1); Pseudouridine synthase I, TruA, C-terminal [IPR020095] (1)	-	-	P_trifoliata_00070_mRNA_94.1
GF0044805	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00070_mRNA_78.1
GF0044804	0	0	1	Hypothetical protein (1)		ABC-transporter extracellular N-terminal domain [IPR029481] (1)	-	-	P_trifoliata_00070_mRNA_76.1
GF0044803	0	0	1	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)	ABC transporter-like [IPR003439] (1); ABC-2 type transporter [IPR013525] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); ABC-transporter extracellular N-terminal domain [IPR029481] (1); Plant PDR ABC transporter associated [IPR013581] (1)	-	-	P_trifoliata_00070_mRNA_75.1
GF0044802	0	0	1	ADP-ribosylation factor A1F (1)	intracellular [GO:0005622 cellular_component] (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 GTP-binding protein domain [IPR005225] (1); Small GTPase superfamily, Rab type [IPR003579] (1); Small GTPase superfamily, ARF type [IPR024156] (1); Small GTPase superfamily, ARF/SAR type [IPR006689] (1)	-	-	P_trifoliata_00070_mRNA_61.1
GF0044801	0	0	1	Hypothetical protein (1)		DnaJ domain [IPR001623] (1); Cleavage inducing molecular chaperone, Jiv [IPR032843] (1)	-	-	P_trifoliata_00070_mRNA_36.2
GF0044800	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00070_mRNA_35.1
GF0044799	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00070_mRNA_31.1
GF0044798	0	0	1	Hypothetical protein (1)	peptidyl-prolyl cis-trans isomerase activity [GO:0003755 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1); nucleotide binding [GO:0000166 molecular_function] (1); protein peptidyl-prolyl isomerization [GO:0000413 biological_process] (1); protein folding [GO:0006457 biological_process] (1)	RNA recognition motif domain [IPR000504] (1); Cyclophilin-type peptidyl-prolyl cis-trans isomerase [IPR024936] (1); Nucleotide-binding alpha-beta plait domain [IPR012677] (1); Cyclophilin-like domain [IPR029000] (1); Cyclophilin-type peptidyl-prolyl cis-trans isomerase domain [IPR002130] (1)	-	-	P_trifoliata_00070_mRNA_30.1
GF0044797	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00069_mRNA_94.1
GF0044796	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00069_mRNA_93.1
GF0044795	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00069_mRNA_91.1
GF0044794	0	0	1	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)	-	-	P_trifoliata_00069_mRNA_9.1
GF0044793	0	0	1	Putative ribonuclease H protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	-	P_trifoliata_00069_mRNA_88.1
GF0044792	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Domain of unknown function DUF4218 [IPR025452] (1)	-	-	P_trifoliata_00069_mRNA_87.1
GF0044791	0	0	1	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1); Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	-	P_trifoliata_00069_mRNA_84.1
GF0044790	0	0	1	UDP-glycosyltransferase 73B5 (1)	transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	-	-	P_trifoliata_00069_mRNA_8.1
GF0044789	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00069_mRNA_78.1
GF0044788	0	0	1	Hypothetical protein (1)		Probable transposase, Ptta/En/Spm, plant [IPR004252] (1)	-	-	P_trifoliata_00069_mRNA_77.1
GF0044787	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00069_mRNA_76.1
GF0044786	0	0	1	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); Transposase, MuDR, plant [IPR004332] (1); Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00069_mRNA_73.1
GF0044785	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00069_mRNA_68.1
GF0044784	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00069_mRNA_66.1
GF0044783	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00069_mRNA_65.1
GF0044782	0	0	1	Pentatricopeptide (PPR) repeat protein (1)	protein binding [GO:0005515 molecular_function] (1)	Pentatricopeptide repeat [IPR002885] (1); Tetratricopeptide-like helical domain [IPR011990] (1)	-	-	P_trifoliata_00069_mRNA_62.1
GF0044781	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00069_mRNA_61.1
GF0044780	0	0	1	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)	-	-	P_trifoliata_00069_mRNA_52.1
GF0044779	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00069_mRNA_5.1
GF0044778	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	-	P_trifoliata_00069_mRNA_45.1
GF0044777	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00069_mRNA_4.1
GF0044776	0	0	1	Phosphoglycerate dehydrogenase (1)	NAD binding [GO:0051287 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); amino acid binding [GO:0016597 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding domain [IPR006140] (1); ACT domain [IPR002912] (1); D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding domain conserved site [IPR029753] (1); NAD(P)-binding domain [IPR016040] (1); Allosteric substrate binding domain [IPR029009] (1); D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding domain conserved site 1 [IPR029752] (1); S-adenosyl-L-homocysteine hydrolase, NAD binding domain [IPR015878] (1)	-	-	P_trifoliata_00069_mRNA_33.1
GF0044775	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00069_mRNA_3.1
GF0044774	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00069_mRNA_28.1
GF0044773	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00069_mRNA_24.1
GF0044772	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00069_mRNA_22.1
GF0044771	0	0	1	Leucine-rich repeat (LRR) family protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00069_mRNA_15.1
GF0044770	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Kelch-type beta propeller [IPR015915] (1); Pentatricopeptide repeat [IPR002885] (1)	-	-	P_trifoliata_00069_mRNA_12.1
GF0044769	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00069_mRNA_1.1
GF0044768	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00068_mRNA_85.1
GF0044767	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00068_mRNA_80.1
GF0044766	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00068_mRNA_7.1
GF0044765	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00068_mRNA_54.1
GF0044764	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00068_mRNA_52.1
GF0044763	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00068_mRNA_51.1
GF0044762	0	0	1	Hypothetical protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	-	P_trifoliata_00068_mRNA_50.1
GF0044761	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00068_mRNA_47.1
GF0044760	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00068_mRNA_46.1
GF0044759	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00068_mRNA_43.1
GF0044758	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00068_mRNA_38.1
GF0044757	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00068_mRNA_34.1
GF0044756	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00068_mRNA_33.1
GF0044755	0	0	1	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	B3 DNA binding domain [IPR003340] (1); DNA-binding pseudobarrel domain [IPR015300] (1)	-	-	P_trifoliata_00068_mRNA_32.1
GF0044754	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00068_mRNA_25.1
GF0044753	0	0	1	CDNA clone:002-110-H12, full insert sequence (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)	-	-	P_trifoliata_00068_mRNA_22.1
GF0044752	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00068_mRNA_21.1
GF0044751	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00068_mRNA_16.1
GF0044750	0	0	1	Feronia receptor-like kinase (1)		Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Malectin-like carbohydrate-binding domain [IPR024788] (1)	-	-	P_trifoliata_00068_mRNA_13.1
GF0044749	0	0	1	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)	-	-	P_trifoliata_00068_mRNA_12.1
GF0044748	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00068_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*
GF0044747	0	0	1	Argininosuccinate synthase (1)	ATP binding [GO:0005524 molecular_function] (1); argininosuccinate synthase activity [GO:0004055 molecular_function] (1); arginine biosynthetic process [GO:0006526 biological_process] (1)	Argininosuccinate synthetase, catalytic/multimerisation domain body [IPR024074] (1); Argininosuccinate synthase, conserved site [IPR018223] (1); Rossmann-like alpha/beta/alpha sandwich fold [IPR014729] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Argininosuccinate synthase [IPR001518] (1)	-	-	P_trifoliata_00067_mRNA_81.1
GF0044746	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00067_mRNA_6.1
GF0044745	0	0	1	Hypothetical protein (1)	transcription, DNA-templated [GO:0006351 biological_process] (1)	Transcription elongation factor S-II, central domain [IPR003618] (1)	-	-	P_trifoliata_00067_mRNA_54.1
GF0044744	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00067_mRNA_53.1
GF0044743	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00067_mRNA_52.1
GF0044742	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00067_mRNA_45.1
GF0044741	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00067_mRNA_38.1
GF0044740	0	0	1	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein (1)		Bifunctional inhibitor/plant lipid transfer protein/seed storage helical domain [IPR016140] (1)	-	-	P_trifoliata_00067_mRNA_32.1
GF0044739	0	0	1	Peptidyl-prolyl cis-trans isomerases isoform 1 (1)	peptidyl-prolyl cis-trans isomerase activity [GO:0003755 molecular_function] (1); protein folding [GO:0006457 biological_process] (1); protein peptidyl-prolyl isomerization [GO:0000413 biological_process] (1)	Cyclophilin-like domain [IPR029000] (1); Cyclophilin-type peptidyl-prolyl cis-trans isomerase domain [IPR002130] (1)	-	-	P_trifoliata_00067_mRNA_31.1
GF0044738	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00067_mRNA_3.1
GF0044737	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00067_mRNA_28.1
GF0044736	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00067_mRNA_14.1
GF0044735	0	0	1	Hypothetical protein (1)	histone binding [GO:0042393 molecular_function] (1)	PUA-like domain [IPR015947] (1); SRA-YDG [IPR003105] (1)	-	-	P_trifoliata_00067_mRNA_12.1
GF0044734	0	0	1	Exostosin family protein (1)		Exostosin-like [IPR004263] (1)	-	-	P_trifoliata_00067_mRNA_1.1
GF0044733	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00066_mRNA_99.1
GF0044732	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00066_mRNA_93.1
GF0044731	0	0	1	Hypothetical protein (1)		NAD(P)-binding domain [IPR016040] (1)	-	-	P_trifoliata_00066_mRNA_91.1
GF0044730	0	0	1	Hypothetical protein (1)		NAD(P)-binding domain [IPR016040] (1)	-	-	P_trifoliata_00066_mRNA_89.1
GF0044729	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00066_mRNA_81.1
GF0044728	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00066_mRNA_47.1
GF0044727	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00066_mRNA_4.1
GF0044726	0	0	1	Hypothetical protein (1)	metal ion binding [GO:0046872 molecular_function] (1)	Metallothionein, family 15, plant [IPR000347] (1)	-	-	P_trifoliata_00066_mRNA_29.1
GF0044725	0	0	1	Putative phosphatase 2C 4-like protein (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)	PPM-type phosphatase domain [IPR001932] (1); Protein phosphatase 2C family [IPR015655] (1)	-	-	P_trifoliata_00066_mRNA_26.1
GF0044724	0	0	1	17.6 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)	-	-	P_trifoliata_00066_mRNA_20.1
GF0044723	0	0	1	SLT1 protein (1)			-	-	P_trifoliata_00066_mRNA_14.1
GF0044722	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00066_mRNA_13.1
GF0044721	0	0	1	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); nucleus [GO:0005634 cellular_component] (1); nucleosome assembly [GO:0006334 biological_process] (1); amino acid binding [GO:0016597 molecular_function] (1); protein heterodimerization activity [GO:0046982 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1); nucleosome [GO:0000786 cellular_component] (1)	Histone-fold [IPR009072] (1); Histone H4 [IPR001951] (1); Histone H4, conserved site [IPR019809] (1); ACT domain [IPR002912] (1)	-	-	P_trifoliata_00066_mRNA_1.1
GF0044720	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00065_mRNA_90.1
GF0044719	0	0	1	Hypothetical protein (1)		NAD(P)-binding domain [IPR016040] (1)	-	-	P_trifoliata_00065_mRNA_87.1
GF0044718	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00065_mRNA_86.1
GF0044717	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00065_mRNA_7.1
GF0044716	0	0	1	Hypothetical protein (1)		Protein of unknown function DUF1191 [IPR010605] (1)	-	-	P_trifoliata_00065_mRNA_62.1
GF0044715	0	0	1	Hypothetical protein (1)		SGNH hydrolase-type esterase domain [IPR013830] (1)	-	-	P_trifoliata_00065_mRNA_61.1
GF0044714	0	0	1	Enhancer of triptychon and caprice 2 (1)	DNA binding [GO:0003677 molecular_function] (1)	SANT/Myb domain [IPR001005] (1); Homeodomain-like [IPR009057] (1)	-	-	P_trifoliata_00065_mRNA_44.1
GF0044713	0	0	1	Thylakoid rhodanese-like, putative isoform 1 (1)		Rhodanese-like domain [IPR001763] (1)	-	-	P_trifoliata_00065_mRNA_42.1
GF0044712	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00065_mRNA_4.1
GF0044711	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00065_mRNA_23.1
GF0044710	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00065_mRNA_20.1
GF0044709	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00065_mRNA_11.1
GF0044708	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00064_mRNA_99.1
GF0044707	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00064_mRNA_93.1
GF0044706	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00064_mRNA_91.1
GF0044705	0	0	1	4-hydroxy-3-methylbut-2-enyl diphosphatereductase (1)	dimethylallyl diphosphate biosynthetic process [GO:0050992 biological_process] (1); metal ion binding [GO:0046872 molecular_function] (1); isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway [GO:0019288 biological_process] (1); 4-hydroxy-3-methylbut-2-en-1-yl diphosphate reductase activity [GO:0051745 molecular_function] (1)	4-hydroxy-3-methylbut-2-enyl diphosphate reductase [IPR003451] (1)	-	-	P_trifoliata_00064_mRNA_79.1
GF0044704	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00064_mRNA_78.1
GF0044703	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00064_mRNA_77.1
GF0044702	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00064_mRNA_76.1
GF0044701	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00064_mRNA_75.1
GF0044700	0	0	1	4-hydroxy-3-methylbut-2-enyl diphosphate reductase (1)	dimethylallyl diphosphate biosynthetic process [GO:0050992 biological_process] (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)	4-hydroxy-3-methylbut-2-enyl diphosphate reductase [IPR003451] (1)	-	-	P_trifoliata_00064_mRNA_73.1
GF0044699	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00064_mRNA_72.1
GF0044698	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00064_mRNA_71.1
GF0044697	0	0	1	4-hydroxy-3-methylbut-2-enyl diphosphate reductase (1)	dimethylallyl diphosphate biosynthetic process [GO:0050992 biological_process] (1); metal ion binding [GO:0046872 molecular_function] (1); isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway [GO:0019288 biological_process] (1); 4-hydroxy-3-methylbut-2-en-1-yl diphosphate reductase activity [GO:0051745 molecular_function] (1)	4-hydroxy-3-methylbut-2-enyl diphosphate reductase [IPR003451] (1)	-	-	P_trifoliata_00064_mRNA_70.1
GF0044696	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00064_mRNA_7.1
GF0044695	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00064_mRNA_64.1
GF0044694	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00064_mRNA_60.1
GF0044693	0	0	1	Hypothetical protein (1)		TB2/DP1/HVA22-related protein [IPR004345] (1)	-	-	P_trifoliata_00064_mRNA_53.1
GF0044692	0	0	1	Phosphate transporter (1)	transmembrane transport [GO:0055085 biological_process] (1); integral component of membrane [GO:0016021 cellular_component] (1); transmembrane transporter activity [GO:0022857 molecular_function] (1)	Major facilitator, sugar transporter-like [IPR005828] (1); Major facilitator superfamily domain [IPR020846] (1)	-	-	P_trifoliata_00064_mRNA_46.1
GF0044691	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00064_mRNA_41.1
GF0044690	0	0	1	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	-	P_trifoliata_00064_mRNA_37.1
GF0044689	0	0	1	Hypothetical protein (1)		Arabidopsis retrotransposon Orf1 [IPR004312] (1)	-	-	P_trifoliata_00064_mRNA_32.1
GF0044688	0	0	1	BURP domain-containing protein (1)		BURP domain [IPR004873] (1)	-	-	P_trifoliata_00064_mRNA_31.1
GF0044687	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00064_mRNA_3.1
GF0044686	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00064_mRNA_28.1
GF0044685	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00064_mRNA_25.1

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*
GF0044684	0	0	1	Hypothetical protein (1)		Myb/SANT-like domain [IPR024752] (1); P-type ATPase, transmembrane domain [IPR023298] (1)	-	-	P_trifoliata_00064_mRNA_103.1
GF0044683	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00064_mRNA_100.1
GF0044682	0	0	1	Hypothetical protein (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)	-	-	P_trifoliata_00063_mRNA_93.1
GF0044681	0	0	1	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); ATPase, AAA-type, core [IPR003959] (1)	-	-	P_trifoliata_00063_mRNA_92.1
GF0044680	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00063_mRNA_77.1
GF0044679	0	0	1	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	-	P_trifoliata_00063_mRNA_75.1
GF0044678	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00063_mRNA_74.1
GF0044677	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00063_mRNA_48.1
GF0044676	0	0	1	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, GRF-type [IPR010666] (1)	-	-	P_trifoliata_00063_mRNA_45.1
GF0044675	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00063_mRNA_42.1
GF0044674	0	0	1	Hypothetical protein (1)	strictosidine synthase activity [GO:0016844 molecular_function] (1); biosynthetic process [GO:0009058 biological_process] (1)	Six-bladed beta-propeller, TolB-like [IPR011042] (1); Strictosidine synthase [IPR004141] (1)	-	-	P_trifoliata_00063_mRNA_4.1
GF0044673	0	0	1	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)	-	-	P_trifoliata_00063_mRNA_32.1
GF0044672	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00063_mRNA_3.1
GF0044671	0	0	1	Hypothetical protein (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)	-	-	P_trifoliata_00063_mRNA_25.1
GF0044670	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00063_mRNA_22.1
GF0044669	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00063_mRNA_21.1
GF0044668	0	0	1	Monosacharide transport protein (1)			-	-	P_trifoliata_00063_mRNA_20.1
GF0044667	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00063_mRNA_15.1
GF0044666	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	CCT domain [IPR010402] (1)	-	-	P_trifoliata_00063_mRNA_11.1
GF0044665	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00062_mRNA_9.1
GF0044664	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00062_mRNA_86.1
GF0044663	0	0	1	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); Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00062_mRNA_83.1
GF0044662	0	0	1	Probably inactive leucine-rich repeat receptor-like protein 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)	-	-	P_trifoliata_00062_mRNA_82.1
GF0044661	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00062_mRNA_74.1
GF0044660	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00062_mRNA_73.1
GF0044659	0	0	1	Hypothetical protein (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)	-	-	P_trifoliata_00062_mRNA_69.1
GF0044658	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00062_mRNA_65.1
GF0044657	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00062_mRNA_61.1
GF0044656	0	0	1	Dicer-like protein isoform 6 (1)	endoribonuclease activity, producing 5'-phosphomonoesters [GO:0016891 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1); ribonuclease III activity [GO:0004525 molecular_function] (1); RNA processing [GO:0006396 biological_process] (1); RNA binding [GO:0003723 molecular_function] (1)	PAZ domain [IPR003100] (1); Helicase, C-terminal [IPR001650] (1); Double-stranded RNA-binding domain [IPR014720] (1); Dicer dimerisation domain [IPR005034] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Ribonuclease III domain [IPR000999] (1)	-	-	P_trifoliata_00062_mRNA_6.1
GF0044655	0	0	1	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)	-	-	P_trifoliata_00062_mRNA_57.1
GF0044654	0	0	1	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	-	P_trifoliata_00062_mRNA_54.1
GF0044653	0	0	1	Polynucleotidyl transferase, Ribonuclease H fold (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	-	P_trifoliata_00062_mRNA_32.1
GF0044652	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00062_mRNA_19.1
GF0044651	0	0	1	LRR receptor-like serine/threonine-protein kinase EFR (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); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1)	-	-	P_trifoliata_00062_mRNA_18.1
GF0044650	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00062_mRNA_12.1
GF0044649	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00062_mRNA_11.1
GF0044648	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00062_mRNA_10.1
GF0044647	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00061_mRNA_69.1
GF0044646	0	0	1	Hypothetical protein (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 family 17 [IPR000490] (1); Glycoside hydrolase superfamily [IPR017853] (1)	-	-	P_trifoliata_00061_mRNA_68.1
GF0044645	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00061_mRNA_66.1
GF0044644	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00061_mRNA_57.1
GF0044643	0	0	1	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)	-	-	P_trifoliata_00061_mRNA_46.1
GF0044642	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00061_mRNA_45.1
GF0044641	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00061_mRNA_44.1
GF0044640	0	0	1	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 binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (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)	-	-	P_trifoliata_00061_mRNA_43.1
GF0044639	0	0	1	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)	-	-	P_trifoliata_00061_mRNA_4.1
GF0044638	0	0	1	Hypothetical protein (1)	transport [GO:0006810 biological_process] (1); intracellular [GO:0005622 cellular_component] (1)	Nuclear transport factor 2 [IPR002075] (1); Nuclear transport factor 2, eukaryote [IPR018222] (1); NTF2-like domain [IPR032710] (1)	-	-	P_trifoliata_00061_mRNA_37.1
GF0044637	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00061_mRNA_31.1
GF0044636	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00061_mRNA_30.1
GF0044635	0	0	1	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	-	P_trifoliata_00061_mRNA_3.1
GF0044634	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00061_mRNA_27.1
GF0044633	0	0	1	Hypothetical protein (1)		P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	-	P_trifoliata_00061_mRNA_25.1
GF0044632	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00061_mRNA_22.1
GF0044631	0	0	1	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); ATPase activity [GO:0016887 molecular_function] (1)	ABC transporter-like [IPR003439] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	-	P_trifoliata_00061_mRNA_21.1
GF0044630	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00061_mRNA_16.1
GF0044629	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00061_mRNA_1.1
GF0044628	0	0	1	Hypothetical protein (1)		Hydrophobic seed protein [IPR027923] (1); Bifunctional inhibitor/plant lipid transfer protein/seed storage helical domain [IPR016140] (1)	-	-	P_trifoliata_00060_mRNA_87.1

