Supplemental Table 3. *C. clementina* 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*
GF0000787	7	0	0	Integrase (5); Hypothetical protein (2)		Aspartic peptidase domain [IPR021109] (7)	scaffold_1_mRNA_1802.1,scaffold_3_mRNA_1921.1,scaffold_3_mRNA_815.1,scaffold_5_mRNA_4186.1,scaffold_8_mRNA_1156.1,scaffold_9_mRNA_1777.1, scaffold_9_mRNA_1997.1	-	-
GF0004025	4	0	0	Hypothetical protein (4)	carotenoid biosynthetic process [GO:0016117 biological_process] (4); carotene 7,8-desaturase activity [GO:0016719 molecular_function] (4); oxidoreductase activity [GO:0016491 molecular_function] (4); oxidation-reduction process [GO:0055114 biological_process] (4)	Zeta-carotene desaturase [IPR014103] (4); Amine oxidase [IPR002937] (4); FAD/NAD(P)-binding domain [IPR023753] (4)	scaffold_5_mRNA_3317.1,scaffold_5_mRNA_3333.1,scaffold_5_mRNA_3335.1, scaffold_5_mRNA_3340.1	-	-
GF0009842	3	0	0	Monosacharide transport protein (3)			scaffold_3_mRNA_4804.1,scaffold_3_mRNA_5074.1,scaffold_5_mRNA_3631.1	-	-
GF0005687	3	0	0	Monosacharide transport protein (3)			scaffold_1_mRNA_2569.1,scaffold_2_mRNA_1391.1,scaffold_3_mRNA_4257.1	-	-
GF0033628	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Aspartic peptidase domain [IPR021109] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_9_mRNA_996.1	-	-
GF0033627	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_995.1	-	-
GF0033626	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_994.1	-	-
GF0033625	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_993.1	-	-
GF0033624	1	0	0	Hypothetical protein (1)	translation [GO:0006412 biological_process] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1); ribosome [GO:0005840 cellular_component] (1)	Ribosomal protein L14P [IPR000218] (1); Ribosomal protein L14P, conserved site [IPR019972] (1)	scaffold_9_mRNA_970.1	-	-
GF0033623	1	0	0	Caleosin (1)		Caleosin-related [IPR007736] (1)	scaffold_9_mRNA_967.1	-	-
GF0033622	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_9_mRNA_948.1	-	-
GF0033621	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Domain of unknown function DUF4219 [IPR025314] (1); Zinc finger, CCHC-type [IPR001878] (1)	scaffold_9_mRNA_945.1	-	-
GF0033620	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_943.1	-	-
GF0033619	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_9_mRNA_938.1	-	-
GF0033618	1	0	0	Peptide transporter PTR3-A (1)	transport [GO:0006810 biological_process] (1); membrane [GO:0016020 cellular_component] (1); transporter activity [GO:0005215 molecular_function] (1)	Major facilitator superfamily domain [IPR020846] (1); Proton-dependent oligopeptide transporter family [IPR000109] (1)	scaffold_9_mRNA_931.1	-	-
GF0033617	1	0	0	Hypothetical protein (1)	cyanate hydratase activity [GO:0008824 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1); cyanate metabolic process [GO:0009439 biological_process] (1); sequence-specific DNA binding [GO:0043565 molecular_function] (1)	Cyanate hydratase [IPR008076] (1); Lambda repressor-like, DNA-binding domain [IPR010982] (1); Cyanate lyase, C-terminal [IPR003712] (1); Cro/C1-type helix-turn-helix domain [IPR001387] (1)	scaffold_9_mRNA_924.1	-	-
GF0033616	1	0	0	Putative retroelement pol polyprotein (1)			scaffold_9_mRNA_908.1	-	-
GF0033615	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_904.1	-	-
GF0033614	1	0	0	Exosome complex component RRP4 (1)	exosome (RNase complex) [GO:0000178 cellular_component] (1); RNA binding [GO:0003723 molecular_function] (1)	Exosome complex RNA-binding protein 1/RRP40/RRP4 [IPR026699] (1); K Homology domain, type 1 [IPR004088] (1)	scaffold_9_mRNA_901.1	-	-
GF0033613	1	0	0	Desiccation PCC13-like protein (1)		Ferritin-related [IPR012347] (1)	scaffold_9_mRNA_90.1	-	-
GF0033612	1	0	0	Thioesterase family protein (1)		Phenylacetic acid degradation-related domain [IPR003736] (1); Thioesterase domain [IPR006683] (1); HotDog domain [IPR029069] (1)	scaffold_9_mRNA_9.1	-	-
GF0033611	1	0	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	scaffold_9_mRNA_897.1	-	-
GF0033610	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_895.1	-	-
GF0033609	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_894.1	-	-
GF0033608	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_893.1	-	-
GF0033607	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_891.1	-	-
GF0033606	1	0	0	Hypothetical protein (1)		Transposase-associated domain [IPR029480] (1)	scaffold_9_mRNA_890.1	-	-
GF0033605	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_889.1	-	-
GF0033604	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_886.1	-	-
GF0033603	1	0	0	Hypothetical protein (1)		Ubiquitin-related domain [IPR029071] (1)	scaffold_9_mRNA_884.1	-	-
GF0033602	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_9_mRNA_880.1	-	-
GF0033601	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4216 [IPR025312] (1)	scaffold_9_mRNA_878.1	-	-
GF0033600	1	0	0	Tau 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)	scaffold_9_mRNA_843.2	-	-
GF0033599	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_828.1	-	-
GF0033598	1	0	0	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	scaffold_9_mRNA_827.1	-	-
GF0033597	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_825.1	-	-
GF0033596	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_823.1	-	-
GF0033595	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_820.1	-	-
GF0033594	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_817.1	-	-
GF0033593	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_813.1	-	-
GF0033592	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_809.1	-	-
GF0033591	1	0	0	1-aminocyclopropane-1-carboxylate oxidase like 12 (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)	scaffold_9_mRNA_799.1	-	-
GF0033590	1	0	0	1-aminocyclopropane-1-carboxylate oxidase like 12 (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)	scaffold_9_mRNA_797.1	-	-
GF0033589	1	0	0	Desacetoxyvindoline 4-hydroxylase, putative (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)	scaffold_9_mRNA_795.1	-	-
GF0033588	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_794.1	-	-
GF0033587	1	0	0	1-aminocyclopropane-1-carboxylate oxidase homolog 11 (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Isopenicillin N synthase-like [IPR027443] (1); Non-haem dioxygenase N-terminal domain [IPR026992] (1); Oxoglutarate/iron-dependent dioxygenase [IPR005123] (1)	scaffold_9_mRNA_791.1	-	-
GF0033586	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_9_mRNA_790.1	-	-
GF0033585	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_789.1	-	-
GF0033584	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_9_mRNA_780.1	-	-
GF0033583	1	0	0	DNA repair protein XRCC4 (1)	DNA binding [GO:0003677 molecular_function] (1); nucleus [GO:0005634 cellular_component] (1); DNA recombination [GO:0006310 biological_process] (1); double-strand break repair [GO:0006302 biological_process] (1)	DNA repair protein XRCC4 [IPR010585] (1)	scaffold_9_mRNA_778.1	-	-
GF0033582	1	0	0	Hypothetical protein (1)	hydrolase activity [GO:0016787 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Peptidase M20 [IPR002933] (1)	scaffold_9_mRNA_775.1	-	-
GF0033581	1	0	0	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	scaffold_9_mRNA_768.1	-	-
GF0033580	1	0	0	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)	scaffold_9_mRNA_764.1	-	-
GF0033579	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_744.1	-	-
GF0033578	1	0	0	Enoyl-CoA delta isomerase 2, peroxisomal (1)	catalytic activity [GO:0003824 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Crotonase superfamily [IPR001753] (1); ClpP/crotonase-like domain [IPR029045] (1)	scaffold_9_mRNA_743.1	-	-
GF0033577	1	0	0	Enoyl-CoA delta isomerase 2, peroxisomal (1)	catalytic activity [GO:0003824 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	ClpP/crotonase-like domain [IPR029045] (1); Crotonase superfamily [IPR001753] (1)	scaffold_9_mRNA_742.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0033576	1	0	0	Hypothetical protein (1)	regulation of defense response [GO:0031347 biological_process] (1); regulation of salicylic acid mediated signaling pathway [GO:2000031 biological_process] (1); cellular response to salicylic acid stimulus [GO:0071446 biological_process] (1); integral component of membrane [GO:0016021 cellular_component] (1); protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat [IPR002110] (1); Ankyrin repeat-containing domain [IPR020683] (1); Protein accelerated cell death 6 [IPR032846] (1)	scaffold_9_mRNA_740.1	-	-
GF0033575	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_739.1	-	-
GF0033574	1	0	0	Ankyrin repeat family protein, putative (1)	integral component of membrane [GO:0016021 cellular_component] (1); cellular response to salicylic acid stimulus [GO:0071446 biological_process] (1); protein binding [GO:0005515 molecular_function] (1); regulation of defense response [GO:0031347 biological_process] (1); regulation of salicylic acid mediated signaling pathway [GO:2000031 biological_process] (1)	Ankyrin repeat [IPR002110] (1); Protein accelerated cell death 6 [IPR032846] (1); PGG domain [IPR026961] (1); Ankyrin repeat-containing domain [IPR020683] (1)	scaffold_9_mRNA_738.1	-	-
GF0033573	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_732.1	-	-
GF0033572	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_726.1	-	-
GF0033571	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_721.1	-	-
GF0033570	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_718.1	-	-
GF0033569	1	0	0	Hypothetical protein (1)	regulation of salicylic acid mediated signaling pathway [GO:2000031 biological_process] (1); regulation of defense response [GO:0031347 biological_process] (1); protein binding [GO:0005515 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1); cellular response to salicylic acid stimulus [GO:0071446 biological_process] (1)	Ankyrin repeat [IPR002110] (1); Ankyrin repeat-containing domain [IPR020683] (1); Protein accelerated cell death 6 [IPR032846] (1)	scaffold_9_mRNA_715.1	-	-
GF0033568	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_713.1	-	-
GF0033567	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4219 [IPR025314] (1)	scaffold_9_mRNA_688.1	-	-
GF0033566	1	0	0	Monosacharide transport protein (1)			scaffold_9_mRNA_686.1	-	-
GF0033565	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_9_mRNA_685.1	-	-
GF0033564	1	0	0	3-ketoacyl-CoA synthase 2 (1)	catalytic activity [GO:0003824 molecular_function] (1); fatty acid biosynthetic process [GO:0006633 biological_process] (1); transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (1); membrane [GO:0016020 cellular_component] (1); metabolic process [GO:0008152 biological_process] (1)	FAE1/Type III polyketide synthase-like protein [IPR013601] (1); Thiolase-like [IPR016039] (1); Chalcone/stilbene synthase, C-terminal [IPR012328] (1); Very-long-chain 3-ketoacyl-CoA synthase [IPR012392] (1)	scaffold_9_mRNA_682.1	-	-
GF0033563	1	0	0	Hypothetical protein (1)	chromatin remodeling [GO:0006338 biological_process] (1); BAF-type complex [GO:0090544 cellular_component] (1); binding [GO:0005488 molecular_function] (1)	SWI/SNF-like complex subunit BAF250/Osa [IPR021906] (1); Armadillo-type fold [IPR016024] (1); Armadillo-like helical [IPR011989] (1)	scaffold_9_mRNA_681.1	-	-
GF0033562	1	0	0	3-ketoacyl-CoA synthase 11 (1)	membrane [GO:0016020 cellular_component] (1); metabolic process [GO:0008152 biological_process] (1); transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (1); fatty acid biosynthetic process [GO:0006633 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1)	Thiolase-like [IPR016039] (1); Very-long-chain 3-ketoacyl-CoA synthase [IPR012392] (1); FAE1/Type III polyketide synthase-like protein [IPR013601] (1)	scaffold_9_mRNA_678.1	-	-
GF0033561	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_670.1	-	-
GF0033560	1	0	0	TSA: Wollemia nobilis transcribed RNA sequence (1)	sulfate adenylyltransferase (ATP) activity [GO:0004781 molecular_function] (1)	Sulphate adenylyltransferase catalytic domain [IPR024951] (1); Rossmann-like alpha/beta/alpha sandwich fold [IPR014729] (1)	scaffold_9_mRNA_664.1	-	-
GF0033559	1	0	0	Cation transport 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)	Cation-transporting P-type ATPase, N-terminal [IPR004014] (1); P-type ATPase, A domain [IPR008250] (1); P-type ATPase, transmembrane domain [IPR023298] (1); P-type ATPase, cytoplasmic domain N [IPR023299] (1); P-type ATPase [IPR001757] (1); P-type ATPase, phosphorylation site [IPR018303] (1)	scaffold_9_mRNA_663.1	-	-
GF0033558	1	0	0	Glutaminase (1)			scaffold_9_mRNA_661.1	-	-
GF0033557	1	0	0	Cation transport 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)	HAD-like domain [IPR023214] (1); Cation-transporting P-type ATPase, N-terminal [IPR004014] (1); P-type ATPase, A domain [IPR008250] (1); P-type ATPase, phosphorylation site [IPR018303] (1); Cation-transporting P-type ATPase, C-terminal [IPR006068] (1); P-type ATPase, transmembrane domain [IPR023298] (1); P-type ATPase [IPR001757] (1)	scaffold_9_mRNA_660.1	-	-
GF0033556	1	0	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	scaffold_9_mRNA_653.1	-	-
GF0033555	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_629.1	-	-
GF0033554	1	0	0	Hypothetical protein (1)		FAR1 DNA binding domain [IPR004330] (1)	scaffold_9_mRNA_625.1	-	-
GF0033553	1	0	0	ADP-ribosylation factor A1F (1)	small GTPase mediated signal transduction [GO:0007264 biological_process] (1); GTP binding [GO:0005525 molecular_function] (1); intracellular [GO:0005622 cellular_component] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Small GTP-binding protein domain [IPR005225] (1); Small GTPase superfamily, ARF type [IPR024156] (1); Small GTPase superfamily, ARF/SAR type [IPR006689] (1)	scaffold_9_mRNA_62.1	-	-
GF0033552	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_6.1	-	-
GF0033551	1	0	0	Monosacharide transport protein (1)			scaffold_9_mRNA_599.1	-	-
GF0033550	1	0	0	Hypothetical protein (1)		Glyoxalase/fosfomycin resistance/dioxygenase domain [IPR004360] (1); Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase [IPR029068] (1)	scaffold_9_mRNA_586.1	-	-
GF0033549	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_584.1	-	-
GF0033548	1	0	0	Hypothetical protein (1)		Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase [IPR029068] (1)	scaffold_9_mRNA_583.1	-	-
GF0033547	1	0	0	Late embryogenesis abundant D-like protein (1)		Seed maturation protein [IPR007011] (1)	scaffold_9_mRNA_582.1	-	-
GF0033546	1	0	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Domain of unknown function DUF1985 [IPR015410] (1); Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	scaffold_9_mRNA_563.1	-	-
GF0033545	1	0	0	Hypothetical protein (1)		MULE transposase domain [IPR018289] (1); Transposase, MuDR, plant [IPR004332] (1)	scaffold_9_mRNA_562.1	-	-
GF0033544	1	0	0	Transposable element Ac (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_9_mRNA_551.1	-	-
GF0033543	1	0	0	Amino-terminal domain cyclin (1)		Cyclin, N-terminal [IPR006671] (1); Cyclin-like [IPR013763] (1)	scaffold_9_mRNA_534.1	-	-
GF0033542	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_9_mRNA_527.1	-	-
GF0033541	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_521.1	-	-
GF0033540	1	0	0	Type II peroxiredoxin (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); cell redox homeostasis [GO:0045454 biological_process] (1)	Thioredoxin domain [IPR013766] (1); Thioredoxin-like fold [IPR012336] (1); Redoxin [IPR013740] (1)	scaffold_9_mRNA_502.1	-	-
GF0033539	1	0	0	Bidirectional sugar transporter SWEET6b (1)	integral component of membrane [GO:0016021 cellular_component] (1)	SWEET sugar transporter [IPR004316] (1)	scaffold_9_mRNA_50.1	-	-
GF0033538	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_495.1	-	-
GF0033537	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_489.1	-	-
GF0033536	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_9_mRNA_487.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0033535	1	0	0	Basic 7S globulin (1)	proteolysis [GO:0006508 biological_process] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1)	Aspartic peptidase A1 family [IPR001461] (1); Xylanase inhibitor, N-terminal [IPR032861] (1); Xylanase inhibitor, C-terminal [IPR032799] (1); Xylanase inhibitor I-like [IPR033868] (1); Aspartic peptidase domain [IPR021109] (1); Peptidase family A1 domain [IPR033121] (1)	scaffold_9_mRNA_486.1	-	-
GF0033534	1	0	0	Basic 7S globulin (1)	proteolysis [GO:0006508 biological_process] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1)	Peptidase family A1 domain [IPR033121] (1); Aspartic peptidase domain [IPR021109] (1); Xylanase inhibitor I-like [IPR033868] (1); Aspartic peptidase A1 family [IPR001461] (1); Xylanase inhibitor, C-terminal [IPR032799] (1); Xylanase inhibitor, N-terminal [IPR032861] (1)	scaffold_9_mRNA_484.1	-	-
GF0033533	1	0	0	Basic 7S globulin (1)	proteolysis [GO:0006508 biological_process] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1)	Xylanase inhibitor I-like [IPR033868] (1); Xylanase inhibitor, C-terminal [IPR032799] (1); Xylanase inhibitor, N-terminal [IPR032861] (1); Aspartic peptidase A1 family [IPR001461] (1); Aspartic peptidase domain [IPR021109] (1); Peptidase family A1 domain [IPR033121] (1)	scaffold_9_mRNA_483.1	-	-
GF0033532	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_482.1	-	-
GF0033531	1	0	0	Hypothetical protein (1)	calcium ion binding [GO:0005509 molecular_function] (1)	EF-hand domain pair [IPR011992] (1); EF-hand domain [IPR002048] (1); EF-Hand 1, calcium-binding site [IPR018247] (1)	scaffold_9_mRNA_456.1	-	-
GF0033530	1	0	0	Hypothetical protein (1)	calcium ion binding [GO:0005509 molecular_function] (1)	EF-hand domain [IPR002048] (1); EF-Hand 1, calcium-binding site [IPR018247] (1); EF-hand domain pair [IPR011992] (1)	scaffold_9_mRNA_452.1	-	-
GF0033529	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_447.1	-	-
GF0033528	1	0	0	Dienelactone hydrolase family, putative (1)	hydrolase activity [GO:0016787 molecular_function] (1)	Dienelactone hydrolase [IPR002925] (1); Alpha/Beta hydrolase fold [IPR029058] (1)	scaffold_9_mRNA_445.1	-	-
GF0033527	1	0	0	Hypothetical protein (1)	metabolic process [GO:0008152 biological_process] (1); transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	scaffold_9_mRNA_442.1	-	-
GF0033526	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_44.1	-	-
GF0033525	1	0	0	Ankyrin repeat plant-like protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat [IPR002110] (1); Ankyrin repeat-containing domain [IPR020683] (1)	scaffold_9_mRNA_436.1	-	-
GF0033524	1	0	0	Hypothetical protein (1)		F-box associated interaction domain [IPR017451] (1)	scaffold_9_mRNA_435.1	-	-
GF0033523	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_420.1	-	-
GF0033522	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_9_mRNA_42.1	-	-
GF0033521	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_419.1	-	-
GF0033520	1	0	0	Hypothetical protein (1)		Pectin lyase fold [IPR012334] (1); Pectate lyase superfamily protein [IPR024535] (1); Pectin lyase fold/virulence factor [IPR011050] (1)	scaffold_9_mRNA_414.1	-	-
GF0033519	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_41.1	-	-
GF0033518	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_406.1	-	-
GF0033517	1	0	0	T-complex protein 1 subunit gamma (1)	ATP binding [GO:0005524 molecular_function] (1); unfolded protein binding [GO:0051082 molecular_function] (1); protein folding [GO:0006457 biological_process] (1)	Chaperonin TCP-1, conserved site [IPR002194] (1); Chaperone tailless complex polypeptide 1 (TCP-1) [IPR017998] (1); T-complex protein 1, gamma subunit [IPR012719] (1); GroEL-like equatorial domain [IPR027413] (1); Chaperonin Cpn60/TCP-1 family [IPR002423] (1); GroEL-like apical domain [IPR027409] (1)	scaffold_9_mRNA_3839.1	-	-
GF0033516	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3813.1	-	-
GF0033515	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3812.1	-	-
GF0033514	1	0	0	Polynucleotidyl transferase, Ribonuclease H fold (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_9_mRNA_3811.1	-	-
GF0033513	1	0	0	Ribosomal protein L33 family 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)	Zinc-binding ribosomal protein [IPR011332] (1); Ribosomal protein L33 [IPR001705] (1)	scaffold_9_mRNA_377.2	-	-
GF0033512	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3755.1	-	-
GF0033511	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	NAC domain [IPR003441] (1); Zinc finger, BED-type [IPR003656] (1); hAT-like transposase, RNase-H fold [IPR025525] (1); Ribonuclease H-like domain [IPR012337] (1); Zinc finger C2H2-type [IPR013087] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	scaffold_9_mRNA_3730.1	-	-
GF0033510	1	0	0	Elongation factor 2 (1)	GTPase activity [GO:0003924 molecular_function] (1); GTP binding [GO:0005525 molecular_function] (1)	Small GTP-binding protein domain [IPR005225] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Translation elongation factor EFG/EF2, domain IV [IPR005517] (1); Translation protein, beta-barrel domain [IPR009000] (1); Translation elongation factor EFG, V domain [IPR000640] (1); Ribosomal protein S5 domain 2-type fold, subgroup [IPR014721] (1); Tr-type G domain, conserved site [IPR031157] (1); Translation elongation factor EFTu-like, domain 2 [IPR004161] (1); Transcription factor, GTP-binding domain [IPR000795] (1); Exostosin-like [IPR004263] (1); Elongation factor G, III-V domain [IPR009022] (1); Ribosomal protein S5 domain 2-type fold [IPR020568] (1)	scaffold_9_mRNA_3726.1	-	-
GF0033509	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3718.1	-	-
GF0033508	1	0	0	Cyclic nucleotide-gated ion channel 1 (1)		Cyclic nucleotide-binding-like [IPR018490] (1); RmlC-like jelly roll fold [IPR014710] (1); Cyclic nucleotide-binding domain [IPR000595] (1)	scaffold_9_mRNA_3712.1	-	-
GF0033507	1	0	0	Hypothetical protein (1)		Isopenicillin N synthase-like [IPR027443] (1)	scaffold_9_mRNA_3701.1	-	-
GF0033506	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3698.1	-	-
GF0033505	1	0	0	Cyclic nucleotide-gated ion channel, putative (1)		RmlC-like jelly roll fold [IPR014710] (1); Cyclic nucleotide-binding-like [IPR018490] (1); Cyclic nucleotide-binding domain [IPR000595] (1)	scaffold_9_mRNA_3697.1	-	-
GF0033504	1	0	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	scaffold_9_mRNA_3690.1	-	-
GF0033503	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_9_mRNA_3689.1	-	-
GF0033502	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF1985 [IPR015410] (1)	scaffold_9_mRNA_3688.1	-	-
GF0033501	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3670.1	-	-
GF0033500	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3662.1	-	-
GF0033499	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3642.1	-	-
GF0033498	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_9_mRNA_3641.1	-	-
GF0033497	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1); DNA integration [GO:0015074 biological_process] (1)	Retrotransposon gag domain [IPR005162] (1); Integrase, catalytic core [IPR001584] (1); Ribonuclease H-like domain [IPR012337] (1); Ribonuclease H domain [IPR002156] (1)	scaffold_9_mRNA_3638.1	-	-
GF0033496	1	0	0	LRR receptor-like kinase family protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	scaffold_9_mRNA_3636.1	-	-

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GF0033495	1	0	0	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)	scaffold_9_mRNA_3634.1	-	-
GF0033494	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_363.1	-	-
GF0033493	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1); Aspartic peptidase domain [IPR021109] (1)	scaffold_9_mRNA_3619.1	-	-
GF0033492	1	0	0	3-isopropylmalate dehydratase large subunit (1)			scaffold_9_mRNA_3594.1	-	-
GF0033491	1	0	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	NAD(P)-binding domain [IPR016040] (1); B3 DNA binding domain [IPR003340] (1); Short-chain dehydrogenase/reductase SDR [IPR002347] (1); DNA-binding pseudobarrel domain [IPR015300] (1)	scaffold_9_mRNA_3575.1	-	-
GF0033490	1	0	0	Hypothetical protein (1)		Gag-polypeptide of LTR copia-type [IPR029472] (1)	scaffold_9_mRNA_3567.1	-	-
GF0033489	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_9_mRNA_3563.1	-	-
GF0033488	1	0	0	Retinol dehydrogenase 14 (1)		Short-chain dehydrogenase/reductase SDR [IPR002347] (1); NAD(P)-binding domain [IPR016040] (1)	scaffold_9_mRNA_3555.1	-	-
GF0033487	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3543.1	-	-
GF0033486	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, GRF-type [IPR010666] (1)	scaffold_9_mRNA_353.1	-	-
GF0033485	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3514.1	-	-
GF0033484	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3513.1	-	-
GF0033483	1	0	0	Monosacharide transport protein (1)			scaffold_9_mRNA_3512.1	-	-
GF0033482	1	0	0	Heavy metal-associated domain protein, putative (1)	metal ion binding [GO:0046872 molecular_function] (1); metal ion transport [GO:0030001 biological_process] (1)	Heavy metal-associated domain, HMA [IPR006121] (1)	scaffold_9_mRNA_3510.1	-	-
GF0033481	1	0	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Domain of unknown function DUF1985 [IPR015410] (1); Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	scaffold_9_mRNA_3493.1	-	-
GF0033480	1	0	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1); Domain of unknown function DUF1985 [IPR015410] (1)	scaffold_9_mRNA_3484.1	-	-
GF0033479	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3436.1	-	-
GF0033478	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Domain of unknown function DUF4283 [IPR025558] (1); Zinc knuckle CX2CX4HX4C [IPR025836] (1); Zinc finger, CCHC-type [IPR001878] (1)	scaffold_9_mRNA_3427.1	-	-
GF0033477	1	0	0	Putative non-LTR retrolelement reverse transcriptase (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_9_mRNA_3426.1	-	-
GF0033476	1	0	0	Gibberellin receptor GID1, putative (1)	hydrolase activity [GO:0016787 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Alpha/Beta hydrolase fold [IPR029058] (1); Lipase, GDXG, putative histidine active site [IPR002168] (1); Alpha/beta hydrolase fold-3 [IPR013094] (1)	scaffold_9_mRNA_3424.1	-	-
GF0033475	1	0	0	Gibberellin receptor GID1, putative (1)	hydrolase activity [GO:0016787 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Alpha/Beta hydrolase fold [IPR029058] (1); Alpha/beta hydrolase fold-3 [IPR013094] (1)	scaffold_9_mRNA_3423.1	-	-
GF0033474	1	0	0	Proline-rich receptor-like protein kinase PERK15 (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)	scaffold_9_mRNA_342.1	-	-
GF0033473	1	0	0	Basic helix-loop-helix DNA-binding superfamily protein, putative (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)	scaffold_9_mRNA_3415.1	-	-
GF0033472	1	0	0	Monosacharide transport protein (1)			scaffold_9_mRNA_3410.1	-	-
GF0033471	1	0	0	Hypothetical protein (1)	RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H domain [IPR002156] (1); Ribonuclease H-like domain [IPR012337] (1); Domain of unknown function DUF4283 [IPR025558] (1)	scaffold_9_mRNA_3402.1	-	-
GF0033470	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3400.1	-	-
GF0033469	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	Zinc finger, A20-type [IPR002653] (1); Zinc finger, AN1-type [IPR000058] (1); Eukaryotic rRNA processing [IPR008610] (1)	scaffold_9_mRNA_3381.1	-	-
GF0033468	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3366.1	-	-
GF0033467	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_336.1	-	-
GF0033466	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3358.1	-	-
GF0033465	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3356.1	-	-
GF0033464	1	0	0	Hypothetical protein (1)	iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1)	Cytochrome P450 [IPR001128] (1)	scaffold_9_mRNA_3355.1	-	-
GF0033463	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3354.1	-	-
GF0033462	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3334.1	-	-
GF0033461	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3333.1	-	-
GF0033460	1	0	0	Hypothetical protein (1)	enzyme inhibitor activity [GO:0004857 molecular_function] (1)	Pectinesterase inhibitor domain [IPR006501] (1)	scaffold_9_mRNA_3330.1	-	-
GF0033459	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3328.1	-	-
GF0033458	1	0	0	Heat stress transcription factor B-2b (1)		Heat shock transcription factor family [IPR027725] (1)	scaffold_9_mRNA_3322.1	-	-
GF0033457	1	0	0	Hypothetical protein (1)		Protein of unknown function DUF594 [IPR007658] (1)	scaffold_9_mRNA_3318.1	-	-
GF0033456	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3317.1	-	-
GF0033455	1	0	0	DUF1680 domain protein (1)	alpha-L-arabinofuranosidase activity [GO:0046556 molecular_function] (1); L-arabinose metabolic process [GO:0046373 biological_process] (1)	Beta-L-arabinofuranosidase, GH127 [IPR012878] (1); Alpha-L-arabinofuranosidase B, arabinose-binding domain [IPR007934] (1)	scaffold_9_mRNA_3316.1	-	-
GF0033454	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_9_mRNA_3307.1	-	-
GF0033453	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3306.1	-	-
GF0033452	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3303.1	-	-
GF0033451	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3301.1	-	-
GF0033450	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3300.1	-	-
GF0033449	1	0	0	Oxidoreductase 2-oxoglutarate-Iron(II)-dependent oxygenase (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)	scaffold_9_mRNA_3299.1	-	-
GF0033448	1	0	0	Hypothetical protein (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Isopenicillin N synthase-like [IPR027443] (1); Non-haem dioxygenase N-terminal domain [IPR026992] (1); Oxoglutarate/iron-dependent dioxygenase [IPR005123] (1)	scaffold_9_mRNA_3296.1	-	-
GF0033447	1	0	0	Wall-associated receptor kinase-like 9 (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)	scaffold_9_mRNA_3295.1	-	-
GF0033446	1	0	0	2-oxoglutarate and Fe(II)-dependent oxygenase superfamily protein, putative (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); Non-haem dioxygenase N-terminal domain [IPR026992] (1)	scaffold_9_mRNA_3294.1	-	-
GF0033445	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3288.1	-	-
GF0033444	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3283.1	-	-
GF0033443	1	0	0	Hypothetical protein (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); polysaccharide binding [GO:0030247 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase-like domain [IPR011009] (1); Wall-associated receptor kinase, galacturonan-binding domain [IPR025287] (1); Protein kinase domain [IPR000719] (1)	scaffold_9_mRNA_3281.1	-	-
GF0033442	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3280.1	-	-
GF0033441	1	0	0	Hypothetical protein (1)		Nucleic acid-binding, OB-fold [IPR012340] (1)	scaffold_9_mRNA_3277.1	-	-
GF0033440	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3271.1	-	-
GF0033439	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3260.1	-	-

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GF0033438	1	0	0	Anthocyanin 5-aromatic acyltransferase (1)	transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (1)	Transferase [IPR003480] (1)	scaffold_9_mRNA_3249.1	-	-
GF0033437	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3248.1	-	-
GF0033436	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_9_mRNA_3246.1	-	-
GF0033435	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_9_mRNA_3244.1	-	-
GF0033434	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_323.1	-	-
GF0033433	1	0	0	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)	scaffold_9_mRNA_3228.1	-	-
GF0033432	1	0	0	Hypothetical protein (1)	transporter activity [GO:0005215 molecular_function] (1); transmembrane transport [GO:0055085 biological_process] (1); substrate-specific transmembrane transporter activity [GO:0022891 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1); transmembrane transporter activity [GO:0022857 molecular_function] (1); membrane [GO:0016020 cellular_component] (1)	Sugar/inositol transporter [IPR003663] (1); Major facilitator, sugar transporter-like [IPR005828] (1); Major facilitator superfamily domain [IPR020846] (1); Sugar transporter, conserved site [IPR005829] (1)	scaffold_9_mRNA_3218.1	-	-
GF0033431	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Domain of unknown function DUF4283 [IPR025558] (1)	scaffold_9_mRNA_3214.1	-	-
GF0033430	1	0	0	Hypothetical protein (1)	transporter activity [GO:0005215 molecular_function] (1); transmembrane transport [GO:0055085 biological_process] (1); substrate-specific transmembrane transporter activity [GO:0022891 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1); transmembrane transporter activity [GO:0022857 molecular_function] (1); membrane [GO:0016020 cellular_component] (1)	Sugar/inositol transporter [IPR003663] (1); Major facilitator, sugar transporter-like [IPR005828] (1); Major facilitator superfamily domain [IPR020846] (1); Sugar transporter, conserved site [IPR005829] (1)	scaffold_9_mRNA_3211.1	-	-
GF0033429	1	0	0	Retrotransposon protein, putative, unclassified (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_9_mRNA_3210.1	-	-
GF0033428	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_321.1	-	-
GF0033427	1	0	0	Hexose carrier protein HEX6 (1)	integral component of membrane [GO:0016021 cellular_component] (1); substrate-specific transmembrane transporter activity [GO:0022891 molecular_function] (1); membrane [GO:0016020 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); Sugar/inositol transporter [IPR003663] (1); Major facilitator superfamily domain [IPR020846] (1)	scaffold_9_mRNA_3207.1	-	-
GF0033426	1	0	0	DUF4283 domain protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	scaffold_9_mRNA_3206.1	-	-
GF0033425	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3194.1	-	-
GF0033424	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_9_mRNA_3190.1	-	-
GF0033423	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3189.1	-	-
GF0033422	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3188.1	-	-
GF0033421	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_9_mRNA_3187.1	-	-
GF0033420	1	0	0	Hypothetical protein (1)		Tubulin/FtsZ, 2-layer sandwich domain [IPR018316] (1)	scaffold_9_mRNA_3185.1	-	-
GF0033419	1	0	0	Proteinase inhibitor (1)	response to wounding [GO:0009611 biological_process] (1); serine-type endopeptidase inhibitor activity [GO:0004867 molecular_function] (1)	Proteinase inhibitor I13, potato inhibitor I [IPR000864] (1)	scaffold_9_mRNA_3184.1	-	-
GF0033418	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3177.1	-	-
GF0033417	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1); Aspartic peptidase domain [IPR021109] (1)	scaffold_9_mRNA_3173.1	-	-
GF0033416	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3172.1	-	-
GF0033415	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3165.1	-	-
GF0033414	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3159.1	-	-
GF0033413	1	0	0	Hypothetical protein (1)		Ankyrin repeat-containing domain [IPR020683] (1)	scaffold_9_mRNA_3156.1	-	-
GF0033412	1	0	0	Ankyrin repeat family protein, putative (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat [IPR002110] (1); Ankyrin repeat-containing domain [IPR020683] (1)	scaffold_9_mRNA_3155.1	-	-
GF0033411	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3149.1	-	-
GF0033410	1	0	0	Hypothetical protein (1)		Transposase, MuDR, plant [IPR004332] (1)	scaffold_9_mRNA_3145.1	-	-
GF0033409	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3141.1	-	-
GF0033408	1	0	0	F-box protein At5g07610 (1)	protein binding [GO:0005515 molecular_function] (1)	F-box associated interaction domain [IPR017451] (1); F-box domain [IPR001810] (1); Kelch-type beta propeller [IPR015915] (1)	scaffold_9_mRNA_3138.1	-	-
GF0033407	1	0	0	Mutator-like transposase (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, SWIM-type [IPR007527] (1); Transposase, MuDR, plant [IPR004332] (1); Zinc finger, PMZ-type [IPR006564] (1); MULE transposase domain [IPR018289] (1)	scaffold_9_mRNA_3131.1	-	-
GF0033406	1	0	0	Serine esterase family protein (1)		Domain of unknown function DUF676, lipase-like [IPR007751] (1); Alpha/Beta hydrolase fold [IPR029058] (1)	scaffold_9_mRNA_3130.1	-	-
GF0033405	1	0	0	Mavicyanin (1)	electron carrier activity [GO:0009055 molecular_function] (1)	Blue (type 1) copper protein, binding site [IPR028871] (1); Phytocyanin domain [IPR003245] (1); Cupredoxin [IPR008972] (1)	scaffold_9_mRNA_3123.1	-	-
GF0033404	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3122.1	-	-
GF0033403	1	0	0	Hypothetical protein (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)	scaffold_9_mRNA_3121.1	-	-
GF0033402	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3110.1	-	-
GF0033401	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3107.1	-	-
GF0033400	1	0	0	Glutaredoxin (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)	Glutaredoxin subgroup [IPR014025] (1); Glutaredoxin [IPR002109] (1); Glutaredoxin, eukaryotic/virial [IPR011899] (1); Thioredoxin-like fold [IPR012336] (1)	scaffold_9_mRNA_3094.1	-	-
GF0033399	1	0	0	Hypothetical protein (1)	DNA ligase activity [GO:0003909 molecular_function] (1); DNA ligation involved in DNA repair [GO:0051103 biological_process] (1)	Domain of unknown function DUF4283 [IPR025558] (1); DNA ligase, ATP-dependent, conserved site [IPR016059] (1)	scaffold_9_mRNA_3089.1	-	-
GF0033398	1	0	0	Protein SRC2 (1)	protein binding [GO:0005515 molecular_function] (1)	C2 domain [IPR000008] (1)	scaffold_9_mRNA_308.1	-	-
GF0033397	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_9_mRNA_3079.1	-	-
GF0033396	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3066.1	-	-
GF0033395	1	0	0	Glycoside hydrolase family 28 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)	scaffold_9_mRNA_3063.1	-	-
GF0033394	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3055.1	-	-
GF0033393	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3048.1	-	-
GF0033392	1	0	0	Non-LTR retroelement reverse transcriptase (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1); TB2/DP1/HVA22-related protein [IPR004345] (1)	scaffold_9_mRNA_3040.1	-	-
GF0033391	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3032.1	-	-
GF0033390	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3030.1	-	-
GF0033389	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3028.1	-	-
GF0033388	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3027.1	-	-
GF0033387	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3019.1	-	-
GF0033386	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3015.1	-	-
GF0033385	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_3008.1	-	-
GF0033384	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_9_mRNA_2999.1	-	-
GF0033383	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2997.1	-	-
GF0033382	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2985.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0033381	1	0	0	DUF642 family protein (1)		Domain of unknown function DUF642 [IPR006946] (1); Galactose-binding domain-like [IPR008979] (1)	scaffold_9_mRNA_2982.1	-	-
GF0033380	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_9_mRNA_2981.1	-	-
GF0033379	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2979.1	-	-
GF0033378	1	0	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_9_mRNA_2978.1	-	-
GF0033377	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2977.1	-	-
GF0033376	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_9_mRNA_2967.1	-	-
GF0033375	1	0	0	Hypothetical 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)	Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase, ATP binding site [IPR017441] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1); Protein kinase domain [IPR000719] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Protein kinase-like domain [IPR011009] (1); Leucine-rich repeat, typical subtype [IPR003591] (1)	scaffold_9_mRNA_2961.1	-	-
GF0033374	1	0	0	Hypothetical protein (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1)	Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	scaffold_9_mRNA_2960.1	-	-
GF0033373	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2958.1	-	-
GF0033372	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2957.1	-	-
GF0033371	1	0	0	Hypothetical protein (1)	RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Aspartic peptidase domain [IPR021109] (1); Ribonuclease H-like domain [IPR012337] (1); Ribonuclease H domain [IPR002156] (1)	scaffold_9_mRNA_2955.1	-	-
GF0033370	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2954.1	-	-
GF0033369	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2946.1	-	-
GF0033368	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2943.1	-	-
GF0033367	1	0	0	Putative disease resistance RGA1 (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_9_mRNA_2942.1	-	-
GF0033366	1	0	0	NB-ARC domain disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1)	scaffold_9_mRNA_2940.1	-	-
GF0033365	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2937.1	-	-
GF0033364	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2936.1	-	-
GF0033363	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2933.1	-	-
GF0033362	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1); Aspartic peptidase domain [IPR021109] (1)	scaffold_9_mRNA_2928.1	-	-
GF0033361	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2927.1	-	-
GF0033360	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2926.1	-	-
GF0033359	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2920.1	-	-
GF0033358	1	0	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (1)	DNA-binding domain [IPR016177] (1); AP2/ERF domain [IPR001471] (1)	scaffold_9_mRNA_2917.1	-	-
GF0033357	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2915.1	-	-
GF0033356	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2913.1	-	-
GF0033355	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); DNA integration [GO:0015074 biological_process] (1)	Integrase, catalytic core [IPR001584] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_9_mRNA_2909.1	-	-
GF0033354	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2907.1	-	-
GF0033353	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2901.1	-	-
GF0033352	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2900.1	-	-
GF0033351	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2896.1	-	-
GF0033350	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1); FAR1 DNA binding domain [IPR004330] (1); Zinc finger, SWIM-type [IPR007527] (1); MULE transposase domain [IPR018289] (1)	scaffold_9_mRNA_2895.1	-	-
GF0033349	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2894.1	-	-
GF0033348	1	0	0	Fragile histidine triad isoform 1 (1)	catalytic activity [GO:0003824 molecular_function] (1)	Histidine triad (HIT) protein [IPR001310] (1); HIT-like domain [IPR011146] (1); Histidine triad, conserved site [IPR019808] (1)	scaffold_9_mRNA_2890.1	-	-
GF0033347	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2887.1	-	-
GF0033346	1	0	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	scaffold_9_mRNA_2883.1	-	-
GF0033345	1	0	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	Transcription factor, MADS-box [IPR002100] (1)	scaffold_9_mRNA_2877.1	-	-
GF0033344	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2875.1	-	-
GF0033343	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2871.1	-	-
GF0033342	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2870.1	-	-
GF0033341	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2869.1	-	-
GF0033340	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2862.1	-	-
GF0033339	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2861.1	-	-
GF0033338	1	0	0	Polygalacturonase (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1); polygalacturonase activity [GO:0004650 molecular_function] (1)	Pectin lyase fold/virulence factor [IPR011050] (1); Pectin lyase fold [IPR012334] (1); Parallel beta-helix repeat [IPR006626] (1); Glycoside hydrolase, family 28 [IPR000743] (1)	scaffold_9_mRNA_2856.1	-	-
GF0033337	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2855.1	-	-
GF0033336	1	0	0	MADS-box transcription factor family protein (1)	DNA binding [GO:0003677 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	Transcription factor, MADS-box [IPR002100] (1)	scaffold_9_mRNA_2852.1	-	-
GF0033335	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2850.1	-	-
GF0033334	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2849.1	-	-
GF0033333	1	0	0	MADS-box transcription factor family protein (1)	RNA polymerase II regulatory region sequence-specific DNA binding [GO:0000977 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1); MAPK cascade [GO:0000165 biological_process] (1); positive regulation of transcription from RNA polymerase II promoter [GO:0045944 biological_process] (1)	MADS MEF2-like [IPR033896] (1); Transcription factor, MADS-box [IPR002100] (1)	scaffold_9_mRNA_2847.1	-	-
GF0033332	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2846.1	-	-
GF0033331	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_9_mRNA_2845.1	-	-
GF0033330	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2842.1	-	-
GF0033329	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4218 [IPR025452] (1)	scaffold_9_mRNA_2838.1	-	-
GF0033328	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_9_mRNA_2837.1	-	-
GF0033327	1	0	0	MADS-box transcription factor family protein (1)	DNA binding [GO:0003677 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	Transcription factor, MADS-box [IPR002100] (1)	scaffold_9_mRNA_2834.1	-	-
GF0033326	1	0	0	Polypepetide with reverse transcriptase and RNaseH domains (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	scaffold_9_mRNA_2833.1	-	-
GF0033325	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2832.1	-	-
GF0033324	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2830.1	-	-
GF0033323	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_9_mRNA_2829.1	-	-
GF0033322	1	0	0	Putative wall-associated receptor kinase-like 16 (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)	scaffold_9_mRNA_2822.1	-	-
GF0033321	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2821.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0033320	1	0	0	MADS-box transcription factor family protein (1)	DNA binding [GO:0003677 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	Transcription factor, MADS-box [IPR002100] (1)	scaffold_9_mRNA_2818.1	-	-
GF0033319	1	0	0	Copia-like retrotransposon Hopscotch polyprotein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); DNA integration [GO:0015074 biological_process] (1)	GAG-pre-integrase domain [IPR025724] (1); Integrase, catalytic core [IPR001584] (1); Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_9_mRNA_2816.1	-	-
GF0033318	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_9_mRNA_2815.1	-	-
GF0033317	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2814.1	-	-
GF0033316	1	0	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	Transcription factor, MADS-box [IPR002100] (1)	scaffold_9_mRNA_2808.1	-	-
GF0033315	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_9_mRNA_2807.1	-	-
GF0033314	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2803.1	-	-
GF0033313	1	0	0	F-box protein interaction domain protein (1)	protein binding [GO:0005515 molecular_function] (1)	Kelch-type beta propeller [IPR015915] (1); F-box associated interaction domain [IPR017451] (1); Galactose oxidase/kelch, beta-propeller [IPR011043] (1)	scaffold_9_mRNA_280.1	-	-
GF0033312	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2792.1	-	-
GF0033311	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2787.1	-	-
GF0033310	1	0	0	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)	scaffold_9_mRNA_2786.1	-	-
GF0033309	1	0	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, BED-type [IPR003656] (1); Zinc finger C2H2-type [IPR013087] (1)	scaffold_9_mRNA_2779.1	-	-
GF0033308	1	0	0	MuDR family transposase isoform 1 (1)	DNA binding [GO:0003677 molecular_function] (1); transposition, DNA-mediated [GO:0006313 biological_process] (1); zinc ion binding [GO:0008270 molecular_function] (1); transposase activity [GO:0004803 molecular_function] (1)	Zinc finger, SWIM-type [IPR007527] (1); Transposase, mutator type [IPR001207] (1); Transposase, MuDR, plant [IPR004332] (1); Zinc finger, PMZ-type [IPR006564] (1); MULE transposase domain [IPR018289] (1)	scaffold_9_mRNA_2777.1	-	-
GF0033307	1	0	0	Hypothetical protein (1)	calmodulin binding [GO:0005516 molecular_function] (1)	Probable transposase, Ptta/En/Spm, plant [IPR004252] (1); Calcium-transporting P-type ATPase, N-terminal autoinhibitory domain [IPR024750] (1); Transposase, Tnp1/En/Spm-like [IPR004264] (1)	scaffold_9_mRNA_2770.1	-	-
GF0033306	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2769.1	-	-
GF0033305	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2763.1	-	-
GF0033304	1	0	0	Hypothetical protein (1)	metabolic process [GO:0008152 biological_process] (1); methyltransferase activity [GO:0008168 molecular_function] (1)	Methyltransferase type 11 [IPR013216] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); Viral movement protein [IPR028919] (1)	scaffold_9_mRNA_2761.1	-	-
GF0033303	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2759.1	-	-
GF0033302	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_9_mRNA_2756.1	-	-
GF0033301	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_9_mRNA_2751.1	-	-
GF0033300	1	0	0	Embryonic abundant protein-like (1)	protein dimerization activity [GO:0046983 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	scaffold_9_mRNA_2750.1	-	-
GF0033299	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2748.1	-	-
GF0033298	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2747.1	-	-
GF0033297	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2745.1	-	-
GF0033296	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2744.1	-	-
GF0033295	1	0	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Carlavirus nucleic acid-binding protein [IPR002568] (1)	scaffold_9_mRNA_2718.1	-	-
GF0033294	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2712.1	-	-
GF0033293	1	0	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1); Peptidase C57, Vaccinia virus protein I7 [IPR004970] (1); Transposase-associated domain [IPR029480] (1)	scaffold_9_mRNA_2709.1	-	-
GF0033292	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2708.1	-	-
GF0033291	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2707.1	-	-
GF0033290	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_9_mRNA_2706.1	-	-
GF0033289	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2696.1	-	-
GF0033288	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2694.1	-	-
GF0033287	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2693.1	-	-
GF0033286	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2681.1	-	-
GF0033285	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2679.1	-	-
GF0033284	1	0	0	Hypothetical protein (1)		Transposon, En/Spm-like [IPR004242] (1); Probable transposase, Ptta/En/Spm, plant [IPR004252] (1); Transposase-associated domain [IPR029480] (1)	scaffold_9_mRNA_2678.1	-	-
GF0033283	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2677.1	-	-
GF0033282	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2670.1	-	-
GF0033281	1	0	0	Putative muDR family transposase-like (1)		MULE transposase domain [IPR018289] (1)	scaffold_9_mRNA_2666.1	-	-
GF0033280	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2663.1	-	-
GF0033279	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	RNA recognition motif domain [IPR000504] (1)	scaffold_9_mRNA_2660.1	-	-
GF0033278	1	0	0	U3 small nucleolar rna-associated protein 18 (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)	scaffold_9_mRNA_2657.1	-	-
GF0033277	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Zinc finger, PMZ-type [IPR006564] (1); Zinc finger, SWIM-type [IPR007527] (1)	scaffold_9_mRNA_2655.1	-	-
GF0033276	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2649.1	-	-
GF0033275	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2645.1	-	-
GF0033274	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2641.1	-	-
GF0033273	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2635.1	-	-
GF0033272	1	0	0	Auxin-induced in root cultures protein 12 (1)		DOMON domain [IPR005018] (1); Cytochrome b561/ferric reductase transmembrane [IPR006593] (1); Cytochrome b561 and DOMON domain-containing protein [IPR017214] (1)	scaffold_9_mRNA_2630.1	-	-
GF0033271	1	0	0	Ribonuclease H protein, putative (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	scaffold_9_mRNA_2629.1	-	-
GF0033270	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1); Endonuclease/exonuclease/phosphatase [IPR005135] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_9_mRNA_2627.1	-	-
GF0033269	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	scaffold_9_mRNA_2626.1	-	-
GF0033268	1	0	0	Auxin-induced in root cultures protein 12 (1)		Cytochrome b561 and DOMON domain-containing protein [IPR017214] (1); Cytochrome b561/ferric reductase transmembrane [IPR006593] (1); DOMON domain [IPR005018] (1)	scaffold_9_mRNA_2622.1	-	-
GF0033267	1	0	0	SLG-Sc and SLA-Sc genes and Melmoth retrotransposon sequence (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)	scaffold_9_mRNA_2621.1	-	-
GF0033266	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2616.1	-	-
GF0033265	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_9_mRNA_2615.1	-	-
GF0033264	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2602.1	-	-
GF0033263	1	0	0	Putative retroelement pol polyprotein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_9_mRNA_2598.1	-	-
GF0033262	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2597.1	-	-
GF0033261	1	0	0	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	scaffold_9_mRNA_2596.1	-	-
GF0033260	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2592.1	-	-

ID	**Num. in *C. celementine***	**Num in *C. unshiu***	**Num in *P.trifoliata***	**Note**	**GO**	**InterPro**	**Members in *C.clementine***	**Members in *C.unshiu***	**Members in *P.trifoliata***
GF0033259	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2591.1	-	-
GF0033258	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4216 [IPR025312] (1); Transposase-associated domain [IPR029480] (1)	scaffold_9_mRNA_2589.1	-	-
GF0033257	1	0	0	Hypothetical protein (1)	single-stranded DNA binding [GO:0003697 molecular_function] (1); DNA metabolic process [GO:0006259 biological_process] (1); DNA-dependent ATPase activity [GO:0008094 molecular_function] (1); DNA repair [GO:0006281 biological_process] (1); DNA binding [GO:0003677 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	DNA recombination and repair protein RecA [IPR013765] (1); DNA recombination and repair protein RecA, monomer-monomer interface [IPR020587] (1)	scaffold_9_mRNA_2588.1	-	-
GF0033256	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2583.1	-	-
GF0033255	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_9_mRNA_2579.1	-	-
GF0033254	1	0	0	Hypothetical protein (1)	calcium ion binding [GO:0005509 molecular_function] (1)	EF-Hand 1, calcium-binding site [IPR018247] (1); EF-hand domain [IPR002048] (1); EF-hand domain pair [IPR011992] (1)	scaffold_9_mRNA_2562.1	-	-
GF0033253	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2555.1	-	-
GF0033252	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2553.1	-	-
GF0033251	1	0	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1); Transposon, En/Spm-like [IPR004242] (1)	scaffold_9_mRNA_2551.1	-	-
GF0033250	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2550.1	-	-
GF0033249	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2542.1	-	-
GF0033248	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2537.1	-	-
GF0033247	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_9_mRNA_2536.1	-	-
GF0033246	1	0	0	LRR receptor-like kinase family protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_9_mRNA_2535.1	-	-
GF0033245	1	0	0	Monosacharide transport protein (1)			scaffold_9_mRNA_2533.1	-	-
GF0033244	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2532.1	-	-
GF0033243	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2531.1	-	-
GF0033242	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2530.1	-	-
GF0033241	1	0	0	Leucine-rich repeat receptor protein kinase EXS (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_9_mRNA_2525.1	-	-
GF0033240	1	0	0	Hypothetical protein (1)	metabolic process [GO:0008152 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1)	Fumarylacetoacetase, C-terminal-related [IPR011234] (1)	scaffold_9_mRNA_252.1	-	-
GF0033239	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2512.1	-	-
GF0033238	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2510.1	-	-
GF0033237	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2508.1	-	-
GF0033236	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2507.1	-	-
GF0033235	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_9_mRNA_2503.1	-	-
GF0033234	1	0	0	Putative muDR family transposase-like (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, PMZ-type [IPR006564] (1); MULE transposase domain [IPR018289] (1); Zinc finger, SWIM-type [IPR007527] (1)	scaffold_9_mRNA_2498.1	-	-
GF0033233	1	0	0	Hypothetical protein (1)		HSP20-like chaperone [IPR008978] (1)	scaffold_9_mRNA_2495.1	-	-
GF0033232	1	0	0	Hypothetical protein (1)		HSP20-like chaperone [IPR008978] (1)	scaffold_9_mRNA_2494.1	-	-
GF0033231	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2492.1	-	-
GF0033230	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_9_mRNA_2491.1	-	-
GF0033229	1	0	0	Hypothetical protein (1)		Small heat shock protein HSP20 [IPR031107] (1); Alpha crystallin/Hsp20 domain [IPR002068] (1); HSP20-like chaperone [IPR008978] (1)	scaffold_9_mRNA_2489.1	-	-
GF0033228	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2487.1	-	-
GF0033227	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2484.1	-	-
GF0033226	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2483.1	-	-
GF0033225	1	0	0	Ribonuclease H (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Domain of unknown function DUF4283 [IPR025558] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1)	scaffold_9_mRNA_2481.1	-	-
GF0033224	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2480.1	-	-
GF0033223	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2478.1	-	-
GF0033222	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2477.1	-	-
GF0033221	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2475.1	-	-
GF0033220	1	0	0	Hypothetical protein (1)		HSP20-like chaperone [IPR008978] (1)	scaffold_9_mRNA_2474.1	-	-
GF0033219	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_247.1	-	-
GF0033218	1	0	0	Transcription factor ORG2 (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)	scaffold_9_mRNA_2467.1	-	-
GF0033217	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2462.1	-	-
GF0033216	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_9_mRNA_2453.1	-	-
GF0033215	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2452.1	-	-
GF0033214	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_9_mRNA_2450.1	-	-
GF0033213	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2449.1	-	-
GF0033212	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_9_mRNA_2433.1	-	-
GF0033211	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2431.1	-	-
GF0033210	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_9_mRNA_2430.1	-	-
GF0033209	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_9_mRNA_2429.1	-	-
GF0033208	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2428.1	-	-
GF0033207	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_9_mRNA_2427.1	-	-
GF0033206	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2425.1	-	-
GF0033205	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2424.1	-	-
GF0033204	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2420.1	-	-
GF0033203	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_9_mRNA_2416.1	-	-
GF0033202	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_9_mRNA_2415.1	-	-
GF0033201	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2414.1	-	-
GF0033200	1	0	0	Gag non-LTR retrotransposase (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)	scaffold_9_mRNA_2412.1	-	-
GF0033199	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2406.1	-	-
GF0033198	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_9_mRNA_2405.1	-	-
GF0033197	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2401.1	-	-
GF0033196	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2399.1	-	-
GF0033195	1	0	0	RNA-directed DNA polymerase (Reverse transcriptase) (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_9_mRNA_2392.1	-	-
GF0033194	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2386.1	-	-
GF0033193	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2385.1	-	-
GF0033192	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2377.1	-	-
GF0033191	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_9_mRNA_2373.1	-	-
GF0033190	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2372.1	-	-
GF0033189	1	0	0	Hypothetical protein (1)	DNA integration [GO:0015074 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Integrase, catalytic core [IPR001584] (1); Reverse transcriptase domain [IPR000477] (1); Aspartic peptidase domain [IPR021109] (1)	scaffold_9_mRNA_2371.1	-	-
GF0033188	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2370.1	-	-
GF0033187	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2367.1	-	-
GF0033186	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2364.1	-	-
GF0033185	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2363.1	-	-
GF0033184	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_9_mRNA_2358.1	-	-
GF0033183	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2345.1	-	-
GF0033182	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2342.1	-	-
GF0033181	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2340.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0033180	1	0	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_9_mRNA_2333.1	-	-
GF0033179	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2323.1	-	-
GF0033178	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2320.1	-	-
GF0033177	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_232.1	-	-
GF0033176	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2317.1	-	-
GF0033175	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_231.1	-	-
GF0033174	1	0	0	Putative RNA-directed DNA polymerase (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_9_mRNA_2305.1	-	-
GF0033173	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2301.1	-	-
GF0033172	1	0	0	Monosacharide transport protein (1)			scaffold_9_mRNA_230.1	-	-
GF0033171	1	0	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_9_mRNA_2299.1	-	-
GF0033170	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2288.1	-	-
GF0033169	1	0	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	scaffold_9_mRNA_2284.1	-	-
GF0033168	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2283.1	-	-
GF0033167	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2282.1	-	-
GF0033166	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2281.1	-	-
GF0033165	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_9_mRNA_2278.1	-	-
GF0033164	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2275.1	-	-
GF0033163	1	0	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_9_mRNA_2269.1	-	-
GF0033162	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2267.1	-	-
GF0033161	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2265.1	-	-
GF0033160	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2263.1	-	-
GF0033159	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2262.1	-	-
GF0033158	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2261.1	-	-
GF0033157	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_9_mRNA_226.1	-	-
GF0033156	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2254.1	-	-
GF0033155	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2253.1	-	-
GF0033154	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2251.1	-	-
GF0033153	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2250.1	-	-
GF0033152	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2248.1	-	-
GF0033151	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_9_mRNA_2247.1	-	-
GF0033150	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2246.1	-	-
GF0033149	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2245.1	-	-
GF0033148	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_9_mRNA_2244.1	-	-
GF0033147	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2243.1	-	-
GF0033146	1	0	0	Hypothetical protein (1)		Paraneoplastic antigen Ma [IPR026523] (1); Reverse transcriptase domain [IPR000477] (1)	scaffold_9_mRNA_2240.1	-	-
GF0033145	1	0	0	Hypothetical protein (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Peptidase A2A, retrovirus, catalytic [IPR001995] (1)	scaffold_9_mRNA_2236.1	-	-
GF0033144	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2235.1	-	-
GF0033143	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2232.1	-	-
GF0033142	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2231.1	-	-
GF0033141	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2227.1	-	-
GF0033140	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2226.1	-	-
GF0033139	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2225.1	-	-
GF0033138	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2224.1	-	-
GF0033137	1	0	0	Hypothetical protein (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Aspartic peptidase domain [IPR021109] (1); Reverse transcriptase domain [IPR000477] (1); Peptidase A2A, retrovirus, catalytic [IPR001995] (1)	scaffold_9_mRNA_2223.1	-	-
GF0033136	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); DNA integration [GO:0015074 biological_process] (1)	Integrase, catalytic core [IPR001584] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_9_mRNA_2222.1	-	-
GF0033135	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2221.1	-	-
GF0033134	1	0	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_9_mRNA_2220.1	-	-
GF0033133	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_9_mRNA_2216.1	-	-
GF0033132	1	0	0	Phosphoglucan, water dikinase (1)	ATP binding [GO:0005524 molecular_function] (1); catalytic activity [GO:0003824 molecular_function] (1); phosphorylation [GO:0016310 biological_process] (1); kinase activity [GO:0016301 molecular_function] (1)	Pyruvate phosphate dikinase, PEP/pyruvate-binding [IPR002192] (1); ATP-grasp fold, subdomain 1 [IPR013815] (1)	scaffold_9_mRNA_2214.1	-	-
GF0033131	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1); Retrotransposon gag domain [IPR005162] (1)	scaffold_9_mRNA_2210.1	-	-
GF0033130	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2207.1	-	-
GF0033129	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2202.1	-	-
GF0033128	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2201.1	-	-
GF0033127	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc knuckle CX2CX4HX4C [IPR025836] (1); Zinc finger, CCHC-type [IPR001878] (1)	scaffold_9_mRNA_2200.1	-	-
GF0033126	1	0	0	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	scaffold_9_mRNA_2199.1	-	-
GF0033125	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2189.1	-	-
GF0033124	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2187.1	-	-
GF0033123	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2181.1	-	-
GF0033122	1	0	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	scaffold_9_mRNA_2164.1	-	-
GF0033121	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2159.1	-	-
GF0033120	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2153.1	-	-
GF0033119	1	0	0	Transposase (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); Zinc finger C2H2-type [IPR013087] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	scaffold_9_mRNA_2144.1	-	-
GF0033118	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2143.1	-	-
GF0033117	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2141.1	-	-
GF0033116	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2140.1	-	-
GF0033115	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2136.1	-	-
GF0033114	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2132.1	-	-
GF0033113	1	0	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1)	scaffold_9_mRNA_2129.1	-	-
GF0033112	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2122.1	-	-
GF0033111	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, PMZ-type [IPR006564] (1)	scaffold_9_mRNA_2121.1	-	-
GF0033110	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2099.1	-	-
GF0033109	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2098.1	-	-
GF0033108	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_9_mRNA_2097.1	-	-
GF0033107	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2095.1	-	-
GF0033106	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_9_mRNA_2094.1	-	-
GF0033105	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2088.1	-	-
GF0033104	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2087.1	-	-
GF0033103	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2084.1	-	-
GF0033102	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc knuckle CX2CX4HX4C [IPR025836] (1); Zinc finger, CCHC-type [IPR001878] (1)	scaffold_9_mRNA_2082.1	-	-
GF0033101	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2080.1	-	-
GF0033100	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2074.1	-	-
GF0033099	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2058.1	-	-
GF0033098	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2053.1	-	-
GF0033097	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2051.1	-	-
GF0033096	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_9_mRNA_2049.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0033095	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_9_mRNA_2048.1	-	-
GF0033094	1	0	0	Isoflavone 7-O-methyltransferase (1)	O-methyltransferase activity [GO:0008171 molecular_function] (1); methyltransferase activity [GO:0008168 molecular_function] (1)	O-methyltransferase COMT-type [IPR016461] (1); O-methyltransferase, family 2 [IPR001077] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	scaffold_9_mRNA_2046.1	-	-
GF0033093	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2044.1	-	-
GF0033092	1	0	0	Hypothetical protein (1)		Harbinger transposase-derived nuclease domain [IPR027806] (1)	scaffold_9_mRNA_2031.1	-	-
GF0033091	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2010.1	-	-
GF0033090	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_2005.1	-	-
GF0033089	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1999.1	-	-
GF0033088	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_9_mRNA_1998.1	-	-
GF0033087	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1996.1	-	-
GF0033086	1	0	0	CwfJ-like family protein, putative isoform 3 (1)	catalytic activity [GO:0003824 molecular_function] (1)	Cwf19-like protein, C-terminal domain-2 [IPR006767] (1); Cwf19-like, C-terminal domain-1 [IPR006768] (1); HIT-like domain [IPR011146] (1)	scaffold_9_mRNA_1995.1	-	-
GF0033085	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1992.1	-	-
GF0033084	1	0	0	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); Reverse transcriptase domain [IPR000477] (1)	scaffold_9_mRNA_1991.1	-	-
GF0033083	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			scaffold_9_mRNA_1987.1	-	-
GF0033082	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1986.1	-	-
GF0033081	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1985.1	-	-
GF0033080	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1983.1	-	-
GF0033079	1	0	0	Disease resistance family protein / LRR family protein, putative (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1); proteolysis [GO:0006508 biological_process] (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); Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	scaffold_9_mRNA_1982.1	-	-
GF0033078	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1980.1	-	-
GF0033077	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_9_mRNA_1979.1	-	-
GF0033076	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_9_mRNA_1978.1	-	-
GF0033075	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1970.1	-	-
GF0033074	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_9_mRNA_1969.1	-	-
GF0033073	1	0	0	Hypothetical protein (1)		PGG domain [IPR026961] (1)	scaffold_9_mRNA_1968.1	-	-
GF0033072	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); zinc ion binding [GO:0008270 molecular_function] (1)	FAR1 DNA binding domain [IPR004330] (1); Zinc finger, CCHC-type [IPR001878] (1); FHY3/FAR1 family [IPR031052] (1)	scaffold_9_mRNA_1967.1	-	-
GF0033071	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1965.1	-	-
GF0033070	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1962.1	-	-
GF0033069	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1961.1	-	-
GF0033068	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1953.1	-	-
GF0033067	1	0	0	Hypothetical protein (1)		Bud13 [IPR018609] (1)	scaffold_9_mRNA_1949.1	-	-
GF0033066	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1947.1	-	-
GF0033065	1	0	0	LRR receptor-like kinase (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat [IPR001611] (1)	scaffold_9_mRNA_1944.1	-	-
GF0033064	1	0	0	Caffeic acid O-methyltransferase (1)	O-methyltransferase activity [GO:0008171 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1); methyltransferase activity [GO:0008168 molecular_function] (1)	S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); Plant methyltransferase dimerisation [IPR012967] (1); O-methyltransferase COMT-type [IPR016461] (1); O-methyltransferase, family 2 [IPR001077] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1)	scaffold_9_mRNA_1941.1	-	-
GF0033063	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1940.1	-	-
GF0033062	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_9_mRNA_1939.1	-	-
GF0033061	1	0	0	Hypothetical protein (1)		Metallo-dependent phosphatase-like [IPR029052] (1)	scaffold_9_mRNA_1937.1	-	-
GF0033060	1	0	0	Polynucleotidyl transferase, ribonuclease H-like superfamily protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_9_mRNA_1933.1	-	-
GF0033059	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1923.1	-	-
GF0033058	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1919.1	-	-
GF0033057	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_9_mRNA_1915.1	-	-
GF0033056	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1)	scaffold_9_mRNA_1912.1	-	-
GF0033055	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1900.1	-	-
GF0033054	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_9_mRNA_1897.1	-	-
GF0033053	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc knuckle CX2CX4HX4C [IPR025836] (1); Zinc finger, CCHC-type [IPR001878] (1); Aspartic peptidase domain [IPR021109] (1); Domain of unknown function DUF4283 [IPR025558] (1); Reverse transcriptase domain [IPR000477] (1)	scaffold_9_mRNA_1895.1	-	-
GF0033052	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1894.1	-	-
GF0033051	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1888.1	-	-
GF0033050	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1883.1	-	-
GF0033049	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1882.1	-	-
GF0033048	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_9_mRNA_1874.1	-	-
GF0033047	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1873.1	-	-
GF0033046	1	0	0	Hypothetical protein (1)		NAD(P)-binding domain [IPR016040] (1); NmrA-like domain [IPR008030] (1)	scaffold_9_mRNA_1872.1	-	-
GF0033045	1	0	0	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)	Translation protein SH3-like domain [IPR008991] (1); Ribosomal protein L14e domain [IPR002784] (1); Ribosomal protein L2 domain 2 [IPR014722] (1)	scaffold_9_mRNA_1871.1	-	-
GF0033044	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1870.1	-	-
GF0033043	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1868.1	-	-
GF0033042	1	0	0	Phloem protein 2-B2 (1)	protein binding [GO:0005515 molecular_function] (1)	F-box domain [IPR001810] (1); Phloem protein 2-like [IPR025886] (1)	scaffold_9_mRNA_1859.1	-	-
GF0033041	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_9_mRNA_1853.1	-	-
GF0033040	1	0	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Carlavirus nucleic acid-binding protein [IPR002568] (1)	scaffold_9_mRNA_1852.1	-	-
GF0033039	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_9_mRNA_1841.1	-	-
GF0033038	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1840.1	-	-
GF0033037	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1830.1	-	-
GF0033036	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1827.1	-	-
GF0033035	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1823.1	-	-
GF0033034	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1821.1	-	-
GF0033033	1	0	0	BED zinc finger,hAT family dimerization domain isoform 1 (1)	DNA binding [GO:0003677 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1); Zinc finger C2H2-type [IPR013087] (1); hAT-like transposase, RNase-H fold [IPR025525] (1); Ribonuclease H-like domain [IPR012337] (1); Zinc finger, BED-type [IPR003656] (1)	scaffold_9_mRNA_1812.1	-	-
GF0033032	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1811.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0033031	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Retrotransposon gag domain [IPR005162] (1); Zinc finger, CCHC-type [IPR001878] (1)	scaffold_9_mRNA_1804.1	-	-
GF0033030	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_9_mRNA_1803.1	-	-
GF0033029	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1802.1	-	-
GF0033028	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1801.1	-	-
GF0033027	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_18.1	-	-
GF0033026	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_9_mRNA_1799.1	-	-
GF0033025	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1798.1	-	-
GF0033024	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1); Arabidopsis retrotransposon Orf1 [IPR004312] (1)	scaffold_9_mRNA_1797.1	-	-
GF0033023	1	0	0	Zinc finger family protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger C2H2-type [IPR013087] (1)	scaffold_9_mRNA_1794.1	-	-
GF0033022	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_9_mRNA_1776.1	-	-
GF0033021	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1772.1	-	-
GF0033020	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1769.1	-	-
GF0033019	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1756.1	-	-
GF0033018	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_9_mRNA_1755.1	-	-
GF0033017	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1754.1	-	-
GF0033016	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_9_mRNA_1748.1	-	-
GF0033015	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1747.1	-	-
GF0033014	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1746.1	-	-
GF0033013	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1731.1	-	-
GF0033012	1	0	0	Hypothetical protein (1)	glycine-tRNA ligase activity [GO:0004820 molecular_function] (1); nucleotide binding [GO:0000166 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1); cytoplasm [GO:0005737 cellular_component] (1); glycyl-tRNA aminoacylation [GO:0006426 biological_process] (1)	Glycyl-tRNA synthetase/DNA polymerase subunit gamma-2 [IPR027031] (1); Glycyl-tRNA synthetase [IPR002315] (1); Anticodon-binding [IPR004154] (1)	scaffold_9_mRNA_1730.1	-	-
GF0033011	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1729.1	-	-
GF0033010	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_9_mRNA_1728.1	-	-
GF0033009	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1718.1	-	-
GF0033008	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1711.1	-	-
GF0033007	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_9_mRNA_1710.1	-	-
GF0033006	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1697.1	-	-
GF0033005	1	0	0	SOUL heme-binding family protein (1)		SOUL haem-binding protein [IPR006917] (1)	scaffold_9_mRNA_1695.1	-	-
GF0033004	1	0	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1); MULE transposase domain [IPR018289] (1)	scaffold_9_mRNA_1690.1	-	-
GF0033003	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1689.1	-	-
GF0033002	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1682.1	-	-
GF0033001	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1677.1	-	-
GF0033000	1	0	0	Uridine 5'-monophosphate synthase (1)	'de novo' UMP biosynthetic process [GO:0044205 biological_process] (1); orotate phosphoribosyltransferase activity [GO:0004588 molecular_function] (1); orotidine-5'-phosphate decarboxylase activity [GO:0004590 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1); nucleoside metabolic process [GO:0009116 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1); 'de novo' pyrimidine nucleobase biosynthetic process [GO:0006207 biological_process] (1)	Phosphoribosyltransferase domain [IPR000836] (1); Aldolase-type TIM barrel [IPR013785] (1); Orotidine 5'-phosphate decarboxylase, active site [IPR018089] (1); Orotidine 5'-phosphate decarboxylase domain [IPR001754] (1); Phosphoribosyltransferase-like [IPR029057] (1); Orotidine 5'-phosphate decarboxylase [IPR014732] (1); Orotate phosphoribosyl transferase domain [IPR004467] (1); Ribulose-phosphate binding barrel [IPR011060] (1)	scaffold_9_mRNA_1670.1	-	-
GF0032999	1	0	0	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)	scaffold_9_mRNA_1668.1	-	-
GF0032998	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_9_mRNA_1667.1	-	-
GF0032997	1	0	0	Hypothetical protein (1)		Myb domain, plants [IPR006447] (1)	scaffold_9_mRNA_1666.1	-	-
GF0032996	1	0	0	Putative non-LTR retroelement reverse transcriptase (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Endonuclease/exonuclease/phosphatase [IPR005135] (1); Ribonuclease H-like domain [IPR012337] (1); Reverse transcriptase domain [IPR000477] (1)	scaffold_9_mRNA_1665.1	-	-
GF0032995	1	0	0	RNA-directed DNA polymerase (Reverse transcriptase) (1)		Reverse transcriptase domain [IPR000477] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1)	scaffold_9_mRNA_1663.1	-	-
GF0032994	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1660.1	-	-
GF0032993	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1658.1	-	-
GF0032992	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1657.1	-	-
GF0032991	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1652.1	-	-
GF0032990	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1650.1	-	-
GF0032989	1	0	0	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	scaffold_9_mRNA_1647.1	-	-
GF0032988	1	0	0	Zinc knuckle family protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_9_mRNA_1645.1	-	-
GF0032987	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1641.1	-	-
GF0032986	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1637.1	-	-
GF0032985	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1635.1	-	-
GF0032984	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1634.1	-	-
GF0032983	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1628.1	-	-
GF0032982	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1625.1	-	-
GF0032981	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1624.1	-	-
GF0032980	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			scaffold_9_mRNA_1621.1	-	-
GF0032979	1	0	0	Hypothetical protein (1)		Cation efflux protein, cytoplasmic domain [IPR027470] (1)	scaffold_9_mRNA_1619.1	-	-
GF0032978	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1603.1	-	-
GF0032977	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1602.1	-	-
GF0032976	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); DNA integration [GO:0015074 biological_process] (1)	Ribonuclease H-like domain [IPR012337] (1); Integrase, catalytic core [IPR001584] (1)	scaffold_9_mRNA_1595.1	-	-
GF0032975	1	0	0	Non-ltr retrotransposon reverse transcriptase-like protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1); Reverse transcriptase domain [IPR000477] (1)	scaffold_9_mRNA_1585.1	-	-
GF0032974	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	UBX domain [IPR001012] (1)	scaffold_9_mRNA_1581.1	-	-
GF0032973	1	0	0	E3 ubiquitin-protein ligase RBBP6 (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_9_mRNA_1568.1	-	-
GF0032972	1	0	0	Hypothetical protein (1)	heme binding [GO:0020037 molecular_function] (1); response to oxidative stress [GO:0006979 biological_process] (1); peroxidase activity [GO:0004601 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Haem peroxidase, plant/fungal/bacterial [IPR002016] (1); Plant peroxidase [IPR000823] (1); Haem peroxidase [IPR010255] (1)	scaffold_9_mRNA_1558.1	-	-
GF0032971	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_9_mRNA_1554.1	-	-
GF0032970	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1552.1	-	-
GF0032969	1	0	0	Hypothetical protein (1)		Arabidopsis retrotransposon Orf1 [IPR004312] (1)	scaffold_9_mRNA_1543.1	-	-
GF0032968	1	0	0	Hypothetical protein (1)	peroxidase activity [GO:0004601 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); heme binding [GO:0020037 molecular_function] (1); response to oxidative stress [GO:0006979 biological_process] (1)	Haem peroxidase [IPR010255] (1); Plant peroxidase [IPR000823] (1); Peroxidases heam-ligand binding site [IPR019793] (1); Haem peroxidase, plant/fungal/bacterial [IPR002016] (1)	scaffold_9_mRNA_1542.1	-	-
GF0032967	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1534.1	-	-
GF0032966	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1533.1	-	-

