**Supplemental Table 6. Mandarin (*C. clementina and C. unshiu* ) specific gene groups and annotation**

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0000019 | 21 | 10 | 0 | Hypothetical protein (31) | | | scaffold_1_mRNA_511.1,scaffold_3_mRNA_14.1,scaffold_3_mRNA_1514.1,scaffold_3_mRNA_220.1,scaffold_3_mRNA_3574.1,scaffold_3_mRNA_3785.1,scaffold_4_mRNA_760.1,scaffold_5_mRNA_3887.1,scaffold_5_mRNA_4369.1,scaffold_5_mRNA_4932.1,scaffold_6_mRNA_1884.1,scaffold_7_mRNA_1009.1,scaffold_7_mRNA_1036.1,scaffold_7_mRNA_1928.1,scaffold_7_mRNA_1995.1,scaffold_7_mRNA_460.1,scaffold_7_mRNA_501.1,scaffold_7_mRNA_864.1,scaffold_8_mRNA_3093.1,scaffold_9_mRNA_229.1,scaffold_9_mRNA_3409.1 | C_unshiu_00008_mRNA_15.1,C_unshiu_00016_mRNA_48.1,C_unshiu_00141_mRNA_26.1,C_unshiu_00185_mRNA_9.1,C_unshiu_00217_mRNA_43.1,C_unshiu_00310_mRNA_22.1,C_unshiu_00514_mRNA_15.1,C_unshiu_00627_mRNA_3.1,C_unshiu_00919_mRNA_9.1,C_unshiu_01313_mRNA_3.1 | - |
| GF0000066 | 12 | 7 | 0 | Hypothetical protein (19) | nucleic acid binding [GO:0003676 molecular_function] (10); zinc ion binding [GO:0008270 molecular_function] (10); proteolysis [GO:0006508 biological_process] (7); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (7) | Zinc finger, CCHC-type [IPR001878] (10); Peptidase A2A, retrovirus, catalytic [IPR001995] (7); Viral movement protein [IPR028919] (6); Aspartic peptidase domain [IPR021109] (6); Reverse transcriptase domain [IPR000477] (5); Retropepsins [IPR018061] (1) | scaffold_1_mRNA_1502.1,scaffold_2_mRNA_324.1,scaffold_6_mRNA_441.1,scaffold_6_mRNA_530.1,scaffold_6_mRNA_635.1,scaffold_8_mRNA_1564.1,scaffold_8_mRNA_1587.1,scaffold_8_mRNA_1595.1,scaffold_8_mRNA_1635.1,scaffold_8_mRNA_1691.1,scaffold_9_mRNA_2229.1,scaffold_9_mRNA_2297.1 | C_unshiu_00128_mRNA_34.1,C_unshiu_00219_mRNA_10.1,C_unshiu_00219_mRNA_13.1,C_unshiu_00538_mRNA_13.1,C_unshiu_00724_mRNA_19.1,C_unshiu_01568_mRNA_13.1,C_unshiu_01925_mRNA_6.1 | - |
| GF0000242 | 10 | 1 | 0 | Hypothetical protein (11) | | | scaffold_1_mRNA_1036.1,scaffold_1_mRNA_963.1,scaffold_2_mRNA_2490.1,scaffold_3_mRNA_1756.1,scaffold_3_mRNA_3222.1,scaffold_3_mRNA_4688.1,scaffold_6_mRNA_290.1,scaffold_6_mRNA_604.1,scaffold_7_mRNA_1891.1,scaffold_9_mRNA_1608.1 | C_unshiu_00170_mRNA_44.1 | - |
| GF0000111 | 10 | 6 | 0 | Hypothetical protein (16) | | | scaffold_4_mRNA_1603.1,scaffold_4_mRNA_1606.1,scaffold_5_mRNA_3949.1,scaffold_5_mRNA_3954.1,scaffold_6_mRNA_669.1,scaffold_7_mRNA_1910.1,scaffold_8_mRNA_1431.1,scaffold_9_mRNA_3174.1,scaffold_9_mRNA_3287.1,scaffold_9_mRNA_3332.1 | C_unshiu_00041_mRNA_39.1,C_unshiu_00218_mRNA_32.1,C_unshiu_00298_mRNA_26.1,C_unshiu_00447_mRNA_32.1,C_unshiu_00582_mRNA_5.1,C_unshiu_02743_mRNA_3.1 | - |
| GF0000477 | 8 | 1 | 0 | Hypothetical protein (9) | | | scaffold_2_mRNA_954.1,scaffold_3_mRNA_12.1,scaffold_3_mRNA_3572.1,scaffold_5_mRNA_4934.1,scaffold_6_mRNA_170.1,scaffold_7_mRNA_2644.1,scaffold_8_mRNA_1523.1,scaffold_8_mRNA_2176.1 | C_unshiu_00627_mRNA_1.1 | - |
| GF0000499 | 7 | 2 | 0 | Hypothetical protein (9) | | | scaffold_3_mRNA_3570.1,scaffold_4_mRNA_756.1,scaffold_5_mRNA_4367.1,scaffold_5_mRNA_486.1,scaffold_5_mRNA_4935.1,scaffold_7_mRNA_1535.1,scaffold_8_mRNA_3091.1 | C_unshiu_00404_mRNA_12.1,C_unshiu_01313_mRNA_7.1 | - |
| GF0000387 | 7 | 3 | 0 | Hypothetical protein (9); Monosacharide transport protein (1) | DNA binding [GO:0003677 molecular_function] (1) | Myb-like domain [IPR017877] (1); Homeobox domain-like [IPR009057] (1) | scaffold_5_mRNA_2779.1,scaffold_5_mRNA_2857.1,scaffold_5_mRNA_438.1,scaffold_8_mRNA_480.1,scaffold_8_mRNA_957.1,scaffold_9_mRNA_1498.1,scaffold_9_mRNA_3365.1 | C_unshiu_00004_mRNA_3.1,C_unshiu_00271_mRNA_7.1,C_unshiu_00378_mRNA_20.1 | - |
| GF0000275 | 6 | 5 | 0 | Hypothetical protein (11) | | | scaffold_3_mRNA_1363.1,scaffold_3_mRNA_5073.1,scaffold_5_mRNA_1401.1,scaffold_5_mRNA_3344.1,scaffold_6_mRNA_1789.1,scaffold_9_mRNA_2959.1 | C_unshiu_00137_mRNA_4.1,C_unshiu_00760_mRNA_4.1,C_unshiu_01260_mRNA_8.1,C_unshiu_01382_mRNA_2.1,C_unshiu_02154_mRNA_2.1 | - |
| GF0000949 | 5 | 2 | 0 | Retrotransposon protein, putative, Ty1-copia subclass (6); Cysteine-rich RLK (RECEPTOR-like protein kinase) 8 (1) | nucleic acid binding [GO:0003676 molecular_function] (5); zinc ion binding [GO:0008270 molecular_function] (4); DNA integration [GO:0015074 biological_process] (4) | Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (7); Ribonuclease H-like domain [IPR012337] (5); Integrase, catalytic core [IPR001584] (4); Zinc finger, CCHC-type [IPR001878] (4); GAG-pre-integrase domain [IPR025724] (3); Viral movement protein [IPR028919] (1) | scaffold_4_mRNA_1134.1,scaffold_5_mRNA_1957.1,scaffold_6_mRNA_1003.1,scaffold_8_mRNA_1396.1,scaffold_8_mRNA_1625.1 | C_unshiu_00323_mRNA_5.1,C_unshiu_00413_mRNA_4.1 | - |
| GF0000805 | 5 | 2 | 0 | Monosacharide transport protein (7) | | | scaffold_1_mRNA_306.1,scaffold_5_mRNA_1301.1,scaffold_5_mRNA_2602.1,scaffold_8_mRNA_472.1,scaffold_9_mRNA_3209.1 | C_unshiu_00233_mRNA_12.1,C_unshiu_00800_mRNA_3.1 | - |
| GF0000784 | 5 | 2 | 0 | Retrotransposon protein, putative, Ty1-copia subclass (6); Putative retroelement pol polyprotein (1) | nucleic acid binding [GO:0003676 molecular_function] (6); zinc ion binding [GO:0008270 molecular_function] (6); DNA integration [GO:0015074 biological_process] (3) | GAG-pre-integrase domain [IPR025724] (6); Zinc finger, CCHC-type [IPR001878] (6); Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (4); Ribonuclease H-like domain [IPR012337] (4); Integrase, catalytic core [IPR001584] (3) | scaffold_1_mRNA_1631.1,scaffold_4_mRNA_1135.1,scaffold_5_mRNA_3554.1,scaffold_9_mRNA_1737.1,scaffold_9_mRNA_2941.1 | C_unshiu_00424_mRNA_4.1,C_unshiu_00434_mRNA_24.1 | - |
| GF0000326 | 5 | 5 | 0 | Hypothetical protein (10) | | LOG family [IPR031100] (10) | scaffold_2_mRNA_172.1,scaffold_3_mRNA_2036.1,scaffold_3_mRNA_4464.1,scaffold_4_mRNA_1996.1,scaffold_5_mRNA_601.1 | C_unshiu_00361_mRNA_9.1,C_unshiu_01106_mRNA_1.1,C_unshiu_02358_mRNA_1.1,C_unshiu_02458_mRNA_3.1,C_unshiu_02747_mRNA_1.1 | - |
| GF0002260 | 4 | 1 | 0 | Hypothetical protein (5) | | | scaffold_5_mRNA_2696.1,scaffold_6_mRNA_2058.1,scaffold_6_mRNA_2059.1,scaffold_6_mRNA_319.1 | C_unshiu_01636_mRNA_5.1 | - |
| GF0001952 | 4 | 1 | 0 | Hypothetical protein (5) | | | scaffold_2_mRNA_839.1,scaffold_3_mRNA_3305.1,scaffold_5_mRNA_1156.1,scaffold_8_mRNA_2127.1 | C_unshiu_00066_mRNA_20.1 | - |
| GF0001907 | 4 | 1 | 0 | Putative retroelement pol polyprotein (4); Hypothetical protein (1) | hydrolase activity [GO:0016787 molecular_function] (1) | Pectinacetylesterase/NOTUM [IPR004963] (1) | scaffold_2_mRNA_3057.1,scaffold_3_mRNA_3146.1,scaffold_5_mRNA_3216.1,scaffold_6_mRNA_117.1 | C_unshiu_00003_mRNA_1.1 | - |
| GF0001883 | 4 | 1 | 0 | Hypothetical protein (5) | | | scaffold_2_mRNA_2323.1,scaffold_3_mRNA_1910.1,scaffold_3_mRNA_1986.1,scaffold_9_mRNA_2255.1 | C_unshiu_00138_mRNA_38.1 | - |
| GF0001765 | 4 | 1 | 0 | Gag protease polyprotein (3); Cellular nucleic acid-binding protein (1); DNA/RNA polymerases superfamily protein (1) | nucleic acid binding [GO:0003676 molecular_function] (5); zinc ion binding [GO:0008270 molecular_function] (5) | Retrotransposon gag domain [IPR005162] (5); Zinc finger, CCHC-type [IPR001878] (5); LDOC1-related [IPR032567] (2); Aspartic peptidase domain [IPR021109] (1); Retroviral aspartyl protease [IPR013242] (1) | scaffold_1_mRNA_1954.1,scaffold_2_mRNA_187.1,scaffold_9_mRNA_2057.1,scaffold_9_mRNA_2916.1 | C_unshiu_00016_mRNA_9.1 | - |
| GF0001444 | 4 | 2 | 0 | Orf764 protein (6) | DNA integration [GO:0015074 biological_process] (6); nucleic acid binding [GO:0003676 molecular_function] (6); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (4) | Ribonuclease H-like domain [IPR012337] (6); Integrase, catalytic core [IPR001584] (6); Ribonuclease H domain [IPR002156] (4); Retrotransposon gag domain [IPR005162] (1) | scaffold_4_mRNA_1666.1,scaffold_5_mRNA_1151.1,scaffold_7_mRNA_1363.1,scaffold_7_mRNA_2242.1 | C_unshiu_00140_mRNA_28.1,C_unshiu_00716_mRNA_14.1 | - |
| GF0001186 | 4 | 2 | 0 | Putative retroelement pol polyprotein (6) | | | scaffold_1_mRNA_751.1,scaffold_2_mRNA_661.1,scaffold_3_mRNA_705.1,scaffold_5_mRNA_615.1 | C_unshiu_00947_mRNA_4.1,C_unshiu_01928_mRNA_5.1 | - |
| GF0000142 | 4 | 10 | 0 | Hypothetical protein (14) | | LOG family [IPR031100] (1) | scaffold_2_mRNA_2854.1,scaffold_2_mRNA_2860.1,scaffold_6_mRNA_310.1,scaffold_8_mRNA_1550.1 | C_unshiu_00124_mRNA_19.1,C_unshiu_00215_mRNA_2.1,C_unshiu_00406_mRNA_9.1,C_unshiu_00556_mRNA_19.1,C_unshiu_00722_mRNA_10.1,C_unshiu_01049_mRNA_5.1,C_unshiu_01704_mRNA_1.1,C_unshiu_01716_mRNA_1.1,C_unshiu_02577_mRNA_3.1,C_unshiu_02711_mRNA_1.1 | - |
| GF0004477 | 3 | 1 | 0 | Eukaryotic translation initiation factor 3 subunit, putative (2); Hypothetical protein (2) | protein binding [GO:0005515 molecular_function] (4) | Tetratricopeptide-like helical domain [IPR011990] (4); Tetratricopeptide repeat [IPR019734] (4); Tetratricopeptide repeat-containing domain [IPR013026] (4); CLU central domain [IPR033646] (3); Winged helix-turn-helix DNA-binding domain [IPR011991] (3) | scaffold_7_mRNA_1733.1,scaffold_7_mRNA_1742.1,scaffold_7_mRNA_1759.1 | C_unshiu_00766_mRNA_2.1 | - |
| GF0004380 | 3 | 1 | 0 | BED zinc finger,hAT family dimerization domain isoform 1 (4) | nucleic acid binding [GO:0003676 molecular_function] (4); protein dimerization activity [GO:0046983 molecular_function] (4); DNA binding [GO:0003677 molecular_function] (4) | Ribonuclease H-like domain [IPR012337] (4); hAT-like transposase, RNase-H fold [IPR025525] (4); HAT, C-terminal dimerisation domain [IPR008906] (4); Zinc finger, BED-type [IPR003656] (3); Zinc finger C2H2-type [IPR013087] (2) | scaffold_6_mRNA_388.1,scaffold_8_mRNA_2483.1,scaffold_9_mRNA_1810.1 | C_unshiu_00474_mRNA_21.1 | - |
| GF0003948 | 3 | 1 | 0 | Hypothetical protein (4) | | Galactose-binding domain-like [IPR008979] (1) | scaffold_5_mRNA_2044.1,scaffold_5_mRNA_2064.1,scaffold_6_mRNA_573.1 | C_unshiu_00691_mRNA_1.1 | - |
| GF0003941 | 3 | 1 | 0 | Hypothetical protein (4) | | | scaffold_5_mRNA_1968.1,scaffold_5_mRNA_1971.1,scaffold_5_mRNA_583.1 | C_unshiu_00358_mRNA_1.1 | - |
| GF0003728 | 3 | 1 | 0 | Hypothetical protein (4) | protein tyrosine phosphatase activity [GO:0004725 molecular_function] (2); dephosphorylation [GO:0016311 biological_process] (2); phosphatase activity [GO:0016791 molecular_function] (2) | Myotubularin-like phosphatase domain [IPR010569] (4); Myotubularin family [IPR030564] (4); Protein-tyrosine phosphatase-like [IPR029021] (4); Protein-tyrosine phosphatase, active site [IPR016130] (2) | scaffold_4_mRNA_1269.1,scaffold_4_mRNA_1276.1,scaffold_4_mRNA_1283.1 | C_unshiu_02303_mRNA_3.1 | - |
| GF0003724 | 3 | 1 | 0 | Hypothetical protein (4) | nucleic acid binding [GO:0003676 molecular_function] (4); zinc ion binding [GO:0008270 molecular_function] (4); proteolysis [GO:0006508 biological_process] (3); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (3) | Zinc finger, CCHC-type [IPR001878] (4); Viral movement protein [IPR028919] (3); Reverse transcriptase domain [IPR000477] (3); Retropepsins [IPR018061] (3); Aspartic peptidase, active site [IPR001969] (3); Aspartic peptidase domain [IPR021109] (3) | scaffold_4_mRNA_1218.1,scaffold_6_mRNA_305.1,scaffold_9_mRNA_1317.1 | C_unshiu_00618_mRNA_28.1 | - |
| GF0003412 | 3 | 1 | 0 | Hypothetical protein (4) | | | scaffold_3_mRNA_3633.1,scaffold_4_mRNA_896.1,scaffold_8_mRNA_1143.1 | C_unshiu_00682_mRNA_19.1 | - |
| GF0002883 | 3 | 1 | 0 | Hypothetical protein (4) | | | scaffold_1_mRNA_791.1,scaffold_6_mRNA_1581.1,scaffold_9_mRNA_2956.1 | C_unshiu_00924_mRNA_12.1 | - |
| GF0002882 | 3 | 1 | 0 | Hypothetical protein (4) | | | scaffold_1_mRNA_786.1,scaffold_1_mRNA_792.1,scaffold_3_mRNA_882.1 | C_unshiu_01463_mRNA_9.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0002863 | 3 | 1 | 0 | Hypothetical protein (4) | | | scaffold_1_mRNA_551.1,scaffold_3_mRNA_2558.1,scaffold_9_mRNA_2646.1 | C_unshiu_00131_mRNA_14.1 | - |
| GF0002740 | 3 | 1 | 0 | Hypothetical protein (4) | | | scaffold_1_mRNA_192.1,scaffold_4_mRNA_2570.1,scaffold_4_mRNA_2572.1 | C_unshiu_01598_mRNA_2.1 | - |
| GF0002733 | 3 | 1 | 0 | Copia protein (2); Opie3 pol polyprotein (1); Orf490 protein (1) | DNA integration [GO:0015074 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1) | Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (4); Integrase, catalytic core [IPR001584] (1); Ribonuclease H-like domain [IPR012337] (1) | scaffold_1_mRNA_1787.1,scaffold_1_mRNA_2785.1,scaffold_5_mRNA_981.1 | C_unshiu_00083_mRNA_36.1 | - |
| GF0002719 | 3 | 1 | 0 | Mutator-like transposase (3); MuDR family transposase isoform 1 (1) | zinc ion binding [GO:0008270 molecular_function] (4); nucleic acid binding [GO:0003676 molecular_function] (2) | Transposase, MuDR, plant [IPR004332] (4); MULE transposase domain [IPR018289] (4); Zinc finger, PMZ-type [IPR006564] (4); Zinc finger, SWIM-type [IPR007527] (4); Zinc finger, CCHC-type [IPR001878] (2) | scaffold_1_mRNA_1535.1,scaffold_2_mRNA_3553.1,scaffold_8_mRNA_146.1 | C_unshiu_00273_mRNA_31.1 | - |
| GF0002696 | 3 | 1 | 0 | Hypothetical protein (4) | | Aspartic peptidase domain [IPR021109] (3) | scaffold_1_mRNA_1206.1,scaffold_2_mRNA_2279.1,scaffold_3_mRNA_1790.1 | C_unshiu_01671_mRNA_7.1 | - |
| GF0002524 | 3 | 2 | 0 | Hypothetical protein (4); Putative polyprotein (Aspartic proteinase, reverse transcriptase, ribonuclease H) (1) | aspartic-type endopeptidase activity [GO:0004190 molecular_function] (4); proteolysis [GO:0006508 biological_process] (4); zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1) | Retropepsins [IPR018061] (4); Aspartic peptidase, active site [IPR001969] (4); Aspartic peptidase domain [IPR021109] (3); Zinc finger, CCHC-type [IPR001878] (1); Reverse transcriptase domain [IPR000477] (1) | scaffold_8_mRNA_1934.1,scaffold_8_mRNA_1985.1,scaffold_9_mRNA_3760.1 | C_unshiu_00469_mRNA_5.1,C_unshiu_02183_mRNA_2.1 | - |
| GF0002169 | 3 | 2 | 0 | Hypothetical protein (5) | zinc ion binding [GO:0008270 molecular_function] (4); nucleic acid binding [GO:0003676 molecular_function] (4) | Domain of unknown function DUF4283 [IPR025558] (5); Zinc knuckle CX2CX4HX4C [IPR025836] (5); Zinc finger, CCHC-type [IPR001878] (4) | scaffold_4_mRNA_2241.1,scaffold_5_mRNA_2218.1,scaffold_5_mRNA_3752.1 | C_unshiu_00028_mRNA_13.1,C_unshiu_00175_mRNA_26.1 | - |
| GF0002138 | 3 | 2 | 0 | Hypothetical protein (5) | | Myotubularin family [IPR030564] (3); Myotubularin-like phosphatase domain [IPR010569] (1) | scaffold_4_mRNA_1047.1,scaffold_4_mRNA_1246.1,scaffold_4_mRNA_1277.1 | C_unshiu_00809_mRNA_6.1,C_unshiu_03085_mRNA_1.1 | - |
| GF0002109 | 3 | 2 | 0 | Hypothetical protein (5) | | Repeat of unknown function XGLTT [IPR008164] (1) | scaffold_3_mRNA_5230.1,scaffold_8_mRNA_56.1,scaffold_9_mRNA_1503.1 | C_unshiu_00787_mRNA_19.1,C_unshiu_01396_mRNA_2.1 | - |
| GF0001919 | 3 | 2 | 0 | Hypothetical protein (5) | proteolysis [GO:0006508 biological_process] (5); cysteine-type peptidase activity [GO:0008234 molecular_function] (5) | Domain of unknown function DUF1985 [IPR015410] (5); Ulp1 protease family, C-terminal catalytic domain [IPR003653] (5) | scaffold_2_mRNA_3518.1,scaffold_3_mRNA_1454.1,scaffold_9_mRNA_3653.1 | C_unshiu_00026_mRNA_32.1,C_unshiu_00112_mRNA_5.1 | - |
| GF0001886 | 3 | 2 | 0 | Hypothetical protein (5) | | | scaffold_2_mRNA_2433.1,scaffold_5_mRNA_2052.1,scaffold_9_mRNA_2300.1 | C_unshiu_00118_mRNA_12.1,C_unshiu_00145_mRNA_12.1 | - |
| GF0001838 | 3 | 2 | 0 | Hypothetical protein (4); Disease resistance protein family (1) | | Leucine-rich repeat domain, L domain-like [IPR032675] (1) | scaffold_2_mRNA_1189.1,scaffold_2_mRNA_3629.1,scaffold_7_mRNA_1631.1 | C_unshiu_00870_mRNA_13.1,C_unshiu_01092_mRNA_11.1 | - |
| GF0001748 | 3 | 2 | 0 | Hypothetical protein (5) | | Viral movement protein [IPR028919] (1) | scaffold_1_mRNA_1387.1,scaffold_1_mRNA_1412.1,scaffold_1_mRNA_1459.1 | C_unshiu_00138_mRNA_9.1,C_unshiu_00470_mRNA_27.1 | - |
| GF0001615 | 3 | 3 | 0 | Disease resistance protein (3); Disease resistance protein RPS2 (1); LRR and NB-ARC domains-containing disease resistance protein, putative (1); NB-ARC domain-containing disease resistance protein, putative isoform 1 (1) | protein binding [GO:0005515 molecular_function] (6); ADP binding [GO:0043531 molecular_function] (5) | Leucine-rich repeat domain, L domain-like [IPR032675] (6); Leucine-rich repeat [IPR001611] (6); NB-ARC [IPR002182] (5); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (5); Winged helix-turn-helix DNA-binding domain [IPR011991] (3); Leucine-rich repeat, typical subtype [IPR003591] (1); AAA+ ATPase domain [IPR003593] (1) | scaffold_7_mRNA_1896.1,scaffold_7_mRNA_1971.1,scaffold_7_mRNA_1976.1 | C_unshiu_00050_mRNA_1.1,C_unshiu_00245_mRNA_10.1,C_unshiu_01710_mRNA_4.1 | - |
| GF0001514 | 3 | 3 | 0 | Disease resistance protein (3); Disease resistance protein (CC-NBS-LRR class) family protein (1); Putative disease resistance gene NBS-LRR family protein (1); Putative disease resistance protein (1) | ADP binding [GO:0043531 molecular_function] (6) | NB-ARC [IPR002182] (6); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (6); Leucine-rich repeat domain, L domain-like [IPR032675] (3); Winged helix-turn-helix DNA-binding domain [IPR011991] (2); AAA+ ATPase domain [IPR003593] (2) | scaffold_5_mRNA_2639.1,scaffold_5_mRNA_2652.1,scaffold_5_mRNA_2663.1 | C_unshiu_00906_mRNA_7.1,C_unshiu_01119_mRNA_1.1,C_unshiu_01443_mRNA_1.1 | - |
| GF0001482 | 3 | 3 | 0 | Hypothetical protein (6) | | | scaffold_5_mRNA_1098.1,scaffold_8_mRNA_1428.1,scaffold_9_mRNA_3758.1 | C_unshiu_00033_mRNA_38.1,C_unshiu_00582_mRNA_6.1,C_unshiu_00825_mRNA_4.1 | - |
| GF0001298 | 3 | 3 | 0 | Monosacharide transport protein (6) | | | scaffold_3_mRNA_1011.1,scaffold_8_mRNA_293.1,scaffold_9_mRNA_2930.1 | C_unshiu_00068_mRNA_31.1,C_unshiu_01467_mRNA_3.1,C_unshiu_02089_mRNA_8.1 | - |
| GF0001250 | 3 | 3 | 0 | Hypothetical protein (6) | | | scaffold_2_mRNA_319.1,scaffold_9_mRNA_2268.1,scaffold_9_mRNA_2368.1 | C_unshiu_00529_mRNA_21.1,C_unshiu_01568_mRNA_7.1,C_unshiu_01730_mRNA_5.1 | - |
| GF0001159 | 3 | 3 | 0 | Hypothetical protein (6) | | RuvA domain 2-like [IPR010994] (1) | scaffold_1_mRNA_2556.1,scaffold_3_mRNA_1508.1,scaffold_4_mRNA_2110.1 | C_unshiu_00017_mRNA_29.1,C_unshiu_00224_mRNA_14.1,C_unshiu_02217_mRNA_4.1 | - |
| GF0000616 | 3 | 5 | 0 | Hypothetical protein (8) | | | scaffold_2_mRNA_2287.1,scaffold_5_mRNA_2471.1,scaffold_6_mRNA_195.1 | C_unshiu_00138_mRNA_65.1,C_unshiu_00377_mRNA_2.1,C_unshiu_00689_mRNA_17.1,C_unshiu_00871_mRNA_5.1,C_unshiu_01585_mRNA_8.1 | - |
| GF0018573 | 2 | 1 | 0 | Hypothetical protein (3) | nucleic acid binding [GO:0003676 molecular_function] (2); oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1) | Non-haem dioxygenase N-terminal domain [IPR026992] (2); Isopenicillin N synthase-like [IPR027443] (2); Reverse transcriptase domain [IPR000477] (2); Ribonuclease H-like domain [IPR012337] (2); Oxoglutarate/iron-dependent dioxygenase [IPR005123] (1) | scaffold_9_mRNA_3284.1,scaffold_9_mRNA_3285.1 | C_unshiu_00741_mRNA_2.1 | - |
| GF0018556 | 2 | 1 | 0 | LRR receptor-like kinase family protein (2); CDNA clone:J023022C01, full insert sequence (1) | protein phosphorylation [GO:0006468 biological_process] (3); protein kinase activity [GO:0004672 molecular_function] (3); ATP binding [GO:0005524 molecular_function] (3); protein binding [GO:0005515 molecular_function] (2) | Protein kinase, ATP binding site [IPR017441] (3); Tyrosine-protein kinase, active site [IPR008266] (3); Protein kinase-like domain [IPR011009] (3); Leucine-rich repeat domain, L domain-like [IPR032675] (3); Protein kinase domain [IPR000719] (3); Leucine-rich repeat [IPR001611] (2); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (2); Leucine-rich repeat, typical subtype [IPR003591] (2); Concanavalin A-like lectin/glucanase domain [IPR013320] (1) | scaffold_9_mRNA_3252.1,scaffold_9_mRNA_3253.1 | C_unshiu_00095_mRNA_16.1 | - |
| GF0018304 | 2 | 1 | 0 | Hypothetical protein (3) | | HSP20-like chaperone [IPR008978] (3); Alpha crystallin/Hsp20 domain [IPR002068] (3); Small heat shock protein HSP20 [IPR031107] (2) | scaffold_9_mRNA_2488.1,scaffold_9_mRNA_2496.1 | C_unshiu_00104_mRNA_34.1 | - |
| GF0018277 | 2 | 1 | 0 | Putative polyprotein (Aspartic proteinase, reverse transcriptase, ribonuclease H) (2); Hypothetical protein (1) | | Reverse transcriptase domain [IPR000477] (3) | scaffold_9_mRNA_2383.1,scaffold_9_mRNA_2384.1 | C_unshiu_00763_mRNA_20.1 | - |
| GF0018065 | 2 | 1 | 0 | Hypothetical protein (3) | | | scaffold_9_mRNA_1578.1,scaffold_9_mRNA_2138.1 | C_unshiu_01433_mRNA_9.1 | - |
| GF0017943 | 2 | 1 | 0 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein, putative (3) | | Isopenicillin N synthase-like [IPR027443] (3); Non-haem dioxygenase N-terminal domain [IPR026992] (3) | scaffold_9_mRNA_1112.1,scaffold_9_mRNA_1134.1 | C_unshiu_00334_mRNA_12.1 | - |
| GF0017165 | 2 | 1 | 0 | Germin-like protein subfamily 2 member 2 (3) | manganese ion binding [GO:0030145 molecular_function] (3); nutrient reservoir activity [GO:0045735 molecular_function] (3) | RmlC-like cupin domain [IPR011051] (3); Cupin 1 [IPR006045] (3); RmlC-like jelly roll fold [IPR014710] (3); Germin [IPR001929] (3) | scaffold_8_mRNA_2458.1,scaffold_8_mRNA_2461.1 | C_unshiu_00814_mRNA_15.1 | - |
| GF0016545 | 2 | 1 | 0 | Hypothetical protein (3) | | Domain of unknown function DUF4283 [IPR025558] (3) | scaffold_7_mRNA_567.1,scaffold_8_mRNA_2690.1 | C_unshiu_00858_mRNA_4.1 | - |
| GF0016296 | 2 | 1 | 0 | Disease resistance protein (3) | ADP binding [GO:0043531 molecular_function] (3) | Leucine-rich repeat domain, L domain-like [IPR032675] (3); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (3); NB-ARC [IPR002182] (3); Winged helix-turn-helix DNA-binding domain [IPR011991] (2); Pentatricopeptide repeat [IPR002885] (1) | scaffold_7_mRNA_2616.1,scaffold_7_mRNA_2621.1 | C_unshiu_01041_mRNA_2.1 | - |
| GF0015996 | 2 | 1 | 0 | Hypothetical protein (3) | | | scaffold_7_mRNA_1752.1,scaffold_7_mRNA_1757.1 | C_unshiu_00055_mRNA_49.1 | - |
| GF0015676 | 2 | 1 | 0 | Putative non-LTR reverse transcriptase (1); Putative non-LTR retroelement reverse transcriptase (1); Putative non-LTR retrolelement reverse transcriptase (1) | nucleic acid binding [GO:0003676 molecular_function] (3) | Ribonuclease H-like domain [IPR012337] (3); Reverse transcriptase zinc-binding domain [IPR026960] (3) | scaffold_6_mRNA_91.1,scaffold_8_mRNA_1231.1 | C_unshiu_00329_mRNA_14.1 | - |
| GF0015624 | 2 | 1 | 0 | Hypothetical protein (3) | | | scaffold_6_mRNA_654.1,scaffold_9_mRNA_458.1 | C_unshiu_00648_mRNA_17.1 | - |
| GF0015590 | 2 | 1 | 0 | Hypothetical protein (3) | | | scaffold_6_mRNA_360.1,scaffold_8_mRNA_1379.1 | C_unshiu_00060_mRNA_66.1 | - |
| GF0015578 | 2 | 1 | 0 | Hypothetical protein (3) | | | scaffold_6_mRNA_3186.1,scaffold_7_mRNA_2.1 | C_unshiu_00051_mRNA_12.1 | - |
| GF0015344 | 2 | 1 | 0 | TCP transcription factor CYC1C (1); Hypothetical protein (1); Transcription factor CYC1 (1) | | CYC/TB1, R domain [IPR017888] (3); Transcription factor TCP subgroup [IPR017887] (3); Transcription factor, TCP [IPR005333] (3) | scaffold_6_mRNA_2849.1,scaffold_9_mRNA_2986.1 | C_unshiu_00098_mRNA_25.1 | - |
| GF0014704 | 2 | 1 | 0 | Hypothetical protein (3) | zinc ion binding [GO:0008270 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | Zinc finger, CCHC-type [IPR001878] (2) | scaffold_6_mRNA_193.1,scaffold_6_mRNA_429.1 | C_unshiu_00145_mRNA_35.1 | - |
| GF0014655 | 2 | 1 | 0 | Hypothetical protein (3) | | | scaffold_6_mRNA_1834.1,scaffold_8_mRNA_2504.1 | C_unshiu_00020_mRNA_59.1 | - |
| GF0014605 | 2 | 1 | 0 | Hypothetical protein (3) | | Retrotransposon gag domain [IPR005162] (3) | scaffold_6_mRNA_171.1,scaffold_7_mRNA_1092.1 | C_unshiu_00053_mRNA_11.1 | - |
| GF0014380 | 2 | 1 | 0 | Hypothetical protein (3) | cysteine-type peptidase activity [GO:0008234 molecular_function] (3); proteolysis [GO:0006508 biological_process] (3) | Domain of unknown function DUF1985 [IPR015410] (3); Ulp1 protease family, C-terminal catalytic domain [IPR003653] (3) | scaffold_6_mRNA_1098.1,scaffold_9_mRNA_2090.1 | C_unshiu_00781_mRNA_14.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0013772 | 2 | 1 | 0 | Hypothetical protein (2); Putative disease resistance protein RGA1 (1) |  | Leucine-rich repeat domain, L domain-like [IPR032675] (3); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); GPN-loop GTPase [IPR004130] (2); GPN-loop GTPase 2 [IPR030231] (2) | scaffold_5_mRNA_445.1,scaffold_5_mRNA_461.1 | C_unshiu_01064_mRNA_8.1 | - |
| GF0013233 | 2 | 1 | 0 | Hypothetical protein (3) | oxidation-reduction process [GO:0055114 biological_process] (3); oxidoreductase activity [GO:0016491 molecular_function] (3); carotene 7,8-desaturase activity [GO:0016719 molecular_function] (2); carotenoid biosynthetic process [GO:0016117 biological_process] (2) | Amine oxidase [IPR002937] (3); Zeta-carotene desaturase [IPR014103] (2); FAD/NAD(P)-binding domain [IPR023753] (1) | scaffold_5_mRNA_3320.1,scaffold_5_mRNA_3350.1 | C_unshiu_00021_mRNA_1.1 | - |
| GF0013184 | 2 | 1 | 0 | Disease resistance family protein / LRR family protein, putative (1); LRR receptor-like serine/threonine-protein kinase GSO1 (1); LRR receptor-like serine/threonine-protein kinase GSO2 (1) | protein binding [GO:0005515 molecular_function] (3) | Leucine-rich repeat domain, L domain-like [IPR032675] (3); Leucine-rich repeat, typical subtype [IPR003591] (3); Leucine-rich repeat [IPR001611] (3); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (2) | scaffold_5_mRNA_3146.1,scaffold_5_mRNA_3154.1 | C_unshiu_02984_mRNA_2.1 | - |
| GF0013047 | 2 | 1 | 0 | Hypothetical protein (3) |  |  | scaffold_5_mRNA_2479.1,scaffold_6_mRNA_585.1 | C_unshiu_01124_mRNA_7.1 | - |
| GF0013019 | 2 | 1 | 0 | MuDR family transposase isoform 1 (2); Putative muDR family transposase-like (1) | zinc ion binding [GO:0008270 molecular_function] (3); transposase activity [GO:0004803 molecular_function] (2); transposition, DNA-mediated [GO:0006313 biological_process] (2); DNA binding [GO:0003677 molecular_function] (2) | Transposase, MuDR, plant [IPR004332] (3); Zinc finger, PMZ-type [IPR006564] (3); MULE transposase domain [IPR018289] (3); Zinc finger, SWIM-type [IPR007527] (3); Transposase, mutator type [IPR001207] (2) | scaffold_5_mRNA_2368.1,scaffold_5_mRNA_2656.1 | C_unshiu_01916_mRNA_3.1 | - |
| GF0012975 | 2 | 1 | 0 | Hypothetical protein (3) | chromatin binding [GO:0003682 molecular_function] (3); methyltransferase activity [GO:0008168 molecular_function] (1) | S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (3); DNA (cytosine-5)-methyltransferase 1, replication foci domain [IPR022702] (3); Bromo adjacent homology (BAH) domain [IPR001025] (3); DNA methylase, C-5 cytosine-specific, conserved site [IPR031303] (2); C-5 cytosine methyltransferase [IPR001525] (1) | scaffold_5_mRNA_218.1,scaffold_5_mRNA_226.1 | C_unshiu_00904_mRNA_5.1 | - |
| GF0012863 | 2 | 1 | 0 | SLG-Sc and SLA-Sc genes and Melmoth retrotransposon sequence (3) | nucleic acid binding [GO:0003676 molecular_function] (1) | Ribonuclease H-like domain [IPR012337] (1) | scaffold_5_mRNA_170.1,scaffold_5_mRNA_982.1 | C_unshiu_00083_mRNA_35.1 | - |
| GF0012828 | 2 | 1 | 0 | Hypothetical protein (3) |  | Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (2) | scaffold_5_mRNA_1436.1,scaffold_8_mRNA_1637.1 | C_unshiu_02887_mRNA_2.1 | - |
| GF0012770 | 2 | 1 | 0 | Putative disease resistance RGA1 (1); TIR-NBS-LRR type disease resistance protein (1); Disease resistance protein RGA4 (1) | ADP binding [GO:0043531 molecular_function] (3) | Leucine-rich repeat domain, L domain-like [IPR032675] (3); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (3); NB-ARC [IPR002182] (3) | scaffold_5_mRNA_1173.1,scaffold_5_mRNA_1174.1 | C_unshiu_01250_mRNA_2.1 | - |
| GF0012769 | 2 | 1 | 0 | Solute carrier family 25 member 44 (2); Hypothetical protein (1) |  | Mitochondrial carrier domain [IPR023395] (3); Mitochondrial substrate/solute carrier [IPR018108] (3) | scaffold_5_mRNA_1170.1,scaffold_5_mRNA_1706.1 | C_unshiu_01766_mRNA_4.1 | - |
| GF0012630 | 2 | 1 | 0 | Caffeic acid 3-O-methyltransferase (2); Caffeic acid O-methyltransferase (1) | O-methyltransferase activity [GO:0008171 molecular_function] (3); methyltransferase activity [GO:0008168 molecular_function] (3) | Winged helix-turn-helix DNA-binding domain [IPR011991] (3); O-methyltransferase, family 2 [IPR001077] (3); O-methyltransferase COMT-type [IPR016461] (3); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (3) | scaffold_4_mRNA_786.1,scaffold_5_mRNA_2803.1 | C_unshiu_00980_mRNA_9.1 | - |
| GF0012628 | 2 | 1 | 0 | Hypothetical protein (3) |  |  | scaffold_4_mRNA_775.1,scaffold_6_mRNA_940.1 | C_unshiu_00407_mRNA_20.1 | - |
| GF0012598 | 2 | 1 | 0 | Hypothetical protein (3) |  |  | scaffold_4_mRNA_625.1,scaffold_4_mRNA_797.1 | C_unshiu_00607_mRNA_7.1 | - |
| GF0012597 | 2 | 1 | 0 | Hypothetical protein (3) |  | Thioredoxin-like fold [IPR012336] (1) | scaffold_4_mRNA_624.1,scaffold_4_mRNA_796.1 | C_unshiu_00607_mRNA_9.1 | - |
| GF0011727 | 2 | 1 | 0 | Hypothetical protein (3) | nucleic acid binding [GO:0003676 molecular_function] (3); zinc ion binding [GO:0008270 molecular_function] (3); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1) | Domain of unknown function DUF4283 [IPR025558] (3); Zinc finger, CCHC-type [IPR001878] (3); Zinc knuckle CX2CX4HX4C [IPR025836] (3); Ribonuclease H-like domain [IPR012337] (1); Ribonuclease H domain [IPR002156] (1) | scaffold_4_mRNA_2432.1,scaffold_8_mRNA_2525.1 | C_unshiu_00011_mRNA_23.1 | - |
| GF0011508 | 2 | 1 | 0 | Hypothetical protein (3) |  |  | scaffold_4_mRNA_2068.1,scaffold_5_mRNA_4596.1 | C_unshiu_00216_mRNA_7.1 | - |
| GF0011505 | 2 | 1 | 0 | MATE efflux family protein, expressed (2); Protein TRANSPARENT TESTA 12-like protein (1) | drug transmembrane transport [GO:0006855 biological_process] (3); membrane [GO:0016020 cellular_component] (3); antiporter activity [GO:0015297 molecular_function] (3); drug transmembrane transporter activity [GO:0015238 molecular_function] (3); transmembrane transport [GO:0055085 biological_process] (3) | Multi antimicrobial extrusion protein [IPR002528] (3) | scaffold_4_mRNA_2051.1,scaffold_4_mRNA_2062.1 | C_unshiu_00700_mRNA_5.1 | - |
| GF0010919 | 2 | 1 | 0 | Putative non-LTR retroelement reverse transcriptase (2); RNA-directed DNA polymerase (Reverse transcriptase), Polynucleotidyl transferase, Ribonuclease H fold-like protein (1) | nucleic acid binding [GO:0003676 molecular_function] (3); zinc ion binding [GO:0008270 molecular_function] (1) | Ribonuclease H-like domain [IPR012337] (3); Reverse transcriptase zinc-binding domain [IPR026960] (3); Reverse transcriptase domain [IPR000477] (2); Domain of unknown function DUF4283 [IPR025558] (1); Zinc finger, CCHC-type [IPR001878] (1); Zinc knuckle CX2CX4HX4C [IPR025836] (1) | scaffold_3_mRNA_74.1,scaffold_8_mRNA_1800.1 | C_unshiu_01059_mRNA_1.1 | - |
| GF0010055 | 2 | 1 | 0 | Hypothetical protein (3) | cysteine-type peptidase activity [GO:0008234 molecular_function] (3); proteolysis [GO:0006508 biological_process] (3) | Ulp1 protease family, C-terminal catalytic domain [IPR003653] (3) | scaffold_3_mRNA_5152.1,scaffold_8_mRNA_779.1 | C_unshiu_00016_mRNA_54.1 | - |
| GF0009624 | 2 | 1 | 0 | Hypothetical protein (3) |  |  | scaffold_3_mRNA_4218.1,scaffold_3_mRNA_4219.1 | C_unshiu_02578_mRNA_6.1 | - |
| GF0009518 | 2 | 1 | 0 | Receptor like protein 33 (2); Receptor like protein 27 (1) | protein binding [GO:0005515 molecular_function] (2) | Leucine-rich repeat domain, L domain-like [IPR032675] (3); Leucine-rich repeat [IPR001611] (2) | scaffold_3_mRNA_3779.1,scaffold_3_mRNA_3794.1 | C_unshiu_00188_mRNA_19.1 | - |
| GF0009483 | 2 | 1 | 0 | Secologanin synthase (2); Putative cytochrome P450 monooxygenase CYP72A5 (1) | oxidation-reduction process [GO:0055114 biological_process] (3); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (3); iron ion binding [GO:0005506 molecular_function] (3); heme binding [GO:0020037 molecular_function] (3) | Cytochrome P450 [IPR001128] (3); Cytochrome P450, E-class, group I [IPR002401] (3); Cytochrome P450, conserved site [IPR017972] (2) | scaffold_3_mRNA_3640.1,scaffold_3_mRNA_3641.1 | C_unshiu_01261_mRNA_7.1 | - |
| GF0009446 | 2 | 1 | 0 | Hypothetical protein (2); Putative Ty-1 copia retrotransposon (1) | DNA integration [GO:0015074 biological_process] (3); nucleic acid binding [GO:0003676 molecular_function] (3) | Ribonuclease H-like domain [IPR012337] (3); Integrase, catalytic core [IPR001584] (3); GAG-pre-integrase domain [IPR025724] (2); Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1) | scaffold_3_mRNA_3484.1,scaffold_9_mRNA_3298.1 | C_unshiu_00381_mRNA_12.1 | - |
| GF0009410 | 2 | 1 | 0 | Retrotransposon protein, putative, Ty3-gypsy subclass, expressed (3) |  | Aspartic peptidase domain [IPR021109] (3) | scaffold_3_mRNA_3354.1,scaffold_8_mRNA_866.1 | C_unshiu_01045_mRNA_10.1 | - |
| GF0009400 | 2 | 1 | 0 | Protein FAR1-RELATED SEQUENCE 5 (2); Protein FAR1-RELATED SEQUENCE 9 (1) | zinc ion binding [GO:0008270 molecular_function] (3); regulation of transcription, DNA-templated [GO:0006355 biological_process] (3); nucleic acid binding [GO:0003676 molecular_function] (2) | FHY3/FAR1 family [IPR031052] (3); MULE transposase domain [IPR018289] (3); Zinc finger, SWIM-type [IPR007527] (3); FAR1 DNA binding domain [IPR004330] (2); Zinc finger, CCHC-type [IPR001878] (2) | scaffold_3_mRNA_3289.1,scaffold_6_mRNA_789.1 | C_unshiu_00120_mRNA_8.1 | - |
| GF0009265 | 2 | 1 | 0 | Hypothetical protein (3) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2); Retrotransposon gag domain [IPR005162] (1) | scaffold_3_mRNA_2694.1,scaffold_9_mRNA_1410.1 | C_unshiu_00423_mRNA_2.1 | - |
| GF0009264 | 2 | 1 | 0 | Hypothetical protein (3) |  | Leucine-rich repeat domain, L domain-like [IPR032675] (3) | scaffold_3_mRNA_2691.1,scaffold_3_mRNA_2707.1 | C_unshiu_01233_mRNA_2.1 | - |
| GF0009198 | 2 | 1 | 0 | Hypothetical protein (2); Transposable element Ac (1) | DNA binding [GO:0003677 molecular_function] (3); nucleic acid binding [GO:0003676 molecular_function] (3) | Ribonuclease H-like domain [IPR012337] (3); hAT-like transposase, RNase-H fold [IPR025525] (3) | scaffold_3_mRNA_2488.1,scaffold_5_mRNA_1866.1 | C_unshiu_00242_mRNA_15.1 | - |
| GF0009195 | 2 | 1 | 0 | Hypothetical protein (3) |  | Domain of unknown function DUF223 [IPR003871] (2); Nucleic acid-binding, OB-fold [IPR012340] (1) | scaffold_3_mRNA_2478.1,scaffold_4_mRNA_917.1 | C_unshiu_00013_mRNA_37.1 | - |
| GF0009188 | 2 | 1 | 0 | Hypothetical protein (3) |  | Retrotransposon gag domain [IPR005162] (3) | scaffold_3_mRNA_2439.1,scaffold_7_mRNA_1159.1 | C_unshiu_01265_mRNA_13.1 | - |
| GF0009180 | 2 | 1 | 0 | Hypothetical protein (2); Ulp1 protease family, carboxy-terminal domain protein (1) | cysteine-type peptidase activity [GO:0008234 molecular_function] (3); proteolysis [GO:0006508 biological_process] (3) | Ulp1 protease family, C-terminal catalytic domain [IPR003653] (3) | scaffold_3_mRNA_2404.1,scaffold_8_mRNA_1860.1 | C_unshiu_00413_mRNA_5.1 | - |
| GF0009158 | 2 | 1 | 0 | Hypothetical protein (3) |  |  | scaffold_3_mRNA_2326.1,scaffold_3_mRNA_2349.1 | C_unshiu_00625_mRNA_9.1 | - |
| GF0009117 | 2 | 1 | 0 | Hypothetical protein (3) |  | LOG family [IPR031100] (1) | scaffold_3_mRNA_2217.1,scaffold_3_mRNA_3407.1 | C_unshiu_01549_mRNA_4.1 | - |
| GF0009052 | 2 | 1 | 0 | Hypothetical protein (3) |  |  | scaffold_3_mRNA_1879.1,scaffold_3_mRNA_1896.1 | C_unshiu_01678_mRNA_9.1 | - |
| GF0008956 | 2 | 1 | 0 | Hypothetical protein (3) |  |  | scaffold_3_mRNA_1523.1,scaffold_5_mRNA_1158.1 | C_unshiu_00101_mRNA_47.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0008931 | 2 | 1 | 0 | Putative muDR family transposase-like (2); AtpA (1) | zinc ion binding [GO:0008270 molecular_function] (3); nucleic acid binding [GO:0003676 molecular_function] (3); transposition, DNA-mediated [GO:0006313 biological_process] (2); transposase activity [GO:0004803 molecular_function] (2); DNA binding [GO:0003677 molecular_function] (2) | Zinc finger, CCHC-type [IPR001878] (3); Zinc finger, PMZ-type [IPR006564] (3); Zinc finger, SWIM-type [IPR007527] (3); Transposase, mutator type [IPR001207] (2); MULE transposase domain [IPR018289] (2) | scaffold_3_mRNA_1439.1,scaffold_6_mRNA_1954.1 | C_unshiu_00259_mRNA_39.1 | - |
| GF0008733 | 2 | 1 | 0 | Hypothetical protein (2); UDP-glycosyltransferase 83A1 (1) | metabolic process [GO:0008152 biological_process] (3); transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (3) | UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (3) | scaffold_3_mRNA_1039.1,scaffold_3_mRNA_1065.1 | C_unshiu_00030_mRNA_76.1 | - |
| GF0008535 | 2 | 1 | 0 | Retrotransposon protein, putative, Ty3-gypsy subclass (1); DNA/RNA polymerases superfamily protein (1); Hypothetical protein (1) | proteolysis [GO:0006508 biological_process] (3); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (3) | Aspartic peptidase, active site [IPR001969] (3); Aspartic peptidase domain [IPR021109] (3); Retrotransposon gag domain [IPR005162] (3) | scaffold_2_mRNA_558.1,scaffold_7_mRNA_1250.1 | C_unshiu_00646_mRNA_16.1 | - |
| GF0008407 | 2 | 1 | 0 | Hypothetical protein (3) | | | scaffold_2_mRNA_4605.1,scaffold_8_mRNA_2654.1 | C_unshiu_00337_mRNA_15.1 | - |
| GF0008271 | 2 | 1 | 0 | Hypothetical protein (3) | | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1) | scaffold_2_mRNA_443.1,scaffold_4_mRNA_1594.1 | C_unshiu_00244_mRNA_24.1 | - |
| GF0007901 | 2 | 1 | 0 | Hypothetical protein (3) | zinc ion binding [GO:0008270 molecular_function] (3); nucleic acid binding [GO:0003676 molecular_function] (3); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1) | Zinc finger, CCHC-type [IPR001878] (3); Viral movement protein [IPR028919] (2); Aspartic peptidase domain [IPR021109] (1); Aspartic peptidase, active site [IPR001969] (1); Retropepsins [IPR018061] (1) | scaffold_2_mRNA_392.1,scaffold_5_mRNA_1015.1 | C_unshiu_00246_mRNA_9.1 | - |
| GF0007847 | 2 | 1 | 0 | Hypothetical protein (3) | | | scaffold_2_mRNA_3838.1,scaffold_9_mRNA_1959.1 | C_unshiu_00089_mRNA_37.1 | - |
| GF0007476 | 2 | 1 | 0 | Putative non-LTR retroelement reverse transcriptase (2); RNA-directed DNA polymerase ; Ribonuclease H, putative (1) | nucleic acid binding [GO:0003676 molecular_function] (1) | Endonuclease/exonuclease/phosphatase [IPR005135] (3); Reverse transcriptase zinc-binding domain [IPR026960] (2); Reverse transcriptase domain [IPR000477] (2); Ribonuclease H-like domain [IPR012337] (1) | scaffold_2_mRNA_3224.1,scaffold_7_mRNA_2536.1 | C_unshiu_00141_mRNA_10.1 | - |
| GF0007244 | 2 | 1 | 0 | Heat shock protein 60 isoform 2 (2); Chaperonin-60 kDa protein isoform 2 (1) | ATP binding [GO:0005524 molecular_function] (2) | GroEL-like apical domain [IPR027409] (3); Chaperonin Cpn60/TCP-1 family [IPR002423] (2); TCP-1-like chaperonin intermediate domain [IPR027410] (1) | scaffold_2_mRNA_2653.1,scaffold_2_mRNA_2656.1 | C_unshiu_00417_mRNA_3.1 | - |
| GF0007243 | 2 | 1 | 0 | Hypothetical protein (3) | rRNA processing [GO:0006364 biological_process] (3); nucleobase-containing compound metabolic process [GO:0006139 biological_process] (3); nucleic acid binding [GO:0003676 molecular_function] (3) | Ribonuclease H-like domain [IPR012337] (3); Putative pre-16S rRNA nuclease [IPR005227] (3); YqgF/RNase H-like domain [IPR006641] (3) | scaffold_2_mRNA_2652.1,scaffold_2_mRNA_2655.1 | C_unshiu_00417_mRNA_2.1 | - |
| GF0007136 | 2 | 1 | 0 | Hypothetical protein (3) | | | scaffold_2_mRNA_198.1,scaffold_9_mRNA_2423.1 | C_unshiu_00464_mRNA_5.1 | - |
| GF0006671 | 2 | 1 | 0 | Hypothetical protein (2); Putative Ty3-gypsy-like retroelement pol polyprotein (1) | nucleic acid binding [GO:0003676 molecular_function] (3) | Ribonuclease H-like domain [IPR012337] (3) | scaffold_1_mRNA_976.1,scaffold_5_mRNA_1006.1 | C_unshiu_00641_mRNA_10.1 | - |
| GF0005994 | 2 | 1 | 0 | Myb domain protein 5 (2); Myb domain protein 5 isoform 1 (1) | DNA binding [GO:0003677 molecular_function] (3) | Myb domain [IPR017930] (3); SANT/Myb domain [IPR001005] (3); Homeobox domain-like [IPR009057] (2); Homeodomain-like [IPR009057] (1) | scaffold_1_mRNA_3085.1,scaffold_3_mRNA_737.1 | C_unshiu_00442_mRNA_24.1 | - |
| GF0005648 | 2 | 1 | 0 | Hypothetical protein (3) | | | scaffold_1_mRNA_2443.1,scaffold_9_mRNA_2472.1 | C_unshiu_00626_mRNA_15.1 | - |
| GF0005611 | 2 | 1 | 0 | Hypothetical protein (3) | | | scaffold_1_mRNA_2300.1,scaffold_3_mRNA_45.1 | C_unshiu_01237_mRNA_10.1 | - |
| GF0005508 | 2 | 1 | 0 | Hypothetical protein (3) | | Retrotransposon gag domain [IPR005162] (3) | scaffold_1_mRNA_2055.1,scaffold_2_mRNA_1138.1 | C_unshiu_00044_mRNA_25.1 | - |
| GF0005416 | 2 | 1 | 0 | Hypothetical protein (3) | | | scaffold_1_mRNA_1782.1,scaffold_8_mRNA_1541.1 | C_unshiu_00441_mRNA_22.1 | - |
| GF0005413 | 2 | 1 | 0 | Hypothetical protein (3) | | | scaffold_1_mRNA_1764.1,scaffold_5_mRNA_5226.1 | C_unshiu_00464_mRNA_9.1 | - |
| GF0005360 | 2 | 1 | 0 | Hypothetical protein (3) | | | scaffold_1_mRNA_1606.1,scaffold_3_mRNA_4360.1 | C_unshiu_01294_mRNA_2.1 | - |
| GF0005303 | 2 | 1 | 0 | Putative nuclease HARBI1 (2); Hypothetical protein (1) | carbohydrate metabolic process [GO:0005975 biological_process] (2); hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (2) | Harbinger transposase-derived nuclease domain [IPR027806] (3); Glycoside hydrolase family 17 [IPR000490] (2); Glycoside hydrolase superfamily [IPR017853] (2); Myb/SANT-like domain [IPR024752] (1); Glycoside hydrolase, catalytic domain [IPR013781] (1) | scaffold_1_mRNA_1334.1,scaffold_3_mRNA_6170.1 | C_unshiu_01540_mRNA_2.1 | - |
| GF0005249 | 2 | 1 | 0 | Hypothetical protein (3) | | | scaffold_1_mRNA_1170.1,scaffold_6_mRNA_299.1 | C_unshiu_00385_mRNA_5.1 | - |
| GF0004997 | 2 | 2 | 0 | Glucan endo-1,3-beta-glucosidase, basic isoform (4) | hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (4); carbohydrate metabolic process [GO:0005975 biological_process] (4) | Glycoside hydrolase family 17 [IPR000490] (4); Glycoside hydrolase superfamily [IPR017853] (4); Glycoside hydrolase, catalytic domain [IPR013781] (2) | scaffold_9_mRNA_2586.1,scaffold_9_mRNA_2587.1 | C_unshiu_00046_mRNA_10.1,C_unshiu_00046_mRNA_7.1 | - |
| GF0004968 | 2 | 2 | 0 | Hypothetical protein (4) | | LOG family [IPR031100] (2) | scaffold_9_mRNA_197.1,scaffold_9_mRNA_2713.1 | C_unshiu_00355_mRNA_10.1,C_unshiu_01190_mRNA_3.1 | - |
| GF0004873 | 2 | 2 | 0 | Hypothetical protein (4) | | | scaffold_8_mRNA_583.1,scaffold_9_mRNA_3186.1 | C_unshiu_00599_mRNA_9.1,C_unshiu_01091_mRNA_3.1 | - |
| GF0004739 | 2 | 2 | 0 | Hypothetical protein (4) | | Protein of unknown function DUF4598 [IPR027921] (4) | scaffold_8_mRNA_232.1,scaffold_8_mRNA_256.1 | C_unshiu_00024_mRNA_97.2,C_unshiu_00116_mRNA_11.1 | - |
| GF0004715 | 2 | 2 | 0 | Hypothetical protein (4) | cysteine-type peptidase activity [GO:0008234 molecular_function] (4); proteolysis [GO:0006508 biological_process] (4) | Ulp1 protease family, C-terminal catalytic domain [IPR003653] (4) | scaffold_8_mRNA_1986.1,scaffold_9_mRNA_2674.1 | C_unshiu_00032_mRNA_55.1,C_unshiu_00093_mRNA_40.1 | - |
| GF0004703 | 2 | 2 | 0 | Hypothetical protein (4) | | | scaffold_8_mRNA_1593.1,scaffold_9_mRNA_2335.1 | C_unshiu_00118_mRNA_50.1,C_unshiu_01343_mRNA_2.1 | - |
| GF0004698 | 2 | 2 | 0 | Hypothetical protein (4) | | | scaffold_8_mRNA_1558.1,scaffold_9_mRNA_2357.1 | C_unshiu_00118_mRNA_69.1,C_unshiu_01687_mRNA_11.1 | - |
| GF0004577 | 2 | 2 | 0 | Tyrosine decarboxylase (4) | carboxylic acid metabolic process [GO:0019752 biological_process] (4); carboxy-lyase activity [GO:0016831 molecular_function] (4); pyridoxal phosphate binding [GO:0030170 molecular_function] (4); catalytic activity [GO:0003824 molecular_function] (4); cellular amino acid metabolic process [GO:0006520 biological_process] (4) | Pyridoxal phosphate-dependent transferase, major region, subdomain 1 [IPR015421] (4); Pyridoxal phosphate-dependent decarboxylase [IPR002129] (4); Pyridoxal-phosphate binding site [IPR021115] (4); Pyridoxal phosphate-dependent transferase [IPR015424] (4); Aromatic-L-amino-acid decarboxylase [IPR010977] (4); Pyridoxal phosphate-dependent transferase, subdomain 2 [IPR015422] (2); Pyridoxal phosphate-dependent transferase, major region, subdomain 2 [IPR015422] (2) | scaffold_7_mRNA_2706.1,scaffold_7_mRNA_2711.1 | C_unshiu_01382_mRNA_3.1,C_unshiu_01382_mRNA_9.1 | - |
| GF0004474 | 2 | 2 | 0 | Hypothetical protein (4) | | Leucine-rich repeat domain, L domain-like [IPR032675] (2) | scaffold_7_mRNA_1639.1,scaffold_7_mRNA_1677.1 | C_unshiu_00352_mRNA_16.1,C_unshiu_02190_mRNA_3.1 | - |
| GF0004365 | 2 | 2 | 0 | Hypothetical protein (4) | proteolysis [GO:0006508 biological_process] (2); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (2) | Aspartic peptidase domain [IPR021109] (4); Aspartic peptidase, active site [IPR001969] (2) | scaffold_6_mRNA_297.1,scaffold_9_mRNA_2638.1 | C_unshiu_00444_mRNA_8.1,C_unshiu_00611_mRNA_1.1 | - |
| GF0004242 | 2 | 2 | 0 | Hypothetical protein (4) | | | scaffold_5_mRNA_907.1,scaffold_5_mRNA_910.1 | C_unshiu_00292_mRNA_17.1,C_unshiu_00292_mRNA_20.1 | - |
| GF0004238 | 2 | 2 | 0 | Phloem protein 2-B5 (4) | protein binding [GO:0005515 molecular_function] (2) | Phloem protein 2-like [IPR025886] (4); F-box domain [IPR001810] (2) | scaffold_5_mRNA_895.1,scaffold_5_mRNA_903.1 | C_unshiu_00292_mRNA_14.1,C_unshiu_00292_mRNA_7.1 | - |
| GF0004204 | 2 | 2 | 0 | Putative pectinesterase/pectinesterase inhibitor 38 (2); Pectinesterase 2 (2) | cell wall [GO:0005618 cellular_component] (4); cell wall modification [GO:0042545 biological_process] (4); pectinesterase activity [GO:0030599 molecular_function] (4) | Pectinesterase, Asp active site [IPR033131] (4); Pectinesterase, catalytic [IPR000070] (4); Pectin lyase fold [IPR012334] (4); Pectin lyase fold/virulence factor [IPR011050] (4) | scaffold_5_mRNA_521.1,scaffold_5_mRNA_526.1 | C_unshiu_00561_mRNA_11.1,C_unshiu_00710_mRNA_14.1 | - |
| GF0004099 | 2 | 2 | 0 | Putative non-LTR retroelement reverse transcriptase (3); RNA-directed DNA polymerase (Reverse transcriptase), Polynucleotidyl transferase, Ribonuclease H fold-like protein (1) | nucleic acid binding [GO:0003676 molecular_function] (4) | Ribonuclease H-like domain [IPR012337] (4); Reverse transcriptase zinc-binding domain [IPR026960] (4); Reverse transcriptase domain [IPR000477] (3) | scaffold_5_mRNA_4157.1,scaffold_9_mRNA_45.1 | C_unshiu_00053_mRNA_69.1,C_unshiu_00174_mRNA_11.1 | - |
| GF0004058 | 2 | 2 | 0 | Hypothetical protein (4) | | | scaffold_5_mRNA_3813.1,scaffold_5_mRNA_3825.1 | C_unshiu_00442_mRNA_2.1,C_unshiu_00442_mRNA_4.1 | - |
| GF0004048 | 2 | 2 | 0 | Hypothetical protein (4) | zinc ion binding [GO:0008270 molecular_function] (1); damaged DNA binding [GO:0003684 molecular_function] (1); nucleus [GO:0005634 cellular_component] (1); DNA repair [GO:0006281 biological_process] (1); endonuclease activity [GO:0004519 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1) | Zinc finger, CCHC-type [IPR001878] (1); ERCC1/RAD10/SWI10 family [IPR004579] (1); Restriction endonuclease type II-like [IPR011335] (1) | scaffold_5_mRNA_3671.1,scaffold_7_mRNA_1856.1 | C_unshiu_00006_mRNA_78.1,C_unshiu_01813_mRNA_1.1 | - |
| GF0004017 | 2 | 2 | 0 | Putative non-LTR retroelement reverse transcriptase (3); Putative RNA-directed DNA polymerase (1) | nucleic acid binding [GO:0003676 molecular_function] (3); zinc ion binding [GO:0008270 molecular_function] (1) | Reverse transcriptase zinc-binding domain [IPR026960] (4); Reverse transcriptase domain [IPR000477] (4); Ribonuclease H-like domain [IPR012337] (3); Endonuclease/exonuclease/phosphatase [IPR005135] (3); Zinc knuckle CX2CX4HX4C [IPR025836] (1); Zinc finger, CCHC-type [IPR001878] (1) | scaffold_5_mRNA_3259.1,scaffold_5_mRNA_3754.1 | C_unshiu_00028_mRNA_14.1,C_unshiu_00161_mRNA_16.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0003936 | 2 | 2 | 0 | Hypothetical protein (4) | response to auxin [GO:0009733 biological_process] (1) | Small auxin-up RNA [IPR003676] (1) | scaffold_5_mRNA_1946.1,scaffold_8_mRNA_1070.1 | C_unshiu_01302_mRNA_3.1,C_unshiu_01849_mRNA_3.1 | - |
| GF0003902 | 2 | 2 | 0 | Hypothetical protein (4) |  | Viral movement protein [IPR028919] (1) | scaffold_5_mRNA_1638.1,scaffold_5_mRNA_2041.1 | C_unshiu_00128_mRNA_41.1,C_unshiu_00531_mRNA_3.1 | - |
| GF0003880 | 2 | 2 | 0 | Hypothetical protein (4) |  |  | scaffold_5_mRNA_1402.1,scaffold_9_mRNA_2527.1 | C_unshiu_00101_mRNA_48.1,C_unshiu_00484_mRNA_5.1 | - |
| GF0003851 | 2 | 2 | 0 | Hypothetical protein (4) |  |  | scaffold_4_mRNA_837.1,scaffold_5_mRNA_1144.1 | C_unshiu_00258_mRNA_10.1,C_unshiu_00258_mRNA_6.1 | - |
| GF0003836 | 2 | 2 | 0 | Hypothetical protein (4) |  | Alpha/Beta hydrolase fold [IPR029058] (1) | scaffold_4_mRNA_614.1,scaffold_4_mRNA_799.1 | C_unshiu_01014_mRNA_3.1,C_unshiu_01202_mRNA_1.1 | - |
| GF0003835 | 2 | 2 | 0 | CDNA clone:002-110-H12, full insert sequence (4) | nucleic acid binding [GO:0003676 molecular_function] (4) | Ribonuclease H-like domain [IPR012337] (4) | scaffold_4_mRNA_605.1,scaffold_4_mRNA_630.1 | C_unshiu_00794_mRNA_5.1,C_unshiu_01014_mRNA_13.1 | - |
| GF0003832 | 2 | 2 | 0 | Hypothetical protein (4) | cysteine-type peptidase activity [GO:0008234 molecular_function] (4); proteolysis [GO:0006508 biological_process] (4) | Ulp1 protease family, C-terminal catalytic domain [IPR003653] (4); Domain of unknown function DUF1985 [IPR015410] (4) | scaffold_4_mRNA_536.1,scaffold_7_mRNA_1689.1 | C_unshiu_00236_mRNA_34.1,C_unshiu_00334_mRNA_3.1 | - |
| GF0003817 | 2 | 2 | 0 | Potassium transporter (4) | membrane [GO:0016020 cellular_component] (4); potassium ion transmembrane transport [GO:0071805 biological_process] (4); potassium ion transmembrane transporter activity [GO:0015079 molecular_function] (4) | Potassium transporter [IPR003855] (4) | scaffold_4_mRNA_3165.1,scaffold_4_mRNA_3167.1 | C_unshiu_00001_mRNA_292.1,C_unshiu_00001_mRNA_293.1 | - |
| GF0003816 | 2 | 2 | 0 | Homogentisate solanesyltransferase (2); Homogentisate phytyltransferase (1); Homogentisate phytyltransferase 1, chloroplastic (1) | integral component of membrane [GO:0016021 cellular_component] (4); prenyltransferase activity [GO:0004659 molecular_function] (2); transferase activity, transferring alkyl or aryl (other than methyl) groups [GO:0016765 molecular_function] (2) | UbiA prenyltransferase family [IPR000537] (4) | scaffold_4_mRNA_3116.1,scaffold_9_mRNA_3566.1 | C_unshiu_00001_mRNA_240.1,C_unshiu_01328_mRNA_3.1 | - |
| GF0003771 | 2 | 2 | 0 | Nepenthesin II (3); Putative aspartic protease (1) | aspartic-type endopeptidase activity [GO:0004190 molecular_function] (4); proteolysis [GO:0006508 biological_process] (4) | Peptidase family A1 domain [IPR033121] (4); Aspartic peptidase domain [IPR021109] (4); Aspartic peptidase, active site [IPR001969] (4); Xylanase inhibitor, N-terminal [IPR032861] (4); Xylanase inhibitor, C-terminal [IPR032799] (4); Aspartic peptidase A1 family [IPR001461] (4); Pepsin-like domain, plant [IPR034161] (2) | scaffold_4_mRNA_2108.1,scaffold_4_mRNA_2111.1 | C_unshiu_00020_mRNA_6.1,C_unshiu_00020_mRNA_8.1 | - |
| GF0003761 | 2 | 2 | 0 | Hypothetical protein (4) |  | NPR1/NIM1-like, C-terminal [IPR021094] (2) | scaffold_4_mRNA_1861.1,scaffold_4_mRNA_1866.1 | C_unshiu_00384_mRNA_14.1,C_unshiu_01556_mRNA_11.1 | - |
| GF0003760 | 2 | 2 | 0 | Nonexpressor of pathogenesis-related protein 1 (3); Ankyrin repeat BTB/POZ domain-containing protein (1) | protein binding [GO:0005515 molecular_function] (4) | Regulatory protein NPR, central domain [IPR024228] (4); Ankyrin repeat [IPR002110] (4); Ankyrin repeat-containing domain [IPR020683] (4); NPR1/NIM1-like, C-terminal [IPR021094] (4); SKP1/BTB/POZ domain [IPR011333] (3); BTB/POZ domain [IPR000210] (3) | scaffold_4_mRNA_1860.1,scaffold_4_mRNA_1868.1 | C_unshiu_01584_mRNA_3.1,C_unshiu_02053_mRNA_3.1 | - |
| GF0003758 | 2 | 2 | 0 | Flavone synthase II (4) | iron ion binding [GO:0005506 molecular_function] (4); heme binding [GO:0020037 molecular_function] (4); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (4); oxidation-reduction process [GO:0055114 biological_process] (4) | Cytochrome P450 [IPR001128] (4); Cytochrome P450, conserved site [IPR017972] (4); Cytochrome P450, E-class, group I [IPR002401] (4) | scaffold_4_mRNA_1836.1,scaffold_4_mRNA_1838.1 | C_unshiu_00428_mRNA_1.1,C_unshiu_02739_mRNA_1.1 | - |
| GF0003751 | 2 | 2 | 0 | Hypothetical protein (4) | heme binding [GO:0020037 molecular_function] (4); iron ion binding [GO:0005506 molecular_function] (4); oxidation-reduction process [GO:0055114 biological_process] (4); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (4) | Cytochrome P450 [IPR001128] (4) | scaffold_4_mRNA_1691.1,scaffold_7_mRNA_1336.1 | C_unshiu_00240_mRNA_24.1,C_unshiu_01151_mRNA_5.1 | - |
| GF0003740 | 2 | 2 | 0 | BED zinc finger,hAT family dimerization domain isoform 1 (2); Hypothetical protein (1); Putative zinc finger BED domain-containing protein DAYSLEEPER-like (1) | DNA binding [GO:0003677 molecular_function] (4); nucleic acid binding [GO:0003676 molecular_function] (4); protein dimerization activity [GO:0046983 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (4); hAT-like transposase, RNase-H fold [IPR025525] (4); Zinc finger, BED-type [IPR003656] (2); HAT, C-terminal dimerisation domain [IPR008906] (2); Zinc finger C2H2-type [IPR013087] (1) | scaffold_4_mRNA_1402.1,scaffold_9_mRNA_788.1 | C_unshiu_00019_mRNA_15.1,C_unshiu_00386_mRNA_2.1 | - |
| GF0003739 | 2 | 2 | 0 | Hypothetical protein (4) |  | Transposase, Tnp1/En/Spm-like [IPR004264] (4) | scaffold_4_mRNA_140.1,scaffold_6_mRNA_1418.1 | C_unshiu_00012_mRNA_17.1,C_unshiu_01022_mRNA_9.1 | - |
| GF0003714 | 2 | 2 | 0 | MuDR family transposase isoform 1 (4) | zinc ion binding [GO:0008270 molecular_function] (4) | Zinc finger, SWIM-type [IPR007527] (4); MULE transposase domain [IPR018289] (4); Transposase, MuDR, plant [IPR004332] (4); Zinc finger, PMZ-type [IPR006564] (2) | scaffold_4_mRNA_1061.1,scaffold_5_mRNA_1060.1 | C_unshiu_00111_mRNA_26.1,C_unshiu_01132_mRNA_13.1 | - |
| GF0003712 | 2 | 2 | 0 | Hypothetical protein (4) |  |  | scaffold_4_mRNA_1037.1,scaffold_6_mRNA_111.1 | C_unshiu_00885_mRNA_10.1,C_unshiu_00932_mRNA_10.1 | - |
| GF0003711 | 2 | 2 | 0 | Hypothetical protein (3); Retrotransposon gag protein (1) |  | Retrotransposon gag domain [IPR005162] (2) | scaffold_4_mRNA_1032.1,scaffold_4_mRNA_1086.1 | C_unshiu_00057_mRNA_1.1,C_unshiu_00097_mRNA_52.1 | - |
| GF0003659 | 2 | 2 | 0 | Metalloendoproteinase 1 (3); Matrix metalloproteinase (1) | zinc ion binding [GO:0008270 molecular_function] (4); metalloendopeptidase activity [GO:0004222 molecular_function] (4); metallopeptidase activity [GO:0008237 molecular_function] (4); extracellular matrix [GO:0031012 cellular_component] (4); proteolysis [GO:0006508 biological_process] (4) | Peptidase, metallopeptidase [IPR006026] (4); Peptidase M10A [IPR021190] (4); Metallopeptidase, catalytic domain [IPR024079] (4); Peptidase M10, metallopeptidase [IPR001818] (4); Peptidase M10A, catalytic domain [IPR033739] (2); Peptidoglycan binding-like [IPR002477] (1); Peptidase M10A, cysteine switch, zinc binding site [IPR021158] (1) | scaffold_3_mRNA_6167.1,scaffold_3_mRNA_756.1 | C_unshiu_00001_mRNA_21.1,C_unshiu_03023_mRNA_1.1 | - |
| GF0003511 | 2 | 2 | 0 | Hypothetical protein (4) |  |  | scaffold_3_mRNA_4637.1,scaffold_3_mRNA_4643.1 | C_unshiu_01029_mRNA_1.1,C_unshiu_01827_mRNA_4.1 | - |
| GF0003497 | 2 | 2 | 0 | Hypothetical protein (4) | metal ion binding [GO:0046872 molecular_function] (4); glutathione gamma-glutamylcysteinyltransferase activity [GO:0016756 molecular_function] (4); phytochelatin biosynthetic process [GO:0046938 biological_process] (4); response to metal ion [GO:0010038 biological_process] (4) | Phytochelatin synthase, C-terminal [IPR015407] (4) | scaffold_3_mRNA_4550.1,scaffold_5_mRNA_28.1 | C_unshiu_00230_mRNA_51.1,C_unshiu_00258_mRNA_22.1 | - |
| GF0003492 | 2 | 2 | 0 | Hypothetical protein (4) | 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_4499.1,scaffold_6_mRNA_93.1 | C_unshiu_00471_mRNA_5.1,C_unshiu_00711_mRNA_1.1 | - |
| GF0003353 | 2 | 2 | 0 | Hypothetical protein (4) |  |  | scaffold_3_mRNA_3007.1,scaffold_3_mRNA_3015.1 | C_unshiu_01094_mRNA_6.1,C_unshiu_03067_mRNA_1.1 | - |
| GF0003313 | 2 | 2 | 0 | BED zinc finger,hAT family dimerization domain isoform 1 (2); Putative zinc finger BED domain-containing protein DAYSLEEPER-like (2) | protein dimerization activity [GO:0046983 molecular_function] (4); nucleic acid binding [GO:0003676 molecular_function] (4); DNA binding [GO:0003677 molecular_function] (4) | HAT, C-terminal dimerisation domain [IPR008906] (4); Ribonuclease H-like domain [IPR012337] (4); hAT-like transposase, RNase-H fold [IPR025525] (4); Zinc finger C2H2-type [IPR013087] (1); Zinc finger, BED-type [IPR003656] (1) | scaffold_3_mRNA_2615.1,scaffold_7_mRNA_1176.1 | C_unshiu_00071_mRNA_13.1,C_unshiu_00775_mRNA_7.1 | - |
| GF0003279 | 2 | 2 | 0 | Hypothetical protein (4) |  |  | scaffold_3_mRNA_2175.1,scaffold_9_mRNA_2692.1 | C_unshiu_00226_mRNA_15.1,C_unshiu_00930_mRNA_9.1 | - |
| GF0003143 | 2 | 2 | 0 | Hypothetical protein (4) |  |  | scaffold_2_mRNA_77.1,scaffold_2_mRNA_80.1 | C_unshiu_00062_mRNA_43.1,C_unshiu_01410_mRNA_2.1 | - |
| GF0003121 | 2 | 2 | 0 | Hypothetical protein (4) | protein binding [GO:0005515 molecular_function] (4) | Leucine-rich repeat domain, L domain-like [IPR032675] (4); Leucine-rich repeat [IPR001611] (4) | scaffold_2_mRNA_492.1,scaffold_5_mRNA_4187.1 | C_unshiu_00992_mRNA_4.1,C_unshiu_02006_mRNA_5.1 | - |
| GF0003118 | 2 | 2 | 0 | Retrotransposon gag protein (4) |  | Retrotransposon gag domain [IPR005162] (4) | scaffold_2_mRNA_470.1,scaffold_4_mRNA_493.1 | C_unshiu_00061_mRNA_14.1,C_unshiu_01651_mRNA_2.1 | - |
| GF0003106 | 2 | 2 | 0 | Retrotransposon protein, putative, unclassified (1); Hypothetical protein (1); Non-LTR retroelement reverse transcriptase-like protein (1); RNA-directed DNA polymerase ; Ribonuclease H, putative (1) | nucleic acid binding [GO:0003676 molecular_function] (2) | Endonuclease/exonuclease/phosphatase [IPR005135] (4); Reverse transcriptase domain [IPR000477] (2); Reverse transcriptase zinc-binding domain [IPR026960] (2); Ribonuclease H-like domain [IPR012337] (2); Zinc knuckle CX2CX4HX4C [IPR025836] (1); Domain of unknown function DUF4283 [IPR025558] (1) | scaffold_2_mRNA_438.1,scaffold_6_mRNA_1770.1 | C_unshiu_00187_mRNA_4.1,C_unshiu_00244_mRNA_30.1 | - |
| GF0003101 | 2 | 2 | 0 | Hypothetical protein (4) | nucleic acid binding [GO:0003676 molecular_function] (4); zinc ion binding [GO:0008270 molecular_function] (4) | Zinc finger, CCHC-type [IPR001878] (4) | scaffold_2_mRNA_424.1,scaffold_3_mRNA_2484.1 | C_unshiu_00526_mRNA_8.1,C_unshiu_01871_mRNA_3.1 | - |
| GF0003082 | 2 | 2 | 0 | Hypothetical protein (4) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_2_mRNA_378.1,scaffold_8_mRNA_1796.1 | C_unshiu_00246_mRNA_22.1,C_unshiu_01290_mRNA_8.1 | - |
| GF0003039 | 2 | 2 | 0 | Hypothetical protein (4) |  |  | scaffold_2_mRNA_306.1,scaffold_6_mRNA_228.1 | C_unshiu_00392_mRNA_23.1,C_unshiu_02445_mRNA_4.1 | - |
| GF0003038 | 2 | 2 | 0 | Receptor like protein 33 (2); Receptor like protein 27 (2) | protein binding [GO:0005515 molecular_function] (2) | Leucine-rich repeat domain, L domain-like [IPR032675] (4); Leucine-rich repeat [IPR001611] (2); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat, typical subtype [IPR003591] (1) | scaffold_2_mRNA_3059.1,scaffold_2_mRNA_3067.1 | C_unshiu_00863_mRNA_4.1,C_unshiu_01163_mRNA_8.1 | - |
| GF0003026 | 2 | 2 | 0 | Hypothetical protein (4) |  |  | scaffold_2_mRNA_2857.1,scaffold_2_mRNA_2858.1 | C_unshiu_00722_mRNA_7.1,C_unshiu_00722_mRNA_8.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0003001 | 2 | 2 | 0 | Hypothetical protein (3); Protein FAR1-RELATED SEQUENCE 6 (1) | regulation of transcription, DNA-templated [GO:0006355 biological_process] (4); zinc ion binding [GO:0008270 molecular_function] (2) | FHY3/FAR1 family [IPR031052] (4); Zinc finger, SWIM-type [IPR007527] (2); Zinc finger, PMZ-type [IPR006564] (2); FAR1 DNA binding domain [IPR004330] (2) | scaffold_2_mRNA_2561.1,scaffold_8_mRNA_1152.1 | C_unshiu_00211_mRNA_22.1,C_unshiu_00682_mRNA_10.1 | - |
| GF0002991 | 2 | 2 | 0 | Hypothetical protein (4) | | | scaffold_2_mRNA_2384.1,scaffold_7_mRNA_1319.1 | C_unshiu_00138_mRNA_11.1,C_unshiu_00655_mRNA_6.1 | - |
| GF0002985 | 2 | 2 | 0 | Hypothetical protein (4) | | Retrotransposon gag domain [IPR005162] (1) | scaffold_2_mRNA_2203.1,scaffold_9_mRNA_1680.1 | C_unshiu_00508_mRNA_7.1,C_unshiu_00683_mRNA_4.1 | - |
| GF0002961 | 2 | 2 | 0 | UDP-glycosyltransferase 74E2 (4) | metabolic process [GO:0008152 biological_process] (4); transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (4) | UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (4) | scaffold_2_mRNA_1959.1,scaffold_2_mRNA_3226.1 | C_unshiu_00030_mRNA_34.1,C_unshiu_00141_mRNA_12.1 | - |
| GF0002894 | 2 | 2 | 0 | Syntaxin 81 (3); Hypothetical protein (1) | vesicle-mediated transport [GO:0016192 biological_process] (4); membrane [GO:0016020 cellular_component] (4); 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) | SNARE-complex protein Syntaxin-18, N-terminal [IPR019529] (4); t-SNARE [IPR010989] (2); SNARE [IPR010989] (2); Translation protein, beta-barrel domain [IPR009000] (1); Ribosomal protein L35A [IPR001780] (1) | scaffold_2_mRNA_1064.1,scaffold_4_mRNA_40.1 | C_unshiu_00168_mRNA_31.1,C_unshiu_00235_mRNA_13.1 | - |
| GF0002879 | 2 | 2 | 0 | Hypothetical protein (4) | | | scaffold_1_mRNA_760.1,scaffold_1_mRNA_770.1 | C_unshiu_00075_mRNA_3.1,C_unshiu_01122_mRNA_2.1 | - |
| GF0002851 | 2 | 2 | 0 | Hypothetical protein (3); Protein FAR1-RELATED SEQUENCE 11 (1) | regulation of transcription, DNA-templated [GO:0006355 biological_process] (4); zinc ion binding [GO:0008270 molecular_function] (2) | FAR1 DNA binding domain [IPR004330] (4); FHY3/FAR1 family [IPR031052] (4); Zinc finger, PMZ-type [IPR006564] (2); Zinc finger, SWIM-type [IPR007527] (2) | scaffold_1_mRNA_355.1,scaffold_7_mRNA_1193.1 | C_unshiu_00365_mRNA_19.1,C_unshiu_02037_mRNA_3.1 | - |
| GF0002838 | 2 | 2 | 0 | Hypothetical protein (2); Putative sugar phosphate/phosphate translocator (2) | | Acyl-CoA N-acyltransferase [IPR016181] (1); Peptidogalycan biosysnthesis/recognition [IPR007434] (1) | scaffold_1_mRNA_3476.1,scaffold_5_mRNA_262.1 | C_unshiu_00164_mRNA_28.1,C_unshiu_00449_mRNA_14.1 | - |
| GF0002807 | 2 | 2 | 0 | Hypothetical protein (4) | strictosidine synthase activity [GO:0016844 molecular_function] (4); biosynthetic process [GO:0009058 biological_process] (4) | Six-bladed beta-propeller, TolB-like [IPR011042] (4); Strictosidine synthase, conserved region [IPR018119] (4); Strictosidine synthase [IPR004141] (4) | scaffold_1_mRNA_292.1,scaffold_1_mRNA_298.1 | C_unshiu_01113_mRNA_1.1,C_unshiu_02657_mRNA_3.1 | - |
| GF0002780 | 2 | 2 | 0 | Hypothetical protein (4) | | Transposase-associated domain [IPR029480] (1) | scaffold_1_mRNA_2549.1,scaffold_9_mRNA_1981.1 | C_unshiu_00036_mRNA_53.1,C_unshiu_02530_mRNA_1.1 | - |
| GF0002758 | 2 | 2 | 0 | Hypothetical protein (4) | | | scaffold_1_mRNA_2266.1,scaffold_5_mRNA_3824.1 | C_unshiu_00274_mRNA_32.1,C_unshiu_01384_mRNA_2.1 | - |