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*
GF0044627	0	0	1	14 kDa proline-rich protein DC2.15 (1)		Hydrophobic seed protein [IPR027923] (1); Bifunctional inhibitor/plant lipid transfer protein/seed storage helical domain [IPR016140] (1)	-	-	P_trifoliata_00060_mRNA_85.1
GF0044626	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00060_mRNA_73.1
GF0044625	0	0	1	Plant VAP (1)	endoplasmic reticulum membrane [GO:0005789 cellular_component] (1)	PapD-like [IPR008962] (1); Vesicle-associated membrane-protein-associated protein [IPR016763] (1); Major sperm protein (MSP) domain [IPR000535] (1); Alpha crystallin/Hsp20 domain [IPR002068] (1); HSP20-like chaperone [IPR008978] (1)	-	-	P_trifoliata_00060_mRNA_70.1
GF0044624	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00060_mRNA_6.1
GF0044623	0	0	1	Ribosomal protein L15 (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 L23/L15e core domain [IPR012678] (1); Ribosomal protein L15e core domain [IPR024794] (1); Ribosomal protein L15e [IPR000439] (1)	-	-	P_trifoliata_00060_mRNA_43.1
GF0044622	0	0	1	Ethylene response factor 2 (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 [GO:0003677 molecular_function] (1)	DNA-binding domain [IPR016177] (1); AP2/ERF domain [IPR001471] (1)	-	-	P_trifoliata_00060_mRNA_35.1
GF0044621	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00060_mRNA_27.1
GF0044620	0	0	1	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	-	P_trifoliata_00060_mRNA_2.1
GF0044619	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00060_mRNA_17.1
GF0044618	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00060_mRNA_14.1
GF0044617	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00060_mRNA_13.1
GF0044616	0	0	1	Putative wall-associated receptor kinase-like 16 (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); 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)	-	-	P_trifoliata_00060_mRNA_11.1
GF0044615	0	0	1	Hypothetical protein (1)	GTPase activity [GO:0003924 molecular_function] (1); GTP binding [GO:0005525 molecular_function] (1)	Transcription factor, GTP-binding domain [IPR000795] (1); Tr-type G domain, conserved site [IPR031157] (1); Translation protein, beta-barrel domain [IPR009000] (1); Small GTP-binding protein domain [IPR005225] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	-	P_trifoliata_00060_mRNA_1.1
GF0044614	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00059_mRNA_8.1
GF0044613	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00059_mRNA_7.1
GF0044612	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00059_mRNA_6.1
GF0044611	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00059_mRNA_47.1
GF0044610	0	0	1	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)	-	-	P_trifoliata_00059_mRNA_41.1
GF0044609	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00059_mRNA_4.1
GF0044608	0	0	1	Ribonuclease H (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	-	P_trifoliata_00059_mRNA_27.1
GF0044607	0	0	1	Hypothetical protein (1)		Zinc knuckle CX2CX4HX4C [IPR025836] (1)	-	-	P_trifoliata_00059_mRNA_26.1
GF0044606	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00059_mRNA_22.1
GF0044605	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00059_mRNA_19.1
GF0044604	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00059_mRNA_15.1
GF0044603	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00059_mRNA_13.1
GF0044602	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00059_mRNA_12.1
GF0044601	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00059_mRNA_11.1
GF0044600	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00059_mRNA_10.1
GF0044599	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00058_mRNA_88.1
GF0044598	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00058_mRNA_71.1
GF0044597	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00058_mRNA_70.1
GF0044596	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00058_mRNA_69.1
GF0044595	0	0	1	Hypothetical protein (1)		Prolamin-like domain [IPR008502] (1)	-	-	P_trifoliata_00058_mRNA_65.1
GF0044594	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00058_mRNA_6.1
GF0044593	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00058_mRNA_56.1
GF0044592	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00058_mRNA_5.1
GF0044591	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00058_mRNA_43.1
GF0044590	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00058_mRNA_38.1
GF0044589	0	0	1	Hypothetical protein (1)		Protein of unknown function DUF789 [IPR008507] (1)	-	-	P_trifoliata_00058_mRNA_36.1
GF0044588	0	0	1	Hypothetical protein (1)		AIR synthase-related protein, C-terminal domain [IPR010918] (1)	-	-	P_trifoliata_00058_mRNA_32.1
GF0044587	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00058_mRNA_29.1
GF0044586	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00058_mRNA_28.1
GF0044585	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00058_mRNA_26.1
GF0044584	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00058_mRNA_2.1
GF0044583	0	0	1	Hypothetical protein (1)	protein geranylgeranylation [GO:0018344 biological_process] (1); Rab geranylgeranyltransferase activity [GO:0004663 molecular_function] (1)	Geranylgeranyl transferase type-2 subunit beta [IPR026873] (1); Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (1)	-	-	P_trifoliata_00058_mRNA_15.1
GF0044582	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00058_mRNA_13.1
GF0044581	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00057_mRNA_99.1
GF0044580	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00057_mRNA_97.1
GF0044579	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00057_mRNA_96.1
GF0044578	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00057_mRNA_87.1
GF0044577	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00057_mRNA_80.1
GF0044576	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00057_mRNA_77.1
GF0044575	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00057_mRNA_76.1
GF0044574	0	0	1	Hypothetical protein (1)	exocyst [GO:0000145 cellular_component] (1); vesicle docking involved in exocytosis [GO:0006904 biological_process] (1)	Exocyst complex subunit Sec15-like [IPR007225] (1)	-	-	P_trifoliata_00057_mRNA_59.1
GF0044573	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00057_mRNA_56.1
GF0044572	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00057_mRNA_48.1
GF0044571	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00057_mRNA_47.1
GF0044570	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00057_mRNA_23.1
GF0044569	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00057_mRNA_16.1
GF0044568	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00057_mRNA_111.1
GF0044567	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00057_mRNA_110.1
GF0044566	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00057_mRNA_11.1
GF0044565	0	0	1	Cytochrome P450 86B1 (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)	-	-	P_trifoliata_00057_mRNA_104.1
GF0044564	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00057_mRNA_103.1
GF0044563	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00057_mRNA_102.1
GF0044562	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00057_mRNA_100.1
GF0044561	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00057_mRNA_1.1
GF0044560	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00056_mRNA_91.1
GF0044559	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00056_mRNA_85.1
GF0044558	0	0	1	E3 ubiquitin-protein ligase (1)	ubiquitin-dependent protein catabolic process [GO:0006511 biological_process] (1); ubiquitin-protein transferase activity [GO:0004842 molecular_function] (1); nucleus [GO:0005634 cellular_component] (1); protein ubiquitination [GO:0016567 biological_process] (1); multicellular organismal development [GO:0007275 biological_process] (1); zinc ion binding [GO:0008270 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Zinc finger, RING/FYVE/PHD-type [IPR013083] (1); SIAH-type domain [IPR013323] (1); Seven-in-absentia protein, TRAF-like domain [IPR018121] (1); Zinc finger, SIAH-type [IPR013010] (1); TRAF-like [IPR008974] (1); Zinc finger, RING-type [IPR001841] (1); E3 ubiquitin-protein ligase SIN-like [IPR004162] (1)	-	-	P_trifoliata_00056_mRNA_40.1
GF0044557	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00056_mRNA_32.1
GF0044556	0	0	1	Hypothetical protein (1)		WEB family [IPR008545] (1)	-	-	P_trifoliata_00056_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*
GF0044555	0	0	1	MATE efflux family protein 9 (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)	-	-	P_trifoliata_00056_mRNA_13.1
GF0044554	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00056_mRNA_12.1
GF0044553	0	0	1	Salutaridinol 7-O-acetyltransferase (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)	-	-	P_trifoliata_00056_mRNA_108.1
GF0044552	0	0	1	Protein trichome birefringence-like 33 (1)		PC-Esterase [IPR026057] (1); PMR5 N-terminal domain [IPR025846] (1); Trichome birefringence-like family [IPR029962] (1); Chloramphenicol acetyltransferase-like domain [IPR023213] (1)	-	-	P_trifoliata_00056_mRNA_107.1
GF0044551	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00055_mRNA_96.1
GF0044550	0	0	1	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FAR1 DNA binding domain [IPR004330] (1); FHY3/FAR1 family [IPR031052] (1)	-	-	P_trifoliata_00055_mRNA_94.1
GF0044549	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00055_mRNA_93.1
GF0044548	0	0	1	Hypothetical protein (1)		GroEL-like equatorial domain [IPR027413] (1); GroEL-like apical domain [IPR027409] (1)	-	-	P_trifoliata_00055_mRNA_73.1
GF0044547	0	0	1	Hypothetical protein (1)	actin filament binding [GO:0051015 molecular_function] (1); actin filament bundle assembly [GO:0051017 biological_process] (1); actin binding [GO:0003779 molecular_function] (1)	ADF-H/Gelsolin-like domain [IPR029006] (1); Villin-2/3/4/5, plant [IPR030009] (1); Gelsolin-like domain [IPR007123] (1); Villin/Gelsolin [IPR007122] (1)	-	-	P_trifoliata_00055_mRNA_61.1
GF0044546	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00055_mRNA_56.1
GF0044545	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00055_mRNA_38.1
GF0044544	0	0	1	Hypothetical protein (1)		Glycine-rich domain-containing protein-like [IPR009836] (1)	-	-	P_trifoliata_00055_mRNA_20.1
GF0044543	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00055_mRNA_18.1
GF0044542	0	0	1	Phosphomutase PMU1 (1)		Histidine phosphatase superfamily [IPR029033] (1); Histidine phosphatase superfamily, clade-1 [IPR013078] (1)	-	-	P_trifoliata_00055_mRNA_15.1
GF0044541	0	0	1	Phosphoglycerate mutase family protein (1)	catalytic activity [GO:0003824 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Phosphoglycerate/bisphosphoglycerate mutase, active site [IPR001345] (1); Histidine phosphatase superfamily, clade-1 [IPR013078] (1); Histidine phosphatase superfamily [IPR029033] (1)	-	-	P_trifoliata_00055_mRNA_13.1
GF0044540	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00055_mRNA_100.1
GF0044539	0	0	1	Phosphoglycerate mutase family protein (1)	metabolic process [GO:0008152 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1)	Histidine phosphatase superfamily [IPR029033] (1); Phosphoglycerate/bisphosphoglycerate mutase, active site [IPR001345] (1)	-	-	P_trifoliata_00055_mRNA_10.1
GF0044538	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00054_mRNA_90.1
GF0044537	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00054_mRNA_81.1
GF0044536	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00054_mRNA_65.1
GF0044535	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00054_mRNA_63.1
GF0044534	0	0	1	Vesicle-associated membrane protein 713 (1)	transport [GO:0006810 biological_process] (1)	Longin domain [IPR010908] (1); Longin-like domain [IPR011012] (1)	-	-	P_trifoliata_00054_mRNA_54.1
GF0044533	0	0	1	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)	-	-	P_trifoliata_00054_mRNA_50.1
GF0044532	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00054_mRNA_48.1
GF0044531	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00054_mRNA_43.1
GF0044530	0	0	1	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)	-	-	P_trifoliata_00054_mRNA_3.1
GF0044529	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00054_mRNA_108.1
GF0044528	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00053_mRNA_98.1
GF0044527	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00053_mRNA_97.1
GF0044526	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00053_mRNA_93.1
GF0044525	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00053_mRNA_84.1
GF0044524	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00053_mRNA_77.1
GF0044523	0	0	1	Cytochrome P450 82A4 (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 [IPR001128] (1)	-	-	P_trifoliata_00053_mRNA_75.1
GF0044522	0	0	1	Ninja-family protein AFP3 (1)	signal transduction [GO:0007165 biological_process] (1)	Jas TPL-binding domain [IPR032308] (1); Ninja family [IPR031307] (1)	-	-	P_trifoliata_00053_mRNA_73.1
GF0044521	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00053_mRNA_60.1
GF0044520	0	0	1	Cytochrome b5 (1)	heme binding [GO:0020037 molecular_function] (1)	Cytochrome b5, heme-binding site [IPR018506] (1); Cytochrome b5-like heme/steroid binding domain [IPR001199] (1)	-	-	P_trifoliata_00053_mRNA_42.1
GF0044519	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00053_mRNA_39.1
GF0044518	0	0	1	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1)	Chaperonin Cpn60/TCP-1 family [IPR002423] (1); GroEL-like equatorial domain [IPR027413] (1)	-	-	P_trifoliata_00053_mRNA_38.1
GF0044517	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00053_mRNA_33.1
GF0044516	0	0	1	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	MULE transposase domain [IPR018289] (1); FHY3/FAR1 family [IPR031052] (1)	-	-	P_trifoliata_00053_mRNA_31.1
GF0044515	0	0	1	AT3G24740 protein (1)		Protein of unknown function DUF1644 [IPR012866] (1); Zinc finger, RING/FYVE/PHD-type [IPR013083] (1)	-	-	P_trifoliata_00053_mRNA_16.1
GF0044514	0	0	1	Hypothetical protein (1)		Ubiquitin-conjugating enzyme E2 [IPR000608] (1); Ubiquitin-conjugating enzyme/RWD-like [IPR016135] (1); Ubiquitin-conjugating enzyme, active site [IPR023313] (1)	-	-	P_trifoliata_00053_mRNA_123.1
GF0044513	0	0	1	LOB domain-containing protein 20 (1)		Lateral organ boundaries, LOB [IPR004883] (1)	-	-	P_trifoliata_00053_mRNA_122.1
GF0044512	0	0	1	Histone-lysine N-methyltransferase SUVR3 (1)	histone-lysine N-methyltransferase activity [GO:0018024 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1); histone lysine methylation [GO:0034968 biological_process] (1); nucleus [GO:0005634 cellular_component] (1)	Post-SET domain [IPR003616] (1); Pre-SET domain [IPR007728] (1); SET domain [IPR001214] (1)	-	-	P_trifoliata_00053_mRNA_121.1
GF0044511	0	0	1	Condensin complex subunit 3 (1)			-	-	P_trifoliata_00053_mRNA_12.1
GF0044510	0	0	1	Hypothetical protein (1)		Phosphoribosyltransferase C-terminal [IPR013583] (1)	-	-	P_trifoliata_00053_mRNA_104.1
GF0044509	0	0	1	Hypothetical protein (1)		AmbAllergen [IPR018082] (1); Pectin lyase fold/virulence factor [IPR011050] (1); Pectin lyase fold [IPR012334] (1)	-	-	P_trifoliata_00053_mRNA_10.1
GF0044508	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00052_mRNA_9.1
GF0044507	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00052_mRNA_83.1
GF0044506	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00052_mRNA_81.1
GF0044505	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00052_mRNA_79.1
GF0044504	0	0	1	Putative xyloglucan endotransglucosylase/hydrolase protein 23 (1)	xyloglucan:xyloglucosyl transferase activity [GO:0016762 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1); hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (1); cell wall [GO:0005618 cellular_component] (1); cellular glucan metabolic process [GO:0006073 biological_process] (1); apoplast [GO:0048046 cellular_component] (1)	Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Glycoside hydrolase family 16 [IPR000757] (1); Xyloglucan endo-transglycosylase, C-terminal [IPR010713] (1)	-	-	P_trifoliata_00052_mRNA_76.1
GF0044503	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00052_mRNA_74.1
GF0044502	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00052_mRNA_72.1
GF0044501	0	0	1	Putative disease resistance protein RGA1 (1)			-	-	P_trifoliata_00052_mRNA_71.1
GF0044500	0	0	1	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	-	P_trifoliata_00052_mRNA_70.1

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*
GF0044499	0	0	1	Ankyrin repeat family protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat [IPR002110] (1); Ankyrin repeat-containing domain [IPR020683] (1)	-	-	P_trifoliata_00052_mRNA_68.1
GF0044498	0	0	1	Truncated putative heavy metal transporter variant 2 (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, A domain [IPR008250] (1); P-type ATPase [IPR001757] (1)	-	-	P_trifoliata_00052_mRNA_63.1
GF0044497	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00052_mRNA_61.1
GF0044496	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00052_mRNA_60.1
GF0044495	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00052_mRNA_6.1
GF0044494	0	0	1	ABC transporter G family member 29 (1)	membrane [GO:0016020 cellular_component] (1)	ABC-2 type transporter [IPR013525] (1)	-	-	P_trifoliata_00052_mRNA_4.1
GF0044493	0	0	1	Orf258 protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	-	P_trifoliata_00052_mRNA_39.1
GF0044492	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00052_mRNA_37.1
GF0044491	0	0	1	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)	-	-	P_trifoliata_00052_mRNA_36.1
GF0044490	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00052_mRNA_35.1
GF0044489	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00052_mRNA_34.1
GF0044488	0	0	1	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	-	P_trifoliata_00052_mRNA_26.1
GF0044487	0	0	1	Deacetylvindoline O-acetyltransferase (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)	-	-	P_trifoliata_00052_mRNA_25.1
GF0044486	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00052_mRNA_24.1
GF0044485	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00052_mRNA_21.1
GF0044484	0	0	1	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 domain [IPR000477] (1); Viral movement protein [IPR028919] (1)	-	-	P_trifoliata_00052_mRNA_13.1
GF0044483	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00052_mRNA_12.1
GF0044482	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00052_mRNA_10.1
GF0044481	0	0	1	AP2/B3 transcriptional factor family protein (1)		DNA-binding pseudobarrel domain [IPR015300] (1)	-	-	P_trifoliata_00051_mRNA_91.1
GF0044480	0	0	1	AP2/B3 transcriptional factor family protein (1)		DNA-binding pseudobarrel domain [IPR015300] (1)	-	-	P_trifoliata_00051_mRNA_88.1
GF0044479	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00051_mRNA_84.1
GF0044478	0	0	1	Homogentisate phytyltransferase 2 (1)	prenyltransferase activity [GO:0004659 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1)	UbiA prenyltransferase family [IPR000537] (1)	-	-	P_trifoliata_00051_mRNA_83.1
GF0044477	0	0	1	Mitogen activated protein kinase kinase kinase 3, mapkkk3, mekk3, 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/dual specificity protein kinase, catalytic domain [IPR002290] (1); Protein kinase, ATP binding site [IPR017441] (1); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1)	-	-	P_trifoliata_00051_mRNA_76.1
GF0044476	0	0	1	Short-chain dehydrogenase TIC 32, chloroplastic (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)	-	-	P_trifoliata_00051_mRNA_73.1
GF0044475	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	-	P_trifoliata_00051_mRNA_60.1
GF0044474	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00051_mRNA_52.1
GF0044473	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00051_mRNA_51.1
GF0044472	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (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); Sec63 domain [IPR004179] (1); DEAD/DEAH box helicase domain [IPR011545] (1); Helicase, C-terminal [IPR001650] (1); C2 domain [IPR000008] (1); Immunoglobulin E-set [IPR014756] (1)	-	-	P_trifoliata_00051_mRNA_46.1
GF0044471	0	0	1	Hypothetical protein (1)	protein folding [GO:0006457 biological_process] (1); unfolded protein binding [GO:0051082 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1); response to stress [GO:0006950 biological_process] (1)	Heat shock protein Hsp90 family [IPR001404] (1)	-	-	P_trifoliata_00051_mRNA_112.1
GF0044470	0	0	1	Glutaminyl-peptide cyclotransferase (1)	protein binding [GO:0005515 molecular_function] (1)	WD40/YVTN repeat-like-containing domain [IPR015943] (1); Glutamine cyclotransferase [IPR007788] (1)	-	-	P_trifoliata_00051_mRNA_110.1
GF0044469	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00051_mRNA_101.1
GF0044468	0	0	1	Hydroxyproline-rich glycoprotein family protein, putative (1)		Late embryogenesis abundant protein, LEA-14 [IPR004864] (1)	-	-	P_trifoliata_00050_mRNA_98.1
GF0044467	0	0	1	Exocyst complex component 7 (1)	exocyst [GO:0000145 cellular_component] (1); exocytosis [GO:0006887 biological_process] (1)	Cullin repeat-like-containing domain [IPR016159] (1); Exocyst complex protein Exo70 [IPR004140] (1)	-	-	P_trifoliata_00050_mRNA_97.1
GF0044466	0	0	1	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein (1)		Bifunctional inhibitor/plant lipid transfer protein/seed storage helical domain [IPR016140] (1)	-	-	P_trifoliata_00050_mRNA_7.1
GF0044465	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00050_mRNA_67.1
GF0044464	0	0	1	Hypothetical protein (1)	activation of anaphase-promoting complex activity [GO:0051488 biological_process] (1); anaphase-promoting complex binding [GO:0010997 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1); ubiquitin-protein transferase activator activity [GO:0097027 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); The WD repeat Cdc20/Fizzy family [IPR033010] (1)	-	-	P_trifoliata_00050_mRNA_47.1
GF0044463	0	0	1	Hypothetical protein (1)	fatty-acyl-CoA reductase (alcohol-forming) activity [GO:0080019 molecular_function] (1)	Fatty acyl-CoA reductase [IPR026055] (1); Male sterility, NAD-binding [IPR013120] (1); NAD(P)-binding domain [IPR016040] (1)	-	-	P_trifoliata_00050_mRNA_16.1
GF0044462	0	0	1	Hypothetical protein (1)	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase activity [GO:0003871 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1); methionine biosynthetic process [GO:0009086 biological_process] (1)	Cobalamin-independent methionine synthase MetE, C-terminal/archaeal [IPR002629] (1)	-	-	P_trifoliata_00050_mRNA_109.1
GF0044461	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00050_mRNA_107.1
GF0044460	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00050_mRNA_1.1
GF0044459	0	0	1	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)	NADH:flavin oxidoreductase/NADH oxidase, N-terminal [IPR001155] (1); Aldolase-type TIM barrel [IPR013785] (1)	-	-	P_trifoliata_00049_mRNA_64.1
GF0044458	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00049_mRNA_63.1
GF0044457	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00049_mRNA_60.1
GF0044456	0	0	1	Hypothetical protein (1)		Retroviral aspartyl protease [IPR013242] (1); Retrotransposon gag domain [IPR005162] (1)	-	-	P_trifoliata_00049_mRNA_59.1
GF0044455	0	0	1	Cation proton exchanger, putative (1)			-	-	P_trifoliata_00049_mRNA_55.1
GF0044454	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00049_mRNA_49.1
GF0044453	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00049_mRNA_37.1
GF0044452	0	0	1	Hypothetical protein (1)	response to oxidative stress [GO:0006979 biological_process] (1); heme binding [GO:0020037 molecular_function] (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); Peroxidases heam-ligand binding site [IPR019793] (1)	-	-	P_trifoliata_00049_mRNA_36.1
GF0044451	0	0	1	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)	Plant peroxidase [IPR000823] (1); Haem peroxidase, plant/fungal/bacterial [IPR002016] (1); Haem peroxidase [IPR010255] (1)	-	-	P_trifoliata_00049_mRNA_35.1
GF0044450	0	0	1	Hypothetical protein (1)	heme binding [GO:0020037 molecular_function] (1); response to oxidative stress [GO:0006979 biological_process] (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)	-	-	P_trifoliata_00049_mRNA_34.1
GF0044449	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00049_mRNA_27.1