ID	**Num. in *C. celementine***	**Num in *C. unshiu***	**Num in *P.trifoliata***	**Note**	**GO**	**InterPro**	**Members in *C.clementine***	**Members in *C.unshiu***	**Members in *P.trifoliata***
GF0032965	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_9_mRNA_1532.1	-	-
GF0032964	1	0	0	P-loop nucleoside triphosphate hydrolase superfamily protein (1)		P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_9_mRNA_1527.1	-	-
GF0032963	1	0	0	Phospholipase A2 family protein (1)	lipid catabolic process [GO:0016042 biological_process] (1); calcium ion binding [GO:0005509 molecular_function] (1); phospholipid metabolic process [GO:0006644 biological_process] (1); arachidonic acid secretion [GO:0050482 biological_process] (1); phospholipase A2 activity [GO:0004623 molecular_function] (1)	Phospholipase A2 domain [IPR016090] (1); Phospholipase A2, histidine active site [IPR033113] (1); Phospholipase A2 [IPR001211] (1)	scaffold_9_mRNA_1526.1	-	-
GF0032962	1	0	0	Monosacharide transport protein (1)			scaffold_9_mRNA_1525.1	-	-
GF0032961	1	0	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1); Domain of unknown function DUF1985 [IPR015410] (1)	scaffold_9_mRNA_1521.1	-	-
GF0032960	1	0	0	(Rice Genome Annotation Project) transposon protein (1)			scaffold_9_mRNA_1520.1	-	-
GF0032959	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1518.1	-	-
GF0032958	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1514.1	-	-
GF0032957	1	0	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Domain of unknown function DUF1985 [IPR015410] (1); Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	scaffold_9_mRNA_1512.1	-	-
GF0032956	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1504.1	-	-
GF0032955	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1497.1	-	-
GF0032954	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1493.1	-	-
GF0032953	1	0	0	Hypothetical protein (1)	structural constituent of ribosome [GO:0003735 molecular_function] (1); translation [GO:0006412 biological_process] (1); ribosome [GO:0005840 cellular_component] (1)	Ribosomal protein L14P [IPR000218] (1)	scaffold_9_mRNA_1492.1	-	-
GF0032952	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1488.1	-	-
GF0032951	1	0	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_9_mRNA_1487.1	-	-
GF0032950	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1481.1	-	-
GF0032949	1	0	0	Amino Acid-Polyamine-Organocation (APC) Family (1)	base-excision repair [GO:0006284 biological_process] (1); DNA repair [GO:0006281 biological_process] (1); hydrolase activity, hydrolyzing N-glycosyl compounds [GO:0016799 molecular_function] (1); uracil DNA N-glycosylase activity [GO:0004844 molecular_function] (1)	Uracil-DNA glycosylase, active site [IPR018085] (1); Uracil-DNA glycosylase-like [IPR005122] (1); Uracil-DNA glycosylase family 1 [IPR002043] (1)	scaffold_9_mRNA_1480.1	-	-
GF0032948	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1475.1	-	-
GF0032947	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1472.1	-	-
GF0032946	1	0	0	Limonene synthase (1)	magnesium ion binding [GO:0000287 molecular_function] (1); terpene synthase activity [GO:0010333 molecular_function] (1); lyase activity [GO:0016829 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	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)	scaffold_9_mRNA_1470.1	-	-
GF0032945	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1468.1	-	-
GF0032944	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1467.1	-	-
GF0032943	1	0	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_9_mRNA_1466.1	-	-
GF0032942	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_9_mRNA_1465.1	-	-
GF0032941	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1460.1	-	-
GF0032940	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1457.1	-	-
GF0032939	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1456.1	-	-
GF0032938	1	0	0	RNA-directed DNA polymerase (Reverse transcriptase) (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_9_mRNA_1454.1	-	-
GF0032937	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1); Chromo domain [IPR023780] (1)	scaffold_9_mRNA_1453.1	-	-
GF0032936	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1452.1	-	-
GF0032935	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1449.1	-	-
GF0032934	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_9_mRNA_1447.1	-	-
GF0032933	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1440.1	-	-
GF0032932	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1436.1	-	-
GF0032931	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1433.1	-	-
GF0032930	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1432.1	-	-
GF0032929	1	0	0	Nucleolar GTP-binding protein 1 (1)	nucleolus [GO:0005730 cellular_component] (1); GTP binding [GO:0005525 molecular_function] (1)	NOG, C-terminal [IPR012973] (1); OBG-type guanine nucleotide-binding (G) domain [IPR031167] (1); Nucleolar GTP-binding protein 1 [IPR024926] (1); GTP binding domain [IPR006073] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_9_mRNA_1426.1	-	-
GF0032928	1	0	0	Phloem protein 2-B13 (1)	protein binding [GO:0005515 molecular_function] (1)	Phloem protein 2-like [IPR025886] (1); F-box domain [IPR001810] (1)	scaffold_9_mRNA_1418.1	-	-
GF0032927	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1415.1	-	-
GF0032926	1	0	0	Hypothetical protein (1)		Gag-polypeptide of LTR copia-type [IPR029472] (1)	scaffold_9_mRNA_1414.1	-	-
GF0032925	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); GAG-pre-integrase domain [IPR025724] (1)	scaffold_9_mRNA_1413.1	-	-
GF0032924	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1409.1	-	-
GF0032923	1	0	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1)	scaffold_9_mRNA_1407.1	-	-
GF0032922	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1406.1	-	-
GF0032921	1	0	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_9_mRNA_1395.1	-	-
GF0032920	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1394.1	-	-
GF0032919	1	0	0	UPF0481 protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	scaffold_9_mRNA_1378.1	-	-
GF0032918	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1377.1	-	-
GF0032917	1	0	0	Hypothetical protein (1)		Zinc knuckle CX2CX4HX4C [IPR025836] (1)	scaffold_9_mRNA_1376.1	-	-
GF0032916	1	0	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_9_mRNA_1373.1	-	-
GF0032915	1	0	0	UPF0481 protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	scaffold_9_mRNA_1372.1	-	-
GF0032914	1	0	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	scaffold_9_mRNA_1371.1	-	-
GF0032913	1	0	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	scaffold_9_mRNA_1359.1	-	-
GF0032912	1	0	0	UPF0481 protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	scaffold_9_mRNA_1353.1	-	-
GF0032911	1	0	0	Hypothetical protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	scaffold_9_mRNA_1352.1	-	-
GF0032910	1	0	0	Hypothetical protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	scaffold_9_mRNA_1350.1	-	-
GF0032909	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1344.1	-	-
GF0032908	1	0	0	RNA-directed DNA polymerase (Reverse transcriptase) (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Reverse transcriptase domain [IPR000477] (1); Ribonuclease H-like domain [IPR012337] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1)	scaffold_9_mRNA_1343.1	-	-
GF0032907	1	0	0	Zinc knuckle family protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_9_mRNA_1342.1	-	-
GF0032906	1	0	0	Hypothetical protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	scaffold_9_mRNA_1336.1	-	-
GF0032905	1	0	0	DUF247 domain protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	scaffold_9_mRNA_1335.1	-	-
GF0032904	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1323.1	-	-
GF0032903	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1322.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0032902	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1316.1	-	-
GF0032901	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_9_mRNA_1315.1	-	-
GF0032900	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	scaffold_9_mRNA_1313.1	-	-
GF0032899	1	0	0	Hypothetical protein (1)		Plant self-incompatibility S1 [IPR010264] (1)	scaffold_9_mRNA_1309.1	-	-
GF0032898	1	0	0	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)	scaffold_9_mRNA_1308.1	-	-
GF0032897	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1307.1	-	-
GF0032896	1	0	0	Hypothetical protein (1)		Plant self-incompatibility S1 [IPR010264] (1)	scaffold_9_mRNA_1304.1	-	-
GF0032895	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1302.1	-	-
GF0032894	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1300.1	-	-
GF0032893	1	0	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Carlavirus nucleic acid-binding protein [IPR002568] (1)	scaffold_9_mRNA_1295.1	-	-
GF0032892	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1294.1	-	-
GF0032891	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_9_mRNA_1293.1	-	-
GF0032890	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1292.1	-	-
GF0032889	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1289.1	-	-
GF0032888	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1280.1	-	-
GF0032887	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	Zinc finger, BED-type [IPR003656] (1); Zinc finger C2H2-type [IPR013087] (1)	scaffold_9_mRNA_1279.1	-	-
GF0032886	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1278.1	-	-
GF0032885	1	0	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Carlavirus nucleic acid-binding protein [IPR002568] (1)	scaffold_9_mRNA_1277.1	-	-
GF0032884	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_9_mRNA_1276.1	-	-
GF0032883	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1275.1	-	-
GF0032882	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_127.1	-	-
GF0032881	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_9_mRNA_1259.1	-	-
GF0032880	1	0	0	Hypothetical protein (1)		Transposon, En/Spm-like [IPR004242] (1); Transposase-associated domain [IPR029480] (1)	scaffold_9_mRNA_1258.1	-	-
GF0032879	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1250.1	-	-
GF0032878	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1246.1	-	-
GF0032877	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1244.1	-	-
GF0032876	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1243.1	-	-
GF0032875	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1242.1	-	-
GF0032874	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1237.1	-	-
GF0032873	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1236.1	-	-
GF0032872	1	0	0	BED zinc finger,hAT family dimerization domain isoform 1 (1)	nucleic acid binding [GO:0003676 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); hAT-like transposase, RNase-H fold [IPR025525] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	scaffold_9_mRNA_1234.1	-	-
GF0032871	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1233.1	-	-
GF0032870	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1231.1	-	-
GF0032869	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			scaffold_9_mRNA_1230.1	-	-
GF0032868	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1228.1	-	-
GF0032867	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_9_mRNA_1227.1	-	-
GF0032866	1	0	0	Hypothetical protein (1)	signal transduction [GO:0007165 biological_process] (1); protein binding [GO:0005515 molecular_function] (1)	Winged helix-turn-helix DNA-binding domain [IPR011991] (1); DDRGK domain containing protein [IPR019153] (1); Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1)	scaffold_9_mRNA_1222.1	-	-
GF0032865	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1215.1	-	-
GF0032864	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	F-box domain [IPR001810] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_9_mRNA_1197.1	-	-
GF0032863	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_9_mRNA_1195.1	-	-
GF0032862	1	0	0	Hypothetical protein (1)		Chromo domain-like [IPR016197] (1)	scaffold_9_mRNA_1190.1	-	-
GF0032861	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_9_mRNA_1183.1	-	-
GF0032860	1	0	0	Monosacharide transport protein (1)			scaffold_9_mRNA_1182.1	-	-
GF0032859	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	F-box domain [IPR001810] (1)	scaffold_9_mRNA_1181.1	-	-
GF0032858	1	0	0	Hypothetical protein (1)	regulation of defense response [GO:0031347 biological_process] (1); regulation of salicylic acid mediated signaling pathway [GO:2000031 biological_process] (1); cellular response to salicylic acid stimulus [GO:0071446 biological_process] (1); integral component of membrane [GO:0016021 cellular_component] (1)	PGG domain [IPR026961] (1); Protein accelerated cell death 6 [IPR032846] (1)	scaffold_9_mRNA_1180.1	-	-
GF0032857	1	0	0	Ankyrin repeat family protein, putative (1)	regulation of salicylic acid mediated signaling pathway [GO:2000031 biological_process] (1); regulation of defense response [GO:0031347 biological_process] (1); protein binding [GO:0005515 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1); cellular response to salicylic acid stimulus [GO:0071446 biological_process] (1)	Ankyrin repeat [IPR002110] (1); Protein accelerated cell death 6 [IPR032846] (1); PGG domain [IPR026961] (1); Ankyrin repeat-containing domain [IPR020683] (1)	scaffold_9_mRNA_1179.1	-	-
GF0032856	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1177.1	-	-
GF0032855	1	0	0	Hypothetical protein (1)	transport [GO:0006810 biological_process] (1); membrane [GO:0016020 cellular_component] (1); transporter activity [GO:0005215 molecular_function] (1)	Proton-dependent oligopeptide transporter family [IPR000109] (1)	scaffold_9_mRNA_1167.1	-	-
GF0032854	1	0	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1)	Aspartic peptidase, active site [IPR001969] (1); Aspartic peptidase domain [IPR021109] (1)	scaffold_9_mRNA_1165.1	-	-
GF0032853	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1164.1	-	-
GF0032852	1	0	0	Reverse transcriptase, related (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Endonuclease/exonuclease/phosphatase [IPR005135] (1)	scaffold_9_mRNA_1163.1	-	-
GF0032851	1	0	0	MATE efflux family protein 9 (1)	antiporter activity [GO:0015297 molecular_function] (1); drug transmembrane transporter activity [GO:0015238 molecular_function] (1); membrane [GO:0016020 cellular_component] (1); drug transmembrane transport [GO:0006855 biological_process] (1); transmembrane transport [GO:0055085 biological_process] (1)	Multi antimicrobial extrusion protein [IPR002528] (1)	scaffold_9_mRNA_1155.1	-	-
GF0032850	1	0	0	Hypothetical protein (1)		Isopenicillin N synthase-like [IPR027443] (1)	scaffold_9_mRNA_1149.1	-	-
GF0032849	1	0	0	Putative MATE efflux family protein 5-like (1)	drug transmembrane transport [GO:0006855 biological_process] (1); antiporter activity [GO:0015297 molecular_function] (1); drug transmembrane transporter activity [GO:0015238 molecular_function] (1); membrane [GO:0016020 cellular_component] (1); transmembrane transport [GO:0055085 biological_process] (1)	Multi antimicrobial extrusion protein [IPR002528] (1)	scaffold_9_mRNA_1143.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0032848	1	0	0	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, N-terminal [IPR004045] (1); Glutathione S-transferase, C-terminal-like [IPR010987] (1)	scaffold_9_mRNA_1142.1	-	-
GF0032847	1	0	0	Tau 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)	scaffold_9_mRNA_1141.1	-	-
GF0032846	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1139.1	-	-
GF0032845	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1138.1	-	-
GF0032844	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_9_mRNA_1137.1	-	-
GF0032843	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1136.1	-	-
GF0032842	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1133.1	-	-
GF0032841	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1131.1	-	-
GF0032840	1	0	0	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, N-terminal [IPR004045] (1); Glutathione S-transferase, C-terminal-like [IPR010987] (1)	scaffold_9_mRNA_1129.1	-	-
GF0032839	1	0	0	Glutathione S-transferase tau 7, putative (1)		Glutathione S-transferase, C-terminal-like [IPR010987] (1); Glutathione S-transferase, C-terminal [IPR004046] (1)	scaffold_9_mRNA_1124.1	-	-
GF0032838	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	Zinc finger, BED-type [IPR003656] (1); Zinc finger C2H2-type [IPR013087] (1)	scaffold_9_mRNA_1119.1	-	-
GF0032837	1	0	0	Hypothetical protein (1)	transport [GO:0006810 biological_process] (1); membrane [GO:0016020 cellular_component] (1); transporter activity [GO:0005215 molecular_function] (1)	Proton-dependent oligopeptide transporter family [IPR000109] (1)	scaffold_9_mRNA_1113.1	-	-
GF0032836	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Thioredoxin-like fold [IPR012336] (1); Glutathione S-transferase, N-terminal [IPR004045] (1)	scaffold_9_mRNA_1109.1	-	-
GF0032835	1	0	0	MATE efflux family protein 9 (1)	transmembrane transport [GO:0055085 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); drug transmembrane transport [GO:0006855 biological_process] (1)	Multi antimicrobial extrusion protein [IPR002528] (1)	scaffold_9_mRNA_1108.1	-	-
GF0032834	1	0	0	Tau 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); Glutathione S-transferase, C-terminal [IPR004046] (1)	scaffold_9_mRNA_1107.1	-	-
GF0032833	1	0	0	Tau class glutathione S-transferase (1)	protein binding [GO:0005515 molecular_function] (1)	Glutathione S-transferase, C-terminal-like [IPR010987] (1); Glutathione S-transferase, N-terminal [IPR004045] (1); Glutathione S-transferase, C-terminal [IPR004046] (1); Thioredoxin-like fold [IPR012336] (1)	scaffold_9_mRNA_1105.1	-	-
GF0032832	1	0	0	Transposon-like ORF protein (1)		Domain of unknown function DUF4216 [IPR025312] (1); Transposon, En/Spm-like [IPR004242] (1)	scaffold_9_mRNA_1104.1	-	-
GF0032831	1	0	0	Tau class glutathione S-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)	scaffold_9_mRNA_1103.1	-	-
GF0032830	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1099.1	-	-
GF0032829	1	0	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	B3 DNA binding domain [IPR003340] (1); NAC domain [IPR003441] (1); DNA-binding pseudobarrel domain [IPR015300] (1)	scaffold_9_mRNA_1098.1	-	-
GF0032828	1	0	0	Glutathione S-transferase tau 7, putative (1)		Glutathione S-transferase, C-terminal-like [IPR010987] (1)	scaffold_9_mRNA_1096.1	-	-
GF0032827	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	scaffold_9_mRNA_1090.1	-	-
GF0032826	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1088.1	-	-
GF0032825	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_9_mRNA_1087.1	-	-
GF0032824	1	0	0	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	scaffold_9_mRNA_1084.1	-	-
GF0032823	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1083.1	-	-
GF0032822	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Pentatricopeptide repeat [IPR002885] (1); Tetratricopeptide-like helical domain [IPR011990] (1)	scaffold_9_mRNA_1079.1	-	-
GF0032821	1	0	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	scaffold_9_mRNA_1065.1	-	-
GF0032820	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1064.1	-	-
GF0032819	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_9_mRNA_1063.1	-	-
GF0032818	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1062.1	-	-
GF0032817	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1060.1	-	-
GF0032816	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1054.1	-	-
GF0032815	1	0	0	RNA-directed DNA polymerase (Reverse transcriptase) (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_9_mRNA_1048.1	-	-
GF0032814	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1043.1	-	-
GF0032813	1	0	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Carlavirus nucleic acid-binding protein [IPR002568] (1)	scaffold_9_mRNA_1042.1	-	-
GF0032812	1	0	0	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	scaffold_9_mRNA_1040.1	-	-
GF0032811	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1038.1	-	-
GF0032810	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H-like domain [IPR012337] (1); Endonuclease/exonuclease/phosphatase [IPR005135] (1)	scaffold_9_mRNA_1016.1	-	-
GF0032809	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1013.1	-	-
GF0032808	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Zinc finger C2H2-type [IPR013087] (1); Zinc finger, BED-type [IPR003656] (1)	scaffold_9_mRNA_1010.1	-	-
GF0032807	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_101.1	-	-
GF0032806	1	0	0	Hypothetical protein (1)		MULE transposase domain [IPR018289] (1)	scaffold_9_mRNA_1007.1	-	-
GF0032805	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1006.1	-	-
GF0032804	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1001.1	-	-
GF0032803	1	0	0	Hypothetical protein (1)			scaffold_9_mRNA_1000.1	-	-
GF0032802	1	0	0	Hypothetical protein (1)	proton-transporting two-sector ATPase complex, proton-transporting domain [GO:0033177 cellular_component] (1); proton-transporting V-type ATPase, V0 domain [GO:0033179 cellular_component] (1); hydrogen ion transmembrane transporter activity [GO:0015078 molecular_function] (1); ATP hydrolysis coupled proton transport [GO:0015991 biological_process] (1)	V-ATPase proteolipid subunit C, eukaryotic [IPR011555] (1); V-ATPase proteolipid subunit [IPR000245] (1); V-ATPase proteolipid subunit C-like domain [IPR002379] (1)	scaffold_8_mRNA_998.1	-	-
GF0032801	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_995.1	-	-
GF0032800	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_993.1	-	-
GF0032799	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_8_mRNA_982.1	-	-
GF0032798	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_976.1	-	-
GF0032797	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_97.1	-	-
GF0032796	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_969.1	-	-
GF0032795	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_968.1	-	-
GF0032794	1	0	0	Hypothetical protein (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); Zinc finger C2H2-type [IPR013087] (1)	scaffold_8_mRNA_962.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0032793	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_8_mRNA_959.1	-	-
GF0032792	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_956.1	-	-
GF0032791	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_955.1	-	-
GF0032790	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_954.1	-	-
GF0032789	1	0	0	Monosacharide transport protein (1)			scaffold_8_mRNA_952.1	-	-
GF0032788	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_8_mRNA_951.1	-	-
GF0032787	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_949.1	-	-
GF0032786	1	0	0	BED zinc finger,hAT family dimerization domain (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); hAT-like transposase, RNase-H fold [IPR025525] (1); Zinc finger C2H2-type [IPR013087] (1); Zinc finger, BED-type [IPR003656] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	scaffold_8_mRNA_942.1	-	-
GF0032785	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_940.1	-	-
GF0032784	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_939.1	-	-
GF0032783	1	0	0	Pentatricopeptide (PPR) repeat protein (1)		Pentatricopeptide repeat [IPR002885] (1)	scaffold_8_mRNA_938.1	-	-
GF0032782	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_933.1	-	-
GF0032781	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_932.1	-	-
GF0032780	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	SH3 domain [IPR001452] (1); Arfaptin homology (AH) domain/BAR domain [IPR027267] (1)	scaffold_8_mRNA_931.1	-	-
GF0032779	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_8_mRNA_921.1	-	-
GF0032778	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_920.1	-	-
GF0032777	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_919.1	-	-
GF0032776	1	0	0	Hypothetical protein (1)	ligase activity, forming aminoacyl-tRNA and related compounds [GO:0016876 molecular_function] (1); tRNA aminoacylation [GO:0043039 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1)	Rossmann-like alpha/beta/alpha sandwich fold [IPR014729] (1); Glutamyl/glutaminyl-tRNA synthetase, class Ib, catalytic domain [IPR020058] (1)	scaffold_8_mRNA_918.1	-	-
GF0032775	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_914.1	-	-
GF0032774	1	0	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_8_mRNA_905.1	-	-
GF0032773	1	0	0	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	scaffold_8_mRNA_892.1	-	-
GF0032772	1	0	0	Monosacharide transport protein (1)			scaffold_8_mRNA_891.1	-	-
GF0032771	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_890.1	-	-
GF0032770	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_874.1	-	-
GF0032769	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_870.1	-	-
GF0032768	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_8_mRNA_867.1	-	-
GF0032767	1	0	0	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-type ATPase, N-terminal domain [IPR025753] (1); ATPase, AAA-type, conserved site [IPR003960] (1)	scaffold_8_mRNA_849.1	-	-
GF0032766	1	0	0	Hypothetical protein (1)		AAA-type ATPase, N-terminal domain [IPR025753] (1)	scaffold_8_mRNA_844.1	-	-
GF0032765	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Domain of unknown function DUF4283 [IPR025558] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1); Endonuclease/exonuclease/phosphatase [IPR005135] (1); Zinc finger, CCHC-type [IPR001878] (1)	scaffold_8_mRNA_837.1	-	-
GF0032764	1	0	0	Pollen-specific protein SF3 (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, LIM-type [IPR001781] (1)	scaffold_8_mRNA_828.1	-	-
GF0032763	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_826.1	-	-
GF0032762	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_8_mRNA_825.1	-	-
GF0032761	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_824.1	-	-
GF0032760	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1); DNA integration [GO:0015074 biological_process] (1)	Integrase, catalytic core [IPR001584] (1); Ribonuclease H-like domain [IPR012337] (1); Ribonuclease H domain [IPR002156] (1); Retrotransposon gag domain [IPR005162] (1)	scaffold_8_mRNA_822.1	-	-
GF0032759	1	0	0	Phenylcoumaran benzylic ether reductase (1)		NAD(P)-binding domain [IPR016040] (1); NmrA-like domain [IPR008030] (1)	scaffold_8_mRNA_821.1	-	-
GF0032758	1	0	0	Phenylcoumaran benzylic ether reductase (1)		NAD(P)-binding domain [IPR016040] (1); NmrA-like domain [IPR008030] (1)	scaffold_8_mRNA_820.1	-	-
GF0032757	1	0	0	Phenylcoumaran benzylic ether reductase (1)		NAD(P)-binding domain [IPR016040] (1); NmrA-like domain [IPR008030] (1)	scaffold_8_mRNA_819.1	-	-
GF0032756	1	0	0	Phenylcoumaran benzylic ether reductase (1)		NmrA-like domain [IPR008030] (1); NAD(P)-binding domain [IPR016040] (1)	scaffold_8_mRNA_815.1	-	-
GF0032755	1	0	0	UDP-glycosyltransferase 85A7 (1)	metabolic process [GO:0008152 biological_process] (1); transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	scaffold_8_mRNA_811.1	-	-
GF0032754	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_810.1	-	-
GF0032753	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_806.1	-	-
GF0032752	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_805.1	-	-
GF0032751	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_804.1	-	-
GF0032750	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			scaffold_8_mRNA_803.1	-	-
GF0032749	1	0	0	Probable pectinesterase 67 (1)	pectinesterase activity [GO:0030599 molecular_function] (1); cell wall modification [GO:0042545 biological_process] (1); cell wall [GO:0005618 cellular_component] (1)	Pectinesterase, Asp active site [IPR033131] (1); Pectinesterase, catalytic [IPR000070] (1); Pectin lyase fold [IPR012334] (1); Pectin lyase fold/virulence factor [IPR011050] (1)	scaffold_8_mRNA_800.1	-	-
GF0032748	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_8.1	-	-
GF0032747	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_799.1	-	-
GF0032746	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_794.1	-	-
GF0032745	1	0	0	Glutaminase (1)			scaffold_8_mRNA_793.1	-	-
GF0032744	1	0	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	scaffold_8_mRNA_789.1	-	-
GF0032743	1	0	0	Mutator-like transposase (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, SWIM-type [IPR007527] (1); Zinc finger, PMZ-type [IPR006564] (1); MULE transposase domain [IPR018289] (1); Transposase, MuDR, plant [IPR004332] (1)	scaffold_8_mRNA_778.1	-	-
GF0032742	1	0	0	BURP domain-containing protein (1)		BURP domain [IPR004873] (1)	scaffold_8_mRNA_755.1	-	-
GF0032741	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_753.1	-	-
GF0032740	1	0	0	Non-LTR retroelement reverse transcriptase-like (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1); Domain of unknown function DUF4283 [IPR025558] (1)	scaffold_8_mRNA_749.1	-	-
GF0032739	1	0	0	Yellow stripe 1A transporter (1)	transmembrane transport [GO:0055085 biological_process] (1)	Oligopeptide transporter, OPT superfamily [IPR004813] (1)	scaffold_8_mRNA_748.1	-	-
GF0032738	1	0	0	Endochitinase (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)	Glycoside hydrolase, family 19, catalytic [IPR000726] (1); Lysozyme-like domain [IPR023346] (1)	scaffold_8_mRNA_74.1	-	-
GF0032737	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_739.1	-	-
GF0032736	1	0	0	Hypothetical protein (1)	protein serine/threonine kinase activity [GO:0004674 molecular_function] (1); nuclear-transcribed mRNA catabolic process, nonsense-mediated decay [GO:0000184 biological_process] (1); phosphorylation [GO:0016310 biological_process] (1); binding [GO:0005488 molecular_function] (1)	Armadillo-like helical [IPR011989] (1); Serine/threonine-protein kinase SMG1 [IPR031559] (1); Armadillo-type fold [IPR016024] (1)	scaffold_8_mRNA_735.1	-	-
GF0032735	1	0	0	Monosacharide transport protein (1)			scaffold_8_mRNA_732.1	-	-
GF0032734	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_713.1	-	-
GF0032733	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_712.1	-	-
GF0032732	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_702.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0032731	1	0	0	4-hydroxy-3-methylbut-2-enyl diphosphate reductase (1)	dimethylallyl diphosphate biosynthetic process [GO:0050992 biological_process] (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-en-1-yl diphosphate reductase activity [GO:0051745 molecular_function] (1)	4-hydroxy-3-methylbut-2-enyl diphosphate reductase [IPR003451] (1)	scaffold_8_mRNA_701.1	-	-
GF0032730	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_697.1	-	-
GF0032729	1	0	0	Mutator-like transposase (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, SWIM-type [IPR007527] (1); Transposase, MuDR, plant [IPR004332] (1); MULE transposase domain [IPR018289] (1); Zinc finger, PMZ-type [IPR006564] (1)	scaffold_8_mRNA_685.1	-	-
GF0032728	1	0	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1); Domain of unknown function DUF1985 [IPR015410] (1)	scaffold_8_mRNA_684.1	-	-
GF0032727	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_683.1	-	-
GF0032726	1	0	0	Retrotransposon protein, putative, Ty1-copia subclass (1)			scaffold_8_mRNA_678.1	-	-
GF0032725	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_676.1	-	-
GF0032724	1	0	0	BiP isoform A family protein (1)		Heat shock protein 70kD, peptide-binding domain [IPR029047] (1); Heat shock protein 70 family [IPR013126] (1); Heat shock protein 70, conserved site [IPR018181] (1); Heat shock protein 70kD, C-terminal domain [IPR029048] (1)	scaffold_8_mRNA_675.1	-	-
GF0032723	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_667.1	-	-
GF0032722	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF1985 [IPR015410] (1)	scaffold_8_mRNA_665.1	-	-
GF0032721	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_647.1	-	-
GF0032720	1	0	0	B3 domain-containing transcription factor VRN1-like protein (1)	DNA binding [GO:0003677 molecular_function] (1)	B3 DNA binding domain [IPR003340] (1); DNA-binding pseudobarrel domain [IPR015300] (1)	scaffold_8_mRNA_634.1	-	-
GF0032719	1	0	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	scaffold_8_mRNA_631.1	-	-
GF0032718	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_626.1	-	-
GF0032717	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_621.1	-	-
GF0032716	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_617.1	-	-
GF0032715	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_615.1	-	-
GF0032714	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_607.1	-	-
GF0032713	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_596.1	-	-
GF0032712	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_8_mRNA_595.1	-	-
GF0032711	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_591.1	-	-
GF0032710	1	0	0	Disease resistance family protein / LRR family protein, putative (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	scaffold_8_mRNA_589.1	-	-
GF0032709	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_586.1	-	-
GF0032708	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_58.1	-	-
GF0032707	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_572.1	-	-
GF0032706	1	0	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); serine-type carboxypeptidase activity [GO:0004185 molecular_function] (1)	Alpha/Beta hydrolase fold [IPR029058] (1); Peptidase S10, serine carboxypeptidase [IPR001563] (1); Serine carboxypeptidases, histidine active site [IPR033124] (1)	scaffold_8_mRNA_566.1	-	-
GF0032705	1	0	0	Putative carboxylesterase 2 (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)	scaffold_8_mRNA_560.1	-	-
GF0032704	1	0	0	CXE carboxylesterase (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)	scaffold_8_mRNA_557.1	-	-
GF0032703	1	0	0	60s ribosomal protein (1)	ribosome [GO:0005840 cellular_component] (1); metabolic process [GO:0008152 biological_process] (1); intracellular [GO:0005622 cellular_component] (1); translation [GO:0006412 biological_process] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1); hydrolase activity [GO:0016787 molecular_function] (1)	Ribosomal protein L2 domain 2 [IPR014722] (1); Alpha/Beta hydrolase fold [IPR029058] (1); Alpha/beta hydrolase fold-3 [IPR013094] (1); Translation protein SH3-like domain [IPR008991] (1); Ribosomal protein L14e domain [IPR002784] (1)	scaffold_8_mRNA_552.1	-	-
GF0032702	1	0	0	Hypothetical protein (1)	hydrolase activity [GO:0016787 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Alpha/beta hydrolase fold-3 [IPR013094] (1); Alpha/Beta hydrolase fold [IPR029058] (1)	scaffold_8_mRNA_549.1	-	-
GF0032701	1	0	0	Putative carboxylesterase 2 (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)	scaffold_8_mRNA_548.1	-	-
GF0032700	1	0	0	Hypothetical protein (1)	DNA integration [GO:0015074 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Integrase, catalytic core [IPR001584] (1); Ribonuclease H-like domain [IPR012337] (1); GAG-pre-integrase domain [IPR025724] (1)	scaffold_8_mRNA_540.1	-	-
GF0032699	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_538.1	-	-
GF0032698	1	0	0	Hypothetical protein (1)	catalytic activity [GO:0003824 molecular_function] (1); metal ion binding [GO:0046872 molecular_function] (1)	Peptidase M16, N-terminal [IPR011765] (1); Peptidase M16, C-terminal [IPR007863] (1); Metalloenzyme, LuxS/M16 peptidase-like [IPR011249] (1)	scaffold_8_mRNA_534.1	-	-
GF0032697	1	0	0	CXE carboxylesterase (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)	scaffold_8_mRNA_532.1	-	-
GF0032696	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1); Reverse transcriptase domain [IPR000477] (1)	scaffold_8_mRNA_531.1	-	-
GF0032695	1	0	0	Hypothetical protein (1)	DNA integration [GO:0015074 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Integrase, catalytic core [IPR001584] (1)	scaffold_8_mRNA_528.1	-	-
GF0032694	1	0	0	Hypothetical protein (1)		Fumarase/histidase, N-terminal [IPR024083] (1)	scaffold_8_mRNA_527.1	-	-
GF0032693	1	0	0	Hypothetical protein (1)	hydrolase activity [GO:0016787 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Alpha/Beta hydrolase fold [IPR029058] (1); Alpha/beta hydrolase fold-3 [IPR013094] (1)	scaffold_8_mRNA_524.1	-	-
GF0032692	1	0	0	Hypothetical protein (1)	catalytic activity [GO:0003824 molecular_function] (1)	Gag-polypeptide of LTR copia-type [IPR029472] (1); Aldolase-type TIM barrel [IPR013785] (1)	scaffold_8_mRNA_522.1	-	-
GF0032691	1	0	0	CXE carboxylesterase (1)	metabolic process [GO:0008152 biological_process] (1); hydrolase activity [GO:0016787 molecular_function] (1)	Alpha/Beta hydrolase fold [IPR029058] (1); Lipase, GDXG, putative serine active site [IPR033140] (1); Alpha/beta hydrolase fold-3 [IPR013094] (1)	scaffold_8_mRNA_520.1	-	-
GF0032690	1	0	0	Hypothetical protein (1)		Short-chain dehydrogenase/reductase SDR [IPR002347] (1); NAD(P)-binding domain [IPR016040] (1)	scaffold_8_mRNA_510.1	-	-
GF0032689	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_492.1	-	-
GF0032688	1	0	0	Monosacharide transport protein (1)			scaffold_8_mRNA_490.1	-	-
GF0032687	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_8_mRNA_478.1	-	-
GF0032686	1	0	0	Vacuolar ATPase assembly integral membrane protein VMA21 homolog (1)	vacuolar proton-transporting V-type ATPase complex assembly [GO:0070072 biological_process] (1)	Vacuolar ATPase assembly integral membrane protein Vma21 [IPR019013] (1)	scaffold_8_mRNA_474.1	-	-
GF0032685	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_8_mRNA_473.1	-	-
GF0032684	1	0	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1)	Myc-type, basic helix-loop-helix (bHLH) domain [IPR011598] (1)	scaffold_8_mRNA_465.1	-	-
GF0032683	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4219 [IPR025314] (1)	scaffold_8_mRNA_452.1	-	-
GF0032682	1	0	0	Patched family protein (1)	integral component of membrane [GO:0016021 cellular_component] (1); lipid transporter activity [GO:0005319 molecular_function] (1)	Niemann-Pick C type protein [IPR004765] (1); Sterol-sensing domain [IPR000731] (1); Protein patched/dispatched [IPR003392] (1); Niemann-Pick C1, N-terminal [IPR032190] (1)	scaffold_8_mRNA_45.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0032681	1	0	0	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)	scaffold_8_mRNA_449.1	-	-
GF0032680	1	0	0	UDP-glucosyltransferase 73B2 (1)	metabolic process [GO:0008152 biological_process] (1); transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	scaffold_8_mRNA_448.1	-	-
GF0032679	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_44.1	-	-
GF0032678	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, PMZ-type [IPR006564] (1); Zinc finger, SWIM-type [IPR007527] (1)	scaffold_8_mRNA_433.1	-	-
GF0032677	1	0	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	scaffold_8_mRNA_432.1	-	-
GF0032676	1	0	0	Pentatricopeptide repeat-containing family protein (1)	protein binding [GO:0005515 molecular_function] (1)	Pentatricopeptide repeat [IPR002885] (1); Tetratricopeptide-like helical domain [IPR011990] (1)	scaffold_8_mRNA_43.1	-	-
GF0032675	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_429.1	-	-
GF0032674	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_8_mRNA_413.1	-	-
GF0032673	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_411.1	-	-
GF0032672	1	0	0	Hypothetical protein (1)		Protein kinase-like domain [IPR011009] (1); Aminoglycoside phosphotransferase [IPR002575] (1)	scaffold_8_mRNA_401.1	-	-
GF0032671	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_38.1	-	-
GF0032670	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_8_mRNA_371.1	-	-
GF0032669	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_370.1	-	-
GF0032668	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_366.1	-	-
GF0032667	1	0	0	Drought responsive protein 2 (1)		At2g23090-like [IPR026939] (1)	scaffold_8_mRNA_357.1	-	-
GF0032666	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_354.1	-	-
GF0032665	1	0	0	Hypothetical protein (1)	hydrolase activity [GO:0016787 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Alpha/Beta hydrolase fold [IPR029058] (1); Alpha/beta hydrolase fold-3 [IPR013094] (1)	scaffold_8_mRNA_352.1	-	-
GF0032664	1	0	0	Hypothetical protein (1)		Fibronectin type III-like domain [IPR026891] (1); Immunoglobulin-like fold [IPR013783] (1)	scaffold_8_mRNA_335.1	-	-
GF0032663	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_332.1	-	-
GF0032662	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_331.1	-	-
GF0032661	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_330.1	-	-
GF0032660	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_329.1	-	-
GF0032659	1	0	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1); FAR1 DNA binding domain [IPR004330] (1)	scaffold_8_mRNA_3249.1	-	-
GF0032658	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_3248.1	-	-
GF0032657	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_324.1	-	-
GF0032656	1	0	0	UDP-glycosyltransferase 87A1 (1)	metabolic process [GO:0008152 biological_process] (1); transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	scaffold_8_mRNA_3220.1	-	-
GF0032655	1	0	0	ADP-ribosylation factor-like A1D (1)	GTP binding [GO:0005525 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Small GTPase superfamily, ARF/SAR type [IPR006689] (1)	scaffold_8_mRNA_319.2	-	-
GF0032654	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_315.1	-	-
GF0032653	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_314.1	-	-
GF0032652	1	0	0	Putative hexose transporter (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); transmembrane transport [GO:0055085 biological_process] (1); transporter activity [GO:0005215 molecular_function] (1)	Sugar/inositol transporter [IPR003663] (1); Major facilitator, sugar transporter-like [IPR005828] (1); Major facilitator superfamily domain [IPR020846] (1); Sugar transporter, conserved site [IPR005829] (1)	scaffold_8_mRNA_3133.1	-	-
GF0032651	1	0	0	Serine/arginine-rich splicing factor SR45a (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	RNA recognition motif domain [IPR000504] (1)	scaffold_8_mRNA_3124.1	-	-
GF0032650	1	0	0	17.5 kDa class I heat shock protein (1)		Alpha crystallin/Hsp20 domain [IPR002068] (1); HSP20-like chaperone [IPR008978] (1); Small heat shock protein HSP20 [IPR031107] (1)	scaffold_8_mRNA_3099.1	-	-
GF0032649	1	0	0	Monosacharide transport protein (1)			scaffold_8_mRNA_3098.1	-	-
GF0032648	1	0	0	Monosacharide transport protein (1)			scaffold_8_mRNA_3092.1	-	-
GF0032647	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1); Aspartic peptidase domain [IPR021109] (1)	scaffold_8_mRNA_3090.1	-	-
GF0032646	1	0	0	Subtilase family protein, putative (1)	serine-type endopeptidase activity [GO:0004252 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Peptidase S8 propeptide/proteinase inhibitor I9 [IPR010259] (1); Peptidase S8/S53 domain [IPR000209] (1)	scaffold_8_mRNA_3073.1	-	-
GF0032645	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_3068.1	-	-
GF0032644	1	0	0	NAD(P)-binding Rossmann-fold superfamily protein isoform 1 (1)		NAD(P)-binding domain [IPR016040] (1); Short-chain dehydrogenase/reductase SDR [IPR002347] (1)	scaffold_8_mRNA_3061.1	-	-
GF0032643	1	0	0	Hypothetical protein (1)	oxidoreductase activity [GO:0016491 molecular_function] (1)	Short-chain dehydrogenase/reductase, conserved site [IPR020904] (1); NAD(P)-binding domain [IPR016040] (1); Short-chain dehydrogenase/reductase SDR [IPR002347] (1)	scaffold_8_mRNA_3057.1	-	-
GF0032642	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_3054.1	-	-
GF0032641	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_3052.1	-	-
GF0032640	1	0	0	Peptide/nitrate transporter plant (1)	transporter activity [GO:0005215 molecular_function] (1); membrane [GO:0016020 cellular_component] (1); transport [GO:0006810 biological_process] (1)	Proton-dependent oligopeptide transporter family [IPR000109] (1); Major facilitator superfamily domain [IPR020846] (1)	scaffold_8_mRNA_305.1	-	-
GF0032639	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_3039.1	-	-
GF0032638	1	0	0	Probable L-type lectin-domain containing receptor kinase II.1 (1)	ATP binding [GO:0005524 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); carbohydrate binding [GO:0030246 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1)	Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Protein kinase-like domain [IPR011009] (1); Legume lectin domain [IPR001220] (1); Protein kinase domain [IPR000719] (1); Protein kinase, ATP binding site [IPR017441] (1)	scaffold_8_mRNA_3038.1	-	-
GF0032637	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_3037.1	-	-
GF0032636	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_3005.1	-	-
GF0032635	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2998.1	-	-
GF0032634	1	0	0	Actin (1)		Actin family [IPR004000] (1); Actin/actin-like conserved site [IPR020902] (1); Actin, conserved site [IPR004001] (1)	scaffold_8_mRNA_2983.1	-	-
GF0032633	1	0	0	Heat shock protein 70 (1)		Heat shock protein 70kD, peptide-binding domain [IPR029047] (1); Heat shock protein 70kD, C-terminal domain [IPR029048] (1); Heat shock protein 70 family [IPR013126] (1); Heat shock protein 70, conserved site [IPR018181] (1)	scaffold_8_mRNA_2972.1	-	-
GF0032632	1	0	0	Mutator-like transposase (1)		MULE transposase domain [IPR018289] (1); Transposase, MuDR, plant [IPR004332] (1)	scaffold_8_mRNA_2969.1	-	-
GF0032631	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2964.1	-	-
GF0032630	1	0	0	Serine carboxypeptidase 1 (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)	scaffold_8_mRNA_295.1	-	-
GF0032629	1	0	0	17.5 kDa class I heat shock protein (1)		Small heat shock protein HSP20 [IPR031107] (1); Alpha crystallin/Hsp20 domain [IPR002068] (1); HSP20-like chaperone [IPR008978] (1)	scaffold_8_mRNA_2947.1	-	-
GF0032628	1	0	0	40S ribosomal protein S15a (1)	structural constituent of ribosome [GO:0003735 molecular_function] (1); translation [GO:0006412 biological_process] (1); ribosome [GO:0005840 cellular_component] (1)	Ribosomal protein S8 [IPR000630] (1)	scaffold_8_mRNA_2942.1	-	-
GF0032627	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2941.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0032626	1	0	0	Ras-related protein RABE1c (1)	GTPase activity [GO:0003924 molecular_function] (1); GTP binding [GO:0005525 molecular_function] (1)	Small GTPase superfamily [IPR001806] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Small GTP-binding protein domain [IPR005225] (1)	scaffold_8_mRNA_2940.2	-	-
GF0032625	1	0	0	Disease resistance-responsive, dirigent domain protein (1)		Plant disease resistance response protein [IPR004265] (1)	scaffold_8_mRNA_2926.1	-	-
GF0032624	1	0	0	Hypothetical protein (1)		Plant disease resistance response protein [IPR004265] (1)	scaffold_8_mRNA_2925.1	-	-
GF0032623	1	0	0	Histone H4 (1)	nucleosome [GO:0000786 cellular_component] (1); protein heterodimerization activity [GO:0046982 molecular_function] (1); nucleosome assembly [GO:0006334 biological_process] (1); nucleus [GO:0005634 cellular_component] (1); DNA binding [GO:0003677 molecular_function] (1)	Histone H4 [IPR001951] (1); Histone-fold [IPR009072] (1); Histone H4, conserved site [IPR019809] (1)	scaffold_8_mRNA_2910.1	-	-
GF0032622	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_289.1	-	-
GF0032621	1	0	0	Serine carboxypeptidase-like 8 (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)	scaffold_8_mRNA_288.1	-	-
GF0032620	1	0	0	Hypothetical protein (1)	transporter activity [GO:0005215 molecular_function] (1); membrane [GO:0016020 cellular_component] (1); transport [GO:0006810 biological_process] (1)	Proton-dependent oligopeptide transporter family [IPR000109] (1)	scaffold_8_mRNA_2868.1	-	-
GF0032619	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_8_mRNA_2860.1	-	-
GF0032618	1	0	0	RNA-directed DNA polymerase ; Ribonuclease H, putative (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	scaffold_8_mRNA_2856.1	-	-
GF0032617	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2832.1	-	-
GF0032616	1	0	0	Elongation factor 1-alpha (1)	GTP binding [GO:0005525 molecular_function] (1); translational elongation [GO:0006414 biological_process] (1); GTPase activity [GO:0003924 molecular_function] (1); cytoplasm [GO:0005737 cellular_component] (1); translation elongation factor activity [GO:0003746 molecular_function] (1)	Transcription factor, GTP-binding domain [IPR000795] (1); Translation elongation factor EF1A/initiation factor IF2gamma, C-terminal [IPR009001] (1); Translation elongation factor EFTu-like, domain 2 [IPR004161] (1); Tr-type G domain, conserved site [IPR031157] (1); Translation elongation factor EF1A, eukaryotic/archaeal [IPR004539] (1); Translation protein, beta-barrel domain [IPR009000] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Translation elongation factor EFTu/EF1A, C-terminal [IPR004160] (1)	scaffold_8_mRNA_2826.1	-	-
GF0032615	1	0	0	Elongation factor 1-alpha (1)	GTPase activity [GO:0003924 molecular_function] (1); cytoplasm [GO:0005737 cellular_component] (1); translation elongation factor activity [GO:0003746 molecular_function] (1); translational elongation [GO:0006414 biological_process] (1); GTP binding [GO:0005525 molecular_function] (1)	Transcription factor, GTP-binding domain [IPR000795] (1); Translation elongation factor EF1A/initiation factor IF2gamma, C-terminal [IPR009001] (1); Translation elongation factor EFTu-like, domain 2 [IPR004161] (1); Tr-type G domain, conserved site [IPR031157] (1); Translation elongation factor EF1A, eukaryotic/archaeal [IPR004539] (1); Translation protein, beta-barrel domain [IPR009000] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Translation elongation factor EFTu/EF1A, C-terminal [IPR004160] (1)	scaffold_8_mRNA_2824.1	-	-
GF0032614	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_282.1	-	-
GF0032613	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2800.1	-	-
GF0032612	1	0	0	F-box/kelch-repeat protein SKIP11 (1)	protein binding [GO:0005515 molecular_function] (1)	Kelch repeat type 1 [IPR006652] (1); Kelch-type beta propeller [IPR015915] (1)	scaffold_8_mRNA_2799.1	-	-
GF0032611	1	0	0	Ankyrin repeat plant-like protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat [IPR002110] (1); Ankyrin repeat-containing domain [IPR020683] (1); PGG domain [IPR026961] (1)	scaffold_8_mRNA_2783.1	-	-
GF0032610	1	0	0	Ankyrin repeat family protein (1)		Ankyrin repeat-containing domain [IPR020683] (1); PGG domain [IPR026961] (1)	scaffold_8_mRNA_2782.1	-	-
GF0032609	1	0	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	Winged helix-turn-helix DNA-binding domain [IPR011991] (1); NB-ARC [IPR002182] (1)	scaffold_8_mRNA_2774.1	-	-
GF0032608	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF588 [IPR006702] (1)	scaffold_8_mRNA_2771.1	-	-
GF0032607	1	0	0	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); ABC-transporter extracellular N-terminal domain [IPR029481] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); AAA+ ATPase domain [IPR003593] (1); ATP-binding cassette transporter, PDR-like subfamily G, domain 1 [IPR034001] (1); ABC transporter-like [IPR003439] (1); ABC-2 type transporter [IPR013525] (1)	scaffold_8_mRNA_2770.1	-	-
GF0032606	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2753.1	-	-
GF0032605	1	0	0	Hypothetical protein (1)	catalytic activity [GO:0003824 molecular_function] (1)	L-Aspartase-like [IPR008948] (1); Fumarase/histidase, N-terminal [IPR024083] (1); Aromatic amino acid lyase [IPR001106] (1)	scaffold_8_mRNA_2750.1	-	-
GF0032604	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2734.1	-	-
GF0032603	1	0	0	High-affinity nitrate transporter (1)	integral component of membrane [GO:0016021 cellular_component] (1); transmembrane transport [GO:0055085 biological_process] (1)	Major facilitator superfamily [IPR011701] (1); Major facilitator superfamily domain [IPR020846] (1)	scaffold_8_mRNA_2730.1	-	-
GF0032602	1	0	0	Polynucleotidyl transferase, ribonuclease H-like superfamily protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_8_mRNA_2717.1	-	-
GF0032601	1	0	0	Probable xyloglucan endotransglucosylase/hydrolase protein 32 (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); cell wall biogenesis [GO:0042546 biological_process] (1); xyloglucan metabolic process [GO:0010411 biological_process] (1)	Xyloglucan endotransglucosylase/hydrolase [IPR016455] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Glycoside hydrolase family 16 [IPR000757] (1); Xyloglucan endo-transglycosylase, C-terminal [IPR010713] (1)	scaffold_8_mRNA_2704.1	-	-
GF0032600	1	0	0	Ribonuclease H-like superfamily protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_8_mRNA_2703.1	-	-
GF0032599	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_270.1	-	-
GF0032598	1	0	0	Hypothetical protein (1)		Transposase, MuDR, plant [IPR004332] (1)	scaffold_8_mRNA_2696.1	-	-
GF0032597	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2688.1	-	-
GF0032596	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2675.1	-	-
GF0032595	1	0	0	Lysosomal Pro-Xaa carboxypeptidase (1)	proteolysis [GO:0006508 biological_process] (1); serine-type peptidase activity [GO:0008236 molecular_function] (1)	Peptidase S28 [IPR008758] (1)	scaffold_8_mRNA_2666.1	-	-
GF0032594	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2663.1	-	-
GF0032593	1	0	0	Lysosomal Pro-Xaa carboxypeptidase (1)			scaffold_8_mRNA_2661.1	-	-
GF0032592	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2655.1	-	-
GF0032591	1	0	0	Lysosomal Pro-Xaa carboxypeptidase (1)	proteolysis [GO:0006508 biological_process] (1); serine-type peptidase activity [GO:0008236 molecular_function] (1)	Alpha/Beta hydrolase fold [IPR029058] (1); Peptidase S28 [IPR008758] (1)	scaffold_8_mRNA_2653.1	-	-
GF0032590	1	0	0	Argonaute 1 (1)	protein binding [GO:0005515 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Argonaute, linker 1 domain [IPR014811] (1); Ribonuclease H-like domain [IPR012337] (1); Zinc finger, PMZ-type [IPR006564] (1); Argonaute linker 2 domain [IPR032472] (1); Zinc finger, SWIM-type [IPR007527] (1); PAZ domain [IPR003100] (1); Piwi domain [IPR003165] (1); Protein argonaute, N-terminal [IPR032474] (1)	scaffold_8_mRNA_2648.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0032589	1	0	0	Argonaute 1 (1)	protein binding [GO:0005515 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Piwi domain [IPR003165] (1); Protein argonaute, N-terminal [IPR032474] (1); Argonaute linker 2 domain [IPR032472] (1); Argonaute, linker 1 domain [IPR014811] (1); Ribonuclease H-like domain [IPR012337] (1); Protein argonaute, Mid domain [IPR032473] (1); PAZ domain [IPR003100] (1)	scaffold_8_mRNA_2642.1	-	-
GF0032588	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2633.1	-	-
GF0032587	1	0	0	Cysteine-rich RLK 34, putative isoform 1 (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1); chitin binding [GO:0008061 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Chitinase II [IPR011583] (1); Protein kinase-like domain [IPR011009] (1); Glycoside hydrolase superfamily [IPR017853] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Chitinase insertion domain [IPR029070] (1); Glycoside hydrolase family 18, catalytic domain [IPR001223] (1)	scaffold_8_mRNA_2631.1	-	-
GF0032586	1	0	0	DUF3128 family protein (1)		Protein of unknown function DUF3128 [IPR021475] (1)	scaffold_8_mRNA_2616.1	-	-
GF0032585	1	0	0	Hypothetical protein (1)	terpene synthase activity [GO:0010333 molecular_function] (1); lyase activity [GO:0016829 molecular_function] (1); magnesium ion binding [GO:0000287 molecular_function] (1)	Terpene synthase, metal-binding domain [IPR005630] (1); Isoprenoid synthase domain [IPR008949] (1)	scaffold_8_mRNA_2607.1	-	-
GF0032584	1	0	0	Putative muDR family transposase-like (1)	transposase activity [GO:0004803 molecular_function] (1); transposition, DNA-mediated [GO:0006313 biological_process] (1); zinc ion binding [GO:0008270 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	Transposase, mutator type [IPR001207] (1); Zinc finger, PMZ-type [IPR006564] (1); Zinc finger, SWIM-type [IPR007527] (1)	scaffold_8_mRNA_2601.1	-	-
GF0032583	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2588.1	-	-
GF0032582	1	0	0	Non-LTR retroelement reverse transcriptase-like (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_8_mRNA_2582.1	-	-
GF0032581	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2580.1	-	-
GF0032580	1	0	0	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)	scaffold_8_mRNA_2578.1	-	-
GF0032579	1	0	0	Unspecific monooxygenase (1)	heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450 [IPR001128] (1)	scaffold_8_mRNA_2554.1	-	-
GF0032578	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2544.1	-	-
GF0032577	1	0	0	Fatty acyl-CoA reductase 3 (1)	fatty-acyl-CoA reductase (alcohol-forming) activity [GO:0080019 molecular_function] (1)	Male sterility, NAD-binding [IPR013120] (1); Fatty acyl-CoA reductase [IPR026055] (1)	scaffold_8_mRNA_2542.1	-	-
GF0032576	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_8_mRNA_2540.1	-	-
GF0032575	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2539.1	-	-
GF0032574	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2538.1	-	-
GF0032573	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2533.1	-	-
GF0032572	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2520.1	-	-
GF0032571	1	0	0	Myricetin O-methyltransferase (1)	O-methyltransferase activity [GO:0008171 molecular_function] (1)	O-methyltransferase, family 2 [IPR001077] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1)	scaffold_8_mRNA_2515.1	-	-
GF0032570	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2514.1	-	-
GF0032569	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_8_mRNA_2513.1	-	-
GF0032568	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2511.1	-	-
GF0032567	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2510.1	-	-
GF0032566	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2505.1	-	-
GF0032565	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2503.1	-	-
GF0032564	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_8_mRNA_2502.1	-	-
GF0032563	1	0	0	Putative muDR family transposase-like (1)	zinc ion binding [GO:0008270 molecular_function] (1)	MULE transposase domain [IPR018289] (1); Zinc finger, PMZ-type [IPR006564] (1); Zinc finger, SWIM-type [IPR007527] (1)	scaffold_8_mRNA_2500.1	-	-
GF0032562	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2499.1	-	-
GF0032561	1	0	0	Hypothetical protein (1)	root development [GO:0048364 biological_process] (1)	C-terminally encoded peptide [IPR033250] (1)	scaffold_8_mRNA_2494.1	-	-
GF0032560	1	0	0	Branched-chain-amino-acid transaminase (1)	branched-chain-amino-acid transaminase activity [GO:0004084 molecular_function] (1); branched-chain amino acid metabolic process [GO:0009081 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Branched-chain amino acid aminotransferase II [IPR005786] (1); Aminotransferase class IV [IPR001544] (1); Aminotransferase, class IV, conserved site [IPR018300] (1); Branched-chain aminotransferase [IPR033939] (1)	scaffold_8_mRNA_249.1	-	-
GF0032559	1	0	0	Hypothetical protein (1)	viral process [GO:0016032 biological_process] (1)	Retroviral nucleocapsid protein Gag [IPR000721] (1); Retrovirus capsid, C-terminal [IPR008916] (1)	scaffold_8_mRNA_2489.1	-	-
GF0032558	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2477.1	-	-
GF0032557	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_8_mRNA_2476.1	-	-
GF0032556	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2469.1	-	-
GF0032555	1	0	0	Hypothetical protein (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Retroviral aspartyl protease [IPR013242] (1); Aspartic peptidase domain [IPR021109] (1); Aspartic peptidase, active site [IPR001969] (1)	scaffold_8_mRNA_2460.1	-	-
GF0032554	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2459.1	-	-
GF0032553	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2448.1	-	-
GF0032552	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2444.1	-	-
GF0032551	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2443.1	-	-
GF0032550	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_8_mRNA_2442.1	-	-
GF0032549	1	0	0	LRR receptor-like serine/threonine-protein kinase GSO1 (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1)	scaffold_8_mRNA_2436.1	-	-
GF0032548	1	0	0	Dcp1-like decapping family 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)	scaffold_8_mRNA_2433.1	-	-
GF0032547	1	0	0	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)	scaffold_8_mRNA_2426.1	-	-
GF0032546	1	0	0	Hypothetical protein (1)		Leucine rich repeat 4 [IPR025875] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_8_mRNA_2422.1	-	-
GF0032545	1	0	0	NF-kappa-B inhibitor-like protein 2 isoform 1 (1)		FAM192A/Fyv6, N-terminal [IPR019331] (1)	scaffold_8_mRNA_2421.1	-	-
GF0032544	1	0	0	Protein phosphatase 1 regulatory subunit SDS22, putative (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Pectin lyase fold/virulence factor [IPR011050] (1); Pectin lyase fold [IPR012334] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_8_mRNA_2420.1	-	-
GF0032543	1	0	0	Probable F-box protein At1g60180 (1)	protein binding [GO:0005515 molecular_function] (1)	F-box domain [IPR001810] (1)	scaffold_8_mRNA_2418.1	-	-
GF0032542	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2417.1	-	-
GF0032541	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2413.1	-	-
GF0032540	1	0	0	Probable F-box protein At1g60180 (1)	protein binding [GO:0005515 molecular_function] (1)	F-box domain [IPR001810] (1)	scaffold_8_mRNA_2411.1	-	-
GF0032539	1	0	0	Disease resistance family protein / LRR family protein, putative (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1)	scaffold_8_mRNA_2409.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0032538	1	0	0	Polygalacturonase (1)	polygalacturonase activity [GO:0004650 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1)	Parallel beta-helix repeat [IPR006626] (1); Glycoside hydrolase, family 28 [IPR000743] (1); Pectin lyase fold/virulence factor [IPR011050] (1); Pectin lyase fold [IPR012334] (1)	scaffold_8_mRNA_2406.1	-	-
GF0032537	1	0	0	Disease resistance family protein / LRR family protein, putative (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)	scaffold_8_mRNA_2405.1	-	-
GF0032536	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_8_mRNA_2395.1	-	-
GF0032535	1	0	0	Short chain alcohol dehydrogenase, putative (1)	oxidoreductase activity [GO:0016491 molecular_function] (1)	NAD(P)-binding domain [IPR016040] (1); Short-chain dehydrogenase/reductase, conserved site [IPR020904] (1); Short-chain dehydrogenase/reductase SDR [IPR002347] (1)	scaffold_8_mRNA_2393.1	-	-
GF0032534	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2391.1	-	-
GF0032533	1	0	0	RNA-binding protein pno1 (1)	nucleic acid binding [GO:0003676 molecular_function] (1); RNA binding [GO:0003723 molecular_function] (1)	K Homology domain [IPR004087] (1); K Homology domain, type 1 [IPR004088] (1)	scaffold_8_mRNA_2389.1	-	-
GF0032532	1	0	0	Monosacharide transport protein (1)			scaffold_8_mRNA_238.1	-	-
GF0032531	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, PMZ-type [IPR006564] (1); Zinc finger, SWIM-type [IPR007527] (1)	scaffold_8_mRNA_2378.1	-	-
GF0032530	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_236.1	-	-
GF0032529	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2355.1	-	-
GF0032528	1	0	0	Hypothetical protein (1)	nucleus [GO:0005634 cellular_component] (1); ribosome biogenesis [GO:0042254 biological_process] (1)	AARP2CN [IPR012948] (1)	scaffold_8_mRNA_2354.1	-	-
GF0032527	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2353.1	-	-
GF0032526	1	0	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_8_mRNA_2350.1	-	-
GF0032525	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2349.1	-	-
GF0032524	1	0	0	LRR receptor-like kinase family protein (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Protein kinase-like domain [IPR011009] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Tyrosine-protein kinase, active site [IPR008266] (1); Leucine-rich repeat [IPR001611] (1)	scaffold_8_mRNA_2347.1	-	-
GF0032523	1	0	0	Putative non-LTR retroelement reverse transcriptase (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_8_mRNA_2345.1	-	-
GF0032522	1	0	0	Polynucleotidyl transferase, Ribonuclease H fold (1)			scaffold_8_mRNA_2344.1	-	-
GF0032521	1	0	0	Hypothetical protein (1)	metal ion binding [GO:0046872 molecular_function] (1); superoxide metabolic process [GO:0006801 biological_process] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Superoxide dismutase, copper/zinc binding domain [IPR001424] (1)	scaffold_8_mRNA_2340.1	-	-
GF0032520	1	0	0	Pathogenesis-related maize seed protein (1)	extracellular region [GO:0005576 cellular_component] (1)	Cysteine-rich secretory protein, allergen V5/Tpx-1-related [IPR001283] (1); CAP domain [IPR014044] (1); Allergen V5/Tpx-1-related, conserved site [IPR018244] (1); Pathogenesis-related protein 1-like, SCP domain [IPR034111] (1)	scaffold_8_mRNA_234.1	-	-
GF0032519	1	0	0	Squalene monooxygenase (1)	extracellular region [GO:0005576 cellular_component] (1); integral component of membrane [GO:0016021 cellular_component] (1); squalene monooxygenase activity [GO:0004506 molecular_function] (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)	Allergen V5/Tpx-1-related, conserved site [IPR018244] (1); Squalene epoxidase [IPR013698] (1); FAD/NAD(P)-binding domain [IPR023753] (1); CAP domain [IPR014044] (1)	scaffold_8_mRNA_233.1	-	-
GF0032518	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2328.1	-	-
GF0032517	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2324.1	-	-
GF0032516	1	0	0	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)	scaffold_8_mRNA_2318.1	-	-
GF0032515	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2314.1	-	-
GF0032514	1	0	0	Egg cell-secreted protein 1.4 (1)		Prolamin-like domain [IPR008502] (1)	scaffold_8_mRNA_2310.1	-	-
GF0032513	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_231.1	-	-
GF0032512	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2300.1	-	-
GF0032511	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2299.1	-	-
GF0032510	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2297.1	-	-
GF0032509	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2293.1	-	-
GF0032508	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2290.1	-	-
GF0032507	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2288.1	-	-
GF0032506	1	0	0	Hypothetical protein (1)		Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_8_mRNA_2280.1	-	-
GF0032505	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2277.1	-	-
GF0032504	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2269.1	-	-
GF0032503	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2265.1	-	-
GF0032502	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_8_mRNA_2264.1	-	-
GF0032501	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2259.1	-	-
GF0032500	1	0	0	RNA-directed DNA polymerase (Reverse transcriptase) (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Reverse transcriptase domain [IPR000477] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_8_mRNA_2254.1	-	-
GF0032499	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2246.1	-	-
GF0032498	1	0	0	Hypothetical protein (1)		Alpha crystallin/Hsp20 domain [IPR002068] (1); HSP20-like chaperone [IPR008978] (1); Small heat shock protein HSP20 [IPR031107] (1)	scaffold_8_mRNA_2235.1	-	-
GF0032497	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2233.1	-	-
GF0032496	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2232.1	-	-
GF0032495	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2229.1	-	-
GF0032494	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2225.1	-	-
GF0032493	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2216.1	-	-
GF0032492	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2213.1	-	-
GF0032491	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2212.1	-	-
GF0032490	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2207.1	-	-
GF0032489	1	0	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	scaffold_8_mRNA_2199.1	-	-
GF0032488	1	0	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_8_mRNA_2195.1	-	-
GF0032487	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2190.1	-	-
GF0032486	1	0	0	Non-LTR retroelement reverse transcriptase-like (1)	nucleic acid binding [GO:0003676 molecular_function] (1); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1)	TB2/DP1/HVA22-related protein [IPR004345] (1); Ribonuclease H domain [IPR002156] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_8_mRNA_2183.1	-	-
GF0032485	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2179.1	-	-
GF0032484	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Retrotransposon gag domain [IPR005162] (1)	scaffold_8_mRNA_2177.1	-	-
GF0032483	1	0	0	Monosacharide transport protein (1)			scaffold_8_mRNA_2175.1	-	-
GF0032482	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2174.1	-	-
GF0032481	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2170.1	-	-
GF0032480	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2168.1	-	-
GF0032479	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2167.1	-	-
GF0032478	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2157.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0032477	1	0	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Zinc finger C2H2-type [IPR013087] (1); Zinc finger, BED-type [IPR003656] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	scaffold_8_mRNA_2156.1	-	-
GF0032476	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2143.1	-	-
GF0032475	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2136.1	-	-
GF0032474	1	0	0	Monosacharide transport protein (1)			scaffold_8_mRNA_2126.1	-	-
GF0032473	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2125.1	-	-
GF0032472	1	0	0	Monosacharide transport protein (1)			scaffold_8_mRNA_2122.1	-	-
GF0032471	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2119.1	-	-
GF0032470	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2118.1	-	-
GF0032469	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_8_mRNA_2117.1	-	-
GF0032468	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2113.1	-	-
GF0032467	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2109.1	-	-
GF0032466	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_8_mRNA_2108.1	-	-
GF0032465	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2107.1	-	-
GF0032464	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2106.1	-	-
GF0032463	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2103.1	-	-
GF0032462	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_8_mRNA_2102.1	-	-
GF0032461	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2099.1	-	-
GF0032460	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2097.1	-	-
GF0032459	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2092.1	-	-
GF0032458	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2091.1	-	-
GF0032457	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF1985 [IPR015410] (1)	scaffold_8_mRNA_209.1	-	-
GF0032456	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_8_mRNA_2087.1	-	-
GF0032455	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2086.1	-	-
GF0032454	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2084.1	-	-
GF0032453	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2073.1	-	-
GF0032452	1	0	0	BED zinc finger,hAT family dimerization domain (1)	nucleic acid binding [GO:0003676 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Zinc finger C2H2-type [IPR013087] (1); Zinc finger, BED-type [IPR003656] (1)	scaffold_8_mRNA_2072.1	-	-
GF0032451	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2071.1	-	-
GF0032450	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2070.1	-	-
GF0032449	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2069.1	-	-
GF0032448	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2066.1	-	-
GF0032447	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2062.1	-	-
GF0032446	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2059.1	-	-
GF0032445	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2058.1	-	-
GF0032444	1	0	0	Transposable element protein, putative, (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_8_mRNA_2054.1	-	-
GF0032443	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_8_mRNA_2053.1	-	-
GF0032442	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_8_mRNA_2052.1	-	-
GF0032441	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2051.1	-	-
GF0032440	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2048.1	-	-
GF0032439	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_8_mRNA_2047.1	-	-
GF0032438	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2046.1	-	-
GF0032437	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2045.1	-	-
GF0032436	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2042.1	-	-
GF0032435	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2030.1	-	-
GF0032434	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2029.1	-	-
GF0032433	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			scaffold_8_mRNA_2027.1	-	-
GF0032432	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2026.1	-	-
GF0032431	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2024.1	-	-
GF0032430	1	0	0	Integrase (1)		Aspartic peptidase domain [IPR021109] (1); LOG family [IPR031100] (1)	scaffold_8_mRNA_2022.1	-	-
GF0032429	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_8_mRNA_2019.1	-	-
GF0032428	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2018.1	-	-
GF0032427	1	0	0	Retrotransposon gag protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_8_mRNA_2017.1	-	-
GF0032426	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_201.1	-	-
GF0032425	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2009.1	-	-
GF0032424	1	0	0	Caffeic acid 3-O-methyltransferase (1)	O-methyltransferase activity [GO:0008171 molecular_function] (1); methyltransferase activity [GO:0008168 molecular_function] (1)	S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); O-methyltransferase, family 2 [IPR001077] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); O-methyltransferase COMT-type [IPR016461] (1)	scaffold_8_mRNA_2006.1	-	-
GF0032423	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_2005.1	-	-
GF0032422	1	0	0	Chromo domain protein (1)		Chromo domain-like [IPR016197] (1); Chromo domain [IPR023780] (1); Retrotransposon gag domain [IPR005162] (1)	scaffold_8_mRNA_2004.1	-	-
GF0032421	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1999.1	-	-
GF0032420	1	0	0	Hypothetical protein (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Retroviral aspartyl protease [IPR013242] (1); Aspartic peptidase domain [IPR021109] (1); Aspartic peptidase, active site [IPR001969] (1)	scaffold_8_mRNA_1996.1	-	-
GF0032419	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			scaffold_8_mRNA_1991.1	-	-
GF0032418	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_199.1	-	-
GF0032417	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1987.1	-	-
GF0032416	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1983.1	-	-
GF0032415	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1982.1	-	-
GF0032414	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1981.1	-	-
GF0032413	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1979.1	-	-
GF0032412	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1975.1	-	-
GF0032411	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1971.1	-	-
GF0032410	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1965.1	-	-
GF0032409	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1961.1	-	-
GF0032408	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1960.1	-	-
GF0032407	1	0	0	Retrotransposon protein, putative, Ty3-gypsy subclass (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_8_mRNA_1956.1	-	-
GF0032406	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1954.1	-	-
GF0032405	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1953.1	-	-
GF0032404	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1951.1	-	-
GF0032403	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_8_mRNA_1950.1	-	-
GF0032402	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1946.1	-	-
GF0032401	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1943.1	-	-
GF0032400	1	0	0	Hypothetical protein (1)		Retroviral aspartyl protease [IPR013242] (1); Aspartic peptidase domain [IPR021109] (1)	scaffold_8_mRNA_1939.1	-	-
GF0032399	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1938.1	-	-
GF0032398	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1937.1	-	-
GF0032397	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1936.1	-	-
GF0032396	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1935.1	-	-
GF0032395	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1931.1	-	-
GF0032394	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_8_mRNA_1928.1	-	-
GF0032393	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1927.1	-	-
GF0032392	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_8_mRNA_1926.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0032391	1	0	0	Probable xyloglucan endotransglucosylase/hydrolase protein B (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, active site [IPR008263] (1); Protein of unknown function DUF241, plant [IPR004320] (1); Xyloglucan endo-transglycosylase, C-terminal [IPR010713] (1); Glycoside hydrolase family 16 [IPR000757] (1)	scaffold_8_mRNA_1924.1	-	-
GF0032390	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1923.1	-	-
GF0032389	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Retropepsins [IPR018061] (1); Aspartic peptidase, active site [IPR001969] (1); Aspartic peptidase domain [IPR021109] (1); Zinc finger, CCHC-type [IPR001878] (1)	scaffold_8_mRNA_1922.1	-	-
GF0032388	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1920.1	-	-
GF0032387	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1919.1	-	-
GF0032386	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_8_mRNA_1917.1	-	-
GF0032385	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1916.1	-	-
GF0032384	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_8_mRNA_1915.1	-	-
GF0032383	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1912.1	-	-
GF0032382	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1909.1	-	-
GF0032381	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_8_mRNA_1908.1	-	-
GF0032380	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1902.1	-	-
GF0032379	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_8_mRNA_1901.1	-	-
GF0032378	1	0	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Carlavirus nucleic acid-binding protein [IPR002568] (1)	scaffold_8_mRNA_1900.1	-	-
GF0032377	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_8_mRNA_1898.1	-	-
GF0032376	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1897.1	-	-
GF0032375	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1896.1	-	-
GF0032374	1	0	0	Retrotransposon gag protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_8_mRNA_1895.1	-	-
GF0032373	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1893.1	-	-
GF0032372	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1892.1	-	-
GF0032371	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_8_mRNA_1889.1	-	-
GF0032370	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1887.1	-	-
GF0032369	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1881.1	-	-
GF0032368	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1879.1	-	-
GF0032367	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_8_mRNA_1872.1	-	-
GF0032366	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1871.1	-	-
GF0032365	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1869.1	-	-
GF0032364	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_8_mRNA_1868.1	-	-
GF0032363	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1866.1	-	-
GF0032362	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1865.1	-	-
GF0032361	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1864.1	-	-
GF0032360	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_8_mRNA_1863.1	-	-
GF0032359	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1861.1	-	-
GF0032358	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1859.1	-	-
GF0032357	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1858.1	-	-
GF0032356	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); DNA integration [GO:0015074 biological_process] (1)	Integrase, catalytic core [IPR001584] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_8_mRNA_1855.1	-	-
GF0032355	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1846.1	-	-
GF0032354	1	0	0	Hypothetical protein (1)		Transposase-associated domain [IPR029480] (1)	scaffold_8_mRNA_1843.1	-	-
GF0032353	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1842.1	-	-
GF0032352	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1841.1	-	-
GF0032351	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_8_mRNA_1839.1	-	-
GF0032350	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_8_mRNA_1837.1	-	-
GF0032349	1	0	0	Hypothetical protein (1)		EF-Hand 1, calcium-binding site [IPR018247] (1)	scaffold_8_mRNA_1835.1	-	-
GF0032348	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1829.1	-	-
GF0032347	1	0	0	Tobamovirus multiplication 1 (1)		Domain of unknown function DUF1084 [IPR009457] (1)	scaffold_8_mRNA_1827.1	-	-
GF0032346	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_8_mRNA_1826.1	-	-
GF0032345	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_8_mRNA_1824.1	-	-
GF0032344	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1822.1	-	-
GF0032343	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1820.1	-	-
GF0032342	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1817.1	-	-
GF0032341	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1812.1	-	-
GF0032340	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1811.1	-	-
GF0032339	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1810.1	-	-
GF0032338	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_8_mRNA_1807.1	-	-
GF0032337	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1806.1	-	-
GF0032336	1	0	0	RNA-directed DNA polymerase , related (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	scaffold_8_mRNA_1803.1	-	-
GF0032335	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1801.1	-	-
GF0032334	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Tetratricopeptide-like helical domain [IPR011990] (1)	scaffold_8_mRNA_1794.1	-	-
GF0032333	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_8_mRNA_1791.1	-	-
GF0032332	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_8_mRNA_1790.1	-	-
GF0032331	1	0	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Carlavirus nucleic acid-binding protein [IPR002568] (1)	scaffold_8_mRNA_1789.1	-	-
GF0032330	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1784.1	-	-
GF0032329	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1777.1	-	-
GF0032328	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_8_mRNA_1772.1	-	-
GF0032327	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_8_mRNA_1771.1	-	-
GF0032326	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1770.1	-	-
GF0032325	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_8_mRNA_1769.1	-	-
GF0032324	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1763.1	-	-
GF0032323	1	0	0	Retrotransposon gag protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_8_mRNA_1760.1	-	-
GF0032322	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1758.1	-	-
GF0032321	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	Zinc finger, SWIM-type [IPR007527] (1); FHY3/FAR1 family [IPR031052] (1)	scaffold_8_mRNA_1757.1	-	-
GF0032320	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1755.1	-	-
GF0032319	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1754.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0032318	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1751.1	-	-
GF0032317	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_8_mRNA_1740.1	-	-
GF0032316	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1739.1	-	-
GF0032315	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1738.1	-	-
GF0032314	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1736.1	-	-
GF0032313	1	0	0	ABC transporter G family member 11 (1)	ATP binding [GO:0005524 molecular_function] (1); ATPase activity [GO:0016887 molecular_function] (1); membrane [GO:0016020 cellular_component] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); ABC transporter-like [IPR003439] (1); ABC-2 type transporter [IPR013525] (1); AAA+ ATPase domain [IPR003593] (1); ABC transporter, conserved site [IPR017871] (1)	scaffold_8_mRNA_1735.1	-	-
GF0032312	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1734.1	-	-
GF0032311	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_8_mRNA_1733.1	-	-
GF0032310	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1732.1	-	-
GF0032309	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_8_mRNA_1731.1	-	-
GF0032308	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1730.1	-	-
GF0032307	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1729.1	-	-
GF0032306	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_8_mRNA_1728.1	-	-
GF0032305	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1727.1	-	-
GF0032304	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1724.1	-	-
GF0032303	1	0	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_8_mRNA_1720.1	-	-
GF0032302	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1716.1	-	-
GF0032301	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1715.1	-	-
GF0032300	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1711.1	-	-
GF0032299	1	0	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_8_mRNA_1708.1	-	-
GF0032298	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1706.1	-	-
GF0032297	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_8_mRNA_1705.1	-	-
GF0032296	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1703.1	-	-
GF0032295	1	0	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1)	Aspartic peptidase, active site [IPR001969] (1)	scaffold_8_mRNA_1702.1	-	-
GF0032294	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1701.1	-	-
GF0032293	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1700.1	-	-
GF0032292	1	0	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Carlavirus nucleic acid-binding protein [IPR002568] (1); Retrotransposon gag domain [IPR005162] (1)	scaffold_8_mRNA_1698.1	-	-
GF0032291	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, PMZ-type [IPR006564] (1); Zinc finger, SWIM-type [IPR007527] (1)	scaffold_8_mRNA_1696.1	-	-
GF0032290	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1695.1	-	-
GF0032289	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_8_mRNA_1694.1	-	-
GF0032288	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1692.1	-	-
GF0032287	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_8_mRNA_1690.1	-	-
GF0032286	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_8_mRNA_1689.1	-	-
GF0032285	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1685.1	-	-
GF0032284	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_8_mRNA_1683.1	-	-
GF0032283	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_8_mRNA_1681.1	-	-
GF0032282	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_8_mRNA_1680.1	-	-
GF0032281	1	0	0	BED zinc finger,hAT family dimerization domain (1)	nucleic acid binding [GO:0003676 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); hAT-like transposase, RNase-H fold [IPR025525] (1)	scaffold_8_mRNA_1674.1	-	-
GF0032280	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1672.1	-	-
GF0032279	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1671.1	-	-
GF0032278	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1670.1	-	-
GF0032277	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1669.1	-	-
GF0032276	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_8_mRNA_1666.1	-	-
GF0032275	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1665.1	-	-
GF0032274	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1664.1	-	-
GF0032273	1	0	0	Gag protease polyprotein, putative (1)		Aspartic peptidase domain [IPR021109] (1); Retroviral aspartyl protease [IPR013242] (1)	scaffold_8_mRNA_1663.1	-	-
GF0032272	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1662.1	-	-
GF0032271	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_8_mRNA_1661.1	-	-
GF0032270	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_8_mRNA_1660.1	-	-
GF0032269	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4219 [IPR025314] (1)	scaffold_8_mRNA_1658.1	-	-
GF0032268	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_8_mRNA_1656.1	-	-
GF0032267	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1654.1	-	-
GF0032266	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1653.1	-	-
GF0032265	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1652.1	-	-
GF0032264	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1649.1	-	-
GF0032263	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1648.1	-	-
GF0032262	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1647.1	-	-
GF0032261	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1645.1	-	-
GF0032260	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1644.1	-	-
GF0032259	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1640.1	-	-
GF0032258	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1638.1	-	-
GF0032257	1	0	0	Hypothetical protein (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Retropepsins [IPR018061] (1); Peptidase A2A, retrovirus, catalytic [IPR001995] (1); Aspartic peptidase domain [IPR021109] (1); Zinc finger, CCHC-type [IPR001878] (1)	scaffold_8_mRNA_1634.1	-	-
GF0032256	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_8_mRNA_1633.1	-	-
GF0032255	1	0	0	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); Aspartic peptidase domain [IPR021109] (1)	scaffold_8_mRNA_1632.1	-	-
GF0032254	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1630.1	-	-
GF0032253	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_8_mRNA_1629.1	-	-
GF0032252	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1628.1	-	-
GF0032251	1	0	0	Metacaspase 1 isoform 1 (1)		Metacaspase type I, plant [IPR033180] (1); Caspase-like domain [IPR029030] (1)	scaffold_8_mRNA_1624.1	-	-
GF0032250	1	0	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); protein binding [GO:0005515 molecular_function] (1)	WD40-repeat-containing domain [IPR017986] (1); WD40 repeat [IPR001680] (1); Topless family [IPR027728] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_8_mRNA_1621.1	-	-
GF0032249	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1620.1	-	-
GF0032248	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1619.1	-	-
GF0032247	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1609.1	-	-
GF0032246	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1603.1	-	-
GF0032245	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1602.1	-	-
GF0032244	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1600.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0032243	1	0	0	Putative anion transporter 5 (1)	transmembrane transport [GO:0055085 biological_process] (1); integral component of membrane [GO:0016021 cellular_component] (1)	Major facilitator superfamily domain [IPR020846] (1); Major facilitator superfamily [IPR011701] (1)	scaffold_8_mRNA_16.1	-	-
GF0032242	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_8_mRNA_1599.1	-	-
GF0032241	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1598.1	-	-
GF0032240	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1597.1	-	-
GF0032239	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1592.1	-	-
GF0032238	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1588.1	-	-
GF0032237	1	0	0	Hypothetical protein (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Aspartic peptidase domain [IPR021109] (1); Zinc finger, CCHC-type [IPR001878] (1); Retropepsins [IPR018061] (1); Reverse transcriptase domain [IPR000477] (1); Peptidase A2A, retrovirus, catalytic [IPR001995] (1)	scaffold_8_mRNA_1586.1	-	-
GF0032236	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1584.1	-	-
GF0032235	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1583.1	-	-
GF0032234	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1582.1	-	-
GF0032233	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_8_mRNA_1581.1	-	-
GF0032232	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1580.1	-	-
GF0032231	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1577.1	-	-
GF0032230	1	0	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_8_mRNA_1575.1	-	-
GF0032229	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1574.1	-	-
GF0032228	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1573.1	-	-
GF0032227	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1567.1	-	-
GF0032226	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1566.1	-	-
GF0032225	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1565.1	-	-
GF0032224	1	0	0	LRR receptor-like serine/threonine-protein kinase GSO1 (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	scaffold_8_mRNA_1560.1	-	-
GF0032223	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1559.1	-	-
GF0032222	1	0	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	scaffold_8_mRNA_1556.1	-	-
GF0032221	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Transposase, MuDR, plant [IPR004332] (1); MULE transposase domain [IPR018289] (1)	scaffold_8_mRNA_1555.1	-	-
GF0032220	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1553.1	-	-
GF0032219	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1551.1	-	-
GF0032218	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1549.1	-	-
GF0032217	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1544.1	-	-
GF0032216	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1539.1	-	-
GF0032215	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1538.1	-	-
GF0032214	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1536.1	-	-
GF0032213	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1534.1	-	-
GF0032212	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1528.1	-	-
GF0032211	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1527.1	-	-
GF0032210	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1526.1	-	-
GF0032209	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1525.1	-	-
GF0032208	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1524.1	-	-
GF0032207	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1520.1	-	-
GF0032206	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1519.1	-	-
GF0032205	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1518.1	-	-
GF0032204	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1517.1	-	-
GF0032203	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1511.1	-	-
GF0032202	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1); LOG family [IPR031100] (1)	scaffold_8_mRNA_1509.1	-	-
GF0032201	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1507.1	-	-
GF0032200	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1503.1	-	-
GF0032199	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1498.1	-	-
GF0032198	1	0	0	Transposon protein, putative, unclassified, expressed (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1); MULE transposase domain [IPR018289] (1)	scaffold_8_mRNA_1493.1	-	-
GF0032197	1	0	0	NBS type disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_8_mRNA_1487.1	-	-
GF0032196	1	0	0	Sugar carrier protein C (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)	scaffold_8_mRNA_1482.1	-	-
GF0032195	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1478.1	-	-
GF0032194	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_8_mRNA_1472.1	-	-
GF0032193	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1471.1	-	-
GF0032192	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1469.1	-	-
GF0032191	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_8_mRNA_1468.1	-	-
GF0032190	1	0	0	Zinc knuckle family protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Domain of unknown function DUF4219 [IPR025314] (1)	scaffold_8_mRNA_1467.1	-	-
GF0032189	1	0	0	RNA-directed DNA polymerase (1)	nucleic acid binding [GO:0003676 molecular_function] (1); DNA integration [GO:0015074 biological_process] (1); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1)	Ribonuclease H domain [IPR002156] (1); Ribonuclease H-like domain [IPR012337] (1); Integrase, catalytic core [IPR001584] (1)	scaffold_8_mRNA_1466.1	-	-
GF0032188	1	0	0	Monosacharide transport protein (1)			scaffold_8_mRNA_1465.1	-	-
GF0032187	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1463.1	-	-
GF0032186	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1461.1	-	-
GF0032185	1	0	0	Hypothetical protein (1)		NADP-dependent oxidoreductase domain [IPR023210] (1); Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	scaffold_8_mRNA_1460.1	-	-
GF0032184	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1456.1	-	-
GF0032183	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1435.1	-	-
GF0032182	1	0	0	Naringenin-chalcone synthase (1)	metabolic process [GO:0008152 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1)	Chalcone/stilbene synthase, N-terminal [IPR001099] (1); Thiolase-like [IPR016039] (1); Chalcone/stilbene synthase, C-terminal [IPR012328] (1)	scaffold_8_mRNA_1432.1	-	-
GF0032181	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1430.1	-	-
GF0032180	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1429.1	-	-
GF0032179	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1424.1	-	-
GF0032178	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1422.1	-	-
GF0032177	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_8_mRNA_1416.1	-	-
GF0032176	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1415.1	-	-
GF0032175	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1414.1	-	-
GF0032174	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1413.1	-	-
GF0032173	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1411.1	-	-
GF0032172	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1410.1	-	-
GF0032171	1	0	0	Hypothetical protein (1)		Arabidopsis retrotransposon Orf1 [IPR004312] (1)	scaffold_8_mRNA_1403.1	-	-
GF0032170	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_8_mRNA_1402.1	-	-
GF0032169	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1401.1	-	-
GF0032168	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1400.1	-	-
GF0032167	1	0	0	Hypothetical protein (1)		Transposon, En/Spm-like [IPR004242] (1)	scaffold_8_mRNA_1398.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0032166	1	0	0	Hypothetical protein (1)	iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1)	Cytochrome P450 [IPR001128] (1); Cytochrome P450, E-class, group I [IPR002401] (1)	scaffold_8_mRNA_1395.1	-	-
GF0032165	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_8_mRNA_1394.1	-	-
GF0032164	1	0	0	Hypothetical protein (1)	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1)	Cytochrome P450 [IPR001128] (1)	scaffold_8_mRNA_1393.1	-	-
GF0032163	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_8_mRNA_1391.1	-	-
GF0032162	1	0	0	Transposable element protein, putative, (1)		Aspartic peptidase domain [IPR021109] (1); Retrotransposon gag domain [IPR005162] (1)	scaffold_8_mRNA_1390.1	-	-
GF0032161	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1388.1	-	-
GF0032160	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1386.1	-	-
GF0032159	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); DNA integration [GO:0015074 biological_process] (1)	Ribonuclease H-like domain [IPR012337] (1); Integrase, catalytic core [IPR001584] (1)	scaffold_8_mRNA_1383.1	-	-
GF0032158	1	0	0	Spc97/Spc98 family of spindle pole body (SBP) component, putative (1)	microtubule organizing center [GO:0005815 cellular_component] (1); gamma-tubulin binding [GO:0043015 molecular_function] (1); microtubule nucleation [GO:0007020 biological_process] (1); microtubule cytoskeleton organization [GO:0000226 biological_process] (1); spindle pole [GO:0000922 cellular_component] (1)	Gamma-tubulin complex component protein [IPR007259] (1)	scaffold_8_mRNA_138.1	-	-
GF0032157	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1378.1	-	-
GF0032156	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1377.1	-	-
GF0032155	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1376.1	-	-
GF0032154	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1374.1	-	-
GF0032153	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_8_mRNA_1373.1	-	-
GF0032152	1	0	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	scaffold_8_mRNA_1372.1	-	-
GF0032151	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1370.1	-	-
GF0032150	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1369.1	-	-
GF0032149	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1368.1	-	-
GF0032148	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_8_mRNA_1367.1	-	-
GF0032147	1	0	0	Hypothetical protein (1)		MULE transposase domain [IPR018289] (1)	scaffold_8_mRNA_1366.1	-	-
GF0032146	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_8_mRNA_1360.1	-	-
GF0032145	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1359.1	-	-
GF0032144	1	0	0	40S ribosomal protein S2 (1)	structural constituent of ribosome [GO:0003735 molecular_function] (1); translation [GO:0006412 biological_process] (1); small ribosomal subunit [GO:0015935 cellular_component] (1); ribosome [GO:0005840 cellular_component] (1); RNA binding [GO:0003723 molecular_function] (1)	Ribosomal protein S5 domain 2-type fold [IPR020568] (1); Ribosomal protein S5 [IPR000851] (1); Ribosomal protein S5 domain 2-type fold, subgroup [IPR014721] (1); Ribosomal protein S5, N-terminal [IPR013810] (1); Ribosomal protein S5, eukaryotic/archaeal [IPR005711] (1); Ribosomal protein S5, C-terminal [IPR005324] (1)	scaffold_8_mRNA_1350.1	-	-
GF0032143	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1349.1	-	-
GF0032142	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1342.1	-	-
GF0032141	1	0	0	Ribonuclease H-like superfamily protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_8_mRNA_1335.1	-	-
GF0032140	1	0	0	Cytochrome P450 76AD1-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); 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)	scaffold_8_mRNA_1329.1	-	-
GF0032139	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1328.1	-	-
GF0032138	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_8_mRNA_1326.1	-	-
GF0032137	1	0	0	Cytochrome P450 76AD1-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, E-class, group I [IPR002401] (1); Cytochrome P450, conserved site [IPR017972] (1); Cytochrome P450 [IPR001128] (1)	scaffold_8_mRNA_1325.1	-	-
GF0032136	1	0	0	Putative retroelement pol polyprotein (1)			scaffold_8_mRNA_1324.1	-	-
GF0032135	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1322.1	-	-
GF0032134	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1317.1	-	-
GF0032133	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1)	Ribonuclease H domain [IPR002156] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_8_mRNA_1316.1	-	-
GF0032132	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1314.1	-	-
GF0032131	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1311.1	-	-
GF0032130	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1306.1	-	-
GF0032129	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1303.1	-	-
GF0032128	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1302.1	-	-
GF0032127	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1301.1	-	-
GF0032126	1	0	0	Cytochrome P450 76AD1-like protein (1)	heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1)	Peptidase family A1 domain [IPR033121] (1); Cytochrome P450, conserved site [IPR017972] (1); Pepsin-like domain, plant [IPR034161] (1); Cytochrome P450, E-class, group I [IPR002401] (1); Aspartic peptidase domain [IPR021109] (1); Cytochrome P450 [IPR001128] (1); Xylanase inhibitor, N-terminal [IPR032861] (1); Xylanase inhibitor, C-terminal [IPR032799] (1)	scaffold_8_mRNA_1300.1	-	-
GF0032125	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_13.1	-	-
GF0032124	1	0	0	40S ribosomal protein S2 (1)	structural constituent of ribosome [GO:0003735 molecular_function] (1); translation [GO:0006412 biological_process] (1); ribosome [GO:0005840 cellular_component] (1); RNA binding [GO:0003723 molecular_function] (1); small ribosomal subunit [GO:0015935 cellular_component] (1)	Ribosomal protein S5 [IPR000851] (1); Ribosomal protein S5 domain 2-type fold [IPR020568] (1); Ribosomal protein S5, eukaryotic/archaeal [IPR005711] (1); Ribosomal protein S5, N-terminal [IPR013810] (1); Ribosomal protein S5, C-terminal [IPR005324] (1); Ribosomal protein S5 domain 2-type fold, subgroup [IPR014721] (1)	scaffold_8_mRNA_1299.1	-	-
GF0032123	1	0	0	Ac-like transposase THELMA13 (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)	scaffold_8_mRNA_1297.1	-	-
GF0032122	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_8_mRNA_1294.1	-	-
GF0032121	1	0	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Carlavirus nucleic acid-binding protein [IPR002568] (1)	scaffold_8_mRNA_1293.1	-	-
GF0032120	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1292.1	-	-
GF0032119	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1291.1	-	-
GF0032118	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1289.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0032117	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_8_mRNA_1288.1	-	-
GF0032116	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1287.1	-	-
GF0032115	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1286.1	-	-
GF0032114	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1284.1	-	-
GF0032113	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1283.1	-	-
GF0032112	1	0	0	Monosacharide transport protein (1)			scaffold_8_mRNA_1281.1	-	-
GF0032111	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1274.1	-	-
GF0032110	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1); LOG family [IPR031100] (1)	scaffold_8_mRNA_1272.1	-	-
GF0032109	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1271.1	-	-
GF0032108	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_8_mRNA_1270.1	-	-
GF0032107	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1269.1	-	-
GF0032106	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_8_mRNA_1268.1	-	-
GF0032105	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1263.1	-	-
GF0032104	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1262.1	-	-
GF0032103	1	0	0	40S ribosomal protein S15a-5 (1)	structural constituent of ribosome [GO:0003735 molecular_function] (1); translation [GO:0006412 biological_process] (1); ribosome [GO:0005840 cellular_component] (1)	Ribosomal protein S8 [IPR000630] (1)	scaffold_8_mRNA_1261.1	-	-
GF0032102	1	0	0	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, conserved site [IPR017972] (1); Cytochrome P450, E-class, group I [IPR002401] (1)	scaffold_8_mRNA_1258.1	-	-
GF0032101	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1257.1	-	-
GF0032100	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Domain of unknown function DUF4371 [IPR025398] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_8_mRNA_1256.1	-	-
GF0032099	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1255.1	-	-
GF0032098	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_8_mRNA_1254.1	-	-
GF0032097	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1253.1	-	-
GF0032096	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1249.1	-	-
GF0032095	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_8_mRNA_1248.1	-	-
GF0032094	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1245.1	-	-
GF0032093	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_8_mRNA_1244.1	-	-
GF0032092	1	0	0	Hypothetical protein (1)		Gag-polypeptide of LTR copia-type [IPR029472] (1)	scaffold_8_mRNA_1243.1	-	-
GF0032091	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1242.1	-	-
GF0032090	1	0	0	DUF313 domain protein (1)		DNA-binding pseudobarrel domain [IPR015300] (1); B3 domain-containing protein [IPR005508] (1)	scaffold_8_mRNA_1239.1	-	-
GF0032089	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, SWIM-type [IPR007527] (1); Zinc finger, PMZ-type [IPR006564] (1); MULE transposase domain [IPR018289] (1)	scaffold_8_mRNA_1236.1	-	-
GF0032088	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1235.1	-	-
GF0032087	1	0	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	DNA-binding pseudobarrel domain [IPR015300] (1); B3 DNA binding domain [IPR003340] (1)	scaffold_8_mRNA_1234.1	-	-
GF0032086	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_8_mRNA_1224.1	-	-
GF0032085	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1217.1	-	-
GF0032084	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_8_mRNA_1216.1	-	-
GF0032083	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1214.1	-	-
GF0032082	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1211.1	-	-
GF0032081	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_8_mRNA_1210.1	-	-
GF0032080	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1209.1	-	-
GF0032079	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1201.1	-	-
GF0032078	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1200.1	-	-
GF0032077	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1194.1	-	-
GF0032076	1	0	0	Hypothetical protein (1)		Plant disease resistance response protein [IPR004265] (1)	scaffold_8_mRNA_1193.1	-	-
GF0032075	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_119.1	-	-
GF0032074	1	0	0	Hypothetical protein (1)		Plant disease resistance response protein [IPR004265] (1)	scaffold_8_mRNA_1187.1	-	-
GF0032073	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1183.1	-	-
GF0032072	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1182.1	-	-
GF0032071	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_8_mRNA_1181.1	-	-
GF0032070	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1180.1	-	-
GF0032069	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1178.1	-	-
GF0032068	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1164.2	-	-
GF0032067	1	0	0	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	scaffold_8_mRNA_1155.1	-	-
GF0032066	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1149.1	-	-
GF0032065	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_8_mRNA_1142.1	-	-
GF0032064	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1141.1	-	-
GF0032063	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1140.1	-	-
GF0032062	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1138.1	-	-
GF0032061	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1137.1	-	-
GF0032060	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1133.1	-	-
GF0032059	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1130.1	-	-
GF0032058	1	0	0	Putative disease resistance gene NBS-LRR family protein (1)	ADP binding [GO:0043531 molecular_function] (1); calcium ion binding [GO:0005509 molecular_function] (1)	Class I glutamine amidotransferase-like [IPR029062] (1); Glutamine amidotransferase [IPR017926] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); EF-hand domain [IPR002048] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1); EF-Hand 1, calcium-binding site [IPR018247] (1); AAA+ ATPase domain [IPR003593] (1)	scaffold_8_mRNA_1121.1	-	-
GF0032057	1	0	0	Disease resistance protein (CC-NBS-LRR class) family protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1); AAA+ ATPase domain [IPR003593] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1)	scaffold_8_mRNA_1111.1	-	-
GF0032056	1	0	0	Hypothetical protein (1)	lipid metabolic process [GO:0006629 biological_process] (1)	Alpha/Beta hydrolase fold [IPR029058] (1); Fungal lipase-like domain [IPR002921] (1)	scaffold_8_mRNA_1109.1	-	-
GF0032055	1	0	0	Auxin-induced protein X10A (1)	response to auxin [GO:0009733 biological_process] (1)	Small auxin-up RNA [IPR003676] (1)	scaffold_8_mRNA_1100.1	-	-
GF0032054	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1); Aspartic peptidase domain [IPR021109] (1)	scaffold_8_mRNA_1090.1	-	-
GF0032053	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1089.1	-	-
GF0032052	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_8_mRNA_1084.1	-	-
GF0032051	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1081.1	-	-
GF0032050	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1080.1	-	-
GF0032049	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1076.1	-	-
GF0032048	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1075.1	-	-
GF0032047	1	0	0	Putative retroelement pol polyprotein (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)	scaffold_8_mRNA_1072.1	-	-
GF0032046	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_8_mRNA_1067.1	-	-
GF0032045	1	0	0	Retrotransposon gag protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_8_mRNA_1065.1	-	-
GF0032044	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1064.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0032043	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1063.1	-	-
GF0032042	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_8_mRNA_1062.1	-	-
GF0032041	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1058.1	-	-
GF0032040	1	0	0	Putative RNA-directed DNA polymerase (1)			scaffold_8_mRNA_1056.1	-	-
GF0032039	1	0	0	Hypothetical protein (1)		Zinc knuckle CX2CX4HX4C [IPR025836] (1)	scaffold_8_mRNA_1055.1	-	-
GF0032038	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1052.1	-	-
GF0032037	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1050.1	-	-
GF0032036	1	0	0	Monosacharide transport protein (1)			scaffold_8_mRNA_1049.1	-	-
GF0032035	1	0	0	Auxin-induced protein X10A (1)	response to auxin [GO:0009733 biological_process] (1)	Small auxin-up RNA [IPR003676] (1)	scaffold_8_mRNA_1046.1	-	-
GF0032034	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1044.1	-	-
GF0032033	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_103.1	-	-
GF0032032	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1028.1	-	-
GF0032031	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1027.1	-	-
GF0032030	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1021.1	-	-
GF0032029	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_102.1	-	-
GF0032028	1	0	0	NBS-LRR type disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Glutamine amidotransferase type 2 domain [IPR017932] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1); Nucleophile aminohydrolases, N-terminal [IPR029055] (1); Phosphoribosyltransferase-like [IPR029057] (1); AAA+ ATPase domain [IPR003593] (1)	scaffold_8_mRNA_1016.1	-	-
GF0032027	1	0	0	Putative retroelement pol polyprotein (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); Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_8_mRNA_1014.1	-	-
GF0032026	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Endonuclease/exonuclease/phosphatase [IPR005135] (1); Aldo/keto reductase, conserved site [IPR018170] (1); Zinc finger, CCHC-type [IPR001878] (1); NADP-dependent oxidoreductase domain [IPR023210] (1); Aldo/keto reductase [IPR020471] (1); Viral movement protein [IPR028919] (1)	scaffold_8_mRNA_1005.1	-	-
GF0032025	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1002.1	-	-
GF0032024	1	0	0	Hypothetical protein (1)			scaffold_8_mRNA_1000.1	-	-
GF0032023	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_995.1	-	-
GF0032022	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_982.1	-	-
GF0032021	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_977.1	-	-
GF0032020	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_972.1	-	-
GF0032019	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_961.1	-	-
GF0032018	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_955.1	-	-
GF0032017	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat-containing domain [IPR020683] (1); Ankyrin repeat [IPR002110] (1)	scaffold_7_mRNA_951.1	-	-
GF0032016	1	0	0	Aconitate hydratase (1)	metabolic process [GO:0008152 biological_process] (1)	Aconitase family, 4Fe-4S cluster binding site [IPR018136] (1); Aconitase A/isopropylmalate dehydratase small subunit, swivel domain [IPR000573] (1); Aconitase/3-isopropylmalate dehydratase large subunit, alpha/beta/alpha domain [IPR001030] (1); Aconitase/3-isopropylmalate dehydratase large subunit, alpha/beta/alpha, subdomain 1/3 [IPR015931] (1); Aconitase/3-isopropylmalate dehydratase, swivel [IPR015928] (1); Aconitase/Iron-responsive element-binding protein 2 [IPR006249] (1)	scaffold_7_mRNA_94.1	-	-
GF0032015	1	0	0	Hypothetical protein (1)	nucleosome [GO:0000786 cellular_component] (1); nucleus [GO:0005634 cellular_component] (1); DNA binding [GO:0003677 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1); nucleosome assembly [GO:0006334 biological_process] (1)	DEAD/DEAH box helicase domain [IPR011545] (1); ATP-dependent RNA helicase DEAD-box, conserved site [IPR000629] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Helicase superfamily 1/2, ATP-binding domain [IPR014001] (1); RNA helicase, DEAD-box type, Q motif [IPR014014] (1); Linker histone H1/H5, domain H15 [IPR005818] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); SANT/Myb domain [IPR001005] (1); Helicase, C-terminal [IPR001650] (1); Myb domain [IPR017930] (1); Homeobox domain-like [IPR009057] (1)	scaffold_7_mRNA_935.1	-	-
GF0032014	1	0	0	50S ribosomal protein L34 (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 L34, conserved site [IPR020939] (1); Ribosomal protein L34 [IPR000271] (1)	scaffold_7_mRNA_924.1	-	-
GF0032013	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_899.1	-	-
GF0032012	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_895.1	-	-
GF0032011	1	0	0	Hypothetical protein (1)	phosphatase activity [GO:0016791 molecular_function] (1)	Phosphatase PHOSPHO-type [IPR016965] (1)	scaffold_7_mRNA_876.1	-	-
GF0032010	1	0	0	Hypothetical protein (1)	phosphatase activity [GO:0016791 molecular_function] (1)	Phosphatase PHOSPHO-type [IPR016965] (1)	scaffold_7_mRNA_875.1	-	-
GF0032009	1	0	0	NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial (1)	NADH dehydrogenase (ubiquinone) activity [GO:0008137 molecular_function] (1); quinone binding [GO:0048038 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); iron-sulfur cluster binding [GO:0051536 molecular_function] (1); 4 iron, 4 sulfur cluster binding [GO:0051539 molecular_function] (1)	NADH:ubiquinone oxidoreductase-like, 20kDa subunit [IPR006137] (1); NADH-ubiquinone oxidoreductase, 20 Kd subunit [IPR006138] (1)	scaffold_7_mRNA_870.1	-	-
GF0032008	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_87.1	-	-
GF0032007	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_867.1	-	-
GF0032006	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_863.1	-	-
GF0032005	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_862.1	-	-
GF0032004	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_861.1	-	-
GF0032003	1	0	0	Retrotransposon protein, putative, Ty3-gypsy subclass (1)	DNA integration [GO:0015074 biological_process] (1); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Retrotransposon gag domain [IPR005162] (1); Aspartic peptidase domain [IPR021109] (1); Ribonuclease H domain [IPR002156] (1); Integrase, catalytic core [IPR001584] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_7_mRNA_860.1	-	-
GF0032002	1	0	0	Serine/arginine-rich-splicing factor SR45A (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	RNA recognition motif domain [IPR000504] (1)	scaffold_7_mRNA_86.1	-	-
GF0032001	1	0	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_7_mRNA_855.1	-	-
GF0032000	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_843.1	-	-
GF0031999	1	0	0	Pre-mrna-splicing factor rse1 (1)		Neprosin [IPR004314] (1); Neprosin activation peptide [IPR025521] (1)	scaffold_7_mRNA_840.1	-	-
GF0031998	1	0	0	Monosacharide transport protein (1)			scaffold_7_mRNA_816.1	-	-
GF0031997	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_7_mRNA_815.1	-	-
GF0031996	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_806.1	-	-
GF0031995	1	0	0	GDSL-like Lipase/Acylhydrolase superfamily protein isoform 2 (1)	hydrolase activity, acting on ester bonds [GO:0016788 molecular_function] (1)	GDSL lipase/esterase [IPR001087] (1); SGNH hydrolase-type esterase domain [IPR013830] (1)	scaffold_7_mRNA_796.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0031994	1	0	0	Hypothetical protein (1)	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen [GO:0016701 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); cellular aromatic compound metabolic process [GO:0006725 biological_process] (1); ferrous iron binding [GO:0008198 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Extradiol ring-cleavage dioxygenase, class III enzyme, subunit B [IPR004183] (1); Extradiol aromatic ring-opening dioxygenase, DODA-type [IPR014436] (1)	scaffold_7_mRNA_791.1	-	-
GF0031993	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_778.1	-	-
GF0031992	1	0	0	UDP-glycosyltransferase 85A1 (1)	transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	scaffold_7_mRNA_776.2	-	-
GF0031991	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_7_mRNA_768.1	-	-
GF0031990	1	0	0	ABC transporter G family member 11 (1)	ATP binding [GO:0005524 molecular_function] (1); membrane [GO:0016020 cellular_component] (1); ATPase activity [GO:0016887 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); AAA+ ATPase domain [IPR003593] (1); ABC-2 type transporter [IPR013525] (1); ABC transporter-like [IPR003439] (1); ABC transporter, conserved site [IPR017871] (1)	scaffold_7_mRNA_767.1	-	-
GF0031989	1	0	0	Hypothetical protein (1)		Zinc finger, TTF-type [IPR006580] (1); Domain of unknown function DUF4371 [IPR025398] (1)	scaffold_7_mRNA_746.1	-	-
GF0031988	1	0	0	Histone H3 (1)	protein heterodimerization activity [GO:0046982 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1); nucleosome [GO:0000786 cellular_component] (1)	Histone-fold [IPR009072] (1); Histone H3/CENP-A [IPR000164] (1); Histone H2A/H2B/H3 [IPR007125] (1)	scaffold_7_mRNA_742.1	-	-
GF0031987	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_729.1	-	-
GF0031986	1	0	0	Hypothetical protein (1)	metabolic process [GO:0008152 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1)	Alkaline phosphatase-like, alpha/beta/alpha [IPR017849] (1)	scaffold_7_mRNA_716.1	-	-
GF0031985	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_7_mRNA_706.1	-	-
GF0031984	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_702.1	-	-
GF0031983	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_7.1	-	-
GF0031982	1	0	0	L-type lectin-domain containing receptor kinase IX.1 (1)	ATP binding [GO:0005524 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1)	Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1)	scaffold_7_mRNA_683.1	-	-
GF0031981	1	0	0	L-type lectin-domain containing receptor kinase IX.1 (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)	scaffold_7_mRNA_681.1	-	-
GF0031980	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_7_mRNA_648.1	-	-
GF0031979	1	0	0	Tubulin alpha chain (1)	GTP binding [GO:0005525 molecular_function] (1); microtubule [GO:0005874 cellular_component] (1); structural constituent of cytoskeleton [GO:0005200 molecular_function] (1); microtubule-based process [GO:0007017 biological_process] (1); GTPase activity [GO:0003924 molecular_function] (1)	Tubulin/FtsZ, GTPase domain [IPR003008] (1); Tubulin, conserved site [IPR017975] (1); Tubulin/FtsZ, C-terminal [IPR008280] (1); Tubulin [IPR000217] (1); Tubulin/FtsZ, 2-layer sandwich domain [IPR018316] (1); Alpha tubulin [IPR002452] (1)	scaffold_7_mRNA_646.1	-	-
GF0031978	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_58.1	-	-
GF0031977	1	0	0	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	scaffold_7_mRNA_569.1	-	-
GF0031976	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc knuckle CX2CX4HX4C [IPR025836] (1); Zinc finger, CCHC-type [IPR001878] (1)	scaffold_7_mRNA_568.1	-	-
GF0031975	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_534.1	-	-
GF0031974	1	0	0	Cytochrome P450, family 81, subfamily D, polypeptide 8, putative (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); Cytochrome P450, conserved site [IPR017972] (1)	scaffold_7_mRNA_530.1	-	-
GF0031973	1	0	0	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1)	Cytochrome P450 [IPR001128] (1)	scaffold_7_mRNA_529.1	-	-
GF0031972	1	0	0	UDP-glycosyltransferase 74E1 (1)	metabolic process [GO:0008152 biological_process] (1); transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	scaffold_7_mRNA_525.1	-	-
GF0031971	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_524.1	-	-
GF0031970	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_522.1	-	-
GF0031969	1	0	0	Zinc finger family protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger C2H2-type [IPR013087] (1)	scaffold_7_mRNA_52.1	-	-
GF0031968	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_509.1	-	-
GF0031967	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1); Aspartic peptidase domain [IPR021109] (1)	scaffold_7_mRNA_499.1	-	-
GF0031966	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_486.1	-	-
GF0031965	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_479.1	-	-
GF0031964	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_463.1	-	-
GF0031963	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_462.1	-	-
GF0031962	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_461.1	-	-
GF0031961	1	0	0	Abscisic acid 8'-hydroxylase 1 (1)	monooxygenase activity [GO:0004497 molecular_function] (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 [IPR001128] (1); Cytochrome P450, E-class, group IV [IPR002403] (1)	scaffold_7_mRNA_445.1	-	-
GF0031960	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_430.1	-	-
GF0031959	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_421.1	-	-
GF0031958	1	0	0	Mitogen-activated protein kinase kinase kinase ANP1 (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)	scaffold_7_mRNA_418.1	-	-
GF0031957	1	0	0	LOB domain-containing protein 36 (1)		Lateral organ boundaries, LOB [IPR004883] (1)	scaffold_7_mRNA_416.1	-	-
GF0031956	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_415.1	-	-
GF0031955	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_403.1	-	-
GF0031954	1	0	0	Hypothetical protein (1)	autophagy [GO:0006914 biological_process] (1)	Autophagy-related protein 101 [IPR012445] (1)	scaffold_7_mRNA_398.1	-	-
GF0031953	1	0	0	Methyl esterase 1 (1)		Alpha/beta hydrolase fold-1 [IPR000073] (1); Alpha/Beta hydrolase fold [IPR029058] (1)	scaffold_7_mRNA_396.1	-	-
GF0031952	1	0	0	Farnesyltranstransferase (1)	isoprenoid biosynthetic process [GO:0008299 biological_process] (1)	Polyprenyl synthetase, conserved site [IPR033749] (1); Polyprenyl synthetase [IPR000092] (1); Isoprenoid synthase domain [IPR008949] (1)	scaffold_7_mRNA_352.1	-	-
GF0031951	1	0	0	RUB1-conjugating enzyme 2, E2 (1)		Ubiquitin-conjugating enzyme E2 [IPR000608] (1); Ubiquitin-conjugating enzyme, active site [IPR023313] (1); Ubiquitin-conjugating enzyme/RWD-like [IPR016135] (1)	scaffold_7_mRNA_350.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0031950	1	0	0	Anthocyanidin 3-O-glucosyltransferase 5 (1)	metabolic process [GO:0008152 biological_process] (1); transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	scaffold_7_mRNA_346.1	-	-
GF0031949	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_343.1	-	-
GF0031948	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_7_mRNA_342.1	-	-
GF0031947	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_33.1	-	-
GF0031946	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_308.1	-	-
GF0031945	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_307.1	-	-
GF0031944	1	0	0	Zinc-finger homeodomain protein 6 (1)		ZF-HD homeobox protein, Cys/His-rich dimerisation domain [IPR006456] (1)	scaffold_7_mRNA_291.1	-	-
GF0031943	1	0	0	Pentatricopeptide (1)	protein binding [GO:0005515 molecular_function] (1)	Tetratricopeptide-like helical domain [IPR011990] (1); Pentatricopeptide repeat [IPR002885] (1)	scaffold_7_mRNA_275.1	-	-
GF0031942	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2725.1	-	-
GF0031941	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2715.1	-	-
GF0031940	1	0	0	Tyrosine decarboxylase (1)	carboxy-lyase activity [GO:0016831 molecular_function] (1); carboxylic acid metabolic process [GO:0019752 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1); cellular amino acid metabolic process [GO:0006520 biological_process] (1); pyridoxal phosphate binding [GO:0030170 molecular_function] (1)	Pyridoxal phosphate-dependent transferase, subdomain 2 [IPR015422] (1); Pyridoxal phosphate-dependent decarboxylase [IPR002129] (1); Pyridoxal phosphate-dependent transferase, major region, subdomain 1 [IPR015421] (1); Pyridoxal-phosphate binding site [IPR021115] (1); Pyridoxal phosphate-dependent transferase [IPR015424] (1); Aromatic-L-amino-acid decarboxylase [IPR010977] (1)	scaffold_7_mRNA_2708.1	-	-
GF0031939	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2697.1	-	-
GF0031938	1	0	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	scaffold_7_mRNA_2694.1	-	-
GF0031937	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2692.1	-	-
GF0031936	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2685.1	-	-
GF0031935	1	0	0	Protein spinster (1)	integral component of membrane [GO:0016021 cellular_component] (1); transmembrane transport [GO:0055085 biological_process] (1)	Major facilitator superfamily [IPR011701] (1); Major facilitator superfamily domain [IPR020846] (1)	scaffold_7_mRNA_2679.1	-	-
GF0031934	1	0	0	Monosacharide transport protein (1)			scaffold_7_mRNA_2678.1	-	-
GF0031933	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_7_mRNA_2677.1	-	-
GF0031932	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_7_mRNA_2670.1	-	-
GF0031931	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2667.1	-	-
GF0031930	1	0	0	Hypothetical protein (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1); actin filament binding [GO:0051015 molecular_function] (1); hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (1); actin filament organization [GO:0007015 biological_process] (1)	HotDog domain [IPR029069] (1); Glycoside hydrolase, family 5 [IPR001547] (1); Actin cross-linking [IPR008999] (1); Fascin [IPR010431] (1); Glycoside hydrolase superfamily [IPR017853] (1)	scaffold_7_mRNA_2655.1	-	-
GF0031929	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2648.1	-	-
GF0031928	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2645.1	-	-
GF0031927	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2643.1	-	-
GF0031926	1	0	0	Hypothetical protein (1)	RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H domain [IPR002156] (1); Ribonuclease H-like domain [IPR012337] (1); Aspartic peptidase domain [IPR021109] (1); Retrotransposon gag domain [IPR005162] (1)	scaffold_7_mRNA_2642.1	-	-
GF0031925	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	scaffold_7_mRNA_2630.1	-	-
GF0031924	1	0	0	Hypothetical protein (1)		Adenosylhomocysteinase-like [IPR000043] (1); S-adenosyl-L-homocysteine hydrolase, NAD binding domain [IPR015878] (1); NAD(P)-binding domain [IPR016040] (1)	scaffold_7_mRNA_2620.1	-	-
GF0031923	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2618.1	-	-
GF0031922	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2617.1	-	-
GF0031921	1	0	0	Hypothetical protein (1)		Short-chain dehydrogenase/reductase SDR [IPR002347] (1); NAD(P)-binding domain [IPR016040] (1)	scaffold_7_mRNA_2596.1	-	-
GF0031920	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_7_mRNA_2595.1	-	-
GF0031919	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2591.1	-	-
GF0031918	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2587.1	-	-
GF0031917	1	0	0	Mitogen activated protein kinase 3 (1)	ATP binding [GO:0005524 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); MAP kinase activity [GO:0004707 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1)	Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase, ATP binding site [IPR017441] (1); Protein kinase-like domain [IPR011009] (1); Mitogen-activated protein (MAP) kinase, conserved site [IPR003527] (1); Protein kinase domain [IPR000719] (1)	scaffold_7_mRNA_258.1	-	-
GF0031916	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2578.1	-	-
GF0031915	1	0	0	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)	scaffold_7_mRNA_2574.1	-	-
GF0031914	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2571.1	-	-
GF0031913	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_257.1	-	-
GF0031912	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2554.1	-	-
GF0031911	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2550.1	-	-
GF0031910	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Zinc knuckle CX2CX4HX4C [IPR025836] (1); Domain of unknown function DUF4283 [IPR025558] (1)	scaffold_7_mRNA_2537.1	-	-
GF0031909	1	0	0	RnaseH protein (1)	RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	TB2/DP1/HVA22-related protein [IPR004345] (1); Ribonuclease H-like domain [IPR012337] (1); Ribonuclease H domain [IPR002156] (1)	scaffold_7_mRNA_2532.1	-	-
GF0031908	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2529.1	-	-
GF0031907	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2524.1	-	-
GF0031906	1	0	0	Monosacharide transport 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)	scaffold_7_mRNA_2523.1	-	-
GF0031905	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2517.1	-	-
GF0031904	1	0	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); double-stranded DNA binding [GO:0003690 molecular_function] (1)	Transcription termination factor, mitochondrial/chloroplastic [IPR003690] (1)	scaffold_7_mRNA_2513.1	-	-
GF0031903	1	0	0	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); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase, ATP binding site [IPR017441] (1); Leucine-rich repeat [IPR001611] (1)	scaffold_7_mRNA_2508.1	-	-
GF0031902	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2503.1	-	-
GF0031901	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2501.1	-	-
GF0031900	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2487.1	-	-
GF0031899	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_248.1	-	-
GF0031898	1	0	0	Elongation factor 1-beta (1)	translational elongation [GO:0006414 biological_process] (1); translation elongation factor activity [GO:0003746 molecular_function] (1)	Translation elongation factor EF1B/ribosomal protein S6 [IPR014717] (1); Translation elongation factor EF1B, beta/delta subunit, guanine nucleotide exchange domain [IPR014038] (1); Glutathione S-transferase, C-terminal-like [IPR010987] (1)	scaffold_7_mRNA_2475.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0031897	1	0	0	Guanylate kinase (1)	purine nucleotide metabolic process [GO:0006163 biological_process] (1); guanylate kinase activity [GO:0004385 molecular_function] (1)	Guanylate kinase, conserved site [IPR020590] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Guanylate kinase/L-type calcium channel beta subunit [IPR008145] (1); Guanylate kinase-like domain [IPR008144] (1); Guanylate kinase [IPR017665] (1)	scaffold_7_mRNA_2474.1	-	-
GF0031896	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_7_mRNA_2467.1	-	-
GF0031895	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2466.1	-	-
GF0031894	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2465.1	-	-
GF0031893	1	0	0	Vinorine synthase (1)	transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (1)	Transferase [IPR003480] (1)	scaffold_7_mRNA_2463.1	-	-
GF0031892	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2453.1	-	-
GF0031891	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_7_mRNA_2445.1	-	-
GF0031890	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_7_mRNA_2442.1	-	-
GF0031889	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2437.1	-	-
GF0031888	1	0	0	Hypothetical protein (1)	methyltransferase activity [GO:0008168 molecular_function] (1); O-methyltransferase activity [GO:0008171 molecular_function] (1)	S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); O-methyltransferase COMT-type [IPR016461] (1); O-methyltransferase, family 2 [IPR001077] (1)	scaffold_7_mRNA_2435.1	-	-
GF0031887	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2434.1	-	-
GF0031886	1	0	0	Caffeic acid O-methyltransferase (1)	O-methyltransferase activity [GO:0008171 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1); methyltransferase activity [GO:0008168 molecular_function] (1)	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)	scaffold_7_mRNA_2432.1	-	-
GF0031885	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2429.1	-	-
GF0031884	1	0	0	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1)	Oxoglutarate/iron-dependent dioxygenase [IPR005123] (1); Thiamin diphosphate-binding fold [IPR029061] (1); Non-haem dioxygenase N-terminal domain [IPR026992] (1); Isopenicillin N synthase-like [IPR027443] (1)	scaffold_7_mRNA_2407.1	-	-
GF0031883	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2405.1	-	-
GF0031882	1	0	0	Monosacharide transport protein (1)			scaffold_7_mRNA_2401.1	-	-
GF0031881	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_7_mRNA_2400.1	-	-
GF0031880	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2378.1	-	-
GF0031879	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2372.1	-	-
GF0031878	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2366.1	-	-
GF0031877	1	0	0	Hypothetical protein (1)		Ribosomal protein L18e/L15P [IPR021131] (1)	scaffold_7_mRNA_2365.1	-	-
GF0031876	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2363.1	-	-
GF0031875	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2361.1	-	-
GF0031874	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2359.1	-	-
GF0031873	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2358.1	-	-
GF0031872	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2350.1	-	-
GF0031871	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2348.1	-	-
GF0031870	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_7_mRNA_2340.1	-	-
GF0031869	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2330.1	-	-
GF0031868	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	Zinc finger C2H2-type [IPR013087] (1); Zinc finger, BED-type [IPR003656] (1)	scaffold_7_mRNA_2323.1	-	-
GF0031867	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2316.1	-	-
GF0031866	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2313.1	-	-
GF0031865	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2299.1	-	-
GF0031864	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2295.1	-	-
GF0031863	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2293.1	-	-
GF0031862	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_7_mRNA_2292.1	-	-
GF0031861	1	0	0	Hypothetical protein (1)		Possible tRNA binding domain [IPR027992] (1)	scaffold_7_mRNA_2290.1	-	-
GF0031860	1	0	0	Hypothetical protein (1)	U2AF [GO:0089701 cellular_component] (1); RNA binding [GO:0003723 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1); mRNA splicing, via spliceosome [GO:0000398 biological_process] (1)	U2 auxiliary factor small subunit [IPR009145] (1); RNA recognition motif domain, eukaryote [IPR003954] (1); RNA recognition motif domain [IPR000504] (1)	scaffold_7_mRNA_2267.1	-	-
GF0031859	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2252.1	-	-
GF0031858	1	0	0	Non-LTR retroelement reverse transcriptase-like (1)	RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H domain [IPR002156] (1); TB2/DP1/HVA22-related protein [IPR004345] (1)	scaffold_7_mRNA_225.1	-	-
GF0031857	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2249.1	-	-
GF0031856	1	0	0	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	scaffold_7_mRNA_2248.1	-	-
GF0031855	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2244.1	-	-
GF0031854	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2239.1	-	-
GF0031853	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2235.1	-	-
GF0031852	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2230.1	-	-
GF0031851	1	0	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1)	scaffold_7_mRNA_2229.1	-	-
GF0031850	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2226.1	-	-
GF0031849	1	0	0	G-type lectin S-receptor-like serine/threonine-protein kinase (1)	ATP binding [GO:0005524 molecular_function] (1); protein serine/threonine kinase activity [GO:0004674 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1)	Serine/threonine-protein kinase, active site [IPR008271] (1); S-locus receptor kinase, C-terminal [IPR021820] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1)	scaffold_7_mRNA_2217.1	-	-
GF0031848	1	0	0	Hypothetical protein (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	PAN/Apple domain [IPR003609] (1); Protein kinase, ATP binding site [IPR017441] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	scaffold_7_mRNA_2214.1	-	-
GF0031847	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2209.1	-	-
GF0031846	1	0	0	Retrotransposon gag protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_7_mRNA_2204.1	-	-
GF0031845	1	0	0	Hypothetical protein (1)		Mitochondrial substrate/solute carrier [IPR018108] (1); Mitochondrial carrier domain [IPR023395] (1)	scaffold_7_mRNA_22.1	-	-
GF0031844	1	0	0	LRR receptor-like kinase family protein (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase, ATP binding site [IPR017441] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1); 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)	scaffold_7_mRNA_2199.1	-	-
GF0031843	1	0	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_7_mRNA_2197.1	-	-
GF0031842	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2196.1	-	-
GF0031841	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_7_mRNA_2180.1	-	-
GF0031840	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2179.1	-	-
GF0031839	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2178.1	-	-
GF0031838	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2176.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0031837	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	scaffold_7_mRNA_2171.1	-	-
GF0031836	1	0	0	Hypothetical protein (1)	intracellular [GO:0005622 cellular_component] (1); translation [GO:0006412 biological_process] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1); ribosome [GO:0005840 cellular_component] (1)	Ribosomal protein L37ae [IPR002674] (1); Ribosomal protein L37ae/L37e [IPR011331] (1); Zinc-binding ribosomal protein [IPR011332] (1)	scaffold_7_mRNA_2167.1	-	-
GF0031835	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat [IPR002110] (1); Ankyrin repeat-containing domain [IPR020683] (1)	scaffold_7_mRNA_2166.1	-	-
GF0031834	1	0	0	Hypothetical protein (1)	cellular response to salicylic acid stimulus [GO:0071446 biological_process] (1); integral component of membrane [GO:0016021 cellular_component] (1); regulation of salicylic acid mediated signaling pathway [GO:2000031 biological_process] (1); regulation of defense response [GO:0031347 biological_process] (1)	PGG domain [IPR026961] (1); Protein accelerated cell death 6 [IPR032846] (1)	scaffold_7_mRNA_2163.1	-	-
GF0031833	1	0	0	Putative ribonuclease H 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)	scaffold_7_mRNA_2162.1	-	-
GF0031832	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2161.1	-	-
GF0031831	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2145.1	-	-
GF0031830	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2134.1	-	-
GF0031829	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2122.1	-	-
GF0031828	1	0	0	B-box type zinc finger family protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); intracellular [GO:0005622 cellular_component] (1)	B-box-type zinc finger [IPR000315] (1)	scaffold_7_mRNA_212.2	-	-
GF0031827	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2113.1	-	-
GF0031826	1	0	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1); Domain of unknown function DUF1985 [IPR015410] (1)	scaffold_7_mRNA_2106.1	-	-
GF0031825	1	0	0	Mutator-like transposase (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, SWIM-type [IPR007527] (1); Zinc finger, PMZ-type [IPR006564] (1); MULE transposase domain [IPR018289] (1); Transposase, MuDR, plant [IPR004332] (1)	scaffold_7_mRNA_2105.1	-	-
GF0031824	1	0	0	Hypothetical protein (1)	spliceosomal complex [GO:0005681 cellular_component] (1); mRNA splicing, via spliceosome [GO:0000398 biological_process] (1)	LSM domain [IPR010920] (1); Small nuclear ribonucleoprotein E [IPR027078] (1); LSM domain, eukaryotic/archaea-type [IPR001163] (1)	scaffold_7_mRNA_2100.1	-	-
GF0031823	1	0	0	Flavonoid 3'-monooxygenase (1)	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1)	Cytochrome P450 [IPR001128] (1); Cytochrome P450, conserved site [IPR017972] (1); Cytochrome P450, E-class, group I [IPR002401] (1)	scaffold_7_mRNA_2098.1	-	-
GF0031822	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2090.1	-	-
GF0031821	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2086.1	-	-
GF0031820	1	0	0	Disease resistance RPS5-like protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	scaffold_7_mRNA_2083.1	-	-
GF0031819	1	0	0	Disease resistance protein RPS2 (1)	ADP binding [GO:0043531 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Leucine-rich repeat [IPR001611] (1); NB-ARC [IPR002182] (1)	scaffold_7_mRNA_2082.1	-	-
GF0031818	1	0	0	C6HC-type zinc finger RING/U-box protein (1)	protein ubiquitination [GO:0016567 biological_process] (1); ubiquitin-protein transferase activity [GO:0004842 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, RING-type [IPR001841] (1); E3 ubiquitin ligase RBR family [IPR031127] (1); Zinc finger, RING-type, conserved site [IPR017907] (1); Zinc finger, RING/FYVE/PHD-type [IPR013083] (1); IBR domain [IPR002867] (1)	scaffold_7_mRNA_2078.1	-	-
GF0031817	1	0	0	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	scaffold_7_mRNA_2073.1	-	-
GF0031816	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2072.1	-	-
GF0031815	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2071.1	-	-
GF0031814	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_207.1	-	-
GF0031813	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2067.1	-	-
GF0031812	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2047.1	-	-
GF0031811	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2044.1	-	-
GF0031810	1	0	0	Histone H3 (1)	protein heterodimerization activity [GO:0046982 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1); nucleosome [GO:0000786 cellular_component] (1)	Histone H2A/H2B/H3 [IPR007125] (1); Histone H3/CENP-A [IPR000164] (1); Histone-fold [IPR009072] (1)	scaffold_7_mRNA_204.1	-	-
GF0031809	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2037.1	-	-
GF0031808	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2036.1	-	-
GF0031807	1	0	0	Retrotransposon protein, putative, Ty1-copia subclass (1)			scaffold_7_mRNA_2030.1	-	-
GF0031806	1	0	0	Histone H1 (1)	nucleosome [GO:0000786 cellular_component] (1); nucleosome assembly [GO:0006334 biological_process] (1); nucleus [GO:0005634 cellular_component] (1); DNA binding [GO:0003677 molecular_function] (1)	Linker histone H1/H5, domain H15 [IPR005818] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Histone H5 [IPR005819] (1)	scaffold_7_mRNA_203.1	-	-
GF0031805	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2025.1	-	-
GF0031804	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2014.1	-	-
GF0031803	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_7_mRNA_2009.1	-	-
GF0031802	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2007.1	-	-
GF0031801	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_7_mRNA_2006.1	-	-
GF0031800	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_2001.1	-	-
GF0031799	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1997.1	-	-
GF0031798	1	0	0	Monosacharide transport protein (1)			scaffold_7_mRNA_1996.1	-	-
GF0031797	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_199.1	-	-
GF0031796	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1988.1	-	-
GF0031795	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1982.1	-	-
GF0031794	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1978.1	-	-
GF0031793	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1977.1	-	-
GF0031792	1	0	0	Putative ribonuclease H protein (1)	RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	TB2/DP1/HVA22-related protein [IPR004345] (1); Ribonuclease H-like domain [IPR012337] (1); Ribonuclease H domain [IPR002156] (1)	scaffold_7_mRNA_1975.1	-	-
GF0031791	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1)	Ribonuclease H domain [IPR002156] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_7_mRNA_1973.1	-	-
GF0031790	1	0	0	Disease resistance related protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_7_mRNA_1970.1	-	-
GF0031789	1	0	0	Defective in cullin neddylation protein (1)		Defective-in-cullin neddylation protein [IPR014764] (1); Potentiating neddylation domain [IPR005176] (1); EF-hand domain pair [IPR011992] (1)	scaffold_7_mRNA_1953.2	-	-
GF0031788	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1950.1	-	-
GF0031787	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1949.1	-	-
GF0031786	1	0	0	Monosacharide transport protein (1)			scaffold_7_mRNA_1947.1	-	-
GF0031785	1	0	0	Hypothetical protein (1)		Protein kinase-like domain [IPR011009] (1)	scaffold_7_mRNA_1934.1	-	-
GF0031784	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	WD40-repeat-containing domain [IPR017986] (1)	scaffold_7_mRNA_1931.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0031783	1	0	0	Cysteine-rich RLK (Receptor-like kinase) protein (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein serine/threonine kinase activity [GO:0004674 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); S-locus receptor kinase, C-terminal [IPR021820] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	scaffold_7_mRNA_1930.1	-	-
GF0031782	1	0	0	Monosacharide transport protein (1)			scaffold_7_mRNA_1927.1	-	-
GF0031781	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1926.1	-	-
GF0031780	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_7_mRNA_1925.1	-	-
GF0031779	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1922.1	-	-
GF0031778	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_7_mRNA_1918.1	-	-
GF0031777	1	0	0	Verticillium wilt resistance-like protein (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); ATP binding [GO:0005524 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat, typical subtype [IPR003591] (1); Protein kinase-like domain [IPR011009] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Protein kinase domain [IPR000719] (1); Leucine-rich repeat [IPR001611] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); S-locus receptor kinase, C-terminal [IPR021820] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1)	scaffold_7_mRNA_1916.1	-	-
GF0031776	1	0	0	Verticillium wilt resistance-like protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1)	scaffold_7_mRNA_1915.1	-	-
GF0031775	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1912.1	-	-
GF0031774	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1909.1	-	-
GF0031773	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc knuckle CX2CX4HX4C [IPR025836] (1); Zinc finger, CCHC-type [IPR001878] (1)	scaffold_7_mRNA_1906.1	-	-
GF0031772	1	0	0	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	scaffold_7_mRNA_1905.1	-	-
GF0031771	1	0	0	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	scaffold_7_mRNA_1903.1	-	-
GF0031770	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, SWIM-type [IPR007527] (1); Zinc finger, PMZ-type [IPR006564] (1)	scaffold_7_mRNA_1899.1	-	-
GF0031769	1	0	0	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	scaffold_7_mRNA_1895.1	-	-
GF0031768	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_7_mRNA_1892.1	-	-
GF0031767	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1890.1	-	-
GF0031766	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1889.1	-	-
GF0031765	1	0	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1)	scaffold_7_mRNA_1879.1	-	-
GF0031764	1	0	0	LRR receptor-like serine/threonine-protein kinase GSO1 (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat [IPR001611] (1)	scaffold_7_mRNA_1878.1	-	-
GF0031763	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1876.1	-	-
GF0031762	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_7_mRNA_1875.1	-	-
GF0031761	1	0	0	Hypothetical protein (1)		MULE transposase domain [IPR018289] (1)	scaffold_7_mRNA_1871.1	-	-
GF0031760	1	0	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1); Domain of unknown function DUF1985 [IPR015410] (1)	scaffold_7_mRNA_1870.1	-	-
GF0031759	1	0	0	Mutator-like transposase (1)	zinc ion binding [GO:0008270 molecular_function] (1)	MULE transposase domain [IPR018289] (1); Zinc finger, PMZ-type [IPR006564] (1); Zinc finger, SWIM-type [IPR007527] (1)	scaffold_7_mRNA_1869.1	-	-
GF0031758	1	0	0	Non-LTR reverse transcriptase (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1); Protein of unknown function DUF247, plant [IPR004158] (1)	scaffold_7_mRNA_1857.1	-	-
GF0031757	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1834.1	-	-
GF0031756	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1832.1	-	-
GF0031755	1	0	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_7_mRNA_1831.1	-	-
GF0031754	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1829.1	-	-
GF0031753	1	0	0	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)	scaffold_7_mRNA_1822.1	-	-
GF0031752	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1821.1	-	-
GF0031751	1	0	0	Phytosulfokine receptor 2-like protein (1)		Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine rich repeat 4 [IPR025875] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_7_mRNA_1813.1	-	-
GF0031750	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_7_mRNA_1809.1	-	-
GF0031749	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine rich repeat 4 [IPR025875] (1)	scaffold_7_mRNA_1807.1	-	-
GF0031748	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_7_mRNA_1805.1	-	-
GF0031747	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1803.1	-	-
GF0031746	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1801.1	-	-
GF0031745	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_7_mRNA_1800.1	-	-
GF0031744	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1797.1	-	-
GF0031743	1	0	0	Putative disease resistance protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1)	scaffold_7_mRNA_1787.1	-	-
GF0031742	1	0	0	Hypothetical protein (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1); phosphotransferase activity, alcohol group as acceptor [GO:0016773 molecular_function] (1)	Carbohydrate kinase, FGGY, N-terminal [IPR018484] (1); Carbohydrate kinase, FGGY, C-terminal [IPR018485] (1)	scaffold_7_mRNA_1786.1	-	-
GF0031741	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1781.1	-	-
GF0031740	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Domain of unknown function DUF4283 [IPR025558] (1); Zinc finger, CCHC-type [IPR001878] (1); Zinc knuckle CX2CX4HX4C [IPR025836] (1)	scaffold_7_mRNA_1779.1	-	-
GF0031739	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1776.1	-	-
GF0031738	1	0	0	Phytosulfokine receptor (1)		Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_7_mRNA_1773.1	-	-
GF0031737	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_177.1	-	-
GF0031736	1	0	0	Monosacharide transport protein (1)			scaffold_7_mRNA_1769.1	-	-
GF0031735	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1); Aspartic peptidase domain [IPR021109] (1)	scaffold_7_mRNA_1768.1	-	-
GF0031734	1	0	0	Hypothetical protein (1)		Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	scaffold_7_mRNA_1766.1	-	-
GF0031733	1	0	0	Hypothetical protein (1)		Winged helix-turn-helix DNA-binding domain [IPR011991] (1)	scaffold_7_mRNA_1764.1	-	-
GF0031732	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1762.1	-	-
GF0031731	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_7_mRNA_176.1	-	-
GF0031730	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Domain of unknown function DUF4283 [IPR025558] (1); Zinc knuckle CX2CX4HX4C [IPR025836] (1); Zinc finger, CCHC-type [IPR001878] (1)	scaffold_7_mRNA_1750.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0031729	1	0	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_7_mRNA_1747.1	-	-
GF0031728	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1741.1	-	-
GF0031727	1	0	0	Hypothetical protein (1)		P-type ATPase, transmembrane domain [IPR023298] (1)	scaffold_7_mRNA_174.1	-	-
GF0031726	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_7_mRNA_1737.1	-	-
GF0031725	1	0	0	LRR receptor-like serine/threonine-protein kinase GSO1 (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)	scaffold_7_mRNA_1735.1	-	-
GF0031724	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1734.1	-	-
GF0031723	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	scaffold_7_mRNA_1731.1	-	-
GF0031722	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1730.1	-	-
GF0031721	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1729.1	-	-
GF0031720	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1728.1	-	-
GF0031719	1	0	0	Eukaryotic translation initiation factor 3 subunit (1)	protein binding [GO:0005515 molecular_function] (1)	Tetratricopeptide-like helical domain [IPR011990] (1); Tetratricopeptide repeat-containing domain [IPR013026] (1); Tetratricopeptide repeat [IPR019734] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); CLU central domain [IPR033646] (1)	scaffold_7_mRNA_1723.1	-	-
GF0031718	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1722.1	-	-
GF0031717	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1); Retrotransposon gag domain [IPR005162] (1)	scaffold_7_mRNA_1721.1	-	-
GF0031716	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1719.1	-	-
GF0031715	1	0	0	Disease resistance protein RPS2 (1)	ADP binding [GO:0043531 molecular_function] (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 domain, L domain-like [IPR032675] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1)	scaffold_7_mRNA_1713.1	-	-
GF0031714	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1712.1	-	-
GF0031713	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1711.1	-	-
GF0031712	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1707.1	-	-
GF0031711	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1702.1	-	-
GF0031710	1	0	0	Disease resistance protein RPS2 (1)	ADP binding [GO:0043531 molecular_function] (1)	Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_7_mRNA_1700.1	-	-
GF0031709	1	0	0	Caffeic acid 3-O-methyltransferase (1)	O-methyltransferase activity [GO:0008171 molecular_function] (1); methyltransferase activity [GO:0008168 molecular_function] (1)	O-methyltransferase COMT-type [IPR016461] (1); O-methyltransferase, family 2 [IPR001077] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	scaffold_7_mRNA_170.1	-	-
GF0031708	1	0	0	Disease resistance protein RPS2 (1)	ADP binding [GO:0043531 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	scaffold_7_mRNA_1698.1	-	-
GF0031707	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1697.1	-	-
GF0031706	1	0	0	Disease resistance protein RPS2 (1)	protein binding [GO:0005515 molecular_function] (1); ADP binding [GO:0043531 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Leucine-rich repeat [IPR001611] (1); NB-ARC [IPR002182] (1)	scaffold_7_mRNA_1696.1	-	-
GF0031705	1	0	0	Disease resistance protein family (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_7_mRNA_1695.1	-	-
GF0031704	1	0	0	Disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1)	scaffold_7_mRNA_1694.1	-	-
GF0031703	1	0	0	Hypothetical protein (1)	DNA damage checkpoint [GO:0000077 biological_process] (1); checkpoint clamp complex [GO:0030896 cellular_component] (1)	Checkpoint protein Hus1/Mec3 [IPR007150] (1); Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	scaffold_7_mRNA_1691.1	-	-
GF0031702	1	0	0	Disease resistance protein RPS2 (1)	ADP binding [GO:0043531 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_7_mRNA_1690.1	-	-
GF0031701	1	0	0	Mutator-like transposase (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, SWIM-type [IPR007527] (1); Transposase, MuDR, plant [IPR004332] (1); Zinc finger, PMZ-type [IPR006564] (1); MULE transposase domain [IPR018289] (1)	scaffold_7_mRNA_1688.1	-	-
GF0031700	1	0	0	Hus1 domain-containing protein (1)	DNA damage checkpoint [GO:0000077 biological_process] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); checkpoint clamp complex [GO:0030896 cellular_component] (1)	FHY3/FAR1 family [IPR031052] (1); Checkpoint protein Hus1/Mec3 [IPR007150] (1)	scaffold_7_mRNA_1686.1	-	-
GF0031699	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_7_mRNA_1680.1	-	-
GF0031698	1	0	0	Disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Winged helix-turn-helix DNA-binding domain [IPR011991] (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)	scaffold_7_mRNA_1676.1	-	-
GF0031697	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1675.1	-	-
GF0031696	1	0	0	Hypothetical 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); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_7_mRNA_1674.1	-	-
GF0031695	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1); FAR1 DNA binding domain [IPR004330] (1); Zinc finger, PMZ-type [IPR006564] (1); Zinc finger, SWIM-type [IPR007527] (1)	scaffold_7_mRNA_1672.1	-	-
GF0031694	1	0	0	HUS1 checkpoint protein (1)	DNA damage checkpoint [GO:0000077 biological_process] (1); checkpoint clamp complex [GO:0030896 cellular_component] (1); nucleolus [GO:0005730 cellular_component] (1)	Cell cycle checkpoint, Hus1 [IPR016580] (1); Checkpoint protein Hus1/Mec3 [IPR007150] (1)	scaffold_7_mRNA_1671.1	-	-
GF0031693	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_167.1	-	-
GF0031692	1	0	0	NBS-LRR type disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1)	scaffold_7_mRNA_1669.1	-	-
GF0031691	1	0	0	Disease resistance RPS5-like protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_7_mRNA_1667.1	-	-
GF0031690	1	0	0	Disease resistance protein RPS2 (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); Winged helix-turn-helix DNA-binding domain [IPR011991] (1)	scaffold_7_mRNA_1664.1	-	-
GF0031689	1	0	0	HUS1 checkpoint protein (1)	checkpoint clamp complex [GO:0030896 cellular_component] (1); DNA damage checkpoint [GO:0000077 biological_process] (1); nucleolus [GO:0005730 cellular_component] (1)	Checkpoint protein Hus1/Mec3 [IPR007150] (1); Cell cycle checkpoint, Hus1 [IPR016580] (1)	scaffold_7_mRNA_1663.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0031688	1	0	0	Disease resistance protein RPS2 (1)	protein binding [GO:0005515 molecular_function] (1); ADP binding [GO:0043531 molecular_function] (1)	Winged helix-turn-helix DNA-binding domain [IPR011991] (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)	scaffold_7_mRNA_1662.1	-	-
GF0031687	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1661.1	-	-
GF0031686	1	0	0	Hypothetical protein (1)		Myb/SANT-like domain [IPR024752] (1); Harbinger transposase-derived nuclease domain [IPR027806] (1)	scaffold_7_mRNA_1657.1	-	-
GF0031685	1	0	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	scaffold_7_mRNA_1656.1	-	-
GF0031684	1	0	0	Disease resistance protein RPS2 (1)	ADP binding [GO:0043531 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); NB-ARC [IPR002182] (1); Leucine-rich repeat [IPR001611] (1); AAA+ ATPase domain [IPR003593] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_7_mRNA_1654.1	-	-
GF0031683	1	0	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	scaffold_7_mRNA_1653.1	-	-
GF0031682	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1652.1	-	-
GF0031681	1	0	0	Disease resistance protein RPS2 (1)	ADP binding [GO:0043531 molecular_function] (1)	AAA+ ATPase domain [IPR003593] (1); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_7_mRNA_1649.1	-	-
GF0031680	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1648.1	-	-
GF0031679	1	0	0	HUS1 checkpoint protein (1)	nucleolus [GO:0005730 cellular_component] (1); DNA damage checkpoint [GO:0000077 biological_process] (1); checkpoint clamp complex [GO:0030896 cellular_component] (1)	Checkpoint protein Hus1/Mec3 [IPR007150] (1); Cell cycle checkpoint, Hus1 [IPR016580] (1)	scaffold_7_mRNA_1647.1	-	-
GF0031678	1	0	0	RNA-directed DNA polymerase (Reverse transcriptase) (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1); Reverse transcriptase domain [IPR000477] (1)	scaffold_7_mRNA_1642.1	-	-
GF0031677	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_7_mRNA_164.1	-	-
GF0031676	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_7_mRNA_1638.1	-	-
GF0031675	1	0	0	Disease resistance protein RPS2 (1)	ADP binding [GO:0043531 molecular_function] (1)	Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_7_mRNA_1636.1	-	-
GF0031674	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1633.1	-	-
GF0031673	1	0	0	HUS1 checkpoint protein (1)	DNA damage checkpoint [GO:0000077 biological_process] (1); checkpoint clamp complex [GO:0030896 cellular_component] (1); nucleolus [GO:0005730 cellular_component] (1)	Cell cycle checkpoint, Hus1 [IPR016580] (1); Checkpoint protein Hus1/Mec3 [IPR007150] (1)	scaffold_7_mRNA_1628.1	-	-
GF0031672	1	0	0	Hypothetical protein (1)	checkpoint clamp complex [GO:0030896 cellular_component] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); DNA damage checkpoint [GO:0000077 biological_process] (1)	FAR1 DNA binding domain [IPR004330] (1); FHY3/FAR1 family [IPR031052] (1); Checkpoint protein Hus1/Mec3 [IPR007150] (1)	scaffold_7_mRNA_1625.1	-	-
GF0031671	1	0	0	Disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_7_mRNA_1624.1	-	-
GF0031670	1	0	0	Disease resistance protein RPS2 (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_7_mRNA_1623.1	-	-
GF0031669	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_162.1	-	-
GF0031668	1	0	0	NBS-LRR type disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_7_mRNA_1619.1	-	-
GF0031667	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF1985 [IPR015410] (1)	scaffold_7_mRNA_1618.1	-	-
GF0031666	1	0	0	Hypothetical protein (1)		CBS domain [IPR000644] (1)	scaffold_7_mRNA_1596.1	-	-
GF0031665	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1591.1	-	-
GF0031664	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1587.1	-	-
GF0031663	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1585.1	-	-
GF0031662	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1584.1	-	-
GF0031661	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1579.1	-	-
GF0031660	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1577.1	-	-
GF0031659	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_7_mRNA_1568.1	-	-
GF0031658	1	0	0	Ribonuclease H-like superfamily protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_7_mRNA_1566.1	-	-
GF0031657	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1565.1	-	-
GF0031656	1	0	0	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein isoform 2 (1)	O-methyltransferase activity [GO:0008171 molecular_function] (1)	S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); O-methyltransferase, family 3 [IPR002935] (1)	scaffold_7_mRNA_1559.1	-	-
GF0031655	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1557.1	-	-
GF0031654	1	0	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_7_mRNA_1555.1	-	-
GF0031653	1	0	0	Putative non-LTR retroelement reverse transcriptase (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	TB2/DP1/HVA22-related protein [IPR004345] (1); Ribonuclease H-like domain [IPR012337] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1)	scaffold_7_mRNA_1554.1	-	-
GF0031652	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_7_mRNA_1536.1	-	-
GF0031651	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1534.1	-	-
GF0031650	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1533.1	-	-
GF0031649	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1532.1	-	-
GF0031648	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_7_mRNA_1515.1	-	-
GF0031647	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1514.1	-	-
GF0031646	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1); Retrotransposon gag domain [IPR005162] (1)	scaffold_7_mRNA_1513.1	-	-
GF0031645	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_149.1	-	-
GF0031644	1	0	0	Mutator-like transposase (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, PMZ-type [IPR006564] (1); MULE transposase domain [IPR018289] (1); Transposase, MuDR, plant [IPR004332] (1); Zinc finger, SWIM-type [IPR007527] (1)	scaffold_7_mRNA_1481.1	-	-
GF0031643	1	0	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Domain of unknown function DUF1985 [IPR015410] (1); Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	scaffold_7_mRNA_1480.1	-	-
GF0031642	1	0	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	scaffold_7_mRNA_1475.1	-	-
GF0031641	1	0	0	Disease resistance RPS5-like protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_7_mRNA_1471.1	-	-
GF0031640	1	0	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_7_mRNA_1462.1	-	-
GF0031639	1	0	0	Disease resistance protein family, putative (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_7_mRNA_1461.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0031638	1	0	0	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); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); AAA+ ATPase domain [IPR003593] (1); Leucine-rich repeat [IPR001611] (1); NB-ARC [IPR002182] (1)	scaffold_7_mRNA_1460.1	-	-
GF0031637	1	0	0	Hypothetical protein (1)	membrane [GO:0016020 cellular_component] (1)	ABC-2 type transporter [IPR013525] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_7_mRNA_1449.1	-	-
GF0031636	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1445.1	-	-
GF0031635	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1444.1	-	-
GF0031634	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1443.1	-	-
GF0031633	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1426.1	-	-
GF0031632	1	0	0	Wall-associated receptor kinase 2 (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1); polysaccharide binding [GO:0030247 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); Wall-associated receptor kinase, galacturonan-binding domain [IPR025287] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1)	scaffold_7_mRNA_1424.1	-	-
GF0031631	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	scaffold_7_mRNA_1423.1	-	-
GF0031630	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1422.1	-	-
GF0031629	1	0	0	Polynucleotidyl transferase, Ribonuclease H fold (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_7_mRNA_1421.1	-	-
GF0031628	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1420.1	-	-
GF0031627	1	0	0	Wall-associated receptor kinase 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-protein kinase, active site [IPR008271] (1); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1)	scaffold_7_mRNA_1419.1	-	-
GF0031626	1	0	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	scaffold_7_mRNA_1418.1	-	-
GF0031625	1	0	0	Monosacharide transport protein (1)			scaffold_7_mRNA_1416.1	-	-
GF0031624	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1415.1	-	-
GF0031623	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_7_mRNA_1414.1	-	-
GF0031622	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1410.1	-	-
GF0031621	1	0	0	Cyclin A2 (1)	nucleus [GO:0005634 cellular_component] (1)	Cyclin, N-terminal [IPR006671] (1); Cyclin, C-terminal domain [IPR004367] (1); Cyclin-like [IPR013763] (1)	scaffold_7_mRNA_1409.1	-	-
GF0031620	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1405.1	-	-
GF0031619	1	0	0	DNA repair protein XRCC1 (1)		BRCT domain [IPR001357] (1)	scaffold_7_mRNA_1399.1	-	-
GF0031618	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_7_mRNA_1397.1	-	-
GF0031617	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1396.1	-	-
GF0031616	1	0	0	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); Domain of unknown function DUF4283 [IPR025558] (1); Zinc finger, CCHC-type [IPR001878] (1)	scaffold_7_mRNA_1391.1	-	-
GF0031615	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1386.1	-	-
GF0031614	1	0	0	LRR receptor-like kinase family protein (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Protein kinase, ATP binding site [IPR017441] (1); Serine/threonine-protein kinase, active site [IPR008271] (1)	scaffold_7_mRNA_1384.1	-	-
GF0031613	1	0	0	SLG-Sc and SLA-Sc genes and Melmoth retrotransposon sequence (1)	DNA integration [GO:0015074 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Integrase, catalytic core [IPR001584] (1); Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1); Ribonuclease H-like domain [IPR012337] (1); GAG-pre-integrase domain [IPR025724] (1)	scaffold_7_mRNA_1379.1	-	-
GF0031612	1	0	0	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1); Gag-polypeptide of LTR copia-type [IPR029472] (1)	scaffold_7_mRNA_1376.1	-	-
GF0031611	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1370.1	-	-
GF0031610	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_7_mRNA_1369.1	-	-
GF0031609	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_7_mRNA_1366.1	-	-
GF0031608	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1350.1	-	-
GF0031607	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	scaffold_7_mRNA_1349.1	-	-
GF0031606	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1348.1	-	-
GF0031605	1	0	0	To encode a PR protein, Belongs to the plant thionin family with the following members:, putative (1)			scaffold_7_mRNA_1346.1	-	-
GF0031604	1	0	0	To encode a PR protein, Belongs to the plant thionin family with the following members:, putative (1)			scaffold_7_mRNA_1345.1	-	-
GF0031603	1	0	0	LRR receptor-like kinase family protein (1)	proteolysis [GO:0006508 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); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Protein kinase-like domain [IPR011009] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Aspartic peptidase, active site [IPR001969] (1); Leucine rich repeat 4 [IPR025875] (1); Protein kinase domain [IPR000719] (1); Leucine-rich repeat [IPR001611] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase, ATP binding site [IPR017441] (1); Aspartic peptidase domain [IPR021109] (1)	scaffold_7_mRNA_1339.1	-	-
GF0031602	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1335.1	-	-
GF0031601	1	0	0	DEAD-box ATP-dependent RNA helicase 1 (1)	nucleic acid binding [GO:0003676 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Helicase superfamily 1/2, ATP-binding domain [IPR014001] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); DEAD/DEAH box helicase domain [IPR011545] (1)	scaffold_7_mRNA_1324.1	-	-
GF0031600	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1321.1	-	-
GF0031599	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1320.1	-	-
GF0031598	1	0	0	Hypothetical protein (1)	transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (1)	Transferase [IPR003480] (1)	scaffold_7_mRNA_1318.1	-	-
GF0031597	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1314.1	-	-
GF0031596	1	0	0	Pseudo response regulator (1)	phosphorelay signal transduction system [GO:0000160 biological_process] (1)	CheY-like superfamily [IPR011006] (1); Signal transduction response regulator, receiver domain [IPR001789] (1)	scaffold_7_mRNA_131.1	-	-
GF0031595	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1309.1	-	-
GF0031594	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_130.1	-	-
GF0031593	1	0	0	Histidine kinase 1 (1)	transferase activity, transferring phosphorus-containing groups [GO:0016772 molecular_function] (1); phosphorylation [GO:0016310 biological_process] (1); signal transduction [GO:0007165 biological_process] (1); phosphorelay sensor kinase activity [GO:0000155 molecular_function] (1); phosphorelay signal transduction system [GO:0000160 biological_process] (1)	Histidine kinase-like ATPase, C-terminal domain [IPR003594] (1); Signal transduction histidine kinase, dimerisation/phosphoacceptor domain [IPR003661] (1); Signal transduction response regulator, receiver domain [IPR001789] (1); Signal transduction histidine kinase-related protein, C-terminal [IPR004358] (1); Histidine kinase domain [IPR005467] (1)	scaffold_7_mRNA_129.1	-	-
GF0031592	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1289.1	-	-
GF0031591	1	0	0	Hypothetical protein (1)		Zf-FLZ domain [IPR007650] (1)	scaffold_7_mRNA_128.1	-	-
GF0031590	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1278.1	-	-
GF0031589	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1277.1	-	-
GF0031588	1	0	0	Sulfite exporter TauE/SafE family protein (1)	integral component of membrane [GO:0016021 cellular_component] (1)	Transmembrane protein TauE-like [IPR002781] (1)	scaffold_7_mRNA_1271.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0031587	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1270.1	-	-
GF0031586	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1268.1	-	-
GF0031585	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1267.1	-	-
GF0031584	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1243.1	-	-
GF0031583	1	0	0	Hypothetical protein (1)		Thioredoxin-like fold [IPR012336] (1)	scaffold_7_mRNA_1236.1	-	-
GF0031582	1	0	0	Tonoplast intrinsic protein (1)	transporter activity [GO:0005215 molecular_function] (1); membrane [GO:0016020 cellular_component] (1); transport [GO:0006810 biological_process] (1)	Major intrinsic protein [IPR000425] (1); Aquaporin transporter [IPR034294] (1); Major intrinsic protein, conserved site [IPR022357] (1); Aquaporin-like [IPR023271] (1)	scaffold_7_mRNA_1226.1	-	-
GF0031581	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc knuckle CX2CX4HX4C [IPR025836] (1); Zinc finger, CCHC-type [IPR001878] (1); Domain of unknown function DUF4283 [IPR025558] (1)	scaffold_7_mRNA_1212.1	-	-
GF0031580	1	0	0	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	scaffold_7_mRNA_1210.1	-	-
GF0031579	1	0	0	Histidine-containing phosphotransfer protein 4 (1)	phosphorelay signal transduction system [GO:0000160 biological_process] (1); signal transducer activity [GO:0004871 molecular_function] (1)	Signal transduction histidine kinase, phosphotransfer (Hpt) domain [IPR008207] (1)	scaffold_7_mRNA_1192.1	-	-
GF0031578	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1184.1	-	-
GF0031577	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1175.1	-	-
GF0031576	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1161.1	-	-
GF0031575	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1155.1	-	-
GF0031574	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1147.1	-	-
GF0031573	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1146.1	-	-
GF0031572	1	0	0	Hypothetical protein (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_7_mRNA_1144.1	-	-
GF0031571	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1140.1	-	-
GF0031570	1	0	0	Isopentenyl transferase IPT2 (1)	tRNA processing [GO:0008033 biological_process] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); tRNA dimethylallyltransferase [IPR018022] (1)	scaffold_7_mRNA_114.1	-	-
GF0031569	1	0	0	LRR receptor-like kinase plant (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); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Malectin-like carbohydrate-binding domain [IPR024788] (1); Protein kinase domain [IPR000719] (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)	scaffold_7_mRNA_1138.1	-	-
GF0031568	1	0	0	LRR receptor-like kinase plant (1)	ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Malectin-like carbohydrate-binding domain [IPR024788] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Protein kinase-like domain [IPR011009] (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); Leucine-rich repeat [IPR001611] (1)	scaffold_7_mRNA_1136.1	-	-
GF0031567	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1132.1	-	-
GF0031566	1	0	0	Plasma membrane ATPase (1)	ATP biosynthetic process [GO:0006754 biological_process] (1); nucleotide binding [GO:0000166 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1); ATPase activity [GO:0016887 molecular_function] (1); metal ion binding [GO:0046872 molecular_function] (1)	P-type ATPase, subfamily IIIA [IPR006534] (1); P-type ATPase, transmembrane domain [IPR023298] (1); P-type ATPase, cytoplasmic domain N [IPR023299] (1); P-type ATPase [IPR001757] (1); Cation-transporting P-type ATPase, N-terminal [IPR004014] (1); HAD-like domain [IPR023214] (1); P-type ATPase, A domain [IPR008250] (1)	scaffold_7_mRNA_1130.1	-	-
GF0031565	1	0	0	Triacylglycerol lipase (1)	lipid metabolic process [GO:0006629 biological_process] (1)	Alpha/Beta hydrolase fold [IPR029058] (1); Fungal lipase-like domain [IPR002921] (1)	scaffold_7_mRNA_1128.1	-	-
GF0031564	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1121.1	-	-
GF0031563	1	0	0	1-phosphatidylinositol-3-phosphate 5-kinase FAB1 (1)	ATP binding [GO:0005524 molecular_function] (1); metal ion binding [GO:0046872 molecular_function] (1); phosphatidylinositol phosphate kinase activity [GO:0016307 molecular_function] (1); phosphatidylinositol metabolic process [GO:0046488 biological_process] (1)	FYVE zinc finger [IPR000306] (1); Phosphatidylinositol-4-phosphate 5-kinase, core [IPR002498] (1); Zinc finger, FYVE-related [IPR017455] (1); Zinc finger, FYVE/PHD-type [IPR011011] (1); GroEL-like apical domain [IPR027409] (1); Zinc finger, RING/FYVE/PHD-type [IPR013083] (1); Chaperonin Cpn60/TCP-1 family [IPR002423] (1); GroEL-like equatorial domain [IPR027413] (1); Phosphatidylinositol-4-phosphate 5-kinase, N-terminal domain [IPR027484] (1); Phosphatidylinositol-4-phosphate 5-kinase, C-terminal [IPR027483] (1)	scaffold_7_mRNA_1111.1	-	-
GF0031562	1	0	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_7_mRNA_1099.1	-	-
GF0031561	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1095.1	-	-
GF0031560	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1093.1	-	-
GF0031559	1	0	0	(S)-2-hydroxy-acid oxidase (1)	catalytic activity [GO:0003824 molecular_function] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); FMN binding [GO:0010181 molecular_function] (1)	Alpha-hydroxy acid dehydrogenase, FMN-dependent [IPR012133] (1); Aldolase-type TIM barrel [IPR013785] (1); FMN-dependent dehydrogenase [IPR000262] (1)	scaffold_7_mRNA_1073.1	-	-
GF0031558	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_7_mRNA_1071.1	-	-
GF0031557	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1068.1	-	-
GF0031556	1	0	0	Hypothetical protein (1)	4 iron, 4 sulfur cluster binding [GO:0051539 molecular_function] (1); lipoate synthase activity [GO:0016992 molecular_function] (1); lipoate biosynthetic process [GO:0009107 biological_process] (1)	Lipoyl synthase [IPR003698] (1)	scaffold_7_mRNA_1063.1	-	-
GF0031555	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1061.1	-	-
GF0031554	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1060.1	-	-
GF0031553	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1059.1	-	-
GF0031552	1	0	0	Monosacharide transport protein (1)			scaffold_7_mRNA_1058.1	-	-
GF0031551	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1057.1	-	-
GF0031550	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1056.1	-	-
GF0031549	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_7_mRNA_1054.1	-	-
GF0031548	1	0	0	Beta-ketoacyl-acyl-carrier-protein synthase II (1)	metabolic process [GO:0008152 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (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)	Polyketide synthase, beta-ketoacyl synthase domain [IPR020841] (1); Thiolase-like [IPR016039] (1); Beta-ketoacyl synthase, active site [IPR018201] (1); Beta-ketoacyl synthase, N-terminal [IPR014030] (1); 3-oxoacyl-[acyl-carrier-protein] synthase 2 [IPR017568] (1); Beta-ketoacyl synthase, C-terminal [IPR014031] (1)	scaffold_7_mRNA_1049.1	-	-
GF0031547	1	0	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_7_mRNA_1048.1	-	-
GF0031546	1	0	0	Putative non-LTR retroelement reverse transcriptase (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H-like domain [IPR012337] (1); Reverse transcriptase domain [IPR000477] (1); Endonuclease/exonuclease/phosphatase [IPR005135] (1)	scaffold_7_mRNA_1046.1	-	-
GF0031545	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1032.1	-	-