| GF0002725 | 2 | 2 | 0 | Hypothetical protein (3); Cysteine-rich RLK (RECEPTOR-like protein kinase) 8 (1) | | Gag-polypeptide of LTR copia-type [IPR029472] (4); Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1) | scaffold_1_mRNA_1614.1,scaffold_8_mRNA_1191.1 | C_unshiu_00910_mRNA_7.1,C_unshiu_02557_mRNA_2.1 | - |
| GF0002716 | 2 | 2 | 0 | Hypothetical protein (4) | | | scaffold_1_mRNA_1514.1,scaffold_6_mRNA_572.1 | C_unshiu_00756_mRNA_14.1,C_unshiu_01623_mRNA_6.1 | - |
| GF0002713 | 2 | 2 | 0 | Hypothetical protein (4) | | | scaffold_1_mRNA_1487.1,scaffold_5_mRNA_2508.1 | C_unshiu_00145_mRNA_68.1,C_unshiu_00756_mRNA_12.1 | - |
| GF0002711 | 2 | 2 | 0 | Hypothetical protein (4) | nucleic acid binding [GO:0003676 molecular_function] (4); zinc ion binding [GO:0008270 molecular_function] (4) | Zinc finger, CCHC-type [IPR001878] (4) | scaffold_1_mRNA_1461.1,scaffold_3_mRNA_1927.1 | C_unshiu_00374_mRNA_1.1,C_unshiu_01568_mRNA_16.1 | - |
| GF0002701 | 2 | 2 | 0 | Hypothetical protein (4) | | | scaffold_1_mRNA_1260.1,scaffold_1_mRNA_1313.1 | C_unshiu_00242_mRNA_21.1,C_unshiu_00270_mRNA_18.1 | - |
| GF0002693 | 2 | 2 | 0 | Hypothetical protein (4) | | | scaffold_1_mRNA_1143.1,scaffold_5_mRNA_1278.1 | C_unshiu_00191_mRNA_3.1,C_unshiu_00899_mRNA_12.1 | - |
| GF0002689 | 2 | 2 | 0 | Hypothetical protein (4) | nucleic acid binding [GO:0003676 molecular_function] (4) | Ribonuclease H-like domain [IPR012337] (4) | scaffold_1_mRNA_1106.1,scaffold_9_mRNA_1664.1 | C_unshiu_00087_mRNA_11.1,C_unshiu_00308_mRNA_2.1 | - |
| GF0002441 | 2 | 3 | 0 | Non-LTR retroelement reverse transcriptase-like (2); RNA-directed DNA polymerase (Reverse transcriptase), Polynucleotidyl transferase, Ribonuclease H fold-like protein (1); Putative non-LTR retroelement reverse transcriptase (1); RNA-directed DNA polymerase (Reverse transcriptase) (1) | RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (4); nucleic acid binding [GO:0003676 molecular_function] (4) | Ribonuclease H domain [IPR002156] (4); Ribonuclease H-like domain [IPR012337] (4); Reverse transcriptase zinc-binding domain [IPR026960] (4); Reverse transcriptase domain [IPR000477] (2); Endonuclease/exonuclease/phosphatase [IPR005135] (1) | scaffold_7_mRNA_1209.1,scaffold_9_mRNA_1975.1 | C_unshiu_00290_mRNA_23.1,C_unshiu_00458_mRNA_12.1,C_unshiu_00957_mRNA_8.1 | - |
| GF0002386 | 2 | 3 | 0 | Lactosylceramide 4-alpha-galactosyltransferase, putative (5) | | Glycosyltransferase, DXD sugar-binding motif [IPR007577] (5); Alpha 1,4-glycosyltransferase domain [IPR007652] (5); Nucleotide-diphospho-sugar transferases [IPR029044] (5) | scaffold_6_mRNA_1763.1,scaffold_6_mRNA_1764.1 | C_unshiu_00473_mRNA_22.1,C_unshiu_00473_mRNA_24.1,C_unshiu_00779_mRNA_12.1 | - |
| GF0002298 | 2 | 3 | 0 | Hypothetical protein (5) | | | scaffold_5_mRNA_3565.1,scaffold_7_mRNA_2585.1 | C_unshiu_00372_mRNA_25.1,C_unshiu_00618_mRNA_8.1,C_unshiu_01187_mRNA_3.1 | - |
| GF0002047 | 2 | 3 | 0 | Hypothetical protein (5) | | | scaffold_3_mRNA_3478.2,scaffold_3_mRNA_3482.1 | C_unshiu_00381_mRNA_10.1,C_unshiu_01092_mRNA_1.1,C_unshiu_02920_mRNA_1.2 | - |
| GF0001924 | 2 | 3 | 0 | Verticillium wilt resistance-like protein (4); Receptor like protein 33 (1) | protein binding [GO:0005515 molecular_function] (5) | Leucine-rich repeat domain, L domain-like [IPR032675] (5); Leucine-rich repeat, typical subtype [IPR003591] (5); Leucine-rich repeat [IPR001611] (5); Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1); Leucine rich repeat 4 [IPR025875] (1) | scaffold_2_mRNA_3837.1,scaffold_2_mRNA_3842.1 | C_unshiu_00185_mRNA_30.1,C_unshiu_00185_mRNA_32.1,C_unshiu_00185_mRNA_34.1 | - |
| GF0001870 | 2 | 3 | 0 | UDP-glycosyltransferase 74E2 (5) | metabolic process [GO:0008152 biological_process] (5); transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (5) | UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (5) | scaffold_2_mRNA_1966.1,scaffold_2_mRNA_3228.1 | C_unshiu_00030_mRNA_27.1,C_unshiu_00141_mRNA_14.1,C_unshiu_01801_mRNA_3.1 | - |
| GF0001786 | 2 | 3 | 0 | Hypothetical protein (2); Transposase (1); Putative zinc finger BED domain-containing protein DAYSLEEPER-like (1); Transposable element Ac (1) | nucleic acid binding [GO:0003676 molecular_function] (5); protein dimerization activity [GO:0046983 molecular_function] (4); DNA binding [GO:0003677 molecular_function] (4); metabolic process [GO:0008152 biological_process] (2); lyase activity [GO:0016829 molecular_function] (2); terpene synthase activity [GO:0010333 molecular_function] (2); magnesium ion binding [GO:0000287 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (5); HAT, C-terminal dimerisation domain [IPR008906] (4); hAT-like transposase, RNase-H fold [IPR025525] (3); Zinc finger, BED-type [IPR003656] (3); Terpene synthase, metal-binding domain [IPR005630] (2); Terpene synthase, N-terminal domain [IPR001906] (2); Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (2); Isoprenoid synthase domain [IPR008949] (2); Transposase, MuDR, plant [IPR004332] (1); Zinc finger C2H2-type [IPR013087] (1) | scaffold_1_mRNA_2390.1,scaffold_9_mRNA_1011.1 | C_unshiu_01083_mRNA_2.1,C_unshiu_01083_mRNA_3.1,C_unshiu_01818_mRNA_5.1 | - |
| GF0001752 | 2 | 3 | 0 | Hypothetical protein (5) | | | scaffold_1_mRNA_1626.1,scaffold_5_mRNA_588.1 | C_unshiu_00667_mRNA_12.1,C_unshiu_01140_mRNA_20.1,C_unshiu_01753_mRNA_3.1 | - |
| GF0001570 | 2 | 4 | 0 | Hypothetical protein (3); Ulp1 protease family, carboxy-terminal domain protein (2); Recombination RecR (1) | ADP binding [GO:0043531 molecular_function] (1) | Transposase, Tnp1/En/Spm-like [IPR004264] (6); Probable transposase, Ptta/En/Spm, plant [IPR004252] (4); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1) | scaffold_6_mRNA_1077.1,scaffold_8_mRNA_2227.1 | C_unshiu_00167_mRNA_2.1,C_unshiu_00328_mRNA_13.1,C_unshiu_00365_mRNA_30.1,C_unshiu_01555_mRNA_1.1 | - |
| GF0001561 | 2 | 4 | 0 | Hypothetical protein (6) | | | scaffold_5_mRNA_679.1,scaffold_6_mRNA_66.1 | C_unshiu_00458_mRNA_4.1,C_unshiu_02240_mRNA_2.1,C_unshiu_02240_mRNA_7.1,C_unshiu_02495_mRNA_2.1 | - |
| GF0001535 | 2 | 4 | 0 | Hypothetical protein (2); Polynucleotidyl transferase, Ribonuclease H fold (2); Non-LTR retroelement reverse transcriptase-like (1); Putative non-LTR retroelement reverse transcriptase (1) | nucleic acid binding [GO:0003676 molecular_function] (6) | Ribonuclease H-like domain [IPR012337] (6); Reverse transcriptase zinc-binding domain [IPR026960] (6); Endonuclease/exonuclease/phosphatase [IPR005135] (2) | scaffold_5_mRNA_3483.1,scaffold_7_mRNA_1291.1 | C_unshiu_00010_mRNA_35.1,C_unshiu_00049_mRNA_23.1,C_unshiu_00199_mRNA_10.1,C_unshiu_01929_mRNA_8.1 | - |
| GF0001519 | 2 | 4 | 0 | Disease resistance protein (CC-NBS-LRR class) family protein (3); NBS-LRR type disease resistance protein (2); Disease resistance protein (1) | ADP binding [GO:0043531 molecular_function] (6) | Leucine-rich repeat domain, L domain-like [IPR032675] (6); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (6); NB-ARC [IPR002182] (6); AAA+ ATPase domain [IPR003593] (5); Winged helix-turn-helix DNA-binding domain [IPR011991] (2) | scaffold_5_mRNA_2795.1,scaffold_5_mRNA_2837.1 | C_unshiu_00263_mRNA_25.1,C_unshiu_01408_mRNA_2.1,C_unshiu_01783_mRNA_5.1,C_unshiu_02128_mRNA_2.1 | - |
| GF0001463 | 2 | 4 | 0 | Hypothetical protein (6) | | | scaffold_4_mRNA_2630.1,scaffold_8_mRNA_2098.1 | C_unshiu_00010_mRNA_95.1,C_unshiu_00111_mRNA_11.1,C_unshiu_00178_mRNA_18.1,C_unshiu_01364_mRNA_4.1 | - |
| GF0001454 | 2 | 4 | 0 | Hypothetical protein (6) | 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_4_mRNA_2055.1,scaffold_5_mRNA_988.1 | C_unshiu_00083_mRNA_29.1,C_unshiu_00104_mRNA_23.1,C_unshiu_00387_mRNA_5.1,C_unshiu_00830_mRNA_3.1 | - |
| GF0001431 | 2 | 4 | 0 | Adipocyte plasma membrane-associated protein (4); Putative strictosidine synthase (2) | strictosidine synthase activity [GO:0016844 molecular_function] (6); biosynthetic process [GO:0009058 biological_process] (6) | Strictosidine synthase, conserved region [IPR018119] (6); Strictosidine synthase [IPR004141] (6); Six-bladed beta-propeller, TolB-like [IPR011042] (6) | scaffold_4_mRNA_1046.1,scaffold_4_mRNA_1278.1 | C_unshiu_00777_mRNA_8.1,C_unshiu_00809_mRNA_5.1,C_unshiu_00932_mRNA_1.1,C_unshiu_02303_mRNA_6.1 | - |
| GF0001283 | 2 | 4 | 0 | Hypothetical protein (6) | | Transposase, MuDR, plant [IPR004332] (6); MULE transposase domain [IPR018289] (3) | scaffold_2_mRNA_511.1,scaffold_5_mRNA_355.1 | C_unshiu_00015_mRNA_61.1,C_unshiu_00016_mRNA_55.1,C_unshiu_00062_mRNA_25.1,C_unshiu_00147_mRNA_6.1 | - |
| GF0001280 | 2 | 4 | 0 | Hypothetical protein (6) | | | scaffold_2_mRNA_473.1,scaffold_8_mRNA_1389.1 | C_unshiu_00056_mRNA_53.1,C_unshiu_00061_mRNA_17.1,C_unshiu_00489_mRNA_3.1,C_unshiu_00944_mRNA_1.1 | - |
| GF0001272 | 2 | 4 | 0 | Hypothetical protein (6) | | Leucine-rich repeat domain, L domain-like [IPR032675] (4) | scaffold_2_mRNA_4295.1,scaffold_2_mRNA_4417.1 | C_unshiu_00015_mRNA_76.1,C_unshiu_00151_mRNA_7.1,C_unshiu_00667_mRNA_7.1,C_unshiu_01889_mRNA_4.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0001231 | 2 | 4 | 0 | Hypothetical protein (6) | | | scaffold_2_mRNA_2444.1,scaffold_9_mRNA_2230.1 | C_unshiu_00128_mRNA_15.1,C_unshiu_00174_mRNA_36.1,C_unshiu_01765_mRNA_3.1,C_unshiu_02091_mRNA_2.1 | - |
| GF0001157 | 2 | 4 | 0 | Hypothetical protein (6) | | | scaffold_1_mRNA_2521.1,scaffold_8_mRNA_2294.1 | C_unshiu_00364_mRNA_19.1,C_unshiu_00702_mRNA_9.1,C_unshiu_02577_mRNA_1.1,C_unshiu_02841_mRNA_1.1 | - |
| GF0001146 | 2 | 4 | 0 | Hypothetical protein (6) | | | scaffold_1_mRNA_2214.1,scaffold_1_mRNA_782.1 | C_unshiu_00247_mRNA_29.1,C_unshiu_00247_mRNA_31.1,C_unshiu_00888_mRNA_3.1,C_unshiu_01591_mRNA_10.1 | - |
| GF0000971 | 2 | 5 | 0 | Retrotransposon gag protein (7) | | Retrotransposon gag domain [IPR005162] (7) | scaffold_5_mRNA_1502.1,scaffold_6_mRNA_858.1 | C_unshiu_00187_mRNA_2.1,C_unshiu_00228_mRNA_45.1,C_unshiu_00274_mRNA_2.1,C_unshiu_00304_mRNA_15.1,C_unshiu_02726_mRNA_3.1 | - |
| GF0000942 | 2 | 5 | 0 | Hypothetical protein (7) | | | scaffold_3_mRNA_6280.1,scaffold_5_mRNA_5232.1 | C_unshiu_00051_mRNA_14.1,C_unshiu_00051_mRNA_15.1,C_unshiu_00309_mRNA_22.1,C_unshiu_01212_mRNA_6.1,C_unshiu_03148_mRNA_1.1 | - |
| GF0000835 | 2 | 5 | 0 | Hypothetical protein (7) | | | scaffold_2_mRNA_1892.1,scaffold_6_mRNA_472.1 | C_unshiu_00104_mRNA_17.1,C_unshiu_00470_mRNA_25.1,C_unshiu_01424_mRNA_5.1,C_unshiu_02033_mRNA_3.1,C_unshiu_02338_mRNA_5.1 | - |
| GF0000748 | 2 | 6 | 0 | Hypothetical protein (4); Polyprotein (2); RNA-directed DNA polymerase (Reverse transcriptase); Zinc finger, CCHC-type; Peptidase aspartic, active site; Retrotransposon gag protein (1); Putative polyprotein (Aspartic proteinase, reverse transcriptase, ribonuclease H) (1) | zinc ion binding [GO:0008270 molecular_function] (7); nucleic acid binding [GO:0003676 molecular_function] (7); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (5); proteolysis [GO:0006508 biological_process] (5) | Zinc finger, CCHC-type [IPR001878] (7); Peptidase A2A, retrovirus, catalytic [IPR001995] (5); Reverse transcriptase domain [IPR000477] (5); Retropepsins [IPR018061] (5); Aspartic peptidase domain [IPR021109] (3) | scaffold_8_mRNA_1614.1,scaffold_9_mRNA_2228.1 | C_unshiu_00074_mRNA_66.1,C_unshiu_00074_mRNA_68.1,C_unshiu_00138_mRNA_51.1,C_unshiu_00145_mRNA_13.1,C_unshiu_00479_mRNA_5.1,C_unshiu_01893_mRNA_8.1 | - |
| GF0000731 | 2 | 6 | 0 | Hypothetical protein (8) | | | scaffold_6_mRNA_457.1,scaffold_8_mRNA_1570.1 | C_unshiu_00350_mRNA_3.1,C_unshiu_00350_mRNA_32.1,C_unshiu_00408_mRNA_16.1,C_unshiu_01245_mRNA_11.1,C_unshiu_01374_mRNA_8.1,C_unshiu_01503_mRNA_7.1 | - |
| GF0000623 | 2 | 6 | 0 | Hypothetical protein (8) | | | scaffold_2_mRNA_2938.1,scaffold_4_mRNA_1091.1 | C_unshiu_00014_mRNA_116.1,C_unshiu_00029_mRNA_87.1,C_unshiu_00055_mRNA_48.1,C_unshiu_00271_mRNA_44.1,C_unshiu_00984_mRNA_13.1,C_unshiu_01350_mRNA_3.1 | - |
| GF0000566 | 2 | 7 | 0 | Hypothetical protein (7); Specific tissue protein 1, putative (1); Pea shoot-specific protein (1) | | Organ specific protein [IPR024489] (9) | scaffold_8_mRNA_741.1,scaffold_8_mRNA_756.1 | C_unshiu_00085_mRNA_8.1,C_unshiu_00432_mRNA_17.1,C_unshiu_01007_mRNA_3.1,C_unshiu_01565_mRNA_1.1,C_unshiu_01565_mRNA_2.1,C_unshiu_02149_mRNA_3.1,C_unshiu_02763_mRNA_2.1 | - |
| GF0024944 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_992.1 | C_unshiu_00161_mRNA_30.1 | - |
| GF0024943 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_990.1 | C_unshiu_00161_mRNA_34.1 | - |
| GF0024941 | 1 | 1 | 0 | LRR receptor-like kinase family protein (2) | protein binding [GO:0005515 molecular_function] (2) | Leucine-rich repeat domain, L domain-like [IPR032675] (2); Leucine-rich repeat [IPR001611] (2); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (2) | scaffold_9_mRNA_987.1 | C_unshiu_00307_mRNA_6.1 | - |
| GF0024940 | 1 | 1 | 0 | Hypothetical protein (2) | serine-type endopeptidase activity [GO:0004252 molecular_function] (2); proteolysis [GO:0006508 biological_process] (2) | Peptidase S8/S53 domain [IPR000209] (2); Peptidase S8, subtilisin-related [IPR015500] (1) | scaffold_9_mRNA_986.1 | C_unshiu_00287_mRNA_19.1 | - |
| GF0024939 | 1 | 1 | 0 | Hypothetical protein (2) | protein binding [GO:0005515 molecular_function] (2) | Leucine-rich repeat [IPR001611] (2); Leucine-rich repeat, typical subtype [IPR003591] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2) | scaffold_9_mRNA_985.1 | C_unshiu_00307_mRNA_7.1 | - |
| GF0024938 | 1 | 1 | 0 | Nuclear transport factor 2 family protein with RNA binding domain isoform 2 (2) | nucleic acid binding [GO:0003676 molecular_function] (2); intracellular [GO:0005622 cellular_component] (2); transport [GO:0006810 biological_process] (2); nucleotide binding [GO:0000166 molecular_function] (1) | NTF2-like domain [IPR032710] (2); Nuclear transport factor 2 [IPR002075] (2); Nuclear transport factor 2, eukaryote [IPR018222] (2); RNA recognition motif domain [IPR000504] (2); Nucleotide-binding alpha-beta plait domain [IPR012677] (1) | scaffold_9_mRNA_982.1 | C_unshiu_00307_mRNA_10.1 | - |
| GF0024937 | 1 | 1 | 0 | Pentatricopeptide (PPR) repeat protein (2) | protein binding [GO:0005515 molecular_function] (2) | Pentatricopeptide repeat [IPR002885] (2); Tetratricopeptide-like helical domain [IPR011990] (2) | scaffold_9_mRNA_980.1 | C_unshiu_00307_mRNA_12.1 | - |
| GF0024936 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_979.1 | C_unshiu_00307_mRNA_13.1 | - |
| GF0024935 | 1 | 1 | 0 | Zinc finger protein CONSTANS-LIKE 4 (2) | protein binding [GO:0005515 molecular_function] (2) | CCT domain [IPR010402] (2) | scaffold_9_mRNA_972.1 | C_unshiu_00307_mRNA_21.1 | - |
| GF0024934 | 1 | 1 | 0 | Peptide transporter PTR3-A (2) | membrane [GO:0016020 cellular_component] (2); transport [GO:0006810 biological_process] (2); transporter activity [GO:0005215 molecular_function] (2) | Proton-dependent oligopeptide transporter family [IPR000109] (2); Major facilitator superfamily domain [IPR020846] (2) | scaffold_9_mRNA_957.1 | C_unshiu_01048_mRNA_5.1 | - |
| GF0024933 | 1 | 1 | 0 | Hypothetical protein (2) | | S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1) | scaffold_9_mRNA_950.1 | C_unshiu_01048_mRNA_11.1 | - |
| GF0024932 | 1 | 1 | 0 | Hypothetical protein (2) | | Leucine-rich repeat domain, L domain-like [IPR032675] (2) | scaffold_9_mRNA_947.1 | C_unshiu_00959_mRNA_12.1 | - |
| GF0024931 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_944.1 | C_unshiu_00146_mRNA_1.1 | - |
| GF0024930 | 1 | 1 | 0 | Hypothetical protein (2) | ATPase activity [GO:0016887 molecular_function] (2); ATP binding [GO:0005524 molecular_function] (2) | ABC transporter-like [IPR003439] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2) | scaffold_9_mRNA_937.1 | C_unshiu_00146_mRNA_8.1 | - |
| GF0024929 | 1 | 1 | 0 | Cyclopropane-fatty-acyl-phospholipid synthase (1); Hypothetical protein (1) | oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1) | S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (2); FAD/NAD(P)-binding domain [IPR023753] (1) | scaffold_9_mRNA_936.1 | C_unshiu_00146_mRNA_7.1 | - |
| GF0024928 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_934.1 | C_unshiu_00146_mRNA_11.1 | - |
| GF0024926 | 1 | 1 | 0 | Hypothetical protein (2) | protein peptidyl-prolyl isomerization [GO:0000413 biological_process] (2); protein folding [GO:0006457 biological_process] (2); nucleic acid binding [GO:0003676 molecular_function] (2); peptidyl-prolyl cis-trans isomerase activity [GO:0003755 molecular_function] (2); nucleotide binding [GO:0000166 molecular_function] (1) | RNA recognition motif domain [IPR000504] (2); Cyclophilin-like domain [IPR029000] (2); Cyclophilin-type peptidyl-prolyl cis-trans isomerase domain [IPR002130] (2); Ferritin-related [IPR012347] (1); Nucleotide-binding alpha-beta plait domain [IPR012677] (1); Cyclophilin-type peptidyl-prolyl cis-trans isomerase [IPR024936] (1) | scaffold_9_mRNA_93.1 | C_unshiu_00007_mRNA_94.1 | - |
| GF0024924 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_913.1 | C_unshiu_00146_mRNA_32.1 | - |
| GF0024923 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_907.1 | C_unshiu_00146_mRNA_37.1 | - |
| GF0024922 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_902.1 | C_unshiu_01125_mRNA_1.1 | - |
| GF0024920 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_888.1 | C_unshiu_00329_mRNA_9.1 | - |
| GF0024918 | 1 | 1 | 0 | 60S ribosomal protein L36 (2) | translation [GO:0006412 biological_process] (2); intracellular [GO:0005622 cellular_component] (2); structural constituent of ribosome [GO:0003735 molecular_function] (2); ribosome [GO:0005840 cellular_component] (2) | Ribosomal protein L36e [IPR000509] (2) | scaffold_9_mRNA_879.1 | C_unshiu_00396_mRNA_1.1 | - |
| GF0024917 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_875.1 | C_unshiu_00396_mRNA_4.1 | - |
| GF0024916 | 1 | 1 | 0 | Hypothetical protein (2) | ubiquitin protein ligase binding [GO:0031625 molecular_function] (2); ubiquitin-dependent protein catabolic process [GO:0006511 biological_process] (2) | Cullin, N-terminal [IPR001373] (2); Cullin repeat-like-containing domain [IPR016159] (2) | scaffold_9_mRNA_872.1 | C_unshiu_00396_mRNA_7.1 | - |
| GF0024914 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_87.1 | C_unshiu_00007_mRNA_99.1 | - |
| GF0024913 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_867.1 | C_unshiu_00396_mRNA_12.1 | - |
| GF0024912 | 1 | 1 | 0 | Hypothetical protein (2) | | Splicing factor 3B subunit 5/RDS3 complex subunit 10 [IPR009846] (2) | scaffold_9_mRNA_854.1 | C_unshiu_00057_mRNA_56.1 | - |
| GF0024910 | 1 | 1 | 0 | 11S globulin (2) | nutrient reservoir activity [GO:0045735 molecular_function] (2) | RmlC-like cupin domain [IPR011051] (2); RmlC-like jelly roll fold [IPR014710] (2); 11-S seed storage protein, conserved site [IPR022379] (2); Cupin 1 [IPR006045] (2); 11-S seed storage protein, plant [IPR006044] (2) | scaffold_9_mRNA_845.2 | C_unshiu_00057_mRNA_47.1 | - |
| GF0024908 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_824.1 | C_unshiu_00164_mRNA_15.1 | - |
| GF0024907 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_822.1 | C_unshiu_00164_mRNA_16.1 | - |
| GF0024906 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_821.1 | C_unshiu_00164_mRNA_17.1 | - |
| GF0024905 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_819.1 | C_unshiu_00164_mRNA_19.1 | - |
| GF0024904 | 1 | 1 | 0 | Repetitive proline-rich cell wall protein 1 (2) | | | scaffold_9_mRNA_818.1 | C_unshiu_00164_mRNA_20.1 | - |
| GF0024903 | 1 | 1 | 0 | Putative retroelement pol polyprotein (2) | | | scaffold_9_mRNA_815.1 | C_unshiu_00164_mRNA_22.1 | - |
| GF0024902 | 1 | 1 | 0 | Hypothetical protein (2) | | Domain of unknown function DUF4283 [IPR025558] (2); Endonuclease/exonuclease/phosphatase [IPR005135] (1); Zinc knuckle CX2CX4HX4C [IPR025836] (1) | scaffold_9_mRNA_812.1 | C_unshiu_00164_mRNA_25.1 | - |
| GF0024901 | 1 | 1 | 0 | Ethylene-responsive transcription factor ERF098 (2) | DNA binding [GO:0003677 molecular_function] (2); regulation of transcription, DNA-templated [GO:0006355 biological_process] (2); transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (2) | AP2/ERF domain [IPR001471] (2); DNA-binding domain [IPR016177] (2) | scaffold_9_mRNA_810.1 | C_unshiu_00164_mRNA_27.1 | - |
| GF0024898 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_796.1 | C_unshiu_01106_mRNA_8.1 | - |
| GF0024897 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_792.1 | C_unshiu_01106_mRNA_4.1 | - |

| **ID** | **Num. in *C. celementine*** | **Num in *C. unshiu*** | **Num in *P.trifoliata*** | **Note** | **GO** | **InterPro** | **Members in *C.clementine*** | **Members in *C.unshiu*** | **Members in *P.trifoliata*** |
|---|---|---|---|---|---|---|---|---|---|
| GF0024896 | 1 | 1 | 0 | 1-aminocyclopropane-1-carboxylate oxidase like 12 (2) | oxidoreductase activity [GO:0016491 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2) | Isopenicillin N synthase-like [IPR027443] (2); Non-haem dioxygenase N-terminal domain [IPR026992] (2); Oxoglutarate/iron-dependent dioxygenase [IPR005123] (2) | scaffold_9_mRNA_787.1 | C_unshiu_00386_mRNA_3.1 | - |
| GF0024895 | 1 | 1 | 0 | Hypothetical protein (2) | DNA binding [GO:0003677 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (1) | Zinc finger, BED-type [IPR003656] (2); Zinc finger C2H2-type [IPR013087] (1) | scaffold_9_mRNA_786.1 | C_unshiu_00386_mRNA_4.1 | - |
| GF0024894 | 1 | 1 | 0 | Hypothetical protein (2) |  | Pentatricopeptide repeat [IPR002885] (2) | scaffold_9_mRNA_773.1 | C_unshiu_00410_mRNA_4.1 | - |
| GF0024893 | 1 | 1 | 0 | Hypothetical protein (2) |  | Cwf19-like, C-terminal domain-1 [IPR006768] (2); Cwf19-like protein, C-terminal domain-2 [IPR006767] (2) | scaffold_9_mRNA_772.1 | C_unshiu_00410_mRNA_2.1 | - |
| GF0024891 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_759.1 | C_unshiu_00032_mRNA_67.1 | - |
| GF0024889 | 1 | 1 | 0 | Hypothetical protein (2) | cellulose biosynthetic process [GO:0030244 biological_process] (1); membrane [GO:0016020 cellular_component] (1); cellulose synthase (UDP-forming) activity [GO:0016760 molecular_function] (1) | Protein of unknown function DUF247, plant [IPR004158] (2); Cellulose synthase [IPR005150] (1) | scaffold_9_mRNA_751.1 | C_unshiu_00032_mRNA_57.1 | - |
| GF0024887 | 1 | 1 | 0 | StAR-related lipid transfer protein 7, mitochondrial (2) | lipid binding [GO:0008289 molecular_function] (2) | START-like domain [IPR023393] (2); START domain [IPR002913] (2) | scaffold_9_mRNA_734.1 | C_unshiu_00445_mRNA_14.1 | - |
| GF0024886 | 1 | 1 | 0 | P-loop nucleoside triphosphate hydrolase superfamily protein (2) | ATP binding [GO:0005524 molecular_function] (2); kinase activity [GO:0016301 molecular_function] (2) | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); Zeta toxin domain [IPR010488] (2) | scaffold_9_mRNA_731.1 | C_unshiu_00445_mRNA_12.1 | - |
| GF0024885 | 1 | 1 | 0 | Histone H1 (2) | nucleosome [GO:0000786 cellular_component] (2); nucleosome assembly [GO:0006334 biological_process] (2); DNA binding [GO:0003677 molecular_function] (2); nucleus [GO:0005634 cellular_component] (2) | Histone H5 [IPR005819] (2); Linker histone H1/H5, domain H15 [IPR005818] (2); Winged helix-turn-helix DNA-binding domain [IPR011991] (2) | scaffold_9_mRNA_730.1 | C_unshiu_00445_mRNA_11.1 | - |
| GF0024884 | 1 | 1 | 0 | 40S ribosomal protein S15 (2) | ribosome [GO:0005840 cellular_component] (2); RNA binding [GO:0003723 molecular_function] (2); small ribosomal subunit [GO:0015935 cellular_component] (2); structural constituent of ribosome [GO:0003735 molecular_function] (2); translation [GO:0006412 biological_process] (2) | Ribosomal protein S19 conserved site [IPR020934] (2); Ribosomal protein S19, superfamily [IPR023575] (2); Ribosomal protein S19A/S15e [IPR005713] (2); Ribosomal protein S19/S15 [IPR002222] (2) | scaffold_9_mRNA_729.2 | C_unshiu_00445_mRNA_10.2 | - |
| GF0024883 | 1 | 1 | 0 | Ankyrin repeat family protein, putative (2) | protein binding [GO:0005515 molecular_function] (2); integral component of membrane [GO:0016021 cellular_component] (1); cellular response to salicylic acid stimulus [GO:0071446 biological_process] (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] (2); Ankyrin repeat-containing domain [IPR020683] (2); Ankyrin repeat [IPR002110] (2); Protein accelerated cell death 6 [IPR032846] (1) | scaffold_9_mRNA_722.1 | C_unshiu_01876_mRNA_3.1 | - |
| GF0024882 | 1 | 1 | 0 | Ankyrin repeat family protein, putative (2) | protein binding [GO:0005515 molecular_function] (2); regulation of salicylic acid mediated signaling pathway [GO:2000031 biological_process] (1); regulation of defense response [GO:0031347 biological_process] (1); integral component of membrane [GO:0016021 cellular_component] (1); cellular response to salicylic acid stimulus [GO:0071446 biological_process] (1) | Ankyrin repeat [IPR002110] (2); PGG domain [IPR026961] (2); Ankyrin repeat-containing domain [IPR020683] (2); Protein accelerated cell death 6 [IPR032846] (1) | scaffold_9_mRNA_711.1 | C_unshiu_00436_mRNA_30.1 | - |
| GF0024881 | 1 | 1 | 0 | Hypothetical protein (2) | protein binding [GO:0005515 molecular_function] (2) | Ankyrin repeat [IPR002110] (2); Ankyrin repeat-containing domain [IPR020683] (2) | scaffold_9_mRNA_710.1 | C_unshiu_00436_mRNA_28.1 | - |
| GF0024878 | 1 | 1 | 0 | NAD(P)H dehydrogenase 18 (2) | response to oxidative stress [GO:0006979 biological_process] (1); chloroplast [GO:0009507 cellular_component] (1) | Photosynthetic NDH subunit of subcomplex B 5, chloroplastic [IPR034569] (1) | scaffold_9_mRNA_695.1 | C_unshiu_00436_mRNA_12.1 | - |
| GF0024877 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_683.1 | C_unshiu_00436_mRNA_3.1 | - |
| GF0024874 | 1 | 1 | 0 | Calmodulin (2) | calcium ion binding [GO:0005509 molecular_function] (2) | EF-Hand 1, calcium-binding site [IPR018247] (2); EF-hand domain [IPR002048] (2); EF-hand domain pair [IPR011992] (2) | scaffold_9_mRNA_667.1 | C_unshiu_00298_mRNA_14.1 | - |
| GF0024873 | 1 | 1 | 0 | 1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase 4 (1); 1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase 2 (1) | acireductone dioxygenase [iron(II)-requiring] activity [GO:0010309 molecular_function] (1); L-methionine salvage from methylthioadenosine [GO:0019509 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1) | RmlC-like jelly roll fold [IPR014710] (1); RmlC-like cupin domain [IPR011051] (1); 1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase, eukaryotes [IPR027496] (1); Acireductone dioxygenase ARD family [IPR004313] (1) | scaffold_9_mRNA_644.2 | C_unshiu_00101_mRNA_29.1 | - |
| GF0024872 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_639.1 | C_unshiu_00101_mRNA_34.1 | - |
| GF0024871 | 1 | 1 | 0 | Leucine-rich repeat receptor-like protein kinase family (2) | protein binding [GO:0005515 molecular_function] (2) | Leucine-rich repeat domain, L domain-like [IPR032675] (2); Leucine-rich repeat [IPR001611] (2); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (2) | scaffold_9_mRNA_627.1 | C_unshiu_00101_mRNA_53.1 | - |
| GF0024870 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_626.1 | C_unshiu_00085_mRNA_51.1 | - |
| GF0024869 | 1 | 1 | 0 | Hypothetical protein (2) | ATP binding [GO:0005524 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2); protein kinase activity [GO:0004672 molecular_function] (2) | Protein kinase-like domain [IPR011009] (2); Protein kinase domain [IPR000719] (2); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1) | scaffold_9_mRNA_614.1 | C_unshiu_00369_mRNA_7.1 | - |
| GF0024868 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_605.1 | C_unshiu_00369_mRNA_17.1 | - |
| GF0024867 | 1 | 1 | 0 | Ribosomal protein L19 (2) | translation [GO:0006412 biological_process] (2); intracellular [GO:0005622 cellular_component] (2); structural constituent of ribosome [GO:0003735 molecular_function] (2); ribosome [GO:0005840 cellular_component] (2); cytosolic large ribosomal subunit [GO:0022625 cellular_component] (1) | Ribosomal protein L19/L19e, domain 3 [IPR015974] (2); Ribosomal protein L19/L19e, domain 1 [IPR015972] (2); Ribosomal protein L19/L19e conserved site [IPR023638] (2); Ribosomal protein L19/L19e, domain 2 [IPR015973] (1); Ribosomal protein L19/L19e [IPR000196] (1); Ribosomal protein L19/L19e domain [IPR000196] (1); Ribosomal protein L19, eukaryotic [IPR033935] (1) | scaffold_9_mRNA_602.1 | C_unshiu_00369_mRNA_20.1 | - |
| GF0024866 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_597.1 | C_unshiu_00254_mRNA_42.1 | - |
| GF0024864 | 1 | 1 | 0 | Cysteine synthase (2) | cysteine biosynthetic process from serine [GO:0006535 biological_process] (2); cysteine synthase activity [GO:0004124 molecular_function] (2) | Cysteine synthase [IPR005856] (2); Cysteine synthase/cystathionine beta-synthase, pyridoxal-phosphate attachment site [IPR001216] (2); Tryptophan synthase beta subunit-like PLP-dependent enzyme [IPR001926] (2); Cysteine synthase CysK [IPR005859] (2) | scaffold_9_mRNA_575.1 | C_unshiu_00254_mRNA_24.1 | - |
| GF0024861 | 1 | 1 | 0 | Amine oxidase (flavin-containing) (2) | primary amine oxidase activity [GO:0008131 molecular_function] (2); copper ion binding [GO:0005507 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2); quinone binding [GO:0048038 molecular_function] (2); amine metabolic process [GO:0009308 biological_process] (2) | Copper amine oxidase, C-terminal [IPR015798] (2); Copper amine oxidase, N-terminal [IPR016182] (2); Copper amine oxidase, N3-terminal [IPR015802] (2); Copper amine oxidase, N2-terminal [IPR015800] (2); Copper amine oxidase [IPR000269] (2) | scaffold_9_mRNA_554.1 | C_unshiu_00254_mRNA_4.1 | - |
| GF0024860 | 1 | 1 | 0 | Amine oxidase (flavin-containing) (2) | amine metabolic process [GO:0009308 biological_process] (2); quinone binding [GO:0048038 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2); copper ion binding [GO:0005507 molecular_function] (2); primary amine oxidase activity [GO:0008131 molecular_function] (2) | Copper amine oxidase [IPR000269] (2); Copper amine oxidase, N2-terminal [IPR015800] (2); Copper amine oxidase, N3-terminal [IPR015802] (2); Copper amine oxidase, N-terminal [IPR016182] (2); Copper amine oxidase, C-terminal [IPR015798] (2) | scaffold_9_mRNA_553.1 | C_unshiu_00254_mRNA_3.1 | - |
| GF0024859 | 1 | 1 | 0 | G-type lectin S-receptor-like serine/threonine-protein kinase RLK1 (1); Hypothetical protein (1) | protein phosphorylation [GO:0006468 biological_process] (2); protein kinase activity [GO:0004672 molecular_function] (2); ATP binding [GO:0005524 molecular_function] (2) | Protein kinase-like domain [IPR011009] (2); Protein kinase domain [IPR000719] (2) | scaffold_9_mRNA_548.1 | C_unshiu_00126_mRNA_56.1 | - |
| GF0024858 | 1 | 1 | 0 | Amine oxidase (flavin-containing) (2) | primary amine oxidase activity [GO:0008131 molecular_function] (2); amine metabolic process [GO:0009308 biological_process] (2); quinone binding [GO:0048038 molecular_function] (2); copper ion binding [GO:0005507 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2) | Copper amine oxidase, C-terminal [IPR015798] (2); Copper amine oxidase [IPR000269] (2); Copper amine oxidase, N-terminal [IPR016182] (1); Copper amine oxidase, N2-terminal [IPR015800] (1) | scaffold_9_mRNA_546.1 | C_unshiu_00126_mRNA_58.1 | - |
| GF0024856 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_523.1 | C_unshiu_00051_mRNA_51.1 | - |
| GF0024855 | 1 | 1 | 0 | Ribonuclease P/MRP protein subunit POP5 (2) | ribonuclease activity [GO:0004540 molecular_function] (1); tRNA processing [GO:0008033 biological_process] (1) | Ribonuclease P/MRP protein subunit [IPR002759] (1) | scaffold_9_mRNA_522.1 | C_unshiu_00051_mRNA_50.1 | - |
| GF0024854 | 1 | 1 | 0 | Odontogenic ameloblast-associated (2) |  |  | scaffold_9_mRNA_500.1 | C_unshiu_00051_mRNA_32.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0024853 | 1 | 1 | 0 | NEDD8-activating enzyme E1 catalytic subunit (2) | NEDD8 activating enzyme activity [GO:0019781 molecular_function] (2); small protein activating enzyme activity [GO:0008641 molecular_function] (2); ATP binding [GO:0005524 molecular_function] (2); acid-amino acid ligase activity [GO:0016881 molecular_function] (2); protein neddylation [GO:0045116 biological_process] (2) | THIF-type NAD/FAD binding fold [IPR000594] (2); E2 binding [IPR014929] (2); NEDD8-activating enzyme E1 catalytic subunit [IPR030468] (2); Ubiquitin-activating enzyme E1, Cys active site [IPR033127] (2); NAD(P)-binding domain [IPR016040] (1); Ubiquitin activating enzyme, alpha domain [IPR023318] (1) | scaffold_9_mRNA_499.2 | C_unshiu_00051_mRNA_31.2 | - |
| GF0024852 | 1 | 1 | 0 | Basic 7S globulin (2) | proteolysis [GO:0006508 biological_process] (2); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (2) | Peptidase family A1 domain [IPR033121] (2); Aspartic peptidase domain [IPR021109] (2); Xylanase inhibitor, N-terminal [IPR032861] (2); Xylanase inhibitor, C-terminal [IPR032799] (2); Aspartic peptidase A1 family [IPR001461] (2); Xylanase inhibitor I-like [IPR033868] (1) | scaffold_9_mRNA_493.1 | C_unshiu_00051_mRNA_26.1 | - |
| GF0024850 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_488.1 | C_unshiu_00051_mRNA_23.1 | - |
| GF0024849 | 1 | 1 | 0 | Basic 7S globulin (2) | proteolysis [GO:0006508 biological_process] (2); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (2) | Aspartic peptidase domain [IPR021109] (2); Peptidase family A1 domain [IPR033121] (2); Aspartic peptidase A1 family [IPR001461] (2); Xylanase inhibitor, C-terminal [IPR032799] (2); Xylanase inhibitor, N-terminal [IPR032861] (2); Xylanase inhibitor I-like [IPR033868] (1) | scaffold_9_mRNA_485.1 | C_unshiu_00702_mRNA_6.1 | - |
| GF0024848 | 1 | 1 | 0 | Hypothetical protein (2) | metal ion transport [GO:0030001 biological_process] (2); metal ion binding [GO:0046872 molecular_function] (2) | Heavy metal-associated domain, HMA [IPR006121] (2) | scaffold_9_mRNA_476.1 | C_unshiu_00097_mRNA_16.1 | - |
| GF0024846 | 1 | 1 | 0 | Ribonucleoside-diphosphate reductase small chain (2) | oxidation-reduction process [GO:0055114 biological_process] (2); deoxyribonucleoside diphosphate metabolic process [GO:0009186 biological_process] (1); deoxyribonucleotide biosynthetic process [GO:0009263 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1) | Ferritin-like superfamily [IPR009078] (2); Ribonucleotide reductase small subunit, acitve site [IPR030475] (2); Ribonucleotide reductase small subunit [IPR033909] (1); Ribonucleotide reductase-related [IPR012348] (1); Ribonucleotide reductase small subunit [IPR000358] (1); Ribonucleotide reductase small subunit family [IPR000358] (1) | scaffold_9_mRNA_460.1 | C_unshiu_00097_mRNA_30.1 | - |
| GF0024844 | 1 | 1 | 0 | Dienelactone hydrolase family, putative (2) | hydrolase activity [GO:0016787 molecular_function] (1) | Alpha/Beta hydrolase fold [IPR029058] (2); Dienelactone hydrolase [IPR002925] (1) | scaffold_9_mRNA_454.1 | C_unshiu_00097_mRNA_37.1 | - |
| GF0024843 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_453.1 | C_unshiu_00097_mRNA_38.1 | - |
| GF0024842 | 1 | 1 | 0 | EF-hand, calcium binding motif-containing protein (2) | calcium ion binding [GO:0005509 molecular_function] (2) | EF-hand domain [IPR002048] (2); EF-Hand 1, calcium-binding site [IPR018247] (2); EF-hand domain pair [IPR011992] (2) | scaffold_9_mRNA_450.1 | C_unshiu_01541_mRNA_2.1 | - |
| GF0024840 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_434.1 | C_unshiu_00040_mRNA_71.1 | - |
| GF0024839 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_422.1 | C_unshiu_00040_mRNA_57.1 | - |
| GF0024838 | 1 | 1 | 0 | Glutamate binding protein (1); Hypothetical protein (1) | | Bax inhibitor 1-related [IPR006214] (1) | scaffold_9_mRNA_410.1 | C_unshiu_00366_mRNA_24.1 | - |
| GF0024837 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_408.1 | C_unshiu_00366_mRNA_26.1 | - |
| GF0024836 | 1 | 1 | 0 | Hypothetical protein (2) | | Nucleotide-diphospho-sugar transferases [IPR029044] (2); Domain of unknown function DUF4283 [IPR025558] (2) | scaffold_9_mRNA_401.1 | C_unshiu_00366_mRNA_32.1 | - |
| GF0024835 | 1 | 1 | 0 | Pentatricopeptide repeat-containing protein, chloroplastic (2) | protein binding [GO:0005515 molecular_function] (1) | Pentatricopeptide repeat [IPR002885] (2); Tetratricopeptide-like helical domain [IPR011990] (1) | scaffold_9_mRNA_40.1 | C_unshiu_00007_mRNA_143.1 | - |
| GF0024831 | 1 | 1 | 0 | Histidine-containing phosphotransfer protein 4 (2) | signal transducer activity [GO:0004871 molecular_function] (2); phosphorelay signal transduction system [GO:0000160 biological_process] (2) | Signal transduction histidine kinase, phosphotransfer (Hpt) domain [IPR008207] (2) | scaffold_9_mRNA_386.1 | C_unshiu_00394_mRNA_22.1 | - |
| GF0024830 | 1 | 1 | 0 | Hypothetical protein (2) | ATP binding [GO:0005524 molecular_function] (2); unfolded protein binding [GO:0051082 molecular_function] (2); protein folding [GO:0006457 biological_process] (2) | Chaperonin Cpn60/TCP-1 family [IPR002423] (2); GroEL-like equatorial domain [IPR027413] (2); T-complex protein 1, gamma subunit [IPR012719] (2); Chaperone tailless complex polypeptide 1 (TCP-1) [IPR017998] (2); Chaperonin TCP-1, conserved site [IPR002194] (2) | scaffold_9_mRNA_3840.1 | C_unshiu_00003_mRNA_118.1 | - |
| GF0024829 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_3837.1 | C_unshiu_00003_mRNA_115.1 | - |
| GF0024828 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_3833.1 | C_unshiu_00003_mRNA_111.1 | - |
| GF0024826 | 1 | 1 | 0 | Hypothetical protein (2) | | Major facilitator superfamily domain [IPR020846] (2) | scaffold_9_mRNA_3808.1 | C_unshiu_00003_mRNA_89.1 | - |
| GF0024825 | 1 | 1 | 0 | Nuclear transcription factor Y subunit C-2 (1); Nuclear transcription factor Y subunit C-9 (1) | protein heterodimerization activity [GO:0046982 molecular_function] (2) | Transcription factor CBF/NF-Y/archaeal histone domain [IPR003958] (2); Histone-fold [IPR009072] (2) | scaffold_9_mRNA_3796.1 | C_unshiu_00003_mRNA_76.1 | - |
| GF0024822 | 1 | 1 | 0 | Splicing factor, arginine/serine-rich 12 (2) | | | scaffold_9_mRNA_3766.1 | C_unshiu_00003_mRNA_49.1 | - |
| GF0024821 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_3764.1 | C_unshiu_00334_mRNA_14.1 | - |
| GF0024818 | 1 | 1 | 0 | FUSICOCCIN receptor protein s (2) | protein domain specific binding [GO:0019904 molecular_function] (2) | 14-3-3 domain [IPR023410] (2); 14-3-3 protein [IPR000308] (2) | scaffold_9_mRNA_3743.1 | C_unshiu_00003_mRNA_32.1 | - |
| GF0024816 | 1 | 1 | 0 | LOB domain-containing protein 4 (2) | | Lateral organ boundaries, LOB [IPR004883] (2) | scaffold_9_mRNA_3736.1 | C_unshiu_00003_mRNA_26.1 | - |
| GF0024815 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_3734.1 | C_unshiu_00003_mRNA_23.1 | - |
| GF0024813 | 1 | 1 | 0 | Cyclic nucleotide-gated ion channel 1 (2) | nucleic acid binding [GO:0003676 molecular_function] (2); protein dimerization activity [GO:0046983 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2); Cyclic nucleotide-binding-like [IPR018490] (2); RmlC-like jelly roll fold [IPR014710] (2); Cyclic nucleotide-binding domain [IPR000595] (2); HAT, C-terminal dimerisation domain [IPR008906] (2) | scaffold_9_mRNA_3714.1 | C_unshiu_00003_mRNA_3.1 | - |
| GF0024812 | 1 | 1 | 0 | Hypothetical protein (2) | | RmlC-like jelly roll fold [IPR014710] (2); Cyclic nucleotide-binding-like [IPR018490] (2); Cyclic nucleotide-binding domain [IPR000595] (2); Gag-polypeptide of LTR copia-type [IPR029472] (1) | scaffold_9_mRNA_3711.1 | C_unshiu_01726_mRNA_1.1 | - |
| GF0024811 | 1 | 1 | 0 | Cyclic nucleotide gated channel 5 isoform 1 (1); Hypothetical protein (1) | | Cyclic nucleotide-binding domain [IPR000595] (2); RmlC-like jelly roll fold [IPR014710] (2); Cyclic nucleotide-binding-like [IPR018490] (2) | scaffold_9_mRNA_3710.1 | C_unshiu_01726_mRNA_2.1 | - |
| GF0024809 | 1 | 1 | 0 | Non-LTR retroelement reverse transcriptase-like protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (2) | Ribonuclease H domain [IPR002156] (2); Ribonuclease H-like domain [IPR012337] (2) | scaffold_9_mRNA_3705.1 | C_unshiu_00740_mRNA_11.1 | - |
| GF0024808 | 1 | 1 | 0 | Cyclic nucleotide-gated ion channel-like protein (2) | trehalose biosynthetic process [GO:0005992 biological_process] (2); ion channel activity [GO:0005216 molecular_function] (2); catalytic activity [GO:0003824 molecular_function] (2); membrane [GO:0016020 cellular_component] (2); ion transport [GO:0006811 biological_process] (2); transmembrane transport [GO:0055085 biological_process] (2) | HAD-superfamily hydrolase, subfamily IIB [IPR006379] (2); Trehalose-phosphatase [IPR003337] (2); Cyclic nucleotide-binding domain [IPR000595] (2); Cyclic nucleotide-binding-like [IPR018490] (2); Ion transport domain [IPR005821] (2); HAD-like domain [IPR023214] (2); RmlC-like jelly roll fold [IPR014710] (2) | scaffold_9_mRNA_3696.1 | C_unshiu_00134_mRNA_2.1 | - |
| GF0024807 | 1 | 1 | 0 | Pentatricopeptide repeat-containing family protein (1); PPR containing plant-like protein (1) | protein binding [GO:0005515 molecular_function] (2) | Pentatricopeptide repeat [IPR002885] (2); Tetratricopeptide-like helical domain [IPR011990] (2) | scaffold_9_mRNA_3676.1 | C_unshiu_00134_mRNA_19.1 | - |
| GF0024806 | 1 | 1 | 0 | TRNA dimethylallyltransferase (2) | | Protein of unknown function DUF3143 [IPR021489] (2) | scaffold_9_mRNA_3650.1 | C_unshiu_00134_mRNA_44.1 | - |
| GF0024805 | 1 | 1 | 0 | Disease resistance family protein / LRR family protein, putative (1); LRR receptor-like kinase family protein (1) | protein binding [GO:0005515 molecular_function] (2) | Leucine-rich repeat [IPR001611] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Leucine-rich repeat, typical subtype [IPR003591] (1) | scaffold_9_mRNA_3645.1 | C_unshiu_00134_mRNA_51.1 | - |
| GF0024802 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_3622.1 | C_unshiu_00056_mRNA_50.1 | - |
| GF0024801 | 1 | 1 | 0 | Disease resistance family protein / LRR family protein, putative (2) | protein binding [GO:0005515 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (1) | Leucine-rich repeat domain, L domain-like [IPR032675] (2); Leucine-rich repeat [IPR001611] (2); Ribonuclease H-like domain [IPR012337] (1) | scaffold_9_mRNA_3620.1 | C_unshiu_00056_mRNA_48.1 | - |
| GF0024800 | 1 | 1 | 0 | Salutaridinol 7-O-acetyltransferase (1); Salutaridinol 7-O-acetyltransferase, putative (1) | transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (2) | Transferase [IPR003480] (2); Chloramphenicol acetyltransferase-like domain [IPR023213] (1) | scaffold_9_mRNA_3615.1 | C_unshiu_00056_mRNA_45.1 | - |
| GF0024799 | 1 | 1 | 0 | Beta-carotene hydroxylase 1 (2) | iron ion binding [GO:0005506 molecular_function] (2); oxidoreductase activity [GO:0016491 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2); fatty acid biosynthetic process [GO:0006633 biological_process] (1); lipid biosynthetic process [GO:0008610 biological_process] (1) | Fatty acid hydroxylase [IPR006694] (2) | scaffold_9_mRNA_3593.1 | C_unshiu_00056_mRNA_20.1 | - |
| GF0024798 | 1 | 1 | 0 | Putative membrane yjcL (2) | | Protein of unknown function DUF819 [IPR008537] (2) | scaffold_9_mRNA_3586.1 | C_unshiu_00056_mRNA_13.1 | - |
| GF0024797 | 1 | 1 | 0 | Putative membrane yjcL (2) | | Protein of unknown function DUF819 [IPR008537] (2) | scaffold_9_mRNA_3585.1 | C_unshiu_00056_mRNA_12.1 | - |
| GF0024795 | 1 | 1 | 0 | Hypothetical protein (1); Retinol dehydrogenase 14 (1) | | NAD(P)-binding domain [IPR016040] (2) | scaffold_9_mRNA_3568.1 | C_unshiu_01328_mRNA_5.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0024793 | 1 | 1 | 0 | Short-chain dehydrogenase TIC 32, chloroplastic (2) | oxidoreductase activity [GO:0016491 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1) | NAD(P)-binding domain [IPR016040] (2); Short-chain dehydrogenase/reductase SDR [IPR002347] (1); Short-chain dehydrogenase/reductase SDR [IPR002198] (1) | scaffold_9_mRNA_3554.1 | C_unshiu_01221_mRNA_6.1 | - |
| GF0024790 | 1 | 1 | 0 | Putative Prolyl 4-hydroxylase alpha subunit (2) | L-ascorbic acid binding [GO:0031418 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (2); iron ion binding [GO:0005506 molecular_function] (2); oxidoreductase activity [GO:0016491 molecular_function] (1) | ShKT domain [IPR003582] (2); Prolyl 4-hydroxylase, alpha subunit [IPR006620] (2); Oxoglutarate/iron-dependent dioxygenase [IPR005123] (1) | scaffold_9_mRNA_3541.1 | C_unshiu_01810_mRNA_6.1 | - |
| GF0024789 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_3530.1 | C_unshiu_00045_mRNA_91.1 | - |
| GF0024788 | 1 | 1 | 0 | KDEL motif-containing protein 1 (2) |  | Lipopolysaccharide-modifying protein [IPR006598] (2) | scaffold_9_mRNA_3515.1 | C_unshiu_00045_mRNA_74.1 | - |
| GF0024785 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_9_mRNA_3499.1 | C_unshiu_00045_mRNA_61.1 | - |
| GF0024784 | 1 | 1 | 0 | Serine/threonine-protein kinase PBS1 (1); G-type lectin S-receptor-like serine/threonine-protein kinase RKS1 (1) | ATP binding [GO:0005524 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2); protein kinase activity [GO:0004672 molecular_function] (2) | Protein kinase-like domain [IPR011009] (2); Protein kinase domain [IPR000719] (2); Protein kinase, ATP binding site [IPR017441] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1) | scaffold_9_mRNA_3481.1 | C_unshiu_00045_mRNA_47.1 | - |
| GF0024781 | 1 | 1 | 0 | Hypothetical protein (2) | oxidation-reduction process [GO:0055114 biological_process] (2); oxidoreductase activity [GO:0016491 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1) | NAD(P)-binding domain [IPR016040] (2); GroES-like [IPR011032] (2); Alcohol dehydrogenase, C-terminal [IPR013149] (2); Alcohol dehydrogenase, N-terminal [IPR013154] (2); Intein C-terminal splicing region [IPR030934] (1); Alcohol dehydrogenase superfamily, zinc-type [IPR002085] (1) | scaffold_9_mRNA_3449.1 | C_unshiu_00045_mRNA_16.1 | - |
| GF0024780 | 1 | 1 | 0 | Hypothetical protein (2) | transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (2); metabolic process [GO:0008152 biological_process] (2) | UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (2) | scaffold_9_mRNA_3445.1 | C_unshiu_00045_mRNA_12.1 | - |
| GF0024779 | 1 | 1 | 0 | Hydroxymethylglutaryl-CoA synthase (2) | catalytic activity [GO:0003824 molecular_function] (2); isoprenoid biosynthetic process [GO:0008299 biological_process] (2); metabolic process [GO:0008152 biological_process] (2); hydroxymethylglutaryl-CoA synthase activity [GO:0004421 molecular_function] (2) | Thiolase-like [IPR016039] (2); Hydroxymethylglutaryl-coenzyme A synthase, N-terminal [IPR013528] (2); Hydroxymethylglutaryl-CoA synthase, eukaryotic [IPR010122] (2); Hydroxymethylglutaryl-coenzyme A synthase, active site [IPR000590] (2); Hydroxymethylglutaryl-coenzyme A synthase C-terminal domain [IPR013746] (2) | scaffold_9_mRNA_3441.1 | C_unshiu_00045_mRNA_8.1 | - |
| GF0024778 | 1 | 1 | 0 | TCP family transcription factor (2) |  | Transcription factor, TCP [IPR005333] (2); Transcription factor TCP subgroup [IPR017887] (2) | scaffold_9_mRNA_3440.1 | C_unshiu_00045_mRNA_7.1 | - |
| GF0024777 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_3432.1 | C_unshiu_01380_mRNA_5.1 | - |
| GF0024776 | 1 | 1 | 0 | Gibberellin receptor GID1, putative (2) | hydrolase activity [GO:0016787 molecular_function] (2); metabolic process [GO:0008152 biological_process] (2) | Lipase, GDXG, putative histidine active site [IPR002168] (2); Alpha/Beta hydrolase fold [IPR029058] (2); Alpha/beta hydrolase fold-3 [IPR013094] (2) | scaffold_9_mRNA_3421.1 | C_unshiu_01050_mRNA_2.1 | - |
| GF0024775 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_3416.1 | C_unshiu_01050_mRNA_6.1 | - |
| GF0024773 | 1 | 1 | 0 | Cytochrome P450 704C1 (2) | oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2); iron ion binding [GO:0005506 molecular_function] (2); heme binding [GO:0020037 molecular_function] (2) | Cytochrome P450, E-class, group I [IPR002401] (2); Cytochrome P450 [IPR001128] (2) | scaffold_9_mRNA_3394.1 | C_unshiu_00182_mRNA_44.1 | - |
| GF0024770 | 1 | 1 | 0 | LRR receptor-like serine/threonine-protein kinase ERL1 (2) | ATP binding [GO:0005524 molecular_function] (2); protein kinase activity [GO:0004672 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2); protein binding [GO:0005515 molecular_function] (2) | Protein kinase domain [IPR000719] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Protein kinase-like domain [IPR011009] (2); Leucine-rich repeat, typical subtype [IPR003591] (2); Serine/threonine-protein kinase, active site [IPR008271] (2); Protein kinase, ATP binding site [IPR017441] (2); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (2); Leucine-rich repeat [IPR001611] (2); Leucine rich repeat 4 [IPR025875] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1) | scaffold_9_mRNA_3385.1 | C_unshiu_00182_mRNA_35.1 | - |
| GF0024767 | 1 | 1 | 0 | Hypothetical protein (2) |  | Protein kinase-like domain [IPR011009] (2) | scaffold_9_mRNA_333.1 | C_unshiu_00085_mRNA_25.1 | - |
| GF0024764 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_3319.1 | C_unshiu_00252_mRNA_22.1 | - |
| GF0024763 | 1 | 1 | 0 | Probable pectinesterase/pectinesterase inhibitor 60 (2) | pectinesterase activity [GO:0030599 molecular_function] (2); enzyme inhibitor activity [GO:0004857 molecular_function] (2); cell wall [GO:0005618 cellular_component] (2); cell wall modification [GO:0042545 biological_process] (2) | Pectinesterase, Asp active site [IPR033131] (2); Pectin lyase fold [IPR012334] (2); Pectinesterase inhibitor domain [IPR006501] (2); Pectinesterase, catalytic [IPR000070] (2); Pectin lyase fold/virulence factor [IPR011050] (2); Pectinesterase, Tyr active site [IPR018040] (2) | scaffold_9_mRNA_3312.1 | C_unshiu_00252_mRNA_29.1 | - |
| GF0024761 | 1 | 1 | 0 | Wall-associated receptor kinase 2 (2) | protein kinase activity [GO:0004672 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2); polysaccharide binding [GO:0030247 molecular_function] (2); ATP binding [GO:0005524 molecular_function] (2) | Serine/threonine-protein kinase, active site [IPR008271] (2); Wall-associated receptor kinase, galacturonan-binding domain [IPR025287] (2); Protein kinase-like domain [IPR011009] (2); Protein kinase domain [IPR000719] (2); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1) | scaffold_9_mRNA_3304.1 | C_unshiu_00252_mRNA_36.1 | - |
| GF0024760 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_3302.1 | C_unshiu_02743_mRNA_1.1 | - |
| GF0024759 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_3286.1 | C_unshiu_00741_mRNA_1.1 | - |
| GF0024758 | 1 | 1 | 0 | RING finger and CHY zinc finger domain-containing protein 1 isoform 1 (2) |  |  | scaffold_9_mRNA_328.1 | C_unshiu_00085_mRNA_29.1 | - |
| GF0024757 | 1 | 1 | 0 | Acidic endochitinase (2) | carbohydrate metabolic process [GO:0005975 biological_process] (2); hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (2) | Glycoside hydrolase family 18, catalytic domain [IPR001223] (2); Glycoside hydrolase, chitinase active site [IPR001579] (2); Glycoside hydrolase superfamily [IPR017853] (2); Glycoside hydrolase, catalytic domain [IPR013781] (1) | scaffold_9_mRNA_3267.1 | C_unshiu_00433_mRNA_15.1 | - |
| GF0024756 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_326.1 | C_unshiu_00085_mRNA_31.1 | - |
| GF0024755 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_3256.1 | C_unshiu_00433_mRNA_3.1 | - |
| GF0024754 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_3254.1 | C_unshiu_00161_mRNA_41.1 | - |
| GF0024753 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_3238.1 | C_unshiu_00095_mRNA_28.1 | - |
| GF0024752 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_3236.1 | C_unshiu_00095_mRNA_31.1 | - |
| GF0024748 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_3216.1 | C_unshiu_00095_mRNA_44.1 | - |
| GF0024747 | 1 | 1 | 0 | RNA-directed DNA polymerase (Reverse transcriptase) (2) |  | Reverse transcriptase domain [IPR000477] (2) | scaffold_9_mRNA_3205.1 | C_unshiu_00599_mRNA_20.1 | - |
| GF0024746 | 1 | 1 | 0 | Hexose carrier protein HEX6 (2) | integral component of membrane [GO:0016021 cellular_component] (2); substrate-specific transmembrane transporter activity [GO:0022891 molecular_function] (2); transmembrane transporter activity [GO:0022857 molecular_function] (2); membrane [GO:0016020 cellular_component] (2); transporter activity [GO:0005215 molecular_function] (2); transmembrane transport [GO:0055085 biological_process] (2) | Sugar transporter, conserved site [IPR005829] (2); Major facilitator superfamily domain [IPR020846] (2); Major facilitator, sugar transporter-like [IPR005828] (2); Sugar/inositol transporter [IPR003663] (2) | scaffold_9_mRNA_3203.1 | C_unshiu_00599_mRNA_18.1 | - |
| GF0024743 | 1 | 1 | 0 | DERLIN-1 isoform 1 (2) | serine-type endopeptidase activity [GO:0004252 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1) | Derlin [IPR007599] (2); Peptidase S54, rhomboid domain [IPR022764] (1) | scaffold_9_mRNA_3199.1 | C_unshiu_00599_mRNA_16.1 | - |
| GF0024742 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_3192.1 | C_unshiu_00599_mRNA_11.1 | - |
| GF0024741 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_3191.1 | C_unshiu_00599_mRNA_10.1 | - |
| GF0024739 | 1 | 1 | 0 | Ankyrin repeat family protein, putative (1); Ankyrin repeat protein (1) | protein binding [GO:0005515 molecular_function] (2) | Ankyrin repeat [IPR002110] (2); Ankyrin repeat-containing domain [IPR020683] (2) | scaffold_9_mRNA_3169.1 | C_unshiu_00060_mRNA_6.1 | - |
| GF0024738 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_3163.1 | C_unshiu_00060_mRNA_12.1 | - |
| GF0024737 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_3154.1 | C_unshiu_00060_mRNA_20.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0024736 | 1 | 1 | 0 | Hypothetical protein (2) | ATP binding [GO:0005524 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2); protein kinase activity [GO:0004672 molecular_function] (2) | Protein kinase domain [IPR000719] (2); Protein kinase-like domain [IPR011009] (2); Serine/threonine-protein kinase, active site [IPR008271] (2); PGG domain [IPR026961] (2) | scaffold_9_mRNA_3153.1 | C_unshiu_00060_mRNA_21.1 | - |
| GF0024735 | 1 | 1 | 0 | FAD-binding Berberine family protein (2) | flavin adenine dinucleotide binding [GO:0050660 molecular_function] (2); oxidoreductase activity [GO:0016491 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2); catalytic activity [GO:0003824 molecular_function] (2); oxidoreductase activity, acting on CH-OH group of donors [GO:0016614 molecular_function] (2) | Berberine/berberine-like [IPR012951] (2); FAD-binding, type 2, subdomain 1 [IPR016167] (2); CO dehydrogenase flavoprotein-like, FAD-binding, subdomain 2 [IPR016169] (2); FAD linked oxidase, N-terminal [IPR006094] (2); FAD-binding, type 2 [IPR016166] (2) | scaffold_9_mRNA_3148.1 | C_unshiu_00060_mRNA_26.1 | - |
| GF0024734 | 1 | 1 | 0 | Tetratricopeptide repeat-like superfamily protein (2) | zinc ion binding [GO:0008270 molecular_function] (2); protein binding [GO:0005515 molecular_function] (2) | DYW domain [IPR032867] (2); Ubiquinol-cytochrome c chaperone/UPF0174 [IPR021150] (2); Pentatricopeptide repeat [IPR002885] (2); Tetratricopeptide-like helical domain [IPR011990] (2) | scaffold_9_mRNA_3139.1 | C_unshiu_00577_mRNA_11.1 | - |
| GF0024733 | 1 | 1 | 0 | FAD-binding Berberine family protein (2) | catalytic activity [GO:0003824 molecular_function] (2); oxidoreductase activity, acting on CH-OH group of donors [GO:0016614 molecular_function] (2); flavin adenine dinucleotide binding [GO:0050660 molecular_function] (2); oxidoreductase activity [GO:0016491 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2) | FAD-binding, type 2, subdomain 1 [IPR016167] (2); CO dehydrogenase flavoprotein-like, FAD-binding, subdomain 2 [IPR016169] (2); FAD linked oxidase, N-terminal [IPR006094] (2); FAD-binding, type 2 [IPR016166] (2); Berberine/berberine-like [IPR012951] (1) | scaffold_9_mRNA_3135.1 | C_unshiu_00577_mRNA_7.1 | - |
| GF0024732 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_3133.1 | C_unshiu_00577_mRNA_5.1 | - |
| GF0024731 | 1 | 1 | 0 | Ankyrin repeat family protein (2) |  | PGG domain [IPR026961] (2); Ankyrin repeat-containing domain [IPR020683] (1) | scaffold_9_mRNA_3129.1 | C_unshiu_00577_mRNA_2.1 | - |
| GF0024730 | 1 | 1 | 0 | Ethylene responsive element binding factor, putative (2) | transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (2); regulation of transcription, DNA-templated [GO:0006355 biological_process] (2); DNA binding [GO:0003677 molecular_function] (2) | DNA-binding domain [IPR016177] (2); AP2/ERF domain [IPR001471] (2) | scaffold_9_mRNA_3126.1 | C_unshiu_02129_mRNA_1.1 | - |
| GF0024729 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_3124.1 | C_unshiu_01744_mRNA_1.1 | - |
| GF0024728 | 1 | 1 | 0 | Hypothetical protein (2) |  | Transposase, MuDR, plant [IPR004332] (2) | scaffold_9_mRNA_3119.1 | C_unshiu_00504_mRNA_19.1 | - |
| GF0024726 | 1 | 1 | 0 | Polynucleotidyl transferase, ribonuclease H-like superfamily protein (1); Putative RNA-directed DNA polymerase (1) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_9_mRNA_3112.1 | C_unshiu_00504_mRNA_11.1 | - |
| GF0024724 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_3109.1 | C_unshiu_00504_mRNA_7.1 | - |
| GF0024723 | 1 | 1 | 0 | Hypothetical protein (1); Polynucleotidyl transferase, ribonuclease H-like superfamily protein (1) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_9_mRNA_3106.1 | C_unshiu_00504_mRNA_5.1 | - |
| GF0024722 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_3100.1 | C_unshiu_01088_mRNA_3.1 | - |
| GF0024720 | 1 | 1 | 0 | Cyclin p4 (2) | protein kinase binding [GO:0019901 molecular_function] (2); regulation of cyclin-dependent protein serine/threonine kinase activity [GO:0000079 biological_process] (2) | Cyclin-like [IPR013763] (2); Cyclin PHO80-like [IPR013922] (2) | scaffold_9_mRNA_3093.1 | C_unshiu_01088_mRNA_9.1 | - |
| GF0024719 | 1 | 1 | 0 | YDG domain-containing protein At5g47150 (1); Hypothetical protein (1) | histone binding [GO:0042393 molecular_function] (2) | SRA-YDG [IPR003105] (2); PUA-like domain [IPR015947] (2); Reverse transcriptase zinc-binding domain [IPR026960] (1) | scaffold_9_mRNA_3090.1 | C_unshiu_01196_mRNA_3.1 | - |
| GF0024718 | 1 | 1 | 0 | Protein GIGAS CELL1 (2) | negative regulation of ubiquitin protein ligase activity [GO:1904667 biological_process] (1); nucleus [GO:0005634 cellular_component] (1); regulation of nuclear division [GO:0051783 biological_process] (1) | POLYCHOME/GIGAS CELL1 [IPR034590] (1) | scaffold_9_mRNA_3074.1 | C_unshiu_00115_mRNA_23.1 | - |
| GF0024715 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_3065.1 | C_unshiu_00115_mRNA_30.1 | - |
| GF0024713 | 1 | 1 | 0 | Hypothetical protein (2) | zinc ion binding [GO:0008270 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | Reverse transcriptase zinc-binding domain [IPR026960] (2); Ribonuclease H-like domain [IPR012337] (2); Zinc knuckle CX2CX4HX4C [IPR025836] (2); Zinc finger, CCHC-type [IPR001878] (2); Domain of unknown function DUF4283 [IPR025558] (1) | scaffold_9_mRNA_3045.1 | C_unshiu_01621_mRNA_4.1 | - |
| GF0024712 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_3037.1 | C_unshiu_00119_mRNA_5.1 | - |
| GF0024711 | 1 | 1 | 0 | Adenylosuccinate synthetase, chloroplastic (2) | GTP binding [GO:0005525 molecular_function] (2); adenylosuccinate synthase activity [GO:0004019 molecular_function] (2); purine nucleotide biosynthetic process [GO:0006164 biological_process] (2) | Adenylosuccinate synthetase [IPR001114] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); Adenylosuccinate synthase,  active site [IPR033128] (2); Adenylosuccinate synthase, GTP-binding site [IPR018220] (2) | scaffold_9_mRNA_3036.1 | C_unshiu_00119_mRNA_6.1 | - |
| GF0024710 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2); TB2/DP1/HVA22-related protein [IPR004345] (1) | scaffold_9_mRNA_3029.1 | C_unshiu_00119_mRNA_12.1 | - |
| GF0024707 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_2998.1 | C_unshiu_00119_mRNA_41.1 | - |
| GF0024706 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_2987.1 | C_unshiu_01689_mRNA_5.1 | - |
| GF0024705 | 1 | 1 | 0 | Hypothetical protein (2) |  | Domain of unknown function DUF4283 [IPR025558] (2); Zinc knuckle CX2CX4HX4C [IPR025836] (2) | scaffold_9_mRNA_2984.1 | C_unshiu_00751_mRNA_12.1 | - |
| GF0024704 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_2983.1 | C_unshiu_00751_mRNA_11.1 | - |
| GF0024702 | 1 | 1 | 0 | Hypothetical protein (2) |  | Viral movement protein [IPR028919] (2) | scaffold_9_mRNA_2939.1 | C_unshiu_01777_mRNA_4.1 | - |
| GF0024701 | 1 | 1 | 0 | Truncated RB (1); Hypothetical protein (1) | ADP binding [GO:0043531 molecular_function] (2); 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) | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); NB-ARC [IPR002182] (2); AP2/ERF domain [IPR001471] (1); DNA-binding domain [IPR016177] (1) | scaffold_9_mRNA_2931.1 | C_unshiu_01467_mRNA_2.1 | - |
| GF0024699 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_2912.1 | C_unshiu_00132_mRNA_6.1 | - |
| GF0024698 | 1 | 1 | 0 | LRR receptor-like kinase family protein (2) | protein binding [GO:0005515 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1) | Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (2); Leucine-rich repeat [IPR001611] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); Protein kinase-like domain [IPR011009] (1) | scaffold_9_mRNA_2903.1 | C_unshiu_00132_mRNA_9.1 | - |
| GF0024697 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_2902.1 | C_unshiu_00132_mRNA_10.1 | - |
| GF0024695 | 1 | 1 | 0 | Fragile histidine triad protein (2) | catalytic activity [GO:0003824 molecular_function] (2) | HIT-like domain [IPR011146] (2); Histidine triad (HIT) protein [IPR001310] (2); Histidine triad, conserved site [IPR019808] (2) | scaffold_9_mRNA_2891.1 | C_unshiu_02647_mRNA_1.1 | - |
| GF0024694 | 1 | 1 | 0 | Hypothetical protein (2) | protein kinase activity [GO:0004672 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2); ATP binding [GO:0005524 molecular_function] (2) | Protein kinase domain [IPR000719] (2); Protein kinase-like domain [IPR011009] (2) | scaffold_9_mRNA_2881.1 | C_unshiu_00132_mRNA_30.1 | - |
| GF0024693 | 1 | 1 | 0 | Hypothetical protein (2) | cysteine-type peptidase activity [GO:0008234 molecular_function] (2); proteolysis [GO:0006508 biological_process] (2) | Transposon, En/Spm-like [IPR004242] (2); Ulp1 protease family, C-terminal catalytic domain [IPR003653] (2) | scaffold_9_mRNA_2880.1 | C_unshiu_00132_mRNA_32.1 | - |
| GF0024692 | 1 | 1 | 0 | Hypothetical protein (2) | cation transmembrane transporter activity [GO:0008324 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1); cation transport [GO:0006812 biological_process] (1); transmembrane transport [GO:0055085 biological_process] (1) | Cation efflux protein transmembrane domain [IPR027469] (1); Cation efflux protein [IPR002524] (1) | scaffold_9_mRNA_2878.1 | C_unshiu_00132_mRNA_34.1 | - |
| GF0024691 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_2876.1 | C_unshiu_01177_mRNA_8.1 | - |