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*
GF0044448	0	0	1	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)	Plant peroxidase [IPR000823] (1); Peroxidase, active site [IPR019794] (1); Haem peroxidase, plant/fungal/bacterial [IPR002016] (1); Haem peroxidase [IPR010255] (1)	-	-	P_trifoliata_00049_mRNA_26.1
GF0044447	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00049_mRNA_19.1
GF0044446	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF641, plant [IPR006943] (1)	-	-	P_trifoliata_00049_mRNA_12.1
GF0044445	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00048_mRNA_9.1
GF0044444	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00048_mRNA_71.1
GF0044443	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00048_mRNA_69.1
GF0044442	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00048_mRNA_65.1
GF0044441	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00048_mRNA_62.1
GF0044440	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00048_mRNA_60.1
GF0044439	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00048_mRNA_58.1
GF0044438	0	0	1	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); Reverse transcriptase domain [IPR000477] (1)	-	-	P_trifoliata_00048_mRNA_57.1
GF0044437	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00048_mRNA_56.1
GF0044436	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00048_mRNA_53.1
GF0044435	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00048_mRNA_52.1
GF0044434	0	0	1	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)	-	-	P_trifoliata_00048_mRNA_49.1
GF0044433	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00048_mRNA_41.1
GF0044432	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00048_mRNA_4.1
GF0044431	0	0	1	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	-	P_trifoliata_00048_mRNA_34.1
GF0044430	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00048_mRNA_30.1
GF0044429	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00048_mRNA_28.1
GF0044428	0	0	1	UDP-arabinopyranose mutase 1 (1)	intramolecular transferase activity [GO:0016866 molecular_function] (1); cellulose biosynthetic process [GO:0030244 biological_process] (1)	Reversibly glycosylated polypeptide family [IPR004901] (1)	-	-	P_trifoliata_00048_mRNA_22.1
GF0044427	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00048_mRNA_19.1
GF0044426	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00048_mRNA_18.1
GF0044425	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00048_mRNA_10.1
GF0044424	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00047_mRNA_99.1
GF0044423	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00047_mRNA_88.1
GF0044422	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00047_mRNA_84.1
GF0044421	0	0	1	Phosphatase 2C family protein (1)	catalytic activity [GO:0003824 molecular_function] (1); cation binding [GO:0043169 molecular_function] (1); protein dephosphorylation [GO:0006470 biological_process] (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)	-	-	P_trifoliata_00047_mRNA_81.1
GF0044420	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00047_mRNA_68.1
GF0044419	0	0	1	60S ribosomal protein L39 (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 L39e domain [IPR023626] (1); Ribosomal protein L39e [IPR000077] (1); Ribosomal protein L39e, conserved site [IPR020083] (1)	-	-	P_trifoliata_00047_mRNA_56.1
GF0044418	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00047_mRNA_39.1
GF0044417	0	0	1	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)	-	-	P_trifoliata_00047_mRNA_3.1
GF0044416	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00047_mRNA_120.1
GF0044415	0	0	1	Hypothetical protein (1)	gamma-glutamyltransferase activity [GO:0003840 molecular_function] (1); glutathione metabolic process [GO:0006749 biological_process] (1)	Gamma-glutamyltranspeptidase [IPR000101] (1); Nucleophile aminohydrolases, N-terminal [IPR029055] (1)	-	-	P_trifoliata_00047_mRNA_116.1
GF0044414	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4220 [IPR025315] (1)	-	-	P_trifoliata_00047_mRNA_115.1
GF0044413	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00047_mRNA_112.1
GF0044412	0	0	1	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 domain [IPR002156] (1); Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00047_mRNA_107.1
GF0044411	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00047_mRNA_105.1
GF0044410	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00047_mRNA_104.1
GF0044409	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00047_mRNA_102.1
GF0044408	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00047_mRNA_101.1
GF0044407	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00047_mRNA_100.1
GF0044406	0	0	1	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)	-	-	P_trifoliata_00047_mRNA_1.1
GF0044405	0	0	1	MATE efflux family protein 9 (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)	-	-	P_trifoliata_00046_mRNA_98.1
GF0044404	0	0	1	Putative AC9 transposase (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)	-	-	P_trifoliata_00046_mRNA_8.1
GF0044403	0	0	1	Farnesylated protein 2 (1)	metal ion binding [GO:0046872 molecular_function] (1); metal ion transport [GO:0030001 biological_process] (1)	Heavy metal-associated domain, HMA [IPR006121] (1)	-	-	P_trifoliata_00046_mRNA_73.1
GF0044402	0	0	1	Spore coat protein A (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); copper ion binding [GO:0005507 molecular_function] (1)	Cupredoxin [IPR008972] (1); Multicopper oxidase, type 1 [IPR001117] (1); Multicopper oxidase, type 3 [IPR011707] (1)	-	-	P_trifoliata_00046_mRNA_70.1
GF0044401	0	0	1	Retrotransposon protein, putative, unclassified (1)			-	-	P_trifoliata_00046_mRNA_7.1
GF0044400	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00046_mRNA_67.1
GF0044399	0	0	1	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)	-	-	P_trifoliata_00046_mRNA_48.1
GF0044398	0	0	1	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	-	P_trifoliata_00046_mRNA_47.1
GF0044397	0	0	1	Hypothetical protein (1)	binding [GO:0005488 molecular_function] (1)	Armadillo-type fold [IPR016024] (1); Armadillo-like helical [IPR011989] (1)	-	-	P_trifoliata_00046_mRNA_19.1
GF0044396	0	0	1	Hypothetical protein (1)		Chromo domain [IPR023780] (1); Chromo domain-like [IPR016197] (1); Chromo/chromo shadow domain [IPR000953] (1)	-	-	P_trifoliata_00046_mRNA_111.1
GF0044395	0	0	1	CDNA clone:J023022E20, full insert sequence (1)			-	-	P_trifoliata_00046_mRNA_109.1
GF0044394	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00046_mRNA_108.1
GF0044393	0	0	1	Chloroplast acyl-ACP thioesterase A (1)	fatty acid biosynthetic process [GO:0006633 biological_process] (1); thiolester hydrolase activity [GO:0016790 molecular_function] (1)	Acyl-ACP thioesterase [IPR002864] (1); HotDog domain [IPR029069] (1)	-	-	P_trifoliata_00046_mRNA_102.1
GF0044392	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00046_mRNA_10.1
GF0044391	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00045_mRNA_94.1
GF0044390	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00045_mRNA_92.1
GF0044389	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00045_mRNA_91.1
GF0044388	0	0	1	Hypothetical protein (1)		MEKHLA [IPR013978] (1)	-	-	P_trifoliata_00045_mRNA_90.1
GF0044387	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00045_mRNA_77.1
GF0044386	0	0	1	Photosystem I reaction center subunit psaK, chloroplastic (1)	chlorophyll binding [GO:0016168 molecular_function] (1); photosynthesis [GO:0015979 biological_process] (1); membrane [GO:0016020 cellular_component] (1); photosystem I [GO:0009522 cellular_component] (1)	Photosystem I PsaK, reaction centre, plant [IPR017493] (1); Photosystem I PsaG/PsaK protein [IPR000549] (1); Photosystem I PsaG/PsaK domain [IPR023618] (1)	-	-	P_trifoliata_00045_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*
GF0044385	0	0	1	Hypothetical protein (1)	extracellular matrix [GO:0031012 cellular_component] (1); proteolysis [GO:0006508 biological_process] (1); metallopeptidase activity [GO:0008237 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1); metalloendopeptidase activity [GO:0004222 molecular_function] (1)	Peptidase M10, metallopeptidase [IPR001818] (1); Peptidase, metallopeptidase [IPR006026] (1); Peptidase M10A [IPR021190] (1); Metallopeptidase, catalytic domain [IPR024079] (1)	-	-	P_trifoliata_00045_mRNA_67.1
GF0044384	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00045_mRNA_66.1
GF0044383	0	0	1	Hypothetical protein (1)	metallopeptidase activity [GO:0008237 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1); extracellular matrix [GO:0031012 cellular_component] (1); metalloendopeptidase activity [GO:0004222 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Peptidase M10, metallopeptidase [IPR001818] (1); Metallopeptidase, catalytic domain [IPR024079] (1); Peptidase M10A [IPR021190] (1); Peptidase, metallopeptidase [IPR006026] (1)	-	-	P_trifoliata_00045_mRNA_65.1
GF0044382	0	0	1	Hypothetical protein (1)		Alpha/Beta hydrolase fold [IPR029058] (1)	-	-	P_trifoliata_00045_mRNA_51.1
GF0044381	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1); metal ion binding [GO:0046872 molecular_function] (1)	Zinc finger, RING-type [IPR001841] (1); Pentatricopeptide repeat [IPR002885] (1); Zinc finger, RING-type, conserved site [IPR017907] (1); Zinc finger, C3HC4 RING-type [IPR018957] (1); Zinc finger, RING/FYVE/PHD-type [IPR013083] (1)	-	-	P_trifoliata_00045_mRNA_46.1
GF0044380	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00045_mRNA_39.1
GF0044379	0	0	1	CBL-interacting protein kinase 3 isoform 2 (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-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	-	-	P_trifoliata_00045_mRNA_38.1
GF0044378	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00045_mRNA_29.1
GF0044377	0	0	1	-glutaredoxin subgroup III (1)	cell redox homeostasis [GO:0045454 biological_process] (1); electron carrier activity [GO:0009055 molecular_function] (1); protein disulfide oxidoreductase activity [GO:0015035 molecular_function] (1)	Thioredoxin-like fold [IPR012336] (1); Glutaredoxin-like, plant II [IPR011905] (1); Glutaredoxin [IPR002109] (1); Glutaredoxin subgroup [IPR014025] (1)	-	-	P_trifoliata_00045_mRNA_27.1
GF0044376	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00045_mRNA_26.1
GF0044375	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00045_mRNA_2.1
GF0044374	0	0	1	O-methyltransferase ZRP4 (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)	-	-	P_trifoliata_00045_mRNA_128.1
GF0044373	0	0	1	Orcinol 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); O-methyltransferase, family 2 [IPR001077] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	-	P_trifoliata_00045_mRNA_126.1
GF0044372	0	0	1	Phosphatase 2C family protein (1)	protein dephosphorylation [GO:0006470 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1); protein serine/threonine phosphatase activity [GO:0004722 molecular_function] (1)	RmlC-like jelly roll fold [IPR014710] (1); PPM-type phosphatase domain [IPR001932] (1); Protein phosphatase 2C family [IPR015655] (1)	-	-	P_trifoliata_00045_mRNA_115.1
GF0044371	0	0	1	Receptor-like protein kinase FERONIA (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); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Malectin-like carbohydrate-binding domain [IPR024788] (1); Protein kinase domain [IPR000719] (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); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1)	-	-	P_trifoliata_00045_mRNA_109.1
GF0044370	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00045_mRNA_108.1
GF0044369	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00045_mRNA_106.1
GF0044368	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00045_mRNA_102.1
GF0044367	0	0	1	Reverse transcriptase, related (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	-	P_trifoliata_00044_mRNA_9.1
GF0044366	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00044_mRNA_8.1
GF0044365	0	0	1	Isoflavone reductase (1)		NmrA-like domain [IPR008030] (1); NAD(P)-binding domain [IPR016040] (1)	-	-	P_trifoliata_00044_mRNA_67.1
GF0044364	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00044_mRNA_66.1
GF0044363	0	0	1	COBW domain-containing protein 1 (1)		Cobalamin (vitamin B12) biosynthesis CobW-like, C-terminal [IPR011629] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); CobW/HypB/UreG domain [IPR003495] (1)	-	-	P_trifoliata_00044_mRNA_63.1
GF0044362	0	0	1	Hypothetical protein (1)	methyltransferase activity [GO:0008168 molecular_function] (1)	C-5 cytosine methyltransferase [IPR001525] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	-	P_trifoliata_00044_mRNA_62.1
GF0044361	0	0	1	Hypothetical protein (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	OTU domain [IPR003323] (1); Aldehyde oxidase/xanthine dehydrogenase, molybdopterin binding [IPR008274] (1)	-	-	P_trifoliata_00044_mRNA_60.1
GF0044360	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00044_mRNA_52.1
GF0044359	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	F-box domain [IPR001810] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00044_mRNA_47.1
GF0044358	0	0	1	Hypothetical protein (1)		P-type ATPase, transmembrane domain [IPR023298] (1); Cation-transporting P-type ATPase, C-terminal [IPR006068] (1)	-	-	P_trifoliata_00044_mRNA_41.1
GF0044357	0	0	1	Calcium-transporting ATPase 9, plasma membrane-type protein (1)		Cation-transporting P-type ATPase, C-terminal [IPR006068] (1); P-type ATPase, transmembrane domain [IPR023298] (1)	-	-	P_trifoliata_00044_mRNA_38.1
GF0044356	0	0	1	Putative calcium-transporting ATPase 9, plasma membrane-type-like (1)	nucleotide binding [GO:0000166 molecular_function] (1); metal ion binding [GO:0046872 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1)	P-type ATPase [IPR001757] (1); P-type ATPase, transmembrane domain [IPR023298] (1); P-type ATPase, cytoplasmic domain N [IPR023299] (1); P-type ATPase, phosphorylation site [IPR018303] (1); P-type ATPase, A domain [IPR008250] (1); Cation-transporting P-type ATPase, N-terminal [IPR004014] (1)	-	-	P_trifoliata_00044_mRNA_37.1
GF0044355	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00044_mRNA_36.1
GF0044354	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00044_mRNA_35.1
GF0044353	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00044_mRNA_32.1
GF0044352	0	0	1	Pentatricopeptide (PPR) repeat protein (1)	protein binding [GO:0005515 molecular_function] (1)	Pentatricopeptide repeat [IPR002885] (1); Tetratricopeptide-like helical domain [IPR011990] (1)	-	-	P_trifoliata_00044_mRNA_3.1
GF0044351	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00044_mRNA_28.1
GF0044350	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00044_mRNA_25.1
GF0044349	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (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); Ankyrin repeat [IPR002110] (1); Ankyrin repeat-containing domain [IPR020683] (1)	-	-	P_trifoliata_00044_mRNA_20.1
GF0044348	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00044_mRNA_18.1
GF0044347	0	0	1	Ankyrin repeat plant-like protein (1)		PGG domain [IPR026961] (1); Ankyrin repeat-containing domain [IPR020683] (1)	-	-	P_trifoliata_00044_mRNA_17.1
GF0044346	0	0	1	Hypothetical protein (1)		Malectin [IPR021720] (1)	-	-	P_trifoliata_00044_mRNA_1.1
GF0044345	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00043_mRNA_98.1
GF0044344	0	0	1	Cysteine proteinase inhibitor (1)	cysteine-type endopeptidase inhibitor activity [GO:0004869 molecular_function] (1)	Proteinase inhibitor I25, cystatin, conserved region [IPR020381] (1); Proteinase inhibitor I25, cystatin, conserved site [IPR018073] (1); Cystatin [IPR027214] (1); Cystatin domain [IPR000010] (1)	-	-	P_trifoliata_00043_mRNA_96.1
GF0044343	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00043_mRNA_94.1

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*
GF0044342	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00043_mRNA_91.1
GF0044341	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00043_mRNA_79.1
GF0044340	0	0	1	TRAF-like family protein isoform 2 (1)	protein binding [GO:0005515 molecular_function] (1)	MATH/TRAF domain [IPR002083] (1); TRAF-like [IPR008974] (1)	-	-	P_trifoliata_00043_mRNA_78.1
GF0044339	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00043_mRNA_75.1
GF0044338	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00043_mRNA_66.1
GF0044337	0	0	1	Hypothetical protein (1)		Early nodulin 93 ENOD93 protein [IPR005050] (1)	-	-	P_trifoliata_00043_mRNA_51.1
GF0044336	0	0	1	Ribosomal protein S8e family protein (1)	structural constituent of ribosome [GO:0003735 molecular_function] (1); translation [GO:0006412 biological_process] (1); intracellular [GO:0005622 cellular_component] (1); ribosome [GO:0005840 cellular_component] (1)	Ribosomal protein S8e [IPR001047] (1); Ribosomal protein S8e/ribosomal biogenesis NSA2 [IPR022309] (1)	-	-	P_trifoliata_00043_mRNA_5.1
GF0044335	0	0	1	Calcineurin B-like protein 02 (1)	calcium ion binding [GO:0005509 molecular_function] (1)	EF-hand domain pair [IPR011992] (1); EF-hand domain [IPR002048] (1)	-	-	P_trifoliata_00043_mRNA_4.1
GF0044334	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00043_mRNA_3.1
GF0044333	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00043_mRNA_25.1
GF0044332	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00043_mRNA_24.1
GF0044331	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00043_mRNA_21.1
GF0044330	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00043_mRNA_2.1
GF0044329	0	0	1	Mitochondrial ATP synthase g subunit family protein (1)	hydrogen ion transmembrane transporter activity [GO:0015078 molecular_function] (1); ATP synthesis coupled proton transport [GO:0015986 biological_process] (1); mitochondrial proton-transporting ATP synthase complex, coupling factor F(o) [GO:0000276 cellular_component] (1)	ATPase, F0 complex, subunit G, mitochondrial [IPR006808] (1)	-	-	P_trifoliata_00043_mRNA_19.1
GF0044328	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00043_mRNA_111.1
GF0044327	0	0	1	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)	-	-	P_trifoliata_00043_mRNA_100.1
GF0044326	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00042_mRNA_94.1
GF0044325	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00042_mRNA_9.1
GF0044324	0	0	1	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1)	-	-	P_trifoliata_00042_mRNA_81.1
GF0044323	0	0	1	Somatic embryogenesis 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)	-	-	P_trifoliata_00042_mRNA_8.1
GF0044322	0	0	1	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)	-	-	P_trifoliata_00042_mRNA_73.1
GF0044321	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00042_mRNA_69.1
GF0044320	0	0	1	Hypothetical protein (1)		Zinc knuckle CX2CX4HX4C [IPR025836] (1)	-	-	P_trifoliata_00042_mRNA_67.1
GF0044319	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00042_mRNA_64.1
GF0044318	0	0	1	Hypothetical protein (1)	serine-type endopeptidase activity [GO:0004252 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Peptidase S8/S53 domain [IPR000209] (1); Peptidase S8, subtilisin-related [IPR015500] (1); Peptidase S8, subtilisin, Ser-active site [IPR023828] (1)	-	-	P_trifoliata_00042_mRNA_60.1
GF0044317	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00042_mRNA_53.1
GF0044316	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00042_mRNA_52.1
GF0044315	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00042_mRNA_50.1
GF0044314	0	0	1	Probably inactive leucine-rich repeat receptor-like protein kinase (1)		Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00042_mRNA_5.1
GF0044313	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00042_mRNA_49.1
GF0044312	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00042_mRNA_48.1
GF0044311	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00042_mRNA_47.1
GF0044310	0	0	1	CCT motif family protein, expressed (1)	protein binding [GO:0005515 molecular_function] (1)	CCT domain [IPR010402] (1)	-	-	P_trifoliata_00042_mRNA_42.1
GF0044309	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00042_mRNA_36.1
GF0044308	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00042_mRNA_32.1
GF0044307	0	0	1	Putative RNA-directed DNA polymerase (1)		Reverse transcriptase domain [IPR000477] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	-	P_trifoliata_00042_mRNA_23.1
GF0044306	0	0	1	60S ribosomal protein L8 (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 L2 [IPR002171] (1); Ribosomal protein L2, C-terminal [IPR022669] (1); Ribosomal protein L2, domain 3 [IPR014726] (1); Ribosomal protein L2 domain 2 [IPR014722] (1); Translation protein SH3-like domain [IPR008991] (1)	-	-	P_trifoliata_00042_mRNA_21.1
GF0044305	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00042_mRNA_20.1
GF0044304	0	0	1	Hypothetical protein (1)		GAG-pre-integrase domain [IPR025724] (1)	-	-	P_trifoliata_00042_mRNA_19.1
GF0044303	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00042_mRNA_18.1
GF0044302	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00042_mRNA_17.1
GF0044301	0	0	1	Hypothetical protein (1)		B3 domain-containing protein [IPR005508] (1)	-	-	P_trifoliata_00042_mRNA_15.1
GF0044300	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00042_mRNA_13.1
GF0044299	0	0	1	Hypothetical protein (1)		Glycosyltransferase family 92 [IPR008166] (1)	-	-	P_trifoliata_00042_mRNA_12.1
GF0044298	0	0	1	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)	-	-	P_trifoliata_00042_mRNA_104.1
GF0044297	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00042_mRNA_102.1
GF0044296	0	0	1	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)	-	-	P_trifoliata_00042_mRNA_1.1
GF0044295	0	0	1	Hypothetical protein (1)	malate transport [GO:0015743 biological_process] (1)	Aluminum-activated malate transporter [IPR020966] (1)	-	-	P_trifoliata_00041_mRNA_96.1
GF0044294	0	0	1	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	-	P_trifoliata_00041_mRNA_95.1
GF0044293	0	0	1	Hypothetical protein (1)		LOG family [IPR031100] (1)	-	-	P_trifoliata_00041_mRNA_84.1
GF0044292	0	0	1	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); Glutathione S-transferase, C-terminal-like [IPR010987] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Glutathione S-transferase, C-terminal [IPR004046] (1)	-	-	P_trifoliata_00041_mRNA_80.1
GF0044291	0	0	1	Tetratricopeptide repeat protein 27-like protein (1)	protein binding [GO:0005515 molecular_function] (1)	Tetratricopeptide repeat-containing domain [IPR013026] (1); Tetratricopeptide repeat [IPR019734] (1); Tetratricopeptide repeat 2 [IPR013105] (1); Tetratricopeptide-like helical domain [IPR011990] (1)	-	-	P_trifoliata_00041_mRNA_79.1
GF0044290	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00041_mRNA_76.1
GF0044289	0	0	1	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)	-	-	P_trifoliata_00041_mRNA_72.1
GF0044288	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00041_mRNA_71.1
GF0044287	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00041_mRNA_70.1
GF0044286	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00041_mRNA_68.1
GF0044285	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00041_mRNA_67.1
GF0044284	0	0	1	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)	-	-	P_trifoliata_00041_mRNA_65.1
GF0044283	0	0	1	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 [IPR020471] (1); Aldo/keto reductase/potassium channel subunit beta [IPR001395] (1); NADP-dependent oxidoreductase domain [IPR023210] (1); Aldo/keto reductase, conserved site [IPR018170] (1)	-	-	P_trifoliata_00041_mRNA_58.1
GF0044282	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00041_mRNA_52.1
GF0044281	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00041_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*
GF0044280	0	0	1	Putative somatic embryogenesis protein kinase 1 (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); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	-	-	P_trifoliata_00041_mRNA_14.1
GF0044279	0	0	1	Hypothetical protein (1)	hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1)	Aldolase-type TIM barrel [IPR013785] (1); Glycoside hydrolase family 27/36, conserved site [IPR000111] (1); Glycoside hydrolase, family 27 [IPR002241] (1); Glycoside hydrolase superfamily [IPR017853] (1); Glycosyl hydrolase, family 13, all-beta [IPR013780] (1)	-	-	P_trifoliata_00040_mRNA_62.1
GF0044278	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00040_mRNA_57.1
GF0044277	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00040_mRNA_45.1
GF0044276	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00040_mRNA_39.1
GF0044275	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00040_mRNA_27.1
GF0044274	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00040_mRNA_120.1
GF0044273	0	0	1	UDP-glycosyltransferase 71C4 (1)	transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	-	-	P_trifoliata_00040_mRNA_119.1
GF0044272	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00040_mRNA_117.1
GF0044271	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00039_mRNA_80.1
GF0044270	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00039_mRNA_8.1
GF0044269	0	0	1	Cysteine proteinase inhibitor (1)	cysteine-type endopeptidase inhibitor activity [GO:0004869 molecular_function] (1)	Cystatin [IPR027214] (1); Cystatin domain [IPR000010] (1); Proteinase inhibitor I25, cystatin, conserved region [IPR020381] (1)	-	-	P_trifoliata_00039_mRNA_78.1
GF0044268	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00039_mRNA_75.1
GF0044267	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00039_mRNA_73.1
GF0044266	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00039_mRNA_65.1
GF0044265	0	0	1	Hypothetical protein (1)		LOG family [IPR031100] (1)	-	-	P_trifoliata_00039_mRNA_61.1
GF0044264	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00039_mRNA_58.1
GF0044263	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00039_mRNA_54.1
GF0044262	0	0	1	UDP-glycosyltransferase 73D1 (1)	metabolic process [GO:0008152 biological_process] (1); transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	-	-	P_trifoliata_00039_mRNA_51.1
GF0044261	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00039_mRNA_50.1
GF0044260	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00039_mRNA_48.1
GF0044259	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00039_mRNA_42.1
GF0044258	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00039_mRNA_41.1
GF0044257	0	0	1	Hypothetical protein (1)		CWC16 protein [IPR007590] (1)	-	-	P_trifoliata_00039_mRNA_40.1
GF0044256	0	0	1	Hypothetical protein (1)		Thiamin diphosphate-binding fold [IPR029061] (1)	-	-	P_trifoliata_00039_mRNA_39.1
GF0044255	0	0	1	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)	-	-	P_trifoliata_00039_mRNA_36.1
GF0044254	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00039_mRNA_31.1
GF0044253	0	0	1	Hypothetical protein (1)	heme binding [GO:0020037 molecular_function] (1); response to oxidative stress [GO:0006979 biological_process] (1); oxidation-reduction process [GO:0055114 biological_process] (1); peroxidase activity [GO:0004601 molecular_function] (1)	Haem peroxidase [IPR010255] (1); Haem peroxidase, animal [IPR019791] (1)	-	-	P_trifoliata_00039_mRNA_3.1
GF0044252	0	0	1	22.0 kDa class IV heat shock 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)	HSP20-like chaperone [IPR008978] (1); Alpha crystallin/Hsp20 domain [IPR002068] (1); Ribosomal protein L27e [IPR001141] (1); Small heat shock protein HSP20 [IPR031107] (1)	-	-	P_trifoliata_00039_mRNA_29.1
GF0044251	0	0	1	Retrotransposon protein, putative, unclassified, expressed (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Reverse transcriptase domain [IPR000477] (1); Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00039_mRNA_24.1
GF0044250	0	0	1	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)	-	-	P_trifoliata_00039_mRNA_23.1
GF0044249	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00039_mRNA_21.1
GF0044248	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00039_mRNA_18.1
GF0044247	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00039_mRNA_17.1
GF0044246	0	0	1	66 kDa stress 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 [IPR001680] (1); WD40-repeat-containing domain [IPR017986] (1)	-	-	P_trifoliata_00039_mRNA_11.1
GF0044245	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00038_mRNA_99.1
GF0044244	0	0	1	Polyubiquitin (1)	protein binding [GO:0005515 molecular_function] (1)	Ubiquitin domain [IPR000626] (1); Ubiquitin-related domain [IPR029071] (1); Ubiquitin [IPR019956] (1)	-	-	P_trifoliata_00038_mRNA_98.1
GF0044243	0	0	1	F-box protein interaction domain protein (1)	protein binding [GO:0005515 molecular_function] (1)	F-box domain [IPR001810] (1); Galactose oxidase/kelch, beta-propeller [IPR011043] (1); F-box associated interaction domain [IPR017451] (1)	-	-	P_trifoliata_00038_mRNA_97.1
GF0044242	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00038_mRNA_93.1
GF0044241	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00038_mRNA_77.1
GF0044240	0	0	1	Hypothetical protein (1)		Splicing factor 3B subunit 5/RDS3 complex subunit 10 [IPR009846] (1)	-	-	P_trifoliata_00038_mRNA_72.1
GF0044239	0	0	1	Hypothetical protein (1)		Protein of unknown function DUF3475 [IPR021864] (1)	-	-	P_trifoliata_00038_mRNA_7.1
GF0044238	0	0	1	11S seed storage globulin (1)	nutrient reservoir activity [GO:0045735 molecular_function] (1)	RmlC-like cupin domain [IPR011051] (1); RmlC-like jelly roll fold [IPR014710] (1); Cupin 1 [IPR006045] (1)	-	-	P_trifoliata_00038_mRNA_63.1
GF0044237	0	0	1	Hypothetical protein (1)		Glutathione S-transferase, C-terminal-like [IPR010987] (1)	-	-	P_trifoliata_00038_mRNA_61.1
GF0044236	0	0	1	Actin-depolymerizing factor 6 (1)	actin cytoskeleton [GO:0015629 cellular_component] (1); actin binding [GO:0003779 molecular_function] (1); actin filament depolymerization [GO:0030042 biological_process] (1); intracellular [GO:0005622 cellular_component] (1)	Actin-depolymerising factor homology domain [IPR002108] (1); ADF/Cofilin/Destrin [IPR017904] (1); ADF-H/Gelsolin-like domain [IPR029006] (1)	-	-	P_trifoliata_00038_mRNA_53.1
GF0044235	0	0	1	Gag non-LTR retrotransposase (1)	nucleic acid binding [GO:0003676 molecular_function] (1); ribosome [GO:0005840 cellular_component] (1); zinc ion binding [GO:0008270 molecular_function] (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 [IPR002171] (1); Ribosomal protein L2, C-terminal [IPR022669] (1); Domain of unknown function DUF4283 [IPR025558] (1); Ribosomal protein L2, domain 3 [IPR014726] (1); Ribosomal protein L2 domain 2 [IPR014722] (1); Zinc knuckle CX2CX4HX4C [IPR025836] (1); Zinc finger, CCHC-type [IPR001878] (1); Translation protein SH3-like domain [IPR008991] (1)	-	-	P_trifoliata_00038_mRNA_46.1
GF0044234	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00038_mRNA_42.1
GF0044233	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00038_mRNA_4.1
GF0044232	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00038_mRNA_39.1
GF0044231	0	0	1	Deacetoxyvindoline 4-hydroxylase (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)	-	-	P_trifoliata_00038_mRNA_32.1
GF0044230	0	0	1	Hypothetical protein (1)		Isopenicillin N synthase-like [IPR027443] (1)	-	-	P_trifoliata_00038_mRNA_31.1
GF0044229	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00038_mRNA_3.1
GF0044228	0	0	1	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)	-	-	P_trifoliata_00038_mRNA_29.1
GF0044227	0	0	1	Hypothetical protein (1)		Isopenicillin N synthase-like [IPR027443] (1)	-	-	P_trifoliata_00038_mRNA_28.1
GF0044226	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00038_mRNA_27.1
GF0044225	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00038_mRNA_26.1
GF0044224	0	0	1	Hypothetical protein (1)		Isopenicillin N synthase-like [IPR027443] (1)	-	-	P_trifoliata_00038_mRNA_25.1
GF0044223	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00038_mRNA_22.1
GF0044222	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00038_mRNA_21.1
GF0044221	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00038_mRNA_20.1