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GF0031544	1	0	0	Subtilisin-like serine protease (1)	serine-type endopeptidase activity [GO:0004252 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Peptidase S8, subtilisin, Ser-active site [IPR023828] (1); Peptidase S8 propeptide/proteinase inhibitor I9 [IPR010259] (1); Peptidase S8, subtilisin-related [IPR015500] (1); Protease propeptides/proteinase inhibitor I9 [IPR009020] (1); Peptidase S8/S53 domain [IPR000209] (1); PA domain [IPR003137] (1); Cucumisin-like catalytic domain [IPR034197] (1)	scaffold_7_mRNA_1015.1	-	-
GF0031543	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1012.1	-	-
GF0031542	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1011.1	-	-
GF0031541	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1010.1	-	-
GF0031540	1	0	0	Hypothetical protein (1)			scaffold_7_mRNA_1006.1	-	-
GF0031539	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_7_mRNA_1001.1	-	-
GF0031538	1	0	0	Monosacharide transport protein (1)			scaffold_6_mRNA_997.1	-	-
GF0031537	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_994.1	-	-
GF0031536	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_990.1	-	-
GF0031535	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_6_mRNA_989.1	-	-
GF0031534	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_986.1	-	-
GF0031533	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_984.1	-	-
GF0031532	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_983.1	-	-
GF0031531	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_6_mRNA_980.1	-	-
GF0031530	1	0	0	LRR receptor-like kinase family protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Protein kinase domain [IPR000719] (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); Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase, ATP binding site [IPR017441] (1)	scaffold_6_mRNA_98.1	-	-
GF0031529	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_978.1	-	-
GF0031528	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	Zinc finger, BED-type [IPR003656] (1); Zinc finger C2H2-type [IPR013087] (1)	scaffold_6_mRNA_976.1	-	-
GF0031527	1	0	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	scaffold_6_mRNA_974.1	-	-
GF0031526	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_967.1	-	-
GF0031525	1	0	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_6_mRNA_966.1	-	-
GF0031524	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_964.1	-	-
GF0031523	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF1985 [IPR015410] (1)	scaffold_6_mRNA_962.1	-	-
GF0031522	1	0	0	Mutator-like transposase (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, PMZ-type [IPR006564] (1); MULE transposase domain [IPR018289] (1); Transposase, MuDR, plant [IPR004332] (1); Zinc finger, SWIM-type [IPR007527] (1)	scaffold_6_mRNA_961.1	-	-
GF0031521	1	0	0	Hypothetical protein (1)		Arabidopsis retrotransposon Orf1 [IPR004312] (1)	scaffold_6_mRNA_960.1	-	-
GF0031520	1	0	0	LRR receptor-like kinase family protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1)	Protein kinase-like domain [IPR011009] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Protein kinase domain [IPR000719] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Serine/threonine-protein kinase, active site [IPR008271] (1)	scaffold_6_mRNA_96.1	-	-
GF0031519	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_959.1	-	-
GF0031518	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1); Chromo domain [IPR023780] (1); Chromo domain-like [IPR016197] (1)	scaffold_6_mRNA_955.1	-	-
GF0031517	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_951.1	-	-
GF0031516	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_95.1	-	-
GF0031515	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_946.1	-	-
GF0031514	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_941.1	-	-
GF0031513	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_94.1	-	-
GF0031512	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_937.1	-	-
GF0031511	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_932.1	-	-
GF0031510	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, SWIM-type [IPR007527] (1); Zinc finger, PMZ-type [IPR006564] (1)	scaffold_6_mRNA_929.1	-	-
GF0031509	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_928.1	-	-
GF0031508	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_920.1	-	-
GF0031507	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_918.1	-	-
GF0031506	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_911.1	-	-
GF0031505	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_908.1	-	-
GF0031504	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_907.1	-	-
GF0031503	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_906.1	-	-
GF0031502	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_900.1	-	-
GF0031501	1	0	0	Auxin efflux carrier component (1)	transmembrane transport [GO:0055085 biological_process] (1); integral component of membrane [GO:0016021 cellular_component] (1)	Membrane transport protein [IPR004776] (1)	scaffold_6_mRNA_891.1	-	-
GF0031500	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_889.1	-	-
GF0031499	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_888.1	-	-
GF0031498	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_884.1	-	-
GF0031497	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_876.1	-	-
GF0031496	1	0	0	DNA-damage-repair/toleration protein DRT100 (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)	scaffold_6_mRNA_875.1	-	-
GF0031495	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_867.1	-	-
GF0031494	1	0	0	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	scaffold_6_mRNA_865.1	-	-
GF0031493	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_863.1	-	-
GF0031492	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_6_mRNA_862.1	-	-
GF0031491	1	0	0	CDNA clone:002-112-G06, full insert sequence (1)			scaffold_6_mRNA_861.1	-	-
GF0031490	1	0	0	LRR receptor-like kinase family protein (1)	protein binding [GO:0005515 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase, ATP binding site [IPR017441] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1)	scaffold_6_mRNA_86.1	-	-
GF0031489	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_856.1	-	-
GF0031488	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_855.1	-	-
GF0031487	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	Zinc finger, BED-type [IPR003656] (1); Zinc finger C2H2-type [IPR013087] (1)	scaffold_6_mRNA_853.1	-	-
GF0031486	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_850.1	-	-
GF0031485	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_85.1	-	-
GF0031484	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_6_mRNA_849.1	-	-
GF0031483	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_846.1	-	-
GF0031482	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_845.1	-	-
GF0031481	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_844.1	-	-
GF0031480	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_839.1	-	-
GF0031479	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_838.1	-	-

ID	**Num. in *C. celementine***	**Num in *C. unshiu***	**Num in *P.trifoliata***	**Note**	**GO**	**InterPro**	**Members in *C.clementine***	**Members in *C.unshiu***	**Members in *P.trifoliata***
GF0031478	1	0	0	Hypothetical protein (1)	structural constituent of ribosome [GO:0003735 molecular_function] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1); intracellular [GO:0005622 cellular_component] (1); translation [GO:0006412 biological_process] (1); ribosome [GO:0005840 cellular_component] (1); proteolysis [GO:0006508 biological_process] (1)	Translation protein SH3-like domain [IPR008991] (1); Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1); Ribosomal protein L14e domain [IPR002784] (1); Ribosomal protein L2 domain 2 [IPR014722] (1)	scaffold_6_mRNA_832.1	-	-
GF0031477	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_83.1	-	-
GF0031476	1	0	0	BED zinc finger,hAT family dimerization domain isoform 1 (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-like transposase, RNase-H fold [IPR025525] (1); Ribonuclease H-like domain [IPR012337] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	scaffold_6_mRNA_829.1	-	-
GF0031475	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_828.1	-	-
GF0031474	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_826.1	-	-
GF0031473	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_824.1	-	-
GF0031472	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_823.1	-	-
GF0031471	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_821.1	-	-
GF0031470	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_820.1	-	-
GF0031469	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_82.1	-	-
GF0031468	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_818.1	-	-
GF0031467	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_813.1	-	-
GF0031466	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_812.1	-	-
GF0031465	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_6_mRNA_811.1	-	-
GF0031464	1	0	0	Monosacharide transport protein (1)			scaffold_6_mRNA_81.1	-	-
GF0031463	1	0	0	Putative AC 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)	scaffold_6_mRNA_809.1	-	-
GF0031462	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_806.1	-	-
GF0031461	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_804.1	-	-
GF0031460	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_802.1	-	-
GF0031459	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Eukaryotic translation initiation factor 3 subunit G, N-terminal [IPR024675] (1); Zinc finger, CCHC-type [IPR001878] (1)	scaffold_6_mRNA_800.1	-	-
GF0031458	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_796.1	-	-
GF0031457	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_6_mRNA_795.1	-	-
GF0031456	1	0	0	Hypothetical protein (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1)	scaffold_6_mRNA_793.1	-	-
GF0031455	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_787.1	-	-
GF0031454	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_785.1	-	-
GF0031453	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_780.1	-	-
GF0031452	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_779.1	-	-
GF0031451	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_778.1	-	-
GF0031450	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_777.1	-	-
GF0031449	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_775.1	-	-
GF0031448	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_6_mRNA_768.1	-	-
GF0031447	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_767.1	-	-
GF0031446	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	scaffold_6_mRNA_766.1	-	-
GF0031445	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_765.1	-	-
GF0031444	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_763.1	-	-
GF0031443	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_762.1	-	-
GF0031442	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_6_mRNA_751.1	-	-
GF0031441	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_6_mRNA_748.1	-	-
GF0031440	1	0	0	Retrotransposon gag protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_6_mRNA_742.1	-	-
GF0031439	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_6_mRNA_739.1	-	-
GF0031438	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_6_mRNA_738.1	-	-
GF0031437	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_737.1	-	-
GF0031436	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_734.1	-	-
GF0031435	1	0	0	Neutral alpha-glucosidase (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); protein binding [GO:0005515 molecular_function] (1); carbohydrate binding [GO:0030246 molecular_function] (1)	Glycoside hydrolase family 31 [IPR000322] (1); Galactose mutarotase-like domain [IPR011013] (1); Domain of unknown function DUF5110 [IPR033403] (1); Glycoside hydrolase superfamily [IPR017853] (1); WW domain [IPR001202] (1)	scaffold_6_mRNA_730.1	-	-
GF0031434	1	0	0	Pentatricopeptide repeat-containing family protein (1)		Pentatricopeptide repeat [IPR002885] (1)	scaffold_6_mRNA_729.1	-	-
GF0031433	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_6_mRNA_719.1	-	-
GF0031432	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_718.1	-	-
GF0031431	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_717.1	-	-
GF0031430	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_714.1	-	-
GF0031429	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_6_mRNA_713.1	-	-
GF0031428	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_711.1	-	-
GF0031427	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_709.1	-	-
GF0031426	1	0	0	UDP-glycosyltransferase 73C5 (1)	transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	scaffold_6_mRNA_708.1	-	-
GF0031425	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_702.1	-	-
GF0031424	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_6_mRNA_701.1	-	-
GF0031423	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_700.1	-	-
GF0031422	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_695.1	-	-
GF0031421	1	0	0	UDP-glycosyltransferase 73D1 (1)	transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	scaffold_6_mRNA_694.1	-	-
GF0031420	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_6_mRNA_690.1	-	-
GF0031419	1	0	0	BED zinc finger,hAT family dimerization domain (1)	nucleic acid binding [GO:0003676 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	Zinc finger C2H2-type [IPR013087] (1); Ribonuclease H-like domain [IPR012337] (1); Zinc finger, BED-type [IPR003656] (1)	scaffold_6_mRNA_689.1	-	-
GF0031418	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_688.1	-	-
GF0031417	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_686.1	-	-
GF0031416	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_6_mRNA_685.1	-	-
GF0031415	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_684.1	-	-
GF0031414	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_683.1	-	-
GF0031413	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_68.1	-	-
GF0031412	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_6_mRNA_677.1	-	-
GF0031411	1	0	0	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	scaffold_6_mRNA_676.1	-	-
GF0031410	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_674.1	-	-
GF0031409	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_673.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0031408	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); DNA integration [GO:0015074 biological_process] (1)	Ribonuclease H-like domain [IPR012337] (1); Integrase, catalytic core [IPR001584] (1)	scaffold_6_mRNA_670.1	-	-
GF0031407	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_664.1	-	-
GF0031406	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_6_mRNA_662.1	-	-
GF0031405	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_661.1	-	-
GF0031404	1	0	0	RAB GTPase-like protein A5B (1)	GTPase activity [GO:0003924 molecular_function] (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 [IPR001806] (1)	scaffold_6_mRNA_656.1	-	-
GF0031403	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_650.1	-	-
GF0031402	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_649.1	-	-
GF0031401	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_6_mRNA_648.1	-	-
GF0031400	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			scaffold_6_mRNA_646.1	-	-
GF0031399	1	0	0	Integrase (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_6_mRNA_645.1	-	-
GF0031398	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_6_mRNA_644.1	-	-
GF0031397	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_643.1	-	-
GF0031396	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_642.1	-	-
GF0031395	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_6_mRNA_641.1	-	-
GF0031394	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_639.1	-	-
GF0031393	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); DNA integration [GO:0015074 biological_process] (1)	Integrase, catalytic core [IPR001584] (1); Ribonuclease H-like domain [IPR012337] (1); GAG-pre-integrase domain [IPR025724] (1)	scaffold_6_mRNA_638.1	-	-
GF0031392	1	0	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Aspartic peptidase domain [IPR021109] (1); Peptidase A2A, retrovirus, catalytic [IPR001995] (1); Reverse transcriptase domain [IPR000477] (1); Retropepsins [IPR018061] (1)	scaffold_6_mRNA_636.1	-	-
GF0031391	1	0	0	Hypothetical protein (1)		Paraneoplastic antigen Ma [IPR026523] (1); Reverse transcriptase domain [IPR000477] (1)	scaffold_6_mRNA_632.1	-	-
GF0031390	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_6_mRNA_629.1	-	-
GF0031389	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_628.1	-	-
GF0031388	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_6_mRNA_627.1	-	-
GF0031387	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_626.1	-	-
GF0031386	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_625.1	-	-
GF0031385	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1); Domain of unknown function DUF4219 [IPR025314] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_6_mRNA_624.1	-	-
GF0031384	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_623.1	-	-
GF0031383	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_6_mRNA_622.1	-	-
GF0031382	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_6_mRNA_621.1	-	-
GF0031381	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_62.1	-	-
GF0031380	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_6_mRNA_619.1	-	-
GF0031379	1	0	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Carlavirus nucleic acid-binding protein [IPR002568] (1)	scaffold_6_mRNA_618.1	-	-
GF0031378	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			scaffold_6_mRNA_616.1	-	-
GF0031377	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_615.1	-	-
GF0031376	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_6_mRNA_614.1	-	-
GF0031375	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_613.1	-	-
GF0031374	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_612.1	-	-
GF0031373	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_610.1	-	-
GF0031372	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_6_mRNA_609.1	-	-
GF0031371	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_607.1	-	-
GF0031370	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_6_mRNA_603.1	-	-
GF0031369	1	0	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_6_mRNA_602.1	-	-
GF0031368	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_601.1	-	-
GF0031367	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_6_mRNA_600.1	-	-
GF0031366	1	0	0	Retrotransposon protein, putative, Ty3-gypsy subclass, expressed (1)		Reverse transcriptase domain [IPR000477] (1); Aspartic peptidase domain [IPR021109] (1)	scaffold_6_mRNA_60.1	-	-
GF0031365	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_598.1	-	-
GF0031364	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_596.1	-	-
GF0031363	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_592.1	-	-
GF0031362	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_6_mRNA_591.1	-	-
GF0031361	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_589.1	-	-
GF0031360	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_588.1	-	-
GF0031359	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_6_mRNA_587.1	-	-
GF0031358	1	0	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); serine-type endopeptidase activity [GO:0004252 molecular_function] (1)	Viral movement protein [IPR028919] (1); Trichovirus movement protein [IPR001815] (1)	scaffold_6_mRNA_584.1	-	-
GF0031357	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_583.1	-	-
GF0031356	1	0	0	Transmembrane protein 136 (1)			scaffold_6_mRNA_579.1	-	-
GF0031355	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_6_mRNA_578.1	-	-
GF0031354	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_577.1	-	-
GF0031353	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_576.1	-	-
GF0031352	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_575.1	-	-
GF0031351	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_6_mRNA_570.1	-	-
GF0031350	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_569.1	-	-
GF0031349	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_568.1	-	-
GF0031348	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_6_mRNA_567.1	-	-
GF0031347	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_565.1	-	-
GF0031346	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_564.1	-	-
GF0031345	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_561.1	-	-
GF0031344	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_560.1	-	-
GF0031343	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			scaffold_6_mRNA_559.1	-	-
GF0031342	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_558.1	-	-
GF0031341	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_555.1	-	-
GF0031340	1	0	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_6_mRNA_554.1	-	-
GF0031339	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_552.1	-	-
GF0031338	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4218 [IPR025452] (1)	scaffold_6_mRNA_551.1	-	-
GF0031337	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_55.1	-	-
GF0031336	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_6_mRNA_549.1	-	-
GF0031335	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Domain of unknown function DUF4219 [IPR025314] (1)	scaffold_6_mRNA_548.1	-	-
GF0031334	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_546.1	-	-
GF0031333	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_6_mRNA_545.1	-	-
GF0031332	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_543.1	-	-
GF0031331	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_542.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0031330	1	0	0	Hypothetical protein (1)		Arabidopsis retrotransposon Orf1 [IPR004312] (1)	scaffold_6_mRNA_54.1	-	-
GF0031329	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_6_mRNA_539.1	-	-
GF0031328	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_538.1	-	-
GF0031327	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_536.1	-	-
GF0031326	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_535.1	-	-
GF0031325	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_534.1	-	-
GF0031324	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_531.1	-	-
GF0031323	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_6_mRNA_526.1	-	-
GF0031322	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_525.1	-	-
GF0031321	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_522.1	-	-
GF0031320	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_6_mRNA_521.1	-	-
GF0031319	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_6_mRNA_520.1	-	-
GF0031318	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_515.1	-	-
GF0031317	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_512.1	-	-
GF0031316	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_6_mRNA_511.1	-	-
GF0031315	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_510.1	-	-
GF0031314	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_507.1	-	-
GF0031313	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_6_mRNA_505.1	-	-
GF0031312	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_504.1	-	-
GF0031311	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_502.1	-	-
GF0031310	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_500.1	-	-
GF0031309	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_6_mRNA_499.1	-	-
GF0031308	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_6_mRNA_497.1	-	-
GF0031307	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_493.1	-	-
GF0031306	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_491.1	-	-
GF0031305	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_490.1	-	-
GF0031304	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_49.1	-	-
GF0031303	1	0	0	Retrotransposon protein, putative, Ty1-copia subclass (1)	DNA integration [GO:0015074 biological_process] (1); zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Integrase, catalytic core [IPR001584] (1); Ribonuclease H-like domain [IPR012337] (1); Zinc finger, CCHC-type [IPR001878] (1); GAG-pre-integrase domain [IPR025724] (1)	scaffold_6_mRNA_487.1	-	-
GF0031302	1	0	0	Hypothetical protein (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 domain 2 [IPR014722] (1); Ribosomal protein L27e [IPR001141] (1)	scaffold_6_mRNA_480.1	-	-
GF0031301	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4219 [IPR025314] (1)	scaffold_6_mRNA_48.1	-	-
GF0031300	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_479.1	-	-
GF0031299	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_478.1	-	-
GF0031298	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_6_mRNA_474.1	-	-
GF0031297	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_473.1	-	-
GF0031296	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_469.1	-	-
GF0031295	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Pentatricopeptide repeat [IPR002885] (1); Tetratricopeptide-like helical domain [IPR011990] (1)	scaffold_6_mRNA_466.1	-	-
GF0031294	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_464.1	-	-
GF0031293	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_6_mRNA_463.1	-	-
GF0031292	1	0	0	Hypothetical protein (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Aspartic peptidase domain [IPR021109] (1); Peptidase A2A, retrovirus, catalytic [IPR001995] (1); Retropepsins [IPR018061] (1)	scaffold_6_mRNA_462.1	-	-
GF0031291	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_456.1	-	-
GF0031290	1	0	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1); Domain of unknown function DUF1985 [IPR015410] (1)	scaffold_6_mRNA_450.1	-	-
GF0031289	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_447.1	-	-
GF0031288	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_446.1	-	-
GF0031287	1	0	0	Retrotransposon protein, putative, Ty3-gypsy subclass (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_6_mRNA_444.1	-	-
GF0031286	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_442.1	-	-
GF0031285	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_6_mRNA_440.1	-	-
GF0031284	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_6_mRNA_437.1	-	-
GF0031283	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_6_mRNA_435.1	-	-
GF0031282	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_434.1	-	-
GF0031281	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_425.1	-	-
GF0031280	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_423.1	-	-
GF0031279	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_6_mRNA_422.1	-	-
GF0031278	1	0	0	Hypothetical protein (1)		Probable transposase, Ptta/En/Spm, plant [IPR004252] (1)	scaffold_6_mRNA_421.1	-	-
GF0031277	1	0	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1); FAR1 DNA binding domain [IPR004330] (1)	scaffold_6_mRNA_42.1	-	-
GF0031276	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_419.1	-	-
GF0031275	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_6_mRNA_411.1	-	-
GF0031274	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_410.1	-	-
GF0031273	1	0	0	Hypothetical protein (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Aspartic peptidase, active site [IPR001969] (1); Peptidase A2A, retrovirus, catalytic [IPR001995] (1)	scaffold_6_mRNA_407.1	-	-
GF0031272	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Retropepsins [IPR018061] (1); Aspartic peptidase domain [IPR021109] (1); Zinc finger, CCHC-type [IPR001878] (1)	scaffold_6_mRNA_406.1	-	-
GF0031271	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_405.1	-	-
GF0031270	1	0	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger C2H2-type [IPR013087] (1); Ribonuclease H-like domain [IPR012337] (1); Zinc finger, BED-type [IPR003656] (1)	scaffold_6_mRNA_399.1	-	-
GF0031269	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_398.1	-	-
GF0031268	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_6_mRNA_396.1	-	-
GF0031267	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_6_mRNA_395.1	-	-
GF0031266	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_392.1	-	-
GF0031265	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_385.1	-	-
GF0031264	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_38.1	-	-
GF0031263	1	0	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	scaffold_6_mRNA_372.1	-	-
GF0031262	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_368.1	-	-
GF0031261	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	Zinc finger, BED-type [IPR003656] (1); Zinc finger C2H2-type [IPR013087] (1)	scaffold_6_mRNA_364.1	-	-
GF0031260	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_362.1	-	-
GF0031259	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_6_mRNA_36.1	-	-
GF0031258	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_355.1	-	-
GF0031257	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_352.1	-	-
GF0031256	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_35.1	-	-
GF0031255	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4218 [IPR025452] (1); Transposon, En/Spm-like [IPR004242] (1)	scaffold_6_mRNA_346.1	-	-
GF0031254	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_344.1	-	-
GF0031253	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_342.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0031252	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_338.1	-	-
GF0031251	1	0	0	Transposable element protein, putative (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_6_mRNA_336.1	-	-
GF0031250	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_333.1	-	-
GF0031249	1	0	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_6_mRNA_330.1	-	-
GF0031248	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_329.1	-	-
GF0031247	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_328.1	-	-
GF0031246	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_326.1	-	-
GF0031245	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_325.1	-	-
GF0031244	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_323.1	-	-
GF0031243	1	0	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); hAT-like transposase, RNase-H fold [IPR025525] (1)	scaffold_6_mRNA_320.1	-	-
GF0031242	1	0	0	Transposable element protein, putative, (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_6_mRNA_3189.1	-	-
GF0031241	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_3187.1	-	-
GF0031240	1	0	0	Transposon protein, putative, Mutator sub-class, expressed (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, PMZ-type [IPR006564] (1); Transposase, MuDR, plant [IPR004332] (1); Zinc finger, SWIM-type [IPR007527] (1); Zinc finger, CCHC-type [IPR001878] (1)	scaffold_6_mRNA_3178.1	-	-
GF0031239	1	0	0	Hydroxyproline-rich glycoprotein family protein (1)		Spo12 [IPR007727] (1)	scaffold_6_mRNA_3167.1	-	-
GF0031238	1	0	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_6_mRNA_3091.1	-	-
GF0031237	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4219 [IPR025314] (1)	scaffold_6_mRNA_308.1	-	-
GF0031236	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_3073.1	-	-
GF0031235	1	0	0	60S ribosomal protein L34 (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 L34Ae [IPR008195] (1); Ribosomal protein L34e, conserved site [IPR018065] (1)	scaffold_6_mRNA_3067.1	-	-
GF0031234	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_3066.1	-	-
GF0031233	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_3064.1	-	-
GF0031232	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_3062.1	-	-
GF0031231	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Domain of unknown function DUF627, N-terminal [IPR006866] (1); Tetratricopeptide-like helical domain [IPR011990] (1)	scaffold_6_mRNA_3061.1	-	-
GF0031230	1	0	0	Hypothetical protein (1)		Quinoprotein alcohol dehydrogenase-like superfamily [IPR011047] (1); Pyrrolo-quinoline quinone repeat [IPR002372] (1)	scaffold_6_mRNA_3036.1	-	-
GF0031229	1	0	0	Ubiquitin-conjugating enzyme E2 2 (1)		Ubiquitin-conjugating enzyme E2 [IPR000608] (1); Ubiquitin-conjugating enzyme/RWD-like [IPR016135] (1)	scaffold_6_mRNA_3034.1	-	-
GF0031228	1	0	0	Hypothetical protein (1)		AmbAllergen [IPR018082] (1); Pectin lyase fold/virulence factor [IPR011050] (1); Pectin lyase fold [IPR012334] (1)	scaffold_6_mRNA_3024.1	-	-
GF0031227	1	0	0	Hypothetical protein (1)		Pectin lyase fold [IPR012334] (1)	scaffold_6_mRNA_3021.1	-	-
GF0031226	1	0	0	Nucleic acid binding protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_6_mRNA_302.1	-	-
GF0031225	1	0	0	Hypothetical protein (1)		Pectin lyase fold/virulence factor [IPR011050] (1); Pectin lyase fold [IPR012334] (1)	scaffold_6_mRNA_3018.1	-	-
GF0031224	1	0	0	Hypothetical protein (1)	DNA integration [GO:0015074 biological_process] (1); nucleus [GO:0005634 cellular_component] (1); nucleosome assembly [GO:0006334 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Nucleosome assembly protein (NAP) [IPR002164] (1); Domain of unknown function DUF4371 [IPR025398] (1); Ribonuclease H-like domain [IPR012337] (1); Integrase, catalytic core [IPR001584] (1)	scaffold_6_mRNA_3017.1	-	-
GF0031223	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_3015.1	-	-
GF0031222	1	0	0	Hypothetical protein (1)	transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (1)	Transferase [IPR003480] (1)	scaffold_6_mRNA_3014.1	-	-
GF0031221	1	0	0	Hypothetical protein (1)	acylphosphatase activity [GO:0003998 molecular_function] (1)	Acylphosphatase, conserved site [IPR017968] (1); Acylphosphatase-like domain [IPR001792] (1); Reverse transcriptase domain [IPR000477] (1); Acylphosphatase [IPR020456] (1)	scaffold_6_mRNA_301.1	-	-
GF0031220	1	0	0	LRR and NB-ARC domain disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	Receptor L-domain [IPR000494] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	scaffold_6_mRNA_30.1	-	-
GF0031219	1	0	0	Putative inactive receptor 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)	scaffold_6_mRNA_2985.1	-	-
GF0031218	1	0	0	Hypothetical protein (1)		Protein of unknown function DUF761, plant [IPR008480] (1)	scaffold_6_mRNA_2983.1	-	-
GF0031217	1	0	0	Hypothetical protein (1)		Gibberellin regulated protein [IPR003854] (1)	scaffold_6_mRNA_2976.1	-	-
GF0031216	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_2973.1	-	-
GF0031215	1	0	0	Protein CREG2 (1)	FMN binding [GO:0010181 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1)	FMN-binding split barrel [IPR012349] (1); Cellular repressor of E1A-stimulated genes (CREG) [IPR014631] (1)	scaffold_6_mRNA_2965.1	-	-
GF0031214	1	0	0	F-box protein interaction domain protein (1)	protein binding [GO:0005515 molecular_function] (1)	Galactose oxidase/kelch, beta-propeller [IPR011043] (1); F-box associated interaction domain [IPR017451] (1); F-box domain [IPR001810] (1); F-box associated domain, type 1 [IPR006527] (1); Kelch-type beta propeller [IPR015915] (1)	scaffold_6_mRNA_2939.1	-	-
GF0031213	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	F-box domain [IPR001810] (1)	scaffold_6_mRNA_2938.1	-	-
GF0031212	1	0	0	Pollen Ole e 1 allergen and extensin (1)			scaffold_6_mRNA_2927.1	-	-
GF0031211	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_289.1	-	-
GF0031210	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_2884.1	-	-
GF0031209	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_2872.1	-	-
GF0031208	1	0	0	NAD(P)-binding Rossmann-fold superfamily protein isoform 2 (1)		NAD(P)-binding domain [IPR016040] (1)	scaffold_6_mRNA_2871.2	-	-
GF0031207	1	0	0	Putative nuclear matrix constituent protein 1-like protein (1)			scaffold_6_mRNA_2854.1	-	-
GF0031206	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_285.1	-	-
GF0031205	1	0	0	Cytochrome c oxidase biogenesis protein Cmc1-like (1)		Cytochrome c oxidase biogenesis protein Cmc1-like [IPR013892] (1)	scaffold_6_mRNA_2836.1	-	-
GF0031204	1	0	0	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	scaffold_6_mRNA_2832.1	-	-
GF0031203	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_283.1	-	-
GF0031202	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_2820.1	-	-
GF0031201	1	0	0	Transmembrane isoform 1 (1)			scaffold_6_mRNA_2815.1	-	-
GF0031200	1	0	0	Hypothetical protein (1)	transmembrane transport [GO:0055085 biological_process] (1); thiamine pyrophosphate binding [GO:0030976 molecular_function] (1); drug transmembrane transporter activity [GO:0015238 molecular_function] (1); antiporter activity [GO:0015297 molecular_function] (1); membrane [GO:0016020 cellular_component] (1); drug transmembrane transport [GO:0006855 biological_process] (1); magnesium ion binding [GO:0000287 molecular_function] (1); catalytic activity [GO:0003824 molecular_function] (1)	Thiamine pyrophosphate enzyme, C-terminal TPP-binding [IPR011766] (1); Thiamine pyrophosphate enzyme, central domain [IPR012000] (1); DHS-like NAD/FAD-binding domain [IPR029035] (1); Multi antimicrobial extrusion protein [IPR002528] (1); Thiamine pyrophosphate enzyme, N-terminal TPP-binding domain [IPR012001] (1); TPP-binding enzyme, conserved site [IPR000399] (1); Thiamin diphosphate-binding fold [IPR029061] (1)	scaffold_6_mRNA_2777.1	-	-
GF0031199	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_2775.1	-	-
GF0031198	1	0	0	Sugar transport protein 1 (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)	scaffold_6_mRNA_2774.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0031197	1	0	0	SNW domain-containing protein 1 (1)	mRNA splicing, via spliceosome [GO:0000398 biological_process] (1); spliceosomal complex [GO:0005681 cellular_component] (1)	SKI-interacting protein SKIP, SNW domain [IPR004015] (1); SKI-interacting protein, SKIP [IPR017862] (1)	scaffold_6_mRNA_2773.1	-	-
GF0031196	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_2772.1	-	-
GF0031195	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_2771.1	-	-
GF0031194	1	0	0	Retrotransposon protein, putative, Ty3-gypsy subclass, expressed (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_6_mRNA_2770.1	-	-
GF0031193	1	0	0	Putative MATE efflux family protein (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)	scaffold_6_mRNA_2769.1	-	-
GF0031192	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_276.1	-	-
GF0031191	1	0	0	E3 ubiquitin-protein ligase (1)	multicellular organism development [GO:0007275 biological_process] (1); protein binding [GO:0005515 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1); ubiquitin-dependent protein catabolic process [GO:0006511 biological_process] (1); nucleus [GO:0005634 cellular_component] (1)	TRAF-like [IPR008974] (1); Zinc finger, SIAH-type [IPR013010] (1); E3 ubiquitin-protein ligase SIN-like [IPR004162] (1); Zinc finger, RING-type [IPR001841] (1); Zinc finger, RING/FYVE/PHD-type [IPR013083] (1); Seven-in-absentia protein, TRAF-like domain [IPR018121] (1)	scaffold_6_mRNA_2742.1	-	-
GF0031190	1	0	0	Hypothetical protein (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1); hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (1)	Glycoside hydrolase family 1 [IPR001360] (1); Glycoside hydrolase superfamily [IPR017853] (1)	scaffold_6_mRNA_2739.1	-	-
GF0031189	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_273.1	-	-
GF0031188	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_6_mRNA_2729.1	-	-
GF0031187	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_6_mRNA_2712.1	-	-
GF0031186	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_2711.1	-	-
GF0031185	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_2710.1	-	-
GF0031184	1	0	0	An2 truncated protein (1)	DNA binding [GO:0003677 molecular_function] (1)	SANT/Myb domain [IPR001005] (1); Homeobox domain-like [IPR009057] (1); Myb domain [IPR017930] (1)	scaffold_6_mRNA_2708.1	-	-
GF0031183	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_270.1	-	-
GF0031182	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_2671.1	-	-
GF0031181	1	0	0	Hypothetical protein (1)		Transposase, MuDR, plant [IPR004332] (1)	scaffold_6_mRNA_267.1	-	-
GF0031180	1	0	0	Gibberellic acid-stimulated protein 1 (1)		Gibberellin regulated protein [IPR003854] (1)	scaffold_6_mRNA_2666.1	-	-
GF0031179	1	0	0	Salutaridinol 7-O-acetyltransferase (1)	transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (1)	Transferase [IPR003480] (1)	scaffold_6_mRNA_2664.1	-	-
GF0031178	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_264.1	-	-
GF0031177	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_262.1	-	-
GF0031176	1	0	0	Putative exocyst complex component 6 (1)	vesicle docking involved in exocytosis [GO:0006904 biological_process] (1); exocyst [GO:0000145 cellular_component] (1)	Exocyst complex component EXOC6/Sec15 [IPR007225] (1)	scaffold_6_mRNA_2616.1	-	-
GF0031175	1	0	0	Hypothetical protein (1)	integral component of membrane [GO:0016021 cellular_component] (1); membrane [GO:0016020 cellular_component] (1); transmembrane transporter activity [GO:0022857 molecular_function] (1)	EamA domain [IPR000620] (1); WAT1-related protein [IPR030184] (1)	scaffold_6_mRNA_2612.1	-	-
GF0031174	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Tetratricopeptide repeat [IPR019734] (1); Tetratricopeptide repeat-containing domain [IPR013026] (1); Peptidyl-prolyl cis-trans isomerase, FKBP-type [IPR023566] (1); Tetratricopeptide-like helical domain [IPR011990] (1)	scaffold_6_mRNA_2611.1	-	-
GF0031173	1	0	0	NAC transcription factor (1)	DNA binding [GO:0003677 molecular_function] (1); transcription, DNA-templated [GO:0006351 biological_process] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	NAC domain [IPR003441] (1); Transcription elongation factor S-II, central domain [IPR003618] (1)	scaffold_6_mRNA_2603.1	-	-
GF0031172	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_6_mRNA_26.1	-	-
GF0031171	1	0	0	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)	Malectin-like carbohydrate-binding domain [IPR024788] (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); Protein kinase, ATP binding site [IPR017441] (1)	scaffold_6_mRNA_2590.1	-	-
GF0031170	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_2585.1	-	-
GF0031169	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_2570.1	-	-
GF0031168	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_256.1	-	-
GF0031167	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_2554.1	-	-
GF0031166	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	PAZ domain [IPR003100] (1); Argonaute, linker 1 domain [IPR014811] (1)	scaffold_6_mRNA_2553.1	-	-
GF0031165	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_253.1	-	-
GF0031164	1	0	0	Retrotransposon gag protein (1)		Paraneoplastic antigen Ma [IPR026523] (1); Aspartic peptidase domain [IPR021109] (1); Retrotransposon gag domain [IPR005162] (1); LOG family [IPR031100] (1); Reverse transcriptase domain [IPR000477] (1)	scaffold_6_mRNA_252.1	-	-
GF0031163	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_2511.1	-	-
GF0031162	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_25.1	-	-
GF0031161	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_6_mRNA_2496.1	-	-
GF0031160	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_2484.1	-	-
GF0031159	1	0	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	scaffold_6_mRNA_2483.1	-	-
GF0031158	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_248.1	-	-
GF0031157	1	0	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); ATPase activity [GO:0016887 molecular_function] (1); membrane [GO:0016020 cellular_component] (1)	Plant PDR ABC transporter associated [IPR013581] (1); ABC-transporter extracellular N-terminal domain [IPR029481] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); AAA+ ATPase domain [IPR003593] (1); ABC-2 type transporter [IPR013525] (1); ATP-binding cassette transporter, PDR-like subfamily G, domain 1 [IPR034001] (1); ABC transporter-like [IPR003439] (1)	scaffold_6_mRNA_2473.1	-	-
GF0031156	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_247.1	-	-
GF0031155	1	0	0	Cytochrome P450 94A1 (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)	scaffold_6_mRNA_2464.1	-	-
GF0031154	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_2461.1	-	-
GF0031153	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_246.1	-	-
GF0031152	1	0	0	Solute carrier family 35 member F2 isoform 4 (1)	integral component of membrane [GO:0016021 cellular_component] (1); transport [GO:0006810 biological_process] (1)	Solute carrier family 35 member SLC35F1/F2/F6 [IPR009262] (1)	scaffold_6_mRNA_2452.1	-	-
GF0031151	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_245.1	-	-
GF0031150	1	0	0	Hypothetical protein (1)		Alpha/Beta hydrolase fold [IPR029058] (1)	scaffold_6_mRNA_2442.1	-	-
GF0031149	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_6_mRNA_244.1	-	-
GF0031148	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_2435.1	-	-
GF0031147	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_243.1	-	-
GF0031146	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_2429.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0031145	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_6_mRNA_242.1	-	-
GF0031144	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_241.1	-	-
GF0031143	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_240.1	-	-
GF0031142	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_24.1	-	-
GF0031141	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_239.1	-	-
GF0031140	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_238.1	-	-
GF0031139	1	0	0	RNA binding family protein isoform 1 (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	RNA recognition motif domain [IPR000504] (1)	scaffold_6_mRNA_2376.1	-	-
GF0031138	1	0	0	Embryo defective 2735 (1)			scaffold_6_mRNA_2372.1	-	-
GF0031137	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_6_mRNA_237.1	-	-
GF0031136	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	Zinc finger C2H2-type [IPR013087] (1); Zinc finger, BED-type [IPR003656] (1)	scaffold_6_mRNA_2363.1	-	-
GF0031135	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_236.1	-	-
GF0031134	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_233.1	-	-
GF0031133	1	0	0	Dof zinc finger protein DOF3.5 (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); DNA binding [GO:0003677 molecular_function] (1)	Zinc finger, Dof-type [IPR003851] (1)	scaffold_6_mRNA_2321.1	-	-
GF0031132	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_232.1	-	-
GF0031131	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_231.1	-	-
GF0031130	1	0	0	40S ribosomal protein S5 (1)	translation [GO:0006412 biological_process] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1); RNA binding [GO:0003723 molecular_function] (1); small ribosomal subunit [GO:0015935 cellular_component] (1)	Ribosomal protein S7, conserved site [IPR020606] (1); Ribosomal protein S7 domain [IPR023798] (1); Ribosomal protein S5/S7 [IPR000235] (1); Ribosomal protein S5/S7, eukaryotic/archaeal [IPR005716] (1)	scaffold_6_mRNA_2285.1	-	-
GF0031129	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_226.1	-	-
GF0031128	1	0	0	Programmed cell death protein, putative (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	RNA-binding domain, S1 [IPR022967] (1); S1 domain [IPR003029] (1); Nucleic acid-binding, OB-fold [IPR012340] (1)	scaffold_6_mRNA_2258.1	-	-
GF0031127	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_225.1	-	-
GF0031126	1	0	0	ATP-dependent RNA helicase (1)	ATP binding [GO:0005524 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	DEAD/DEAH box helicase domain [IPR011545] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); RNA helicase, DEAD-box type, Q motif [IPR014014] (1); Helicase superfamily 1/2, ATP-binding domain [IPR014001] (1)	scaffold_6_mRNA_2245.1	-	-
GF0031125	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_2244.1	-	-
GF0031124	1	0	0	Hypothetical protein (1)	phytochelatin biosynthetic process [GO:0046938 biological_process] (1); glutathione gamma-glutamylcysteinyltransferase activity [GO:0016756 molecular_function] (1); metal ion binding [GO:0046872 molecular_function] (1); response to metal ion [GO:0010038 biological_process] (1)	Phytochelatin synthase, C-terminal [IPR015407] (1)	scaffold_6_mRNA_2243.1	-	-
GF0031123	1	0	0	Hypothetical protein (1)		Protein kinase-like domain [IPR011009] (1)	scaffold_6_mRNA_224.1	-	-
GF0031122	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_2239.1	-	-
GF0031121	1	0	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	scaffold_6_mRNA_223.1	-	-
GF0031120	1	0	0	Serine/threonine-protein kinase PBS1 (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, ATP binding site [IPR017441] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	scaffold_6_mRNA_2228.1	-	-
GF0031119	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_6_mRNA_220.1	-	-
GF0031118	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_22.1	-	-
GF0031117	1	0	0	Basic 7S globulin, putative (1)	proteolysis [GO:0006508 biological_process] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1)	Aspartic peptidase A1 family [IPR001461] (1); Xylanase inhibitor, N-terminal [IPR032861] (1); Aspartic peptidase domain [IPR021109] (1)	scaffold_6_mRNA_2197.1	-	-
GF0031116	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_2195.1	-	-
GF0031115	1	0	0	Diaminohydroxyphosphoribosylaminopyrimidine deaminase (1)	diaminohydroxyphosphoribosylaminopyrimidine deaminase activity [GO:0008835 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); hydrolase activity [GO:0016787 molecular_function] (1); catalytic activity [GO:0003824 molecular_function] (1); riboflavin biosynthetic process [GO:0009231 biological_process] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Cytidine deaminase-like [IPR016193] (1); Riboflavin biosynthesis protein RibD [IPR004794] (1); Cytidine and deoxycytidylate deaminases, zinc-binding [IPR002125] (1); Dihydrofolate reductase-like domain [IPR024072] (1); APOBEC/CMP deaminase, zinc-binding [IPR016192] (1)	scaffold_6_mRNA_2184.1	-	-
GF0031114	1	0	0	Putative polyprotein (Aspartic proteinase, reverse transcriptase, ribonuclease H) (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Aspartic peptidase domain [IPR021109] (1); Peptidase A2A, retrovirus, catalytic [IPR001995] (1); Aspartic peptidase, active site [IPR001969] (1); Reverse transcriptase domain [IPR000477] (1); Retropepsins [IPR018061] (1)	scaffold_6_mRNA_218.1	-	-
GF0031113	1	0	0	Hypothetical protein (1)	transcription, DNA-templated [GO:0006351 biological_process] (1)	Transcription elongation factor S-II, central domain [IPR003618] (1)	scaffold_6_mRNA_2170.1	-	-
GF0031112	1	0	0	Hypothetical protein (1)	transcription, DNA-templated [GO:0006351 biological_process] (1)	Transcription elongation factor S-II, central domain [IPR003618] (1)	scaffold_6_mRNA_2169.1	-	-
GF0031111	1	0	0	Hypothetical protein (1)		Sugar phosphate transporter domain [IPR004853] (1)	scaffold_6_mRNA_2167.1	-	-
GF0031110	1	0	0	Hypothetical protein (1)	transcription, DNA-templated [GO:0006351 biological_process] (1)	Transcription elongation factor S-II, central domain [IPR003618] (1)	scaffold_6_mRNA_2166.1	-	-
GF0031109	1	0	0	Hypothetical protein (1)	transcription, DNA-templated [GO:0006351 biological_process] (1)	Transcription elongation factor S-II, central domain [IPR003618] (1)	scaffold_6_mRNA_2164.1	-	-
GF0031108	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_2163.1	-	-
GF0031107	1	0	0	Hypothetical protein (1)	transcription, DNA-templated [GO:0006351 biological_process] (1)	Transcription elongation factor S-II, central domain [IPR003618] (1)	scaffold_6_mRNA_2162.1	-	-
GF0031106	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_6_mRNA_216.1	-	-
GF0031105	1	0	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_6_mRNA_215.1	-	-
GF0031104	1	0	0	Hybrid proline-rich protein (1)		Hydrophobic seed protein [IPR027923] (1); Bifunctional inhibitor/plant lipid transfer protein/seed storage helical domain [IPR016140] (1)	scaffold_6_mRNA_2148.1	-	-
GF0031103	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_2147.1	-	-
GF0031102	1	0	0	Hypothetical protein (1)		Hydrophobic seed protein [IPR027923] (1); Bifunctional inhibitor/plant lipid transfer protein/seed storage helical domain [IPR016140] (1)	scaffold_6_mRNA_2146.2	-	-
GF0031101	1	0	0	Hypothetical protein (1)		Bifunctional inhibitor/plant lipid transfer protein/seed storage helical domain [IPR016140] (1); Hydrophobic seed protein [IPR027923] (1)	scaffold_6_mRNA_2144.1	-	-
GF0031100	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_2140.1	-	-
GF0031099	1	0	0	60S ribosomal protein L27 (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 L27e, conserved site [IPR018262] (1); Ribosomal protein L27e [IPR001141] (1); Ribosomal protein L2 domain 2 [IPR014722] (1)	scaffold_6_mRNA_2125.1	-	-
GF0031098	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_2113.1	-	-
GF0031097	1	0	0	Hypothetical protein (1)	metabolic process [GO:0008152 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1)	AMP-binding enzyme C-terminal domain [IPR025110] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); AMP-dependent synthetase/ligase [IPR000873] (1); Protein kinase-like domain [IPR011009] (1)	scaffold_6_mRNA_2111.1	-	-
GF0031096	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_210.1	-	-
GF0031095	1	0	0	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)	scaffold_6_mRNA_2096.1	-	-
GF0031094	1	0	0	Hypothetical protein (1)		FBD domain [IPR006566] (1)	scaffold_6_mRNA_2088.1	-	-
GF0031093	1	0	0	Hypothetical protein (1)		Rossmann-like alpha/beta/alpha sandwich fold [IPR014729] (1)	scaffold_6_mRNA_2073.1	-	-
GF0031092	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_6_mRNA_207.1	-	-
GF0031091	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_205.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0031090	1	0	0	Hypothetical protein (1)		Protein of unknown function DUF1191 [IPR010605] (1)	scaffold_6_mRNA_2048.1	-	-
GF0031089	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_204.1	-	-
GF0031088	1	0	0	Eukaryotic translation initiation factor 2 beta subunit, putative, expressed (1)	translational initiation [GO:0006413 biological_process] (1); translation initiation factor activity [GO:0003743 molecular_function] (1)	Translation initiation factor IF2/IF5 [IPR002735] (1); Translation initiation factor IF2/IF5, zinc-binding [IPR016190] (1); Translation initiation factor IF2/IF5, N-terminal [IPR016189] (1)	scaffold_6_mRNA_2033.1	-	-
GF0031087	1	0	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_6_mRNA_2031.1	-	-
GF0031086	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_6_mRNA_203.1	-	-
GF0031085	1	0	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1)	Peptidase A2A, retrovirus, catalytic [IPR001995] (1); Retropepsins [IPR018061] (1); Aspartic peptidase domain [IPR021109] (1)	scaffold_6_mRNA_202.1	-	-
GF0031084	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_2006.1	-	-
GF0031083	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_20.1	-	-
GF0031082	1	0	0	Hypothetical protein (1)	peroxidase activity [GO:0004601 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); response to oxidative stress [GO:0006979 biological_process] (1); heme binding [GO:0020037 molecular_function] (1)	Haem peroxidase [IPR010255] (1)	scaffold_6_mRNA_1982.1	-	-
GF0031081	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF1985 [IPR015410] (1)	scaffold_6_mRNA_1981.1	-	-
GF0031080	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_198.1	-	-
GF0031079	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1977.1	-	-
GF0031078	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1969.1	-	-
GF0031077	1	0	0	Hypothetical protein (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Viral movement protein [IPR028919] (1); Aspartic peptidase, active site [IPR001969] (1)	scaffold_6_mRNA_196.1	-	-
GF0031076	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_6_mRNA_1944.1	-	-
GF0031075	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_194.1	-	-
GF0031074	1	0	0	Macrophage migration inhibitory factor family protein (1)		Macrophage migration inhibitory factor [IPR001398] (1); Tautomerase/MIF superfamily [IPR014347] (1)	scaffold_6_mRNA_1936.2	-	-
GF0031073	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1929.1	-	-
GF0031072	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1925.1	-	-
GF0031071	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_191.1	-	-
GF0031070	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1909.1	-	-
GF0031069	1	0	0	Verticillium wilt resistance-like protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_6_mRNA_1891.1	-	-
GF0031068	1	0	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1); Endonuclease/exonuclease/phosphatase [IPR005135] (1)	scaffold_6_mRNA_1888.1	-	-
GF0031067	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1); Aspartic peptidase domain [IPR021109] (1)	scaffold_6_mRNA_1886.1	-	-
GF0031066	1	0	0	Monosacharide transport protein (1)			scaffold_6_mRNA_1885.1	-	-
GF0031065	1	0	0	Hypothetical protein (1)	protein serine/threonine kinase activity [GO:0004674 molecular_function] (1)	S-locus receptor kinase, C-terminal [IPR021820] (1); Protein kinase-like domain [IPR011009] (1)	scaffold_6_mRNA_1874.1	-	-
GF0031064	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_187.1	-	-
GF0031063	1	0	0	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	scaffold_6_mRNA_185.1	-	-
GF0031062	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1847.1	-	-
GF0031061	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1846.1	-	-
GF0031060	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1845.1	-	-
GF0031059	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1844.1	-	-
GF0031058	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1842.1	-	-
GF0031057	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1833.1	-	-
GF0031056	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_6_mRNA_1832.1	-	-
GF0031055	1	0	0	Hypothetical protein (1)		Gag-polypeptide of LTR copia-type [IPR029472] (1)	scaffold_6_mRNA_1831.1	-	-
GF0031054	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1828.1	-	-
GF0031053	1	0	0	Mutator-like transposase (1)		MULE transposase domain [IPR018289] (1); Transposase, MuDR, plant [IPR004332] (1)	scaffold_6_mRNA_1821.1	-	-
GF0031052	1	0	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Domain of unknown function DUF1985 [IPR015410] (1); Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	scaffold_6_mRNA_1820.1	-	-
GF0031051	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1809.1	-	-
GF0031050	1	0	0	RNA-directed DNA polymerase (Reverse transcriptase) (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_6_mRNA_1808.1	-	-
GF0031049	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1797.1	-	-
GF0031048	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_179.1	-	-
GF0031047	1	0	0	Monosacharide transport protein (1)			scaffold_6_mRNA_1788.1	-	-
GF0031046	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1787.1	-	-
GF0031045	1	0	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1)	scaffold_6_mRNA_1785.1	-	-
GF0031044	1	0	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_6_mRNA_1784.1	-	-
GF0031043	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1780.1	-	-
GF0031042	1	0	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_6_mRNA_1777.1	-	-
GF0031041	1	0	0	LRR receptor-like kinase (1)	protein binding [GO:0005515 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Protein kinase domain [IPR000719] (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/tyrosine-protein kinase, catalytic domain [IPR001245] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Leucine-rich repeat [IPR001611] (1)	scaffold_6_mRNA_1775.1	-	-
GF0031040	1	0	0	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)	scaffold_6_mRNA_1774.1	-	-
GF0031039	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1773.1	-	-
GF0031038	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_6_mRNA_1772.1	-	-
GF0031037	1	0	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_6_mRNA_1768.1	-	-
GF0031036	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1762.1	-	-
GF0031035	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1758.1	-	-
GF0031034	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1757.1	-	-
GF0031033	1	0	0	Potassium channel tetramerization domain-containing protein (1)	protein binding [GO:0005515 molecular_function] (1); protein homooligomerization [GO:0051260 biological_process] (1)	Six-bladed beta-propeller, TolB-like [IPR011042] (1); WD40/YVTN repeat-like-containing domain [IPR015943] (1); Potassium channel tetramerisation-type BTB domain [IPR003131] (1); WD40-repeat-containing domain [IPR017986] (1); SKP1/BTB/POZ domain [IPR011333] (1)	scaffold_6_mRNA_1754.1	-	-
GF0031032	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1753.1	-	-
GF0031031	1	0	0	Hypothetical protein (1)	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor [GO:0016620 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Glyceraldehyde/Erythrose phosphate dehydrogenase family [IPR020831] (1)	scaffold_6_mRNA_1751.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0031030	1	0	0	Putative peptide transporter, Protein NRT1/ PTR FAMILY 8.3 (1)	oligopeptide transport [GO:0006857 biological_process] (1); transporter activity [GO:0005215 molecular_function] (1); transport [GO:0006810 biological_process] (1); membrane [GO:0016020 cellular_component] (1)	PTR2 family proton/oligopeptide symporter, conserved site [IPR018456] (1); Major facilitator superfamily domain [IPR020846] (1); Proton-dependent oligopeptide transporter family [IPR000109] (1)	scaffold_6_mRNA_1741.1	-	-
GF0031029	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1738.1	-	-
GF0031028	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1735.1	-	-
GF0031027	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1731.1	-	-
GF0031026	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1729.1	-	-
GF0031025	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1728.1	-	-
GF0031024	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1727.1	-	-
GF0031023	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1726.1	-	-
GF0031022	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1721.1	-	-
GF0031021	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1720.1	-	-
GF0031020	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1719.1	-	-
GF0031019	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_6_mRNA_1718.1	-	-
GF0031018	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1717.1	-	-
GF0031017	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_6_mRNA_1699.1	-	-
GF0031016	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1698.1	-	-
GF0031015	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_169.1	-	-
GF0031014	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_168.1	-	-
GF0031013	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1652.1	-	-
GF0031012	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_165.1	-	-
GF0031011	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1); Endonuclease/exonuclease/phosphatase [IPR005135] (1)	scaffold_6_mRNA_1640.1	-	-
GF0031010	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1630.1	-	-
GF0031009	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_163.1	-	-
GF0031008	1	0	0	Putative receptor protein kinase ZmPK1 (1)	protein binding [GO:0005515 molecular_function] (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); recognition of pollen [GO:0048544 biological_process] (1); protein phosphorylation [GO:0006468 biological_process] (1)	Bulb-type lectin domain [IPR001480] (1); PAN/Apple domain [IPR003609] (1); Protein kinase, ATP binding site [IPR017441] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); S-locus glycoprotein domain [IPR000858] (1); EGF-like domain [IPR000742] (1); Protein kinase-like domain [IPR011009] (1); S-receptor-like serine/threonine-protein kinase [IPR024171] (1); Protein kinase domain [IPR000719] (1)	scaffold_6_mRNA_1629.1	-	-
GF0031007	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1628.1	-	-
GF0031006	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1624.1	-	-
GF0031005	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1623.1	-	-
GF0031004	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1617.1	-	-
GF0031003	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1610.1	-	-
GF0031002	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_6_mRNA_1609.1	-	-
GF0031001	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1608.1	-	-
GF0031000	1	0	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); zinc ion binding [GO:0008270 molecular_function] (1); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Ribonuclease H-like domain [IPR012337] (1); Domain of unknown function DUF4283 [IPR025558] (1); Protein kinase-like domain [IPR011009] (1); Ribonuclease H domain [IPR002156] (1); Zinc finger, CCHC-type [IPR001878] (1)	scaffold_6_mRNA_1600.1	-	-
GF0030999	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_160.1	-	-
GF0030998	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_16.1	-	-
GF0030997	1	0	0	Protein FAR1-RELATED SEQUENCE 6 (1)	zinc ion binding [GO:0008270 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	Zinc finger, SWIM-type [IPR007527] (1); MULE transposase domain [IPR018289] (1); Zinc finger, PMZ-type [IPR006564] (1); FAR1 DNA binding domain [IPR004330] (1); FHY3/FAR1 family [IPR031052] (1)	scaffold_6_mRNA_1597.1	-	-
GF0030996	1	0	0	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	scaffold_6_mRNA_1592.1	-	-
GF0030995	1	0	0	Short chain alcohol dehydrogenase-like protein (1)		Short-chain dehydrogenase/reductase SDR [IPR002347] (1); NAD(P)-binding domain [IPR016040] (1)	scaffold_6_mRNA_1591.1	-	-
GF0030994	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1586.1	-	-
GF0030993	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1583.1	-	-
GF0030992	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1582.1	-	-
GF0030991	1	0	0	Monosacharide transport protein (1)			scaffold_6_mRNA_1580.1	-	-
GF0030990	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1576.1	-	-
GF0030989	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1573.1	-	-
GF0030988	1	0	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	scaffold_6_mRNA_1565.1	-	-
GF0030987	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1564.1	-	-
GF0030986	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_156.1	-	-
GF0030985	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_6_mRNA_1547.1	-	-
GF0030984	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1546.1	-	-
GF0030983	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1545.1	-	-
GF0030982	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, SWIM-type [IPR007527] (1); Zinc finger, PMZ-type [IPR006564] (1)	scaffold_6_mRNA_1544.1	-	-
GF0030981	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1543.1	-	-
GF0030980	1	0	0	Disease resistance protein (CC-NBS-LRR class) family 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); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1)	scaffold_6_mRNA_154.1	-	-
GF0030979	1	0	0	Hypothetical protein (1)		Arabidopsis retrotransposon Orf1 [IPR004312] (1)	scaffold_6_mRNA_1532.1	-	-
GF0030978	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_153.1	-	-
GF0030977	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_6_mRNA_1527.1	-	-
GF0030976	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1526.1	-	-
GF0030975	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1524.1	-	-
GF0030974	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1523.1	-	-
GF0030973	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1522.1	-	-
GF0030972	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_6_mRNA_152.1	-	-
GF0030971	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1515.1	-	-
GF0030970	1	0	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); AAA+ ATPase domain [IPR003593] (1); NB-ARC [IPR002182] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1)	scaffold_6_mRNA_151.1	-	-
GF0030969	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1508.1	-	-
GF0030968	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1507.1	-	-
GF0030967	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1506.1	-	-
GF0030966	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1503.1	-	-
GF0030965	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1502.1	-	-
GF0030964	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_6_mRNA_1501.1	-	-
GF0030963	1	0	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_6_mRNA_15.1	-	-
GF0030962	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1497.1	-	-
GF0030961	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1496.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0030960	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1490.1	-	-
GF0030959	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1476.1	-	-
GF0030958	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_6_mRNA_1472.1	-	-
GF0030957	1	0	0	MADS-box transcription factor family protein (1)	positive regulation of transcription from RNA polymerase II promoter [GO:0045944 biological_process] (1); MAPK cascade [GO:0000165 biological_process] (1); protein dimerization activity [GO:0046983 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1); RNA polymerase II regulatory region sequence-specific DNA binding [GO:0000977 molecular_function] (1)	MADS MEF2-like [IPR033896] (1); Transcription factor, MADS-box [IPR002100] (1)	scaffold_6_mRNA_1462.1	-	-
GF0030956	1	0	0	NAD(P)-binding Rossmann-fold superfamily protein isoform 2 (1)		NAD(P)-binding domain [IPR016040] (1); Short-chain dehydrogenase/reductase SDR [IPR002347] (1)	scaffold_6_mRNA_1461.1	-	-
GF0030955	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1458.1	-	-
GF0030954	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1448.1	-	-
GF0030953	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_6_mRNA_1447.1	-	-
GF0030952	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1446.1	-	-
GF0030951	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1445.1	-	-
GF0030950	1	0	0	Histone H4 (1)	nucleosome [GO:0000786 cellular_component] (1); protein heterodimerization activity [GO:0046982 molecular_function] (1); nucleus [GO:0005634 cellular_component] (1); DNA binding [GO:0003677 molecular_function] (1); nucleosome assembly [GO:0006334 biological_process] (1)	Histone H4, conserved site [IPR019809] (1); Histone H4 [IPR001951] (1); Histone-fold [IPR009072] (1)	scaffold_6_mRNA_1439.1	-	-
GF0030949	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_6_mRNA_1424.1	-	-
GF0030948	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1412.1	-	-
GF0030947	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1411.1	-	-
GF0030946	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_6_mRNA_1410.1	-	-
GF0030945	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1); Zinc knuckle CX2CX4HX4C [IPR025836] (1)	scaffold_6_mRNA_141.1	-	-
GF0030944	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1400.1	-	-
GF0030943	1	0	0	Ta11 non-LTR retroelement protein-like (1)		Domain of unknown function DUF4283 [IPR025558] (1); Zinc knuckle CX2CX4HX4C [IPR025836] (1)	scaffold_6_mRNA_140.1	-	-
GF0030942	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_139.1	-	-
GF0030941	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1385.1	-	-
GF0030940	1	0	0	Transposable element protein, putative, (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_6_mRNA_1384.1	-	-
GF0030939	1	0	0	RNA-directed DNA polymerase (Reverse transcriptase) (1)		Reverse transcriptase domain [IPR000477] (1); Endonuclease/exonuclease/phosphatase [IPR005135] (1)	scaffold_6_mRNA_138.1	-	-
GF0030938	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1379.1	-	-
GF0030937	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	scaffold_6_mRNA_1373.1	-	-
GF0030936	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_6_mRNA_1362.1	-	-
GF0030935	1	0	0	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	scaffold_6_mRNA_1360.1	-	-
GF0030934	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1354.1	-	-
GF0030933	1	0	0	Subtilisin-like protease SDD1 (1)	proteolysis [GO:0006508 biological_process] (1); serine-type endopeptidase activity [GO:0004252 molecular_function] (1)	Peptidase S8 propeptide/proteinase inhibitor I9 [IPR010259] (1); Peptidase S8, subtilisin-related [IPR015500] (1); Cucumisin-like catalytic domain [IPR034197] (1); PA domain [IPR003137] (1); Peptidase S8/S53 domain [IPR000209] (1)	scaffold_6_mRNA_1344.1	-	-
GF0030932	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1343.1	-	-
GF0030931	1	0	0	Hypothetical protein (1)	transcription, DNA-templated [GO:0006351 biological_process] (1); DNA-directed 5'-3' RNA polymerase activity [GO:0003899 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1); ribonucleoside binding [GO:0032549 molecular_function] (1)	DNA-directed RNA polymerase, subunit 2 [IPR015712] (1); RNA polymerase Rpb2, domain 7 [IPR007641] (1)	scaffold_6_mRNA_1330.1	-	-
GF0030930	1	0	0	Monosacharide transport protein (1)			scaffold_6_mRNA_1320.1	-	-
GF0030929	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1317.1	-	-
GF0030928	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1315.1	-	-
GF0030927	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_6_mRNA_1314.1	-	-
GF0030926	1	0	0	Hypothetical protein (1)		Tubulin/FtsZ, 2-layer sandwich domain [IPR018316] (1)	scaffold_6_mRNA_1313.1	-	-
GF0030925	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ubiquitin domain [IPR000626] (1); Aspartic peptidase domain [IPR021109] (1); Ubiquitin [IPR019956] (1); Ubiquitin-related domain [IPR029071] (1); Ubiquitin conserved site [IPR019954] (1)	scaffold_6_mRNA_1309.1	-	-
GF0030924	1	0	0	Hypothetical protein (1)		Protein kinase-like domain [IPR011009] (1)	scaffold_6_mRNA_1304.1	-	-
GF0030923	1	0	0	RNA-directed DNA polymerase (Reverse transcriptase); Polynucleotidyl transferase, Ribonuclease H fold (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Reverse transcriptase zinc-binding domain [IPR026960] (1); Domain of unknown function DUF4283 [IPR025558] (1); Ribonuclease H-like domain [IPR012337] (1); Reverse transcriptase domain [IPR000477] (1); Zinc finger, CCHC-type [IPR001878] (1)	scaffold_6_mRNA_1299.1	-	-
GF0030922	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1297.1	-	-
GF0030921	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_6_mRNA_1296.1	-	-
GF0030920	1	0	0	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 L2 domain 2 [IPR014722] (1); Ribosomal protein L27e [IPR001141] (1); Translation protein SH3-like domain [IPR008991] (1)	scaffold_6_mRNA_129.1	-	-
GF0030919	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1285.1	-	-
GF0030918	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1284.1	-	-
GF0030917	1	0	0	LRR receptor-like kinase family protein (1)	protein binding [GO:0005515 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Protein kinase, ATP binding site [IPR017441] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1); Protein kinase domain [IPR000719] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Protein kinase-like domain [IPR011009] (1)	scaffold_6_mRNA_128.1	-	-
GF0030916	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1274.1	-	-
GF0030915	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1273.1	-	-
GF0030914	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_127.1	-	-
GF0030913	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1268.1	-	-
GF0030912	1	0	0	40S ribosomal protein S23 (1)	small ribosomal subunit [GO:0015935 cellular_component] (1); ribosome [GO:0005840 cellular_component] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1); translation [GO:0006412 biological_process] (1); intracellular [GO:0005622 cellular_component] (1)	Ribosomal protein S23, eukaryotic/archaeal [IPR005680] (1); Ribosomal protein S12/S23 [IPR006032] (1); Nucleic acid-binding, OB-fold [IPR012340] (1)	scaffold_6_mRNA_1261.1	-	-
GF0030911	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_126.1	-	-
GF0030910	1	0	0	Protein FAR1-RELATED SEQUENCE 5 (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, PMZ-type [IPR006564] (1); Zinc finger, SWIM-type [IPR007527] (1); FHY3/FAR1 family [IPR031052] (1)	scaffold_6_mRNA_1258.1	-	-
GF0030909	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1256.1	-	-

ID	**Num. in *C. celementine***	**Num in *C. unshiu***	**Num in *P.trifoliata***	**Note**	**GO**	**InterPro**	**Members in *C.clementine***	**Members in *C.unshiu***	**Members in *P.trifoliata***
GF0030908	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1253.1	-	-
GF0030907	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_6_mRNA_1252.1	-	-
GF0030906	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_125.1	-	-
GF0030905	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1248.1	-	-
GF0030904	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1245.1	-	-
GF0030903	1	0	0	Alpha/beta-Hydrolases superfamily protein isoform 3 (1)		Alpha/Beta hydrolase fold [IPR029058] (1)	scaffold_6_mRNA_1240.1	-	-
GF0030902	1	0	0	Cysteine-rich RLK (RECEPTOR-like protein kinase) 8 (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	scaffold_6_mRNA_124.1	-	-
GF0030901	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1239.1	-	-
GF0030900	1	0	0	LRR receptor-like kinase family protein, putative (1)	integral component of membrane [GO:0016021 cellular_component] (1); dolichyl-diphosphooligosaccharide-protein glycotransferase activity [GO:0004579 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); oligosaccharyltransferase complex [GO:0008250 cellular_component] (1)	Leucine-rich repeat [IPR001611] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); DAD/Ost2 [IPR003038] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Protein kinase-like domain [IPR011009] (1)	scaffold_6_mRNA_1237.1	-	-
GF0030899	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Pentatricopeptide repeat [IPR002885] (1); Tetratricopeptide-like helical domain [IPR011990] (1)	scaffold_6_mRNA_1236.1	-	-
GF0030898	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Tetratricopeptide-like helical domain [IPR011990] (1); Pentatricopeptide repeat [IPR002885] (1)	scaffold_6_mRNA_1234.1	-	-
GF0030897	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1232.1	-	-
GF0030896	1	0	0	TRNA synthetase class I (C) family protein (1)	aminoacyl-tRNA ligase activity [GO:0004812 molecular_function] (1); nucleotide binding [GO:0000166 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1); tRNA aminoacylation for protein translation [GO:0006418 biological_process] (1)	tRNA synthetases class I, catalytic domain [IPR032678] (1); Cysteinyl-tRNA synthetase/mycothiol ligase [IPR024909] (1); Rossmann-like alpha/beta/alpha sandwich fold [IPR014729] (1); Aminoacyl-tRNA synthetase, class Ia, anticodon-binding [IPR009080] (1)	scaffold_6_mRNA_123.1	-	-
GF0030895	1	0	0	LRR receptor-like kinase family protein (1)	protein binding [GO:0005515 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Protein kinase, ATP binding site [IPR017441] (1); Tyrosine-protein kinase, active site [IPR008266] (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)	scaffold_6_mRNA_1224.1	-	-
GF0030894	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_122.1	-	-
GF0030893	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1219.1	-	-
GF0030892	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1212.1	-	-
GF0030891	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_6_mRNA_1206.1	-	-
GF0030890	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1203.1	-	-
GF0030889	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1201.1	-	-
GF0030888	1	0	0	Polyubiquitin (1)	protein binding [GO:0005515 molecular_function] (1)	Ubiquitin conserved site [IPR019954] (1); Ubiquitin-related domain [IPR029071] (1); Ubiquitin [IPR019956] (1); Ubiquitin domain [IPR000626] (1)	scaffold_6_mRNA_1200.1	-	-
GF0030887	1	0	0	Hypothetical protein (1)		Cactin, central domain [IPR018816] (1)	scaffold_6_mRNA_1199.1	-	-
GF0030886	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1198.1	-	-
GF0030885	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_6_mRNA_1196.1	-	-
GF0030884	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1195.1	-	-
GF0030883	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1194.1	-	-
GF0030882	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Cactin, C-terminal [IPR019134] (1); Cactin, central domain [IPR018816] (1)	scaffold_6_mRNA_1193.1	-	-
GF0030881	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1191.1	-	-
GF0030880	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1190.1	-	-
GF0030879	1	0	0	Hypothetical protein (1)	DNA integration [GO:0015074 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); GAG-pre-integrase domain [IPR025724] (1); Ribonuclease H-like domain [IPR012337] (1); LOG family [IPR031100] (1); Integrase, catalytic core [IPR001584] (1)	scaffold_6_mRNA_119.1	-	-
GF0030878	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1189.1	-	-
GF0030877	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1188.1	-	-
GF0030876	1	0	0	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	scaffold_6_mRNA_1186.1	-	-
GF0030875	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1181.1	-	-
GF0030874	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); DNA integration [GO:0015074 biological_process] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Ribonuclease H-like domain [IPR012337] (1); Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1); Integrase, catalytic core [IPR001584] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	scaffold_6_mRNA_118.1	-	-
GF0030873	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_6_mRNA_1178.1	-	-
GF0030872	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1173.1	-	-
GF0030871	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1172.1	-	-
GF0030870	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_6_mRNA_1171.1	-	-
GF0030869	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1170.1	-	-
GF0030868	1	0	0	Hypothetical protein (1)		Transposase-associated domain [IPR029480] (1)	scaffold_6_mRNA_1169.1	-	-
GF0030867	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1164.1	-	-
GF0030866	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_6_mRNA_1163.1	-	-
GF0030865	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1162.1	-	-
GF0030864	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1160.1	-	-
GF0030863	1	0	0	Putative non-LTR retrolelement reverse transcriptase (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_6_mRNA_116.1	-	-
GF0030862	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_115.1	-	-
GF0030861	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_6_mRNA_1149.1	-	-
GF0030860	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1148.1	-	-
GF0030859	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1147.1	-	-
GF0030858	1	0	0	RnaseH protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_6_mRNA_1141.1	-	-
GF0030857	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_114.1	-	-
GF0030856	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Domain of unknown function DUF4216 [IPR025312] (1)	scaffold_6_mRNA_113.1	-	-
GF0030855	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1128.1	-	-
GF0030854	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_6_mRNA_1125.1	-	-
GF0030853	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1123.1	-	-
GF0030852	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_6_mRNA_1119.1	-	-
GF0030851	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1118.1	-	-
GF0030850	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1117.1	-	-
GF0030849	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1115.1	-	-
GF0030848	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1111.1	-	-
GF0030847	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1110.1	-	-
GF0030846	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1107.1	-	-
GF0030845	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Zinc finger, PMZ-type [IPR006564] (1)	scaffold_6_mRNA_1104.1	-	-
GF0030844	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1101.1	-	-