| GF0024690 | 1 | 1 | 0 | Hypothetical protein (2) | DNA binding [GO:0003677 molecular_function] (2); protein dimerization activity [GO:0046983 molecular_function] (2) | Transcription factor, MADS-box [IPR002100] (2) | scaffold_9_mRNA_2872.1 | C_unshiu_01156_mRNA_10.1 | - |
| GF0024689 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_2865.1 | C_unshiu_00879_mRNA_4.1 | - |
| GF0024688 | 1 | 1 | 0 | MADS-box transcription factor family protein (2) | DNA binding [GO:0003677 molecular_function] (2); protein dimerization activity [GO:0046983 molecular_function] (2) | Transcription factor, MADS-box [IPR002100] (2) | scaffold_9_mRNA_2864.1 | C_unshiu_00879_mRNA_5.1 | - |
| GF0024687 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_2859.1 | C_unshiu_01550_mRNA_2.1 | - |
| GF0024686 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_2857.1 | C_unshiu_01550_mRNA_4.1 | - |
| GF0024685 | 1 | 1 | 0 | Hypothetical protein (2) |  | Transposase-associated domain [IPR029480] (2) | scaffold_9_mRNA_2840.1 | C_unshiu_01096_mRNA_7.1 | - |
| GF0024681 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_2820.1 | C_unshiu_00451_mRNA_3.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0024680 | 1 | 1 | 0 | MADS-box transcription factor family protein (1); Hypothetical protein (1) | protein dimerization activity [GO:0046983 molecular_function] (2); DNA binding [GO:0003677 molecular_function] (2) | Transcription factor, MADS-box [IPR002100] (2) | scaffold_9_mRNA_2819.1 | C_unshiu_00829_mRNA_1.1 | - |
| GF0024679 | 1 | 1 | 0 | Hypothetical protein (2) | protein phosphorylation [GO:0006468 biological_process] (2); protein kinase activity [GO:0004672 molecular_function] (2); ATP binding [GO:0005524 molecular_function] (2) | Protein kinase-like domain [IPR011009] (2); Protein kinase domain [IPR000719] (2); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1) | scaffold_9_mRNA_2817.1 | C_unshiu_00222_mRNA_25.1 | - |
| GF0024678 | 1 | 1 | 0 | AP2 type transcription factor (2) | DNA binding [GO:0003677 molecular_function] (2); regulation of transcription, DNA-templated [GO:0006355 biological_process] (2); transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (2); multicellular organismal development [GO:0007275 biological_process] (1); multicellular organism development [GO:0007275 biological_process] (1) | DNA-binding domain [IPR016177] (2); AP2-like ethylene-responsive transcription factor [IPR031112] (2); AP2/ERF domain [IPR001471] (2) | scaffold_9_mRNA_2804.1 | C_unshiu_00222_mRNA_19.1 | - |
| GF0024677 | 1 | 1 | 0 | Hypothetical protein (2) | ATP binding [GO:0005524 molecular_function] (2); transporter activity [GO:0005215 molecular_function] (2); transport [GO:0006810 biological_process] (2); ATPase activity [GO:0016887 molecular_function] (2); integral component of membrane [GO:0016021 cellular_component] (2) | AAA+ ATPase domain [IPR003593] (2); ABC transporter A, ABCA [IPR026082] (2); ABC transporter-like [IPR003439] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); ABC transporter, conserved site [IPR017871] (2) | scaffold_9_mRNA_2801.2 | C_unshiu_00222_mRNA_15.2 | - |
| GF0024676 | 1 | 1 | 0 | Hypothetical protein (2) |  | Gag-polypeptide of LTR copia-type [IPR029472] (1) | scaffold_9_mRNA_2800.1 | C_unshiu_00222_mRNA_14.1 | - |
| GF0024675 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_2793.1 | C_unshiu_00222_mRNA_7.1 | - |
| GF0024674 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_2780.1 | C_unshiu_01023_mRNA_2.1 | - |
| GF0024673 | 1 | 1 | 0 | Glycoprotein family protein (2) | mitochondrial matrix [GO:0005759 cellular_component] (2) | Mitochondrial glycoprotein [IPR003428] (2) | scaffold_9_mRNA_2772.2 | C_unshiu_00148_mRNA_17.2 | - |
| GF0024672 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_9_mRNA_2771.1 | C_unshiu_02385_mRNA_2.1 | - |
| GF0024671 | 1 | 1 | 0 | Plasma membrane-type calcium ATPase (1); Hypothetical protein (1) | calmodulin binding [GO:0005516 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1) | P-type ATPase, transmembrane domain [IPR023298] (2); Cation-transporting P-type ATPase, C-terminal [IPR006068] (2); P-type ATPase [IPR001757] (1); Probable transposase, Ptta/En/Spm, plant [IPR004252] (1); Calcium-transporting P-type ATPase, N-terminal autoinhibitory domain [IPR024750] (1); HAD-like domain [IPR023214] (1) | scaffold_9_mRNA_2767.1 | C_unshiu_02385_mRNA_1.1 | - |
| GF0024669 | 1 | 1 | 0 | Hypothetical protein (2) |  | Retroviral aspartyl protease [IPR013242] (2); Aspartic peptidase domain [IPR021109] (2) | scaffold_9_mRNA_2757.1 | C_unshiu_00645_mRNA_8.1 | - |
| GF0024668 | 1 | 1 | 0 | Hypothetical protein (2) |  | Domain of unknown function DUF4216 [IPR025312] (2); Probable transposase, Ptta/En/Spm, plant [IPR004252] (2); Domain of unknown function DUF4218 [IPR025452] (1); LOG family [IPR031100] (1); Transposase-associated domain [IPR029480] (1) | scaffold_9_mRNA_2752.1 | C_unshiu_02971_mRNA_1.1 | - |
| GF0024666 | 1 | 1 | 0 | Hypothetical protein (2) |  | Endonuclease/exonuclease/phosphatase [IPR005135] (2) | scaffold_9_mRNA_2738.1 | C_unshiu_00295_mRNA_15.1 | - |
| GF0024665 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_2736.1 | C_unshiu_00295_mRNA_13.1 | - |
| GF0024664 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_2735.1 | C_unshiu_00295_mRNA_12.1 | - |
| GF0024663 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_2734.1 | C_unshiu_00295_mRNA_11.1 | - |
| GF0024662 | 1 | 1 | 0 | Hypothetical protein (2) |  | Cysteine-rich transmembrane CYSTM domain [IPR028144] (1) | scaffold_9_mRNA_2731.1 | C_unshiu_00295_mRNA_9.1 | - |
| GF0024661 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_2730.1 | C_unshiu_00295_mRNA_8.1 | - |
| GF0024660 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_273.1 | C_unshiu_00036_mRNA_16.1 | - |
| GF0024659 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2); protein dimerization activity [GO:0046983 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2); HAT, C-terminal dimerisation domain [IPR008906] (2) | scaffold_9_mRNA_2727.1 | C_unshiu_00295_mRNA_5.1 | - |
| GF0024658 | 1 | 1 | 0 | Ribonuclease H protein, putative (1); Hypothetical protein (1) |  | Reverse transcriptase zinc-binding domain [IPR026960] (2); Reverse transcriptase domain [IPR000477] (1); Chromo domain-like [IPR016197] (1) | scaffold_9_mRNA_2723.1 | C_unshiu_00295_mRNA_2.1 | - |
| GF0024657 | 1 | 1 | 0 | Hypothetical protein (2) |  | Domain of unknown function DUF4283 [IPR025558] (1) | scaffold_9_mRNA_2721.1 | C_unshiu_00295_mRNA_1.1 | - |
| GF0024656 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_2715.1 | C_unshiu_00331_mRNA_15.1 | - |
| GF0024655 | 1 | 1 | 0 | Putative COX1/OXI3 intron 2 protein (2) | metabolic process [GO:0008152 biological_process] (2); catalytic activity [GO:0003824 molecular_function] (2); mRNA processing [GO:0006397 biological_process] (2) | Domain X [IPR024937] (2); ClpP/crotonase-like domain [IPR029045] (2); Crotonase superfamily [IPR001753] (2); Reverse transcriptase domain [IPR000477] (2) | scaffold_9_mRNA_2714.1 | C_unshiu_00331_mRNA_16.1 | - |
| GF0024654 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_2711.1 | C_unshiu_00391_mRNA_20.1 | - |
| GF0024653 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2); protein dimerization activity [GO:0046983 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2); HAT, C-terminal dimerisation domain [IPR008906] (2) | scaffold_9_mRNA_2705.1 | C_unshiu_00391_mRNA_17.1 | - |
| GF0024652 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_2703.1 | C_unshiu_00391_mRNA_15.1 | - |
| GF0024651 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_2702.1 | C_unshiu_00391_mRNA_14.1 | - |
| GF0024650 | 1 | 1 | 0 | Hypothetical protein (2) |  | Endonuclease/exonuclease/phosphatase [IPR005135] (2) | scaffold_9_mRNA_2701.1 | C_unshiu_00391_mRNA_13.1 | - |
| GF0024649 | 1 | 1 | 0 | UDP-glucuronic acid decarboxylase 1 (2) |  | NAD(P)-binding domain [IPR016040] (2) | scaffold_9_mRNA_270.1 | C_unshiu_00036_mRNA_19.1 | - |
| GF0024648 | 1 | 1 | 0 | Xyloglucan galactosyltransferase KATAMARI1 (1); Hypothetical protein (1) |  | Exostosin-like [IPR004263] (2) | scaffold_9_mRNA_2698.1 | C_unshiu_00391_mRNA_9.1 | - |
| GF0024647 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_2691.1 | C_unshiu_00391_mRNA_5.1 | - |
| GF0024646 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_2684.1 | C_unshiu_01282_mRNA_9.1 | - |
| GF0024645 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_2683.1 | C_unshiu_01282_mRNA_8.1 | - |
| GF0024644 | 1 | 1 | 0 | Phylloplanin (1); Hypothetical protein (1) |  |  | scaffold_9_mRNA_268.1 | C_unshiu_00036_mRNA_23.1 | - |
| GF0024643 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_2661.1 | C_unshiu_00093_mRNA_26.1 | - |
| GF0024642 | 1 | 1 | 0 | Hypothetical protein (2) |  | Viral movement protein [IPR028919] (2) | scaffold_9_mRNA_2648.1 | C_unshiu_00280_mRNA_12.1 | - |
| GF0024641 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_2640.1 | C_unshiu_00444_mRNA_6.1 | - |
| GF0024639 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_2623.1 | C_unshiu_01247_mRNA_10.1 | - |
| GF0024638 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_2620.1 | C_unshiu_01247_mRNA_8.1 | - |
| GF0024637 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_2618.1 | C_unshiu_01247_mRNA_6.1 | - |
| GF0024635 | 1 | 1 | 0 | Hypothetical protein (2) |  | Domain of unknown function DUF4283 [IPR025558] (1) | scaffold_9_mRNA_2601.1 | C_unshiu_00454_mRNA_10.1 | - |
| GF0024634 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_2595.1 | C_unshiu_00046_mRNA_3.1 | - |
| GF0024633 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_2581.1 | C_unshiu_00160_mRNA_41.1 | - |
| GF0024632 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_2580.1 | C_unshiu_00160_mRNA_40.1 | - |
| GF0024631 | 1 | 1 | 0 | Beta 1,3 glucanase (2) | carbohydrate metabolic process [GO:0005975 biological_process] (2); hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (2) | Glycoside hydrolase superfamily [IPR017853] (2); Glycoside hydrolase family 17 [IPR000490] (2); Glycoside hydrolase, catalytic domain [IPR013781] (1) | scaffold_9_mRNA_2578.1 | C_unshiu_00160_mRNA_38.1 | - |
| GF0024630 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_2567.1 | C_unshiu_00160_mRNA_27.1 | - |
| GF0024629 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_2566.1 | C_unshiu_00160_mRNA_26.1 | - |
| GF0024628 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_2554.1 | C_unshiu_01758_mRNA_8.1 | - |
| GF0024625 | 1 | 1 | 0 | Hypothetical protein (2) |  | Protein kinase-like domain [IPR011009] (2) | scaffold_9_mRNA_2539.1 | C_unshiu_00064_mRNA_66.1 | - |
| GF0024624 | 1 | 1 | 0 | Epoxide hydrolase (2) | catalytic activity [GO:0003824 molecular_function] (2) | Alpha/Beta hydrolase fold [IPR029058] (2); Alpha/beta hydrolase fold-1 [IPR000073] (2); Epoxide hydrolase-like [IPR000639] (2) | scaffold_9_mRNA_253.1 | C_unshiu_00614_mRNA_23.1 | - |
| GF0024623 | 1 | 1 | 0 | Protein FAR1-RELATED SEQUENCE 6 (2) | regulation of transcription, DNA-templated [GO:0006355 biological_process] (2); zinc ion binding [GO:0008270 molecular_function] (2) | FAR1 DNA binding domain [IPR004330] (2); FHY3/FAR1 family [IPR031052] (2); Zinc finger, SWIM-type [IPR007527] (2); MULE transposase domain [IPR018289] (2); Zinc finger, PMZ-type [IPR006564] (2) | scaffold_9_mRNA_2520.1 | C_unshiu_00345_mRNA_15.1 | - |
| GF0024622 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_2513.1 | C_unshiu_02090_mRNA_2.1 | - |
| GF0024621 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_9_mRNA_2505.1 | C_unshiu_00082_mRNA_26.1 | - |
| GF0024620 | 1 | 1 | 0 | LRR receptor-like kinase family protein (2) | protein binding [GO:0005515 molecular_function] (2) | Leucine-rich repeat [IPR001611] (2); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Leucine-rich repeat, typical subtype [IPR003591] (2) | scaffold_9_mRNA_2502.1 | C_unshiu_00148_mRNA_2.1 | - |
| GF0024619 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_9_mRNA_2500.1 | C_unshiu_00148_mRNA_6.1 | - |
| GF0024618 | 1 | 1 | 0 | Epoxide hydrolase 2 (1); Epoxide hydrolase (1) | catalytic activity [GO:0003824 molecular_function] (2) | Epoxide hydrolase-like [IPR000639] (2); Alpha/beta hydrolase fold-1 [IPR000073] (2); Alpha/Beta hydrolase fold [IPR029058] (2) | scaffold_9_mRNA_250.1 | C_unshiu_00846_mRNA_5.1 | - |
| GF0024615 | 1 | 1 | 0 | Non-LTR retroelement reverse transcriptase-like (1); Hypothetical protein (1) | nucleic acid binding [GO:0003676 molecular_function] (2); DNA binding [GO:0003677 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1) | Ribonuclease H-like domain [IPR012337] (2); Reverse transcriptase zinc-binding domain [IPR026960] (2); Achaete-scute transcription factor-related [IPR015660] (1); Myc-type, basic helix-loop-helix (bHLH) domain [IPR011598] (1); TB2/DP1/HVA22-related protein [IPR004345] (1) | scaffold_9_mRNA_2468.1 | C_unshiu_00011_mRNA_86.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0024614 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2466.1 | C_unshiu_00011_mRNA_85.1 | - |
| GF0024613 | 1 | 1 | 0 | Cytokinin riboside 5'-monophosphate phosphoribohydrolase (2) | | LOG family [IPR031100] (2) | scaffold_9_mRNA_2464.1 | C_unshiu_00011_mRNA_83.1 | - |
| GF0024612 | 1 | 1 | 0 | Hypothetical protein (2) | | Aspartic peptidase domain [IPR021109] (1) | scaffold_9_mRNA_2463.1 | C_unshiu_00011_mRNA_82.1 | - |
| GF0024611 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2457.1 | C_unshiu_00011_mRNA_75.1 | - |
| GF0024610 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2455.1 | C_unshiu_00011_mRNA_72.1 | - |
| GF0024609 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2448.1 | C_unshiu_00170_mRNA_42.1 | - |
| GF0024608 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2444.1 | C_unshiu_00170_mRNA_37.1 | - |
| GF0024607 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2442.1 | C_unshiu_00170_mRNA_35.1 | - |
| GF0024606 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2441.1 | C_unshiu_00170_mRNA_34.1 | - |
| GF0024604 | 1 | 1 | 0 | Hypothetical protein (2) | methyltransferase activity [GO:0008168 molecular_function] (1) | SAM dependent carboxyl methyltransferase [IPR005299] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1) | scaffold_9_mRNA_2417.1 | C_unshiu_00486_mRNA_12.1 | - |
| GF0024603 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2407.1 | C_unshiu_00336_mRNA_18.1 | - |
| GF0024602 | 1 | 1 | 0 | Zinc knuckle family protein (2) | zinc ion binding [GO:0008270 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | Zinc finger, CCHC-type [IPR001878] (2) | scaffold_9_mRNA_2404.1 | C_unshiu_00336_mRNA_14.1 | - |
| GF0024601 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2402.1 | C_unshiu_00336_mRNA_10.1 | - |
| GF0024600 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2400.1 | C_unshiu_00336_mRNA_8.1 | - |
| GF0024599 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2397.1 | C_unshiu_00336_mRNA_6.1 | - |
| GF0024597 | 1 | 1 | 0 | Hemopexin (1); Hypothetical protein (1) | | Endonuclease/exonuclease/phosphatase [IPR005135] (2) | scaffold_9_mRNA_2393.1 | C_unshiu_00336_mRNA_4.1 | - |
| GF0024596 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2382.1 | C_unshiu_00156_mRNA_32.1 | - |
| GF0024595 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2381.1 | C_unshiu_00156_mRNA_33.1 | - |
| GF0024594 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2379.1 | C_unshiu_00156_mRNA_37.1 | - |
| GF0024593 | 1 | 1 | 0 | Hypothetical protein (2) | | LOG family [IPR031100] (1) | scaffold_9_mRNA_2374.1 | C_unshiu_00156_mRNA_41.1 | - |
| GF0024592 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_237.1 | C_unshiu_00614_mRNA_11.1 | - |
| GF0024591 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2369.1 | C_unshiu_00529_mRNA_20.1 | - |
| GF0024590 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2366.1 | C_unshiu_00529_mRNA_23.1 | - |
| GF0024588 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2362.1 | C_unshiu_01129_mRNA_11.1 | - |
| GF0024587 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2361.1 | C_unshiu_01129_mRNA_12.1 | - |
| GF0024586 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2360.1 | C_unshiu_01129_mRNA_13.1 | - |
| GF0024585 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_236.1 | C_unshiu_00614_mRNA_10.1 | - |
| GF0024584 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2355.1 | C_unshiu_00118_mRNA_68.1 | - |
| GF0024583 | 1 | 1 | 0 | Hypothetical protein (2) | proteolysis [GO:0006508 biological_process] (2); nucleic acid binding [GO:0003676 molecular_function] (2); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (2); zinc ion binding [GO:0008270 molecular_function] (2) | Zinc finger, CCHC-type [IPR001878] (2); Aspartic peptidase, active site [IPR001969] (2) | scaffold_9_mRNA_2353.1 | C_unshiu_00118_mRNA_66.1 | - |
| GF0024582 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2351.1 | C_unshiu_00118_mRNA_65.1 | - |
| GF0024581 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2348.1 | C_unshiu_00118_mRNA_60.1 | - |
| GF0024580 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2347.1 | C_unshiu_00118_mRNA_58.1 | - |
| GF0024579 | 1 | 1 | 0 | Hypothetical protein (2) | | Viral movement protein [IPR028919] (2) | scaffold_9_mRNA_2346.1 | C_unshiu_00118_mRNA_57.1 | - |
| GF0024578 | 1 | 1 | 0 | Hypothetical protein (2) | zinc ion binding [GO:0008270 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | Zinc finger, CCHC-type [IPR001878] (2) | scaffold_9_mRNA_2343.1 | C_unshiu_00118_mRNA_55.1 | - |
| GF0024577 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2341.1 | C_unshiu_00118_mRNA_54.1 | - |
| GF0024575 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2); zinc ion binding [GO:0008270 molecular_function] (2) | Zinc finger, CCHC-type [IPR001878] (2) | scaffold_9_mRNA_2337.1 | C_unshiu_00118_mRNA_52.1 | - |
| GF0024574 | 1 | 1 | 0 | Hypothetical protein (2) | spindle [GO:0005819 cellular_component] (1); microtubule [GO:0005874 cellular_component] (1); regulation of mitotic spindle organization [GO:0060236 biological_process] (1); activation of protein kinase activity [GO:0032147 biological_process] (1) | TPX2, C-terminal [IPR027329] (1); TPX2 [IPR009675] (1) | scaffold_9_mRNA_2331.1 | C_unshiu_00118_mRNA_45.1 | - |
| GF0024573 | 1 | 1 | 0 | Hypothetical protein (2) | | Viral movement protein [IPR028919] (2) | scaffold_9_mRNA_2329.1 | C_unshiu_00118_mRNA_42.1 | - |
| GF0024572 | 1 | 1 | 0 | STELAR K+ outward rectifier isoform 2 (1); Potassium channel SKOR (1) | membrane [GO:0016020 cellular_component] (2); protein binding [GO:0005515 molecular_function] (2); ion channel activity [GO:0005216 molecular_function] (2); transmembrane transport [GO:0055085 biological_process] (2); potassium ion transport [GO:0006813 biological_process] (2); voltage-gated potassium channel activity [GO:0005249 molecular_function] (2); ion transport [GO:0006811 biological_process] (2) | Potassium channel, voltage-dependent, EAG/ELK/ERG [IPR003938] (2); Ankyrin repeat [IPR002110] (2); Cyclic nucleotide-binding-like [IPR018490] (2); Ion transport domain [IPR005821] (2); Ankyrin repeat-containing domain [IPR020683] (2); Cyclic nucleotide-binding domain [IPR000595] (2); RmlC-like jelly roll fold [IPR014710] (1) | scaffold_9_mRNA_2321.1 | C_unshiu_00118_mRNA_33.1 | - |
| GF0024571 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2318.1 | C_unshiu_00118_mRNA_31.1 | - |
| GF0024570 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2314.1 | C_unshiu_00118_mRNA_27.1 | - |
| GF0024569 | 1 | 1 | 0 | Hypothetical protein (2) | | Viral movement protein [IPR028919] (2) | scaffold_9_mRNA_2313.1 | C_unshiu_00118_mRNA_26.1 | - |
| GF0024568 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2312.1 | C_unshiu_00118_mRNA_25.1 | - |
| GF0024567 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2311.1 | C_unshiu_00118_mRNA_24.1 | - |
| GF0024566 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2310.1 | C_unshiu_00118_mRNA_23.1 | - |
| GF0024565 | 1 | 1 | 0 | Hypothetical protein (2) | | Viral movement protein [IPR028919] (2) | scaffold_9_mRNA_2309.1 | C_unshiu_00118_mRNA_22.1 | - |
| GF0024564 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2308.1 | C_unshiu_00118_mRNA_21.1 | - |
| GF0024563 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2307.1 | C_unshiu_00118_mRNA_20.1 | - |
| GF0024562 | 1 | 1 | 0 | Hypothetical protein (2) | | Viral movement protein [IPR028919] (2) | scaffold_9_mRNA_2306.1 | C_unshiu_00118_mRNA_19.1 | - |
| GF0024561 | 1 | 1 | 0 | Hypothetical protein (2) | | Viral movement protein [IPR028919] (2) | scaffold_9_mRNA_2302.1 | C_unshiu_00118_mRNA_15.1 | - |
| GF0024560 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2296.1 | C_unshiu_00470_mRNA_6.1 | - |
| GF0024559 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2295.1 | C_unshiu_00118_mRNA_4.1 | - |
| GF0024558 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2294.1 | C_unshiu_00118_mRNA_3.1 | - |
| GF0024557 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2291.1 | C_unshiu_01462_mRNA_3.1 | - |
| GF0024556 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2287.1 | C_unshiu_01462_mRNA_6.1 | - |
| GF0024555 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2286.1 | C_unshiu_01462_mRNA_7.1 | - |
| GF0024554 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2285.1 | C_unshiu_01462_mRNA_8.1 | - |
| GF0024553 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2276.1 | C_unshiu_00138_mRNA_19.1 | - |
| GF0024552 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2274.1 | C_unshiu_00138_mRNA_24.1 | - |
| GF0024551 | 1 | 1 | 0 | Hypothetical protein (2) | | Transposase, MuDR, plant [IPR004332] (2) | scaffold_9_mRNA_2273.1 | C_unshiu_00138_mRNA_25.1 | - |
| GF0024550 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2272.1 | C_unshiu_00138_mRNA_26.1 | - |
| GF0024549 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_227.1 | C_unshiu_00614_mRNA_6.1 | - |
| GF0024548 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2266.1 | C_unshiu_00138_mRNA_30.1 | - |
| GF0024547 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2264.1 | C_unshiu_00871_mRNA_27.1 | - |
| GF0024546 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2252.1 | C_unshiu_00138_mRNA_40.1 | - |
| GF0024545 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2219.1 | C_unshiu_01188_mRNA_6.1 | - |
| GF0024544 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2218.1 | C_unshiu_01188_mRNA_4.1 | - |
| GF0024543 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2213.1 | C_unshiu_01618_mRNA_1.1 | - |
| GF0024541 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2205.1 | C_unshiu_00556_mRNA_16.1 | - |
| GF0024540 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2190.1 | C_unshiu_00241_mRNA_15.1 | - |
| GF0024539 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2182.1 | C_unshiu_01204_mRNA_7.1 | - |
| GF0024538 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2); zinc ion binding [GO:0008270 molecular_function] (2) | Zinc finger, CCHC-type [IPR001878] (2) | scaffold_9_mRNA_2179.1 | C_unshiu_00921_mRNA_5.1 | - |
| GF0024537 | 1 | 1 | 0 | Nucleic acid-binding proteins superfamily isoform 1 (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | S1 domain [IPR003029] (2); Nucleic acid-binding, OB-fold [IPR012340] (2); RNA-binding domain, S1 [IPR022967] (2) | scaffold_9_mRNA_2178.1 | C_unshiu_00921_mRNA_6.1 | - |
| GF0024536 | 1 | 1 | 0 | Hypothetical protein (2) | | Reverse transcriptase zinc-binding domain [IPR026960] (1) | scaffold_9_mRNA_2176.1 | C_unshiu_00098_mRNA_2.1 | - |
| GF0024535 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2173.1 | C_unshiu_00380_mRNA_21.1 | - |
| GF0024532 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2166.1 | C_unshiu_00380_mRNA_13.1 | - |
| GF0024531 | 1 | 1 | 0 | Hypothetical protein (2) | zinc ion binding [GO:0008270 molecular_function] (2) | Zinc finger, PMZ-type [IPR006564] (2); Transposase, MuDR, plant [IPR004332] (2); Zinc finger, SWIM-type [IPR007527] (2) | scaffold_9_mRNA_2162.1 | C_unshiu_00107_mRNA_35.1 | - |
| GF0024530 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2161.1 | C_unshiu_00036_mRNA_65.1 | - |
| GF0024529 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2158.1 | C_unshiu_00107_mRNA_37.1 | - |
| GF0024528 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2157.1 | C_unshiu_00107_mRNA_38.1 | - |
| GF0024527 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2154.1 | C_unshiu_00107_mRNA_41.1 | - |
| GF0024526 | 1 | 1 | 0 | Xyloglucan endotransglucosylase/hydrolase protein 15 (2) | apoplast [GO:0048046 cellular_component] (2); cellular glucan metabolic process [GO:0006073 biological_process] (2); xyloglucan metabolic process [GO:0010411 biological_process] (2); cell wall biogenesis [GO:0042546 biological_process] (2); xyloglucan:xyloglucosyl transferase activity [GO:0016762 molecular_function] (2); hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (2); cell wall [GO:0005618 cellular_component] (2); carbohydrate metabolic process [GO:0005975 biological_process] (2) | Glycoside hydrolase, family 16, active site [IPR008263] (2); Concanavalin A-like lectin/glucanase domain [IPR013320] (2); Xyloglucan endotransglucosylase/hydrolase [IPR016455] (2); Glycoside hydrolase family 16 [IPR000757] (2); Xyloglucan endo-transglycosylase, C-terminal [IPR010713] (2) | scaffold_9_mRNA_2147.1 | C_unshiu_00107_mRNA_48.1 | - |
| GF0024523 | 1 | 1 | 0 | Pentatricopeptide repeat (PPR) superfamily protein (1); Pentatricopeptide repeat-containing family protein (1) | zinc ion binding [GO:0008270 molecular_function] (2); protein binding [GO:0005515 molecular_function] (2) | DYW domain [IPR032867] (2); Tetratricopeptide-like helical domain [IPR011990] (2); Pentatricopeptide repeat [IPR002885] (2) | scaffold_9_mRNA_2127.1 | C_unshiu_00122_mRNA_15.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0024522 | 1 | 1 | 0 | Glycoside hydrolase family 28 protein (2) | carbohydrate metabolic process [GO:0005975 biological_process] (2); polygalacturonase activity [GO:0004650 molecular_function] (2) | Protein of unknown function DUF4602 [IPR027973] (2); Pectin lyase fold/virulence factor [IPR011050] (2); Pectin lyase fold [IPR012334] (2); Glycoside hydrolase, family 28 [IPR000743] (2); Parallel beta-helix repeat [IPR006626] (2) | scaffold_9_mRNA_212.2 | C_unshiu_00355_mRNA_23.2 | - |
| GF0024521 | 1 | 1 | 0 | Pol polyprotein (1); Copia ltr rider (1) | | Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (2) | scaffold_9_mRNA_2115.1 | C_unshiu_00122_mRNA_30.1 | - |
| GF0024520 | 1 | 1 | 0 | Hypothetical protein (2) | | GAG-pre-integrase domain [IPR025724] (2) | scaffold_9_mRNA_2114.1 | C_unshiu_00122_mRNA_31.1 | - |
| GF0024519 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2108.1 | C_unshiu_00122_mRNA_37.1 | - |
| GF0024518 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2106.1 | C_unshiu_00122_mRNA_39.1 | - |
| GF0024517 | 1 | 1 | 0 | Glycine hydroxymethyltransferase (2) | L-serine metabolic process [GO:0006563 biological_process] (2); glycine metabolic process [GO:0006544 biological_process] (2); pyridoxal phosphate binding [GO:0030170 molecular_function] (2); transferase activity [GO:0016740 molecular_function] (2); catalytic activity [GO:0003824 molecular_function] (2); glycine hydroxymethyltransferase activity [GO:0004372 molecular_function] (2) | Pyridoxal phosphate-dependent transferase, major region, subdomain 1 [IPR015421] (2); Serine hydroxymethyltransferase, pyridoxal phosphate binding site [IPR019798] (2); Pyridoxal phosphate-dependent transferase [IPR015424] (2); Serine hydroxymethyltransferase [IPR001085] (2); Pyridoxal phosphate-dependent transferase, subdomain 2 [IPR015422] (1); Pyridoxal phosphate-dependent transferase, major region, subdomain 2 [IPR015422] (1) | scaffold_9_mRNA_2103.1 | C_unshiu_00122_mRNA_42.1 | - |
| GF0024516 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2101.1 | C_unshiu_00122_mRNA_44.1 | - |
| GF0024515 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2100.1 | C_unshiu_00122_mRNA_45.1 | - |
| GF0024513 | 1 | 1 | 0 | Hypothetical protein (2) | 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_2093.1 | C_unshiu_00781_mRNA_17.1 | - |
| GF0024512 | 1 | 1 | 0 | Hypothetical protein (2) | metal ion binding [GO:0046872 molecular_function] (2); metal ion transport [GO:0030001 biological_process] (2) | Heavy metal-associated domain, HMA [IPR006121] (2) | scaffold_9_mRNA_209.1 | C_unshiu_00355_mRNA_20.1 | - |
| GF0024511 | 1 | 1 | 0 | PR10 protein (2) | defense response [GO:0006952 biological_process] (2); response to biotic stimulus [GO:0009607 biological_process] (2) | Bet v I type allergen [IPR024949] (2); Bet v I/Major latex protein [IPR000916] (2); START-like domain [IPR023393] (2); Major latex protein domain [IPR024948] (1) | scaffold_9_mRNA_208.1 | C_unshiu_00355_mRNA_19.1 | - |
| GF0024510 | 1 | 1 | 0 | Putative retroelement pol polyprotein (1); Hypothetical protein (1) | | Gag-polypeptide of LTR copia-type [IPR029472] (2) | scaffold_9_mRNA_2079.1 | C_unshiu_01797_mRNA_1.1 | - |
| GF0024509 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2075.1 | C_unshiu_00268_mRNA_21.1 | - |
| GF0024508 | 1 | 1 | 0 | Hypothetical protein (2) | | Aspartic peptidase domain [IPR021109] (1) | scaffold_9_mRNA_2073.1 | C_unshiu_00268_mRNA_20.1 | - |
| GF0024507 | 1 | 1 | 0 | Bet v 1 allergen (1); Hypothetical protein (1) | response to biotic stimulus [GO:0009607 biological_process] (1); defense response [GO:0006952 biological_process] (1) | START-like domain [IPR023393] (2); Bet v I type allergen [IPR024949] (2); Bet v I/Major latex protein [IPR000916] (1) | scaffold_9_mRNA_207.1 | C_unshiu_00355_mRNA_18.1 | - |
| GF0024506 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2065.1 | C_unshiu_00268_mRNA_10.1 | - |
| GF0024505 | 1 | 1 | 0 | 6a-hydroxymaackiain methyltransferase family protein (2) | O-methyltransferase activity [GO:0008171 molecular_function] (2); protein dimerization activity [GO:0046983 molecular_function] (2); methyltransferase activity [GO:0008168 molecular_function] (2) | S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (2); Plant methyltransferase dimerisation [IPR012967] (2); O-methyltransferase COMT-type [IPR016461] (2); O-methyltransferase, family 2 [IPR001077] (2); Winged helix-turn-helix DNA-binding domain [IPR011991] (2) | scaffold_9_mRNA_2064.1 | C_unshiu_00268_mRNA_9.1 | - |
| GF0024504 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2062.1 | C_unshiu_00268_mRNA_7.1 | - |
| GF0024503 | 1 | 1 | 0 | Hypothetical protein (2) | proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1) | Domain of unknown function DUF4218 [IPR025452] (2); Domain of unknown function DUF4216 [IPR025312] (2); Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1) | scaffold_9_mRNA_2052.1 | C_unshiu_00268_mRNA_2.1 | - |
| GF0024502 | 1 | 1 | 0 | Fra a 2 allergen (1); Major allergen Pru ar, putative (1) | response to biotic stimulus [GO:0009607 biological_process] (2); defense response [GO:0006952 biological_process] (2) | Bet v I type allergen [IPR024949] (2); Bet v I/Major latex protein [IPR000916] (2); START-like domain [IPR023393] (2) | scaffold_9_mRNA_205.1 | C_unshiu_00355_mRNA_16.1 | - |
| GF0024501 | 1 | 1 | 0 | Cytokinin riboside 5'-monophosphate phosphoribohydrolase (2) | | LOG family [IPR031100] (2) | scaffold_9_mRNA_2045.1 | C_unshiu_00094_mRNA_38.1 | - |
| GF0024500 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2042.1 | C_unshiu_00094_mRNA_35.1 | - |
| GF0024499 | 1 | 1 | 0 | UV radiation resistance-associated protein (2) | | | scaffold_9_mRNA_2038.1 | C_unshiu_00094_mRNA_31.1 | - |
| GF0024498 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2037.1 | C_unshiu_00094_mRNA_30.1 | - |
| GF0024497 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2034.1 | C_unshiu_00094_mRNA_27.1 | - |
| GF0024496 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2030.1 | C_unshiu_00094_mRNA_24.1 | - |
| GF0024495 | 1 | 1 | 0 | Putative UMUC-like DNA repair family protein (2) | | | scaffold_9_mRNA_2028.1 | C_unshiu_00094_mRNA_21.1 | - |
| GF0024494 | 1 | 1 | 0 | Autophagy protein 5 (2) | autophagy [GO:0006914 biological_process] (2); cytoplasm [GO:0005737 cellular_component] (2) | Autophagy-related protein 5 [IPR007239] (2) | scaffold_9_mRNA_2027.1 | C_unshiu_00094_mRNA_20.1 | - |
| GF0024493 | 1 | 1 | 0 | Hypothetical protein (2) | cytoplasm [GO:0005737 cellular_component] (2); autophagy [GO:0006914 biological_process] (2) | Autophagy-related protein 5 [IPR007239] (2) | scaffold_9_mRNA_2023.1 | C_unshiu_00094_mRNA_17.1 | - |
| GF0024492 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2016.1 | C_unshiu_00094_mRNA_7.1 | - |
| GF0024491 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2015.1 | C_unshiu_00094_mRNA_6.1 | - |
| GF0024490 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2012.1 | C_unshiu_00094_mRNA_2.1 | - |
| GF0024489 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2008.1 | C_unshiu_00679_mRNA_3.1 | - |
| GF0024488 | 1 | 1 | 0 | Alkaline ceramidase 3 (2) | ceramide metabolic process [GO:0006672 biological_process] (2); hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides [GO:0016811 molecular_function] (2); integral component of membrane [GO:0016021 cellular_component] (2) | Ceramidase [IPR008901] (2) | scaffold_9_mRNA_2006.1 | C_unshiu_00679_mRNA_5.1 | - |
| GF0024487 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2004.1 | C_unshiu_00679_mRNA_6.1 | - |
| GF0024486 | 1 | 1 | 0 | Hypothetical protein (2) | proteolysis [GO:0006508 biological_process] (2); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1) | Viral movement protein [IPR028919] (2); Aspartic peptidase, active site [IPR001969] (2); Aspartic peptidase domain [IPR021109] (1); Zinc finger, CCHC-type [IPR001878] (1) | scaffold_9_mRNA_2002.1 | C_unshiu_00679_mRNA_9.1 | - |
| GF0024485 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_2.1 | C_unshiu_00230_mRNA_30.1 | - |
| GF0024483 | 1 | 1 | 0 | Major allergen Mal d 1 (2) | defense response [GO:0006952 biological_process] (2); response to biotic stimulus [GO:0009607 biological_process] (2) | Bet v I/Major latex protein [IPR000916] (2); START-like domain [IPR023393] (2); Bet v I type allergen [IPR024949] (2); Major latex protein domain [IPR024948] (1) | scaffold_9_mRNA_198.1 | C_unshiu_00355_mRNA_11.1 | - |
| GF0024481 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1971.1 | C_unshiu_00393_mRNA_16.1 | - |
| GF0024480 | 1 | 1 | 0 | Hypothetical protein (2) | | Leucine-rich repeat domain, L domain-like [IPR032675] (1) | scaffold_9_mRNA_1951.1 | C_unshiu_00015_mRNA_12.1 | - |
| GF0024479 | 1 | 1 | 0 | Hypothetical protein (2) | | Transposase-associated domain [IPR029480] (2) | scaffold_9_mRNA_195.1 | C_unshiu_00355_mRNA_9.1 | - |
| GF0024476 | 1 | 1 | 0 | Hypothetical protein (2) | hydrolase activity [GO:0016787 molecular_function] (2) | Iron/zinc purple acid phosphatase-like C-terminal domain [IPR025733] (2); Metallo-dependent phosphatase-like [IPR029052] (2); Calcineurin-like phosphoesterase domain, ApaH type [IPR004843] (1); Calcineurin-like phosphoesterase domain, apaH type [IPR004843] (1) | scaffold_9_mRNA_1936.1 | C_unshiu_00567_mRNA_1.1 | - |
| GF0024475 | 1 | 1 | 0 | Hypothetical protein (1); BED zinc finger,hAT family dimerization domain (1) | DNA binding [GO:0003677 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1) | hAT-like transposase, RNase-H fold [IPR025525] (2); HAT, C-terminal dimerisation domain [IPR008906] (1); Ribonuclease H-like domain [IPR012337] (1) | scaffold_9_mRNA_1931.1 | C_unshiu_00567_mRNA_7.1 | - |
| GF0024474 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (1) | Ribonuclease H-like domain [IPR012337] (1) | scaffold_9_mRNA_1925.1 | C_unshiu_00567_mRNA_13.1 | - |
| GF0024473 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1918.1 | C_unshiu_00170_mRNA_21.1 | - |
| GF0024471 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1898.1 | C_unshiu_00057_mRNA_65.1 | - |
| GF0024470 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1896.1 | C_unshiu_00057_mRNA_63.1 | - |
| GF0024469 | 1 | 1 | 0 | DUF247 domain protein (2) | | Protein of unknown function DUF247, plant [IPR004158] (2) | scaffold_9_mRNA_1892.1 | C_unshiu_00701_mRNA_3.1 | - |
| GF0024468 | 1 | 1 | 0 | Hypothetical protein (2) | | Protein of unknown function DUF247, plant [IPR004158] (2) | scaffold_9_mRNA_1890.1 | C_unshiu_00701_mRNA_5.1 | - |
| GF0024467 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1889.1 | C_unshiu_00701_mRNA_6.1 | - |
| GF0024466 | 1 | 1 | 0 | UPF0481 protein (2) | | Protein of unknown function DUF247, plant [IPR004158] (2) | scaffold_9_mRNA_1887.1 | C_unshiu_02148_mRNA_5.1 | - |
| GF0024465 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1886.1 | C_unshiu_02148_mRNA_4.1 | - |
| GF0024464 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (1) | Ribonuclease H-like domain [IPR012337] (1) | scaffold_9_mRNA_1885.1 | C_unshiu_02148_mRNA_3.1 | - |
| GF0024463 | 1 | 1 | 0 | Hypothetical protein (2) | | Retrotransposon gag domain [IPR005162] (2) | scaffold_9_mRNA_1884.1 | C_unshiu_02148_mRNA_2.1 | - |
| GF0024462 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1881.1 | C_unshiu_00287_mRNA_13.1 | - |
| GF0024461 | 1 | 1 | 0 | Hypothetical protein (2) | | Aspartic peptidase domain [IPR021109] (1) | scaffold_9_mRNA_1880.1 | C_unshiu_00287_mRNA_12.1 | - |

| **ID** | **Num. in *C. celementine*** | **Num in *C. unshiu*** | **Num in *P.trifoliata*** | **Note** | **GO** | **InterPro** | **Members in *C.clementine*** | **Members in *C.unshiu*** | **Members in *P.trifoliata*** |
|---|---|---|---|---|---|---|---|---|---|
| GF0024460 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2); Reverse transcriptase zinc-binding domain [IPR026960] (2); Endonuclease/exonuclease/phosphatase [IPR005135] (2) | scaffold_9_mRNA_1864.1 | C_unshiu_00124_mRNA_27.1 | - |
| GF0024459 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1862.1 | C_unshiu_00124_mRNA_25.1 | - |
| GF0024457 | 1 | 1 | 0 | Two-component response regulator ARR12-like protein (2) | DNA binding [GO:0003677 molecular_function] (2); phosphorelay signal transduction system [GO:0000160 biological_process] (2) | Signal transduction response regulator, receiver domain [IPR001789] (2); CheY-like superfamily [IPR011006] (2); Myb domain [IPR017930] (2); Myb domain, plants [IPR006447] (2); SANT/Myb domain [IPR001005] (2); Homeobox domain-like [IPR009057] (1); Homeodomain-like [IPR009057] (1) | scaffold_9_mRNA_186.1 | C_unshiu_00007_mRNA_2.1 | - |
| GF0024456 | 1 | 1 | 0 | Hypothetical protein (2) | | Transposase, MuDR, plant [IPR004332] (2) | scaffold_9_mRNA_1858.1 | C_unshiu_00480_mRNA_4.1 | - |
| GF0024455 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1849.1 | C_unshiu_00351_mRNA_17.1 | - |
| GF0024454 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1847.1 | C_unshiu_00351_mRNA_16.1 | - |
| GF0024452 | 1 | 1 | 0 | Hypothetical protein (2) | | Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (2) | scaffold_9_mRNA_1843.1 | C_unshiu_00351_mRNA_13.1 | - |
| GF0024451 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1838.1 | C_unshiu_00015_mRNA_3.1 | - |
| GF0024449 | 1 | 1 | 0 | Hypothetical protein (2) | | Alpha/Beta hydrolase fold [IPR029058] (1) | scaffold_9_mRNA_1832.1 | C_unshiu_01152_mRNA_5.1 | - |
| GF0024448 | 1 | 1 | 0 | Cytokinin riboside 5'-monophosphate phosphoribohydrolase (2) | | | scaffold_9_mRNA_1822.1 | C_unshiu_01121_mRNA_7.1 | - |
| GF0024447 | 1 | 1 | 0 | Leukocyte receptor cluster member 1 (2) | | CBF1-interacting co-repressor CIR, N-terminal domain [IPR019339] (2) | scaffold_9_mRNA_1815.1 | C_unshiu_00323_mRNA_6.1 | - |
| GF0024446 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1813.1 | C_unshiu_01046_mRNA_3.1 | - |
| GF0024445 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1808.1 | C_unshiu_01596_mRNA_2.1 | - |
| GF0024444 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1807.1 | C_unshiu_01596_mRNA_1.1 | - |
| GF0024443 | 1 | 1 | 0 | Putative AC transposase (2) | DNA binding [GO:0003677 molecular_function] (2); protein dimerization activity [GO:0046983 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | HAT, C-terminal dimerisation domain [IPR008906] (2); Zinc finger, BED-type [IPR003656] (2); Ribonuclease H-like domain [IPR012337] (2); Zinc finger C2H2-type [IPR013087] (1) | scaffold_9_mRNA_1806.1 | C_unshiu_00645_mRNA_13.1 | - |
| GF0024442 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1805.1 | C_unshiu_00645_mRNA_14.1 | - |
| GF0024441 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_9_mRNA_1789.1 | C_unshiu_00506_mRNA_13.1 | - |
| GF0024440 | 1 | 1 | 0 | Hypothetical protein (2) | protein binding [GO:0005515 molecular_function] (1) | Transposase-associated domain [IPR029480] (2); WD40/YVTN repeat-like-containing domain [IPR015943] (1); WD40-repeat-containing domain [IPR017986] (1) | scaffold_9_mRNA_1788.1 | C_unshiu_00506_mRNA_12.1 | - |
| GF0024439 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1782.1 | C_unshiu_00920_mRNA_3.1 | - |
| GF0024438 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1781.1 | C_unshiu_00920_mRNA_2.1 | - |
| GF0024437 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1780.1 | C_unshiu_00351_mRNA_11.1 | - |
| GF0024436 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1779.1 | C_unshiu_00920_mRNA_1.1 | - |
| GF0024435 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1778.1 | C_unshiu_00013_mRNA_1.1 | - |
| GF0024434 | 1 | 1 | 0 | Hypothetical protein (2) | | Calcium/calmodulin-dependent/calcium-dependent protein kinase [IPR020636] (2) | scaffold_9_mRNA_1775.1 | C_unshiu_00506_mRNA_5.1 | - |
| GF0024433 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1770.1 | C_unshiu_00062_mRNA_40.1 | - |
| GF0024432 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1768.1 | C_unshiu_01039_mRNA_2.1 | - |
| GF0024431 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1765.1 | C_unshiu_00309_mRNA_17.1 | - |
| GF0024430 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1752.1 | C_unshiu_02379_mRNA_1.1 | - |
| GF0024429 | 1 | 1 | 0 | Transcription factor MYB12 (2) | DNA binding [GO:0003677 molecular_function] (2) | SANT/Myb domain [IPR001005] (2); Myb domain [IPR017930] (2); Homeodomain-like [IPR009057] (1); Homeobox domain-like [IPR009057] (1) | scaffold_9_mRNA_175.1 | C_unshiu_00007_mRNA_13.1 | - |
| GF0024428 | 1 | 1 | 0 | Hypothetical protein (2) | regulation of transcription, DNA-templated [GO:0006355 biological_process] (2) | FAR1 DNA binding domain [IPR004330] (2); FHY3/FAR1 family [IPR031052] (2) | scaffold_9_mRNA_1743.1 | C_unshiu_00424_mRNA_10.1 | - |
| GF0024427 | 1 | 1 | 0 | Transposon protein, putative, unclassified (1); Protein FAR-RED IMPAIRED RESPONSE 1 (1) | regulation of transcription, DNA-templated [GO:0006355 biological_process] (2); zinc ion binding [GO:0008270 molecular_function] (2) | FHY3/FAR1 family [IPR031052] (2); Zinc finger, SWIM-type [IPR007527] (2); MULE transposase domain [IPR018289] (2) | scaffold_9_mRNA_1742.1 | C_unshiu_00424_mRNA_9.1 | - |
| GF0024426 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1740.1 | C_unshiu_00424_mRNA_7.1 | - |
| GF0024425 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1738.1 | C_unshiu_00424_mRNA_5.1 | - |
| GF0024423 | 1 | 1 | 0 | Hypothetical protein (2) | | Retrotransposon gag domain [IPR005162] (1) | scaffold_9_mRNA_1732.1 | C_unshiu_01199_mRNA_3.1 | - |
| GF0024422 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1721.1 | C_unshiu_00620_mRNA_10.1 | - |
| GF0024421 | 1 | 1 | 0 | Hypothetical protein (1); Ethylene-responsive transcription factor ERF114 (1) | DNA binding [GO:0003677 molecular_function] (1); transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1) | DNA-binding domain [IPR016177] (1); AP2/ERF domain [IPR001471] (1) | scaffold_9_mRNA_1720.1 | C_unshiu_00620_mRNA_11.2 | - |
| GF0024420 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1714.1 | C_unshiu_00063_mRNA_6.1 | - |
| GF0024419 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_171.1 | C_unshiu_00007_mRNA_18.1 | - |
| GF0024418 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1709.1 | C_unshiu_00211_mRNA_1.1 | - |
| GF0024417 | 1 | 1 | 0 | 60S ribosomal protein L30 (2) | ribosome [GO:0005840 cellular_component] (2); intracellular [GO:0005622 cellular_component] (2); translation [GO:0006412 biological_process] (2); structural constituent of ribosome [GO:0003735 molecular_function] (2) | Ribosomal protein L30e, conserved site [IPR022991] (2); Ribosomal protein L7Ae/L30e/S12e/Gadd45 [IPR004038] (2); 50S ribosomal protein L30e-like [IPR029064] (2); Ribosomal protein L30e [IPR000231] (2) | scaffold_9_mRNA_1708.1 | C_unshiu_00211_mRNA_2.1 | - |
| GF0024416 | 1 | 1 | 0 | Putative non-LTR reverse transcriptase (1); Hypothetical protein (1) | nucleic acid binding [GO:0003676 molecular_function] (2) | Reverse transcriptase zinc-binding domain [IPR026960] (2); Ribonuclease H-like domain [IPR012337] (2); Domain of unknown function DUF4283 [IPR025558] (1) | scaffold_9_mRNA_1704.1 | C_unshiu_00211_mRNA_9.1 | - |
| GF0024415 | 1 | 1 | 0 | TMV resistance protein N (2) | ADP binding [GO:0043531 molecular_function] (2); signal transduction [GO:0007165 biological_process] (1); protein binding [GO:0005515 molecular_function] (1) | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); NB-ARC [IPR002182] (2); Leucine-rich repeat 3 [IPR011713] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1) | scaffold_9_mRNA_1701.1 | C_unshiu_00211_mRNA_13.1 | - |
| GF0024414 | 1 | 1 | 0 | Hypothetical protein (2) | | Reverse transcriptase zinc-binding domain [IPR026960] (2) | scaffold_9_mRNA_1699.1 | C_unshiu_00211_mRNA_15.1 | - |
| GF0024413 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (1) | Ribonuclease H-like domain [IPR012337] (1) | scaffold_9_mRNA_1698.1 | C_unshiu_00211_mRNA_16.1 | - |
| GF0024410 | 1 | 1 | 0 | E3 ubiquitin-protein ligase (2) | nucleus [GO:0005634 cellular_component] (2); ubiquitin-dependent protein catabolic process [GO:0006511 biological_process] (2); protein binding [GO:0005515 molecular_function] (2); zinc ion binding [GO:0008270 molecular_function] (2); multicellular organismal development [GO:0007275 biological_process] (1); protein ubiquitination [GO:0016567 biological_process] (1); ubiquitin-protein transferase activity [GO:0004842 molecular_function] (1); multicellular organism development [GO:0007275 biological_process] (1) | Zinc finger, RING/FYVE/PHD-type [IPR013083] (2); Seven-in-absentia protein, TRAF-like domain [IPR018121] (2); TRAF-like [IPR008974] (2); Zinc finger, SIAH-type [IPR013010] (2); E3 ubiquitin-protein ligase SIN-like [IPR004162] (2); Zinc finger, RING-type [IPR001841] (2); SIAH-type domain [IPR013323] (1) | scaffold_9_mRNA_1671.1 | C_unshiu_00294_mRNA_14.1 | - |
| GF0024409 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2); zinc ion binding [GO:0008270 molecular_function] (2) | Domain of unknown function DUF4283 [IPR025558] (2); Zinc knuckle CX2CX4HX4C [IPR025836] (2); Zinc finger, CCHC-type [IPR001878] (2) | scaffold_9_mRNA_1661.1 | C_unshiu_00294_mRNA_7.1 | - |
| GF0024407 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1640.1 | C_unshiu_00603_mRNA_8.1 | - |
| GF0024406 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1638.1 | C_unshiu_00603_mRNA_6.1 | - |
| GF0024403 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1631.1 | C_unshiu_02459_mRNA_1.1 | - |
| GF0024402 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1629.1 | C_unshiu_00354_mRNA_21.1 | - |
| GF0024400 | 1 | 1 | 0 | Putative amidohydrolase ytcJ (2) | hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds [GO:0016810 molecular_function] (2) | Metal-dependent hydrolase, composite domain [IPR011059] (2); Amidohydrolase 3 [IPR013108] (2); Metal-dependent hydrolase [IPR032466] (2); YtcJ like [IPR033932] (1) | scaffold_9_mRNA_1616.1 | C_unshiu_00952_mRNA_1.1 | - |
| GF0024399 | 1 | 1 | 0 | Hypothetical protein (2) | GTPase activity [GO:0003924 molecular_function] (2); signal recognition particle receptor complex [GO:0005785 cellular_component] (2); intracellular protein transport [GO:0006886 biological_process] (2); GTP binding [GO:0005525 molecular_function] (2); signal recognition particle binding [GO:0005047 molecular_function] (2); SRP-dependent cotranslational protein targeting to membrane [GO:0006614 biological_process] (1) | Signal recognition particle receptor, alpha subunit, N-terminal [IPR007222] (2); Signal recognition particle, SRP54 subunit, helical bundle [IPR013822] (1) | scaffold_9_mRNA_1612.1 | C_unshiu_00512_mRNA_13.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0024398 | 1 | 1 | 0 | Leucine-rich repeat protein kinase family protein (2) | protein binding [GO:0005515 molecular_function] (2); protein kinase activity [GO:0004672 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2); ATP binding [GO:0005524 molecular_function] (2) | Leucine-rich repeat [IPR001611] (2); Protein kinase-like domain [IPR011009] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Protein kinase domain [IPR000719] (2); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase, ATP binding site [IPR017441] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1) | scaffold_9_mRNA_1611.1 | C_unshiu_02063_mRNA_3.1 | - |
| GF0024397 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1610.1 | C_unshiu_02063_mRNA_4.1 | - |
| GF0024396 | 1 | 1 | 0 | Hypothetical protein (2) | protein binding [GO:0005515 molecular_function] (2) | Leucine-rich repeat [IPR001611] (2); Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2) | scaffold_9_mRNA_1609.1 | C_unshiu_00512_mRNA_11.1 | - |
| GF0024395 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1607.1 | C_unshiu_00512_mRNA_8.1 | - |
| GF0024394 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1601.1 | C_unshiu_00926_mRNA_3.1 | - |
| GF0024393 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1594.1 | C_unshiu_00926_mRNA_8.1 | - |
| GF0024392 | 1 | 1 | 0 | Hypothetical protein (1); RNA-directed DNA polymerase (Reverse transcriptase) (1) | | Aspartic peptidase domain [IPR021109] (2); Reverse transcriptase domain [IPR000477] (1) | scaffold_9_mRNA_1593.1 | C_unshiu_00926_mRNA_9.1 | - |
| GF0024391 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1588.1 | C_unshiu_01176_mRNA_2.1 | - |
| GF0024390 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1584.1 | C_unshiu_01176_mRNA_5.1 | - |
| GF0024389 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1583.1 | C_unshiu_01176_mRNA_6.1 | - |
| GF0024388 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1576.1 | C_unshiu_01433_mRNA_7.1 | - |
| GF0024387 | 1 | 1 | 0 | Hypothetical protein (2) | | Transposase, MuDR, plant [IPR004332] (2) | scaffold_9_mRNA_1575.1 | C_unshiu_01433_mRNA_6.1 | - |
| GF0024386 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1574.1 | C_unshiu_01433_mRNA_5.1 | - |
| GF0024385 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1572.1 | C_unshiu_01870_mRNA_1.1 | - |
| GF0024384 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_9_mRNA_1570.1 | C_unshiu_01870_mRNA_3.1 | - |
| GF0024383 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1563.1 | C_unshiu_01433_mRNA_1.1 | - |
| GF0024381 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1559.1 | C_unshiu_01680_mRNA_3.1 | - |
| GF0024380 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1557.1 | C_unshiu_01680_mRNA_5.1 | - |
| GF0024378 | 1 | 1 | 0 | UDP-glucoronosyl/UDP-glucosyl transferase family protein (1); Pentatricopeptide repeat-containing protein, chloroplastic (1) | protein binding [GO:0005515 molecular_function] (2) | Tetratricopeptide-like helical domain [IPR011990] (2); Pentatricopeptide repeat [IPR002885] (2) | scaffold_9_mRNA_1553.1 | C_unshiu_01796_mRNA_5.1 | - |
| GF0024376 | 1 | 1 | 0 | P-loop nucleoside triphosphate hydrolase superfamily protein (2) | | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2) | scaffold_9_mRNA_1549.1 | C_unshiu_00747_mRNA_17.1 | - |
| GF0024375 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1547.1 | C_unshiu_00747_mRNA_16.1 | - |
| GF0024374 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1545.1 | C_unshiu_00747_mRNA_14.1 | - |
| GF0024373 | 1 | 1 | 0 | Hypothetical protein (2) | nucleobase-containing compound metabolic process [GO:0006139 biological_process] (2); 3'-5' exonuclease activity [GO:0008408 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2); 3'-5' exonuclease domain [IPR002562] (2) | scaffold_9_mRNA_1544.1 | C_unshiu_00747_mRNA_13.1 | - |
| GF0024372 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1540.1 | C_unshiu_01191_mRNA_2.1 | - |
| GF0024371 | 1 | 1 | 0 | Hypothetical protein (2) | ubiquitin-dependent protein catabolic process [GO:0006511 biological_process] (2) | SKP1 component, dimerisation [IPR016072] (2) | scaffold_9_mRNA_1536.1 | C_unshiu_01191_mRNA_7.1 | - |
| GF0024370 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1530.1 | C_unshiu_01126_mRNA_11.1 | - |
| GF0024368 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1513.1 | C_unshiu_01938_mRNA_5.1 | - |
| GF0024367 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1502.1 | C_unshiu_00787_mRNA_18.1 | - |
| GF0024365 | 1 | 1 | 0 | Hypothetical protein (1); Chloroplast lumen common family protein (1) | protein binding [GO:0005515 molecular_function] (2) | Tetratricopeptide repeat-containing domain [IPR013026] (2); Tetratricopeptide-like helical domain [IPR011990] (2); Tetratricopeptide repeat 2 [IPR013105] (1) | scaffold_9_mRNA_1495.1 | C_unshiu_00963_mRNA_7.1 | - |
| GF0024364 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_149.1 | C_unshiu_00007_mRNA_38.1 | - |
| GF0024363 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1462.1 | C_unshiu_00351_mRNA_10.1 | - |
| GF0024362 | 1 | 1 | 0 | Phloem protein 2-B5 (2) | protein binding [GO:0005515 molecular_function] (2) | Phloem protein 2-like [IPR025886] (2); F-box domain [IPR001810] (2) | scaffold_9_mRNA_1461.1 | C_unshiu_00351_mRNA_9.1 | - |
| GF0024361 | 1 | 1 | 0 | Putative non-LTR retrolelement reverse transcriptase (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_9_mRNA_1455.1 | C_unshiu_01074_mRNA_10.1 | - |
| GF0024360 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1446.1 | C_unshiu_00094_mRNA_45.1 | - |
| GF0024359 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1445.1 | C_unshiu_00094_mRNA_44.1 | - |
| GF0024358 | 1 | 1 | 0 | Hypothetical protein (2) | DNA binding [GO:0003677 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (1) | hAT-like transposase, RNase-H fold [IPR025525] (2); Ribonuclease H-like domain [IPR012337] (1) | scaffold_9_mRNA_1444.1 | C_unshiu_00094_mRNA_43.1 | - |
| GF0024357 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1443.1 | C_unshiu_00094_mRNA_42.1 | - |
| GF0024355 | 1 | 1 | 0 | Hypothetical protein (2) | | LOG family [IPR031100] (2) | scaffold_9_mRNA_1427.1 | C_unshiu_00124_mRNA_20.1 | - |
| GF0024354 | 1 | 1 | 0 | Pentatricopeptide repeat-containing family protein (2) | protein binding [GO:0005515 molecular_function] (1) | Pentatricopeptide repeat [IPR002885] (2); Tetratricopeptide-like helical domain [IPR011990] (1) | scaffold_9_mRNA_1425.1 | C_unshiu_00124_mRNA_16.1 | - |
| GF0024353 | 1 | 1 | 0 | Type II peroxiredoxin (2) | oxidoreductase activity [GO:0016491 molecular_function] (2) | Redoxin [IPR013740] (2); Thioredoxin-like fold [IPR012336] (2) | scaffold_9_mRNA_1424.1 | C_unshiu_00124_mRNA_15.1 | - |
| GF0024352 | 1 | 1 | 0 | Phloem protein 2-B5 (2) | protein binding [GO:0005515 molecular_function] (2) | F-box domain [IPR001810] (2); Phloem protein 2-like [IPR025886] (2) | scaffold_9_mRNA_1421.1 | C_unshiu_00124_mRNA_12.1 | - |
| GF0024351 | 1 | 1 | 0 | Hypothetical protein (2) | | Cyclic nucleotide-binding-like [IPR018490] (2); RmlC-like jelly roll fold [IPR014710] (2); Cyclic nucleotide-binding domain [IPR000595] (2) | scaffold_9_mRNA_1420.1 | C_unshiu_00124_mRNA_11.1 | - |
| GF0024350 | 1 | 1 | 0 | Phloem protein 2-B5 (2) | protein binding [GO:0005515 molecular_function] (2) | F-box domain [IPR001810] (2); Phloem protein 2-like [IPR025886] (2) | scaffold_9_mRNA_1416.1 | C_unshiu_00124_mRNA_5.1 | - |
| GF0024349 | 1 | 1 | 0 | Hypothetical protein (2) | DNA binding [GO:0003677 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (1) | Zinc finger, BED-type [IPR003656] (2); Zinc finger C2H2-type [IPR013087] (1) | scaffold_9_mRNA_1404.1 | C_unshiu_00367_mRNA_15.1 | - |
| GF0024348 | 1 | 1 | 0 | Hypothetical protein (2) | | Domain of unknown function DUF4283 [IPR025558] (2) | scaffold_9_mRNA_1403.1 | C_unshiu_00367_mRNA_14.1 | - |
| GF0024347 | 1 | 1 | 0 | Progesterone 5-beta-reductase (2) | | NAD(P)-binding domain [IPR016040] (2) | scaffold_9_mRNA_1402.1 | C_unshiu_00367_mRNA_13.1 | - |
| GF0024346 | 1 | 1 | 0 | Hypothetical protein (2) | zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1) | Zinc knuckle CX2CX4HX4C [IPR025836] (2); Domain of unknown function DUF4283 [IPR025558] (2); Zinc finger, CCHC-type [IPR001878] (1) | scaffold_9_mRNA_1370.1 | C_unshiu_00344_mRNA_41.1 | - |
| GF0024345 | 1 | 1 | 0 | UPF0481 protein (2) | | Protein of unknown function DUF247, plant [IPR004158] (2) | scaffold_9_mRNA_1365.1 | C_unshiu_00057_mRNA_4.1 | - |
| GF0024344 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1358.1 | C_unshiu_00057_mRNA_11.1 | - |
| GF0024343 | 1 | 1 | 0 | Hypothetical protein (2) | calcium ion binding [GO:0005509 molecular_function] (2) | EF-hand domain pair [IPR011992] (2); EF-Hand 1, calcium-binding site [IPR018247] (2); EF-hand domain [IPR002048] (2) | scaffold_9_mRNA_1357.1 | C_unshiu_00057_mRNA_12.1 | - |
| GF0024342 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1355.1 | C_unshiu_00057_mRNA_14.1 | - |
| GF0024341 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1354.1 | C_unshiu_00057_mRNA_16.1 | - |
| GF0024340 | 1 | 1 | 0 | Hypothetical protein (2) | | Gag-polypeptide of LTR copia-type [IPR029472] (1); Wall-associated receptor kinase, C-terminal [IPR032872] (1) | scaffold_9_mRNA_135.1 | C_unshiu_00007_mRNA_51.1 | - |
| GF0024339 | 1 | 1 | 0 | Hypothetical protein (1); AtpA (1) | zinc ion binding [GO:0008270 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (1) | Zinc finger, SWIM-type [IPR007527] (2); Zinc finger, PMZ-type [IPR006564] (2); Zinc finger, CCHC-type [IPR001878] (1) | scaffold_9_mRNA_1348.1 | C_unshiu_01146_mRNA_2.1 | - |
| GF0024335 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1337.1 | C_unshiu_00057_mRNA_23.1 | - |
| GF0024334 | 1 | 1 | 0 | Hypothetical protein (1); AT4g04660 protein (1) | nucleic acid binding [GO:0003676 molecular_function] (2); zinc ion binding [GO:0008270 molecular_function] (2) | Domain of unknown function DUF4283 [IPR025558] (2); Zinc knuckle CX2CX4HX4C [IPR025836] (2); Zinc finger, CCHC-type [IPR001878] (2) | scaffold_9_mRNA_1319.1 | C_unshiu_00451_mRNA_15.1 | - |
| GF0024333 | 1 | 1 | 0 | Hypothetical protein (2) | | LOG family [IPR031100] (1) | scaffold_9_mRNA_1312.1 | C_unshiu_00178_mRNA_40.1 | - |
| GF0024332 | 1 | 1 | 0 | 60S ribosomal protein L14-2 (1); Hypothetical protein (1) | intracellular [GO:0005622 cellular_component] (2); translation [GO:0006412 biological_process] (2); structural constituent of ribosome [GO:0003735 molecular_function] (2); ribosome [GO:0005840 cellular_component] (2) | Translation protein SH3-like domain [IPR008991] (2); Ribosomal protein L2 domain 2 [IPR014722] (2); Ribosomal protein L14e domain [IPR002784] (1); Ribosomal protein L14 [IPR002784] (1) | scaffold_9_mRNA_1310.1 | C_unshiu_00178_mRNA_38.1 | - |
| GF0024329 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1303.1 | C_unshiu_00311_mRNA_26.1 | - |
| GF0024327 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1282.1 | C_unshiu_01632_mRNA_10.1 | - |
| GF0024326 | 1 | 1 | 0 | Hypothetical protein (2) | | Transposon, En/Spm-like [IPR004242] (2) | scaffold_9_mRNA_1281.1 | C_unshiu_01632_mRNA_9.1 | - |
| GF0024325 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_128.1 | C_unshiu_00007_mRNA_59.1 | - |
| GF0024322 | 1 | 1 | 0 | Hypothetical protein (2) | | MULE transposase domain [IPR018289] (1) | scaffold_9_mRNA_1268.1 | C_unshiu_00998_mRNA_13.1 | - |
| GF0024321 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1267.1 | C_unshiu_02381_mRNA_1.1 | - |
| GF0024319 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1257.1 | C_unshiu_00040_mRNA_18.1 | - |
| GF0024318 | 1 | 1 | 0 | Hypothetical protein (2) | integral component of membrane [GO:0016021 cellular_component] (2); transferase activity, transferring alkyl or aryl (other than methyl) groups [GO:0016765 molecular_function] (1); prenyltransferase activity [GO:0004659 molecular_function] (1) | UbiA prenyltransferase family [IPR000537] (2) | scaffold_9_mRNA_1255.1 | C_unshiu_00193_mRNA_14.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0024317 | 1 | 1 | 0 | Hypothetical protein (1); Nucleic acid binding protein, putative (1) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2); TB2/DP1/HVA22-related protein [IPR004345] (1) | scaffold_9_mRNA_1254.1 | C_unshiu_00193_mRNA_16.1 | - |
| GF0024316 | 1 | 1 | 0 | Hypothetical protein (2) | | Plant self-incompatibility S1 [IPR010264] (2); DnaJ domain [IPR001623] (2); DnaJ domain, conserved site [IPR018253] (2); Class I glutamine amidotransferase-like [IPR029062] (2); Glutamine amidotransferase [IPR017926] (2) | scaffold_9_mRNA_1251.1 | C_unshiu_00193_mRNA_20.1 | - |
| GF0024315 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1249.1 | C_unshiu_00193_mRNA_22.1 | - |
| GF0024314 | 1 | 1 | 0 | Retrotransposon protein, putative, Ty1-copia subclass (2) | zinc ion binding [GO:0008270 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | Zinc finger, CCHC-type [IPR001878] (2) | scaffold_9_mRNA_1247.1 | C_unshiu_00193_mRNA_25.1 | - |
| GF0024313 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1245.1 | C_unshiu_00193_mRNA_27.1 | - |
| GF0024312 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1) | Domain of unknown function DUF4219 [IPR025314] (2); Zinc finger, CCHC-type [IPR001878] (1) | scaffold_9_mRNA_1240.1 | C_unshiu_00634_mRNA_17.1 | - |
| GF0024311 | 1 | 1 | 0 | Cytokinin riboside 5'-monophosphate phosphoribohydrolase (2) | | | scaffold_9_mRNA_1239.1 | C_unshiu_00634_mRNA_18.1 | - |
| GF0024310 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1238.1 | C_unshiu_00634_mRNA_19.1 | - |
| GF0024309 | 1 | 1 | 0 | Hypothetical protein (2) | | Mitochondrial substrate/solute carrier [IPR018108] (2); Mitochondrial carrier domain [IPR023395] (2) | scaffold_9_mRNA_1219.1 | C_unshiu_00112_mRNA_44.1 | - |
| GF0024308 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1218.1 | C_unshiu_00112_mRNA_43.1 | - |
| GF0024307 | 1 | 1 | 0 | Hypothetical protein (2) | proteolysis [GO:0006508 biological_process] (2); cysteine-type peptidase activity [GO:0008234 molecular_function] (2) | Ulp1 protease family, C-terminal catalytic domain [IPR003653] (2) | scaffold_9_mRNA_1214.1 | C_unshiu_00112_mRNA_41.1 | - |
| GF0024306 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1213.1 | C_unshiu_00112_mRNA_40.1 | - |
| GF0024305 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1212.1 | C_unshiu_00112_mRNA_39.1 | - |