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*
GF0044220	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Domain of unknown function DUF4283 [IPR025558] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	-	P_trifoliata_00038_mRNA_119.1
GF0044219	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00038_mRNA_116.1
GF0044218	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00038_mRNA_115.1
GF0044217	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00038_mRNA_114.1
GF0044216	0	0	1	Hypothetical protein (1)	membrane [GO:0016020 cellular_component] (1); protein transport [GO:0015031 biological_process] (1)	SecY subunit domain [IPR023201] (1); SecY/SEC61-alpha family [IPR002208] (1)	-	-	P_trifoliata_00038_mRNA_113.1
GF0044215	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00038_mRNA_112.1
GF0044214	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00038_mRNA_105.1
GF0044213	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00038_mRNA_102.1
GF0044212	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00038_mRNA_10.1
GF0044211	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00037_mRNA_9.1
GF0044210	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00037_mRNA_76.1
GF0044209	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00037_mRNA_75.1
GF0044208	0	0	1	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)	-	-	P_trifoliata_00037_mRNA_60.1
GF0044207	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00037_mRNA_6.1
GF0044206	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00037_mRNA_54.1
GF0044205	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00037_mRNA_35.1
GF0044204	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00037_mRNA_32.1
GF0044203	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00037_mRNA_20.1
GF0044202	0	0	1	Somatic embryogenesis receptor kinase 1 (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)	-	-	P_trifoliata_00037_mRNA_111.1
GF0044201	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00037_mRNA_106.1
GF0044200	0	0	1	Hypothetical protein (1)	binding [GO:0005488 molecular_function] (1)	Armadillo-like helical [IPR011989] (1); Armadillo-type fold [IPR016024] (1)	-	-	P_trifoliata_00037_mRNA_103.1
GF0044199	0	0	1	Pre-mrna-splicing factor rse1 (1)		Domain of unknown function DUF4409 [IPR025521] (1); Domain of unknown function DUF239 [IPR004314] (1)	-	-	P_trifoliata_00036_mRNA_96.1
GF0044198	0	0	1	Peroxidase 21 (1)	response to oxidative stress [GO:0006979 biological_process] (1); heme binding [GO:0020037 molecular_function] (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)	-	-	P_trifoliata_00036_mRNA_81.1
GF0044197	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00036_mRNA_79.1
GF0044196	0	0	1	NADH-ubiquinone oxidoreductase 20 kDa subunit, mitochondrial (1)	quinone binding [GO:0048038 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); NADH dehydrogenase (ubiquinone) activity [GO:0008137 molecular_function] (1); iron-sulfur cluster binding [GO:0051536 molecular_function] (1); 4 iron, 4 sulfur cluster binding [GO:0051539 molecular_function] (1)	NADH-ubiquinone oxidoreductase, 20 Kd subunit [IPR006138] (1); NADH:ubiquinone oxidoreductase-like, 20kDa subunit [IPR006137] (1)	-	-	P_trifoliata_00036_mRNA_76.1
GF0044195	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00036_mRNA_75.1
GF0044194	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00036_mRNA_71.1
GF0044193	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00036_mRNA_70.1
GF0044192	0	0	1	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	Topless family [IPR027728] (1)	-	-	P_trifoliata_00036_mRNA_7.1
GF0044191	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Kelch-type beta propeller [IPR015915] (1)	-	-	P_trifoliata_00036_mRNA_68.1
GF0044190	0	0	1	Hypothetical protein (1)	transport [GO:0006810 biological_process] (1); ATPase activity [GO:0016887 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (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)	ABC transporter, conserved site [IPR017871] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); ABC transporter type 1, transmembrane domain [IPR011527] (1); ABC transporter-like [IPR003439] (1); AAA+ ATPase domain [IPR003593] (1)	-	-	P_trifoliata_00036_mRNA_64.1
GF0044189	0	0	1	ABC transporter C family protein (1)	ATPase activity, coupled to transmembrane movement of substances [GO:0042626 molecular_function] (1); transmembrane transport [GO:0055085 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1); ATPase activity [GO:0016887 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1); transport [GO:0006810 biological_process] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); ABC transporter-like [IPR003439] (1); ABC transporter type 1, transmembrane domain [IPR011527] (1); AAA+ ATPase domain [IPR003593] (1)	-	-	P_trifoliata_00036_mRNA_63.1
GF0044188	0	0	1	Adenine nucleotide alpha hydrolase-like domain 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-like domain [IPR011009] (1); Rossmann-like alpha/beta/alpha sandwich fold [IPR014729] (1); Protein kinase domain [IPR000719] (1); Tyrosine-protein kinase, active site [IPR008266] (1)	-	-	P_trifoliata_00036_mRNA_62.1
GF0044187	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00036_mRNA_60.1
GF0044186	0	0	1	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	-	-	P_trifoliata_00036_mRNA_55.1
GF0044185	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00036_mRNA_53.1
GF0044184	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00036_mRNA_42.1
GF0044183	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00036_mRNA_4.1
GF0044182	0	0	1	Hypothetical protein (1)		DnaJ domain [IPR001623] (1)	-	-	P_trifoliata_00036_mRNA_3.1
GF0044181	0	0	1	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)	Pectinesterase, Asp active site [IPR033131] (1); Pectinesterase, catalytic [IPR000070] (1); Pectin lyase fold [IPR012334] (1); Pectin lyase fold/virulence factor [IPR011050] (1)	-	-	P_trifoliata_00036_mRNA_28.1
GF0044180	0	0	1	Disease resistance protein (TIR-NBS-LRR class) (1)	ADP binding [GO:0043531 molecular_function] (1); signal transduction [GO:0007165 biological_process] (1); protein binding [GO:0005515 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat 3 [IPR011713] (1); Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00036_mRNA_15.1
GF0044179	0	0	1	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1)	Myc-type, basic helix-loop-helix (bHLH) domain [IPR011598] (1)	-	-	P_trifoliata_00036_mRNA_104.1
GF0044178	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00036_mRNA_1.1
GF0044177	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00035_mRNA_91.1
GF0044176	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00035_mRNA_90.1
GF0044175	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00035_mRNA_89.1
GF0044174	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00035_mRNA_87.1
GF0044173	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00035_mRNA_85.1
GF0044172	0	0	1	LRR receptor-like serine/threonine-protein kinase FLS2 (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)	-	-	P_trifoliata_00035_mRNA_84.1
GF0044171	0	0	1	Hypothetical protein (1)	transcription factor TFIID complex [GO:0005669 cellular_component] (1); transcription initiation from RNA polymerase II promoter [GO:0006367 biological_process] (1)	TAFII55 protein, conserved region [IPR006751] (1)	-	-	P_trifoliata_00035_mRNA_83.1
GF0044170	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00035_mRNA_8.1
GF0044169	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00035_mRNA_77.1
GF0044168	0	0	1	60S ribosomal protein L29-1 (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 L29e [IPR002673] (1)	-	-	P_trifoliata_00035_mRNA_73.1
GF0044167	0	0	1	Hypothetical protein (1)	iron-sulfur cluster binding [GO:0051536 molecular_function] (1); electron carrier activity [GO:0009055 molecular_function] (1)	Beta-grasp domain [IPR012675] (1); 2Fe-2S ferredoxin-type iron-sulfur binding domain [IPR001041] (1)	-	-	P_trifoliata_00035_mRNA_46.1
GF0044166	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00035_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***
GF0044165	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00035_mRNA_39.1
GF0044164	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00035_mRNA_38.1
GF0044163	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00035_mRNA_35.1
GF0044162	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00035_mRNA_33.1
GF0044161	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00035_mRNA_31.1
GF0044160	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00035_mRNA_3.1
GF0044159	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00035_mRNA_29.1
GF0044158	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00035_mRNA_27.1
GF0044157	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00035_mRNA_24.1
GF0044156	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00035_mRNA_22.1
GF0044155	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00035_mRNA_21.1
GF0044154	0	0	1	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)	-	-	P_trifoliata_00035_mRNA_18.1
GF0044153	0	0	1	Hypothetical protein (1)		Ribosomal protein L5, N-terminal [IPR031310] (1); Ribosomal protein L5 domain [IPR022803] (1)	-	-	P_trifoliata_00035_mRNA_17.1
GF0044152	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00035_mRNA_16.1
GF0044151	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00035_mRNA_15.1
GF0044150	0	0	1	Polyketide cyclase/dehydrase and lipid transport superfamily protein (1)		Polyketide cyclase/dehydrase [IPR019587] (1); START-like domain [IPR023393] (1)	-	-	P_trifoliata_00035_mRNA_119.1
GF0044149	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00035_mRNA_113.1
GF0044148	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00035_mRNA_1.1
GF0044147	0	0	1	Ribosomal protein L23 (1)	structural constituent of ribosome [GO:0003735 molecular_function] (1); translation [GO:0006412 biological_process] (1); ribosome [GO:0005840 cellular_component] (1)	Ribosomal protein L14 domain [IPR023571] (1); Ribosomal protein L14 conserved site [IPR019972] (1); PGG domain [IPR026961] (1); Ribosomal protein L14b/L23e [IPR000218] (1)	-	-	P_trifoliata_00034_mRNA_60.1
GF0044146	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00034_mRNA_6.1
GF0044145	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00034_mRNA_43.1
GF0044144	0	0	1	F-box protein interaction domain protein (1)	protein binding [GO:0005515 molecular_function] (1)	F-box associated interaction domain [IPR017451] (1); F-box associated domain, type 1 [IPR006527] (1); F-box domain [IPR001810] (1)	-	-	P_trifoliata_00034_mRNA_28.1
GF0044143	0	0	1	Putative E3 ubiquitin-protein ligase XBAT35 (1)	zinc ion binding [GO:0008270 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Zinc finger, RING/FYVE/PHD-type [IPR013083] (1); Ankyrin repeat [IPR002110] (1); Ankyrin repeat-containing domain [IPR020683] (1); Zinc finger, RING-type [IPR001841] (1)	-	-	P_trifoliata_00034_mRNA_12.1
GF0044142	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00034_mRNA_106.1
GF0044141	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00034_mRNA_105.1
GF0044140	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00034_mRNA_104.1
GF0044139	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00034_mRNA_100.1
GF0044138	0	0	1	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)	-	-	P_trifoliata_00033_mRNA_99.1
GF0044137	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00033_mRNA_92.1
GF0044136	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00033_mRNA_91.1
GF0044135	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00033_mRNA_90.1
GF0044134	0	0	1	G-type lectin S-receptor-like serine/threonine-protein kinase RLK1 (1)		Bulb-type lectin domain [IPR001480] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1)	-	-	P_trifoliata_00033_mRNA_89.1
GF0044133	0	0	1	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 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/dual specificity protein kinase, catalytic domain [IPR002290] (1)	-	-	P_trifoliata_00033_mRNA_87.1
GF0044132	0	0	1	G-type lectin S-receptor-like serine/threonine-protein kinase RLK1 (1)		Bulb-type lectin domain [IPR001480] (1)	-	-	P_trifoliata_00033_mRNA_86.1
GF0044131	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00033_mRNA_84.1
GF0044130	0	0	1	Cysteine synthase (1)	cysteine biosynthetic process from serine [GO:0006535 biological_process] (1)	Cysteine synthase/cystathionine beta-synthase, pyridoxal-phosphate attachment site [IPR001216] (1); Tryptophan synthase beta subunit-like PLP-dependent enzyme [IPR001926] (1)	-	-	P_trifoliata_00033_mRNA_71.1
GF0044129	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00033_mRNA_7.1
GF0044128	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00033_mRNA_6.1
GF0044127	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00033_mRNA_59.1
GF0044126	0	0	1	Early light-induced protein, chloroplastic (1)		Chlorophyll A-B binding protein [IPR022796] (1); Chlorophyll a/b binding protein domain [IPR023329] (1)	-	-	P_trifoliata_00033_mRNA_5.1
GF0044125	0	0	1	Pentatricopeptide repeat-containing family protein (1)	protein binding [GO:0005515 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Pentatricopeptide repeat [IPR002885] (1); Tetratricopeptide-like helical domain [IPR011990] (1); DYW domain [IPR032867] (1)	-	-	P_trifoliata_00033_mRNA_33.1
GF0044124	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00033_mRNA_3.1
GF0044123	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00033_mRNA_24.1
GF0044122	0	0	1	Hypothetical protein (1)		Dymeclin [IPR019142] (1); Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	-	P_trifoliata_00033_mRNA_2.1
GF0044121	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00033_mRNA_17.1
GF0044120	0	0	1	Guanylate kinase (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)	-	-	P_trifoliata_00033_mRNA_127.1
GF0044119	0	0	1	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	-	P_trifoliata_00033_mRNA_120.1
GF0044118	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00033_mRNA_118.1
GF0044117	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00033_mRNA_116.1
GF0044116	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00033_mRNA_115.1
GF0044115	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00033_mRNA_108.1
GF0044114	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00033_mRNA_107.1
GF0044113	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00033_mRNA_104.1
GF0044112	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00033_mRNA_103.1
GF0044111	0	0	1	Early light-induced protein, chloroplastic (1)		Chlorophyll a/b binding protein domain [IPR023329] (1)	-	-	P_trifoliata_00033_mRNA_1.1
GF0044110	0	0	1	Acid phosphatase 1 (1)		Sieve element occlusion, C-terminal [IPR027944] (1); Sieve element occlusion, N-terminal [IPR027942] (1)	-	-	P_trifoliata_00032_mRNA_97.1
GF0044109	0	0	1	Hypothetical protein (1)	catalytic activity [GO:0003824 molecular_function] (1)	Aldolase-type TIM barrel [IPR013785] (1); Glycosyl hydrolases 36 [IPR008811] (1)	-	-	P_trifoliata_00032_mRNA_94.1
GF0044108	0	0	1	Hypothetical protein (1)		Glyoxal oxidase, N-terminal [IPR009880] (1)	-	-	P_trifoliata_00032_mRNA_88.1
GF0044107	0	0	1	Terpene synthase 21, putative (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); Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (1); Terpene synthase, N-terminal domain [IPR001906] (1); Terpene synthase, metal-binding domain [IPR005630] (1)	-	-	P_trifoliata_00032_mRNA_80.1
GF0044106	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00032_mRNA_64.1
GF0044105	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00032_mRNA_57.1
GF0044104	0	0	1	Hypothetical protein (1)	anaphase-promoting complex [GO:0005680 cellular_component] (1); regulation of mitotic cell cycle spindle assembly checkpoint [GO:0090266 biological_process] (1)	Anaphase-promoting complex subunit 15 [IPR026182] (1)	-	-	P_trifoliata_00032_mRNA_56.1
GF0044103	0	0	1	Armadillo repeat only 2 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)	-	-	P_trifoliata_00032_mRNA_48.1
GF0044102	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00032_mRNA_112.1
GF0044101	0	0	1	Peptidase C78, ubiquitin fold modifier-specific peptidase 1/ 2 isoform 1 (1)		Pentatricopeptide repeat [IPR002885] (1); Peptidase C78, ubiquitin fold modifier-specific peptidase 1/ 2 [IPR012462] (1)	-	-	P_trifoliata_00032_mRNA_108.1
GF0044100	0	0	1	Hypothetical protein (1)		Sieve element occlusion, N-terminal [IPR027942] (1)	-	-	P_trifoliata_00032_mRNA_102.1
GF0044099	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00031_mRNA_99.1
GF0044098	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00031_mRNA_94.1
GF0044097	0	0	1	Bifunctional dihydroflavonol 4-reductase/flavanone 4-reductase (1)	coenzyme binding [GO:0050662 molecular_function] (1); catalytic activity [GO:0003824 molecular_function] (1)	NAD-dependent epimerase/dehydratase, N-terminal domain [IPR001509] (1); NAD(P)-binding domain [IPR016040] (1)	-	-	P_trifoliata_00031_mRNA_81.1