ID	**Num. in *C. celementine***	**Num in *C. unshiu***	**Num in *P.trifoliata***	**Note**	**GO**	**InterPro**	**Members in *C.clementine***	**Members in *C.unshiu***	**Members in *P.trifoliata***
GF0030843	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1099.1	-	-
GF0030842	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ubiquitin conserved site [IPR019954] (1); Ubiquitin-related domain [IPR029071] (1); Ubiquitin [IPR019956] (1); Ubiquitin domain [IPR000626] (1)	scaffold_6_mRNA_1095.1	-	-
GF0030841	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			scaffold_6_mRNA_1094.1	-	-
GF0030840	1	0	0	Hypothetical protein (1)	catalytic activity [GO:0003824 molecular_function] (1)	Glycoside hydrolase superfamily [IPR017853] (1); Aldolase-type TIM barrel [IPR013785] (1)	scaffold_6_mRNA_1082.1	-	-
GF0030839	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1079.1	-	-
GF0030838	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1076.1	-	-
GF0030837	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1074.1	-	-
GF0030836	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_6_mRNA_1071.1	-	-
GF0030835	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_6_mRNA_1070.1	-	-
GF0030834	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_107.1	-	-
GF0030833	1	0	0	Hypothetical protein (1)		Transposon, En/Spm-like [IPR004242] (1)	scaffold_6_mRNA_1067.1	-	-
GF0030832	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_6_mRNA_1065.1	-	-
GF0030831	1	0	0	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)	scaffold_6_mRNA_1064.1	-	-
GF0030830	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1063.1	-	-
GF0030829	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1055.1	-	-
GF0030828	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1054.1	-	-
GF0030827	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1053.1	-	-
GF0030826	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_6_mRNA_1045.1	-	-
GF0030825	1	0	0	Hypothetical protein (1)	catalytic activity [GO:0003824 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	AMP-dependent synthetase/ligase [IPR000873] (1)	scaffold_6_mRNA_1044.1	-	-
GF0030824	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1043.1	-	-
GF0030823	1	0	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_6_mRNA_104.1	-	-
GF0030822	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1039.1	-	-
GF0030821	1	0	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	Zinc finger C2H2-type [IPR013087] (1); Ribonuclease H-like domain [IPR012337] (1); Zinc finger, BED-type [IPR003656] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	scaffold_6_mRNA_1038.1	-	-
GF0030820	1	0	0	Hypothetical protein (1)	transcription factor TFIID complex [GO:0005669 cellular_component] (1); DNA-templated transcription, initiation [GO:0006352 biological_process] (1)	Transcription initiation factor TFIID component TAF4 [IPR007900] (1)	scaffold_6_mRNA_1036.1	-	-
GF0030819	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1031.1	-	-
GF0030818	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1026.1	-	-
GF0030817	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1025.1	-	-
GF0030816	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1020.1	-	-
GF0030815	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_1017.1	-	-
GF0030814	1	0	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1)	scaffold_6_mRNA_1013.1	-	-
GF0030813	1	0	0	General transcription factor-like zinc finger protein, putative (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_6_mRNA_1007.1	-	-
GF0030812	1	0	0	Hydroquinone glucosyltransferase (1)	metabolic process [GO:0008152 biological_process] (1); transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	scaffold_6_mRNA_1005.1	-	-
GF0030811	1	0	0	Hypothetical protein (1)			scaffold_6_mRNA_10.1	-	-
GF0030810	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_991.1	-	-
GF0030809	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_985.1	-	-
GF0030808	1	0	0	Putative disease resistance RPP13-like protein 1 (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_5_mRNA_98.1	-	-
GF0030807	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_978.1	-	-
GF0030806	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_975.1	-	-
GF0030805	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_969.1	-	-
GF0030804	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_959.1	-	-
GF0030803	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_5_mRNA_955.1	-	-
GF0030802	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_951.1	-	-
GF0030801	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_938.1	-	-
GF0030800	1	0	0	Putative Ruda gag-pol polyprotein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_5_mRNA_923.1	-	-
GF0030799	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_922.1	-	-
GF0030798	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_92.1	-	-
GF0030797	1	0	0	Hypothetical protein (1)	enzyme inhibitor activity [GO:0004857 molecular_function] (1)	Pectinesterase inhibitor domain [IPR006501] (1)	scaffold_5_mRNA_916.1	-	-
GF0030796	1	0	0	Orf764 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)	scaffold_5_mRNA_908.1	-	-
GF0030795	1	0	0	Phloem protein 2-B5 (1)	protein binding [GO:0005515 molecular_function] (1)	Phloem protein 2-like [IPR025886] (1); F-box domain [IPR001810] (1)	scaffold_5_mRNA_899.1	-	-
GF0030794	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_5_mRNA_897.1	-	-
GF0030793	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_893.1	-	-
GF0030792	1	0	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Carlavirus nucleic acid-binding protein [IPR002568] (1)	scaffold_5_mRNA_889.1	-	-
GF0030791	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_5_mRNA_888.1	-	-
GF0030790	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_886.1	-	-
GF0030789	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_885.1	-	-
GF0030788	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_5_mRNA_883.1	-	-
GF0030787	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_882.1	-	-
GF0030786	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_881.1	-	-
GF0030785	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_880.1	-	-
GF0030784	1	0	0	Monosacharide transport protein (1)			scaffold_5_mRNA_88.1	-	-
GF0030783	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_878.1	-	-
GF0030782	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_877.1	-	-
GF0030781	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_876.1	-	-
GF0030780	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_875.1	-	-
GF0030779	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_871.1	-	-
GF0030778	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_5_mRNA_87.1	-	-
GF0030777	1	0	0	Ubiquitin carboxyl-terminal hydrolase 12 (1)	protein binding [GO:0005515 molecular_function] (1)	MATH/TRAF domain [IPR002083] (1); TRAF-like [IPR008974] (1)	scaffold_5_mRNA_868.1	-	-
GF0030776	1	0	0	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	scaffold_5_mRNA_863.1	-	-
GF0030775	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_5_mRNA_862.1	-	-
GF0030774	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_860.1	-	-
GF0030773	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Endonuclease/exonuclease/phosphatase [IPR005135] (1); Ribonuclease H-like domain [IPR012337] (1); Domain of unknown function DUF4283 [IPR025558] (1)	scaffold_5_mRNA_86.1	-	-
GF0030772	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_858.1	-	-
GF0030771	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_855.1	-	-
GF0030770	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_854.1	-	-
GF0030769	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_852.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0030768	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	MATH/TRAF domain [IPR002083] (1); TRAF-like [IPR008974] (1); Ribokinase-like [IPR029056] (1)	scaffold_5_mRNA_850.1	-	-
GF0030767	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	scaffold_5_mRNA_849.1	-	-
GF0030766	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_847.1	-	-
GF0030765	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_828.1	-	-
GF0030764	1	0	0	Hypothetical protein (1)		Arabidopsis retrotransposon Orf1 [IPR004312] (1)	scaffold_5_mRNA_825.1	-	-
GF0030763	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Aspartic peptidase domain [IPR021109] (1)	scaffold_5_mRNA_824.1	-	-
GF0030762	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_822.1	-	-
GF0030761	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	TRAF-like [IPR008974] (1); MATH/TRAF domain [IPR002083] (1)	scaffold_5_mRNA_820.1	-	-
GF0030760	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_82.1	-	-
GF0030759	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_819.1	-	-
GF0030758	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_5_mRNA_818.1	-	-
GF0030757	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_815.1	-	-
GF0030756	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_5_mRNA_814.1	-	-
GF0030755	1	0	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Carlavirus nucleic acid-binding protein [IPR002568] (1)	scaffold_5_mRNA_813.1	-	-
GF0030754	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_812.1	-	-
GF0030753	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_808.1	-	-
GF0030752	1	0	0	Disease resistance protein (TIR-NBS-LRR class) (1)	signal transduction [GO:0007165 biological_process] (1); ADP binding [GO:0043531 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1)	scaffold_5_mRNA_803.1	-	-
GF0030751	1	0	0	TMV resistance N (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_5_mRNA_802.1	-	-
GF0030750	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_80.1	-	-
GF0030749	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_8.1	-	-
GF0030748	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_795.1	-	-
GF0030747	1	0	0	Hypothetical protein (1)		Gcp-like domain [IPR000905] (1)	scaffold_5_mRNA_79.1	-	-
GF0030746	1	0	0	Polypeptide with an integrase domain (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)	scaffold_5_mRNA_784.1	-	-
GF0030745	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_5_mRNA_783.1	-	-
GF0030744	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_768.1	-	-
GF0030743	1	0	0	Contains similarity to reverse trancriptase , related (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_5_mRNA_766.1	-	-
GF0030742	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_5_mRNA_764.1	-	-
GF0030741	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_762.1	-	-
GF0030740	1	0	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_5_mRNA_758.1	-	-
GF0030739	1	0	0	Disease resistance protein RPM1 (1)	ADP binding [GO:0043531 molecular_function] (1)	Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_5_mRNA_755.1	-	-
GF0030738	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_753.1	-	-
GF0030737	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_744.1	-	-
GF0030736	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_741.1	-	-
GF0030735	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_740.1	-	-
GF0030734	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_74.1	-	-
GF0030733	1	0	0	Transcription repressor TRM protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, RING/FYVE/PHD-type [IPR013083] (1); Zinc finger C2H2-type [IPR013087] (1)	scaffold_5_mRNA_736.1	-	-
GF0030732	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_728.1	-	-
GF0030731	1	0	0	Polynucleotidyl transferase, Ribonuclease H fold, putative (1)			scaffold_5_mRNA_712.1	-	-
GF0030730	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_5_mRNA_711.1	-	-
GF0030729	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF1605 [IPR011709] (1)	scaffold_5_mRNA_704.1	-	-
GF0030728	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_703.1	-	-
GF0030727	1	0	0	Orcinol 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)	scaffold_5_mRNA_700.1	-	-
GF0030726	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_696.1	-	-
GF0030725	1	0	0	40S ribosomal protein S2 (1)	translation [GO:0006412 biological_process] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1); RNA binding [GO:0003723 molecular_function] (1); ribosome [GO:0005840 cellular_component] (1); small ribosomal subunit [GO:0015935 cellular_component] (1)	Ribosomal protein S5 domain 2-type fold, subgroup [IPR014721] (1); Ribosomal protein S5, eukaryotic/archaeal [IPR005711] (1); Ribosomal protein S5, N-terminal [IPR013810] (1); Ribosomal protein S5, C-terminal [IPR005324] (1); Ribosomal protein S5 domain 2-type fold [IPR020568] (1); Ribosomal protein S5 [IPR000851] (1)	scaffold_5_mRNA_695.1	-	-
GF0030724	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_5_mRNA_694.1	-	-
GF0030723	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_690.1	-	-
GF0030722	1	0	0	Serine/threonine-protein kinase PBS1 (1)			scaffold_5_mRNA_688.1	-	-
GF0030721	1	0	0	NBS-LRR class resistance protein Fy1-Ry1 (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)	scaffold_5_mRNA_686.1	-	-
GF0030720	1	0	0	Disease resistance protein RPM1 (1)	ADP binding [GO:0043531 molecular_function] (1)	Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_5_mRNA_684.1	-	-
GF0030719	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_683.1	-	-
GF0030718	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_681.1	-	-
GF0030717	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_680.1	-	-
GF0030716	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_68.1	-	-
GF0030715	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_677.1	-	-
GF0030714	1	0	0	Cytochrome P450 82A4 (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); Cytochrome P450, E-class, group I [IPR002401] (1)	scaffold_5_mRNA_660.1	-	-
GF0030713	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_659.1	-	-
GF0030712	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_651.1	-	-
GF0030711	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_643.1	-	-
GF0030710	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_640.1	-	-
GF0030709	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_634.1	-	-
GF0030708	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_632.1	-	-
GF0030707	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_630.1	-	-
GF0030706	1	0	0	LRR and NB-ARC domain disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_5_mRNA_63.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0030705	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_5_mRNA_629.1	-	-
GF0030704	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_626.1	-	-
GF0030703	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_606.1	-	-
GF0030702	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_603.1	-	-
GF0030701	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_5_mRNA_602.1	-	-
GF0030700	1	0	0	FAD-binding Berberine 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); catalytic activity [GO:0003824 molecular_function] (1)	Berberine/berberine-like [IPR012951] (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); FAD-binding, type 2 [IPR016166] (1); FAD linked oxidase, N-terminal [IPR006094] (1)	scaffold_5_mRNA_593.1	-	-
GF0030699	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_592.1	-	-
GF0030698	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_591.1	-	-
GF0030697	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_590.1	-	-
GF0030696	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_589.1	-	-
GF0030695	1	0	0	Hypothetical 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)	Leucine-rich repeat domain, L domain-like [IPR032675] (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); FAD-binding, type 2 [IPR016166] (1); FAD linked oxidase, N-terminal [IPR006094] (1)	scaffold_5_mRNA_585.1	-	-
GF0030694	1	0	0	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	scaffold_5_mRNA_567.1	-	-
GF0030693	1	0	0	Hypothetical protein (1)	calcium ion binding [GO:0005509 molecular_function] (1)	EGF-like calcium-binding domain [IPR001881] (1)	scaffold_5_mRNA_564.1	-	-
GF0030692	1	0	0	Disease resistance protein (1)	protein binding [GO:0005515 molecular_function] (1); ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1); Leucine-rich repeat [IPR001611] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_5_mRNA_550.1	-	-
GF0030691	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_549.1	-	-
GF0030690	1	0	0	Putative pectinesterase/pectinesterase inhibitor 38 (1)	pectinesterase activity [GO:0030599 molecular_function] (1); cell wall [GO:0005618 cellular_component] (1); cell wall modification [GO:0042545 biological_process] (1)	Pectin lyase fold/virulence factor [IPR011050] (1); Pectin lyase fold [IPR012334] (1); Pectinesterase, catalytic [IPR000070] (1); Pectinesterase, Asp active site [IPR033131] (1)	scaffold_5_mRNA_544.1	-	-
GF0030689	1	0	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1)	scaffold_5_mRNA_543.1	-	-
GF0030688	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_542.1	-	-
GF0030687	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_541.1	-	-
GF0030686	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_540.1	-	-
GF0030685	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_539.1	-	-
GF0030684	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_533.1	-	-
GF0030683	1	0	0	Hypothetical protein (1)	enzyme inhibitor activity [GO:0004857 molecular_function] (1)	Pectinesterase inhibitor domain [IPR006501] (1)	scaffold_5_mRNA_531.1	-	-
GF0030682	1	0	0	Hypothetical protein (1)		Ankyrin repeat-containing domain [IPR020683] (1)	scaffold_5_mRNA_528.1	-	-
GF0030681	1	0	0	Hypothetical protein (1)	response to auxin [GO:0009733 biological_process] (1)	Small auxin-up RNA [IPR003676] (1)	scaffold_5_mRNA_5228.1	-	-
GF0030680	1	0	0	Histone deacetylase 9 isoform 11 (1)		Histone deacetylase superfamily [IPR000286] (1); Histone deacetylase domain [IPR023801] (1)	scaffold_5_mRNA_5220.1	-	-
GF0030679	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_5212.1	-	-
GF0030678	1	0	0	Hypothetical protein (1)	metabolic process [GO:0008152 biological_process] (1); transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	scaffold_5_mRNA_5204.1	-	-
GF0030677	1	0	0	Putative disease resistance protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_5_mRNA_519.1	-	-
GF0030676	1	0	0	RING-H2 finger protein ATL1L (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)	scaffold_5_mRNA_5178.1	-	-
GF0030675	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_5_mRNA_516.1	-	-
GF0030674	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_5149.1	-	-
GF0030673	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_5148.1	-	-
GF0030672	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_5146.1	-	-
GF0030671	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc knuckle CX2CX4HX4C [IPR025836] (1); Zinc finger, CCHC-type [IPR001878] (1); Domain of unknown function DUF4283 [IPR025558] (1)	scaffold_5_mRNA_511.1	-	-
GF0030670	1	0	0	Heavy metal ATPase transporter (1)	cation transport [GO:0006812 biological_process] (1); metal ion binding [GO:0046872 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1); cation-transporting ATPase activity [GO:0019829 molecular_function] (1); nucleotide binding [GO:0000166 molecular_function] (1)	HAD-like domain [IPR023214] (1); P-type ATPase, A domain [IPR008250] (1); P-type ATPase, subfamily IB [IPR027256] (1); P-type ATPase, phosphorylation site [IPR018303] (1); P-type ATPase, cytoplasmic domain N [IPR023299] (1); P-type ATPase, transmembrane domain [IPR023298] (1); P-type ATPase [IPR001757] (1)	scaffold_5_mRNA_510.1	-	-
GF0030669	1	0	0	Enoyl-CoA hydratase 2, peroxisomal (1)		MaoC-like domain [IPR002539] (1); HotDog domain [IPR029069] (1)	scaffold_5_mRNA_5099.1	-	-
GF0030668	1	0	0	Prolyl endopeptidase (1)	serine-type exopeptidase activity [GO:0070008 molecular_function] (1); serine-type endopeptidase activity [GO:0004252 molecular_function] (1)	Peptidase S9A, N-terminal domain [IPR023302] (1)	scaffold_5_mRNA_5097.1	-	-
GF0030667	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_5094.1	-	-
GF0030666	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_5083.1	-	-
GF0030665	1	0	0	Flavonoid 3',5'-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)	scaffold_5_mRNA_508.1	-	-
GF0030664	1	0	0	Hypothetical protein (1)	enzyme regulator activity [GO:0030234 molecular_function] (1); proteasome complex [GO:0000502 cellular_component] (1); regulation of protein catabolic process [GO:0042176 biological_process] (1)	26S proteasome regulatory subunit, C-terminal [IPR013586] (1)	scaffold_5_mRNA_5071.1	-	-
GF0030663	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_5063.1	-	-
GF0030662	1	0	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	scaffold_5_mRNA_5058.1	-	-
GF0030661	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_504.1	-	-
GF0030660	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_5033.1	-	-
GF0030659	1	0	0	Hypothetical protein (1)	catalytic activity [GO:0003824 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	ATP-grasp fold, subdomain 1 [IPR013815] (1)	scaffold_5_mRNA_5032.1	-	-
GF0030658	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_501.1	-	-
GF0030657	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_5000.1	-	-
GF0030656	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_4994.1	-	-
GF0030655	1	0	0	Cell growth defect factor 2 (1)			scaffold_5_mRNA_4985.1	-	-
GF0030654	1	0	0	Histone H3 (1)	DNA binding [GO:0003677 molecular_function] (1); protein heterodimerization activity [GO:0046982 molecular_function] (1); nucleosome [GO:0000786 cellular_component] (1)	Histone-fold [IPR009072] (1); Histone H3/CENP-A [IPR000164] (1); Histone H2A/H2B/H3 [IPR007125] (1)	scaffold_5_mRNA_4984.1	-	-
GF0030653	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_4954.1	-	-
GF0030652	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_495.1	-	-
GF0030651	1	0	0	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	scaffold_5_mRNA_494.1	-	-