| GF0024304 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1211.1 | C_unshiu_00112_mRNA_38.1 | - |
| GF0024303 | 1 | 1 | 0 | Isoleucine N-monooxygenase 2 (2) | oxidation-reduction process [GO:0055114 biological_process] (2); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (2); heme binding [GO:0020037 molecular_function] (2); iron ion binding [GO:0005506 molecular_function] (2) | Cytochrome P450, E-class, group I [IPR002401] (2); Cytochrome P450, conserved site [IPR017972] (2); Cytochrome P450 [IPR001128] (2) | scaffold_9_mRNA_1205.1 | C_unshiu_00112_mRNA_32.1 | - |
| GF0024302 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1194.1 | C_unshiu_00112_mRNA_16.1 | - |
| GF0024301 | 1 | 1 | 0 | Hypothetical protein (2) | protein binding [GO:0005515 molecular_function] (2) | F-box domain [IPR001810] (2) | scaffold_9_mRNA_1191.1 | C_unshiu_00112_mRNA_9.1 | - |
| GF0024300 | 1 | 1 | 0 | Ankyrin repeat family protein, putative (2) | protein binding [GO:0005515 molecular_function] (2); integral component of membrane [GO:0016021 cellular_component] (1); cellular response to salicylic acid stimulus [GO:0071446 biological_process] (1); regulation of salicylic acid mediated signaling pathway [GO:2000031 biological_process] (1); regulation of defense response [GO:0031347 biological_process] (1) | Ankyrin repeat [IPR002110] (2); Ankyrin repeat-containing domain [IPR020683] (2); PGG domain [IPR026961] (2); Protein accelerated cell death 6 [IPR032846] (1) | scaffold_9_mRNA_1184.1 | C_unshiu_00112_mRNA_4.1 | - |
| GF0024299 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1175.1 | C_unshiu_00334_mRNA_35.1 | - |
| GF0024298 | 1 | 1 | 0 | E3 ubiquitin-protein ligase mind-bomb (2) | protein binding [GO:0005515 molecular_function] (2); 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) | Ankyrin repeat [IPR002110] (2); Ankyrin repeat-containing domain [IPR020683] (2); Protein accelerated cell death 6 [IPR032846] (1) | scaffold_9_mRNA_1174.1 | C_unshiu_00334_mRNA_34.1 | - |
| GF0024297 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_9_mRNA_1170.1 | C_unshiu_00334_mRNA_30.1 | - |
| GF0024296 | 1 | 1 | 0 | Hypothetical protein (2) | protein binding [GO:0005515 molecular_function] (2); integral component of membrane [GO:0016021 cellular_component] (1); cellular response to salicylic acid stimulus [GO:0071446 biological_process] (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] (2); Ankyrin repeat-containing domain [IPR020683] (2); Endonuclease/exonuclease/phosphatase [IPR005135] (1); Protein accelerated cell death 6 [IPR032846] (1) | scaffold_9_mRNA_1169.1 | C_unshiu_00334_mRNA_29.1 | - |
| GF0024295 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_116.1 | C_unshiu_00007_mRNA_71.1 | - |
| GF0024294 | 1 | 1 | 0 | Putative peptide transporter, Protein NRT1/ PTR FAMILY 5.6 (2) | transporter activity [GO:0005215 molecular_function] (2); transport [GO:0006810 biological_process] (2); membrane [GO:0016020 cellular_component] (2) | Proton-dependent oligopeptide transporter family [IPR000109] (2) | scaffold_9_mRNA_1158.1 | C_unshiu_00334_mRNA_24.1 | - |
| GF0024290 | 1 | 1 | 0 | Hypothetical protein (2) | protein binding [GO:0005515 molecular_function] (2) | Thioredoxin-like fold [IPR012336] (2); Glutathione S-transferase, N-terminal [IPR004045] (2); Glutathione S-transferase, C-terminal-like [IPR010987] (1) | scaffold_9_mRNA_1117.1 | C_unshiu_00334_mRNA_7.1 | - |
| GF0024289 | 1 | 1 | 0 | Glutathione S-transferase tau 7, putative (2) | | Glutathione S-transferase, C-terminal [IPR004046] (2); Glutathione S-transferase, C-terminal-like [IPR010987] (2) | scaffold_9_mRNA_1116.1 | C_unshiu_00017_mRNA_5.1 | - |
| GF0024288 | 1 | 1 | 0 | Tau class glutathione S-transferase (2) | protein binding [GO:0005515 molecular_function] (2) | Glutathione S-transferase, N-terminal [IPR004045] (2); Glutathione S-transferase, C-terminal-like [IPR010987] (2); Thioredoxin-like fold [IPR012336] (2); Glutathione S-transferase, C-terminal [IPR004046] (2) | scaffold_9_mRNA_1102.1 | C_unshiu_00721_mRNA_1.1 | - |
| GF0024287 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_11.1 | C_unshiu_00007_mRNA_171.1 | - |
| GF0024286 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1081.1 | C_unshiu_00063_mRNA_62.1 | - |
| GF0024285 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1077.1 | C_unshiu_00063_mRNA_59.1 | - |
| GF0024284 | 1 | 1 | 0 | BED zinc finger,hAT family dimerization domain (2) | DNA binding [GO:0003677 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2); protein dimerization activity [GO:0046983 molecular_function] (2) | HAT, C-terminal dimerisation domain [IPR008906] (2); Ribonuclease H-like domain [IPR012337] (2); hAT-like transposase, RNase-H fold [IPR025525] (2) | scaffold_9_mRNA_1075.1 | C_unshiu_00063_mRNA_57.1 | - |
| GF0024283 | 1 | 1 | 0 | Hypothetical protein (2) | | Reverse transcriptase zinc-binding domain [IPR026960] (2) | scaffold_9_mRNA_1074.1 | C_unshiu_00063_mRNA_56.1 | - |
| GF0024282 | 1 | 1 | 0 | Peptidase S41 family protein (2) | protein binding [GO:0005515 molecular_function] (2); serine-type peptidase activity [GO:0008236 molecular_function] (2); proteolysis [GO:0006508 biological_process] (2) | PDZ domain [IPR001478] (2); C-terminal-processing peptidase S41A [IPR004447] (2); Tail specific protease [IPR005151] (2); ClpP/crotonase-like domain [IPR029045] (2) | scaffold_9_mRNA_1071.1 | C_unshiu_00063_mRNA_53.1 | - |
| GF0024281 | 1 | 1 | 0 | Ammonium transporter (2) | ammonium transport [GO:0015696 biological_process] (2); membrane [GO:0016020 cellular_component] (2); ammonium transmembrane transport [GO:0072488 biological_process] (2); ammonium transmembrane transporter activity [GO:0008519 molecular_function] (2) | Ammonium transporter AmtB-like domain [IPR024041] (2); Ammonium transporter, conserved site [IPR018047] (2); Ammonium transporter [IPR001905] (2); Ammonium/urea transporter [IPR029020] (1) | scaffold_9_mRNA_1070.1 | C_unshiu_00063_mRNA_52.1 | - |
| GF0024278 | 1 | 1 | 0 | Hypothetical protein (2) | | Gag-polypeptide of LTR copia-type [IPR029472] (1) | scaffold_9_mRNA_1055.1 | C_unshiu_00063_mRNA_43.1 | - |
| GF0024277 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1052.1 | C_unshiu_00063_mRNA_38.1 | - |
| GF0024275 | 1 | 1 | 0 | Glycerol kinase (2) | | | scaffold_9_mRNA_1036.1 | C_unshiu_00063_mRNA_22.1 | - |
| GF0024274 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1025.1 | C_unshiu_00161_mRNA_6.1 | - |
| GF0024273 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_9_mRNA_1020.1 | C_unshiu_00161_mRNA_11.1 | - |
| GF0024272 | 1 | 1 | 0 | Hypothetical protein (2) | catalytic activity [GO:0003824 molecular_function] (2); thiamine pyrophosphate binding [GO:0030976 molecular_function] (2) | Thiamin diphosphate-binding fold [IPR029061] (2); Thiamine pyrophosphate enzyme, C-terminal TPP-binding [IPR011766] (2) | scaffold_9_mRNA_1002.1 | C_unshiu_00161_mRNA_25.1 | - |
| GF0024271 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_9_mRNA_1.1 | C_unshiu_00309_mRNA_26.1 | - |
| GF0024270 | 1 | 1 | 0 | Tetratricopeptide repeat (TPR)-like superfamily protein, putative (1); Pentatricopeptide (PPR) repeat protein | | Pentatricopeptide repeat [IPR002885] (2) | scaffold_8_mRNA_994.1 | C_unshiu_00778_mRNA_11.1 | - |
| GF0024268 | 1 | 1 | 0 | Hypothetical protein (2) | protein dimerization activity [GO:0046983 molecular_function] (1) | HAT, C-terminal dimerisation domain [IPR008906] (1) | scaffold_8_mRNA_983.1 | C_unshiu_00845_mRNA_9.1 | - |
| GF0024266 | 1 | 1 | 0 | Altered inheritance of mitochondria 23, mitochondrial (2) | | | scaffold_8_mRNA_971.1 | C_unshiu_00624_mRNA_10.1 | - |
| GF0024265 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_967.1 | C_unshiu_01451_mRNA_5.1 | - |
| GF0024262 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_929.1 | C_unshiu_00117_mRNA_75.1 | - |
| GF0024261 | 1 | 1 | 0 | Hypothetical protein (1); Retrotransposon protein, putative, unclassified (1) | nucleic acid binding [GO:0003676 molecular_function] (1) | Ribonuclease H-like domain [IPR012337] (1) | scaffold_8_mRNA_912.1 | C_unshiu_00220_mRNA_15.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0024260 | 1 | 1 | 0 | DNA replication licensing factor MCM4 (2) | ATP binding [GO:0005524 molecular_function] (2); DNA binding [GO:0003677 molecular_function] (2); DNA replication initiation [GO:0006270 biological_process] (2); MCM complex [GO:0042555 cellular_component] (2); DNA replication [GO:0006260 biological_process] (2); DNA helicase activity [GO:0003678 molecular_function] (2) | MCM N-terminal domain [IPR027925] (2); Nucleic acid-binding, OB-fold [IPR012340] (2); Mini-chromosome maintenance protein [IPR031327] (2); Mini-chromosome maintenance complex protein 4 [IPR008047] (2); MCM domain [IPR001208] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); Mini-chromosome maintenance, conserved site [IPR018525] (2); MCM OB domain [IPR033762] (1); Rubredoxin-type fold [IPR004039] (1) | scaffold_8_mRNA_911.1 | C_unshiu_00220_mRNA_14.1 | - |
| GF0024259 | 1 | 1 | 0 | Hypothetical protein (2) | 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_8_mRNA_906.1 | C_unshiu_01161_mRNA_6.1 | - |
| GF0024258 | 1 | 1 | 0 | Hypothetical protein (2) | cysteine-type peptidase activity [GO:0008234 molecular_function] (2) | Peptidase C1A [IPR013128] (2); Cathepsin propeptide inhibitor domain (I29) [IPR013201] (2) | scaffold_8_mRNA_904.1 | C_unshiu_01161_mRNA_7.1 | - |
| GF0024257 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_903.1 | C_unshiu_01161_mRNA_8.1 | - |
| GF0024256 | 1 | 1 | 0 | Pentatricopeptide (PPR) repeat protein (2) | protein binding [GO:0005515 molecular_function] (2) | Pentatricopeptide repeat [IPR002885] (2); Tetratricopeptide-like helical domain [IPR011990] (2) | scaffold_8_mRNA_894.1 | C_unshiu_00874_mRNA_2.1 | - |
| GF0024255 | 1 | 1 | 0 | Tetratricopeptide repeat (TPR)-like superfamily protein, putative (2) | | Pentatricopeptide repeat [IPR002885] (2) | scaffold_8_mRNA_889.1 | C_unshiu_00125_mRNA_3.1 | - |
| GF0024253 | 1 | 1 | 0 | GDSL esterase/lipase APG (2) | hydrolase activity, acting on ester bonds [GO:0016788 molecular_function] (2) | GDSL lipase/esterase [IPR001087] (2); SGNH hydrolase-type esterase domain [IPR013830] (1) | scaffold_8_mRNA_87.1 | C_unshiu_00041_mRNA_26.1 | - |
| GF0024252 | 1 | 1 | 0 | Verticillium wilt resistance-like protein (1); Putative verticillium wilt disease resistance protein (1) | protein binding [GO:0005515 molecular_function] (2) | Leucine-rich repeat domain, L domain-like [IPR032675] (2); Leucine-rich repeat, typical subtype [IPR003591] (2); Leucine-rich repeat [IPR001611] (2) | scaffold_8_mRNA_864.1 | C_unshiu_00060_mRNA_52.1 | - |
| GF0024251 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_862.1 | C_unshiu_00637_mRNA_3.1 | - |
| GF0024249 | 1 | 1 | 0 | Putative mitochondrial chaperone BCS1-B (2) | ATP binding [GO:0005524 molecular_function] (2) | AAA+ ATPase domain [IPR003593] (2); ATPase, AAA-type, core [IPR003959] (2); AAA-type ATPase, N-terminal domain [IPR025753] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); ATPase, AAA-type, conserved site [IPR003960] (1) | scaffold_8_mRNA_846.1 | C_unshiu_01593_mRNA_1.1 | - |
| GF0024248 | 1 | 1 | 0 | Hypothetical protein (2) | defense response [GO:0006952 biological_process] (2) | Knottin, scorpion toxin-like [IPR003614] (2); Gamma-thionin [IPR008176] (1); Defensin, plant [IPR008176] (1) | scaffold_8_mRNA_839.1 | C_unshiu_00815_mRNA_5.1 | - |
| GF0024246 | 1 | 1 | 0 | Hypothetical protein (2) | | Reverse transcriptase zinc-binding domain [IPR026960] (2) | scaffold_8_mRNA_827.1 | C_unshiu_01879_mRNA_3.1 | - |
| GF0024245 | 1 | 1 | 0 | Isoflavone reductase family protein (1); Hypothetical protein (1) | | NmrA-like domain [IPR008030] (2); NAD(P)-binding domain [IPR016040] (2) | scaffold_8_mRNA_818.1 | C_unshiu_01879_mRNA_1.1 | - |
| GF0024244 | 1 | 1 | 0 | Probable pectinesterase 68 (1); Pectinesterase 31 (1) | cell wall modification [GO:0042545 biological_process] (2); cell wall [GO:0005618 cellular_component] (2); pectinesterase activity [GO:0030599 molecular_function] (2) | Pectinesterase, catalytic [IPR000070] (2); Pectin lyase fold [IPR012334] (2); Pectin lyase fold/virulence factor [IPR011050] (2) | scaffold_8_mRNA_809.1 | C_unshiu_00511_mRNA_5.1 | - |
| GF0024243 | 1 | 1 | 0 | Hypothetical protein (2) | | Retrotransposon gag domain [IPR005162] (2) | scaffold_8_mRNA_798.1 | C_unshiu_02198_mRNA_3.1 | - |
| GF0024242 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_790.1 | C_unshiu_02286_mRNA_3.1 | - |
| GF0024240 | 1 | 1 | 0 | Hypothetical protein (2) | protein binding [GO:0005515 molecular_function] (1) | Pentatricopeptide repeat [IPR002885] (2); Tetratricopeptide-like helical domain [IPR011990] (1) | scaffold_8_mRNA_781.1 | C_unshiu_00444_mRNA_21.1 | - |
| GF0024238 | 1 | 1 | 0 | Hypothetical protein (2) | ATP binding [GO:0005524 molecular_function] (1); ATPase activity [GO:0016887 molecular_function] (1) | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); ABC transporter-like [IPR003439] (1) | scaffold_8_mRNA_776.1 | C_unshiu_00362_mRNA_20.1 | - |
| GF0024237 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_760.1 | C_unshiu_02149_mRNA_1.1 | - |
| GF0024235 | 1 | 1 | 0 | Hypothetical protein (2) | cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1) | Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1); Organ specific protein [IPR024489] (1) | scaffold_8_mRNA_747.1 | C_unshiu_00438_mRNA_4.1 | - |
| GF0024234 | 1 | 1 | 0 | Hypothetical protein (2) | | Organ specific protein [IPR024489] (2) | scaffold_8_mRNA_745.1 | C_unshiu_01007_mRNA_1.1 | - |
| GF0024233 | 1 | 1 | 0 | Polynucleotidyl transferase, Ribonuclease H fold (1); Ribonuclease H-like superfamily protein (1) | nucleic acid binding [GO:0003676 molecular_function] (1) | Reverse transcriptase zinc-binding domain [IPR026960] (2); Ribonuclease H-like domain [IPR012337] (1) | scaffold_8_mRNA_744.1 | C_unshiu_02999_mRNA_2.1 | - |
| GF0024232 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_743.1 | C_unshiu_02999_mRNA_1.1 | - |
| GF0024231 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_733.1 | C_unshiu_01713_mRNA_8.1 | - |
| GF0024228 | 1 | 1 | 0 | UDP-glycosyltransferase 83A1 (2) | transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (2); metabolic process [GO:0008152 biological_process] (2) | UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (2) | scaffold_8_mRNA_70.1 | C_unshiu_00041_mRNA_12.1 | - |
| GF0024226 | 1 | 1 | 0 | Hypothetical protein (1); DUF241 domain protein (1) | | Protein of unknown function DUF241, plant [IPR004320] (2) | scaffold_8_mRNA_69.1 | C_unshiu_00041_mRNA_11.1 | - |
| GF0024225 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2); DNA integration [GO:0015074 biological_process] (2) | GAG-pre-integrase domain [IPR025724] (2); Ribonuclease H-like domain [IPR012337] (2); Integrase, catalytic core [IPR001584] (2) | scaffold_8_mRNA_687.1 | C_unshiu_00140_mRNA_27.1 | - |
| GF0024223 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_661.1 | C_unshiu_01175_mRNA_8.1 | - |
| GF0024221 | 1 | 1 | 0 | Cytochrome b6-f complex subunit 7 (2) | cytochrome b6f complex [GO:0009512 cellular_component] (2) | PetM of cytochrome b6/f complex subunit 7 [IPR012595] (2) | scaffold_8_mRNA_639.1 | C_unshiu_00560_mRNA_11.1 | - |
| GF0024220 | 1 | 1 | 0 | B3 domain-containing transcription factor VRN1 (2) | DNA binding [GO:0003677 molecular_function] (2) | B3 DNA binding domain [IPR003340] (2); DNA-binding pseudobarrel domain [IPR015300] (2) | scaffold_8_mRNA_628.1 | C_unshiu_00630_mRNA_5.1 | - |
| GF0024218 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_619.1 | C_unshiu_00308_mRNA_10.1 | - |
| GF0024217 | 1 | 1 | 0 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (2) | oxidoreductase activity [GO:0016491 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2); iron ion binding [GO:0005506 molecular_function] (1) | Isopenicillin N synthase-like [IPR027443] (2); Non-haem dioxygenase N-terminal domain [IPR026992] (2); Oxoglutarate/iron-dependent dioxygenase [IPR005123] (2); Isopenicillin N synthase [IPR002283] (1) | scaffold_8_mRNA_616.1 | C_unshiu_00308_mRNA_13.1 | - |
| GF0024216 | 1 | 1 | 0 | Putative inactive receptor kinase (2) | ATP binding [GO:0005524 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2); protein kinase activity [GO:0004672 molecular_function] (2) | Protein kinase domain [IPR000719] (2); Protein kinase-like domain [IPR011009] (2); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1) | scaffold_8_mRNA_606.1 | C_unshiu_00630_mRNA_15.1 | - |
| GF0024215 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_605.1 | C_unshiu_01911_mRNA_4.1 | - |
| GF0024214 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_602.1 | C_unshiu_00589_mRNA_17.1 | - |
| GF0024213 | 1 | 1 | 0 | Hypothetical protein (1); Sorting nexin carboxy-terminal protein (1) | zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1) | Sorting nexin, C-terminal [IPR013937] (1); Zinc finger, SWIM-type [IPR007527] (1); Zinc finger, PMZ-type [IPR006564] (1); Zinc finger, CCHC-type [IPR001878] (1); Phox-associated domain [IPR003114] (1) | scaffold_8_mRNA_598.1 | C_unshiu_00589_mRNA_16.1 | - |
| GF0024212 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_587.1 | C_unshiu_00015_mRNA_5.1 | - |
| GF0024211 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_582.1 | C_unshiu_01091_mRNA_2.1 | - |
| GF0024210 | 1 | 1 | 0 | Hypothetical protein (1); Polynucleotidyl transferase, ribonuclease H-like superfamily protein (1) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_8_mRNA_578.1 | C_unshiu_01293_mRNA_6.1 | - |
| GF0024208 | 1 | 1 | 0 | CXE carboxylesterase (2) | metabolic process [GO:0008152 biological_process] (2); hydrolase activity [GO:0016787 molecular_function] (2) | Alpha/Beta hydrolase fold [IPR029058] (2); Alpha/beta hydrolase fold-3 [IPR013094] (2) | scaffold_8_mRNA_563.1 | C_unshiu_00736_mRNA_8.1 | - |
| GF0024206 | 1 | 1 | 0 | Putative carboxylesterase 2 (2) | hydrolase activity [GO:0016787 molecular_function] (2); metabolic process [GO:0008152 biological_process] (2) | Alpha/Beta hydrolase fold [IPR029058] (2); Alpha/beta hydrolase fold-3 [IPR013094] (2) | scaffold_8_mRNA_559.1 | C_unshiu_00736_mRNA_4.1 | - |
| GF0024205 | 1 | 1 | 0 | Hypothetical protein (2) | hydrolase activity [GO:0016787 molecular_function] (2); metabolic process [GO:0008152 biological_process] (2) | Alpha/beta hydrolase fold-3 [IPR013094] (2); Alpha/Beta hydrolase fold [IPR029058] (2) | scaffold_8_mRNA_556.1 | C_unshiu_01210_mRNA_1.1 | - |
| GF0024204 | 1 | 1 | 0 | Hypothetical protein (2) | | Alpha/Beta hydrolase fold [IPR029058] (2) | scaffold_8_mRNA_554.1 | C_unshiu_01210_mRNA_3.1 | - |
| GF0024203 | 1 | 1 | 0 | Hypothetical protein (2) | metabolic process [GO:0008152 biological_process] (2); hydrolase activity [GO:0016787 molecular_function] (2) | Alpha/beta hydrolase fold-3 [IPR013094] (2); Alpha/Beta hydrolase fold [IPR029058] (2) | scaffold_8_mRNA_553.1 | C_unshiu_01210_mRNA_4.1 | - |
| GF0024202 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_550.1 | C_unshiu_01210_mRNA_9.1 | - |
| GF0024201 | 1 | 1 | 0 | Hypothetical protein (2) | | Reverse transcriptase zinc-binding domain [IPR026960] (1) | scaffold_8_mRNA_544.1 | C_unshiu_02219_mRNA_1.1 | - |
| GF0024200 | 1 | 1 | 0 | Hypothetical protein (2) | metabolic process [GO:0008152 biological_process] (2); hydrolase activity [GO:0016787 molecular_function] (2) | Alpha/beta hydrolase fold-3 [IPR013094] (2); Alpha/Beta hydrolase fold [IPR029058] (2) | scaffold_8_mRNA_536.1 | C_unshiu_02622_mRNA_5.1 | - |
| GF0024199 | 1 | 1 | 0 | Hypothetical protein (2) | | Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1) | scaffold_8_mRNA_523.1 | C_unshiu_01576_mRNA_9.1 | - |
| GF0024198 | 1 | 1 | 0 | Hypothetical protein (2) | metal ion binding [GO:0046872 molecular_function] (2); catalytic activity [GO:0003824 molecular_function] (2) | Metalloenzyme, LuxS/M16 peptidase-like [IPR011249] (2); Peptidase M16, C-terminal [IPR007863] (2); Peptidase M16, N-terminal [IPR011765] (2); Peptidase M16 domain [IPR011237] (1) | scaffold_8_mRNA_521.1 | C_unshiu_02622_mRNA_3.1 | - |
| GF0024195 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_497.1 | C_unshiu_01315_mRNA_3.1 | - |
| GF0024194 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_491.1 | C_unshiu_00646_mRNA_3.1 | - |
| GF0024193 | 1 | 1 | 0 | Subtilisin-like serine protease (2) | serine-type endopeptidase activity [GO:0004252 molecular_function] (2); proteolysis [GO:0006508 biological_process] (2) | Peptidase S8, subtilisin, Ser-active site [IPR023828] (2); Peptidase S8/S53 domain [IPR000209] (2); Peptidase S8, subtilisin-related [IPR015500] (1) | scaffold_8_mRNA_481.1 | C_unshiu_00827_mRNA_12.1 | - |
| GF0024192 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_479.1 | C_unshiu_00827_mRNA_14.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0024190 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_476.1 | C_unshiu_00827_mRNA_16.1 | - |
| GF0024188 | 1 | 1 | 0 | Hypothetical protein (2) | | Peptidase S8 propeptide/proteinase inhibitor I9 [IPR010259] (2); Peptidase S8, subtilisin-related [IPR015500] (1) | scaffold_8_mRNA_469.1 | C_unshiu_00152_mRNA_4.1 | - |
| GF0024187 | 1 | 1 | 0 | Putative nuclease HARBI1 (2) | | Harbinger transposase-derived nuclease domain [IPR027806] (2) | scaffold_8_mRNA_463.1 | C_unshiu_00152_mRNA_10.1 | - |
| GF0024185 | 1 | 1 | 0 | Pentatricopeptide (PPR) repeat protein (2) | protein binding [GO:0005515 molecular_function] (1) | Pentatricopeptide repeat [IPR002885] (2); Tetratricopeptide-like helical domain [IPR011990] (1) | scaffold_8_mRNA_451.1 | C_unshiu_00152_mRNA_23.1 | - |
| GF0024182 | 1 | 1 | 0 | Cyclin D (2) | nucleus [GO:0005634 cellular_component] (2) | Cyclin, C-terminal domain [IPR004367] (2); Cyclin-like [IPR013763] (2); Cyclin, N-terminal [IPR006671] (2) | scaffold_8_mRNA_436.1 | C_unshiu_00152_mRNA_35.1 | - |
| GF0024180 | 1 | 1 | 0 | Phosphoglycerate dehydrogenase (2) | metabolic process [GO:0008152 biological_process] (2); L-serine biosynthetic process [GO:0006564 biological_process] (2); amino acid binding [GO:0016597 molecular_function] (2); phosphoglycerate dehydrogenase activity [GO:0004617 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2); oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor [GO:0016616 molecular_function] (2); NAD binding [GO:0051287 molecular_function] (2) | D-isomer specific 2-hydroxyacid dehydrogenase, catalytic domain [IPR006139] (2); S-adenosyl-L-homocysteine hydrolase, NAD binding domain [IPR015878] (2); D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding domain [IPR006140] (2); ACT domain [IPR002912] (2); D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding domain conserved site [IPR029753] (2); NAD(P)-binding domain [IPR016040] (2); Allosteric substrate binding domain [IPR029009] (2); D-3-phosphoglycerate dehydrogenase [IPR006236] (2); D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding domain conserved site 1 [IPR029752] (2) | scaffold_8_mRNA_421.1 | C_unshiu_00152_mRNA_44.1 | - |
| GF0024179 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_408.1 | C_unshiu_00152_mRNA_56.1 | - |
| GF0024176 | 1 | 1 | 0 | RNA polymerase-associated protein RTF1 like (2) | transcription elongation from RNA polymerase II promoter [GO:0006368 biological_process] (2); histone modification [GO:0016570 biological_process] (2); Cdc73/Paf1 complex [GO:0016593 cellular_component] (2); DNA binding [GO:0003677 molecular_function] (2); DNA-templated transcription, initiation [GO:0006352 biological_process] (1); nucleus [GO:0005634 cellular_component] (1) | Plus-3 domain [IPR004343] (2); RNA polymerase-associated protein Rtf1 [IPR031102] (2); Plus-3 domain, subgroup [IPR018144] (1) | scaffold_8_mRNA_391.1 | C_unshiu_00363_mRNA_16.1 | - |
| GF0024175 | 1 | 1 | 0 | F-box protein interaction domain protein (2) | protein binding [GO:0005515 molecular_function] (2) | F-box domain [IPR001810] (2); F-box associated interaction domain [IPR017451] (2); F-box associated domain, type 1 [IPR006527] (1) | scaffold_8_mRNA_388.1 | C_unshiu_00363_mRNA_19.1 | - |
| GF0024174 | 1 | 1 | 0 | Carboxy-terminal domain cyclin (2) | nucleus [GO:0005634 cellular_component] (2) | Cyclin, N-terminal [IPR006671] (2); Cyclin-like [IPR013763] (2); Cyclin, C-terminal domain [IPR004367] (2); Cyclin A, plant [IPR029507] (1) | scaffold_8_mRNA_378.1 | C_unshiu_00363_mRNA_30.1 | - |
| GF0024173 | 1 | 1 | 0 | Vignain (2) | cysteine-type peptidase activity [GO:0008234 molecular_function] (2); proteolysis [GO:0006508 biological_process] (2) | Cysteine peptidase, histidine active site [IPR025660] (2); Peptidase C1A [IPR013128] (2); Peptidase C1A, papain C-terminal [IPR000668] (2); Cysteine peptidase, asparagine active site [IPR025661] (2); Cathepsin propeptide inhibitor domain (I29) [IPR013201] (1) | scaffold_8_mRNA_376.1 | C_unshiu_00363_mRNA_32.1 | - |
| GF0024172 | 1 | 1 | 0 | Class II metallothionein-like protein 1A (2) | zinc ion binding [GO:0008270 molecular_function] (2) | Plant EC metallothionein-like protein, family 15 [IPR000316] (2) | scaffold_8_mRNA_37.1 | C_unshiu_00376_mRNA_12.1 | - |
| GF0024170 | 1 | 1 | 0 | SWIB complex BAF60b domain-containing family protein (2) | protein binding [GO:0005515 molecular_function] (2) | SWIB/MDM2 domain [IPR003121] (2); SWIB domain [IPR019835] (2) | scaffold_8_mRNA_365.1 | C_unshiu_00024_mRNA_8.1 | - |
| GF0024168 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_36.1 | C_unshiu_00376_mRNA_13.1 | - |
| GF0024167 | 1 | 1 | 0 | Somatic embryogenesis receptor kinase 1 (2) | transmembrane receptor protein kinase activity [GO:0019199 molecular_function] (1) | Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Somatic embryogenesis receptor-like kinase [IPR031048] (1) | scaffold_8_mRNA_356.2 | C_unshiu_00024_mRNA_15.1 | - |
| GF0024166 | 1 | 1 | 0 | Amino acid permease family protein (2) | amino acid transmembrane transporter activity [GO:0015171 molecular_function] (2); amino acid transmembrane transport [GO:0003333 biological_process] (2); membrane [GO:0016020 cellular_component] (2) | Amino acid/polyamine transporter I [IPR002293] (2) | scaffold_8_mRNA_351.1 | C_unshiu_00024_mRNA_18.1 | - |
| GF0024160 | 1 | 1 | 0 | High chlorophyll fluorescence phenotype 173 protein (2) | | Galactose-binding domain-like [IPR008979] (2); NAD(P)-binding domain [IPR016040] (2); NADH:ubiquinone oxidoreductase intermediate-associated protein 30 [IPR013857] (2); NmrA-like domain [IPR008030] (1) | scaffold_8_mRNA_3245.1 | C_unshiu_00211_mRNA_24.1 | - |
| GF0024158 | 1 | 1 | 0 | Laccase (2) | lignin catabolic process [GO:0046274 biological_process] (2); hydroquinone:oxygen oxidoreductase activity [GO:0052716 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2); oxidoreductase activity [GO:0016491 molecular_function] (2); apoplast [GO:0048046 cellular_component] (2); copper ion binding [GO:0005507 molecular_function] (2) | Multicopper oxidase, copper-binding site [IPR002355] (2); Multicopper oxidase, type 3 [IPR011707] (2); Multicopper oxidases, conserved site [IPR033138] (2); Laccase [IPR017761] (2); Multicopper oxidase, type 2 [IPR011706] (2); Multicopper oxidase, type 1 [IPR001117] (2); Cupredoxin [IPR008972] (2); Laccase, third cupredoxin domain [IPR034289] (1); Laccase, first cupredoxin domain [IPR034288] (1); Laccase, second cupredoxin domain [IPR034285] (1) | scaffold_8_mRNA_3227.1 | C_unshiu_00271_mRNA_23.1 | - |
| GF0024156 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_320.1 | C_unshiu_00024_mRNA_45.1 | - |
| GF0024155 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_3191.1 | C_unshiu_00021_mRNA_110.1 | - |
| GF0024151 | 1 | 1 | 0 | Hypothetical protein (2) | metabolic process [GO:0008152 biological_process] (2); transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (2) | UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (2) | scaffold_8_mRNA_3149.1 | C_unshiu_00021_mRNA_70.1 | - |
| GF0024150 | 1 | 1 | 0 | Transcription factor MYB98 (1); Hypothetical protein (1) | DNA binding [GO:0003677 molecular_function] (1) | SANT/Myb domain [IPR001005] (1); Myb domain [IPR017930] (1); Homeobox domain-like [IPR009057] (1) | scaffold_8_mRNA_3145.1 | C_unshiu_00021_mRNA_66.1 | - |
| GF0024149 | 1 | 1 | 0 | Thioesterase superfamily protein (2) | | HotDog domain [IPR029069] (2); Thioesterase domain [IPR006683] (2) | scaffold_8_mRNA_3127.1 | C_unshiu_00021_mRNA_49.1 | - |
| GF0024148 | 1 | 1 | 0 | Hypothetical protein (2) | proteolysis [GO:0006508 biological_process] (2); cysteine-type peptidase activity [GO:0008234 molecular_function] (2) | Ulp1 protease family, C-terminal catalytic domain [IPR003653] (2) | scaffold_8_mRNA_3121.1 | C_unshiu_00021_mRNA_43.1 | - |
| GF0024147 | 1 | 1 | 0 | Putative sugar phosphate/phosphate translocator (2) | | Sugar phosphate transporter domain [IPR004853] (2) | scaffold_8_mRNA_3114.1 | C_unshiu_00021_mRNA_35.1 | - |
| GF0024145 | 1 | 1 | 0 | UDP-glucoronosyl/UDP-glucosyl transferase family protein (2) | metabolic process [GO:0008152 biological_process] (2); transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (2); 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) | UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (2); Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450 [IPR001128] (1) | scaffold_8_mRNA_3104.1 | C_unshiu_00021_mRNA_24.1 | - |
| GF0024144 | 1 | 1 | 0 | Copper transporter (2) | copper ion transmembrane transport [GO:0035434 biological_process] (2); integral component of membrane [GO:0016021 cellular_component] (2); copper ion transmembrane transporter activity [GO:0005375 molecular_function] (2) | Ctr copper transporter [IPR007274] (2) | scaffold_8_mRNA_3083.1 | C_unshiu_00117_mRNA_27.1 | - |
| GF0024143 | 1 | 1 | 0 | Cucumisin (1); Hypothetical 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/S53 domain [IPR000209] (1); Peptidase S8, subtilisin-related [IPR015500] (1) | scaffold_8_mRNA_3074.1 | C_unshiu_00117_mRNA_38.1 | - |
| GF0024142 | 1 | 1 | 0 | DNA-directed RNA polymerase II non-catalytic subunit (2) | nucleic acid binding [GO:0003676 molecular_function] (2); transcription, DNA-templated [GO:0006351 biological_process] (2); DNA-directed RNA polymerase activity [GO:0003899 molecular_function] (1); DNA-directed 5'-3' RNA polymerase activity [GO:0003899 molecular_function] (1) | S1 domain [IPR003029] (2); RNA polymerase Rpb7, N-terminal [IPR005576] (2); Nucleic acid-binding, OB-fold [IPR012340] (2) | scaffold_8_mRNA_3067.1 | C_unshiu_00117_mRNA_48.1 | - |
| GF0024141 | 1 | 1 | 0 | Hypothetical protein (2) | metabolic process [GO:0008152 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1) | NAD(P)-binding domain [IPR016040] (2); Short-chain dehydrogenase/reductase SDR [IPR002198] (1) | scaffold_8_mRNA_3055.1 | C_unshiu_00117_mRNA_59.1 | - |
| GF0024140 | 1 | 1 | 0 | Plastid transcriptionally active 16 (2) | | NAD(P)-binding domain [IPR016040] (2); NmrA-like domain [IPR008030] (1) | scaffold_8_mRNA_3050.1 | C_unshiu_00117_mRNA_62.1 | - |
| GF0024139 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_3036.1 | C_unshiu_00281_mRNA_43.1 | - |
| GF0024138 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_3035.1 | C_unshiu_02529_mRNA_5.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0024135 | 1 | 1 | 0 | Zinc transporter 1 (1); Hypothetical protein (1) | membrane [GO:0016020 cellular_component] (2); metal ion transmembrane transporter activity [GO:0046873 molecular_function] (2); metal ion transport [GO:0030001 biological_process] (2); transmembrane transport [GO:0055085 biological_process] (2) | Zinc/iron permease [IPR003689] (2) | scaffold_8_mRNA_3026.1 | C_unshiu_00281_mRNA_34.1 | - |
| GF0024134 | 1 | 1 | 0 | Haloacid dehalogenase-like hydrolase (2) | metabolic process [GO:0008152 biological_process] (2); hydrolase activity [GO:0016787 molecular_function] (2) | HAD hydrolase, subfamily IA [IPR006439] (2); HAD-like domain [IPR023214] (2); Pyrimidine 5-nucleotidase [IPR010237] (2) | scaffold_8_mRNA_3020.1 | C_unshiu_00281_mRNA_27.1 | - |
| GF0024133 | 1 | 1 | 0 | Haloacid dehalogenase-like hydrolase (2) | metabolic process [GO:0008152 biological_process] (2); hydrolase activity [GO:0016787 molecular_function] (2) | HAD hydrolase, subfamily IA [IPR006439] (2); HAD-like domain [IPR023214] (2); Pyrimidine 5-nucleotidase [IPR010237] (2) | scaffold_8_mRNA_3019.1 | C_unshiu_00281_mRNA_26.2 | - |
| GF0024132 | 1 | 1 | 0 | Photosystem I reaction center subunit N (2) | photosystem I [GO:0009522 cellular_component] (2); photosynthesis [GO:0015979 biological_process] (2) | Photosystem I reaction centre subunit N, chloroplastic [IPR008796] (2) | scaffold_8_mRNA_301.1 | C_unshiu_00024_mRNA_62.1 | - |
| GF0024131 | 1 | 1 | 0 | Hypothetical protein (2) | oxidation-reduction process [GO:0055114 biological_process] (2); oxidoreductase activity [GO:0016491 molecular_function] (2); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1) | Aldehyde oxidase/xanthine dehydrogenase, molybdopterin binding [IPR008274] (2); FHY3/FAR1 family [IPR031052] (1) | scaffold_8_mRNA_3007.1 | C_unshiu_00281_mRNA_13.1 | - |
| GF0024130 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2); zinc ion binding [GO:0008270 molecular_function] (1) | Ribonuclease H-like domain [IPR012337] (1); Zinc finger, CCHC-type [IPR001878] (1) | scaffold_8_mRNA_2997.1 | C_unshiu_00281_mRNA_3.1 | - |
| GF0024129 | 1 | 1 | 0 | Serine carboxypeptidase 1 (2) | proteolysis [GO:0006508 biological_process] (2); serine-type carboxypeptidase activity [GO:0004185 molecular_function] (2) | Serine carboxypeptidases, histidine active site [IPR033124] (2); Peptidase S10, serine carboxypeptidase [IPR001563] (2); Alpha/Beta hydrolase fold [IPR029058] (2) | scaffold_8_mRNA_298.1 | C_unshiu_00024_mRNA_65.1 | - |
| GF0024128 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_2977.1 | C_unshiu_00571_mRNA_9.1 | - |
| GF0024127 | 1 | 1 | 0 | Hypothetical protein (2) | 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_2971.1 | C_unshiu_00571_mRNA_22.1 | - |
| GF0024125 | 1 | 1 | 0 | Histone H2A (2) | nucleus [GO:0005634 cellular_component] (2); DNA binding [GO:0003677 molecular_function] (2); protein heterodimerization activity [GO:0046982 molecular_function] (2); nucleosome [GO:0000786 cellular_component] (2) | Histone H2A/H2B/H3 [IPR007125] (2); Histone H2A, C-terminal domain [IPR032454] (2); Histone H2A conserved site [IPR032458] (2); Histone-fold [IPR009072] (2); Histone H2A [IPR002119] (2) | scaffold_8_mRNA_2950.1 | C_unshiu_00525_mRNA_15.1 | - |
| GF0024124 | 1 | 1 | 0 | RNA recognition motif (2) | nucleic acid binding [GO:0003676 molecular_function] (2); nucleotide binding [GO:0000166 molecular_function] (1) | RNA recognition motif domain [IPR000504] (2); Nucleotide-binding alpha-beta plait domain [IPR012677] (1) | scaffold_8_mRNA_2949.1 | C_unshiu_00525_mRNA_14.1 | - |
| GF0024122 | 1 | 1 | 0 | Histone H2B (2) | nucleosome [GO:0000786 cellular_component] (2); DNA binding [GO:0003677 molecular_function] (2); protein heterodimerization activity [GO:0046982 molecular_function] (2) | Histone-fold [IPR009072] (2); Histone H2B [IPR000558] (2); Histone H2A/H2B/H3 [IPR007125] (2) | scaffold_8_mRNA_2944.1 | C_unshiu_00525_mRNA_11.1 | - |
| GF0024120 | 1 | 1 | 0 | Disease resistance response/dirigent-like protein (2) |  | Plant disease resistance response protein [IPR004265] (2) | scaffold_8_mRNA_2924.1 | C_unshiu_00158_mRNA_48.1 | - |
| GF0024119 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_291.1 | C_unshiu_01074_mRNA_5.1 | - |
| GF0024118 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_2907.1 | C_unshiu_00858_mRNA_7.1 | - |
| GF0024117 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_2899.1 | C_unshiu_00158_mRNA_24.1 | - |
| GF0024116 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_2896.1 | C_unshiu_00158_mRNA_22.1 | - |
| GF0024110 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_286.1 | C_unshiu_00024_mRNA_67.1 | - |
| GF0024108 | 1 | 1 | 0 | ATP synthase subunit d, mitochondrial (1); Hypothetical protein (1) | ATP synthesis coupled proton transport [GO:0015986 biological_process] (2); mitochondrial proton-transporting ATP synthase complex, coupling factor F(o) [GO:0000276 cellular_component] (2); hydrogen ion transmembrane transporter activity [GO:0015078 molecular_function] (2) | ATPase, F0 complex, subunit D, mitochondrial [IPR008689] (1); ATP synthase, F0 complex, subunit D, mitochondrial [IPR008689] (1) | scaffold_8_mRNA_2843.1 | C_unshiu_00082_mRNA_44.1 | - |
| GF0024107 | 1 | 1 | 0 | Hypothetical protein (1); Translation elongation factor EF-1 alpha (1) |  |  | scaffold_8_mRNA_2837.1 | C_unshiu_00639_mRNA_21.1 | - |
| GF0024106 | 1 | 1 | 0 | Tetratricopeptide repeat-like superfamily protein, putative (1); Pentatricopeptide repeat-containing protein, mitochondrial (1) |  | Pentatricopeptide repeat [IPR002885] (2) | scaffold_8_mRNA_2825.1 | C_unshiu_00639_mRNA_11.1 | - |
| GF0024103 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_2812.1 | C_unshiu_01354_mRNA_6.1 | - |
| GF0024100 | 1 | 1 | 0 | Proline-rich receptor-like protein kinase PERK15 (2) | protein kinase activity [GO:0004672 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2); ATP binding [GO:0005524 molecular_function] (2) | Protein kinase domain [IPR000719] (2); Protein kinase-like domain [IPR011009] (2); Protein kinase, ATP binding site [IPR017441] (2); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1) | scaffold_8_mRNA_2788.1 | C_unshiu_00481_mRNA_12.1 | - |
| GF0024098 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_2778.1 | C_unshiu_01053_mRNA_9.1 | - |
| GF0024097 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_2766.1 | C_unshiu_00500_mRNA_15.1 | - |
| GF0024094 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_2746.1 | C_unshiu_00438_mRNA_23.1 | - |
| GF0024090 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_2694.1 | C_unshiu_00049_mRNA_3.1 | - |
| GF0024089 | 1 | 1 | 0 | Hypothetical protein (2) | membrane [GO:0016020 cellular_component] (2); metal ion binding [GO:0046872 molecular_function] (1); oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen [GO:0016702 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1) | Prohibitin [IPR000163] (2); Lipoxygenase, C-terminal [IPR013819] (1) | scaffold_8_mRNA_2664.1 | C_unshiu_02347_mRNA_2.1 | - |
| GF0024088 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2); nucleotide binding [GO:0000166 molecular_function] (1); RNA binding [GO:0003723 molecular_function] (1) | RNA recognition motif domain [IPR000504] (2); Polyadenylate-binding protein/Hyperplastic disc protein [IPR002004] (1); Nucleotide-binding alpha-beta plait domain [IPR012677] (1) | scaffold_8_mRNA_2647.1 | C_unshiu_00883_mRNA_5.1 | - |
| GF0024086 | 1 | 1 | 0 | Hypothetical protein (1); Cysteine-rich receptor-like protein kinase 10 (1) | protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1) | Protein kinase-like domain [IPR011009] (2); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1) | scaffold_8_mRNA_2628.1 | C_unshiu_01848_mRNA_4.1 | - |
| GF0024085 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_8_mRNA_2624.1 | C_unshiu_01999_mRNA_5.1 | - |
| GF0024084 | 1 | 1 | 0 | Phototropic-responsive NPH3 family protein (2) | protein binding [GO:0005515 molecular_function] (2) | SKP1/BTB/POZ domain [IPR011333] (2); NPH3 domain [IPR027356] (2); BTB/POZ domain [IPR000210] (2) | scaffold_8_mRNA_2622.1 | C_unshiu_00897_mRNA_8.1 | - |
| GF0024080 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_2595.1 | C_unshiu_00320_mRNA_7.1 | - |
| GF0024077 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_2587.1 | C_unshiu_00320_mRNA_16.1 | - |
| GF0024076 | 1 | 1 | 0 | Jerky putative (1); Hypothetical protein (1) | nucleic acid binding [GO:0003676 molecular_function] (1) | DDE superfamily endonuclease domain [IPR004875] (1) | scaffold_8_mRNA_2586.1 | C_unshiu_00320_mRNA_17.1 | - |
| GF0024075 | 1 | 1 | 0 | Hypothetical protein (2) |  | X8 domain [IPR012946] (2) | scaffold_8_mRNA_2575.1 | C_unshiu_00320_mRNA_25.1 | - |
| GF0024074 | 1 | 1 | 0 | Hypothetical protein (2) |  | Domain of unknown function DUF1985 [IPR015410] (2) | scaffold_8_mRNA_2559.1 | C_unshiu_00059_mRNA_47.1 | - |
| GF0024073 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_2557.1 | C_unshiu_00059_mRNA_43.1 | - |
| GF0024072 | 1 | 1 | 0 | Polynucleotidyl transferase, Ribonuclease H fold (1); Putative ribonuclease H protein (1) | nucleic acid binding [GO:0003676 molecular_function] (2) | Reverse transcriptase zinc-binding domain [IPR026960] (2); Ribonuclease H-like domain [IPR012337] (2) | scaffold_8_mRNA_2556.1 | C_unshiu_00059_mRNA_42.1 | - |
| GF0024071 | 1 | 1 | 0 | Fatty acyl-CoA reductase 3 (2) | fatty-acyl-CoA reductase (alcohol-forming) activity [GO:0080019 molecular_function] (2) | Fatty acyl-CoA reductase [IPR026055] (2) | scaffold_8_mRNA_2548.1 | C_unshiu_01814_mRNA_4.1 | - |
| GF0024068 | 1 | 1 | 0 | Non-ltr retrotransposon reverse transcriptase-like protein (1); 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) | Domain of unknown function DUF4283 [IPR025558] (2); Reverse transcriptase domain [IPR000477] (2); Endonuclease/exonuclease/phosphatase [IPR005135] (2); Ribonuclease H domain [IPR002156] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1); Ribonuclease H-like domain [IPR012337] (1); Zinc finger, CCHC-type [IPR001878] (1); Protein of unknown function DUF247, plant [IPR004158] (1) | scaffold_8_mRNA_2537.1 | C_unshiu_00302_mRNA_32.1 | - |
| GF0024067 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_2534.1 | C_unshiu_00011_mRNA_31.1 | - |
| GF0024066 | 1 | 1 | 0 | Hypothetical protein (2) | fatty-acyl-CoA reductase (alcohol-forming) activity [GO:0080019 molecular_function] (2) | Fatty acyl-CoA reductase [IPR026055] (2); Fatty acyl-CoA reductase, C-terminal [IPR033640] (1); NAD(P)-binding domain [IPR016040] (1); Male sterility, NAD-binding [IPR013120] (1) | scaffold_8_mRNA_2531.1 | C_unshiu_00011_mRNA_29.1 | - |
| GF0024065 | 1 | 1 | 0 | Pentatricopeptide repeat-containing family protein (1); Chlororespiratory reduction 21 (1) | protein binding [GO:0005515 molecular_function] (2) | Tetratricopeptide-like helical domain [IPR011990] (2); Pentatricopeptide repeat [IPR002885] (2) | scaffold_8_mRNA_2529.1 | C_unshiu_00011_mRNA_27.1 | - |
| GF0024064 | 1 | 1 | 0 | Subtilisin-like serine protease (1); Subtilisin-like serine endopeptidase family protein (1) | proteolysis [GO:0006508 biological_process] (2); serine-type endopeptidase activity [GO:0004252 molecular_function] (2) | PA domain [IPR003137] (2); Peptidase S8/S53 domain [IPR000209] (2); Peptidase S8, subtilisin, Ser-active site [IPR023828] (1); Peptidase S8, subtilisin-related [IPR015500] (1) | scaffold_8_mRNA_2528.1 | C_unshiu_00011_mRNA_26.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0024063 | 1 | 1 | 0 | Hypothetical protein (2) | proteolysis [GO:0006508 biological_process] (2); serine-type endopeptidase activity [GO:0004252 molecular_function] (2) | Peptidase S8/S53 domain [IPR000209] (2); Peptidase S8, subtilisin-related [IPR015500] (1) | scaffold_8_mRNA_2526.1 | C_unshiu_00011_mRNA_24.1 | - |
| GF0024062 | 1 | 1 | 0 | Hypothetical protein (1); Reticuline oxidase-like protein (1) | | | scaffold_8_mRNA_2518.1 | C_unshiu_00011_mRNA_16.1 | - |
| GF0024061 | 1 | 1 | 0 | Alpha/beta fold hydrolase (2) | | Alpha/beta hydrolase fold-1 [IPR000073] (2); Alpha/Beta hydrolase fold [IPR029058] (2) | scaffold_8_mRNA_2508.1 | C_unshiu_00011_mRNA_10.1 | - |
| GF0024057 | 1 | 1 | 0 | Trichome birefringence-like 14 (1); Hypothetical protein (1) | | Protein trichome birefringence-like 13 [IPR029968] (2); PC-Esterase [IPR026057] (2); Trichome birefringence-like family [IPR029962] (2) | scaffold_8_mRNA_248.1 | C_unshiu_00024_mRNA_105.1 | - |
| GF0024054 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_8_mRNA_2463.1 | C_unshiu_02360_mRNA_2.1 | - |
| GF0024052 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_2454.1 | C_unshiu_00814_mRNA_8.1 | - |
| GF0024051 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_2453.1 | C_unshiu_00814_mRNA_7.1 | - |
| GF0024046 | 1 | 1 | 0 | Hypothetical protein (1); RNA-binding (RRM/RBD/RNP motif) family protein (1) | nucleic acid binding [GO:0003676 molecular_function] (2); nucleotide binding [GO:0000166 molecular_function] (1) | RNA recognition motif domain [IPR000504] (2); Nucleotide-binding alpha-beta plait domain [IPR012677] (1); RNA recognition motif domain, eukaryote [IPR003954] (1) | scaffold_8_mRNA_2424.1 | C_unshiu_00730_mRNA_6.1 | - |
| GF0024045 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_242.1 | C_unshiu_00116_mRNA_2.1 | - |
| GF0024044 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_2419.1 | C_unshiu_01561_mRNA_2.1 | - |
| GF0024042 | 1 | 1 | 0 | Probable F-box protein At1g60180 (2) | protein binding [GO:0005515 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); Ribonuclease H-like domain [IPR012337] (1); F-box domain [IPR001810] (1) | scaffold_8_mRNA_2402.1 | C_unshiu_00426_mRNA_5.1 | - |
| GF0024040 | 1 | 1 | 0 | Tnp (2) | | MULE transposase domain [IPR018289] (2) | scaffold_8_mRNA_2381.1 | C_unshiu_01840_mRNA_5.1 | - |
| GF0024038 | 1 | 1 | 0 | Hypothetical protein (2) | malate transport [GO:0015743 biological_process] (2) | Aluminum-activated malate transporter [IPR020966] (2) | scaffold_8_mRNA_2359.1 | C_unshiu_00949_mRNA_13.1 | - |
| GF0024036 | 1 | 1 | 0 | Leucine-rich repeat receptor-like protein kinase family protein (2) | protein binding [GO:0005515 molecular_function] (2) | Leucine-rich repeat [IPR001611] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Leucine-rich repeat, typical subtype [IPR003591] (2); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1) | scaffold_8_mRNA_2348.1 | C_unshiu_01153_mRNA_11.1 | - |
| GF0024035 | 1 | 1 | 0 | Hypothetical protein (2) | regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); root development [GO:0048364 biological_process] (1); transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (1); nucleus [GO:0005634 cellular_component] (1) | Transcription factor LHW [IPR033260] (1) | scaffold_8_mRNA_2342.1 | C_unshiu_00605_mRNA_15.1 | - |
| GF0024033 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_2323.1 | C_unshiu_00251_mRNA_28.1 | - |
| GF0024032 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_2319.1 | C_unshiu_00251_mRNA_24.1 | - |
| GF0024031 | 1 | 1 | 0 | Hypothetical protein (2) | | Domain of unknown function DUF1985 [IPR015410] (2) | scaffold_8_mRNA_2307.1 | C_unshiu_00251_mRNA_9.1 | - |
| GF0024030 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_23.1 | C_unshiu_00376_mRNA_28.1 | - |
| GF0024028 | 1 | 1 | 0 | 17.5 kDa class I heat shock protein (2) | | Small heat shock protein HSP20 [IPR031107] (2); HSP20-like chaperone [IPR008978] (2); Alpha crystallin/Hsp20 domain [IPR002068] (2) | scaffold_8_mRNA_2296.1 | C_unshiu_02467_mRNA_2.1 | - |
| GF0024026 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_2279.1 | C_unshiu_00826_mRNA_3.1 | - |
| GF0024025 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_2274.1 | C_unshiu_00114_mRNA_4.1 | - |
| GF0024024 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_2273.1 | C_unshiu_00114_mRNA_3.1 | - |
| GF0024023 | 1 | 1 | 0 | Cytokinin riboside 5'-monophosphate phosphoribohydrolase (2) | | | scaffold_8_mRNA_2272.1 | C_unshiu_00114_mRNA_2.1 | - |
| GF0024022 | 1 | 1 | 0 | Hypothetical protein (2) | protein dimerization activity [GO:0046983 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2); HAT, C-terminal dimerisation domain [IPR008906] (2) | scaffold_8_mRNA_2263.1 | C_unshiu_01882_mRNA_4.1 | - |
| GF0024021 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_2258.1 | C_unshiu_01653_mRNA_6.1 | - |
| GF0024020 | 1 | 1 | 0 | Chitinase / Hevein / PR-4 / Wheatwin2 (2) | defense response to bacterium [GO:0042742 biological_process] (2); defense response to fungus [GO:0050832 biological_process] (2) | Barwin, conserved site [IPR018226] (2); Barwin domain [IPR001153] (2); RlpA-like protein, double-psi beta-barrel domain [IPR009009] (1); RlpA-like double-psi beta-barrel domain [IPR009009] (1) | scaffold_8_mRNA_2256.1 | C_unshiu_01653_mRNA_4.1 | - |
| GF0024019 | 1 | 1 | 0 | Chitinase / Hevein / PR-4 / Wheatwin2 (2) | defense response to fungus [GO:0050832 biological_process] (2); defense response to bacterium [GO:0042742 biological_process] (2) | Barwin, conserved site [IPR018226] (2); Barwin domain [IPR001153] (2); RlpA-like protein, double-psi beta-barrel domain [IPR009009] (1); RlpA-like double-psi beta-barrel domain [IPR009009] (1) | scaffold_8_mRNA_2255.1 | C_unshiu_02252_mRNA_2.1 | - |
| GF0024018 | 1 | 1 | 0 | BED zinc finger,hAT family dimerization domain (1); BED zinc finger,hAT family dimerization domain isoform 1 (1) | nucleic acid binding [GO:0003676 molecular_function] (2); DNA binding [GO:0003677 molecular_function] (2); protein dimerization activity [GO:0046983 molecular_function] (1) | Ribonuclease H-like domain [IPR012337] (2); hAT-like transposase, RNase-H fold [IPR025525] (2); Zinc finger, BED-type [IPR003656] (2); Zinc finger C2H2-type [IPR013087] (1); HAT, C-terminal dimerisation domain [IPR008906] (1) | scaffold_8_mRNA_2244.1 | C_unshiu_00962_mRNA_7.1 | - |
| GF0024017 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_2241.1 | C_unshiu_01594_mRNA_6.1 | - |
| GF0024016 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_2234.1 | C_unshiu_01317_mRNA_2.1 | - |
| GF0024015 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_2230.1 | C_unshiu_00427_mRNA_10.1 | - |
| GF0024014 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_2228.1 | C_unshiu_00235_mRNA_1.1 | - |
| GF0024012 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_2217.1 | C_unshiu_00427_mRNA_19.1 | - |
| GF0024011 | 1 | 1 | 0 | Hypothetical protein (2) | zinc ion binding [GO:0008270 molecular_function] (2); regulation of transcription, DNA-templated [GO:0006355 biological_process] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | Zinc finger, SWIM-type [IPR007527] (2); Zinc finger, CCHC-type [IPR001878] (2); FHY3/FAR1 family [IPR031052] (2) | scaffold_8_mRNA_2211.1 | C_unshiu_00427_mRNA_25.1 | - |
| GF0024010 | 1 | 1 | 0 | Hypothetical protein (2) | cysteine-type peptidase activity [GO:0008234 molecular_function] (2); proteolysis [GO:0006508 biological_process] (2) | Ulp1 protease family, C-terminal catalytic domain [IPR003653] (2) | scaffold_8_mRNA_2210.1 | C_unshiu_00427_mRNA_26.1 | - |
| GF0024009 | 1 | 1 | 0 | Hypothetical protein (2) | | HSP20-like chaperone [IPR008978] (2); Alpha crystallin/Hsp20 domain [IPR002068] (2); Small heat shock protein HSP20 [IPR031107] (1) | scaffold_8_mRNA_2208.1 | C_unshiu_02022_mRNA_2.1 | - |
| GF0024008 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_2206.1 | C_unshiu_02022_mRNA_4.1 | - |
| GF0024007 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_2201.1 | C_unshiu_00413_mRNA_22.1 | - |
| GF0024006 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_2200.1 | C_unshiu_00413_mRNA_21.1 | - |
| GF0024005 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_2187.1 | C_unshiu_02155_mRNA_5.1 | - |
| GF0024004 | 1 | 1 | 0 | Hypothetical protein (2) | cysteine-type peptidase activity [GO:0008234 molecular_function] (2); proteolysis [GO:0006508 biological_process] (2) | Ulp1 protease family, C-terminal catalytic domain [IPR003653] (2); Probable transposase, Ptta/En/Spm, plant [IPR004252] (1) | scaffold_8_mRNA_2186.1 | C_unshiu_01073_mRNA_6.1 | - |
| GF0024003 | 1 | 1 | 0 | Hypothetical protein (2) | DNA binding [GO:0003677 molecular_function] (2); nucleus [GO:0005634 cellular_component] (2); integral component of thylakoid membrane [GO:0031361 cellular_component] (1); iron ion binding [GO:0005506 molecular_function] (1); photosynthesis [GO:0015979 biological_process] (1); electron carrier activity [GO:0009055 molecular_function] (1); heme binding [GO:0020037 molecular_function] (1) | Methyl-CpG DNA binding [IPR001739] (2); DNA-binding domain [IPR016177] (2); Cytochrome f [IPR002325] (1) | scaffold_8_mRNA_2180.1 | C_unshiu_02719_mRNA_2.1 | - |
| GF0024002 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_2163.1 | C_unshiu_00507_mRNA_13.1 | - |
| GF0024001 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_2162.1 | C_unshiu_00507_mRNA_12.1 | - |
| GF0024000 | 1 | 1 | 0 | Hypothetical protein (1); Transcription factor MYB86 (1) | DNA binding [GO:0003677 molecular_function] (1) | Myb domain [IPR017930] (1); Homeobox domain-like [IPR009057] (1); SANT/Myb domain [IPR001005] (1) | scaffold_8_mRNA_2160.1 | C_unshiu_00507_mRNA_10.1 | - |
| GF0023999 | 1 | 1 | 0 | Peptide transporter PTR5 (1); Nitrate transporter 1.2 (1) | transporter activity [GO:0005215 molecular_function] (2); membrane [GO:0016020 cellular_component] (2); transport [GO:0006810 biological_process] (2) | Major facilitator superfamily domain [IPR020846] (2); Proton-dependent oligopeptide transporter family [IPR000109] (2) | scaffold_8_mRNA_2158.1 | C_unshiu_00507_mRNA_7.1 | - |
| GF0023998 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_2153.1 | C_unshiu_00110_mRNA_20.1 | - |
| GF0023997 | 1 | 1 | 0 | Hypothetical protein (2) | | Domain of unknown function DUF4283 [IPR025558] (1) | scaffold_8_mRNA_2140.1 | C_unshiu_00110_mRNA_5.1 | - |
| GF0023996 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_2138.1 | C_unshiu_01298_mRNA_3.1 | - |
| GF0023994 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_2112.1 | C_unshiu_00361_mRNA_22.1 | - |
| GF0023993 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_2105.1 | C_unshiu_00361_mRNA_18.1 | - |
| GF0023992 | 1 | 1 | 0 | Hypothetical protein (2) | protein folding [GO:0006457 biological_process] (1); unfolded protein binding [GO:0051082 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1) | Chaperonin Cpn60/TCP-1 family [IPR002423] (1); GroEL-like equatorial domain [IPR027413] (1); Chaperonin TCP-1, conserved site [IPR002194] (1); Chaperone tailless complex polypeptide 1 (TCP-1) [IPR017998] (1) | scaffold_8_mRNA_2104.1 | C_unshiu_00250_mRNA_26.1 | - |
| GF0023991 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_210.1 | C_unshiu_00116_mRNA_34.1 | - |
| GF0023990 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_2090.1 | C_unshiu_00441_mRNA_25.1 | - |
| GF0023989 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1) | Zinc knuckle CX2CX4HX4C [IPR025836] (2); Domain of unknown function DUF4283 [IPR025558] (2); Zinc finger, CCHC-type [IPR001878] (1) | scaffold_8_mRNA_2088.1 | C_unshiu_00694_mRNA_11.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0023987 | 1 | 1 | 0 | Hypothetical protein (2) |  | Aspartic peptidase domain [IPR021109] (2); Retropepsins [IPR018061] (1) | scaffold_8_mRNA_2068.1 | C_unshiu_01948_mRNA_5.1 | - |
| GF0023986 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_2064.1 | C_unshiu_02550_mRNA_2.1 | - |
| GF0023985 | 1 | 1 | 0 | Hypothetical protein (2) |  | Retroviral aspartyl protease [IPR013242] (2); Aspartic peptidase domain [IPR021109] (1) | scaffold_8_mRNA_2060.1 | C_unshiu_02075_mRNA_2.1 | - |
| GF0023984 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_2057.1 | C_unshiu_01704_mRNA_2.1 | - |
| GF0023983 | 1 | 1 | 0 | Hypothetical protein (2) |  | Retrotransposon gag domain [IPR005162] (2) | scaffold_8_mRNA_2056.1 | C_unshiu_01704_mRNA_3.1 | - |
| GF0023982 | 1 | 1 | 0 | Retrotransposon protein, putative, unclassified (2) |  | Retrotransposon gag domain [IPR005162] (2) | scaffold_8_mRNA_2049.1 | C_unshiu_00266_mRNA_7.1 | - |
| GF0023981 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_2044.1 | C_unshiu_00266_mRNA_4.1 | - |
| GF0023980 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_2043.1 | C_unshiu_00266_mRNA_3.1 | - |
| GF0023979 | 1 | 1 | 0 | Hypothetical protein (2) |  | Retrotransposon gag domain [IPR005162] (2) | scaffold_8_mRNA_2040.1 | C_unshiu_01652_mRNA_3.1 | - |
| GF0023978 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_2035.1 | C_unshiu_00083_mRNA_10.1 | - |
| GF0023977 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_2034.1 | C_unshiu_00083_mRNA_9.1 | - |
| GF0023976 | 1 | 1 | 0 | Hypothetical protein (2) |  | Viral movement protein [IPR028919] (2) | scaffold_8_mRNA_2033.1 | C_unshiu_00083_mRNA_8.1 | - |
| GF0023975 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_2032.1 | C_unshiu_00083_mRNA_7.1 | - |
| GF0023974 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_2031.1 | C_unshiu_00083_mRNA_6.1 | - |
| GF0023973 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_2025.1 | C_unshiu_02426_mRNA_2.1 | - |
| GF0023972 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1) | Zinc finger, CCHC-type [IPR001878] (1); Reverse transcriptase domain [IPR000477] (1) | scaffold_8_mRNA_2016.1 | C_unshiu_01267_mRNA_14.1 | - |
| GF0023971 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_2015.1 | C_unshiu_01267_mRNA_13.1 | - |
| GF0023970 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_2013.1 | C_unshiu_01267_mRNA_11.1 | - |
| GF0023969 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_2012.1 | C_unshiu_01267_mRNA_10.1 | - |
| GF0023968 | 1 | 1 | 0 | Hypothetical protein (2) |  | Chromo domain [IPR023780] (2); Chromo domain-like [IPR016197] (2) | scaffold_8_mRNA_1995.1 | C_unshiu_01338_mRNA_8.1 | - |
| GF0023967 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (1) | Domain of unknown function DUF4283 [IPR025558] (2); Ribonuclease H-like domain [IPR012337] (1) | scaffold_8_mRNA_1980.1 | C_unshiu_02098_mRNA_2.1 | - |
| GF0023966 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_1976.1 | C_unshiu_02397_mRNA_1.1 | - |
| GF0023965 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_1968.1 | C_unshiu_00880_mRNA_6.1 | - |
| GF0023964 | 1 | 1 | 0 | Hypothetical protein (2) |  | NADH:quinone oxidoreductase/Mrp antiporter, membrane subunit [IPR001750] (2) | scaffold_8_mRNA_1967.1 | C_unshiu_00914_mRNA_9.1 | - |
| GF0023963 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_1966.1 | C_unshiu_00914_mRNA_10.1 | - |
| GF0023962 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_1958.1 | C_unshiu_02645_mRNA_3.1 | - |
| GF0023961 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_1957.1 | C_unshiu_02645_mRNA_2.1 | - |
| GF0023959 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_1949.1 | C_unshiu_00842_mRNA_1.1 | - |
| GF0023958 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_1940.1 | C_unshiu_01072_mRNA_11.1 | - |
| GF0023957 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_1932.1 | C_unshiu_00485_mRNA_2.1 | - |
| GF0023956 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2); DNA integration [GO:0015074 biological_process] (2) | Integrase, catalytic core [IPR001584] (2); Ribonuclease H-like domain [IPR012337] (2) | scaffold_8_mRNA_1930.1 | C_unshiu_00485_mRNA_3.1 | - |
| GF0023955 | 1 | 1 | 0 | Egg cell-secreted protein 1.4 (2) |  | Prolamin-like domain [IPR008502] (2) | scaffold_8_mRNA_1914.1 | C_unshiu_01096_mRNA_5.1 | - |
| GF0023954 | 1 | 1 | 0 | Hypothetical protein (2) |  | Transposase-associated domain [IPR029480] (1); Transposon, En/Spm-like [IPR004242] (1) | scaffold_8_mRNA_1913.1 | C_unshiu_01096_mRNA_6.1 | - |
| GF0023952 | 1 | 1 | 0 | Far-red impaired response protein-like (2) | regulation of transcription, DNA-templated [GO:0006355 biological_process] (2) | FHY3/FAR1 family [IPR031052] (2); FAR1 DNA binding domain [IPR004330] (2); MULE transposase domain [IPR018289] (2) | scaffold_8_mRNA_1905.1 | C_unshiu_00625_mRNA_23.1 | - |
| GF0023951 | 1 | 1 | 0 | Hypothetical protein (2) | regulation of transcription, DNA-templated [GO:0006355 biological_process] (2) | FHY3/FAR1 family [IPR031052] (2) | scaffold_8_mRNA_1904.1 | C_unshiu_00625_mRNA_22.1 | - |
| GF0023950 | 1 | 1 | 0 | Eukaryotic peptide chain release factor subunit 1-3 (2) | cytoplasm [GO:0005737 cellular_component] (2); translation release factor activity, codon specific [GO:0016149 molecular_function] (2); translational termination [GO:0006415 biological_process] (2) | Peptide Chain Release Factor eRF1/aRF1, N-terminal [IPR024049] (2); 50S ribosomal protein L30e-like [IPR029064] (2); eRF1 domain 3 [IPR005142] (2); eRF1 domain 1/Pelota-like [IPR005140] (2); eRF1 domain 2 [IPR005141] (2); Peptide chain release factor eRF1/aRF1 [IPR004403] (2) | scaffold_8_mRNA_1899.1 | C_unshiu_00966_mRNA_5.1 | - |
| GF0023949 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_1890.1 | C_unshiu_00592_mRNA_8.1 | - |
| GF0023948 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_1885.1 | C_unshiu_00912_mRNA_9.1 | - |
| GF0023947 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_1882.1 | C_unshiu_01503_mRNA_1.1 | - |
| GF0023945 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_1877.1 | C_unshiu_00905_mRNA_3.1 | - |
| GF0023944 | 1 | 1 | 0 | Hypothetical protein (2) |  | Domain of unknown function DUF4216 [IPR025312] (2) | scaffold_8_mRNA_1876.1 | C_unshiu_00266_mRNA_1.1 | - |
| GF0023943 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_1873.1 | C_unshiu_00941_mRNA_14.1 | - |
| GF0023941 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_187.1 | C_unshiu_00116_mRNA_51.1 | - |
| GF0023940 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_1857.1 | C_unshiu_01417_mRNA_2.1 | - |
| GF0023939 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_1856.1 | C_unshiu_01417_mRNA_4.1 | - |
| GF0023938 | 1 | 1 | 0 | Pathogenesis-related thaumatin family protein (2) |  | Thaumatin [IPR001938] (2) | scaffold_8_mRNA_185.1 | C_unshiu_00116_mRNA_53.1 | - |
| GF0023937 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_1849.1 | C_unshiu_01993_mRNA_2.1 | - |
| GF0023936 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_1847.1 | C_unshiu_00204_mRNA_22.1 | - |
| GF0023935 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_1844.1 | C_unshiu_00204_mRNA_20.1 | - |
| GF0023933 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_1830.1 | C_unshiu_01628_mRNA_4.1 | - |
| GF0023932 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_1819.1 | C_unshiu_01419_mRNA_2.1 | - |
| GF0023931 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_1816.1 | C_unshiu_00708_mRNA_16.1 | - |
| GF0023930 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_1814.1 | C_unshiu_00708_mRNA_14.1 | - |
| GF0023929 | 1 | 1 | 0 | Hypothetical protein (2) | zinc ion binding [GO:0008270 molecular_function] (2) | Zinc finger, SWIM-type [IPR007527] (2) | scaffold_8_mRNA_1813.1 | C_unshiu_00708_mRNA_13.1 | - |
| GF0023928 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_181.1 | C_unshiu_00344_mRNA_23.1 | - |
| GF0023927 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_1809.1 | C_unshiu_01072_mRNA_2.1 | - |
| GF0023926 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_1804.1 | C_unshiu_01290_mRNA_2.1 | - |
| GF0023925 | 1 | 1 | 0 | Putative ribonuclease H protein (2) | nucleic acid binding [GO:0003676 molecular_function] (1) | Ribonuclease H-like domain [IPR012337] (1) | scaffold_8_mRNA_1802.1 | C_unshiu_01290_mRNA_3.1 | - |
| GF0023924 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_1781.1 | C_unshiu_00743_mRNA_6.1 | - |
| GF0023923 | 1 | 1 | 0 | BAHD acyltransferase (2) | transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (2) | Transferase [IPR003480] (2); Chloramphenicol acetyltransferase-like domain [IPR023213] (1) | scaffold_8_mRNA_1780.1 | C_unshiu_00331_mRNA_18.1 | - |