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*
GF0044096	0	0	1	Hypothetical protein (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/FYVE/PHD-type [IPR013083] (1)	-	-	P_trifoliata_00031_mRNA_7.1
GF0044095	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00031_mRNA_60.1
GF0044094	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00031_mRNA_58.1
GF0044093	0	0	1	Transcription factor HBP-1b(C1) (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); transcription, DNA-templated [GO:0006351 biological_process] (1)	Basic-leucine zipper domain [IPR004827] (1); Transcription factor TGA like domain [IPR025422] (1)	-	-	P_trifoliata_00031_mRNA_54.1
GF0044092	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00031_mRNA_4.1
GF0044091	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00031_mRNA_35.1
GF0044090	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00031_mRNA_34.1
GF0044089	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00031_mRNA_3.1
GF0044088	0	0	1	Phosphate transporter PHO1-like protein (1)	integral component of membrane [GO:0016021 cellular_component] (1)	EXS, C-terminal [IPR004342] (1)	-	-	P_trifoliata_00031_mRNA_14.1
GF0044087	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF630 [IPR006868] (1)	-	-	P_trifoliata_00030_mRNA_98.1
GF0044086	0	0	1	DUF241 domain protein (1)		Protein of unknown function DUF241, plant [IPR004320] (1)	-	-	P_trifoliata_00030_mRNA_92.1
GF0044085	0	0	1	BRCA1-A complex subunit BRE (1)		Brain/reproductive organ-expressed protein [IPR010358] (1)	-	-	P_trifoliata_00030_mRNA_9.1
GF0044084	0	0	1	Cytoplasmic tRNA 2-thiolation protein 1 (1)	tRNA processing [GO:0008033 biological_process] (1); tRNA wobble uridine modification [GO:0002098 biological_process] (1); tRNA thio-modification [GO:0034227 biological_process] (1); tRNA binding [GO:0000049 molecular_function] (1)	Cytoplasmic tRNA 2-thiolation protein 1 [IPR000541] (1); 2-thiocytidine tRNA biosynthesis protein, TtcA [IPR012089] (1); tRNA(Ile)-lysidine/2-thiocytidine synthase, N-terminal [IPR011063] (1); Cytoplasmic tRNA 2-thiolation protein 1, C-terminal [IPR032442] (1); Rossmann-like alpha/beta/alpha sandwich fold [IPR014729] (1)	-	-	P_trifoliata_00030_mRNA_83.1
GF0044083	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00030_mRNA_73.1
GF0044082	0	0	1	Hypothetical protein (1)		Root cap [IPR009646] (1)	-	-	P_trifoliata_00030_mRNA_72.1
GF0044081	0	0	1	E3 ubiquitin-protein ligase UPL3-like protein (1)		Thioredoxin-like fold [IPR012336] (1)	-	-	P_trifoliata_00030_mRNA_54.1
GF0044080	0	0	1	ER lumen protein retaining receptor (1)	protein retention in ER lumen [GO:0006621 biological_process] (1); ER retention sequence binding [GO:0046923 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1)	ER lumen protein retaining receptor [IPR000133] (1)	-	-	P_trifoliata_00030_mRNA_5.1
GF0044079	0	0	1	Hypothetical protein (1)		RGS domain [IPR016137] (1)	-	-	P_trifoliata_00030_mRNA_4.1
GF0044078	0	0	1	GDSL esterase/lipase EXL3 (1)	hydrolase activity, acting on ester bonds [GO:0016788 molecular_function] (1)	GDSL lipase/esterase [IPR001087] (1); SGNH hydrolase-type esterase domain [IPR013830] (1)	-	-	P_trifoliata_00030_mRNA_39.1
GF0044077	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00030_mRNA_136.1
GF0044076	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00030_mRNA_135.1
GF0044075	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00030_mRNA_134.1
GF0044074	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00030_mRNA_133.1
GF0044073	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00030_mRNA_125.1
GF0044072	0	0	1	Ankyrin repeat family protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat [IPR002110] (1); Ankyrin repeat-containing domain [IPR020683] (1)	-	-	P_trifoliata_00030_mRNA_121.1
GF0044071	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00030_mRNA_117.1
GF0044070	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00030_mRNA_114.1
GF0044069	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00030_mRNA_110.1
GF0044068	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat [IPR002110] (1); Ankyrin repeat-containing domain [IPR020683] (1)	-	-	P_trifoliata_00030_mRNA_109.1
GF0044067	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1); response to stress [GO:0006950 biological_process] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1); UspA [IPR006016] (1); Rossmann-like alpha/beta/alpha sandwich fold [IPR014729] (1); Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00030_mRNA_103.1
GF0044066	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00029_mRNA_95.1
GF0044065	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00029_mRNA_93.1
GF0044064	0	0	1	Hypothetical protein (1)		Ankyrin repeat-containing domain [IPR020683] (1)	-	-	P_trifoliata_00029_mRNA_92.1
GF0044063	0	0	1	Ankyrin repeat protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat [IPR002110] (1); Ankyrin repeat-containing domain [IPR020683] (1); PGG domain [IPR026961] (1)	-	-	P_trifoliata_00029_mRNA_91.1
GF0044062	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00029_mRNA_89.1
GF0044061	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00029_mRNA_88.1
GF0044060	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00029_mRNA_85.1
GF0044059	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00029_mRNA_77.1
GF0044058	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00029_mRNA_76.1
GF0044057	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00029_mRNA_75.1
GF0044056	0	0	1	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	-	P_trifoliata_00029_mRNA_73.1
GF0044055	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00029_mRNA_72.1
GF0044054	0	0	1	Hypothetical protein (1)	nutrient reservoir activity [GO:0045735 molecular_function] (1); manganese ion binding [GO:0030145 molecular_function] (1)	RmlC-like jelly roll fold [IPR014710] (1); Cupin 1 [IPR006045] (1); Germin, manganese binding site [IPR019780] (1); RmlC-like cupin domain [IPR011051] (1)	-	-	P_trifoliata_00029_mRNA_70.1
GF0044053	0	0	1	Pentatricopeptide repeat (PPR) superfamily protein, putative (1)		Pentatricopeptide repeat [IPR002885] (1)	-	-	P_trifoliata_00029_mRNA_67.1
GF0044052	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00029_mRNA_64.1
GF0044051	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00029_mRNA_63.1
GF0044050	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00029_mRNA_61.1
GF0044049	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00029_mRNA_60.1
GF0044048	0	0	1	Hypothetical protein (1)	hydrolase activity [GO:0016787 molecular_function] (1)	Alpha/Beta hydrolase fold [IPR029058] (1); Dienelactone hydrolase [IPR002925] (1)	-	-	P_trifoliata_00029_mRNA_5.1
GF0044047	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00029_mRNA_43.1
GF0044046	0	0	1	Hypothetical protein (1)	chromatin binding [GO:0003682 molecular_function] (1)	Bromo adjacent homology (BAH) domain [IPR001025] (1)	-	-	P_trifoliata_00029_mRNA_42.1
GF0044045	0	0	1	Hypothetical protein (1)	chromatin binding [GO:0003682 molecular_function] (1)	Bromo adjacent homology (BAH) domain [IPR001025] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	-	P_trifoliata_00029_mRNA_41.1
GF0044044	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00029_mRNA_40.1
GF0044043	0	0	1	Putative disease resistance protein RGA1 (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00029_mRNA_39.1
GF0044042	0	0	1	Hypothetical protein (1)		S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	-	P_trifoliata_00029_mRNA_38.1
GF0044041	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	-	P_trifoliata_00029_mRNA_37.1
GF0044040	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00029_mRNA_36.1
GF0044039	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00029_mRNA_35.1
GF0044038	0	0	1	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)	-	-	P_trifoliata_00029_mRNA_34.1
GF0044037	0	0	1	Hypothetical protein (1)	chromatin binding [GO:0003682 molecular_function] (1)	Bromo adjacent homology (BAH) domain [IPR001025] (1)	-	-	P_trifoliata_00029_mRNA_33.1
GF0044036	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00029_mRNA_32.1
GF0044035	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00029_mRNA_30.1
GF0044034	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00029_mRNA_27.1
GF0044033	0	0	1	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	-	P_trifoliata_00029_mRNA_26.1
GF0044032	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00029_mRNA_23.1
GF0044031	0	0	1	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); Retrotransposon gag domain [IPR005162] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1)	-	-	P_trifoliata_00029_mRNA_2.1
GF0044030	0	0	1	UDP-glycosyltransferase 74B1 (1)	transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	-	-	P_trifoliata_00029_mRNA_18.1
GF0044029	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00029_mRNA_17.1
GF0044028	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00029_mRNA_16.1
GF0044027	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00029_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*
GF0044026	0	0	1	Hypothetical protein (1)	protein folding [GO:0006457 biological_process] (1)	Peptidyl-prolyl cis-trans isomerase, FKBP-type [IPR023566] (1); FKBP-type peptidyl-prolyl cis-trans isomerase domain [IPR001179] (1)	-	-	P_trifoliata_00029_mRNA_14.1
GF0044025	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00029_mRNA_12.1
GF0044024	0	0	1	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1)	Myc-type, basic helix-loop-helix (bHLH) domain [IPR011598] (1)	-	-	P_trifoliata_00029_mRNA_11.1
GF0044023	0	0	1	Translocon at the outer envelope membrane ofs 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)	-	-	P_trifoliata_00028_mRNA_80.1
GF0044022	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00028_mRNA_67.1
GF0044021	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00028_mRNA_63.1
GF0044020	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00028_mRNA_52.1
GF0044019	0	0	1	Porphobilinogen deaminase, chloroplastic (1)	peptidyl-pyrromethane cofactor linkage [GO:0018160 biological_process] (1); tetrapyrrole biosynthetic process [GO:0033014 biological_process] (1); hydroxymethylbilane synthase activity [GO:0004418 molecular_function] (1)	Porphobilinogen deaminase [IPR000860] (1); Porphobilinogen deaminase, C-terminal [IPR022418] (1); Porphobilinogen deaminase, N-terminal [IPR022417] (1); Porphobilinogen deaminase, dipyrromethane cofactor binding site [IPR022419] (1)	-	-	P_trifoliata_00028_mRNA_48.1
GF0044018	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00028_mRNA_42.1
GF0044017	0	0	1	Hypothetical protein (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); NB-ARC [IPR002182] (1); AAA+ ATPase domain [IPR003593] (1); Leucine-rich repeat [IPR001611] (1)	-	-	P_trifoliata_00028_mRNA_40.1
GF0044016	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00028_mRNA_39.1
GF0044015	0	0	1	Disease resistance RPS5-like protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	-	P_trifoliata_00028_mRNA_33.1
GF0044014	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00028_mRNA_31.1
GF0044013	0	0	1	Disease resistance protein family (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00028_mRNA_30.1
GF0044012	0	0	1	Disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	-	P_trifoliata_00028_mRNA_28.1
GF0044011	0	0	1	Putative serine/threonine-protein kinase NAK (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); Protein kinase, ATP binding site [IPR017441] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1)	-	-	P_trifoliata_00028_mRNA_131.1
GF0044010	0	0	1	16 kDa. phloem protein 2 (1)	protein binding [GO:0005515 molecular_function] (1)	C2 domain [IPR000008] (1)	-	-	P_trifoliata_00028_mRNA_128.1
GF0044009	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00028_mRNA_102.1
GF0044008	0	0	1	Hypothetical protein (1)		Peptidase S8 propeptide/proteinase inhibitor I9 [IPR010259] (1)	-	-	P_trifoliata_00028_mRNA_101.1
GF0044007	0	0	1	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)	-	-	P_trifoliata_00027_mRNA_99.1
GF0044006	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00027_mRNA_96.1
GF0044005	0	0	1	Hypothetical protein (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)	-	-	P_trifoliata_00027_mRNA_88.1
GF0044004	0	0	1	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)	-	-	P_trifoliata_00027_mRNA_86.1
GF0044003	0	0	1	Putative peptide transporter 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); Major facilitator superfamily domain [IPR020846] (1)	-	-	P_trifoliata_00027_mRNA_85.1
GF0044002	0	0	1	Peptide transporter PTR3-A (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)	-	-	P_trifoliata_00027_mRNA_83.1
GF0044001	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00027_mRNA_80.1
GF0044000	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00027_mRNA_79.1
GF0043999	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00027_mRNA_78.1
GF0043998	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00027_mRNA_77.1
GF0043997	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00027_mRNA_76.1
GF0043996	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00027_mRNA_75.1
GF0043995	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00027_mRNA_74.1
GF0043994	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00027_mRNA_7.1
GF0043993	0	0	1	Hypothetical protein (1)	response to biotic stimulus [GO:0009607 biological_process] (1); defense response [GO:0006952 biological_process] (1)	START-like domain [IPR023393] (1); Bet v I/Major latex protein [IPR000916] (1)	-	-	P_trifoliata_00027_mRNA_69.1
GF0043992	0	0	1	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); Cytochrome P450, conserved site [IPR017972] (1)	-	-	P_trifoliata_00027_mRNA_67.1
GF0043991	0	0	1	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); Helix-turn-helix, base-excision DNA repair, C-terminal [IPR023170] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	-	-	P_trifoliata_00027_mRNA_66.1
GF0043990	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00027_mRNA_62.1
GF0043989	0	0	1	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)	-	-	P_trifoliata_00027_mRNA_61.1
GF0043988	0	0	1	TMV resistance N (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00027_mRNA_6.1
GF0043987	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00027_mRNA_59.1
GF0043986	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00027_mRNA_56.1
GF0043985	0	0	1	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)	-	-	P_trifoliata_00027_mRNA_53.1
GF0043984	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00027_mRNA_52.1
GF0043983	0	0	1	Hypothetical protein (1)		LOG family [IPR031100] (1)	-	-	P_trifoliata_00027_mRNA_51.1
GF0043982	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00027_mRNA_5.1
GF0043981	0	0	1	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)	-	-	P_trifoliata_00027_mRNA_48.1
GF0043980	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00027_mRNA_47.1
GF0043979	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00027_mRNA_44.1
GF0043978	0	0	1	Hypothetical protein (1)		LOG family [IPR031100] (1)	-	-	P_trifoliata_00027_mRNA_42.1
GF0043977	0	0	1	NBS type disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00027_mRNA_4.1
GF0043976	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00027_mRNA_38.1
GF0043975	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00027_mRNA_37.1
GF0043974	0	0	1	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)	-	-	P_trifoliata_00027_mRNA_35.1
GF0043973	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00027_mRNA_34.1
GF0043972	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00027_mRNA_32.1
GF0043971	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00027_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*
GF0043970	0	0	1	Peroxidase 4 (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); Peroxidase, active site [IPR019794] (1); Peroxidases heam-ligand binding site [IPR019793] (1); Plant peroxidase [IPR000823] (1); Haem peroxidase [IPR010255] (1)	-	-	P_trifoliata_00027_mRNA_27.1
GF0043969	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00027_mRNA_26.1
GF0043968	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00027_mRNA_20.1
GF0043967	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00027_mRNA_19.1
GF0043966	0	0	1	Pentatricopeptide (PPR) repeat protein (1)		Pentatricopeptide repeat [IPR002885] (1)	-	-	P_trifoliata_00027_mRNA_14.1
GF0043965	0	0	1	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	-	P_trifoliata_00027_mRNA_1.1
GF0043964	0	0	1	Hypothetical protein (1)	transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (1); sequence-specific DNA binding [GO:0043565 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	Basic-leucine zipper domain [IPR004827] (1)	-	-	P_trifoliata_00026_mRNA_94.1
GF0043963	0	0	1	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)	-	-	P_trifoliata_00026_mRNA_82.1
GF0043962	0	0	1	Endoplasmatic reticulum retrieval protein 1B isoform 1 (1)	integral component of membrane [GO:0016021 cellular_component] (1)	Retrieval of early ER protein Rer1 [IPR004932] (1)	-	-	P_trifoliata_00026_mRNA_72.1
GF0043961	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00026_mRNA_38.1
GF0043960	0	0	1	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); microtubule binding [GO:0008017 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Kinesin-like protein [IPR027640] (1); Kinesin motor domain, conserved site [IPR019821] (1); Kinesin motor domain [IPR001752] (1)	-	-	P_trifoliata_00026_mRNA_138.1
GF0043959	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00026_mRNA_137.1
GF0043958	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00026_mRNA_126.1
GF0043957	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00025_mRNA_98.1
GF0043956	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00025_mRNA_94.1
GF0043955	0	0	1	Nucleoside diphosphate kinase (1)	GTP biosynthetic process [GO:0006183 biological_process] (1); UTP biosynthetic process [GO:0006228 biological_process] (1); nucleoside diphosphate phosphorylation [GO:0006165 biological_process] (1); CTP biosynthetic process [GO:0006241 biological_process] (1); nucleoside diphosphate kinase activity [GO:0004550 molecular_function] (1)	Nucleoside diphosphate kinase [IPR001564] (1)	-	-	P_trifoliata_00025_mRNA_93.1
GF0043954	0	0	1	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	-	-	P_trifoliata_00025_mRNA_9.1
GF0043953	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00025_mRNA_84.1
GF0043952	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00025_mRNA_83.1
GF0043951	0	0	1	S-adenosyl-L-methionine:salicylic acid carboxyl methyltransferase, putative (1)	methyltransferase activity [GO:0008168 molecular_function] (1)	SAM dependent carboxyl methyltransferase [IPR005299] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	-	P_trifoliata_00025_mRNA_81.1
GF0043950	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00025_mRNA_73.1
GF0043949	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00025_mRNA_66.1
GF0043948	0	0	1	Transcriptional adapter ADA2b-like protein (1)	DNA binding [GO:0003677 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Homeodomain-like [IPR009057] (1); SWIRM domain [IPR007526] (1)	-	-	P_trifoliata_00025_mRNA_63.1
GF0043947	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00025_mRNA_6.1
GF0043946	0	0	1	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)	-	-	P_trifoliata_00025_mRNA_56.1
GF0043945	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00025_mRNA_55.1
GF0043944	0	0	1	Dnajc14 protein, putative (1)		DnaJ domain [IPR001623] (1)	-	-	P_trifoliata_00025_mRNA_53.1
GF0043943	0	0	1	Hypothetical protein (1)	nucleotide binding [GO:0000166 molecular_function] (1); metal ion binding [GO:0046872 molecular_function] (1)	Cation-transporting P-type ATPase, N-terminal [IPR004014] (1); P-type ATPase, A domain [IPR008250] (1)	-	-	P_trifoliata_00025_mRNA_50.1
GF0043942	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00025_mRNA_45.1
GF0043941	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00025_mRNA_41.1
GF0043940	0	0	1	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)	-	-	P_trifoliata_00025_mRNA_4.1
GF0043939	0	0	1	Thymidine kinase (1)	thymidine kinase activity [GO:0004797 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Thymidine kinase, conserved site [IPR020633] (1); Thymidine kinase [IPR001267] (1)	-	-	P_trifoliata_00025_mRNA_34.1
GF0043938	0	0	1	Hypothetical protein (1)		Pectin lyase fold [IPR012334] (1); Pectin lyase fold/virulence factor [IPR011050] (1)	-	-	P_trifoliata_00025_mRNA_24.1
GF0043937	0	0	1	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)	-	-	P_trifoliata_00025_mRNA_23.1
GF0043936	0	0	1	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); Parallel beta-helix repeat [IPR006626] (1); Glycoside hydrolase, family 28 [IPR000743] (1)	-	-	P_trifoliata_00025_mRNA_22.1
GF0043935	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00025_mRNA_19.1
GF0043934	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00025_mRNA_18.1
GF0043933	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00025_mRNA_151.1
GF0043932	0	0	1	Hypothetical protein (1)	calcium ion binding [GO:0005509 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	EF-hand domain pair [IPR011992] (1); EH domain [IPR000261] (1); EF-hand domain [IPR002048] (1)	-	-	P_trifoliata_00025_mRNA_131.1
GF0043931	0	0	1	Hypothetical protein (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); N,N-dimethylaniline monooxygenase activity [GO:0004499 molecular_function] (1); NADP binding [GO:0050661 molecular_function] (1)	FAD/NAD(P)-binding domain [IPR023753] (1); Flavin monooxygenase-like [IPR020946] (1)	-	-	P_trifoliata_00025_mRNA_108.1
GF0043930	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00025_mRNA_101.1
GF0043929	0	0	1	Putative intracellular protein transport protein USO1-like (1)		Zein-binding domain [IPR007656] (1)	-	-	P_trifoliata_00024_mRNA_97.1
GF0043928	0	0	1	Photosystem II reaction center W protein, chloroplastic (1)	photosystem II [GO:0009523 cellular_component] (1); photosynthesis [GO:0015979 biological_process] (1); chloroplast [GO:0009507 cellular_component] (1)	Photosystem II PsbW, class 2 [IPR009806] (1)	-	-	P_trifoliata_00024_mRNA_85.1
GF0043927	0	0	1	NAC domain-containing protein 67 (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); DNA binding [GO:0003677 molecular_function] (1)	NAC domain [IPR003441] (1)	-	-	P_trifoliata_00024_mRNA_8.1
GF0043926	0	0	1	Spindle pole body-associated CIK1 (1)			-	-	P_trifoliata_00024_mRNA_7.1
GF0043925	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00024_mRNA_50.1
GF0043924	0	0	1	Divergent CCT motif protein (1)		Tify domain [IPR010399] (1); CO/COL/TOC1, conserved site [IPR018467] (1)	-	-	P_trifoliata_00024_mRNA_45.1
GF0043923	0	0	1	Homocysteine S-methyltransferase-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)	Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Homocysteine-binding domain [IPR003726] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	-	-	P_trifoliata_00024_mRNA_33.1
GF0043922	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00024_mRNA_15.1
GF0043921	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00024_mRNA_142.1
GF0043920	0	0	1	Caffeic acid 3-O-methyltransferase (1)	methyltransferase activity [GO:0008168 molecular_function] (1); O-methyltransferase activity [GO:0008171 molecular_function] (1)	O-methyltransferase, family 2 [IPR001077] (1); O-methyltransferase COMT-type [IPR016461] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	-	P_trifoliata_00024_mRNA_140.1
GF0043919	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00024_mRNA_139.1
GF0043918	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00024_mRNA_138.1
GF0043917	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00024_mRNA_135.1
GF0043916	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00024_mRNA_134.1

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*
GF0043915	0	0	1	Hypothetical protein (1)	cysteine-type endopeptidase inhibitor activity [GO:0004869 molecular_function] (1)	Proteinase inhibitor I25, cystatin, conserved region [IPR020381] (1); Cystatin [IPR027214] (1); Proteinase inhibitor I25, cystatin, conserved site [IPR018073] (1)	-	-	P_trifoliata_00024_mRNA_133.1
GF0043914	0	0	1	Cysteine proteinase inhibitor (1)	cysteine-type endopeptidase inhibitor activity [GO:0004869 molecular_function] (1)	Proteinase inhibitor I25, cystatin, conserved region [IPR020381] (1); Cystatin [IPR027214] (1); Proteinase inhibitor I25, cystatin, conserved site [IPR018073] (1); Cystatin domain [IPR000010] (1)	-	-	P_trifoliata_00024_mRNA_132.1
GF0043913	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00024_mRNA_131.1
GF0043912	0	0	1	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)	-	-	P_trifoliata_00024_mRNA_130.1
GF0043911	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00024_mRNA_129.1
GF0043910	0	0	1	Transcriptional regulator SUPERMAN (1)	metal ion binding [GO:0046872 molecular_function] (1)	Zinc finger, C2H2 [IPR007087] (1)	-	-	P_trifoliata_00024_mRNA_114.1
GF0043909	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00024_mRNA_108.1
GF0043908	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00024_mRNA_107.1
GF0043907	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00024_mRNA_106.1
GF0043906	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00024_mRNA_105.1
GF0043905	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00024_mRNA_104.1
GF0043904	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00024_mRNA_100.1
GF0043903	0	0	1	FAR1 DNA-binding domain protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FAR1 DNA binding domain [IPR004330] (1); FHY3/FAR1 family [IPR031052] (1)	-	-	P_trifoliata_00023_mRNA_99.1
GF0043902	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00023_mRNA_92.1
GF0043901	0	0	1	Embryo defective 2752 protein (1)			-	-	P_trifoliata_00023_mRNA_8.3
GF0043900	0	0	1	Hypothetical protein (1)		Domain unknown function DUF295 [IPR005174] (1); Myb/SANT-like domain [IPR024752] (1)	-	-	P_trifoliata_00023_mRNA_75.1
GF0043899	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00023_mRNA_65.1
GF0043898	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00023_mRNA_57.1
GF0043897	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00023_mRNA_51.1
GF0043896	0	0	1	Hypothetical protein (1)	chromatin binding [GO:0003682 molecular_function] (1)	Bromo adjacent homology (BAH) domain [IPR001025] (1); WLM domain [IPR013536] (1)	-	-	P_trifoliata_00023_mRNA_50.1
GF0043895	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00023_mRNA_46.1
GF0043894	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00023_mRNA_45.1
GF0043893	0	0	1	Tetraspanin family protein (1)	integral component of membrane [GO:0016021 cellular_component] (1)	Tetraspanin [IPR000301] (1); Tetraspanin/Peripherin [IPR018499] (1)	-	-	P_trifoliata_00023_mRNA_4.1
GF0043892	0	0	1	Isoprene synthase, chloroplastic (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)	-	-	P_trifoliata_00023_mRNA_38.1
GF0043891	0	0	1	Probable 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)	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)	-	-	P_trifoliata_00023_mRNA_37.1
GF0043890	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	-	P_trifoliata_00023_mRNA_33.1
GF0043889	0	0	1	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1); Pentatricopeptide repeat [IPR002885] (1); Retroviral aspartyl protease [IPR013242] (1); Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	-	P_trifoliata_00023_mRNA_31.1
GF0043888	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00023_mRNA_28.1
GF0043887	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00023_mRNA_24.1
GF0043886	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00023_mRNA_18.1
GF0043885	0	0	1	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)	-	-	P_trifoliata_00023_mRNA_17.1
GF0043884	0	0	1	Hypothetical protein (1)		Harbinger transposase-derived nuclease domain [IPR027806] (1)	-	-	P_trifoliata_00023_mRNA_14.1
GF0043883	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00023_mRNA_126.1
GF0043882	0	0	1	Hypothetical protein (1)		Protein kinase-like domain [IPR011009] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00023_mRNA_124.1
GF0043881	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00023_mRNA_123.1
GF0043880	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00023_mRNA_121.1
GF0043879	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00023_mRNA_12.1
GF0043878	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00023_mRNA_109.1
GF0043877	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00023_mRNA_108.1
GF0043876	0	0	1	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	-	-	P_trifoliata_00023_mRNA_107.1
GF0043875	0	0	1	Hypothetical protein (1)		Gag-polypeptide of LTR copia-type [IPR029472] (1)	-	-	P_trifoliata_00023_mRNA_106.1
GF0043874	0	0	1	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/tyrosine-protein kinase catalytic domain [IPR001245] (1)	-	-	P_trifoliata_00023_mRNA_105.1
GF0043873	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00023_mRNA_103.1
GF0043872	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00023_mRNA_101.1
GF0043871	0	0	1	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)	-	-	P_trifoliata_00022_mRNA_92.1
GF0043870	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00022_mRNA_91.1
GF0043869	0	0	1	Hypothetical protein (1)		SGNH hydrolase-type esterase domain [IPR013830] (1)	-	-	P_trifoliata_00022_mRNA_76.1
GF0043868	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00022_mRNA_6.1
GF0043867	0	0	1	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)	-	-	P_trifoliata_00022_mRNA_5.1
GF0043866	0	0	1	Hypothetical protein (1)	phosphogluconate dehydrogenase (decarboxylating) activity [GO:0004616 molecular_function] (1); pentose-phosphate shunt [GO:0006098 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	6-phosphogluconate dehydrogenase [IPR006183] (1); NAD(P)-binding domain [IPR016040] (1); 6-phosphogluconate dehydrogenase, C-terminal [IPR006114] (1); 6-phosphogluconate dehydrogenase, domain 2 [IPR013328] (1); 6-phosphogluconate dehydrogenase, NADP-binding [IPR006115] (1); 6-phosphogluconate dehydrogenase C-terminal domain-like [IPR008927] (1)	-	-	P_trifoliata_00022_mRNA_49.1
GF0043865	0	0	1	Hypothetical protein (1)		Major facilitator superfamily domain [IPR020846] (1)	-	-	P_trifoliata_00022_mRNA_44.1
GF0043864	0	0	1	Germination family protein (1)		NADH-ubiquinone reductase complex 1 MLRQ subunit [IPR010530] (1)	-	-	P_trifoliata_00022_mRNA_22.1
GF0043863	0	0	1	PLC-like phosphodiesterases 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); Phosphatidylinositol-specific phospholipase C, X domain [IPR000909] (1)	-	-	P_trifoliata_00022_mRNA_21.1
GF0043862	0	0	1	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)	-	-	P_trifoliata_00022_mRNA_20.1
GF0043861	0	0	1	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	-	-	P_trifoliata_00022_mRNA_2.1
GF0043860	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00022_mRNA_148.1
GF0043859	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00022_mRNA_147.1
GF0043858	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00022_mRNA_146.1
GF0043857	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00022_mRNA_145.1
GF0043856	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00022_mRNA_143.1
GF0043855	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00022_mRNA_142.1
GF0043854	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00022_mRNA_141.1
GF0043853	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00022_mRNA_140.1
GF0043852	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00022_mRNA_139.1
GF0043851	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00022_mRNA_137.1