ID	**Num. in *C. celementine***	**Num in *C. unshiu***	**Num in *P.trifoliata***	**Note**	**GO**	**InterPro**	**Members in *C.clementine***	**Members in *C.unshiu***	**Members in *P.trifoliata***
GF0030650	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_5_mRNA_4936.1	-	-
GF0030649	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_4933.1	-	-
GF0030648	1	0	0	Hypothetical protein (1)	RNA binding [GO:0003723 molecular_function] (1)	K Homology domain, type 1 [IPR004088] (1)	scaffold_5_mRNA_493.1	-	-
GF0030647	1	0	0	Gamma carbonic anhydrase 3 (1)		Hexapeptide repeat [IPR001451] (1); Domain unknown function DUF295 [IPR005174] (1); Trimeric LpxA-like [IPR011004] (1)	scaffold_5_mRNA_4914.1	-	-
GF0030646	1	0	0	Phenylcoumaran benzylic ether reductase (1)		NmrA-like domain [IPR008030] (1); NAD(P)-binding domain [IPR016040] (1)	scaffold_5_mRNA_4910.1	-	-
GF0030645	1	0	0	Armadillo repeat containing protein-like (1)	protein ubiquitination [GO:0016567 biological_process] (1); ubiquitin-protein transferase activity [GO:0004842 molecular_function] (1); binding [GO:0005488 molecular_function] (1)	Armadillo-type fold [IPR016024] (1); U box domain [IPR003613] (1); Armadillo-like helical [IPR011989] (1); Zinc finger, RING/FYVE/PHD-type [IPR013083] (1)	scaffold_5_mRNA_4904.1	-	-
GF0030644	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_490.1	-	-
GF0030643	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_4894.1	-	-
GF0030642	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_489.1	-	-
GF0030641	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_488.1	-	-
GF0030640	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_4852.1	-	-
GF0030639	1	0	0	Hypothetical protein (1)	integral component of membrane [GO:0016021 cellular_component] (1)	ELO family [IPR002076] (1)	scaffold_5_mRNA_4850.1	-	-
GF0030638	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_485.1	-	-
GF0030637	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_484.1	-	-
GF0030636	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	WD40/YVTN repeat-like-containing domain [IPR015943] (1)	scaffold_5_mRNA_482.1	-	-
GF0030635	1	0	0	Sulfotransferase (1)		P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_5_mRNA_4801.1	-	-
GF0030634	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_480.1	-	-
GF0030633	1	0	0	Hypothetical protein (1)	binding [GO:0005488 molecular_function] (1)	Armadillo-type fold [IPR016024] (1)	scaffold_5_mRNA_4797.1	-	-
GF0030632	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_4795.1	-	-
GF0030631	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_4790.1	-	-
GF0030630	1	0	0	Intraflagellar transport protein (1)	protein binding [GO:0005515 molecular_function] (1)	Tetratricopeptide-like helical domain [IPR011990] (1)	scaffold_5_mRNA_4787.1	-	-
GF0030629	1	0	0	Transmembrane 53 (1)		Protein of unknown function DUF829, TMEM53 [IPR008547] (1); Alpha/Beta hydrolase fold [IPR029058] (1)	scaffold_5_mRNA_4785.1	-	-
GF0030628	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_4752.1	-	-
GF0030627	1	0	0	Subtilase family protein (1)	serine-type endopeptidase activity [GO:0004252 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Peptidase S8 propeptide/proteinase inhibitor I9 [IPR010259] (1); Peptidase S8, subtilisin, Ser-active site [IPR023828] (1); Peptidase S8, subtilisin-related [IPR015500] (1); Cucumisin-like catalytic domain [IPR034197] (1); Peptidase S8/S53 domain [IPR000209] (1)	scaffold_5_mRNA_4748.1	-	-
GF0030626	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_4731.1	-	-
GF0030625	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_473.1	-	-
GF0030624	1	0	0	Putative disease resistance RGA3 (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)	scaffold_5_mRNA_472.1	-	-
GF0030623	1	0	0	Hypothetical protein (1)		GPN-loop GTPase 2 [IPR030231] (1); GPN-loop GTPase [IPR004130] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_5_mRNA_468.1	-	-
GF0030622	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_4665.1	-	-
GF0030621	1	0	0	LRR and NB-ARC domain disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_5_mRNA_466.1	-	-
GF0030620	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_5_mRNA_464.1	-	-
GF0030619	1	0	0	Neutral/alkaline invertase (1)	glycopeptide alpha-N-acetylgalactosaminidase activity [GO:0033926 molecular_function] (1); catalytic activity [GO:0003824 molecular_function] (1)	Glycosyl hydrolase family 100 [IPR024746] (1); Six-hairpin glycosidase-like [IPR008928] (1)	scaffold_5_mRNA_4639.1	-	-
GF0030618	1	0	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1)	scaffold_5_mRNA_463.1	-	-
GF0030617	1	0	0	MA3 domain-containing protein (1)	binding [GO:0005488 molecular_function] (1)	Armadillo-type fold [IPR016024] (1); Initiation factor eIF-4 gamma, MA3 [IPR003891] (1)	scaffold_5_mRNA_4617.1	-	-
GF0030616	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); metallocarboxypeptidase activity [GO:0004181 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Peptidase M14, carboxypeptidase A [IPR000834] (1)	scaffold_5_mRNA_4594.1	-	-
GF0030615	1	0	0	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, ATP binding site [IPR017441] (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)	scaffold_5_mRNA_4584.1	-	-
GF0030614	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_458.1	-	-
GF0030613	1	0	0	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)	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)	scaffold_5_mRNA_4569.1	-	-
GF0030612	1	0	0	Cytochrome P450 family 71 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, E-class, group I [IPR002401] (1)	scaffold_5_mRNA_4568.1	-	-
GF0030611	1	0	0	Protein SET DOMAIN GROUP 41 (1)	protein binding [GO:0005515 molecular_function] (1)	SET domain [IPR001214] (1)	scaffold_5_mRNA_4562.1	-	-
GF0030610	1	0	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1); Receptor L-domain [IPR000494] (1)	scaffold_5_mRNA_453.1	-	-
GF0030609	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_4529.1	-	-
GF0030608	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_4514.1	-	-
GF0030607	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_451.1	-	-
GF0030606	1	0	0	Alcohol dehydrogenase (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, C-terminal [IPR013149] (1); Alcohol dehydrogenase, zinc-type, conserved site [IPR002328] (1); Alcohol dehydrogenase, N-terminal [IPR013154] (1); GroES-like [IPR011032] (1); NAD(P)-binding domain [IPR016040] (1)	scaffold_5_mRNA_4502.1	-	-
GF0030605	1	0	0	Retrotransposon protein, putative, unclassified (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_5_mRNA_4491.1	-	-
GF0030604	1	0	0	GPN-loop GTPase 2 (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); GPN-loop GTPase [IPR004130] (1); GPN-loop GTPase 2 [IPR030231] (1)	scaffold_5_mRNA_449.1	-	-
GF0030603	1	0	0	Hypothetical protein (1)		LIM-domain binding protein/SEUSS [IPR029005] (1)	scaffold_5_mRNA_4486.1	-	-
GF0030602	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_5_mRNA_4479.1	-	-
GF0030601	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_4444.1	-	-
GF0030600	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_4443.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0030599	1	0	0	Putative acyl-activating enzyme 6 (1)	catalytic activity [GO:0003824 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	AMP-binding, conserved site [IPR020845] (1); AMP-binding enzyme C-terminal domain [IPR025110] (1); AMP-dependent synthetase/ligase [IPR000873] (1)	scaffold_5_mRNA_4442.1	-	-
GF0030598	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_4427.1	-	-
GF0030597	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_4410.1	-	-
GF0030596	1	0	0	12-oxophytodienoate reductase 1 (1)	catalytic activity [GO:0003824 molecular_function] (1); FMN binding [GO:0010181 molecular_function] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Aldolase-type TIM barrel [IPR013785] (1); NADH:flavin oxidoreductase/NADH oxidase, N-terminal [IPR001155] (1)	scaffold_5_mRNA_441.1	-	-
GF0030595	1	0	0	Carboxy-terminal domain cyclin (1)			scaffold_5_mRNA_4408.1	-	-
GF0030594	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_439.1	-	-
GF0030593	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_4384.1	-	-
GF0030592	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_437.1	-	-
GF0030591	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_5_mRNA_4366.1	-	-
GF0030590	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_4362.1	-	-
GF0030589	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_4344.1	-	-
GF0030588	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_433.1	-	-
GF0030587	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_4316.1	-	-
GF0030586	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_4310.1	-	-
GF0030585	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_431.1	-	-
GF0030584	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Ribonuclease H domain [IPR002156] (1)	scaffold_5_mRNA_430.1	-	-
GF0030583	1	0	0	GrpE protein homolog (1)	adenyl-nucleotide exchange factor activity [GO:0000774 molecular_function] (1); protein homodimerization activity [GO:0042803 molecular_function] (1); protein folding [GO:0006457 biological_process] (1); chaperone binding [GO:0051087 molecular_function] (1)	GrpE nucleotide exchange factor, coiled-coil [IPR013805] (1); GrpE nucleotide exchange factor [IPR000740] (1); GrpE nucleotide exchange factor, head [IPR009012] (1)	scaffold_5_mRNA_4294.1	-	-
GF0030582	1	0	0	Hypothetical protein (1)		Protein of unknown function DUF4750 [IPR031851] (1)	scaffold_5_mRNA_4293.1	-	-
GF0030581	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_4292.1	-	-
GF0030580	1	0	0	Hypothetical protein (1)		Ankyrin repeat-containing domain [IPR020683] (1)	scaffold_5_mRNA_426.1	-	-
GF0030579	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_4252.1	-	-
GF0030578	1	0	0	Random slug protein 5 (1)		CRAL-TRIO lipid binding domain [IPR001251] (1); CRAL/TRIO, N-terminal domain [IPR011074] (1)	scaffold_5_mRNA_4251.1	-	-
GF0030577	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_4249.1	-	-
GF0030576	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_4247.1	-	-
GF0030575	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_424.1	-	-
GF0030574	1	0	0	Hypothetical protein (1)	transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	scaffold_5_mRNA_4226.1	-	-
GF0030573	1	0	0	Hypothetical protein (1)		Ankyrin repeat-containing domain [IPR020683] (1)	scaffold_5_mRNA_422.1	-	-
GF0030572	1	0	0	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)	scaffold_5_mRNA_420.1	-	-
GF0030571	1	0	0	Alcohol dehydrogenase (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, N-terminal [IPR013154] (1); Alcohol dehydrogenase, zinc-type, conserved site [IPR002328] (1); Alcohol dehydrogenase, C-terminal [IPR013149] (1)	scaffold_5_mRNA_4192.1	-	-
GF0030570	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_4191.1	-	-
GF0030569	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_5_mRNA_4190.1	-	-
GF0030568	1	0	0	12-oxophytodienoate reductase 2 (1)	catalytic activity [GO:0003824 molecular_function] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); FMN binding [GO:0010181 molecular_function] (1)	Aldolase-type TIM barrel [IPR013785] (1); NADH:flavin oxidoreductase/NADH oxidase, N-terminal [IPR001155] (1)	scaffold_5_mRNA_419.1	-	-
GF0030567	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_4189.1	-	-
GF0030566	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_5_mRNA_4185.1	-	-
GF0030565	1	0	0	Alcohol dehydrogenase (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, zinc-type, conserved site [IPR002328] (1); Alcohol dehydrogenase, N-terminal [IPR013154] (1); GroES-like [IPR011032] (1); NAD(P)-binding domain [IPR016040] (1)	scaffold_5_mRNA_4184.1	-	-
GF0030564	1	0	0	Ankyrin repeat protein (1)		PGG domain [IPR026961] (1)	scaffold_5_mRNA_415.1	-	-
GF0030563	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_414.1	-	-
GF0030562	1	0	0	12-oxophytodienoate reductase 2 (1)	catalytic activity [GO:0003824 molecular_function] (1); FMN binding [GO:0010181 molecular_function] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	NADH:flavin oxidoreductase/NADH oxidase, N-terminal [IPR001155] (1); Aldolase-type TIM barrel [IPR013785] (1)	scaffold_5_mRNA_413.1	-	-
GF0030561	1	0	0	Hypothetical protein (1)		Rossmann-like alpha/beta/alpha sandwich fold [IPR014729] (1)	scaffold_5_mRNA_4127.1	-	-
GF0030560	1	0	0	Carbonate dehydratase (1)	zinc ion binding [GO:0008270 molecular_function] (1); carbonate dehydratase activity [GO:0004089 molecular_function] (1)	Carbonic anhydrase [IPR001765] (1)	scaffold_5_mRNA_4123.1	-	-
GF0030559	1	0	0	Hypothetical protein (1)	binding [GO:0005488 molecular_function] (1)	Domain of unknown function DUF4704 [IPR031570] (1); Armadillo-type fold [IPR016024] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Armadillo-like helical [IPR011989] (1)	scaffold_5_mRNA_4102.1	-	-
GF0030558	1	0	0	Hydroxyproline-rich glycoprotein family protein (1)		Spo12 [IPR007727] (1)	scaffold_5_mRNA_4089.1	-	-
GF0030557	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_4087.1	-	-
GF0030556	1	0	0	MADS-box transcription factor (1)			scaffold_5_mRNA_4083.1	-	-
GF0030555	1	0	0	Tubulin alpha chain (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); GTPase activity [GO:0003924 molecular_function] (1)	Alpha tubulin [IPR002452] (1); Tubulin/FtsZ, C-terminal [IPR008280] (1); Tubulin [IPR000217] (1); Tubulin/FtsZ, 2-layer sandwich domain [IPR018316] (1); Tubulin, conserved site [IPR017975] (1); Tubulin/FtsZ, GTPase domain [IPR003008] (1)	scaffold_5_mRNA_4053.1	-	-
GF0030554	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_4042.1	-	-
GF0030553	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_4040.1	-	-
GF0030552	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_4039.1	-	-
GF0030551	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_4038.1	-	-
GF0030550	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_4037.1	-	-
GF0030549	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_4036.1	-	-
GF0030548	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_4024.1	-	-
GF0030547	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_4020.1	-	-
GF0030546	1	0	0	RNA-directed DNA polymerase (Reverse transcriptase) (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_5_mRNA_4.1	-	-
GF0030545	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3992.1	-	-
GF0030544	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3989.1	-	-
GF0030543	1	0	0	Hypothetical protein (1)		Uncharacterised protein family SERF [IPR007513] (1); At2g23090-like [IPR026939] (1)	scaffold_5_mRNA_3973.1	-	-
GF0030542	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3953.1	-	-
GF0030541	1	0	0	Monosacharide transport protein (1)			scaffold_5_mRNA_3952.1	-	-
GF0030540	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_5_mRNA_3950.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0030539	1	0	0	Ankyrin repeat family protein, putative (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat [IPR002110] (1); Ankyrin repeat-containing domain [IPR020683] (1); PGG domain [IPR026961] (1)	scaffold_5_mRNA_395.1	-	-
GF0030538	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_392.1	-	-
GF0030537	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_39.1	-	-
GF0030536	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3886.1	-	-
GF0030535	1	0	0	Hypothetical protein (1)		Protein of unknown function DUF3511 [IPR021899] (1)	scaffold_5_mRNA_3878.1	-	-
GF0030534	1	0	0	Phloem protein 2-B5 (1)	protein binding [GO:0005515 molecular_function] (1)	Phloem protein 2-like [IPR025886] (1); F-box domain [IPR001810] (1)	scaffold_5_mRNA_3854.1	-	-
GF0030533	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3853.1	-	-
GF0030532	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3851.1	-	-
GF0030531	1	0	0	Hypothetical protein (1)		Iron hydrogenase [IPR009016] (1); Iron hydrogenase, small subunit [IPR003149] (1); Iron hydrogenase, large subunit, C-terminal [IPR004108] (1)	scaffold_5_mRNA_3847.1	-	-
GF0030530	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3837.1	-	-
GF0030529	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3833.1	-	-
GF0030528	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3832.1	-	-
GF0030527	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3831.1	-	-
GF0030526	1	0	0	Retrotransposon protein, putative, Ty1-copia subclass (1)			scaffold_5_mRNA_383.1	-	-
GF0030525	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3829.1	-	-
GF0030524	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); F-box domain [IPR001810] (1)	scaffold_5_mRNA_3828.1	-	-
GF0030523	1	0	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1); FBD domain [IPR006566] (1)	scaffold_5_mRNA_3827.1	-	-
GF0030522	1	0	0	Monosacharide transport protein (1)			scaffold_5_mRNA_3826.1	-	-
GF0030521	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_382.1	-	-
GF0030520	1	0	0	CXE carboxylesterase (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)	scaffold_5_mRNA_3816.1	-	-
GF0030519	1	0	0	Sugar transporter SWEET (1)	integral component of membrane [GO:0016021 cellular_component] (1)	SWEET sugar transporter [IPR004316] (1)	scaffold_5_mRNA_3815.1	-	-
GF0030518	1	0	0	BiP isoform A family 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)	scaffold_5_mRNA_3814.1	-	-
GF0030517	1	0	0	Retrotransposon protein, putative, Ty1-copia subclass (1)		GAG-pre-integrase domain [IPR025724] (1)	scaffold_5_mRNA_381.1	-	-
GF0030516	1	0	0	BiP isoform A family protein (1)		Heat shock protein 70kD, peptide-binding domain [IPR029047] (1); Heat shock protein 70, conserved site [IPR018181] (1); Heat shock protein 70 family [IPR013126] (1)	scaffold_5_mRNA_3808.1	-	-
GF0030515	1	0	0	22.0 kDa class IV heat shock protein (1)		Alpha crystallin/Hsp20 domain [IPR002068] (1); HSP20-like chaperone [IPR008978] (1); Small heat shock protein HSP20 [IPR031107] (1)	scaffold_5_mRNA_38.1	-	-
GF0030514	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	scaffold_5_mRNA_3797.1	-	-
GF0030513	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3796.1	-	-
GF0030512	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_5_mRNA_3795.1	-	-
GF0030511	1	0	0	Hypothetical protein (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1)	scaffold_5_mRNA_3764.1	-	-
GF0030510	1	0	0	Hypothetical protein (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	scaffold_5_mRNA_3763.1	-	-
GF0030509	1	0	0	Putative wall-associated receptor kinase-like 16 (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)	scaffold_5_mRNA_3759.1	-	-
GF0030508	1	0	0	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)	scaffold_5_mRNA_3758.1	-	-
GF0030507	1	0	0	Hypothetical protein (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1)	scaffold_5_mRNA_3756.1	-	-
GF0030506	1	0	0	Putative wall-associated receptor kinase-like 11 (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)	scaffold_5_mRNA_3755.1	-	-
GF0030505	1	0	0	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	scaffold_5_mRNA_3753.1	-	-
GF0030504	1	0	0	Hypothetical protein (1)		Protein kinase-like domain [IPR011009] (1)	scaffold_5_mRNA_3751.1	-	-
GF0030503	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3746.1	-	-
GF0030502	1	0	0	Putative disease resistance RPP13-like protein 1 (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_5_mRNA_3710.1	-	-
GF0030501	1	0	0	Hypothetical protein (1)	ribosome [GO:0005840 cellular_component] (1); translation [GO:0006412 biological_process] (1); intracellular [GO:0005622 cellular_component] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1)	Ribosomal protein S8e [IPR001047] (1)	scaffold_5_mRNA_3709.1	-	-
GF0030500	1	0	0	Putative disease resistance RGA1 (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1)	scaffold_5_mRNA_3707.1	-	-
GF0030499	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	scaffold_5_mRNA_3698.1	-	-
GF0030498	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_369.1	-	-
GF0030497	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3672.1	-	-
GF0030496	1	0	0	Monosacharide transport protein (1)			scaffold_5_mRNA_3670.1	-	-
GF0030495	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_5_mRNA_367.1	-	-
GF0030494	1	0	0	NB-ARC domain disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_5_mRNA_3668.1	-	-
GF0030493	1	0	0	DNA excision repair protein ERCC-1 (1)	damaged DNA binding [GO:0003684 molecular_function] (1); endonuclease activity [GO:0004519 molecular_function] (1); DNA repair [GO:0006281 biological_process] (1); nucleus [GO:0005634 cellular_component] (1)	ERCC1/RAD10/SWI10 family [IPR004579] (1); Restriction endonuclease type II-like [IPR011335] (1); RuvA domain 2-like [IPR010994] (1)	scaffold_5_mRNA_3667.1	-	-
GF0030492	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Zinc finger, PMZ-type [IPR006564] (1)	scaffold_5_mRNA_3653.1	-	-
GF0030491	1	0	0	Putative disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1); Transposase, MuDR, plant [IPR004332] (1); MULE transposase domain [IPR018289] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_5_mRNA_3652.1	-	-
GF0030490	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3650.1	-	-
GF0030489	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3649.1	-	-
GF0030488	1	0	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_5_mRNA_3648.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0030487	1	0	0	Putative non-LTR retroelement reverse transcriptase (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Reverse transcriptase domain [IPR000477] (1); Ribonuclease H-like domain [IPR012337] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1); Endonuclease/exonuclease/phosphatase [IPR005135] (1)	scaffold_5_mRNA_3644.1	-	-
GF0030486	1	0	0	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); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1)	scaffold_5_mRNA_3643.1	-	-
GF0030485	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1); Retrotransposon gag domain [IPR005162] (1)	scaffold_5_mRNA_3642.1	-	-
GF0030484	1	0	0	Bifunctional dihydroflavonol 4-reductase/flavanone 4-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 [IPR001509] (1)	scaffold_5_mRNA_3634.1	-	-
GF0030483	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1); Retrotransposon gag domain [IPR005162] (1)	scaffold_5_mRNA_3633.1	-	-
GF0030482	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3632.1	-	-
GF0030481	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1); Retrotransposon gag domain [IPR005162] (1)	scaffold_5_mRNA_3622.1	-	-
GF0030480	1	0	0	Magnesium transporter 2 isoform 2 (1)	protein serine/threonine kinase activity [GO:0004674 molecular_function] (1)	S-locus receptor kinase, C-terminal [IPR021820] (1)	scaffold_5_mRNA_3620.1	-	-
GF0030479	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3615.1	-	-
GF0030478	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3614.1	-	-
GF0030477	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3611.1	-	-
GF0030476	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3610.1	-	-
GF0030475	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3609.1	-	-
GF0030474	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3608.1	-	-
GF0030473	1	0	0	Cysteine-rich receptor-like protein kinase 10 (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein serine/threonine kinase activity [GO:0004674 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (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)	scaffold_5_mRNA_3607.1	-	-
GF0030472	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_5_mRNA_3603.1	-	-
GF0030471	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3602.1	-	-
GF0030470	1	0	0	NB-ARC domain-containing disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	scaffold_5_mRNA_36.1	-	-
GF0030469	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_5_mRNA_3597.1	-	-
GF0030468	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3596.1	-	-
GF0030467	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3594.1	-	-
GF0030466	1	0	0	AT1G08890 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)	scaffold_5_mRNA_3593.1	-	-
GF0030465	1	0	0	Sodium/hydrogen exchanger 2 (1)	transmembrane transport [GO:0055085 biological_process] (1); solute:proton antiporter activity [GO:0015299 molecular_function] (1); sodium ion transport [GO:0006814 biological_process] (1); integral component of membrane [GO:0016021 cellular_component] (1); sodium:proton antiporter activity [GO:0015385 molecular_function] (1); regulation of pH [GO:0006885 biological_process] (1); cation transport [GO:0006812 biological_process] (1)	Cation/H+ exchanger [IPR006153] (1); Na+/H+ exchanger [IPR004709] (1); Cation/H+ exchanger, CPA1 family [IPR018422] (1)	scaffold_5_mRNA_3582.1	-	-
GF0030464	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	F-box domain [IPR001810] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_5_mRNA_3578.1	-	-
GF0030463	1	0	0	Phosphoprotein phosphatase (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_5_mRNA_3576.1	-	-
GF0030462	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3573.1	-	-
GF0030461	1	0	0	Disease resistance protein (CC-NBS-LRR class) family protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1)	scaffold_5_mRNA_3572.1	-	-
GF0030460	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3571.1	-	-
GF0030459	1	0	0	Disease resistance RPS2-like protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_5_mRNA_3570.1	-	-
GF0030458	1	0	0	Monosacharide transport protein (1)			scaffold_5_mRNA_3569.1	-	-
GF0030457	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3568.1	-	-
GF0030456	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_5_mRNA_3566.1	-	-
GF0030455	1	0	0	Protein BONZAI 3 (1)	calcium-dependent phospholipid binding [GO:0005544 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1); negative regulation of cell death [GO:0060548 biological_process] (1)	von Willebrand factor, type A [IPR002035] (1); C2 domain [IPR000008] (1); Protein BONZAI [IPR031116] (1); Copine [IPR010734] (1)	scaffold_5_mRNA_3562.1	-	-
GF0030454	1	0	0	Hypothetical protein (1)		P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_5_mRNA_3561.1	-	-
GF0030453	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3560.1	-	-
GF0030452	1	0	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Domain of unknown function DUF1985 [IPR015410] (1); Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	scaffold_5_mRNA_356.1	-	-
GF0030451	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3559.1	-	-
GF0030450	1	0	0	Retrotransposon protein, putative, Ty3-gypsy subclass (1)	nucleic acid binding [GO:0003676 molecular_function] (1); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1); DNA integration [GO:0015074 biological_process] (1)	Ribonuclease H domain [IPR002156] (1); Integrase, catalytic core [IPR001584] (1); Ribonuclease H-like domain [IPR012337] (1); Retrotransposon gag domain [IPR005162] (1); Aspartic peptidase domain [IPR021109] (1)	scaffold_5_mRNA_3558.1	-	-
GF0030449	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3553.1	-	-
GF0030448	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_5_mRNA_3552.1	-	-
GF0030447	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3551.1	-	-
GF0030446	1	0	0	Retrotransposon gag protein (1)			scaffold_5_mRNA_3550.1	-	-
GF0030445	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, PMZ-type [IPR006564] (1); Zinc finger, SWIM-type [IPR007527] (1)	scaffold_5_mRNA_3548.1	-	-
GF0030444	1	0	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Domain of unknown function DUF1985 [IPR015410] (1); Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	scaffold_5_mRNA_3547.1	-	-
GF0030443	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3545.1	-	-
GF0030442	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3543.1	-	-
GF0030441	1	0	0	Protein BONZAI 3 (1)	calcium-dependent phospholipid binding [GO:0005544 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1); negative regulation of cell death [GO:0060548 biological_process] (1)	Protein BONZAI [IPR031116] (1); C2 domain [IPR000008] (1); Copine [IPR010734] (1); von Willebrand factor, type A [IPR002035] (1)	scaffold_5_mRNA_3541.1	-	-
GF0030440	1	0	0	NBS-LRR type disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	scaffold_5_mRNA_3532.1	-	-
GF0030439	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Ribonuclease H domain [IPR002156] (1); Retrotransposon gag domain [IPR005162] (1)	scaffold_5_mRNA_3531.1	-	-
GF0030438	1	0	0	Monosacharide transport protein (1)			scaffold_5_mRNA_3530.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0030437	1	0	0	Disease resistance protein RPS2, 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); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_5_mRNA_3529.1	-	-
GF0030436	1	0	0	Protein BONZAI 1 (1)	protein binding [GO:0005515 molecular_function] (1); calcium-dependent phospholipid binding [GO:0005544 molecular_function] (1); negative regulation of cell death [GO:0060548 biological_process] (1)	von Willebrand factor, type A [IPR002035] (1); Protein BONZAI [IPR031116] (1); C2 domain [IPR000008] (1); Copine [IPR010734] (1)	scaffold_5_mRNA_3525.1	-	-
GF0030435	1	0	0	Hypothetical protein (1)		GAG-pre-integrase domain [IPR025724] (1)	scaffold_5_mRNA_3523.1	-	-
GF0030434	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3521.1	-	-
GF0030433	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3520.1	-	-
GF0030432	1	0	0	Hypothetical protein (1)		P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_5_mRNA_352.1	-	-
GF0030431	1	0	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Domain of unknown function DUF1985 [IPR015410] (1); Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	scaffold_5_mRNA_3519.1	-	-
GF0030430	1	0	0	Similarity to non-LTR retroelement reverse transcriptase (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_5_mRNA_3517.1	-	-
GF0030429	1	0	0	Non-LTR retroelement reverse transcriptase-like (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_5_mRNA_3516.1	-	-
GF0030428	1	0	0	RNA-directed DNA polymerase (Reverse transcriptase) (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Reverse transcriptase domain [IPR000477] (1)	scaffold_5_mRNA_3515.1	-	-
GF0030427	1	0	0	NBS-LRR type disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_5_mRNA_3512.1	-	-
GF0030426	1	0	0	Disease resistance protein (CC-NBS-LRR class) family protein (1)	ADP binding [GO:0043531 molecular_function] (1)	Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_5_mRNA_3511.1	-	-
GF0030425	1	0	0	Hypothetical protein (1)	negative regulation of cell death [GO:0060548 biological_process] (1); calcium-dependent phospholipid binding [GO:0005544 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Copine [IPR010734] (1); Protein BONZAI [IPR031116] (1); C2 domain [IPR000008] (1); von Willebrand factor, type A [IPR002035] (1); Development/cell death domain [IPR013989] (1)	scaffold_5_mRNA_3510.1	-	-
GF0030424	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3498.1	-	-
GF0030423	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3495.1	-	-
GF0030422	1	0	0	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	scaffold_5_mRNA_3490.1	-	-
GF0030421	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1); Zinc knuckle CX2CX4HX4C [IPR025836] (1)	scaffold_5_mRNA_3484.1	-	-
GF0030420	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3482.1	-	-
GF0030419	1	0	0	Superoxide dismutase [Cu-Zn] (1)	superoxide dismutase activity [GO:0004784 molecular_function] (1); metal ion binding [GO:0046872 molecular_function] (1); superoxide metabolic process [GO:0006801 biological_process] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Superoxide dismutase, copper/zinc, binding site [IPR018152] (1); Superoxide dismutase, copper/zinc binding domain [IPR001424] (1)	scaffold_5_mRNA_3481.1	-	-
GF0030418	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3476.1	-	-
GF0030417	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3474.1	-	-
GF0030416	1	0	0	Ras-like GTP-binding protein YPT1 (1)	GTPase activity [GO:0003924 molecular_function] (1); GTP binding [GO:0005525 molecular_function] (1)	Small GTP-binding protein domain [IPR005225] (1); Small GTPase superfamily [IPR001806] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_5_mRNA_347.1	-	-
GF0030415	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3464.1	-	-
GF0030414	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3459.1	-	-
GF0030413	1	0	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1)	Xylanase inhibitor, N-terminal [IPR032861] (1); Xylanase inhibitor, C-terminal [IPR032799] (1); Aspartic peptidase A1 family [IPR001461] (1); Aspartic peptidase, active site [IPR001969] (1); Pepsin-like domain, plant [IPR034161] (1); Aspartic peptidase domain [IPR021109] (1); Peptidase family A1 domain [IPR033121] (1)	scaffold_5_mRNA_3452.1	-	-
GF0030412	1	0	0	Hypothetical protein (1)		Small heat shock protein HSP20 [IPR031107] (1); HSP20-like chaperone [IPR008978] (1); Alpha crystallin/Hsp20 domain [IPR002068] (1)	scaffold_5_mRNA_345.1	-	-
GF0030411	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3445.1	-	-
GF0030410	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3438.1	-	-
GF0030409	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3435.1	-	-
GF0030408	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_5_mRNA_3434.1	-	-
GF0030407	1	0	0	Cysteine synthase (1)	cysteine synthase activity [GO:0004124 molecular_function] (1); cysteine biosynthetic process from serine [GO:0006535 biological_process] (1)	Cysteine synthase CysK [IPR005859] (1); Cysteine synthase [IPR005856] (1); Tryptophan synthase beta subunit-like PLP-dependent enzyme [IPR001926] (1); Cysteine synthase/cystathionine beta-synthase, pyridoxal-phosphate attachment site [IPR001216] (1)	scaffold_5_mRNA_3425.1	-	-
GF0030406	1	0	0	Monosacharide transport protein (1)			scaffold_5_mRNA_342.1	-	-
GF0030405	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3415.1	-	-
GF0030404	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_341.1	-	-
GF0030403	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3399.1	-	-
GF0030402	1	0	0	Disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1); AAA+ ATPase domain [IPR003593] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1)	scaffold_5_mRNA_3398.1	-	-
GF0030401	1	0	0	Disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1); binding [GO:0005488 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	NB-ARC [IPR002182] (1); Armadillo-type fold [IPR016024] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Atypical Arm repeat [IPR032413] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Armadillo [IPR000225] (1); Armadillo-like helical [IPR011989] (1)	scaffold_5_mRNA_3397.1	-	-
GF0030400	1	0	0	NBS-LRR type disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	Winged helix-turn-helix DNA-binding domain [IPR011991] (1); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_5_mRNA_3396.1	-	-
GF0030399	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3395.1	-	-
GF0030398	1	0	0	Disease resistance protein (CC-NBS-LRR class) family protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1)	scaffold_5_mRNA_3394.1	-	-
GF0030397	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3389.1	-	-
GF0030396	1	0	0	Monosacharide transport protein (1)			scaffold_5_mRNA_3377.1	-	-
GF0030395	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1); Aspartic peptidase domain [IPR021109] (1)	scaffold_5_mRNA_3376.1	-	-
GF0030394	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3374.1	-	-
GF0030393	1	0	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	scaffold_5_mRNA_3371.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0030392	1	0	0	Hypothetical protein (1)	RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1); ADP binding [GO:0043531 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H-like domain [IPR012337] (1); Receptor L-domain [IPR000494] (1); Ribonuclease H domain [IPR002156] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_5_mRNA_337.1	-	-
GF0030391	1	0	0	Monosacharide transport protein (1)			scaffold_5_mRNA_3361.1	-	-
GF0030390	1	0	0	LRR and NB-ARC domain disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	scaffold_5_mRNA_336.1	-	-
GF0030389	1	0	0	Retrotransposon protein, putative, Ty3-gypsy subclass (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_5_mRNA_3359.1	-	-
GF0030388	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3357.1	-	-
GF0030387	1	0	0	Hypothetical protein (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	FAD/NAD(P)-binding domain [IPR023753] (1); Lin-54 family [IPR028307] (1)	scaffold_5_mRNA_3351.1	-	-
GF0030386	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3349.1	-	-
GF0030385	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3348.1	-	-
GF0030384	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_5_mRNA_3347.1	-	-
GF0030383	1	0	0	Disease resistance protein (CC-NBS-LRR class) family 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); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_5_mRNA_3343.1	-	-
GF0030382	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_5_mRNA_3342.1	-	-
GF0030381	1	0	0	Disease resistance protein (CC-NBS-LRR class) family protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_5_mRNA_3341.1	-	-
GF0030380	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_334.1	-	-
GF0030379	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1); LOG family [IPR031100] (1)	scaffold_5_mRNA_3331.1	-	-
GF0030378	1	0	0	Disease resistance protein RPS2 (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1)	scaffold_5_mRNA_3330.1	-	-
GF0030377	1	0	0	Importin subunit alpha (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); binding [GO:0005488 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Atypical Arm repeat [IPR032413] (1); Armadillo [IPR000225] (1); Armadillo-like helical [IPR011989] (1); FAD/NAD(P)-binding domain [IPR023753] (1); Armadillo-type fold [IPR016024] (1)	scaffold_5_mRNA_3329.1	-	-
GF0030376	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3327.1	-	-
GF0030375	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_5_mRNA_3326.1	-	-
GF0030374	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3321.1	-	-
GF0030373	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3316.1	-	-
GF0030372	1	0	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1); binding [GO:0005488 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	AAA+ ATPase domain [IPR003593] (1); NB-ARC [IPR002182] (1); Armadillo-type fold [IPR016024] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Atypical Arm repeat [IPR032413] (1); Armadillo [IPR000225] (1); Armadillo-like helical [IPR011989] (1)	scaffold_5_mRNA_3315.1	-	-
GF0030371	1	0	0	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); carotenoid biosynthetic process [GO:0016117 biological_process] (1); carotene 7,8-desaturase activity [GO:0016719 molecular_function] (1)	Zeta-carotene desaturase [IPR014103] (1); FAD/NAD(P)-binding domain [IPR023753] (1)	scaffold_5_mRNA_3311.1	-	-
GF0030370	1	0	0	Phosphoprotein phosphatase (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_5_mRNA_3309.1	-	-
GF0030369	1	0	0	Hypothetical protein (1)	intracellular signal transduction [GO:0035556 biological_process] (1)	DC1 [IPR004146] (1); Protein kinase C-like, phorbol ester/diacylglycerol-binding domain [IPR002219] (1); Zinc finger, RING/FYVE/PHD-type [IPR013083] (1); Domain of unknown function DUF1985 [IPR015410] (1)	scaffold_5_mRNA_3294.1	-	-
GF0030368	1	0	0	Hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyl transferase (1)	transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (1)	Transferase [IPR003480] (1)	scaffold_5_mRNA_3291.1	-	-
GF0030367	1	0	0	Putative perakine reductase-like (1)		NADP-dependent oxidoreductase domain [IPR023210] (1)	scaffold_5_mRNA_3277.1	-	-
GF0030366	1	0	0	Aldo/keto reductase family oxidoreductase (1)		NADP-dependent oxidoreductase domain [IPR023210] (1)	scaffold_5_mRNA_3273.1	-	-
GF0030365	1	0	0	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)	scaffold_5_mRNA_3267.1	-	-
GF0030364	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3261.1	-	-
GF0030363	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_5_mRNA_3252.1	-	-
GF0030362	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3251.1	-	-
GF0030361	1	0	0	LRR and NB-ARC domain disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_5_mRNA_325.1	-	-
GF0030360	1	0	0	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); double-stranded DNA binding [GO:0003690 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	Transcription termination factor, mitochondrial/chloroplastic [IPR003690] (1); Isopenicillin N synthase-like [IPR027443] (1); Non-haem dioxygenase N-terminal domain [IPR026992] (1); Oxoglutarate/iron-dependent dioxygenase [IPR005123] (1)	scaffold_5_mRNA_3242.1	-	-
GF0030359	1	0	0	Ras-like GTP-binding protein YPT1 (1)	GTP binding [GO:0005525 molecular_function] (1); GTPase activity [GO:0003924 molecular_function] (1)	Small GTP-binding protein domain [IPR005225] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Small GTPase superfamily [IPR001806] (1)	scaffold_5_mRNA_324.1	-	-
GF0030358	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3239.1	-	-
GF0030357	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_5_mRNA_3234.1	-	-
GF0030356	1	0	0	Hypothetical protein (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Oxoglutarate/iron-dependent dioxygenase [IPR005123] (1); Isopenicillin N synthase-like [IPR027443] (1); Non-haem dioxygenase N-terminal domain [IPR026992] (1)	scaffold_5_mRNA_3232.1	-	-
GF0030355	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Tetratricopeptide-like helical domain [IPR011990] (1); Pentatricopeptide repeat [IPR002885] (1)	scaffold_5_mRNA_3231.1	-	-
GF0030354	1	0	0	Ras-like GTP-binding protein YPT1 (1)	GTPase activity [GO:0003924 molecular_function] (1); GTP binding [GO:0005525 molecular_function] (1)	Small GTPase superfamily [IPR001806] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_5_mRNA_322.1	-	-
GF0030353	1	0	0	LRR receptor-like serine/threonine-protein kinase GSO1 (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)	scaffold_5_mRNA_3217.1	-	-
GF0030352	1	0	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1); High mobility group box domain [IPR009071] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_5_mRNA_321.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0030351	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3204.1	-	-
GF0030350	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3202.1	-	-
GF0030349	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3200.1	-	-
GF0030348	1	0	0	Hypothetical protein (1)	integral component of membrane [GO:0016021 cellular_component] (1); transmembrane transport [GO:0055085 biological_process] (1)	Membrane transport protein [IPR004776] (1)	scaffold_5_mRNA_320.1	-	-
GF0030347	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3198.1	-	-
GF0030346	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3196.1	-	-
GF0030345	1	0	0	Putative TNP2 like transposable element (1)		Domain of unknown function DUF4218 [IPR025452] (1); Domain of unknown function DUF4216 [IPR025312] (1)	scaffold_5_mRNA_3195.1	-	-
GF0030344	1	0	0	Hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyl transferase (1)	transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (1)	Transferase [IPR003480] (1)	scaffold_5_mRNA_3191.1	-	-
GF0030343	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3189.1	-	-
GF0030342	1	0	0	Ras-like GTP-binding protein YPT1 (1)	GTPase activity [GO:0003924 molecular_function] (1); GTP binding [GO:0005525 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Small GTPase superfamily [IPR001806] (1)	scaffold_5_mRNA_318.1	-	-
GF0030341	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_5_mRNA_3174.1	-	-
GF0030340	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3173.1	-	-
GF0030339	1	0	0	LRR receptor-like serine/threonine-protein kinase GSO1 (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_5_mRNA_3171.1	-	-
GF0030338	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_5_mRNA_317.1	-	-
GF0030337	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3167.1	-	-
GF0030336	1	0	0	Hypothetical protein (1)	mitotic DNA replication checkpoint [GO:0033314 biological_process] (1); DNA replication [GO:0006260 biological_process] (1); response to ionizing radiation [GO:0010212 biological_process] (1); nucleus [GO:0005634 cellular_component] (1)	Treslin [IPR026153] (1)	scaffold_5_mRNA_3166.1	-	-
GF0030335	1	0	0	SH3 domain-containing protein 2 (1)		Arfaptin homology (AH) domain/BAR domain [IPR027267] (1)	scaffold_5_mRNA_3165.1	-	-
GF0030334	1	0	0	LRR receptor-like serine/threonine-protein kinase GSO1 (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat [IPR001611] (1)	scaffold_5_mRNA_3164.1	-	-
GF0030333	1	0	0	LRR receptor-like kinase family protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_5_mRNA_3162.1	-	-
GF0030332	1	0	0	22.7 kDa class IV heat shock protein (1)		Small heat shock protein HSP20 [IPR031107] (1); Alpha crystallin/Hsp20 domain [IPR002068] (1); HSP20-like chaperone [IPR008978] (1)	scaffold_5_mRNA_316.1	-	-
GF0030331	1	0	0	Hypothetical protein (1)		Transposase-associated domain [IPR029480] (1)	scaffold_5_mRNA_3159.1	-	-
GF0030330	1	0	0	LRR receptor-like serine/threonine-protein kinase GSO1 (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1)	scaffold_5_mRNA_3158.1	-	-
GF0030329	1	0	0	SH3 domain-containing protein 2 (1)	protein binding [GO:0005515 molecular_function] (1)	SH3 domain [IPR001452] (1); Arfaptin homology (AH) domain/BAR domain [IPR027267] (1)	scaffold_5_mRNA_3155.1	-	-
GF0030328	1	0	0	Zinc knuckle family protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_5_mRNA_3152.1	-	-
GF0030327	1	0	0	SH3 domain-containing protein 2 (1)	protein binding [GO:0005515 molecular_function] (1)	SH3 domain [IPR001452] (1); Arfaptin homology (AH) domain/BAR domain [IPR027267] (1)	scaffold_5_mRNA_3150.1	-	-
GF0030326	1	0	0	Hypothetical protein (1)	transmembrane transport [GO:0055085 biological_process] (1); membrane [GO:0016020 cellular_component] (1); transport [GO:0006810 biological_process] (1)	Amino acid permease/ SLC12A domain [IPR004841] (1)	scaffold_5_mRNA_3147.1	-	-
GF0030325	1	0	0	Hypothetical protein (1)	polyamine binding [GO:0019808 molecular_function] (1); polyamine transport [GO:0015846 biological_process] (1); periplasmic space [GO:0042597 cellular_component] (1)	Bacterial periplasmic spermidine/putrescine-binding protein [IPR001188] (1)	scaffold_5_mRNA_3145.1	-	-
GF0030324	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3144.1	-	-
GF0030323	1	0	0	SH3 domain-containing protein 2 (1)	protein binding [GO:0005515 molecular_function] (1)	Arfaptin homology (AH) domain/BAR domain [IPR027267] (1); SH3 domain [IPR001452] (1)	scaffold_5_mRNA_3143.1	-	-
GF0030322	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3141.1	-	-
GF0030321	1	0	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	hAT-like transposase, RNase-H fold [IPR025525] (1)	scaffold_5_mRNA_3140.1	-	-
GF0030320	1	0	0	Amino acid permease family protein (1)	amino acid transmembrane transporter activity [GO:0015171 molecular_function] (1); membrane [GO:0016020 cellular_component] (1); amino acid transmembrane transport [GO:0003333 biological_process] (1)	Amino acid/polyamine transporter I [IPR002293] (1)	scaffold_5_mRNA_3139.1	-	-
GF0030319	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	SH3 domain [IPR001452] (1)	scaffold_5_mRNA_3138.1	-	-
GF0030318	1	0	0	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)	scaffold_5_mRNA_3137.1	-	-
GF0030317	1	0	0	Amino acid permease family protein (1)	amino acid transmembrane transport [GO:0003333 biological_process] (1); membrane [GO:0016020 cellular_component] (1); protein binding [GO:0005515 molecular_function] (1); amino acid transmembrane transporter activity [GO:0015171 molecular_function] (1)	SH3 domain [IPR001452] (1); Amino acid/polyamine transporter I [IPR002293] (1)	scaffold_5_mRNA_3135.1	-	-
GF0030316	1	0	0	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)	scaffold_5_mRNA_3134.1	-	-
GF0030315	1	0	0	Retrotransposon protein, putative, unclassified (1)			scaffold_5_mRNA_3132.1	-	-
GF0030314	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_313.1	-	-
GF0030313	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3129.1	-	-
GF0030312	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3128.1	-	-
GF0030311	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3126.1	-	-
GF0030310	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3125.1	-	-
GF0030309	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_5_mRNA_3124.1	-	-
GF0030308	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3121.1	-	-
GF0030307	1	0	0	Hypothetical protein (1)	membrane [GO:0016020 cellular_component] (1); amino acid transmembrane transport [GO:0003333 biological_process] (1); amino acid transmembrane transporter activity [GO:0015171 molecular_function] (1)	Amino acid/polyamine transporter I [IPR002293] (1)	scaffold_5_mRNA_3120.1	-	-
GF0030306	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Arfaptin homology (AH) domain/BAR domain [IPR027267] (1); SH3 domain [IPR001452] (1)	scaffold_5_mRNA_3119.1	-	-
GF0030305	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	scaffold_5_mRNA_3118.1	-	-
GF0030304	1	0	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_5_mRNA_3117.1	-	-
GF0030303	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3116.1	-	-
GF0030302	1	0	0	SH3 domain-containing protein 2 (1)	protein binding [GO:0005515 molecular_function] (1)	SH3 domain [IPR001452] (1); Arfaptin homology (AH) domain/BAR domain [IPR027267] (1)	scaffold_5_mRNA_3115.1	-	-
GF0030301	1	0	0	Hypothetical 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)	scaffold_5_mRNA_3114.1	-	-
GF0030300	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_5_mRNA_3113.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0030299	1	0	0	Hypothetical protein (1)	polyamine transport [GO:0015846 biological_process] (1); periplasmic space [GO:0042597 cellular_component] (1); polyamine binding [GO:0019808 molecular_function] (1)	Bacterial periplasmic spermidine/putrescine-binding protein [IPR001188] (1)	scaffold_5_mRNA_3112.1	-	-
GF0030298	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3110.1	-	-
GF0030297	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_5_mRNA_311.1	-	-
GF0030296	1	0	0	LRR receptor-like serine/threonine-protein kinase GSO1 (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1)	scaffold_5_mRNA_3109.1	-	-
GF0030295	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3108.1	-	-
GF0030294	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3105.1	-	-
GF0030293	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3104.1	-	-
GF0030292	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3103.1	-	-
GF0030291	1	0	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, BED-type [IPR003656] (1); Zinc finger C2H2-type [IPR013087] (1)	scaffold_5_mRNA_3102.1	-	-
GF0030290	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3101.1	-	-
GF0030289	1	0	0	Disease resistance family protein / LRR family protein, putative (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1)	scaffold_5_mRNA_3098.1	-	-
GF0030288	1	0	0	SH3 domain-containing protein 2 (1)	protein binding [GO:0005515 molecular_function] (1)	Arfaptin homology (AH) domain/BAR domain [IPR027267] (1); SH3 domain [IPR001452] (1)	scaffold_5_mRNA_3096.1	-	-
GF0030287	1	0	0	LRR receptor-like serine/threonine-protein kinase GSO1 (1)	polyamine binding [GO:0019808 molecular_function] (1); polyamine transport [GO:0015846 biological_process] (1); periplasmic space [GO:0042597 cellular_component] (1); protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Bacterial periplasmic spermidine/putrescine-binding protein [IPR001188] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1)	scaffold_5_mRNA_3095.1	-	-
GF0030286	1	0	0	Hypothetical protein (1)		Histone deacetylase domain [IPR023801] (1); Histone deacetylase superfamily [IPR000286] (1)	scaffold_5_mRNA_3087.1	-	-
GF0030285	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3086.1	-	-
GF0030284	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3085.1	-	-
GF0030283	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3084.1	-	-
GF0030282	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3082.1	-	-
GF0030281	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_5_mRNA_3081.1	-	-
GF0030280	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3079.1	-	-
GF0030279	1	0	0	Receptor like protein 21 (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)	scaffold_5_mRNA_3073.1	-	-
GF0030278	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3072.1	-	-
GF0030277	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3071.1	-	-
GF0030276	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_5_mRNA_3062.1	-	-
GF0030275	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3058.1	-	-
GF0030274	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3046.1	-	-
GF0030273	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3044.1	-	-
GF0030272	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3043.1	-	-
GF0030271	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			scaffold_5_mRNA_3042.1	-	-
GF0030270	1	0	0	Hypothetical protein (1)	nucleus [GO:0005634 cellular_component] (1)	Retrotransposon gag domain [IPR005162] (1); BUD31/G10-related, conserved site [IPR018230] (1); G10 protein [IPR001748] (1)	scaffold_5_mRNA_3040.1	-	-
GF0030269	1	0	0	Ubiquitin carboxyl-terminal hydrolase 12 (1)	protein binding [GO:0005515 molecular_function] (1)	MATH/TRAF domain [IPR002083] (1); TRAF-like [IPR008974] (1)	scaffold_5_mRNA_3036.1	-	-
GF0030268	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	TRAF-like [IPR008974] (1); MATH/TRAF domain [IPR002083] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_5_mRNA_3034.1	-	-
GF0030267	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	MATH/TRAF domain [IPR002083] (1); TRAF-like [IPR008974] (1); Arabidopsis retrotransposon Orf1 [IPR004312] (1)	scaffold_5_mRNA_3033.1	-	-
GF0030266	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3032.1	-	-
GF0030265	1	0	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); protein binding [GO:0005515 molecular_function] (1)	MULE transposase domain [IPR018289] (1); TRAF-like [IPR008974] (1); MATH/TRAF domain [IPR002083] (1); FAR1 DNA binding domain [IPR004330] (1); FHY3/FAR1 family [IPR031052] (1)	scaffold_5_mRNA_3029.1	-	-
GF0030264	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	MATH/TRAF domain [IPR002083] (1); TRAF-like [IPR008974] (1)	scaffold_5_mRNA_3028.1	-	-
GF0030263	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3026.1	-	-
GF0030262	1	0	0	BTB/POZ and MATH domain protein (1)	protein binding [GO:0005515 molecular_function] (1)	MATH/TRAF domain [IPR002083] (1); TRAF-like [IPR008974] (1)	scaffold_5_mRNA_3024.1	-	-
GF0030261	1	0	0	Envelope glycoprotein (1)	protein binding [GO:0005515 molecular_function] (1)	TRAF-like [IPR008974] (1); MATH/TRAF domain [IPR002083] (1)	scaffold_5_mRNA_3023.1	-	-
GF0030260	1	0	0	Envelope glycoprotein (1)			scaffold_5_mRNA_3021.1	-	-
GF0030259	1	0	0	Hypothetical protein (1)	catalytic activity [GO:0003824 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Type I phosphodiesterase/nucleotide pyrophosphatase/phosphate transferase [IPR002591] (1); Alkaline phosphatase-like, alpha/beta/alpha [IPR017849] (1); Alkaline-phosphatase-like, core domain [IPR017850] (1)	scaffold_5_mRNA_302.1	-	-
GF0030258	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3011.1	-	-
GF0030257	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_3008.1	-	-
GF0030256	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_5_mRNA_3007.1	-	-
GF0030255	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Zinc finger, SWIM-type [IPR007527] (1); Zinc finger, PMZ-type [IPR006564] (1); Transposase, MuDR, plant [IPR004332] (1)	scaffold_5_mRNA_3001.1	-	-
GF0030254	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2996.1	-	-
GF0030253	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			scaffold_5_mRNA_2992.1	-	-
GF0030252	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_299.1	-	-
GF0030251	1	0	0	Cytochrome P450 82A3 (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, conserved site [IPR017972] (1); Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450 [IPR001128] (1)	scaffold_5_mRNA_2986.1	-	-
GF0030250	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2985.1	-	-
GF0030249	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2982.1	-	-
GF0030248	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2980.1	-	-
GF0030247	1	0	0	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)	scaffold_5_mRNA_298.1	-	-
GF0030246	1	0	0	Hypothetical protein (1)		DnaJ domain [IPR001623] (1); DnaJ domain, conserved site [IPR018253] (1)	scaffold_5_mRNA_2973.1	-	-
GF0030245	1	0	0	Cytochrome P450 82A3, putative (1)	iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1)	Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450, conserved site [IPR017972] (1); Cytochrome P450 [IPR001128] (1)	scaffold_5_mRNA_2970.1	-	-
GF0030244	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_297.1	-	-
GF0030243	1	0	0	SLG-Sc and SLA-Sc genes and Melmoth retrotransposon sequence (1)			scaffold_5_mRNA_2969.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0030242	1	0	0	Putative hAT family dimerisation domain containing 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)	HAT, C-terminal dimerisation domain [IPR008906] (1); hAT-like transposase, RNase-H fold [IPR025525] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_5_mRNA_2968.1	-	-
GF0030241	1	0	0	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)	scaffold_5_mRNA_2962.1	-	-
GF0030240	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2961.1	-	-
GF0030239	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2957.1	-	-
GF0030238	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2952.1	-	-
GF0030237	1	0	0	Hypothetical protein (1)		Ankyrin repeat-containing domain [IPR020683] (1)	scaffold_5_mRNA_2941.1	-	-
GF0030236	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_5_mRNA_2939.1	-	-
GF0030235	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2937.1	-	-
GF0030234	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2936.1	-	-
GF0030233	1	0	0	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)	scaffold_5_mRNA_2934.1	-	-
GF0030232	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2930.1	-	-
GF0030231	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2926.1	-	-
GF0030230	1	0	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1); Domain of unknown function DUF3627 [IPR022549] (1)	scaffold_5_mRNA_2925.1	-	-
GF0030229	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2924.1	-	-
GF0030228	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2923.1	-	-
GF0030227	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_5_mRNA_2922.1	-	-
GF0030226	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2919.1	-	-
GF0030225	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_5_mRNA_2914.1	-	-
GF0030224	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2908.1	-	-
GF0030223	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Helicase superfamily 1/2, ATP-binding domain [IPR014001] (1); 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)	scaffold_5_mRNA_2905.1	-	-
GF0030222	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2904.1	-	-
GF0030221	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2903.1	-	-
GF0030220	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_5_mRNA_2897.1	-	-
GF0030219	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2893.1	-	-
GF0030218	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2892.1	-	-
GF0030217	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2890.1	-	-
GF0030216	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2889.1	-	-
GF0030215	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1); Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	scaffold_5_mRNA_2873.1	-	-
GF0030214	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2872.1	-	-
GF0030213	1	0	0	Transposase (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)	scaffold_5_mRNA_2868.1	-	-
GF0030212	1	0	0	Disease resistance protein (CC-NBS-LRR class) family protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1); AAA+ ATPase domain [IPR003593] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_5_mRNA_2866.1	-	-
GF0030211	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2864.1	-	-
GF0030210	1	0	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, BED-type [IPR003656] (1); Zinc finger C2H2-type [IPR013087] (1)	scaffold_5_mRNA_2863.1	-	-
GF0030209	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2862.1	-	-
GF0030208	1	0	0	UPF0481 protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	scaffold_5_mRNA_2861.1	-	-
GF0030207	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_5_mRNA_286.1	-	-
GF0030206	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2858.1	-	-
GF0030205	1	0	0	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); Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_5_mRNA_2853.1	-	-
GF0030204	1	0	0	Hypothetical protein (1)	catalytic activity [GO:0003824 molecular_function] (1); protein dephosphorylation [GO:0006470 biological_process] (1); protein binding [GO:0005515 molecular_function] (1); protein serine/threonine phosphatase activity [GO:0004722 molecular_function] (1)	PPM-type phosphatase domain [IPR001932] (1); Thioredoxin-like fold [IPR012336] (1); Protein phosphatase 2C family [IPR015655] (1); Glutathione S-transferase, N-terminal [IPR004045] (1); Pectin lyase fold [IPR012334] (1)	scaffold_5_mRNA_2851.1	-	-
GF0030203	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2850.1	-	-
GF0030202	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1); Aspartic peptidase domain [IPR021109] (1)	scaffold_5_mRNA_2849.1	-	-
GF0030201	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2848.1	-	-
GF0030200	1	0	0	Hypothetical protein (1)	lipid binding [GO:0008289 molecular_function] (1)	START-like domain [IPR023393] (1); START domain [IPR002913] (1)	scaffold_5_mRNA_2843.1	-	-
GF0030199	1	0	0	Hypothetical protein (1)	transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	scaffold_5_mRNA_2842.1	-	-
GF0030198	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2841.1	-	-
GF0030197	1	0	0	Resistance protein RGC2 (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_5_mRNA_2839.1	-	-
GF0030196	1	0	0	Hypothetical protein (1)		Protein ENHANCED DISEASE RESISTANCE 2, C-terminal [IPR009769] (1)	scaffold_5_mRNA_2836.1	-	-
GF0030195	1	0	0	Hypothetical protein (1)		Arabidopsis retrotransposon Orf1 [IPR004312] (1)	scaffold_5_mRNA_2834.1	-	-
GF0030194	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2832.1	-	-
GF0030193	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2831.1	-	-
GF0030192	1	0	0	Phosphoprotein phosphatase isoform 1 (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_5_mRNA_2829.1	-	-
GF0030191	1	0	0	Hypothetical protein (1)	metabolic process [GO:0008152 biological_process] (1); transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	scaffold_5_mRNA_2828.1	-	-
GF0030190	1	0	0	Disease resistance protein (CC-NBS-LRR class) family protein (1)	ADP binding [GO:0043531 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); AAA+ ATPase domain [IPR003593] (1); NB-ARC [IPR002182] (1)	scaffold_5_mRNA_2826.1	-	-
GF0030189	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2823.1	-	-
GF0030188	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_282.1	-	-
GF0030187	1	0	0	Hypothetical protein (1)		Prolamin-like domain [IPR008502] (1)	scaffold_5_mRNA_2819.1	-	-
GF0030186	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_5_mRNA_2816.1	-	-
GF0030185	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_5_mRNA_2815.1	-	-
GF0030184	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2812.1	-	-
GF0030183	1	0	0	DUF247 domain protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	scaffold_5_mRNA_2811.1	-	-
GF0030182	1	0	0	UDP-glycosyltransferase 73C2 (1)	transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	scaffold_5_mRNA_2810.1	-	-
GF0030181	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_281.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0030180	1	0	0	Disease resistance protein (CC-NBS-LRR class) family protein (1)	ADP binding [GO:0043531 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); AAA+ ATPase domain [IPR003593] (1); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_5_mRNA_2809.1	-	-
GF0030179	1	0	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1); Probable transposase, Ptta/En/Spm, plant [IPR004252] (1)	scaffold_5_mRNA_2805.1	-	-
GF0030178	1	0	0	Glutathione-s-transferase omega (1)	protein binding [GO:0005515 molecular_function] (1)	Thioredoxin-like fold [IPR012336] (1); Glutathione S-transferase, N-terminal [IPR004045] (1)	scaffold_5_mRNA_2800.1	-	-
GF0030177	1	0	0	Disease resistance protein RPS2 (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_5_mRNA_2799.1	-	-
GF0030176	1	0	0	Hypothetical protein (1)		Protein ENHANCED DISEASE RESISTANCE 2, C-terminal [IPR009769] (1)	scaffold_5_mRNA_2798.1	-	-
GF0030175	1	0	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_5_mRNA_2794.1	-	-
GF0030174	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2793.1	-	-
GF0030173	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2792.1	-	-
GF0030172	1	0	0	Hypothetical protein (1)		Protein ENHANCED DISEASE RESISTANCE 2, C-terminal [IPR009769] (1)	scaffold_5_mRNA_2790.1	-	-
GF0030171	1	0	0	Cytochrome c oxidase biogenesis protein Cmc1-like isoform 1 (1)		Cytochrome c oxidase biogenesis protein Cmc1-like [IPR013892] (1)	scaffold_5_mRNA_279.1	-	-
GF0030170	1	0	0	Disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); AAA+ ATPase domain [IPR003593] (1); NB-ARC [IPR002182] (1)	scaffold_5_mRNA_2787.1	-	-
GF0030169	1	0	0	Disease resistance protein RPS2 (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_5_mRNA_2786.1	-	-
GF0030168	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2780.1	-	-
GF0030167	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2778.1	-	-
GF0030166	1	0	0	RNA-directed DNA polymerase (1)	RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H-like domain [IPR012337] (1); Ribonuclease H domain [IPR002156] (1)	scaffold_5_mRNA_2776.1	-	-
GF0030165	1	0	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_5_mRNA_2775.1	-	-
GF0030164	1	0	0	Disease resistance protein (CC-NBS-LRR class) family protein (1)	ADP binding [GO:0043531 molecular_function] (1)	Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); NB-ARC [IPR002182] (1); AAA+ ATPase domain [IPR003593] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_5_mRNA_2769.1	-	-
GF0030163	1	0	0	Hypothetical protein (1)	cell wall macromolecule catabolic process [GO:0016998 biological_process] (1); chitinase activity [GO:0004568 molecular_function] (1); chitin catabolic process [GO:0006032 biological_process] (1)	Lysozyme-like domain [IPR023346] (1); Glycoside hydrolase, family 19, catalytic [IPR000726] (1)	scaffold_5_mRNA_2763.1	-	-
GF0030162	1	0	0	Putative glutamyl endopeptidase, chloroplastic (1)			scaffold_5_mRNA_276.1	-	-
GF0030161	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2759.1	-	-
GF0030160	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_5_mRNA_2758.1	-	-
GF0030159	1	0	0	Non-LTR retroelement reverse transcriptase-like protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	scaffold_5_mRNA_2757.1	-	-
GF0030158	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Piwi domain [IPR003165] (1)	scaffold_5_mRNA_2756.1	-	-
GF0030157	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Piwi domain [IPR003165] (1)	scaffold_5_mRNA_2755.1	-	-
GF0030156	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2752.1	-	-
GF0030155	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2750.1	-	-
GF0030154	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1); Aspartic peptidase domain [IPR021109] (1); Retroviral aspartyl protease [IPR013242] (1)	scaffold_5_mRNA_275.1	-	-
GF0030153	1	0	0	LRR receptor-like kinase family protein (1)	protein binding [GO:0005515 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase, ATP binding site [IPR017441] (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)	scaffold_5_mRNA_2747.1	-	-
GF0030152	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2746.1	-	-
GF0030151	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2745.1	-	-
GF0030150	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2743.1	-	-
GF0030149	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2742.1	-	-
GF0030148	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_274.1	-	-
GF0030147	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_5_mRNA_2739.1	-	-
GF0030146	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, PMZ-type [IPR006564] (1); Zinc finger, SWIM-type [IPR007527] (1)	scaffold_5_mRNA_2738.1	-	-
GF0030145	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2733.1	-	-
GF0030144	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2731.1	-	-
GF0030143	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2729.1	-	-
GF0030142	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2716.1	-	-
GF0030141	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2711.1	-	-
GF0030140	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2710.1	-	-
GF0030139	1	0	0	Putative non-LTR retroelement reverse transcriptase (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1); Reverse transcriptase domain [IPR000477] (1)	scaffold_5_mRNA_2709.1	-	-
GF0030138	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2708.1	-	-
GF0030137	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2705.1	-	-
GF0030136	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2703.1	-	-
GF0030135	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2699.1	-	-
GF0030134	1	0	0	F-box protein CPR30 (1)		F-box associated interaction domain [IPR017451] (1)	scaffold_5_mRNA_2691.1	-	-
GF0030133	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_269.1	-	-
GF0030132	1	0	0	Progesterone 5-beta-reductase (1)		NAD(P)-binding domain [IPR016040] (1)	scaffold_5_mRNA_2683.1	-	-
GF0030131	1	0	0	Progesterone 5-beta-reductase (1)		NAD(P)-binding domain [IPR016040] (1)	scaffold_5_mRNA_2680.1	-	-
GF0030130	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_5_mRNA_268.1	-	-
GF0030129	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2677.1	-	-
GF0030128	1	0	0	Progesterone 5-beta-reductase (1)		NAD(P)-binding domain [IPR016040] (1)	scaffold_5_mRNA_2675.1	-	-
GF0030127	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_5_mRNA_2674.1	-	-
GF0030126	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2673.1	-	-
GF0030125	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2670.1	-	-
GF0030124	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2669.1	-	-
GF0030123	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2667.1	-	-
GF0030122	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_5_mRNA_2666.1	-	-
GF0030121	1	0	0	Hypothetical protein (1)	ubiquitin-dependent protein catabolic process [GO:0006511 biological_process] (1)	Domain of unknown function DUF4216 [IPR025312] (1); SKP1 component, POZ domain [IPR016073] (1); Transposase-associated domain [IPR029480] (1)	scaffold_5_mRNA_2664.1	-	-
GF0030120	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2661.1	-	-
GF0030119	1	0	0	Disease resistance protein (CC-NBS-LRR class) family protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1)	scaffold_5_mRNA_2659.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0030118	1	0	0	Resistance protein RGC2 (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Zinc finger, CCHC-type [IPR001878] (1)	scaffold_5_mRNA_2658.1	-	-
GF0030117	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_5_mRNA_2649.1	-	-
GF0030116	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2646.1	-	-
GF0030115	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_5_mRNA_2645.1	-	-
GF0030114	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2643.1	-	-
GF0030113	1	0	0	Putative muDR family transposase-like (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); MULE transposase domain [IPR018289] (1); Zinc finger, PMZ-type [IPR006564] (1); Zinc finger, SWIM-type [IPR007527] (1)	scaffold_5_mRNA_2641.1	-	-
GF0030112	1	0	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_5_mRNA_2638.1	-	-
GF0030111	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2636.1	-	-
GF0030110	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4219 [IPR025314] (1)	scaffold_5_mRNA_2634.1	-	-
GF0030109	1	0	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Carlavirus nucleic acid-binding protein [IPR002568] (1)	scaffold_5_mRNA_2633.1	-	-
GF0030108	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_5_mRNA_2632.1	-	-
GF0030107	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2631.1	-	-
GF0030106	1	0	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	scaffold_5_mRNA_2628.1	-	-
GF0030105	1	0	0	Disease resistance protein (CC-NBS-LRR class) family protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_5_mRNA_2627.1	-	-
GF0030104	1	0	0	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)	scaffold_5_mRNA_2624.1	-	-
GF0030103	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2622.1	-	-
GF0030102	1	0	0	Disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_5_mRNA_2620.1	-	-
GF0030101	1	0	0	Hypothetical protein (1)	methyltransferase activity [GO:0008168 molecular_function] (1)	Putative S-adenosyl-L-methionine-dependent methyltransferase [IPR004159] (1)	scaffold_5_mRNA_2619.1	-	-
GF0030100	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2618.1	-	-
GF0030099	1	0	0	Disease resistance protein (CC-NBS-LRR class) family protein (1)	ADP binding [GO:0043531 molecular_function] (1)	Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_5_mRNA_2615.1	-	-
GF0030098	1	0	0	Disease resistance protein (CC-NBS-LRR class) family protein (1)	ADP binding [GO:0043531 molecular_function] (1)	Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_5_mRNA_2612.1	-	-
GF0030097	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2611.1	-	-
GF0030096	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_261.1	-	-
GF0030095	1	0	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_5_mRNA_2608.1	-	-
GF0030094	1	0	0	Hypothetical protein (1)		Transposase, MuDR, plant [IPR004332] (1)	scaffold_5_mRNA_2604.1	-	-
GF0030093	1	0	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_5_mRNA_2596.1	-	-
GF0030092	1	0	0	Disease resistance protein (CC-NBS-LRR class) family protein (1)	ADP binding [GO:0043531 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_5_mRNA_2594.1	-	-
GF0030091	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2593.1	-	-
GF0030090	1	0	0	Disease resistance protein (CC-NBS-LRR class) family 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); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1)	scaffold_5_mRNA_2591.1	-	-
GF0030089	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2588.1	-	-
GF0030088	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2580.1	-	-
GF0030087	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2577.1	-	-
GF0030086	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2574.1	-	-
GF0030085	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2573.1	-	-
GF0030084	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2572.1	-	-
GF0030083	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2571.1	-	-
GF0030082	1	0	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_5_mRNA_2570.1	-	-
GF0030081	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2569.1	-	-
GF0030080	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_5_mRNA_2561.1	-	-
GF0030079	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2559.1	-	-
GF0030078	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2558.1	-	-
GF0030077	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2553.1	-	-
GF0030076	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_255.1	-	-
GF0030075	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2548.1	-	-
GF0030074	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2544.1	-	-
GF0030073	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_254.1	-	-
GF0030072	1	0	0	Actin (1)		Actin/actin-like conserved site [IPR020902] (1); Actin, conserved site [IPR004001] (1); Actin family [IPR004000] (1)	scaffold_5_mRNA_2537.1	-	-
GF0030071	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2533.1	-	-
GF0030070	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2530.1	-	-
GF0030069	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2528.1	-	-
GF0030068	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2523.1	-	-
GF0030067	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2522.1	-	-
GF0030066	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_252.1	-	-
GF0030065	1	0	0	Hypothetical protein (1)	ribosome [GO:0005840 cellular_component] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1); translation [GO:0006412 biological_process] (1)	Ribosomal S11, conserved site [IPR018102] (1); Ribosomal protein S11 [IPR001971] (1); Reverse transcriptase domain [IPR000477] (1)	scaffold_5_mRNA_2519.1	-	-
GF0030064	1	0	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_5_mRNA_2514.1	-	-
GF0030063	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2507.1	-	-
GF0030062	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_5_mRNA_2504.1	-	-
GF0030061	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_5_mRNA_2502.1	-	-
GF0030060	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2500.1	-	-
GF0030059	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2499.1	-	-
GF0030058	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_5_mRNA_2498.1	-	-
GF0030057	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2495.1	-	-
GF0030056	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Peptidase A2A, retrovirus, catalytic [IPR001995] (1); Aspartic peptidase, active site [IPR001969] (1); Zinc finger, CCHC-type [IPR001878] (1)	scaffold_5_mRNA_2492.1	-	-
GF0030055	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Immunoglobulin-like domain [IPR007110] (1)	scaffold_5_mRNA_2490.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0030054	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_5_mRNA_2488.1	-	-
GF0030053	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2487.1	-	-
GF0030052	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); DNA integration [GO:0015074 biological_process] (1)	Ribonuclease H-like domain [IPR012337] (1); Integrase, catalytic core [IPR001584] (1)	scaffold_5_mRNA_2485.1	-	-
GF0030051	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2481.1	-	-
GF0030050	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_248.1	-	-
GF0030049	1	0	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_5_mRNA_2478.1	-	-
GF0030048	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2477.1	-	-
GF0030047	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2473.1	-	-
GF0030046	1	0	0	DNA (Cytosine-5) methyltransferase (1)	chromatin binding [GO:0003682 molecular_function] (1); methyltransferase activity [GO:0008168 molecular_function] (1)	C-5 cytosine methyltransferase [IPR001525] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); Bromo adjacent homology (BAH) domain [IPR001025] (1); DNA methylase, C-5 cytosine-specific, active site [IPR018117] (1)	scaffold_5_mRNA_247.1	-	-
GF0030045	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2469.1	-	-
GF0030044	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2468.1	-	-
GF0030043	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_5_mRNA_2467.1	-	-
GF0030042	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_246.1	-	-
GF0030041	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			scaffold_5_mRNA_2456.1	-	-
GF0030040	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_5_mRNA_2451.1	-	-
GF0030039	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2450.1	-	-
GF0030038	1	0	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); DNA (cytosine-5)-methyltransferase 1, replication foci domain [IPR022702] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	scaffold_5_mRNA_245.1	-	-
GF0030037	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2448.1	-	-
GF0030036	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2446.1	-	-
GF0030035	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2444.1	-	-
GF0030034	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2443.1	-	-
GF0030033	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_5_mRNA_2442.1	-	-
GF0030032	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2440.1	-	-
GF0030031	1	0	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); DNA (cytosine-5)-methyltransferase 1, replication foci domain [IPR022702] (1); NB-ARC [IPR002182] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_5_mRNA_244.1	-	-
GF0030030	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_5_mRNA_2439.1	-	-
GF0030029	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2435.1	-	-
GF0030028	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_5_mRNA_2430.1	-	-
GF0030027	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2429.1	-	-
GF0030026	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2427.1	-	-
GF0030025	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_5_mRNA_2424.1	-	-
GF0030024	1	0	0	Cysteine-rich RLK (RECEPTOR-like protein kinase) 8 (1)			scaffold_5_mRNA_2422.1	-	-
GF0030023	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2421.1	-	-
GF0030022	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2415.1	-	-
GF0030021	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2411.1	-	-
GF0030020	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_241.1	-	-
GF0030019	1	0	0	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, plant/fungal/bacterial [IPR002016] (1); Plant peroxidase [IPR000823] (1); Haem peroxidase [IPR010255] (1)	scaffold_5_mRNA_2409.1	-	-
GF0030018	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_5_mRNA_2408.1	-	-
GF0030017	1	0	0	Hypothetical protein (1)		Chromo domain-like [IPR016197] (1); Chromo domain [IPR023780] (1)	scaffold_5_mRNA_2402.1	-	-
GF0030016	1	0	0	Retrotransposon protein, putative, Ty3-gypsy subclass (1)		Aspartic peptidase domain [IPR021109] (1); Retrotransposon gag domain [IPR005162] (1)	scaffold_5_mRNA_240.1	-	-
GF0030015	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			scaffold_5_mRNA_2397.1	-	-
GF0030014	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2396.1	-	-
GF0030013	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_239.1	-	-
GF0030012	1	0	0	DNA (Cytosine-5)-methyltransferase CMT2 (1)	methyltransferase activity [GO:0008168 molecular_function] (1)	S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); C-5 cytosine methyltransferase [IPR001525] (1); DNA methylase, C-5 cytosine-specific, active site [IPR018117] (1)	scaffold_5_mRNA_238.1	-	-
GF0030011	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_237.1	-	-
GF0030010	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2366.1	-	-
GF0030009	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2362.1	-	-
GF0030008	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2360.1	-	-
GF0030007	1	0	0	Hypothetical protein (1)		S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); DNA (cytosine-5)-methyltransferase 1, replication foci domain [IPR022702] (1)	scaffold_5_mRNA_236.1	-	-
GF0030006	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2356.1	-	-
GF0030005	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2355.1	-	-
GF0030004	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2353.1	-	-
GF0030003	1	0	0	Hypothetical protein (1)	transcription, DNA-templated [GO:0006351 biological_process] (1)	Transcription elongation factor S-II, central domain [IPR003618] (1)	scaffold_5_mRNA_2350.1	-	-
GF0030002	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2348.1	-	-
GF0030001	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2342.1	-	-
GF0030000	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2335.1	-	-
GF0029999	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2334.1	-	-
GF0029998	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2331.1	-	-
GF0029997	1	0	0	Auxin-responsive GH3 family protein (1)		GH3 family [IPR004993] (1)	scaffold_5_mRNA_2328.1	-	-
GF0029996	1	0	0	Hypothetical protein (1)		CTLH, C-terminal LisH motif [IPR006595] (1)	scaffold_5_mRNA_2325.1	-	-
GF0029995	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2324.1	-	-
GF0029994	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2320.1	-	-
GF0029993	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2319.1	-	-
GF0029992	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_5_mRNA_2313.1	-	-
GF0029991	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Domain of unknown function DUF4371 [IPR025398] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_5_mRNA_2310.1	-	-
GF0029990	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2306.1	-	-
GF0029989	1	0	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Zinc finger C2H2-type [IPR013087] (1); Zinc finger, BED-type [IPR003656] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	scaffold_5_mRNA_2304.1	-	-
GF0029988	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_230.1	-	-
GF0029987	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2299.1	-	-
GF0029986	1	0	0	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)	scaffold_5_mRNA_2298.1	-	-
GF0029985	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_5_mRNA_2297.1	-	-
GF0029984	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2296.1	-	-
GF0029983	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2295.1	-	-
GF0029982	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2291.1	-	-
GF0029981	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_229.1	-	-
GF0029980	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2285.1	-	-
GF0029979	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2283.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0029978	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2282.1	-	-
GF0029977	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_5_mRNA_2276.1	-	-
GF0029976	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2268.1	-	-
GF0029975	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2264.1	-	-
GF0029974	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2259.1	-	-
GF0029973	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2255.1	-	-
GF0029972	1	0	0	Verticillium wilt resistance-like protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	scaffold_5_mRNA_2250.1	-	-
GF0029971	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_225.1	-	-
GF0029970	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2249.1	-	-
GF0029969	1	0	0	Leucine-rich repeat, plant specific (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)	scaffold_5_mRNA_2245.1	-	-
GF0029968	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2242.1	-	-
GF0029967	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_224.1	-	-
GF0029966	1	0	0	Putative leucine-rich repeat disease resistance protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1)	scaffold_5_mRNA_2239.1	-	-
GF0029965	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	scaffold_5_mRNA_2235.1	-	-
GF0029964	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2234.1	-	-
GF0029963	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2233.1	-	-
GF0029962	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2231.1	-	-
GF0029961	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2229.1	-	-
GF0029960	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2228.1	-	-
GF0029959	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2227.1	-	-
GF0029958	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2226.1	-	-
GF0029957	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, SWIM-type [IPR007527] (1); Nascent polypeptide-associated complex NAC domain [IPR002715] (1); Zinc finger, PMZ-type [IPR006564] (1); Nascent polypeptide-associated complex subunit alpha [IPR016641] (1)	scaffold_5_mRNA_2223.1	-	-
GF0029956	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_222.1	-	-
GF0029955	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2216.1	-	-
GF0029954	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_221.1	-	-
GF0029953	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2205.1	-	-
GF0029952	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2200.1	-	-
GF0029951	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_220.1	-	-
GF0029950	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2198.1	-	-
GF0029949	1	0	0	Hypothetical protein (1)		Protein of unknown function DUF241, plant [IPR004320] (1)	scaffold_5_mRNA_2197.1	-	-
GF0029948	1	0	0	Hypothetical protein (1)		Protein of unknown function DUF241, plant [IPR004320] (1)	scaffold_5_mRNA_2196.1	-	-
GF0029947	1	0	0	LRR and NB-ARC domain disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	Winged helix-turn-helix DNA-binding domain [IPR011991] (1); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_5_mRNA_2195.1	-	-
GF0029946	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_5_mRNA_2193.1	-	-
GF0029945	1	0	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Carlavirus nucleic acid-binding protein [IPR002568] (1)	scaffold_5_mRNA_2192.1	-	-
GF0029944	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2190.1	-	-
GF0029943	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_5_mRNA_2185.1	-	-
GF0029942	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2184.1	-	-
GF0029941	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_5_mRNA_2183.1	-	-
GF0029940	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2182.1	-	-
GF0029939	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2181.1	-	-
GF0029938	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1); Retrotransposon gag domain [IPR005162] (1)	scaffold_5_mRNA_2180.1	-	-
GF0029937	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2179.1	-	-
GF0029936	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2173.1	-	-
GF0029935	1	0	0	Hypothetical protein (1)		Protein of unknown function DUF241, plant [IPR004320] (1)	scaffold_5_mRNA_2171.1	-	-
GF0029934	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_217.1	-	-
GF0029933	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2166.1	-	-
GF0029932	1	0	0	Hypothetical protein (1)		BRCT domain [IPR001357] (1)	scaffold_5_mRNA_2162.1	-	-
GF0029931	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2161.1	-	-
GF0029930	1	0	0	LRR and NB-ARC domain disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Receptor L-domain [IPR000494] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	scaffold_5_mRNA_216.1	-	-
GF0029929	1	0	0	ABSCISIC ACID-INSENSITIVE 5-like protein 2 (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)	scaffold_5_mRNA_2159.1	-	-
GF0029928	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2157.1	-	-
GF0029927	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_5_mRNA_2152.1	-	-
GF0029926	1	0	0	Subtilisin-like serine endopeptidase family protein, putative (1)	serine-type endopeptidase activity [GO:0004252 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Peptidase S8/S53 domain [IPR000209] (1)	scaffold_5_mRNA_2148.1	-	-
GF0029925	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2145.1	-	-
GF0029924	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_214.1	-	-
GF0029923	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_5_mRNA_2136.1	-	-
GF0029922	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_5_mRNA_2134.1	-	-
GF0029921	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_5_mRNA_2132.1	-	-
GF0029920	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_5_mRNA_2129.1	-	-
GF0029919	1	0	0	Hypothetical protein (1)		Protein kinase-like domain [IPR011009] (1)	scaffold_5_mRNA_2124.1	-	-
GF0029918	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_5_mRNA_2122.1	-	-
GF0029917	1	0	0	Hypothetical protein (1)		DNA (cytosine-5)-methyltransferase 1, replication foci domain [IPR022702] (1)	scaffold_5_mRNA_212.1	-	-
GF0029916	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1); Reverse transcriptase domain [IPR000477] (1)	scaffold_5_mRNA_2117.1	-	-
GF0029915	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2116.1	-	-
GF0029914	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2115.1	-	-
GF0029913	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2114.1	-	-
GF0029912	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Viral movement protein [IPR028919] (1); Zinc finger, CCHC-type [IPR001878] (1)	scaffold_5_mRNA_2112.1	-	-
GF0029911	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2111.1	-	-
GF0029910	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_5_mRNA_2110.1	-	-
GF0029909	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2109.1	-	-
GF0029908	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2107.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0029907	1	0	0	Hypothetical protein (1)		Protein kinase-like domain [IPR011009] (1)	scaffold_5_mRNA_2106.1	-	-
GF0029906	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1); transmembrane transporter activity [GO:0022857 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	WAT1-related protein [IPR030184] (1); Zinc finger, CCHC-type [IPR001878] (1)	scaffold_5_mRNA_2105.1	-	-
GF0029905	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2102.1	-	-
GF0029904	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_5_mRNA_2101.1	-	-
GF0029903	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2097.1	-	-
GF0029902	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2095.1	-	-
GF0029901	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2094.1	-	-
GF0029900	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2093.1	-	-
GF0029899	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2090.1	-	-
GF0029898	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2088.1	-	-
GF0029897	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2086.1	-	-
GF0029896	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2085.1	-	-
GF0029895	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2083.1	-	-
GF0029894	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2082.1	-	-
GF0029893	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2079.1	-	-
GF0029892	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_5_mRNA_2074.1	-	-
GF0029891	1	0	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_5_mRNA_2073.1	-	-
GF0029890	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2070.1	-	-
GF0029889	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2068.1	-	-
GF0029888	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2067.1	-	-
GF0029887	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2066.1	-	-
GF0029886	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_206.1	-	-
GF0029885	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2056.1	-	-
GF0029884	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_5_mRNA_2054.1	-	-
GF0029883	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2051.1	-	-
GF0029882	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2050.1	-	-
GF0029881	1	0	0	CDNA clone:002-112-E03, full insert sequence (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_5_mRNA_2048.1	-	-
GF0029880	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2047.1	-	-
GF0029879	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2042.1	-	-
GF0029878	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2038.1	-	-
GF0029877	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_5_mRNA_2030.1	-	-
GF0029876	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2028.1	-	-
GF0029875	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_2025.1	-	-
GF0029874	1	0	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	scaffold_5_mRNA_2022.1	-	-
GF0029873	1	0	0	Hypothetical protein (1)		Prolamin-like domain [IPR008502] (1)	scaffold_5_mRNA_2013.1	-	-
GF0029872	1	0	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1); FAR1 DNA binding domain [IPR004330] (1)	scaffold_5_mRNA_2007.1	-	-
GF0029871	1	0	0	Hypothetical protein (1)	transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (1)	Transferase [IPR003480] (1)	scaffold_5_mRNA_2005.1	-	-
GF0029870	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF1985 [IPR015410] (1)	scaffold_5_mRNA_1998.1	-	-
GF0029869	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_5_mRNA_1997.1	-	-
GF0029868	1	0	0	Hypothetical protein (1)	RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H domain [IPR002156] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_5_mRNA_1996.1	-	-
GF0029867	1	0	0	Acylsugar acyltransferase 3 (1)	transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (1)	Transferase [IPR003480] (1)	scaffold_5_mRNA_1986.1	-	-
GF0029866	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1985.1	-	-
GF0029865	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1977.1	-	-
GF0029864	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1976.1	-	-
GF0029863	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1969.1	-	-
GF0029862	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1963.1	-	-
GF0029861	1	0	0	Hypothetical protein (1)		DNA (cytosine-5)-methyltransferase 1, replication foci domain [IPR022702] (1)	scaffold_5_mRNA_196.1	-	-
GF0029860	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1951.1	-	-
GF0029859	1	0	0	LRR and NB-ARC domains-containing disease resistance protein, putative (1)	ADP binding [GO:0043531 molecular_function] (1)	Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_5_mRNA_195.1	-	-
GF0029858	1	0	0	LRR receptor-like kinase (1)	protein binding [GO:0005515 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Protein kinase-like domain [IPR011009] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Protein kinase domain [IPR000719] (1); Leucine-rich repeat [IPR001611] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase, ATP binding site [IPR017441] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	scaffold_5_mRNA_1947.1	-	-
GF0029857	1	0	0	Hypothetical protein (1)	RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H domain [IPR002156] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_5_mRNA_1943.1	-	-
GF0029856	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1926.1	-	-
GF0029855	1	0	0	Hypothetical protein (1)	transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1); Transposase, MuDR, plant [IPR004332] (1); Zinc finger, PMZ-type [IPR006564] (1); Zinc finger, SWIM-type [IPR007527] (1)	scaffold_5_mRNA_1924.1	-	-
GF0029854	1	0	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_5_mRNA_1921.1	-	-
GF0029853	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1914.1	-	-
GF0029852	1	0	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Carlavirus nucleic acid-binding protein [IPR002568] (1)	scaffold_5_mRNA_1913.1	-	-
GF0029851	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1909.1	-	-
GF0029850	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1908.1	-	-
GF0029849	1	0	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	Zinc finger, BED-type [IPR003656] (1)	scaffold_5_mRNA_1903.1	-	-
GF0029848	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1894.1	-	-
GF0029847	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1889.1	-	-
GF0029846	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_5_mRNA_1888.1	-	-
GF0029845	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1887.1	-	-
GF0029844	1	0	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	scaffold_5_mRNA_1884.1	-	-
GF0029843	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1883.1	-	-
GF0029842	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1877.1	-	-
GF0029841	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1871.1	-	-
GF0029840	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1868.1	-	-
GF0029839	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1867.1	-	-
GF0029838	1	0	0	Putative nuclease HARBI1 (1)		Harbinger transposase-derived nuclease domain [IPR027806] (1)	scaffold_5_mRNA_1865.1	-	-
GF0029837	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1862.1	-	-
GF0029836	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_5_mRNA_1860.1	-	-
GF0029835	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_5_mRNA_1857.1	-	-
GF0029834	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1856.1	-	-
GF0029833	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1855.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0029832	1	0	0	MUDRA-like transposase (1)		MULE transposase domain [IPR018289] (1); Transposase, MuDR, plant [IPR004332] (1)	scaffold_5_mRNA_1850.1	-	-
GF0029831	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_185.1	-	-
GF0029830	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_5_mRNA_1846.1	-	-
GF0029829	1	0	0	Gibberellin 20-oxidase family protein (1)		Isopenicillin N synthase-like [IPR027443] (1); Non-haem dioxygenase N-terminal domain [IPR026992] (1)	scaffold_5_mRNA_1840.1	-	-
GF0029828	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_184.1	-	-
GF0029827	1	0	0	Gibberellin 20 oxidase (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Isopenicillin N synthase-like [IPR027443] (1); Non-haem dioxygenase N-terminal domain [IPR026992] (1); Oxoglutarate/iron-dependent dioxygenase [IPR005123] (1)	scaffold_5_mRNA_1839.1	-	-
GF0029826	1	0	0	Hypothetical protein (1)		LysM domain [IPR018392] (1)	scaffold_5_mRNA_1834.1	-	-
GF0029825	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Domain of unknown function DUF4283 [IPR025558] (1); Ribonuclease H-like domain [IPR012337] (1); TB2/DP1/HVA22-related protein [IPR004345] (1)	scaffold_5_mRNA_1833.1	-	-
GF0029824	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1832.1	-	-
GF0029823	1	0	0	Hypothetical protein (1)	calmodulin binding [GO:0005516 molecular_function] (1)	Calcium-transporting P-type ATPase, N-terminal autoinhibitory domain [IPR024750] (1)	scaffold_5_mRNA_183.1	-	-
GF0029822	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1826.1	-	-
GF0029821	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1823.1	-	-
GF0029820	1	0	0	Integrase (1)		Aspartic peptidase domain [IPR021109] (1); Retrotransposon gag domain [IPR005162] (1)	scaffold_5_mRNA_1814.1	-	-
GF0029819	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1812.1	-	-
GF0029818	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1810.1	-	-
GF0029817	1	0	0	L-type lectin-domain containing receptor kinase IX.1 (1)	ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); carbohydrate binding [GO:0030246 molecular_function] (1)	Protein kinase-like domain [IPR011009] (1); Legume lectin domain [IPR001220] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Protein kinase domain [IPR000719] (1); Protein kinase, ATP binding site [IPR017441] (1)	scaffold_5_mRNA_1807.1	-	-
GF0029816	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1804.1	-	-
GF0029815	1	0	0	Hypothetical protein (1)	metal ion binding [GO:0046872 molecular_function] (1); nucleotide binding [GO:0000166 molecular_function] (1)	HAD-like domain [IPR023214] (1); P-type ATPase, A domain [IPR008250] (1); P-type ATPase, cytoplasmic domain N [IPR023299] (1)	scaffold_5_mRNA_1802.1	-	-
GF0029814	1	0	0	CDNA clone:002-110-H12, full insert sequence (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_5_mRNA_1800.1	-	-
GF0029813	1	0	0	BED zinc finger,hAT family dimerization domain (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	scaffold_5_mRNA_1797.1	-	-
GF0029812	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1796.1	-	-
GF0029811	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1788.1	-	-
GF0029810	1	0	0	Disease resistance protein (CC-NBS-LRR class) family 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); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_5_mRNA_1777.1	-	-
GF0029809	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1772.1	-	-
GF0029808	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1771.1	-	-
GF0029807	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_5_mRNA_1770.1	-	-
GF0029806	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1765.1	-	-
GF0029805	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1760.1	-	-
GF0029804	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_5_mRNA_1755.1	-	-
GF0029803	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1746.1	-	-
GF0029802	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1745.1	-	-
GF0029801	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_5_mRNA_1744.1	-	-
GF0029800	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_5_mRNA_1743.1	-	-
GF0029799	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1742.1	-	-
GF0029798	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1740.1	-	-
GF0029797	1	0	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); hAT-like transposase, RNase-H fold [IPR025525] (1); Major facilitator superfamily domain [IPR020846] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	scaffold_5_mRNA_174.1	-	-
GF0029796	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1738.1	-	-
GF0029795	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1736.1	-	-
GF0029794	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1733.1	-	-
GF0029793	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_5_mRNA_1730.1	-	-
GF0029792	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1729.1	-	-
GF0029791	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1726.1	-	-
GF0029790	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1720.1	-	-
GF0029789	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_172.1	-	-
GF0029788	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1719.1	-	-
GF0029787	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1702.1	-	-
GF0029786	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1700.1	-	-
GF0029785	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1699.1	-	-
GF0029784	1	0	0	Hypothetical protein (1)	GTP biosynthetic process [GO:0006183 biological_process] (1); nucleoside diphosphate kinase activity [GO:0004550 molecular_function] (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 [IPR001564] (1)	scaffold_5_mRNA_1680.1	-	-
GF0029783	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_168.1	-	-
GF0029782	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1678.1	-	-
GF0029781	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1674.1	-	-
GF0029780	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1673.1	-	-
GF0029779	1	0	0	Retrotransposon gag protein (1)			scaffold_5_mRNA_1671.1	-	-
GF0029778	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1669.1	-	-
GF0029777	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_5_mRNA_1665.1	-	-
GF0029776	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1664.1	-	-
GF0029775	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1659.1	-	-
GF0029774	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_5_mRNA_1653.1	-	-
GF0029773	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1651.1	-	-
GF0029772	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_5_mRNA_1650.1	-	-
GF0029771	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1643.1	-	-
GF0029770	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1642.1	-	-
GF0029769	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_5_mRNA_1640.1	-	-
GF0029768	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1639.1	-	-
GF0029767	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1636.1	-	-
GF0029766	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1635.1	-	-
GF0029765	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1634.1	-	-
GF0029764	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1631.1	-	-
GF0029763	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1630.1	-	-
GF0029762	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_5_mRNA_1628.1	-	-
GF0029761	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1627.1	-	-
GF0029760	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1624.1	-	-
GF0029759	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1623.1	-	-
GF0029758	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1621.1	-	-
GF0029757	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1620.1	-	-
GF0029756	1	0	0	Putative polyprotein (Aspartic proteinase, reverse transcriptase, ribonuclease H) (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_5_mRNA_1619.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0029755	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1618.1	-	-
GF0029754	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1617.1	-	-
GF0029753	1	0	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_5_mRNA_1614.1	-	-
GF0029752	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1611.1	-	-
GF0029751	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1606.1	-	-
GF0029750	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1604.1	-	-
GF0029749	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1603.1	-	-
GF0029748	1	0	0	Hypothetical protein (1)		Histone deacetylase superfamily [IPR000286] (1); Histone deacetylase domain [IPR023801] (1)	scaffold_5_mRNA_16.1	-	-
GF0029747	1	0	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_5_mRNA_1598.1	-	-
GF0029746	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1597.1	-	-
GF0029745	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1592.1	-	-
GF0029744	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_5_mRNA_1591.1	-	-
GF0029743	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_159.1	-	-
GF0029742	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1585.1	-	-
GF0029741	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_5_mRNA_1584.1	-	-
GF0029740	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1); zinc ion binding [GO:0008270 molecular_function] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Aspartic peptidase, active site [IPR001969] (1)	scaffold_5_mRNA_1582.1	-	-
GF0029739	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_5_mRNA_1581.1	-	-
GF0029738	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_5_mRNA_1580.1	-	-
GF0029737	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1572.1	-	-
GF0029736	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1569.1	-	-
GF0029735	1	0	0	Hypothetical protein (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Retropepsins [IPR018061] (1); Aspartic peptidase, active site [IPR001969] (1); Peptidase A2A, retrovirus, catalytic [IPR001995] (1); Aspartic peptidase domain [IPR021109] (1)	scaffold_5_mRNA_1568.1	-	-
GF0029734	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1565.1	-	-
GF0029733	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_5_mRNA_1562.1	-	-
GF0029732	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1561.1	-	-
GF0029731	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1560.1	-	-
GF0029730	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1556.1	-	-
GF0029729	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1555.1	-	-
GF0029728	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1552.1	-	-
GF0029727	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_5_mRNA_1551.1	-	-
GF0029726	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1); zinc ion binding [GO:0008270 molecular_function] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1)	Peptidase A2A, retrovirus, catalytic [IPR001995] (1); Aspartic peptidase, active site [IPR001969] (1); Zinc finger, CCHC-type [IPR001878] (1)	scaffold_5_mRNA_1549.1	-	-
GF0029725	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1548.1	-	-
GF0029724	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1544.1	-	-
GF0029723	1	0	0	Hypothetical protein (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Aspartic peptidase, active site [IPR001969] (1); Peptidase A2A, retrovirus, catalytic [IPR001995] (1)	scaffold_5_mRNA_1543.1	-	-
GF0029722	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_5_mRNA_1542.1	-	-
GF0029721	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1541.1	-	-
GF0029720	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1537.1	-	-
GF0029719	1	0	0	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)	scaffold_5_mRNA_1536.1	-	-
GF0029718	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_5_mRNA_1535.1	-	-
GF0029717	1	0	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_5_mRNA_1534.1	-	-
GF0029716	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_5_mRNA_1533.1	-	-
GF0029715	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1532.1	-	-
GF0029714	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1531.1	-	-
GF0029713	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1530.1	-	-
GF0029712	1	0	0	Hypothetical protein (1)	U2AF [GO:0089701 cellular_component] (1); RNA binding [GO:0003723 molecular_function] (1); mRNA splicing, via spliceosome [GO:0000398 biological_process] (1)	U2 auxiliary factor small subunit [IPR009145] (1)	scaffold_5_mRNA_153.1	-	-
GF0029711	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1522.1	-	-
GF0029710	1	0	0	Integrase (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_5_mRNA_1521.1	-	-
GF0029709	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1520.1	-	-
GF0029708	1	0	0	Enhanced disease susceptibility 1 (1)	lipid metabolic process [GO:0006629 biological_process] (1)	Fungal lipase-like domain [IPR002921] (1); Alpha/Beta hydrolase fold [IPR029058] (1)	scaffold_5_mRNA_152.1	-	-
GF0029707	1	0	0	Retrotransposon gag protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_5_mRNA_1518.1	-	-
GF0029706	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1515.1	-	-
GF0029705	1	0	0	Nodulin MtN21 /EamA-like transporter family protein isoform 3 (1)		Sugar phosphate transporter domain [IPR004853] (1)	scaffold_5_mRNA_1513.1	-	-
GF0029704	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1512.1	-	-
GF0029703	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1509.1	-	-
GF0029702	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_5_mRNA_1507.1	-	-
GF0029701	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1506.1	-	-
GF0029700	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_5_mRNA_1505.1	-	-
GF0029699	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1504.1	-	-
GF0029698	1	0	0	Integrase (1)		LOG family [IPR031100] (1); Aspartic peptidase domain [IPR021109] (1)	scaffold_5_mRNA_1501.1	-	-
GF0029697	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_150.1	-	-
GF0029696	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_15.1	-	-
GF0029695	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1497.1	-	-
GF0029694	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_5_mRNA_1496.1	-	-
GF0029693	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_5_mRNA_1495.1	-	-
GF0029692	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_5_mRNA_1491.1	-	-
GF0029691	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1490.1	-	-
GF0029690	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1484.1	-	-
GF0029689	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_5_mRNA_1483.1	-	-
GF0029688	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_5_mRNA_1482.1	-	-
GF0029687	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1481.1	-	-
GF0029686	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1480.1	-	-
GF0029685	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1479.1	-	-
GF0029684	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1478.1	-	-
GF0029683	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1476.1	-	-
GF0029682	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1475.1	-	-
GF0029681	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_5_mRNA_1472.1	-	-
GF0029680	1	0	0	LRR receptor-like kinase family protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	scaffold_5_mRNA_147.1	-	-
GF0029679	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_5_mRNA_1466.1	-	-
GF0029678	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1465.1	-	-
GF0029677	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1464.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0029676	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_5_mRNA_1463.1	-	-
GF0029675	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1462.1	-	-
GF0029674	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1458.1	-	-
GF0029673	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1445.1	-	-
GF0029672	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1444.1	-	-
GF0029671	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_5_mRNA_1438.1	-	-
GF0029670	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			scaffold_5_mRNA_1437.1	-	-
GF0029669	1	0	0	Hypothetical protein (1)		Transposase-associated domain [IPR029480] (1)	scaffold_5_mRNA_1431.1	-	-
GF0029668	1	0	0	Hypothetical protein (1)	heme binding [GO:0020037 molecular_function] (1); response to oxidative stress [GO:0006979 biological_process] (1); peroxidase activity [GO:0004601 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Haem peroxidase, plant/fungal/bacterial [IPR002016] (1); Peroxidase, active site [IPR019794] (1); Plant peroxidase [IPR000823] (1); Haem peroxidase [IPR010255] (1)	scaffold_5_mRNA_1430.1	-	-
GF0029667	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_5_mRNA_1425.1	-	-
GF0029666	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1424.1	-	-
GF0029665	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1415.1	-	-
GF0029664	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1405.1	-	-
GF0029663	1	0	0	Hypothetical protein (1)		Arabidopsis retrotransposon Orf1 [IPR004312] (1)	scaffold_5_mRNA_1404.1	-	-
GF0029662	1	0	0	FRS transcription factor family, putative isoform 8 (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FAR1 DNA binding domain [IPR004330] (1); FHY3/FAR1 family [IPR031052] (1); MULE transposase domain [IPR018289] (1)	scaffold_5_mRNA_1403.1	-	-
GF0029661	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1400.1	-	-
GF0029660	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1396.1	-	-
GF0029659	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_5_mRNA_1395.1	-	-
GF0029658	1	0	0	TSA: Wollemia nobilis transcribed RNA sequence (1)		Arfaptin homology (AH) domain/BAR domain [IPR027267] (1)	scaffold_5_mRNA_1391.1	-	-
GF0029657	1	0	0	Hypothetical protein (1)	DNA integration [GO:0015074 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Integrase, catalytic core [IPR001584] (1); Ribonuclease H-like domain [IPR012337] (1); Domain of unknown function DUF1985 [IPR015410] (1)	scaffold_5_mRNA_1390.1	-	-
GF0029656	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_5_mRNA_1385.1	-	-
GF0029655	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1384.1	-	-
GF0029654	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_138.1	-	-
GF0029653	1	0	0	Copper chaperone (1)	metal ion transport [GO:0030001 biological_process] (1); metal ion binding [GO:0046872 molecular_function] (1)	Heavy metal-associated domain, HMA [IPR006121] (1)	scaffold_5_mRNA_1379.1	-	-
GF0029652	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_5_mRNA_1377.1	-	-
GF0029651	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1372.1	-	-
GF0029650	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1367.1	-	-
GF0029649	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1365.1	-	-
GF0029648	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1363.1	-	-
GF0029647	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_136.1	-	-
GF0029646	1	0	0	Harpin binding protein 1 (1)		Plastid lipid-associated protein/fibrillin conserved domain [IPR006843] (1)	scaffold_5_mRNA_1356.1	-	-
GF0029645	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1355.1	-	-
GF0029644	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_135.1	-	-
GF0029643	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1345.1	-	-
GF0029642	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1340.1	-	-
GF0029641	1	0	0	Athila retroelement ORF1 protein, putative (1)			scaffold_5_mRNA_1339.1	-	-
GF0029640	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1335.1	-	-
GF0029639	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1332.1	-	-
GF0029638	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_5_mRNA_1330.1	-	-
GF0029637	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1329.1	-	-
GF0029636	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1328.1	-	-
GF0029635	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1313.1	-	-
GF0029634	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1312.1	-	-
GF0029633	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1309.1	-	-
GF0029632	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4219 [IPR025314] (1)	scaffold_5_mRNA_1308.1	-	-
GF0029631	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1305.1	-	-
GF0029630	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_5_mRNA_1304.1	-	-
GF0029629	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_5_mRNA_1300.1	-	-
GF0029628	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1299.1	-	-
GF0029627	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1298.1	-	-
GF0029626	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1296.1	-	-
GF0029625	1	0	0	Hypothetical protein (1)	DNA integration [GO:0015074 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); LOG family [IPR031100] (1); Integrase, catalytic core [IPR001584] (1)	scaffold_5_mRNA_1292.1	-	-
GF0029624	1	0	0	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	scaffold_5_mRNA_1290.1	-	-
GF0029623	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Domain of unknown function DUF4219 [IPR025314] (1); Zinc finger, CCHC-type [IPR001878] (1)	scaffold_5_mRNA_1288.1	-	-
GF0029622	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1286.1	-	-
GF0029621	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1285.1	-	-
GF0029620	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_5_mRNA_1284.1	-	-
GF0029619	1	0	0	Ubiquitin carboxyl-terminal hydrolase 12 (1)	protein binding [GO:0005515 molecular_function] (1)	MATH/TRAF domain [IPR002083] (1); TRAF-like [IPR008974] (1)	scaffold_5_mRNA_1283.1	-	-
GF0029618	1	0	0	TRAF-like family protein isoform 2 (1)	protein binding [GO:0005515 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	MATH/TRAF domain [IPR002083] (1); TRAF-like [IPR008974] (1); Zinc finger, SWIM-type [IPR007527] (1); Zinc finger, PMZ-type [IPR006564] (1)	scaffold_5_mRNA_1281.1	-	-
GF0029617	1	0	0	Polypepetide with reverse transcriptase and RNaseH domains (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	scaffold_5_mRNA_1272.1	-	-
GF0029616	1	0	0	Hypothetical protein (1)	mitotic spindle assembly checkpoint [GO:0007094 biological_process] (1)	Spindle assembly checkpoint component Mad1 [IPR008672] (1)	scaffold_5_mRNA_126.1	-	-
GF0029615	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1258.1	-	-
GF0029614	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1257.1	-	-
GF0029613	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1255.1	-	-
GF0029612	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1250.1	-	-
GF0029611	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_125.1	-	-
GF0029610	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_124.1	-	-
GF0029609	1	0	0	Truncated RB (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); Protein RETICULATA-related [IPR021825] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_5_mRNA_1237.1	-	-
GF0029608	1	0	0	Truncated RB (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	scaffold_5_mRNA_1236.1	-	-
GF0029607	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1235.1	-	-
GF0029606	1	0	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_5_mRNA_1233.1	-	-
GF0029605	1	0	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_5_mRNA_1232.1	-	-
GF0029604	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_5_mRNA_1228.1	-	-
GF0029603	1	0	0	Putative disease resistance protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_5_mRNA_1225.1	-	-
GF0029602	1	0	0	Retrotransposon gag protein (1)			scaffold_5_mRNA_1221.1	-	-
GF0029601	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1213.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0029600	1	0	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1)	scaffold_5_mRNA_1211.1	-	-
GF0029599	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_5_mRNA_1204.1	-	-
GF0029598	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1203.1	-	-
GF0029597	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1202.1	-	-
GF0029596	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1); Retrotransposon gag domain [IPR005162] (1)	scaffold_5_mRNA_1201.1	-	-
GF0029595	1	0	0	Hypothetical 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)	scaffold_5_mRNA_1200.1	-	-
GF0029594	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1199.1	-	-
GF0029593	1	0	0	Putative disease resistance protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_5_mRNA_1198.1	-	-
GF0029592	1	0	0	Hypothetical protein (1)	catalytic activity [GO:0003824 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	ATP-grasp fold, subdomain 1 [IPR013815] (1)	scaffold_5_mRNA_1196.1	-	-
GF0029591	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1195.1	-	-
GF0029590	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_5_mRNA_1194.1	-	-
GF0029589	1	0	0	Putative disease resistance protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_5_mRNA_1193.1	-	-
GF0029588	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1191.1	-	-
GF0029587	1	0	0	Zinc finger-homeodomain protein 2 (1)		ZF-HD homeobox protein, Cys/His-rich dimerisation domain [IPR006456] (1)	scaffold_5_mRNA_119.1	-	-
GF0029586	1	0	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_5_mRNA_1188.1	-	-
GF0029585	1	0	0	Putative disease resistance protein RGA1 (1)		Winged helix-turn-helix DNA-binding domain [IPR011991] (1)	scaffold_5_mRNA_1186.1	-	-
GF0029584	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1183.1	-	-
GF0029583	1	0	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_5_mRNA_1179.1	-	-
GF0029582	1	0	0	NB-ARC domain disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_5_mRNA_1177.1	-	-
GF0029581	1	0	0	Putative disease resistance protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_5_mRNA_1175.1	-	-
GF0029580	1	0	0	Putative disease resistance protein RGA1 (1)			scaffold_5_mRNA_1172.1	-	-
GF0029579	1	0	0	Peroxidase 15 (1)	hydrogen peroxide catabolic process [GO:0042744 biological_process] (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); Secretory peroxidase [IPR033905] (1); Haem peroxidase, plant/fungal/bacterial [IPR002016] (1); Plant peroxidase [IPR000823] (1); Peroxidases heam-ligand binding site [IPR019793] (1); Peroxidase, active site [IPR019794] (1)	scaffold_5_mRNA_1171.1	-	-
GF0029578	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1166.1	-	-
GF0029577	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1157.1	-	-
GF0029576	1	0	0	Monosacharide transport protein (1)	binding [GO:0005488 molecular_function] (1)	Armadillo-type fold [IPR016024] (1)	scaffold_5_mRNA_1152.1	-	-
GF0029575	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1149.1	-	-
GF0029574	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_5_mRNA_1148.1	-	-
GF0029573	1	0	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_5_mRNA_1146.1	-	-
GF0029572	1	0	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	scaffold_5_mRNA_1145.1	-	-
GF0029571	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1143.1	-	-
GF0029570	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_5_mRNA_1142.1	-	-
GF0029569	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4216 [IPR025312] (1); Transposon, En/Spm-like [IPR004242] (1); Domain of unknown function DUF4218 [IPR025452] (1); Transposase-associated domain [IPR029480] (1)	scaffold_5_mRNA_1141.1	-	-
GF0029568	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_5_mRNA_1139.1	-	-
GF0029567	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_5_mRNA_1138.1	-	-
GF0029566	1	0	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_5_mRNA_1135.1	-	-
GF0029565	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1132.1	-	-
GF0029564	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1131.1	-	-
GF0029563	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_5_mRNA_1128.1	-	-
GF0029562	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4371 [IPR025398] (1); Protein RETICULATA-related [IPR021825] (1)	scaffold_5_mRNA_1127.1	-	-
GF0029561	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1126.1	-	-
GF0029560	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1125.1	-	-
GF0029559	1	0	0	Putative disease resistance protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1)	scaffold_5_mRNA_1123.1	-	-
GF0029558	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1121.1	-	-
GF0029557	1	0	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_5_mRNA_112.1	-	-
GF0029556	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1119.1	-	-
GF0029555	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1118.1	-	-
GF0029554	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1117.1	-	-
GF0029553	1	0	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1); Small heat shock protein HSP20 [IPR031107] (1); Domain of unknown function DUF1985 [IPR015410] (1); HSP20-like chaperone [IPR008978] (1); Alpha crystallin/Hsp20 domain [IPR002068] (1)	scaffold_5_mRNA_111.1	-	-
GF0029552	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_5_mRNA_1096.1	-	-
GF0029551	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H-like domain [IPR012337] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_5_mRNA_108.1	-	-
GF0029550	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_5_mRNA_1067.1	-	-
GF0029549	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1066.1	-	-
GF0029548	1	0	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	scaffold_5_mRNA_1065.1	-	-
GF0029547	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, PMZ-type [IPR006564] (1); Zinc finger, SWIM-type [IPR007527] (1); FHY3/FAR1 family [IPR031052] (1); Zinc finger, CCHC-type [IPR001878] (1)	scaffold_5_mRNA_1064.1	-	-
GF0029546	1	0	0	Disease resistance protein RPS2 (1)			scaffold_5_mRNA_106.1	-	-
GF0029545	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1056.1	-	-
GF0029544	1	0	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_5_mRNA_1051.1	-	-
GF0029543	1	0	0	Hypothetical protein (1)	methyltransferase activity [GO:0008168 molecular_function] (1)	SAM dependent carboxyl methyltransferase [IPR005299] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	scaffold_5_mRNA_1034.1	-	-
GF0029542	1	0	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_5_mRNA_1021.1	-	-
GF0029541	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1013.1	-	-
GF0029540	1	0	0	Hypothetical protein (1)	RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H domain [IPR002156] (1); Ribonuclease H-like domain [IPR012337] (1); TB2/DP1/HVA22-related protein [IPR004345] (1)	scaffold_5_mRNA_1008.1	-	-
GF0029539	1	0	0	Hypothetical protein (1)		DNA-binding pseudobarrel domain [IPR015300] (1)	scaffold_5_mRNA_1007.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0029538	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1005.1	-	-
GF0029537	1	0	0	Hypothetical protein (1)			scaffold_5_mRNA_1003.1	-	-
GF0029536	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_993.1	-	-
GF0029535	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_992.1	-	-
GF0029534	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_4_mRNA_991.1	-	-
GF0029533	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_4_mRNA_989.1	-	-
GF0029532	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_987.1	-	-
GF0029531	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_4_mRNA_986.1	-	-
GF0029530	1	0	0	LRR receptor-like kinase family protein (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	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); Tyrosine-protein kinase, active site [IPR008266] (1); Protein kinase, ATP binding site [IPR017441] (1); Leucine-rich repeat [IPR001611] (1)	scaffold_4_mRNA_985.1	-	-
GF0029529	1	0	0	Hypothetical 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)	scaffold_4_mRNA_982.1	-	-
GF0029528	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_97.1	-	-
GF0029527	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_966.1	-	-
GF0029526	1	0	0	LRR receptor-like kinase family protein (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Protein kinase, ATP binding site [IPR017441] (1); Tyrosine-protein kinase, active site [IPR008266] (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)	scaffold_4_mRNA_962.1	-	-
GF0029525	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_925.1	-	-
GF0029524	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_924.1	-	-
GF0029523	1	0	0	Putative non-LTR retroelement reverse transcriptase (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Reverse transcriptase domain [IPR000477] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_4_mRNA_923.1	-	-
GF0029522	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Domain of unknown function DUF4219 [IPR025314] (1); Zinc finger, CCHC-type [IPR001878] (1)	scaffold_4_mRNA_918.1	-	-
GF0029521	1	0	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Zinc finger, BED-type [IPR003656] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	scaffold_4_mRNA_905.1	-	-
GF0029520	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_903.1	-	-
GF0029519	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_9.1	-	-
GF0029518	1	0	0	Integrase (1)		Aspartic peptidase domain [IPR021109] (1); LOG family [IPR031100] (1)	scaffold_4_mRNA_884.1	-	-
GF0029517	1	0	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	scaffold_4_mRNA_877.1	-	-
GF0029516	1	0	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_4_mRNA_868.1	-	-
GF0029515	1	0	0	Tropinone reductase I (1)		NAD(P)-binding domain [IPR016040] (1); Short-chain dehydrogenase/reductase SDR [IPR002347] (1)	scaffold_4_mRNA_86.1	-	-
GF0029514	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_843.1	-	-
GF0029513	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4216 [IPR025312] (1)	scaffold_4_mRNA_839.1	-	-
GF0029512	1	0	0	Hypothetical protein (1)		Probable transposase, Ptta/En/Spm, plant [IPR004252] (1)	scaffold_4_mRNA_834.1	-	-
GF0029511	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_8.1	-	-
GF0029510	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_798.1	-	-
GF0029509	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_795.1	-	-
GF0029508	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_793.1	-	-
GF0029507	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_791.1	-	-
GF0029506	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_790.1	-	-
GF0029505	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_789.1	-	-
GF0029504	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_788.1	-	-
GF0029503	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_4_mRNA_787.1	-	-
GF0029502	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_782.1	-	-
GF0029501	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_781.1	-	-
GF0029500	1	0	0	Hypothetical protein (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Aspartic peptidase domain [IPR021109] (1); Aspartic peptidase, active site [IPR001969] (1)	scaffold_4_mRNA_780.1	-	-
GF0029499	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_776.1	-	-
GF0029498	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_773.1	-	-
GF0029497	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_4_mRNA_77.1	-	-
GF0029496	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_763.1	-	-
GF0029495	1	0	0	Putative non-LTR retroelement reverse transcriptase (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1); Reverse transcriptase domain [IPR000477] (1)	scaffold_4_mRNA_761.1	-	-
GF0029494	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_759.1	-	-
GF0029493	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1); Aspartic peptidase domain [IPR021109] (1)	scaffold_4_mRNA_758.1	-	-
GF0029492	1	0	0	Retrotransposon protein, putative, Ty3-gypsy subclass, expressed (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_4_mRNA_757.1	-	-
GF0029491	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_755.1	-	-
GF0029490	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_754.1	-	-
GF0029489	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_4_mRNA_753.1	-	-
GF0029488	1	0	0	Polynucleotidyl transferase, ribonuclease H-like superfamily protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Harbinger transposase-derived nuclease domain [IPR027806] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_4_mRNA_751.1	-	-
GF0029487	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_750.1	-	-
GF0029486	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Domain of unknown function DUF4371 [IPR025398] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_4_mRNA_748.1	-	-
GF0029485	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_747.1	-	-
GF0029484	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_745.1	-	-
GF0029483	1	0	0	Terpene cyclase/mutase family member (1)	intramolecular transferase activity [GO:0016866 molecular_function] (1)	Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (1); Squalene cyclase, C-terminal [IPR032696] (1); Squalene cyclase [IPR018333] (1); Terpene synthase, conserved site [IPR002365] (1)	scaffold_4_mRNA_744.1	-	-
GF0029482	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (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); LOG family [IPR031100] (1)	scaffold_4_mRNA_741.1	-	-
GF0029481	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_740.1	-	-
GF0029480	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (1); Viral movement protein [IPR028919] (1); Zinc finger, CCHC-type [IPR001878] (1); Squalene cyclase, N-terminal [IPR032697] (1)	scaffold_4_mRNA_737.1	-	-
GF0029479	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_736.1	-	-
GF0029478	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_735.1	-	-
GF0029477	1	0	0	Terpene cyclase/mutase family member (1)	intramolecular transferase activity [GO:0016866 molecular_function] (1)	Squalene cyclase, C-terminal [IPR032696] (1); Squalene cyclase [IPR018333] (1); Squalene cyclase, N-terminal [IPR032697] (1); Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (1)	scaffold_4_mRNA_733.1	-	-
GF0029476	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF632 [IPR006867] (1)	scaffold_4_mRNA_731.1	-	-
GF0029475	1	0	0	Terpene cyclase/mutase family member (1)		Squalene cyclase, N-terminal [IPR032697] (1); Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (1)	scaffold_4_mRNA_729.1	-	-
GF0029474	1	0	0	Retrotransposon gag protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_4_mRNA_725.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0029473	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_721.1	-	-
GF0029472	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_4_mRNA_720.1	-	-
GF0029471	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_4_mRNA_719.1	-	-
GF0029470	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_71.1	-	-
GF0029469	1	0	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	scaffold_4_mRNA_702.1	-	-
GF0029468	1	0	0	Hypothetical protein (1)	biosynthetic process [GO:0009058 biological_process] (1); hydrolase activity [GO:0016787 molecular_function] (1); ligase activity [GO:0016874 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1); tetrahydrofolylpolyglutamate synthase activity [GO:0004326 molecular_function] (1); folic acid-containing compound biosynthetic process [GO:0009396 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1)	WD40-repeat-containing domain [IPR017986] (1); WD40 repeat [IPR001680] (1); WD40/YVTN repeat-like-containing domain [IPR015943] (1); Mur ligase, C-terminal [IPR004101] (1); Metallo-dependent phosphatase-like [IPR029052] (1); Folylpolyglutamate synthetase, conserved site [IPR018109] (1); Folylpolyglutamate synthetase [IPR001645] (1); Serine/threonine-specific protein phosphatase/bis(5-nucleosyl)-tetraphosphatase [IPR006186] (1); Serine-threonine protein phosphatase, N-terminal [IPR031675] (1); Calcineurin-like phosphoesterase domain, ApaH type [IPR004843] (1); Mur ligase, central [IPR013221] (1)	scaffold_4_mRNA_70.1	-	-
GF0029467	1	0	0	LRR receptor-like kinase family protein (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	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/tyrosine-protein kinase, catalytic domain [IPR001245] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Leucine-rich repeat [IPR001611] (1)	scaffold_4_mRNA_698.1	-	-
GF0029466	1	0	0	GDSL-motif lipase 7 (1)	hydrolase activity, acting on ester bonds [GO:0016788 molecular_function] (1)	SGNH hydrolase-type esterase domain [IPR013830] (1); GDSL lipase/esterase [IPR001087] (1)	scaffold_4_mRNA_696.1	-	-
GF0029465	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_692.1	-	-
GF0029464	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_690.1	-	-
GF0029463	1	0	0	Hypothetical protein (1)		Transposase-associated domain [IPR029480] (1)	scaffold_4_mRNA_677.1	-	-
GF0029462	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_676.1	-	-
GF0029461	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_671.1	-	-
GF0029460	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	scaffold_4_mRNA_667.1	-	-
GF0029459	1	0	0	LRR receptor-like serine/threonine-protein kinase FLS2 (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	scaffold_4_mRNA_666.1	-	-
GF0029458	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_658.1	-	-
GF0029457	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_655.1	-	-
GF0029456	1	0	0	Ribonuclease H-like superfamily protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_4_mRNA_654.1	-	-
GF0029455	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_653.1	-	-
GF0029454	1	0	0	LRR receptor-like serine/threonine-protein kinase FLS2 (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)	scaffold_4_mRNA_652.1	-	-
GF0029453	1	0	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	scaffold_4_mRNA_651.1	-	-
GF0029452	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_644.1	-	-
GF0029451	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_642.1	-	-
GF0029450	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_64.1	-	-
GF0029449	1	0	0	Caffeic acid 3-O-methyltransferase (1)	O-methyltransferase activity [GO:0008171 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1); methyltransferase activity [GO:0008168 molecular_function] (1)	S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); 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)	scaffold_4_mRNA_639.1	-	-
GF0029448	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_635.1	-	-
GF0029447	1	0	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger C2H2-type [IPR013087] (1); Zinc finger, BED-type [IPR003656] (1)	scaffold_4_mRNA_629.1	-	-
GF0029446	1	0	0	Caffeic acid 3-O-methyltransferase (1)	O-methyltransferase activity [GO:0008171 molecular_function] (1); methyltransferase activity [GO:0008168 molecular_function] (1)	S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); O-methyltransferase COMT-type [IPR016461] (1); O-methyltransferase, family 2 [IPR001077] (1)	scaffold_4_mRNA_628.1	-	-
GF0029445	1	0	0	Hypothetical protein (1)		Alpha/Beta hydrolase fold [IPR029058] (1); Serine aminopeptidase, S33 [IPR022742] (1)	scaffold_4_mRNA_627.1	-	-
GF0029444	1	0	0	Hypothetical protein (1)		Arabidopsis retrotransposon Orf1 [IPR004312] (1)	scaffold_4_mRNA_623.1	-	-
GF0029443	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_621.1	-	-
GF0029442	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_620.1	-	-
GF0029441	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_619.1	-	-
GF0029440	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_617.1	-	-
GF0029439	1	0	0	Putative Ruda gag-pol polyprotein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Domain of unknown function DUF4219 [IPR025314] (1)	scaffold_4_mRNA_607.1	-	-
GF0029438	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); hAT-like transposase, RNase-H fold [IPR025525] (1)	scaffold_4_mRNA_606.1	-	-
GF0029437	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_4_mRNA_597.1	-	-
GF0029436	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_4_mRNA_594.1	-	-
GF0029435	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_593.1	-	-
GF0029434	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_592.1	-	-
GF0029433	1	0	0	Protease inhibitor/seed storage/lipid transfer family protein (1)		Bifunctional inhibitor/plant lipid transfer protein/seed storage helical domain [IPR016140] (1)	scaffold_4_mRNA_58.1	-	-
GF0029432	1	0	0	Mutator-like transposase (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); Transposase, MuDR, plant [IPR004332] (1)	scaffold_4_mRNA_557.1	-	-
GF0029431	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_550.1	-	-
GF0029430	1	0	0	17.5 kDa class I heat shock protein (1)		Small heat shock protein HSP20 [IPR031107] (1); HSP20-like chaperone [IPR008978] (1); Alpha crystallin/Hsp20 domain [IPR002068] (1)	scaffold_4_mRNA_53.1	-	-
GF0029429	1	0	0	SET domain protein (1)			scaffold_4_mRNA_496.1	-	-
GF0029428	1	0	0	Heat shock protein (1)		Alpha crystallin/Hsp20 domain [IPR002068] (1); HSP20-like chaperone [IPR008978] (1); Peptidase S8 propeptide/proteinase inhibitor I9 [IPR010259] (1); Small heat shock protein HSP20 [IPR031107] (1)	scaffold_4_mRNA_49.1	-	-
GF0029427	1	0	0	SCF ubiquitin ligase, SKP1 component (1)	ubiquitin-dependent protein catabolic process [GO:0006511 biological_process] (1)	SKP1/BTB/POZ domain [IPR011333] (1); SKP1 component, dimerisation [IPR016072] (1); SKP1 component, POZ domain [IPR016073] (1); S-phase kinase-associated protein 1 [IPR016897] (1); S-phase kinase-associated protein 1-like [IPR001232] (1)	scaffold_4_mRNA_458.1	-	-
GF0029426	1	0	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1); Domain of unknown function DUF4371 [IPR025398] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_4_mRNA_452.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0029425	1	0	0	F-box protein At2g39490 (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); F-box domain [IPR001810] (1)	scaffold_4_mRNA_432.1	-	-
GF0029424	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_42.1	-	-
GF0029423	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_417.1	-	-
GF0029422	1	0	0	Monosacharide transport protein (1)			scaffold_4_mRNA_41.1	-	-
GF0029421	1	0	0	CASP-like protein 4C1 (1)		Domain of unknown function DUF588 [IPR006702] (1)	scaffold_4_mRNA_409.1	-	-
GF0029420	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_4_mRNA_392.1	-	-
GF0029419	1	0	0	Monosacharide transport protein (1)			scaffold_4_mRNA_391.1	-	-
GF0029418	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_390.1	-	-
GF0029417	1	0	0	Hypothetical protein (1)		F-box associated interaction domain [IPR017451] (1)	scaffold_4_mRNA_384.1	-	-
GF0029416	1	0	0	Cysteine/histidine-rich C1 domain protein (1)	intracellular signal transduction [GO:0035556 biological_process] (1); zinc ion binding [GO:0008270 molecular_function] (1)	DC1 [IPR004146] (1); Zinc finger, ZZ-type [IPR000433] (1); Protein kinase C-like, phorbol ester/diacylglycerol-binding domain [IPR002219] (1)	scaffold_4_mRNA_373.1	-	-
GF0029415	1	0	0	Monosacharide transport protein (1)			scaffold_4_mRNA_363.1	-	-
GF0029414	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_3286.1	-	-
GF0029413	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_3268.1	-	-
GF0029412	1	0	0	Polynucleotidyl transferase, Ribonuclease H fold (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_4_mRNA_3265.1	-	-
GF0029411	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_3264.1	-	-
GF0029410	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_3249.1	-	-
GF0029409	1	0	0	Retrotransposon gag protein (1)			scaffold_4_mRNA_3248.1	-	-
GF0029408	1	0	0	N-terminal asparagine amidohydrolase family protein (1)	protein-N-terminal asparagine amidohydrolase activity [GO:0008418 molecular_function] (1)	Protein N-terminal asparagine amidohydrolase [IPR026750] (1)	scaffold_4_mRNA_3235.1	-	-
GF0029407	1	0	0	Nucleic acid binding / zinc ion binding protein (1)		Zinc knuckle CX2CX4HX4C [IPR025836] (1); Domain of unknown function DUF4283 [IPR025558] (1)	scaffold_4_mRNA_3217.1	-	-
GF0029406	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_3216.1	-	-
GF0029405	1	0	0	DUF946 family protein (1)		Vacuolar protein sorting-associated protein 62 [IPR009291] (1)	scaffold_4_mRNA_3215.1	-	-
GF0029404	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_3212.1	-	-
GF0029403	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_3210.1	-	-
GF0029402	1	0	0	Ribonuclease H (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	TB2/DP1/HVA22-related protein [IPR004345] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_4_mRNA_3209.1	-	-
GF0029401	1	0	0	Hypothetical protein (1)	transmembrane transport [GO:0055085 biological_process] (1)	Oligopeptide transporter, OPT superfamily [IPR004813] (1)	scaffold_4_mRNA_3207.1	-	-
GF0029400	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_3206.1	-	-
GF0029399	1	0	0	Holiday junction resolvase, S1x1p, URI domain nuclease (1)		GIY-YIG nuclease superfamily [IPR000305] (1)	scaffold_4_mRNA_3173.1	-	-
GF0029398	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_4_mRNA_3160.1	-	-
GF0029397	1	0	0	Carboxypeptidase (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); Serine carboxypeptidases, histidine active site [IPR033124] (1)	scaffold_4_mRNA_3159.1	-	-
GF0029396	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_3156.1	-	-
GF0029395	1	0	0	Glycerol-3-phosphate dehydrogenase [NAD(+)] GPDHC1, cytosolic (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1); glycerol-3-phosphate metabolic process [GO:0006072 biological_process] (1); glycerol-3-phosphate dehydrogenase complex [GO:0009331 cellular_component] (1); glycerol-3-phosphate dehydrogenase [NAD+] activity [GO:0004367 molecular_function] (1); glycerol-3-phosphate catabolic process [GO:0046168 biological_process] (1); 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, NAD-dependent, N-terminal [IPR011128] (1); Glycerol-3-phosphate dehydrogenase, NAD-dependent [IPR006168] (1); NAD(P)-binding domain [IPR016040] (1); Glycerol-3-phosphate dehydrogenase, NAD-dependent, C-terminal [IPR006109] (1); 6-phosphogluconate dehydrogenase C-terminal domain-like [IPR008927] (1); 6-phosphogluconate dehydrogenase, domain 2 [IPR013328] (1)	scaffold_4_mRNA_3155.1	-	-
GF0029394	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_312.1	-	-
GF0029393	1	0	0	BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	scaffold_4_mRNA_3110.1	-	-
GF0029392	1	0	0	Isoleucine N-monooxygenase 2 (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)	scaffold_4_mRNA_311.1	-	-
GF0029391	1	0	0	RNA-directed DNA polymerase (Reverse transcriptase) (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_4_mRNA_308.1	-	-
GF0029390	1	0	0	Hypothetical protein (1)		Glycosyl hydrolase, five-bladed beta-propellor domain [IPR023296] (1)	scaffold_4_mRNA_3038.1	-	-
GF0029389	1	0	0	TPR domain containing protein, putative (1)	protein binding [GO:0005515 molecular_function] (1)	SET domain [IPR001214] (1); Tetratricopeptide repeat-containing domain [IPR013026] (1); Tetratricopeptide repeat [IPR019734] (1); Tetratricopeptide-like helical domain [IPR011990] (1)	scaffold_4_mRNA_3034.1	-	-
GF0029388	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_3018.1	-	-
GF0029387	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_3.1	-	-
GF0029386	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_295.1	-	-
GF0029385	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_4_mRNA_294.1	-	-
GF0029384	1	0	0	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1)	Cytochrome P450, E-class, group I [IPR002401] (1); Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1); Cytochrome P450 [IPR001128] (1)	scaffold_4_mRNA_293.1	-	-
GF0029383	1	0	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	scaffold_4_mRNA_2925.1	-	-
GF0029382	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2906.1	-	-
GF0029381	1	0	0	40S ribosomal protein S26-1 (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)	scaffold_4_mRNA_290.1	-	-
GF0029380	1	0	0	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, E-class, group I [IPR002401] (1); Cytochrome P450 [IPR001128] (1)	scaffold_4_mRNA_289.1	-	-
GF0029379	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_286.1	-	-
GF0029378	1	0	0	Putative radical SAM domain-containing protein-like (1)	RNA methyltransferase activity [GO:0008173 molecular_function] (1); rRNA processing [GO:0006364 biological_process] (1); cytoplasm [GO:0005737 cellular_component] (1)	Ribosomal RNA large subunit methyltransferase RlmN/Cfr [IPR004383] (1)	scaffold_4_mRNA_2848.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0029377	1	0	0	Hexosyltransferase (1)	galactose metabolic process [GO:0006012 biological_process] (1); transferase activity, transferring glycosyl groups [GO:0016757 molecular_function] (1); inositol 3-alpha-galactosyltransferase activity [GO:0047216 molecular_function] (1)	Galactinol synthase [IPR030515] (1); Nucleotide-diphospho-sugar transferases [IPR029044] (1); Glycosyl transferase, family 8 [IPR002495] (1)	scaffold_4_mRNA_2825.1	-	-
GF0029376	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2824.1	-	-
GF0029375	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2807.1	-	-
GF0029374	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2786.1	-	-
GF0029373	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2775.1	-	-
GF0029372	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2746.1	-	-
GF0029371	1	0	0	Histone H2B (1)	protein heterodimerization activity [GO:0046982 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1); nucleosome [GO:0000786 cellular_component] (1)	Histone-fold [IPR009072] (1); Histone H2B [IPR000558] (1)	scaffold_4_mRNA_2740.1	-	-
GF0029370	1	0	0	Xylem cysteine peptidase 1 (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)	scaffold_4_mRNA_2730.1	-	-
GF0029369	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2725.1	-	-
GF0029368	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2723.1	-	-
GF0029367	1	0	0	Protein SUR2 , putative (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); lipid biosynthetic process [GO:0008610 biological_process] (1); iron ion binding [GO:0005506 molecular_function] (1)	Fatty acid hydroxylase [IPR006694] (1)	scaffold_4_mRNA_2719.1	-	-
GF0029366	1	0	0	DNA-binding storekeeper protein-related (1)	integral component of membrane [GO:0016021 cellular_component] (1)	TRAM/LAG1/CLN8 homology domain [IPR006634] (1)	scaffold_4_mRNA_2683.1	-	-
GF0029365	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2664.1	-	-
GF0029364	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2653.1	-	-
GF0029363	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2631.1	-	-
GF0029362	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	TB2/DP1/HVA22-related protein [IPR004345] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_4_mRNA_2625.1	-	-
GF0029361	1	0	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Domain of unknown function DUF1985 [IPR015410] (1); Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	scaffold_4_mRNA_2615.1	-	-
GF0029360	1	0	0	Hypothetical protein (1)	RNA polymerase II regulatory region sequence-specific DNA binding [GO:0000977 molecular_function] (1); nucleus [GO:0005634 cellular_component] (1); DNA binding [GO:0003677 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1); transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1); MAPK cascade [GO:0000165 biological_process] (1); positive regulation of transcription from RNA polymerase II promoter [GO:0045944 biological_process] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	MADS MEF2-like [IPR033896] (1); Transcription factor, K-box [IPR002487] (1); Zinc finger, PMZ-type [IPR006564] (1); MULE transposase domain [IPR018289] (1); Transposase, MuDR, plant [IPR004332] (1); Zinc finger, SWIM-type [IPR007527] (1); Transcription factor, MADS-box [IPR002100] (1)	scaffold_4_mRNA_2614.1	-	-
GF0029359	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2578.1	-	-
GF0029358	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_4_mRNA_2577.1	-	-
GF0029357	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2576.1	-	-
GF0029356	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2575.1	-	-
GF0029355	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2574.1	-	-
GF0029354	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2573.1	-	-
GF0029353	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2571.1	-	-
GF0029352	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2565.1	-	-
GF0029351	1	0	0	Retrotransposon protein, putative, Ty3-gypsy subclass, expressed (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_4_mRNA_2564.1	-	-
GF0029350	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_4_mRNA_2563.1	-	-
GF0029349	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2555.1	-	-
GF0029348	1	0	0	PLC-like phosphodiesterase superfamily protein (1)	phosphoric diester hydrolase activity [GO:0008081 molecular_function] (1); lipid metabolic process [GO:0006629 biological_process] (1)	PLC-like phosphodiesterase, TIM beta/alpha-barrel domain [IPR017946] (1)	scaffold_4_mRNA_2533.1	-	-
GF0029347	1	0	0	Hypothetical protein (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1); Serine/threonine-protein kinase, active site [IPR008271] (1)	scaffold_4_mRNA_2519.1	-	-
GF0029346	1	0	0	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1)	Cytochrome P450, conserved site [IPR017972] (1); Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450 [IPR001128] (1)	scaffold_4_mRNA_2517.1	-	-
GF0029345	1	0	0	Putative non-LTR retroelement reverse transcriptase (1)	RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Reverse transcriptase domain [IPR000477] (1); Domain of unknown function DUF4283 [IPR025558] (1); Ribonuclease H-like domain [IPR012337] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H domain [IPR002156] (1); Zinc finger, CCHC-type [IPR001878] (1); Zinc knuckle CX2CX4HX4C [IPR025836] (1); Endonuclease/exonuclease/phosphatase [IPR005135] (1)	scaffold_4_mRNA_2512.1	-	-
GF0029344	1	0	0	Lipid transfer protein 2 (1)	lipid transport [GO:0006869 biological_process] (1); lipid binding [GO:0008289 molecular_function] (1)	Plant lipid transfer protein/Par allergen [IPR000528] (1); Bifunctional inhibitor/plant lipid transfer protein/seed storage helical domain [IPR016140] (1)	scaffold_4_mRNA_2487.1	-	-
GF0029343	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2486.1	-	-
GF0029342	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2483.1	-	-
GF0029341	1	0	0	Verticillium wilt resistance-like protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_4_mRNA_2477.1	-	-
GF0029340	1	0	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	scaffold_4_mRNA_2465.1	-	-
GF0029339	1	0	0	Monosacharide transport protein (1)			scaffold_4_mRNA_2440.1	-	-
GF0029338	1	0	0	Putative non-LTR retroelement reverse transcriptase (1)	nucleic acid binding [GO:0003676 molecular_function] (1); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1)	TB2/DP1/HVA22-related protein [IPR004345] (1); Endonuclease/exonuclease/phosphatase [IPR005135] (1); Ribonuclease H-like domain [IPR012337] (1); Ribonuclease H domain [IPR002156] (1)	scaffold_4_mRNA_2433.1	-	-
GF0029337	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2425.1	-	-
GF0029336	1	0	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1); FAR1 DNA binding domain [IPR004330] (1)	scaffold_4_mRNA_2400.1	-	-
GF0029335	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2397.1	-	-
GF0029334	1	0	0	Putative retroelement pol polyprotein (1)			scaffold_4_mRNA_2396.1	-	-
GF0029333	1	0	0	3-ketoacyl-CoA synthase 6 (1)	catalytic activity [GO:0003824 molecular_function] (1); fatty acid biosynthetic process [GO:0006633 biological_process] (1); transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (1); membrane [GO:0016020 cellular_component] (1); metabolic process [GO:0008152 biological_process] (1)	Thiolase-like [IPR016039] (1); Very-long-chain 3-ketoacyl-CoA synthase [IPR012392] (1); FAE1/Type III polyketide synthase-like protein [IPR013601] (1); 3-Oxoacyl-[acyl-carrier-protein (ACP)] synthase III, C-terminal [IPR013747] (1)	scaffold_4_mRNA_2376.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0029332	1	0	0	Hypothetical protein (1)		Transposase, Tnp1/En/Spm-like [IPR004264] (1)	scaffold_4_mRNA_2372.1	-	-
GF0029331	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	scaffold_4_mRNA_2364.1	-	-
GF0029330	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2363.1	-	-
GF0029329	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2357.1	-	-
GF0029328	1	0	0	Hypothetical protein (1)		Bifunctional inhibitor/plant lipid transfer protein/seed storage helical domain [IPR016140] (1)	scaffold_4_mRNA_2323.1	-	-
GF0029327	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2291.1	-	-
GF0029326	1	0	0	LRR receptor-like kinase family protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein binding [GO:0005515 molecular_function] (1)	Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); Leucine-rich repeat [IPR001611] (1); Protein kinase domain [IPR000719] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Protein kinase-like domain [IPR011009] (1)	scaffold_4_mRNA_2289.1	-	-
GF0029325	1	0	0	Monosacharide transport protein (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1)	scaffold_4_mRNA_2288.1	-	-
GF0029324	1	0	0	Retrotransposon protein, putative, Ty3-gypsy subclass, expressed (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_4_mRNA_2287.1	-	-
GF0029323	1	0	0	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)	scaffold_4_mRNA_2285.1	-	-
GF0029322	1	0	0	Protein prenylyltransferase superfamily 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); Tetratricopeptide repeat 2 [IPR013105] (1)	scaffold_4_mRNA_2281.1	-	-
GF0029321	1	0	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1)	Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Gag-polypeptide of LTR copia-type [IPR029472] (1); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1)	scaffold_4_mRNA_2280.1	-	-
GF0029320	1	0	0	Glutathione 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)	scaffold_4_mRNA_2279.1	-	-
GF0029319	1	0	0	Tetratricopeptide repeat protein 27-like protein (1)	protein binding [GO:0005515 molecular_function] (1)	Tetratricopeptide-like helical domain [IPR011990] (1); Tetratricopeptide repeat 2 [IPR013105] (1); Tetratricopeptide repeat [IPR019734] (1); Tetratricopeptide repeat-containing domain [IPR013026] (1)	scaffold_4_mRNA_2278.1	-	-
GF0029318	1	0	0	Glutathione 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); Glutathione S-transferase, C-terminal [IPR004046] (1)	scaffold_4_mRNA_2275.1	-	-
GF0029317	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2272.1	-	-
GF0029316	1	0	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	MULE transposase domain [IPR018289] (1); FHY3/FAR1 family [IPR031052] (1)	scaffold_4_mRNA_2270.1	-	-
GF0029315	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2269.1	-	-
GF0029314	1	0	0	DUF177 domain protein (1)			scaffold_4_mRNA_2263.1	-	-
GF0029313	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2255.1	-	-
GF0029312	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2254.1	-	-
GF0029311	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2242.1	-	-
GF0029310	1	0	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1)	Aspartic peptidase, active site [IPR001969] (1); Aspartic peptidase domain [IPR021109] (1)	scaffold_4_mRNA_2235.1	-	-
GF0029309	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2228.1	-	-
GF0029308	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2218.1	-	-
GF0029307	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2217.1	-	-
GF0029306	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2215.1	-	-
GF0029305	1	0	0	Hypothetical protein (1)	proton-transporting ATPase activity, rotational mechanism [GO:0046961 molecular_function] (1); vacuolar proton-transporting V-type ATPase, V1 domain [GO:0000221 cellular_component] (1); heme binding [GO:0020037 molecular_function] (1); binding [GO:0005488 molecular_function] (1); ATP hydrolysis coupled proton transport [GO:0015991 biological_process] (1); hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances [GO:0016820 molecular_function] (1)	ATPase, V1 complex, subunit H [IPR004908] (1); ATPase, V1 complex, subunit H, C-terminal [IPR011987] (1); Cytochrome b5, heme-binding site [IPR018506] (1); Armadillo-type fold [IPR016024] (1)	scaffold_4_mRNA_2198.1	-	-
GF0029304	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2184.1	-	-
GF0029303	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2183.1	-	-
GF0029302	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2173.1	-	-
GF0029301	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2166.1	-	-
GF0029300	1	0	0	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	scaffold_4_mRNA_2148.1	-	-
GF0029299	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2147.1	-	-
GF0029298	1	0	0	Hypothetical protein (1)		RlpA-like protein, double-psi beta-barrel domain [IPR009009] (1); Expansin, cellulose-binding-like domain [IPR007117] (1)	scaffold_4_mRNA_2146.1	-	-
GF0029297	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2141.1	-	-
GF0029296	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2129.1	-	-
GF0029295	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2126.1	-	-
GF0029294	1	0	0	Hypothetical protein (1)	photosynthesis, light reaction [GO:0019684 biological_process] (1); plasma membrane light-harvesting complex [GO:0030077 cellular_component] (1); electron transporter, transferring electrons within the cyclic electron transport pathway of photosynthesis activity [GO:0045156 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1)	Antenna complex, alpha/beta subunit [IPR000066] (1)	scaffold_4_mRNA_2125.1	-	-
GF0029293	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4787 [IPR031985] (1)	scaffold_4_mRNA_2121.1	-	-
GF0029292	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2120.1	-	-
GF0029291	1	0	0	Hypothetical protein (1)		Thioredoxin-like fold [IPR012336] (1)	scaffold_4_mRNA_2116.1	-	-
GF0029290	1	0	0	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)	scaffold_4_mRNA_2114.1	-	-
GF0029289	1	0	0	Tau class glutathione S-transferase (1)	protein binding [GO:0005515 molecular_function] (1)	Glutathione S-transferase, C-terminal-like [IPR010987] (1); Glutathione S-transferase, N-terminal [IPR004045] (1); Glutathione S-transferase, C-terminal [IPR004046] (1); Thioredoxin-like fold [IPR012336] (1)	scaffold_4_mRNA_2112.1	-	-
GF0029288	1	0	0	Non-LTR retroelement reverse transcriptase-like (1)	nucleic acid binding [GO:0003676 molecular_function] (1); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1)	Ribonuclease H domain [IPR002156] (1); Ribonuclease H-like domain [IPR012337] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1); TB2/DP1/HVA22-related protein [IPR004345] (1)	scaffold_4_mRNA_2107.1	-	-
GF0029287	1	0	0	Hypothetical protein (1)	selenium binding [GO:0008430 molecular_function] (1)	Selenium-binding protein [IPR008826] (1)	scaffold_4_mRNA_2103.1	-	-
GF0029286	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2087.1	-	-
GF0029285	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2086.1	-	-
GF0029284	1	0	0	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)	scaffold_4_mRNA_2076.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0029283	1	0	0	Hypothetical protein (1)		High mobility group box domain [IPR009071] (1)	scaffold_4_mRNA_2069.2	-	-
GF0029282	1	0	0	Hypothetical protein (1)	membrane [GO:0016020 cellular_component] (1); antiporter activity [GO:0015297 molecular_function] (1); drug transmembrane transporter activity [GO:0015238 molecular_function] (1); drug transmembrane transport [GO:0006855 biological_process] (1); transmembrane transport [GO:0055085 biological_process] (1)	Multi antimicrobial extrusion protein [IPR002528] (1)	scaffold_4_mRNA_2063.1	-	-
GF0029281	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2059.1	-	-
GF0029280	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4005 [IPR025064] (1)	scaffold_4_mRNA_2056.1	-	-
GF0029279	1	0	0	MATE efflux family protein, expressed (1)	transmembrane transport [GO:0055085 biological_process] (1); drug transmembrane transport [GO:0006855 biological_process] (1); antiporter activity [GO:0015297 molecular_function] (1); drug transmembrane transporter activity [GO:0015238 molecular_function] (1); membrane [GO:0016020 cellular_component] (1)	Multi antimicrobial extrusion protein [IPR002528] (1)	scaffold_4_mRNA_2053.1	-	-
GF0029278	1	0	0	MatE family protein, expressed (1)	transmembrane transport [GO:0055085 biological_process] (1); drug transmembrane transport [GO:0006855 biological_process] (1); drug transmembrane transporter activity [GO:0015238 molecular_function] (1); antiporter activity [GO:0015297 molecular_function] (1); membrane [GO:0016020 cellular_component] (1)	Multi antimicrobial extrusion protein [IPR002528] (1)	scaffold_4_mRNA_2052.1	-	-
GF0029277	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2050.1	-	-
GF0029276	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2026.1	-	-
GF0029275	1	0	0	RNA-directed DNA polymerase ; Ribonuclease H, putative (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	scaffold_4_mRNA_2022.1	-	-
GF0029274	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2021.1	-	-
GF0029273	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_4_mRNA_2013.1	-	-
GF0029272	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	scaffold_4_mRNA_2012.1	-	-
GF0029271	1	0	0	Hypothetical protein (1)	intracellular [GO:0005622 cellular_component] (1); translation [GO:0006412 biological_process] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1); ribosome [GO:0005840 cellular_component] (1)	Ribosomal protein S8e, conserved site [IPR018283] (1); Ribosomal protein S8e [IPR001047] (1); Transposase, MuDR, plant [IPR004332] (1); Ribosomal protein S8e/ribosomal biogenesis NSA2 [IPR022309] (1)	scaffold_4_mRNA_2010.1	-	-
GF0029270	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2006.1	-	-
GF0029269	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_2003.1	-	-
GF0029268	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_4_mRNA_2002.1	-	-
GF0029267	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Aspartic peptidase domain [IPR021109] (1); Zinc finger, CCHC-type [IPR001878] (1); Viral movement protein [IPR028919] (1); Retropepsins [IPR018061] (1); Peptidase A2A, retrovirus, catalytic [IPR001995] (1); Aspartic peptidase, active site [IPR001969] (1)	scaffold_4_mRNA_1997.1	-	-
GF0029266	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1985.1	-	-
GF0029265	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1968.1	-	-
GF0029264	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1956.1	-	-
GF0029263	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1952.1	-	-
GF0029262	1	0	0	Hypothetical protein (1)		Arabidopsis retrotransposon Orf1 [IPR004312] (1)	scaffold_4_mRNA_1951.1	-	-
GF0029261	1	0	0	LRR receptor-like kinase family protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1)	scaffold_4_mRNA_1950.1	-	-
GF0029260	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1948.1	-	-
GF0029259	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1947.1	-	-
GF0029258	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_4_mRNA_1946.1	-	-
GF0029257	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1945.1	-	-
GF0029256	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1944.1	-	-
GF0029255	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1941.1	-	-
GF0029254	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1938.1	-	-
GF0029253	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1937.1	-	-
GF0029252	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_4_mRNA_1936.1	-	-
GF0029251	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1933.1	-	-
GF0029250	1	0	0	Putative callose synthase 8 (1)	(1->3)-beta-D-glucan biosynthetic process [GO:0006075 biological_process] (1); 1,3-beta-D-glucan synthase complex [GO:0000148 cellular_component] (1); 1,3-beta-D-glucan synthase activity [GO:0003843 molecular_function] (1); membrane [GO:0016020 cellular_component] (1)	Glycosyl transferase, family 48 [IPR003440] (1); 1,3-beta-glucan synthase subunit FKS1-like, domain-1 [IPR026899] (1)	scaffold_4_mRNA_1930.1	-	-
GF0029249	1	0	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Domain of unknown function DUF1985 [IPR015410] (1); Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	scaffold_4_mRNA_1928.1	-	-
GF0029248	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1924.1	-	-
GF0029247	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1915.1	-	-
GF0029246	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1892.1	-	-
GF0029245	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1886.1	-	-
GF0029244	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1878.1	-	-
GF0029243	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	scaffold_4_mRNA_1875.1	-	-
GF0029242	1	0	0	Phi class glutathione S-transferase (1)		Glutathione S-transferase, C-terminal-like [IPR010987] (1); Glutathione S-transferase, C-terminal [IPR004046] (1); Glutathione S-transferases Phi, C-terminal [IPR034347] (1)	scaffold_4_mRNA_1874.1	-	-
GF0029241	1	0	0	Hypothetical protein (1)	integral component of membrane [GO:0016021 cellular_component] (1); protein binding [GO:0005515 molecular_function] (1)	Regulatory protein NPR, central domain [IPR024228] (1); SKP1/BTB/POZ domain [IPR011333] (1); Ankyrin repeat [IPR002110] (1); BTB/POZ domain [IPR000210] (1); TRAM/LAG1/CLN8 homology domain [IPR006634] (1); NPR1/NIM1-like, C-terminal [IPR021094] (1); Ankyrin repeat-containing domain [IPR020683] (1)	scaffold_4_mRNA_1871.1	-	-
GF0029240	1	0	0	Non-expressor of PR1 (1)	protein binding [GO:0005515 molecular_function] (1)	SKP1/BTB/POZ domain [IPR011333] (1); Regulatory protein NPR, central domain [IPR024228] (1); Ankyrin repeat [IPR002110] (1); BTB/POZ domain [IPR000210] (1); NPR1/NIM1-like, C-terminal [IPR021094] (1); Ankyrin repeat-containing domain [IPR020683] (1)	scaffold_4_mRNA_1867.1	-	-
GF0029239	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1865.1	-	-
GF0029238	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat-containing domain [IPR020683] (1); NPR1/NIM1-like, C-terminal [IPR021094] (1); BTB/POZ domain [IPR000210] (1); SKP1/BTB/POZ domain [IPR011333] (1); Regulatory protein NPR, central domain [IPR024228] (1); Ankyrin repeat [IPR002110] (1)	scaffold_4_mRNA_1864.1	-	-
GF0029237	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1859.1	-	-
GF0029236	1	0	0	Nonexpressor of pathogenesis-related protein 1 (1)	protein binding [GO:0005515 molecular_function] (1)	BTB/POZ domain [IPR000210] (1); NPR1/NIM1-like, C-terminal [IPR021094] (1); Ankyrin repeat-containing domain [IPR020683] (1); SKP1/BTB/POZ domain [IPR011333] (1); Ankyrin repeat [IPR002110] (1)	scaffold_4_mRNA_1857.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0029235	1	0	0	Regulatory protein NPR1 (1)	protein binding [GO:0005515 molecular_function] (1)	BTB/POZ domain [IPR000210] (1); NPR1/NIM1-like, C-terminal [IPR021094] (1); Ankyrin repeat-containing domain [IPR020683] (1); Regulatory protein NPR, central domain [IPR024228] (1); SKP1/BTB/POZ domain [IPR011333] (1); Ankyrin repeat [IPR002110] (1)	scaffold_4_mRNA_1854.1	-	-
GF0029234	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat [IPR002110] (1); SKP1/BTB/POZ domain [IPR011333] (1); Regulatory protein NPR, central domain [IPR024228] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); BTB/POZ domain [IPR000210] (1); NPR1/NIM1-like, C-terminal [IPR021094] (1); Ankyrin repeat-containing domain [IPR020683] (1)	scaffold_4_mRNA_1853.1	-	-
GF0029233	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1847.1	-	-
GF0029232	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1837.1	-	-
GF0029231	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Ribonuclease H-like domain [IPR012337] (1); Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	scaffold_4_mRNA_1835.1	-	-
GF0029230	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1830.1	-	-
GF0029229	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1824.1	-	-
GF0029228	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	C2 domain [IPR000008] (1)	scaffold_4_mRNA_1823.1	-	-
GF0029227	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1821.1	-	-
GF0029226	1	0	0	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	scaffold_4_mRNA_1820.1	-	-
GF0029225	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1814.1	-	-
GF0029224	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1798.1	-	-
GF0029223	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1796.1	-	-
GF0029222	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1791.1	-	-
GF0029221	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1789.1	-	-
GF0029220	1	0	0	Zinc knuckle family protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Domain of unknown function DUF4219 [IPR025314] (1)	scaffold_4_mRNA_1786.1	-	-
GF0029219	1	0	0	Stress up-regulated Nod 19 protein (1)		Stress up-regulated Nod 19 [IPR011692] (1)	scaffold_4_mRNA_1764.1	-	-
GF0029218	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_4_mRNA_1745.1	-	-
GF0029217	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1744.1	-	-
GF0029216	1	0	0	Transporter, Pam16 (1)	protein import into mitochondrial matrix [GO:0030150 biological_process] (1); mitochondrial inner membrane presequence translocase complex [GO:0005744 cellular_component] (1)	Mitochondrial import inner membrane translocase subunit Tim16 [IPR005341] (1)	scaffold_4_mRNA_1735.1	-	-
GF0029215	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_4_mRNA_1719.1	-	-
GF0029214	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1714.1	-	-
GF0029213	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1709.1	-	-
GF0029212	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1708.1	-	-
GF0029211	1	0	0	Polynucleotidyl transferase, Ribonuclease H fold (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_4_mRNA_1705.1	-	-
GF0029210	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc knuckle CX2CX4HX4C [IPR025836] (1); Zinc finger, CCHC-type [IPR001878] (1); Domain of unknown function DUF4283 [IPR025558] (1)	scaffold_4_mRNA_17.1	-	-
GF0029209	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_4_mRNA_1698.1	-	-
GF0029208	1	0	0	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)	scaffold_4_mRNA_1697.1	-	-
GF0029207	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_4_mRNA_1696.1	-	-
GF0029206	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1690.1	-	-
GF0029205	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1688.1	-	-
GF0029204	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1684.1	-	-
GF0029203	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc knuckle CX2CX4HX4C [IPR025836] (1); Zinc finger, CCHC-type [IPR001878] (1); Domain of unknown function DUF4283 [IPR025558] (1)	scaffold_4_mRNA_1678.1	-	-
GF0029202	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1675.1	-	-
GF0029201	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_4_mRNA_1674.1	-	-
GF0029200	1	0	0	Monosacharide transport protein (1)			scaffold_4_mRNA_1665.1	-	-
GF0029199	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_4_mRNA_1662.1	-	-
GF0029198	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1661.1	-	-
GF0029197	1	0	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Carlavirus nucleic acid-binding protein [IPR002568] (1)	scaffold_4_mRNA_1659.1	-	-
GF0029196	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1649.1	-	-
GF0029195	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1648.1	-	-
GF0029194	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1647.1	-	-
GF0029193	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1646.1	-	-
GF0029192	1	0	0	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)	scaffold_4_mRNA_1645.1	-	-
GF0029191	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1644.1	-	-
GF0029190	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1643.1	-	-
GF0029189	1	0	0	Hypothetical protein (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); Retrotransposon gag domain [IPR005162] (1); LOG family [IPR031100] (1)	scaffold_4_mRNA_1642.1	-	-
GF0029188	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); DNA integration [GO:0015074 biological_process] (1)	Integrase, catalytic core [IPR001584] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_4_mRNA_1641.1	-	-
GF0029187	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1640.1	-	-
GF0029186	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1639.1	-	-
GF0029185	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1637.1	-	-
GF0029184	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1635.1	-	-
GF0029183	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_4_mRNA_1634.1	-	-
GF0029182	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1633.1	-	-
GF0029181	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1632.1	-	-
GF0029180	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1629.1	-	-
GF0029179	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1628.1	-	-
GF0029178	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			scaffold_4_mRNA_1627.1	-	-
GF0029177	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_4_mRNA_1625.1	-	-
GF0029176	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Domain of unknown function DUF4283 [IPR025558] (1)	scaffold_4_mRNA_1617.1	-	-
GF0029175	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1616.1	-	-
GF0029174	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1613.1	-	-
GF0029173	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1610.1	-	-
GF0029172	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1609.1	-	-
GF0029171	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_4_mRNA_1608.1	-	-
GF0029170	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1604.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0029169	1	0	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1); FAR1 DNA binding domain [IPR004330] (1); Retrotransposon gag domain [IPR005162] (1)	scaffold_4_mRNA_1589.1	-	-
GF0029168	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1569.1	-	-
GF0029167	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_4_mRNA_1568.1	-	-
GF0029166	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_4_mRNA_1552.1	-	-
GF0029165	1	0	0	Zinc knuckle family protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_4_mRNA_1550.1	-	-
GF0029164	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4219 [IPR025314] (1)	scaffold_4_mRNA_1549.1	-	-
GF0029163	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_4_mRNA_1544.1	-	-
GF0029162	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_4_mRNA_1505.1	-	-
GF0029161	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1504.1	-	-
GF0029160	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1498.1	-	-
GF0029159	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_4_mRNA_1497.1	-	-
GF0029158	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1495.1	-	-
GF0029157	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_4_mRNA_1494.1	-	-
GF0029156	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1493.1	-	-
GF0029155	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1492.1	-	-
GF0029154	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG7 (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_4_mRNA_1491.1	-	-
GF0029153	1	0	0	Alpha,alpha-trehalase (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); Glycoside hydrolase, family 37, conserved site [IPR018232] (1); Six-hairpin glycosidase-like [IPR008928] (1)	scaffold_4_mRNA_1479.1	-	-
GF0029152	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1471.1	-	-
GF0029151	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1453.1	-	-
GF0029150	1	0	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1); MULE transposase domain [IPR018289] (1)	scaffold_4_mRNA_1433.1	-	-
GF0029149	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1416.1	-	-
GF0029148	1	0	0	Hypothetical protein (1)		Transposase-associated domain [IPR029480] (1)	scaffold_4_mRNA_141.1	-	-
GF0029147	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1401.1	-	-
GF0029146	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_14.1	-	-
GF0029145	1	0	0	Putative RNA-directed DNA polymerase (1)			scaffold_4_mRNA_1397.1	-	-
GF0029144	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_4_mRNA_1385.1	-	-
GF0029143	1	0	0	Retrotransposon protein, putative, unclassified (1)			scaffold_4_mRNA_1381.1	-	-
GF0029142	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_4_mRNA_1375.1	-	-
GF0029141	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1373.1	-	-
GF0029140	1	0	0	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1)	Cytochrome P450 [IPR001128] (1); Cytochrome P450, E-class, group I [IPR002401] (1)	scaffold_4_mRNA_1372.1	-	-
GF0029139	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_4_mRNA_1371.1	-	-
GF0029138	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1367.1	-	-
GF0029137	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1356.1	-	-
GF0029136	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_4_mRNA_1355.1	-	-
GF0029135	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_4_mRNA_1354.1	-	-
GF0029134	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1353.1	-	-
GF0029133	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1350.1	-	-
GF0029132	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1349.1	-	-
GF0029131	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1341.1	-	-
GF0029130	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1331.1	-	-
GF0029129	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1330.1	-	-
GF0029128	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1327.1	-	-
GF0029127	1	0	0	Transposase (1)		Domain of unknown function DUF4218 [IPR025452] (1)	scaffold_4_mRNA_1326.1	-	-
GF0029126	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1325.1	-	-
GF0029125	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_4_mRNA_1324.1	-	-
GF0029124	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1322.1	-	-
GF0029123	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1317.1	-	-
GF0029122	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1315.1	-	-
GF0029121	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1314.1	-	-
GF0029120	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1310.1	-	-
GF0029119	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1309.1	-	-
GF0029118	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1307.1	-	-
GF0029117	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1306.1	-	-
GF0029116	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1305.1	-	-
GF0029115	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1301.1	-	-
GF0029114	1	0	0	PLATZ transcription factor family protein (1)	intracellular [GO:0005622 cellular_component] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Protein of unknown function DUF597 [IPR006734] (1); B-box-type zinc finger [IPR000315] (1)	scaffold_4_mRNA_1298.1	-	-
GF0029113	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1296.1	-	-
GF0029112	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1291.1	-	-
GF0029111	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); DNA integration [GO:0015074 biological_process] (1)	Aspartic peptidase domain [IPR021109] (1); Integrase, catalytic core [IPR001584] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_4_mRNA_1290.1	-	-
GF0029110	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_129.1	-	-
GF0029109	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1287.1	-	-
GF0029108	1	0	0	Hypothetical protein (1)		Protein-tyrosine phosphatase-like [IPR029021] (1); Aspartic peptidase domain [IPR021109] (1); Myotubularin-like phosphatase domain [IPR010569] (1)	scaffold_4_mRNA_1286.1	-	-
GF0029107	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_4_mRNA_1285.1	-	-
GF0029106	1	0	0	RNA-directed DNA polymerase (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)	scaffold_4_mRNA_1282.1	-	-
GF0029105	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1281.1	-	-
GF0029104	1	0	0	Hypothetical protein (1)		Aspartate/glutamate/uridylate kinase [IPR001048] (1)	scaffold_4_mRNA_1280.1	-	-
GF0029103	1	0	0	Hypothetical protein (1)	RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Ribonuclease H domain [IPR002156] (1)	scaffold_4_mRNA_1275.1	-	-
GF0029102	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1273.1	-	-
GF0029101	1	0	0	Hypothetical protein (1)		Aspartate/glutamate/uridylate kinase [IPR001048] (1)	scaffold_4_mRNA_1271.1	-	-
GF0029100	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1268.1	-	-
GF0029099	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1266.1	-	-
GF0029098	1	0	0	Hypothetical protein (1)		Aspartate/glutamate/uridylate kinase [IPR001048] (1)	scaffold_4_mRNA_1265.1	-	-
GF0029097	1	0	0	Strictosidine synthase family 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); Strictosidine synthase, conserved region [IPR018119] (1)	scaffold_4_mRNA_1264.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0029096	1	0	0	Retrovirus-related Pol polyprotein from transposon 412 (1)	nucleic acid binding [GO:0003676 molecular_function] (1); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Ribonuclease H domain [IPR002156] (1)	scaffold_4_mRNA_1262.1	-	-
GF0029095	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1260.1	-	-
GF0029094	1	0	0	Hypothetical protein (1)	phosphatase activity [GO:0016791 molecular_function] (1); dephosphorylation [GO:0016311 biological_process] (1); protein tyrosine phosphatase activity [GO:0004725 molecular_function] (1)	Protein-tyrosine phosphatase, active site [IPR016130] (1); Myotubularin-like phosphatase domain [IPR010569] (1); Myotubularin family [IPR030564] (1); Protein-tyrosine phosphatase-like [IPR029021] (1)	scaffold_4_mRNA_1252.1	-	-
GF0029093	1	0	0	Hypothetical protein (1)	RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Ribonuclease H domain [IPR002156] (1)	scaffold_4_mRNA_1251.1	-	-
GF0029092	1	0	0	Hypothetical protein (1)		Aspartate/glutamate/uridylate kinase [IPR001048] (1)	scaffold_4_mRNA_1249.1	-	-
GF0029091	1	0	0	Putative strictosidine synthase (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); Strictosidine synthase, conserved region [IPR018119] (1)	scaffold_4_mRNA_1247.1	-	-
GF0029090	1	0	0	Hypothetical protein (1)		Protein-tyrosine phosphatase-like [IPR029021] (1); Myotubularin family [IPR030564] (1); Myotubularin-like phosphatase domain [IPR010569] (1)	scaffold_4_mRNA_1241.1	-	-
GF0029089	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1240.1	-	-
GF0029088	1	0	0	Hypothetical protein (1)		Myotubularin-like phosphatase domain [IPR010569] (1)	scaffold_4_mRNA_1239.1	-	-
GF0029087	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1236.1	-	-
GF0029086	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1228.1	-	-
GF0029085	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1227.1	-	-
GF0029084	1	0	0	Putative methyltransferase PMT20 (1)	methyltransferase activity [GO:0008168 molecular_function] (1)	Putative S-adenosyl-L-methionine-dependent methyltransferase [IPR004159] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	scaffold_4_mRNA_1225.1	-	-
GF0029083	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger C2H2-type [IPR013087] (1); Zinc finger, RING/FYVE/PHD-type [IPR013083] (1)	scaffold_4_mRNA_1224.1	-	-
GF0029082	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1223.1	-	-
GF0029081	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1222.1	-	-
GF0029080	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1221.1	-	-
GF0029079	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1213.1	-	-
GF0029078	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1204.1	-	-
GF0029077	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1201.1	-	-
GF0029076	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_4_mRNA_1195.1	-	-
GF0029075	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1185.1	-	-
GF0029074	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1177.1	-	-
GF0029073	1	0	0	Hypothetical protein (1)		Prolamin-like domain [IPR008502] (1)	scaffold_4_mRNA_1176.1	-	-
GF0029072	1	0	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_4_mRNA_1162.1	-	-
GF0029071	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1159.1	-	-
GF0029070	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1158.1	-	-
GF0029069	1	0	0	Putative Athila retroelement ORF1 protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_4_mRNA_1156.1	-	-
GF0029068	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1143.1	-	-
GF0029067	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1133.1	-	-
GF0029066	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_4_mRNA_1132.1	-	-
GF0029065	1	0	0	Hypothetical protein (1)	RNA binding [GO:0003723 molecular_function] (1); ribonuclease T2 activity [GO:0033897 molecular_function] (1)	Ribonuclease T2-like [IPR001568] (1)	scaffold_4_mRNA_1131.1	-	-
GF0029064	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1130.1	-	-
GF0029063	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1129.1	-	-
GF0029062	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1126.1	-	-
GF0029061	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1125.1	-	-
GF0029060	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1123.1	-	-
GF0029059	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1120.1	-	-
GF0029058	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1112.1	-	-
GF0029057	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_4_mRNA_1111.1	-	-
GF0029056	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1108.1	-	-
GF0029055	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1107.1	-	-
GF0029054	1	0	0	Hypothetical protein (1)		Transposase, Tnp1/En/Spm-like [IPR004264] (1)	scaffold_4_mRNA_1104.1	-	-
GF0029053	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_4_mRNA_1101.1	-	-
GF0029052	1	0	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1); Serine/threonine-protein kinase, active site [IPR008271] (1)	scaffold_4_mRNA_1095.1	-	-
GF0029051	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1093.1	-	-
GF0029050	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1092.1	-	-
GF0029049	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1089.1	-	-
GF0029048	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_4_mRNA_1088.1	-	-
GF0029047	1	0	0	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)	scaffold_4_mRNA_1087.1	-	-
GF0029046	1	0	0	Hypothetical protein (1)		Gag-polypeptide of LTR copia-type [IPR029472] (1)	scaffold_4_mRNA_1080.1	-	-
GF0029045	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1075.1	-	-
GF0029044	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1070.1	-	-
GF0029043	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1063.1	-	-
GF0029042	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); GAG-pre-integrase domain [IPR025724] (1)	scaffold_4_mRNA_1052.1	-	-
GF0029041	1	0	0	Hypothetical protein (1)		Gag-polypeptide of LTR copia-type [IPR029472] (1)	scaffold_4_mRNA_1051.1	-	-
GF0029040	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1050.1	-	-
GF0029039	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1048.1	-	-
GF0029038	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1024.1	-	-
GF0029037	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1013.1	-	-
GF0029036	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1002.1	-	-
GF0029035	1	0	0	Hypothetical protein (1)			scaffold_4_mRNA_1.1	-	-
GF0029034	1	0	0	Hypothetical protein (1)		P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_3_mRNA_991.1	-	-
GF0029033	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_989.1	-	-
GF0029032	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_3_mRNA_987.1	-	-
GF0029031	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_985.1	-	-
GF0029030	1	0	0	Pentatricopeptide repeat-containing family protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Tetratricopeptide-like helical domain [IPR011990] (1); Pentatricopeptide repeat [IPR002885] (1); DYW domain [IPR032867] (1)	scaffold_3_mRNA_979.1	-	-
GF0029029	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_973.1	-	-
GF0029028	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_97.1	-	-
GF0029027	1	0	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1); Domain of unknown function DUF1985 [IPR015410] (1)	scaffold_3_mRNA_959.1	-	-
GF0029026	1	0	0	Phloem protein 2-A13 (1)	protein binding [GO:0005515 molecular_function] (1)	F-box domain [IPR001810] (1); Phloem protein 2-like [IPR025886] (1)	scaffold_3_mRNA_935.1	-	-
GF0029025	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_932.1	-	-
GF0029024	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_929.1	-	-
GF0029023	1	0	0	RNA-directed DNA polymerase (Reverse transcriptase) (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_3_mRNA_924.1	-	-
GF0029022	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_923.1	-	-
GF0029021	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_922.1	-	-
GF0029020	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_903.1	-	-