| GF0023922 | 1 | 1 | 0 | Cytokinin riboside 5'-monophosphate phosphoribohydrolase (2) |  | LOG family [IPR031100] (2) | scaffold_8_mRNA_1779.1 | C_unshiu_00331_mRNA_17.1 | - |
| GF0023921 | 1 | 1 | 0 | UDP-glycosyltransferase 73C5 (2) | metabolic process [GO:0008152 biological_process] (2); transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (2) | UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (2) | scaffold_8_mRNA_1775.1 | C_unshiu_01736_mRNA_1.1 | - |
| GF0023920 | 1 | 1 | 0 | Hypothetical protein (2) |  | Domain of unknown function DUF4283 [IPR025558] (2); Zinc knuckle CX2CX4HX4C [IPR025836] (1) | scaffold_8_mRNA_1725.1 | C_unshiu_00147_mRNA_33.1 | - |
| GF0023919 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_1723.1 | C_unshiu_02582_mRNA_2.1 | - |
| GF0023917 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_1676.1 | C_unshiu_00581_mRNA_4.1 | - |
| GF0023916 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_1667.1 | C_unshiu_00977_mRNA_12.1 | - |
| GF0023915 | 1 | 1 | 0 | Metacaspase 9 (2) |  | Metacaspase type I, plant [IPR033180] (1); Caspase-like domain [IPR029030] (1) | scaffold_8_mRNA_1657.1 | C_unshiu_00750_mRNA_9.1 | - |
| GF0023913 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_1642.1 | C_unshiu_01687_mRNA_10.1 | - |
| GF0023912 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (1) | Ribonuclease H-like domain [IPR012337] (1) | scaffold_8_mRNA_1636.1 | C_unshiu_00379_mRNA_22.1 | - |
| GF0023911 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_163.1 | C_unshiu_00041_mRNA_96.1 | - |
| GF0023910 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_1626.1 | C_unshiu_02140_mRNA_2.1 | - |
| GF0023909 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_1608.1 | C_unshiu_00724_mRNA_24.1 | - |
| GF0023908 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_1607.1 | C_unshiu_00375_mRNA_21.1 | - |
| GF0023907 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_1596.1 | C_unshiu_00871_mRNA_25.1 | - |
| GF0023906 | 1 | 1 | 0 | Polynucleotidyl transferase, Ribonuclease H fold (2) | nucleic acid binding [GO:0003676 molecular_function] (1) | Reverse transcriptase zinc-binding domain [IPR026960] (2); Ribonuclease H-like domain [IPR012337] (1) | scaffold_8_mRNA_1572.1 | C_unshiu_01374_mRNA_7.1 | - |
| GF0023905 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_1554.1 | C_unshiu_01235_mRNA_3.1 | - |
| GF0023903 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_1548.1 | C_unshiu_00988_mRNA_1.1 | - |
| GF0023902 | 1 | 1 | 0 | Cytokinin riboside 5'-monophosphate phosphoribohydrolase (2) |  |  | scaffold_8_mRNA_1547.1 | C_unshiu_01506_mRNA_3.1 | - |
| GF0023901 | 1 | 1 | 0 | Hypothetical protein (2) | 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_8_mRNA_1533.1 | C_unshiu_01632_mRNA_4.1 | - |
| GF0023899 | 1 | 1 | 0 | Leguminosin group485 secreted peptide (2) |  |  | scaffold_8_mRNA_1501.1 | C_unshiu_02832_mRNA_4.1 | - |
| GF0023898 | 1 | 1 | 0 | Hypothetical protein (1); Nucleolar complex protein 4 (1) | transmembrane transport [GO:0055085 biological_process] (1); ribosome biogenesis [GO:0042254 biological_process] (1); integral component of membrane [GO:0016021 cellular_component] (1) | CCAAT-binding factor [IPR005612] (2); Major facilitator superfamily domain [IPR020846] (1); Major facilitator superfamily [IPR011701] (1); Nucleolar complex protein 4 [IPR027193] (1) | scaffold_8_mRNA_15.1 | C_unshiu_00376_mRNA_35.1 | - |
| GF0023897 | 1 | 1 | 0 | Hypothetical protein (2) |  | Transposase, MuDR, plant [IPR004332] (2) | scaffold_8_mRNA_149.1 | C_unshiu_01872_mRNA_7.1 | - |
| GF0023895 | 1 | 1 | 0 | Hypothetical protein (2) |  | NADP-dependent oxidoreductase domain [IPR023210] (2); Aldo/keto reductase/potassium channel subunit beta [IPR001395] (1) | scaffold_8_mRNA_1458.1 | C_unshiu_00697_mRNA_10.1 | - |
| GF0023894 | 1 | 1 | 0 | Hypothetical protein (2) |  | NADP-dependent oxidoreductase domain [IPR023210] (2); Aldo/keto reductase/potassium channel subunit beta [IPR001395] (1) | scaffold_8_mRNA_1457.1 | C_unshiu_00697_mRNA_11.1 | - |
| GF0023893 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_8_mRNA_1453.1 | C_unshiu_00697_mRNA_14.1 | - |
| GF0023892 | 1 | 1 | 0 | Aldo/keto reductase family oxidoreductase (2) |  | NADP-dependent oxidoreductase domain [IPR023210] (2); Aldo/keto reductase/potassium channel subunit beta [IPR001395] (1) | scaffold_8_mRNA_1450.1 | C_unshiu_01227_mRNA_2.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0023891 | 1 | 1 | 0 | Hypothetical protein (2) | regulation of transcription, DNA-templated [GO:0006355 biological_process] (1) | FHY3/FAR1 family [IPR031052] (1); SCP2 sterol-binding domain [IPR003033] (1) | scaffold_8_mRNA_1449.1 | C_unshiu_00997_mRNA_1.1 | - |
| GF0023890 | 1 | 1 | 0 | Gag protease polyprotein (1); Hypothetical protein (1) | | Retrotransposon gag domain [IPR005162] (1) | scaffold_8_mRNA_1447.1 | C_unshiu_01227_mRNA_4.1 | - |
| GF0023889 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_1445.1 | C_unshiu_01227_mRNA_6.1 | - |
| GF0023888 | 1 | 1 | 0 | Hypothetical protein (2) | | Aspartic peptidase domain [IPR021109] (1) | scaffold_8_mRNA_1443.1 | C_unshiu_00950_mRNA_8.1 | - |
| GF0023887 | 1 | 1 | 0 | Exostosin family protein (1); Xylogalacturonan beta-1,3-xylosyltransferase-like protein (1) | | Exostosin-like [IPR004263] (2) | scaffold_8_mRNA_1439.1 | C_unshiu_00174_mRNA_16.1 | - |
| GF0023885 | 1 | 1 | 0 | Dihydrokaempferol 4-reductase (1); Hypothetical protein (1) | catalytic activity [GO:0003824 molecular_function] (2); coenzyme binding [GO:0050662 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (1) | NAD(P)-binding domain [IPR016040] (2); Domain of unknown function DUF4371 [IPR025398] (2); NAD-dependent epimerase/dehydratase [IPR001509] (1); Ribonuclease H-like domain [IPR012337] (1); NAD-dependent epimerase/dehydratase, N-terminal domain [IPR001509] (1) | scaffold_8_mRNA_1426.1 | C_unshiu_00632_mRNA_11.1 | - |
| GF0023884 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_1423.1 | C_unshiu_00632_mRNA_8.1 | - |
| GF0023882 | 1 | 1 | 0 | Hypothetical protein (2) | | MULE transposase domain [IPR018289] (2) | scaffold_8_mRNA_1409.1 | C_unshiu_01473_mRNA_3.1 | - |
| GF0023881 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_1407.1 | C_unshiu_01302_mRNA_10.1 | - |
| GF0023880 | 1 | 1 | 0 | Naringenin-chalcone synthase (2) | catalytic activity [GO:0003824 molecular_function] (2); transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (2); biosynthetic process [GO:0009058 biological_process] (2); metabolic process [GO:0008152 biological_process] (2) | Chalcone/stilbene synthase, C-terminal [IPR012328] (2); Thiolase-like [IPR016039] (2); Polyketide synthase, type III [IPR011141] (2); Chalcone/stilbene synthase, N-terminal [IPR001099] (2) | scaffold_8_mRNA_1406.1 | C_unshiu_01302_mRNA_9.1 | - |
| GF0023879 | 1 | 1 | 0 | Xylem cysteine peptidase 1 (2) | cysteine-type peptidase activity [GO:0008234 molecular_function] (2); proteolysis [GO:0006508 biological_process] (2) | Peptidase C1A [IPR013128] (2); Cysteine peptidase, cysteine active site [IPR000169] (2); Peptidase C1A, papain C-terminal [IPR000668] (2); Cysteine peptidase, asparagine active site [IPR025661] (2); Cathepsin propeptide inhibitor domain (I29) [IPR013201] (2) | scaffold_8_mRNA_14.1 | C_unshiu_00376_mRNA_36.1 | - |
| GF0023878 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2); DNA binding [GO:0003677 molecular_function] (2) | Zinc finger, BED-type [IPR003656] (2); hAT-like transposase, RNase-H fold [IPR025525] (2); Ribonuclease H-like domain [IPR012337] (2); Zinc finger C2H2-type [IPR013087] (1) | scaffold_8_mRNA_1392.1 | C_unshiu_00601_mRNA_20.1 | - |
| GF0023877 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_1385.1 | C_unshiu_00244_mRNA_9.1 | - |
| GF0023876 | 1 | 1 | 0 | Geraniol 10-hydroxylase-like protein (2) | 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_8_mRNA_1384.1 | C_unshiu_00244_mRNA_8.1 | - |
| GF0023874 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_1362.1 | C_unshiu_01081_mRNA_7.1 | - |
| GF0023871 | 1 | 1 | 0 | Serine/threonine protein phosphatase 2A 57 kDa regulatory subunit B' alpha isoform (1); Serine/threonine protein phosphatase 2A 57 kDa regulatory subunit B' beta isoform (1) | protein phosphatase type 2A complex [GO:0000159 cellular_component] (2); binding [GO:0005488 molecular_function] (2); signal transduction [GO:0007165 biological_process] (2); membrane [GO:0016020 cellular_component] (1); protein phosphatase type 2A regulator activity [GO:0008601 molecular_function] (1); amino acid transmembrane transport [GO:0003333 biological_process] (1); protein phosphatase regulator activity [GO:0019888 molecular_function] (1); amino acid transmembrane transporter activity [GO:0015171 molecular_function] (1) | Protein phosphatase 2A, regulatory B subunit, B56 [IPR002554] (2); Armadillo-type fold [IPR016024] (2); Amino acid/polyamine transporter I [IPR002293] (1); Armadillo-like helical [IPR011989] (1) | scaffold_8_mRNA_134.1 | C_unshiu_00041_mRNA_71.1 | - |
| GF0023870 | 1 | 1 | 0 | Hypothetical protein (2) | DNA binding [GO:0003677 molecular_function] (2) | B3 DNA binding domain [IPR003340] (2); DNA-binding pseudobarrel domain [IPR015300] (2) | scaffold_8_mRNA_1332.1 | C_unshiu_00859_mRNA_17.1 | - |
| GF0023869 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_1330.1 | C_unshiu_00878_mRNA_15.1 | - |
| GF0023868 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_1323.1 | C_unshiu_01071_mRNA_3.1 | - |
| GF0023867 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_1309.1 | C_unshiu_00859_mRNA_10.1 | - |
| GF0023865 | 1 | 1 | 0 | Hypothetical protein (2) | iron ion binding [GO:0005506 molecular_function] (2); heme binding [GO:0020037 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (2) | Cytochrome P450 [IPR001128] (2) | scaffold_8_mRNA_1280.1 | C_unshiu_00264_mRNA_17.1 | - |
| GF0023864 | 1 | 1 | 0 | General transcription factor 2-related zinc finger protein (1); TTF-type zinc finger protein with HAT dimerisation domain (1) | nucleic acid binding [GO:0003676 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1) | Domain of unknown function DUF4371 [IPR025398] (2); HAT, C-terminal dimerisation domain [IPR008906] (1); Ribonuclease H-like domain [IPR012337] (1) | scaffold_8_mRNA_1246.1 | C_unshiu_00245_mRNA_23.1 | - |
| GF0023863 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_1240.1 | C_unshiu_00329_mRNA_25.1 | - |
| GF0023862 | 1 | 1 | 0 | Hypothetical protein (2) | | Transposase, MuDR, plant [IPR004332] (1) | scaffold_8_mRNA_1229.1 | C_unshiu_00329_mRNA_16.1 | - |
| GF0023860 | 1 | 1 | 0 | Hypothetical protein (2) | | Retrotransposon gag domain [IPR005162] (2) | scaffold_8_mRNA_1206.1 | C_unshiu_01085_mRNA_9.1 | - |
| GF0023859 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_1204.1 | C_unshiu_02314_mRNA_1.1 | - |
| GF0023858 | 1 | 1 | 0 | F-box protein interaction domain protein (2) | protein binding [GO:0005515 molecular_function] (2) | F-box associated domain, type 1 [IPR006527] (2); F-box domain [IPR001810] (2); F-box associated interaction domain [IPR017451] (2); Galactose oxidase/kelch, beta-propeller [IPR011043] (2); Kelch-type beta propeller [IPR015915] (1) | scaffold_8_mRNA_120.1 | C_unshiu_00041_mRNA_56.1 | - |
| GF0023855 | 1 | 1 | 0 | Hypothetical protein (2) | | Plant disease resistance response protein [IPR004265] (2) | scaffold_8_mRNA_1188.1 | C_unshiu_02557_mRNA_3.1 | - |
| GF0023854 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_1179.1 | C_unshiu_02525_mRNA_2.1 | - |
| GF0023853 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_1162.1 | C_unshiu_00261_mRNA_37.1 | - |
| GF0023852 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_1159.1 | C_unshiu_02107_mRNA_3.1 | - |
| GF0023848 | 1 | 1 | 0 | Hypothetical protein (2) | transporter activity [GO:0005215 molecular_function] (2); transport [GO:0006810 biological_process] (2); membrane [GO:0016020 cellular_component] (2) | Aquaporin-like [IPR023271] (2); Major intrinsic protein [IPR000425] (2); Aquaporin transporter [IPR034294] (1) | scaffold_8_mRNA_1124.1 | C_unshiu_00887_mRNA_11.1 | - |
| GF0023846 | 1 | 1 | 0 | Hypothetical protein (1); Putative retroelement pol polyprotein (1) | | Gag-polypeptide of LTR copia-type [IPR029472] (1); GAG-pre-integrase domain [IPR025724] (1) | scaffold_8_mRNA_1118.1 | C_unshiu_00161_mRNA_33.1 | - |
| GF0023845 | 1 | 1 | 0 | Hypothetical protein (2) | ADP binding [GO:0043531 molecular_function] (2) | Leucine-rich repeat domain, L domain-like [IPR032675] (2); NB-ARC [IPR002182] (2); AAA+ ATPase domain [IPR003593] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); Winged helix-turn-helix DNA-binding domain [IPR011991] (1) | scaffold_8_mRNA_1105.1 | C_unshiu_01068_mRNA_7.1 | - |
| GF0023842 | 1 | 1 | 0 | Hypothetical protein (1); Retrotransposon protein, putative, Ty3-gypsy subclass (1) | nucleic acid binding [GO:0003676 molecular_function] (1); response to auxin [GO:0009733 biological_process] (1); DNA integration [GO:0015074 biological_process] (1) | Chromo domain-like [IPR016197] (2); Chromo domain [IPR023780] (2); Small auxin-up RNA [IPR003676] (1); Integrase, catalytic core [IPR001584] (1); Ribonuclease H-like domain [IPR012337] (1) | scaffold_8_mRNA_1096.1 | C_unshiu_01043_mRNA_5.1 | - |
| GF0023840 | 1 | 1 | 0 | Auxin-induced protein X10A (2) | response to auxin [GO:0009733 biological_process] (2) | Small auxin-up RNA [IPR003676] (2) | scaffold_8_mRNA_1093.1 | C_unshiu_01086_mRNA_2.1 | - |
| GF0023838 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_1085.1 | C_unshiu_00396_mRNA_29.1 | - |
| GF0023837 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_1071.1 | C_unshiu_00047_mRNA_4.1 | - |
| GF0023836 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_1048.1 | C_unshiu_02412_mRNA_4.1 | - |
| GF0023835 | 1 | 1 | 0 | Auxin-induced protein 10A5 (1); Auxin-induced protein X10A (1) | response to auxin [GO:0009733 biological_process] (2) | Small auxin-up RNA [IPR003676] (2) | scaffold_8_mRNA_1045.1 | C_unshiu_01573_mRNA_6.1 | - |
| GF0023834 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_1037.1 | C_unshiu_00649_mRNA_20.1 | - |
| GF0023833 | 1 | 1 | 0 | Disease resistance protein (CC-NBS-LRR class) family protein (2) | ADP binding [GO:0043531 molecular_function] (2) | Leucine-rich repeat domain, L domain-like [IPR032675] (2); AAA+ ATPase domain [IPR003593] (2); NB-ARC [IPR002182] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); Winged helix-turn-helix DNA-binding domain [IPR011991] (1) | scaffold_8_mRNA_1023.1 | C_unshiu_00873_mRNA_2.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0023832 | 1 | 1 | 0 | Disease resistance protein RPS5-like protein 3 (1); Disease resistance protein (1) | ADP binding [GO:0043531 molecular_function] (2) | Leucine-rich repeat domain, L domain-like [IPR032675] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); NB-ARC [IPR002182] (2); AAA+ ATPase domain [IPR003593] (2); Winged helix-turn-helix DNA-binding domain [IPR011991] (1) | scaffold_8_mRNA_1022.1 | C_unshiu_00272_mRNA_13.1 | - |
| GF0023831 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_8_mRNA_1020.1 | C_unshiu_00090_mRNA_11.1 | - |
| GF0023830 | 1 | 1 | 0 | Disease resistance protein (CC-NBS-LRR class) family protein (2) | ADP binding [GO:0043531 molecular_function] (2); lipid metabolic process [GO:0006629 biological_process] (1) | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); AAA+ ATPase domain [IPR003593] (2); NB-ARC [IPR002182] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Fungal lipase-like domain [IPR002921] (1); Alpha/Beta hydrolase fold [IPR029058] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1) | scaffold_8_mRNA_1018.1 | C_unshiu_02383_mRNA_5.1 | - |
| GF0023828 | 1 | 1 | 0 | Polyprenol reductase 2 (1); Putative polyprenol reductase 2 (1) | integral component of membrane [GO:0016021 cellular_component] (1); oxidoreductase activity, acting on the CH-CH group of donors [GO:0016627 molecular_function] (1); lipid metabolic process [GO:0006629 biological_process] (1); cytoplasm [GO:0005737 cellular_component] (1) | 3-oxo-5-alpha-steroid 4-dehydrogenase, C-terminal [IPR001104] (1) | scaffold_8_mRNA_1006.1 | C_unshiu_00918_mRNA_10.1 | - |
| GF0023825 | 1 | 1 | 0 | Hypothetical protein (2) | | Alpha/Beta hydrolase fold [IPR029058] (2) | scaffold_7_mRNA_992.1 | C_unshiu_00065_mRNA_5.1 | - |
| GF0023824 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_7_mRNA_988.1 | C_unshiu_00065_mRNA_1.1 | - |
| GF0023819 | 1 | 1 | 0 | GDSL esterase/lipase 5 (2) | hydrolase activity, acting on ester bonds [GO:0016788 molecular_function] (2) | GDSL lipase/esterase [IPR001087] (2); SGNH hydrolase-type esterase domain [IPR013830] (2) | scaffold_7_mRNA_966.1 | C_unshiu_00397_mRNA_6.1 | - |
| GF0023816 | 1 | 1 | 0 | Ribosomal protein L18ae family protein (2) | | Membrane associated eicosanoid/glutathione metabolism-like domain [IPR023352] (1) | scaffold_7_mRNA_942.1 | C_unshiu_00166_mRNA_19.1 | - |
| GF0023814 | 1 | 1 | 0 | Hypothetical protein (2) | translation initiation factor activity [GO:0003743 molecular_function] (2); translational initiation [GO:0006413 biological_process] (2) | Translation initiation factor 1A (eIF-1A) [IPR001253] (2); Nucleic acid-binding, OB-fold [IPR012340] (1) | scaffold_7_mRNA_930.1 | C_unshiu_00166_mRNA_33.1 | - |
| GF0023813 | 1 | 1 | 0 | Phospholipase D beta 1 (1); Putative phospholipase D beta 1-like (1) | | Phospholipase D, C-terminal [IPR024632] (2); Phospholipase D family [IPR015679] (2) | scaffold_7_mRNA_929.1 | C_unshiu_00166_mRNA_34.1 | - |
| GF0023812 | 1 | 1 | 0 | Hypothetical protein (2) | translational initiation [GO:0006413 biological_process] (2); translation initiation factor activity [GO:0003743 molecular_function] (2) | Translation initiation factor 1A (eIF-1A) [IPR001253] (2); Nucleic acid-binding, OB-fold [IPR012340] (1) | scaffold_7_mRNA_928.1 | C_unshiu_00166_mRNA_35.1 | - |
| GF0023811 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_7_mRNA_927.1 | C_unshiu_00166_mRNA_36.1 | - |
| GF0023809 | 1 | 1 | 0 | 5'-nucleotidase surE (2) | nucleotidase activity [GO:0008252 molecular_function] (2); hydrolase activity [GO:0016787 molecular_function] (2) | Survival protein SurE [IPR030048] (2); Survival protein SurE-like phosphatase/nucleotidase [IPR002828] (2) | scaffold_7_mRNA_923.1 | C_unshiu_00166_mRNA_38.1 | - |
| GF0023808 | 1 | 1 | 0 | Hypothetical protein (2) | DNA binding [GO:0003677 molecular_function] (2); regulation of transcription, DNA-templated [GO:0006355 biological_process] (2) | NAC domain [IPR003441] (2) | scaffold_7_mRNA_916.1 | C_unshiu_00166_mRNA_44.1 | - |
| GF0023806 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_7_mRNA_900.1 | C_unshiu_00015_mRNA_106.1 | - |
| GF0023803 | 1 | 1 | 0 | Inactive protein kinase (2) | ATP binding [GO:0005524 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2); protein kinase activity [GO:0004672 molecular_function] (2) | Rossmann-like alpha/beta/alpha sandwich fold [IPR014729] (2); Protein kinase-like domain [IPR011009] (2); Protein kinase domain [IPR000719] (2); Tyrosine-protein kinase, active site [IPR008266] (2); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1) | scaffold_7_mRNA_882.1 | C_unshiu_00726_mRNA_10.1 | - |
| GF0023802 | 1 | 1 | 0 | ABC transporter C family member 10 (2) | ATPase activity, coupled to transmembrane movement of substances [GO:0042626 molecular_function] (2); transmembrane transport [GO:0055085 biological_process] (2); ATP binding [GO:0005524 molecular_function] (2); ATPase activity [GO:0016887 molecular_function] (2); integral component of membrane [GO:0016021 cellular_component] (2); transport [GO:0006810 biological_process] (2) | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); AAA+ ATPase domain [IPR003593] (2); ABC transporter type 1, transmembrane domain [IPR011527] (2); ABC transporter-like [IPR003439] (2); ABC transporter, conserved site [IPR017871] (2) | scaffold_7_mRNA_881.1 | C_unshiu_00726_mRNA_9.1 | - |
| GF0023800 | 1 | 1 | 0 | TRNA-splicing ligase RtcB (1); Pre-mrna-splicing factor rse1 (1) | | Domain of unknown function DUF4409 [IPR025521] (1); Neprosin activation peptide [IPR025521] (1); Domain of unknown function DUF239 [IPR004314] (1); Neprosin [IPR004314] (1) | scaffold_7_mRNA_844.1 | C_unshiu_00505_mRNA_27.1 | - |
| GF0023799 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_7_mRNA_841.1 | C_unshiu_00505_mRNA_28.1 | - |
| GF0023796 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_7_mRNA_809.1 | C_unshiu_02546_mRNA_4.1 | - |
| GF0023794 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_7_mRNA_790.1 | C_unshiu_00508_mRNA_15.1 | - |
| GF0023793 | 1 | 1 | 0 | Hypothetical protein (2) | iron ion binding [GO:0005506 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2); oxidoreductase activity [GO:0016491 molecular_function] (2); fatty acid biosynthetic process [GO:0006633 biological_process] (1); lipid biosynthetic process [GO:0008610 biological_process] (1) | Fatty acid hydroxylase [IPR006694] (2) | scaffold_7_mRNA_788.1 | C_unshiu_01120_mRNA_1.1 | - |
| GF0023789 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_7_mRNA_752.1 | C_unshiu_00303_mRNA_21.1 | - |
| GF0023786 | 1 | 1 | 0 | E3 ubiquitin-protein ligase ATL6 (2) | protein binding [GO:0005515 molecular_function] (2); zinc ion binding [GO:0008270 molecular_function] (2) | Zinc finger, RING/FYVE/PHD-type [IPR013083] (2); Zinc finger, RING-type [IPR001841] (2) | scaffold_7_mRNA_741.1 | C_unshiu_00303_mRNA_13.1 | - |
| GF0023784 | 1 | 1 | 0 | Putative cationic peroxidase 1-like (2) | oxidation-reduction process [GO:0055114 biological_process] (2); peroxidase activity [GO:0004601 molecular_function] (2); response to oxidative stress [GO:0006979 biological_process] (2); heme binding [GO:0020037 molecular_function] (2); hydrogen peroxide catabolic process [GO:0042744 biological_process] (1) | Haem peroxidase, plant/fungal/bacterial [IPR002016] (2); Plant peroxidase [IPR000823] (2); Peroxidase, active site [IPR019794] (2); Haem peroxidase [IPR010255] (2); Secretory peroxidase [IPR033905] (1) | scaffold_7_mRNA_727.1 | C_unshiu_00303_mRNA_1.2 | - |
| GF0023783 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_7_mRNA_721.1 | C_unshiu_00288_mRNA_23.1 | - |
| GF0023781 | 1 | 1 | 0 | Putative tRNA/rRNA methyltransferase YsgA (1); Hypothetical protein (1) | RNA processing [GO:0006396 biological_process] (2); RNA binding [GO:0003723 molecular_function] (2); RNA methyltransferase activity [GO:0008173 molecular_function] (2) | tRNA (guanine-N1-)-methyltransferase, N-terminal [IPR029026] (2); tRNA/rRNA methyltransferase, SpoU type [IPR001537] (2); 50S ribosomal protein L30e-like [IPR029064] (2); Alpha/beta knot methyltransferases [IPR029028] (2); Exostosin-like [IPR004263] (1) | scaffold_7_mRNA_694.1 | C_unshiu_00789_mRNA_10.1 | - |
| GF0023778 | 1 | 1 | 0 | Hypothetical protein (2) | oxidation-reduction process [GO:0055114 biological_process] (2); zinc ion binding [GO:0008270 molecular_function] (1); oxidoreductase activity [GO:0016491 molecular_function] (1) | Alcohol dehydrogenase, N-terminal [IPR013154] (2); GroES-like [IPR011032] (2); Alcohol dehydrogenase superfamily, zinc-type [IPR002085] (1) | scaffold_7_mRNA_686.1 | C_unshiu_01662_mRNA_5.1 | - |
| GF0023776 | 1 | 1 | 0 | Cysteine-rich TM module stress tolerance protein (2) | | Cysteine-rich transmembrane CYSTM domain [IPR028144] (2) | scaffold_7_mRNA_667.1 | C_unshiu_00853_mRNA_14.1 | - |
| GF0023774 | 1 | 1 | 0 | Squalene monooxygenase (2) | flavin adenine dinucleotide binding [GO:0050660 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2); oxidoreductase activity [GO:0016491 molecular_function] (2); integral component of membrane [GO:0016021 cellular_component] (2); squalene monooxygenase activity [GO:0004506 molecular_function] (2) | Squalene epoxidase [IPR013698] (2); FAD/NAD(P)-binding domain [IPR023753] (2) | scaffold_7_mRNA_623.1 | C_unshiu_00028_mRNA_65.1 | - |
| GF0023768 | 1 | 1 | 0 | Sigma factor sigB regulation protein rsbQ (2) | strigolactone biosynthetic process [GO:1901601 biological_process] (1); secondary shoot formation [GO:0010223 biological_process] (1) | Alpha/beta hydrolase fold-1 [IPR000073] (2); Alpha/Beta hydrolase fold [IPR029058] (2); Strigolactone esterase D14 family [IPR031143] (1) | scaffold_7_mRNA_546.1 | C_unshiu_00861_mRNA_6.1 | - |
| GF0023767 | 1 | 1 | 0 | Metal transporter Nramp3 (2) | transporter activity [GO:0005215 molecular_function] (2); transport [GO:0006810 biological_process] (2); membrane [GO:0016020 cellular_component] (2) | NRAMP family [IPR001046] (2) | scaffold_7_mRNA_538.1 | C_unshiu_00169_mRNA_18.1 | - |
| GF0023765 | 1 | 1 | 0 | Lipid transfer protein (1); Hypothetical protein (1) | | Bifunctional inhibitor/plant lipid transfer protein/seed storage helical domain [IPR016140] (2); Hydrophobic seed protein [IPR027923] (2) | scaffold_7_mRNA_511.1 | C_unshiu_00169_mRNA_41.1 | - |
| GF0023764 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_7_mRNA_493.1 | C_unshiu_00301_mRNA_15.1 | - |
| GF0023759 | 1 | 1 | 0 | High mobility group (HMG)-box protein (2) | | High mobility group box domain [IPR009071] (2) | scaffold_7_mRNA_45.2 | C_unshiu_00312_mRNA_20.2 | - |
| GF0023757 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_7_mRNA_442.1 | C_unshiu_00084_mRNA_22.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0023755 | 1 | 1 | 0 | Transcription factor (2) |  | Ternary complex factor MIP1, leucine-zipper [IPR025757] (2); Domain of unknown function DUF547 [IPR006869] (2) | scaffold_7_mRNA_427.1 | C_unshiu_00084_mRNA_38.1 | - |
| GF0023750 | 1 | 1 | 0 | Methylesterase (1); Methyl esterase 10, putative (1) |  | Alpha/Beta hydrolase fold [IPR029058] (2); Alpha/beta hydrolase fold-1 [IPR000073] (1) | scaffold_7_mRNA_397.1 | C_unshiu_02661_mRNA_2.1 | - |
| GF0023746 | 1 | 1 | 0 | TPR domain containing protein (1); Hypothetical protein (1) | protein binding [GO:0005515 molecular_function] (2) | Tetratricopeptide-like helical domain [IPR011990] (2); Tetratricopeptide repeat [IPR019734] (1) | scaffold_7_mRNA_378.1 | C_unshiu_00025_mRNA_74.1 | - |
| GF0023745 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_7_mRNA_377.1 | C_unshiu_00025_mRNA_72.1 | - |
| GF0023744 | 1 | 1 | 0 | Cold acclimation protein WCOR413 (2) | integral component of membrane [GO:0016021 cellular_component] (2) | Cold-regulated 413 protein [IPR008892] (2) | scaffold_7_mRNA_375.1 | C_unshiu_00025_mRNA_70.1 | - |
| GF0023736 | 1 | 1 | 0 | Septum formation protein Maf (2) | nucleoside-triphosphate diphosphatase activity [GO:0047429 molecular_function] (1); cytoplasm [GO:0005737 cellular_component] (1) | Maf-like protein [IPR003697] (2); Inosine triphosphate pyrophosphatase-like [IPR029001] (2) | scaffold_7_mRNA_297.1 | C_unshiu_00289_mRNA_35.1 | - |
| GF0023735 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_7_mRNA_287.1 | C_unshiu_00289_mRNA_26.1 | - |
| GF0023734 | 1 | 1 | 0 | Hypothetical protein (2) | protein dimerization activity [GO:0046983 molecular_function] (1) | Myc-type, basic helix-loop-helix (bHLH) domain [IPR011598] (1) | scaffold_7_mRNA_286.1 | C_unshiu_00289_mRNA_25.1 | - |
| GF0023733 | 1 | 1 | 0 | Protein RER1A (2) | integral component of membrane [GO:0016021 cellular_component] (2) | Retrieval of early ER protein Rer1 [IPR004932] (2) | scaffold_7_mRNA_279.1 | C_unshiu_00289_mRNA_15.1 | - |
| GF0023729 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_7_mRNA_2718.1 | C_unshiu_00001_mRNA_409.1 | - |
| GF0023728 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_7_mRNA_2713.1 | C_unshiu_01382_mRNA_10.1 | - |
| GF0023727 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_7_mRNA_2707.1 | C_unshiu_01382_mRNA_4.1 | - |
| GF0023726 | 1 | 1 | 0 | Hypothetical protein (1); 50S ribosomal protein L23 (1) | nucleotide binding [GO:0000166 molecular_function] (1); ribosome [GO:0005840 cellular_component] (1); intracellular [GO:0005622 cellular_component] (1); translation [GO:0006412 biological_process] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1) | Ribosomal protein L25/L23 [IPR013025] (1); Nucleotide-binding alpha-beta plait domain [IPR012677] (1); Ribosomal protein L23/L15e core domain [IPR012678] (1) | scaffold_7_mRNA_2695.1 | C_unshiu_00622_mRNA_11.1 | - |
| GF0023724 | 1 | 1 | 0 | Hypothetical protein (2) |  | Reverse transcriptase domain [IPR000477] (1) | scaffold_7_mRNA_2681.1 | C_unshiu_00940_mRNA_6.1 | - |
| GF0023723 | 1 | 1 | 0 | Protein spinster (2) | transmembrane transport [GO:0055085 biological_process] (2); integral component of membrane [GO:0016021 cellular_component] (2) | Major facilitator superfamily [IPR011701] (2); Major facilitator superfamily domain [IPR020846] (2) | scaffold_7_mRNA_2680.1 | C_unshiu_00940_mRNA_4.1 | - |
| GF0023722 | 1 | 1 | 0 | Tether containing UBX domain for GLUT4, putative (2) |  |  | scaffold_7_mRNA_2665.1 | C_unshiu_00807_mRNA_7.1 | - |
| GF0023721 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_7_mRNA_2664.1 | C_unshiu_00807_mRNA_8.1 | - |
| GF0023720 | 1 | 1 | 0 | Disease resistance protein (2) | ADP binding [GO:0043531 molecular_function] (2) | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); NB-ARC [IPR002182] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Winged helix-turn-helix DNA-binding domain [IPR011991] (1) | scaffold_7_mRNA_2651.1 | C_unshiu_01391_mRNA_3.1 | - |
| GF0023719 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_7_mRNA_2650.1 | C_unshiu_00713_mRNA_1.1 | - |
| GF0023718 | 1 | 1 | 0 | LRR and NB-ARC domain disease resistance protein (1); Disease resistance protein (1) | ADP binding [GO:0043531 molecular_function] (2) | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); NB-ARC [IPR002182] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Winged helix-turn-helix DNA-binding domain [IPR011991] (1) | scaffold_7_mRNA_2649.1 | C_unshiu_02682_mRNA_3.1 | - |
| GF0023717 | 1 | 1 | 0 | Hypothetical protein (2) | copper ion binding [GO:0005507 molecular_function] (2); oxidoreductase activity [GO:0016491 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2) | Multicopper oxidase, type 2 [IPR011706] (2); Cupredoxin [IPR008972] (2) | scaffold_7_mRNA_2632.1 | C_unshiu_02082_mRNA_1.1 | - |
| GF0023716 | 1 | 1 | 0 | Hypothetical protein (2) | copper ion binding [GO:0005507 molecular_function] (2); oxidoreductase activity [GO:0016491 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2) | Cupredoxin [IPR008972] (2); Multicopper oxidase, type 2 [IPR011706] (2) | scaffold_7_mRNA_2629.1 | C_unshiu_02082_mRNA_4.1 | - |
| GF0023715 | 1 | 1 | 0 | Hypothetical protein (2) | protein domain specific binding [GO:0019904 molecular_function] (2) | 14-3-3 protein [IPR000308] (2); 14-3-3 domain [IPR023410] (2); Myo-inositol-1-phosphate synthase, GAPDH-like [IPR013021] (1) | scaffold_7_mRNA_2623.1 | C_unshiu_00760_mRNA_15.1 | - |
| GF0023714 | 1 | 1 | 0 | Hypothetical protein (2) |  | Gag-polypeptide of LTR copia-type [IPR029472] (1) | scaffold_7_mRNA_2615.1 | C_unshiu_00519_mRNA_6.1 | - |
| GF0023713 | 1 | 1 | 0 | Aspartic proteinase-like protein 1 (2) | proteolysis [GO:0006508 biological_process] (2); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (2) | Aspartic peptidase domain [IPR021109] (2); Peptidase family A1 domain [IPR033121] (2); Aspartic peptidase A1 family [IPR001461] (2); Xylanase inhibitor, N-terminal [IPR032861] (2); Xylanase inhibitor, C-terminal [IPR032799] (2); Aspartic peptidase, active site [IPR001969] (2); Pepsin-like domain [IPR034164] (1) | scaffold_7_mRNA_2613.1 | C_unshiu_00519_mRNA_9.1 | - |
| GF0023711 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_7_mRNA_2598.1 | C_unshiu_01312_mRNA_3.1 | - |
| GF0023710 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_7_mRNA_2579.1 | C_unshiu_00854_mRNA_7.1 | - |
| GF0023709 | 1 | 1 | 0 | Hypothetical protein (2) |  | GroEL-like equatorial domain [IPR027413] (1) | scaffold_7_mRNA_2577.1 | C_unshiu_00854_mRNA_6.1 | - |
| GF0023708 | 1 | 1 | 0 | Hypothetical protein (1); Retrotransposon protein, putative, Ty1-copia subclass (1) |  | GAG-pre-integrase domain [IPR025724] (1) | scaffold_7_mRNA_2569.1 | C_unshiu_00434_mRNA_2.1 | - |
| GF0023707 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_7_mRNA_2566.1 | C_unshiu_00434_mRNA_5.1 | - |
| GF0023705 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_7_mRNA_2548.1 | C_unshiu_00434_mRNA_19.1 | - |
| GF0023703 | 1 | 1 | 0 | Hypothetical protein (2) |  | Domain of unknown function DUF4283 [IPR025558] (2) | scaffold_7_mRNA_2527.1 | C_unshiu_00245_mRNA_19.1 | - |
| GF0023701 | 1 | 1 | 0 | Hypothetical protein (2) | 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_7_mRNA_2520.1 | C_unshiu_01469_mRNA_2.1 | - |
| GF0023700 | 1 | 1 | 0 | Somatic embryogenesis receptor kinase 1 (2) | protein binding [GO:0005515 molecular_function] (2); ATP binding [GO:0005524 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2); protein kinase activity [GO:0004672 molecular_function] (2) | Protein kinase-like domain [IPR011009] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Protein kinase domain [IPR000719] (2); Leucine-rich repeat [IPR001611] (2); Serine/threonine-protein kinase, active site [IPR008271] (2); Protein kinase, ATP binding site [IPR017441] (2); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (2); Leucine-rich repeat, typical subtype [IPR003591] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1) | scaffold_7_mRNA_2507.1 | C_unshiu_00441_mRNA_8.1 | - |
| GF0023697 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_7_mRNA_2495.1 | C_unshiu_00594_mRNA_9.1 | - |
| GF0023696 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_7_mRNA_2490.1 | C_unshiu_02139_mRNA_5.2 | - |
| GF0023695 | 1 | 1 | 0 | Hypothetical protein (1); Disease resistance RPM1-like protein (1) | ADP binding [GO:0043531 molecular_function] (1) | Leucine-rich repeat domain, L domain-like [IPR032675] (2); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); NB-ARC [IPR002182] (1) | scaffold_7_mRNA_2486.1 | C_unshiu_00468_mRNA_14.1 | - |
| GF0023694 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (1) | Ribonuclease H-like domain [IPR012337] (1) | scaffold_7_mRNA_2485.1 | C_unshiu_00468_mRNA_15.1 | - |
| GF0023693 | 1 | 1 | 0 | RPM1-interacting protein 4 (RIN4) family protein (2) |  |  | scaffold_7_mRNA_2473.1 | C_unshiu_00468_mRNA_30.2 | - |
| GF0023691 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2); zinc ion binding [GO:0008270 molecular_function] (2) | Zinc finger, CCHC-type [IPR001878] (2) | scaffold_7_mRNA_2456.1 | C_unshiu_00566_mRNA_18.1 | - |
| GF0023690 | 1 | 1 | 0 | Hypothetical protein (2) |  | High mobility group box domain [IPR009071] (1) | scaffold_7_mRNA_2455.1 | C_unshiu_00566_mRNA_17.1 | - |
| GF0023688 | 1 | 1 | 0 | Mechanosensitive ion channel protein 10 (2) | transmembrane transport [GO:0055085 biological_process] (2); calcium ion binding [GO:0005509 molecular_function] (2); membrane [GO:0016020 cellular_component] (2) | Mechanosensitive ion channel MscS [IPR006685] (2); EF-hand domain [IPR002048] (2); LSM domain [IPR010920] (2); Mechanosensitive ion channel MscS-like, plants/fungi [IPR016688] (2); EF-hand domain pair [IPR011992] (1) | scaffold_7_mRNA_2446.1 | C_unshiu_00566_mRNA_7.1 | - |
| GF0023687 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_7_mRNA_2439.1 | C_unshiu_01193_mRNA_2.1 | - |
| GF0023686 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_7_mRNA_2433.1 | C_unshiu_00357_mRNA_14.1 | - |
| GF0023685 | 1 | 1 | 0 | Putative WRKY transcription factor 51 (2) | transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (2); regulation of transcription, DNA-templated [GO:0006355 biological_process] (2); sequence-specific DNA binding [GO:0043565 molecular_function] (2) | WRKY domain [IPR003657] (2) | scaffold_7_mRNA_2425.1 | C_unshiu_00634_mRNA_6.1 | - |
| GF0023684 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_7_mRNA_2417.1 | C_unshiu_01284_mRNA_10.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0023683 | 1 | 1 | 0 | Disease resistance protein RPP13 variant (1); Disease resistance protein RPM1 (1) | ADP binding [GO:0043531 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (1) | Leucine-rich repeat domain, L domain-like [IPR032675] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); NB-ARC [IPR002182] (2); Ribonuclease H-like domain [IPR012337] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1) | scaffold_7_mRNA_2414.1 | C_unshiu_01284_mRNA_8.1 | - |
| GF0023682 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_7_mRNA_2412.1 | C_unshiu_01570_mRNA_1.1 | - |
| GF0023681 | 1 | 1 | 0 | Ribonuclease H protein, putative (2) |  | Reverse transcriptase zinc-binding domain [IPR026960] (2) | scaffold_7_mRNA_2409.1 | C_unshiu_01570_mRNA_3.1 | - |
| GF0023680 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_7_mRNA_2408.1 | C_unshiu_01570_mRNA_4.1 | - |
| GF0023679 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_7_mRNA_2404.1 | C_unshiu_00173_mRNA_38.1 | - |
| GF0023678 | 1 | 1 | 0 | Cellulose synthase-like B3, putative isoform 3 (2) | cellulose biosynthetic process [GO:0030244 biological_process] (2); cellulose synthase (UDP-forming) activity [GO:0016760 molecular_function] (2); membrane [GO:0016020 cellular_component] (2) | Cellulose synthase [IPR005150] (2); Nucleotide-diphospho-sugar transferases [IPR029044] (1) | scaffold_7_mRNA_2403.1 | C_unshiu_00173_mRNA_37.1 | - |
| GF0023677 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_7_mRNA_2397.1 | C_unshiu_00173_mRNA_31.1 | - |
| GF0023676 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_7_mRNA_2396.1 | C_unshiu_00173_mRNA_30.1 | - |
| GF0023675 | 1 | 1 | 0 | Hypothetical protein (1); Cysteine/Histidine-rich C1 domain family protein, putative (1) | protein binding [GO:0005515 molecular_function] (1); protein-disulfide reductase activity [GO:0047134 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1) | Leucine-rich repeat [IPR001611] (1); C1-like [IPR011424] (1); DC1 [IPR004146] (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); Zinc finger, RING/FYVE/PHD-type [IPR013083] (1) | scaffold_7_mRNA_2395.1 | C_unshiu_01539_mRNA_7.1 | - |
| GF0023674 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_7_mRNA_2381.1 | C_unshiu_01813_mRNA_3.1 | - |
| GF0023672 | 1 | 1 | 0 | NBS-LRR type disease resistance protein (2) |  | Leucine-rich repeat domain, L domain-like [IPR032675] (2) | scaffold_7_mRNA_2376.1 | C_unshiu_00173_mRNA_13.1 | - |
| GF0023671 | 1 | 1 | 0 | Hypothetical protein (2) | membrane [GO:0016020 cellular_component] (1); transmembrane transporter activity [GO:0022857 molecular_function] (1); integral component of membrane [GO:0016021 cellular_component] (1) | WAT1-related protein [IPR030184] (1); EamA domain [IPR000620] (1) | scaffold_7_mRNA_237.1 | C_unshiu_00209_mRNA_15.1 | - |
| GF0023670 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_7_mRNA_2369.1 | C_unshiu_00173_mRNA_6.1 | - |
| GF0023669 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_7_mRNA_2367.1 | C_unshiu_00173_mRNA_4.1 | - |
| GF0023667 | 1 | 1 | 0 | Vinorine synthase (1); Salutaridinol 7-O-acetyltransferase (1) | transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (2) | Transferase [IPR003480] (2); Chloramphenicol acetyltransferase-like domain [IPR023213] (1) | scaffold_7_mRNA_2356.1 | C_unshiu_01110_mRNA_6.1 | - |
| GF0023666 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_7_mRNA_2355.1 | C_unshiu_01110_mRNA_5.1 | - |
| GF0023664 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_7_mRNA_2346.1 | C_unshiu_01635_mRNA_3.1 | - |
| GF0023663 | 1 | 1 | 0 | Hypothetical protein (2) |  | Endonuclease/exonuclease/phosphatase [IPR005135] (2) | scaffold_7_mRNA_2341.1 | C_unshiu_02366_mRNA_3.1 | - |
| GF0023661 | 1 | 1 | 0 | General transcription factor 3C-like protein (2) |  | Transcription factor IIIC, subunit 5 [IPR019136] (2) | scaffold_7_mRNA_2333.1 | C_unshiu_00382_mRNA_10.1 | - |
| GF0023660 | 1 | 1 | 0 | Hypothetical protein (2) | mRNA splicing, via spliceosome [GO:0000398 biological_process] (1); spliceosomal complex [GO:0005681 cellular_component] (1) | Intron-binding protein aquarius [IPR032464] (1); CWF11 family [IPR026300] (1) | scaffold_7_mRNA_2327.1 | C_unshiu_00757_mRNA_14.1 | - |
| GF0023659 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_7_mRNA_2324.1 | C_unshiu_00757_mRNA_11.1 | - |
| GF0023658 | 1 | 1 | 0 | Egg cell-secreted protein 1.4 (2) |  | Prolamin-like domain [IPR008502] (2) | scaffold_7_mRNA_2321.1 | C_unshiu_00757_mRNA_9.1 | - |
| GF0023657 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_7_mRNA_2320.1 | C_unshiu_00016_mRNA_22.1 | - |
| GF0023656 | 1 | 1 | 0 | Hypothetical protein (2) | mRNA splicing, via spliceosome [GO:0000398 biological_process] (1); spliceosomal complex [GO:0005681 cellular_component] (1) | CWF11 family [IPR026300] (1) | scaffold_7_mRNA_2319.1 | C_unshiu_00757_mRNA_8.1 | - |
| GF0023655 | 1 | 1 | 0 | Egg cell-secreted protein 1.4 (2) |  | Prolamin-like domain [IPR008502] (2) | scaffold_7_mRNA_2315.1 | C_unshiu_00757_mRNA_5.1 | - |
| GF0023654 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_7_mRNA_2312.1 | C_unshiu_00069_mRNA_4.1 | - |
| GF0023653 | 1 | 1 | 0 | Hypothetical protein (2) | protein binding [GO:0005515 molecular_function] (2) | WD40-repeat-containing domain [IPR017986] (2); WD40 repeat [IPR001680] (2); WD40/YVTN repeat-like-containing domain [IPR015943] (1) | scaffold_7_mRNA_2308.1 | C_unshiu_02029_mRNA_4.1 | - |
| GF0023652 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_7_mRNA_2304.1 | C_unshiu_00016_mRNA_34.1 | - |
| GF0023651 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_7_mRNA_2294.1 | C_unshiu_00514_mRNA_13.1 | - |
| GF0023650 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_7_mRNA_2274.1 | C_unshiu_00925_mRNA_6.1 | - |
| GF0023649 | 1 | 1 | 0 | RING-H2 finger protein ATL78 (2) | zinc ion binding [GO:0008270 molecular_function] (2); protein binding [GO:0005515 molecular_function] (2) | Zinc finger, RING/FYVE/PHD-type [IPR013083] (2); Zinc finger, RING-type [IPR001841] (2) | scaffold_7_mRNA_2251.1 | C_unshiu_00414_mRNA_32.1 | - |
| GF0023648 | 1 | 1 | 0 | Polynucleotidyl transferase, Ribonuclease H fold (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2); Reverse transcriptase zinc-binding domain [IPR026960] (2) | scaffold_7_mRNA_2250.1 | C_unshiu_00414_mRNA_31.1 | - |
| GF0023647 | 1 | 1 | 0 | RING-H2 finger protein ATL78 (2) | zinc ion binding [GO:0008270 molecular_function] (2); protein binding [GO:0005515 molecular_function] (2) | Zinc finger, RING-type [IPR001841] (2); Zinc finger, RING/FYVE/PHD-type [IPR013083] (2) | scaffold_7_mRNA_2246.1 | C_unshiu_00414_mRNA_28.1 | - |
| GF0023646 | 1 | 1 | 0 | RING-H2 finger protein ATL78 (2) | protein binding [GO:0005515 molecular_function] (2); zinc ion binding [GO:0008270 molecular_function] (2) | Zinc finger, RING/FYVE/PHD-type [IPR013083] (2); Zinc finger, RING-type [IPR001841] (2) | scaffold_7_mRNA_2240.1 | C_unshiu_00414_mRNA_26.1 | - |
| GF0023645 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_7_mRNA_2233.1 | C_unshiu_00414_mRNA_13.1 | - |
| GF0023644 | 1 | 1 | 0 | Hypothetical protein (2) | protein phosphorylation [GO:0006468 biological_process] (2); protein kinase activity [GO:0004672 molecular_function] (2) | Protein kinase-like domain [IPR011009] (2); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1) | scaffold_7_mRNA_2228.1 | C_unshiu_00414_mRNA_7.1 | - |
| GF0023643 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_7_mRNA_2223.1 | C_unshiu_00414_mRNA_3.1 | - |
| GF0023642 | 1 | 1 | 0 | Non-LTR retroelement reverse transcriptase-like protein (1); Putative non-LTR retroelement reverse transcriptase (1) | ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1) | Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1); Protein kinase, ATP binding site [IPR017441] (1) | scaffold_7_mRNA_2205.1 | C_unshiu_01046_mRNA_9.1 | - |
| GF0023641 | 1 | 1 | 0 | Hypothetical protein (2) |  | Domain of unknown function DUF1985 [IPR015410] (2) | scaffold_7_mRNA_2187.1 | C_unshiu_01242_mRNA_8.1 | - |
| GF0023639 | 1 | 1 | 0 | Hypothetical protein (2) |  | Protein kinase-like domain [IPR011009] (1) | scaffold_7_mRNA_2170.1 | C_unshiu_00666_mRNA_5.1 | - |
| GF0023638 | 1 | 1 | 0 | UPF0183 protein (2) |  | Uncharacterised protein family UPF0183 [IPR005373] (2) | scaffold_7_mRNA_217.1 | C_unshiu_00218_mRNA_37.1 | - |
| GF0023637 | 1 | 1 | 0 | LRR receptor-like serine/threonine-protein kinase FLS2 (1); LRR receptor-like kinase (1) | protein phosphorylation [GO:0006468 biological_process] (2); protein kinase activity [GO:0004672 molecular_function] (2); ATP binding [GO:0005524 molecular_function] (2); protein binding [GO:0005515 molecular_function] (2) | Protein kinase domain [IPR000719] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Protein kinase-like domain [IPR011009] (2); Leucine-rich repeat, typical subtype [IPR003591] (2); Leucine-rich repeat [IPR001611] (2); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1) | scaffold_7_mRNA_2169.1 | C_unshiu_00666_mRNA_6.1 | - |
| GF0023636 | 1 | 1 | 0 | Hypothetical protein (1); AT4G05040 protein (1) | protein binding [GO:0005515 molecular_function] (2); integral component of membrane [GO:0016021 cellular_component] (2); cellular response to salicylic acid stimulus [GO:0071446 biological_process] (2); regulation of salicylic acid mediated signaling pathway [GO:2000031 biological_process] (2); regulation of defense response [GO:0031347 biological_process] (2) | Ankyrin repeat [IPR002110] (2); Protein accelerated cell death 6 [IPR032846] (2); Ankyrin repeat-containing domain [IPR020683] (2); PGG domain [IPR026961] (1) | scaffold_7_mRNA_2165.1 | C_unshiu_01042_mRNA_3.1 | - |
| GF0023635 | 1 | 1 | 0 | Disease resistance protein family, putative (2) |  | Leucine-rich repeat domain, L domain-like [IPR032675] (2) | scaffold_7_mRNA_2159.1 | C_unshiu_01927_mRNA_4.1 | - |
| GF0023634 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_7_mRNA_2153.1 | C_unshiu_01042_mRNA_10.1 | - |
| GF0023633 | 1 | 1 | 0 | Kelch repeat-containing family protein (2) | protein binding [GO:0005515 molecular_function] (2) | Kelch repeat type 1 [IPR006652] (2); Kelch-type beta propeller [IPR015915] (2) | scaffold_7_mRNA_2151.1 | C_unshiu_00371_mRNA_2.1 | - |
| GF0023630 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_7_mRNA_2135.1 | C_unshiu_00526_mRNA_10.1 | - |
| GF0023629 | 1 | 1 | 0 | Putative calcium-transporting ATPase 8, plasma membrane-type-like (2) | calcium-transporting ATPase activity [GO:0005388 molecular_function] (2); ATP binding [GO:0005524 molecular_function] (2); nucleotide binding [GO:0000166 molecular_function] (2); integral component of membrane [GO:0016021 cellular_component] (2); membrane [GO:0016020 cellular_component] (2); calcium ion transmembrane transport [GO:0070588 biological_process] (2); calmodulin binding [GO:0005516 molecular_function] (1) | HAD-like domain [IPR023214] (2); P-type ATPase [IPR001757] (2); Cation-transporting P-type ATPase, C-terminal [IPR006068] (2); P-type ATPase, cytoplasmic domain N [IPR023299] (2); P-type ATPase, subfamily IIB [IPR006408] (2); P-type ATPase, transmembrane domain [IPR023298] (2); Calcium-transporting P-type ATPase, N-terminal autoinhibitory domain [IPR024750] (1); Cation-transporting P-type ATPase, N-terminal [IPR004014] (1) | scaffold_7_mRNA_2132.1 | C_unshiu_00606_mRNA_12.1 | - |
| GF0023628 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_7_mRNA_2127.1 | C_unshiu_00267_mRNA_6.1 | - |
| GF0023627 | 1 | 1 | 0 | Ubiquitin carboxyl-terminal hydrolase family protein (2) |  | Plant organelle RNA recognition domain [IPR021099] (2) | scaffold_7_mRNA_2120.1 | C_unshiu_00390_mRNA_1.1 | - |
| GF0023626 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_7_mRNA_2115.1 | C_unshiu_00406_mRNA_7.1 | - |
| GF0023624 | 1 | 1 | 0 | Integrase (2) | DNA integration [GO:0015074 biological_process] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | Integrase, catalytic core [IPR001584] (2); Ribonuclease H-like domain [IPR012337] (2) | scaffold_7_mRNA_2112.1 | C_unshiu_00284_mRNA_2.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0023623 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_7_mRNA_2111.1 | C_unshiu_01722_mRNA_4.1 | - |
| GF0023622 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_7_mRNA_2108.1 | C_unshiu_01722_mRNA_1.1 | - |
| GF0023621 | 1 | 1 | 0 | Hypothetical protein (2) | 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_2107.1 | C_unshiu_00968_mRNA_2.1 | - |
| GF0023620 | 1 | 1 | 0 | Flavonoid 3'-monooxygenase (1); Flavonoid 3-monooxygenase (1) | heme binding [GO:0020037 molecular_function] (2); iron ion binding [GO:0005506 molecular_function] (2); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2) | Cytochrome P450 [IPR001128] (2); Cytochrome P450, E-class, group I [IPR002401] (1) | scaffold_7_mRNA_2104.1 | C_unshiu_00968_mRNA_3.1 | - |
| GF0023619 | 1 | 1 | 0 | RNA-binding protein with multiple splicing 2 (2) | nucleic acid binding [GO:0003676 molecular_function] (2); nucleotide binding [GO:0000166 molecular_function] (1) | RNA recognition motif domain [IPR000504] (2); Nucleotide-binding alpha-beta plait domain [IPR012677] (1) | scaffold_7_mRNA_2101.1 | C_unshiu_00968_mRNA_7.1 | - |
| GF0023618 | 1 | 1 | 0 | Flavonoid 3'-monooxygenase (2) | oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2); heme binding [GO:0020037 molecular_function] (2); iron ion binding [GO:0005506 molecular_function] (2) | Cytochrome P450, E-class, group I [IPR002401] (2); Cytochrome P450, conserved site [IPR017972] (2); Cytochrome P450 [IPR001128] (2) | scaffold_7_mRNA_2099.1 | C_unshiu_00968_mRNA_13.1 | - |
| GF0023617 | 1 | 1 | 0 | Phosphoglycerate dehydrogenase (2) | metabolic process [GO:0008152 biological_process] (2); L-serine biosynthetic process [GO:0006564 biological_process] (2); amino acid binding [GO:0016597 molecular_function] (2); phosphoglycerate dehydrogenase activity [GO:0004617 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2); oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor [GO:0016616 molecular_function] (2); NAD binding [GO:0051287 molecular_function] (2) | D-isomer specific 2-hydroxyacid dehydrogenase, catalytic domain [IPR006139] (2); D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding domain conserved site [IPR029753] (2); ACT domain [IPR002912] (2); D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding domain [IPR006140] (2); D-3-phosphoglycerate dehydrogenase [IPR006236] (2); D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding domain conserved site 1 [IPR029752] (2); Allosteric substrate binding domain [IPR029009] (2); NAD(P)-binding domain [IPR016040] (2) | scaffold_7_mRNA_2097.1 | C_unshiu_02401_mRNA_1.1 | - |
| GF0023616 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_7_mRNA_2094.1 | C_unshiu_00690_mRNA_12.1 | - |
| GF0023614 | 1 | 1 | 0 | Disease resistance protein RPS2 (2) | ADP binding [GO:0043531 molecular_function] (2); protein binding [GO:0005515 molecular_function] (2) | Leucine-rich repeat domain, L domain-like [IPR032675] (2); Leucine-rich repeat, typical subtype [IPR003591] (2); Leucine-rich repeat [IPR001611] (2); NB-ARC [IPR002182] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); Winged helix-turn-helix DNA-binding domain [IPR011991] (1) | scaffold_7_mRNA_2084.1 | C_unshiu_02972_mRNA_1.1 | - |
| GF0023612 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_7_mRNA_2061.1 | C_unshiu_00703_mRNA_14.1 | - |
| GF0023611 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_7_mRNA_2056.1 | C_unshiu_01521_mRNA_3.1 | - |
| GF0023610 | 1 | 1 | 0 | Hypothetical protein (2) | heme binding [GO:0020037 molecular_function] (2); iron ion binding [GO:0005506 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (2) | Cytochrome P450 [IPR001128] (2); Domain of unknown function DUF4216 [IPR025312] (1); Cytochrome P450, E-class, group I [IPR002401] (1); Domain of unknown function DUF4218 [IPR025452] (1) | scaffold_7_mRNA_2052.1 | C_unshiu_01894_mRNA_4.1 | - |
| GF0023608 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_7_mRNA_2040.1 | C_unshiu_00763_mRNA_1.1 | - |
| GF0023603 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_7_mRNA_2015.1 | C_unshiu_01047_mRNA_6.1 | - |
| GF0023602 | 1 | 1 | 0 | Cyclic nucleotide-gated ion channel, putative (2) | ion transport [GO:0006811 biological_process] (2); transmembrane transport [GO:0055085 biological_process] (2); ion channel activity [GO:0005216 molecular_function] (2); membrane [GO:0016020 cellular_component] (2) | Cyclic nucleotide-binding domain [IPR000595] (2); RmlC-like jelly roll fold [IPR014710] (2); Cyclic nucleotide-binding-like [IPR018490] (2); Ion transport domain [IPR005821] (2) | scaffold_7_mRNA_2003.1 | C_unshiu_01243_mRNA_1.1 | - |
| GF0023601 | 1 | 1 | 0 | Multidrug resistance associated protein 2 (1); ABC transporter C family member 13 (1) | ATPase activity [GO:0016887 molecular_function] (2); integral component of membrane [GO:0016021 cellular_component] (2); transport [GO:0006810 biological_process] (2); ATPase activity, coupled to transmembrane movement of substances [GO:0042626 molecular_function] (2); transmembrane transport [GO:0055085 biological_process] (2); ATP binding [GO:0005524 molecular_function] (2) | ABC transporter, conserved site [IPR017871] (2); ABC transporter-like [IPR003439] (2); ABC transporter type 1, transmembrane domain [IPR011527] (2); AAA+ ATPase domain [IPR003593] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2) | scaffold_7_mRNA_1993.1 | C_unshiu_01243_mRNA_5.1 | - |
| GF0023600 | 1 | 1 | 0 | Hypothetical protein (2) | | CWC16 protein [IPR007590] (1) | scaffold_7_mRNA_1989.1 | C_unshiu_00637_mRNA_12.1 | - |
| GF0023598 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_7_mRNA_198.1 | C_unshiu_00218_mRNA_17.1 | - |
| GF0023596 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_7_mRNA_1968.1 | C_unshiu_00884_mRNA_8.1 | - |
| GF0023595 | 1 | 1 | 0 | Disease resistance RPS2-like protein (1); Hypothetical protein (1) | ADP binding [GO:0043531 molecular_function] (2) | Leucine-rich repeat domain, L domain-like [IPR032675] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); NB-ARC [IPR002182] (2) | scaffold_7_mRNA_1967.1 | C_unshiu_01884_mRNA_1.1 | - |
| GF0023594 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_7_mRNA_1962.1 | C_unshiu_02045_mRNA_5.1 | - |
| GF0023592 | 1 | 1 | 0 | Hypothetical protein (2) | protein binding [GO:0005515 molecular_function] (2) | WD40/YVTN repeat-like-containing domain [IPR015943] (2); WD40 repeat [IPR001680] (2); WD40-repeat-containing domain [IPR017986] (2) | scaffold_7_mRNA_1936.1 | C_unshiu_01836_mRNA_1.1 | - |
| GF0023590 | 1 | 1 | 0 | Verticillium wilt resistance-like protein (2) | protein binding [GO:0005515 molecular_function] (2) | Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (2); Leucine-rich repeat [IPR001611] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Leucine-rich repeat, typical subtype [IPR003591] (2) | scaffold_7_mRNA_1932.1 | C_unshiu_01728_mRNA_3.1 | - |
| GF0023589 | 1 | 1 | 0 | Hypothetical protein (2) | | Iron hydrogenase [IPR009016] (2); Iron hydrogenase, small subunit [IPR003149] (2); Iron hydrogenase, large subunit, C-terminal [IPR004108] (2) | scaffold_7_mRNA_1921.1 | C_unshiu_00344_mRNA_13.1 | - |
| GF0023588 | 1 | 1 | 0 | Hypothetical protein (1); Cysteine-rich RLK (Receptor-like kinase) protein (1) | ATP binding [GO:0005524 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2); protein kinase activity [GO:0004672 molecular_function] (2); protein binding [GO:0005515 molecular_function] (2); protein serine/threonine kinase activity [GO:0004674 molecular_function] (1) | Protein kinase-like domain [IPR011009] (2); Protein kinase domain [IPR000719] (2); WD40-repeat-containing domain [IPR017986] (2); WD40 repeat [IPR001680] (2); Serine/threonine-protein kinase, active site [IPR008271] (2); WD40/YVTN repeat-like-containing domain [IPR015943] (2); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); S-locus receptor kinase, C-terminal [IPR021820] (1) | scaffold_7_mRNA_1920.1 | C_unshiu_00344_mRNA_14.1 | - |
| GF0023587 | 1 | 1 | 0 | RNA polymerase I-specific transcription initiation factor RRN3 (2) | | RNA polymerase I specific transcription initiation factor RRN3 [IPR007991] (2) | scaffold_7_mRNA_19.1 | C_unshiu_00706_mRNA_7.1 | - |
| GF0023586 | 1 | 1 | 0 | Hypothetical protein (2) | | Plant self-incompatibility S1 [IPR010264] (2) | scaffold_7_mRNA_1888.1 | C_unshiu_00302_mRNA_3.1 | - |
| GF0023585 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_7_mRNA_1886.1 | C_unshiu_00302_mRNA_5.1 | - |
| GF0023584 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_7_mRNA_1866.1 | C_unshiu_00302_mRNA_25.1 | - |
| GF0023583 | 1 | 1 | 0 | UPF0481 plant-like protein (2) | | Protein of unknown function DUF247, plant [IPR004158] (2) | scaffold_7_mRNA_1862.1 | C_unshiu_00302_mRNA_29.1 | - |
| GF0023582 | 1 | 1 | 0 | Ankyrin repeat plant-like protein (1); Ankyrin repeat protein (1) | protein binding [GO:0005515 molecular_function] (1) | Ankyrin repeat-containing domain [IPR020683] (2); PGG domain [IPR026961] (2); Ankyrin repeat [IPR002110] (1) | scaffold_7_mRNA_1847.1 | C_unshiu_02133_mRNA_1.1 | - |
| GF0023581 | 1 | 1 | 0 | NBS-LRR type disease resistance protein (2) | ADP binding [GO:0043531 molecular_function] (2) | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); NB-ARC [IPR002182] (2); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); AAA+ ATPase domain [IPR003593] (1) | scaffold_7_mRNA_1843.1 | C_unshiu_02601_mRNA_4.1 | - |
| GF0023580 | 1 | 1 | 0 | Hypothetical protein (2) | regulation of transcription, DNA-templated [GO:0006355 biological_process] (2); transcription cofactor activity [GO:0003712 molecular_function] (2) | Coactivator CBP, KIX domain [IPR003101] (2) | scaffold_7_mRNA_1841.1 | C_unshiu_02601_mRNA_1.1 | - |
| GF0023579 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_7_mRNA_1839.1 | C_unshiu_01605_mRNA_7.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0023578 | 1 | 1 | 0 | Hypothetical protein (2) | | Leucine-rich repeat domain, L domain-like [IPR032675] (1) | scaffold_7_mRNA_1826.1 | C_unshiu_01319_mRNA_2.1 | - |
| GF0023577 | 1 | 1 | 0 | Miraculin (2) | endopeptidase inhibitor activity [GO:0004866 molecular_function] (2) | Proteinase inhibitor I3, Kunitz legume [IPR002160] (2); Kunitz inhibitor ST1-like [IPR011065] (2) | scaffold_7_mRNA_1802.1 | C_unshiu_01097_mRNA_13.1 | - |
| GF0023572 | 1 | 1 | 0 | Hypothetical protein (2) | | Aspartic peptidase domain [IPR021109] (2) | scaffold_7_mRNA_1744.1 | C_unshiu_00460_mRNA_13.1 | - |
| GF0023571 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_7_mRNA_1709.1 | C_unshiu_00877_mRNA_7.1 | - |
| GF0023569 | 1 | 1 | 0 | Disease resistance protein RFL1, putative (1); Disease resistance RPS5-like protein (1) | protein binding [GO:0005515 molecular_function] (2); ADP binding [GO:0043531 molecular_function] (2) | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); NB-ARC [IPR002182] (2); Leucine-rich repeat [IPR001611] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Winged helix-turn-helix DNA-binding domain [IPR011991] (1) | scaffold_7_mRNA_1683.1 | C_unshiu_00352_mRNA_13.1 | - |
| GF0023566 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_7_mRNA_1634.1 | C_unshiu_00429_mRNA_4.1 | - |
| GF0023565 | 1 | 1 | 0 | Hypothetical protein (2) | zinc ion binding [GO:0008270 molecular_function] (2); regulation of transcription, DNA-templated [GO:0006355 biological_process] (2) | FHY3/FAR1 family [IPR031052] (2); Zinc finger, PMZ-type [IPR006564] (2); Zinc finger, SWIM-type [IPR007527] (2) | scaffold_7_mRNA_1629.1 | C_unshiu_00352_mRNA_18.1 | - |
| GF0023563 | 1 | 1 | 0 | Hypothetical protein (2) | zinc ion binding [GO:0008270 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | Domain of unknown function DUF4283 [IPR025558] (2); Endonuclease/exonuclease/phosphatase [IPR005135] (2); Zinc knuckle CX2CX4HX4C [IPR025836] (2); Zinc finger, CCHC-type [IPR001878] (2); Ribonuclease H-like domain [IPR012337] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1) | scaffold_7_mRNA_1590.1 | C_unshiu_00404_mRNA_8.1 | - |
| GF0023562 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_7_mRNA_1578.1 | C_unshiu_00404_mRNA_20.1 | - |
| GF0023561 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2); zinc ion binding [GO:0008270 molecular_function] (1) | Reverse transcriptase zinc-binding domain [IPR026960] (2); Endonuclease/exonuclease/phosphatase [IPR005135] (2); Domain of unknown function DUF4283 [IPR025558] (1); Ribonuclease H-like domain [IPR012337] (1); Zinc finger, CCHC-type [IPR001878] (1) | scaffold_7_mRNA_1569.1 | C_unshiu_01362_mRNA_6.1 | - |
| GF0023559 | 1 | 1 | 0 | Hypothetical protein (2) | | Protein of unknown function DUF761, plant [IPR008480] (2) | scaffold_7_mRNA_1544.1 | C_unshiu_01309_mRNA_11.1 | - |
| GF0023555 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_7_mRNA_1525.1 | C_unshiu_02526_mRNA_3.1 | - |
| GF0023554 | 1 | 1 | 0 | Disease resistance protein (2) | ADP binding [GO:0043531 molecular_function] (2); protein binding [GO:0005515 molecular_function] (1) | Leucine-rich repeat domain, L domain-like [IPR032675] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); NB-ARC [IPR002182] (2); AAA+ ATPase domain [IPR003593] (1); Leucine-rich repeat [IPR001611] (1) | scaffold_7_mRNA_1517.1 | C_unshiu_00451_mRNA_8.1 | - |
| GF0023551 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_7_mRNA_1506.1 | C_unshiu_00451_mRNA_19.1 | - |
| GF0023550 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_7_mRNA_1493.1 | C_unshiu_01130_mRNA_4.1 | - |
| GF0023549 | 1 | 1 | 0 | Boron transporter (2) | anion transport [GO:0006820 biological_process] (2); membrane [GO:0016020 cellular_component] (2); inorganic anion exchanger activity [GO:0005452 molecular_function] (2); integral component of membrane [GO:0016021 cellular_component] (2) | Bicarbonate transporter, C-terminal [IPR011531] (2); Bicarbonate transporter, eukaryotic [IPR003020] (2) | scaffold_7_mRNA_1491.1 | C_unshiu_01130_mRNA_2.1 | - |
| GF0023548 | 1 | 1 | 0 | ECA1 gametogenesis related family (1); Egg cell-secreted protein 1.4 (1) | | Prolamin-like domain [IPR008502] (2) | scaffold_7_mRNA_1484.1 | C_unshiu_01754_mRNA_3.1 | - |
| GF0023546 | 1 | 1 | 0 | Disease resistance protein RPS2 (1); Disease resistance protein (1) | ADP binding [GO:0043531 molecular_function] (2) | Leucine-rich repeat domain, L domain-like [IPR032675] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); NB-ARC [IPR002182] (2); Alpha/Beta hydrolase fold [IPR029058] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1) | scaffold_7_mRNA_1469.1 | C_unshiu_00989_mRNA_16.1 | - |
| GF0023545 | 1 | 1 | 0 | Molybdate transporter 1-like protein (2) | molybdate ion transport [GO:0015689 biological_process] (2); molybdate ion transmembrane transporter activity [GO:0015098 molecular_function] (2); integral component of membrane [GO:0016021 cellular_component] (1) | Molybdate transporter 1/2 [IPR031563] (2); Molybdate transporter 1, plant [IPR030161] (1) | scaffold_7_mRNA_1453.1 | C_unshiu_00924_mRNA_2.1 | - |
| GF0023544 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_7_mRNA_1439.1 | C_unshiu_00975_mRNA_1.1 | - |