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*
GF0043850	0	0	1	Muconate cycloisomerase, putative (1)	metabolic process [GO:0008152 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1)	Mandelate racemase/muconate lactonizing enzyme, N-terminal domain [IPR013341] (1); Mandelate racemase/muconate lactonizing enzyme/methylaspartate ammonia-lyase [IPR001354] (1); Mandelate racemase/muconate lactonizing enzyme, C-terminal [IPR013342] (1); Enolase N-terminal domain-like [IPR029017] (1); Enolase C-terminal domain-like [IPR029065] (1)	-	-	P_trifoliata_00022_mRNA_134.1
GF0043849	0	0	1	Lipid transfer protein (1)		Bifunctional inhibitor/plant lipid transfer protein/seed storage helical domain [IPR016140] (1)	-	-	P_trifoliata_00022_mRNA_133.1
GF0043848	0	0	1	Lipid transfer protein (1)		Bifunctional inhibitor/plant lipid transfer protein/seed storage helical domain [IPR016140] (1)	-	-	P_trifoliata_00022_mRNA_132.1
GF0043847	0	0	1	Alpha/beta hydrolase family 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 S7e [IPR000554] (1); Alpha/Beta hydrolase fold [IPR029058] (1); Alpha/beta hydrolase fold-1 [IPR000073] (1)	-	-	P_trifoliata_00022_mRNA_108.1
GF0043846	0	0	1	F-box/RNI-like superfamily protein isoform 2 (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); F-box domain [IPR001810] (1)	-	-	P_trifoliata_00021_mRNA_87.1
GF0043845	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00021_mRNA_83.1
GF0043844	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00021_mRNA_8.1
GF0043843	0	0	1	Hydroxyphenylpyruvate reductase (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); NAD(P)-binding domain [IPR016040] (1); D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding domain [IPR006140] (1)	-	-	P_trifoliata_00021_mRNA_75.1
GF0043842	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00021_mRNA_68.1
GF0043841	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00021_mRNA_6.1
GF0043840	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00021_mRNA_55.1
GF0043839	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00021_mRNA_53.1
GF0043838	0	0	1	Secreted glycoprotein 3 (1)		Bulb-type lectin domain [IPR001480] (1)	-	-	P_trifoliata_00021_mRNA_47.1
GF0043837	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00021_mRNA_41.1
GF0043836	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00021_mRNA_33.1
GF0043835	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00021_mRNA_3.1
GF0043834	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00021_mRNA_18.1
GF0043833	0	0	1	Hypothetical protein (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)	-	-	P_trifoliata_00021_mRNA_16.1
GF0043832	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00021_mRNA_144.1
GF0043831	0	0	1	Fe-S cluster assembly protein SufD (1)	iron-sulfur cluster assembly [GO:0016226 biological_process] (1)	SUF system FeS cluster assembly, SufBD [IPR000825] (1); SUF system FeS cluster assembly, SufD [IPR011542] (1)	-	-	P_trifoliata_00021_mRNA_143.1
GF0043830	0	0	1	Hypothetical protein (1)		Harbinger transposase-derived nuclease domain [IPR027806] (1)	-	-	P_trifoliata_00021_mRNA_136.1
GF0043829	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00021_mRNA_119.1
GF0043828	0	0	1	Cytochrome c oxidase assembly protein COX19 (1)		CHCH [IPR010625] (1)	-	-	P_trifoliata_00021_mRNA_106.1
GF0043827	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00020_mRNA_78.1
GF0043826	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00020_mRNA_51.1
GF0043825	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00020_mRNA_4.1
GF0043824	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00020_mRNA_39.1
GF0043823	0	0	1	Hypothetical protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	-	-	P_trifoliata_00020_mRNA_38.1
GF0043822	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00020_mRNA_37.1
GF0043821	0	0	1	Hypothetical protein (1)		Gag-polypeptide of LTR copia-type [IPR029472] (1)	-	-	P_trifoliata_00020_mRNA_28.1
GF0043820	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00020_mRNA_26.1
GF0043819	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00020_mRNA_2.1
GF0043818	0	0	1	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)	-	-	P_trifoliata_00020_mRNA_16.1
GF0043817	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00020_mRNA_128.1
GF0043816	0	0	1	Phospholipase, patatin family (1)	metabolic process [GO:0008152 biological_process] (1)	Acyl transferase/acyl hydrolase/lysophospholipase [IPR016035] (1)	-	-	P_trifoliata_00020_mRNA_125.1
GF0043815	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00020_mRNA_121.1
GF0043814	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00020_mRNA_111.1
GF0043813	0	0	1	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)	-	-	P_trifoliata_00020_mRNA_104.1
GF0043812	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00020_mRNA_101.1
GF0043811	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00019_mRNA_96.1
GF0043810	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00019_mRNA_95.1
GF0043809	0	0	1	Receptor like protein 27 (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00019_mRNA_92.1
GF0043808	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00019_mRNA_91.1
GF0043807	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00019_mRNA_90.1
GF0043806	0	0	1	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)	-	-	P_trifoliata_00019_mRNA_89.1
GF0043805	0	0	1	Putative disease resistance gene NBS-LRR family protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00019_mRNA_87.1
GF0043804	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00019_mRNA_85.1
GF0043803	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00019_mRNA_84.1
GF0043802	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00019_mRNA_83.1
GF0043801	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00019_mRNA_81.1
GF0043800	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00019_mRNA_63.1
GF0043799	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00019_mRNA_59.1
GF0043798	0	0	1	Xylem serine proteinase 1 (1)		Peptidase S8, subtilisin-related [IPR015500] (1)	-	-	P_trifoliata_00019_mRNA_51.1
GF0043797	0	0	1	Basic helix-loop-helix family protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1)	Myc-type, basic helix-loop-helix (bHLH) domain [IPR011598] (1)	-	-	P_trifoliata_00019_mRNA_46.1
GF0043796	0	0	1	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)	-	-	P_trifoliata_00019_mRNA_43.1
GF0043795	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00019_mRNA_32.1
GF0043794	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00019_mRNA_22.1
GF0043793	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00019_mRNA_158.1
GF0043792	0	0	1	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	-	-	P_trifoliata_00019_mRNA_156.1
GF0043791	0	0	1	Hypothetical protein (1)	binding [GO:0005488 molecular_function] (1); mRNA cis splicing, via spliceosome [GO:0045292 biological_process] (1); nuclear cap binding complex [GO:0005846 cellular_component] (1); protein binding [GO:0005515 molecular_function] (1); RNA cap binding [GO:0000339 molecular_function] (1); RNA metabolic process [GO:0016070 biological_process] (1); mRNA transport [GO:0051028 biological_process] (1); RNA binding [GO:0003723 molecular_function] (1)	Nuclear cap-binding protein subunit 1 [IPR027159] (1); MIF4G-like, type 1 [IPR015172] (1); MIF4G-like, type 3 [IPR003890] (1); Armadillo-type fold [IPR016024] (1); MIF4G-like domain [IPR016021] (1)	-	-	P_trifoliata_00019_mRNA_154.1
GF0043790	0	0	1	Hypothetical protein (1)		Bifunctional inhibitor/plant lipid transfer protein/seed storage helical domain [IPR016140] (1)	-	-	P_trifoliata_00019_mRNA_150.1
GF0043789	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00019_mRNA_147.1
GF0043788	0	0	1	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); DNA binding [GO:0003677 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); MULE transposase domain [IPR018289] (1); NAC domain [IPR003441] (1)	-	-	P_trifoliata_00019_mRNA_142.1
GF0043787	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00019_mRNA_141.1
GF0043786	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00019_mRNA_135.1

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*
GF0043785	0	0	1	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	-	P_trifoliata_00019_mRNA_123.1
GF0043784	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00019_mRNA_118.1
GF0043783	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00019_mRNA_115.1
GF0043782	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00019_mRNA_114.1
GF0043781	0	0	1	DUF642 family protein (1)		Domain of unknown function DUF642 [IPR006946] (1)	-	-	P_trifoliata_00019_mRNA_104.1
GF0043780	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00018_mRNA_84.1
GF0043779	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00018_mRNA_70.1
GF0043778	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00018_mRNA_7.1
GF0043777	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00018_mRNA_69.1
GF0043776	0	0	1	C3HC4 type RING-finger 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)	-	-	P_trifoliata_00018_mRNA_55.1
GF0043775	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00018_mRNA_50.1
GF0043774	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00018_mRNA_5.1
GF0043773	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	-	P_trifoliata_00018_mRNA_48.1
GF0043772	0	0	1	Hypothetical protein (1)	lipid metabolic process [GO:0006629 biological_process] (1)	Partial AB-hydrolase lipase domain [IPR006693] (1); Alpha/Beta hydrolase fold [IPR029058] (1)	-	-	P_trifoliata_00018_mRNA_44.1
GF0043771	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00018_mRNA_43.1
GF0043770	0	0	1	Hypothetical protein (1)		Alpha/Beta hydrolase fold [IPR029058] (1)	-	-	P_trifoliata_00018_mRNA_42.1
GF0043769	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00018_mRNA_4.1
GF0043768	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00018_mRNA_39.1
GF0043767	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00018_mRNA_34.1
GF0043766	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00018_mRNA_31.1
GF0043765	0	0	1	Putative mitochondrial chaperone bcs1 (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)	-	-	P_trifoliata_00018_mRNA_3.1
GF0043764	0	0	1	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)	-	-	P_trifoliata_00018_mRNA_2.1
GF0043763	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00018_mRNA_14.1
GF0043762	0	0	1	Hypothetical protein (1)		RIN4, pathogenic type III effector avirulence factor Avr cleavage site [IPR008700] (1)	-	-	P_trifoliata_00018_mRNA_135.1
GF0043761	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00018_mRNA_13.1
GF0043760	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00018_mRNA_123.1
GF0043759	0	0	1	Hypothetical protein (1)	nutrient reservoir activity [GO:0045735 molecular_function] (1)	RmlC-like cupin domain [IPR011051] (1); RmlC-like jelly roll fold [IPR014710] (1); Cupin 1 [IPR006045] (1)	-	-	P_trifoliata_00018_mRNA_121.1
GF0043758	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00018_mRNA_12.1
GF0043757	0	0	1	Hypothetical protein (1)		Glycine rich protein [IPR010800] (1)	-	-	P_trifoliata_00018_mRNA_11.1
GF0043756	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00018_mRNA_103.1
GF0043755	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00018_mRNA_102.1
GF0043754	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00017_mRNA_99.1
GF0043753	0	0	1	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	-	P_trifoliata_00017_mRNA_98.1
GF0043752	0	0	1	Pectinacetylesterase family protein (1)	hydrolase activity [GO:0016787 molecular_function] (1)	Pectinacetylesterase/NOTUM [IPR004963] (1)	-	-	P_trifoliata_00017_mRNA_9.1
GF0043751	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00017_mRNA_88.1
GF0043750	0	0	1	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1)	-	-	P_trifoliata_00017_mRNA_87.1
GF0043749	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00017_mRNA_8.1
GF0043748	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00017_mRNA_79.1
GF0043747	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00017_mRNA_78.1
GF0043746	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00017_mRNA_76.1
GF0043745	0	0	1	Hypothetical protein (1)	3'-5' exonuclease activity [GO:0008408 molecular_function] (1); nucleobase-containing compound metabolic process [GO:0006139 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	3'-5' exonuclease domain [IPR002562] (1); Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00017_mRNA_48.1
GF0043744	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00017_mRNA_47.1
GF0043743	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00017_mRNA_41.1
GF0043742	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00017_mRNA_35.1
GF0043741	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00017_mRNA_28.1
GF0043740	0	0	1	Hypothetical protein (1)	integral component of membrane [GO:0016021 cellular_component] (1); transmembrane transporter activity [GO:0022857 molecular_function] (1); transmembrane transport [GO:0055085 biological_process] (1)	Major facilitator, sugar transporter-like [IPR005828] (1)	-	-	P_trifoliata_00017_mRNA_23.1
GF0043739	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00017_mRNA_19.1
GF0043738	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00017_mRNA_18.1
GF0043737	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00017_mRNA_151.1
GF0043736	0	0	1	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	-	P_trifoliata_00017_mRNA_150.1
GF0043735	0	0	1	Lipid transfer protein (1)		Bifunctional inhibitor/plant lipid transfer protein/seed storage helical domain [IPR016140] (1)	-	-	P_trifoliata_00017_mRNA_144.1
GF0043734	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00017_mRNA_136.1
GF0043733	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00017_mRNA_132.1
GF0043732	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00017_mRNA_12.1
GF0043731	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00017_mRNA_10.1
GF0043730	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00016_mRNA_94.1
GF0043729	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00016_mRNA_92.1
GF0043728	0	0	1	Peptidyl-prolyl cis-trans isomerase CYP37 (1)	protein folding [GO:0006457 biological_process] (1); peptidyl-prolyl cis-trans isomerase activity [GO:0003755 molecular_function] (1)	Cyclophilin-type peptidyl-prolyl cis-trans isomerase [IPR024936] (1); Cyclophilin-like domain [IPR029000] (1)	-	-	P_trifoliata_00016_mRNA_81.1
GF0043727	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00016_mRNA_78.1
GF0043726	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF1985 [IPR015410] (1)	-	-	P_trifoliata_00016_mRNA_75.1
GF0043725	0	0	1	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Transposase, MuDR, plant [IPR004332] (1); Zinc finger, PMZ-type [IPR006564] (1); Zinc finger, SWIM-type [IPR007527] (1)	-	-	P_trifoliata_00016_mRNA_74.1
GF0043724	0	0	1	Cytochrome P450, family 88, subfamily A, polypeptide 3 isoform 3 (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)	-	-	P_trifoliata_00016_mRNA_71.1
GF0043723	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00016_mRNA_7.1
GF0043722	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00016_mRNA_65.1
GF0043721	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00016_mRNA_59.1
GF0043720	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00016_mRNA_58.1
GF0043719	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00016_mRNA_52.1
GF0043718	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00016_mRNA_51.1
GF0043717	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00016_mRNA_50.1
GF0043716	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00016_mRNA_44.1
GF0043715	0	0	1	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1)	Xylanase inhibitor, N-terminal [IPR032861] (1); Aspartic peptidase A1 family [IPR001461] (1); Aspartic peptidase domain [IPR021109] (1)	-	-	P_trifoliata_00016_mRNA_42.1
GF0043714	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00016_mRNA_41.1
GF0043713	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00016_mRNA_39.1
GF0043712	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00016_mRNA_28.1
GF0043711	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00016_mRNA_26.1
GF0043710	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00016_mRNA_24.1
GF0043709	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00016_mRNA_21.1
GF0043708	0	0	1	Cationic amino acid transporter (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)	-	-	P_trifoliata_00016_mRNA_132.1
GF0043707	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00016_mRNA_130.1
GF0043706	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00016_mRNA_128.1

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*
GF0043705	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00016_mRNA_126.1
GF0043704	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00016_mRNA_122.1
GF0043703	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00016_mRNA_120.1
GF0043702	0	0	1	Hypothetical protein (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)	-	-	P_trifoliata_00016_mRNA_115.1
GF0043701	0	0	1	Histone-binding protein RBBP4 (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); Histone-binding protein RBBP4, N-terminal [IPR022052] (1)	-	-	P_trifoliata_00016_mRNA_111.1
GF0043700	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00016_mRNA_1.1
GF0043699	0	0	1	Golgi apparatus membrane protein TVP23 (1)	integral component of membrane [GO:0016021 cellular_component] (1)	Protein of unknown function DUF846, eukaryotic [IPR008564] (1)	-	-	P_trifoliata_00015_mRNA_89.1
GF0043698	0	0	1	Hypothetical protein (1)		Translation protein, beta-barrel domain [IPR009000] (1)	-	-	P_trifoliata_00015_mRNA_86.1
GF0043697	0	0	1	Hypothetical protein (1)	cellular amino acid metabolic process [GO:0006520 biological_process] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Homoserine dehydrogenase, catalytic [IPR001342] (1); Glutathione S-transferase, C-terminal-like [IPR010987] (1); NAD(P)-binding domain [IPR016040] (1)	-	-	P_trifoliata_00015_mRNA_8.1
GF0043696	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00015_mRNA_72.1
GF0043695	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00015_mRNA_68.1
GF0043694	0	0	1	Progesterone 5-beta-reductase (1)	coenzyme binding [GO:0050662 molecular_function] (1); catalytic activity [GO:0003824 molecular_function] (1)	NAD(P)-binding domain [IPR016040] (1); NAD-dependent epimerase/dehydratase, N-terminal domain [IPR001509] (1)	-	-	P_trifoliata_00015_mRNA_59.1
GF0043693	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00015_mRNA_41.1
GF0043692	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00015_mRNA_31.1
GF0043691	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00015_mRNA_24.1
GF0043690	0	0	1	Hypothetical protein (1)	nucleotide binding [GO:0000166 molecular_function] (1); metal ion binding [GO:0046872 molecular_function] (1)	P-type ATPase, A domain [IPR008250] (1)	-	-	P_trifoliata_00015_mRNA_21.1
GF0043689	0	0	1	SAL1 phosphatase-like protein (1)	phosphatidylinositol phosphorylation [GO:0046854 biological_process] (1)	Inositol monophosphatase [IPR000760] (1); Inositol monophosphatase, conserved site [IPR020550] (1)	-	-	P_trifoliata_00015_mRNA_190.1
GF0043688	0	0	1	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	-	-	P_trifoliata_00015_mRNA_189.1
GF0043687	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00015_mRNA_177.1
GF0043686	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00015_mRNA_176.1
GF0043685	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	F-box domain [IPR001810] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Phloem protein 2-like [IPR025886] (1)	-	-	P_trifoliata_00015_mRNA_171.1
GF0043684	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00015_mRNA_166.1
GF0043683	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00015_mRNA_150.1
GF0043682	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00015_mRNA_149.1
GF0043681	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00015_mRNA_148.1
GF0043680	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	-	-	P_trifoliata_00015_mRNA_112.1
GF0043679	0	0	1	Hypothetical protein (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)	-	-	P_trifoliata_00015_mRNA_103.1
GF0043678	0	0	1	Hydroxyproline-rich glycoprotein family protein (1)		Spo12 [IPR007727] (1)	-	-	P_trifoliata_00015_mRNA_100.1
GF0043677	0	0	1	Germin-like protein subfamily 2 member 4 (1)	nutrient reservoir activity [GO:0045735 molecular_function] (1); manganese ion binding [GO:0030145 molecular_function] (1)	RmlC-like cupin domain [IPR011051] (1); Germin, manganese binding site [IPR019780] (1); Cupin 1 [IPR006045] (1); RmlC-like jelly roll fold [IPR014710] (1); Germin [IPR001929] (1)	-	-	P_trifoliata_00014_mRNA_88.1
GF0043676	0	0	1	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)	-	-	P_trifoliata_00014_mRNA_86.1
GF0043675	0	0	1	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)	-	-	P_trifoliata_00014_mRNA_78.1
GF0043674	0	0	1	ASYNAPTIC 3 (1)			-	-	P_trifoliata_00014_mRNA_74.1
GF0043673	0	0	1	WRKY transcription factor 6 (1)	transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (1); sequence-specific DNA binding [GO:0043565 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	WRKY domain [IPR003657] (1)	-	-	P_trifoliata_00014_mRNA_70.1
GF0043672	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00014_mRNA_60.1
GF0043671	0	0	1	Peroxidase 1 (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)	Plant peroxidase [IPR000823] (1); Peroxidase, active site [IPR019794] (1); Haem peroxidase, plant/fungal/bacterial [IPR002016] (1); Haem peroxidase [IPR010255] (1)	-	-	P_trifoliata_00014_mRNA_41.1
GF0043670	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00014_mRNA_4.1
GF0043669	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00014_mRNA_3.1
GF0043668	0	0	1	Heat shock cognate 70 kDa protein 2 (1)		Heat shock protein 70kD, C-terminal domain [IPR029048] (1)	-	-	P_trifoliata_00014_mRNA_26.1
GF0043667	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00014_mRNA_24.1
GF0043666	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00014_mRNA_2.1
GF0043665	0	0	1	DNA-directed RNA polymerase subunit (1)	zinc ion binding [GO:0008270 molecular_function] (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); nucleic acid binding [GO:0003676 molecular_function] (1)	Nudix hydrolase, N-terminal [IPR029401] (1); DNA-directed RNA polymerase subunit/transcription factor S [IPR012164] (1); Zinc finger, TFIIS-type [IPR001222] (1); DNA-directed RNA polymerase, M/15kDa subunit [IPR001529] (1)	-	-	P_trifoliata_00014_mRNA_177.1
GF0043664	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00014_mRNA_172.1
GF0043663	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00014_mRNA_158.1
GF0043662	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00014_mRNA_148.1
GF0043661	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00014_mRNA_138.1
GF0043660	0	0	1	Hypothetical protein (1)	cation transport [GO:0006812 biological_process] (1); cation transmembrane transporter activity [GO:0008324 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1); transmembrane transport [GO:0055085 biological_process] (1)	Cation efflux protein [IPR002524] (1); Cation efflux protein transmembrane domain [IPR027469] (1)	-	-	P_trifoliata_00014_mRNA_129.1
GF0043659	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00014_mRNA_124.1
GF0043658	0	0	1	Hypothetical protein (1)	integral component of membrane [GO:0016021 cellular_component] (1); transmembrane transporter activity [GO:0022857 molecular_function] (1)	WAT1-related protein [IPR030184] (1)	-	-	P_trifoliata_00014_mRNA_108.1
GF0043657	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00013_mRNA_9.1
GF0043656	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00013_mRNA_81.1
GF0043655	0	0	1	Hypothetical protein (1)	actin binding [GO:0003779 molecular_function] (1)	Stomatal closure-related actin-binding protein, actin-binding domain [IPR032012] (1)	-	-	P_trifoliata_00013_mRNA_8.1
GF0043654	0	0	1	F-box and associated interaction domains-containing protein, putative (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 3 [IPR013187] (1)	-	-	P_trifoliata_00013_mRNA_64.1