ID	**Num. in *C. celementine***	**Num in *C. unshiu***	**Num in *P.trifoliata***	**Note**	**GO**	**InterPro**	**Members in *C.clementine***	**Members in *C.unshiu***	**Members in *P.trifoliata***
GF0029019	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_899.1	-	-
GF0029018	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_897.1	-	-
GF0029017	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_896.1	-	-
GF0029016	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_895.1	-	-
GF0029015	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_3_mRNA_881.1	-	-
GF0029014	1	0	0	Geraniol 10-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); Cytochrome P450, E-class, group I [IPR002401] (1)	scaffold_3_mRNA_877.1	-	-
GF0029013	1	0	0	Hypothetical protein (1)	primary amine oxidase activity [GO:0008131 molecular_function] (1); copper ion binding [GO:0005507 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); quinone binding [GO:0048038 molecular_function] (1); amine metabolic process [GO:0009308 biological_process] (1)	Copper amine oxidase, C-terminal [IPR015798] (1); Copper amine oxidase [IPR000269] (1)	scaffold_3_mRNA_838.1	-	-
GF0029012	1	0	0	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1)	scaffold_3_mRNA_834.1	-	-
GF0029011	1	0	0	Protein ODORANT1 (1)	DNA binding [GO:0003677 molecular_function] (1)	SANT/Myb domain [IPR001005] (1); Myb domain [IPR017930] (1); Homeobox domain-like [IPR009057] (1)	scaffold_3_mRNA_828.1	-	-
GF0029010	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_3_mRNA_814.1	-	-
GF0029009	1	0	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1); Domain of unknown function DUF1985 [IPR015410] (1)	scaffold_3_mRNA_801.1	-	-
GF0029008	1	0	0	Zinc finger matrin-type protein 1, putative isoform 1 (1)			scaffold_3_mRNA_77.2	-	-
GF0029007	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_766.1	-	-
GF0029006	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_747.3	-	-
GF0029005	1	0	0	Ribosomal protein L15 (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 L15e core domain [IPR024794] (1); Ribosomal protein L15e, conserved site [IPR020925] (1); Ribosomal protein L23/L15e core domain [IPR012678] (1); Ribosomal protein L15e [IPR000439] (1)	scaffold_3_mRNA_743.1	-	-
GF0029004	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_724.1	-	-
GF0029003	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_711.1	-	-
GF0029002	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_709.1	-	-
GF0029001	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_697.1	-	-
GF0029000	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_694.1	-	-
GF0028999	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_693.1	-	-
GF0028998	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_692.1	-	-
GF0028997	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_3_mRNA_690.1	-	-
GF0028996	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	scaffold_3_mRNA_689.1	-	-
GF0028995	1	0	0	Ubiquitinyl hydrolase 1 (1)	intracellular [GO:0005622 cellular_component] (1); thiol-dependent ubiquitin-specific protease activity [GO:0004843 molecular_function] (1); ubiquitin-dependent protein catabolic process [GO:0006511 biological_process] (1)	Peptidase C12, ubiquitin carboxyl-terminal hydrolase [IPR001578] (1)	scaffold_3_mRNA_686.1	-	-
GF0028994	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_683.1	-	-
GF0028993	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_682.1	-	-
GF0028992	1	0	0	Hypothetical protein (1)	GTP binding [GO:0005525 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); GTPase activity [GO:0003924 molecular_function] (1); FAD binding [GO:0071949 molecular_function] (1)	FAD-binding domain [IPR002938] (1); FAD/NAD(P)-binding domain [IPR023753] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Small GTPase superfamily [IPR001806] (1); Small GTP-binding protein domain [IPR005225] (1)	scaffold_3_mRNA_677.1	-	-
GF0028991	1	0	0	FAR1 DNA-binding domain protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1); FAR1 DNA binding domain [IPR004330] (1)	scaffold_3_mRNA_644.1	-	-
GF0028990	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_640.1	-	-
GF0028989	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_631.1	-	-
GF0028988	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_629.1	-	-
GF0028987	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_628.1	-	-
GF0028986	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_6279.1	-	-
GF0028985	1	0	0	Protein transport protein SEC23 (1)	zinc ion binding [GO:0008270 molecular_function] (1); intracellular protein transport [GO:0006886 biological_process] (1); ER to Golgi vesicle-mediated transport [GO:0006888 biological_process] (1); COPII vesicle coat [GO:0030127 cellular_component] (1)	ADF-H/Gelsolin-like domain [IPR029006] (1); Gelsolin-like domain [IPR007123] (1); Zinc finger, Sec23/Sec24-type [IPR006895] (1); von Willebrand factor, type A [IPR002035] (1); Sec23/Sec24, helical domain [IPR006900] (1); Sec23/Sec24, trunk domain [IPR006896] (1)	scaffold_3_mRNA_6276.2	-	-
GF0028984	1	0	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Domain of unknown function DUF1985 [IPR015410] (1); Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	scaffold_3_mRNA_625.1	-	-
GF0028983	1	0	0	Hypothetical protein (1)	GTPase activity [GO:0003924 molecular_function] (1); GTP binding [GO:0005525 molecular_function] (1)	Small GTPase superfamily [IPR001806] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Small GTP-binding protein domain [IPR005225] (1)	scaffold_3_mRNA_6248.1	-	-
GF0028982	1	0	0	DNA repair recO (1)		Zf-FLZ domain [IPR007650] (1)	scaffold_3_mRNA_6241.1	-	-
GF0028981	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_3_mRNA_6169.1	-	-
GF0028980	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_6168.1	-	-
GF0028979	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_6110.1	-	-
GF0028978	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_6102.1	-	-
GF0028977	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_6096.1	-	-
GF0028976	1	0	0	MADS-box protein SOC1 (1)	positive regulation of transcription from RNA polymerase II promoter [GO:0045944 biological_process] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); MAPK cascade [GO:0000165 biological_process] (1); transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1); nucleus [GO:0005634 cellular_component] (1); DNA binding [GO:0003677 molecular_function] (1); RNA polymerase II regulatory region sequence-specific DNA binding [GO:0000977 molecular_function] (1)	Transcription factor, MADS-box [IPR002100] (1); Transcription factor, K-box [IPR002487] (1); MADS MEF2-like [IPR033896] (1)	scaffold_3_mRNA_6067.1	-	-
GF0028975	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_6060.1	-	-
GF0028974	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_6026.1	-	-
GF0028973	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_6025.1	-	-
GF0028972	1	0	0	Carbonyl reductase 3 (1)		Short-chain dehydrogenase/reductase SDR [IPR002347] (1); NAD(P)-binding domain [IPR016040] (1)	scaffold_3_mRNA_6024.1	-	-
GF0028971	1	0	0	Adenylate kinase (1)	ATP binding [GO:0005524 molecular_function] (1); nucleobase-containing compound kinase activity [GO:0019205 molecular_function] (1); nucleobase-containing compound metabolic process [GO:0006139 biological_process] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Adenylate kinase/UMP-CMP kinase [IPR000850] (1)	scaffold_3_mRNA_602.1	-	-
GF0028970	1	0	0	Myb transcription factor MIXTA-like protein (1)	DNA binding [GO:0003677 molecular_function] (1)	SANT/Myb domain [IPR001005] (1); Myb domain [IPR017930] (1); Homeobox domain-like [IPR009057] (1)	scaffold_3_mRNA_6012.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0028969	1	0	0	Integrin-linked protein kinase family isoform 4 (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)	Ankyrin repeat-containing domain [IPR020683] (1); Protein kinase, ATP binding site [IPR017441] (1); Ankyrin repeat [IPR002110] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	scaffold_3_mRNA_5995.1	-	-
GF0028968	1	0	0	Calcium-dependent lipid-binding (CaLB domain) family protein, putative (1)	protein binding [GO:0005515 molecular_function] (1)	C2 domain [IPR000008] (1)	scaffold_3_mRNA_5987.1	-	-
GF0028967	1	0	0	Unspecific monooxygenase (1)	iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450, conserved site [IPR017972] (1); Cytochrome P450 [IPR001128] (1)	scaffold_3_mRNA_5976.1	-	-
GF0028966	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_5974.1	-	-
GF0028965	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_5935.1	-	-
GF0028964	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc knuckle CX2CX4HX4C [IPR025836] (1); Endonuclease/exonuclease/phosphatase [IPR005135] (1); Domain of unknown function DUF4283 [IPR025558] (1); Ribonuclease H-like domain [IPR012337] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1)	scaffold_3_mRNA_5912.1	-	-
GF0028963	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_5910.1	-	-
GF0028962	1	0	0	Hypothetical protein (1)	metabolic process [GO:0008152 biological_process] (1); transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	scaffold_3_mRNA_5893.1	-	-
GF0028961	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_5891.1	-	-
GF0028960	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_5890.1	-	-
GF0028959	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_581.1	-	-
GF0028958	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_5806.1	-	-
GF0028957	1	0	0	Ubiquitin-40S ribosomal protein S27a (1)	translation [GO:0006412 biological_process] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1); ribosome [GO:0005840 cellular_component] (1)	Ubiquitin domain [IPR000626] (1); Ubiquitin conserved site [IPR019954] (1); Zinc-binding ribosomal protein [IPR011332] (1); Ribosomal protein S27a [IPR002906] (1); Ubiquitin [IPR019956] (1); Ubiquitin-related domain [IPR029071] (1)	scaffold_3_mRNA_5709.1	-	-
GF0028956	1	0	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	scaffold_3_mRNA_5701.1	-	-
GF0028955	1	0	0	Mutator-like transposase (1)	zinc ion binding [GO:0008270 molecular_function] (1)	MULE transposase domain [IPR018289] (1); Zinc finger, PMZ-type [IPR006564] (1); Transposase, MuDR, plant [IPR004332] (1); Zinc finger, SWIM-type [IPR007527] (1)	scaffold_3_mRNA_5700.1	-	-
GF0028954	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_5688.1	-	-
GF0028953	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_5684.1	-	-
GF0028952	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_5671.1	-	-
GF0028951	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Domain of unknown function DUF4283 [IPR025558] (1)	scaffold_3_mRNA_5668.1	-	-
GF0028950	1	0	0	D27 family protein, putative (1)		Domain of unknown function DUF4033 [IPR025114] (1)	scaffold_3_mRNA_5652.1	-	-
GF0028949	1	0	0	Multidrug resistance protein ABC transporter family protein (1)		Protein of unknown function DUF4228, plant [IPR025322] (1)	scaffold_3_mRNA_5626.1	-	-
GF0028948	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_5616.1	-	-
GF0028947	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_5611.1	-	-
GF0028946	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_5603.1	-	-
GF0028945	1	0	0	Hypothetical protein (1)	selenium binding [GO:0008430 molecular_function] (1)	Selenium-binding protein [IPR008826] (1)	scaffold_3_mRNA_5599.1	-	-
GF0028944	1	0	0	GATA transcription factor 15 (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); sequence-specific DNA binding [GO:0043565 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1); transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (1)	Zinc finger, NHR/GATA-type [IPR013088] (1); Zinc finger, GATA-type [IPR000679] (1)	scaffold_3_mRNA_5598.1	-	-
GF0028943	1	0	0	Fumarate hydratase (1)	fumarate metabolic process [GO:0006106 biological_process] (1); tricarboxylic acid cycle [GO:0006099 biological_process] (1); tricarboxylic acid cycle enzyme complex [GO:0045239 cellular_component] (1); lyase activity [GO:0016829 molecular_function] (1); catalytic activity [GO:0003824 molecular_function] (1); fumarate hydratase activity [GO:0004333 molecular_function] (1)	Fumarase/histidase, N-terminal [IPR024083] (1); Fumarate lyase, conserved site [IPR020557] (1); Fumarate lyase family [IPR000362] (1); Fumarate lyase, N-terminal [IPR022761] (1); Fumarase C, C-terminal [IPR018951] (1); Fumarate hydratase, class II [IPR005677] (1); L-Aspartase-like [IPR008948] (1)	scaffold_3_mRNA_5581.2	-	-
GF0028942	1	0	0	Ribosomal protein L19 (1)	structural constituent of ribosome [GO:0003735 molecular_function] (1); intracellular [GO:0005622 cellular_component] (1); translation [GO:0006412 biological_process] (1); cytosolic large ribosomal subunit [GO:0022625 cellular_component] (1); ribosome [GO:0005840 cellular_component] (1)	Ribosomal protein L19/L19e conserved site [IPR023638] (1); Ribosomal protein L19, eukaryotic [IPR033935] (1); Ribosomal protein L19/L19e, domain 3 [IPR015974] (1); Ribosomal protein L19/L19e, domain 2 [IPR015973] (1); Ribosomal protein L19/L19e [IPR000196] (1); Ribosomal protein L19/L19e, domain 1 [IPR015972] (1)	scaffold_3_mRNA_5578.1	-	-
GF0028941	1	0	0	Epoxide hydrolase 2 (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)	scaffold_3_mRNA_5567.1	-	-
GF0028940	1	0	0	Hypothetical protein (1)	regulation of transcription from RNA polymerase II promoter [GO:0006357 biological_process] (1); RNA polymerase II transcription cofactor activity [GO:0001104 molecular_function] (1); mediator complex [GO:0016592 cellular_component] (1)	Mediator complex, subunit Med14 [IPR013947] (1)	scaffold_3_mRNA_5566.1	-	-
GF0028939	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_5552.1	-	-
GF0028938	1	0	0	Poly [ADP-ribose] polymerase (1)	NAD+ ADP-ribosyltransferase activity [GO:0003950 molecular_function] (1); protein ADP-ribosylation [GO:0006471 biological_process] (1)	Poly(ADP-ribose) polymerase, regulatory domain [IPR004102] (1); Poly(ADP-ribose) polymerase, catalytic domain [IPR012317] (1); WGR domain [IPR008893] (1); SAP domain [IPR003034] (1)	scaffold_3_mRNA_5551.1	-	-
GF0028937	1	0	0	Empfindlicher im dunkelroten licht 1 family protein (1)	protein binding [GO:0005515 molecular_function] (1)	F-box domain [IPR001810] (1)	scaffold_3_mRNA_5535.1	-	-
GF0028936	1	0	0	Mutator-like transposase (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); MULE transposase domain [IPR018289] (1); Zinc finger, PMZ-type [IPR006564] (1); Transposase, MuDR, plant [IPR004332] (1); Zinc finger, SWIM-type [IPR007527] (1)	scaffold_3_mRNA_5464.1	-	-
GF0028935	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_5462.1	-	-
GF0028934	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_5455.1	-	-
GF0028933	1	0	0	Sieve element occlusion protein (1)		Sieve element occlusion, N-terminal [IPR027942] (1); Sieve element occlusion, C-terminal [IPR027944] (1)	scaffold_3_mRNA_545.1	-	-
GF0028932	1	0	0	Hypothetical protein (1)	integral component of membrane [GO:0016021 cellular_component] (1); mechanically-gated ion channel activity [GO:0008381 molecular_function] (1)	Piezo family [IPR027272] (1)	scaffold_3_mRNA_5423.1	-	-
GF0028931	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Domain of unknown function DUF4283 [IPR025558] (1); Zinc finger, CCHC-type [IPR001878] (1); Zinc knuckle CX2CX4HX4C [IPR025836] (1)	scaffold_3_mRNA_5413.1	-	-
GF0028930	1	0	0	Non-LTR retroelement reverse transcriptase-like (1)	nucleic acid binding [GO:0003676 molecular_function] (1); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1)	Endonuclease/exonuclease/phosphatase [IPR005135] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H-like domain [IPR012337] (1); Ribonuclease H domain [IPR002156] (1)	scaffold_3_mRNA_5412.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0028929	1	0	0	RNA exonuclease 4 (1)	nucleic acid binding [GO:0003676 molecular_function] (1); metal ion transport [GO:0030001 biological_process] (1); metal ion binding [GO:0046872 molecular_function] (1)	Exonuclease, RNase T/DNA polymerase III [IPR013520] (1); Ribonuclease H-like domain [IPR012337] (1); Heavy metal-associated domain, HMA [IPR006121] (1); Zinc finger C2H2-type [IPR013087] (1)	scaffold_3_mRNA_5404.1	-	-
GF0028928	1	0	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1); Domain of unknown function DUF1985 [IPR015410] (1)	scaffold_3_mRNA_5402.1	-	-
GF0028927	1	0	0	Hypothetical protein (1)		Transposase-associated domain [IPR029480] (1)	scaffold_3_mRNA_5375.1	-	-
GF0028926	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_3_mRNA_5358.1	-	-
GF0028925	1	0	0	Monosacharide transport protein (1)			scaffold_3_mRNA_5353.1	-	-
GF0028924	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_5352.1	-	-
GF0028923	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_5351.1	-	-
GF0028922	1	0	0	Cytochrome P450 71A21 (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)	scaffold_3_mRNA_534.1	-	-
GF0028921	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_533.1	-	-
GF0028920	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_5309.1	-	-
GF0028919	1	0	0	Hypothetical protein (1)	chlorophyll catabolic process [GO:0015996 biological_process] (1); chlorophyllase activity [GO:0047746 molecular_function] (1)	Chlorophyllase [IPR017395] (1)	scaffold_3_mRNA_5306.1	-	-
GF0028918	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_53.1	-	-
GF0028917	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_5293.1	-	-
GF0028916	1	0	0	Retrotransposon protein, putative, Ty3-gypsy subclass (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_3_mRNA_5292.1	-	-
GF0028915	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_5280.1	-	-
GF0028914	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	scaffold_3_mRNA_5272.1	-	-
GF0028913	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_5271.1	-	-
GF0028912	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	Zinc finger, BED-type [IPR003656] (1); Zinc finger C2H2-type [IPR013087] (1)	scaffold_3_mRNA_5247.1	-	-
GF0028911	1	0	0	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)	scaffold_3_mRNA_5229.1	-	-
GF0028910	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_5226.1	-	-
GF0028909	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_5224.1	-	-
GF0028908	1	0	0	Actin-depolymerizing factor 6 (1)	actin binding [GO:0003779 molecular_function] (1); actin filament depolymerization [GO:0030042 biological_process] (1); intracellular [GO:0005622 cellular_component] (1); actin cytoskeleton [GO:0015629 cellular_component] (1)	ADF-H/Gelsolin-like domain [IPR029006] (1); Actin-depolymerising factor homology domain [IPR002108] (1); ADF/Cofilin [IPR017904] (1)	scaffold_3_mRNA_5214.1	-	-
GF0028907	1	0	0	Pollen Ole e I family allergen (1)			scaffold_3_mRNA_5208.1	-	-
GF0028906	1	0	0	Peptidase S24/S26A/S26B/S26C family protein (1)		Peptidase S24/S26A/S26B/S26C [IPR015927] (1)	scaffold_3_mRNA_5203.1	-	-
GF0028905	1	0	0	Hypothetical protein (1)	nucleobase-containing compound metabolic process [GO:0006139 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	YqgF/RNase H-like domain [IPR006641] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_3_mRNA_5202.1	-	-
GF0028904	1	0	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	scaffold_3_mRNA_5188.1	-	-
GF0028903	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_5185.1	-	-
GF0028902	1	0	0	Glutathione gamma-glutamylcysteinyltransferase (1)	response to metal ion [GO:0010038 biological_process] (1); metal ion binding [GO:0046872 molecular_function] (1); glutathione gamma-glutamylcysteinyltransferase activity [GO:0016756 molecular_function] (1); phytochelatin biosynthetic process [GO:0046938 biological_process] (1)	Phytochelatin synthase [IPR007719] (1); Phytochelatin synthase, C-terminal [IPR015407] (1)	scaffold_3_mRNA_5175.1	-	-
GF0028901	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_5169.1	-	-
GF0028900	1	0	0	Mutator-like transposase (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)	scaffold_3_mRNA_5153.1	-	-
GF0028899	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_5119.1	-	-
GF0028898	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_3_mRNA_5114.1	-	-
GF0028897	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_510.1	-	-
GF0028896	1	0	0	S-protein homologue 1 (1)		Plant self-incompatibility S1 [IPR010264] (1)	scaffold_3_mRNA_5098.1	-	-
GF0028895	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_5081.1	-	-
GF0028894	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1); Aspartic peptidase domain [IPR021109] (1)	scaffold_3_mRNA_5076.1	-	-
GF0028893	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_5067.1	-	-
GF0028892	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_5061.1	-	-
GF0028891	1	0	0	60S ribosomal protein L27a (1)	ribosome [GO:0005840 cellular_component] (1); intracellular [GO:0005622 cellular_component] (1); translation [GO:0006412 biological_process] (1); large ribosomal subunit [GO:0015934 cellular_component] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1)	Ribosomal protein L15 [IPR030878] (1); Ribosomal protein L15, conserved site [IPR001196] (1); Ribosomal protein L18e/L15P [IPR021131] (1)	scaffold_3_mRNA_505.1	-	-
GF0028890	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_3_mRNA_5021.1	-	-
GF0028889	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_5020.1	-	-
GF0028888	1	0	0	Hypothetical protein (1)	binding [GO:0005488 molecular_function] (1)	Armadillo-like helical [IPR011989] (1); Armadillo-type fold [IPR016024] (1)	scaffold_3_mRNA_502.1	-	-
GF0028887	1	0	0	Cytochrome P450 82A4 (1)	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); 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)	scaffold_3_mRNA_5018.1	-	-
GF0028886	1	0	0	60S ribosomal protein L36 (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 L36e [IPR000509] (1)	scaffold_3_mRNA_5002.1	-	-
GF0028885	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4989.1	-	-
GF0028884	1	0	0	BTB/POZ and MATH domain-containing protein 4 (1)	protein binding [GO:0005515 molecular_function] (1)	BPM, C-terminal [IPR034090] (1); SKP1/BTB/POZ domain [IPR011333] (1); TRAF-like [IPR008974] (1); MATH/TRAF domain [IPR002083] (1); BTB/POZ domain [IPR000210] (1)	scaffold_3_mRNA_4983.1	-	-
GF0028883	1	0	0	Ubiquitin-conjugating enzyme E2 2 (1)		Ubiquitin-conjugating enzyme, active site [IPR023313] (1); Ubiquitin-conjugating enzyme/RWD-like [IPR016135] (1); Ubiquitin-conjugating enzyme E2 [IPR000608] (1)	scaffold_3_mRNA_4980.1	-	-
GF0028882	1	0	0	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (1)	zinc ion binding [GO:0008270 molecular_function] (1); cellular amino acid biosynthetic process [GO:0008652 biological_process] (1); methionine biosynthetic process [GO:0009086 biological_process] (1); 5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase activity [GO:0003871 molecular_function] (1)	Cobalamin-independent methionine synthase [IPR006276] (1); Cobalamin-independent methionine synthase MetE, N-terminal [IPR013215] (1); Cobalamin-independent methionine synthase MetE, C-terminal/archaeal [IPR002629] (1)	scaffold_3_mRNA_4971.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0028881	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_497.1	-	-
GF0028880	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4948.1	-	-
GF0028879	1	0	0	Photosynthetic NDH subcomplex B 2 (1)	carbohydrate binding [GO:0030246 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1)	Glycoside hydrolase-type carbohydrate-binding [IPR014718] (1); Galactose mutarotase-like domain [IPR011013] (1)	scaffold_3_mRNA_4926.1	-	-
GF0028878	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4918.1	-	-
GF0028877	1	0	0	Hypothetical protein (1)		Transposase, MuDR, plant [IPR004332] (1)	scaffold_3_mRNA_4913.1	-	-
GF0028876	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4912.1	-	-
GF0028875	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4902.1	-	-
GF0028874	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4887.1	-	-
GF0028873	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	scaffold_3_mRNA_4875.1	-	-
GF0028872	1	0	0	Cytochrome P450 83B1 (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)	scaffold_3_mRNA_4873.1	-	-
GF0028871	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4871.1	-	-
GF0028870	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4870.1	-	-
GF0028869	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_3_mRNA_4868.1	-	-
GF0028868	1	0	0	Hypothetical protein (1)	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1)	Cytochrome P450, conserved site [IPR017972] (1); Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450 [IPR001128] (1)	scaffold_3_mRNA_4867.1	-	-
GF0028867	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4865.1	-	-
GF0028866	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_3_mRNA_4864.1	-	-
GF0028865	1	0	0	Germin-like protein subfamily 1 member 7 (1)	nutrient reservoir activity [GO:0045735 molecular_function] (1); manganese ion binding [GO:0030145 molecular_function] (1)	Cupin 1 [IPR006045] (1); Germin, manganese binding site [IPR019780] (1); Germin [IPR001929] (1); RmlC-like jelly roll fold [IPR014710] (1); RmlC-like cupin domain [IPR011051] (1)	scaffold_3_mRNA_4853.1	-	-
GF0028864	1	0	0	Hypothetical protein (1)		RmlC-like jelly roll fold [IPR014710] (1)	scaffold_3_mRNA_4849.1	-	-
GF0028863	1	0	0	Germin-like protein subfamily 1 member 7 (1)	nutrient reservoir activity [GO:0045735 molecular_function] (1); manganese ion binding [GO:0030145 molecular_function] (1)	RmlC-like cupin domain [IPR011051] (1); Cupin 1 [IPR006045] (1); Germin, manganese binding site [IPR019780] (1); Germin [IPR001929] (1); RmlC-like jelly roll fold [IPR014710] (1)	scaffold_3_mRNA_4846.1	-	-
GF0028862	1	0	0	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	scaffold_3_mRNA_4844.1	-	-
GF0028861	1	0	0	Germin-like protein subfamily 1 member 7 (1)	nutrient reservoir activity [GO:0045735 molecular_function] (1); manganese ion binding [GO:0030145 molecular_function] (1)	RmlC-like jelly roll fold [IPR014710] (1); Germin, manganese binding site [IPR019780] (1); Cupin 1 [IPR006045] (1); RmlC-like cupin domain [IPR011051] (1)	scaffold_3_mRNA_4842.1	-	-
GF0028860	1	0	0	LRR receptor-like serine/threonine-protein kinase RCH1 (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); Leucine-rich repeat, typical subtype [IPR003591] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	scaffold_3_mRNA_4837.1	-	-
GF0028859	1	0	0	Plastid transcriptionally active 3 isoform 1 (1)	protein binding [GO:0005515 molecular_function] (1)	Tetratricopeptide-like helical domain [IPR011990] (1); SAP domain [IPR003034] (1)	scaffold_3_mRNA_4835.1	-	-
GF0028858	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_3_mRNA_4829.1	-	-
GF0028857	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4828.1	-	-
GF0028856	1	0	0	GDSL esterase/lipase LTL1 (1)	hydrolase activity, acting on ester bonds [GO:0016788 molecular_function] (1)	SGNH hydrolase-type esterase domain [IPR013830] (1); GDSL lipase/esterase [IPR001087] (1)	scaffold_3_mRNA_4826.1	-	-
GF0028855	1	0	0	Hypothetical protein (1)	catalytic activity [GO:0003824 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	PPM-type phosphatase domain [IPR001932] (1); FHY3/FAR1 family [IPR031052] (1)	scaffold_3_mRNA_4819.1	-	-
GF0028854	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4805.1	-	-
GF0028853	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Aspartic peptidase domain [IPR021109] (1); Retrotransposon gag domain [IPR005162] (1)	scaffold_3_mRNA_4802.1	-	-
GF0028852	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4781.1	-	-
GF0028851	1	0	0	Cytochrome P450 83B1 (1)	iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1)	Cytochrome P450, conserved site [IPR017972] (1); Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450 [IPR001128] (1)	scaffold_3_mRNA_4780.1	-	-
GF0028850	1	0	0	Caffeic acid 3-O-methyltransferase (1)	methyltransferase activity [GO:0008168 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1); O-methyltransferase activity [GO:0008171 molecular_function] (1)	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)	scaffold_3_mRNA_4771.1	-	-
GF0028849	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_3_mRNA_4770.1	-	-
GF0028848	1	0	0	Zinc knuckle family protein (1)			scaffold_3_mRNA_4769.1	-	-
GF0028847	1	0	0	Hypothetical protein (1)	O-methyltransferase activity [GO:0008171 molecular_function] (1); methyltransferase activity [GO:0008168 molecular_function] (1)	S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); O-methyltransferase COMT-type [IPR016461] (1); O-methyltransferase, family 2 [IPR001077] (1)	scaffold_3_mRNA_4767.1	-	-
GF0028846	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4371 [IPR025398] (1)	scaffold_3_mRNA_4763.1	-	-
GF0028845	1	0	0	Phd finger protein, putative (1)			scaffold_3_mRNA_4742.1	-	-
GF0028844	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4734.1	-	-
GF0028843	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4731.1	-	-
GF0028842	1	0	0	Cysteine-rich receptor-like protein kinase 42 (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); Gnk2-homologous domain [IPR002902] (1)	scaffold_3_mRNA_473.1	-	-
GF0028841	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_3_mRNA_4727.1	-	-
GF0028840	1	0	0	Hypothetical protein (1)		Transposase, MuDR, plant [IPR004332] (1)	scaffold_3_mRNA_4724.1	-	-
GF0028839	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4723.1	-	-
GF0028838	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4711.1	-	-
GF0028837	1	0	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); DNA binding [GO:0003677 molecular_function] (1)	NAC domain [IPR003441] (1)	scaffold_3_mRNA_4707.1	-	-
GF0028836	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4701.1	-	-
GF0028835	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4700.1	-	-
GF0028834	1	0	0	Hypothetical protein (1)	RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Ribonuclease H domain [IPR002156] (1)	scaffold_3_mRNA_47.1	-	-
GF0028833	1	0	0	Polynucleotidyl transferase, Ribonuclease H fold, putative (1)			scaffold_3_mRNA_4696.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0028832	1	0	0	Hypothetical protein (1)	catalytic activity [GO:0003824 molecular_function] (1); biotin synthase activity [GO:0004076 molecular_function] (1); iron-sulfur cluster binding [GO:0051536 molecular_function] (1); biotin biosynthetic process [GO:0009102 biological_process] (1)	Biotin synthase [IPR024177] (1); Elongator protein 3/MiaB/NifB [IPR006638] (1); Biotin synthase/Biotin biosynthesis bifunctional protein BioAB [IPR002684] (1); Biotin and thiamin synthesis-associated domain [IPR010722] (1); Aldolase-type TIM barrel [IPR013785] (1); Radical SAM [IPR007197] (1)	scaffold_3_mRNA_4695.1	-	-
GF0028831	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4694.1	-	-
GF0028830	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4693.1	-	-
GF0028829	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4692.1	-	-
GF0028828	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_3_mRNA_4691.1	-	-
GF0028827	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_3_mRNA_4689.1	-	-
GF0028826	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4687.1	-	-
GF0028825	1	0	0	Biotin synthase (1)	biotin biosynthetic process [GO:0009102 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1); biotin synthase activity [GO:0004076 molecular_function] (1); iron-sulfur cluster binding [GO:0051536 molecular_function] (1)	Biotin synthase/Biotin biosynthesis bifunctional protein BioAB [IPR002684] (1); Elongator protein 3/MiaB/NifB [IPR006638] (1); Aldolase-type TIM barrel [IPR013785] (1); Biotin and thiamin synthesis-associated domain [IPR010722] (1); Biotin synthase [IPR024177] (1)	scaffold_3_mRNA_4684.1	-	-
GF0028824	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4683.1	-	-
GF0028823	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4682.1	-	-
GF0028822	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4681.1	-	-
GF0028821	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4679.1	-	-
GF0028820	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4669.1	-	-
GF0028819	1	0	0	Ribonuclease H-like superfamily protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	scaffold_3_mRNA_4663.1	-	-
GF0028818	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4655.1	-	-
GF0028817	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4650.1	-	-
GF0028816	1	0	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	scaffold_3_mRNA_4649.1	-	-
GF0028815	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4647.1	-	-
GF0028814	1	0	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	NAC domain [IPR003441] (1)	scaffold_3_mRNA_4645.1	-	-
GF0028813	1	0	0	NAC domain-containing protein 42 (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); DNA binding [GO:0003677 molecular_function] (1)	NAC domain [IPR003441] (1)	scaffold_3_mRNA_4644.1	-	-
GF0028812	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4639.1	-	-
GF0028811	1	0	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); DNA binding [GO:0003677 molecular_function] (1)	NAC domain [IPR003441] (1)	scaffold_3_mRNA_4638.1	-	-
GF0028810	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4629.1	-	-
GF0028809	1	0	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	Zinc finger, BED-type [IPR003656] (1)	scaffold_3_mRNA_4614.1	-	-
GF0028808	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1); Zinc finger, BED-type [IPR003656] (1); Ribonuclease H-like domain [IPR012337] (1); Viral movement protein [IPR028919] (1); hAT-like transposase, RNase-H fold [IPR025525] (1)	scaffold_3_mRNA_4611.1	-	-
GF0028807	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_3_mRNA_4606.1	-	-
GF0028806	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4601.1	-	-
GF0028805	1	0	0	BED zinc finger,hAT family dimerization domain (1)	DNA binding [GO:0003677 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, BED-type [IPR003656] (1); Ribonuclease H-like domain [IPR012337] (1); hAT-like transposase, RNase-H fold [IPR025525] (1); Zinc finger C2H2-type [IPR013087] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	scaffold_3_mRNA_4599.1	-	-
GF0028804	1	0	0	Hypothetical protein (1)		P-type ATPase, transmembrane domain [IPR023298] (1)	scaffold_3_mRNA_4591.1	-	-
GF0028803	1	0	0	Hypothetical protein (1)	nucleotide binding [GO:0000166 molecular_function] (1)	P-type ATPase, cytoplasmic domain N [IPR023299] (1); HAD-like domain [IPR023214] (1)	scaffold_3_mRNA_4590.1	-	-
GF0028802	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4588.1	-	-
GF0028801	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4587.1	-	-
GF0028800	1	0	0	RNA-directed DNA polymerase ; Ribonuclease H, putative (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	scaffold_3_mRNA_4578.1	-	-
GF0028799	1	0	0	Putative ribonuclease H protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1)	scaffold_3_mRNA_4577.1	-	-
GF0028798	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_3_mRNA_4571.1	-	-
GF0028797	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4570.1	-	-
GF0028796	1	0	0	Monoterpene 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, N-terminal domain [IPR001906] (1); Terpene synthase, metal-binding domain [IPR005630] (1); Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (1)	scaffold_3_mRNA_4569.1	-	-
GF0028795	1	0	0	F-box protein SKIP16 (1)		SMI1/KNR4-like domain [IPR018958] (1); ApaG domain [IPR007474] (1)	scaffold_3_mRNA_4563.1	-	-
GF0028794	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4555.1	-	-
GF0028793	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4535.1	-	-
GF0028792	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4528.1	-	-
GF0028791	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4527.1	-	-
GF0028790	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Reverse transcriptase zinc-binding domain [IPR026960] (1); Domain of unknown function DUF4283 [IPR025558] (1); Ribonuclease H-like domain [IPR012337] (1); Zinc knuckle CX2CX4HX4C [IPR025836] (1); Zinc finger, CCHC-type [IPR001878] (1)	scaffold_3_mRNA_4526.1	-	-
GF0028789	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_3_mRNA_4523.1	-	-
GF0028788	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4520.1	-	-
GF0028787	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_3_mRNA_4518.1	-	-
GF0028786	1	0	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); DNA binding [GO:0003677 molecular_function] (1)	NAC domain [IPR003441] (1)	scaffold_3_mRNA_4517.1	-	-
GF0028785	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4514.1	-	-
GF0028784	1	0	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	Zinc finger, CCHC-type [IPR001878] (1); NAC domain [IPR003441] (1); Zinc finger, BED-type [IPR003656] (1); Zinc finger C2H2-type [IPR013087] (1)	scaffold_3_mRNA_4512.1	-	-
GF0028783	1	0	0	Hypothetical protein (1)	transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); DNA binding [GO:0003677 molecular_function] (1)	DNA-binding domain [IPR016177] (1); AP2/ERF domain [IPR001471] (1)	scaffold_3_mRNA_4510.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0028782	1	0	0	Hypothetical protein (1)	1-deoxy-D-xylulose-5-phosphate reductoisomerase activity [GO:0030604 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); NADPH binding [GO:0070402 molecular_function] (1); isoprenoid biosynthetic process [GO:0008299 biological_process] (1); metal ion binding [GO:0046872 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	1-deoxy-D-xylulose 5-phosphate reductoisomerase, N-terminal [IPR013512] (1); Peroxisome membrane anchor protein Pex14p, N-terminal [IPR006785] (1); 1-deoxy-D-xylulose 5-phosphate reductoisomerase, C-terminal [IPR013644] (1); DXP reductoisomerase C-terminal domain [IPR026877] (1); NAD(P)-binding domain [IPR016040] (1); 1-deoxy-D-xylulose 5-phosphate reductoisomerase [IPR003821] (1)	scaffold_3_mRNA_451.1	-	-
GF0028781	1	0	0	Hypothetical protein (1)		MULE transposase domain [IPR018289] (1); Transposase, MuDR, plant [IPR004332] (1)	scaffold_3_mRNA_4507.1	-	-
GF0028780	1	0	0	Hypothetical protein (1)		Powdery mildew resistance protein, RPW8 domain [IPR008808] (1)	scaffold_3_mRNA_4500.1	-	-
GF0028779	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4498.1	-	-
GF0028778	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4495.1	-	-
GF0028777	1	0	0	Hypothetical protein (1)	RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H domain [IPR002156] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_3_mRNA_4492.1	-	-
GF0028776	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4486.1	-	-
GF0028775	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4480.1	-	-
GF0028774	1	0	0	Hypothetical protein (1)		Non-haem dioxygenase N-terminal domain [IPR026992] (1); Isopenicillin N synthase-like [IPR027443] (1)	scaffold_3_mRNA_4478.1	-	-
GF0028773	1	0	0	Hypothetical protein (1)		Ribosome biogenesis protein BMS1/TSR1, C-terminal [IPR007034] (1)	scaffold_3_mRNA_4477.1	-	-
GF0028772	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4471.1	-	-
GF0028771	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4470.1	-	-
GF0028770	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4468.1	-	-
GF0028769	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	scaffold_3_mRNA_4466.1	-	-
GF0028768	1	0	0	Polynucleotidyl transferase, Ribonuclease H fold (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1)	scaffold_3_mRNA_4461.1	-	-
GF0028767	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4460.1	-	-
GF0028766	1	0	0	Hypothetical protein (1)		MULE transposase domain [IPR018289] (1)	scaffold_3_mRNA_4458.1	-	-
GF0028765	1	0	0	Hypothetical protein (1)		Rab-GTPase-TBC domain [IPR000195] (1)	scaffold_3_mRNA_4457.1	-	-
GF0028764	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4456.1	-	-
GF0028763	1	0	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	scaffold_3_mRNA_4455.1	-	-
GF0028762	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4453.1	-	-
GF0028761	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4448.1	-	-
GF0028760	1	0	0	C6HC-type zinc finger RING/U-box protein (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); protein ubiquitination [GO:0016567 biological_process] (1)	Zinc finger, RING-type, conserved site [IPR017907] (1); E3 ubiquitin ligase RBR family [IPR031127] (1); Zinc finger, RING-type [IPR001841] (1); IBR domain [IPR002867] (1); Zinc finger, RING/FYVE/PHD-type [IPR013083] (1)	scaffold_3_mRNA_4437.1	-	-
GF0028759	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4433.1	-	-
GF0028758	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4430.1	-	-
GF0028757	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4420.1	-	-
GF0028756	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_441.1	-	-
GF0028755	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4397.1	-	-
GF0028754	1	0	0	Probably inactive leucine-rich repeat receptor-like 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-protein kinase, active site [IPR008271] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	scaffold_3_mRNA_4379.1	-	-
GF0028753	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4377.1	-	-
GF0028752	1	0	0	Retrotransposon protein, putative, Ty3-gypsy subclass, expressed (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_3_mRNA_4375.1	-	-
GF0028751	1	0	0	Avr9/Cf-9 rapidly elicited protein (1)		Protein of unknown function DUF668 [IPR007700] (1); Protein of unknown function DUF3475 [IPR021864] (1)	scaffold_3_mRNA_4372.1	-	-
GF0028750	1	0	0	PK (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)	scaffold_3_mRNA_4370.1	-	-
GF0028749	1	0	0	Leucine-rich repeat receptor-like kinase At1g09970 (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)	scaffold_3_mRNA_4369.1	-	-
GF0028748	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4367.1	-	-
GF0028747	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Domain of unknown function DUF4219 [IPR025314] (1)	scaffold_3_mRNA_4366.1	-	-
GF0028746	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_3_mRNA_4364.1	-	-
GF0028745	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4363.1	-	-
GF0028744	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4362.1	-	-
GF0028743	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4361.1	-	-
GF0028742	1	0	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	scaffold_3_mRNA_4359.1	-	-
GF0028741	1	0	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1)	scaffold_3_mRNA_4358.1	-	-
GF0028740	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4357.1	-	-
GF0028739	1	0	0	Hypothetical protein (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase, ATP binding site [IPR017441] (1); Serine/threonine-protein kinase, active site [IPR008271] (1)	scaffold_3_mRNA_4355.1	-	-
GF0028738	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4338.1	-	-
GF0028737	1	0	0	Hypothetical protein (1)		Transposon, En/Spm-like [IPR004242] (1); Domain of unknown function DUF4218 [IPR025452] (1)	scaffold_3_mRNA_4335.1	-	-
GF0028736	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4330.1	-	-
GF0028735	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	VASt domain [IPR031968] (1); C2 domain [IPR000008] (1)	scaffold_3_mRNA_4329.1	-	-
GF0028734	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4325.1	-	-
GF0028733	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4315.1	-	-
GF0028732	1	0	0	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1); Endonuclease/exonuclease/phosphatase [IPR005135] (1)	scaffold_3_mRNA_4301.1	-	-
GF0028731	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4295.1	-	-
GF0028730	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_3_mRNA_4294.1	-	-
GF0028729	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4285.1	-	-
GF0028728	1	0	0	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); ADP binding [GO:0043531 molecular_function] (1); GPI-anchor transamidase complex [GO:0042765 cellular_component] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1); GPI-anchor transamidase [IPR028361] (1); Peptidase C13, legumain [IPR001096] (1)	scaffold_3_mRNA_4283.1	-	-
GF0028727	1	0	0	Hypothetical protein (1)		Arabidopsis retrotransposon Orf1 [IPR004312] (1)	scaffold_3_mRNA_4282.1	-	-
GF0028726	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4281.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0028725	1	0	0	Hypothetical protein (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Protein kinase-like domain [IPR011009] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1)	scaffold_3_mRNA_4280.1	-	-
GF0028724	1	0	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_3_mRNA_4279.1	-	-
GF0028723	1	0	0	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)	scaffold_3_mRNA_4275.1	-	-
GF0028722	1	0	0	LRR receptor-like kinase (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)	Malectin [IPR021720] (1); Protein kinase, ATP binding site [IPR017441] (1); Leucine-rich repeat [IPR001611] (1); Protein kinase domain [IPR000719] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Protein kinase-like domain [IPR011009] (1)	scaffold_3_mRNA_4274.1	-	-
GF0028721	1	0	0	Hypothetical protein (1)	GPI-anchor transamidase activity [GO:0003923 molecular_function] (1); GPI-anchor transamidase complex [GO:0042765 cellular_component] (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 [IPR028361] (1); Peptidase C13, legumain [IPR001096] (1)	scaffold_3_mRNA_4273.1	-	-
GF0028720	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4266.1	-	-
GF0028719	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4265.1	-	-
GF0028718	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4262.1	-	-
GF0028717	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4261.1	-	-
GF0028716	1	0	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_3_mRNA_4256.1	-	-
GF0028715	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4253.1	-	-
GF0028714	1	0	0	Hypothetical protein (1)	protein kinase activity [GO:0004672 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1); peptidase activity [GO:0008233 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); attachment of GPI anchor to protein [GO:0016255 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1); GPI-anchor transamidase activity [GO:0003923 molecular_function] (1); GPI-anchor transamidase complex [GO:0042765 cellular_component] (1)	GPI-anchor transamidase [IPR028361] (1); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); Peptidase C13, legumain [IPR001096] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1)	scaffold_3_mRNA_4252.1	-	-
GF0028713	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4251.1	-	-
GF0028712	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4250.1	-	-
GF0028711	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4249.1	-	-
GF0028710	1	0	0	Pentatricopeptide repeat-containing family protein (1)	protein binding [GO:0005515 molecular_function] (1)	Pentatricopeptide repeat [IPR002885] (1); Tetratricopeptide-like helical domain [IPR011990] (1)	scaffold_3_mRNA_4239.1	-	-
GF0028709	1	0	0	Phospholipase, patatin family (1)	metabolic process [GO:0008152 biological_process] (1)	Acyl transferase/acyl hydrolase/lysophospholipase [IPR016035] (1)	scaffold_3_mRNA_4237.1	-	-
GF0028708	1	0	0	Cysteine-rich RLK (RECEPTOR-like protein kinase) 8 (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	scaffold_3_mRNA_4236.1	-	-
GF0028707	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4233.1	-	-
GF0028706	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4231.1	-	-
GF0028705	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4230.1	-	-
GF0028704	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4228.1	-	-
GF0028703	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_3_mRNA_4227.1	-	-
GF0028702	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4213.1	-	-
GF0028701	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_3_mRNA_4212.1	-	-
GF0028700	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4210.1	-	-
GF0028699	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4207.1	-	-
GF0028698	1	0	0	Zinc knuckle family protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Domain of unknown function DUF4219 [IPR025314] (1); Zinc finger, CCHC-type [IPR001878] (1)	scaffold_3_mRNA_4205.1	-	-
GF0028697	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4204.1	-	-
GF0028696	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4203.1	-	-
GF0028695	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	RNA recognition motif domain [IPR000504] (1)	scaffold_3_mRNA_4202.1	-	-
GF0028694	1	0	0	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	scaffold_3_mRNA_420.1	-	-
GF0028693	1	0	0	Hypothetical protein (1)	methyltransferase activity [GO:0008168 molecular_function] (1)	Putative S-adenosyl-L-methionine-dependent methyltransferase [IPR004159] (1)	scaffold_3_mRNA_4199.1	-	-
GF0028692	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	LOG family [IPR031100] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_3_mRNA_4192.1	-	-
GF0028691	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4191.1	-	-
GF0028690	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4190.1	-	-
GF0028689	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4189.1	-	-
GF0028688	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4180.1	-	-
GF0028687	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Aspartic peptidase domain [IPR021109] (1); Retrotransposon gag domain [IPR005162] (1); Retroviral aspartyl protease [IPR013242] (1); Zinc finger, CCHC-type [IPR001878] (1)	scaffold_3_mRNA_4178.1	-	-
GF0028686	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4169.1	-	-
GF0028685	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4161.1	-	-
GF0028684	1	0	0	Putative retroelement pol polyprotein (1)			scaffold_3_mRNA_4160.1	-	-
GF0028683	1	0	0	Hypothetical leucine rich repeat protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1)	scaffold_3_mRNA_4159.1	-	-
GF0028682	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4156.1	-	-
GF0028681	1	0	0	Hypothetical protein (1)	nucleus [GO:0005634 cellular_component] (1); transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (1); root development [GO:0048364 biological_process] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	Transcription factor LHW [IPR033260] (1)	scaffold_3_mRNA_4152.1	-	-
GF0028680	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_3_mRNA_4151.1	-	-
GF0028679	1	0	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); regulation of microtubule-based process [GO:0032886 biological_process] (1); microtubule binding [GO:0008017 molecular_function] (1); microtubule-based movement [GO:0007018 biological_process] (1); microtubule motor activity [GO:0003777 molecular_function] (1); root development [GO:0048364 biological_process] (1)	Armadillo repeat-containing kinesin-like protein 1/2 [IPR033291] (1); Kinesin motor domain [IPR001752] (1)	scaffold_3_mRNA_4147.1	-	-
GF0028678	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4146.1	-	-
GF0028677	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4145.1	-	-
GF0028676	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_3_mRNA_4144.1	-	-
GF0028675	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4142.1	-	-
GF0028674	1	0	0	AT1G67060 protein (1)			scaffold_3_mRNA_4125.1	-	-
GF0028673	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4122.1	-	-
GF0028672	1	0	0	Hypothetical protein (1)		MULE transposase domain [IPR018289] (1); Transposase, MuDR, plant [IPR004332] (1)	scaffold_3_mRNA_4121.1	-	-
GF0028671	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_3_mRNA_4120.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0028670	1	0	0	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); monooxygenase activity [GO:0004497 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1)	Cytochrome P450, E-class, group IV [IPR002403] (1); Cytochrome P450 [IPR001128] (1); Cytochrome P450, conserved site [IPR017972] (1)	scaffold_3_mRNA_4117.1	-	-
GF0028669	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4116.1	-	-
GF0028668	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4115.1	-	-
GF0028667	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4114.1	-	-
GF0028666	1	0	0	Cytochrome P450 71A1 (1)	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1)	Cytochrome P450 [IPR001128] (1); Cytochrome P450, conserved site [IPR017972] (1); Cytochrome P450, E-class, group I [IPR002401] (1)	scaffold_3_mRNA_4112.1	-	-
GF0028665	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4111.1	-	-
GF0028664	1	0	0	Cytochrome P450 (1)	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); 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)	scaffold_3_mRNA_4110.1	-	-
GF0028663	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4109.1	-	-
GF0028662	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4107.1	-	-
GF0028661	1	0	0	Hypothetical protein (1)	iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Cytochrome P450 [IPR001128] (1); Cytochrome P450, E-class, group I [IPR002401] (1)	scaffold_3_mRNA_4106.1	-	-
GF0028660	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4105.1	-	-
GF0028659	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4104.1	-	-
GF0028658	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4103.1	-	-
GF0028657	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4094.1	-	-
GF0028656	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4093.1	-	-
GF0028655	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4080.1	-	-
GF0028654	1	0	0	Kinase superfamily protein isoform 2 (1)		Wall-associated receptor kinase, C-terminal [IPR032872] (1)	scaffold_3_mRNA_4079.1	-	-
GF0028653	1	0	0	Protein FAR1-RELATED SEQUENCE 6 (1)	magnesium ion binding [GO:0000287 molecular_function] (1); lyase activity [GO:0016829 molecular_function] (1); terpene synthase activity [GO:0010333 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1); FAR1 DNA binding domain [IPR004330] (1); Isoprenoid synthase domain [IPR008949] (1); Zinc finger, SWIM-type [IPR007527] (1); Zinc finger, PMZ-type [IPR006564] (1); MULE transposase domain [IPR018289] (1); Terpene synthase, metal-binding domain [IPR005630] (1)	scaffold_3_mRNA_4077.1	-	-
GF0028652	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4064.1	-	-
GF0028651	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4057.1	-	-
GF0028650	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4056.1	-	-
GF0028649	1	0	0	Class I glutamine amidotransferase-like superfamily protein isoform 2 (1)		Protein DJ-1 [IPR006287] (1); Class I glutamine amidotransferase-like [IPR029062] (1); DJ-1/PfpI [IPR002818] (1)	scaffold_3_mRNA_4052.1	-	-
GF0028648	1	0	0	Hypothetical protein (1)		Class I glutamine amidotransferase-like [IPR029062] (1); Ribosomal protein L9, N-terminal [IPR020070] (1); Ribosomal protein L9, C-terminal [IPR020069] (1); Protein DJ-1 [IPR006287] (1); DJ-1/PfpI [IPR002818] (1)	scaffold_3_mRNA_4044.1	-	-
GF0028647	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4043.1	-	-
GF0028646	1	0	0	Retrotransposon protein, putative, Ty3-gypsy subclass (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Aspartic peptidase domain [IPR021109] (1)	scaffold_3_mRNA_4042.1	-	-
GF0028645	1	0	0	4-methyl-5(B-hydroxyethyl)-thiazole monophosphate biosynthesis (1)		Class I glutamine amidotransferase-like [IPR029062] (1); Protein DJ-1 [IPR006287] (1); DJ-1/PfpI [IPR002818] (1)	scaffold_3_mRNA_4037.1	-	-
GF0028644	1	0	0	4-methyl-5(B-hydroxyethyl)-thiazole monophosphate biosynthesis (1)		DJ-1/PfpI [IPR002818] (1); Class I glutamine amidotransferase-like [IPR029062] (1)	scaffold_3_mRNA_4034.1	-	-
GF0028643	1	0	0	4-methyl-5(B-hydroxyethyl)-thiazole monophosphate biosynthesis (1)		DJ-1/PfpI [IPR002818] (1); Class I glutamine amidotransferase-like [IPR029062] (1)	scaffold_3_mRNA_4032.1	-	-
GF0028642	1	0	0	4-methyl-5(B-hydroxyethyl)-thiazole monophosphate biosynthesis (1)		DJ-1/PfpI [IPR002818] (1); Protein DJ-1 [IPR006287] (1); Class I glutamine amidotransferase-like [IPR029062] (1)	scaffold_3_mRNA_4030.1	-	-
GF0028641	1	0	0	Class I glutamine amidotransferase-like superfamily protein isoform 1 (1)		DJ-1/PfpI [IPR002818] (1); Class I glutamine amidotransferase-like [IPR029062] (1); Protein DJ-1 [IPR006287] (1)	scaffold_3_mRNA_4026.1	-	-
GF0028640	1	0	0	Hypothetical protein (1)		Protein kinase-like domain [IPR011009] (1)	scaffold_3_mRNA_4025.1	-	-
GF0028639	1	0	0	LRR receptor-like kinase family protein (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase, ATP binding site [IPR017441] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Leucine-rich repeat [IPR001611] (1)	scaffold_3_mRNA_4024.1	-	-
GF0028638	1	0	0	LRR receptor-like kinase family protein (1)	protein binding [GO:0005515 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase, ATP binding site [IPR017441] (1); Leucine-rich repeat [IPR001611] (1); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1)	scaffold_3_mRNA_4022.1	-	-
GF0028637	1	0	0	Class I glutamine amidotransferase superfamily protein (1)		DJ-1/PfpI [IPR002818] (1); Protein DJ-1 [IPR006287] (1); Class I glutamine amidotransferase-like [IPR029062] (1)	scaffold_3_mRNA_4019.1	-	-
GF0028636	1	0	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, BED-type [IPR003656] (1); Zinc finger C2H2-type [IPR013087] (1)	scaffold_3_mRNA_4018.1	-	-
GF0028635	1	0	0	Hypothetical protein (1)	binding [GO:0005488 molecular_function] (1)	Armadillo-like helical [IPR011989] (1); Condensin complex subunit 1, C-terminal [IPR032682] (1); Armadillo-type fold [IPR016024] (1)	scaffold_3_mRNA_4015.1	-	-
GF0028634	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4014.1	-	-
GF0028633	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4013.1	-	-
GF0028632	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4011.1	-	-
GF0028631	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_401.1	-	-
GF0028630	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_4005.1	-	-
GF0028629	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Viral movement protein [IPR028919] (1); Zinc finger, CCHC-type [IPR001878] (1)	scaffold_3_mRNA_4001.1	-	-
GF0028628	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1); sulfotransferase activity [GO:0008146 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Sulfotransferase domain [IPR000863] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_3_mRNA_3998.1	-	-
GF0028627	1	0	0	Mads box protein, putative (1)	protein dimerization activity [GO:0046983 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	Transcription factor, MADS-box [IPR002100] (1)	scaffold_3_mRNA_3995.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0028626	1	0	0	MurA transferase2 (1)	catalytic activity [GO:0003824 molecular_function] (1); UDP-N-acetylglucosamine 1-carboxyvinyltransferase activity [GO:0008760 molecular_function] (1); UDP-N-acetylgalactosamine biosynthetic process [GO:0019277 biological_process] (1); transferase activity, transferring alkyl or aryl (other than methyl) groups [GO:0016765 molecular_function] (1)	Enolpyruvate transferase domain [IPR001986] (1); UDP-N-acetylglucosamine 1-carboxyvinyltransferase [IPR005750] (1); RNA 3'-terminal phosphate cyclase/enolpyruvate transferase, alpha/beta [IPR013792] (1)	scaffold_3_mRNA_3994.1	-	-
GF0028625	1	0	0	MADS-box protein MADS2 (1)	protein dimerization activity [GO:0046983 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	Transcription factor, MADS-box [IPR002100] (1)	scaffold_3_mRNA_3993.1	-	-
GF0028624	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_3_mRNA_3988.1	-	-
GF0028623	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3983.1	-	-
GF0028622	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3981.1	-	-
GF0028621	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3977.1	-	-
GF0028620	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3976.1	-	-
GF0028619	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3975.1	-	-
GF0028618	1	0	0	Hypothetical protein (1)		Myb/SANT-like domain [IPR024752] (1)	scaffold_3_mRNA_3972.1	-	-
GF0028617	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3967.1	-	-
GF0028616	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3940.1	-	-
GF0028615	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_3_mRNA_3938.1	-	-
GF0028614	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3926.1	-	-
GF0028613	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3925.1	-	-
GF0028612	1	0	0	Ankyrin repeat protein (1)		Ankyrin repeat-containing domain [IPR020683] (1); PGG domain [IPR026961] (1)	scaffold_3_mRNA_3924.1	-	-
GF0028611	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3920.1	-	-
GF0028610	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3919.1	-	-
GF0028609	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, SWIM-type [IPR007527] (1); Zinc finger, PMZ-type [IPR006564] (1)	scaffold_3_mRNA_3918.1	-	-
GF0028608	1	0	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); protein binding [GO:0005515 molecular_function] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1); Tetratricopeptide-like helical domain [IPR011990] (1); Tetratricopeptide repeat-containing domain [IPR013026] (1)	scaffold_3_mRNA_3917.1	-	-
GF0028607	1	0	0	Putative RNA-directed DNA polymerase (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Domain of unknown function DUF4283 [IPR025558] (1); Ribonuclease H-like domain [IPR012337] (1); Reverse transcriptase domain [IPR000477] (1); Endonuclease/exonuclease/phosphatase [IPR005135] (1)	scaffold_3_mRNA_3916.1	-	-
GF0028606	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat-containing domain [IPR020683] (1); Ankyrin repeat [IPR002110] (1)	scaffold_3_mRNA_3914.1	-	-
GF0028605	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat [IPR002110] (1); Ankyrin repeat-containing domain [IPR020683] (1)	scaffold_3_mRNA_3910.1	-	-
GF0028604	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Tetratricopeptide-like helical domain [IPR011990] (1)	scaffold_3_mRNA_3907.1	-	-
GF0028603	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat-containing domain [IPR020683] (1); Ankyrin repeat [IPR002110] (1)	scaffold_3_mRNA_3906.1	-	-
GF0028602	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3905.1	-	-
GF0028601	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Tetratricopeptide-like helical domain [IPR011990] (1); Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	scaffold_3_mRNA_3903.1	-	-
GF0028600	1	0	0	Cell division cycle protein 16 putative (1)	protein binding [GO:0005515 molecular_function] (1)	Tetratricopeptide repeat [IPR019734] (1); Tetratricopeptide repeat-containing domain [IPR013026] (1); Tetratricopeptide-like helical domain [IPR011990] (1); Tetratricopeptide repeat 1 [IPR001440] (1)	scaffold_3_mRNA_3901.1	-	-
GF0028599	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1)	Ribonuclease H domain [IPR002156] (1); Ribonuclease H-like domain [IPR012337] (1); Domain of unknown function DUF4283 [IPR025558] (1)	scaffold_3_mRNA_3897.1	-	-
GF0028598	1	0	0	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); Germin [IPR001929] (1); Germin, manganese binding site [IPR019780] (1); Cupin 1 [IPR006045] (1); Pentatricopeptide repeat [IPR002885] (1); RmlC-like cupin domain [IPR011051] (1)	scaffold_3_mRNA_3896.1	-	-
GF0028597	1	0	0	Hypothetical protein (1)		RmlC-like jelly roll fold [IPR014710] (1); RmlC-like cupin domain [IPR011051] (1)	scaffold_3_mRNA_3891.1	-	-
GF0028596	1	0	0	Oxalate oxidase (1)		RmlC-like jelly roll fold [IPR014710] (1); RmlC-like cupin domain [IPR011051] (1)	scaffold_3_mRNA_3889.1	-	-
GF0028595	1	0	0	Germin-like protein subfamily 1 member 7 (1)	manganese ion binding [GO:0030145 molecular_function] (1); nutrient reservoir activity [GO:0045735 molecular_function] (1)	RmlC-like cupin domain [IPR011051] (1); Germin [IPR001929] (1); RmlC-like jelly roll fold [IPR014710] (1); Cupin 1 [IPR006045] (1); Germin, manganese binding site [IPR019780] (1)	scaffold_3_mRNA_3885.1	-	-
GF0028594	1	0	0	Ribonuclease H protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	scaffold_3_mRNA_3884.1	-	-
GF0028593	1	0	0	Germin-like protein subfamily 1 member 7 (1)	manganese ion binding [GO:0030145 molecular_function] (1); nutrient reservoir activity [GO:0045735 molecular_function] (1)	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)	scaffold_3_mRNA_3880.1	-	-
GF0028592	1	0	0	RNA-dependent RNA polymerase 6 (1)	RNA-directed 5'-3' RNA polymerase activity [GO:0003968 molecular_function] (1)	RNA-dependent RNA polymerase, eukaryotic-type [IPR007855] (1); Protein kinase-like domain [IPR011009] (1)	scaffold_3_mRNA_3871.1	-	-
GF0028591	1	0	0	Hypothetical protein (1)	RNA-directed 5'-3' RNA polymerase activity [GO:0003968 molecular_function] (1)	RNA-dependent RNA polymerase, eukaryotic-type [IPR007855] (1); Arabidopsis retrotransposon Orf1 [IPR004312] (1)	scaffold_3_mRNA_3870.1	-	-
GF0028590	1	0	0	Hypothetical protein (1)	lipid metabolic process [GO:0006629 biological_process] (1); phosphorelay signal transduction system [GO:0000160 biological_process] (1)	Formin, FH2 domain [IPR015425] (1); Alpha/Beta hydrolase fold [IPR029058] (1); Signal transduction response regulator, receiver domain [IPR001789] (1); CheY-like superfamily [IPR011006] (1); Fungal lipase-like domain [IPR002921] (1)	scaffold_3_mRNA_387.1	-	-
GF0028589	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3869.1	-	-
GF0028588	1	0	0	Hypothetical protein (1)	sigma factor antagonist activity [GO:0016989 molecular_function] (1)	Anti sigma-E protein RseA, N-terminal [IPR005572] (1)	scaffold_3_mRNA_3863.1	-	-
GF0028587	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3862.1	-	-
GF0028586	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_3_mRNA_3860.1	-	-
GF0028585	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3859.1	-	-
GF0028584	1	0	0	Trypsin inhibitor (1)	endopeptidase inhibitor activity [GO:0004866 molecular_function] (1)	Proteinase inhibitor I3, Kunitz legume [IPR002160] (1); Kunitz inhibitor ST1-like [IPR011065] (1)	scaffold_3_mRNA_3841.1	-	-
GF0028583	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3840.1	-	-
GF0028582	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_384.1	-	-
GF0028581	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3837.1	-	-
GF0028580	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_3_mRNA_3836.1	-	-
GF0028579	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3835.1	-	-
GF0028578	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3831.1	-	-
GF0028577	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3830.1	-	-
GF0028576	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3829.1	-	-
GF0028575	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3828.1	-	-
GF0028574	1	0	0	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)	scaffold_3_mRNA_3825.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0028573	1	0	0	Receptor like protein 21 (1)	nucleic acid binding [GO:0003676 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); HAT, C-terminal dimerisation domain [IPR008906] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, cysteine-containing subtype [IPR006553] (1); Leucine rich repeat 4 [IPR025875] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_3_mRNA_3823.1	-	-
GF0028572	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3821.1	-	-
GF0028571	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3819.1	-	-
GF0028570	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3818.1	-	-
GF0028569	1	0	0	Uncharacterized mitochondrial protein AtMg00310 (1)			scaffold_3_mRNA_3816.1	-	-
GF0028568	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3814.1	-	-
GF0028567	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_3_mRNA_3813.1	-	-
GF0028566	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3811.1	-	-
GF0028565	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_3_mRNA_3810.1	-	-
GF0028564	1	0	0	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)	scaffold_3_mRNA_3806.1	-	-
GF0028563	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3805.1	-	-
GF0028562	1	0	0	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)	scaffold_3_mRNA_3804.1	-	-
GF0028561	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3801.1	-	-
GF0028560	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3799.1	-	-
GF0028559	1	0	0	UPF0481 protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	scaffold_3_mRNA_3796.1	-	-
GF0028558	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3791.1	-	-
GF0028557	1	0	0	Type I proteinase inhibitor-like protein (1)	serine-type endopeptidase inhibitor activity [GO:0004867 molecular_function] (1); response to wounding [GO:0009611 biological_process] (1)	Proteinase inhibitor I13, potato inhibitor I [IPR000864] (1)	scaffold_3_mRNA_3790.1	-	-
GF0028556	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_3_mRNA_3788.1	-	-
GF0028555	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3787.1	-	-
GF0028554	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3786.1	-	-
GF0028553	1	0	0	Putative muDR family transposase-like (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, SWIM-type [IPR007527] (1); MULE transposase domain [IPR018289] (1); Zinc finger, PMZ-type [IPR006564] (1)	scaffold_3_mRNA_3783.1	-	-
GF0028552	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3782.1	-	-
GF0028551	1	0	0	LRR receptor-like kinase family protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein binding [GO:0005515 molecular_function] (1)	Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); Protein kinase, ATP binding site [IPR017441] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Leucine-rich repeat [IPR001611] (1); Protein kinase domain [IPR000719] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Protein kinase-like domain [IPR011009] (1)	scaffold_3_mRNA_3775.1	-	-
GF0028550	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	RNA recognition motif domain [IPR000504] (1)	scaffold_3_mRNA_3769.1	-	-
GF0028549	1	0	0	LRR receptor-like serine/threonine-protein kinase GSO1 (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_3_mRNA_3768.1	-	-
GF0028548	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3763.1	-	-
GF0028547	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3755.1	-	-
GF0028546	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3753.1	-	-
GF0028545	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3750.1	-	-
GF0028544	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_3_mRNA_3749.1	-	-
GF0028543	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3741.1	-	-
GF0028542	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3739.1	-	-
GF0028541	1	0	0	Hypothetical protein (1)		GAG-pre-integrase domain [IPR025724] (1)	scaffold_3_mRNA_3738.1	-	-
GF0028540	1	0	0	LRR receptor-like 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); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Protein kinase-like domain [IPR011009] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); Malectin [IPR021720] (1); Serine/threonine-protein kinase, active site [IPR008271] (1)	scaffold_3_mRNA_3736.1	-	-
GF0028539	1	0	0	Hypothetical protein (1)		Transposon, En/Spm-like [IPR004242] (1)	scaffold_3_mRNA_3735.1	-	-
GF0028538	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3734.1	-	-
GF0028537	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3730.1	-	-
GF0028536	1	0	0	Serine/threonine-protein phosphatase PP2A-1 catalytic subunit (1)	hydrolase activity [GO:0016787 molecular_function] (1)	Serine/threonine-specific protein phosphatase/bis(5-nucleosyl)-tetraphosphatase [IPR006186] (1); Calcineurin-like phosphoesterase domain, ApaH type [IPR004843] (1); Metallo-dependent phosphatase-like [IPR029052] (1)	scaffold_3_mRNA_373.1	-	-
GF0028535	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3729.1	-	-
GF0028534	1	0	0	Retrotransposon gag protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_3_mRNA_3728.1	-	-
GF0028533	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_3_mRNA_3727.1	-	-
GF0028532	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3725.1	-	-
GF0028531	1	0	0	LRR receptor-like kinase (1)	ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Malectin [IPR021720] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase-like domain [IPR011009] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Protein kinase domain [IPR000719] (1)	scaffold_3_mRNA_3724.1	-	-
GF0028530	1	0	0	LRR receptor-like kinase (1)	ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Malectin [IPR021720] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase domain [IPR000719] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Protein kinase-like domain [IPR011009] (1)	scaffold_3_mRNA_3721.1	-	-
GF0028529	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3707.1	-	-
GF0028528	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3706.1	-	-
GF0028527	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3705.1	-	-
GF0028526	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_3_mRNA_3703.1	-	-
GF0028525	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3699.1	-	-
GF0028524	1	0	0	Hypothetical protein (1)		Isopenicillin N synthase-like [IPR027443] (1)	scaffold_3_mRNA_3691.1	-	-
GF0028523	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3688.1	-	-
GF0028522	1	0	0	2OG-Fe(II) oxygenase family oxidoreductase (1)		Isopenicillin N synthase-like [IPR027443] (1); Non-haem dioxygenase N-terminal domain [IPR026992] (1)	scaffold_3_mRNA_3687.1	-	-
GF0028521	1	0	0	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); Non-haem dioxygenase N-terminal domain [IPR026992] (1); Isopenicillin N synthase-like [IPR027443] (1)	scaffold_3_mRNA_3684.1	-	-
GF0028520	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3682.1	-	-
GF0028519	1	0	0	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)	scaffold_3_mRNA_3680.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0028518	1	0	0	Senescence-related gene 1 (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Non-haem dioxygenase N-terminal domain [IPR026992] (1); Isopenicillin N synthase-like [IPR027443] (1); Oxoglutarate/iron-dependent dioxygenase [IPR005123] (1)	scaffold_3_mRNA_3679.1	-	-
GF0028517	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3671.1	-	-
GF0028516	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3664.1	-	-
GF0028515	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3659.1	-	-
GF0028514	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3656.1	-	-
GF0028513	1	0	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	scaffold_3_mRNA_3655.1	-	-
GF0028512	1	0	0	LRR receptor-like kinase (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)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1); Leucine-rich repeat [IPR001611] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); Malectin [IPR021720] (1)	scaffold_3_mRNA_3644.1	-	-
GF0028511	1	0	0	Hypothetical protein (1)	RNA-directed 5'-3' RNA polymerase activity [GO:0003968 molecular_function] (1)	RNA-dependent RNA polymerase, eukaryotic-type [IPR007855] (1)	scaffold_3_mRNA_3642.1	-	-
GF0028510	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_3_mRNA_3638.1	-	-
GF0028509	1	0	0	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)	scaffold_3_mRNA_3637.1	-	-
GF0028508	1	0	0	Phosphate import ATP-binding PstB 2 (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_3_mRNA_3634.1	-	-
GF0028507	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3630.1	-	-
GF0028506	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_3_mRNA_3628.1	-	-
GF0028505	1	0	0	Secologanin synthase (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, conserved site [IPR017972] (1); Cytochrome P450, E-class, group IV [IPR002403] (1); Cytochrome P450 [IPR001128] (1)	scaffold_3_mRNA_3627.1	-	-
GF0028504	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3625.1	-	-
GF0028503	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_3_mRNA_3622.1	-	-
GF0028502	1	0	0	Secologanin synthase (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); Cytochrome P450, E-class, group I [IPR002401] (1)	scaffold_3_mRNA_3621.1	-	-
GF0028501	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3620.1	-	-
GF0028500	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3619.1	-	-
GF0028499	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3618.1	-	-
GF0028498	1	0	0	Cytochrome P450 family 72 protein, putative (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)	scaffold_3_mRNA_3616.1	-	-
GF0028497	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3610.1	-	-
GF0028496	1	0	0	Oxalate oxidase 2 (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)	scaffold_3_mRNA_361.1	-	-
GF0028495	1	0	0	Zinc finger MYM-type protein 1 (1)			scaffold_3_mRNA_3607.1	-	-
GF0028494	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4371 [IPR025398] (1)	scaffold_3_mRNA_3606.1	-	-
GF0028493	1	0	0	Cysteine-rich RLK (RECEPTOR-like protein kinase) 8 (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	scaffold_3_mRNA_3600.1	-	-
GF0028492	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_360.1	-	-
GF0028491	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_3_mRNA_3599.1	-	-
GF0028490	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3597.1	-	-
GF0028489	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3596.1	-	-
GF0028488	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_3_mRNA_3595.1	-	-
GF0028487	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_3_mRNA_3594.1	-	-
GF0028486	1	0	0	RNA polymerase II C-terminal domain phosphatase-like 4 (1)		HAD-like domain [IPR023214] (1); BRCT domain [IPR001357] (1); FCP1 homology domain [IPR004274] (1)	scaffold_3_mRNA_359.1	-	-
GF0028485	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3586.1	-	-
GF0028484	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Domain of unknown function DUF4219 [IPR025314] (1); Zinc finger, CCHC-type [IPR001878] (1)	scaffold_3_mRNA_3585.1	-	-
GF0028483	1	0	0	Verticillium wilt disease resistance 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)	scaffold_3_mRNA_3584.1	-	-
GF0028482	1	0	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1); Aspartic peptidase domain [IPR021109] (1)	scaffold_3_mRNA_3582.1	-	-
GF0028481	1	0	0	Monosacharide transport protein (1)			scaffold_3_mRNA_3581.1	-	-
GF0028480	1	0	0	LRR receptor-like kinase (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)	scaffold_3_mRNA_3580.1	-	-
GF0028479	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3579.1	-	-
GF0028478	1	0	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_3_mRNA_3577.1	-	-
GF0028477	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_3_mRNA_3576.1	-	-
GF0028476	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3573.1	-	-
GF0028475	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1); Retrotransposon gag domain [IPR005162] (1)	scaffold_3_mRNA_3569.1	-	-
GF0028474	1	0	0	Putative methyltransferase PMT20 (1)	methyltransferase activity [GO:0008168 molecular_function] (1)	S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); Putative S-adenosyl-L-methionine-dependent methyltransferase [IPR004159] (1)	scaffold_3_mRNA_3567.1	-	-
GF0028473	1	0	0	Verticillium wilt disease resistance protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	scaffold_3_mRNA_3565.1	-	-
GF0028472	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_3_mRNA_3564.1	-	-
GF0028471	1	0	0	Hypothetical protein (1)		SOUL haem-binding protein [IPR006917] (1)	scaffold_3_mRNA_3561.1	-	-
GF0028470	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3558.1	-	-
GF0028469	1	0	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	MULE transposase domain [IPR018289] (1); FHY3/FAR1 family [IPR031052] (1)	scaffold_3_mRNA_3552.1	-	-
GF0028468	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3549.1	-	-
GF0028467	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3543.1	-	-
GF0028466	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3527.1	-	-
GF0028465	1	0	0	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)	scaffold_3_mRNA_3523.1	-	-
GF0028464	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3515.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0028463	1	0	0	Ac-like transposase (1)	nucleic acid binding [GO:0003676 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); hAT-like transposase, RNase-H fold [IPR025525] (1)	scaffold_3_mRNA_3514.1	-	-
GF0028462	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_3_mRNA_3509.1	-	-
GF0028461	1	0	0	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)	scaffold_3_mRNA_3505.1	-	-
GF0028460	1	0	0	Glutathione S-transferase 3 (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)	scaffold_3_mRNA_3504.1	-	-
GF0028459	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_3_mRNA_3503.1	-	-
GF0028458	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3496.1	-	-
GF0028457	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3495.1	-	-
GF0028456	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3493.1	-	-
GF0028455	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3489.1	-	-
GF0028454	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_3_mRNA_3487.1	-	-
GF0028453	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_3_mRNA_3481.1	-	-
GF0028452	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3480.1	-	-
GF0028451	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3479.1	-	-
GF0028450	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3477.1	-	-
GF0028449	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3475.1	-	-
GF0028448	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_3_mRNA_3474.1	-	-
GF0028447	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3469.1	-	-
GF0028446	1	0	0	TMV resistance protein N (1)	signal transduction [GO:0007165 biological_process] (1); ADP binding [GO:0043531 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1); Leucine-rich repeat 3 [IPR011713] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Leucine-rich repeat [IPR001611] (1); NB-ARC [IPR002182] (1)	scaffold_3_mRNA_3468.1	-	-
GF0028445	1	0	0	Hypothetical 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)	scaffold_3_mRNA_3467.1	-	-
GF0028444	1	0	0	Hypothetical protein (1)	signal transduction [GO:0007165 biological_process] (1); ADP binding [GO:0043531 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1)	scaffold_3_mRNA_3466.1	-	-
GF0028443	1	0	0	TMV resistance protein N (1)	ADP binding [GO:0043531 molecular_function] (1); signal transduction [GO:0007165 biological_process] (1); protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1); Leucine-rich repeat 3 [IPR011713] (1)	scaffold_3_mRNA_3461.1	-	-
GF0028442	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3460.1	-	-
GF0028441	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3455.1	-	-
GF0028440	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3448.1	-	-
GF0028439	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3446.1	-	-
GF0028438	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3439.1	-	-
GF0028437	1	0	0	Accelerated cell death 6 (1)	integral component of membrane [GO:0016021 cellular_component] (1); cellular response to salicylic acid stimulus [GO:0071446 biological_process] (1); protein binding [GO:0005515 molecular_function] (1); regulation of defense response [GO:0031347 biological_process] (1); regulation of salicylic acid mediated signaling pathway [GO:2000031 biological_process] (1)	Ankyrin repeat [IPR002110] (1); Protein accelerated cell death 6 [IPR032846] (1); PGG domain [IPR026961] (1); Ankyrin repeat-containing domain [IPR020683] (1)	scaffold_3_mRNA_3437.1	-	-
GF0028436	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3436.1	-	-
GF0028435	1	0	0	TMV resistance protein N (1)	signal transduction [GO:0007165 biological_process] (1); ADP binding [GO:0043531 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	scaffold_3_mRNA_3415.1	-	-
GF0028434	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_3_mRNA_3413.1	-	-
GF0028433	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_3_mRNA_3411.1	-	-
GF0028432	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3410.1	-	-
GF0028431	1	0	0	TMV resistance protein N (1)	protein binding [GO:0005515 molecular_function] (1); signal transduction [GO:0007165 biological_process] (1); ADP binding [GO:0043531 molecular_function] (1)	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-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	scaffold_3_mRNA_3408.1	-	-
GF0028430	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3405.1	-	-
GF0028429	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3404.1	-	-
GF0028428	1	0	0	Disease resistance protein (TIR-NBS-LRR class) (1)	signal transduction [GO:0007165 biological_process] (1); ADP binding [GO:0043531 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1)	scaffold_3_mRNA_3402.1	-	-
GF0028427	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3400.1	-	-
GF0028426	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3398.1	-	-
GF0028425	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3397.1	-	-
GF0028424	1	0	0	TMV resistance protein N (1)	ADP binding [GO:0043531 molecular_function] (1); signal transduction [GO:0007165 biological_process] (1); protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat 3 [IPR011713] (1); Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	scaffold_3_mRNA_3396.1	-	-
GF0028423	1	0	0	Hypothetical protein (1)		Galactose-binding domain-like [IPR008979] (1)	scaffold_3_mRNA_3395.1	-	-
GF0028422	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3394.1	-	-
GF0028421	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3390.1	-	-
GF0028420	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3389.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0028419	1	0	0	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)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Leucine-rich repeat [IPR001611] (1); NB-ARC [IPR002182] (1); Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1); Leucine-rich repeat 3 [IPR011713] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1)	scaffold_3_mRNA_3381.1	-	-
GF0028418	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3380.1	-	-
GF0028417	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3378.1	-	-
GF0028416	1	0	0	Disease resistance protein (TIR-NBS-LRR class) (1)	protein binding [GO:0005515 molecular_function] (1); signal transduction [GO:0007165 biological_process] (1); ADP binding [GO:0043531 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1); NB-ARC [IPR002182] (1); Leucine-rich repeat [IPR001611] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_3_mRNA_3374.1	-	-
GF0028415	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3372.1	-	-
GF0028414	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3371.1	-	-
GF0028413	1	0	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_3_mRNA_3369.1	-	-
GF0028412	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3366.1	-	-
GF0028411	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_3_mRNA_3363.1	-	-
GF0028410	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3362.1	-	-
GF0028409	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_3_mRNA_3356.1	-	-
GF0028408	1	0	0	Monosacharide transport protein (1)			scaffold_3_mRNA_3353.1	-	-
GF0028407	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3352.1	-	-
GF0028406	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3346.1	-	-
GF0028405	1	0	0	LRR receptor-like kinase (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_3_mRNA_3344.1	-	-
GF0028404	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3339.1	-	-
GF0028403	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_3_mRNA_3337.1	-	-
GF0028402	1	0	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_3_mRNA_3336.1	-	-
GF0028401	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4219 [IPR025314] (1)	scaffold_3_mRNA_3329.1	-	-
GF0028400	1	0	0	Monosacharide transport protein (1)			scaffold_3_mRNA_3325.1	-	-
GF0028399	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3324.1	-	-
GF0028398	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3323.1	-	-
GF0028397	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3319.1	-	-
GF0028396	1	0	0	UDP-glycosyltransferase 74E2 (1)	metabolic process [GO:0008152 biological_process] (1); transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	scaffold_3_mRNA_3318.1	-	-
GF0028395	1	0	0	Hypothetical protein (1)	ribosome [GO:0005840 cellular_component] (1); translation [GO:0006412 biological_process] (1); intracellular [GO:0005622 cellular_component] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1)	Ribosomal protein L2, domain 3 [IPR014726] (1); Ribosomal protein L2, C-terminal [IPR022669] (1); Ribosomal protein L2 [IPR002171] (1); Translation protein SH3-like domain [IPR008991] (1)	scaffold_3_mRNA_3315.1	-	-
GF0028394	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3308.1	-	-
GF0028393	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3306.1	-	-
GF0028392	1	0	0	LRR and NB-ARC domain disease resistance protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); ADP binding [GO:0043531 molecular_function] (1)	Alcohol dehydrogenase, C-terminal [IPR013149] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Receptor L-domain [IPR000494] (1); NAD(P)-binding domain [IPR016040] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	scaffold_3_mRNA_3302.1	-	-
GF0028391	1	0	0	LRR and NB-ARC domain disease resistance protein (1)	ADP binding [GO:0043531 molecular_function] (1)	Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	scaffold_3_mRNA_3301.1	-	-
GF0028390	1	0	0	Mutator-like transposase (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Transposase, MuDR, plant [IPR004332] (1); MULE transposase domain [IPR018289] (1); Zinc finger, PMZ-type [IPR006564] (1); Zinc finger, SWIM-type [IPR007527] (1)	scaffold_3_mRNA_3299.1	-	-
GF0028389	1	0	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1); ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_3_mRNA_3298.1	-	-
GF0028388	1	0	0	MuDR family transposase isoform 1 (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, SWIM-type [IPR007527] (1); Zinc finger, PMZ-type [IPR006564] (1); MULE transposase domain [IPR018289] (1)	scaffold_3_mRNA_3290.1	-	-
GF0028387	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3287.1	-	-
GF0028386	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1); Aspartic peptidase domain [IPR021109] (1)	scaffold_3_mRNA_3286.1	-	-
GF0028385	1	0	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1)	Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1)	scaffold_3_mRNA_3281.1	-	-
GF0028384	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3278.1	-	-
GF0028383	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3277.1	-	-
GF0028382	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3275.1	-	-
GF0028381	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_3_mRNA_3274.1	-	-
GF0028380	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3272.1	-	-
GF0028379	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Retroviral aspartyl protease [IPR013242] (1); Aspartic peptidase domain [IPR021109] (1)	scaffold_3_mRNA_3271.1	-	-
GF0028378	1	0	0	Embryonic abundant protein-like (1)	metabolic process [GO:0008152 biological_process] (1); methyltransferase activity [GO:0008168 molecular_function] (1)	S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); Methyltransferase type 11 [IPR013216] (1)	scaffold_3_mRNA_3270.1	-	-
GF0028377	1	0	0	Retrovirus-related Pol polyprotein from transposon TNT 1-94 (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_3_mRNA_3264.1	-	-
GF0028376	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3259.1	-	-
GF0028375	1	0	0	Hypothetical protein (1)		Transposon, En/Spm-like [IPR004242] (1)	scaffold_3_mRNA_3256.1	-	-
GF0028374	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4371 [IPR025398] (1)	scaffold_3_mRNA_3252.1	-	-
GF0028373	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3232.1	-	-
GF0028372	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4219 [IPR025314] (1)	scaffold_3_mRNA_3231.1	-	-
GF0028371	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, GRF-type [IPR010666] (1)	scaffold_3_mRNA_3228.1	-	-
GF0028370	1	0	0	Transposon protein, putative, Mutator sub-class (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Transposase, MuDR, plant [IPR004332] (1); Domain of unknown function DUF4219 [IPR025314] (1); Zinc finger, PMZ-type [IPR006564] (1); MULE transposase domain [IPR018289] (1); Zinc finger, SWIM-type [IPR007527] (1)	scaffold_3_mRNA_3227.1	-	-
GF0028369	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3226.1	-	-
GF0028368	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3224.1	-	-
GF0028367	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3221.1	-	-
GF0028366	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3218.1	-	-