| GF0023542 | 1 | 1 | 0 | Hypothetical protein (2) | polysaccharide binding [GO:0030247 molecular_function] (2) | Wall-associated receptor kinase, galacturonan-binding domain [IPR025287] (2) | scaffold_7_mRNA_1417.1 | C_unshiu_00165_mRNA_16.1 | - |
| GF0023541 | 1 | 1 | 0 | Auxin-induced protein IAA6 (2) | protein binding [GO:0005515 molecular_function] (2); regulation of transcription, DNA-templated [GO:0006355 biological_process] (2); nucleus [GO:0005634 cellular_component] (2) | PB1 domain [IPR000270] (2); AUX/IAA protein [IPR003311] (2); AUX/IAA domain [IPR033389] (1) | scaffold_7_mRNA_1403.1 | C_unshiu_00496_mRNA_5.1 | - |
| GF0023539 | 1 | 1 | 0 | Putative glycosyltransferase ypjH (2) | | Glycosyl transferase, family 1 [IPR001296] (2) | scaffold_7_mRNA_1388.1 | C_unshiu_00496_mRNA_19.1 | - |
| GF0023538 | 1 | 1 | 0 | LRR receptor-like kinase family protein (2) | protein binding [GO:0005515 molecular_function] (2); ATP binding [GO:0005524 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2); protein kinase activity [GO:0004672 molecular_function] (2) | Protein kinase-like domain [IPR011009] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Protein kinase domain [IPR000719] (2); Leucine-rich repeat [IPR001611] (2); Serine/threonine-protein kinase, active site [IPR008271] (2); Protein kinase, ATP binding site [IPR017441] (2); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (2); Leucine-rich repeat, typical subtype [IPR003591] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1) | scaffold_7_mRNA_1383.1 | C_unshiu_00372_mRNA_5.1 | - |
| GF0023537 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_7_mRNA_1382.1 | C_unshiu_01453_mRNA_4.1 | - |
| GF0023536 | 1 | 1 | 0 | LRR receptor-like kinase family protein (2) | protein binding [GO:0005515 molecular_function] (2); protein kinase activity [GO:0004672 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2); ATP binding [GO:0005524 molecular_function] (2) | Leucine-rich repeat domain, L domain-like [IPR032675] (2); Protein kinase-like domain [IPR011009] (2); Leucine-rich repeat, typical subtype [IPR003591] (2); Protein kinase domain [IPR000719] (2); Leucine-rich repeat [IPR001611] (2); Serine/threonine-protein kinase, active site [IPR008271] (2); Protein kinase, ATP binding site [IPR017441] (2); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1) | scaffold_7_mRNA_1374.1 | C_unshiu_00982_mRNA_7.1 | - |
| GF0023535 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_7_mRNA_1372.1 | C_unshiu_01521_mRNA_8.1 | - |
| GF0023534 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_7_mRNA_1367.1 | C_unshiu_02144_mRNA_2.1 | - |
| GF0023533 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_7_mRNA_1364.1 | C_unshiu_00982_mRNA_2.1 | - |
| GF0023532 | 1 | 1 | 0 | RNA-dependent RNA polymerase 1c (2) | RNA-directed RNA polymerase activity [GO:0003968 molecular_function] (1); RNA-directed 5'-3' RNA polymerase activity [GO:0003968 molecular_function] (1) | RNA-dependent RNA polymerase, eukaryotic-type [IPR007855] (2) | scaffold_7_mRNA_1361.1 | C_unshiu_00595_mRNA_26.1 | - |
| GF0023530 | 1 | 1 | 0 | FAD-binding Berberine family protein (2) | oxidoreductase activity [GO:0016491 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2); flavin adenine dinucleotide binding [GO:0050660 molecular_function] (2); catalytic activity [GO:0003824 molecular_function] (2); oxidoreductase activity, acting on CH-OH group of donors [GO:0016614 molecular_function] (2) | Berberine/berberine-like [IPR012951] (2); FAD-binding, type 2, subdomain 1 [IPR016167] (2); CO dehydrogenase flavoprotein-like, FAD-binding, subdomain 2 [IPR016169] (2); FAD linked oxidase, N-terminal [IPR006094] (2); FAD-binding, type 2 [IPR016166] (2) | scaffold_7_mRNA_1358.1 | C_unshiu_00595_mRNA_28.1 | - |
| GF0023529 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_7_mRNA_1357.1 | C_unshiu_00595_mRNA_29.1 | - |
| GF0023528 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_7_mRNA_1338.1 | C_unshiu_01983_mRNA_2.1 | - |
| GF0023526 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_7_mRNA_1317.1 | C_unshiu_00208_mRNA_33.1 | - |
| GF0023525 | 1 | 1 | 0 | Hypothetical protein (1); Mitochondrial-processing peptidase subunit alpha (1) | catalytic activity [GO:0003824 molecular_function] (1); metal ion binding [GO:0046872 molecular_function] (1) | Peptidase M16 domain [IPR011237] (1); Metalloenzyme, LuxS/M16 peptidase-like [IPR011249] (1) | scaffold_7_mRNA_1311.1 | C_unshiu_01958_mRNA_4.1 | - |
| GF0023524 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_7_mRNA_1310.1 | C_unshiu_01958_mRNA_3.1 | - |
| GF0023523 | 1 | 1 | 0 | Hypothetical protein (1); Transposon protein, putative, unclassified, expressed (1) | regulation of transcription, DNA-templated [GO:0006355 biological_process] (2) | FHY3/FAR1 family [IPR031052] (2); MULE transposase domain [IPR018289] (2); FAR1 DNA binding domain [IPR004330] (1) | scaffold_7_mRNA_1307.1 | C_unshiu_00530_mRNA_3.1 | - |
| GF0023522 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_7_mRNA_1306.1 | C_unshiu_00004_mRNA_160.1 | - |
| GF0023521 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_7_mRNA_1273.1 | C_unshiu_00221_mRNA_44.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0023520 | 1 | 1 | 0 | Glyoxylate reductase (2) | metabolic process [GO:0008152 biological_process] (2); NAD binding [GO:0051287 molecular_function] (2); oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor [GO:0016616 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2) | D-isomer specific 2-hydroxyacid dehydrogenase, catalytic domain [IPR006139] (2); D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding domain [IPR006140] (2); NAD(P)-binding domain [IPR016040] (2) | scaffold_7_mRNA_1261.1 | C_unshiu_00221_mRNA_37.1 | - |
| GF0023519 | 1 | 1 | 0 | Glyoxylate reductase (2) | metabolic process [GO:0008152 biological_process] (2); oxidation-reduction process [GO:0055114 biological_process] (2); NAD binding [GO:0051287 molecular_function] (2); oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor [GO:0016616 molecular_function] (2) | D-isomer specific 2-hydroxyacid dehydrogenase, catalytic domain [IPR006139] (2); NAD(P)-binding domain [IPR016040] (2); D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding domain [IPR006140] (2) | scaffold_7_mRNA_1260.1 | C_unshiu_00221_mRNA_36.1 | - |
| GF0023518 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_7_mRNA_1252.1 | C_unshiu_00221_mRNA_26.1 | - |
| GF0023516 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_7_mRNA_1246.1 | C_unshiu_00221_mRNA_21.1 | - |
| GF0023515 | 1 | 1 | 0 | Hypothetical protein (2) | | Leucine-rich repeat domain, L domain-like [IPR032675] (2); Leucine-rich repeat 2 [IPR013101] (2) | scaffold_7_mRNA_1245.1 | C_unshiu_00221_mRNA_20.1 | - |
| GF0023514 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_7_mRNA_1244.1 | C_unshiu_00221_mRNA_19.1 | - |
| GF0023512 | 1 | 1 | 0 | Hypothetical protein (2) | DNA binding [GO:0003677 molecular_function] (2) | Homeodomain-like [IPR009057] (1); Homeobox domain-like [IPR009057] (1) | scaffold_7_mRNA_124.1 | C_unshiu_00353_mRNA_16.1 | - |
| GF0023511 | 1 | 1 | 0 | Hypothetical protein (2) | catalytic activity [GO:0003824 molecular_function] (2); metabolic process [GO:0008152 biological_process] (2) | Isochorismatase-like [IPR000868] (2) | scaffold_7_mRNA_1238.1 | C_unshiu_00221_mRNA_15.1 | - |
| GF0023508 | 1 | 1 | 0 | Hypothetical protein (2) | | Endonuclease/exonuclease/phosphatase [IPR005135] (1) | scaffold_7_mRNA_1211.1 | C_unshiu_00603_mRNA_3.1 | - |
| GF0023502 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_7_mRNA_1156.1 | C_unshiu_00121_mRNA_20.1 | - |
| GF0023501 | 1 | 1 | 0 | Hypothetical protein (1); Carbohydrate-binding protein of the ER protein (1) | ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1) | Malectin-like carbohydrate-binding domain [IPR024788] (2); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1) | scaffold_7_mRNA_1145.1 | C_unshiu_00121_mRNA_28.1 | - |
| GF0023495 | 1 | 1 | 0 | Hypothetical protein (2) | oxygen binding [GO:0019825 molecular_function] (2); heme binding [GO:0020037 molecular_function] (2) | Globin-like [IPR009050] (2); Globin [IPR000971] (2); Globin/Protoglobin [IPR012292] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1) | scaffold_7_mRNA_1108.1 | C_unshiu_00121_mRNA_60.1 | - |
| GF0023494 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_7_mRNA_1100.1 | C_unshiu_00121_mRNA_68.1 | - |
| GF0023488 | 1 | 1 | 0 | Putative disease resistance protein RGA3 (1); Disease resistance protein (1) | ADP binding [GO:0043531 molecular_function] (2) | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); NB-ARC [IPR002182] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Winged helix-turn-helix DNA-binding domain [IPR011991] (1) | scaffold_7_mRNA_1065.1 | C_unshiu_00065_mRNA_55.1 | - |
| GF0023487 | 1 | 1 | 0 | Disease resistance protein RPM1 (2) | ADP binding [GO:0043531 molecular_function] (2) | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); AAA+ ATPase domain [IPR003593] (2); NB-ARC [IPR002182] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Winged helix-turn-helix DNA-binding domain [IPR011991] (1) | scaffold_7_mRNA_1053.1 | C_unshiu_00065_mRNA_60.1 | - |
| GF0023485 | 1 | 1 | 0 | LA-related protein 6 LA RNA-binding domain protein (2) | | Winged helix-turn-helix DNA-binding domain [IPR011991] (2); RNA-binding protein Lupus La [IPR006630] (2) | scaffold_7_mRNA_104.1 | C_unshiu_01418_mRNA_1.1 | - |
| GF0023482 | 1 | 1 | 0 | D6-type cyclin isoform 1 (2) | nucleus [GO:0005634 cellular_component] (2); regulation of cell cycle [GO:0051726 biological_process] (1) | Cyclin, N-terminal [IPR006671] (2); Cyclin-like [IPR013763] (2); Cyclin, C-terminal domain [IPR004367] (2); Cyclin D, plant [IPR031093] (1) | scaffold_7_mRNA_1000.1 | C_unshiu_00065_mRNA_14.1 | - |
| GF0023481 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_7_mRNA_1.1 | C_unshiu_00009_mRNA_100.1 | - |
| GF0023479 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_971.1 | C_unshiu_00232_mRNA_27.1 | - |
| GF0023478 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_970.1 | C_unshiu_00232_mRNA_28.1 | - |
| GF0023477 | 1 | 1 | 0 | Hypothetical protein (2) | zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1) | Gag-polypeptide of LTR copia-type [IPR029472] (1); Zinc finger, CCHC-type [IPR001878] (1) | scaffold_6_mRNA_97.1 | C_unshiu_00378_mRNA_9.1 | - |
| GF0023476 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2); zinc ion binding [GO:0008270 molecular_function] (2) | Zinc finger, CCHC-type [IPR001878] (2); Zinc knuckle CX2CX4HX4C [IPR025836] (2); Domain of unknown function DUF4283 [IPR025558] (2) | scaffold_6_mRNA_954.1 | C_unshiu_00964_mRNA_1.1 | - |
| GF0023475 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_953.1 | C_unshiu_01179_mRNA_1.1 | - |
| GF0023474 | 1 | 1 | 0 | Polynucleotidyl transferase, Ribonuclease H fold (2) | | Reverse transcriptase zinc-binding domain [IPR026960] (2) | scaffold_6_mRNA_952.1 | C_unshiu_01179_mRNA_4.1 | - |
| GF0023473 | 1 | 1 | 0 | Tabersonine 16-O-methyltransferase (2) | O-methyltransferase activity [GO:0008171 molecular_function] (2); methyltransferase activity [GO:0008168 molecular_function] (2) | S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (2); O-methyltransferase, family 2 [IPR001077] (2); O-methyltransferase COMT-type [IPR016461] (2) | scaffold_6_mRNA_949.1 | C_unshiu_00530_mRNA_12.1 | - |
| GF0023472 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_939.1 | C_unshiu_00407_mRNA_19.1 | - |
| GF0023471 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_938.1 | C_unshiu_00407_mRNA_18.1 | - |
| GF0023470 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_936.1 | C_unshiu_00407_mRNA_17.1 | - |
| GF0023469 | 1 | 1 | 0 | Hypothetical protein (2) | 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_924.1 | C_unshiu_00407_mRNA_2.1 | - |
| GF0023467 | 1 | 1 | 0 | Hypothetical protein (2) | transcription, DNA-templated [GO:0006351 biological_process] (2); nucleus [GO:0005634 cellular_component] (1); zinc ion binding [GO:0008270 molecular_function] (1) | Transcription elongation factor S-II, central domain [IPR003618] (2); Transcription elongation factor S-IIM [IPR017890] (1) | scaffold_6_mRNA_902.1 | C_unshiu_00539_mRNA_5.1 | - |
| GF0023466 | 1 | 1 | 0 | Non-LTR retroelement reverse transcriptase (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2); Reverse transcriptase zinc-binding domain [IPR026960] (2) | scaffold_6_mRNA_90.1 | C_unshiu_00646_mRNA_18.1 | - |
| GF0023464 | 1 | 1 | 0 | Zinc finger CCCH domain-containing protein 32 (2) | metal ion binding [GO:0046872 molecular_function] (2) | Zinc finger, CCCH-type [IPR000571] (2) | scaffold_6_mRNA_894.1 | C_unshiu_00104_mRNA_54.1 | - |
| GF0023463 | 1 | 1 | 0 | Lysine ketoglutarate reductase trans-splicing-like protein (2) | | Protein of unknown function DUF707 [IPR007877] (2) | scaffold_6_mRNA_893.1 | C_unshiu_00104_mRNA_53.1 | - |
| GF0023461 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_882.1 | C_unshiu_00222_mRNA_3.1 | - |
| GF0023459 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_872.1 | C_unshiu_00529_mRNA_16.1 | - |
| GF0023458 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_871.1 | C_unshiu_00393_mRNA_13.1 | - |
| GF0023457 | 1 | 1 | 0 | 3-ketoacyl-CoA synthase 11 (2) | catalytic activity [GO:0003824 molecular_function] (2); fatty acid biosynthetic process [GO:0006633 biological_process] (2); transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (2); membrane [GO:0016020 cellular_component] (2); metabolic process [GO:0008152 biological_process] (2) | Thiolase-like [IPR016039] (2); Very-long-chain 3-ketoacyl-CoA synthase [IPR012392] (2); FAE1/Type III polyketide synthase-like protein [IPR013601] (2); 3-Oxoacyl-[acyl-carrier-protein (ACP)] synthase III, C-terminal [IPR013747] (2) | scaffold_6_mRNA_860.1 | C_unshiu_00393_mRNA_21.1 | - |
| GF0023456 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_859.1 | C_unshiu_00446_mRNA_18.1 | - |
| GF0023455 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_848.1 | C_unshiu_00882_mRNA_5.1 | - |
| GF0023454 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_847.1 | C_unshiu_00882_mRNA_6.1 | - |
| GF0023453 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_841.1 | C_unshiu_00882_mRNA_10.1 | - |
| GF0023452 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_84.1 | C_unshiu_01116_mRNA_2.1 | - |
| GF0023451 | 1 | 1 | 0 | Hypothetical protein (2) | | Chromo domain [IPR023780] (2); Chromo domain-like [IPR016197] (2) | scaffold_6_mRNA_835.1 | C_unshiu_00432_mRNA_2.1 | - |
| GF0023450 | 1 | 1 | 0 | Hypothetical protein (2) | | GAG-pre-integrase domain [IPR025724] (2) | scaffold_6_mRNA_825.1 | C_unshiu_00257_mRNA_20.1 | - |
| GF0023448 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_815.1 | C_unshiu_00257_mRNA_15.1 | - |
| GF0023447 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_814.1 | C_unshiu_00257_mRNA_14.1 | - |
| GF0023445 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_798.1 | C_unshiu_00382_mRNA_3.1 | - |
| GF0023444 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_797.1 | C_unshiu_00323_mRNA_19.1 | - |
| GF0023443 | 1 | 1 | 0 | MuDR family transposase isoform 1 (2) | zinc ion binding [GO:0008270 molecular_function] (2) | Zinc finger, SWIM-type [IPR007527] (2); Transposase, MuDR, plant [IPR004332] (2); MULE transposase domain [IPR018289] (2); Zinc finger, PMZ-type [IPR006564] (2) | scaffold_6_mRNA_791.1 | C_unshiu_00120_mRNA_10.1 | - |
| GF0023442 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_783.1 | C_unshiu_01590_mRNA_3.1 | - |
| GF0023441 | 1 | 1 | 0 | 40S ribosomal protein S2 (2) | ribosome [GO:0005840 cellular_component] (2); RNA binding [GO:0003723 molecular_function] (2); small ribosomal subunit [GO:0015935 cellular_component] (2); structural constituent of ribosome [GO:0003735 molecular_function] (2); translation [GO:0006412 biological_process] (2) | Ribosomal protein S5 domain 2-type fold [IPR020568] (2); Ribosomal protein S5 [IPR000851] (2); Ribosomal protein S5 domain 2-type fold, subgroup [IPR014721] (2); Ribosomal protein S5, N-terminal [IPR013810] (2); Ribosomal protein S5, eukaryotic/archaeal [IPR005711] (2); Ribosomal protein S5, C-terminal [IPR005324] (2); Double-stranded RNA-binding domain [IPR014720] (1) | scaffold_6_mRNA_782.1 | C_unshiu_01590_mRNA_2.1 | - |
| GF0023440 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_764.1 | C_unshiu_00147_mRNA_31.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0023439 | 1 | 1 | 0 | Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger domain-containing protein (2) | zinc ion binding [GO:0008270 molecular_function] (2); protein binding [GO:0005515 molecular_function] (2) | Zinc finger, FYVE/PHD-type [IPR011011] (2); Zinc finger, RING/FYVE/PHD-type [IPR013083] (2); Zinc finger, PHD-type, conserved site [IPR019786] (2); Zinc finger, PHD-type [IPR001965] (2); Zinc finger, PHD-finger [IPR019787] (2); Jas TPL-binding domain [IPR032308] (2) | scaffold_6_mRNA_758.1 | C_unshiu_00147_mRNA_24.1 | - |
| GF0023438 | 1 | 1 | 0 | Cysteine-rich RLK (RECEPTOR-like protein kinase) 8 (1); Pol polyprotein (1) |  | Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (2) | scaffold_6_mRNA_755.1 | C_unshiu_00860_mRNA_7.1 | - |
| GF0023437 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_753.1 | C_unshiu_00860_mRNA_5.1 | - |
| GF0023436 | 1 | 1 | 0 | TRNA synthetase class I (C) family protein (2) | nucleotide binding [GO:0000166 molecular_function] (2); ATP binding [GO:0005524 molecular_function] (2); tRNA aminoacylation for protein translation [GO:0006418 biological_process] (2); aminoacyl-tRNA ligase activity [GO:0004812 molecular_function] (2) | Cysteinyl-tRNA synthetase/mycothiol ligase [IPR024909] (2); tRNA synthetases class I, catalytic domain [IPR032678] (2); Rossmann-like alpha/beta/alpha sandwich fold [IPR014729] (2); Aminoacyl-tRNA synthetase, class 1a, anticodon-binding [IPR009080] (1); Aminoacyl-tRNA synthetase, class Ia, anticodon-binding [IPR009080] (1) | scaffold_6_mRNA_75.1 | C_unshiu_01116_mRNA_5.1 | - |
| GF0023435 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_741.1 | C_unshiu_00402_mRNA_19.1 | - |
| GF0023434 | 1 | 1 | 0 | Glycosyl hydrolases family 31 protein isoform 2 (1); Hypothetical protein (1) | carbohydrate binding [GO:0030246 molecular_function] (2); hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (2); carbohydrate metabolic process [GO:0005975 biological_process] (2); catalytic activity [GO:0003824 molecular_function] (2); proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1) | Glycoside hydrolase family 31 [IPR000322] (2); Galactose mutarotase-like domain [IPR011013] (2); Aldolase-type TIM barrel [IPR013785] (2); Glycoside hydrolase superfamily [IPR017853] (2); Glycoside hydrolase family 31, N-terminal domain [IPR025887] (2); Glycosyl hydrolases family 31, active site [IPR030458] (1); Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1) | scaffold_6_mRNA_728.1 | C_unshiu_01112_mRNA_7.1 | - |
| GF0023433 | 1 | 1 | 0 | Hypothetical protein (2) | regulation of transcription, DNA-templated [GO:0006355 biological_process] (2) | FHY3/FAR1 family [IPR031052] (2); MULE transposase domain [IPR018289] (2) | scaffold_6_mRNA_721.1 | C_unshiu_01112_mRNA_1.1 | - |
| GF0023432 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_716.1 | C_unshiu_00287_mRNA_17.1 | - |
| GF0023431 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_715.1 | C_unshiu_00287_mRNA_18.1 | - |
| GF0023429 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_697.1 | C_unshiu_00840_mRNA_1.1 | - |
| GF0023428 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_696.1 | C_unshiu_01532_mRNA_5.1 | - |
| GF0023427 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_693.1 | C_unshiu_00433_mRNA_30.1 | - |
| GF0023426 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_687.1 | C_unshiu_00017_mRNA_54.1 | - |
| GF0023425 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_682.1 | C_unshiu_00422_mRNA_16.1 | - |
| GF0023423 | 1 | 1 | 0 | Hypothetical protein (2) | regulation of transcription, DNA-templated [GO:0006355 biological_process] (2) | FHY3/FAR1 family [IPR031052] (2); MULE transposase domain [IPR018289] (1) | scaffold_6_mRNA_665.1 | C_unshiu_01576_mRNA_5.1 | - |
| GF0023421 | 1 | 1 | 0 | Glutaminase (2) |  | Harbinger transposase-derived nuclease domain [IPR027806] (2) | scaffold_6_mRNA_634.1 | C_unshiu_00858_mRNA_11.1 | - |
| GF0023420 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_620.1 | C_unshiu_02253_mRNA_1.1 | - |
| GF0023418 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_608.1 | C_unshiu_01017_mRNA_9.1 | - |
| GF0023417 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_599.1 | C_unshiu_00763_mRNA_15.1 | - |
| GF0023416 | 1 | 1 | 0 | Hypothetical protein (2) |  | Reverse transcriptase domain [IPR000477] (2) | scaffold_6_mRNA_597.1 | C_unshiu_00479_mRNA_12.1 | - |
| GF0023415 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_574.1 | C_unshiu_00408_mRNA_4.1 | - |
| GF0023413 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_566.1 | C_unshiu_01671_mRNA_6.1 | - |
| GF0023412 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_56.1 | C_unshiu_00545_mRNA_21.1 | - |
| GF0023408 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_544.1 | C_unshiu_00408_mRNA_28.1 | - |
| GF0023407 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_529.1 | C_unshiu_00118_mRNA_5.1 | - |
| GF0023406 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_523.1 | C_unshiu_01616_mRNA_2.1 | - |
| GF0023405 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_519.1 | C_unshiu_02890_mRNA_3.1 | - |
| GF0023404 | 1 | 1 | 0 | Polynucleotidyl transferase, ribonuclease H-like superfamily protein (1); Putative non-LTR retroelement reverse transcriptase (1) | nucleic acid binding [GO:0003676 molecular_function] (1) | Reverse transcriptase zinc-binding domain [IPR026960] (2); Ribonuclease H-like domain [IPR012337] (1) | scaffold_6_mRNA_516.1 | C_unshiu_00020_mRNA_1.1 | - |
| GF0023403 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_51.1 | C_unshiu_01076_mRNA_4.1 | - |
| GF0023402 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_503.1 | C_unshiu_02865_mRNA_2.1 | - |
| GF0023401 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_496.1 | C_unshiu_00470_mRNA_7.1 | - |
| GF0023400 | 1 | 1 | 0 | Hypothetical protein (2) |  | Viral movement protein [IPR028919] (2) | scaffold_6_mRNA_489.1 | C_unshiu_01765_mRNA_6.1 | - |
| GF0023399 | 1 | 1 | 0 | Hypothetical protein (2) | proteolysis [GO:0006508 biological_process] (2); cysteine-type peptidase activity [GO:0008234 molecular_function] (2) | Ulp1 protease family, C-terminal catalytic domain [IPR003653] (2) | scaffold_6_mRNA_485.1 | C_unshiu_01803_mRNA_1.1 | - |
| GF0023397 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_481.1 | C_unshiu_01803_mRNA_4.1 | - |
| GF0023396 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_465.1 | C_unshiu_01388_mRNA_11.1 | - |
| GF0023395 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_461.1 | C_unshiu_00219_mRNA_6.1 | - |
| GF0023394 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_454.1 | C_unshiu_01109_mRNA_7.1 | - |
| GF0023393 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_453.1 | C_unshiu_01547_mRNA_1.1 | - |
| GF0023392 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_445.1 | C_unshiu_01873_mRNA_7.1 | - |
| GF0023391 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_443.1 | C_unshiu_01616_mRNA_3.1 | - |
| GF0023390 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_438.1 | C_unshiu_00145_mRNA_27.1 | - |
| GF0023389 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_431.1 | C_unshiu_00145_mRNA_33.1 | - |
| GF0023388 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_430.1 | C_unshiu_00145_mRNA_34.1 | - |
| GF0023387 | 1 | 1 | 0 | Hypothetical protein (2) |  | Viral movement protein [IPR028919] (2) | scaffold_6_mRNA_428.1 | C_unshiu_00145_mRNA_36.1 | - |
| GF0023386 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_424.1 | C_unshiu_00145_mRNA_41.1 | - |
| GF0023385 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_418.1 | C_unshiu_00145_mRNA_45.1 | - |
| GF0023384 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_417.1 | C_unshiu_00145_mRNA_46.1 | - |
| GF0023383 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_415.1 | C_unshiu_00011_mRNA_93.1 | - |
| GF0023382 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_414.1 | C_unshiu_00011_mRNA_92.1 | - |
| GF0023381 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_413.1 | C_unshiu_00011_mRNA_91.1 | - |
| GF0023380 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_412.1 | C_unshiu_00011_mRNA_90.1 | - |
| GF0023379 | 1 | 1 | 0 | Nucleic acid binding / zinc ion binding protein (1); Zinc finger CCCH domain-containing protein 3 (1) | zinc ion binding [GO:0008270 molecular_function] (2); metal ion binding [GO:0046872 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | Zinc finger, CCCH-type [IPR000571] (2); Zinc finger, U1-C type [IPR013085] (1); Zinc finger, U1-type [IPR003604] (1); Zinc finger C2H2-type [IPR013087] (1); Matrin/U1-C-like, C2H2-type zinc finger [IPR003604] (1); U1-C, C2H2-type zinc finger [IPR013085] (1) | scaffold_6_mRNA_41.1 | C_unshiu_00772_mRNA_3.1 | - |
| GF0023377 | 1 | 1 | 0 | Hypothetical protein (2) | DNA binding [GO:0003677 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (1) | Zinc finger, BED-type [IPR003656] (2); Zinc finger C2H2-type [IPR013087] (1) | scaffold_6_mRNA_408.1 | C_unshiu_00610_mRNA_3.1 | - |
| GF0023376 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_404.1 | C_unshiu_00003_mRNA_170.1 | - |
| GF0023375 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_401.1 | C_unshiu_00003_mRNA_166.1 | - |
| GF0023374 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_393.1 | C_unshiu_00474_mRNA_17.1 | - |
| GF0023373 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_391.1 | C_unshiu_00474_mRNA_18.1 | - |
| GF0023372 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_387.1 | C_unshiu_00474_mRNA_22.1 | - |
| GF0023371 | 1 | 1 | 0 | Hypothetical protein (2) |  | Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (2) | scaffold_6_mRNA_386.1 | C_unshiu_00474_mRNA_23.1 | - |
| GF0023370 | 1 | 1 | 0 | Hypothetical protein (2) |  | Viral movement protein [IPR028919] (2) | scaffold_6_mRNA_384.1 | C_unshiu_00474_mRNA_27.1 | - |
| GF0023369 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_379.1 | C_unshiu_00886_mRNA_7.1 | - |
| GF0023368 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_377.1 | C_unshiu_00321_mRNA_1.1 | - |
| GF0023367 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_371.1 | C_unshiu_00403_mRNA_6.1 | - |
| GF0023366 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_365.1 | C_unshiu_00321_mRNA_11.1 | - |
| GF0023365 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_347.1 | C_unshiu_00106_mRNA_21.1 | - |
| GF0023364 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_34.1 | C_unshiu_00851_mRNA_2.1 | - |
| GF0023363 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_337.1 | C_unshiu_00897_mRNA_13.1 | - |
| GF0023362 | 1 | 1 | 0 | Assimilatory nitrate reductase catalytic subunit (1); Hypothetical protein (1) |  |  | scaffold_6_mRNA_3169.1 | C_unshiu_00009_mRNA_77.1 | - |
| GF0023361 | 1 | 1 | 0 | UDP-glycosyltransferase 83A1 (2) | transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (2); metabolic process [GO:0008152 biological_process] (2) | UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (2); EF-Hand 1, calcium-binding site [IPR018247] (1) | scaffold_6_mRNA_3161.1 | C_unshiu_00009_mRNA_70.1 | - |
| GF0023358 | 1 | 1 | 0 | Hypothetical protein (2) | protein dimerization activity [GO:0046983 molecular_function] (1) | Myc-type, basic helix-loop-helix (bHLH) domain [IPR011598] (1) | scaffold_6_mRNA_3156.1 | C_unshiu_00009_mRNA_68.1 | - |
| GF0023357 | 1 | 1 | 0 | Hypothetical protein (2) | protein kinase activity [GO:0004672 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2); ATP binding [GO:0005524 molecular_function] (2) | Protein kinase, ATP binding site [IPR017441] (2); Protein kinase-like domain [IPR011009] (2); Protein kinase domain [IPR000719] (2); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1) | scaffold_6_mRNA_3143.1 | C_unshiu_00009_mRNA_54.1 | - |
| GF0023356 | 1 | 1 | 0 | Early nodulin-like protein 17 (2) | electron carrier activity [GO:0009055 molecular_function] (2) | Phytocyanin domain [IPR003245] (2); Cupredoxin [IPR008972] (2) | scaffold_6_mRNA_3140.1 | C_unshiu_00009_mRNA_51.1 | - |
| GF0023354 | 1 | 1 | 0 | UPF0301 protein (2) |  | Protein of unknown function UPF0301 [IPR003774] (2) | scaffold_6_mRNA_3137.1 | C_unshiu_00009_mRNA_48.1 | - |
| GF0023353 | 1 | 1 | 0 | Cyclic nucleotide-gated ion channel 2 (2) | ion channel activity [GO:0005216 molecular_function] (1); membrane [GO:0016020 cellular_component] (1); ion transport [GO:0006811 biological_process] (1); transmembrane transport [GO:0055085 biological_process] (1) | Cyclic nucleotide-binding domain [IPR000595] (1); RmlC-like jelly roll fold [IPR014710] (1); Ion transport domain [IPR005821] (1); Cyclic nucleotide-binding-like [IPR018490] (1) | scaffold_6_mRNA_3130.1 | C_unshiu_00009_mRNA_41.1 | - |
| GF0023350 | 1 | 1 | 0 | ERD (Early-responsive to dehydration stress) family protein (2) | membrane [GO:0016020 cellular_component] (2) | Calcium permeable stress-gated cation channel 1, N-terminal transmembrane domain [IPR032880] (2); 10TM putative phosphate transporter, cytosolic domain [IPR027815] (2); Calcium-dependent channel, 7TM region, putative phosphate [IPR003864] (2) | scaffold_6_mRNA_3109.1 | C_unshiu_00009_mRNA_18.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0023349 | 1 | 1 | 0 | Hypothetical protein (2) | glucose metabolic process [GO:0006006 biological_process] (2); oxidation-reduction process [GO:0055114 biological_process] (2); glucose-6-phosphate dehydrogenase activity [GO:0004345 molecular_function] (2); NADP binding [GO:0050661 molecular_function] (2) | Glucose-6-phosphate dehydrogenase [IPR001282] (2); Glucose-6-phosphate dehydrogenase, C-terminal [IPR022675] (2) | scaffold_6_mRNA_31.1 | C_unshiu_00464_mRNA_13.1 | - |
| GF0023348 | 1 | 1 | 0 | Hypothetical protein (1); PLATZ transcription factor family protein (1) | | Protein of unknown function DUF597 [IPR006734] (2) | scaffold_6_mRNA_309.1 | C_unshiu_01082_mRNA_4.1 | - |
| GF0023346 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_307.1 | C_unshiu_01082_mRNA_6.1 | - |
| GF0023345 | 1 | 1 | 0 | Hypothetical protein (2) | | Domain unknown function DUF295 [IPR005174] (1) | scaffold_6_mRNA_3065.1 | C_unshiu_00654_mRNA_6.1 | - |
| GF0023344 | 1 | 1 | 0 | Protein kinase APK1A (2) | ATP binding [GO:0005524 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2); protein kinase activity [GO:0004672 molecular_function] (2) | Serine/threonine-protein kinase, active site [IPR008271] (2); Protein kinase, ATP binding site [IPR017441] (2); Protein kinase-like domain [IPR011009] (2); Protein kinase domain [IPR000719] (2); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1) | scaffold_6_mRNA_3058.1 | C_unshiu_00135_mRNA_16.1 | - |
| GF0023342 | 1 | 1 | 0 | Caffeic acid O-methyltransferase (2) | O-methyltransferase activity [GO:0008171 molecular_function] (2); protein dimerization activity [GO:0046983 molecular_function] (2); methyltransferase activity [GO:0008168 molecular_function] (2) | O-methyltransferase, family 2 [IPR001077] (2); Winged helix-turn-helix DNA-binding domain [IPR011991] (2); O-methyltransferase COMT-type [IPR016461] (2); Plant methyltransferase dimerisation [IPR012967] (2); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (2) | scaffold_6_mRNA_3040.1 | C_unshiu_02673_mRNA_2.1 | - |
| GF0023341 | 1 | 1 | 0 | Polyvinylalcohol dehydrogenase-like protein (2) | | Pyrrolo-quinoline quinone beta-propeller repeat [IPR018391] (2); Quinoprotein alcohol dehydrogenase-like superfamily [IPR011047] (2); Pyrrolo-quinoline quinone repeat [IPR002372] (2); Quinoprotein alcohol dehydrogenase-like domain [IPR027295] (1) | scaffold_6_mRNA_3035.1 | C_unshiu_00135_mRNA_40.1 | - |
| GF0023339 | 1 | 1 | 0 | Hypothetical protein (1); Spo11-3/Rhl2/Bin5/Top6A3 vegetative topoisomerase VIA (1) | DNA binding [GO:0003677 molecular_function] (2); chromosome [GO:0005694 cellular_component] (2); DNA catabolic process, endonucleolytic [GO:0000737 biological_process] (2); DNA topoisomerase type II (ATP-hydrolyzing) activity [GO:0003918 molecular_function] (1); DNA metabolic process [GO:0006259 biological_process] (1); DNA topological change [GO:0006265 biological_process] (1); ATP binding [GO:0005524 molecular_function] (1); catalytic activity [GO:0003824 molecular_function] (1) | Spo11/DNA topoisomerase VI subunit A [IPR002815] (2); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Topoisomerase 6 subunit A/Spo11, TOPRIM domain [IPR034136] (1); Spo11/DNA topoisomerase VI, subunit A, N-terminal [IPR013049] (1); DNA topoisomerase VI, subunit A [IPR004085] (1) | scaffold_6_mRNA_3016.1 | C_unshiu_00135_mRNA_54.1 | - |
| GF0023338 | 1 | 1 | 0 | Putative mitochondrial chaperone BCS1-B (2) | ATP binding [GO:0005524 molecular_function] (2) | ATPase, AAA-type, conserved site [IPR003960] (2); ATPase, AAA-type, core [IPR003959] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); AAA-type ATPase, N-terminal domain [IPR025753] (2); AAA+ ATPase domain [IPR003593] (2) | scaffold_6_mRNA_3000.1 | C_unshiu_00420_mRNA_11.1 | - |
| GF0023332 | 1 | 1 | 0 | Hypothetical protein (2) | | Leucine-rich repeat domain, L domain-like [IPR032675] (1); FBD domain [IPR006566] (1) | scaffold_6_mRNA_2972.1 | C_unshiu_00133_mRNA_46.1 | - |
| GF0023329 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_2957.1 | C_unshiu_00133_mRNA_29.1 | - |
| GF0023328 | 1 | 1 | 0 | Abhydrolase domain-containing protein (2) | | Alpha/Beta hydrolase fold [IPR029058] (2); Alpha/beta hydrolase fold-5 [IPR029059] (1); Serine aminopeptidase, S33 [IPR022742] (1) | scaffold_6_mRNA_2945.1 | C_unshiu_00133_mRNA_14.1 | - |
| GF0023327 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_294.1 | C_unshiu_00178_mRNA_27.1 | - |
| GF0023326 | 1 | 1 | 0 | Hypothetical protein (2) | | GH3 family [IPR004993] (2) | scaffold_6_mRNA_2926.1 | C_unshiu_00253_mRNA_5.1 | - |
| GF0023325 | 1 | 1 | 0 | Receptor-like protein kinase FERONIA (2) | protein phosphorylation [GO:0006468 biological_process] (2); protein kinase activity [GO:0004672 molecular_function] (2); ATP binding [GO:0005524 molecular_function] (2); protein tyrosine kinase activity [GO:0004713 molecular_function] (1) | Protein kinase, ATP binding site [IPR017441] (2); Protein kinase domain [IPR000719] (2); Protein kinase-like domain [IPR011009] (2); Malectin-like carbohydrate-binding domain [IPR024788] (2); Serine/threonine-protein kinase, active site [IPR008271] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Tyrosine-protein kinase, catalytic domain [IPR020635] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1) | scaffold_6_mRNA_2912.1 | C_unshiu_00253_mRNA_19.1 | - |
| GF0023324 | 1 | 1 | 0 | PLC-like phosphodiesterases superfamily protein (2) | phosphoric diester hydrolase activity [GO:0008081 molecular_function] (2); lipid metabolic process [GO:0006629 biological_process] (2) | NADH-ubiquinone reductase complex 1 MLRQ subunit [IPR010530] (2); Phosphatidylinositol-specific phospholipase C, X domain [IPR000909] (2); PLC-like phosphodiesterase, TIM beta/alpha-barrel domain [IPR017946] (2) | scaffold_6_mRNA_2911.1 | C_unshiu_00253_mRNA_20.1 | - |
| GF0023322 | 1 | 1 | 0 | Pentatricopeptide (PPR) repeat protein (2) | protein binding [GO:0005515 molecular_function] (2) | Tetratricopeptide-like helical domain [IPR011990] (2); Pentatricopeptide repeat [IPR002885] (2) | scaffold_6_mRNA_2895.1 | C_unshiu_00253_mRNA_37.1 | - |
| GF0023321 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_2892.1 | C_unshiu_00183_mRNA_23.1 | - |
| GF0023320 | 1 | 1 | 0 | S-adenosylmethionine decarboxylase proenzyme (2) | spermine biosynthetic process [GO:0006597 biological_process] (2); spermidine biosynthetic process [GO:0008295 biological_process] (2); adenosylmethionine decarboxylase activity [GO:0004014 molecular_function] (2) | S-adenosylmethionine decarboxylase [IPR001985] (2); S-adenosylmethionine decarboxylase, conserved site [IPR018166] (2); S-adenosylmethionine decarboxylase, core [IPR016067] (2); S-adenosylmethionine decarboxylase subgroup [IPR018167] (1) | scaffold_6_mRNA_2876.1 | C_unshiu_00098_mRNA_50.1 | - |
| GF0023319 | 1 | 1 | 0 | DUF1262 family protein (2) | | Protein of unknown function DUF1262 [IPR010683] (2) | scaffold_6_mRNA_2869.1 | C_unshiu_00098_mRNA_45.1 | - |
| GF0023318 | 1 | 1 | 0 | Non-LTR retroelement reverse transcriptase-like (1); Ribonuclease H-like superfamily protein (1) | nucleic acid binding [GO:0003676 molecular_function] (2) | Reverse transcriptase zinc-binding domain [IPR026960] (2); Ribonuclease H-like domain [IPR012337] (2) | scaffold_6_mRNA_2868.1 | C_unshiu_00357_mRNA_6.1 | - |
| GF0023317 | 1 | 1 | 0 | Acclimation of photosynthesis to environment (2) | | Protein of unknown function DUF2854 [IPR021275] (2) | scaffold_6_mRNA_2842.1 | C_unshiu_00098_mRNA_18.1 | - |
| GF0023316 | 1 | 1 | 0 | Plasma membrane associated protein (1); ABA induced plasma membrane protein (1) | | AWPM-19-like [IPR008390] (2) | scaffold_6_mRNA_2839.1 | C_unshiu_00098_mRNA_14.1 | - |
| GF0023314 | 1 | 1 | 0 | Neoxanthin synthase (2) | | Protein of unknown function DUF4281 [IPR025461] (1); ABA DEFICIENT 4-like [IPR025461] (1) | scaffold_6_mRNA_2817.1 | C_unshiu_00537_mRNA_16.1 | - |
| GF0023313 | 1 | 1 | 0 | MurB reductase, putative isoform 1 (2) | flavin adenine dinucleotide binding [GO:0050660 molecular_function] (2); oxidoreductase activity [GO:0016491 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2); UDP-N-acetylmuramate dehydrogenase activity [GO:0008762 molecular_function] (2); oxidoreductase activity, acting on CH-OH group of donors [GO:0016614 molecular_function] (2); catalytic activity [GO:0003824 molecular_function] (2) | UDP-N-acetylenolpyruvoylglucosamine reductase [IPR003170] (2); UDP-N-acetylenolpyruvoylglucosamine reductase, C-terminal [IPR011601] (2); FAD linked oxidase, N-terminal [IPR006094] (2); FAD-binding, type 2 [IPR016166] (2); FAD-binding, type 2, subdomain 1 [IPR016167] (2); CO dehydrogenase flavoprotein-like, FAD-binding, subdomain 2 [IPR016169] (2) | scaffold_6_mRNA_2816.1 | C_unshiu_00537_mRNA_15.1 | - |
| GF0023312 | 1 | 1 | 0 | Alpha/beta hydrolase family protein (2) | | Alpha/Beta hydrolase fold [IPR029058] (2); Alpha/beta hydrolase fold-1 [IPR000073] (2) | scaffold_6_mRNA_2813.1 | C_unshiu_00537_mRNA_13.1 | - |
| GF0023311 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_281.1 | C_unshiu_00360_mRNA_15.1 | - |
| GF0023309 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_2784.1 | C_unshiu_00866_mRNA_7.1 | - |
| GF0023307 | 1 | 1 | 0 | Zinc finger protein, putative (1); Zinc finger CCCH domain-containing protein 39 (1) | metal ion binding [GO:0046872 molecular_function] (2) | Zinc finger, CCCH-type [IPR000571] (2) | scaffold_6_mRNA_2780.1 | C_unshiu_00038_mRNA_73.1 | - |
| GF0023306 | 1 | 1 | 0 | DUF4228 domain protein (2) | | Protein of unknown function DUF4228, plant [IPR025322] (2) | scaffold_6_mRNA_2760.1 | C_unshiu_00038_mRNA_59.1 | - |
| GF0023305 | 1 | 1 | 0 | Integrin-linked protein kinase family isoform 1 (2) | protein binding [GO:0005515 molecular_function] (2); ATP binding [GO:0005524 molecular_function] (2); protein kinase activity [GO:0004672 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2) | Ankyrin repeat-containing domain [IPR020683] (2); Protein kinase-like domain [IPR011009] (2); Ankyrin repeat [IPR002110] (2); Protein kinase domain [IPR000719] (2); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Ferritin-related [IPR012347] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1) | scaffold_6_mRNA_2759.1 | C_unshiu_00038_mRNA_58.1 | - |
| GF0023303 | 1 | 1 | 0 | Ubiquitin fusion degradation protein (2) | ubiquitin-dependent protein catabolic process [GO:0006511 biological_process] (2) | Ubiquitin fusion degradation protein UFD1 [IPR004854] (2) | scaffold_6_mRNA_2735.1 | C_unshiu_00038_mRNA_31.1 | - |
| GF0023302 | 1 | 1 | 0 | Transcription factor DYSFUNCTIONAL TAPETUM 1 (2) | protein dimerization activity [GO:0046983 molecular_function] (2) | Myc-type, basic helix-loop-helix (bHLH) domain [IPR011598] (2) | scaffold_6_mRNA_2718.1 | C_unshiu_00038_mRNA_13.1 | - |
| GF0023301 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_2707.1 | C_unshiu_00038_mRNA_6.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0023299 | 1 | 1 | 0 | Farnesyltranstransferase (2) | isoprenoid biosynthetic process [GO:0008299 biological_process] (2) | Isoprenoid synthase domain [IPR008949] (2); Polyprenyl synthetase [IPR000092] (2); Polyprenyl synthetase-related [IPR017446] (1); Polyprenyl synthetase, conserved site [IPR033749] (1) | scaffold_6_mRNA_2698.1 | C_unshiu_00704_mRNA_17.1 | - |
| GF0023298 | 1 | 1 | 0 | Histidine-tRNA ligase/ATP phosphoribosyltransferase regulatory subunit (2) | cytoplasm [GO:0005737 cellular_component] (2) | Histidine-tRNA ligase/ATP phosphoribosyltransferase regulatory subunit [IPR004516] (2); Anticodon-binding [IPR004154] (2) | scaffold_6_mRNA_269.1 | C_unshiu_00176_mRNA_11.1 | - |
| GF0023296 | 1 | 1 | 0 | CCR4-NOT transcription complex subunit 7 (2) | nucleic acid binding [GO:0003676 molecular_function] (2); nucleus [GO:0005634 cellular_component] (1) | Ribonuclease H-like domain [IPR012337] (2); Ribonuclease CAF1 [IPR006941] (2) | scaffold_6_mRNA_2684.1 | C_unshiu_00704_mRNA_1.1 | - |
| GF0023294 | 1 | 1 | 0 | Centromere protein V (2) | carbon-sulfur lyase activity [GO:0016846 molecular_function] (2); metabolic process [GO:0008152 biological_process] (2) | Glutathione-dependent formaldehyde-activating enzyme/centromere protein V [IPR006913] (2); Mss4-like [IPR011057] (2) | scaffold_6_mRNA_2659.1 | C_unshiu_02047_mRNA_4.1 | - |
| GF0023292 | 1 | 1 | 0 | 3-oxoacyl-[acyl-carrier-protein] reductase FabG (2) | oxidoreductase activity [GO:0016491 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1) | NAD(P)-binding domain [IPR016040] (2); Glucose/ribitol dehydrogenase [IPR002347] (1); Short-chain dehydrogenase/reductase SDR [IPR002198] (1); Short-chain dehydrogenase/reductase SDR [IPR002347] (1); Polyketide synthase, ketoreductase domain [IPR013968] (1) | scaffold_6_mRNA_2642.1 | C_unshiu_00079_mRNA_56.1 | - |
| GF0023290 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_2625.1 | C_unshiu_00173_mRNA_7.1 | - |
| GF0023289 | 1 | 1 | 0 | Zinc finger protein, putative (2) | zinc ion binding [GO:0008270 molecular_function] (2); protein binding [GO:0005515 molecular_function] (2) | Zinc finger, RING/FYVE/PHD-type [IPR013083] (2); Zinc finger, RING-type [IPR001841] (2) | scaffold_6_mRNA_2601.1 | C_unshiu_00079_mRNA_19.1 | - |
| GF0023288 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_259.1 | C_unshiu_00380_mRNA_7.1 | - |
| GF0023287 | 1 | 1 | 0 | 50S ribosomal protein L40 (2) | | | scaffold_6_mRNA_2588.1 | C_unshiu_01167_mRNA_15.1 | - |
| GF0023286 | 1 | 1 | 0 | Hypothetical protein (2) | protein binding [GO:0005515 molecular_function] (1) | Pentatricopeptide repeat [IPR002885] (2); Tetratricopeptide-like helical domain [IPR011990] (1) | scaffold_6_mRNA_258.1 | C_unshiu_00380_mRNA_8.1 | - |
| GF0023285 | 1 | 1 | 0 | E3 ubiquitin-protein ligase RING1 (2) | protein binding [GO:0005515 molecular_function] (2); zinc ion binding [GO:0008270 molecular_function] (2) | Zinc finger, RING/FYVE/PHD-type [IPR013083] (2); Zinc finger, RING-type [IPR001841] (2) | scaffold_6_mRNA_2576.1 | C_unshiu_01167_mRNA_5.1 | - |
| GF0023284 | 1 | 1 | 0 | LEM3 (Ligand-effect modulator 3) family protein (2) | membrane [GO:0016020 cellular_component] (2) | CDC50/LEM3 family [IPR005045] (2) | scaffold_6_mRNA_2538.2 | C_unshiu_00037_mRNA_33.2 | - |
| GF0023283 | 1 | 1 | 0 | Uridylate kinase, putative (2) | pyrimidine nucleotide biosynthetic process [GO:0006221 biological_process] (2); UMP kinase activity [GO:0033862 molecular_function] (2); cytoplasm [GO:0005737 cellular_component] (2) | Aspartate/glutamate/uridylate kinase [IPR001048] (2); Uridylate kinase, bacteria [IPR015963] (2) | scaffold_6_mRNA_2513.1 | C_unshiu_00037_mRNA_60.1 | - |
| GF0023282 | 1 | 1 | 0 | Geraniol 10-hydroxylase-like protein (2) | iron ion binding [GO:0005506 molecular_function] (2); heme binding [GO:0020037 molecular_function] (2); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2) | Cytochrome P450, E-class, group I [IPR002401] (2); Cytochrome P450, conserved site [IPR017972] (2); Cytochrome P450 [IPR001128] (2) | scaffold_6_mRNA_2510.1 | C_unshiu_00052_mRNA_18.1 | - |
| GF0023281 | 1 | 1 | 0 | Avr9/Cf-9 rapidly elicited protein 137, putative (1); DUF3475 domain protein (1) | | Protein of unknown function DUF668 [IPR007700] (2); Protein of unknown function DUF3475 [IPR021864] (2) | scaffold_6_mRNA_2509.1 | C_unshiu_00052_mRNA_20.1 | - |
| GF0023278 | 1 | 1 | 0 | PAN domain-containing protein (2) | recognition of pollen [GO:0048544 biological_process] (2) | PAN/Apple domain [IPR003609] (2); Bulb-type lectin domain [IPR001480] (2); S-locus glycoprotein domain [IPR000858] (2) | scaffold_6_mRNA_2492.1 | C_unshiu_00052_mRNA_36.1 | - |
| GF0023277 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_249.1 | C_unshiu_01219_mRNA_6.1 | - |
| GF0023276 | 1 | 1 | 0 | Probable F-box protein At1g60180 (2) | protein binding [GO:0005515 molecular_function] (2) | F-box domain [IPR001810] (2) | scaffold_6_mRNA_2460.1 | C_unshiu_00052_mRNA_66.1 | - |
| GF0023274 | 1 | 1 | 0 | Terminal flower 1 (2) | negative regulation of flower development [GO:0009910 biological_process] (1); transcription cofactor activity [GO:0003712 molecular_function] (1) | Phosphatidylethanolamine-binding, conserved site [IPR001858] (2); Phosphatidylethanolamine-binding protein PEBP [IPR008914] (1); TERMINAL FLOWER 1-like [IPR031114] (1); Phosphatidylethanolamine-binding protein [IPR008914] (1) | scaffold_6_mRNA_2443.1 | C_unshiu_00046_mRNA_45.1 | - |
| GF0023273 | 1 | 1 | 0 | Iron-sulfur cluster assembly protein, putative (2) | structural molecule activity [GO:0005198 molecular_function] (2); iron-sulfur cluster binding [GO:0051536 molecular_function] (2); protein maturation by iron-sulfur cluster transfer [GO:0097428 biological_process] (1); iron-sulfur cluster assembly [GO:0016226 biological_process] (1) | FeS cluster biogenesis [IPR000361] (2); FeS cluster insertion protein [IPR016092] (2); FeS cluster insertion, C-terminal, conserved site [IPR017870] (2) | scaffold_6_mRNA_2439.1 | C_unshiu_02025_mRNA_2.1 | - |
| GF0023272 | 1 | 1 | 0 | Hypothetical protein (2) | protein binding [GO:0005515 molecular_function] (1) | Pentatricopeptide repeat [IPR002885] (2); Tetratricopeptide-like helical domain [IPR011990] (1) | scaffold_6_mRNA_2403.1 | C_unshiu_00215_mRNA_46.1 | - |
| GF0023271 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_2386.1 | C_unshiu_00215_mRNA_26.1 | - |
| GF0023269 | 1 | 1 | 0 | PHD finger transcription factor (2) | N-acetyltransferase activity [GO:0008080 molecular_function] (2); zinc ion binding [GO:0008270 molecular_function] (2); protein binding [GO:0005515 molecular_function] (2) | Zinc finger, FYVE/PHD-type [IPR011011] (2); GNAT domain [IPR000182] (2); Zinc finger, PHD-type [IPR001965] (2); Zinc finger, PHD-type, conserved site [IPR019786] (2); Zinc finger, RING/FYVE/PHD-type [IPR013083] (2); Acyl-CoA N-acyltransferase [IPR016181] (2); Jas TPL-binding domain [IPR032308] (2); Zinc finger, PHD-finger [IPR019787] (2) | scaffold_6_mRNA_2378.1 | C_unshiu_00215_mRNA_19.1 | - |
| GF0023268 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_2364.1 | C_unshiu_00475_mRNA_21.1 | - |
| GF0023263 | 1 | 1 | 0 | Exocyst subunit EXO70 family protein (2) | exocytosis [GO:0006887 biological_process] (2); exocyst [GO:0000145 cellular_component] (2) | Cullin repeat-like-containing domain [IPR016159] (2); Late embryogenesis abundant protein, LEA-14 [IPR004864] (2); Exocyst complex protein Exo70 [IPR004140] (1); Immunoglobulin-like fold [IPR013783] (1); Exocyst complex component Exo70 [IPR004140] (1) | scaffold_6_mRNA_2336.1 | C_unshiu_00043_mRNA_61.1 | - |
| GF0023261 | 1 | 1 | 0 | TatD related DNase (2) | hydrolase activity, acting on ester bonds [GO:0016788 molecular_function] (2) | Metal-dependent hydrolase [IPR032466] (2); TatD family [IPR001130] (2) | scaffold_6_mRNA_2316.1 | C_unshiu_00043_mRNA_39.1 | - |
| GF0023260 | 1 | 1 | 0 | Carotenoid isomerase (2) | oxidoreductase activity [GO:0016491 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2); carotenoid biosynthetic process [GO:0016117 biological_process] (2); isomerase activity [GO:0016853 molecular_function] (1); carotenoid isomerase activity [GO:0046608 molecular_function] (1) | FAD/NAD(P)-binding domain [IPR023753] (2); Amine oxidase [IPR002937] (2); Prolycopene isomerase [IPR014101] (1); Carotene isomerase [IPR014101] (1) | scaffold_6_mRNA_2293.1 | C_unshiu_00043_mRNA_12.1 | - |
| GF0023259 | 1 | 1 | 0 | Pentatricopeptide repeat-containing family protein (1); Tetratricopeptide repeat-like superfamily protein, putative isoform 1 (1) | protein binding [GO:0005515 molecular_function] (2); methyltransferase activity [GO:0008168 molecular_function] (1); methylation [GO:0032259 biological_process] (1); nucleic acid binding [GO:0003676 molecular_function] (1) | Pentatricopeptide repeat [IPR002885] (2); Tetratricopeptide-like helical domain [IPR011990] (2); Protein-lysine N-methyltransferase Efm5 [IPR019369] (1); DNA methylase, N-6 adenine-specific, conserved site [IPR002052] (1) | scaffold_6_mRNA_2269.1 | C_unshiu_00273_mRNA_15.1 | - |
| GF0023258 | 1 | 1 | 0 | Fatty acyl-CoA reductase 3 (1); Fatty acyl-CoA reductase 1 (1) | fatty-acyl-CoA reductase (alcohol-forming) activity [GO:0080019 molecular_function] (2) | Male sterility, NAD-binding [IPR013120] (2); NAD(P)-binding domain [IPR016040] (2); Fatty acyl-CoA reductase [IPR026055] (2); Fatty acyl-CoA reductase, C-terminal [IPR033640] (1) | scaffold_6_mRNA_2254.1 | C_unshiu_00273_mRNA_35.1 | - |
| GF0023257 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_2246.1 | C_unshiu_00089_mRNA_2.1 | - |
| GF0023256 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2); metal ion binding [GO:0046872 molecular_function] (1) | Zinc finger C2H2-type/integrase DNA-binding domain [IPR013087] (1); Zinc finger, C2H2 [IPR007087] (1); Zinc finger C2H2-type [IPR013087] (1) | scaffold_6_mRNA_2233.1 | C_unshiu_00089_mRNA_13.1 | - |
| GF0023254 | 1 | 1 | 0 | Metal tolerance protein 5 (2) | cation transport [GO:0006812 biological_process] (2); integral component of membrane [GO:0016021 cellular_component] (2); cation transmembrane transporter activity [GO:0008324 molecular_function] (2); transmembrane transport [GO:0055085 biological_process] (2) | Cation efflux protein, cytoplasmic domain [IPR027470] (2); Cation efflux protein [IPR002524] (2); Cation efflux protein transmembrane domain [IPR027469] (1) | scaffold_6_mRNA_2231.1 | C_unshiu_00089_mRNA_15.1 | - |
| GF0023253 | 1 | 1 | 0 | WCRKC thioredoxin 1 isoform 1 (2) | cell redox homeostasis [GO:0045454 biological_process] (2); glycerol ether metabolic process [GO:0006662 biological_process] (2); protein disulfide oxidoreductase activity [GO:0015035 molecular_function] (2) | Thioredoxin-like fold [IPR012336] (2); Thioredoxin [IPR005746] (2); Thioredoxin domain [IPR013766] (2) | scaffold_6_mRNA_2223.1 | C_unshiu_00089_mRNA_23.1 | - |
| GF0023252 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_2216.1 | C_unshiu_00089_mRNA_30.1 | - |
| GF0023249 | 1 | 1 | 0 | Hypothetical protein (1); Bimodular protein (1) | | Bifunctional inhibitor/plant lipid transfer protein/seed storage helical domain [IPR016140] (2); Hydrophobic seed protein [IPR027923] (2) | scaffold_6_mRNA_2145.1 | C_unshiu_00248_mRNA_35.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0023247 | 1 | 1 | 0 | UDP-glycosyltransferase 71C4 (2) | transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (2); metabolic process [GO:0008152 biological_process] (2) | UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (2) | scaffold_6_mRNA_2139.1 | C_unshiu_00248_mRNA_30.1 | - |
| GF0023244 | 1 | 1 | 0 | Mitochondrial transcription termination factor family protein (2) | regulation of transcription, DNA-templated [GO:0006355 biological_process] (2); double-stranded DNA binding [GO:0003690 molecular_function] (2); mitochondrion [GO:0005739 cellular_component] (1) | Mitochodrial transcription termination factor [IPR003690] (1); Transcription termination factor, mitochondrial/chloroplastic [IPR003690] (1) | scaffold_6_mRNA_2123.1 | C_unshiu_00248_mRNA_12.1 | - |
| GF0023243 | 1 | 1 | 0 | UPF0586 C9orf41-like protein (2) | | S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (2); N2227-like [IPR012901] (2) | scaffold_6_mRNA_2116.1 | C_unshiu_00248_mRNA_4.1 | - |
| GF0023242 | 1 | 1 | 0 | Hypothetical protein (2) | transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (2); metabolic process [GO:0008152 biological_process] (2) | UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (2); Bifunctional inhibitor/plant lipid transfer protein/seed storage helical domain [IPR016140] (1) | scaffold_6_mRNA_2115.1 | C_unshiu_00248_mRNA_2.1 | - |
| GF0023241 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_2091.1 | C_unshiu_01587_mRNA_5.1 | - |
| GF0023240 | 1 | 1 | 0 | Hypothetical protein (2) | | Agenet domain, plant type [IPR014002] (2); Protein of unknown function DUF724 [IPR007930] (2) | scaffold_6_mRNA_2082.1 | C_unshiu_00865_mRNA_9.1 | - |
| GF0023238 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_208.1 | C_unshiu_01343_mRNA_13.1 | - |
| GF0023234 | 1 | 1 | 0 | Lung seven transmembrane receptor family protein, expressed (2) | integral component of membrane [GO:0016021 cellular_component] (2) | Lung seven transmembrane receptor-like [IPR009637] (2) | scaffold_6_mRNA_2020.1 | C_unshiu_00090_mRNA_53.1 | - |
| GF0023231 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_200.1 | C_unshiu_00138_mRNA_69.1 | - |
| GF0023228 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_1975.1 | C_unshiu_00008_mRNA_111.1 | - |
| GF0023227 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_1970.1 | C_unshiu_00008_mRNA_105.1 | - |
| GF0023226 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_197.1 | C_unshiu_00138_mRNA_67.1 | - |
| GF0023222 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_1947.1 | C_unshiu_00008_mRNA_86.1 | - |
| GF0023220 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_1940.1 | C_unshiu_00008_mRNA_82.1 | - |
| GF0023219 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_1939.1 | C_unshiu_00008_mRNA_81.1 | - |
| GF0023217 | 1 | 1 | 0 | Hypothetical protein (2) | | Endonuclease/exonuclease/phosphatase [IPR005135] (2) | scaffold_6_mRNA_1928.1 | C_unshiu_00008_mRNA_73.1 | - |
| GF0023216 | 1 | 1 | 0 | Hypothetical protein (2) | | Endonuclease/exonuclease/phosphatase [IPR005135] (2) | scaffold_6_mRNA_1927.1 | C_unshiu_00008_mRNA_72.1 | - |
| GF0023215 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_1907.1 | C_unshiu_00008_mRNA_54.1 | - |
| GF0023214 | 1 | 1 | 0 | Nudix hydrolase 15, mitochondrial-like protein (1); Nudix hydrolase 15, mitochondrial (1) | hydrolase activity [GO:0016787 molecular_function] (2) | NUDIX hydrolase domain [IPR000086] (2); NUDIX hydrolase domain-like [IPR015797] (2) | scaffold_6_mRNA_1898.1 | C_unshiu_00008_mRNA_45.1 | - |
| GF0023213 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_1882.1 | C_unshiu_00008_mRNA_35.1 | - |
| GF0023212 | 1 | 1 | 0 | Verticillium wilt resistance-like protein (2) | protein binding [GO:0005515 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1) | Leucine-rich repeat [IPR001611] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Leucine-rich repeat, typical subtype [IPR003591] (2); Zinc finger, CCHC-type [IPR001878] (1) | scaffold_6_mRNA_1881.1 | C_unshiu_00008_mRNA_34.1 | - |
| GF0023211 | 1 | 1 | 0 | Pentatricopeptide repeat-containing protein, putative isoform 3 (2) | | Pentatricopeptide repeat [IPR002885] (2) | scaffold_6_mRNA_1873.1 | C_unshiu_00008_mRNA_27.1 | - |
| GF0023210 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_1864.1 | C_unshiu_00008_mRNA_18.1 | - |
| GF0023208 | 1 | 1 | 0 | Hypothetical protein (2) | | Leucine-rich repeat domain, L domain-like [IPR032675] (1) | scaffold_6_mRNA_1862.1 | C_unshiu_00157_mRNA_6.1 | - |
| GF0023205 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_1859.1 | C_unshiu_00008_mRNA_12.1 | - |
| GF0023203 | 1 | 1 | 0 | Hypothetical protein (2) | aminoacyl-tRNA ligase activity [GO:0004812 molecular_function] (2); lysine-tRNA ligase activity [GO:0004824 molecular_function] (2); lysyl-tRNA aminoacylation [GO:0006430 biological_process] (2); nucleotide binding [GO:0000166 molecular_function] (2); ATP binding [GO:0005524 molecular_function] (2); cytoplasm [GO:0005737 cellular_component] (2); tRNA aminoacylation for protein translation [GO:0006418 biological_process] (2) | Lysyl-tRNA synthetase, class II, C-terminal [IPR018149] (2); Aminoacyl-tRNA synthetase, class II (D/K/N) [IPR004364] (2); Aminoacyl-tRNA synthetase, class II (D/K/N)-like [IPR018150] (1) | scaffold_6_mRNA_1848.1 | C_unshiu_00008_mRNA_1.1 | - |
| GF0023202 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_1843.1 | C_unshiu_00217_mRNA_14.1 | - |
| GF0023201 | 1 | 1 | 0 | 50S ribosomal protein L14, chloroplastic (2) | ribosome [GO:0005840 cellular_component] (2); translation [GO:0006412 biological_process] (2); structural constituent of ribosome [GO:0003735 molecular_function] (2) | Ribosomal protein L14b/L23e [IPR000218] (1); Ribosomal protein L14 domain [IPR023571] (1); Ribosomal protein L14P [IPR000218] (1) | scaffold_6_mRNA_1841.1 | C_unshiu_01534_mRNA_7.1 | - |
| GF0023200 | 1 | 1 | 0 | Selenoprotein t (2) | | Selenoprotein, Rdx type [IPR011893] (2); Thioredoxin-like fold [IPR012336] (2); Selenoprotein T [IPR019389] (2) | scaffold_6_mRNA_1839.1 | C_unshiu_01534_mRNA_5.1 | - |
| GF0023199 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_1815.2 | C_unshiu_00332_mRNA_9.1 | - |
| GF0023198 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_1811.1 | C_unshiu_00332_mRNA_5.1 | - |
| GF0023197 | 1 | 1 | 0 | Hypothetical protein (2) | transmembrane transport [GO:0055085 biological_process] (1); integral component of membrane [GO:0016021 cellular_component] (1) | Sodium/calcium exchanger membrane region [IPR004837] (1) | scaffold_6_mRNA_1806.1 | C_unshiu_00390_mRNA_4.1 | - |
| GF0023195 | 1 | 1 | 0 | Disease resistance protein (2) | | Leucine-rich repeat domain, L domain-like [IPR032675] (2); Receptor L-domain [IPR000494] (1) | scaffold_6_mRNA_18.1 | C_unshiu_01597_mRNA_3.1 | - |
| GF0023194 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_6_mRNA_1795.1 | C_unshiu_00390_mRNA_16.1 | - |
| GF0023193 | 1 | 1 | 0 | LRR receptor-like kinase family protein (2) | protein phosphorylation [GO:0006468 biological_process] (2); protein kinase activity [GO:0004672 molecular_function] (2); ATP binding [GO:0005524 molecular_function] (2); protein binding [GO:0005515 molecular_function] (1) | Protein kinase domain [IPR000719] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Protein kinase-like domain [IPR011009] (2); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Leucine-rich repeat [IPR001611] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1) | scaffold_6_mRNA_1779.1 | C_unshiu_00473_mRNA_13.1 | - |
| GF0023190 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_1725.1 | C_unshiu_02528_mRNA_1.1 | - |
| GF0023189 | 1 | 1 | 0 | Hypothetical protein (1); Ribonuclease H protein (1) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2); Reverse transcriptase zinc-binding domain [IPR026960] (2) | scaffold_6_mRNA_1716.1 | C_unshiu_00034_mRNA_30.1 | - |
| GF0023188 | 1 | 1 | 0 | Hypothetical protein (2) | protein binding [GO:0005515 molecular_function] (2) | F-box domain [IPR001810] (2) | scaffold_6_mRNA_1711.1 | C_unshiu_00034_mRNA_36.1 | - |
| GF0023187 | 1 | 1 | 0 | Hypothetical protein (2) | protein binding [GO:0005515 molecular_function] (1) | WD40/YVTN repeat-like-containing domain [IPR015943] (1) | scaffold_6_mRNA_1710.1 | C_unshiu_00034_mRNA_37.1 | - |
| GF0023186 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_1708.1 | C_unshiu_00034_mRNA_39.1 | - |
| GF0023185 | 1 | 1 | 0 | DNA double-strand break repair rad50 ATPase, putative isoform 2 (2) | | | scaffold_6_mRNA_1684.1 | C_unshiu_00034_mRNA_58.1 | - |
| GF0023184 | 1 | 1 | 0 | UDP-glycosyltransferase 85A7 (2) | transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (2); metabolic process [GO:0008152 biological_process] (2) | UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (2) | scaffold_6_mRNA_1673.1 | C_unshiu_00034_mRNA_69.1 | - |
| GF0023183 | 1 | 1 | 0 | Hypothetical protein (2) | 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_1672.1 | C_unshiu_00034_mRNA_70.1 | - |
| GF0023182 | 1 | 1 | 0 | UDP-glycosyltransferase 85A7 (2) | metabolic process [GO:0008152 biological_process] (2); transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (2) | UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (2) | scaffold_6_mRNA_1671.1 | C_unshiu_00034_mRNA_71.1 | - |
| GF0023180 | 1 | 1 | 0 | Hypothetical protein (2) | | Domain of unknown function DUF4283 [IPR025558] (2) | scaffold_6_mRNA_1655.1 | C_unshiu_01358_mRNA_3.1 | - |
| GF0023179 | 1 | 1 | 0 | Hypothetical protein (1); Non-LTR retroelement reverse transcriptase-like protein (1) | | Reverse transcriptase zinc-binding domain [IPR026960] (2) | scaffold_6_mRNA_1651.1 | C_unshiu_00178_mRNA_15.1 | - |
| GF0023178 | 1 | 1 | 0 | Hypothetical protein (2) | | Bulb-type lectin domain [IPR001480] (2); Protein kinase-like domain [IPR011009] (1) | scaffold_6_mRNA_1641.1 | C_unshiu_00178_mRNA_3.1 | - |
| GF0023177 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_1637.1 | C_unshiu_01603_mRNA_3.1 | - |
| GF0023176 | 1 | 1 | 0 | Hypothetical protein (2) | | Concanavalin A-like lectin/glucanase domain [IPR013320] (1) | scaffold_6_mRNA_1636.1 | C_unshiu_01603_mRNA_2.1 | - |
| GF0023173 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_1616.1 | C_unshiu_00102_mRNA_38.1 | - |
| GF0023172 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_1615.1 | C_unshiu_00102_mRNA_37.1 | - |
| GF0023171 | 1 | 1 | 0 | Aldo-keto reductase family 4 member C9 (2) | oxidoreductase activity [GO:0016491 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2) | Aldo/keto reductase [IPR020471] (2); Aldo/keto reductase, conserved site [IPR018170] (2); NADP-dependent oxidoreductase domain [IPR023210] (2); Aldo/keto reductase/potassium channel subunit beta [IPR001395] (1) | scaffold_6_mRNA_1613.1 | C_unshiu_00102_mRNA_28.1 | - |
| GF0023170 | 1 | 1 | 0 | Aldo-keto reductase family 4 member C9 (2) | oxidation-reduction process [GO:0055114 biological_process] (2); oxidoreductase activity [GO:0016491 molecular_function] (2) | Aldo/keto reductase [IPR020471] (2); Aldo/keto reductase, conserved site [IPR018170] (2); NADP-dependent oxidoreductase domain [IPR023210] (2); Aldo/keto reductase/potassium channel subunit beta [IPR001395] (1) | scaffold_6_mRNA_1607.1 | C_unshiu_00102_mRNA_21.1 | - |