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*
GF0043653	0	0	1	Receptor-like protein kinase FERONIA (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); Protein kinase, ATP binding site [IPR017441] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Protein kinase-like domain [IPR011009] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Malectin-like carbohydrate-binding domain [IPR024788] (1); Protein kinase domain [IPR000719] (1)	-	-	P_trifoliata_00013_mRNA_60.1
GF0043652	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00013_mRNA_55.1
GF0043651	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00013_mRNA_53.1
GF0043650	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00013_mRNA_48.1
GF0043649	0	0	1	Putative cytochrome P450-dependent fatty acid 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 [IPR001128] (1); Cytochrome P450, conserved site [IPR017972] (1)	-	-	P_trifoliata_00013_mRNA_31.1
GF0043648	0	0	1	Cytochrome P450 94A1 (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, E-class, group I [IPR002401] (1); Cytochrome P450 [IPR001128] (1)	-	-	P_trifoliata_00013_mRNA_30.1
GF0043647	0	0	1	Cytochrome P450 94A1 (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, E-class, group I [IPR002401] (1); Cytochrome P450, conserved site [IPR017972] (1)	-	-	P_trifoliata_00013_mRNA_29.1
GF0043646	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00013_mRNA_2.1
GF0043645	0	0	1	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein, putative (1)	methyltransferase activity [GO:0008168 molecular_function] (1)	SAM dependent carboxyl methyltransferase [IPR005299] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	-	P_trifoliata_00013_mRNA_19.1
GF0043644	0	0	1	Pleiotropic drug resistance protein 1 (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); AAA+ ATPase domain [IPR003593] (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)	-	-	P_trifoliata_00013_mRNA_160.1
GF0043643	0	0	1	AP2/B3 transcription factor family protein (1)	DNA binding [GO:0003677 molecular_function] (1)	DNA-binding pseudobarrel domain [IPR015300] (1); B3 DNA binding domain [IPR003340] (1)	-	-	P_trifoliata_00013_mRNA_13.1
GF0043642	0	0	1	Hypothetical protein (1)	protein ubiquitination [GO:0016567 biological_process] (1); ubiquitin-protein transferase activity [GO:0004842 molecular_function] (1)	Zinc finger, RING/FYVE/PHD-type [IPR013083] (1); IBR domain [IPR002867] (1); Zinc finger, RING-type, conserved site [IPR017907] (1); E3 ubiquitin ligase RBR family [IPR031127] (1)	-	-	P_trifoliata_00013_mRNA_12.1
GF0043641	0	0	1	Hypothetical protein (1)		NADP-dependent oxidoreductase domain [IPR023210] (1)	-	-	P_trifoliata_00012_mRNA_99.1
GF0043640	0	0	1	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-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); Concanavalin A-like lectin/glucanase domain [IPR013320] (1)	-	-	P_trifoliata_00012_mRNA_94.1
GF0043639	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00012_mRNA_78.1
GF0043638	0	0	1	Putative invertase inhibitor (1)	enzyme inhibitor activity [GO:0004857 molecular_function] (1)	Pectinesterase inhibitor domain [IPR006501] (1)	-	-	P_trifoliata_00012_mRNA_73.1
GF0043637	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00012_mRNA_61.1
GF0043636	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00012_mRNA_60.1
GF0043635	0	0	1	DNA-directed RNA polymerase II 8.2 kDa polypeptide (1)	zinc ion binding [GO:0008270 molecular_function] (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 subunit RPB10 [IPR023580] (1); DNA-directed RNA polymerase, subunit N/Rpb10 [IPR000268] (1); RNA polymerases, subunit N, zinc binding site [IPR020789] (1); Conserved hypothetical protein CHP01589, plant [IPR006476] (1); Homeodomain-like [IPR009057] (1)	-	-	P_trifoliata_00012_mRNA_57.1
GF0043634	0	0	1	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/virulence factor [IPR011050] (1); Pectin lyase fold [IPR012334] (1)	-	-	P_trifoliata_00012_mRNA_53.1
GF0043633	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00012_mRNA_3.1
GF0043632	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00012_mRNA_16.1
GF0043631	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00012_mRNA_157.1
GF0043630	0	0	1	Hypothetical protein (1)		Uncharacterised domain Wax2, C-terminal [IPR021940] (1)	-	-	P_trifoliata_00012_mRNA_155.1
GF0043629	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00012_mRNA_154.1
GF0043628	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00012_mRNA_151.1
GF0043627	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00012_mRNA_150.1
GF0043626	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00012_mRNA_144.1
GF0043625	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00012_mRNA_143.1
GF0043624	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00012_mRNA_138.1
GF0043623	0	0	1	Hypothetical protein (1)		Sieve element occlusion, N-terminal [IPR027942] (1)	-	-	P_trifoliata_00012_mRNA_137.1
GF0043622	0	0	1	Pedicel, carpel, stamen, petal differentiation and expansion stage, group 2-like protein (1)		Late embryogenesis abundant protein, LEA-14 [IPR004864] (1)	-	-	P_trifoliata_00012_mRNA_125.1
GF0043621	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00012_mRNA_10.1
GF0043620	0	0	1	Fatty acyl-CoA reductase 1 (1)	fatty-acyl-CoA reductase (alcohol-forming) activity [GO:0080019 molecular_function] (1)	Fatty acyl-CoA reductase [IPR026055] (1); Male sterility, NAD-binding [IPR013120] (1); NAD(P)-binding domain [IPR016040] (1)	-	-	P_trifoliata_00012_mRNA_1.1
GF0043619	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00011_mRNA_87.1
GF0043618	0	0	1	Hypothetical protein (1)	RNA polyadenylation [GO:0043631 biological_process] (1); polynucleotide adenylyltransferase activity [GO:0004652 molecular_function] (1); nucleus [GO:0005634 cellular_component] (1)	Poly(A) polymerase [IPR014492] (1)	-	-	P_trifoliata_00011_mRNA_8.1
GF0043617	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00011_mRNA_77.1
GF0043616	0	0	1	Hydroxyproline-rich glycoprotein family protein, putative (1)			-	-	P_trifoliata_00011_mRNA_75.1
GF0043615	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00011_mRNA_44.1
GF0043614	0	0	1	Glycosyl hydrolase family protein (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)	-	-	P_trifoliata_00011_mRNA_25.1
GF0043613	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00011_mRNA_23.1
GF0043612	0	0	1	Putative RING zinc finger domain superfamily 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)	-	-	P_trifoliata_00011_mRNA_17.1
GF0043611	0	0	1	Auxin-induced protein 15A (1)	response to auxin [GO:0009733 biological_process] (1)	Small auxin-up RNA [IPR003676] (1)	-	-	P_trifoliata_00011_mRNA_160.1
GF0043610	0	0	1	4,5-DOPA dioxygenase extradiol (1)	cellular aromatic compound metabolic process [GO:0006725 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); ferrous iron binding [GO:0008198 molecular_function] (1)	Extradiol ring-cleavage dioxygenase, class III enzyme, subunit B [IPR004183] (1)	-	-	P_trifoliata_00011_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*
GF0043609	0	0	1	40S ribosomal protein S6 (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 S6e, conserved site [IPR018282] (1); Ribosomal protein S6e [IPR001377] (1)	-	-	P_trifoliata_00011_mRNA_117.1
GF0043608	0	0	1	Hypothetical protein (1)	nucleotidyltransferase activity [GO:0016779 molecular_function] (1); RNA 3'-end processing [GO:0031123 biological_process] (1); RNA binding [GO:0003723 molecular_function] (1); nucleus [GO:0005634 cellular_component] (1); polynucleotide adenylyltransferase activity [GO:0004652 molecular_function] (1); RNA polyadenylation [GO:0043631 biological_process] (1)	Poly(A) polymerase [IPR014492] (1); Nucleotidyltransferase, class I, C-terminal-like [IPR011068] (1); Poly(A) polymerase, central domain [IPR007012] (1); Poly(A) polymerase, RNA-binding domain [IPR007010] (1)	-	-	P_trifoliata_00011_mRNA_11.1
GF0043607	0	0	1	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	-	P_trifoliata_00010_mRNA_88.1
GF0043606	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00010_mRNA_8.1
GF0043605	0	0	1	Hypothetical protein (1)	integral component of membrane [GO:0016021 cellular_component] (1)	Mpv17/PMP22 [IPR007248] (1)	-	-	P_trifoliata_00010_mRNA_77.1
GF0043604	0	0	1	Hypothetical protein (1)		Stigma-specific protein Stig1 [IPR006969] (1); AmbAllergen [IPR018082] (1); Pectin lyase fold/virulence factor [IPR011050] (1); Pectin lyase fold [IPR012334] (1)	-	-	P_trifoliata_00010_mRNA_70.1
GF0043603	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00010_mRNA_65.1
GF0043602	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00010_mRNA_64.1
GF0043601	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00010_mRNA_62.1
GF0043600	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00010_mRNA_44.1
GF0043599	0	0	1	Hypothetical protein (1)	phosphatidylinositol phosphorylation [GO:0046854 biological_process] (1); binding [GO:0005488 molecular_function] (1)	Armadillo-type fold [IPR016024] (1); Inositol monophosphatase, metal-binding site [IPR020583] (1); Mo25-like [IPR013878] (1); Inositol monophosphatase [IPR000760] (1); Inositol monophosphatase, conserved site [IPR020550] (1); Armadillo-like helical [IPR011989] (1)	-	-	P_trifoliata_00010_mRNA_4.1
GF0043598	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00010_mRNA_36.1
GF0043597	0	0	1	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)	-	-	P_trifoliata_00010_mRNA_35.1
GF0043596	0	0	1	Hypothetical protein (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 domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); Serine/threonine-protein kinase HT1, plant [IPR015783] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1)	-	-	P_trifoliata_00010_mRNA_30.1
GF0043595	0	0	1	Putative 26S protease regulatory subunit 6A like protein (1)		P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	-	P_trifoliata_00010_mRNA_2.1
GF0043594	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00010_mRNA_163.1
GF0043593	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00010_mRNA_162.1
GF0043592	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00010_mRNA_154.1
GF0043591	0	0	1	Hypothetical protein (1)		Transposase, MuDR, plant [IPR004332] (1)	-	-	P_trifoliata_00010_mRNA_150.1
GF0043590	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00010_mRNA_149.1
GF0043589	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00010_mRNA_146.1
GF0043588	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00010_mRNA_133.1
GF0043587	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00010_mRNA_127.1
GF0043586	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00010_mRNA_125.1
GF0043585	0	0	1	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)	-	-	P_trifoliata_00010_mRNA_122.1
GF0043584	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00010_mRNA_121.1
GF0043583	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00010_mRNA_113.1
GF0043582	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00010_mRNA_11.1
GF0043581	0	0	1	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)	-	-	P_trifoliata_00010_mRNA_108.1
GF0043580	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00010_mRNA_100.1
GF0043579	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00010_mRNA_1.1
GF0043578	0	0	1	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1)	NmrA-like domain [IPR008030] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Plant methyltransferase dimerisation [IPR012967] (1); NAD(P)-binding domain [IPR016040] (1)	-	-	P_trifoliata_00009_mRNA_98.1
GF0043577	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00009_mRNA_95.1
GF0043576	0	0	1	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)	GroES-like [IPR011032] (1); Alcohol dehydrogenase superfamily, zinc-type [IPR002085] (1); Alcohol dehydrogenase, N-terminal [IPR013154] (1); Alcohol dehydrogenase, zinc-type, conserved site [IPR002328] (1); Alcohol dehydrogenase, C-terminal [IPR013149] (1); NAD(P)-binding domain [IPR016040] (1)	-	-	P_trifoliata_00009_mRNA_85.1
GF0043575	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00009_mRNA_83.1
GF0043574	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00009_mRNA_74.1
GF0043573	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00009_mRNA_66.1
GF0043572	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00009_mRNA_56.1
GF0043571	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00009_mRNA_28.1
GF0043570	0	0	1	Sesquiterpene synthase (1)	metabolic process [GO:0008152 biological_process] (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, 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)	-	-	P_trifoliata_00009_mRNA_24.1
GF0043569	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00009_mRNA_22.1
GF0043568	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00009_mRNA_170.1
GF0043567	0	0	1	Ribonucleoside-diphosphate reductase large subunit (1)	DNA replication [GO:0006260 biological_process] (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)	Ribonucleotide reductase large subunit, C-terminal [IPR000788] (1); Ribonucleotide reductase large subunit, N-terminal [IPR013509] (1); Ribonucleotide reductase, class I , alpha subunit [IPR013346] (1); Ribonucleotide reductase R1 subunit, N-terminal [IPR008926] (1); ATP-cone domain [IPR005144] (1)	-	-	P_trifoliata_00009_mRNA_17.1
GF0043566	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00009_mRNA_163.1
GF0043565	0	0	1	Basic 7S globulin (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Peptidase family A1 domain [IPR033121] (1); Aspartic peptidase domain [IPR021109] (1); Ribonuclease H domain [IPR002156] (1); Xylanase inhibitor, N-terminal [IPR032861] (1); Xylanase inhibitor, C-terminal [IPR032799] (1); Aspartic peptidase A1 family [IPR001461] (1); Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00009_mRNA_145.1
GF0043564	0	0	1	Basic 7S globulin, putative (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)	-	-	P_trifoliata_00009_mRNA_141.1
GF0043563	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00009_mRNA_139.1
GF0043562	0	0	1	Hypothetical protein (1)	mRNA guanylyltransferase activity [GO:0004484 molecular_function] (1); 7-methylguanosine mRNA capping [GO:0006370 biological_process] (1); mRNA processing [GO:0006397 biological_process] (1)	mRNA capping enzyme, catalytic domain [IPR001339] (1)	-	-	P_trifoliata_00009_mRNA_137.1
GF0043561	0	0	1	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 S24e [IPR001976] (1)	-	-	P_trifoliata_00009_mRNA_115.1
GF0043560	0	0	1	Hypothetical protein (1)	hydrolase activity [GO:0016787 molecular_function] (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); Alpha/Beta hydrolase fold [IPR029058] (1); Dienelactone hydrolase [IPR002925] (1)	-	-	P_trifoliata_00009_mRNA_113.1

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*
GF0043559	0	0	1	Hypothetical protein (1)		Alpha/Beta hydrolase fold [IPR029058] (1)	-	-	P_trifoliata_00009_mRNA_101.1
GF0043558	0	0	1	Hypothetical protein (1)		Alpha/Beta hydrolase fold [IPR029058] (1)	-	-	P_trifoliata_00009_mRNA_100.1
GF0043557	0	0	1	UDP-galactose transporter 2 (1)	nucleotide-sugar transmembrane transporter activity [GO:0005338 molecular_function] (1); nucleotide-sugar transport [GO:0015780 biological_process] (1)	Bi-functional UDP-rhamnose/UDP-galactose transporter [IPR031089] (1); Sugar phosphate transporter domain [IPR004853] (1)	-	-	P_trifoliata_00009_mRNA_1.1
GF0043556	0	0	1	DNA (cytosine-5-)-methyltransferase (1)	methyltransferase activity [GO:0008168 molecular_function] (1)	C-5 cytosine methyltransferase [IPR001525] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	-	-	P_trifoliata_00008_mRNA_92.1
GF0043555	0	0	1	Crooked neck-like protein 1 (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)	-	-	P_trifoliata_00008_mRNA_83.1
GF0043554	0	0	1	Auxin-responsive protein IAA20 (1)	nucleus [GO:0005634 cellular_component] (1); protein binding [GO:0005515 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	AUX/IAA protein [IPR003311] (1); PB1 domain [IPR000270] (1)	-	-	P_trifoliata_00008_mRNA_55.1
GF0043553	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00008_mRNA_4.1
GF0043552	0	0	1	Glucuronidase 3 isoform 2 (1)	membrane [GO:0016020 cellular_component] (1); hydrolase activity, acting on glycosyl bonds [GO:0016798 molecular_function] (1)	Glycoside hydrolase, family 79 [IPR005199] (1); Glycoside hydrolase superfamily [IPR017853] (1)	-	-	P_trifoliata_00008_mRNA_35.1
GF0043551	0	0	1	Nodulin family protein (1)		Flotillin family [IPR027705] (1)	-	-	P_trifoliata_00008_mRNA_29.1
GF0043550	0	0	1	Hyp O-arabinosyltransferase homolog (1)			-	-	P_trifoliata_00008_mRNA_17.1
GF0043549	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00008_mRNA_167.1
GF0043548	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00008_mRNA_166.1
GF0043547	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00008_mRNA_165.1
GF0043546	0	0	1	TSA: Wollemia nobilis transcribed RNA sequence (1)		Frigida-like [IPR012474] (1)	-	-	P_trifoliata_00008_mRNA_164.1
GF0043545	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00008_mRNA_163.1
GF0043544	0	0	1	Putative serine/threonine-protein kinase WNK11 (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)	-	-	P_trifoliata_00008_mRNA_162.1
GF0043543	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00008_mRNA_157.1
GF0043542	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00008_mRNA_147.1
GF0043541	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00008_mRNA_144.1
GF0043540	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00008_mRNA_143.1
GF0043539	0	0	1	Hypothetical protein (1)		SOUL haem-binding protein [IPR006917] (1); Regulatory factor, effector binding domain [IPR011256] (1)	-	-	P_trifoliata_00008_mRNA_139.1
GF0043538	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00008_mRNA_136.1
GF0043537	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00008_mRNA_135.1
GF0043536	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00008_mRNA_128.1
GF0043535	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00008_mRNA_126.1
GF0043534	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00008_mRNA_119.1
GF0043533	0	0	1	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)	Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (1); Terpene synthase, N-terminal domain [IPR001906] (1)	-	-	P_trifoliata_00008_mRNA_116.1
GF0043532	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00008_mRNA_113.1
GF0043531	0	0	1	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)	Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (1); Terpene synthase, N-terminal domain [IPR001906] (1)	-	-	P_trifoliata_00008_mRNA_111.1
GF0043530	0	0	1	Hypothetical protein (1)		Transposon, En/Spm-like [IPR004242] (1)	-	-	P_trifoliata_00008_mRNA_108.1
GF0043529	0	0	1	FscO (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1)	FAD/NAD(P)-binding domain [IPR023753] (1)	-	-	P_trifoliata_00008_mRNA_106.1
GF0043528	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00008_mRNA_1.1
GF0043527	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00007_mRNA_91.1
GF0043526	0	0	1	Hypothetical protein (1)		Chromo domain-like [IPR016197] (1); Chromo domain [IPR023780] (1)	-	-	P_trifoliata_00007_mRNA_8.1
GF0043525	0	0	1	JmjC domain containing protein, expressed (1)		JmjN domain [IPR003349] (1); JmjC domain [IPR003347] (1)	-	-	P_trifoliata_00007_mRNA_76.1
GF0043524	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00007_mRNA_74.1
GF0043523	0	0	1	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, PMZ-type [IPR006564] (1); Zinc finger, SWIM-type [IPR007527] (1); Zinc finger, CCHC-type [IPR001878] (1)	-	-	P_trifoliata_00007_mRNA_71.1
GF0043522	0	0	1	Cytokinin dehydrogenase 3 (1)	cytokinin dehydrogenase activity [GO:0019139 molecular_function] (1); catalytic activity [GO:0003824 molecular_function] (1); cytokinin metabolic process [GO:0009690 biological_process] (1); oxidoreductase activity, acting on CH-OH group of donors [GO:0016614 molecular_function] (1); flavin adenine dinucleotide binding [GO:0050660 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Vanillyl-alcohol oxidase/Cytokinin dehydrogenase C-terminal domain [IPR016170] (1); FAD-binding, type 2 [IPR016166] (1); Cytokinin dehydrogenase 1, FAD/cytokinin binding domain [IPR015345] (1); FAD-linked oxidase-like, C-terminal [IPR016164] (1)	-	-	P_trifoliata_00007_mRNA_7.1
GF0043521	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00007_mRNA_51.1
GF0043520	0	0	1	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)	-	-	P_trifoliata_00007_mRNA_5.1
GF0043519	0	0	1	Hypothetical protein (1)	nucleotidyltransferase activity [GO:0016779 molecular_function] (1)	Polymerase, nucleotidyl transferase domain [IPR002934] (1)	-	-	P_trifoliata_00007_mRNA_42.1
GF0043518	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00007_mRNA_41.1
GF0043517	0	0	1	Disease resistance RPS2-like protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00007_mRNA_40.1
GF0043516	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00007_mRNA_4.1
GF0043515	0	0	1	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)	-	-	P_trifoliata_00007_mRNA_39.1
GF0043514	0	0	1	Disease resistance protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00007_mRNA_36.1
GF0043513	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00007_mRNA_34.1
GF0043512	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00007_mRNA_32.1
GF0043511	0	0	1	Retrotransposon protein, putative, unclassified (1)		Reverse transcriptase domain [IPR000477] (1)	-	-	P_trifoliata_00007_mRNA_3.1
GF0043510	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00007_mRNA_25.1
GF0043509	0	0	1	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	-	P_trifoliata_00007_mRNA_2.1
GF0043508	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00007_mRNA_19.1
GF0043507	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00007_mRNA_18.1
GF0043506	0	0	1	Condensin complex subunit 3 (1)			-	-	P_trifoliata_00007_mRNA_17.1
GF0043505	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00007_mRNA_156.1
GF0043504	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00007_mRNA_155.1
GF0043503	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00007_mRNA_152.1
GF0043502	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00007_mRNA_149.1
GF0043501	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00007_mRNA_148.1
GF0043500	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00007_mRNA_145.1
GF0043499	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00007_mRNA_144.1
GF0043498	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00007_mRNA_143.1
GF0043497	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00007_mRNA_142.1
GF0043496	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00007_mRNA_139.1
GF0043495	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00007_mRNA_136.1
GF0043494	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00007_mRNA_134.1
GF0043493	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00007_mRNA_132.1

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***
GF0043492	0	0	1	Hypothetical protein (1)	1-deoxy-D-xylulose-5-phosphate reductoisomerase activity [GO:0030604 molecular_function] (1); NADPH binding [GO:0070402 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); isoprenoid biosynthetic process [GO:0008299 biological_process] (1); metal ion binding [GO:0046872 molecular_function] (1)	1-deoxy-D-xylulose 5-phosphate reductoisomerase, N-terminal [IPR013512] (1); 1-deoxy-D-xylulose 5-phosphate reductoisomerase [IPR003821] (1); NAD(P)-binding domain [IPR016040] (1); DXP reductoisomerase C-terminal domain [IPR026877] (1)	-	-	P_trifoliata_00007_mRNA_125.1
GF0043491	0	0	1	Carbonate dehydratase (1)	zinc ion binding [GO:0008270 molecular_function] (1); carbonate dehydratase activity [GO:0004089 molecular_function] (1); carbon utilization [GO:0015976 biological_process] (1)	Carbonic anhydrase, prokaryotic-like, conserved site [IPR015892] (1); Carbonic anhydrase [IPR001765] (1)	-	-	P_trifoliata_00007_mRNA_122.1
GF0043490	0	0	1	Hypothetical protein (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)	Peroxisome membrane anchor protein Pex14p, N-terminal [IPR006785] (1); Peroxisomal membrane protein 14 [IPR025655] (1)	-	-	P_trifoliata_00007_mRNA_121.1
GF0043489	0	0	1	Putative polygalacturonase non-catalytic subunit (1)			-	-	P_trifoliata_00007_mRNA_112.1
GF0043488	0	0	1	Hypothetical protein (1)		Zinc knuckle CX2CX4HX4C [IPR025836] (1)	-	-	P_trifoliata_00007_mRNA_1.1
GF0043487	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00006_mRNA_73.1
GF0043486	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF2828 [IPR024553] (1)	-	-	P_trifoliata_00006_mRNA_67.1
GF0043485	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00006_mRNA_61.1
GF0043484	0	0	1	Glycerol-3-phosphate dehydrogenase [NAD(+)] GPDHC1, cytosolic (1)	glycerol-3-phosphate metabolic process [GO:0006072 biological_process] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (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); glycerol-3-phosphate dehydrogenase complex [GO:0009331 cellular_component] (1); glycerol-3-phosphate catabolic process [GO:0046168 biological_process] (1); glycerol-3-phosphate dehydrogenase [NAD+] activity [GO:0004367 molecular_function] (1)	NAD(P)-binding domain [IPR016040] (1); Glycerol-3-phosphate dehydrogenase, NAD-dependent [IPR006168] (1); Glycerol-3-phosphate dehydrogenase, NAD-dependent, C-terminal [IPR006109] (1); Glycerol-3-phosphate dehydrogenase, NAD-dependent, N-terminal [IPR011128] (1); 6-phosphogluconate dehydrogenase, domain 2 [IPR013328] (1); 6-phosphogluconate dehydrogenase C-terminal domain-like [IPR008927] (1)	-	-	P_trifoliata_00006_mRNA_27.2
GF0043483	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00006_mRNA_235.1
GF0043482	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00006_mRNA_226.1
GF0043481	0	0	1	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); ATP-dependent RNA helicase DEAD-box, conserved site [IPR000629] (1)	-	-	P_trifoliata_00006_mRNA_203.1
GF0043480	0	0	1	Wax synthase isoform 1 (1)		Wax synthase domain [IPR032805] (1)	-	-	P_trifoliata_00006_mRNA_20.1
GF0043479	0	0	1	Hypothetical protein (1)		Uncharacterised protein family UPF0114 [IPR005134] (1)	-	-	P_trifoliata_00006_mRNA_2.1
GF0043478	0	0	1	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1); MULE transposase domain [IPR018289] (1)	-	-	P_trifoliata_00006_mRNA_187.1
GF0043477	0	0	1	Clavata3/ESR (CLE) gene family member MtCLE24 (1)			-	-	P_trifoliata_00006_mRNA_169.1
GF0043476	0	0	1	DUF679 domain membrane protein (1)		Protein of unknown function DUF679 [IPR007770] (1)	-	-	P_trifoliata_00006_mRNA_162.1
GF0043475	0	0	1	Hypothetical protein (1)	oxidoreductase activity, acting on CH-OH group of donors [GO:0016614 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1)	FAD/NAD(P)-binding domain [IPR023753] (1); Glucose-methanol-choline oxidoreductase, C-terminal [IPR007867] (1)	-	-	P_trifoliata_00006_mRNA_158.1
GF0043474	0	0	1	Glucose-methanol-choline (GMC) oxidoreductase family 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); oxidoreductase activity, acting on CH-OH group of donors [GO:0016614 molecular_function] (1)	Glucose-methanol-choline oxidoreductase, N-terminal [IPR000172] (1); FAD/NAD(P)-binding domain [IPR023753] (1)	-	-	P_trifoliata_00006_mRNA_157.1
GF0043473	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00006_mRNA_153.1
GF0043472	0	0	1	Potassium transporter (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)	-	-	P_trifoliata_00006_mRNA_15.1
GF0043471	0	0	1	Serine carboxypeptidase (1)	transferase activity, transferring glycosyl groups [GO:0016757 molecular_function] (1)	Glycosyltransferase AER61, uncharacterised [IPR007657] (1)	-	-	P_trifoliata_00006_mRNA_108.1
GF0043470	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00006_mRNA_100.1
GF0043469	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00005_mRNA_99.1
GF0043468	0	0	1	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1); FAR1 DNA binding domain [IPR004330] (1)	-	-	P_trifoliata_00005_mRNA_97.1
GF0043467	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00005_mRNA_93.1
GF0043466	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00005_mRNA_90.1
GF0043465	0	0	1	Auxin-induced protein 10A5 (1)	response to auxin [GO:0009733 biological_process] (1)	Small auxin-up RNA [IPR003676] (1)	-	-	P_trifoliata_00005_mRNA_86.1
GF0043464	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00005_mRNA_81.1
GF0043463	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00005_mRNA_80.1
GF0043462	0	0	1	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 [IPR001128] (1); Cytochrome P450, E-class, group I [IPR002401] (1)	-	-	P_trifoliata_00005_mRNA_78.1
GF0043461	0	0	1	Hypothetical protein (1)	integral component of membrane [GO:0016021 cellular_component] (1)	TRAM/LAG1/CLN8 homology domain [IPR006634] (1)	-	-	P_trifoliata_00005_mRNA_68.1
GF0043460	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00005_mRNA_67.1
GF0043459	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00005_mRNA_66.1
GF0043458	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00005_mRNA_62.1
GF0043457	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00005_mRNA_61.1
GF0043456	0	0	1	BAHD acyltransferase (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)	-	-	P_trifoliata_00005_mRNA_59.1
GF0043455	0	0	1	Hypothetical protein (1)	GTP biosynthetic process [GO:0006183 biological_process] (1); CTP biosynthetic process [GO:0006241 biological_process] (1); nucleoside diphosphate phosphorylation [GO:0006165 biological_process] (1); UTP biosynthetic process [GO:0006228 biological_process] (1); nucleoside diphosphate kinase activity [GO:0004550 molecular_function] (1)	Nucleoside diphosphate kinase [IPR001564] (1)	-	-	P_trifoliata_00005_mRNA_56.1
GF0043454	0	0	1	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)	-	-	P_trifoliata_00005_mRNA_55.1
GF0043453	0	0	1	Geraniol 10-hydroxylase-like 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 [IPR001128] (1); Cytochrome P450, E-class, group I [IPR002401] (1)	-	-	P_trifoliata_00005_mRNA_54.1