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GF0028365	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_3_mRNA_3217.1	-	-
GF0028364	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3215.1	-	-
GF0028363	1	0	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FAR1 DNA binding domain [IPR004330] (1); FHY3/FAR1 family [IPR031052] (1)	scaffold_3_mRNA_3213.1	-	-
GF0028362	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3210.1	-	-
GF0028361	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			scaffold_3_mRNA_3209.1	-	-
GF0028360	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3204.1	-	-
GF0028359	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3203.1	-	-
GF0028358	1	0	0	Hypothetical protein (1)		Pectin lyase fold/virulence factor [IPR011050] (1); Pectin lyase fold [IPR012334] (1)	scaffold_3_mRNA_3199.1	-	-
GF0028357	1	0	0	Hypothetical protein (1)	polygalacturonase activity [GO:0004650 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1)	Pectin lyase fold [IPR012334] (1); Pectin lyase fold/virulence factor [IPR011050] (1); Glycoside hydrolase, family 28 [IPR000743] (1); Parallel beta-helix repeat [IPR006626] (1)	scaffold_3_mRNA_3195.1	-	-
GF0028356	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3194.1	-	-
GF0028355	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_3_mRNA_3190.1	-	-
GF0028354	1	0	0	Polygalacturonase (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1); polygalacturonase activity [GO:0004650 molecular_function] (1)	Pectin lyase fold/virulence factor [IPR011050] (1); Pectin lyase fold [IPR012334] (1); Parallel beta-helix repeat [IPR006626] (1); Glycoside hydrolase, family 28 [IPR000743] (1)	scaffold_3_mRNA_3188.1	-	-
GF0028353	1	0	0	Monosacharide transport protein (1)			scaffold_3_mRNA_3187.1	-	-
GF0028352	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3186.1	-	-
GF0028351	1	0	0	Hypothetical protein (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)	scaffold_3_mRNA_3184.1	-	-
GF0028350	1	0	0	Polygalacturonase (1)	polygalacturonase activity [GO:0004650 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1)	Pectin lyase fold [IPR012334] (1); Pectin lyase fold/virulence factor [IPR011050] (1); Glycoside hydrolase, family 28 [IPR000743] (1); Parallel beta-helix repeat [IPR006626] (1)	scaffold_3_mRNA_3182.1	-	-
GF0028349	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3180.1	-	-
GF0028348	1	0	0	Monosacharide transport protein (1)			scaffold_3_mRNA_3179.1	-	-
GF0028347	1	0	0	Retrotransposon protein, putative, Ty3-gypsy subclass (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_3_mRNA_3178.1	-	-
GF0028346	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3176.1	-	-
GF0028345	1	0	0	Polygalacturonase (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1); polygalacturonase activity [GO:0004650 molecular_function] (1)	Pectin lyase fold [IPR012334] (1); Pectin lyase fold/virulence factor [IPR011050] (1); Parallel beta-helix repeat [IPR006626] (1); Glycoside hydrolase, family 28 [IPR000743] (1)	scaffold_3_mRNA_3175.1	-	-
GF0028344	1	0	0	Putative Leucine Rich Repeat Protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_3_mRNA_3173.1	-	-
GF0028343	1	0	0	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); Parallel beta-helix repeat [IPR006626] (1)	scaffold_3_mRNA_3172.1	-	-
GF0028342	1	0	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_3_mRNA_3171.1	-	-
GF0028341	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3170.1	-	-
GF0028340	1	0	0	Polygalacturonase (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)	scaffold_3_mRNA_3167.1	-	-
GF0028339	1	0	0	Hypothetical protein (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_3_mRNA_3166.1	-	-
GF0028338	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3160.1	-	-
GF0028337	1	0	0	Polygalacturonase (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1); polygalacturonase activity [GO:0004650 molecular_function] (1)	Pectin lyase fold [IPR012334] (1); Pectin lyase fold/virulence factor [IPR011050] (1); Glycoside hydrolase, family 28 [IPR000743] (1); Parallel beta-helix repeat [IPR006626] (1)	scaffold_3_mRNA_3157.1	-	-
GF0028336	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3155.1	-	-
GF0028335	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_3_mRNA_3154.1	-	-
GF0028334	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3153.1	-	-
GF0028333	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3152.1	-	-
GF0028332	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3151.1	-	-
GF0028331	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3150.1	-	-
GF0028330	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3148.1	-	-
GF0028329	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3143.1	-	-
GF0028328	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Ribonuclease H domain [IPR002156] (1)	scaffold_3_mRNA_3140.1	-	-
GF0028327	1	0	0	KINASE 2B 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 kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); Calcineurin-like phosphoesterase domain, lpxH type [IPR024654] (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); Phosphodiesterase MJ0936/Vps29 [IPR000979] (1); Metallo-dependent phosphatase-like [IPR029052] (1)	scaffold_3_mRNA_313.1	-	-
GF0028326	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3126.1	-	-
GF0028325	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3123.1	-	-
GF0028324	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3122.1	-	-
GF0028323	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3119.1	-	-
GF0028322	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3117.1	-	-
GF0028321	1	0	0	Monosacharide transport protein (1)			scaffold_3_mRNA_3116.1	-	-
GF0028320	1	0	0	ABC transporter G family member 33 (1)	riboflavin synthase complex [GO:0009349 cellular_component] (1); riboflavin biosynthetic process [GO:0009231 biological_process] (1)	6,7-dimethyl-8-ribityllumazine synthase [IPR002180] (1)	scaffold_3_mRNA_3108.1	-	-
GF0028319	1	0	0	Disease resistance N'-like protein (1)	ADP binding [GO:0043531 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_3_mRNA_3102.1	-	-
GF0028318	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3098.1	-	-
GF0028317	1	0	0	Disease resistance N'-like protein (1)	ADP binding [GO:0043531 molecular_function] (1)	Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Receptor L-domain [IPR000494] (1); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_3_mRNA_3092.1	-	-
GF0028316	1	0	0	Hypothetical protein (1)		Transposon, En/Spm-like [IPR004242] (1)	scaffold_3_mRNA_3091.1	-	-
GF0028315	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4218 [IPR025452] (1)	scaffold_3_mRNA_3090.1	-	-
GF0028314	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3083.1	-	-
GF0028313	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3079.1	-	-
GF0028312	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3077.1	-	-
GF0028311	1	0	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	MULE transposase domain [IPR018289] (1); FHY3/FAR1 family [IPR031052] (1); FAR1 DNA binding domain [IPR004330] (1)	scaffold_3_mRNA_3076.1	-	-
GF0028310	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3072.1	-	-
GF0028309	1	0	0	Putative retrotransposable elements TNP2 (1)			scaffold_3_mRNA_3071.1	-	-
GF0028308	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_3_mRNA_3070.1	-	-
GF0028307	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3069.1	-	-
GF0028306	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_3_mRNA_3058.1	-	-
GF0028305	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3057.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0028304	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3054.1	-	-
GF0028303	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3052.1	-	-
GF0028302	1	0	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_3_mRNA_3050.1	-	-
GF0028301	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Domain of unknown function DUF4283 [IPR025558] (1); Zinc knuckle CX2CX4HX4C [IPR025836] (1); Zinc finger, CCHC-type [IPR001878] (1)	scaffold_3_mRNA_3042.1	-	-
GF0028300	1	0	0	RNA-directed DNA polymerase (Reverse transcriptase) (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_3_mRNA_3040.1	-	-
GF0028299	1	0	0	Hypothetical protein (1)		Ankyrin repeat-containing domain [IPR020683] (1)	scaffold_3_mRNA_3027.1	-	-
GF0028298	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3024.1	-	-
GF0028297	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3023.1	-	-
GF0028296	1	0	0	Hydrolase, alpha/beta domain protein (1)		Alpha/Beta hydrolase fold [IPR029058] (1); Alpha/beta hydrolase fold-1 [IPR000073] (1)	scaffold_3_mRNA_3016.1	-	-
GF0028295	1	0	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	scaffold_3_mRNA_3009.1	-	-
GF0028294	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3004.1	-	-
GF0028293	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3003.1	-	-
GF0028292	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_3000.1	-	-
GF0028291	1	0	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_3_mRNA_2995.1	-	-
GF0028290	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2993.1	-	-
GF0028289	1	0	0	Aluminum-activated malate transporter 4 (1)	malate transport [GO:0015743 biological_process] (1)	Aluminum-activated malate transporter [IPR020966] (1)	scaffold_3_mRNA_2992.1	-	-
GF0028288	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2990.1	-	-
GF0028287	1	0	0	Hypothetical protein (1)		Arabidopsis retrotransposon Orf1 [IPR004312] (1)	scaffold_3_mRNA_2987.1	-	-
GF0028286	1	0	0	Disease resistance protein (TIR-NBS-LRR class) (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1); Leucine-rich repeat 3 [IPR011713] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1)	scaffold_3_mRNA_2984.1	-	-
GF0028285	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_3_mRNA_2982.1	-	-
GF0028284	1	0	0	Hypothetical protein (1)		Alpha/Beta hydrolase fold [IPR029058] (1)	scaffold_3_mRNA_2975.1	-	-
GF0028283	1	0	0	Disease resistance protein (TIR-NBS-LRR class) (1)	signal transduction [GO:0007165 biological_process] (1); ADP binding [GO:0043531 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1); GAG-pre-integrase domain [IPR025724] (1); Zinc finger, CCHC-type [IPR001878] (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)	scaffold_3_mRNA_2973.1	-	-
GF0028282	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2972.1	-	-
GF0028281	1	0	0	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)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1)	scaffold_3_mRNA_2964.1	-	-
GF0028280	1	0	0	Disease resistance protein (TIR-NBS-LRR class) (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); 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)	scaffold_3_mRNA_2963.1	-	-
GF0028279	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2961.1	-	-
GF0028278	1	0	0	Disease resistance protein (TIR-NBS-LRR class) (1)	protein binding [GO:0005515 molecular_function] (1); signal transduction [GO:0007165 biological_process] (1); ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1); Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1)	scaffold_3_mRNA_2960.1	-	-
GF0028277	1	0	0	Hypothetical protein (1)	translation release factor activity [GO:0003747 molecular_function] (1); translational termination [GO:0006415 biological_process] (1)	Peptide chain release factor class I/class II [IPR000352] (1)	scaffold_3_mRNA_2958.1	-	-
GF0028276	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1); signal transduction [GO:0007165 biological_process] (1)	Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1)	scaffold_3_mRNA_2957.1	-	-
GF0028275	1	0	0	Hypothetical protein (1)		Alpha/Beta hydrolase fold [IPR029058] (1)	scaffold_3_mRNA_2956.1	-	-
GF0028274	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2953.1	-	-
GF0028273	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2952.1	-	-
GF0028272	1	0	0	Peptide chain release factor 1 (1)	translational termination [GO:0006415 biological_process] (1); translation release factor activity [GO:0003747 molecular_function] (1)	Peptide chain release factor class I/class II [IPR000352] (1)	scaffold_3_mRNA_2950.1	-	-
GF0028271	1	0	0	Putative hydrolase yugF (1)		Alpha/Beta hydrolase fold [IPR029058] (1)	scaffold_3_mRNA_2949.1	-	-
GF0028270	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1); signal transduction [GO:0007165 biological_process] (1); ADP binding [GO:0043531 molecular_function] (1)	Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1); NB-ARC [IPR002182] (1); Arabidopsis retrotransposon Orf1 [IPR004312] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_3_mRNA_2947.1	-	-
GF0028269	1	0	0	Hypothetical protein (1)	translation release factor activity [GO:0003747 molecular_function] (1); translational termination [GO:0006415 biological_process] (1)	Peptide chain release factor class I/class II [IPR000352] (1)	scaffold_3_mRNA_2946.1	-	-
GF0028268	1	0	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine rich repeat 4 [IPR025875] (1)	scaffold_3_mRNA_2943.1	-	-
GF0028267	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2942.1	-	-
GF0028266	1	0	0	Hypothetical protein (1)	RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H domain [IPR002156] (1); Domain of unknown function DUF4283 [IPR025558] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_3_mRNA_2940.1	-	-
GF0028265	1	0	0	Hypothetical protein (1)	signal transduction [GO:0007165 biological_process] (1); protein binding [GO:0005515 molecular_function] (1)	Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1)	scaffold_3_mRNA_2936.1	-	-
GF0028264	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2935.1	-	-
GF0028263	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_3_mRNA_2931.1	-	-
GF0028262	1	0	0	R 4 protein (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); Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1)	scaffold_3_mRNA_2929.1	-	-
GF0028261	1	0	0	Hypothetical protein (1)		Repeat of unknown function XGLTT [IPR008164] (1)	scaffold_3_mRNA_2925.1	-	-
GF0028260	1	0	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	scaffold_3_mRNA_2924.1	-	-
GF0028259	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_3_mRNA_2917.1	-	-
GF0028258	1	0	0	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); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_3_mRNA_2912.1	-	-
GF0028257	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2907.1	-	-
GF0028256	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2906.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0028255	1	0	0	Hypothetical protein (1)	metal ion transport [GO:0030001 biological_process] (1); metal ion binding [GO:0046872 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1)	Heavy-metal-associated, conserved site [IPR017969] (1); Heavy metal-associated domain, HMA [IPR006121] (1); HAD-like domain [IPR023214] (1); P-type ATPase [IPR001757] (1); P-type ATPase, transmembrane domain [IPR023298] (1)	scaffold_3_mRNA_290.1	-	-
GF0028254	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2896.1	-	-
GF0028253	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_3_mRNA_2895.1	-	-
GF0028252	1	0	0	Disease resistance protein (TIR-NBS-LRR class) (1)	signal transduction [GO:0007165 biological_process] (1); ADP binding [GO:0043531 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (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)	scaffold_3_mRNA_2894.1	-	-
GF0028251	1	0	0	Hypothetical protein (1)	translation release factor activity [GO:0003747 molecular_function] (1); translational termination [GO:0006415 biological_process] (1)	Peptide chain release factor class I/class II [IPR000352] (1)	scaffold_3_mRNA_2893.1	-	-
GF0028250	1	0	0	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); Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1)	scaffold_3_mRNA_2892.1	-	-
GF0028249	1	0	0	Protein phosphatase 2A regulatory subunit A (1)	protein complex assembly [GO:0006461 biological_process] (1); binding [GO:0005488 molecular_function] (1); protein phosphatase regulator activity [GO:0019888 molecular_function] (1)	Armadillo-type fold [IPR016024] (1); Serine/threonine-protein phosphatase 2A subunit A, metazoa [IPR031090] (1); HEAT, type 2 [IPR021133] (1); Armadillo-like helical [IPR011989] (1)	scaffold_3_mRNA_2891.1	-	-
GF0028248	1	0	0	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); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1)	scaffold_3_mRNA_2887.1	-	-
GF0028247	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_3_mRNA_2871.1	-	-
GF0028246	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2870.1	-	-
GF0028245	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2868.1	-	-
GF0028244	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_3_mRNA_2867.1	-	-
GF0028243	1	0	0	Hypothetical protein (1)	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1)	Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450 [IPR001128] (1)	scaffold_3_mRNA_2866.1	-	-
GF0028242	1	0	0	Hypothetical protein (1)	signal transduction [GO:0007165 biological_process] (1); ADP binding [GO:0043531 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H-like domain [IPR012337] (1); Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_3_mRNA_2865.1	-	-
GF0028241	1	0	0	Flavone synthase II (1)	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1)	Cytochrome P450 [IPR001128] (1); Cytochrome P450, conserved site [IPR017972] (1); Cytochrome P450, E-class, group I [IPR002401] (1)	scaffold_3_mRNA_2864.1	-	-
GF0028240	1	0	0	TMV resistance protein N (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); Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_3_mRNA_2858.1	-	-
GF0028239	1	0	0	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)	Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_3_mRNA_2857.1	-	-
GF0028238	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2852.1	-	-
GF0028237	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2851.1	-	-
GF0028236	1	0	0	Hypothetical protein (1)	structural constituent of ribosome [GO:0003735 molecular_function] (1); intracellular [GO:0005622 cellular_component] (1); translation [GO:0006412 biological_process] (1); ribosome [GO:0005840 cellular_component] (1)	Ribosomal protein L13e [IPR001380] (1); Ribosomal protein L13, eukaryotic [IPR034295] (1); Ribosomal protein L13e, conserved site [IPR018256] (1)	scaffold_3_mRNA_2850.1	-	-
GF0028235	1	0	0	Hypothetical protein (1)		DNA methylase, C-5 cytosine-specific, active site [IPR018117] (1)	scaffold_3_mRNA_2843.1	-	-
GF0028234	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2836.1	-	-
GF0028233	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2835.1	-	-
GF0028232	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); protein glycosylation [GO:0006486 biological_process] (1); galactosyltransferase activity [GO:0008378 molecular_function] (1); membrane [GO:0016020 cellular_component] (1)	Glycosyl transferase, family 31 [IPR002659] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_3_mRNA_2830.1	-	-
GF0028231	1	0	0	N-acetyllactosaminide 3-alpha-galactosyltransferase (1)	protein glycosylation [GO:0006486 biological_process] (1); membrane [GO:0016020 cellular_component] (1); galactosyltransferase activity [GO:0008378 molecular_function] (1)	Glycosyl transferase, family 31 [IPR002659] (1)	scaffold_3_mRNA_2829.1	-	-
GF0028230	1	0	0	Protein AIG1 (1)	GTP binding [GO:0005525 molecular_function] (1)	AIG1-type guanine nucleotide-binding (G) domain [IPR006703] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_3_mRNA_2819.1	-	-
GF0028229	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2817.1	-	-
GF0028228	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2815.1	-	-
GF0028227	1	0	0	Protein AIG1 (1)	GTP binding [GO:0005525 molecular_function] (1)	AIG1-type guanine nucleotide-binding (G) domain [IPR006703] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_3_mRNA_2813.1	-	-
GF0028226	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2800.1	-	-
GF0028225	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_3_mRNA_2799.1	-	-
GF0028224	1	0	0	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	scaffold_3_mRNA_2798.1	-	-
GF0028223	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2791.1	-	-
GF0028222	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2790.1	-	-
GF0028221	1	0	0	Putative non-LTR retrolelement reverse transcriptase (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_3_mRNA_2783.1	-	-
GF0028220	1	0	0	Gibberellin receptor GID1C (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)	scaffold_3_mRNA_2782.1	-	-
GF0028219	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2764.1	-	-
GF0028218	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2763.1	-	-
GF0028217	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2762.1	-	-
GF0028216	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2760.1	-	-
GF0028215	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			scaffold_3_mRNA_2752.1	-	-
GF0028214	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_3_mRNA_2744.1	-	-
GF0028213	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2743.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0028212	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2742.1	-	-
GF0028211	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2741.1	-	-
GF0028210	1	0	0	Retrotransposon protein, putative, Ty1-copia subclass (1)			scaffold_3_mRNA_2739.1	-	-
GF0028209	1	0	0	Disease resistance protein (TIR-NBS-LRR class) (1)	protein binding [GO:0005515 molecular_function] (1); signal transduction [GO:0007165 biological_process] (1); ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1); Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1)	scaffold_3_mRNA_2736.1	-	-
GF0028208	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2734.1	-	-
GF0028207	1	0	0	Putative non-LTR retroelement reverse transcriptase (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Reverse transcriptase domain [IPR000477] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_3_mRNA_2732.1	-	-
GF0028206	1	0	0	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	scaffold_3_mRNA_2731.1	-	-
GF0028205	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	scaffold_3_mRNA_2724.1	-	-
GF0028204	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2706.1	-	-
GF0028203	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2699.1	-	-
GF0028202	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2698.1	-	-
GF0028201	1	0	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_3_mRNA_2696.1	-	-
GF0028200	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2692.1	-	-
GF0028199	1	0	0	TMV resistance N (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_3_mRNA_2684.1	-	-
GF0028198	1	0	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_3_mRNA_2682.1	-	-
GF0028197	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2681.1	-	-
GF0028196	1	0	0	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	scaffold_3_mRNA_2678.1	-	-
GF0028195	1	0	0	Chalcone reductase (1)	catalytic activity [GO:0003824 molecular_function] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); omega peptidase activity [GO:0008242 molecular_function] (1); glutamine metabolic process [GO:0006541 biological_process] (1)	NADP-dependent oxidoreductase domain [IPR023210] (1); Peptidase C26, gamma-glutamyl hydrolase [IPR015527] (1); Aldo/keto reductase, conserved site [IPR018170] (1); Class I glutamine amidotransferase-like [IPR029062] (1); Aldo/keto reductase [IPR020471] (1)	scaffold_3_mRNA_2667.1	-	-
GF0028194	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2662.1	-	-
GF0028193	1	0	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Protein kinase, ATP binding site [IPR017441] (1); Protein kinase-like domain [IPR011009] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Protein kinase domain [IPR000719] (1)	scaffold_3_mRNA_2659.1	-	-
GF0028192	1	0	0	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)	scaffold_3_mRNA_2658.1	-	-
GF0028191	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2656.1	-	-
GF0028190	1	0	0	Ankyrin repeat family protein, putative (1)	regulation of salicylic acid mediated signaling pathway [GO:2000031 biological_process] (1); regulation of defense response [GO:0031347 biological_process] (1); protein binding [GO:0005515 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1); cellular response to salicylic acid stimulus [GO:0071446 biological_process] (1)	Ankyrin repeat-containing domain [IPR020683] (1); PGG domain [IPR026961] (1); Protein accelerated cell death 6 [IPR032846] (1); Ankyrin repeat [IPR002110] (1)	scaffold_3_mRNA_2655.1	-	-
GF0028189	1	0	0	Retrotransposon protein, putative, Ty1-copia subclass (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	scaffold_3_mRNA_2650.1	-	-
GF0028188	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_265.1	-	-
GF0028187	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2640.1	-	-
GF0028186	1	0	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_3_mRNA_2629.1	-	-
GF0028185	1	0	0	Hypothetical protein (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1); amino acid binding [GO:0016597 molecular_function] (1); cellular amino acid biosynthetic process [GO:0008652 biological_process] (1); metabolic process [GO:0008152 biological_process] (1); NADP binding [GO:0050661 molecular_function] (1); aspartate kinase activity [GO:0004072 molecular_function] (1); cellular amino acid metabolic process [GO:0006520 biological_process] (1)	Aspartate kinase, conserved site [IPR018042] (1); Zinc finger, TTF-type [IPR006580] (1); Ribonuclease H-like domain [IPR012337] (1); GATS-like ACT domain [IPR027795] (1); Homoserine dehydrogenase, catalytic [IPR001342] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Aspartate/glutamate/uridylate kinase [IPR001048] (1); NAD(P)-binding domain [IPR016040] (1); HAT, C-terminal dimerisation domain [IPR008906] (1); Aspartate/homoserine dehydrogenase, NAD-binding [IPR005106] (1); ACT domain [IPR002912] (1); Homoserine dehydrogenase, conserved site [IPR019811] (1); Aspartate kinase domain [IPR001341] (1); Domain of unknown function DUF4371 [IPR025398] (1)	scaffold_3_mRNA_2613.1	-	-
GF0028184	1	0	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); AAA+ ATPase domain [IPR003593] (1); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1)	scaffold_3_mRNA_2611.1	-	-
GF0028183	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2610.1	-	-
GF0028182	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2608.1	-	-
GF0028181	1	0	0	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	scaffold_3_mRNA_2606.1	-	-
GF0028180	1	0	0	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	scaffold_3_mRNA_2604.1	-	-
GF0028179	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2600.1	-	-
GF0028178	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2599.1	-	-
GF0028177	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2598.1	-	-
GF0028176	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2596.1	-	-
GF0028175	1	0	0	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)	scaffold_3_mRNA_2589.1	-	-
GF0028174	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2587.1	-	-
GF0028173	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Zinc finger, SWIM-type [IPR007527] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Zinc finger, PMZ-type [IPR006564] (1); F-box domain [IPR001810] (1)	scaffold_3_mRNA_2582.1	-	-
GF0028172	1	0	0	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	scaffold_3_mRNA_2573.1	-	-
GF0028171	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_3_mRNA_2559.1	-	-
GF0028170	1	0	0	TMV resistance N (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_3_mRNA_2531.1	-	-
GF0028169	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2529.1	-	-
GF0028168	1	0	0	General transcription factor 2-related zinc finger protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Domain of unknown function DUF4371 [IPR025398] (1); Zinc finger, TTF-type [IPR006580] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_3_mRNA_2525.1	-	-
GF0028167	1	0	0	TSA: Wollemia nobilis transcribed RNA sequence (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)	scaffold_3_mRNA_2523.1	-	-
GF0028166	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2521.1	-	-
GF0028165	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2520.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0028164	1	0	0	Caffeic acid 3-O-methyltransferase (1)	O-methyltransferase activity [GO:0008171 molecular_function] (1); methyltransferase activity [GO:0008168 molecular_function] (1)	S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); O-methyltransferase COMT-type [IPR016461] (1); O-methyltransferase, family 2 [IPR001077] (1)	scaffold_3_mRNA_2506.1	-	-
GF0028163	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2504.1	-	-
GF0028162	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2503.1	-	-
GF0028161	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2501.1	-	-
GF0028160	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2500.1	-	-
GF0028159	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2495.1	-	-
GF0028158	1	0	0	Retrotransposon ty1-copia subclass (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	scaffold_3_mRNA_2490.1	-	-
GF0028157	1	0	0	Caffeic acid O-methyltransferase (1)	methyltransferase activity [GO:0008168 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1); O-methyltransferase activity [GO:0008171 molecular_function] (1)	S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); 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)	scaffold_3_mRNA_2486.1	-	-
GF0028156	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2483.1	-	-
GF0028155	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2482.1	-	-
GF0028154	1	0	0	Hypothetical protein (1)	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1)	Cytochrome P450 [IPR001128] (1)	scaffold_3_mRNA_2481.1	-	-
GF0028153	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_3_mRNA_2473.1	-	-
GF0028152	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2471.1	-	-
GF0028151	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2468.1	-	-
GF0028150	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2466.1	-	-
GF0028149	1	0	0	Caffeic acid O-methyltransferase (1)	O-methyltransferase activity [GO:0008171 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1); methyltransferase activity [GO:0008168 molecular_function] (1)	S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); O-methyltransferase, family 2 [IPR001077] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Plant methyltransferase dimerisation [IPR012967] (1); O-methyltransferase COMT-type [IPR016461] (1)	scaffold_3_mRNA_2465.1	-	-
GF0028148	1	0	0	GDSL esterase/lipase 7 (1)	hydrolase activity, acting on ester bonds [GO:0016788 molecular_function] (1)	GDSL lipase/esterase [IPR001087] (1)	scaffold_3_mRNA_2463.1	-	-
GF0028147	1	0	0	GDSL esterase/lipase 7 (1)	hydrolase activity, acting on ester bonds [GO:0016788 molecular_function] (1)	GDSL lipase/esterase [IPR001087] (1)	scaffold_3_mRNA_2456.1	-	-
GF0028146	1	0	0	GDSL-like Lipase/Acylhydrolase superfamily protein, putative isoform 2 (1)			scaffold_3_mRNA_2454.1	-	-
GF0028145	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2453.1	-	-
GF0028144	1	0	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_3_mRNA_2452.1	-	-
GF0028143	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2450.1	-	-
GF0028142	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2446.1	-	-
GF0028141	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2444.1	-	-
GF0028140	1	0	0	Monosacharide transport protein (1)			scaffold_3_mRNA_2440.1	-	-
GF0028139	1	0	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_3_mRNA_2437.1	-	-
GF0028138	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2436.1	-	-
GF0028137	1	0	0	Hypothetical protein (1)	catalytic activity [GO:0003824 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); FMN binding [GO:0010181 molecular_function] (1)	Aldolase-type TIM barrel [IPR013785] (1); NADH:flavin oxidoreductase/NADH oxidase, N-terminal [IPR001155] (1)	scaffold_3_mRNA_2432.1	-	-
GF0028136	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2420.1	-	-
GF0028135	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2416.1	-	-
GF0028134	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_3_mRNA_2415.1	-	-
GF0028133	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2412.1	-	-
GF0028132	1	0	0	Hypothetical protein (1)	GTP binding [GO:0005525 molecular_function] (1)	AIG1-type guanine nucleotide-binding (G) domain [IPR006703] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_3_mRNA_2411.1	-	-
GF0028131	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2410.1	-	-
GF0028130	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_3_mRNA_2406.1	-	-
GF0028129	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2405.1	-	-
GF0028128	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_3_mRNA_2401.1	-	-
GF0028127	1	0	0	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)	scaffold_3_mRNA_2395.1	-	-
GF0028126	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_3_mRNA_2388.1	-	-
GF0028125	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2385.1	-	-
GF0028124	1	0	0	Hypothetical protein (1)		Transposon, En/Spm-like [IPR004242] (1)	scaffold_3_mRNA_2383.1	-	-
GF0028123	1	0	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1); Probable transposase, Ptta/En/Spm, plant [IPR004252] (1); Domain of unknown function DUF4218 [IPR025452] (1)	scaffold_3_mRNA_2382.1	-	-
GF0028122	1	0	0	Protein AIG1 (1)	GTP binding [GO:0005525 molecular_function] (1)	AIG1-type guanine nucleotide-binding (G) domain [IPR006703] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_3_mRNA_2368.1	-	-
GF0028121	1	0	0	Hypothetical protein (1)	nucleus [GO:0005634 cellular_component] (1); nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (1)	Transcription factor, K-box [IPR002487] (1); Zinc finger, CCHC-type [IPR001878] (1)	scaffold_3_mRNA_2367.1	-	-
GF0028120	1	0	0	Hypothetical protein (1)	GTP binding [GO:0005525 molecular_function] (1); hydrolase activity, acting on ester bonds [GO:0016788 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Harbinger transposase-derived protein [IPR006912] (1); AIG1-type guanine nucleotide-binding (G) domain [IPR006703] (1)	scaffold_3_mRNA_2366.1	-	-
GF0028119	1	0	0	Hypothetical protein (1)		Regulator of nonsense-mediated decay, UPF3 [IPR005120] (1)	scaffold_3_mRNA_2363.1	-	-
GF0028118	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2354.1	-	-
GF0028117	1	0	0	Pre-mRNA-processing factor 17 (1)	catalytic step 2 spliceosome [GO:0071013 cellular_component] (1); mRNA splicing, via spliceosome [GO:0000398 biological_process] (1); protein binding [GO:0005515 molecular_function] (1)	WD40-repeat-containing domain [IPR017986] (1); WD40 repeat [IPR001680] (1); WD40 repeat, conserved site [IPR019775] (1); WD40/YVTN repeat-like-containing domain [IPR015943] (1); G-protein beta WD-40 repeat [IPR020472] (1); Pre-mRNA-processing factor 17 [IPR032847] (1)	scaffold_3_mRNA_2353.1	-	-
GF0028116	1	0	0	Isoflavone reductase-like protein 4 isoform 2 (1)		NAD(P)-binding domain [IPR016040] (1); NmrA-like domain [IPR008030] (1)	scaffold_3_mRNA_2350.1	-	-
GF0028115	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2341.1	-	-
GF0028114	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2338.1	-	-
GF0028113	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2337.1	-	-
GF0028112	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2336.1	-	-
GF0028111	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2331.1	-	-
GF0028110	1	0	0	Phenylcoumaran benzylic ether reductase (1)		NAD(P)-binding domain [IPR016040] (1); NmrA-like domain [IPR008030] (1)	scaffold_3_mRNA_2329.1	-	-
GF0028109	1	0	0	Polynucleotidyl transferase, Ribonuclease H fold (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1)	scaffold_3_mRNA_2302.1	-	-
GF0028108	1	0	0	Putative ribonuclease H protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	scaffold_3_mRNA_2301.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0028107	1	0	0	Monosacharide transport protein (1)			scaffold_3_mRNA_2298.1	-	-
GF0028106	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2296.1	-	-
GF0028105	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2294.1	-	-
GF0028104	1	0	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (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); zinc ion binding [GO:0008270 molecular_function] (1); transposition, DNA-mediated [GO:0006313 biological_process] (1); transposase activity [GO:0004803 molecular_function] (1)	Glycoside hydrolase superfamily [IPR017853] (1); Zinc finger, SWIM-type [IPR007527] (1); Zinc finger, PMZ-type [IPR006564] (1); Transposase, mutator type [IPR001207] (1); Glycoside hydrolase, family 27 [IPR002241] (1); Aldolase-type TIM barrel [IPR013785] (1)	scaffold_3_mRNA_2290.1	-	-
GF0028103	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2288.1	-	-
GF0028102	1	0	0	Hypothetical protein (1)	membrane [GO:0016020 cellular_component] (1); transport [GO:0006810 biological_process] (1); transporter activity [GO:0005215 molecular_function] (1)	Major intrinsic protein [IPR000425] (1); Aquaporin transporter [IPR034294] (1); Major intrinsic protein, conserved site [IPR022357] (1); Aquaporin-like [IPR023271] (1)	scaffold_3_mRNA_2283.1	-	-
GF0028101	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	scaffold_3_mRNA_2272.1	-	-
GF0028100	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_3_mRNA_2269.1	-	-
GF0028099	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); DNA integration [GO:0015074 biological_process] (1)	Ribonuclease H-like domain [IPR012337] (1); Integrase, catalytic core [IPR001584] (1)	scaffold_3_mRNA_2249.1	-	-
GF0028098	1	0	0	DNA/RNA polymerases superfamily protein (1)			scaffold_3_mRNA_2247.1	-	-
GF0028097	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2246.1	-	-
GF0028096	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2244.1	-	-
GF0028095	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_3_mRNA_2243.1	-	-
GF0028094	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2241.1	-	-
GF0028093	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2239.1	-	-
GF0028092	1	0	0	Kunitz trypsin inhibitor (1)	endopeptidase inhibitor activity [GO:0004866 molecular_function] (1)	Kunitz inhibitor ST1-like [IPR011065] (1); Proteinase inhibitor I3, Kunitz legume [IPR002160] (1)	scaffold_3_mRNA_2232.1	-	-
GF0028091	1	0	0	Kunitz trypsin inhibitor (1)	endopeptidase inhibitor activity [GO:0004866 molecular_function] (1)	Kunitz inhibitor ST1-like [IPR011065] (1); Proteinase inhibitor I3, Kunitz legume [IPR002160] (1)	scaffold_3_mRNA_2230.1	-	-
GF0028090	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2228.1	-	-
GF0028089	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); GRAM domain [IPR004182] (1)	scaffold_3_mRNA_2220.1	-	-
GF0028088	1	0	0	Miraculin (1)	endopeptidase inhibitor activity [GO:0004866 molecular_function] (1)	Proteinase inhibitor I3, Kunitz legume [IPR002160] (1); Kunitz inhibitor ST1-like [IPR011065] (1)	scaffold_3_mRNA_2219.1	-	-
GF0028087	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			scaffold_3_mRNA_2216.1	-	-
GF0028086	1	0	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Carlavirus nucleic acid-binding protein [IPR002568] (1)	scaffold_3_mRNA_2215.1	-	-
GF0028085	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2214.1	-	-
GF0028084	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			scaffold_3_mRNA_2213.1	-	-
GF0028083	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2211.1	-	-
GF0028082	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2210.1	-	-
GF0028081	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2208.1	-	-
GF0028080	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2202.1	-	-
GF0028079	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2201.1	-	-
GF0028078	1	0	0	Hypothetical protein (1)	endopeptidase inhibitor activity [GO:0004866 molecular_function] (1)	Proteinase inhibitor I3, Kunitz legume [IPR002160] (1); Kunitz inhibitor ST1-like [IPR011065] (1)	scaffold_3_mRNA_2199.1	-	-
GF0028077	1	0	0	Miraculin (1)	endopeptidase inhibitor activity [GO:0004866 molecular_function] (1)	Proteinase inhibitor I3, Kunitz legume [IPR002160] (1); Kunitz inhibitor ST1-like [IPR011065] (1)	scaffold_3_mRNA_2195.1	-	-
GF0028076	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2193.1	-	-
GF0028075	1	0	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	scaffold_3_mRNA_2192.1	-	-
GF0028074	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	scaffold_3_mRNA_2190.1	-	-
GF0028073	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_3_mRNA_218.1	-	-
GF0028072	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2176.1	-	-
GF0028071	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2174.1	-	-
GF0028070	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_3_mRNA_2173.1	-	-
GF0028069	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2172.1	-	-
GF0028068	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2171.1	-	-
GF0028067	1	0	0	LRR receptor-like serine/threonine-protein kinase GSO1 (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	scaffold_3_mRNA_2169.1	-	-
GF0028066	1	0	0	Nodulin MtN21/EamA-like transporter family protein (1)	transmembrane transporter activity [GO:0022857 molecular_function] (1); membrane [GO:0016020 cellular_component] (1); integral component of membrane [GO:0016021 cellular_component] (1)	WAT1-related protein [IPR030184] (1); Aspartic peptidase domain [IPR021109] (1); EamA domain [IPR000620] (1)	scaffold_3_mRNA_2166.1	-	-
GF0028065	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2159.1	-	-
GF0028064	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2156.1	-	-
GF0028063	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2152.1	-	-
GF0028062	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2146.1	-	-
GF0028061	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_3_mRNA_2145.1	-	-
GF0028060	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2144.1	-	-
GF0028059	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2143.1	-	-
GF0028058	1	0	0	Hypothetical protein (1)	omega peptidase activity [GO:0008242 molecular_function] (1); glutamine metabolic process [GO:0006541 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1)	Peptidase C26, gamma-glutamyl hydrolase [IPR015527] (1)	scaffold_3_mRNA_2134.1	-	-
GF0028057	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2133.1	-	-
GF0028056	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2132.1	-	-
GF0028055	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2131.1	-	-
GF0028054	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2129.1	-	-
GF0028053	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2128.1	-	-
GF0028052	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_3_mRNA_2127.1	-	-
GF0028051	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2126.1	-	-
GF0028050	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2125.1	-	-
GF0028049	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2124.1	-	-
GF0028048	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2123.1	-	-
GF0028047	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_3_mRNA_2120.1	-	-
GF0028046	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2119.1	-	-
GF0028045	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2117.1	-	-
GF0028044	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2115.1	-	-
GF0028043	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2108.1	-	-
GF0028042	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_3_mRNA_2105.1	-	-
GF0028041	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2104.1	-	-
GF0028040	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2103.1	-	-
GF0028039	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2101.1	-	-
GF0028038	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2100.1	-	-
GF0028037	1	0	0	Hypothetical protein (1)			scaffold_3_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***
GF0028036	1	0	0	Putative muDR family transposase-like (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); MULE transposase domain [IPR018289] (1); Zinc finger, PMZ-type [IPR006564] (1); Zinc finger, SWIM-type [IPR007527] (1)	scaffold_3_mRNA_2096.1	-	-
GF0028035	1	0	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	scaffold_3_mRNA_2095.1	-	-
GF0028034	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); signal transduction [GO:0007165 biological_process] (1); zinc ion binding [GO:0008270 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1); Zinc finger, CCHC-type [IPR001878] (1)	scaffold_3_mRNA_2087.1	-	-
GF0028033	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2084.1	-	-
GF0028032	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2083.1	-	-
GF0028031	1	0	0	Hypothetical protein (1)	ATPase activity [GO:0016887 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Plant PDR ABC transporter associated [IPR013581] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); AAA+ ATPase domain [IPR003593] (1); ATP-binding cassette transporter, PDR-like subfamily G, domain 2 [IPR034003] (1); ABC transporter-like [IPR003439] (1)	scaffold_3_mRNA_2081.1	-	-
GF0028030	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2080.1	-	-
GF0028029	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2075.1	-	-
GF0028028	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_3_mRNA_2074.1	-	-
GF0028027	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2070.1	-	-
GF0028026	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_3_mRNA_2069.1	-	-
GF0028025	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2067.1	-	-
GF0028024	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2064.1	-	-
GF0028023	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2062.1	-	-
GF0028022	1	0	0	Hypothetical protein (1)		Probable transposase, Ptta/En/Spm, plant [IPR004252] (1)	scaffold_3_mRNA_2061.1	-	-
GF0028021	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2055.1	-	-
GF0028020	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_3_mRNA_2046.1	-	-
GF0028019	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2045.1	-	-
GF0028018	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2041.1	-	-
GF0028017	1	0	0	Triose-phosphate isomerase (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)	scaffold_3_mRNA_2037.1	-	-
GF0028016	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2033.1	-	-
GF0028015	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2032.1	-	-
GF0028014	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2026.1	-	-
GF0028013	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2025.1	-	-
GF0028012	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2024.1	-	-
GF0028011	1	0	0	BED zinc finger,hAT family dimerization domain isoform 1 (1)	DNA binding [GO:0003677 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	hAT-like transposase, RNase-H fold [IPR025525] (1); Ribonuclease H-like domain [IPR012337] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	scaffold_3_mRNA_2023.1	-	-
GF0028010	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2020.1	-	-
GF0028009	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2017.1	-	-
GF0028008	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2016.1	-	-
GF0028007	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2015.1	-	-
GF0028006	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2012.1	-	-
GF0028005	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2011.1	-	-
GF0028004	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_2005.1	-	-
GF0028003	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_3_mRNA_2003.1	-	-
GF0028002	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1999.1	-	-
GF0028001	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1998.1	-	-
GF0028000	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1997.1	-	-
GF0027999	1	0	0	Retrotransposon protein, putative, Ty3-gypsy subclass (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_3_mRNA_1995.1	-	-
GF0027998	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1994.1	-	-
GF0027997	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1993.1	-	-
GF0027996	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_3_mRNA_1989.1	-	-
GF0027995	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1988.1	-	-
GF0027994	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1987.1	-	-
GF0027993	1	0	0	Hypothetical protein (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Peptidase A2A, retrovirus, catalytic [IPR001995] (1)	scaffold_3_mRNA_1985.1	-	-
GF0027992	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1984.1	-	-
GF0027991	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1983.1	-	-
GF0027990	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1976.1	-	-
GF0027989	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1975.1	-	-
GF0027988	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1974.1	-	-
GF0027987	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1973.1	-	-
GF0027986	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1972.1	-	-
GF0027985	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1970.1	-	-
GF0027984	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1969.1	-	-
GF0027983	1	0	0	CDNA clone:002-112-E03, full insert sequence (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_3_mRNA_1968.1	-	-
GF0027982	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1967.1	-	-
GF0027981	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_3_mRNA_1966.1	-	-
GF0027980	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1965.1	-	-
GF0027979	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1956.1	-	-
GF0027978	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1952.1	-	-
GF0027977	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1948.1	-	-
GF0027976	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_3_mRNA_1947.1	-	-
GF0027975	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_3_mRNA_1946.1	-	-
GF0027974	1	0	0	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)	scaffold_3_mRNA_1945.1	-	-
GF0027973	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1944.1	-	-
GF0027972	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1943.1	-	-
GF0027971	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1941.1	-	-
GF0027970	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1939.1	-	-
GF0027969	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1937.1	-	-
GF0027968	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1936.1	-	-
GF0027967	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1935.1	-	-
GF0027966	1	0	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_3_mRNA_1934.1	-	-
GF0027965	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_3_mRNA_1933.1	-	-
GF0027964	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1931.1	-	-
GF0027963	1	0	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_3_mRNA_1930.1	-	-
GF0027962	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1929.1	-	-
GF0027961	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1928.1	-	-
GF0027960	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1925.1	-	-
GF0027959	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1922.1	-	-
GF0027958	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1920.1	-	-
GF0027957	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1917.1	-	-
GF0027956	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1913.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0027955	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1912.1	-	-
GF0027954	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1911.1	-	-
GF0027953	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1904.1	-	-
GF0027952	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_3_mRNA_1901.1	-	-
GF0027951	1	0	0	Cation/H(+) antiporter 15 (1)	cation transport [GO:0006812 biological_process] (1); integral component of membrane [GO:0016021 cellular_component] (1); transmembrane transport [GO:0055085 biological_process] (1); solute:proton antiporter activity [GO:0015299 molecular_function] (1)	Cation/H+ exchanger [IPR006153] (1); Rossmann-like alpha/beta/alpha sandwich fold [IPR014729] (1)	scaffold_3_mRNA_190.1	-	-
GF0027950	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_19.1	-	-
GF0027949	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1895.1	-	-
GF0027948	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1892.1	-	-
GF0027947	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1891.1	-	-
GF0027946	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1885.1	-	-
GF0027945	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1884.1	-	-
GF0027944	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1883.1	-	-
GF0027943	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1880.1	-	-
GF0027942	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1877.1	-	-
GF0027941	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1875.1	-	-
GF0027940	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1873.1	-	-
GF0027939	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1871.1	-	-
GF0027938	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_3_mRNA_1867.1	-	-
GF0027937	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1866.1	-	-
GF0027936	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1864.1	-	-
GF0027935	1	0	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_3_mRNA_1862.1	-	-
GF0027934	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1858.1	-	-
GF0027933	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1857.1	-	-
GF0027932	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1856.1	-	-
GF0027931	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_3_mRNA_1855.1	-	-
GF0027930	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1854.1	-	-
GF0027929	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1853.1	-	-
GF0027928	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1850.1	-	-
GF0027927	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1849.1	-	-
GF0027926	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1846.1	-	-
GF0027925	1	0	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_3_mRNA_1843.1	-	-
GF0027924	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1840.1	-	-
GF0027923	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1); Viral movement protein [IPR028919] (1)	scaffold_3_mRNA_1838.1	-	-
GF0027922	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1837.1	-	-
GF0027921	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Aspartic peptidase domain [IPR021109] (1); Retropepsins [IPR018061] (1)	scaffold_3_mRNA_1836.1	-	-
GF0027920	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1835.1	-	-
GF0027919	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Zinc finger, CCHC-type [IPR001878] (1); Aspartic peptidase domain [IPR021109] (1); Peptidase A2A, retrovirus, catalytic [IPR001995] (1); Zinc finger, BED-type [IPR003656] (1); Retropepsins [IPR018061] (1)	scaffold_3_mRNA_1833.1	-	-
GF0027918	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1831.1	-	-
GF0027917	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1830.1	-	-
GF0027916	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1825.1	-	-
GF0027915	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_3_mRNA_1824.1	-	-
GF0027914	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1823.1	-	-
GF0027913	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1820.1	-	-
GF0027912	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1813.1	-	-
GF0027911	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_3_mRNA_1811.1	-	-
GF0027910	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1809.1	-	-
GF0027909	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1807.1	-	-
GF0027908	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); DNA integration [GO:0015074 biological_process] (1)	Ribonuclease H-like domain [IPR012337] (1); Integrase, catalytic core [IPR001584] (1)	scaffold_3_mRNA_1804.1	-	-
GF0027907	1	0	0	Retrotransposon gag protein (1)			scaffold_3_mRNA_1803.1	-	-
GF0027906	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_3_mRNA_1801.1	-	-
GF0027905	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1798.1	-	-
GF0027904	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1792.1	-	-
GF0027903	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1791.1	-	-
GF0027902	1	0	0	Retrovirus-related Pol polyprotein from transposon TNT 1-94 (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_3_mRNA_1788.1	-	-
GF0027901	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_3_mRNA_1787.1	-	-
GF0027900	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4216 [IPR025312] (1); Transposase-associated domain [IPR029480] (1)	scaffold_3_mRNA_1785.1	-	-
GF0027899	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1783.1	-	-
GF0027898	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1782.1	-	-
GF0027897	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1781.1	-	-
GF0027896	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1780.1	-	-
GF0027895	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_3_mRNA_1779.1	-	-
GF0027894	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_3_mRNA_1778.1	-	-
GF0027893	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1776.1	-	-
GF0027892	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1773.1	-	-
GF0027891	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1769.1	-	-
GF0027890	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1768.1	-	-
GF0027889	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1767.1	-	-
GF0027888	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1759.1	-	-
GF0027887	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1758.1	-	-
GF0027886	1	0	0	Integrase (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_3_mRNA_1757.1	-	-
GF0027885	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_3_mRNA_1755.1	-	-
GF0027884	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1747.1	-	-
GF0027883	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_3_mRNA_1746.1	-	-
GF0027882	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1745.1	-	-
GF0027881	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1743.1	-	-
GF0027880	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1739.1	-	-
GF0027879	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_3_mRNA_1738.1	-	-
GF0027878	1	0	0	Hypothetical protein (1)	endopeptidase inhibitor activity [GO:0004866 molecular_function] (1)	Kunitz inhibitor ST1-like [IPR011065] (1); Proteinase inhibitor I3, Kunitz legume [IPR002160] (1)	scaffold_3_mRNA_1736.1	-	-
GF0027877	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_3_mRNA_1734.1	-	-
GF0027876	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1730.1	-	-
GF0027875	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1723.1	-	-
GF0027874	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1722.1	-	-
GF0027873	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1716.1	-	-
GF0027872	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1703.1	-	-
GF0027871	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1702.1	-	-
GF0027870	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			scaffold_3_mRNA_1701.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0027869	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_17.1	-	-
GF0027868	1	0	0	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)	scaffold_3_mRNA_1695.1	-	-
GF0027867	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_3_mRNA_1694.1	-	-
GF0027866	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1692.1	-	-
GF0027865	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1691.1	-	-
GF0027864	1	0	0	Putative non-LTR retroelement reverse transcriptase (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1); sequence-specific DNA binding [GO:0043565 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (1)	Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H-like domain [IPR012337] (1); Zinc finger, GATA-type [IPR000679] (1); Reverse transcriptase domain [IPR000477] (1); Endonuclease/exonuclease/phosphatase [IPR005135] (1)	scaffold_3_mRNA_1689.1	-	-
GF0027863	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1680.1	-	-
GF0027862	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_3_mRNA_1679.1	-	-
GF0027861	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1678.1	-	-
GF0027860	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1677.1	-	-
GF0027859	1	0	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1); Probable transposase, Ptta/En/Spm, plant [IPR004252] (1)	scaffold_3_mRNA_1676.1	-	-
GF0027858	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_167.1	-	-
GF0027857	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1666.1	-	-
GF0027856	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1665.1	-	-
GF0027855	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1662.1	-	-
GF0027854	1	0	0	Hypothetical protein (1)	intracellular signal transduction [GO:0035556 biological_process] (1)	DEP domain [IPR000591] (1)	scaffold_3_mRNA_1661.1	-	-
GF0027853	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_3_mRNA_1660.1	-	-
GF0027852	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1657.1	-	-
GF0027851	1	0	0	Hypothetical protein (1)		Transposase, MuDR, plant [IPR004332] (1)	scaffold_3_mRNA_1654.1	-	-
GF0027850	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_3_mRNA_1651.1	-	-
GF0027849	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1650.1	-	-
GF0027848	1	0	0	Hypothetical protein (1)		Myb/SANT-like domain [IPR024752] (1)	scaffold_3_mRNA_1642.1	-	-
GF0027847	1	0	0	Putative nuclease HARBI1 (1)		Harbinger transposase-derived nuclease domain [IPR027806] (1); Myb/SANT-like domain [IPR024752] (1)	scaffold_3_mRNA_1640.1	-	-
GF0027846	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1635.1	-	-
GF0027845	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_3_mRNA_1634.1	-	-
GF0027844	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1633.1	-	-
GF0027843	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1632.1	-	-
GF0027842	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1631.1	-	-
GF0027841	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1629.1	-	-
GF0027840	1	0	0	Retrotransposon gag protein (1)			scaffold_3_mRNA_1626.1	-	-
GF0027839	1	0	0	Phenazine biosynthesis PhzC/PhzF family protein (1)	catalytic activity [GO:0003824 molecular_function] (1); biosynthetic process [GO:0009058 biological_process] (1)	Phenazine biosynthesis PhzF protein [IPR003719] (1)	scaffold_3_mRNA_1604.1	-	-
GF0027838	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_16.1	-	-
GF0027837	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1598.1	-	-
GF0027836	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1591.1	-	-
GF0027835	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1590.1	-	-
GF0027834	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1588.1	-	-
GF0027833	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1587.1	-	-
GF0027832	1	0	0	Hypothetical protein (1)		Zinc knuckle CX2CX4HX4C [IPR025836] (1)	scaffold_3_mRNA_1584.1	-	-
GF0027831	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_3_mRNA_1583.1	-	-
GF0027830	1	0	0	Hypothetical protein (1)	metabolic process [GO:0008152 biological_process] (1); branched-chain amino acid biosynthetic process [GO:0009082 biological_process] (1); acetolactate synthase activity [GO:0003984 molecular_function] (1); serine-type endopeptidase activity [GO:0004252 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1); amino acid binding [GO:0016597 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	ACT domain [IPR002912] (1); Peptidase S1, PA clan [IPR009003] (1); Acetolactate synthase, small subunit [IPR004789] (1); Peptidase S1C [IPR001940] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_3_mRNA_1578.1	-	-
GF0027829	1	0	0	Far-red impaired responsive family protein isoform 1 (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1); FAR1 DNA binding domain [IPR004330] (1)	scaffold_3_mRNA_1577.1	-	-
GF0027828	1	0	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	scaffold_3_mRNA_1576.1	-	-
GF0027827	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1574.1	-	-
GF0027826	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1571.1	-	-
GF0027825	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1570.1	-	-
GF0027824	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1565.1	-	-
GF0027823	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1555.1	-	-
GF0027822	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1553.1	-	-
GF0027821	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1552.1	-	-
GF0027820	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1547.1	-	-
GF0027819	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1546.1	-	-
GF0027818	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1545.1	-	-
GF0027817	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_3_mRNA_1541.1	-	-
GF0027816	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1540.1	-	-
GF0027815	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1532.1	-	-
GF0027814	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1527.1	-	-
GF0027813	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1526.1	-	-
GF0027812	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1525.1	-	-
GF0027811	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1524.1	-	-
GF0027810	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1521.1	-	-
GF0027809	1	0	0	Hypothetical protein (1)		Alpha/Beta hydrolase fold [IPR029058] (1)	scaffold_3_mRNA_1520.1	-	-
GF0027808	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1519.1	-	-
GF0027807	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_3_mRNA_1518.1	-	-
GF0027806	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_3_mRNA_1516.1	-	-
GF0027805	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1511.1	-	-
GF0027804	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1510.1	-	-
GF0027803	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_151.1	-	-
GF0027802	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1506.1	-	-
GF0027801	1	0	0	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	scaffold_3_mRNA_1503.1	-	-
GF0027800	1	0	0	RNA-directed DNA polymerase (Reverse transcriptase) (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_3_mRNA_1502.1	-	-
GF0027799	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1501.1	-	-
GF0027798	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1500.1	-	-
GF0027797	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1498.1	-	-
GF0027796	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1492.1	-	-
GF0027795	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_3_mRNA_1491.1	-	-
GF0027794	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1488.1	-	-
GF0027793	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1485.1	-	-
GF0027792	1	0	0	Hydrolase, alpha/beta fold family protein-like (1)		Alpha/Beta hydrolase fold [IPR029058] (1)	scaffold_3_mRNA_1483.1	-	-
GF0027791	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1481.1	-	-
GF0027790	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1469.1	-	-
GF0027789	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1467.1	-	-
GF0027788	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	Zinc finger, BED-type [IPR003656] (1); Zinc finger C2H2-type [IPR013087] (1)	scaffold_3_mRNA_1457.1	-	-
GF0027787	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1456.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0027786	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1449.1	-	-
GF0027785	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1447.1	-	-
GF0027784	1	0	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Carlavirus nucleic acid-binding protein [IPR002568] (1)	scaffold_3_mRNA_1444.1	-	-
GF0027783	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1443.1	-	-
GF0027782	1	0	0	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)	Protein kinase, ATP binding site [IPR017441] (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); Malectin-like carbohydrate-binding domain [IPR024788] (1)	scaffold_3_mRNA_1440.1	-	-
GF0027781	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1438.1	-	-
GF0027780	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1437.1	-	-
GF0027779	1	0	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1)	Retropepsins [IPR018061] (1); Aspartic peptidase, active site [IPR001969] (1); Aspartic peptidase domain [IPR021109] (1)	scaffold_3_mRNA_1431.1	-	-
GF0027778	1	0	0	Retrotransposon gag protein (1)			scaffold_3_mRNA_1426.1	-	-
GF0027777	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1419.1	-	-
GF0027776	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); TB2/DP1/HVA22-related protein [IPR004345] (1)	scaffold_3_mRNA_1418.1	-	-
GF0027775	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1409.1	-	-
GF0027774	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1408.1	-	-
GF0027773	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1404.1	-	-
GF0027772	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1403.1	-	-
GF0027771	1	0	0	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1)	NAD(P)-binding domain [IPR016040] (1); Alcohol dehydrogenase, C-terminal [IPR013149] (1)	scaffold_3_mRNA_1401.1	-	-
GF0027770	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1395.1	-	-
GF0027769	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1394.1	-	-
GF0027768	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_3_mRNA_1393.1	-	-
GF0027767	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1391.1	-	-
GF0027766	1	0	0	Hypothetical protein (1)	response to metal ion [GO:0010038 biological_process] (1); phytochelatin biosynthetic process [GO:0046938 biological_process] (1); glutathione gamma-glutamylcysteinyltransferase activity [GO:0016756 molecular_function] (1); metal ion binding [GO:0046872 molecular_function] (1)	Phytochelatin synthase, C-terminal [IPR015407] (1)	scaffold_3_mRNA_1390.1	-	-
GF0027765	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1386.1	-	-
GF0027764	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_3_mRNA_1385.1	-	-
GF0027763	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1383.1	-	-
GF0027762	1	0	0	Zinc finger containing preotein, putative (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, PMZ-type [IPR006564] (1); Zinc finger, SWIM-type [IPR007527] (1)	scaffold_3_mRNA_1382.1	-	-
GF0027761	1	0	0	Hypothetical protein (1)		Non-haem dioxygenase N-terminal domain [IPR026992] (1); Isopenicillin N synthase-like [IPR027443] (1)	scaffold_3_mRNA_1380.1	-	-
GF0027760	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1379.1	-	-
GF0027759	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1378.1	-	-
GF0027758	1	0	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	scaffold_3_mRNA_1377.1	-	-
GF0027757	1	0	0	Hypothetical protein (1)		Transposase-associated domain [IPR029480] (1)	scaffold_3_mRNA_1376.1	-	-
GF0027756	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1375.1	-	-
GF0027755	1	0	0	Syn-copalyl-diphosphate synthase (1)		Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (1)	scaffold_3_mRNA_1369.1	-	-
GF0027754	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1361.1	-	-
GF0027753	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Reverse transcriptase domain [IPR000477] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_3_mRNA_1359.1	-	-
GF0027752	1	0	0	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	scaffold_3_mRNA_1358.1	-	-
GF0027751	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1353.1	-	-
GF0027750	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1352.1	-	-
GF0027749	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1347.1	-	-
GF0027748	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1341.1	-	-
GF0027747	1	0	0	Hexadecanal dehydrogenase (acylating) (1)	fatty-acyl-CoA reductase (alcohol-forming) activity [GO:0080019 molecular_function] (1)	NAD(P)-binding domain [IPR016040] (1); Male sterility, NAD-binding [IPR013120] (1); Fatty acyl-CoA reductase [IPR026055] (1); Fatty acyl-CoA reductase, C-terminal [IPR033640] (1)	scaffold_3_mRNA_1333.1	-	-
GF0027746	1	0	0	Retrotransposon protein, putative, Ty1-copia subclass (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	scaffold_3_mRNA_1329.1	-	-
GF0027745	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1325.1	-	-
GF0027744	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1324.1	-	-
GF0027743	1	0	0	VQ motif-containing family protein (1)		VQ [IPR008889] (1)	scaffold_3_mRNA_1313.1	-	-
GF0027742	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1306.1	-	-
GF0027741	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1302.1	-	-
GF0027740	1	0	0	Monosacharide transport protein (1)			scaffold_3_mRNA_13.1	-	-
GF0027739	1	0	0	Putative disease resistance protein (TMV N-like) (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); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	scaffold_3_mRNA_1296.1	-	-
GF0027738	1	0	0	Hypothetical protein (1)		Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_3_mRNA_1295.1	-	-
GF0027737	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1294.1	-	-
GF0027736	1	0	0	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); Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	scaffold_3_mRNA_1293.1	-	-
GF0027735	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1288.1	-	-
GF0027734	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_3_mRNA_1287.1	-	-
GF0027733	1	0	0	Serine/threonine protein phosphatase 2A regulatory subunit A (1)	binding [GO:0005488 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	HEAT, type 2 [IPR021133] (1); HEAT repeat [IPR000357] (1); Armadillo-like helical [IPR011989] (1); Armadillo-type fold [IPR016024] (1)	scaffold_3_mRNA_1274.1	-	-
GF0027732	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1272.1	-	-
GF0027731	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1269.1	-	-
GF0027730	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1267.1	-	-
GF0027729	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_3_mRNA_1266.1	-	-
GF0027728	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1265.1	-	-
GF0027727	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1264.1	-	-
GF0027726	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_3_mRNA_1263.1	-	-
GF0027725	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_3_mRNA_1261.1	-	-
GF0027724	1	0	0	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)	scaffold_3_mRNA_1254.1	-	-
GF0027723	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1253.1	-	-
GF0027722	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1252.1	-	-
GF0027721	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1246.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0027720	1	0	0	Carbon catabolite repressor-like protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	scaffold_3_mRNA_1245.1	-	-
GF0027719	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1244.1	-	-
GF0027718	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1240.1	-	-
GF0027717	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1237.1	-	-
GF0027716	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_3_mRNA_1226.1	-	-
GF0027715	1	0	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	Zinc finger C2H2-type [IPR013087] (1); Zinc finger, BED-type [IPR003656] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	scaffold_3_mRNA_1225.1	-	-
GF0027714	1	0	0	General transcription factor 2-related zinc finger 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); Domain of unknown function DUF4371 [IPR025398] (1)	scaffold_3_mRNA_1223.1	-	-
GF0027713	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1201.1	-	-
GF0027712	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1199.1	-	-
GF0027711	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1196.1	-	-
GF0027710	1	0	0	Retrotransposon protein, putative, Ty3-gypsy subclass (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_3_mRNA_1188.1	-	-
GF0027709	1	0	0	Pre-mRNA-splicing factor syf2 (1)		mRNA splicing factor SYF2 [IPR013260] (1)	scaffold_3_mRNA_1159.1	-	-
GF0027708	1	0	0	Hypothetical protein (1)	metabolic process [GO:0008152 biological_process] (1); transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	scaffold_3_mRNA_1158.1	-	-
GF0027707	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1155.1	-	-
GF0027706	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	TB2/DP1/HVA22-related protein [IPR004345] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_3_mRNA_1142.1	-	-
GF0027705	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_3_mRNA_1131.1	-	-
GF0027704	1	0	0	Phytochelatin synthetase-like protein (1)	cell growth [GO:0016049 biological_process] (1); cellulose microfibril organization [GO:0010215 biological_process] (1); anchored component of membrane [GO:0031225 cellular_component] (1)	COBRA, plant [IPR006918] (1)	scaffold_3_mRNA_1127.1	-	-
GF0027703	1	0	0	COBRA-like extracellular glycosyl-phosphatidyl inositol-anchored protein family isoform 2 (1)	cellulose microfibril organization [GO:0010215 biological_process] (1); anchored component of membrane [GO:0031225 cellular_component] (1); cell growth [GO:0016049 biological_process] (1)	COBRA, plant [IPR006918] (1)	scaffold_3_mRNA_1124.1	-	-
GF0027702	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_3_mRNA_11.1	-	-
GF0027701	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1097.1	-	-
GF0027700	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1088.1	-	-
GF0027699	1	0	0	Putative non-LTR reverse transcriptase (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_3_mRNA_1085.1	-	-
GF0027698	1	0	0	ATP-dependent chaperone ClpB (1)	ATP binding [GO:0005524 molecular_function] (1)	AAA+ ATPase domain [IPR003593] (1); ClpA/B, conserved site 1 [IPR018368] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Clp ATPase, C-terminal [IPR019489] (1); ATPase, AAA-type, core [IPR003959] (1)	scaffold_3_mRNA_1075.1	-	-
GF0027697	1	0	0	UDP-glycosyltransferase 83A1 (1)	metabolic process [GO:0008152 biological_process] (1); transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	scaffold_3_mRNA_1066.1	-	-
GF0027696	1	0	0	UDP-glycosyltransferase 83A1 (1)	transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	scaffold_3_mRNA_1064.1	-	-
GF0027695	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1062.1	-	-
GF0027694	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_3_mRNA_1061.1	-	-
GF0027693	1	0	0	Bidirectional sugar transporter SWEET4 (1)	integral component of membrane [GO:0016021 cellular_component] (1)	SWEET sugar transporter [IPR004316] (1)	scaffold_3_mRNA_105.1	-	-
GF0027692	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1046.1	-	-
GF0027691	1	0	0	AT hook motif-containing protein, putative (1)	telomere maintenance [GO:0000723 biological_process] (1); DNA helicase activity [GO:0003678 molecular_function] (1); DNA repair [GO:0006281 biological_process] (1)	DNA helicase Pif1-like [IPR010285] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_3_mRNA_1027.1	-	-
GF0027690	1	0	0	Hypothetical protein (1)			scaffold_3_mRNA_1014.1	-	-
GF0027689	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1)	Aspartic peptidase domain [IPR021109] (1); Ribonuclease H-like domain [IPR012337] (1); Ribonuclease H domain [IPR002156] (1)	scaffold_3_mRNA_1012.1	-	-
GF0027688	1	0	0	Hypothetical protein (1)	GTP binding [GO:0005525 molecular_function] (1); transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (1)	Small GTPase superfamily, ARF/SAR type [IPR006689] (1); Transferase [IPR003480] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_2_mRNA_996.1	-	-
GF0027687	1	0	0	Hypothetical protein (1)		Bifunctional inhibitor/plant lipid transfer protein/seed storage helical domain [IPR016140] (1)	scaffold_2_mRNA_959.1	-	-
GF0027686	1	0	0	Kinase family protein with leucine-rich repeat domain (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)	scaffold_2_mRNA_957.1	-	-
GF0027685	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_2_mRNA_955.1	-	-
GF0027684	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_946.1	-	-
GF0027683	1	0	0	Hypothetical protein (1)	integral component of membrane [GO:0016021 cellular_component] (1); transporter activity [GO:0005215 molecular_function] (1)	Purine permease, plant [IPR030182] (1)	scaffold_2_mRNA_936.1	-	-
GF0027682	1	0	0	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1)	Saccharopine dehydrogenase, NADP binding domain [IPR005097] (1); NAD(P)-binding domain [IPR016040] (1)	scaffold_2_mRNA_927.1	-	-
GF0027681	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_925.1	-	-
GF0027680	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_924.1	-	-
GF0027679	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_921.1	-	-
GF0027678	1	0	0	Receptor like protein 33 (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)	scaffold_2_mRNA_918.1	-	-
GF0027677	1	0	0	Retrotransposon protein, putative, unclassified (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Endonuclease/exonuclease/phosphatase [IPR005135] (1); Reverse transcriptase domain [IPR000477] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_2_mRNA_91.1	-	-
GF0027676	1	0	0	Transposon protein, putative, Pong sub-class, expressed (1)		No apical meristem-associated, C-terminal domain [IPR029466] (1)	scaffold_2_mRNA_902.1	-	-
GF0027675	1	0	0	Disease resistance protein (CC-NBS-LRR class) family protein, putative (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_2_mRNA_895.1	-	-
GF0027674	1	0	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	scaffold_2_mRNA_894.1	-	-
GF0027673	1	0	0	Disease resistance protein (CC-NBS-LRR class) family 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); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1)	scaffold_2_mRNA_893.1	-	-
GF0027672	1	0	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_2_mRNA_891.1	-	-
GF0027671	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_890.1	-	-
GF0027670	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_86.1	-	-
GF0027669	1	0	0	Protein TRANSPARENT TESTA 1 (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger C2H2-type [IPR013087] (1)	scaffold_2_mRNA_844.1	-	-
GF0027668	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_843.1	-	-
GF0027667	1	0	0	Hypothetical protein (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	scaffold_2_mRNA_840.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0027666	1	0	0	Monosacharide transport protein (1)			scaffold_2_mRNA_838.1	-	-
GF0027665	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_837.1	-	-
GF0027664	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_833.1	-	-
GF0027663	1	0	0	LRR receptor-like kinase family protein (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Tyrosine-protein kinase, active site [IPR008266] (1); Protein kinase, ATP binding site [IPR017441] (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)	scaffold_2_mRNA_832.1	-	-
GF0027662	1	0	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1)	Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1)	scaffold_2_mRNA_830.1	-	-
GF0027661	1	0	0	LRR receptor-like kinase family protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Tyrosine-protein kinase, active site [IPR008266] (1); Protein kinase, ATP binding site [IPR017441] (1); Leucine-rich repeat [IPR001611] (1)	scaffold_2_mRNA_829.1	-	-
GF0027660	1	0	0	Ulp1 protease family, carboxy-terminal domain protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Probable transposase, Ptta/En/Spm, plant [IPR004252] (1); Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	scaffold_2_mRNA_82.1	-	-
GF0027659	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_819.1	-	-
GF0027658	1	0	0	Hypothetical protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	scaffold_2_mRNA_817.1	-	-
GF0027657	1	0	0	Hypothetical protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	scaffold_2_mRNA_814.1	-	-
GF0027656	1	0	0	Putative muDR family transposase-like (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	MULE transposase domain [IPR018289] (1); Zinc finger, PMZ-type [IPR006564] (1); Zinc finger, SWIM-type [IPR007527] (1); Zinc finger, CCHC-type [IPR001878] (1)	scaffold_2_mRNA_812.1	-	-
GF0027655	1	0	0	Hypothetical protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	scaffold_2_mRNA_808.1	-	-
GF0027654	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_806.1	-	-
GF0027653	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			scaffold_2_mRNA_804.1	-	-
GF0027652	1	0	0	DUF594 family protein (1)		Protein of unknown function DUF594 [IPR007658] (1); Domain of unknown function DUF4220 [IPR025315] (1)	scaffold_2_mRNA_789.1	-	-
GF0027651	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1)	Endonuclease/exonuclease/phosphatase [IPR005135] (1); Zinc knuckle CX2CX4HX4C [IPR025836] (1); Zinc finger, CCHC-type [IPR001878] (1); Ribonuclease H domain [IPR002156] (1); Domain of unknown function DUF4283 [IPR025558] (1); Ribonuclease H-like domain [IPR012337] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1)	scaffold_2_mRNA_779.1	-	-
GF0027650	1	0	0	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)	scaffold_2_mRNA_778.1	-	-
GF0027649	1	0	0	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1)	Cytochrome P450, conserved site [IPR017972] (1); Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450 [IPR001128] (1)	scaffold_2_mRNA_771.1	-	-
GF0027648	1	0	0	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1)	Cytochrome P450 [IPR001128] (1)	scaffold_2_mRNA_768.1	-	-
GF0027647	1	0	0	Cytochrome P450 71D8 (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)	scaffold_2_mRNA_767.1	-	-
GF0027646	1	0	0	Flavonoid 3'-monooxygenase (1)	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1)	Cytochrome P450 [IPR001128] (1)	scaffold_2_mRNA_766.1	-	-
GF0027645	1	0	0	TMV resistance protein N (1)	signal transduction [GO:0007165 biological_process] (1); protein binding [GO:0005515 molecular_function] (1)	Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1)	scaffold_2_mRNA_760.1	-	-
GF0027644	1	0	0	UDP-glycosyltransferase 92A1 (1)	transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	scaffold_2_mRNA_754.1	-	-
GF0027643	1	0	0	UDP-glucose flavonoid 3-O-glucosyltransferase 7 (1)	transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	scaffold_2_mRNA_749.1	-	-
GF0027642	1	0	0	Hypothetical protein (1)	transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	scaffold_2_mRNA_747.1	-	-
GF0027641	1	0	0	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)	scaffold_2_mRNA_744.1	-	-
GF0027640	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_737.1	-	-
GF0027639	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_734.1	-	-
GF0027638	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_733.1	-	-
GF0027637	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_732.1	-	-
GF0027636	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_731.1	-	-
GF0027635	1	0	0	Hypothetical protein (1)		GAG-pre-integrase domain [IPR025724] (1)	scaffold_2_mRNA_728.1	-	-
GF0027634	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_723.1	-	-
GF0027633	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_720.1	-	-
GF0027632	1	0	0	Monosacharide transport protein (1)			scaffold_2_mRNA_719.1	-	-
GF0027631	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_714.1	-	-
GF0027630	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc knuckle CX2CX4HX4C [IPR025836] (1); Zinc finger, CCHC-type [IPR001878] (1); Domain of unknown function DUF4283 [IPR025558] (1); Ribonuclease H-like domain [IPR012337] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1)	scaffold_2_mRNA_713.1	-	-
GF0027629	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_706.1	-	-
GF0027628	1	0	0	Non-LTR reverse transcriptase (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Endonuclease/exonuclease/phosphatase [IPR005135] (1); Zinc finger, CCHC-type [IPR001878] (1)	scaffold_2_mRNA_699.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0027627	1	0	0	Hypothetical protein (1)	lyase activity [GO:0016829 molecular_function] (1); terpene synthase activity [GO:0010333 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Terpene synthase, N-terminal domain [IPR001906] (1); Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (1)	scaffold_2_mRNA_688.1	-	-
GF0027626	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_687.1	-	-
GF0027625	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_686.1	-	-
GF0027624	1	0	0	Hypothetical protein (1)		Protein kinase-like domain [IPR011009] (1)	scaffold_2_mRNA_677.1	-	-
GF0027623	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_673.1	-	-
GF0027622	1	0	0	G-type lectin S-receptor-like serine/threonine-protein kinase RLK1 (1)	ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1); Bulb-type lectin domain [IPR001480] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase, ATP binding site [IPR017441] (1)	scaffold_2_mRNA_666.1	-	-
GF0027621	1	0	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1)	Bulb-type lectin domain [IPR001480] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	scaffold_2_mRNA_665.1	-	-
GF0027620	1	0	0	Hypothetical protein (1)		GAG-pre-integrase domain [IPR025724] (1)	scaffold_2_mRNA_662.1	-	-
GF0027619	1	0	0	G-type lectin S-receptor-like serine/threonine-protein kinase RLK1 (1)	ATP binding [GO:0005524 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase, ATP binding site [IPR017441] (1); Serine/threonine-protein kinase, active site [IPR008271] (1)	scaffold_2_mRNA_659.1	-	-
GF0027618	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_657.1	-	-
GF0027617	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_656.1	-	-
GF0027616	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_654.1	-	-
GF0027615	1	0	0	2-oxoglutarate and Fe(II)-dependent oxygenase superfamily protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1)	Isopenicillin N synthase-like [IPR027443] (1); Non-haem dioxygenase N-terminal domain [IPR026992] (1); Oxoglutarate/iron-dependent dioxygenase [IPR005123] (1)	scaffold_2_mRNA_65.1	-	-
GF0027614	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_638.1	-	-
GF0027613	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_634.1	-	-
GF0027612	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, SWIM-type [IPR007527] (1); Zinc finger, PMZ-type [IPR006564] (1); MULE transposase domain [IPR018289] (1)	scaffold_2_mRNA_627.1	-	-
GF0027611	1	0	0	Callose synthase 3 (1)	membrane [GO:0016020 cellular_component] (1); 1,3-beta-D-glucan synthase complex [GO:0000148 cellular_component] (1); 1,3-beta-D-glucan synthase activity [GO:0003843 molecular_function] (1); (1->3)-beta-D-glucan biosynthetic process [GO:0006075 biological_process] (1)	Glycosyl transferase, family 48 [IPR003440] (1); 1,3-beta-glucan synthase subunit FKS1-like, domain-1 [IPR026899] (1); Vacuolar protein sorting-associate protein Vta1/Callose synthase, N-terminal domain [IPR023175] (1)	scaffold_2_mRNA_625.1	-	-
GF0027610	1	0	0	Peroxidase 15 (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); hydrogen peroxide catabolic process [GO:0042744 biological_process] (1)	Haem peroxidase [IPR010255] (1); Haem peroxidase, plant/fungal/bacterial [IPR002016] (1); Secretory peroxidase [IPR033905] (1); Peroxidase, active site [IPR019794] (1); Peroxidases heam-ligand binding site [IPR019793] (1); Plant peroxidase [IPR000823] (1)	scaffold_2_mRNA_618.1	-	-
GF0027609	1	0	0	Peroxidase 15 (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); hydrogen peroxide catabolic process [GO:0042744 biological_process] (1)	Secretory peroxidase [IPR033905] (1); Haem peroxidase, plant/fungal/bacterial [IPR002016] (1); Peroxidase, active site [IPR019794] (1); Plant peroxidase [IPR000823] (1); Haem peroxidase [IPR010255] (1)	scaffold_2_mRNA_617.1	-	-
GF0027608	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_599.1	-	-
GF0027607	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_2_mRNA_591.1	-	-
GF0027606	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_590.1	-	-
GF0027605	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_588.1	-	-
GF0027604	1	0	0	DUF247 domain protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	scaffold_2_mRNA_586.1	-	-
GF0027603	1	0	0	Hypothetical protein (1)		GAG-pre-integrase domain [IPR025724] (1)	scaffold_2_mRNA_585.1	-	-
GF0027602	1	0	0	UPF0481 protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	scaffold_2_mRNA_583.1	-	-
GF0027601	1	0	0	PPR containing plant-like protein (1)	protein binding [GO:0005515 molecular_function] (1)	Protein kinase-like domain [IPR011009] (1); Pentatricopeptide repeat [IPR002885] (1); Tetratricopeptide-like helical domain [IPR011990] (1)	scaffold_2_mRNA_581.1	-	-
GF0027600	1	0	0	Hypothetical protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	scaffold_2_mRNA_578.1	-	-
GF0027599	1	0	0	UPF0481 protein (1)		Protein of unknown function DUF247, plant [IPR004158] (1)	scaffold_2_mRNA_575.1	-	-
GF0027598	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_570.1	-	-
GF0027597	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_569.1	-	-
GF0027596	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_2_mRNA_568.1	-	-
GF0027595	1	0	0	Cytochrome P450 83B1 (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); iron ion binding [GO:0005506 molecular_function] (1)	Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450 [IPR001128] (1)	scaffold_2_mRNA_559.1	-	-
GF0027594	1	0	0	Caffeic acid 3-O-methyltransferase (1)	protein dimerization activity [GO:0046983 molecular_function] (1); O-methyltransferase activity [GO:0008171 molecular_function] (1); methyltransferase activity [GO:0008168 molecular_function] (1)	S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); O-methyltransferase COMT-type [IPR016461] (1); Plant methyltransferase dimerisation [IPR012967] (1); O-methyltransferase, family 2 [IPR001077] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1)	scaffold_2_mRNA_556.1	-	-
GF0027593	1	0	0	Hypothetical protein (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)	scaffold_2_mRNA_551.1	-	-
GF0027592	1	0	0	Transmembrane protein 45B (1)		Protein of unknown function DUF716 (TMEM45) [IPR006904] (1)	scaffold_2_mRNA_549.1	-	-
GF0027591	1	0	0	Cytochrome P450 83B1 (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, conserved site [IPR017972] (1); Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450 [IPR001128] (1)	scaffold_2_mRNA_546.1	-	-
GF0027590	1	0	0	Hypothetical protein (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); cytoplasm [GO:0005737 cellular_component] (1); lipid metabolic process [GO:0006629 biological_process] (1)	3-oxo-5-alpha-steroid 4-dehydrogenase, C-terminal [IPR001104] (1)	scaffold_2_mRNA_527.1	-	-
GF0027589	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_526.1	-	-
GF0027588	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_504.1	-	-
GF0027587	1	0	0	Hypothetical protein (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Aspartic peptidase domain [IPR021109] (1); Aspartic peptidase, active site [IPR001969] (1)	scaffold_2_mRNA_503.1	-	-
GF0027586	1	0	0	Hypothetical protein (1)	mitochondrial matrix [GO:0005759 cellular_component] (1)	Mitochondrial glycoprotein [IPR003428] (1)	scaffold_2_mRNA_501.1	-	-
GF0027585	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_496.1	-	-
GF0027584	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_2_mRNA_495.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0027583	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc knuckle CX2CX4HX4C [IPR025836] (1); Ribonuclease H-like domain [IPR012337] (1); Domain of unknown function DUF4283 [IPR025558] (1)	scaffold_2_mRNA_478.1	-	-
GF0027582	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_4712.1	-	-
GF0027581	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	DYW domain [IPR032867] (1); Tetratricopeptide-like helical domain [IPR011990] (1)	scaffold_2_mRNA_4707.1	-	-
GF0027580	1	0	0	Hexosyltransferase (1)	polygalacturonate 4-alpha-galacturonosyltransferase activity [GO:0047262 molecular_function] (1); transferase activity, transferring glycosyl groups [GO:0016757 molecular_function] (1)	Nucleotide-diphospho-sugar transferases [IPR029044] (1); Plant galacturonosyltransferase GAUT [IPR029993] (1); Glycosyl transferase, family 8 [IPR002495] (1)	scaffold_2_mRNA_4706.1	-	-
GF0027579	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_47.1	-	-
GF0027578	1	0	0	RNA-directed DNA polymerase , related (1)			scaffold_2_mRNA_466.1	-	-
GF0027577	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_4642.1	-	-
GF0027576	1	0	0	ER membrane protein complex subunit 3 (1)	membrane [GO:0016020 cellular_component] (1)	ER membrane protein complex subunit 3 [IPR008568] (1); Integral membrane protein EMC3/TMCO1-like [IPR002809] (1)	scaffold_2_mRNA_4637.1	-	-
GF0027575	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_4636.1	-	-
GF0027574	1	0	0	Hypothetical protein (1)	oxidoreductase activity [GO:0016491 molecular_function] (1)	Short-chain dehydrogenase/reductase, conserved site [IPR020904] (1); NAD(P)-binding domain [IPR016040] (1); Short-chain dehydrogenase/reductase SDR [IPR002347] (1)	scaffold_2_mRNA_4615.1	-	-
GF0027573	1	0	0	RPM1 interacting protein 4 transcript 2 (1)		RIN4, pathogenic type III effector avirulence factor Avr cleavage site [IPR008700] (1)	scaffold_2_mRNA_4612.1	-	-
GF0027572	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_4510.1	-	-
GF0027571	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_4508.1	-	-
GF0027570	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_2_mRNA_4506.1	-	-
GF0027569	1	0	0	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 3 C-terminal domain [IPR002772] (1); Immunoglobulin-like fold [IPR013783] (1); Fibronectin type III-like domain [IPR026891] (1)	scaffold_2_mRNA_4487.1	-	-
GF0027568	1	0	0	Chlorophyll a/b binding protein (1)	membrane [GO:0016020 cellular_component] (1); photosynthesis, light harvesting [GO:0009765 biological_process] (1)	Chlorophyll a/b binding protein domain [IPR023329] (1); Chlorophyll A-B binding protein, plant [IPR001344] (1); Chlorophyll A-B binding protein [IPR022796] (1)	scaffold_2_mRNA_4483.1	-	-
GF0027567	1	0	0	Chlorophyll a/b binding protein (1)	membrane [GO:0016020 cellular_component] (1); photosynthesis, light harvesting [GO:0009765 biological_process] (1)	Chlorophyll a/b binding protein domain [IPR023329] (1); Chlorophyll A-B binding protein, plant [IPR001344] (1); Chlorophyll A-B binding protein [IPR022796] (1)	scaffold_2_mRNA_4481.1	-	-
GF0027566	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_4455.1	-	-
GF0027565	1	0	0	Leucine-rich repeat protein kinase family protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_2_mRNA_4403.1	-	-
GF0027564	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_4402.1	-	-
GF0027563	1	0	0	LRR receptor-like kinase family protein (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase, ATP binding site [IPR017441] (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)	scaffold_2_mRNA_4401.1	-	-
GF0027562	1	0	0	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	scaffold_2_mRNA_4400.1	-	-
GF0027561	1	0	0	Hypothetical protein (1)	protein domain specific binding [GO:0019904 molecular_function] (1)	14-3-3 protein, conserved site [IPR023409] (1); 14-3-3 protein [IPR000308] (1); Agenet domain, plant type [IPR014002] (1); 14-3-3 domain [IPR023410] (1); Agenet-like domain [IPR008395] (1)	scaffold_2_mRNA_4380.1	-	-
GF0027560	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_4359.1	-	-
GF0027559	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, PMZ-type [IPR006564] (1); Zinc finger, SWIM-type [IPR007527] (1); Zinc finger, CCHC-type [IPR001878] (1); FHY3/FAR1 family [IPR031052] (1)	scaffold_2_mRNA_4337.1	-	-
GF0027558	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_4303.1	-	-
GF0027557	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_4285.1	-	-
GF0027556	1	0	0	Callose synthase 1 catalytic subunit-like 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)	Histidine phosphatase superfamily, clade-1 [IPR013078] (1); Glycosyl transferase, family 48 [IPR003440] (1); Histidine phosphatase superfamily [IPR029033] (1)	scaffold_2_mRNA_4273.1	-	-
GF0027555	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_426.1	-	-
GF0027554	1	0	0	ABC transporter G family member 9 (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)	scaffold_2_mRNA_4229.1	-	-
GF0027553	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_4210.1	-	-
GF0027552	1	0	0	Nuclease S1 (1)	DNA catabolic process [GO:0006308 biological_process] (1); hydrolase activity, acting on ester bonds [GO:0016788 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1); endonuclease activity [GO:0004519 molecular_function] (1)	S1/P1 nuclease [IPR003154] (1); Phospholipase C/P1 nuclease domain [IPR008947] (1)	scaffold_2_mRNA_4206.1	-	-
GF0027551	1	0	0	Quinone oxidoreductase PIG3 (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1)	Quinone oxidoreductase PIG3 [IPR014189] (1); NAD(P)-binding domain [IPR016040] (1); Polyketide synthase, enoylreductase domain [IPR020843] (1); Alcohol dehydrogenase, N-terminal [IPR013154] (1); Alcohol dehydrogenase, C-terminal [IPR013149] (1); GroES-like [IPR011032] (1)	scaffold_2_mRNA_4205.1	-	-
GF0027550	1	0	0	Hypothetical protein (1)		Protein of unknown function DUF761, plant [IPR008480] (1); Organic solute transporter subunit alpha/Transmembrane protein 184 [IPR005178] (1)	scaffold_2_mRNA_4200.1	-	-
GF0027549	1	0	0	Nucleolar protein 12, 25 kDa protein (1)		Nucleolar protein 12 [IPR019186] (1)	scaffold_2_mRNA_4193.1	-	-
GF0027548	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_4192.1	-	-
GF0027547	1	0	0	Hypothetical protein (1)	structural molecule activity [GO:0005198 molecular_function] (1)	Polyhedrin [IPR001746] (1)	scaffold_2_mRNA_4183.1	-	-
GF0027546	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_4180.1	-	-
GF0027545	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_418.1	-	-
GF0027544	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_4162.1	-	-
GF0027543	1	0	0	Cysteine-rich RLK (Receptor-like kinase) protein (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1)	Protein kinase-like domain [IPR011009] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1)	scaffold_2_mRNA_4153.1	-	-
GF0027542	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_2_mRNA_415.1	-	-
GF0027541	1	0	0	Adipocyte plasma membrane-associated 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)	scaffold_2_mRNA_413.1	-	-
GF0027540	1	0	0	Cysteine-rich receptor-like protein kinase 25 (1)		Protein kinase-like domain [IPR011009] (1); Gnk2-homologous domain [IPR002902] (1)	scaffold_2_mRNA_4129.1	-	-
GF0027539	1	0	0	Monosacharide transport protein (1)			scaffold_2_mRNA_4127.1	-	-
GF0027538	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_4126.1	-	-

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GF0027537	1	0	0	Hypothetical protein (1)	viral process [GO:0016032 biological_process] (1)	Retrovirus capsid, C-terminal [IPR008916] (1); Retrotransposon gag domain [IPR005162] (1); Retroviral nucleocapsid protein Gag [IPR000721] (1)	scaffold_2_mRNA_4125.1	-	-
GF0027536	1	0	0	Hypothetical protein (1)		Gnk2-homologous domain [IPR002902] (1)	scaffold_2_mRNA_4124.1	-	-
GF0027535	1	0	0	Vacuolar iron transporter like 4 (1)		Ccc1 family [IPR008217] (1)	scaffold_2_mRNA_4096.1	-	-
GF0027534	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_408.1	-	-
GF0027533	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_4078.1	-	-
GF0027532	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_2_mRNA_405.1	-	-
GF0027531	1	0	0	Hypothetical protein (1)	metalloendopeptidase activity [GO:0004222 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1); metallopeptidase activity [GO:0008237 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1); extracellular matrix [GO:0031012 cellular_component] (1)	Peptidase M10A, cysteine switch, zinc binding site [IPR021158] (1); Metallopeptidase, catalytic domain [IPR024079] (1); Peptidoglycan binding-like [IPR002477] (1)	scaffold_2_mRNA_4031.1	-	-
GF0027530	1	0	0	ABC transporter C family member 2 (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-like [IPR003439] (1); ABC transporter type 1, transmembrane domain [IPR011527] (1); AAA+ ATPase domain [IPR003593] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); ABC transporter, conserved site [IPR017871] (1)	scaffold_2_mRNA_4028.1	-	-
GF0027529	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_402.1	-	-
GF0027528	1	0	0	Glycolipid transfer protein domain-containing protein 1 (1)	glycolipid transport [GO:0046836 biological_process] (1); glycolipid transporter activity [GO:0017089 molecular_function] (1); glycolipid binding [GO:0051861 molecular_function] (1); cytoplasm [GO:0005737 cellular_component] (1)	Glycolipid transfer protein domain [IPR014830] (1)	scaffold_2_mRNA_4019.1	-	-
GF0027527	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_4000.1	-	-
GF0027526	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3999.1	-	-
GF0027525	1	0	0	Tubulin beta-9 chain (1)	GTPase activity [GO:0003924 molecular_function] (1); microtubule-based process [GO:0007017 biological_process] (1); GTP binding [GO:0005525 molecular_function] (1); microtubule [GO:0005874 cellular_component] (1); structural constituent of cytoskeleton [GO:0005200 molecular_function] (1)	Tubulin [IPR000217] (1); Beta tubulin, autoregulation binding site [IPR013838] (1); Beta tubulin [IPR002453] (1); Tubulin, conserved site [IPR017975] (1); Tubulin/FtsZ, GTPase domain [IPR003008] (1)	scaffold_2_mRNA_3988.1	-	-
GF0027524	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3984.1	-	-
GF0027523	1	0	0	Hypothetical protein (1)	iron ion binding [GO:0005506 molecular_function] (1); lipid biosynthetic process [GO:0008610 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Fatty acid hydroxylase [IPR006694] (1)	scaffold_2_mRNA_3983.1	-	-
GF0027522	1	0	0	FAD-binding Berberine family protein (1)	catalytic activity [GO:0003824 molecular_function] (1); oxidoreductase activity, acting on CH-OH group of donors [GO:0016614 molecular_function] (1); flavin adenine dinucleotide binding [GO:0050660 molecular_function] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Berberine/berberine-like [IPR012951] (1); FAD-binding, type 2, subdomain 1 [IPR016167] (1); CO dehydrogenase flavoprotein-like, FAD-binding, subdomain 2 [IPR016169] (1); FAD linked oxidase, N-terminal [IPR006094] (1); FAD-binding, type 2 [IPR016166] (1)	scaffold_2_mRNA_3980.1	-	-
GF0027521	1	0	0	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, subdomain 1 [IPR016167] (1); CO dehydrogenase flavoprotein-like, FAD-binding, subdomain 2 [IPR016169] (1); FAD linked oxidase, N-terminal [IPR006094] (1); FAD-binding, type 2 [IPR016166] (1); Berberine/berberine-like [IPR012951] (1)	scaffold_2_mRNA_3975.1	-	-
GF0027520	1	0	0	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); flavin adenine dinucleotide binding [GO:0050660 molecular_function] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (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); Berberine/berberine-like [IPR012951] (1)	scaffold_2_mRNA_3974.1	-	-
GF0027519	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_2_mRNA_3971.1	-	-
GF0027518	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3970.1	-	-
GF0027517	1	0	0	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); 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 linked oxidase, N-terminal [IPR006094] (1); FAD-binding, type 2 [IPR016166] (1)	scaffold_2_mRNA_3969.1	-	-
GF0027516	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3957.1	-	-
GF0027515	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3955.1	-	-
GF0027514	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3924.1	-	-
GF0027513	1	0	0	DNA/RNA polymerases superfamily protein (1)			scaffold_2_mRNA_3922.1	-	-
GF0027512	1	0	0	Leucine-rich repeat transmembrane protein kinase (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1); Malectin [IPR021720] (1)	scaffold_2_mRNA_3918.1	-	-
GF0027511	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3912.1	-	-
GF0027510	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3881.1	-	-
GF0027509	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3880.1	-	-
GF0027508	1	0	0	Hypothetical protein (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Retrotransposon gag domain [IPR005162] (1); Aspartic peptidase domain [IPR021109] (1); Peptidase A2A, retrovirus, catalytic [IPR001995] (1)	scaffold_2_mRNA_3879.1	-	-
GF0027507	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3878.1	-	-
GF0027506	1	0	0	Hypothetical protein (1)	carbohydrate binding [GO:0030246 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1); hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (1)	Galactose mutarotase-like domain [IPR011013] (1); Glycoside hydrolase family 31 [IPR000322] (1)	scaffold_2_mRNA_3866.1	-	-
GF0027505	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_2_mRNA_3863.1	-	-
GF0027504	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3862.1	-	-
GF0027503	1	0	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_2_mRNA_3858.1	-	-
GF0027502	1	0	0	Glutathione transferase (1)		Glutathione S-transferase, C-terminal-like [IPR010987] (1); Glutathione S-transferase (GST) [IPR016639] (1)	scaffold_2_mRNA_3856.1	-	-
GF0027501	1	0	0	Verticillium wilt resistance-like 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)	scaffold_2_mRNA_3840.1	-	-
GF0027500	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_2_mRNA_3839.1	-	-
GF0027499	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3835.1	-	-
GF0027498	1	0	0	Verticillium wilt disease resistance 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)	scaffold_2_mRNA_3831.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0027497	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); threonine-type endopeptidase activity [GO:0004298 molecular_function] (1); proteolysis involved in cellular protein catabolic process [GO:0051603 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1); proteasome core complex [GO:0005839 cellular_component] (1)	Zinc knuckle CX2CX4HX4C [IPR025836] (1); Proteasome, subunit alpha/beta [IPR001353] (1); Zinc finger, CCHC-type [IPR001878] (1); Endonuclease/exonuclease/phosphatase [IPR005135] (1); Nucleophile aminohydrolases, N-terminal [IPR029055] (1); Domain of unknown function DUF4283 [IPR025558] (1)	scaffold_2_mRNA_3779.1	-	-
GF0027496	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_371.1	-	-
GF0027495	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_370.1	-	-
GF0027494	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3673.1	-	-
GF0027493	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_2_mRNA_3672.1	-	-
GF0027492	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_367.1	-	-
GF0027491	1	0	0	Hypothetical 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)	PPM-type phosphatase domain [IPR001932] (1); Protein phosphatase 2C family [IPR015655] (1)	scaffold_2_mRNA_3666.1	-	-
GF0027490	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3641.1	-	-
GF0027489	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_364.1	-	-
GF0027488	1	0	0	Receptor kinase (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1); polysaccharide binding [GO:0030247 molecular_function] (1)	Protein kinase, ATP binding site [IPR017441] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); Protein kinase-like domain [IPR011009] (1); Wall-associated receptor kinase, galacturonan-binding domain [IPR025287] (1)	scaffold_2_mRNA_3630.1	-	-
GF0027487	1	0	0	Monosacharide transport protein (1)			scaffold_2_mRNA_3628.1	-	-
GF0027486	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_2_mRNA_3627.1	-	-
GF0027485	1	0	0	Hypothetical protein (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1); Protein kinase, ATP binding site [IPR017441] (1); Wall-associated receptor kinase, C-terminal [IPR032872] (1)	scaffold_2_mRNA_3623.1	-	-
GF0027484	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3622.1	-	-
GF0027483	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3621.1	-	-
GF0027482	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3620.1	-	-
GF0027481	1	0	0	Hypothetical protein (1)	sigma factor antagonist activity [GO:0016989 molecular_function] (1)	Anti sigma-E protein RseA, N-terminal [IPR005572] (1)	scaffold_2_mRNA_3619.1	-	-
GF0027480	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3618.1	-	-
GF0027479	1	0	0	Hypothetical protein (1)	polysaccharide binding [GO:0030247 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); Protein kinase-like domain [IPR011009] (1); Wall-associated receptor kinase, galacturonan-binding domain [IPR025287] (1); Zinc finger, SWIM-type [IPR007527] (1); MULE transposase domain [IPR018289] (1); Zinc finger, PMZ-type [IPR006564] (1)	scaffold_2_mRNA_3614.1	-	-
GF0027478	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3613.1	-	-
GF0027477	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3612.1	-	-
GF0027476	1	0	0	Hypothetical protein (1)	polysaccharide binding [GO:0030247 molecular_function] (1)	Wall-associated receptor kinase, galacturonan-binding domain [IPR025287] (1); Aspartic peptidase domain [IPR021109] (1)	scaffold_2_mRNA_3610.1	-	-
GF0027475	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3606.1	-	-
GF0027474	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3605.1	-	-
GF0027473	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3604.1	-	-
GF0027472	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3601.1	-	-
GF0027471	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3596.1	-	-
GF0027470	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3594.1	-	-
GF0027469	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			scaffold_2_mRNA_3593.1	-	-
GF0027468	1	0	0	Hypothetical protein (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1); polysaccharide binding [GO:0030247 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); Wall-associated receptor kinase, galacturonan-binding domain [IPR025287] (1); Serine/threonine-protein kinase, active site [IPR008271] (1)	scaffold_2_mRNA_3592.1	-	-
GF0027467	1	0	0	PR5-like 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-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1); Serine/threonine-protein kinase, active site [IPR008271] (1)	scaffold_2_mRNA_3591.1	-	-
GF0027466	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3590.1	-	-
GF0027465	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_359.1	-	-
GF0027464	1	0	0	Hypothetical protein (1)	polysaccharide binding [GO:0030247 molecular_function] (1)	Wall-associated receptor kinase, galacturonan-binding domain [IPR025287] (1)	scaffold_2_mRNA_3589.1	-	-
GF0027463	1	0	0	Hypothetical protein (1)	transmembrane transport [GO:0055085 biological_process] (1); antiporter activity [GO:0015297 molecular_function] (1); drug transmembrane transporter activity [GO:0015238 molecular_function] (1); membrane [GO:0016020 cellular_component] (1); drug transmembrane transport [GO:0006855 biological_process] (1)	Multi antimicrobial extrusion protein [IPR002528] (1)	scaffold_2_mRNA_3577.1	-	-
GF0027462	1	0	0	Hypothetical protein (1)	cytoplasm [GO:0005737 cellular_component] (1); protein folding [GO:0006457 biological_process] (1)	GroES-like [IPR011032] (1); GroES chaperonin family [IPR020818] (1)	scaffold_2_mRNA_3525.1	-	-
GF0027461	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3523.1	-	-
GF0027460	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, SWIM-type [IPR007527] (1); Zinc finger, PMZ-type [IPR006564] (1); Zinc finger, CCHC-type [IPR001878] (1)	scaffold_2_mRNA_3519.1	-	-
GF0027459	1	0	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	scaffold_2_mRNA_3506.1	-	-
GF0027458	1	0	0	Hypothetical protein (1)	response to biotic stimulus [GO:0009607 biological_process] (1); defense response [GO:0006952 biological_process] (1)	Bet v I/Major latex protein [IPR000916] (1); START-like domain [IPR023393] (1)	scaffold_2_mRNA_3505.1	-	-
GF0027457	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3485.1	-	-
GF0027456	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3482.1	-	-
GF0027455	1	0	0	Hypothetical protein (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1); hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (1)	Glycoside hydrolase superfamily [IPR017853] (1); Glycoside hydrolase family 17 [IPR000490] (1); Reverse transcriptase domain [IPR000477] (1); X8 domain [IPR012946] (1); Endonuclease/exonuclease/phosphatase [IPR005135] (1)	scaffold_2_mRNA_3475.1	-	-
GF0027454	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3467.1	-	-
GF0027453	1	0	0	Hypothetical protein (1)	ubiquitin protein ligase binding [GO:0031625 molecular_function] (1); ubiquitin-dependent protein catabolic process [GO:0006511 biological_process] (1)	Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Cullin homology [IPR016158] (1); Cullin, N-terminal [IPR001373] (1)	scaffold_2_mRNA_3460.1	-	-
GF0027452	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3456.1	-	-
GF0027451	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3455.1	-	-
GF0027450	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3440.1	-	-
GF0027449	1	0	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); DNA repair [GO:0006281 biological_process] (1); DNA recombination [GO:0006310 biological_process] (1); DNA ligase (ATP) activity [GO:0003910 molecular_function] (1)	DNA ligase, ATP-dependent, N-terminal [IPR012308] (1)	scaffold_2_mRNA_3438.1	-	-
GF0027448	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3437.1	-	-
GF0027447	1	0	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Domain of unknown function DUF1985 [IPR015410] (1); Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	scaffold_2_mRNA_3423.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0027446	1	0	0	Transposable element protein, putative, (1)		LOG family [IPR031100] (1); Retrotransposon gag domain [IPR005162] (1)	scaffold_2_mRNA_3422.1	-	-
GF0027445	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_2_mRNA_3416.1	-	-
GF0027444	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3404.1	-	-
GF0027443	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_2_mRNA_3402.1	-	-
GF0027442	1	0	0	Putative receptor protein kinase TMK1 (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)	scaffold_2_mRNA_3397.1	-	-
GF0027441	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_339.1	-	-
GF0027440	1	0	0	Transmembrane ascorbate ferrireductase 1 (1)		Cytochrome b561/ferric reductase transmembrane [IPR006593] (1)	scaffold_2_mRNA_3389.1	-	-
GF0027439	1	0	0	Monosacharide transport protein (1)			scaffold_2_mRNA_337.1	-	-
GF0027438	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3367.1	-	-
GF0027437	1	0	0	Hypothetical protein (1)	integral component of membrane [GO:0016021 cellular_component] (1)	Nonaspanin (TM9SF) [IPR004240] (1)	scaffold_2_mRNA_3353.1	-	-
GF0027436	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_2_mRNA_3352.1	-	-
GF0027435	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3351.1	-	-
GF0027434	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3347.1	-	-
GF0027433	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3346.1	-	-
GF0027432	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3339.1	-	-
GF0027431	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_2_mRNA_3316.1	-	-
GF0027430	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); ubiquinone biosynthetic process [GO:0006744 biological_process] (1); 2-polyprenyl-6-methoxy-1,4-benzoquinone methyltransferase activity [GO:0008425 molecular_function] (1)	S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); Zinc finger, SWIM-type [IPR007527] (1); Ubiquinone biosynthesis O-methyltransferase [IPR010233] (1); Transposase, MuDR, plant [IPR004332] (1); Zinc finger, PMZ-type [IPR006564] (1); MULE transposase domain [IPR018289] (1)	scaffold_2_mRNA_3312.1	-	-
GF0027429	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4219 [IPR025314] (1)	scaffold_2_mRNA_331.1	-	-
GF0027428	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3294.1	-	-
GF0027427	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3285.1	-	-
GF0027426	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3282.1	-	-
GF0027425	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3281.1	-	-
GF0027424	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3280.1	-	-
GF0027423	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3277.1	-	-
GF0027422	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3261.1	-	-
GF0027421	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_2_mRNA_326.1	-	-
GF0027420	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_2_mRNA_3255.1	-	-
GF0027419	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3254.1	-	-
GF0027418	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3253.1	-	-
GF0027417	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3242.1	-	-
GF0027416	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3241.1	-	-
GF0027415	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3239.1	-	-
GF0027414	1	0	0	Hypothetical protein (1)	metabolic process [GO:0008152 biological_process] (1); transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1)	GAG-pre-integrase domain [IPR025724] (1); UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	scaffold_2_mRNA_3227.1	-	-
GF0027413	1	0	0	UDP-glycosyltransferase 74E2 (1)	transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	scaffold_2_mRNA_3221.1	-	-
GF0027412	1	0	0	Hypothetical protein (1)	transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	scaffold_2_mRNA_3220.1	-	-
GF0027411	1	0	0	Hypothetical protein (1)	metabolic process [GO:0008152 biological_process] (1); transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1); Endonuclease/exonuclease/phosphatase [IPR005135] (1)	scaffold_2_mRNA_3216.1	-	-
GF0027410	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_321.1	-	-
GF0027409	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3203.1	-	-
GF0027408	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_320.1	-	-
GF0027407	1	0	0	Putative auxin-induced in root cultures protein 12-like (1)		Cytochrome b561/ferric reductase transmembrane [IPR006593] (1)	scaffold_2_mRNA_3196.1	-	-
GF0027406	1	0	0	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); DNA/RNA helicase, ATP-dependent, DEAH-box type, conserved site [IPR002464] (1); Helicase superfamily 1/2, ATP-binding domain [IPR014001] (1)	scaffold_2_mRNA_3178.1	-	-
GF0027405	1	0	0	Hypothetical protein (1)		Zinc finger, FYVE/PHD-type [IPR011011] (1); Zinc finger, PHD-type, conserved site [IPR019786] (1); Zinc finger, RING/FYVE/PHD-type [IPR013083] (1)	scaffold_2_mRNA_3175.1	-	-
GF0027404	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3173.1	-	-
GF0027403	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3172.1	-	-
GF0027402	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			scaffold_2_mRNA_317.1	-	-
GF0027401	1	0	0	Hypothetical protein (1)	DNA integration [GO:0015074 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Integrase, catalytic core [IPR001584] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_2_mRNA_3169.1	-	-
GF0027400	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3166.1	-	-
GF0027399	1	0	0	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	scaffold_2_mRNA_3165.1	-	-
GF0027398	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3164.1	-	-
GF0027397	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_316.1	-	-
GF0027396	1	0	0	Hypothetical protein (1)		Transposase-associated domain [IPR029480] (1)	scaffold_2_mRNA_3158.1	-	-
GF0027395	1	0	0	Exostosin family protein (1)		Exostosin-like [IPR004263] (1); Domain of unknown function DUF2431 [IPR019446] (1)	scaffold_2_mRNA_3131.1	-	-
GF0027394	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_312.1	-	-
GF0027393	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3112.1	-	-
GF0027392	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	Zinc finger C2H2-type [IPR013087] (1); Zinc finger, BED-type [IPR003656] (1)	scaffold_2_mRNA_3107.1	-	-
GF0027391	1	0	0	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)	scaffold_2_mRNA_3093.1	-	-
GF0027390	1	0	0	Salicylate O-methyltransferase (1)	methyltransferase activity [GO:0008168 molecular_function] (1)	SAM dependent carboxyl methyltransferase [IPR005299] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	scaffold_2_mRNA_3090.1	-	-
GF0027389	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3081.1	-	-
GF0027388	1	0	0	Receptor like protein 33 (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1)	scaffold_2_mRNA_3075.1	-	-
GF0027387	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	scaffold_2_mRNA_3074.1	-	-
GF0027386	1	0	0	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)	scaffold_2_mRNA_3073.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0027385	1	0	0	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, C-terminal [IPR022675] (1); Glucose-6-phosphate dehydrogenase [IPR001282] (1)	scaffold_2_mRNA_3072.1	-	-
GF0027384	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_2_mRNA_3069.1	-	-
GF0027383	1	0	0	LRR receptor-like serine/threonine-protein kinase GSO1 (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_2_mRNA_3066.1	-	-
GF0027382	1	0	0	Receptor like protein 33 (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	scaffold_2_mRNA_3064.1	-	-
GF0027381	1	0	0	Hypothetical protein (1)	glucose-6-phosphate dehydrogenase activity [GO:0004345 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); glucose metabolic process [GO:0006006 biological_process] (1); NADP binding [GO:0050661 molecular_function] (1)	NAD(P)-binding domain [IPR016040] (1); Glucose-6-phosphate dehydrogenase, C-terminal [IPR022675] (1); Glucose-6-phosphate dehydrogenase [IPR001282] (1); Glucose-6-phosphate dehydrogenase, NAD-binding [IPR022674] (1)	scaffold_2_mRNA_3062.1	-	-
GF0027380	1	0	0	Leucine-rich repeat, plant specific (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1)	scaffold_2_mRNA_3061.1	-	-
GF0027379	1	0	0	Putative disease resistance 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)	scaffold_2_mRNA_3058.1	-	-
GF0027378	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3056.1	-	-
GF0027377	1	0	0	LRR receptor-like serine/threonine-protein kinase EFR (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_2_mRNA_3055.1	-	-
GF0027376	1	0	0	ABC transporter G family member 14 (1)	membrane [GO:0016020 cellular_component] (1); ATPase activity [GO:0016887 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); ABC-2 type transporter [IPR013525] (1); ABC transporter-like [IPR003439] (1)	scaffold_2_mRNA_3054.1	-	-
GF0027375	1	0	0	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)	scaffold_2_mRNA_3053.1	-	-
GF0027374	1	0	0	Hypothetical protein (1)	NADP binding [GO:0050661 molecular_function] (1); glucose-6-phosphate dehydrogenase activity [GO:0004345 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); glucose metabolic process [GO:0006006 biological_process] (1)	Glucose-6-phosphate dehydrogenase, NAD-binding [IPR022674] (1); NAD(P)-binding domain [IPR016040] (1); Glucose-6-phosphate dehydrogenase [IPR001282] (1)	scaffold_2_mRNA_3050.1	-	-
GF0027373	1	0	0	Hypothetical protein (1)	glucose metabolic process [GO:0006006 biological_process] (1); oxidation-reduction process [GO:0055114 biological_process] (1); glucose-6-phosphate dehydrogenase activity [GO:0004345 molecular_function] (1); NADP binding [GO:0050661 molecular_function] (1)	Glucose-6-phosphate dehydrogenase, active site [IPR019796] (1); Glucose-6-phosphate dehydrogenase, NAD-binding [IPR022674] (1); Glucose-6-phosphate dehydrogenase [IPR001282] (1); Glucose-6-phosphate dehydrogenase, C-terminal [IPR022675] (1); NAD(P)-binding domain [IPR016040] (1)	scaffold_2_mRNA_3047.1	-	-
GF0027372	1	0	0	Verticillium wilt resistance-like protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat [IPR001611] (1)	scaffold_2_mRNA_3046.1	-	-
GF0027371	1	0	0	Glucose-6-phosphate 1-dehydrogenase, cytoplasmic isoform (1)	NADP binding [GO:0050661 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); glucose-6-phosphate dehydrogenase activity [GO:0004345 molecular_function] (1); glucose metabolic process [GO:0006006 biological_process] (1)	Glucose-6-phosphate dehydrogenase, NAD-binding [IPR022674] (1); Glucose-6-phosphate dehydrogenase [IPR001282] (1); Glucose-6-phosphate dehydrogenase, C-terminal [IPR022675] (1); NAD(P)-binding domain [IPR016040] (1)	scaffold_2_mRNA_3045.1	-	-
GF0027370	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1)	scaffold_2_mRNA_3044.1	-	-
GF0027369	1	0	0	Receptor like protein 33 (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)	scaffold_2_mRNA_3042.1	-	-
GF0027368	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_3041.1	-	-
GF0027367	1	0	0	Receptor like protein 33 (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)	scaffold_2_mRNA_3039.1	-	-
GF0027366	1	0	0	Verticillium wilt resistance-like protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	scaffold_2_mRNA_3038.1	-	-
GF0027365	1	0	0	Cytochrome P450 71D8 (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)	scaffold_2_mRNA_3032.1	-	-
GF0027364	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_303.1	-	-
GF0027363	1	0	0	Monosacharide transport protein (1)			scaffold_2_mRNA_2996.1	-	-
GF0027362	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_2_mRNA_2994.1	-	-
GF0027361	1	0	0	Transposase tnp2 (1)		Transposon, En/Spm-like [IPR004242] (1)	scaffold_2_mRNA_2970.1	-	-
GF0027360	1	0	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	scaffold_2_mRNA_2965.1	-	-
GF0027359	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2960.1	-	-
GF0027358	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2957.1	-	-
GF0027357	1	0	0	Pol polyprotein (1)			scaffold_2_mRNA_2954.1	-	-
GF0027356	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_2_mRNA_295.1	-	-
GF0027355	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_294.1	-	-
GF0027354	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2919.1	-	-
GF0027353	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	scaffold_2_mRNA_2902.1	-	-
GF0027352	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_290.1	-	-
GF0027351	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			scaffold_2_mRNA_2898.1	-	-
GF0027350	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2897.1	-	-
GF0027349	1	0	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1); FAR1 DNA binding domain [IPR004330] (1)	scaffold_2_mRNA_2894.1	-	-
GF0027348	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2893.1	-	-
GF0027347	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_2_mRNA_2892.1	-	-
GF0027346	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_289.1	-	-
GF0027345	1	0	0	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)	scaffold_2_mRNA_2885.1	-	-
GF0027344	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2884.1	-	-
GF0027343	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_288.1	-	-

ID	**Num. in *C. celementine***	**Num in *C. unshiu***	**Num in *P.trifoliata***	**Note**	**GO**	**InterPro**	**Members in *C.clementine***	**Members in *C.unshiu***	**Members in *P.trifoliata***
GF0027342	1	0	0	RNA-directed DNA polymerase , related (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Reverse transcriptase domain [IPR000477] (1)	scaffold_2_mRNA_2873.1	-	-
GF0027341	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_2_mRNA_2856.1	-	-
GF0027340	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2853.1	-	-
GF0027339	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_285.1	-	-
GF0027338	1	0	0	Stress responsive alpha-beta barrel domain protein isoform 2 (1)		Stress responsive alpha-beta barrel [IPR013097] (1); Dimeric alpha-beta barrel [IPR011008] (1)	scaffold_2_mRNA_2843.1	-	-
GF0027337	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2832.1	-	-
GF0027336	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_283.1	-	-
GF0027335	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_2_mRNA_2826.1	-	-
GF0027334	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2825.1	-	-
GF0027333	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2823.1	-	-
GF0027332	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2822.1	-	-
GF0027331	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2821.1	-	-
GF0027330	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			scaffold_2_mRNA_2818.1	-	-
GF0027329	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2814.1	-	-
GF0027328	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_2_mRNA_2813.1	-	-
GF0027327	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2812.1	-	-
GF0027326	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_2_mRNA_281.1	-	-
GF0027325	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2806.1	-	-
GF0027324	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_2_mRNA_2805.1	-	-
GF0027323	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2799.1	-	-
GF0027322	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2793.1	-	-
GF0027321	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2792.1	-	-
GF0027320	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2790.1	-	-
GF0027319	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2776.1	-	-
GF0027318	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2774.1	-	-
GF0027317	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2762.1	-	-
GF0027316	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_2_mRNA_2753.1	-	-
GF0027315	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2749.1	-	-
GF0027314	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_2_mRNA_2748.1	-	-
GF0027313	1	0	0	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	scaffold_2_mRNA_2741.1	-	-
GF0027312	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2739.1	-	-
GF0027311	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_2_mRNA_2736.1	-	-
GF0027310	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2733.1	-	-
GF0027309	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_273.1	-	-
GF0027308	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2721.1	-	-
GF0027307	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2720.1	-	-
GF0027306	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2719.1	-	-
GF0027305	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2718.1	-	-
GF0027304	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2717.1	-	-
GF0027303	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2716.1	-	-
GF0027302	1	0	0	CDNA clone:001-127-C06, full insert sequence (1)		Trichome birefringence-like family [IPR029962] (1); PC-Esterase [IPR026057] (1)	scaffold_2_mRNA_2712.1	-	-
GF0027301	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_2_mRNA_2683.1	-	-
GF0027300	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2666.1	-	-
GF0027299	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_2_mRNA_2665.1	-	-
GF0027298	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2663.1	-	-
GF0027297	1	0	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1)	Chaperonin Cpn60/TCP-1 family [IPR002423] (1); GroEL-like equatorial domain [IPR027413] (1)	scaffold_2_mRNA_2661.1	-	-
GF0027296	1	0	0	Hypothetical protein (1)	cell redox homeostasis [GO:0045454 biological_process] (1)	Thioredoxin-like fold [IPR012336] (1); NADP-dependent oxidoreductase domain [IPR023210] (1); Thioredoxin domain [IPR013766] (1)	scaffold_2_mRNA_2660.1	-	-
GF0027295	1	0	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1); Domain of unknown function DUF1985 [IPR015410] (1)	scaffold_2_mRNA_266.1	-	-
GF0027294	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2659.1	-	-
GF0027293	1	0	0	Mutator-like transposase (1)	zinc ion binding [GO:0008270 molecular_function] (1)	MULE transposase domain [IPR018289] (1); Zinc finger, PMZ-type [IPR006564] (1); Transposase, MuDR, plant [IPR004332] (1); Zinc finger, SWIM-type [IPR007527] (1)	scaffold_2_mRNA_265.1	-	-
GF0027292	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2649.1	-	-
GF0027291	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2647.1	-	-
GF0027290	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2646.1	-	-
GF0027289	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_2_mRNA_2645.1	-	-
GF0027288	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			scaffold_2_mRNA_2644.1	-	-
GF0027287	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2643.1	-	-
GF0027286	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_264.1	-	-
GF0027285	1	0	0	Putative retroelement pol polyprotein (1)	DNA integration [GO:0015074 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	GAG-pre-integrase domain [IPR025724] (1); Ribonuclease H-like domain [IPR012337] (1); Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1); Integrase, catalytic core [IPR001584] (1)	scaffold_2_mRNA_2639.1	-	-
GF0027284	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_2_mRNA_2637.1	-	-
GF0027283	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_2_mRNA_2636.1	-	-
GF0027282	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2635.1	-	-
GF0027281	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2634.1	-	-
GF0027280	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2630.1	-	-
GF0027279	1	0	0	Hypothetical protein (1)		Transposon, En/Spm-like [IPR004242] (1)	scaffold_2_mRNA_2629.1	-	-
GF0027278	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2625.1	-	-
GF0027277	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2621.1	-	-
GF0027276	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2616.1	-	-
GF0027275	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2614.1	-	-
GF0027274	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2613.1	-	-
GF0027273	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2612.1	-	-
GF0027272	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2611.1	-	-
GF0027271	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2610.1	-	-
GF0027270	1	0	0	G-type lectin S-receptor-like serine/threonine-protein kinase (1)	protein binding [GO:0005515 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein serine/threonine kinase activity [GO:0004674 molecular_function] (1); recognition of pollen [GO:0048544 biological_process] (1); protein phosphorylation [GO:0006468 biological_process] (1)	Protein kinase domain [IPR000719] (1); S-receptor-like serine/threonine-protein kinase [IPR024171] (1); Protein kinase-like domain [IPR011009] (1); S-locus glycoprotein domain [IPR000858] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); EGF-like domain [IPR000742] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); PAN/Apple domain [IPR003609] (1); Bulb-type lectin domain [IPR001480] (1)	scaffold_2_mRNA_2603.1	-	-
GF0027269	1	0	0	Frataxin (1)	ferric iron binding [GO:0008199 molecular_function] (1); mitochondrion [GO:0005739 cellular_component] (1); oxidation-reduction process [GO:0055114 biological_process] (1); ferroxidase activity [GO:0004322 molecular_function] (1); iron-sulfur cluster assembly [GO:0016226 biological_process] (1)	Frataxin conserved site [IPR020895] (1); Frataxin [IPR017789] (1); Frataxin/CyaY [IPR002908] (1)	scaffold_2_mRNA_2602.1	-	-
GF0027268	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_260.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0027267	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, GRF-type [IPR010666] (1)	scaffold_2_mRNA_2599.1	-	-
GF0027266	1	0	0	Hypothetical protein (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1)	scaffold_2_mRNA_2595.1	-	-
GF0027265	1	0	0	BED zinc finger,hAT family dimerization domain (1)	DNA binding [GO:0003677 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	hAT-like transposase, RNase-H fold [IPR025525] (1); Ribonuclease H-like domain [IPR012337] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	scaffold_2_mRNA_2591.1	-	-
GF0027264	1	0	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1); Zinc finger, BED-type [IPR003656] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_2_mRNA_2585.1	-	-
GF0027263	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	scaffold_2_mRNA_2583.1	-	-
GF0027262	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_2_mRNA_2582.1	-	-
GF0027261	1	0	0	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	scaffold_2_mRNA_258.1	-	-
GF0027260	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_2_mRNA_2579.1	-	-
GF0027259	1	0	0	Equilibrative nucleoside transporter 4 (1)	transport [GO:0006810 biological_process] (1); integral component of membrane [GO:0016021 cellular_component] (1); nucleoside transmembrane transporter activity [GO:0005337 molecular_function] (1)	Equilibrative nucleoside transporter [IPR002259] (1); Major facilitator superfamily domain [IPR020846] (1); Nucleoside transporter, plants [IPR030200] (1)	scaffold_2_mRNA_2574.1	-	-
GF0027258	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2571.1	-	-
GF0027257	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_257.1	-	-
GF0027256	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2567.1	-	-
GF0027255	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2566.1	-	-
GF0027254	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2557.1	-	-
GF0027253	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_2_mRNA_2556.1	-	-
GF0027252	1	0	0	Hypothetical protein (1)		Protein of unknown function wound-induced [IPR022251] (1)	scaffold_2_mRNA_2552.1	-	-
GF0027251	1	0	0	Putative wound induced protein-like (1)		Protein of unknown function wound-induced [IPR022251] (1)	scaffold_2_mRNA_2551.1	-	-
GF0027250	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Viral movement protein [IPR028919] (1); Zinc finger, CCHC-type [IPR001878] (1)	scaffold_2_mRNA_2550.1	-	-
GF0027249	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2540.1	-	-
GF0027248	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_254.1	-	-
GF0027247	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2539.1	-	-
GF0027246	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_2_mRNA_2533.1	-	-
GF0027245	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2531.1	-	-
GF0027244	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2529.1	-	-
GF0027243	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_2_mRNA_2528.1	-	-
GF0027242	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2526.1	-	-
GF0027241	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2525.1	-	-
GF0027240	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2524.1	-	-
GF0027239	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2523.1	-	-
GF0027238	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2522.1	-	-
GF0027237	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2521.1	-	-
GF0027236	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_2_mRNA_2520.1	-	-
GF0027235	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_2_mRNA_2518.1	-	-
GF0027234	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2517.1	-	-
GF0027233	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_2_mRNA_2516.1	-	-
GF0027232	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2514.1	-	-
GF0027231	1	0	0	Hypothetical protein (1)		Transposon, En/Spm-like [IPR004242] (1)	scaffold_2_mRNA_2511.1	-	-
GF0027230	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2509.1	-	-
GF0027229	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2504.1	-	-
GF0027228	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_2_mRNA_2494.1	-	-
GF0027227	1	0	0	Hypothetical protein (1)	DNA integration [GO:0015074 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Aspartic peptidase domain [IPR021109] (1); Paraneoplastic antigen Ma [IPR026523] (1); Ribonuclease H-like domain [IPR012337] (1); Reverse transcriptase domain [IPR000477] (1); Integrase, catalytic core [IPR001584] (1)	scaffold_2_mRNA_2489.1	-	-
GF0027226	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2488.1	-	-
GF0027225	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_2_mRNA_2482.1	-	-
GF0027224	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2479.1	-	-
GF0027223	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2469.1	-	-
GF0027222	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_2_mRNA_2468.1	-	-
GF0027221	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2467.1	-	-
GF0027220	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2466.1	-	-
GF0027219	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2465.1	-	-
GF0027218	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2463.1	-	-
GF0027217	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Peptidase A2A, retrovirus, catalytic [IPR001995] (1); Viral movement protein [IPR028919] (1); Reverse transcriptase domain [IPR000477] (1); Zinc finger, CCHC-type [IPR001878] (1); Aspartic peptidase domain [IPR021109] (1)	scaffold_2_mRNA_2462.1	-	-
GF0027216	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2461.1	-	-
GF0027215	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_2_mRNA_2460.1	-	-
GF0027214	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2457.1	-	-
GF0027213	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2452.1	-	-
GF0027212	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2451.1	-	-
GF0027211	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2448.1	-	-
GF0027210	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2446.1	-	-
GF0027209	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2442.1	-	-
GF0027208	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2441.1	-	-
GF0027207	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2440.1	-	-
GF0027206	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2439.1	-	-
GF0027205	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2438.1	-	-
GF0027204	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_2_mRNA_2437.1	-	-
GF0027203	1	0	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_2_mRNA_2432.1	-	-
GF0027202	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2427.1	-	-
GF0027201	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_2_mRNA_2426.1	-	-
GF0027200	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2425.1	-	-
GF0027199	1	0	0	Putative polyprotein (Aspartic proteinase, reverse transcriptase, ribonuclease H) (1)		Retropepsins [IPR018061] (1); Reverse transcriptase domain [IPR000477] (1); Aspartic peptidase domain [IPR021109] (1)	scaffold_2_mRNA_2421.1	-	-
GF0027198	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2418.1	-	-
GF0027197	1	0	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_2_mRNA_2410.1	-	-
GF0027196	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2407.1	-	-
GF0027195	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_2_mRNA_2395.1	-	-
GF0027194	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2393.1	-	-
GF0027193	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2380.1	-	-
GF0027192	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_238.1	-	-
GF0027191	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2379.1	-	-
GF0027190	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2378.1	-	-
GF0027189	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2375.1	-	-
GF0027188	1	0	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_2_mRNA_2373.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0027187	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2372.1	-	-
GF0027186	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2371.1	-	-
GF0027185	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2369.1	-	-
GF0027184	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2368.1	-	-
GF0027183	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_2_mRNA_2367.1	-	-
GF0027182	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_2_mRNA_2365.1	-	-
GF0027181	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2363.1	-	-
GF0027180	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2358.1	-	-
GF0027179	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2355.1	-	-
GF0027178	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2354.1	-	-
GF0027177	1	0	0	Putative retroelement pol polyprotein (1)			scaffold_2_mRNA_2351.1	-	-
GF0027176	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2350.1	-	-
GF0027175	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2341.1	-	-
GF0027174	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_2_mRNA_2340.1	-	-
GF0027173	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2334.1	-	-
GF0027172	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_2_mRNA_2330.1	-	-
GF0027171	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2328.1	-	-
GF0027170	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2326.1	-	-
GF0027169	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2324.1	-	-
GF0027168	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2320.1	-	-
GF0027167	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2319.1	-	-
GF0027166	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2316.1	-	-
GF0027165	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2313.1	-	-
GF0027164	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_231.1	-	-
GF0027163	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2303.1	-	-
GF0027162	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2302.1	-	-
GF0027161	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_2_mRNA_230.1	-	-
GF0027160	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2294.1	-	-
GF0027159	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2292.1	-	-
GF0027158	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2289.1	-	-
GF0027157	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2286.1	-	-
GF0027156	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_2_mRNA_2285.1	-	-
GF0027155	1	0	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Retrotransposon gag domain [IPR005162] (1); Carlavirus nucleic acid-binding protein [IPR002568] (1)	scaffold_2_mRNA_2284.1	-	-
GF0027154	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_2_mRNA_2282.1	-	-
GF0027153	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2274.1	-	-
GF0027152	1	0	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_2_mRNA_2273.1	-	-
GF0027151	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_2_mRNA_2270.1	-	-
GF0027150	1	0	0	Retrotransposon gag protein (1)			scaffold_2_mRNA_227.1	-	-
GF0027149	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2269.1	-	-
GF0027148	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2268.1	-	-
GF0027147	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2267.1	-	-
GF0027146	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2266.1	-	-
GF0027145	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2264.1	-	-
GF0027144	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_2_mRNA_2263.1	-	-
GF0027143	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2261.1	-	-
GF0027142	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_2_mRNA_2260.1	-	-
GF0027141	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_226.1	-	-
GF0027140	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2255.1	-	-
GF0027139	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2251.1	-	-
GF0027138	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2247.1	-	-
GF0027137	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2245.1	-	-
GF0027136	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2244.1	-	-
GF0027135	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2243.1	-	-
GF0027134	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_2_mRNA_2242.1	-	-
GF0027133	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2233.1	-	-
GF0027132	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2225.1	-	-
GF0027131	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2224.1	-	-
GF0027130	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_2_mRNA_2222.1	-	-
GF0027129	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2220.1	-	-
GF0027128	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4219 [IPR025314] (1)	scaffold_2_mRNA_2219.1	-	-
GF0027127	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2218.1	-	-
GF0027126	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2217.1	-	-
GF0027125	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_2_mRNA_2216.1	-	-
GF0027124	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2215.1	-	-
GF0027123	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2214.1	-	-
GF0027122	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_2_mRNA_2213.1	-	-
GF0027121	1	0	0	Hypothetical protein (1)		Ribosomal protein L9/RNase H1, N-terminal [IPR009027] (1); Ribonuclease H1, N-terminal [IPR011320] (1)	scaffold_2_mRNA_2210.1	-	-
GF0027120	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_2_mRNA_2202.1	-	-
GF0027119	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2198.1	-	-
GF0027118	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_2_mRNA_2196.1	-	-
GF0027117	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2191.1	-	-
GF0027116	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_219.1	-	-
GF0027115	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2189.1	-	-
GF0027114	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2188.1	-	-
GF0027113	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2187.1	-	-
GF0027112	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2186.1	-	-
GF0027111	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_2_mRNA_2185.1	-	-
GF0027110	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2184.1	-	-
GF0027109	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_2_mRNA_2183.1	-	-
GF0027108	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2179.1	-	-
GF0027107	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_2_mRNA_2177.1	-	-
GF0027106	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2176.1	-	-
GF0027105	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2175.1	-	-
GF0027104	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2174.1	-	-
GF0027103	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_2_mRNA_2173.1	-	-
GF0027102	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2172.1	-	-
GF0027101	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2171.1	-	-
GF0027100	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2168.1	-	-
GF0027099	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_2_mRNA_2167.1	-	-
GF0027098	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2162.1	-	-
GF0027097	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_2_mRNA_216.1	-	-
GF0027096	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2155.1	-	-
GF0027095	1	0	0	Hypothetical protein (1)		Zinc knuckle CX2CX4HX4C [IPR025836] (1)	scaffold_2_mRNA_2153.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0027094	1	0	0	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)	scaffold_2_mRNA_2152.1	-	-
GF0027093	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_2_mRNA_2151.1	-	-
GF0027092	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_215.1	-	-
GF0027091	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2148.1	-	-
GF0027090	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_2_mRNA_2146.1	-	-
GF0027089	1	0	0	Putative Ty3-gypsy-like retroelement pol polyprotein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_2_mRNA_2142.1	-	-
GF0027088	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_214.1	-	-
GF0027087	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_2_mRNA_2139.1	-	-
GF0027086	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2138.1	-	-
GF0027085	1	0	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1); Probable transposase, Ptta/En/Spm, plant [IPR004252] (1); Transposon, En/Spm-like [IPR004242] (1); Domain of unknown function DUF4218 [IPR025452] (1); Domain of unknown function DUF4216 [IPR025312] (1)	scaffold_2_mRNA_2131.1	-	-
GF0027084	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2130.1	-	-
GF0027083	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_213.1	-	-
GF0027082	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_2_mRNA_2126.1	-	-
GF0027081	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2125.1	-	-
GF0027080	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_2_mRNA_2124.1	-	-
GF0027079	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2123.1	-	-
GF0027078	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2122.1	-	-
GF0027077	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_2_mRNA_2121.1	-	-
GF0027076	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2120.1	-	-
GF0027075	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2117.1	-	-
GF0027074	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_2_mRNA_2116.1	-	-
GF0027073	1	0	0	BED zinc finger,hAT family dimerization domain isoform 1 (1)	DNA binding [GO:0003677 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1); Zinc finger, BED-type [IPR003656] (1); hAT-like transposase, RNase-H fold [IPR025525] (1); Ribonuclease H-like domain [IPR012337] (1); Zinc finger C2H2-type [IPR013087] (1)	scaffold_2_mRNA_2114.1	-	-
GF0027072	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_211.1	-	-
GF0027071	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_2_mRNA_2109.1	-	-
GF0027070	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2108.1	-	-
GF0027069	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2101.1	-	-
GF0027068	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_2_mRNA_210.1	-	-
GF0027067	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2099.1	-	-
GF0027066	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2098.1	-	-
GF0027065	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2090.1	-	-
GF0027064	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_2_mRNA_2085.1	-	-
GF0027063	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2084.1	-	-
GF0027062	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2072.1	-	-
GF0027061	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_2_mRNA_2071.1	-	-
GF0027060	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2070.1	-	-
GF0027059	1	0	0	60S ribosomal protein L14 (1)	ribosome [GO:0005840 cellular_component] (1); translation [GO:0006412 biological_process] (1); intracellular [GO:0005622 cellular_component] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1)	Ribosomal protein L2 domain 2 [IPR014722] (1); Ribosomal protein L14e domain [IPR002784] (1); Translation protein SH3-like domain [IPR008991] (1)	scaffold_2_mRNA_2066.1	-	-
GF0027058	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2061.1	-	-
GF0027057	1	0	0	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)	scaffold_2_mRNA_2060.1	-	-
GF0027056	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_2_mRNA_206.1	-	-
GF0027055	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2054.1	-	-
GF0027054	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2052.1	-	-
GF0027053	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			scaffold_2_mRNA_2050.1	-	-
GF0027052	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_205.1	-	-
GF0027051	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2049.1	-	-
GF0027050	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2045.1	-	-
GF0027049	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2044.1	-	-
GF0027048	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2043.1	-	-
GF0027047	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2042.1	-	-
GF0027046	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_2_mRNA_204.1	-	-
GF0027045	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1); Paraneoplastic antigen Ma [IPR026523] (1); Reverse transcriptase domain [IPR000477] (1)	scaffold_2_mRNA_2036.1	-	-
GF0027044	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2035.1	-	-
GF0027043	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2033.1	-	-
GF0027042	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2030.1	-	-
GF0027041	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_203.1	-	-
GF0027040	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_2_mRNA_2027.1	-	-
GF0027039	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2025.1	-	-
GF0027038	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			scaffold_2_mRNA_202.1	-	-
GF0027037	1	0	0	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)	scaffold_2_mRNA_2015.1	-	-
GF0027036	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_2013.1	-	-
GF0027035	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_201.1	-	-
GF0027034	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_2_mRNA_2007.1	-	-
GF0027033	1	0	0	Hypothetical protein (1)		Arabidopsis retrotransposon Orf1 [IPR004312] (1)	scaffold_2_mRNA_2002.1	-	-
GF0027032	1	0	0	Putative Athila retroelement ORF1 protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_2_mRNA_2000.1	-	-
GF0027031	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1997.1	-	-
GF0027030	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1996.1	-	-
GF0027029	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1995.1	-	-
GF0027028	1	0	0	Protein FAR1-RELATED SEQUENCE 6 (1)	zinc ion binding [GO:0008270 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FAR1 DNA binding domain [IPR004330] (1); FHY3/FAR1 family [IPR031052] (1); Zinc finger, SWIM-type [IPR007527] (1); Zinc finger, PMZ-type [IPR006564] (1); MULE transposase domain [IPR018289] (1)	scaffold_2_mRNA_1994.1	-	-
GF0027027	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1984.1	-	-
GF0027026	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_2_mRNA_1983.1	-	-
GF0027025	1	0	0	RNA-directed DNA polymerase (Reverse transcriptase) (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_2_mRNA_1980.1	-	-
GF0027024	1	0	0	Ribonuclease H-like superfamily protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	scaffold_2_mRNA_1979.1	-	-
GF0027023	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1971.1	-	-
GF0027022	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_2_mRNA_196.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0027021	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_2_mRNA_1958.1	-	-
GF0027020	1	0	0	Tyrosine/nicotianamine family aminotransferase (1)	biosynthetic process [GO:0009058 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1); pyridoxal phosphate binding [GO:0030170 molecular_function] (1)	Pyridoxal phosphate-dependent transferase, major region, subdomain 1 [IPR015421] (1); Pyridoxal phosphate-dependent transferase, subdomain 2 [IPR015422] (1); Aminotransferase, class I/classII [IPR004839] (1); Pyridoxal phosphate-dependent transferase [IPR015424] (1)	scaffold_2_mRNA_1957.1	-	-
GF0027019	1	0	0	Hypothetical protein (1)	mRNA splicing, via spliceosome [GO:0000398 biological_process] (1); RNA binding [GO:0003723 molecular_function] (1); metal ion binding [GO:0046872 molecular_function] (1); U2AF [GO:0089701 cellular_component] (1)	Zinc finger, CCCH-type [IPR000571] (1); U2 auxiliary factor small subunit [IPR009145] (1)	scaffold_2_mRNA_1951.1	-	-
GF0027018	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1950.1	-	-
GF0027017	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_195.1	-	-
GF0027016	1	0	0	Hypothetical protein (1)	RNA binding [GO:0003723 molecular_function] (1); mRNA splicing, via spliceosome [GO:0000398 biological_process] (1); metal ion binding [GO:0046872 molecular_function] (1); U2AF [GO:0089701 cellular_component] (1)	U2 auxiliary factor small subunit [IPR009145] (1); Zinc finger, CCCH-type [IPR000571] (1)	scaffold_2_mRNA_1949.1	-	-
GF0027015	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1935.1	-	-
GF0027014	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1932.1	-	-
GF0027013	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1931.1	-	-
GF0027012	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_193.1	-	-
GF0027011	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1929.1	-	-
GF0027010	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1928.1	-	-
GF0027009	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_2_mRNA_1927.1	-	-
GF0027008	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1923.1	-	-
GF0027007	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1922.1	-	-
GF0027006	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1920.1	-	-
GF0027005	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_192.1	-	-
GF0027004	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1914.1	-	-
GF0027003	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1911.1	-	-
GF0027002	1	0	0	CAI-1 autoinducer sensor kinase/phosphatase cqsS isoform 3 (1)		Harbinger transposase-derived nuclease domain [IPR027806] (1)	scaffold_2_mRNA_1909.1	-	-
GF0027001	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			scaffold_2_mRNA_190.1	-	-
GF0027000	1	0	0	Hypothetical protein (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, 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)	scaffold_2_mRNA_1898.1	-	-
GF0026999	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_2_mRNA_1891.1	-	-
GF0026998	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1890.1	-	-
GF0026997	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_189.1	-	-
GF0026996	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1884.1	-	-
GF0026995	1	0	0	Zinc knuckle family protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Domain of unknown function DUF4219 [IPR025314] (1)	scaffold_2_mRNA_1883.1	-	-
GF0026994	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_2_mRNA_1881.1	-	-
GF0026993	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1880.1	-	-
GF0026992	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_188.1	-	-
GF0026991	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1879.1	-	-
GF0026990	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1878.1	-	-
GF0026989	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1875.1	-	-
GF0026988	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1874.1	-	-
GF0026987	1	0	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Carlavirus nucleic acid-binding protein [IPR002568] (1)	scaffold_2_mRNA_1872.1	-	-
GF0026986	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1871.1	-	-
GF0026985	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1869.1	-	-
GF0026984	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1868.1	-	-
GF0026983	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1867.1	-	-
GF0026982	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_2_mRNA_1866.1	-	-
GF0026981	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1863.1	-	-
GF0026980	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			scaffold_2_mRNA_1862.1	-	-
GF0026979	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_186.1	-	-
GF0026978	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1858.1	-	-
GF0026977	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_2_mRNA_1857.1	-	-
GF0026976	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_2_mRNA_1842.1	-	-
GF0026975	1	0	0	BED zinc finger,hAT family dimerization domain (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1); Ribonuclease H-like domain [IPR012337] (1); hAT-like transposase, RNase-H fold [IPR025525] (1)	scaffold_2_mRNA_1839.1	-	-
GF0026974	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_183.1	-	-
GF0026973	1	0	0	RNA-directed DNA polymerase (Reverse transcriptase) (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_2_mRNA_1826.1	-	-
GF0026972	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Zinc knuckle CX2CX4HX4C [IPR025836] (1)	scaffold_2_mRNA_1825.1	-	-
GF0026971	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_2_mRNA_182.1	-	-
GF0026970	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1818.1	-	-
GF0026969	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1816.1	-	-
GF0026968	1	0	0	Similarity to non-LTR retroelement reverse transcriptase (1)			scaffold_2_mRNA_1811.1	-	-
GF0026967	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	scaffold_2_mRNA_1809.1	-	-
GF0026966	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4219 [IPR025314] (1)	scaffold_2_mRNA_180.1	-	-
GF0026965	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Domain of unknown function DUF4283 [IPR025558] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1); Zinc knuckle CX2CX4HX4C [IPR025836] (1); Endonuclease/exonuclease/phosphatase [IPR005135] (1)	scaffold_2_mRNA_18.1	-	-
GF0026964	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1798.1	-	-
GF0026963	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_2_mRNA_1796.1	-	-
GF0026962	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1793.1	-	-
GF0026961	1	0	0	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	scaffold_2_mRNA_1789.1	-	-
GF0026960	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1788.1	-	-
GF0026959	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1780.1	-	-
GF0026958	1	0	0	MuDR family transposase containing protein (1)		MULE transposase domain [IPR018289] (1)	scaffold_2_mRNA_1777.1	-	-
GF0026957	1	0	0	Disease resistance family protein / LRR family protein (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_2_mRNA_1752.1	-	-
GF0026956	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1751.1	-	-
GF0026955	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); DNA integration [GO:0015074 biological_process] (1)	Ribonuclease H-like domain [IPR012337] (1); Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1); Integrase, catalytic core [IPR001584] (1)	scaffold_2_mRNA_175.1	-	-