| GF0023168 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_1588.1 | C_unshiu_00032_mRNA_49.1 | - |
| GF0023167 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_6_mRNA_1584.1 | C_unshiu_00032_mRNA_44.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0023166 | 1 | 1 | 0 | Hypothetical protein (2) | protein binding [GO:0005515 molecular_function] (1) | PB1 domain [IPR000270] (1) | scaffold_6_mRNA_158.1 | C_unshiu_02589_mRNA_5.1 | - |
| GF0023164 | 1 | 1 | 0 | Putative non-LTR retroelement reverse transcriptase (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Reverse transcriptase domain [IPR000477] (2); Reverse transcriptase zinc-binding domain [IPR026960] (2); Ribonuclease H-like domain [IPR012337] (2) | scaffold_6_mRNA_1513.1 | C_unshiu_01718_mRNA_7.1 | - |
| GF0023163 | 1 | 1 | 0 | Hypothetical protein (2) |  | Endonuclease/exonuclease/phosphatase [IPR005135] (2) | scaffold_6_mRNA_1512.1 | C_unshiu_01718_mRNA_6.1 | - |
| GF0023162 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_1510.1 | C_unshiu_01718_mRNA_4.1 | - |
| GF0023161 | 1 | 1 | 0 | Transposase tnp2 (1); Hypothetical protein (1) |  | Transposon, En/Spm-like [IPR004242] (2) | scaffold_6_mRNA_1509.1 | C_unshiu_01718_mRNA_3.1 | - |
| GF0023160 | 1 | 1 | 0 | Hypothetical protein (2) |  | Gag-polypeptide of LTR copia-type [IPR029472] (1) | scaffold_6_mRNA_1505.1 | C_unshiu_01171_mRNA_5.1 | - |
| GF0023159 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_150.1 | C_unshiu_01748_mRNA_2.1 | - |
| GF0023158 | 1 | 1 | 0 | Hypothetical protein (2) | DNA binding [GO:0003677 molecular_function] (2); nucleus [GO:0005634 cellular_component] (1) | DNA-binding domain [IPR016177] (2); Methyl-CpG DNA binding [IPR001739] (1) | scaffold_6_mRNA_1498.1 | C_unshiu_00597_mRNA_9.1 | - |
| GF0023157 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_1495.1 | C_unshiu_00597_mRNA_7.1 | - |
| GF0023156 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_1494.1 | C_unshiu_00597_mRNA_6.1 | - |
| GF0023154 | 1 | 1 | 0 | Hypothetical protein (2) | DNA binding [GO:0003677 molecular_function] (2) | hAT-like transposase, RNase-H fold [IPR025525] (2) | scaffold_6_mRNA_1491.1 | C_unshiu_00597_mRNA_3.1 | - |
| GF0023152 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_1487.1 | C_unshiu_00155_mRNA_3.1 | - |
| GF0023150 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_1481.1 | C_unshiu_00155_mRNA_8.1 | - |
| GF0023148 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2); TB2/DP1/HVA22-related protein [IPR004345] (1) | scaffold_6_mRNA_1459.1 | C_unshiu_00155_mRNA_31.1 | - |
| GF0023147 | 1 | 1 | 0 | Cation/H(+) antiporter 15 (2) | cation transport [GO:0006812 biological_process] (2); integral component of membrane [GO:0016021 cellular_component] (2); transmembrane transport [GO:0055085 biological_process] (2); solute:proton antiporter activity [GO:0015299 molecular_function] (2) | Cation/H+ exchanger [IPR006153] (2); Rossmann-like alpha/beta/alpha sandwich fold [IPR014729] (1) | scaffold_6_mRNA_1444.1 | C_unshiu_00277_mRNA_28.1 | - |
| GF0023146 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_1422.1 | C_unshiu_01022_mRNA_4.1 | - |
| GF0023145 | 1 | 1 | 0 | G-type lectin S-receptor-like serine/threonine-protein kinase RLK1 (2) | ATP binding [GO:0005524 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2); recognition of pollen [GO:0048544 biological_process] (2); protein serine/threonine kinase activity [GO:0004674 molecular_function] (2); protein kinase activity [GO:0004672 molecular_function] (2) | Protein kinase domain [IPR000719] (2); S-receptor-like serine/threonine-protein kinase [IPR024171] (2); Protein kinase-like domain [IPR011009] (2); S-locus glycoprotein domain [IPR000858] (2); Serine/threonine-protein kinase, active site [IPR008271] (2); Protein kinase, ATP binding site [IPR017441] (2); PAN/Apple domain [IPR003609] (2); Bulb-type lectin domain [IPR001480] (2); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1) | scaffold_6_mRNA_1419.1 | C_unshiu_01022_mRNA_7.1 | - |
| GF0023144 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_1415.1 | C_unshiu_01675_mRNA_6.1 | - |
| GF0023142 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_1402.1 | C_unshiu_00219_mRNA_40.1 | - |
| GF0023141 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_1383.1 | C_unshiu_01785_mRNA_2.1 | - |
| GF0023140 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_6_mRNA_137.1 | C_unshiu_01830_mRNA_5.1 | - |
| GF0023139 | 1 | 1 | 0 | Hypothetical protein (2) | 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_1369.1 | C_unshiu_02605_mRNA_1.1 | - |
| GF0023138 | 1 | 1 | 0 | Hypothetical protein (2) | transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (2) | Transferase [IPR003480] (2); Chloramphenicol acetyltransferase-like domain [IPR023213] (1) | scaffold_6_mRNA_1367.1 | C_unshiu_00178_mRNA_35.1 | - |
| GF0023134 | 1 | 1 | 0 | Hypothetical protein (2) |  | Pentatricopeptide repeat [IPR002885] (2) | scaffold_6_mRNA_1337.1 | C_unshiu_01367_mRNA_7.1 | - |
| GF0023133 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2); DNA-directed 5'-3' RNA polymerase activity [GO:0003899 molecular_function] (1); transcription, DNA-templated [GO:0006351 biological_process] (1); ribonucleoside binding [GO:0032549 molecular_function] (1) | Ribonuclease H-like domain [IPR012337] (2); DNA-directed RNA polymerase, subunit 2 [IPR015712] (1) | scaffold_6_mRNA_1331.1 | C_unshiu_02941_mRNA_2.1 | - |
| GF0023132 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_1326.1 | C_unshiu_00748_mRNA_12.1 | - |
| GF0023131 | 1 | 1 | 0 | Hypothetical protein (2) | phosphotransferase activity, alcohol group as acceptor [GO:0016773 molecular_function] (1) | Ribokinase-like [IPR029056] (2); Carbohydrate kinase PfkB [IPR011611] (2); Carbohydrate/puine kinase, PfkB, conserved site [IPR002173] (1) | scaffold_6_mRNA_1312.1 | C_unshiu_00405_mRNA_15.1 | - |
| GF0023130 | 1 | 1 | 0 | Hypothetical protein (2) | protein binding [GO:0005515 molecular_function] (1) | PB1 domain [IPR000270] (1) | scaffold_6_mRNA_1307.1 | C_unshiu_00315_mRNA_3.1 | - |
| GF0023129 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_1292.1 | C_unshiu_00207_mRNA_26.1 | - |
| GF0023127 | 1 | 1 | 0 | Hypothetical protein (2) |  | Domain of unknown function DUF4283 [IPR025558] (1) | scaffold_6_mRNA_1276.1 | C_unshiu_01124_mRNA_3.1 | - |
| GF0023125 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_1267.1 | C_unshiu_00149_mRNA_3.1 | - |
| GF0023124 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_1254.1 | C_unshiu_02458_mRNA_1.1 | - |
| GF0023122 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_1230.1 | C_unshiu_00936_mRNA_7.1 | - |
| GF0023121 | 1 | 1 | 0 | Hypothetical protein (2) |  | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1) | scaffold_6_mRNA_1228.1 | C_unshiu_00936_mRNA_9.1 | - |
| GF0023120 | 1 | 1 | 0 | Hypothetical protein (2) | protein binding [GO:0005515 molecular_function] (1) | Pentatricopeptide repeat [IPR002885] (2); Tetratricopeptide-like helical domain [IPR011990] (1) | scaffold_6_mRNA_1222.1 | C_unshiu_03013_mRNA_1.1 | - |
| GF0023119 | 1 | 1 | 0 | DNA-binding protein S1FA2 (2) | regulation of transcription, DNA-templated [GO:0006355 biological_process] (2); nucleus [GO:0005634 cellular_component] (2); DNA binding [GO:0003677 molecular_function] (2) | DNA binding protein S1FA [IPR006779] (2) | scaffold_6_mRNA_1210.1 | C_unshiu_00028_mRNA_15.1 | - |
| GF0023118 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_1208.1 | C_unshiu_00028_mRNA_11.1 | - |
| GF0023117 | 1 | 1 | 0 | Hypothetical protein (1); UBX domain protein (1) | zinc ion binding [GO:0008270 molecular_function] (1) | Thioredoxin-like fold [IPR012336] (2); UAS [IPR006577] (2); Zinc finger, SWIM-type [IPR007527] (1); Zinc finger, PMZ-type [IPR006564] (1) | scaffold_6_mRNA_1202.1 | C_unshiu_01324_mRNA_4.1 | - |
| GF0023116 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_120.1 | C_unshiu_01119_mRNA_7.1 | - |
| GF0023115 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_1180.1 | C_unshiu_00196_mRNA_37.1 | - |
| GF0023114 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_1175.1 | C_unshiu_01055_mRNA_6.1 | - |
| GF0023112 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_1140.1 | C_unshiu_00231_mRNA_43.1 | - |
| GF0023111 | 1 | 1 | 0 | Hypothetical protein (2) |  | Domain of unknown function DUF588 [IPR006702] (2) | scaffold_6_mRNA_1130.1 | C_unshiu_02282_mRNA_1.1 | - |
| GF0023110 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_1126.1 | C_unshiu_01001_mRNA_2.1 | - |
| GF0023109 | 1 | 1 | 0 | Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1); Hypothetical protein (1) | nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1) | LOG family [IPR031100] (2); Zinc finger, CCHC-type [IPR001878] (1) | scaffold_6_mRNA_1122.1 | C_unshiu_01151_mRNA_2.1 | - |
| GF0023107 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_1096.1 | C_unshiu_02915_mRNA_1.1 | - |
| GF0023106 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_1091.1 | C_unshiu_00279_mRNA_4.1 | - |
| GF0023105 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_1090.1 | C_unshiu_00629_mRNA_1.1 | - |
| GF0023103 | 1 | 1 | 0 | Hypothetical protein (2) |  | Transposase-associated domain [IPR029480] (2) | scaffold_6_mRNA_1087.1 | C_unshiu_00629_mRNA_3.1 | - |
| GF0023102 | 1 | 1 | 0 | Retrotransposon protein, putative, Ty3-gypsy subclass (1); Hypothetical protein (1) |  | Chromo domain [IPR023780] (2); Chromo domain-like [IPR016197] (2) | scaffold_6_mRNA_1069.1 | C_unshiu_00393_mRNA_20.1 | - |
| GF0023101 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_1068.1 | C_unshiu_00912_mRNA_17.1 | - |
| GF0023099 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_1033.1 | C_unshiu_01025_mRNA_13.1 | - |
| GF0023098 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_1032.1 | C_unshiu_00848_mRNA_1.1 | - |
| GF0023096 | 1 | 1 | 0 | Cytochrome b-c1 complex subunit 8 (2) | ubiquinol-cytochrome-c reductase activity [GO:0008121 molecular_function] (2); respiratory chain [GO:0070469 cellular_component] (2); electron transport chain [GO:0022900 biological_process] (2); mitochondrial inner membrane [GO:0005743 cellular_component] (2) | Cytochrome b-c1 complex subunit 8 [IPR004205] (2); Cytochrome b-c1 complex subunit 8, plants [IPR020101] (2) | scaffold_6_mRNA_1021.1 | C_unshiu_01984_mRNA_4.1 | - |
| GF0023095 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_1018.1 | C_unshiu_00402_mRNA_3.1 | - |
| GF0023094 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_6_mRNA_1012.1 | C_unshiu_00402_mRNA_8.1 | - |
| GF0023093 | 1 | 1 | 0 | Hypothetical protein (2) | protein binding [GO:0005515 molecular_function] (2) | Leucine-rich repeat [IPR001611] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2) | scaffold_5_mRNA_999.1 | C_unshiu_00083_mRNA_20.1 | - |
| GF0023092 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_996.1 | C_unshiu_00083_mRNA_23.1 | - |
| GF0023090 | 1 | 1 | 0 | Hypothetical protein (2) |  | Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1) | scaffold_5_mRNA_992.1 | C_unshiu_00083_mRNA_27.1 | - |
| GF0023089 | 1 | 1 | 0 | Hypothetical protein (2) | ATP binding [GO:0005524 molecular_function] (1) | Phosphoribosylglycinamide synthetase, ATP-grasp (A) domain [IPR020561] (2); ATP-grasp fold, subdomain 2 [IPR013816] (1) | scaffold_5_mRNA_99.1 | C_unshiu_00760_mRNA_11.1 | - |
| GF0023087 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_987.1 | C_unshiu_00083_mRNA_31.1 | - |
| GF0023086 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_984.1 | C_unshiu_00083_mRNA_33.1 | - |
| GF0023085 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_983.1 | C_unshiu_00083_mRNA_34.1 | - |
| GF0023084 | 1 | 1 | 0 | Oxalate oxidase 2 (2) | nutrient reservoir activity [GO:0045735 molecular_function] (2); manganese ion binding [GO:0030145 molecular_function] (2) | RmlC-like cupin domain [IPR011051] (2); RmlC-like jelly roll fold [IPR014710] (2); Germin [IPR001929] (2); Cupin 1 [IPR006045] (2) | scaffold_5_mRNA_980.1 | C_unshiu_00083_mRNA_37.1 | - |
| GF0023083 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_979.1 | C_unshiu_00083_mRNA_38.1 | - |
| GF0023082 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_974.1 | C_unshiu_00540_mRNA_5.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0023081 | 1 | 1 | 0 | Hypothetical protein (2) | integral component of membrane [GO:0016021 cellular_component] (2); prenyltransferase activity [GO:0004659 molecular_function] (1); transferase activity, transferring alkyl or aryl (other than methyl) groups [GO:0016765 molecular_function] (1) | UbiA prenyltransferase family [IPR000537] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2) | scaffold_5_mRNA_973.1 | C_unshiu_00540_mRNA_6.1 | - |
| GF0023080 | 1 | 1 | 0 | Small heat shock protein (2) | | HSP20-like chaperone [IPR008978] (1); Small heat shock protein HSP20 [IPR031107] (1) | scaffold_5_mRNA_97.1 | C_unshiu_00633_mRNA_11.1 | - |
| GF0023078 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_964.1 | C_unshiu_00540_mRNA_13.1 | - |
| GF0023077 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_962.1 | C_unshiu_00540_mRNA_15.1 | - |
| GF0023076 | 1 | 1 | 0 | Hypothetical protein (2) | 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_960.1 | C_unshiu_00540_mRNA_17.1 | - |
| GF0023075 | 1 | 1 | 0 | LRR and NB-ARC domain disease resistance protein (2) | ADP binding [GO:0043531 molecular_function] (2) | Leucine-rich repeat domain, L domain-like [IPR032675] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); NB-ARC [IPR002182] (2); Winged helix-turn-helix DNA-binding domain [IPR011991] (1) | scaffold_5_mRNA_96.1 | C_unshiu_00633_mRNA_10.1 | - |
| GF0023074 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_957.1 | C_unshiu_00033_mRNA_18.1 | - |
| GF0023073 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_956.1 | C_unshiu_00033_mRNA_17.1 | - |
| GF0023072 | 1 | 1 | 0 | Tyrosine-sulfated glycopeptide receptor 1 (2) | protein binding [GO:0005515 molecular_function] (2) | Leucine-rich repeat [IPR001611] (2); Leucine-rich repeat, typical subtype [IPR003591] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2) | scaffold_5_mRNA_954.1 | C_unshiu_00033_mRNA_15.1 | - |
| GF0023071 | 1 | 1 | 0 | Beta-glucosidase 44 (2) | hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (2); carbohydrate metabolic process [GO:0005975 biological_process] (2) | Glycoside hydrolase family 1 [IPR001360] (2); Glycoside hydrolase superfamily [IPR017853] (2); Glycoside hydrolase, catalytic domain [IPR013781] (1) | scaffold_5_mRNA_953.1 | C_unshiu_00033_mRNA_14.1 | - |
| GF0023069 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_941.1 | C_unshiu_00033_mRNA_2.1 | - |
| GF0023068 | 1 | 1 | 0 | Transposable element Ac (1); Hypothetical protein (1) | nucleic acid binding [GO:0003676 molecular_function] (2); protein dimerization activity [GO:0046983 molecular_function] (2) | HAT, C-terminal dimerisation domain [IPR008906] (2); LOG family [IPR031100] (2); Ribonuclease H-like domain [IPR012337] (2) | scaffold_5_mRNA_940.1 | C_unshiu_01003_mRNA_5.1 | - |
| GF0023067 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_94.1 | C_unshiu_03124_mRNA_1.1 | - |
| GF0023065 | 1 | 1 | 0 | Seven transmembrane MLO family protein (1); MLO protein homolog 1 (1) | integral component of membrane [GO:0016021 cellular_component] (2); defense response [GO:0006952 biological_process] (2) | Mlo-related protein [IPR004326] (2) | scaffold_5_mRNA_933.1 | C_unshiu_01044_mRNA_3.1 | - |
| GF0023064 | 1 | 1 | 0 | Hypothetical protein (1); Geranylgeranyl diphosphate synthase (1) | isoprenoid biosynthetic process [GO:0008299 biological_process] (2) | Polyprenyl synthetase [IPR000092] (2); Isoprenoid synthase domain [IPR008949] (2); Polyprenyl synthetase-related [IPR017446] (1); Polyprenyl synthetase, conserved site [IPR033749] (1) | scaffold_5_mRNA_932.1 | C_unshiu_01044_mRNA_4.1 | - |
| GF0023063 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_927.1 | C_unshiu_01044_mRNA_8.1 | - |
| GF0023062 | 1 | 1 | 0 | GGPP synthase 2 family protein (2) | isoprenoid biosynthetic process [GO:0008299 biological_process] (2) | Polyprenyl synthetase [IPR000092] (2); Isoprenoid synthase domain [IPR008949] (2); Polyprenyl synthetase-related [IPR017446] (1) | scaffold_5_mRNA_921.1 | C_unshiu_00292_mRNA_31.1 | - |
| GF0023061 | 1 | 1 | 0 | Putative non-LTR reverse transcriptase (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Reverse transcriptase zinc-binding domain [IPR026960] (2); Ribonuclease H-like domain [IPR012337] (2); Reverse transcriptase domain [IPR000477] (2) | scaffold_5_mRNA_919.1 | C_unshiu_00292_mRNA_29.1 | - |
| GF0023060 | 1 | 1 | 0 | Hypothetical protein (2) | zinc ion binding [GO:0008270 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | Domain of unknown function DUF4283 [IPR025558] (2); Zinc finger, CCHC-type [IPR001878] (2); Zinc knuckle CX2CX4HX4C [IPR025836] (2) | scaffold_5_mRNA_917.1 | C_unshiu_00292_mRNA_27.1 | - |
| GF0023059 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_915.1 | C_unshiu_00292_mRNA_25.1 | - |
| GF0023058 | 1 | 1 | 0 | Monosacharide transport protein (2) | | | scaffold_5_mRNA_909.1 | C_unshiu_00292_mRNA_19.1 | - |
| GF0023057 | 1 | 1 | 0 | Hypothetical protein (2) | DNA integration [GO:0015074 biological_process] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2); Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (2); Integrase, catalytic core [IPR001584] (2); GAG-pre-integrase domain [IPR025724] (2) | scaffold_5_mRNA_901.1 | C_unshiu_00292_mRNA_12.1 | - |
| GF0023056 | 1 | 1 | 0 | Putative retroelement pol polyprotein (2) | | | scaffold_5_mRNA_900.1 | C_unshiu_00292_mRNA_11.1 | - |
| GF0023055 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_9.1 | C_unshiu_00230_mRNA_31.1 | - |
| GF0023054 | 1 | 1 | 0 | Hypothetical protein (2) | O-methyltransferase activity [GO:0008171 molecular_function] (2) | O-methyltransferase, family 3 [IPR002935] (2); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1) | scaffold_5_mRNA_891.1 | C_unshiu_00292_mRNA_3.1 | - |
| GF0023053 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_890.1 | C_unshiu_00292_mRNA_2.1 | - |
| GF0023052 | 1 | 1 | 0 | Hypothetical protein (2) | protein binding [GO:0005515 molecular_function] (2) | TRAF-like [IPR008974] (2); MATH/TRAF domain [IPR002083] (2) | scaffold_5_mRNA_887.1 | C_unshiu_00771_mRNA_1.1 | - |
| GF0023051 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_874.1 | C_unshiu_00769_mRNA_15.1 | - |
| GF0023050 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_873.1 | C_unshiu_00769_mRNA_16.1 | - |
| GF0023049 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_872.1 | C_unshiu_00769_mRNA_17.1 | - |
| GF0023048 | 1 | 1 | 0 | Hypothetical protein (2) | cysteine-type peptidase activity [GO:0008234 molecular_function] (2); proteolysis [GO:0006508 biological_process] (2) | Ulp1 protease family, C-terminal catalytic domain [IPR003653] (2); Domain of unknown function DUF4216 [IPR025312] (1) | scaffold_5_mRNA_866.1 | C_unshiu_00256_mRNA_20.1 | - |
| GF0023047 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_856.1 | C_unshiu_00896_mRNA_2.1 | - |
| GF0023046 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_85.1 | C_unshiu_01059_mRNA_2.1 | - |
| GF0023045 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_844.1 | C_unshiu_00405_mRNA_7.1 | - |
| GF0023044 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_842.1 | C_unshiu_00405_mRNA_5.1 | - |
| GF0023043 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_840.1 | C_unshiu_00405_mRNA_3.1 | - |
| GF0023042 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_839.1 | C_unshiu_00405_mRNA_2.1 | - |
| GF0023041 | 1 | 1 | 0 | Hypothetical protein (2) | DNA integration [GO:0015074 biological_process] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | Integrase, catalytic core [IPR001584] (2); Ribonuclease H-like domain [IPR012337] (2) | scaffold_5_mRNA_835.1 | C_unshiu_00638_mRNA_12.1 | - |
| GF0023040 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_830.1 | C_unshiu_00638_mRNA_6.1 | - |
| GF0023039 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_829.1 | C_unshiu_00638_mRNA_5.1 | - |
| GF0023038 | 1 | 1 | 0 | Hypothetical protein (2) | | Chromo/chromo shadow domain [IPR000953] (2); Chromo domain-like [IPR016197] (2); Chromo domain [IPR023780] (2) | scaffold_5_mRNA_826.1 | C_unshiu_00638_mRNA_2.1 | - |
| GF0023037 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_823.1 | C_unshiu_00373_mRNA_32.1 | - |
| GF0023036 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_821.1 | C_unshiu_00373_mRNA_29.1 | - |
| GF0023034 | 1 | 1 | 0 | TNL (1); TMV resistance N (1) | ADP binding [GO:0043531 molecular_function] (1) | Leucine-rich repeat domain, L domain-like [IPR032675] (2); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1) | scaffold_5_mRNA_807.1 | C_unshiu_01566_mRNA_9.1 | - |
| GF0023033 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2); protein dimerization activity [GO:0046983 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2); HAT, C-terminal dimerisation domain [IPR008906] (2) | scaffold_5_mRNA_801.1 | C_unshiu_00583_mRNA_5.1 | - |
| GF0023032 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_800.1 | C_unshiu_00583_mRNA_6.1 | - |
| GF0023031 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_799.1 | C_unshiu_00583_mRNA_7.1 | - |
| GF0023030 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_798.1 | C_unshiu_00583_mRNA_8.1 | - |
| GF0023029 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_793.1 | C_unshiu_00583_mRNA_11.1 | - |
| GF0023028 | 1 | 1 | 0 | Putative ribonuclease H protein (1); Putative non-LTR retroelement reverse transcriptase (1) | nucleic acid binding [GO:0003676 molecular_function] (2) | Reverse transcriptase zinc-binding domain [IPR026960] (2); Ribonuclease H-like domain [IPR012337] (2) | scaffold_5_mRNA_792.1 | C_unshiu_00195_mRNA_40.1 | - |
| GF0023027 | 1 | 1 | 0 | Hypothetical protein (2) | ADP binding [GO:0043531 molecular_function] (2) | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); NB-ARC [IPR002182] (2) | scaffold_5_mRNA_782.1 | C_unshiu_00195_mRNA_30.1 | - |
| GF0023026 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_781.1 | C_unshiu_00195_mRNA_29.1 | - |
| GF0023025 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_778.1 | C_unshiu_00195_mRNA_26.1 | - |
| GF0023024 | 1 | 1 | 0 | Disease resistance protein RPM1 (1); NBS-LRR class resistance protein Fy1-Ry1 (1) | ADP binding [GO:0043531 molecular_function] (2) | Leucine-rich repeat domain, L domain-like [IPR032675] (2); NB-ARC [IPR002182] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); Winged helix-turn-helix DNA-binding domain [IPR011991] (1) | scaffold_5_mRNA_776.1 | C_unshiu_00195_mRNA_23.1 | - |
| GF0023023 | 1 | 1 | 0 | Hypothetical protein (1); Aldose reductase (1) | oxidoreductase activity [GO:0016491 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2) | Aldo/keto reductase, conserved site [IPR018170] (2); NADP-dependent oxidoreductase domain [IPR023210] (2); Aldo/keto reductase/potassium channel subunit beta [IPR001395] (1); Aldo/keto reductase [IPR020471] (1) | scaffold_5_mRNA_77.1 | C_unshiu_01059_mRNA_5.1 | - |
| GF0023022 | 1 | 1 | 0 | Hypothetical protein (2) | ADP binding [GO:0043531 molecular_function] (2) | NB-ARC [IPR002182] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2) | scaffold_5_mRNA_761.1 | C_unshiu_00195_mRNA_10.1 | - |
| GF0023021 | 1 | 1 | 0 | NBS-LRR class resistance protein Fy1-Ry1 (1); Disease resistance protein RPM1 (1) | ADP binding [GO:0043531 molecular_function] (2) | NB-ARC [IPR002182] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Winged helix-turn-helix DNA-binding domain [IPR011991] (1) | scaffold_5_mRNA_757.1 | C_unshiu_00195_mRNA_7.1 | - |
| GF0023020 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_734.1 | C_unshiu_00892_mRNA_7.1 | - |
| GF0023019 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_730.1 | C_unshiu_00892_mRNA_3.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0023018 | 1 | 1 | 0 | LRR receptor-like kinase family protein (2) | ATP binding [GO:0005524 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2); protein kinase activity [GO:0004672 molecular_function] (2); protein binding [GO:0005515 molecular_function] (2) | Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (2); Serine/threonine-protein kinase, active site [IPR008271] (2); Protein kinase, ATP binding site [IPR017441] (2); Leucine-rich repeat [IPR001611] (2); Protein kinase domain [IPR000719] (2); Protein kinase-like domain [IPR011009] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Leucine-rich repeat, typical subtype [IPR003591] (2); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1) | scaffold_5_mRNA_729.1 | C_unshiu_00034_mRNA_1.1 | - |
| GF0023017 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_727.1 | C_unshiu_00034_mRNA_2.1 | - |
| GF0023016 | 1 | 1 | 0 | Retrovirus-related pol polyprotein from transposon tnt 1-94 (2) | DNA integration [GO:0015074 biological_process] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | Integrase, catalytic core [IPR001584] (2); Ribonuclease H-like domain [IPR012337] (2) | scaffold_5_mRNA_726.1 | C_unshiu_00034_mRNA_3.1 | - |
| GF0023015 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (1) | Ribonuclease H-like domain [IPR012337] (1) | scaffold_5_mRNA_718.1 | C_unshiu_00034_mRNA_11.1 | - |
| GF0023013 | 1 | 1 | 0 | WEB family protein (2) | | | scaffold_5_mRNA_714.1 | C_unshiu_00034_mRNA_14.1 | - |
| GF0023012 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_710.1 | C_unshiu_00034_mRNA_16.1 | - |
| GF0023011 | 1 | 1 | 0 | O-methyltransferase ZRP4 (2) | O-methyltransferase activity [GO:0008171 molecular_function] (2); methyltransferase activity [GO:0008168 molecular_function] (2) | O-methyltransferase, family 2 [IPR001077] (2); O-methyltransferase COMT-type [IPR016461] (2); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (2) | scaffold_5_mRNA_705.1 | C_unshiu_00486_mRNA_21.1 | - |
| GF0023010 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_7.1 | C_unshiu_00230_mRNA_24.1 | - |
| GF0023009 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_698.1 | C_unshiu_00486_mRNA_19.1 | - |
| GF0023005 | 1 | 1 | 0 | Hypothetical protein (2) | metal ion binding [GO:0046872 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1) | Zinc finger, CCCH-type [IPR000571] (2); Zinc finger, CCHC-type [IPR001878] (1) | scaffold_5_mRNA_676.1 | C_unshiu_00486_mRNA_1.1 | - |
| GF0023004 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_673.1 | C_unshiu_00324_mRNA_14.1 | - |
| GF0023003 | 1 | 1 | 0 | Embryogenesis-associated EMB8 (2) | | Alpha/Beta hydrolase fold [IPR029058] (2) | scaffold_5_mRNA_670.1 | C_unshiu_00324_mRNA_17.1 | - |
| GF0023002 | 1 | 1 | 0 | Hypothetical protein (2) | | Domain of unknown function DUF4283 [IPR025558] (2) | scaffold_5_mRNA_663.1 | C_unshiu_00324_mRNA_25.1 | - |
| GF0023001 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (1) | Ribonuclease H-like domain [IPR012337] (1) | scaffold_5_mRNA_662.1 | C_unshiu_00324_mRNA_26.1 | - |
| GF0023000 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1) | Ribonuclease H-like domain [IPR012337] (2); Ribonuclease H domain [IPR002156] (1) | scaffold_5_mRNA_661.1 | C_unshiu_00695_mRNA_15.1 | - |
| GF0022999 | 1 | 1 | 0 | Retrotransposon protein, putative, Ty1-copia subclass (1); Hypothetical protein (1) | | | scaffold_5_mRNA_657.1 | C_unshiu_00269_mRNA_31.1 | - |
| GF0022998 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_655.1 | C_unshiu_00269_mRNA_27.1 | - |
| GF0022997 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_654.1 | C_unshiu_01868_mRNA_2.1 | - |
| GF0022996 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_649.1 | C_unshiu_00269_mRNA_19.1 | - |
| GF0022995 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_647.1 | C_unshiu_00269_mRNA_17.1 | - |
| GF0022994 | 1 | 1 | 0 | Hypothetical protein (2) | 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_639.1 | C_unshiu_00269_mRNA_11.1 | - |
| GF0022993 | 1 | 1 | 0 | Hypothetical protein (2) | zinc ion binding [GO:0008270 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | Zinc finger, CCHC-type [IPR001878] (2) | scaffold_5_mRNA_636.1 | C_unshiu_00492_mRNA_3.1 | - |
| GF0022991 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_627.1 | C_unshiu_00234_mRNA_4.1 | - |
| GF0022990 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_625.1 | C_unshiu_00234_mRNA_2.1 | - |
| GF0022989 | 1 | 1 | 0 | Hypothetical protein (2) | | Ribokinase-like [IPR029056] (2) | scaffold_5_mRNA_623.1 | C_unshiu_00636_mRNA_9.1 | - |
| GF0022988 | 1 | 1 | 0 | Hypothetical protein (2) | protein binding [GO:0005515 molecular_function] (2); RNA processing [GO:0006396 biological_process] (2) | HAT (Half-A-TPR) repeat [IPR003107] (2); Tetratricopeptide-like helical domain [IPR011990] (2) | scaffold_5_mRNA_62.1 | C_unshiu_00231_mRNA_21.1 | - |
| GF0022987 | 1 | 1 | 0 | HAT family dimerization domain containing protein (2) | protein dimerization activity [GO:0046983 molecular_function] (2) | HAT, C-terminal dimerisation domain [IPR008906] (2) | scaffold_5_mRNA_619.1 | C_unshiu_00354_mRNA_1.1 | - |
| GF0022985 | 1 | 1 | 0 | Retrotransposon protein, putative, unclassified (1); Hypothetical protein (1) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_5_mRNA_610.1 | C_unshiu_00354_mRNA_4.1 | - |
| GF0022984 | 1 | 1 | 0 | Hypothetical protein (2) | | Arabidopsis retrotransposon Orf1 [IPR004312] (2) | scaffold_5_mRNA_609.1 | C_unshiu_00354_mRNA_7.1 | - |
| GF0022983 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_6.1 | C_unshiu_00230_mRNA_28.1 | - |
| GF0022982 | 1 | 1 | 0 | Disease resistance protein (CC-NBS-LRR class) family protein (2) | ADP binding [GO:0043531 molecular_function] (2) | Leucine-rich repeat domain, L domain-like [IPR032675] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); NB-ARC [IPR002182] (2); AAA+ ATPase domain [IPR003593] (2); Winged helix-turn-helix DNA-binding domain [IPR011991] (1) | scaffold_5_mRNA_594.1 | C_unshiu_01036_mRNA_4.1 | - |
| GF0022981 | 1 | 1 | 0 | FAD-binding Berberine family protein (2) | flavin adenine dinucleotide binding [GO:0050660 molecular_function] (2); oxidoreductase activity [GO:0016491 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2); oxidoreductase activity, acting on CH-OH group of donors [GO:0016614 molecular_function] (2); catalytic activity [GO:0003824 molecular_function] (2) | Berberine/berberine-like [IPR012951] (2); FAD-binding, type 2 [IPR016166] (2); FAD linked oxidase, N-terminal [IPR006094] (1); Oxygen oxidoreductase covalent FAD-binding site [IPR006093] (1); FAD-binding, type 2, subdomain 1 [IPR016167] (1); CO dehydrogenase flavoprotein-like, FAD-binding, subdomain 2 [IPR016169] (1) | scaffold_5_mRNA_587.1 | C_unshiu_00108_mRNA_15.1 | - |
| GF0022980 | 1 | 1 | 0 | 60S ribosomal protein L3 (2) | ribosome [GO:0005840 cellular_component] (2); translation [GO:0006412 biological_process] (2); intracellular [GO:0005622 cellular_component] (2); structural constituent of ribosome [GO:0003735 molecular_function] (2) | Ribosomal protein L3 [IPR000597] (2); Translation protein, beta-barrel domain [IPR009000] (2); Ribosomal protein L3, conserved site [IPR019926] (2) | scaffold_5_mRNA_579.1 | C_unshiu_00108_mRNA_11.1 | - |
| GF0022979 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_572.1 | C_unshiu_00108_mRNA_4.1 | - |
| GF0022978 | 1 | 1 | 0 | Hypothetical protein (1); Transposase (1) | DNA binding [GO:0003677 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1) | hAT-like transposase, RNase-H fold [IPR025525] (2); Ribonuclease H-like domain [IPR012337] (1); HAT, C-terminal dimerisation domain [IPR008906] (1) | scaffold_5_mRNA_571.1 | C_unshiu_00108_mRNA_3.1 | - |
| GF0022975 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_557.1 | C_unshiu_00710_mRNA_4.1 | - |
| GF0022974 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_556.1 | C_unshiu_00710_mRNA_5.1 | - |
| GF0022973 | 1 | 1 | 0 | Hypothetical protein (2) | | Ankyrin repeat-containing domain [IPR020683] (2) | scaffold_5_mRNA_555.1 | C_unshiu_00710_mRNA_6.1 | - |
| GF0022972 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_55.1 | C_unshiu_00231_mRNA_13.1 | - |
| GF0022971 | 1 | 1 | 0 | Hypothetical protein (2) | | Aspartic peptidase domain [IPR021109] (1) | scaffold_5_mRNA_548.1 | C_unshiu_00035_mRNA_73.1 | - |
| GF0022970 | 1 | 1 | 0 | Hypothetical protein (2) | | Aspartic peptidase domain [IPR021109] (1) | scaffold_5_mRNA_532.1 | C_unshiu_00561_mRNA_14.1 | - |
| GF0022965 | 1 | 1 | 0 | Hypothetical protein (2) | ADP binding [GO:0043531 molecular_function] (2) | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); NB-ARC [IPR002182] (2); Winged helix-turn-helix DNA-binding domain [IPR011991] (1) | scaffold_5_mRNA_520.1 | C_unshiu_00561_mRNA_12.1 | - |
| GF0022964 | 1 | 1 | 0 | Hypothetical protein (2) | | Leucine-rich repeat domain, L domain-like [IPR032675] (1) | scaffold_5_mRNA_52.1 | C_unshiu_00231_mRNA_10.1 | - |
| GF0022963 | 1 | 1 | 0 | Hypothetical protein (2) | regulation of transcription, DNA-templated [GO:0006355 biological_process] (2); zinc ion binding [GO:0008270 molecular_function] (2) | FHY3/FAR1 family [IPR031052] (2); FAR1 DNA binding domain [IPR004330] (2); Zinc finger, PMZ-type [IPR006564] (2); Zinc finger, SWIM-type [IPR007527] (2) | scaffold_5_mRNA_5195.1 | C_unshiu_00697_mRNA_2.2 | - |
| GF0022961 | 1 | 1 | 0 | Xylem cysteine peptidase 1 (2) | cysteine-type peptidase activity [GO:0008234 molecular_function] (2); proteolysis [GO:0006508 biological_process] (2) | Peptidase C1A [IPR013128] (2); Cysteine peptidase, cysteine active site [IPR000169] (2); Cysteine peptidase, histidine active site [IPR025660] (2); Peptidase C1A, papain C-terminal [IPR000668] (2); Cysteine peptidase, asparagine active site [IPR025661] (2); Cathepsin propeptide inhibitor domain (I29) [IPR013201] (2) | scaffold_5_mRNA_5185.1 | C_unshiu_00370_mRNA_21.1 | - |
| GF0022958 | 1 | 1 | 0 | Hypothetical protein (2) | enzyme inhibitor activity [GO:0004857 molecular_function] (1) | Pectinesterase inhibitor domain [IPR006501] (1) | scaffold_5_mRNA_515.1 | C_unshiu_00561_mRNA_15.1 | - |
| GF0022957 | 1 | 1 | 0 | Dimethylaniline monooxygenase, putative (2) | oxidoreductase activity [GO:0016491 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2); flavin adenine dinucleotide binding [GO:0050660 molecular_function] (2); NADP binding [GO:0050661 molecular_function] (2); N,N-dimethylaniline monooxygenase activity [GO:0004499 molecular_function] (2) | Dimethylaniline monooxygenase, N-oxide-forming [IPR012143] (2); FAD/NAD(P)-binding domain [IPR023753] (2); Flavin monooxygenase-like [IPR020946] (2) | scaffold_5_mRNA_5133.1 | C_unshiu_00623_mRNA_11.1 | - |
| GF0022956 | 1 | 1 | 0 | Hypothetical protein (1); BAHD acyltransferase (1) | transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (1) | Transferase [IPR003480] (1); Chloramphenicol acetyltransferase-like domain [IPR023213] (1) | scaffold_5_mRNA_5128.1 | C_unshiu_00623_mRNA_6.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0022955 | 1 | 1 | 0 | Acylsugar acyltransferase 3 (2) | transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (2) | Transferase [IPR003480] (2); Chloramphenicol acetyltransferase-like domain [IPR023213] (1) | scaffold_5_mRNA_5127.1 | C_unshiu_00623_mRNA_5.1 | - |
| GF0022954 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_5120.1 | C_unshiu_01461_mRNA_5.1 | - |
| GF0022952 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_5112.1 | C_unshiu_00409_mRNA_15.1 | - |
| GF0022948 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_5105.1 | C_unshiu_00409_mRNA_10.1 | - |
| GF0022946 | 1 | 1 | 0 | Hypothetical protein (1); U11/U12 small nuclear ribonucleoprotein 25 kDa (1) | | Ubiquitin-related domain [IPR029071] (2) | scaffold_5_mRNA_5089.1 | C_unshiu_00527_mRNA_21.1 | - |
| GF0022941 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_5046.1 | C_unshiu_00192_mRNA_34.1 | - |
| GF0022940 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_5038.1 | C_unshiu_00061_mRNA_51.1 | - |
| GF0022938 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_503.1 | C_unshiu_02469_mRNA_2.1 | - |
| GF0022936 | 1 | 1 | 0 | Hypothetical protein (2) | GTP binding [GO:0005525 molecular_function] (2); microtubule [GO:0005874 cellular_component] (2); structural constituent of cytoskeleton [GO:0005200 molecular_function] (2); microtubule-based process [GO:0007017 biological_process] (2); GTPase activity [GO:0003924 molecular_function] (2) | Beta tubulin [IPR002453] (2); Tubulin/FtsZ, GTPase domain [IPR003008] (2); Tubulin [IPR000217] (2); Tubulin/FtsZ, 2-layer sandwich domain [IPR018316] (2); Tubulin/FtsZ, C-terminal [IPR008280] (2); Brain/reproductive organ-expressed protein [IPR010358] (2); Tubulin, conserved site [IPR017975] (1); Tubulin, C-terminal [IPR023123] (1) | scaffold_5_mRNA_5025.1 | C_unshiu_00192_mRNA_14.1 | - |
| GF0022935 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_5023.2 | C_unshiu_00192_mRNA_12.2 | - |
| GF0022934 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_5022.1 | C_unshiu_00192_mRNA_11.1 | - |
| GF0022933 | 1 | 1 | 0 | Hypothetical protein (2) | protein retention in ER lumen [GO:0006621 biological_process] (2); glycopeptide alpha-N-acetylgalactosaminidase activity [GO:0033926 molecular_function] (2); catalytic activity [GO:0003824 molecular_function] (2); integral component of membrane [GO:0016021 cellular_component] (2); ER retention sequence binding [GO:0046923 molecular_function] (2) | ER lumen protein retaining receptor [IPR000133] (2); Six-hairpin glycosidase-like [IPR008928] (2); Glycosyl hydrolase family 100 [IPR024746] (2) | scaffold_5_mRNA_5020.1 | C_unshiu_00192_mRNA_9.1 | - |
| GF0022932 | 1 | 1 | 0 | Protein disulfide-isomerase LQY1 (2) | heat shock protein binding [GO:0031072 molecular_function] (2); unfolded protein binding [GO:0051082 molecular_function] (2) | Heat shock protein DnaJ, cysteine-rich domain [IPR001305] (2) | scaffold_5_mRNA_5009.1 | C_unshiu_00009_mRNA_158.1 | - |
| GF0022931 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_5.1 | C_unshiu_00230_mRNA_29.1 | - |
| GF0022928 | 1 | 1 | 0 | Transmembrane and coiled-coil protein (2) | | Protein of unknown function DUF726 [IPR007941] (2); Alpha/Beta hydrolase fold [IPR029058] (2) | scaffold_5_mRNA_4975.1 | C_unshiu_00009_mRNA_123.1 | - |
| GF0022926 | 1 | 1 | 0 | S-type anion channel SLAH1 (2) | transmembrane transport [GO:0055085 biological_process] (2); integral component of membrane [GO:0016021 cellular_component] (2); voltage-gated anion channel activity [GO:0008308 molecular_function] (1); cellular ion homeostasis [GO:0006873 biological_process] (1) | Voltage-dependent anion channel [IPR004695] (2); S-type anion channel [IPR030183] (1) | scaffold_5_mRNA_4970.1 | C_unshiu_00009_mRNA_120.1 | - |
| GF0022925 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_4964.1 | C_unshiu_00009_mRNA_114.1 | - |
| GF0022922 | 1 | 1 | 0 | Hypothetical protein (2) | | Cyclin-like [IPR013763] (1) | scaffold_5_mRNA_4930.1 | C_unshiu_00127_mRNA_33.1 | - |
| GF0022921 | 1 | 1 | 0 | Hypothetical protein (2) | | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2) | scaffold_5_mRNA_4927.1 | C_unshiu_00127_mRNA_36.1 | - |
| GF0022919 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_4911.1 | C_unshiu_00127_mRNA_50.1 | - |
| GF0022918 | 1 | 1 | 0 | Zinc finger homeodomain protein 1 (1); Zinc-finger homeodomain protein 1 (1) | DNA binding [GO:0003677 molecular_function] (2) | ZF-HD homeobox protein, Cys/His-rich dimerisation domain [IPR006456] (2); Homeodomain, ZF-HD class [IPR006455] (2); Homeodomain-like [IPR009057] (1); Homeobox domain-like [IPR009057] (1) | scaffold_5_mRNA_4902.1 | C_unshiu_00079_mRNA_4.1 | - |
| GF0022917 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_4900.1 | C_unshiu_01543_mRNA_5.1 | - |
| GF0022911 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_4847.1 | C_unshiu_00234_mRNA_23.1 | - |
| GF0022909 | 1 | 1 | 0 | DUF617 family protein (2) | | Protein of unknown function DUF617, plant [IPR006460] (1); Protein MIZU-KUSSEI 1-like, plant [IPR006460] (1) | scaffold_5_mRNA_4811.1 | C_unshiu_00013_mRNA_108.1 | - |
| GF0022908 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_4796.1 | C_unshiu_00951_mRNA_18.1 | - |
| GF0022905 | 1 | 1 | 0 | Putative succinate dehydrogenase 5-like (1); Succinate dehydrogenase 5 (1) | | Protein of unknown function DUF4370 [IPR025397] (2) | scaffold_5_mRNA_4789.1 | C_unshiu_00951_mRNA_12.1 | - |
| GF0022902 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_478.1 | C_unshiu_00308_mRNA_3.1 | - |
| GF0022901 | 1 | 1 | 0 | Hypothetical protein (2) | protein binding [GO:0005515 molecular_function] (2); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1) | WD40/YVTN repeat-like-containing domain [IPR015943] (2); WD40-repeat-containing domain [IPR017986] (2); WD40 repeat [IPR001680] (1); Ribonuclease H domain [IPR002156] (1); Ribonuclease H-like domain [IPR012337] (1) | scaffold_5_mRNA_477.1 | C_unshiu_00610_mRNA_8.1 | - |
| GF0022899 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_4756.1 | C_unshiu_00096_mRNA_42.1 | - |
| GF0022898 | 1 | 1 | 0 | Baculoviral IAP repeat-containing protein 3 (2) | regulation of defense response [GO:0031347 biological_process] (2); ubiquitin-protein transferase activity [GO:0004842 molecular_function] (2); nucleus [GO:0005634 cellular_component] (2); protein ubiquitination [GO:0016567 biological_process] (2); zinc ion binding [GO:0008270 molecular_function] (2); protein binding [GO:0005515 molecular_function] (2) | Zinc finger, RING-type [IPR001841] (2); E3 ubiquitin-protein ligase BOI [IPR017066] (2); Zinc finger, RING/FYVE/PHD-type [IPR013083] (1) | scaffold_5_mRNA_4751.1 | C_unshiu_00096_mRNA_38.1 | - |
| GF0022897 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_475.1 | C_unshiu_00646_mRNA_7.1 | - |
| GF0022895 | 1 | 1 | 0 | Poly(A) binding protein 6, putative isoform 1 (2) | RNA binding [GO:0003723 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2); nucleotide binding [GO:0000166 molecular_function] (1) | Polyadenylate-binding protein/Hyperplastic disc protein [IPR002004] (2); RNA recognition motif domain, eukaryote [IPR003954] (2); RNA recognition motif domain [IPR000504] (2); Polyadenylate binding protein, human types 1, 2, 3, 4 [IPR006515] (2); Nucleotide-binding alpha-beta plait domain [IPR012677] (1) | scaffold_5_mRNA_4741.1 | C_unshiu_00096_mRNA_31.1 | - |
| GF0022893 | 1 | 1 | 0 | Serine/threonine-protein kinase WNK (2) | | Transcription factor MYC/MYB N-terminal [IPR025610] (2) | scaffold_5_mRNA_4730.1 | C_unshiu_00096_mRNA_19.1 | - |
| GF0022892 | 1 | 1 | 0 | Cyclin D (2) | nucleus [GO:0005634 cellular_component] (2) | Cyclin, C-terminal domain [IPR004367] (2); Cyclin-like [IPR013763] (2); Cyclin, N-terminal [IPR006671] (2) | scaffold_5_mRNA_4726.1 | C_unshiu_00096_mRNA_13.1 | - |
| GF0022890 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_4705.1 | C_unshiu_01089_mRNA_10.1 | - |
| GF0022888 | 1 | 1 | 0 | C3HC4-type RING finger protein (2) | protein binding [GO:0005515 molecular_function] (2); zinc ion binding [GO:0008270 molecular_function] (2) | Zinc finger, RING/FYVE/PHD-type [IPR013083] (2); Protein of unknown function DUF1232 [IPR010652] (2); Zinc finger, RING-type [IPR001841] (2); Zinc finger, RING-type, conserved site [IPR017907] (2) | scaffold_5_mRNA_4696.1 | C_unshiu_01089_mRNA_17.1 | - |
| GF0022886 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_4687.1 | C_unshiu_01033_mRNA_11.1 | - |
| GF0022885 | 1 | 1 | 0 | Epidermal patterning factor (2) | | | scaffold_5_mRNA_4681.1 | C_unshiu_01033_mRNA_5.1 | - |
| GF0022884 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_4676.1 | C_unshiu_00457_mRNA_31.1 | - |
| GF0022881 | 1 | 1 | 0 | Hypothetical protein (2) | histidinol-phosphate transaminase activity [GO:0004400 molecular_function] (1); biosynthetic process [GO:0009058 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1); pyridoxal phosphate binding [GO:0030170 molecular_function] (1); histidine biosynthetic process [GO:0000105 biological_process] (1) | Protein of unknown function DUF616 [IPR006852] (2); Pyridoxal phosphate-dependent transferase, major region, subdomain 1 [IPR015421] (1); Aminotransferase, class I/classII [IPR004839] (1); Pyridoxal phosphate-dependent transferase, major region, subdomain 2 [IPR015422] (1); Pyridoxal phosphate-dependent transferase [IPR015424] (1); Histidinol-phosphate aminotransferase family [IPR005861] (1) | scaffold_5_mRNA_4657.1 | C_unshiu_00457_mRNA_11.1 | - |
| GF0022880 | 1 | 1 | 0 | Similar to ATP-binding domain 1 family member B (1); GPN-loop GTPase 2 (1) | | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); GPN-loop GTPase [IPR004130] (2); GPN-loop GTPase 2 [IPR030231] (2) | scaffold_5_mRNA_465.1 | C_unshiu_00646_mRNA_10.1 | - |
| GF0022879 | 1 | 1 | 0 | CCA tRNA nucleotidyltransferase, mitochondrial (2) | RNA binding [GO:0003723 molecular_function] (2); RNA processing [GO:0006396 biological_process] (2); nucleotidyltransferase activity [GO:0016779 molecular_function] (2) | Poly A polymerase, head domain [IPR002646] (2) | scaffold_5_mRNA_4642.1 | C_unshiu_00802_mRNA_5.1 | - |
| GF0022875 | 1 | 1 | 0 | Hypothetical protein (1); F-actin capping protein beta subunit (1) | F-actin capping protein complex [GO:0008290 cellular_component] (2); actin cytoskeleton organization [GO:0030036 biological_process] (2); actin binding [GO:0003779 molecular_function] (2); cytoplasm [GO:0005737 cellular_component] (2); barbed-end actin filament capping [GO:0051016 biological_process] (2) | F-actin-capping protein subunit beta [IPR001698] (2); F-actin capping protein, beta subunit, conserved site [IPR019771] (2) | scaffold_5_mRNA_4619.1 | C_unshiu_00495_mRNA_17.1 | - |
| GF0022873 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_4615.1 | C_unshiu_00046_mRNA_29.1 | - |
| GF0022872 | 1 | 1 | 0 | Hypothetical protein (2) | regulation of transcription, DNA-templated [GO:0006355 biological_process] (2) | FHY3/FAR1 family [IPR031052] (2); FAR1 DNA binding domain [IPR004330] (2) | scaffold_5_mRNA_4614.1 | C_unshiu_00046_mRNA_28.1 | - |
| GF0022870 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_460.1 | C_unshiu_00646_mRNA_22.1 | - |
| GF0022869 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_46.1 | C_unshiu_00407_mRNA_25.1 | - |
| GF0022868 | 1 | 1 | 0 | Hypothetical protein (2) | enzyme inhibitor activity [GO:0004857 molecular_function] (1) | Pectinesterase inhibitor domain [IPR006501] (1) | scaffold_5_mRNA_4580.1 | C_unshiu_00278_mRNA_25.1 | - |
| GF0022867 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_4571.1 | C_unshiu_00556_mRNA_1.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0022865 | 1 | 1 | 0 | Cupredoxin superfamily protein, putative (2) |  | Cupredoxin [IPR008972] (2) | scaffold_5_mRNA_4554.1 | C_unshiu_00430_mRNA_18.1 | - |
| GF0022863 | 1 | 1 | 0 | Dof domain zinc finger protein (2) | regulation of transcription, DNA-templated [GO:0006355 biological_process] (2); DNA binding [GO:0003677 molecular_function] (2) | Zinc finger, Dof-type [IPR003851] (2) | scaffold_5_mRNA_4521.1 | C_unshiu_00183_mRNA_14.1 | - |
| GF0022862 | 1 | 1 | 0 | Hypothetical protein (2) |  | PGG domain [IPR026961] (2) | scaffold_5_mRNA_4520.1 | C_unshiu_00183_mRNA_15.1 | - |
| GF0022861 | 1 | 1 | 0 | EF1 protein (2) |  | NTF2-like domain [IPR032710] (2) | scaffold_5_mRNA_4513.1 | C_unshiu_00183_mRNA_22.1 | - |
| GF0022859 | 1 | 1 | 0 | Retrotransposon protein, putative, Ty1-copia subclass (1); Putative retroelement pol polyprotein (1) |  |  | scaffold_5_mRNA_450.1 | C_unshiu_01064_mRNA_9.1 | - |
| GF0022858 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (1) | Ribonuclease H-like domain [IPR012337] (1) | scaffold_5_mRNA_4498.1 | C_unshiu_00183_mRNA_39.1 | - |
| GF0022857 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2); zinc ion binding [GO:0008270 molecular_function] (1) | Reverse transcriptase zinc-binding domain [IPR026960] (2); Zinc knuckle CX2CX4HX4C [IPR025836] (1); Zinc finger, CCHC-type [IPR001878] (1); Ribonuclease H-like domain [IPR012337] (1) | scaffold_5_mRNA_4492.1 | C_unshiu_00183_mRNA_45.1 | - |
| GF0022856 | 1 | 1 | 0 | Geraniol dehydrogenase 1 (2) | oxidation-reduction process [GO:0055114 biological_process] (2); oxidoreductase activity [GO:0016491 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1) | GroES-like [IPR011032] (2); Alcohol dehydrogenase, N-terminal [IPR013154] (2); NAD(P)-binding domain [IPR016040] (1); Alcohol dehydrogenase superfamily, zinc-type [IPR002085] (1) | scaffold_5_mRNA_4485.1 | C_unshiu_00319_mRNA_40.1 | - |
| GF0022855 | 1 | 1 | 0 | Hypothetical protein (2) | protein dimerization activity [GO:0046983 molecular_function] (2) | NAD(P)-binding domain [IPR016040] (2); Winged helix-turn-helix DNA-binding domain [IPR011991] (2); NmrA-like domain [IPR008030] (2); Plant methyltransferase dimerisation [IPR012967] (2) | scaffold_5_mRNA_4482.1 | C_unshiu_00319_mRNA_37.1 | - |
| GF0022854 | 1 | 1 | 0 | Hypothetical protein (2) |  | Leucine-rich repeat domain, L domain-like [IPR032675] (2) | scaffold_5_mRNA_447.1 | C_unshiu_01064_mRNA_6.1 | - |
| GF0022853 | 1 | 1 | 0 | Hypothetical protein (2) | protein kinase activity [GO:0004672 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2); ATP binding [GO:0005524 molecular_function] (2) | Protein kinase, ATP binding site [IPR017441] (2); Protein kinase-like domain [IPR011009] (2); Protein kinase domain [IPR000719] (2); Serine/threonine/dual specificity protein kinase, catalytic  domain [IPR002290] (1) | scaffold_5_mRNA_4456.1 | C_unshiu_02773_mRNA_1.1 | - |
| GF0022852 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_4451.1 | C_unshiu_00238_mRNA_36.1 | - |
| GF0022851 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_4449.1 | C_unshiu_00277_mRNA_6.1 | - |
| GF0022850 | 1 | 1 | 0 | Preprotein translocase SecA family protein, putative isoform 8 (2) | zinc ion binding [GO:0008270 molecular_function] (2); protein binding [GO:0005515 molecular_function] (2) | Zinc finger, RING-type [IPR001841] (2); WD40/YVTN repeat-like-containing domain [IPR015943] (2); WD40 repeat [IPR001680] (2); WD40-repeat-containing domain [IPR017986] (2); Protein kinase-like domain [IPR011009] (2); Zinc finger, RING/FYVE/PHD-type [IPR013083] (2); G-protein beta WD-40 repeat [IPR020472] (1); RING-type zinc-finger, LisH dimerisation motif [IPR027370] (1) | scaffold_5_mRNA_4418.1 | C_unshiu_00238_mRNA_7.1 | - |
| GF0022849 | 1 | 1 | 0 | Acyl-CoA N-acyltransferases (NAT) superfamily protein isoform 1 (2) |  | Yjdj-type Gcn5-related N-acetyltransferase [IPR031165] (2); Acyl-CoA N-acyltransferase [IPR016181] (2) | scaffold_5_mRNA_4382.1 | C_unshiu_00477_mRNA_19.1 | - |
| GF0022847 | 1 | 1 | 0 | Small glutamine-rich tetratricopeptide repeat-containing protein alpha (2) | protein binding [GO:0005515 molecular_function] (2) | Tetratricopeptide-like helical domain [IPR011990] (2); Tetratricopeptide repeat 2 [IPR013105] (2); Tetratricopeptide repeat [IPR019734] (2); Tetratricopeptide repeat-containing domain [IPR013026] (2) | scaffold_5_mRNA_4363.1 | C_unshiu_00144_mRNA_7.1 | - |
| GF0022846 | 1 | 1 | 0 | Hypothetical protein (2) |  | Aspartic peptidase domain [IPR021109] (1) | scaffold_5_mRNA_436.1 | C_unshiu_00378_mRNA_6.1 | - |
| GF0022845 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_4355.1 | C_unshiu_02644_mRNA_3.1 | - |
| GF0022842 | 1 | 1 | 0 | Putative calcium-binding protein CML29 (1); Putative calcium-binding protein CML25 (1) | calcium ion binding [GO:0005509 molecular_function] (2) | EF-hand domain pair [IPR011992] (2); EF-Hand 1, calcium-binding site [IPR018247] (2); EF-hand domain [IPR002048] (2) | scaffold_5_mRNA_4308.1 | C_unshiu_00088_mRNA_11.1 | - |
| GF0022841 | 1 | 1 | 0 | Glycosyl hydrolase family 17 family protein (1); Hypothetical protein (1) | hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1) | Glycoside hydrolase superfamily [IPR017853] (2); Glycoside hydrolase family 17 [IPR000490] (1); Glycoside hydrolase, catalytic domain [IPR013781] (1) | scaffold_5_mRNA_4303.1 | C_unshiu_00088_mRNA_18.1 | - |
| GF0022840 | 1 | 1 | 0 | Transmembrane protein 50A (2) |  | Uncharacterised protein family UPF0220 [IPR007919] (2) | scaffold_5_mRNA_4300.1 | C_unshiu_00088_mRNA_20.1 | - |
| GF0022839 | 1 | 1 | 0 | Hypothetical protein (2) |  | DNA-binding pseudobarrel domain [IPR015300] (2) | scaffold_5_mRNA_43.1 | C_unshiu_00231_mRNA_2.1 | - |
| GF0022837 | 1 | 1 | 0 | Galactosyltransferase family protein (2) | galactosyltransferase activity [GO:0008378 molecular_function] (2); membrane [GO:0016020 cellular_component] (2); protein glycosylation [GO:0006486 biological_process] (2) | Domain of unknown function DUF4094 [IPR025298] (2); Glycosyl transferase, family 31 [IPR002659] (2) | scaffold_5_mRNA_4296.1 | C_unshiu_00088_mRNA_23.1 | - |
| GF0022836 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_429.1 | C_unshiu_00378_mRNA_28.1 | - |
| GF0022835 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_428.1 | C_unshiu_00378_mRNA_27.1 | - |
| GF0022832 | 1 | 1 | 0 | Farnesylated protein 2 (2) | metal ion transport [GO:0030001 biological_process] (2); metal ion binding [GO:0046872 molecular_function] (2) | Heavy metal-associated domain, HMA [IPR006121] (2) | scaffold_5_mRNA_4266.1 | C_unshiu_00088_mRNA_45.1 | - |
| GF0022831 | 1 | 1 | 0 | Hypothetical protein (1); MADS-box protein AGL66 (1) | RNA polymerase II regulatory region sequence-specific DNA binding [GO:0000977 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1); nucleus [GO:0005634 cellular_component] (1); protein dimerization activity [GO:0046983 molecular_function] (1); transcription factor activity, sequence-specific DNA binding [GO:0003700 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) | Transcription factor, MADS-box [IPR002100] (1); Transcription factor, K-box [IPR002487] (1); MADS MEF2-like [IPR033896] (1) | scaffold_5_mRNA_4265.1 | C_unshiu_00088_mRNA_46.1 | - |
| GF0022830 | 1 | 1 | 0 | 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase (2) | metabolic process [GO:0008152 biological_process] (2); intramolecular transferase activity, phosphotransferases [GO:0016868 molecular_function] (2); catalytic activity [GO:0003824 molecular_function] (2); phosphoglycerate mutase activity [GO:0004619 molecular_function] (2); glycolytic process [GO:0006096 biological_process] (2) | Histidine phosphatase superfamily, clade-1 [IPR013078] (2); Phosphoglycerate/bisphosphoglycerate mutase, active site [IPR001345] (2); Histidine phosphatase superfamily [IPR029033] (2); Phosphoglycerate mutase 1 [IPR005952] (2) | scaffold_5_mRNA_4254.1 | C_unshiu_00088_mRNA_64.1 | - |
| GF0022829 | 1 | 1 | 0 | Monoacylglycerol lipase ABHD6 (2) | catalytic activity [GO:0003824 molecular_function] (2) | Alpha/beta hydrolase fold-1 [IPR000073] (2); Alpha/Beta hydrolase fold [IPR029058] (2); Epoxide hydrolase-like [IPR000639] (2); Alpha/beta hydrolase fold-5 [IPR029059] (1) | scaffold_5_mRNA_4218.1 | C_unshiu_00241_mRNA_14.1 | - |
| GF0022825 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_421.1 | C_unshiu_00059_mRNA_40.1 | - |
| GF0022824 | 1 | 1 | 0 | UDP-glycosyltransferase 85A1 (2) | transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (2); metabolic process [GO:0008152 biological_process] (2) | UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (2) | scaffold_5_mRNA_4205.1 | C_unshiu_02009_mRNA_2.1 | - |
| GF0022823 | 1 | 1 | 0 | Hypothetical protein (2) |  | Phosphate-induced protein 1 [IPR006766] (2) | scaffold_5_mRNA_4203.1 | C_unshiu_02009_mRNA_3.1 | - |
| GF0022822 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_4179.1 | C_unshiu_00406_mRNA_25.1 | - |
| GF0022819 | 1 | 1 | 0 | Putative MATE efflux family protein (2) | transmembrane transport [GO:0055085 biological_process] (2); drug transmembrane transport [GO:0006855 biological_process] (2); antiporter activity [GO:0015297 molecular_function] (2); drug transmembrane transporter activity [GO:0015238 molecular_function] (2); membrane [GO:0016020 cellular_component] (2) | Multi antimicrobial extrusion protein [IPR002528] (2) | scaffold_5_mRNA_4159.1 | C_unshiu_02304_mRNA_4.1 | - |
| GF0022814 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_4131.1 | C_unshiu_00255_mRNA_12.1 | - |
| GF0022813 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_4130.1 | C_unshiu_00255_mRNA_11.1 | - |
| GF0022812 | 1 | 1 | 0 | Hypothetical protein (1); Peptide upstream ORF protein (1) |  |  | scaffold_5_mRNA_4128.1 | C_unshiu_00255_mRNA_9.1 | - |
| GF0022811 | 1 | 1 | 0 | AT4G38060 protein (1); Ribosomal RNA small subunit methyltransferase A (1) |  |  | scaffold_5_mRNA_4113.1 | C_unshiu_00718_mRNA_10.1 | - |
| GF0022810 | 1 | 1 | 0 | Hypothetical protein (1); Putative CAI-1 autoinducer sensor kinase/phosphatase cqsS-like (1) | zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1) | Harbinger transposase-derived nuclease domain [IPR027806] (2); Zinc finger, CCHC-type [IPR001878] (1) | scaffold_5_mRNA_410.1 | C_unshiu_01699_mRNA_4.1 | - |
| GF0022806 | 1 | 1 | 0 | Ankyrin repeat protein (2) | protein binding [GO:0005515 molecular_function] (2) | Ankyrin repeat [IPR002110] (2); Ankyrin repeat-containing domain [IPR020683] (2); PGG domain [IPR026961] (2) | scaffold_5_mRNA_408.1 | C_unshiu_00664_mRNA_11.1 | - |
| GF0022805 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_4075.1 | C_unshiu_00042_mRNA_50.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0022802 | 1 | 1 | 0 | Hypothetical protein (2) | NAD+ ADP-ribosyltransferase activity [GO:0003950 molecular_function] (2) | Poly(ADP-ribose) polymerase, catalytic domain [IPR012317] (2) | scaffold_5_mRNA_4048.1 | C_unshiu_00042_mRNA_20.1 | - |
| GF0022801 | 1 | 1 | 0 | 50S ribosomal protein 6, chloroplastic (2) | structural constituent of ribosome [GO:0003735 molecular_function] (2); translation [GO:0006412 biological_process] (2); rRNA binding [GO:0019843 molecular_function] (2); ribosome [GO:0005840 cellular_component] (2); chloroplast [GO:0009507 cellular_component] (2) | Ribosomal protein L6, chloroplast [IPR020526] (2) | scaffold_5_mRNA_4046.1 | C_unshiu_00042_mRNA_18.1 | - |
| GF0022800 | 1 | 1 | 0 | Hypothetical protein (2) | protein binding [GO:0005515 molecular_function] (1) | Pentatricopeptide repeat [IPR002885] (2); Tetratricopeptide-like helical domain [IPR011990] (1) | scaffold_5_mRNA_404.1 | C_unshiu_00664_mRNA_9.1 | - |
| GF0022799 | 1 | 1 | 0 | F-box protein interaction domain protein (2) | protein binding [GO:0005515 molecular_function] (2) | F-box domain [IPR001810] (2); F-box associated interaction domain [IPR017451] (2) | scaffold_5_mRNA_4034.1 | C_unshiu_00484_mRNA_3.1 | - |
| GF0022797 | 1 | 1 | 0 | Hypothetical protein (2) |  | Retrotransposon gag domain [IPR005162] (2) | scaffold_5_mRNA_403.1 | C_unshiu_00664_mRNA_8.1 | - |
| GF0022795 | 1 | 1 | 0 | Heptahelical protein (2) | integral component of membrane [GO:0016021 cellular_component] (2) | AdipoR/Haemolysin-III-related [IPR004254] (2) | scaffold_5_mRNA_4003.1 | C_unshiu_00190_mRNA_13.1 | - |
| GF0022793 | 1 | 1 | 0 | Transcription factor bHLH85 (2) | protein dimerization activity [GO:0046983 molecular_function] (2) | Myc-type, basic helix-loop-helix (bHLH) domain [IPR011598] (2) | scaffold_5_mRNA_3984.1 | C_unshiu_00190_mRNA_32.1 | - |
| GF0022792 | 1 | 1 | 0 | Hypothetical protein (1); Elongation factor 4 (1) |  |  | scaffold_5_mRNA_3978.1 | C_unshiu_00190_mRNA_38.1 | - |
| GF0022791 | 1 | 1 | 0 | Hypothetical protein (2) | regulation of transcription, DNA-templated [GO:0006355 biological_process] (1) | FHY3/FAR1 family [IPR031052] (1) | scaffold_5_mRNA_3963.1 | C_unshiu_02775_mRNA_2.1 | - |
| GF0022790 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_3960.1 | C_unshiu_00321_mRNA_17.1 | - |
| GF0022788 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_3941.1 | C_unshiu_02182_mRNA_2.1 | - |
| GF0022787 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_394.1 | C_unshiu_00397_mRNA_2.1 | - |
| GF0022786 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_3919.1 | C_unshiu_00067_mRNA_60.1 | - |
| GF0022785 | 1 | 1 | 0 | Hypothetical protein (2) |  | Munc13 homology 1 [IPR014770] (2); Protein of unknown function DUF810 [IPR008528] (2) | scaffold_5_mRNA_3918.1 | C_unshiu_00067_mRNA_61.1 | - |
| GF0022784 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_5_mRNA_3917.1 | C_unshiu_00067_mRNA_62.1 | - |
| GF0022782 | 1 | 1 | 0 | Ankyrin repeat family protein, putative (1); Ankyrin repeat protein (1) | protein binding [GO:0005515 molecular_function] (2) | Ankyrin repeat-containing domain [IPR020683] (2); PGG domain [IPR026961] (2); Ankyrin repeat [IPR002110] (2) | scaffold_5_mRNA_390.1 | C_unshiu_00165_mRNA_20.1 | - |
| GF0022781 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_388.1 | C_unshiu_00165_mRNA_24.1 | - |
| GF0022779 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_385.1 | C_unshiu_00165_mRNA_27.1 | - |
| GF0022778 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_3848.1 | C_unshiu_01774_mRNA_4.1 | - |
| GF0022777 | 1 | 1 | 0 | Epoxide hydrolase 2 (2) | catalytic activity [GO:0003824 molecular_function] (2) | Alpha/beta hydrolase fold-1 [IPR000073] (2); Alpha/Beta hydrolase fold [IPR029058] (2); Epoxide hydrolase-like [IPR000639] (2) | scaffold_5_mRNA_3841.1 | C_unshiu_01107_mRNA_4.1 | - |
| GF0022775 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_3821.1 | C_unshiu_00170_mRNA_2.1 | - |
| GF0022774 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_3820.1 | C_unshiu_00214_mRNA_48.1 | - |
| GF0022772 | 1 | 1 | 0 | Translationally-controlled tumor protein homolog (2) |  | Translationally controlled tumour protein [IPR018105] (2); Mss4-like [IPR011057] (2); Translationally controlled tumour protein, conserved site [IPR018103] (2); Mss4/translationally controlled tumour-associated TCTP [IPR011323] (1); Translationally controlled tumor protein (TCTP) domain [IPR034737] (1) | scaffold_5_mRNA_3799.1 | C_unshiu_00214_mRNA_33.1 | - |
| GF0022771 | 1 | 1 | 0 | Hypothetical protein (1); Desiccation PCC13-like protein (1) |  | Ferritin-related [IPR012347] (1) | scaffold_5_mRNA_3784.1 | C_unshiu_00214_mRNA_21.1 | - |
| GF0022770 | 1 | 1 | 0 | Zinc finger protein MAGPIE (2) | nucleic acid binding [GO:0003676 molecular_function] (2); metal ion binding [GO:0046872 molecular_function] (1) | Zinc finger C2H2-type [IPR013087] (1); Zinc finger, C2H2 [IPR007087] (1); Zinc finger C2H2-type/integrase DNA-binding domain [IPR013087] (1); Zinc finger, C2H2-like [IPR015880] (1); Zinc finger, double-stranded RNA binding [IPR022755] (1) | scaffold_5_mRNA_3770.1 | C_unshiu_00214_mRNA_6.1 | - |
| GF0022769 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_377.1 | C_unshiu_00328_mRNA_10.1 | - |
| GF0022767 | 1 | 1 | 0 | 3-ketoacyl-CoA synthase 7 (2) | catalytic activity [GO:0003824 molecular_function] (2); fatty acid biosynthetic process [GO:0006633 biological_process] (2); transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (2); membrane [GO:0016020 cellular_component] (2); metabolic process [GO:0008152 biological_process] (2) | 3-Oxoacyl-[acyl-carrier-protein (ACP)] synthase III, C-terminal [IPR013747] (2); FAE1/Type III polyketide synthase-like protein [IPR013601] (2); Very-long-chain 3-ketoacyl-CoA synthase [IPR012392] (2); Thiolase-like [IPR016039] (2) | scaffold_5_mRNA_3765.1 | C_unshiu_00214_mRNA_1.1 | - |