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*
GF0043452	0	0	1	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)	-	-	P_trifoliata_00005_mRNA_52.1
GF0043451	0	0	1	Hypothetical protein (1)		DNA-binding pseudobarrel domain [IPR015300] (1); B3 domain-containing protein [IPR005508] (1)	-	-	P_trifoliata_00005_mRNA_50.1
GF0043450	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00005_mRNA_45.1
GF0043449	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00005_mRNA_4.1
GF0043448	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00005_mRNA_38.1
GF0043447	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1); Reverse transcriptase domain [IPR000477] (1)	-	-	P_trifoliata_00005_mRNA_34.1
GF0043446	0	0	1	Hypothetical protein (1)	carbohydrate binding [GO:0030246 molecular_function] (1)	Legume lectin domain [IPR001220] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1)	-	-	P_trifoliata_00005_mRNA_33.1
GF0043445	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00005_mRNA_31.1
GF0043444	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	-	-	P_trifoliata_00005_mRNA_26.1
GF0043443	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00005_mRNA_25.1
GF0043442	0	0	1	Hypothetical protein (1)	GTPase activator activity [GO:0005096 molecular_function] (1)	Arf GTPase activating protein [IPR001164] (1)	-	-	P_trifoliata_00005_mRNA_22.1
GF0043441	0	0	1	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Pentatricopeptide repeat [IPR002885] (1); Tetratricopeptide-like helical domain [IPR011990] (1)	-	-	P_trifoliata_00005_mRNA_16.1
GF0043440	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00005_mRNA_148.1
GF0043439	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00005_mRNA_146.1
GF0043438	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00005_mRNA_144.1
GF0043437	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00005_mRNA_140.1
GF0043436	0	0	1	Agamous-like MADS-box protein AGL61 (1)	protein dimerization activity [GO:0046983 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	Transcription factor, MADS-box [IPR002100] (1)	-	-	P_trifoliata_00005_mRNA_14.1
GF0043435	0	0	1	Lectin receptor kinase (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); carbohydrate binding [GO:0030246 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Legume lectin domain [IPR001220] (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)	-	-	P_trifoliata_00005_mRNA_138.1
GF0043434	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00005_mRNA_134.1
GF0043433	0	0	1	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)	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)	-	-	P_trifoliata_00005_mRNA_131.1
GF0043432	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00005_mRNA_130.1
GF0043431	0	0	1	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1)	Protein kinase, ATP binding site [IPR017441] (1); Protein kinase-like domain [IPR011009] (1); Leucine-rich repeat 3 [IPR011713] (1)	-	-	P_trifoliata_00005_mRNA_129.1
GF0043430	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00005_mRNA_127.1
GF0043429	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00005_mRNA_125.1
GF0043428	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00005_mRNA_124.1
GF0043427	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00005_mRNA_122.1
GF0043426	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00005_mRNA_12.1
GF0043425	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00005_mRNA_119.1
GF0043424	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00005_mRNA_117.1
GF0043423	0	0	1	Hypothetical protein (1)	hydrolase activity, acting on ester bonds [GO:0016788 molecular_function] (1)	Harbinger transposase-derived protein [IPR006912] (1)	-	-	P_trifoliata_00005_mRNA_115.1
GF0043422	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00005_mRNA_113.1
GF0043421	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00005_mRNA_103.1
GF0043420	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00005_mRNA_101.1
GF0043419	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00005_mRNA_100.1
GF0043418	0	0	1	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 Rpb2, domain 2 [IPR007642] (1)	-	-	P_trifoliata_00004_mRNA_95.1
GF0043417	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00004_mRNA_92.1
GF0043416	0	0	1	Hypothetical protein (1)		Protein kinase-like domain [IPR011009] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1)	-	-	P_trifoliata_00004_mRNA_67.1
GF0043415	0	0	1	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); protein ubiquitination [GO:0016567 biological_process] (1); nucleus [GO:0005634 cellular_component] (1)	SIAH-type domain [IPR013323] (1); Seven-in-absentia protein, TRAF-like domain [IPR018121] (1); TRAF-like [IPR008974] (1); E3 ubiquitin-protein ligase SIN-like [IPR004162] (1)	-	-	P_trifoliata_00004_mRNA_63.1
GF0043414	0	0	1	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)	-	-	P_trifoliata_00004_mRNA_54.1
GF0043413	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00004_mRNA_4.1
GF0043412	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00004_mRNA_34.1
GF0043411	0	0	1	Hypothetical protein (1)		Domain of unknown function DUF4782 [IPR031968] (1)	-	-	P_trifoliata_00004_mRNA_3.1
GF0043410	0	0	1	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 [IPR001128] (1)	-	-	P_trifoliata_00004_mRNA_190.1
GF0043409	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00004_mRNA_178.1
GF0043408	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00004_mRNA_175.1
GF0043407	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00004_mRNA_174.1
GF0043406	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00004_mRNA_17.1
GF0043405	0	0	1	Hypothetical protein (1)		Protein of unknown function DUF594 [IPR007658] (1)	-	-	P_trifoliata_00004_mRNA_169.1
GF0043404	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00004_mRNA_167.1
GF0043403	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00004_mRNA_166.1
GF0043402	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00004_mRNA_165.1
GF0043401	0	0	1	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	Paired amphipathic helix [IPR003822] (1)	-	-	P_trifoliata_00004_mRNA_164.1
GF0043400	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00004_mRNA_161.1
GF0043399	0	0	1	Hypothetical protein (1)		Mitochondrial carrier domain [IPR023395] (1); Mitochondrial substrate/solute carrier [IPR018108] (1)	-	-	P_trifoliata_00004_mRNA_158.1
GF0043398	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00004_mRNA_153.1
GF0043397	0	0	1	Hypothetical protein (1)		Cwf19-like protein, C-terminal domain-2 [IPR006767] (1); Cwf19-like, C-terminal domain-1 [IPR006768] (1)	-	-	P_trifoliata_00004_mRNA_152.1
GF0043396	0	0	1	CwfJ-like family protein, putative isoform 4 (1)			-	-	P_trifoliata_00004_mRNA_150.1
GF0043395	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00004_mRNA_149.1
GF0043394	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00004_mRNA_148.1
GF0043393	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00004_mRNA_145.1
GF0043392	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00004_mRNA_144.1
GF0043391	0	0	1	Hypothetical protein (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)	-	-	P_trifoliata_00004_mRNA_143.1
GF0043390	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00004_mRNA_140.1
GF0043389	0	0	1	Leucine-rich repeat receptor-like protein CLAVATA2 (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)	-	-	P_trifoliata_00004_mRNA_139.1
GF0043388	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00004_mRNA_135.1
GF0043387	0	0	1	Dormancy/auxin associated family protein (1)		Dormancyauxin associated [IPR008406] (1)	-	-	P_trifoliata_00004_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*
GF0043386	0	0	1	Hypothetical protein (1)		Rapid ALkalinization Factor [IPR008801] (1)	-	-	P_trifoliata_00004_mRNA_112.1
GF0043385	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00004_mRNA_109.1
GF0043384	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00004_mRNA_106.1
GF0043383	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00004_mRNA_1.1
GF0043382	0	0	1	Hypothetical protein (1)		GAG-pre-integrase domain [IPR025724] (1)	-	-	P_trifoliata_00003_mRNA_89.1
GF0043381	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00003_mRNA_83.1
GF0043380	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00003_mRNA_81.1
GF0043379	0	0	1	UDP-glycosyltransferase 89B1 (1)	metabolic process [GO:0008152 biological_process] (1); transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	-	-	P_trifoliata_00003_mRNA_68.1
GF0043378	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00003_mRNA_58.1
GF0043377	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00003_mRNA_56.1
GF0043376	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00003_mRNA_47.1
GF0043375	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00003_mRNA_44.1
GF0043374	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00003_mRNA_42.1
GF0043373	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00003_mRNA_39.1
GF0043372	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00003_mRNA_37.1
GF0043371	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00003_mRNA_32.1
GF0043370	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00003_mRNA_30.1
GF0043369	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00003_mRNA_29.1
GF0043368	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00003_mRNA_26.1
GF0043367	0	0	1	Mitochondrial thiamine pyrophosphate carrier 1 (1)		Mitochondrial carrier domain [IPR023395] (1); Mitochondrial substrate/solute carrier [IPR018108] (1)	-	-	P_trifoliata_00003_mRNA_25.1
GF0043366	0	0	1	Solute carrier family 25 member 44 (1)		Repeat of unknown function XGLTT [IPR008164] (1); Mitochondrial substrate/solute carrier [IPR018108] (1); Mitochondrial carrier domain [IPR023395] (1)	-	-	P_trifoliata_00003_mRNA_24.1
GF0043365	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00003_mRNA_23.1
GF0043364	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00003_mRNA_22.1
GF0043363	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00003_mRNA_21.1
GF0043362	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00003_mRNA_20.1
GF0043361	0	0	1	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)	-	-	P_trifoliata_00003_mRNA_193.1
GF0043360	0	0	1	Hypothetical protein (1)	positive regulation of catalytic activity [GO:0043085 biological_process] (1); deadenylation-dependent decapping of nuclear-transcribed mRNA [GO:0000290 biological_process] (1); enzyme activator activity [GO:0008047 molecular_function] (1)	mRNA-decapping enzyme subunit 1 [IPR010334] (1); PH domain-like [IPR011993] (1)	-	-	P_trifoliata_00003_mRNA_192.1
GF0043359	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00003_mRNA_19.1
GF0043358	0	0	1	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	-	P_trifoliata_00003_mRNA_168.1
GF0043357	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00003_mRNA_159.1
GF0043356	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00003_mRNA_155.1
GF0043355	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00003_mRNA_15.1
GF0043354	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00003_mRNA_149.1
GF0043353	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00003_mRNA_141.1
GF0043352	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00003_mRNA_14.1
GF0043351	0	0	1	Disease resistance protein (1)	protein binding [GO:0005515 molecular_function] (1); ADP binding [GO:0043531 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)	-	-	P_trifoliata_00003_mRNA_137.1
GF0043350	0	0	1	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FAR1 DNA binding domain [IPR004330] (1); FHY3/FAR1 family [IPR031052] (1)	-	-	P_trifoliata_00003_mRNA_136.1
GF0043349	0	0	1	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	-	-	P_trifoliata_00003_mRNA_13.1
GF0043348	0	0	1	Hypothetical protein (1)		Isopenicillin N synthase-like [IPR027443] (1)	-	-	P_trifoliata_00003_mRNA_126.1
GF0043347	0	0	1	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); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Domain of unknown function DUF1985 [IPR015410] (1); Protein kinase domain [IPR000719] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Protein kinase, ATP binding site [IPR017441] (1)	-	-	P_trifoliata_00003_mRNA_114.1
GF0043346	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00003_mRNA_105.1
GF0043345	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00003_mRNA_102.1
GF0043344	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00003_mRNA_1.1
GF0043343	0	0	1	Protein pleiotropic regulatory locus 1 (1)	protein binding [GO:0005515 molecular_function] (1)	G-protein beta WD-40 repeat [IPR020472] (1); WD40 repeat, conserved site [IPR019775] (1); WD40/YVTN repeat-like-containing domain [IPR015943] (1); WD40 repeat [IPR001680] (1); WD40-repeat-containing domain [IPR017986] (1)	-	-	P_trifoliata_00002_mRNA_99.1
GF0043342	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00002_mRNA_90.1
GF0043341	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00002_mRNA_9.1
GF0043340	0	0	1	DEAD-box ATP-dependent RNA helicase 20 (1)	ATP binding [GO:0005524 molecular_function] (1); nucleic acid binding [GO:0003676 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)	-	-	P_trifoliata_00002_mRNA_89.1
GF0043339	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00002_mRNA_8.1
GF0043338	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00002_mRNA_69.1
GF0043337	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00002_mRNA_68.1
GF0043336	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00002_mRNA_67.1
GF0043335	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00002_mRNA_66.1
GF0043334	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00002_mRNA_62.1
GF0043333	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00002_mRNA_57.1
GF0043332	0	0	1	Pectolytic enzyme, Pectin lyase fold (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)	-	-	P_trifoliata_00002_mRNA_56.1
GF0043331	0	0	1	Imidazole glycerol phosphate synthase subunit HisH (1)		Protein of unknown function DUF4602 [IPR027973] (1)	-	-	P_trifoliata_00002_mRNA_41.1
GF0043330	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00002_mRNA_4.1
GF0043329	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00002_mRNA_33.1
GF0043328	0	0	1	Ribosomal protein S4 (1)		Ribosomal protein S4/S9 [IPR022801] (1)	-	-	P_trifoliata_00002_mRNA_32.1
GF0043327	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00002_mRNA_31.1
GF0043326	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00002_mRNA_30.1
GF0043325	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00002_mRNA_28.1
GF0043324	0	0	1	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	-	-	P_trifoliata_00002_mRNA_244.1
GF0043323	0	0	1	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1); FAR1 DNA binding domain [IPR004330] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1)	-	-	P_trifoliata_00002_mRNA_232.1
GF0043322	0	0	1	Polygalacturonase (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)	-	-	P_trifoliata_00002_mRNA_228.1
GF0043321	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00002_mRNA_227.1
GF0043320	0	0	1	Hypothetical protein (1)	transferase activity, transferring glycosyl groups [GO:0016757 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Glycosyl transferase, family 8 [IPR002495] (1); Ribonuclease H-like domain [IPR012337] (1); Nucleotide-diphospho-sugar transferases [IPR029044] (1)	-	-	P_trifoliata_00002_mRNA_220.1
GF0043319	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00002_mRNA_22.1
GF0043318	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00002_mRNA_21.1
GF0043317	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00002_mRNA_20.1

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*
GF0043316	0	0	1	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)	Plant peroxidase [IPR000823] (1); Haem peroxidase, plant/fungal/bacterial [IPR002016] (1); Haem peroxidase [IPR010255] (1)	-	-	P_trifoliata_00002_mRNA_196.1
GF0043315	0	0	1	Orf105b protein (1)			-	-	P_trifoliata_00002_mRNA_19.1
GF0043314	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00002_mRNA_187.1
GF0043313	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00002_mRNA_18.1
GF0043312	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00002_mRNA_17.1
GF0043311	0	0	1	Serine/threonine-protein kinase PBS1 (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/dual specificity protein kinase, catalytic domain [IPR002290] (1)	-	-	P_trifoliata_00002_mRNA_159.1
GF0043310	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00002_mRNA_14.1
GF0043309	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00002_mRNA_134.1
GF0043308	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00002_mRNA_132.1
GF0043307	0	0	1	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1); FAR1 DNA binding domain [IPR004330] (1)	-	-	P_trifoliata_00002_mRNA_130.1
GF0043306	0	0	1	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	Myb domain [IPR017930] (1); Homeodomain-like [IPR009057] (1); SANT/Myb domain [IPR001005] (1)	-	-	P_trifoliata_00002_mRNA_12.1
GF0043305	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00002_mRNA_11.1
GF0043304	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00002_mRNA_102.1
GF0043303	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	-	-	P_trifoliata_00002_mRNA_10.1
GF0043302	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00002_mRNA_1.1
GF0043301	0	0	1	Hypothetical protein (1)	nucleotide binding [GO:0000166 molecular_function] (1); metal ion binding [GO:0046872 molecular_function] (1)	P-type ATPase, A domain [IPR008250] (1)	-	-	P_trifoliata_00001_mRNA_83.1
GF0043300	0	0	1	P-type ATPase superfamily (1)	nucleotide binding [GO:0000166 molecular_function] (1); metal ion binding [GO:0046872 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1)	P-type ATPase, A domain [IPR008250] (1); HAD-like domain [IPR023214] (1); P-type ATPase [IPR001757] (1); P-type ATPase, cytoplasmic domain N [IPR023299] (1)	-	-	P_trifoliata_00001_mRNA_82.1
GF0043299	0	0	1	Theta 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); Thioredoxin-like fold [IPR012336] (1)	-	-	P_trifoliata_00001_mRNA_81.1
GF0043298	0	0	1	Theta class glutathione S-transferase (1)	protein binding [GO:0005515 molecular_function] (1)	Glutathione S-transferase, C-terminal [IPR004046] (1); Thioredoxin-like fold [IPR012336] (1); Glutathione S-transferase, N-terminal [IPR004045] (1); Glutathione S-transferase, C-terminal-like [IPR010987] (1)	-	-	P_trifoliata_00001_mRNA_80.1
GF0043297	0	0	1	Xyloglucan galactosyltransferase KATAMARI1 (1)		Exostosin-like [IPR004263] (1)	-	-	P_trifoliata_00001_mRNA_78.1
GF0043296	0	0	1	Probable phospholipid hydroperoxide 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); Glutathione peroxidase conserved site [IPR029760] (1); Glutathione peroxidase active site [IPR029759] (1)	-	-	P_trifoliata_00001_mRNA_77.1
GF0043295	0	0	1	Protein kinase protein with tetratricopeptide repeat domain (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); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1)	-	-	P_trifoliata_00001_mRNA_75.1
GF0043294	0	0	1	Pollen-specific protein SF3 (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, LIM-type [IPR001781] (1)	-	-	P_trifoliata_00001_mRNA_74.1
GF0043293	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00001_mRNA_55.1
GF0043292	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00001_mRNA_30.1
GF0043291	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00001_mRNA_279.1
GF0043290	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00001_mRNA_244.1
GF0043289	0	0	1	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); FAE1/Type III polyketide synthase-like protein [IPR013601] (1)	-	-	P_trifoliata_00001_mRNA_242.1
GF0043288	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00001_mRNA_240.1
GF0043287	0	0	1	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); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1)	-	-	P_trifoliata_00001_mRNA_238.1
GF0043286	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00001_mRNA_234.1
GF0043285	0	0	1	Hypothetical protein (1)	serine-type carboxypeptidase activity [GO:0004185 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Alpha/Beta hydrolase fold [IPR029058] (1); Peptidase S10, serine carboxypeptidase [IPR001563] (1)	-	-	P_trifoliata_00001_mRNA_227.1
GF0043284	0	0	1	Hypothetical protein (1)	methionine biosynthetic process [GO:0009086 biological_process] (1); zinc ion binding [GO:0008270 molecular_function] (1); 5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase activity [GO:0003871 molecular_function] (1)	Cobalamin-independent methionine synthase MetE, C-terminal/archaeal [IPR002629] (1)	-	-	P_trifoliata_00001_mRNA_226.1
GF0043283	0	0	1	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Piwi domain [IPR003165] (1)	-	-	P_trifoliata_00001_mRNA_217.1
GF0043282	0	0	1	Early nodulin-like protein 20 (1)	electron carrier activity [GO:0009055 molecular_function] (1)	Phytocyanin domain [IPR003245] (1); Cupredoxin [IPR008972] (1)	-	-	P_trifoliata_00001_mRNA_216.1
GF0043281	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00001_mRNA_208.1
GF0043280	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00001_mRNA_205.1
GF0043279	0	0	1	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)	-	-	P_trifoliata_00001_mRNA_203.1
GF0043278	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00001_mRNA_201.1
GF0043277	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00001_mRNA_190.1
GF0043276	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00001_mRNA_19.1
GF0043275	0	0	1	Multidrug resistance protein ABC transporter family protein (1)	ATPase activity, coupled to transmembrane movement of substances [GO:0042626 molecular_function] (1); transmembrane transport [GO:0055085 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1); ATPase activity [GO:0016887 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1); transport [GO:0006810 biological_process] (1)	ABC transporter, conserved site [IPR017871] (1); AAA+ ATPase domain [IPR003593] (1); ABC transporter type 1, transmembrane domain [IPR011527] (1); ABC transporter-like [IPR003439] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	-	-	P_trifoliata_00001_mRNA_189.1
GF0043274	0	0	1	Hypothetical protein (1)	translational initiation [GO:0006413 biological_process] (1); integral component of membrane [GO:0016021 cellular_component] (1); cation transport [GO:0006812 biological_process] (1); transmembrane transport [GO:0055085 biological_process] (1); translation initiation factor activity [GO:0003743 molecular_function] (1); solute:proton antiporter activity [GO:0015299 molecular_function] (1); RNA binding [GO:0003723 molecular_function] (1)	Translation initiation factor IF-1 [IPR004368] (1); Nucleic acid-binding, OB-fold [IPR012340] (1); RNA-binding domain, S1, IF1 type [IPR006196] (1); Cation/H+ exchanger [IPR006153] (1); RNA-binding domain, S1 [IPR022967] (1)	-	-	P_trifoliata_00001_mRNA_182.1
GF0043273	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00001_mRNA_177.1
GF0043272	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00001_mRNA_131.1
GF0043271	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00001_mRNA_123.1
GF0043270	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00001_mRNA_122.1
GF0043269	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00001_mRNA_12.1
GF0043268	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00001_mRNA_107.1
GF0043267	0	0	1	Hypothetical protein (1)			-	-	P_trifoliata_00001_mRNA_102.1
GF0043266	0	0	1	TSA: Wollemia nobilis transcribed RNA sequence (1)		Protein of unknown function DUF2039 [IPR019351] (1); YfgJ-like [IPR029037] (1)	-	-	P_trifoliata_00001_mRNA_1.1