ID	**Num. in *C. celementine***	**Num in *C. unshiu***	**Num in *P.trifoliata***	**Note**	**GO**	**InterPro**	**Members in *C.clementine***	**Members in *C.unshiu***	**Members in *P.trifoliata***
GF0026954	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_2_mRNA_1746.1	-	-
GF0026953	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_2_mRNA_1741.1	-	-
GF0026952	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1735.1	-	-
GF0026951	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1734.1	-	-
GF0026950	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1728.1	-	-
GF0026949	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1727.1	-	-
GF0026948	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1721.1	-	-
GF0026947	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1720.1	-	-
GF0026946	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1718.1	-	-
GF0026945	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_2_mRNA_171.1	-	-
GF0026944	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Domain of unknown function DUF4219 [IPR025314] (1)	scaffold_2_mRNA_1701.1	-	-
GF0026943	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_2_mRNA_170.1	-	-
GF0026942	1	0	0	Hypothetical protein (1)		Protein of unknown function DUF3339 [IPR021775] (1)	scaffold_2_mRNA_1691.1	-	-
GF0026941	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_2_mRNA_169.1	-	-
GF0026940	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1681.1	-	-
GF0026939	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, SWIM-type [IPR007527] (1); Zinc finger, PMZ-type [IPR006564] (1)	scaffold_2_mRNA_1674.1	-	-
GF0026938	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_167.1	-	-
GF0026937	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1668.1	-	-
GF0026936	1	0	0	Hypothetical protein (1)		ABC-transporter extension domain [IPR032781] (1)	scaffold_2_mRNA_1666.1	-	-
GF0026935	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_166.1	-	-
GF0026934	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1659.1	-	-
GF0026933	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_2_mRNA_1656.1	-	-
GF0026932	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1655.1	-	-
GF0026931	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1652.1	-	-
GF0026930	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1651.1	-	-
GF0026929	1	0	0	Retrotransposon protein, putative, Ty3-gypsy subclass (1)	DNA integration [GO:0015074 biological_process] (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); Integrase, catalytic core [IPR001584] (1); Aspartic peptidase domain [IPR021109] (1); Retrotransposon gag domain [IPR005162] (1)	scaffold_2_mRNA_1650.1	-	-
GF0026928	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1); Retrotransposon gag domain [IPR005162] (1)	scaffold_2_mRNA_165.1	-	-
GF0026927	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1647.1	-	-
GF0026926	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1643.1	-	-
GF0026925	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1642.1	-	-
GF0026924	1	0	0	Mutator-like transposase (1)		Transposase, MuDR, plant [IPR004332] (1); MULE transposase domain [IPR018289] (1)	scaffold_2_mRNA_1636.1	-	-
GF0026923	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4371 [IPR025398] (1)	scaffold_2_mRNA_1623.1	-	-
GF0026922	1	0	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Domain of unknown function DUF1985 [IPR015410] (1); Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	scaffold_2_mRNA_1620.1	-	-
GF0026921	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_2_mRNA_162.1	-	-
GF0026920	1	0	0	Putative muDR family transposase-like (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, SWIM-type [IPR007527] (1); Zinc finger, PMZ-type [IPR006564] (1); MULE transposase domain [IPR018289] (1)	scaffold_2_mRNA_1619.1	-	-
GF0026919	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1617.1	-	-
GF0026918	1	0	0	Homogentisate phytyltransferase (1)	integral component of membrane [GO:0016021 cellular_component] (1); transferase activity, transferring alkyl or aryl (other than methyl) groups [GO:0016765 molecular_function] (1)	UbiA prenyltransferase family [IPR000537] (1)	scaffold_2_mRNA_1616.1	-	-
GF0026917	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1); Retroviral aspartyl protease [IPR013242] (1)	scaffold_2_mRNA_1615.1	-	-
GF0026916	1	0	0	Hypothetical protein (1)		Alpha/Beta hydrolase fold [IPR029058] (1)	scaffold_2_mRNA_1611.1	-	-
GF0026915	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1610.1	-	-
GF0026914	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_161.1	-	-
GF0026913	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1606.1	-	-
GF0026912	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1601.1	-	-
GF0026911	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_160.1	-	-
GF0026910	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1596.1	-	-
GF0026909	1	0	0	Monosacharide transport protein (1)			scaffold_2_mRNA_1595.1	-	-
GF0026908	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1594.1	-	-
GF0026907	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1593.1	-	-
GF0026906	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1591.1	-	-
GF0026905	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1590.1	-	-
GF0026904	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_2_mRNA_159.1	-	-
GF0026903	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_2_mRNA_1587.1	-	-
GF0026902	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1580.1	-	-
GF0026901	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_2_mRNA_158.1	-	-
GF0026900	1	0	0	Polynucleotidyl transferase, ribonuclease H-like superfamily protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_2_mRNA_1579.1	-	-
GF0026899	1	0	0	ATP-dependent Clp protease ATP-binding subunit clpC (1)	protein binding [GO:0005515 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); ClpA/B, conserved site 1 [IPR018368] (1); ATPase, AAA-type, core [IPR003959] (1); AAA+ ATPase domain [IPR003593] (1); F-box domain [IPR001810] (1); ClpA/B family [IPR001270] (1)	scaffold_2_mRNA_1572.1	-	-
GF0026898	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1568.1	-	-
GF0026897	1	0	0	Subtilisin-like serine protease (1)	serine-type endopeptidase activity [GO:0004252 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Peptidase S8, subtilisin-related [IPR015500] (1); Peptidase S8, subtilisin, Asp-active site [IPR023827] (1); PA domain [IPR003137] (1); Peptidase S8/S53 domain [IPR000209] (1); Cucumisin-like catalytic domain [IPR034197] (1); Peptidase S8 propeptide/proteinase inhibitor I9 [IPR010259] (1)	scaffold_2_mRNA_1566.1	-	-
GF0026896	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1565.1	-	-
GF0026895	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_2_mRNA_1564.1	-	-
GF0026894	1	0	0	Subtilisin-like serine protease (1)	serine-type endopeptidase activity [GO:0004252 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Peptidase S8 propeptide/proteinase inhibitor I9 [IPR010259] (1); Peptidase S8, subtilisin-related [IPR015500] (1); Peptidase S8, subtilisin, Asp-active site [IPR023827] (1); Peptidase S8/S53 domain [IPR000209] (1); Cucumisin-like catalytic domain [IPR034197] (1)	scaffold_2_mRNA_1562.1	-	-
GF0026893	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1558.1	-	-
GF0026892	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1553.1	-	-
GF0026891	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1549.1	-	-
GF0026890	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1545.1	-	-
GF0026889	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1540.1	-	-
GF0026888	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1528.1	-	-
GF0026887	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1527.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0026886	1	0	0	Hypothetical protein (1)	transmembrane transport [GO:0055085 biological_process] (1); calcium ion binding [GO:0005509 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	EF-Hand 1, calcium-binding site [IPR018247] (1); EF-hand domain [IPR002048] (1); Mitochondrial carrier protein [IPR002067] (1); Zinc finger, GRF-type [IPR010666] (1); Mitochondrial carrier domain [IPR023395] (1); EF-hand domain pair [IPR011992] (1); Mitochondrial substrate/solute carrier [IPR018108] (1)	scaffold_2_mRNA_1523.1	-	-
GF0026885	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1521.1	-	-
GF0026884	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_2_mRNA_152.1	-	-
GF0026883	1	0	0	Polynucleotidyl transferase, Ribonuclease H fold (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_2_mRNA_1511.1	-	-
GF0026882	1	0	0	Pentatricopeptide (1)	zinc ion binding [GO:0008270 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Tetratricopeptide-like helical domain [IPR011990] (1); Pentatricopeptide repeat [IPR002885] (1); DYW domain [IPR032867] (1)	scaffold_2_mRNA_1506.1	-	-
GF0026881	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1502.1	-	-
GF0026880	1	0	0	Glyceraldehyde-3-phosphate dehydrogenase (NADP+) (Phosphorylating) (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor [GO:0016620 molecular_function] (1)	Glyceraldehyde 3-phosphate dehydrogenase, catalytic domain [IPR020829] (1); Glyceraldehyde 3-phosphate dehydrogenase, NAD(P) binding domain [IPR020828] (1); Glyceraldehyde/Erythrose phosphate dehydrogenase family [IPR020831] (1); Glyceraldehyde 3-phosphate dehydrogenase, active site [IPR020830] (1); NAD(P)-binding domain [IPR016040] (1)	scaffold_2_mRNA_1497.1	-	-
GF0026879	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1496.1	-	-
GF0026878	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Pentatricopeptide repeat [IPR002885] (1); Tetratricopeptide-like helical domain [IPR011990] (1)	scaffold_2_mRNA_1492.1	-	-
GF0026877	1	0	0	Hypothetical protein (1)	translation elongation factor activity [GO:0003746 molecular_function] (1); translational elongation [GO:0006414 biological_process] (1)	Translation elongation factor EF1B, beta/delta subunit, guanine nucleotide exchange domain [IPR014038] (1); Prolamin-like domain [IPR008502] (1); Translation elongation factor EF1B/ribosomal protein S6 [IPR014717] (1)	scaffold_2_mRNA_1490.1	-	-
GF0026876	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_149.1	-	-
GF0026875	1	0	0	Eukaryotic peptide chain release factor subunit 1-3 (1)	cytoplasm [GO:0005737 cellular_component] (1); translation release factor activity, codon specific [GO:0016149 molecular_function] (1); translational termination [GO:0006415 biological_process] (1)	Peptide Chain Release Factor eRF1/aRF1, N-terminal [IPR024049] (1); 50S ribosomal protein L30e-like [IPR029064] (1); eRF1 domain 3 [IPR005142] (1); eRF1 domain 2 [IPR005141] (1); Peptide chain release factor eRF1/aRF1 [IPR004403] (1); eRF1 domain 1/Pelota-like [IPR005140] (1)	scaffold_2_mRNA_1484.1	-	-
GF0026874	1	0	0	Protein TRANSPARENT TESTA 12 (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)	scaffold_2_mRNA_1478.1	-	-
GF0026873	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1)	scaffold_2_mRNA_1477.1	-	-
GF0026872	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1474.1	-	-
GF0026871	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1468.1	-	-
GF0026870	1	0	0	Ras-related protein RABA1f (1)	GTPase activity [GO:0003924 molecular_function] (1); GTP binding [GO:0005525 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Small GTP-binding protein domain [IPR005225] (1); Small GTPase superfamily [IPR001806] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); DYW domain [IPR032867] (1)	scaffold_2_mRNA_1464.1	-	-
GF0026869	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1463.1	-	-
GF0026868	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1459.1	-	-
GF0026867	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_2_mRNA_1445.1	-	-
GF0026866	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1444.1	-	-
GF0026865	1	0	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Peptidase C1A [IPR013128] (1); Peptidase C1A, papain C-terminal [IPR000668] (1)	scaffold_2_mRNA_1434.1	-	-
GF0026864	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_2_mRNA_1432.1	-	-
GF0026863	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1429.1	-	-
GF0026862	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1422.1	-	-
GF0026861	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1414.1	-	-
GF0026860	1	0	0	Hypothetical protein (1)		14-3-3 domain [IPR023410] (1)	scaffold_2_mRNA_1412.1	-	-
GF0026859	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1410.1	-	-
GF0026858	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1409.1	-	-
GF0026857	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1399.1	-	-
GF0026856	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1395.1	-	-
GF0026855	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1); Retrotransposon gag domain [IPR005162] (1)	scaffold_2_mRNA_1390.1	-	-
GF0026854	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)	protein binding [GO:0005515 molecular_function] (1); membrane [GO:0016020 cellular_component] (1); intracellular protein transport [GO:0006886 biological_process] (1); SNAP receptor activity [GO:0005484 molecular_function] (1)	LOG family [IPR031100] (1); Syntaxin/epimorphin, conserved site [IPR006012] (1); Target SNARE coiled-coil homology domain [IPR000727] (1)	scaffold_2_mRNA_139.1	-	-
GF0026853	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1389.1	-	-
GF0026852	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1382.1	-	-
GF0026851	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1381.1	-	-
GF0026850	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1380.1	-	-
GF0026849	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_2_mRNA_138.1	-	-
GF0026848	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_137.1	-	-
GF0026847	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_2_mRNA_136.1	-	-
GF0026846	1	0	0	O-methyltransferase ZRP4 (1)	O-methyltransferase activity [GO:0008171 molecular_function] (1); methyltransferase activity [GO:0008168 molecular_function] (1)	S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); O-methyltransferase, family 2 [IPR001077] (1); O-methyltransferase COMT-type [IPR016461] (1)	scaffold_2_mRNA_1353.1	-	-
GF0026845	1	0	0	Orcinol O-methyltransferase (1)	methyltransferase activity [GO:0008168 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1); O-methyltransferase activity [GO:0008171 molecular_function] (1)	S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); O-methyltransferase COMT-type [IPR016461] (1); Plant methyltransferase dimerisation [IPR012967] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); O-methyltransferase, family 2 [IPR001077] (1)	scaffold_2_mRNA_1352.1	-	-
GF0026844	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1350.1	-	-
GF0026843	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_135.1	-	-
GF0026842	1	0	0	Alcohol acyltransferase (1)	transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (1)	Transferase [IPR003480] (1)	scaffold_2_mRNA_1342.1	-	-
GF0026841	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_2_mRNA_1339.1	-	-
GF0026840	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1338.1	-	-
GF0026839	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_2_mRNA_132.1	-	-
GF0026838	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1319.1	-	-
GF0026837	1	0	0	Disease resistance family protein / LRR family protein, putative (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	scaffold_2_mRNA_1313.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0026836	1	0	0	Disease resistance family protein / LRR family protein, putative (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_2_mRNA_1312.1	-	-
GF0026835	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1311.1	-	-
GF0026834	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_2_mRNA_1310.1	-	-
GF0026833	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_131.1	-	-
GF0026832	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1309.1	-	-
GF0026831	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1308.1	-	-
GF0026830	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_2_mRNA_1307.1	-	-
GF0026829	1	0	0	Hypothetical protein (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)	scaffold_2_mRNA_1303.1	-	-
GF0026828	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_2_mRNA_129.1	-	-
GF0026827	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1289.1	-	-
GF0026826	1	0	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, BED-type [IPR003656] (1); Zinc finger C2H2-type [IPR013087] (1)	scaffold_2_mRNA_1288.1	-	-
GF0026825	1	0	0	HAT family dimerisation domain containing 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)	hAT-like transposase, RNase-H fold [IPR025525] (1); Ribonuclease H-like domain [IPR012337] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	scaffold_2_mRNA_1284.1	-	-
GF0026824	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_128.1	-	-
GF0026823	1	0	0	Non-LTR retroelement reverse transcriptase (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	scaffold_2_mRNA_1274.1	-	-
GF0026822	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1271.1	-	-
GF0026821	1	0	0	Pre-rrna-processing protein esf2 (1)			scaffold_2_mRNA_1270.1	-	-
GF0026820	1	0	0	Early nodulin 8 family protein (1)	protein binding [GO:0005515 molecular_function] (1); hydrolase activity, acting on ester bonds [GO:0016788 molecular_function] (1)	Tetratricopeptide-like helical domain [IPR011990] (1); Pentatricopeptide repeat [IPR002885] (1); GDSL lipase/esterase [IPR001087] (1)	scaffold_2_mRNA_1264.1	-	-
GF0026819	1	0	0	Hypothetical protein (1)	generation of catalytic spliceosome for second transesterification step [GO:0000350 biological_process] (1)	Pre-mRNA-splicing factor Isy1 [IPR009360] (1)	scaffold_2_mRNA_1262.1	-	-
GF0026818	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1261.1	-	-
GF0026817	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_126.1	-	-
GF0026816	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1228.1	-	-
GF0026815	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1204.1	-	-
GF0026814	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1201.1	-	-
GF0026813	1	0	0	RNA-directed DNA polymerase , related (1)			scaffold_2_mRNA_1199.1	-	-
GF0026812	1	0	0	Phosphate/phosphoenolpyruvate translocator (1)		Sugar phosphate transporter domain [IPR004853] (1)	scaffold_2_mRNA_1190.1	-	-
GF0026811	1	0	0	Alpha-amylase type B isozyme (1)	alpha-amylase activity [GO:0004556 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1); calcium ion binding [GO:0005509 molecular_function] (1); cation binding [GO:0043169 molecular_function] (1)	Glycoside hydrolase superfamily [IPR017853] (1); Alpha amylase [IPR006046] (1); Glycosyl hydrolase, family 13, catalytic domain [IPR006047] (1); Alpha-amylase, C-terminal beta-sheet [IPR012850] (1); Alpha-amylase, plant [IPR013775] (1)	scaffold_2_mRNA_1183.1	-	-
GF0026810	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_2_mRNA_117.1	-	-
GF0026809	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_116.1	-	-
GF0026808	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_115.1	-	-
GF0026807	1	0	0	UDP-glycosyltransferase 73C5 (1)	metabolic process [GO:0008152 biological_process] (1); transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (1)	UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (1)	scaffold_2_mRNA_1142.1	-	-
GF0026806	1	0	0	Monosacharide transport protein (1)			scaffold_2_mRNA_1137.1	-	-
GF0026805	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_113.1	-	-
GF0026804	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1117.1	-	-
GF0026803	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_111.1	-	-
GF0026802	1	0	0	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); Protein kinase-like domain [IPR011009] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat [IPR001611] (1)	scaffold_2_mRNA_1104.1	-	-
GF0026801	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_110.1	-	-
GF0026800	1	0	0	Non-LTR retroelement reverse transcriptase (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1); LOG family [IPR031100] (1)	scaffold_2_mRNA_1094.1	-	-
GF0026799	1	0	0	Hypothetical protein (1)		EF-hand domain pair [IPR011992] (1)	scaffold_2_mRNA_1080.1	-	-
GF0026798	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_108.1	-	-
GF0026797	1	0	0	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)	scaffold_2_mRNA_1046.1	-	-
GF0026796	1	0	0	Transcription factor bHLH36 (1)	protein dimerization activity [GO:0046983 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	Achaete-scute transcription factor-related [IPR015660] (1); Myc-type, basic helix-loop-helix (bHLH) domain [IPR011598] (1)	scaffold_2_mRNA_1045.1	-	-
GF0026795	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_103.1	-	-
GF0026794	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1029.1	-	-
GF0026793	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1017.1	-	-
GF0026792	1	0	0	Hypothetical protein (1)			scaffold_2_mRNA_1008.1	-	-
GF0026791	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_997.1	-	-
GF0026790	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_995.1	-	-
GF0026789	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_974.1	-	-
GF0026788	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_954.1	-	-
GF0026787	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_95.1	-	-
GF0026786	1	0	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_1_mRNA_939.1	-	-
GF0026785	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_934.1	-	-
GF0026784	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_921.1	-	-
GF0026783	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_920.1	-	-
GF0026782	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_918.1	-	-
GF0026781	1	0	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	hAT-like transposase, RNase-H fold [IPR025525] (1)	scaffold_1_mRNA_914.1	-	-
GF0026780	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_899.1	-	-
GF0026779	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_898.1	-	-
GF0026778	1	0	0	Hypothetical protein (1)	methyltransferase activity [GO:0008168 molecular_function] (1)	S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); Bin3-type S-adenosyl-L-methionine binding domain [IPR024160] (1)	scaffold_1_mRNA_884.1	-	-
GF0026777	1	0	0	30S ribosomal protein S1 like (1)	nucleic acid binding [GO:0003676 molecular_function] (1); translation elongation factor activity [GO:0003746 molecular_function] (1); translational elongation [GO:0006414 biological_process] (1); intracellular [GO:0005622 cellular_component] (1)	RNA-binding domain, S1 [IPR022967] (1); Translation elongation factor EFTs/EF1B [IPR001816] (1); Nucleic acid-binding, OB-fold [IPR012340] (1); S1 domain [IPR003029] (1)	scaffold_1_mRNA_875.1	-	-
GF0026776	1	0	0	Translation elongation factor Ts (1)	translation elongation factor activity [GO:0003746 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1); translational elongation [GO:0006414 biological_process] (1); intracellular [GO:0005622 cellular_component] (1)	Translation elongation factor EFTs/EF1B, dimerisation [IPR014039] (1); UBA-like [IPR009060] (1); Translation elongation factor EFTs/EF1B [IPR001816] (1); Translation elongation factor Ts, conserved site [IPR018101] (1)	scaffold_1_mRNA_874.1	-	-
GF0026775	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_869.1	-	-
GF0026774	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_854.1	-	-
GF0026773	1	0	0	Transposable element protein, putative (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_1_mRNA_849.1	-	-
GF0026772	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_848.1	-	-
GF0026771	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_833.1	-	-
GF0026770	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_830.1	-	-
GF0026769	1	0	0	Putative retroelement pol polyprotein (1)			scaffold_1_mRNA_83.1	-	-
GF0026768	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_1_mRNA_829.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0026767	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_828.1	-	-
GF0026766	1	0	0	Hypothetical protein (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); Receptor, ligand binding region [IPR001828] (1); Periplasmic binding protein-like I [IPR028082] (1)	scaffold_1_mRNA_81.1	-	-
GF0026765	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_794.1	-	-
GF0026764	1	0	0	Monosacharide transport protein (1)			scaffold_1_mRNA_793.1	-	-
GF0026763	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_789.1	-	-
GF0026762	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_788.1	-	-
GF0026761	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_1_mRNA_787.1	-	-
GF0026760	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_785.1	-	-
GF0026759	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_1_mRNA_783.1	-	-
GF0026758	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_781.1	-	-
GF0026757	1	0	0	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)	scaffold_1_mRNA_771.1	-	-
GF0026756	1	0	0	General transcription factor IIH subunit 4 (1)	core TFIIH complex [GO:0000439 cellular_component] (1); nucleotide-excision repair [GO:0006289 biological_process] (1); nucleus [GO:0005634 cellular_component] (1); ATP-dependent DNA helicase activity [GO:0004003 molecular_function] (1)	Transcription factor TFIIH subunit p52/Tfb2 [IPR004598] (1)	scaffold_1_mRNA_768.1	-	-
GF0026755	1	0	0	Hypothetical protein (1)	nucleus [GO:0005634 cellular_component] (1); ATP-dependent DNA helicase activity [GO:0004003 molecular_function] (1); nucleotide-excision repair [GO:0006289 biological_process] (1); core TFIIH complex [GO:0000439 cellular_component] (1)	Transcription factor TFIIH subunit p52/Tfb2 [IPR004598] (1)	scaffold_1_mRNA_761.1	-	-
GF0026754	1	0	0	Terpene synthase 21, putative isoform 3 (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)	scaffold_1_mRNA_759.1	-	-
GF0026753	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_758.1	-	-
GF0026752	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_755.1	-	-
GF0026751	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_736.1	-	-
GF0026750	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_733.1	-	-
GF0026749	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_725.1	-	-
GF0026748	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_723.1	-	-
GF0026747	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_722.1	-	-
GF0026746	1	0	0	Retrotransposon protein, putative, Ty1-copia subclass (1)			scaffold_1_mRNA_721.1	-	-
GF0026745	1	0	0	NAD-dependent aldehyde dehydrogenase family protein (1)	metabolic process [GO:0008152 biological_process] (1); oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1)	Aldehyde dehydrogenase N-terminal domain [IPR016162] (1); Aldehyde dehydrogenase, glutamic acid active site [IPR029510] (1); Aldehyde dehydrogenase domain [IPR015590] (1); Aldehyde/histidinol dehydrogenase [IPR016161] (1)	scaffold_1_mRNA_719.1	-	-
GF0026744	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_707.1	-	-
GF0026743	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_695.1	-	-
GF0026742	1	0	0	Nudix hydrolase 24 (1)		Domain of unknown function DUF4743 [IPR031804] (1)	scaffold_1_mRNA_694.1	-	-
GF0026741	1	0	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1); Domain of unknown function DUF1985 [IPR015410] (1)	scaffold_1_mRNA_692.1	-	-
GF0026740	1	0	0	MuDR family transposase containing protein (1)		MULE transposase domain [IPR018289] (1); Transposase, MuDR, plant [IPR004332] (1)	scaffold_1_mRNA_691.1	-	-
GF0026739	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_682.1	-	-
GF0026738	1	0	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1); Domain of unknown function DUF1985 [IPR015410] (1)	scaffold_1_mRNA_675.1	-	-
GF0026737	1	0	0	Gibberellin 3 beta-hydroxylase family protein (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)	scaffold_1_mRNA_672.1	-	-
GF0026736	1	0	0	Hypothetical protein (1)		Protein of unknown function DUF2921 [IPR021319] (1)	scaffold_1_mRNA_667.1	-	-
GF0026735	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_661.1	-	-
GF0026734	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	Zinc finger, BED-type [IPR003656] (1); Zinc finger C2H2-type [IPR013087] (1)	scaffold_1_mRNA_659.1	-	-
GF0026733	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_658.1	-	-
GF0026732	1	0	0	Hypothetical protein (1)		Pentatricopeptide repeat [IPR002885] (1)	scaffold_1_mRNA_654.1	-	-
GF0026731	1	0	0	Hypothetical protein (1)	membrane [GO:0016020 cellular_component] (1); metabolic process [GO:0008152 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1); fatty acid biosynthetic process [GO:0006633 biological_process] (1); transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (1)	Thiolase-like [IPR016039] (1); SOUL haem-binding protein [IPR006917] (1); Protein of unknown function DUF2358 [IPR018790] (1); Very-long-chain 3-ketoacyl-CoA synthase [IPR012392] (1); FAE1/Type III polyketide synthase-like protein [IPR013601] (1); 3-Oxoacyl-[acyl-carrier-protein (ACP)] synthase III, C-terminal [IPR013747] (1)	scaffold_1_mRNA_653.1	-	-
GF0026730	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_647.1	-	-
GF0026729	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, GRF-type [IPR010666] (1)	scaffold_1_mRNA_645.1	-	-
GF0026728	1	0	0	DUF761 domain protein (1)		Protein of unknown function DUF761, plant [IPR008480] (1)	scaffold_1_mRNA_63.1	-	-
GF0026727	1	0	0	Hypothetical protein (1)	translation [GO:0006412 biological_process] (1); intracellular [GO:0005622 cellular_component] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1); ribosome [GO:0005840 cellular_component] (1)	Ribosomal protein L36 [IPR000473] (1)	scaffold_1_mRNA_582.1	-	-
GF0026726	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Domain of unknown function DUF4283 [IPR025558] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_1_mRNA_571.1	-	-
GF0026725	1	0	0	COP9 signalosome complex subunit 5b (1)	protein binding [GO:0005515 molecular_function] (1)	JAB1/MPN/MOV34 metalloenzyme domain [IPR000555] (1)	scaffold_1_mRNA_55.3	-	-
GF0026724	1	0	0	Hypothetical protein (1)	carbohydrate binding [GO:0030246 molecular_function] (1)	Legume lectin domain [IPR001220] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1)	scaffold_1_mRNA_515.1	-	-
GF0026723	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_510.1	-	-
GF0026722	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_509.1	-	-
GF0026721	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_508.1	-	-
GF0026720	1	0	0	Green ripe-like 1 (1)		Protein of unknown function DUF778 [IPR008496] (1)	scaffold_1_mRNA_504.1	-	-
GF0026719	1	0	0	Ribonuclease H-like superfamily protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_1_mRNA_501.1	-	-
GF0026718	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_482.1	-	-
GF0026717	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_1_mRNA_475.1	-	-
GF0026716	1	0	0	Derlin-1.1 isoform 1 (1)	integral component of membrane [GO:0016021 cellular_component] (1); serine-type endopeptidase activity [GO:0004252 molecular_function] (1)	Derlin [IPR007599] (1); Peptidase S54, rhomboid domain [IPR022764] (1)	scaffold_1_mRNA_460.1	-	-
GF0026715	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_414.1	-	-
GF0026714	1	0	0	E3 ubiquitin-protein ligase ATL42 (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)	scaffold_1_mRNA_409.1	-	-
GF0026713	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat-containing protein At2g01680 [IPR027002] (1); Ankyrin repeat-containing domain [IPR020683] (1); Ankyrin repeat [IPR002110] (1)	scaffold_1_mRNA_406.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0026712	1	0	0	Hypothetical protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1)	Protein kinase, ATP binding site [IPR017441] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Domain of unknown function DUF828 [IPR008546] (1); Pleckstrin-like, plant [IPR013666] (1); PH domain-like [IPR011993] (1); Pleckstrin homology domain [IPR001849] (1); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1)	scaffold_1_mRNA_400.1	-	-
GF0026711	1	0	0	Peptide/nitrate transporter plant (1)	transport [GO:0006810 biological_process] (1); membrane [GO:0016020 cellular_component] (1); transporter activity [GO:0005215 molecular_function] (1)	Major facilitator superfamily domain [IPR020846] (1); Proton-dependent oligopeptide transporter family [IPR000109] (1)	scaffold_1_mRNA_398.1	-	-
GF0026710	1	0	0	ARM repeat superfamily protein, putative (1)		Armadillo-like helical [IPR011989] (1)	scaffold_1_mRNA_392.1	-	-
GF0026709	1	0	0	Hemopexin (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	scaffold_1_mRNA_372.1	-	-
GF0026708	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_3597.1	-	-
GF0026707	1	0	0	Hypothetical protein (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1)	Glycoside hydrolase superfamily [IPR017853] (1); Glycoside hydrolase family 18, catalytic domain [IPR001223] (1)	scaffold_1_mRNA_3565.1	-	-
GF0026706	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_3548.1	-	-
GF0026705	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_3547.1	-	-
GF0026704	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, RING/FYVE/PHD-type [IPR013083] (1); Zinc finger, RING-type [IPR001841] (1)	scaffold_1_mRNA_3533.1	-	-
GF0026703	1	0	0	Tetratricopeptide repeat (TPR)-like superfamily protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	DYW domain [IPR032867] (1); Tetratricopeptide-like helical domain [IPR011990] (1); Pentatricopeptide repeat [IPR002885] (1)	scaffold_1_mRNA_349.1	-	-
GF0026702	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_3478.1	-	-
GF0026701	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_3468.1	-	-
GF0026700	1	0	0	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)	scaffold_1_mRNA_3444.1	-	-
GF0026699	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_3430.1	-	-
GF0026698	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_3420.1	-	-
GF0026697	1	0	0	Hypothetical protein (1)		Periplasmic binding protein-like I [IPR028082] (1); Receptor, ligand binding region [IPR001828] (1)	scaffold_1_mRNA_3414.1	-	-
GF0026696	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_1_mRNA_3408.1	-	-
GF0026695	1	0	0	Hypothetical protein (1)	terpenoid biosynthetic process [GO:0016114 biological_process] (1); 1-deoxy-D-xylulose-5-phosphate synthase activity [GO:0008661 molecular_function] (1)	Transketolase-like, pyrimidine-binding domain [IPR005475] (1); Transketolase binding site [IPR020826] (1); Deoxyxylulose-5-phosphate synthase [IPR005477] (1); Thiamin diphosphate-binding fold [IPR029061] (1)	scaffold_1_mRNA_3402.1	-	-
GF0026694	1	0	0	ADP-ribosylation factor 2 (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)	scaffold_1_mRNA_3401.1	-	-
GF0026693	1	0	0	Hypothetical protein (1)	xyloglucan:xyloglucosyl transferase activity [GO:0016762 molecular_function] (1); hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (1); cell wall [GO:0005618 cellular_component] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1); apoplast [GO:0048046 cellular_component] (1); cellular glucan metabolic process [GO:0006073 biological_process] (1)	Xyloglucan endo-transglycosylase, C-terminal [IPR010713] (1); Beta-glucanase [IPR008264] (1); Glycoside hydrolase family 16 [IPR000757] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Glycoside hydrolase, family 16, active site [IPR008263] (1)	scaffold_1_mRNA_3381.1	-	-
GF0026692	1	0	0	Probable xyloglucan endotransglucosylase/hydrolase protein 23 (1)	xyloglucan:xyloglucosyl transferase activity [GO:0016762 molecular_function] (1); hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (1); cell wall [GO:0005618 cellular_component] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1); apoplast [GO:0048046 cellular_component] (1); cellular glucan metabolic process [GO:0006073 biological_process] (1)	Xyloglucan endo-transglycosylase, C-terminal [IPR010713] (1); Glycoside hydrolase family 16 [IPR000757] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1)	scaffold_1_mRNA_3378.1	-	-
GF0026691	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_3369.1	-	-
GF0026690	1	0	0	Syntaxin/t-SNARE family protein, putative isoform 1 (1)	membrane [GO:0016020 cellular_component] (1); vesicle-mediated transport [GO:0016192 biological_process] (1); Golgi vesicle transport [GO:0048193 biological_process] (1)	SNARE [IPR010989] (1); Syntaxin 6, N-terminal [IPR015260] (1)	scaffold_1_mRNA_3358.1	-	-
GF0026689	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_3356.1	-	-
GF0026688	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_1_mRNA_3330.1	-	-
GF0026687	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_3317.1	-	-
GF0026686	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_1_mRNA_33.1	-	-
GF0026685	1	0	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FAR1 DNA binding domain [IPR004330] (1); FHY3/FAR1 family [IPR031052] (1)	scaffold_1_mRNA_3299.1	-	-
GF0026684	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_3270.1	-	-
GF0026683	1	0	0	Neuronal acetylcholine receptor subunit alpha-5 (1)			scaffold_1_mRNA_3243.1	-	-
GF0026682	1	0	0	Squalene monooxygenase isoform 3 (1)	squalene monooxygenase activity [GO:0004506 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (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)	Squalene epoxidase [IPR013698] (1); FAD/NAD(P)-binding domain [IPR023753] (1)	scaffold_1_mRNA_3224.1	-	-
GF0026681	1	0	0	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	scaffold_1_mRNA_3223.1	-	-
GF0026680	1	0	0	Squalene monooxygenase (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); squalene monooxygenase activity [GO:0004506 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1)	FAD/NAD(P)-binding domain [IPR023753] (1); Squalene epoxidase [IPR013698] (1)	scaffold_1_mRNA_3221.1	-	-
GF0026679	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_1_mRNA_319.1	-	-
GF0026678	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_1_mRNA_3181.1	-	-
GF0026677	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_3179.1	-	-
GF0026676	1	0	0	Vesicle-associated membrane protein 713 (1)	vesicle-mediated transport [GO:0016192 biological_process] (1); integral component of membrane [GO:0016021 cellular_component] (1); transport [GO:0006810 biological_process] (1)	Longin domain [IPR010908] (1); Longin-like domain [IPR011012] (1); Synaptobrevin [IPR001388] (1)	scaffold_1_mRNA_3156.1	-	-
GF0026675	1	0	0	Copia-like retroelement pol polyprotein-like (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	scaffold_1_mRNA_315.1	-	-
GF0026674	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_3140.1	-	-
GF0026673	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_314.1	-	-
GF0026672	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_3132.1	-	-
GF0026671	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_313.1	-	-
GF0026670	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_3123.1	-	-
GF0026669	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_3121.1	-	-
GF0026668	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_312.1	-	-

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GF0026667	1	0	0	Hypothetical protein (1)		Prolamin-like domain [IPR008502] (1)	scaffold_1_mRNA_3119.1	-	-
GF0026666	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_1_mRNA_3118.1	-	-
GF0026665	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_3117.1	-	-
GF0026664	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_3116.1	-	-
GF0026663	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat [IPR002110] (1); Ankyrin repeat-containing domain [IPR020683] (1)	scaffold_1_mRNA_3111.1	-	-
GF0026662	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_1_mRNA_311.1	-	-
GF0026661	1	0	0	Ankyrin repeat family protein (1)	protein binding [GO:0005515 molecular_function] (1)	Ankyrin repeat [IPR002110] (1); Ankyrin repeat-containing domain [IPR020683] (1)	scaffold_1_mRNA_3107.1	-	-
GF0026660	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_3102.1	-	-
GF0026659	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_310.1	-	-
GF0026658	1	0	0	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	scaffold_1_mRNA_308.1	-	-
GF0026657	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_3074.1	-	-
GF0026656	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_3073.1	-	-
GF0026655	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_1_mRNA_3072.1	-	-
GF0026654	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_3053.1	-	-
GF0026653	1	0	0	F-box domain containing protein, expressed (1)	protein binding [GO:0005515 molecular_function] (1)	F-box domain [IPR001810] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); FBD domain [IPR006566] (1)	scaffold_1_mRNA_3039.1	-	-
GF0026652	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_3030.1	-	-
GF0026651	1	0	0	Hypothetical protein (1)	pectinesterase activity [GO:0030599 molecular_function] (1); cell wall modification [GO:0042545 biological_process] (1); cell wall [GO:0005618 cellular_component] (1)	Pectinesterase, Asp active site [IPR033131] (1); Pectin lyase fold [IPR012334] (1); Pectinesterase, catalytic [IPR000070] (1); Pectin lyase fold/virulence factor [IPR011050] (1)	scaffold_1_mRNA_3029.1	-	-
GF0026650	1	0	0	C6HC-type zinc finger RING/U-box protein (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); protein ubiquitination [GO:0016567 biological_process] (1)	Zinc finger, RING/FYVE/PHD-type [IPR013083] (1); IBR domain [IPR002867] (1); Zinc finger, RING-type [IPR001841] (1); Zinc finger, RING-type, conserved site [IPR017907] (1); E3 ubiquitin ligase RBR family [IPR031127] (1)	scaffold_1_mRNA_3020.1	-	-
GF0026649	1	0	0	Auxin-induced protein 15A (1)	response to auxin [GO:0009733 biological_process] (1)	Small auxin-up RNA [IPR003676] (1)	scaffold_1_mRNA_3006.1	-	-
GF0026648	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_300.1	-	-
GF0026647	1	0	0	Salicylate 1-monooxygenase (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); FAD binding [GO:0071949 molecular_function] (1)	FAD-binding domain [IPR002938] (1); FAD/NAD(P)-binding domain [IPR023753] (1)	scaffold_1_mRNA_299.1	-	-
GF0026646	1	0	0	Adipocyte plasma membrane-associated 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)	scaffold_1_mRNA_2972.1	-	-
GF0026645	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2946.1	-	-
GF0026644	1	0	0	Myb domain protein 4 (1)			scaffold_1_mRNA_2928.1	-	-
GF0026643	1	0	0	Hypothetical protein (1)	monolayer-surrounded lipid storage body [GO:0012511 cellular_component] (1); integral component of membrane [GO:0016021 cellular_component] (1)	Oleosin [IPR000136] (1)	scaffold_1_mRNA_2925.1	-	-
GF0026642	1	0	0	Subtilisin-like serine protease (1)	proteolysis [GO:0006508 biological_process] (1); serine-type endopeptidase activity [GO:0004252 molecular_function] (1)	Peptidase S8, subtilisin, Ser-active site [IPR023828] (1); Peptidase S8 propeptide/proteinase inhibitor I9 [IPR010259] (1); PA domain [IPR003137] (1); Peptidase S8/S53 domain [IPR000209] (1); Cucumisin-like catalytic domain [IPR034197] (1); Peptidase S8, subtilisin-related [IPR015500] (1)	scaffold_1_mRNA_2915.1	-	-
GF0026641	1	0	0	Salicylate 1-monooxygenase (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); FAD binding [GO:0071949 molecular_function] (1)	FAD/NAD(P)-binding domain [IPR023753] (1); FAD-binding domain [IPR002938] (1)	scaffold_1_mRNA_291.1	-	-
GF0026640	1	0	0	Putative non-LTR reverse transcriptase (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_1_mRNA_2908.1	-	-
GF0026639	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Reverse transcriptase domain [IPR000477] (1); Domain of unknown function DUF4283 [IPR025558] (1); Zinc finger, CCHC-type [IPR001878] (1); Domain of unknown function DUF2431 [IPR019446] (1); Endonuclease/exonuclease/phosphatase [IPR005135] (1)	scaffold_1_mRNA_2902.1	-	-
GF0026638	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2899.1	-	-
GF0026637	1	0	0	Hypothetical protein (1)		Reverse transcriptase zinc-binding domain [IPR026960] (1)	scaffold_1_mRNA_2898.1	-	-
GF0026636	1	0	0	Hypothetical protein (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Isopenicillin N synthase-like [IPR027443] (1); Oxoglutarate/iron-dependent dioxygenase [IPR005123] (1)	scaffold_1_mRNA_2897.1	-	-
GF0026635	1	0	0	Senescence-related gene 1 (1)	oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Oxoglutarate/iron-dependent dioxygenase [IPR005123] (1); Isopenicillin N synthase-like [IPR027443] (1); Non-haem dioxygenase N-terminal domain [IPR026992] (1)	scaffold_1_mRNA_2895.1	-	-
GF0026634	1	0	0	Hypothetical protein (1)		Non-haem dioxygenase N-terminal domain [IPR026992] (1); Isopenicillin N synthase-like [IPR027443] (1)	scaffold_1_mRNA_2893.1	-	-
GF0026633	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_289.1	-	-
GF0026632	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_288.1	-	-
GF0026631	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_1_mRNA_2878.1	-	-
GF0026630	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2877.1	-	-
GF0026629	1	0	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	scaffold_1_mRNA_2875.1	-	-
GF0026628	1	0	0	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); FAD binding [GO:0071949 molecular_function] (1)	FAD/NAD(P)-binding domain [IPR023753] (1); FAD-binding domain [IPR002938] (1)	scaffold_1_mRNA_286.1	-	-
GF0026627	1	0	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Carlavirus nucleic acid-binding protein [IPR002568] (1)	scaffold_1_mRNA_2848.1	-	-
GF0026626	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_1_mRNA_2847.1	-	-
GF0026625	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2841.1	-	-
GF0026624	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_284.1	-	-
GF0026623	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2826.1	-	-
GF0026622	1	0	0	Hypothetical protein (1)		AmbAllergen [IPR018082] (1); Pectin lyase fold/virulence factor [IPR011050] (1); Pectin lyase fold [IPR012334] (1)	scaffold_1_mRNA_2824.1	-	-
GF0026621	1	0	0	Hypothetical protein (1)		Potassium channel domain [IPR013099] (1)	scaffold_1_mRNA_2815.1	-	-
GF0026620	1	0	0	Hypothetical protein (1)		Potassium channel domain [IPR013099] (1)	scaffold_1_mRNA_2814.1	-	-
GF0026619	1	0	0	Cytochrome P450 (1)	iron ion binding [GO:0005506 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1)	Cytochrome P450 [IPR001128] (1); Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450, conserved site [IPR017972] (1)	scaffold_1_mRNA_2802.1	-	-
GF0026618	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2795.1	-	-
GF0026617	1	0	0	Polypeptide with a gag-like domain (1)			scaffold_1_mRNA_2787.1	-	-
GF0026616	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Retrotransposon gag domain [IPR005162] (1)	scaffold_1_mRNA_2781.1	-	-
GF0026615	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2780.1	-	-
GF0026614	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2774.1	-	-
GF0026613	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_1_mRNA_2754.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0026612	1	0	0	Monosacharide transport protein (1)			scaffold_1_mRNA_2753.1	-	-
GF0026611	1	0	0	Hypothetical protein (1)	carbohydrate metabolic process [GO:0005975 biological_process] (1); polygalacturonase activity [GO:0004650 molecular_function] (1)	Pectin lyase fold [IPR012334] (1); Pectin lyase fold/virulence factor [IPR011050] (1); Glycoside hydrolase, family 28 [IPR000743] (1)	scaffold_1_mRNA_2748.1	-	-
GF0026610	1	0	0	F-box and associated interaction domains-containing protein, putative isoform 1 (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)	scaffold_1_mRNA_2747.1	-	-
GF0026609	1	0	0	Mutator-like transposase isoform 1 (1)		Transposase, MuDR, plant [IPR004332] (1); MULE transposase domain [IPR018289] (1)	scaffold_1_mRNA_273.1	-	-
GF0026608	1	0	0	SWIb domain-containing protein (1)	protein binding [GO:0005515 molecular_function] (1)	SWIB domain [IPR019835] (1); SWIB/MDM2 domain [IPR003121] (1)	scaffold_1_mRNA_2725.1	-	-
GF0026607	1	0	0	Short chain alcohol dehydrogenase, putative (1)		NAD(P)-binding domain [IPR016040] (1); Short-chain dehydrogenase/reductase SDR [IPR002347] (1)	scaffold_1_mRNA_271.1	-	-
GF0026606	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2700.1	-	-
GF0026605	1	0	0	Hypothetical protein (1)		Transposase, MuDR, plant [IPR004332] (1)	scaffold_1_mRNA_2687.1	-	-
GF0026604	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2680.1	-	-
GF0026603	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2679.1	-	-
GF0026602	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_1_mRNA_2674.1	-	-
GF0026601	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2673.1	-	-
GF0026600	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2672.1	-	-
GF0026599	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2671.1	-	-
GF0026598	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2670.1	-	-
GF0026597	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	scaffold_1_mRNA_2668.1	-	-
GF0026596	1	0	0	AT4G05040 protein (1)	regulation of salicylic acid mediated signaling pathway [GO:2000031 biological_process] (1); regulation of defense response [GO:0031347 biological_process] (1); protein binding [GO:0005515 molecular_function] (1); cellular response to salicylic acid stimulus [GO:0071446 biological_process] (1); integral component of membrane [GO:0016021 cellular_component] (1)	Ankyrin repeat-containing domain [IPR020683] (1); PGG domain [IPR026961] (1); Protein accelerated cell death 6 [IPR032846] (1); Ankyrin repeat [IPR002110] (1)	scaffold_1_mRNA_2653.1	-	-
GF0026595	1	0	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger C2H2-type [IPR013087] (1); Zinc finger, BED-type [IPR003656] (1)	scaffold_1_mRNA_2648.1	-	-
GF0026594	1	0	0	Monosacharide transport protein (1)			scaffold_1_mRNA_2644.1	-	-
GF0026593	1	0	0	Hypothetical protein (1)	calcium ion binding [GO:0005509 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1); EF-hand domain pair [IPR011992] (1); EF-Hand 1, calcium-binding site [IPR018247] (1); EF-hand domain [IPR002048] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase, ATP binding site [IPR017441] (1)	scaffold_1_mRNA_2641.1	-	-
GF0026592	1	0	0	Calcium-dependent protein kinase 29 (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-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	scaffold_1_mRNA_2636.1	-	-
GF0026591	1	0	0	Calcium-dependent protein kinase 20 (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)	scaffold_1_mRNA_2630.1	-	-
GF0026590	1	0	0	Endoribonuclease L-PSP family protein (1)		Endoribonuclease L-PSP/chorismate mutase-like [IPR013813] (1); RidA, conserved site [IPR019897] (1); RidA family [IPR006056] (1); YjgF/YER057c/UK114 family [IPR006175] (1)	scaffold_1_mRNA_2626.1	-	-
GF0026589	1	0	0	Hypothetical protein (1)		P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1)	scaffold_1_mRNA_2608.1	-	-
GF0026588	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2607.1	-	-
GF0026587	1	0	0	NBS-LRR class resistance protein Fy1-Ry1 (1)	ADP binding [GO:0043531 molecular_function] (1)	Leucine-rich repeat domain, L domain-like [IPR032675] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	scaffold_1_mRNA_2606.1	-	-
GF0026586	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2604.1	-	-
GF0026585	1	0	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1); membrane [GO:0016020 cellular_component] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1); Ribonuclease H-like domain [IPR012337] (1); TMEM14 family [IPR005349] (1)	scaffold_1_mRNA_2596.1	-	-
GF0026584	1	0	0	Disease resistance family protein / LRR family protein, putative (1)	protein binding [GO:0005515 molecular_function] (1)	Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	scaffold_1_mRNA_2585.1	-	-
GF0026583	1	0	0	Plant natriuretic peptide A (1)		RlpA-like protein, double-psi beta-barrel domain [IPR009009] (1); Expansin/pollen allergen, DPBB domain [IPR007112] (1)	scaffold_1_mRNA_258.1	-	-
GF0026582	1	0	0	MuDR family transposase isoform 1 (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, SWIM-type [IPR007527] (1); Transposase, MuDR, plant [IPR004332] (1); MULE transposase domain [IPR018289] (1); Zinc finger, PMZ-type [IPR006564] (1)	scaffold_1_mRNA_2579.1	-	-
GF0026581	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2575.1	-	-
GF0026580	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2568.1	-	-
GF0026579	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2561.1	-	-
GF0026578	1	0	0	Serine/threonine-protein phosphatase 7 long form like (1)		Protein of unknown function DUF716 (TMEM45) [IPR006904] (1); Aminotransferase-like, plant mobile domain [IPR019557] (1)	scaffold_1_mRNA_2557.1	-	-
GF0026577	1	0	0	Ankyrin repeat-containing protein, putative isoform 1 (1)	protein binding [GO:0005515 molecular_function] (1)	PGG domain [IPR026961] (1); Ankyrin repeat-containing domain [IPR020683] (1); Ankyrin repeat [IPR002110] (1)	scaffold_1_mRNA_2545.1	-	-
GF0026576	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2544.1	-	-
GF0026575	1	0	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_1_mRNA_2543.1	-	-
GF0026574	1	0	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_1_mRNA_2542.1	-	-
GF0026573	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2539.1	-	-
GF0026572	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2538.1	-	-
GF0026571	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1); Xylanase inhibitor, C-terminal [IPR032799] (1)	scaffold_1_mRNA_2520.1	-	-
GF0026570	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2502.1	-	-
GF0026569	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2501.1	-	-
GF0026568	1	0	0	Sesquiterpene synthase (1)	magnesium ion binding [GO:0000287 molecular_function] (1); terpene synthase activity [GO:0010333 molecular_function] (1); lyase activity [GO:0016829 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1)	Terpene synthase, N-terminal domain [IPR001906] (1); Terpene synthase, metal-binding domain [IPR005630] (1); Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (1); Isoprenoid synthase domain [IPR008949] (1)	scaffold_1_mRNA_2497.1	-	-
GF0026567	1	0	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1)	scaffold_1_mRNA_2496.1	-	-
GF0026566	1	0	0	S-locus lectin kinase family protein (1)	recognition of pollen [GO:0048544 biological_process] (1)	S-locus glycoprotein domain [IPR000858] (1); Bulb-type lectin domain [IPR001480] (1); PAN/Apple domain [IPR003609] (1)	scaffold_1_mRNA_2480.1	-	-
GF0026565	1	0	0	Polyubiquitin (1)	protein binding [GO:0005515 molecular_function] (1)	Ubiquitin conserved site [IPR019954] (1); Ubiquitin [IPR019956] (1); Ubiquitin-related domain [IPR029071] (1); Ubiquitin domain [IPR000626] (1)	scaffold_1_mRNA_2477.2	-	-
GF0026564	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2474.1	-	-
GF0026563	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2468.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0026562	1	0	0	Hypothetical protein (1)	protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Serine/threonine-protein kinase, active site [IPR008271] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); LysM domain [IPR018392] (1); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1)	scaffold_1_mRNA_246.1	-	-
GF0026561	1	0	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_1_mRNA_2459.1	-	-
GF0026560	1	0	0	Lectin receptor 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); Concanavalin A-like lectin/glucanase domain [IPR013320] (1)	scaffold_1_mRNA_245.1	-	-
GF0026559	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2448.1	-	-
GF0026558	1	0	0	Vetispiradiene synthase (1)	metabolic process [GO:0008152 biological_process] (1); magnesium ion binding [GO:0000287 molecular_function] (1); terpene synthase activity [GO:0010333 molecular_function] (1); lyase activity [GO:0016829 molecular_function] (1)	Isoprenoid synthase domain [IPR008949] (1); Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (1); Terpene synthase, metal-binding domain [IPR005630] (1); Terpene synthase, N-terminal domain [IPR001906] (1)	scaffold_1_mRNA_2446.1	-	-
GF0026557	1	0	0	Pentatricopeptide repeat-containing protein, mitochondrial (1)			scaffold_1_mRNA_2445.1	-	-
GF0026556	1	0	0	Putative retroelement pol polyprotein (1)	DNA integration [GO:0015074 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Integrase, catalytic core [IPR001584] (1); Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1); Ribonuclease H-like domain [IPR012337] (1); GAG-pre-integrase domain [IPR025724] (1)	scaffold_1_mRNA_2440.1	-	-
GF0026555	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2437.1	-	-
GF0026554	1	0	0	Hypothetical protein (1)		Ataxin-2, C-terminal [IPR009818] (1)	scaffold_1_mRNA_2432.1	-	-
GF0026553	1	0	0	Lectin (1)	carbohydrate binding [GO:0030246 molecular_function] (1)	Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Legume lectin domain [IPR001220] (1)	scaffold_1_mRNA_243.1	-	-
GF0026552	1	0	0	Hypothetical protein (1)		Endonuclease/exonuclease/phosphatase [IPR005135] (1)	scaffold_1_mRNA_2428.1	-	-
GF0026551	1	0	0	Hypothetical protein (1)	lyase activity [GO:0016829 molecular_function] (1); terpene synthase activity [GO:0010333 molecular_function] (1); magnesium ion binding [GO:0000287 molecular_function] (1)	Isoprenoid synthase domain [IPR008949] (1); Terpene synthase, metal-binding domain [IPR005630] (1)	scaffold_1_mRNA_2424.1	-	-
GF0026550	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2421.1	-	-
GF0026549	1	0	0	Lectin (1)	carbohydrate binding [GO:0030246 molecular_function] (1)	Legume lectin domain [IPR001220] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Legume lectin, beta chain, Mn/Ca-binding site [IPR019825] (1)	scaffold_1_mRNA_240.1	-	-
GF0026548	1	0	0	(+)-delta-cadinene synthase isozyme A (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)	Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (1); Terpene synthase, N-terminal domain [IPR001906] (1); Terpene synthase, metal-binding domain [IPR005630] (1); Isoprenoid synthase domain [IPR008949] (1)	scaffold_1_mRNA_2399.1	-	-
GF0026547	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2397.1	-	-
GF0026546	1	0	0	Cysteine-rich RLK (RECEPTOR-like protein kinase) 8 (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); Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	scaffold_1_mRNA_2386.1	-	-
GF0026545	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_1_mRNA_2385.1	-	-
GF0026544	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2384.1	-	-
GF0026543	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2383.1	-	-
GF0026542	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_238.1	-	-
GF0026541	1	0	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	scaffold_1_mRNA_2370.1	-	-
GF0026540	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_1_mRNA_237.1	-	-
GF0026539	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2363.1	-	-
GF0026538	1	0	0	S-locus lectin protein kinase family protein, putative (1)		Bulb-type lectin domain [IPR001480] (1)	scaffold_1_mRNA_2360.1	-	-
GF0026537	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2357.1	-	-
GF0026536	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2356.1	-	-
GF0026535	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2355.1	-	-
GF0026534	1	0	0	Cysteine-rich RLK (Receptor-like kinase) protein (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); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); S-locus receptor kinase, C-terminal [IPR021820] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1)	scaffold_1_mRNA_2354.1	-	-
GF0026533	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_235.1	-	-
GF0026532	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2341.1	-	-
GF0026531	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_1_mRNA_2339.1	-	-
GF0026530	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2336.1	-	-
GF0026529	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_1_mRNA_2334.1	-	-
GF0026528	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2333.1	-	-
GF0026527	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2331.1	-	-
GF0026526	1	0	0	Hypothetical protein (1)		Bulb-type lectin domain [IPR001480] (1)	scaffold_1_mRNA_2329.1	-	-
GF0026525	1	0	0	S-locus lectin kinase family protein, putative (1)	recognition of pollen [GO:0048544 biological_process] (1)	S-locus glycoprotein domain [IPR000858] (1); Bulb-type lectin domain [IPR001480] (1)	scaffold_1_mRNA_2327.1	-	-
GF0026524	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_1_mRNA_2325.1	-	-
GF0026523	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2324.1	-	-
GF0026522	1	0	0	Hypothetical protein (1)		PAN/Apple domain [IPR003609] (1); Protein kinase-like domain [IPR011009] (1)	scaffold_1_mRNA_2323.1	-	-
GF0026521	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Retrotransposon gag domain [IPR005162] (1)	scaffold_1_mRNA_2321.1	-	-
GF0026520	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2320.1	-	-
GF0026519	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2319.1	-	-
GF0026518	1	0	0	Hypothetical protein (1)	recognition of pollen [GO:0048544 biological_process] (1)	Bulb-type lectin domain [IPR001480] (1); S-locus glycoprotein domain [IPR000858] (1)	scaffold_1_mRNA_2318.1	-	-
GF0026517	1	0	0	Monosacharide transport protein (1)			scaffold_1_mRNA_2316.1	-	-
GF0026516	1	0	0	Hypothetical protein (1)	RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Retrotransposon gag domain [IPR005162] (1); Ribonuclease H-like domain [IPR012337] (1); Ribonuclease H domain [IPR002156] (1)	scaffold_1_mRNA_2315.1	-	-
GF0026515	1	0	0	G-type lectin S-receptor-like serine/threonine-protein kinase (1)	protein serine/threonine kinase activity [GO:0004674 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); recognition of pollen [GO:0048544 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1)	Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); S-locus receptor kinase, C-terminal [IPR021820] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); S-locus glycoprotein domain [IPR000858] (1); EGF-like domain [IPR000742] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); Bulb-type lectin domain [IPR001480] (1)	scaffold_1_mRNA_2313.1	-	-
GF0026514	1	0	0	Monosacharide transport protein (1)			scaffold_1_mRNA_2311.1	-	-
GF0026513	1	0	0	G-type lectin S-receptor-like serine/threonine-protein kinase (1)	recognition of pollen [GO:0048544 biological_process] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Serine/threonine-protein kinase, active site [IPR008271] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); S-locus glycoprotein domain [IPR000858] (1); PAN/Apple domain [IPR003609] (1); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1)	scaffold_1_mRNA_2309.1	-	-
GF0026512	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_1_mRNA_2307.1	-	-
GF0026511	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2304.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0026510	1	0	0	Disease resistance N'-like protein (1)	ADP binding [GO:0043531 molecular_function] (1)	Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1)	scaffold_1_mRNA_2302.1	-	-
GF0026509	1	0	0	Hypothetical protein (1)	protein serine/threonine kinase activity [GO:0004674 molecular_function] (1)	S-locus receptor kinase, C-terminal [IPR021820] (1)	scaffold_1_mRNA_2296.1	-	-
GF0026508	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_1_mRNA_2290.1	-	-
GF0026507	1	0	0	S-locus lectin kinase family protein (1)	ATP binding [GO:0005524 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); recognition of pollen [GO:0048544 biological_process] (1)	PAN/Apple domain [IPR003609] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); S-locus glycoprotein domain [IPR000858] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	scaffold_1_mRNA_2288.1	-	-
GF0026506	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_1_mRNA_2286.1	-	-
GF0026505	1	0	0	Transposase family tnp2, putative (1)		Domain of unknown function DUF4218 [IPR025452] (1); Transposon, En/Spm-like [IPR004242] (1); Probable transposase, Ptta/En/Spm, plant [IPR004252] (1); Transposase, Tnp1/En/Spm-like [IPR004264] (1); Transposase-associated domain [IPR029480] (1)	scaffold_1_mRNA_2281.1	-	-
GF0026504	1	0	0	G-type lectin S-receptor-like serine/threonine-protein kinase (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)	Serine/threonine-protein kinase, active site [IPR008271] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); S-locus glycoprotein domain [IPR000858] (1); PAN/Apple domain [IPR003609] (1); Bulb-type lectin domain [IPR001480] (1); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); S-receptor-like serine/threonine-protein kinase [IPR024171] (1)	scaffold_1_mRNA_2280.1	-	-
GF0026503	1	0	0	Hypothetical protein (1)		Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_1_mRNA_228.1	-	-
GF0026502	1	0	0	G-type lectin S-receptor-like serine/threonine-protein kinase (1)	ATP binding [GO:0005524 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein serine/threonine kinase activity [GO:0004674 molecular_function] (1); recognition of pollen [GO:0048544 biological_process] (1); protein phosphorylation [GO:0006468 biological_process] (1)	PAN/Apple domain [IPR003609] (1); Bulb-type lectin domain [IPR001480] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); S-locus receptor kinase, C-terminal [IPR021820] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); S-locus glycoprotein domain [IPR000858] (1); Protein kinase-like domain [IPR011009] (1); S-receptor-like serine/threonine-protein kinase [IPR024171] (1); Protein kinase domain [IPR000719] (1)	scaffold_1_mRNA_2277.1	-	-
GF0026501	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2276.1	-	-
GF0026500	1	0	0	Hypothetical protein (1)		Bulb-type lectin domain [IPR001480] (1)	scaffold_1_mRNA_2273.1	-	-
GF0026499	1	0	0	Monosacharide transport protein (1)			scaffold_1_mRNA_2271.1	-	-
GF0026498	1	0	0	G-type lectin S-receptor-like serine/threonine-protein kinase (1)	ATP binding [GO:0005524 molecular_function] (1); protein serine/threonine kinase activity [GO:0004674 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); recognition of pollen [GO:0048544 biological_process] (1)	Protein kinase-like domain [IPR011009] (1); S-receptor-like serine/threonine-protein kinase [IPR024171] (1); Protein kinase domain [IPR000719] (1); Bulb-type lectin domain [IPR001480] (1); PAN/Apple domain [IPR003609] (1); S-locus receptor kinase, C-terminal [IPR021820] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); S-locus glycoprotein domain [IPR000858] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1)	scaffold_1_mRNA_2269.1	-	-
GF0026497	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_1_mRNA_2268.1	-	-
GF0026496	1	0	0	Cysteine-rich RLK 10 (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/tyrosine-protein kinase, catalytic domain [IPR001245] (1); Aspartic peptidase domain [IPR021109] (1); Protein kinase, ATP binding site [IPR017441] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); S-locus receptor kinase, C-terminal [IPR021820] (1)	scaffold_1_mRNA_2265.1	-	-
GF0026495	1	0	0	Retrotransposon gag protein (1)		Retrotransposon gag domain [IPR005162] (1); OAR domain [IPR003654] (1)	scaffold_1_mRNA_2264.1	-	-
GF0026494	1	0	0	G-type lectin S-receptor-like serine/threonine-protein kinase (1)	recognition of pollen [GO:0048544 biological_process] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein serine/threonine kinase activity [GO:0004674 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1)	Protein kinase-like domain [IPR011009] (1); S-receptor-like serine/threonine-protein kinase [IPR024171] (1); Protein kinase domain [IPR000719] (1); PAN/Apple domain [IPR003609] (1); Bulb-type lectin domain [IPR001480] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); S-locus glycoprotein domain [IPR000858] (1)	scaffold_1_mRNA_2261.1	-	-
GF0026493	1	0	0	Retrotransposon gag protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_1_mRNA_2256.1	-	-
GF0026492	1	0	0	G-type lectin S-receptor-like serine/threonine-protein kinase (1)	protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1)	PAN/Apple domain [IPR003609] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	scaffold_1_mRNA_2252.1	-	-
GF0026491	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1); Retrotransposon gag domain [IPR005162] (1)	scaffold_1_mRNA_2251.1	-	-
GF0026490	1	0	0	Hypothetical protein (1)		Bulb-type lectin domain [IPR001480] (1); PAN/Apple domain [IPR003609] (1)	scaffold_1_mRNA_2250.1	-	-
GF0026489	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2246.1	-	-
GF0026488	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_1_mRNA_2244.1	-	-
GF0026487	1	0	0	Monosacharide transport protein (1)			scaffold_1_mRNA_2242.1	-	-
GF0026486	1	0	0	G-type lectin S-receptor-like serine/threonine-protein kinase (1)	ATP binding [GO:0005524 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)	PAN/Apple domain [IPR003609] (1); Bulb-type lectin domain [IPR001480] (1); S-locus glycoprotein domain [IPR000858] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1)	scaffold_1_mRNA_2241.1	-	-
GF0026485	1	0	0	Peroxisomal ascorbate peroxidase (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); Plant ascorbate peroxidase [IPR002207] (1); Peroxidase, active site [IPR019794] (1); Peroxidases heam-ligand binding site [IPR019793] (1); Haem peroxidase, plant/fungal/bacterial [IPR002016] (1)	scaffold_1_mRNA_224.1	-	-
GF0026484	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2239.1	-	-
GF0026483	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2237.1	-	-
GF0026482	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2233.1	-	-
GF0026481	1	0	0	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)	scaffold_1_mRNA_2232.1	-	-
GF0026480	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_1_mRNA_2231.1	-	-
GF0026479	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2223.1	-	-
GF0026478	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2222.1	-	-
GF0026477	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_1_mRNA_2216.1	-	-
GF0026476	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2215.1	-	-

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GF0026475	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2208.1	-	-
GF0026474	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2205.1	-	-
GF0026473	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2197.1	-	-
GF0026472	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2193.1	-	-
GF0026471	1	0	0	Protein FAR1-RELATED SEQUENCE 6 (1)	zinc ion binding [GO:0008270 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	Zinc finger, SWIM-type [IPR007527] (1); Zinc finger, PMZ-type [IPR006564] (1); FAR1 DNA binding domain [IPR004330] (1); FHY3/FAR1 family [IPR031052] (1)	scaffold_1_mRNA_2192.1	-	-
GF0026470	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2184.1	-	-
GF0026469	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2180.1	-	-
GF0026468	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2177.1	-	-
GF0026467	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2168.1	-	-
GF0026466	1	0	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_1_mRNA_2166.1	-	-
GF0026465	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2159.1	-	-
GF0026464	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Reverse transcriptase domain [IPR000477] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_1_mRNA_2158.1	-	-
GF0026463	1	0	0	Monosacharide transport protein (1)	sigma factor antagonist activity [GO:0016989 molecular_function] (1)	Anti sigma-E protein RseA, N-terminal [IPR005572] (1)	scaffold_1_mRNA_2153.1	-	-
GF0026462	1	0	0	Protein ULTRAPETALA 2 (1)		Developmental regulator, ULTRAPETALA [IPR020533] (1)	scaffold_1_mRNA_2142.1	-	-
GF0026461	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2137.1	-	-
GF0026460	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2134.1	-	-
GF0026459	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2130.1	-	-
GF0026458	1	0	0	Retrotransposon protein, putative, Ty3-gypsy subclass, expressed (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_1_mRNA_2129.1	-	-
GF0026457	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2128.1	-	-
GF0026456	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2127.1	-	-
GF0026455	1	0	0	Peptidyl-prolyl cis-trans isomerase chloroplast (1)	protein folding [GO:0006457 biological_process] (1); protein peptidyl-prolyl isomerization [GO:0000413 biological_process] (1); peptidyl-prolyl cis-trans isomerase activity [GO:0003755 molecular_function] (1)	Cyclophilin-type peptidyl-prolyl cis-trans isomerase domain [IPR002130] (1); Cyclophilin-like domain [IPR029000] (1); Cyclophilin-type peptidyl-prolyl cis-trans isomerase [IPR024936] (1)	scaffold_1_mRNA_2125.1	-	-
GF0026454	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2120.1	-	-
GF0026453	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2105.1	-	-
GF0026452	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2103.1	-	-
GF0026451	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2090.1	-	-
GF0026450	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			scaffold_1_mRNA_2089.1	-	-
GF0026449	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2088.1	-	-
GF0026448	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	scaffold_1_mRNA_2085.1	-	-
GF0026447	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2081.1	-	-
GF0026446	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2073.1	-	-
GF0026445	1	0	0	Nucleotidyltransferase family protein (1)	nucleotidyltransferase activity [GO:0016779 molecular_function] (1)	Polymerase, nucleotidyl transferase domain [IPR002934] (1); PAP/25A-associated [IPR002058] (1)	scaffold_1_mRNA_2070.1	-	-
GF0026444	1	0	0	Hypothetical protein (1)	nucleotidyltransferase activity [GO:0016779 molecular_function] (1)	Polymerase, nucleotidyl transferase domain [IPR002934] (1); Aspartic peptidase domain [IPR021109] (1)	scaffold_1_mRNA_2067.1	-	-
GF0026443	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_1_mRNA_2064.1	-	-
GF0026442	1	0	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1)	scaffold_1_mRNA_2061.1	-	-
GF0026441	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2056.1	-	-
GF0026440	1	0	0	Monosacharide transport protein (1)			scaffold_1_mRNA_2053.1	-	-
GF0026439	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2051.1	-	-
GF0026438	1	0	0	Hypothetical protein (1)		Protein of unknown function DUF2921 [IPR021319] (1)	scaffold_1_mRNA_2046.1	-	-
GF0026437	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2030.1	-	-
GF0026436	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1)	scaffold_1_mRNA_2024.1	-	-
GF0026435	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2020.1	-	-
GF0026434	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2019.1	-	-
GF0026433	1	0	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_1_mRNA_2007.1	-	-
GF0026432	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2005.1	-	-
GF0026431	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_2003.1	-	-
GF0026430	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1997.1	-	-
GF0026429	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1994.1	-	-
GF0026428	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Ribonuclease H-like domain [IPR012337] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1)	scaffold_1_mRNA_1988.1	-	-
GF0026427	1	0	0	Monosacharide transport protein (1)			scaffold_1_mRNA_1982.1	-	-
GF0026426	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1979.1	-	-
GF0026425	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1977.1	-	-
GF0026424	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1972.1	-	-
GF0026423	1	0	0	Disease resistance protein family, putative isoform 2 (1)	ADP binding [GO:0043531 molecular_function] (1)	P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1)	scaffold_1_mRNA_1971.1	-	-
GF0026422	1	0	0	Hypothetical protein (1)	ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1)	scaffold_1_mRNA_1962.1	-	-
GF0026421	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1961.1	-	-
GF0026420	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_1_mRNA_1960.1	-	-
GF0026419	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1953.1	-	-
GF0026418	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1952.1	-	-
GF0026417	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1946.1	-	-
GF0026416	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1943.1	-	-
GF0026415	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1942.1	-	-
GF0026414	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1941.1	-	-
GF0026413	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1940.1	-	-
GF0026412	1	0	0	Nodulin family protein (1)		Flotillin family [IPR027705] (1); Band 7 domain [IPR001107] (1)	scaffold_1_mRNA_194.1	-	-
GF0026411	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1938.1	-	-
GF0026410	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1935.1	-	-
GF0026409	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1933.1	-	-
GF0026408	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1930.1	-	-
GF0026407	1	0	0	Ribosomal protein L11 methyltransferase (1)		S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1)	scaffold_1_mRNA_1924.1	-	-
GF0026406	1	0	0	Disease resistance protein RPP13 variant (1)	nucleic acid binding [GO:0003676 molecular_function] (1); ADP binding [GO:0043531 molecular_function] (1)	NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_1_mRNA_1923.1	-	-
GF0026405	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1916.1	-	-
GF0026404	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1900.1	-	-
GF0026403	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_190.1	-	-
GF0026402	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1896.1	-	-
GF0026401	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_189.1	-	-
GF0026400	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1); hydrolase activity [GO:0016787 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Alpha/Beta hydrolase fold [IPR029058] (1); Viral movement protein [IPR028919] (1); Ribonuclease H-like domain [IPR012337] (1); Alpha/beta hydrolase fold-3 [IPR013094] (1); Exonuclease, RNase T/DNA polymerase III [IPR013520] (1); Zinc finger, CCHC-type [IPR001878] (1)	scaffold_1_mRNA_1883.1	-	-
GF0026399	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1882.1	-	-
GF0026398	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1873.1	-	-
GF0026397	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1871.1	-	-
GF0026396	1	0	0	Hypothetical protein (1)		Chromo domain [IPR023780] (1); Chromo domain-like [IPR016197] (1); Chromo/chromo shadow domain [IPR000953] (1)	scaffold_1_mRNA_1863.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0026395	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1862.1	-	-
GF0026394	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Endonuclease/exonuclease/phosphatase [IPR005135] (1); Zinc knuckle CX2CX4HX4C [IPR025836] (1); Zinc finger, CCHC-type [IPR001878] (1); Domain of unknown function DUF4283 [IPR025558] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_1_mRNA_1858.1	-	-
GF0026393	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_1_mRNA_1855.1	-	-
GF0026392	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1853.1	-	-
GF0026391	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Zinc finger, PMZ-type [IPR006564] (1); Zinc finger, SWIM-type [IPR007527] (1)	scaffold_1_mRNA_1851.1	-	-
GF0026390	1	0	0	Mutator-like transposase (1)		MULE transposase domain [IPR018289] (1); Transposase, MuDR, plant [IPR004332] (1)	scaffold_1_mRNA_1850.1	-	-
GF0026389	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1847.1	-	-
GF0026388	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1846.1	-	-
GF0026387	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1839.1	-	-
GF0026386	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1832.1	-	-
GF0026385	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1829.1	-	-
GF0026384	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			scaffold_1_mRNA_1827.1	-	-
GF0026383	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1826.1	-	-
GF0026382	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1825.1	-	-
GF0026381	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1824.1	-	-
GF0026380	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Eukaryotic translation initiation factor 3 subunit G, N-terminal [IPR024675] (1); Zinc finger, CCHC-type [IPR001878] (1)	scaffold_1_mRNA_1809.1	-	-
GF0026379	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_1_mRNA_1808.1	-	-
GF0026378	1	0	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	FHY3/FAR1 family [IPR031052] (1); Zinc finger, CCHC-type [IPR001878] (1); Zinc finger, PMZ-type [IPR006564] (1); MULE transposase domain [IPR018289] (1); Zinc finger, SWIM-type [IPR007527] (1)	scaffold_1_mRNA_1805.1	-	-
GF0026377	1	0	0	FAR1 DNA-binding domain protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1)	FHY3/FAR1 family [IPR031052] (1); FAR1 DNA binding domain [IPR004330] (1)	scaffold_1_mRNA_1804.1	-	-
GF0026376	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_1_mRNA_1801.1	-	-
GF0026375	1	0	0	Elongator complex protein 4 (1)	Elongator holoenzyme complex [GO:0033588 cellular_component] (1)	Elongator complex protein 4 [IPR008728] (1)	scaffold_1_mRNA_1800.1	-	-
GF0026374	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_18.1	-	-
GF0026373	1	0	0	Hypothetical protein (1)	transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (1)	Transferase [IPR003480] (1); Transposase-associated domain [IPR029480] (1); Probable transposase, Ptta/En/Spm, plant [IPR004252] (1)	scaffold_1_mRNA_1797.1	-	-
GF0026372	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1796.1	-	-
GF0026371	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1795.1	-	-
GF0026370	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1794.1	-	-
GF0026369	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1793.1	-	-
GF0026368	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1788.1	-	-
GF0026367	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1785.1	-	-
GF0026366	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1784.1	-	-
GF0026365	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_1_mRNA_1783.1	-	-
GF0026364	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, PMZ-type [IPR006564] (1)	scaffold_1_mRNA_1778.1	-	-
GF0026363	1	0	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1)	Aspartic peptidase, active site [IPR001969] (1); Peptidase A2A, retrovirus, catalytic [IPR001995] (1); Viral movement protein [IPR028919] (1)	scaffold_1_mRNA_1774.1	-	-
GF0026362	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1)	Reverse transcriptase domain [IPR000477] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_1_mRNA_1773.1	-	-
GF0026361	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1768.1	-	-
GF0026360	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_1_mRNA_1767.1	-	-
GF0026359	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_1_mRNA_1763.1	-	-
GF0026358	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1760.1	-	-
GF0026357	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1759.1	-	-
GF0026356	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1756.1	-	-
GF0026355	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_1_mRNA_1755.1	-	-
GF0026354	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1754.1	-	-
GF0026353	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_175.1	-	-
GF0026352	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1749.1	-	-
GF0026351	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1747.1	-	-
GF0026350	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1744.1	-	-
GF0026349	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1741.1	-	-
GF0026348	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1738.1	-	-
GF0026347	1	0	0	Sesquiterpene 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); Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (1); Terpene synthase, N-terminal domain [IPR001906] (1); Terpene synthase, metal-binding domain [IPR005630] (1)	scaffold_1_mRNA_1722.1	-	-
GF0026346	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1719.1	-	-
GF0026345	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1710.1	-	-
GF0026344	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1691.1	-	-
GF0026343	1	0	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1)	Domain of unknown function DUF4371 [IPR025398] (1); HAT, C-terminal dimerisation domain [IPR008906] (1)	scaffold_1_mRNA_1690.1	-	-
GF0026342	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1688.1	-	-
GF0026341	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1686.1	-	-
GF0026340	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			scaffold_1_mRNA_1675.1	-	-
GF0026339	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1674.1	-	-
GF0026338	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_1_mRNA_1666.1	-	-
GF0026337	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1665.1	-	-
GF0026336	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1664.1	-	-
GF0026335	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1661.1	-	-
GF0026334	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1660.1	-	-
GF0026333	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1659.1	-	-
GF0026332	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1657.1	-	-
GF0026331	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1655.1	-	-
GF0026330	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1654.1	-	-
GF0026329	1	0	0	60S ribosomal protein L14 (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)	Translation protein SH3-like domain [IPR008991] (1); Ribosomal protein L14e domain [IPR002784] (1); Ribosomal protein L2 domain 2 [IPR014722] (1)	scaffold_1_mRNA_1652.1	-	-
GF0026328	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1651.1	-	-
GF0026327	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1649.1	-	-
GF0026326	1	0	0	Putative retroelement pol polyprotein (1)			scaffold_1_mRNA_1646.1	-	-
GF0026325	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1636.1	-	-
GF0026324	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1)	scaffold_1_mRNA_1634.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0026323	1	0	0	Ras-related protein RABA6a (1)	GTPase activity [GO:0003924 molecular_function] (1); GTP binding [GO:0005525 molecular_function] (1)	Small GTPase superfamily [IPR001806] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Small GTP-binding protein domain [IPR005225] (1)	scaffold_1_mRNA_1633.1	-	-
GF0026322	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_1_mRNA_1620.1	-	-
GF0026321	1	0	0	Hypothetical protein (1)	GTPase activity [GO:0003924 molecular_function] (1); GTP binding [GO:0005525 molecular_function] (1); microtubule [GO:0005874 cellular_component] (1); structural constituent of cytoskeleton [GO:0005200 molecular_function] (1); microtubule-based process [GO:0007017 biological_process] (1)	Tubulin [IPR000217] (1); Beta tubulin [IPR002453] (1); Tubulin/FtsZ, GTPase domain [IPR003008] (1)	scaffold_1_mRNA_1618.1	-	-
GF0026320	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_1_mRNA_1611.1	-	-
GF0026319	1	0	0	Umbelliferone 8-geranyltransferase (1)			scaffold_1_mRNA_161.1	-	-
GF0026318	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_1_mRNA_1609.1	-	-
GF0026317	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_1_mRNA_1608.1	-	-
GF0026316	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1607.1	-	-
GF0026315	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_1_mRNA_1602.1	-	-
GF0026314	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1601.1	-	-
GF0026313	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_16.1	-	-
GF0026312	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1597.1	-	-
GF0026311	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1595.1	-	-
GF0026310	1	0	0	Integrase (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_1_mRNA_1594.1	-	-
GF0026309	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_1_mRNA_1593.1	-	-
GF0026308	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1590.1	-	-
GF0026307	1	0	0	Hypothetical protein (1)	protein binding [GO:0005515 molecular_function] (1)	C2 domain [IPR000008] (1)	scaffold_1_mRNA_1589.1	-	-
GF0026306	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1588.1	-	-
GF0026305	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_1_mRNA_1586.1	-	-
GF0026304	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1577.1	-	-
GF0026303	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	scaffold_1_mRNA_1571.1	-	-
GF0026302	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1570.1	-	-
GF0026301	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_1_mRNA_1569.1	-	-
GF0026300	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1557.1	-	-
GF0026299	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1556.1	-	-
GF0026298	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1550.1	-	-
GF0026297	1	0	0	Fructose-bisphosphate aldolase, class II (1)	zinc ion binding [GO:0008270 molecular_function] (1); catalytic activity [GO:0003824 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1); aldehyde-lyase activity [GO:0016832 molecular_function] (1)	Fructose-bisphosphate aldolase, class-II [IPR000771] (1); Aldolase-type TIM barrel [IPR013785] (1)	scaffold_1_mRNA_1545.1	-	-
GF0026296	1	0	0	Hypothetical protein (1)	cysteine-type peptidase activity [GO:0008234 molecular_function] (1); chitin binding [GO:0008061 molecular_function] (1); hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1); proteolysis [GO:0006508 biological_process] (1)	Chitinase insertion domain [IPR029070] (1); Glycoside hydrolase family 18, catalytic domain [IPR001223] (1); Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1); Chitinase II [IPR011583] (1); Domain of unknown function DUF1985 [IPR015410] (1); Glycoside hydrolase, chitinase active site [IPR001579] (1); Glycoside hydrolase superfamily [IPR017853] (1)	scaffold_1_mRNA_154.1	-	-
GF0026295	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1539.1	-	-
GF0026294	1	0	0	Retrotransposon protein, putative, Ty1-copia subclass (1)	nucleic acid binding [GO:0003676 molecular_function] (1); DNA integration [GO:0015074 biological_process] (1); zinc ion binding [GO:0008270 molecular_function] (1)	GAG-pre-integrase domain [IPR025724] (1); Zinc finger, CCHC-type [IPR001878] (1); Ribonuclease H-like domain [IPR012337] (1); Integrase, catalytic core [IPR001584] (1)	scaffold_1_mRNA_1537.1	-	-
GF0026293	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1526.1	-	-
GF0026292	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1524.1	-	-
GF0026291	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1522.1	-	-
GF0026290	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1518.1	-	-
GF0026289	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1517.1	-	-
GF0026288	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1513.1	-	-
GF0026287	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1511.1	-	-
GF0026286	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1509.1	-	-
GF0026285	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_1_mRNA_1506.1	-	-
GF0026284	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1503.1	-	-
GF0026283	1	0	0	Hypothetical protein (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1); Aspartic peptidase domain [IPR021109] (1); Peptidase A2A, retrovirus, catalytic [IPR001995] (1); Reverse transcriptase domain [IPR000477] (1); Retropepsins [IPR018061] (1)	scaffold_1_mRNA_1501.1	-	-
GF0026282	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1500.1	-	-
GF0026281	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1498.1	-	-
GF0026280	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1497.1	-	-
GF0026279	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1496.1	-	-
GF0026278	1	0	0	Gag protease polyprotein (1)			scaffold_1_mRNA_1495.1	-	-
GF0026277	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1492.1	-	-
GF0026276	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_1_mRNA_1489.1	-	-
GF0026275	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1488.1	-	-
GF0026274	1	0	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_1_mRNA_1486.1	-	-
GF0026273	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1483.1	-	-
GF0026272	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1480.1	-	-
GF0026271	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_148.1	-	-
GF0026270	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1478.1	-	-
GF0026269	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1474.1	-	-
GF0026268	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1473.1	-	-
GF0026267	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1469.1	-	-
GF0026266	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1464.1	-	-
GF0026265	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1463.1	-	-
GF0026264	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1462.1	-	-
GF0026263	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_146.1	-	-
GF0026262	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1457.1	-	-
GF0026261	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1452.1	-	-
GF0026260	1	0	0	Hypothetical protein (1)		Retropepsins [IPR018061] (1); Aspartic peptidase domain [IPR021109] (1)	scaffold_1_mRNA_1450.1	-	-
GF0026259	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1449.1	-	-
GF0026258	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1447.1	-	-
GF0026257	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_1_mRNA_1445.1	-	-
GF0026256	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_1_mRNA_1440.1	-	-
GF0026255	1	0	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1)	scaffold_1_mRNA_1435.1	-	-
GF0026254	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1434.1	-	-
GF0026253	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1429.1	-	-
GF0026252	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1424.1	-	-
GF0026251	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1420.1	-	-
GF0026250	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1419.1	-	-
GF0026249	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1418.1	-	-
GF0026248	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1417.1	-	-
GF0026247	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1416.1	-	-
GF0026246	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1415.1	-	-
GF0026245	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1413.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0026244	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1411.1	-	-
GF0026243	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_1_mRNA_1410.1	-	-
GF0026242	1	0	0	RNA polymerase I-specific transcription initiation factor RRN3 (1)		RNA polymerase I specific transcription initiation factor RRN3 [IPR007991] (1)	scaffold_1_mRNA_141.1	-	-
GF0026241	1	0	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1)	Peptidase A2A, retrovirus, catalytic [IPR001995] (1)	scaffold_1_mRNA_1409.1	-	-
GF0026240	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_1_mRNA_1408.1	-	-
GF0026239	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1407.1	-	-
GF0026238	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1406.1	-	-
GF0026237	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1401.1	-	-
GF0026236	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1400.1	-	-
GF0026235	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1399.1	-	-
GF0026234	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1394.1	-	-
GF0026233	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_1_mRNA_1390.1	-	-
GF0026232	1	0	0	Hypothetical protein (1)	aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1)	Aspartic peptidase, active site [IPR001969] (1); Peptidase A2A, retrovirus, catalytic [IPR001995] (1)	scaffold_1_mRNA_1389.1	-	-
GF0026231	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1388.1	-	-
GF0026230	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1385.1	-	-
GF0026229	1	0	0	Hypothetical protein (1)	proteolysis [GO:0006508 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1)	Aspartic peptidase, active site [IPR001969] (1); Zinc finger, CCHC-type [IPR001878] (1)	scaffold_1_mRNA_1384.1	-	-
GF0026228	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_1_mRNA_1381.1	-	-
GF0026227	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1380.1	-	-
GF0026226	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1376.1	-	-
GF0026225	1	0	0	Hypothetical protein (1)	nucleic acid binding [GO:0003676 molecular_function] (1); DNA integration [GO:0015074 biological_process] (1)	Ribonuclease H-like domain [IPR012337] (1); Integrase, catalytic core [IPR001584] (1); Aspartic peptidase domain [IPR021109] (1); Retrotransposon gag domain [IPR005162] (1)	scaffold_1_mRNA_1373.1	-	-
GF0026224	1	0	0	Hypothetical protein (1)	nucleus [GO:0005634 cellular_component] (1); DNA binding [GO:0003677 molecular_function] (1); DNA replication [GO:0006260 biological_process] (1)	Nucleic acid-binding, OB-fold [IPR012340] (1); Replication factor-A protein 1, N-terminal [IPR007199] (1)	scaffold_1_mRNA_1371.1	-	-
GF0026223	1	0	0	Hypothetical protein (1)	lipid metabolic process [GO:0006629 biological_process] (1)	Alpha/Beta hydrolase fold [IPR029058] (1); Fungal lipase-like domain [IPR002921] (1)	scaffold_1_mRNA_137.1	-	-
GF0026222	1	0	0	Hypothetical protein (1)		Transposase-associated domain [IPR029480] (1)	scaffold_1_mRNA_1364.1	-	-
GF0026221	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1363.1	-	-
GF0026220	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1362.1	-	-
GF0026219	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1361.1	-	-
GF0026218	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1360.1	-	-
GF0026217	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1357.1	-	-
GF0026216	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1355.1	-	-
GF0026215	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1353.1	-	-
GF0026214	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_135.1	-	-
GF0026213	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1347.1	-	-
GF0026212	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1344.1	-	-
GF0026211	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1341.1	-	-
GF0026210	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Domain of unknown function DUF4219 [IPR025314] (1); Zinc finger, CCHC-type [IPR001878] (1)	scaffold_1_mRNA_1340.1	-	-
GF0026209	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1338.1	-	-
GF0026208	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_1_mRNA_1337.1	-	-
GF0026207	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1336.1	-	-
GF0026206	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_1_mRNA_1332.1	-	-
GF0026205	1	0	0	Integrase (1)		Aspartic peptidase domain [IPR021109] (1)	scaffold_1_mRNA_1331.1	-	-
GF0026204	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1326.1	-	-
GF0026203	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1324.1	-	-
GF0026202	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1323.1	-	-
GF0026201	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1321.1	-	-
GF0026200	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1315.1	-	-
GF0026199	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_1_mRNA_1314.1	-	-
GF0026198	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1310.1	-	-
GF0026197	1	0	0	Putative AC9 transposase (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)	scaffold_1_mRNA_1308.1	-	-
GF0026196	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1300.1	-	-
GF0026195	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1298.1	-	-
GF0026194	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_1_mRNA_1297.1	-	-
GF0026193	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1294.1	-	-
GF0026192	1	0	0	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); Rossmann-like alpha/beta/alpha sandwich fold [IPR014729] (1)	scaffold_1_mRNA_1274.1	-	-
GF0026191	1	0	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	hAT-like transposase, RNase-H fold [IPR025525] (1)	scaffold_1_mRNA_1273.1	-	-
GF0026190	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1270.1	-	-
GF0026189	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1268.1	-	-
GF0026188	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1264.1	-	-
GF0026187	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1257.1	-	-
GF0026186	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_1_mRNA_1255.1	-	-
GF0026185	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4283 [IPR025558] (1)	scaffold_1_mRNA_1252.1	-	-
GF0026184	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1250.1	-	-
GF0026183	1	0	0	Hypothetical protein (1)		Transposase, MuDR, plant [IPR004332] (1)	scaffold_1_mRNA_1249.1	-	-
GF0026182	1	0	0	Hypothetical protein (1)		Viral movement protein [IPR028919] (1)	scaffold_1_mRNA_1248.1	-	-
GF0026181	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1246.1	-	-
GF0026180	1	0	0	Hypothetical protein (1)	mitochondrial inner membrane [GO:0005743 cellular_component] (1); ubiquinol-cytochrome-c reductase activity [GO:0008121 molecular_function] (1); respiratory chain [GO:0070469 cellular_component] (1); electron transport chain [GO:0022900 biological_process] (1)	Cytochrome b-c1 complex subunit 8 [IPR004205] (1); Cytochrome b-c1 complex subunit 8, plants [IPR020101] (1)	scaffold_1_mRNA_1239.1	-	-
GF0026179	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1230.1	-	-
GF0026178	1	0	0	Hypothetical protein (1)		Aspartic peptidase domain [IPR021109] (1); Retropepsins [IPR018061] (1)	scaffold_1_mRNA_1228.1	-	-
GF0026177	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_1_mRNA_1221.1	-	-
GF0026176	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1217.1	-	-
GF0026175	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1211.1	-	-
GF0026174	1	0	0	Hypothetical protein (1)		Reverse transcriptase domain [IPR000477] (1); Aspartic peptidase domain [IPR021109] (1)	scaffold_1_mRNA_1208.1	-	-
GF0026173	1	0	0	Hypothetical protein (1)	regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Carlavirus nucleic acid-binding protein [IPR002568] (1)	scaffold_1_mRNA_1205.1	-	-
GF0026172	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_1_mRNA_1204.1	-	-
GF0026171	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1203.1	-	-
GF0026170	1	0	0	Chaperone protein dnaJ 11 (1)		DnaJ domain, conserved site [IPR018253] (1); DnaJ domain [IPR001623] (1)	scaffold_1_mRNA_1201.1	-	-

ID	Num. in *C. celementine*	Num in *C. unshiu*	Num in *P.trifoliata*	Note	GO	InterPro	Members in *C.clementine*	Members in *C.unshiu*	Members in *P.trifoliata*
GF0026169	1	0	0	Cytokinin dehydrogenase 3 (1)	flavin adenine dinucleotide binding [GO:0050660 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1); cytokinin dehydrogenase activity [GO:0019139 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)	CO dehydrogenase flavoprotein-like, FAD-binding, subdomain 2 [IPR016169] (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)	scaffold_1_mRNA_1196.1	-	-
GF0026168	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc finger, CCHC-type [IPR001878] (1)	scaffold_1_mRNA_1195.1	-	-
GF0026167	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1194.1	-	-
GF0026166	1	0	0	Hypothetical protein (1)		Domain of unknown function DUF4216 [IPR025312] (1); Domain of unknown function DUF4218 [IPR025452] (1); Transposon, En/Spm-like [IPR004242] (1)	scaffold_1_mRNA_1193.1	-	-
GF0026165	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_1_mRNA_1190.1	-	-
GF0026164	1	0	0	Hypothetical protein (1)		Transposon, En/Spm-like [IPR004242] (1)	scaffold_1_mRNA_1189.1	-	-
GF0026163	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Zinc knuckle CX2CX4HX4C [IPR025836] (1); Zinc finger, CCHC-type [IPR001878] (1); Endonuclease/exonuclease/phosphatase [IPR005135] (1)	scaffold_1_mRNA_1188.1	-	-
GF0026162	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1176.1	-	-
GF0026161	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1167.1	-	-
GF0026160	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1165.1	-	-
GF0026159	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)			scaffold_1_mRNA_1164.1	-	-
GF0026158	1	0	0	Hypothetical protein (1)	protein dimerization activity [GO:0046983 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1)	HAT, C-terminal dimerisation domain [IPR008906] (1); hAT-like transposase, RNase-H fold [IPR025525] (1); Ribonuclease H-like domain [IPR012337] (1)	scaffold_1_mRNA_1153.1	-	-
GF0026157	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1142.1	-	-
GF0026156	1	0	0	Hypothetical protein (1)		Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1)	scaffold_1_mRNA_1137.1	-	-
GF0026155	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1134.1	-	-
GF0026154	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1133.1	-	-
GF0026153	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_1_mRNA_1132.1	-	-
GF0026152	1	0	0	Mutator-like transposase (1)		MULE transposase domain [IPR018289] (1); Transposase, MuDR, plant [IPR004332] (1)	scaffold_1_mRNA_1103.1	-	-
GF0026151	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1101.1	-	-
GF0026150	1	0	0	Hypothetical protein (1)	DNA binding [GO:0003677 molecular_function] (1)	hAT-like transposase, RNase-H fold [IPR025525] (1)	scaffold_1_mRNA_1099.1	-	-
GF0026149	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1098.1	-	-
GF0026148	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1093.1	-	-
GF0026147	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1092.1	-	-
GF0026146	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_1_mRNA_1091.1	-	-
GF0026145	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1086.1	-	-
GF0026144	1	0	0	Hypothetical protein (1)		Retrotransposon gag domain [IPR005162] (1)	scaffold_1_mRNA_1071.1	-	-
GF0026143	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (1); LOG family [IPR031100] (1)	scaffold_1_mRNA_1070.1	-	-
GF0026142	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1068.1	-	-
GF0026141	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1052.1	-	-
GF0026140	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_1_mRNA_1049.1	-	-
GF0026139	1	0	0	Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1)		LOG family [IPR031100] (1)	scaffold_1_mRNA_1035.1	-	-
GF0026138	1	0	0	Hypothetical protein (1)		LOG family [IPR031100] (1)	scaffold_1_mRNA_1033.1	-	-
GF0026137	1	0	0	Hypothetical protein (1)	zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1)	Domain of unknown function DUF4283 [IPR025558] (1); Zinc finger, CCHC-type [IPR001878] (1)	scaffold_1_mRNA_1031.1	-	-
GF0026136	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1030.1	-	-
GF0026135	1	0	0	Hypothetical protein (1)			scaffold_1_mRNA_1026.1	-	-
GF0026134	1	0	0	Hypothetical protein (1)	oxidation-reduction process [GO:0055114 biological_process] (1); cytoplasm [GO:0005737 cellular_component] (1); inositol catabolic process [GO:0019310 biological_process] (1); iron ion binding [GO:0005506 molecular_function] (1); inositol oxygenase activity [GO:0050113 molecular_function] (1)	Inositol oxygenase [IPR007828] (1)	scaffold_1_mRNA_1005.1	-	-