| GF0022765 | 1 | 1 | 0 | Hypothetical protein (2) |  | Arabidopsis retrotransposon Orf1 [IPR004312] (2) | scaffold_5_mRNA_376.1 | C_unshiu_00328_mRNA_8.1 | - |
| GF0022764 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_3745.1 | C_unshiu_00907_mRNA_3.1 | - |
| GF0022762 | 1 | 1 | 0 | Hypothetical protein (2) | ATP binding [GO:0005524 molecular_function] (2); protein kinase activity [GO:0004672 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2) | Protein kinase domain [IPR000719] (2); Protein kinase-like domain [IPR011009] (2); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1) | scaffold_5_mRNA_3733.1 | C_unshiu_00229_mRNA_24.1 | - |
| GF0022761 | 1 | 1 | 0 | Hypothetical protein (2) | nucleosome [GO:0000786 cellular_component] (2); DNA binding [GO:0003677 molecular_function] (2); protein heterodimerization activity [GO:0046982 molecular_function] (1) | Histone H3/CENP-A [IPR000164] (2); Histone-fold [IPR009072] (1) | scaffold_5_mRNA_373.1 | C_unshiu_00328_mRNA_7.1 | - |
| GF0022758 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_370.1 | C_unshiu_00328_mRNA_4.1 | - |
| GF0022756 | 1 | 1 | 0 | Hypothetical protein (2) |  | HSP20-like chaperone [IPR008978] (1) | scaffold_5_mRNA_3684.1 | C_unshiu_00224_mRNA_31.1 | - |
| GF0022755 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_3683.1 | C_unshiu_00224_mRNA_30.1 | - |
| GF0022753 | 1 | 1 | 0 | Hypothetical protein (2) |  | Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1) | scaffold_5_mRNA_3662.1 | C_unshiu_00213_mRNA_53.1 | - |
| GF0022751 | 1 | 1 | 0 | Hypothetical protein (2) | protein binding [GO:0005515 molecular_function] (2); mRNA splicing, via spliceosome [GO:0000398 biological_process] (1) | Tetratricopeptide-like helical domain [IPR011990] (2); Pre-mRNA-processing factor 6/Prp1/STA1 [IPR027108] (1) | scaffold_5_mRNA_3660.1 | C_unshiu_00224_mRNA_7.1 | - |
| GF0022750 | 1 | 1 | 0 | Hypothetical protein (2) | protein binding [GO:0005515 molecular_function] (2); mRNA splicing, via spliceosome [GO:0000398 biological_process] (2); RNA processing [GO:0006396 biological_process] (1) | Tetratricopeptide-like helical domain [IPR011990] (2); Pre-mRNA-processing factor 6/Prp1/STA1 [IPR027108] (2); HAT (Half-A-TPR) repeat [IPR003107] (1); Tetratricopeptide repeat-containing domain [IPR013026] (1) | scaffold_5_mRNA_3659.1 | C_unshiu_00224_mRNA_6.1 | - |
| GF0022749 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_3656.1 | C_unshiu_00224_mRNA_1.1 | - |
| GF0022748 | 1 | 1 | 0 | Inosine-uridine preferring nucleoside hydrolase (2) |  | Inosine/uridine-preferring nucleoside hydrolase [IPR023186] (2); Inosine/uridine-preferring nucleoside hydrolase domain [IPR001910] (2) | scaffold_5_mRNA_3629.1 | C_unshiu_00453_mRNA_3.1 | - |
| GF0022747 | 1 | 1 | 0 | Histidine-containing phosphotransfer protein 4 (2) | signal transducer activity [GO:0004871 molecular_function] (2); phosphorelay signal transduction system [GO:0000160 biological_process] (2) | Signal transduction histidine kinase, phosphotransfer (Hpt) domain [IPR008207] (2) | scaffold_5_mRNA_3627.1 | C_unshiu_00226_mRNA_4.1 | - |
| GF0022745 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_3623.1 | C_unshiu_01771_mRNA_8.1 | - |
| GF0022744 | 1 | 1 | 0 | Hypothetical protein (1); Sugar transporter ERD6-like 16 (1) | integral component of membrane [GO:0016021 cellular_component] (2); transmembrane transporter activity [GO:0022857 molecular_function] (2); transmembrane transport [GO:0055085 biological_process] (2) | Major facilitator, sugar transporter-like [IPR005828] (2); Major facilitator superfamily domain [IPR020846] (2) | scaffold_5_mRNA_3621.1 | C_unshiu_00226_mRNA_1.1 | - |
| GF0022741 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_358.1 | C_unshiu_00036_mRNA_72.1 | - |
| GF0022740 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_3546.1 | C_unshiu_00433_mRNA_23.1 | - |
| GF0022736 | 1 | 1 | 0 | Hypothetical protein (2) | regulation of transcription, DNA-templated [GO:0006355 biological_process] (2); transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (2); DNA binding [GO:0003677 molecular_function] (2) | AP2/ERF domain [IPR001471] (2); DNA-binding domain [IPR016177] (2); Frigida-like [IPR012474] (1) | scaffold_5_mRNA_3506.1 | C_unshiu_00339_mRNA_22.1 | - |
| GF0022735 | 1 | 1 | 0 | Hypothetical protein (2) |  | Frigida-like [IPR012474] (2) | scaffold_5_mRNA_3502.1 | C_unshiu_00339_mRNA_13.1 | - |
| GF0022730 | 1 | 1 | 0 | Pentatricopeptide repeat-containing family protein (2) | zinc ion binding [GO:0008270 molecular_function] (2); protein binding [GO:0005515 molecular_function] (2) | DYW domain [IPR032867] (2); Tetratricopeptide-like helical domain [IPR011990] (2); Pentatricopeptide repeat [IPR002885] (2) | scaffold_5_mRNA_3439.1 | C_unshiu_00205_mRNA_16.1 | - |
| GF0022727 | 1 | 1 | 0 | Glutathione S-transferase zeta class (2) | protein binding [GO:0005515 molecular_function] (2) | Thioredoxin-like fold [IPR012336] (2); Glutathione S-transferase, N-terminal [IPR004045] (2); Glutathione S-transferase, C-terminal-like [IPR010987] (2) | scaffold_5_mRNA_34.1 | C_unshiu_00230_mRNA_57.1 | - |
| GF0022726 | 1 | 1 | 0 | Hypothetical protein (2) | ADP binding [GO:0043531 molecular_function] (2) | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); NB-ARC [IPR002182] (2) | scaffold_5_mRNA_3382.1 | C_unshiu_02124_mRNA_1.1 | - |
| GF0022725 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_3373.1 | C_unshiu_02124_mRNA_2.1 | - |
| GF0022724 | 1 | 1 | 0 | Disease resistance protein (1); Disease resistance protein RPS2 (1) |  | Leucine-rich repeat domain, L domain-like [IPR032675] (2); Winged helix-turn-helix DNA-binding domain [IPR011991] (1) | scaffold_5_mRNA_3368.1 | C_unshiu_00660_mRNA_13.1 | - |
| GF0022723 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_3366.1 | C_unshiu_02743_mRNA_4.1 | - |
| GF0022722 | 1 | 1 | 0 | Phosphoprotein phosphatase isoform 3 (1); Cc-nbs-lrr resistance protein, putative isoform 1 (1) |  | Leucine-rich repeat domain, L domain-like [IPR032675] (2) | scaffold_5_mRNA_3364.1 | C_unshiu_00304_mRNA_19.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0022721 | 1 | 1 | 0 | NBS-LRR type disease resistance protein (2) | ADP binding [GO:0043531 molecular_function] (2) | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); NB-ARC [IPR002182] (2) | scaffold_5_mRNA_3352.1 | C_unshiu_00570_mRNA_20.1 | - |
| GF0022720 | 1 | 1 | 0 | Hypothetical protein (2) | GTP binding [GO:0005525 molecular_function] (2); small GTPase mediated signal transduction [GO:0007264 biological_process] (2) | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); Mitochondrial Rho-like [IPR013684] (1); Small GTPase superfamily [IPR001806] (1) | scaffold_5_mRNA_335.1 | C_unshiu_02337_mRNA_3.1 | - |
| GF0022719 | 1 | 1 | 0 | Disease resistance protein (CC-NBS-LRR class) family protein (1); Hypothetical protein (1) | protein binding [GO:0005515 molecular_function] (2); binding [GO:0005488 molecular_function] (2); ADP binding [GO:0043531 molecular_function] (1) | Armadillo-like helical [IPR011989] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Atypical Arm repeat [IPR032413] (2); Armadillo [IPR000225] (2); Armadillo-type fold [IPR016024] (2); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1) | scaffold_5_mRNA_3334.1 | C_unshiu_00812_mRNA_2.1 | - |
| GF0022717 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_3319.1 | C_unshiu_00570_mRNA_21.1 | - |
| GF0022714 | 1 | 1 | 0 | Hypothetical protein (2) | protein folding [GO:0006457 biological_process] (2); unfolded protein binding [GO:0051082 molecular_function] (2) | HSP40/DnaJ peptide-binding [IPR008971] (2); Chaperone DnaJ, C-terminal [IPR002939] (1) | scaffold_5_mRNA_3284.1 | C_unshiu_00731_mRNA_13.1 | - |
| GF0022709 | 1 | 1 | 0 | Hypothetical protein (2) | ubiquitin-protein transferase activity [GO:0004842 molecular_function] (2); protein ubiquitination [GO:0016567 biological_process] (2); zinc ion binding [GO:0008270 molecular_function] (2); protein binding [GO:0005515 molecular_function] (2) | Zinc finger, RING/FYVE/PHD-type [IPR013083] (2); E3 ubiquitin ligase RBR family [IPR031127] (2); Zinc finger, RING-type [IPR001841] (2) | scaffold_5_mRNA_3265.1 | C_unshiu_01493_mRNA_10.1 | - |
| GF0022708 | 1 | 1 | 0 | Hypothetical protein (2) | DNA-directed RNA polymerase activity [GO:0003899 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1); transcription, DNA-templated [GO:0006351 biological_process] (1) | RNA polymerase Rpb1, domain 1 [IPR007080] (1) | scaffold_5_mRNA_3264.1 | C_unshiu_01156_mRNA_4.1 | - |
| GF0022707 | 1 | 1 | 0 | Hypothetical protein (2) | DNA binding [GO:0003677 molecular_function] (2); transcription, DNA-templated [GO:0006351 biological_process] (2); DNA-directed RNA polymerase activity [GO:0003899 molecular_function] (1); DNA-directed 5'-3' RNA polymerase activity [GO:0003899 molecular_function] (1) | RNA polymerase Rpb1, domain 5 [IPR007081] (2) | scaffold_5_mRNA_3263.1 | C_unshiu_01156_mRNA_3.1 | - |
| GF0022706 | 1 | 1 | 0 | Small rubber particle protein (2) | | Rubber elongation factor [IPR008802] (2) | scaffold_5_mRNA_326.1 | C_unshiu_02040_mRNA_3.1 | - |
| GF0022704 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_3236.1 | C_unshiu_00451_mRNA_12.1 | - |
| GF0022703 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_3233.1 | C_unshiu_00852_mRNA_7.1 | - |
| GF0022699 | 1 | 1 | 0 | Putative non-LTR reverse transcriptase (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Reverse transcriptase zinc-binding domain [IPR026960] (2); Ribonuclease H-like domain [IPR012337] (2) | scaffold_5_mRNA_3199.1 | C_unshiu_00361_mRNA_12.1 | - |
| GF0022693 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_314.1 | C_unshiu_01061_mRNA_15.1 | - |
| GF0022692 | 1 | 1 | 0 | Hypothetical protein (2) | metal ion binding [GO:0046872 molecular_function] (1) | Zinc finger, CCCH-type [IPR000571] (1) | scaffold_5_mRNA_3136.1 | C_unshiu_00888_mRNA_13.1 | - |
| GF0022691 | 1 | 1 | 0 | Hypothetical protein (2) | | Leucine-rich repeat domain, L domain-like [IPR032675] (2) | scaffold_5_mRNA_3130.1 | C_unshiu_01691_mRNA_5.1 | - |
| GF0022690 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_3127.1 | C_unshiu_00755_mRNA_2.1 | - |
| GF0022689 | 1 | 1 | 0 | Hypothetical protein (2) | protein binding [GO:0005515 molecular_function] (2) | SH3 domain [IPR001452] (2) | scaffold_5_mRNA_3123.1 | C_unshiu_00961_mRNA_2.1 | - |
| GF0022687 | 1 | 1 | 0 | Cytochrome P450 (1); Cytochrome P450 71D10, putative (1) | iron ion binding [GO:0005506 molecular_function] (2); heme binding [GO:0020037 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (2); monooxygenase activity [GO:0004497 molecular_function] (1) | Cytochrome P450, conserved site [IPR017972] (2); Cytochrome P450 [IPR001128] (2); Cytochrome P450, E-class, group I [IPR002401] (1); Cytochrome P450, E-class, group IV [IPR002403] (1) | scaffold_5_mRNA_31.1 | C_unshiu_00230_mRNA_54.1 | - |
| GF0022686 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_3097.1 | C_unshiu_02001_mRNA_3.1 | - |
| GF0022685 | 1 | 1 | 0 | Ras-like GTP-binding protein YPT1 (2) | GTP binding [GO:0005525 molecular_function] (2); GTPase activity [GO:0003924 molecular_function] (2); signal transduction [GO:0007165 biological_process] (1); intracellular protein transport [GO:0006886 biological_process] (1); intracellular [GO:0005622 cellular_component] (1); nucleocytoplasmic transport [GO:0006913 biological_process] (1); small GTPase mediated signal transduction [GO:0007264 biological_process] (1); membrane [GO:0016020 cellular_component] (1); protein transport [GO:0015031 biological_process] (1) | Small GTP-binding protein domain [IPR005225] (2); Small GTPase superfamily [IPR001806] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); Ran GTPase [IPR002041] (1); Small GTPase superfamily, ARF type [IPR024156] (1); Small GTPase superfamily, Rab type [IPR003579] (1); Small GTPase superfamily, Rho type [IPR003578] (1); Small GTPase superfamily, Ras type [IPR020849] (1) | scaffold_5_mRNA_309.1 | C_unshiu_00127_mRNA_4.1 | - |
| GF0022684 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_3083.1 | C_unshiu_00219_mRNA_38.1 | - |
| GF0022683 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_3076.1 | C_unshiu_00734_mRNA_7.1 | - |
| GF0022682 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_3069.1 | C_unshiu_02141_mRNA_1.1 | - |
| GF0022681 | 1 | 1 | 0 | Leucine Rich Repeat family protein, expressed (1); LRR receptor-like kinase family protein (1) | protein binding [GO:0005515 molecular_function] (2) | Leucine-rich repeat [IPR001611] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Leucine-rich repeat, typical subtype [IPR003591] (2) | scaffold_5_mRNA_3068.1 | C_unshiu_00961_mRNA_9.1 | - |
| GF0022680 | 1 | 1 | 0 | Acyl-CoA binding protein 6 (2) | fatty-acyl-CoA binding [GO:0000062 molecular_function] (2) | Acyl-CoA-binding protein, ACBP, conserved site [IPR022408] (2); Acyl-CoA-binding protein, ACBP [IPR000582] (2); FERM/acyl-CoA-binding protein, 3-helical bundle [IPR014352] (2) | scaffold_5_mRNA_3066.1 | C_unshiu_00061_mRNA_32.1 | - |
| GF0022678 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_3055.1 | C_unshiu_00061_mRNA_45.1 | - |
| GF0022677 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_3054.1 | C_unshiu_00061_mRNA_46.1 | - |
| GF0022676 | 1 | 1 | 0 | Transcription factor MYB39 (2) | DNA binding [GO:0003677 molecular_function] (2) | Myb domain [IPR017930] (2); SANT/Myb domain [IPR001005] (2); Homeobox domain-like [IPR009057] (1); Homeodomain-like [IPR009057] (1) | scaffold_5_mRNA_3048.1 | C_unshiu_00671_mRNA_11.1 | - |
| GF0022672 | 1 | 1 | 0 | Calmodulin (2) | calcium ion binding [GO:0005509 molecular_function] (2) | EF-Hand 1, calcium-binding site [IPR018247] (2); EF-hand domain [IPR002048] (2); EF-hand domain pair [IPR011992] (2) | scaffold_5_mRNA_3016.1 | C_unshiu_00078_mRNA_37.1 | - |
| GF0022671 | 1 | 1 | 0 | Putative transcription factor KAN2 (2) | DNA binding [GO:0003677 molecular_function] (2) | SANT/Myb domain [IPR001005] (2); Myb domain, plants [IPR006447] (2); Homeodomain-like [IPR009057] (1); Homeobox domain-like [IPR009057] (1) | scaffold_5_mRNA_3012.1 | C_unshiu_00078_mRNA_33.1 | - |
| GF0022670 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_3004.1 | C_unshiu_00078_mRNA_29.1 | - |
| GF0022668 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2); TB2/DP1/HVA22-related protein [IPR004345] (1) | scaffold_5_mRNA_3.1 | C_unshiu_02167_mRNA_1.1 | - |
| GF0022662 | 1 | 1 | 0 | Ankyrin repeat plant-like protein (2) | protein binding [GO:0005515 molecular_function] (2) | Ankyrin repeat [IPR002110] (2); Ankyrin repeat-containing domain [IPR020683] (2); PGG domain [IPR026961] (2) | scaffold_5_mRNA_2931.1 | C_unshiu_00040_mRNA_14.1 | - |
| GF0022661 | 1 | 1 | 0 | Putative retroelement pol polyprotein (1); Retrovirus-related Pol polyprotein from transposon TNT 1-94 (1) | DNA integration [GO:0015074 biological_process] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2); Integrase, catalytic core [IPR001584] (2); GAG-pre-integrase domain [IPR025724] (2) | scaffold_5_mRNA_2906.1 | C_unshiu_01150_mRNA_1.1 | - |
| GF0022659 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_290.1 | C_unshiu_00159_mRNA_20.1 | - |
| GF0022658 | 1 | 1 | 0 | Cytochrome P450 71D8 (2) | oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2); iron ion binding [GO:0005506 molecular_function] (2); heme binding [GO:0020037 molecular_function] (2) | Cytochrome P450, conserved site [IPR017972] (2); Cytochrome P450, E-class, group I [IPR002401] (2); Cytochrome P450 [IPR001128] (2) | scaffold_5_mRNA_29.1 | C_unshiu_00230_mRNA_52.1 | - |
| GF0022657 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_2888.1 | C_unshiu_00389_mRNA_17.1 | - |
| GF0022656 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_2879.1 | C_unshiu_01065_mRNA_7.1 | - |
| GF0022652 | 1 | 1 | 0 | Hypothetical protein (1); PAB-dependent poly(A)-specific ribonuclease subunit PAN3 (1) | | Domain of unknown function DUF1336 [IPR009769] (1); Protein ENHANCED DISEASE RESISTANCE 2, C-terminal [IPR009769] (1) | scaffold_5_mRNA_2859.1 | C_unshiu_01037_mRNA_4.1 | - |
| GF0022651 | 1 | 1 | 0 | Putative disease resistance gene NBS-LRR family protein (2) | ADP binding [GO:0043531 molecular_function] (2) | Leucine-rich repeat domain, L domain-like [IPR032675] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); NB-ARC [IPR002182] (2); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); AAA+ ATPase domain [IPR003593] (1) | scaffold_5_mRNA_2840.1 | C_unshiu_01806_mRNA_3.1 | - |
| GF0022650 | 1 | 1 | 0 | Hypothetical protein (2) | | Protein ENHANCED DISEASE RESISTANCE 2, C-terminal [IPR009769] (1); Domain of unknown function DUF1336 [IPR009769] (1) | scaffold_5_mRNA_2833.1 | C_unshiu_01783_mRNA_3.1 | - |
| GF0022649 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_283.1 | C_unshiu_00159_mRNA_11.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0022647 | 1 | 1 | 0 | UPF0481 protein (2) | | Protein of unknown function DUF247, plant [IPR004158] (2) | scaffold_5_mRNA_2820.1 | C_unshiu_00465_mRNA_3.1 | - |
| GF0022646 | 1 | 1 | 0 | Disease resistance protein (CC-NBS-LRR class) family protein (2) | ADP binding [GO:0043531 molecular_function] (2) | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); NB-ARC [IPR002182] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Winged helix-turn-helix DNA-binding domain [IPR011991] (1) | scaffold_5_mRNA_2818.1 | C_unshiu_00465_mRNA_4.1 | - |
| GF0022645 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_2808.1 | C_unshiu_02128_mRNA_1.1 | - |
| GF0022644 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_2788.1 | C_unshiu_01306_mRNA_7.1 | - |
| GF0022642 | 1 | 1 | 0 | Hypothetical protein (2) | | Pectin lyase fold [IPR012334] (2); Pectin lyase fold/virulence factor [IPR011050] (2) | scaffold_5_mRNA_2773.1 | C_unshiu_01439_mRNA_7.1 | - |
| GF0022641 | 1 | 1 | 0 | Hypothetical protein (2) | protein serine/threonine phosphatase activity [GO:0004722 molecular_function] (2); protein binding [GO:0005515 molecular_function] (2); protein dephosphorylation [GO:0006470 biological_process] (2); catalytic activity [GO:0003824 molecular_function] (2) | PPM-type phosphatase domain [IPR001932] (2); Thioredoxin-like fold [IPR012336] (2); Protein phosphatase 2C family [IPR015655] (2); Glutathione S-transferase, N-terminal [IPR004045] (2) | scaffold_5_mRNA_2772.1 | C_unshiu_01439_mRNA_6.1 | - |
| GF0022640 | 1 | 1 | 0 | Hypothetical protein (2) | | Protein ENHANCED DISEASE RESISTANCE 2, C-terminal [IPR009769] (1); Domain of unknown function DUF1336 [IPR009769] (1) | scaffold_5_mRNA_2771.1 | C_unshiu_01150_mRNA_2.1 | - |
| GF0022639 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_2770.1 | C_unshiu_01783_mRNA_6.1 | - |
| GF0022638 | 1 | 1 | 0 | Ribosomal protein L15 (2) | structural constituent of ribosome [GO:0003735 molecular_function] (2); translation [GO:0006412 biological_process] (2); intracellular [GO:0005622 cellular_component] (2); ribosome [GO:0005840 cellular_component] (2) | Ribosomal protein L15e [IPR000439] (2); Ribosomal protein L23/L15e core domain [IPR012678] (2); Ribosomal protein L15e, conserved site [IPR020925] (2); Ribosomal protein L15e core domain [IPR024794] (2) | scaffold_5_mRNA_277.1 | C_unshiu_00159_mRNA_4.1 | - |
| GF0022635 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_2754.1 | C_unshiu_00435_mRNA_15.1 | - |
| GF0022634 | 1 | 1 | 0 | Hypothetical protein (2) | | Aspartic peptidase domain [IPR021109] (1) | scaffold_5_mRNA_2753.1 | C_unshiu_00435_mRNA_16.1 | - |
| GF0022633 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_2751.1 | C_unshiu_00435_mRNA_17.1 | - |
| GF0022632 | 1 | 1 | 0 | BED zinc finger,hAT family dimerization domain (2) | DNA binding [GO:0003677 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2); protein dimerization activity [GO:0046983 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2); hAT-like transposase, RNase-H fold [IPR025525] (2); HAT, C-terminal dimerisation domain [IPR008906] (2) | scaffold_5_mRNA_2749.1 | C_unshiu_00435_mRNA_18.1 | - |
| GF0022631 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_2748.1 | C_unshiu_02394_mRNA_2.1 | - |
| GF0022630 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (1) | Piwi domain [IPR003165] (1); Ribonuclease H-like domain [IPR012337] (1) | scaffold_5_mRNA_2744.1 | C_unshiu_01625_mRNA_1.1 | - |
| GF0022629 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_2736.1 | C_unshiu_00686_mRNA_3.1 | - |
| GF0022628 | 1 | 1 | 0 | Protein BREVIS RADIX (2) | | Transcription factor BREVIS RADIX, N-terminal domain [IPR027988] (2); Brevis radix (BRX) domain [IPR013591] (2) | scaffold_5_mRNA_2735.1 | C_unshiu_00686_mRNA_4.1 | - |
| GF0022626 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_2730.1 | C_unshiu_02469_mRNA_3.1 | - |
| GF0022625 | 1 | 1 | 0 | Hypothetical protein (1); Protein FAR1-RELATED SEQUENCE 3 (1) | regulation of transcription, DNA-templated [GO:0006355 biological_process] (2) | FHY3/FAR1 family [IPR031052] (2); FAR1 DNA binding domain [IPR004330] (2) | scaffold_5_mRNA_2723.1 | C_unshiu_00686_mRNA_17.1 | - |
| GF0022624 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_2715.1 | C_unshiu_01349_mRNA_2.1 | - |
| GF0022623 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_2712.1 | C_unshiu_00343_mRNA_2.1 | - |
| GF0022621 | 1 | 1 | 0 | Replication factor-A carboxy-terminal domain protein (1); Animal RPA1 domain protein (1) | | Nucleic acid-binding, OB-fold [IPR012340] (2); Domain of unknown function DUF223 [IPR003871] (1); Replication factor A, C-terminal [IPR013955] (1) | scaffold_5_mRNA_2706.1 | C_unshiu_00794_mRNA_10.1 | - |
| GF0022620 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_2704.1 | C_unshiu_00011_mRNA_64.1 | - |
| GF0022619 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_2702.1 | C_unshiu_00011_mRNA_62.1 | - |
| GF0022618 | 1 | 1 | 0 | Putative non-LTR retroelement reverse transcriptase (2) | | Reverse transcriptase domain [IPR000477] (2) | scaffold_5_mRNA_270.1 | C_unshiu_00449_mRNA_6.1 | - |
| GF0022617 | 1 | 1 | 0 | Probable pectinesterase/pectinesterase inhibitor 46 (2) | pectinesterase activity [GO:0030599 molecular_function] (2); cell wall modification [GO:0042545 biological_process] (2); cell wall [GO:0005618 cellular_component] (2); enzyme inhibitor activity [GO:0004857 molecular_function] (2) | Pectinesterase, Asp active site [IPR033131] (2); Pectin lyase fold [IPR012334] (2); Pectinesterase inhibitor domain [IPR006501] (2); Pectinesterase, catalytic [IPR000070] (2); Pectin lyase fold/virulence factor [IPR011050] (2); Pectinesterase, Tyr active site [IPR018040] (2) | scaffold_5_mRNA_2692.1 | C_unshiu_00011_mRNA_54.1 | - |
| GF0022615 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_2672.1 | C_unshiu_00867_mRNA_1.1 | - |
| GF0022614 | 1 | 1 | 0 | Phosphoprotein phosphatase (2) | | Leucine-rich repeat domain, L domain-like [IPR032675] (2) | scaffold_5_mRNA_2662.1 | C_unshiu_01931_mRNA_1.1 | - |
| GF0022613 | 1 | 1 | 0 | Hypothetical protein (2) | | Transposon, En/Spm-like [IPR004242] (1) | scaffold_5_mRNA_2623.1 | C_unshiu_02552_mRNA_1.1 | - |
| GF0022612 | 1 | 1 | 0 | NBS-LRR type disease resistance protein (2) | | | scaffold_5_mRNA_2617.1 | C_unshiu_02523_mRNA_4.1 | - |
| GF0022611 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_2606.1 | C_unshiu_01443_mRNA_3.1 | - |
| GF0022610 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_2605.1 | C_unshiu_01443_mRNA_6.1 | - |
| GF0022608 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_2595.1 | C_unshiu_00831_mRNA_11.1 | - |
| GF0022607 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_259.1 | C_unshiu_00449_mRNA_16.1 | - |
| GF0022605 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_258.1 | C_unshiu_00449_mRNA_17.1 | - |
| GF0022604 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_2578.1 | C_unshiu_00374_mRNA_5.1 | - |
| GF0022603 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_2575.1 | C_unshiu_00374_mRNA_8.1 | - |
| GF0022602 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_2565.1 | C_unshiu_00374_mRNA_23.1 | - |
| GF0022601 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_2560.1 | C_unshiu_00592_mRNA_6.1 | - |
| GF0022600 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_2556.1 | C_unshiu_00374_mRNA_29.1 | - |
| GF0022599 | 1 | 1 | 0 | Hypothetical protein (2) | zinc ion binding [GO:0008270 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | Zinc finger, CCHC-type [IPR001878] (2) | scaffold_5_mRNA_2555.1 | C_unshiu_00374_mRNA_31.1 | - |
| GF0022598 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_2554.1 | C_unshiu_00374_mRNA_32.1 | - |
| GF0022597 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_5_mRNA_2551.1 | C_unshiu_00374_mRNA_35.1 | - |
| GF0022596 | 1 | 1 | 0 | RNA-directed DNA polymerase , related (2) | | | scaffold_5_mRNA_2550.1 | C_unshiu_00374_mRNA_36.1 | - |
| GF0022595 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_2543.1 | C_unshiu_00374_mRNA_41.1 | - |
| GF0022594 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_2541.1 | C_unshiu_00374_mRNA_43.1 | - |
| GF0022593 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_2517.1 | C_unshiu_00377_mRNA_41.1 | - |
| GF0022592 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_2515.1 | C_unshiu_00377_mRNA_39.1 | - |
| GF0022591 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_2512.1 | C_unshiu_00377_mRNA_35.1 | - |
| GF0022590 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_251.1 | C_unshiu_00449_mRNA_21.1 | - |
| GF0022589 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_2506.1 | C_unshiu_00377_mRNA_30.1 | - |
| GF0022587 | 1 | 1 | 0 | Endoglucanase (2) | hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (2); catalytic activity [GO:0003824 molecular_function] (2); carbohydrate metabolic process [GO:0005975 biological_process] (2) | Glycoside hydrolase family 9 [IPR001701] (2); Six-hairpin glycosidase-like [IPR008928] (2); Six-hairpin glycosidase [IPR012341] (1) | scaffold_5_mRNA_25.1 | C_unshiu_00230_mRNA_48.1 | - |
| GF0022586 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_2497.1 | C_unshiu_00377_mRNA_22.1 | - |
| GF0022583 | 1 | 1 | 0 | Hypothetical protein (2) | nucleus [GO:0005634 cellular_component] (2); regulation of transcription from RNA polymerase II promoter [GO:0006357 biological_process] (2); cell cycle [GO:0007049 biological_process] (2); transcription, DNA-templated [GO:0006351 biological_process] (2); regulation of cell cycle [GO:0051726 biological_process] (2) | Retinoblastoma-related protein [IPR015652] (2); Cyclin-like [IPR013763] (2); Retinoblastoma-associated protein, A-box [IPR002720] (2); Retinoblastoma protein family [IPR028309] (2) | scaffold_5_mRNA_2491.1 | C_unshiu_00377_mRNA_15.1 | - |
| GF0022581 | 1 | 1 | 0 | Hypothetical protein (2) | | Viral movement protein [IPR028919] (1) | scaffold_5_mRNA_2482.1 | C_unshiu_00377_mRNA_12.1 | - |
| GF0022580 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_2480.1 | C_unshiu_00377_mRNA_11.1 | - |
| GF0022579 | 1 | 1 | 0 | Hypothetical protein (1); BED zinc finger,hAT family dimerization domain (1) | DNA binding [GO:0003677 molecular_function] (2); protein dimerization activity [GO:0046983 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | HAT, C-terminal dimerisation domain [IPR008906] (2); Ribonuclease H-like domain [IPR012337] (2); hAT-like transposase, RNase-H fold [IPR025525] (2); GH3 family [IPR004993] (1) | scaffold_5_mRNA_2474.1 | C_unshiu_00377_mRNA_5.1 | - |
| GF0022578 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_2472.1 | C_unshiu_00377_mRNA_3.1 | - |
| GF0022576 | 1 | 1 | 0 | Clade XI lectin receptor kinase (2) | ATP binding [GO:0005524 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2); protein kinase activity [GO:0004672 molecular_function] (2); carbohydrate binding [GO:0030246 molecular_function] (2) | Protein kinase, ATP binding site [IPR017441] (2); Serine/threonine-protein kinase, active site [IPR008271] (2); Protein kinase domain [IPR000719] (2); Concanavalin A-like lectin/glucanase domain [IPR013320] (2); Protein kinase-like domain [IPR011009] (2); Legume lectin domain [IPR001220] (2); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1) | scaffold_5_mRNA_2458.1 | C_unshiu_00114_mRNA_16.1 | - |
| GF0022575 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_2433.1 | C_unshiu_02744_mRNA_2.1 | - |
| GF0022574 | 1 | 1 | 0 | Hypothetical protein (2) | | Plant disease resistance response protein [IPR004265] (2) | scaffold_5_mRNA_2425.1 | C_unshiu_02134_mRNA_1.1 | - |
| GF0022573 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_2418.1 | C_unshiu_00327_mRNA_14.1 | - |
| GF0022572 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_2414.1 | C_unshiu_00327_mRNA_11.1 | - |
| GF0022571 | 1 | 1 | 0 | Hypothetical protein (2) | | MULE transposase domain [IPR018289] (2) | scaffold_5_mRNA_2412.1 | C_unshiu_00327_mRNA_9.1 | - |
| GF0022570 | 1 | 1 | 0 | Hypothetical protein (2) | | Retrotransposon gag domain [IPR005162] (2) | scaffold_5_mRNA_2406.1 | C_unshiu_00327_mRNA_5.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0022569 | 1 | 1 | 0 | Putative clathrin assembly protein (2) | clathrin-coated vesicle [GO:0030136 cellular_component] (2); 1-phosphatidylinositol binding [GO:0005545 molecular_function] (2); clathrin coat assembly [GO:0048268 biological_process] (2); phospholipid binding [GO:0005543 molecular_function] (2); clathrin binding [GO:0030276 molecular_function] (2) | ENTH domain [IPR013809] (2); Phosphoinositide-binding clathrin adaptor, domain 2 [IPR014712] (2); AP180 N-terminal homology (ANTH) domain [IPR011417] (2); ENTH/VHS [IPR008942] (2) | scaffold_5_mRNA_2404.1 | C_unshiu_00327_mRNA_4.1 | - |
| GF0022568 | 1 | 1 | 0 | Hypothetical protein (2) |  | Chromo domain-like [IPR016197] (1); Chromo domain [IPR023780] (1) | scaffold_5_mRNA_2403.1 | C_unshiu_00327_mRNA_3.1 | - |
| GF0022567 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_2398.1 | C_unshiu_00327_mRNA_1.1 | - |
| GF0022566 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_2394.1 | C_unshiu_00201_mRNA_1.1 | - |
| GF0022565 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_2391.1 | C_unshiu_00201_mRNA_4.1 | - |
| GF0022564 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_2390.1 | C_unshiu_00957_mRNA_2.1 | - |
| GF0022563 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_2385.1 | C_unshiu_00201_mRNA_9.1 | - |
| GF0022562 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_2381.1 | C_unshiu_00201_mRNA_14.1 | - |
| GF0022561 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_2377.1 | C_unshiu_00912_mRNA_8.1 | - |
| GF0022560 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_2374.1 | C_unshiu_00912_mRNA_4.1 | - |
| GF0022559 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_2364.1 | C_unshiu_00020_mRNA_73.1 | - |
| GF0022558 | 1 | 1 | 0 | ERI1 exoribonuclease 2 (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2); Exonuclease, RNase T/DNA polymerase III [IPR013520] (2) | scaffold_5_mRNA_2358.1 | C_unshiu_00020_mRNA_78.1 | - |
| GF0022557 | 1 | 1 | 0 | RNase P Rpr2/Rpp21 subunit domain protein (2) | chromatin binding [GO:0003682 molecular_function] (1) | RNAse P, Rpr2/Rpp21 subunit [IPR007175] (2); Bromo adjacent homology (BAH) domain [IPR001025] (1) | scaffold_5_mRNA_2351.1 | C_unshiu_00020_mRNA_82.1 | - |
| GF0022556 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_2341.1 | C_unshiu_00842_mRNA_4.1 | - |
| GF0022554 | 1 | 1 | 0 | Urease accessory protein UreF (2) | nickel cation binding [GO:0016151 molecular_function] (2); nitrogen compound metabolic process [GO:0006807 biological_process] (2) | Urease accessory protein UreF [IPR002639] (2) | scaffold_5_mRNA_2326.1 | C_unshiu_00196_mRNA_32.1 | - |
| GF0022553 | 1 | 1 | 0 | Hypothetical protein (2) |  | MULE transposase domain [IPR018289] (2) | scaffold_5_mRNA_2318.1 | C_unshiu_00360_mRNA_20.1 | - |
| GF0022552 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_2317.1 | C_unshiu_00360_mRNA_21.1 | - |
| GF0022551 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_2309.1 | C_unshiu_00360_mRNA_28.1 | - |
| GF0022549 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_5_mRNA_2303.1 | C_unshiu_01673_mRNA_4.1 | - |
| GF0022548 | 1 | 1 | 0 | Hypothetical protein (2) | oxidation-reduction process [GO:0055114 biological_process] (2); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (2); iron ion binding [GO:0005506 molecular_function] (2); heme binding [GO:0020037 molecular_function] (2) | Cytochrome P450 [IPR001128] (2); Retrotransposon gag domain [IPR005162] (2) | scaffold_5_mRNA_2288.1 | C_unshiu_00359_mRNA_7.1 | - |
| GF0022547 | 1 | 1 | 0 | Cytochrome P450 98A2 (2) | heme binding [GO:0020037 molecular_function] (2); iron ion binding [GO:0005506 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (2) | Cytochrome P450 [IPR001128] (2); Cytochrome P450, E-class, group I [IPR002401] (2); Cytochrome P450, conserved site [IPR017972] (2) | scaffold_5_mRNA_2287.1 | C_unshiu_00359_mRNA_8.1 | - |
| GF0022546 | 1 | 1 | 0 | Hypothetical protein (2) | protein heterodimerization activity [GO:0046982 molecular_function] (1) | Transcription factor CBF/NF-Y/archaeal histone domain [IPR003958] (2); Histone-fold [IPR009072] (1) | scaffold_5_mRNA_2277.1 | C_unshiu_00913_mRNA_6.1 | - |
| GF0022545 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_2273.1 | C_unshiu_01277_mRNA_2.1 | - |
| GF0022544 | 1 | 1 | 0 | Hypothetical protein (1); Similarity to non-LTR retroelement reverse transcriptase (1) |  |  | scaffold_5_mRNA_2271.1 | C_unshiu_00258_mRNA_3.1 | - |
| GF0022542 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_2266.1 | C_unshiu_01255_mRNA_6.1 | - |
| GF0022541 | 1 | 1 | 0 | Hypothetical protein (2) | ATP binding [GO:0005524 molecular_function] (2); metal ion binding [GO:0046872 molecular_function] (2); catalytic activity [GO:0003824 molecular_function] (2) | Pre-ATP-grasp domain [IPR016185] (2); ATP-grasp fold, subdomain 1 [IPR013815] (2); ATP-grasp fold [IPR011761] (2); ATP-grasp fold, ATP-dependent carboxylate-amine ligase-type [IPR003135] (2) | scaffold_5_mRNA_2265.1 | C_unshiu_01255_mRNA_8.1 | - |
| GF0022540 | 1 | 1 | 0 | Hypothetical protein (2) | galactoside 2-alpha-L-fucosyltransferase activity [GO:0008107 molecular_function] (2); cell wall biogenesis [GO:0042546 biological_process] (2); membrane [GO:0016020 cellular_component] (2); nucleic acid binding [GO:0003676 molecular_function] (1) | Xyloglucan fucosyltransferase [IPR004938] (2); Ribonuclease H-like domain [IPR012337] (1) | scaffold_5_mRNA_2258.1 | C_unshiu_00581_mRNA_18.1 | - |
| GF0022539 | 1 | 1 | 0 | Hypothetical protein (2) | galactoside 2-alpha-L-fucosyltransferase activity [GO:0008107 molecular_function] (2); membrane [GO:0016020 cellular_component] (2); cell wall biogenesis [GO:0042546 biological_process] (2) | Xyloglucan fucosyltransferase [IPR004938] (2) | scaffold_5_mRNA_2257.1 | C_unshiu_00581_mRNA_17.1 | - |
| GF0022536 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_2206.1 | C_unshiu_00031_mRNA_25.1 | - |
| GF0022535 | 1 | 1 | 0 | COP9 signalosome complex subunit 8 (1); Hypothetical protein (1) |  | Winged helix-turn-helix DNA-binding domain [IPR011991] (1) | scaffold_5_mRNA_2204.1 | C_unshiu_00031_mRNA_23.1 | - |
| GF0022534 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_2203.1 | C_unshiu_00031_mRNA_22.1 | - |
| GF0022532 | 1 | 1 | 0 | Hypothetical protein (2) |  | Transposase, MuDR, plant [IPR004332] (2); Domain of unknown function DUF1985 [IPR015410] (2) | scaffold_5_mRNA_22.1 | C_unshiu_00230_mRNA_45.1 | - |
| GF0022529 | 1 | 1 | 0 | Hypothetical protein (2) |  | Retrotransposon gag domain [IPR005162] (2) | scaffold_5_mRNA_2174.1 | C_unshiu_00243_mRNA_38.1 | - |
| GF0022528 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_2169.1 | C_unshiu_01087_mRNA_4.1 | - |
| GF0022527 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_2155.1 | C_unshiu_00517_mRNA_7.1 | - |
| GF0022523 | 1 | 1 | 0 | Hypothetical protein (2) | integral component of membrane [GO:0016021 cellular_component] (2); transmembrane transporter activity [GO:0022857 molecular_function] (2) | WAT1-related protein [IPR030184] (2) | scaffold_5_mRNA_2139.1 | C_unshiu_00100_mRNA_22.1 | - |
| GF0022522 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_2138.1 | C_unshiu_00100_mRNA_21.1 | - |
| GF0022521 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2); zinc ion binding [GO:0008270 molecular_function] (2) | Zinc finger, CCHC-type [IPR001878] (2) | scaffold_5_mRNA_2137.1 | C_unshiu_00100_mRNA_19.1 | - |
| GF0022520 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_2133.1 | C_unshiu_00174_mRNA_57.1 | - |
| GF0022519 | 1 | 1 | 0 | Hypothetical protein (2) | zinc ion binding [GO:0008270 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | Zinc finger, CCHC-type [IPR001878] (2) | scaffold_5_mRNA_2130.1 | C_unshiu_00350_mRNA_14.1 | - |
| GF0022518 | 1 | 1 | 0 | Nodulin MtN21/EamA-like transporter family protein (2) | transmembrane transporter activity [GO:0022857 molecular_function] (2); membrane [GO:0016020 cellular_component] (2); integral component of membrane [GO:0016021 cellular_component] (2) | WAT1-related protein [IPR030184] (2); EamA domain [IPR000620] (2) | scaffold_5_mRNA_2123.2 | C_unshiu_00264_mRNA_4.1 | - |
| GF0022517 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_2120.1 | C_unshiu_01932_mRNA_1.1 | - |
| GF0022516 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_2099.1 | C_unshiu_00226_mRNA_18.1 | - |
| GF0022515 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_2091.1 | C_unshiu_00226_mRNA_20.1 | - |
| GF0022514 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_2089.1 | C_unshiu_00074_mRNA_64.1 | - |
| GF0022513 | 1 | 1 | 0 | Hypothetical protein (2) | aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1) | Peptidase A2A, retrovirus, catalytic [IPR001995] (1) | scaffold_5_mRNA_2087.1 | C_unshiu_00226_mRNA_23.1 | - |
| GF0022512 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2); proteolysis [GO:0006508 biological_process] (2); zinc ion binding [GO:0008270 molecular_function] (2); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (2) | Peptidase A2A, retrovirus, catalytic [IPR001995] (2); Zinc finger, CCHC-type [IPR001878] (2); Reverse transcriptase domain [IPR000477] (1); Aspartic peptidase domain [IPR021109] (1) | scaffold_5_mRNA_2078.1 | C_unshiu_00226_mRNA_30.1 | - |
| GF0022511 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_2076.1 | C_unshiu_00226_mRNA_32.1 | - |
| GF0022510 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_2072.1 | C_unshiu_00226_mRNA_37.1 | - |
| GF0022509 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_2062.1 | C_unshiu_00531_mRNA_1.1 | - |
| GF0022508 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_2060.1 | C_unshiu_00531_mRNA_5.1 | - |
| GF0022507 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_2059.1 | C_unshiu_00531_mRNA_6.1 | - |
| GF0022506 | 1 | 1 | 0 | Hypothetical protein (2) |  | Reverse transcriptase domain [IPR000477] (2) | scaffold_5_mRNA_2045.1 | C_unshiu_01903_mRNA_2.1 | - |
| GF0022504 | 1 | 1 | 0 | Hypothetical protein (2) | chromatin binding [GO:0003682 molecular_function] (2); methyltransferase activity [GO:0008168 molecular_function] (2) | DNA methylase, C-5 cytosine-specific, active site [IPR018117] (2); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (2); C-5 cytosine methyltransferase [IPR001525] (2); Bromo adjacent homology (BAH) domain [IPR001025] (2) | scaffold_5_mRNA_204.1 | C_unshiu_01769_mRNA_5.1 | - |
| GF0022503 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_2029.1 | C_unshiu_00028_mRNA_41.1 | - |
| GF0022502 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (1) | Ribonuclease H-like domain [IPR012337] (1) | scaffold_5_mRNA_2027.1 | C_unshiu_00028_mRNA_38.1 | - |
| GF0022501 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_2023.1 | C_unshiu_00668_mRNA_8.1 | - |
| GF0022500 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Domain of unknown function DUF4283 [IPR025558] (2); Ribonuclease H-like domain [IPR012337] (2) | scaffold_5_mRNA_202.1 | C_unshiu_01769_mRNA_3.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0022499 | 1 | 1 | 0 | Narbonin (1); Chitinase 2 (1) | carbohydrate metabolic process [GO:0005975 biological_process] (2); hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (1) | 2S globulin [IPR000677] (2); Glycoside hydrolase superfamily [IPR017853] (2); Glycoside hydrolase family 18, catalytic domain [IPR001223] (1); Glycoside hydrolase, catalytic domain [IPR013781] (1); Glycoside hydrolase, chitinase active site [IPR001579] (1) | scaffold_5_mRNA_2016.1 | C_unshiu_00524_mRNA_13.1 | - |
| GF0022498 | 1 | 1 | 0 | LRR and NB-ARC domain disease resistance protein (2) | ADP binding [GO:0043531 molecular_function] (2) | Leucine-rich repeat domain, L domain-like [IPR032675] (2); NB-ARC [IPR002182] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); Winged helix-turn-helix DNA-binding domain [IPR011991] (1) | scaffold_5_mRNA_201.1 | C_unshiu_01769_mRNA_2.1 | - |
| GF0022497 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_20.1 | C_unshiu_00230_mRNA_42.1 | - |
| GF0022496 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_1999.1 | C_unshiu_00983_mRNA_3.1 | - |
| GF0022495 | 1 | 1 | 0 | Polynucleotidyl transferase, Ribonuclease H fold (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Reverse transcriptase zinc-binding domain [IPR026960] (2); Ribonuclease H-like domain [IPR012337] (2) | scaffold_5_mRNA_1995.1 | C_unshiu_00605_mRNA_11.1 | - |
| GF0022494 | 1 | 1 | 0 | Hypothetical protein (2) | | Winged helix-turn-helix DNA-binding domain [IPR011991] (1) | scaffold_5_mRNA_1993.1 | C_unshiu_00559_mRNA_1.1 | - |
| GF0022493 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_1983.1 | C_unshiu_00559_mRNA_8.1 | - |
| GF0022491 | 1 | 1 | 0 | Hypothetical protein (2) | aspartic-type endopeptidase activity [GO:0004190 molecular_function] (2); proteolysis [GO:0006508 biological_process] (2) | Aspartic peptidase domain [IPR021109] (2); Retrotransposon gag domain [IPR005162] (2); Aspartic peptidase, active site [IPR001969] (2) | scaffold_5_mRNA_198.1 | C_unshiu_00060_mRNA_33.1 | - |
| GF0022490 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_1970.1 | C_unshiu_00029_mRNA_97.1 | - |
| GF0022489 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_1967.1 | C_unshiu_00516_mRNA_1.1 | - |
| GF0022488 | 1 | 1 | 0 | Hypothetical protein (2) | proteolysis [GO:0006508 biological_process] (1); cysteine-type peptidase activity [GO:0008234 molecular_function] (1) | Transposon, En/Spm-like [IPR004242] (2); Domain of unknown function DUF4218 [IPR025452] (2); Probable transposase, Ptta/En/Spm, plant [IPR004252] (2); Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1); Transposase-associated domain [IPR029480] (1) | scaffold_5_mRNA_1962.1 | C_unshiu_00698_mRNA_12.1 | - |
| GF0022487 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_1959.1 | C_unshiu_01392_mRNA_11.1 | - |
| GF0022486 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_1952.1 | C_unshiu_00282_mRNA_15.1 | - |
| GF0022484 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_1945.1 | C_unshiu_01849_mRNA_2.1 | - |
| GF0022483 | 1 | 1 | 0 | Hypothetical protein (2) | | FAR1 DNA binding domain [IPR004330] (1) | scaffold_5_mRNA_1932.1 | C_unshiu_00243_mRNA_4.1 | - |
| GF0022482 | 1 | 1 | 0 | Hypothetical protein (2) | | Retrotransposon gag domain [IPR005162] (2) | scaffold_5_mRNA_1931.1 | C_unshiu_00243_mRNA_5.1 | - |
| GF0022481 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_1930.1 | C_unshiu_00243_mRNA_7.1 | - |
| GF0022479 | 1 | 1 | 0 | Hypothetical protein (2) | | Leucine-rich repeat domain, L domain-like [IPR032675] (2) | scaffold_5_mRNA_1916.1 | C_unshiu_01964_mRNA_3.1 | - |
| GF0022478 | 1 | 1 | 0 | Hypothetical protein (2) | | GAG-pre-integrase domain [IPR025724] (1) | scaffold_5_mRNA_1915.1 | C_unshiu_01964_mRNA_4.1 | - |
| GF0022477 | 1 | 1 | 0 | Hypothetical protein (2) | | Retrotransposon gag domain [IPR005162] (1); Aspartic peptidase domain [IPR021109] (1) | scaffold_5_mRNA_1910.1 | C_unshiu_00880_mRNA_9.1 | - |
| GF0022476 | 1 | 1 | 0 | Hypothetical protein (2) | 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_1907.1 | C_unshiu_00880_mRNA_8.1 | - |
| GF0022475 | 1 | 1 | 0 | Kunitz trypsin inhibitor (2) | endopeptidase inhibitor activity [GO:0004866 molecular_function] (2) | Proteinase inhibitor I3, Kunitz legume [IPR002160] (2); Kunitz inhibitor ST1-like [IPR011065] (2) | scaffold_5_mRNA_1906.1 | C_unshiu_00880_mRNA_7.1 | - |
| GF0022474 | 1 | 1 | 0 | Hypothetical protein (2) | | Transposase-associated domain [IPR029480] (2); Transposon, En/Spm-like [IPR004242] (2) | scaffold_5_mRNA_1904.1 | C_unshiu_00880_mRNA_4.1 | - |
| GF0022473 | 1 | 1 | 0 | Putative COX1/OXI3 intron 2 protein (2) | mRNA processing [GO:0006397 biological_process] (2) | Domain X [IPR024937] (2) | scaffold_5_mRNA_1900.1 | C_unshiu_00819_mRNA_6.1 | - |
| GF0022472 | 1 | 1 | 0 | Disease resistance protein (2) | ADP binding [GO:0043531 molecular_function] (2) | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); NB-ARC [IPR002182] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Winged helix-turn-helix DNA-binding domain [IPR011991] (1) | scaffold_5_mRNA_1899.1 | C_unshiu_00819_mRNA_7.1 | - |
| GF0022471 | 1 | 1 | 0 | Hypothetical protein (2) | regulation of transcription, DNA-templated [GO:0006355 biological_process] (2); DNA binding [GO:0003677 molecular_function] (2) | NAC domain [IPR003441] (2) | scaffold_5_mRNA_1863.1 | C_unshiu_00083_mRNA_1.1 | - |
| GF0022468 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_5_mRNA_1851.1 | C_unshiu_00798_mRNA_5.1 | - |
| GF0022467 | 1 | 1 | 0 | LRR receptor-like kinase (2) | protein binding [GO:0005515 molecular_function] (2) | Leucine-rich repeat domain, L domain-like [IPR032675] (2); Leucine-rich repeat, typical subtype [IPR003591] (2); Leucine-rich repeat [IPR001611] (2) | scaffold_5_mRNA_1848.1 | C_unshiu_00798_mRNA_9.1 | - |
| GF0022466 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_1835.1 | C_unshiu_00654_mRNA_8.1 | - |
| GF0022463 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_1821.1 | C_unshiu_00588_mRNA_8.1 | - |
| GF0022461 | 1 | 1 | 0 | Hypothetical protein (1); Retrotransposon Tto1 DNA (1) | | Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (2) | scaffold_5_mRNA_1811.1 | C_unshiu_00056_mRNA_75.1 | - |
| GF0022460 | 1 | 1 | 0 | Calcium-transporting ATPase 8, plasma membrane-type-like protein (1); Plasma membrane-type calcium ATPase (1) | integral component of membrane [GO:0016021 cellular_component] (2) | HAD-like domain [IPR023214] (2); P-type ATPase [IPR001757] (2); Cation-transporting P-type ATPase, C-terminal [IPR006068] (2); P-type ATPase, transmembrane domain [IPR023298] (2) | scaffold_5_mRNA_1803.1 | C_unshiu_00180_mRNA_33.1 | - |
| GF0022459 | 1 | 1 | 0 | Hypothetical protein (2) | zinc ion binding [GO:0008270 molecular_function] (2) | Zinc finger, PMZ-type [IPR006564] (2); Zinc finger, SWIM-type [IPR007527] (2) | scaffold_5_mRNA_18.1 | C_unshiu_00230_mRNA_40.1 | - |
| GF0022457 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_1791.1 | C_unshiu_00180_mRNA_24.1 | - |
| GF0022455 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_1780.1 | C_unshiu_00275_mRNA_25.1 | - |
| GF0022454 | 1 | 1 | 0 | Glycosyl hydrolase family 35 protein isoform 2 (1); Hypothetical protein (1) | hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (2); carbohydrate metabolic process [GO:0005975 biological_process] (2); ATP binding [GO:0005524 molecular_function] (1) | Glycoside hydrolase 35, catalytic domain [IPR031330] (2); Galactose-binding domain-like [IPR008979] (2); Glycoside hydrolase superfamily [IPR017853] (2); Glycoside hydrolase, family 35 [IPR001944] (2); Glycoside hydrolase, family 35, conserved site [IPR019801] (2); Beta-galactosidase jelly roll domain [IPR025300] (1); Glycoside hydrolase, catalytic domain [IPR013781] (1); GroEL-like apical domain [IPR027409] (1); Chaperonin Cpn60/TCP-1 family [IPR002423] (1) | scaffold_5_mRNA_1768.1 | C_unshiu_00293_mRNA_12.1 | - |
| GF0022453 | 1 | 1 | 0 | Nucleic acid binding / zinc ion binding protein (2) | | Zinc knuckle CX2CX4HX4C [IPR025836] (2); Domain of unknown function DUF4283 [IPR025558] (2) | scaffold_5_mRNA_1756.1 | C_unshiu_00468_mRNA_8.1 | - |
| GF0022452 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_1754.1 | C_unshiu_00533_mRNA_17.1 | - |
| GF0022451 | 1 | 1 | 0 | Hypothetical protein (2) | calmodulin binding [GO:0005516 molecular_function] (2) | Calcium-transporting P-type ATPase, N-terminal autoinhibitory domain [IPR024750] (2) | scaffold_5_mRNA_175.1 | C_unshiu_00033_mRNA_70.1 | - |
| GF0022449 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_1734.1 | C_unshiu_02044_mRNA_2.1 | - |
| GF0022448 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_1732.1 | C_unshiu_02268_mRNA_1.1 | - |
| GF0022447 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_1728.1 | C_unshiu_00492_mRNA_4.1 | - |
| GF0022446 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_1727.1 | C_unshiu_00492_mRNA_5.1 | - |
| GF0022445 | 1 | 1 | 0 | Kinase interacting family protein, putative isoform 1 (1); Hypothetical protein (1) | actin binding [GO:0003779 molecular_function] (2) | Protein Networked (NET), actin-binding (NAB) domain [IPR011684] (2) | scaffold_5_mRNA_1724.1 | C_unshiu_00492_mRNA_8.1 | - |
| GF0022444 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_1723.1 | C_unshiu_01749_mRNA_1.1 | - |
| GF0022443 | 1 | 1 | 0 | Chaperone protein dnaJ 11 (2) | | DnaJ domain, conserved site [IPR018253] (2); DnaJ domain [IPR001623] (2) | scaffold_5_mRNA_1721.1 | C_unshiu_01749_mRNA_3.1 | - |
| GF0022442 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_1717.1 | C_unshiu_01018_mRNA_7.1 | - |
| GF0022441 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_1716.1 | C_unshiu_01018_mRNA_6.1 | - |
| GF0022440 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_1715.1 | C_unshiu_01018_mRNA_5.1 | - |
| GF0022439 | 1 | 1 | 0 | Hypothetical protein (2) | | Domain of unknown function DUF4283 [IPR025558] (2) | scaffold_5_mRNA_1713.1 | C_unshiu_01018_mRNA_3.1 | - |
| GF0022437 | 1 | 1 | 0 | 26S protease regulatory subunit 6B (1); 26S protease regulatory subunit 6B-like protein (1) | ATP binding [GO:0005524 molecular_function] (2); cytoplasm [GO:0005737 cellular_component] (1); protein catabolic process [GO:0030163 biological_process] (1); hydrolase activity [GO:0016787 molecular_function] (1) | ATPase, AAA-type, core [IPR003959] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); ATPase, AAA-type, conserved site [IPR003960] (2); CDC48 domain 2-like [IPR029067] (1); AAA+ ATPase domain [IPR003593] (1); 26S proteasome subunit P45 [IPR005937] (1) | scaffold_5_mRNA_1705.1 | C_unshiu_01766_mRNA_5.1 | - |
| GF0022436 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_1701.1 | C_unshiu_00097_mRNA_7.1 | - |
| GF0022435 | 1 | 1 | 0 | LRR receptor-like kinase (2) | protein binding [GO:0005515 molecular_function] (2); protein kinase activity [GO:0004672 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2); ATP binding [GO:0005524 molecular_function] (2) | Protein kinase domain [IPR000719] (2); Leucine-rich repeat, typical subtype [IPR003591] (2); Protein kinase-like domain [IPR011009] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Serine/threonine-protein kinase, active site [IPR008271] (2); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (2); Leucine-rich repeat [IPR001611] (2); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Protein kinase, ATP binding site [IPR017441] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1) | scaffold_5_mRNA_1696.1 | C_unshiu_00608_mRNA_6.1 | - |
| GF0022434 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_1684.1 | C_unshiu_01634_mRNA_1.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0022433 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_1677.1 | C_unshiu_00211_mRNA_20.1 | - |
| GF0022432 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_1676.1 | C_unshiu_00211_mRNA_19.1 | - |
| GF0022431 | 1 | 1 | 0 | Hypothetical protein (2) |  | Domain of unknown function DUF4219 [IPR025314] (1) | scaffold_5_mRNA_1672.1 | C_unshiu_03081_mRNA_1.1 | - |
| GF0022429 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_1666.1 | C_unshiu_00588_mRNA_3.1 | - |
| GF0022426 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_1658.1 | C_unshiu_01752_mRNA_8.1 | - |
| GF0022425 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_1654.1 | C_unshiu_01752_mRNA_4.1 | - |
| GF0022424 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_1647.1 | C_unshiu_00145_mRNA_4.1 | - |
| GF0022423 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_1633.1 | C_unshiu_01669_mRNA_3.1 | - |
| GF0022422 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_1632.1 | C_unshiu_00830_mRNA_18.1 | - |
| GF0022421 | 1 | 1 | 0 | Auxin response factor (2) | regulation of transcription, DNA-templated [GO:0006355 biological_process] (2); DNA binding [GO:0003677 molecular_function] (2); nucleus [GO:0005634 cellular_component] (2); response to hormone [GO:0009725 biological_process] (2); ATP binding [GO:0005524 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2); protein kinase activity [GO:0004672 molecular_function] (2) | Protein kinase-like domain [IPR011009] (2); DNA-binding pseudobarrel domain [IPR015300] (2); Auxin response factor [IPR010525] (2); Protein kinase domain [IPR000719] (2); Protein kinase, ATP binding site [IPR017441] (2); Serine/threonine-protein kinase, active site [IPR008271] (2); B3 DNA binding domain [IPR003340] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1) | scaffold_5_mRNA_163.1 | C_unshiu_00033_mRNA_56.1 | - |
| GF0022420 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_1610.1 | C_unshiu_00576_mRNA_24.1 | - |
| GF0022419 | 1 | 1 | 0 | Hypothetical protein (2) | protein kinase activity [GO:0004672 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2); ATP binding [GO:0005524 molecular_function] (2) | Protein kinase domain [IPR000719] (2); Protein kinase-like domain [IPR011009] (2) | scaffold_5_mRNA_161.1 | C_unshiu_00033_mRNA_60.1 | - |
| GF0022418 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_1602.1 | C_unshiu_00346_mRNA_37.1 | - |
| GF0022417 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2); zinc ion binding [GO:0008270 molecular_function] (2) | Zinc finger, CCHC-type [IPR001878] (2); Aspartic peptidase domain [IPR021109] (2); Retropepsins [IPR018061] (2) | scaffold_5_mRNA_1601.1 | C_unshiu_00346_mRNA_36.1 | - |
| GF0022416 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_1600.1 | C_unshiu_00346_mRNA_35.1 | - |
| GF0022415 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_1594.1 | C_unshiu_00346_mRNA_24.1 | - |
| GF0022414 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_1590.1 | C_unshiu_00138_mRNA_71.1 | - |
| GF0022413 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_1589.1 | C_unshiu_00138_mRNA_72.1 | - |
| GF0022412 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_1588.1 | C_unshiu_00138_mRNA_73.1 | - |
| GF0022411 | 1 | 1 | 0 | Hypothetical protein (2) |  | Viral movement protein [IPR028919] (1) | scaffold_5_mRNA_1587.1 | C_unshiu_00576_mRNA_28.1 | - |
| GF0022410 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_1586.1 | C_unshiu_00576_mRNA_27.1 | - |
| GF0022409 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_1579.1 | C_unshiu_01678_mRNA_1.1 | - |
| GF0022408 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_1577.1 | C_unshiu_01678_mRNA_3.1 | - |
| GF0022407 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_1576.1 | C_unshiu_01678_mRNA_4.1 | - |
| GF0022406 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_1574.1 | C_unshiu_01678_mRNA_6.1 | - |
| GF0022405 | 1 | 1 | 0 | Zinc finger C-x8-C-x5-C-x3-H type family protein isoform 3 (2) | mRNA splicing, via spliceosome [GO:0000398 biological_process] (2); RNA binding [GO:0003723 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2); metal ion binding [GO:0046872 molecular_function] (2); U2AF [GO:0089701 cellular_component] (2); nucleotide binding [GO:0000166 molecular_function] (1) | U2 auxiliary factor small subunit [IPR009145] (2); RNA recognition motif domain, eukaryote [IPR003954] (2); RNA recognition motif domain [IPR000504] (2); Zinc finger, CCCH-type [IPR000571] (2); Nucleotide-binding alpha-beta plait domain [IPR012677] (1) | scaffold_5_mRNA_157.1 | C_unshiu_00033_mRNA_53.1 | - |
| GF0022404 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_1559.1 | C_unshiu_00745_mRNA_14.1 | - |
| GF0022403 | 1 | 1 | 0 | Hypothetical protein (2) |  | Viral movement protein [IPR028919] (2) | scaffold_5_mRNA_1554.1 | C_unshiu_00346_mRNA_16.1 | - |
| GF0022402 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_1550.1 | C_unshiu_00346_mRNA_14.1 | - |
| GF0022401 | 1 | 1 | 0 | Retrotransposon protein, putative, unclassified (1); Retrotransposon protein, putative, Ty3-gypsy subclass (1) | nucleic acid binding [GO:0003676 molecular_function] (1) | Chromo domain [IPR023780] (2); Chromo domain-like [IPR016197] (2); Chromo/chromo shadow domain [IPR000953] (1); Ribonuclease H-like domain [IPR012337] (1) | scaffold_5_mRNA_1540.1 | C_unshiu_00317_mRNA_5.1 | - |
| GF0022400 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_1525.1 | C_unshiu_01886_mRNA_2.1 | - |
| GF0022399 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_1524.1 | C_unshiu_01886_mRNA_3.1 | - |
| GF0022398 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_1519.1 | C_unshiu_02752_mRNA_3.1 | - |
| GF0022397 | 1 | 1 | 0 | Hypothetical protein (2) |  | LOG family [IPR031100] (2) | scaffold_5_mRNA_1517.1 | C_unshiu_02752_mRNA_1.1 | - |
| GF0022396 | 1 | 1 | 0 | Ac-like transposase THELMA13 (1); Hypothetical protein (1) | nucleic acid binding [GO:0003676 molecular_function] (2); DNA binding [GO:0003677 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2); Zinc finger, BED-type [IPR003656] (2); Zinc finger C2H2-type [IPR013087] (1) | scaffold_5_mRNA_1510.1 | C_unshiu_01355_mRNA_2.1 | - |
| GF0022394 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_1508.1 | C_unshiu_02377_mRNA_1.1 | - |
| GF0022392 | 1 | 1 | 0 | Hypothetical protein (2) |  | Viral movement protein [IPR028919] (2) | scaffold_5_mRNA_1487.1 | C_unshiu_01648_mRNA_2.1 | - |
| GF0022391 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_1486.1 | C_unshiu_01648_mRNA_1.1 | - |
| GF0022390 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_1477.1 | C_unshiu_00263_mRNA_20.1 | - |
| GF0022389 | 1 | 1 | 0 | DUF641 family protein (2) |  | Domain of unknown function DUF641, plant [IPR006943] (2) | scaffold_5_mRNA_1473.1 | C_unshiu_00263_mRNA_16.1 | - |
| GF0022387 | 1 | 1 | 0 | LRR receptor-like kinase family protein (2) | ATP binding [GO:0005524 molecular_function] (2); protein kinase activity [GO:0004672 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2); protein binding [GO:0005515 molecular_function] (2) | Protein kinase domain [IPR000719] (2); Protein kinase-like domain [IPR011009] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Leucine-rich repeat, typical subtype [IPR003591] (2); Serine/threonine-protein kinase, active site [IPR008271] (2); Protein kinase, ATP binding site [IPR017441] (2); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (2); Leucine-rich repeat [IPR001611] (2); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1) | scaffold_5_mRNA_145.1 | C_unshiu_00033_mRNA_46.1 | - |
| GF0022385 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_1439.1 | C_unshiu_01184_mRNA_5.1 | - |
| GF0022384 | 1 | 1 | 0 | Hypothetical protein (2) | 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_1435.1 | C_unshiu_00418_mRNA_2.1 | - |
| GF0022382 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_1433.1 | C_unshiu_00678_mRNA_3.1 | - |
| GF0022381 | 1 | 1 | 0 | Hypothetical protein (1); Putative muDR family transposase-like (1) | zinc ion binding [GO:0008270 molecular_function] (2) | Zinc finger, PMZ-type [IPR006564] (2); Zinc finger, SWIM-type [IPR007527] (2); MULE transposase domain [IPR018289] (1) | scaffold_5_mRNA_1422.1 | C_unshiu_00762_mRNA_16.1 | - |
| GF0022380 | 1 | 1 | 0 | Hypothetical protein (2) | regulation of transcription, DNA-templated [GO:0006355 biological_process] (2) | FHY3/FAR1 family [IPR031052] (2) | scaffold_5_mRNA_1421.1 | C_unshiu_00762_mRNA_15.1 | - |
| GF0022379 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2); zinc ion binding [GO:0008270 molecular_function] (2) | Zinc finger, CCHC-type [IPR001878] (2) | scaffold_5_mRNA_1420.1 | C_unshiu_00762_mRNA_14.1 | - |
| GF0022378 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_1418.1 | C_unshiu_02568_mRNA_1.1 | - |
| GF0022377 | 1 | 1 | 0 | Hypothetical protein (2) |  | LURP1-related protein domain [IPR007612] (2); Tubby C-terminal-like domain [IPR025659] (2); Transposase, MuDR, plant [IPR004332] (2); MULE transposase domain [IPR018289] (1) | scaffold_5_mRNA_1417.1 | C_unshiu_00762_mRNA_11.1 | - |
| GF0022376 | 1 | 1 | 0 | Protein FAR1-RELATED SEQUENCE 3 (2) | zinc ion binding [GO:0008270 molecular_function] (2); regulation of transcription, DNA-templated [GO:0006355 biological_process] (2) | FHY3/FAR1 family [IPR031052] (2); Zinc finger, SWIM-type [IPR007527] (2); Zinc finger, PMZ-type [IPR006564] (2) | scaffold_5_mRNA_1410.1 | C_unshiu_01316_mRNA_6.1 | - |
| GF0022374 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_14.1 | C_unshiu_00230_mRNA_36.1 | - |
| GF0022373 | 1 | 1 | 0 | Hypothetical protein (2) |  | FAS1 domain [IPR000782] (1) | scaffold_5_mRNA_1399.1 | C_unshiu_00578_mRNA_4.1 | - |
| GF0022372 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_1398.1 | C_unshiu_00578_mRNA_2.1 | - |
| GF0022371 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_1387.1 | C_unshiu_00379_mRNA_13.1 | - |
| GF0022370 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_1386.1 | C_unshiu_00379_mRNA_12.1 | - |
| GF0022369 | 1 | 1 | 0 | Hypothetical protein (2) |  | Leucine-rich repeat domain, L domain-like [IPR032675] (2) | scaffold_5_mRNA_1381.1 | C_unshiu_00379_mRNA_5.1 | - |
| GF0022368 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_1368.1 | C_unshiu_00031_mRNA_37.1 | - |
| GF0022366 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_5_mRNA_1362.1 | C_unshiu_00031_mRNA_42.1 | - |
| GF0022365 | 1 | 1 | 0 | LRR and NB-ARC domain disease resistance protein (2) | ADP binding [GO:0043531 molecular_function] (2) | Leucine-rich repeat domain, L domain-like [IPR032675] (2); NB-ARC [IPR002182] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); Winged helix-turn-helix DNA-binding domain [IPR011991] (1) | scaffold_5_mRNA_1361.1 | C_unshiu_00031_mRNA_43.1 | - |
| GF0022364 | 1 | 1 | 0 | Egg cell-secreted protein 1.4 (2) |  | Prolamin-like domain [IPR008502] (2) | scaffold_5_mRNA_1358.1 | C_unshiu_00031_mRNA_46.1 | - |
| GF0022363 | 1 | 1 | 0 | Hypothetical protein (2) | regulation of transcription, DNA-templated [GO:0006355 biological_process] (1) | Plastid lipid-associated protein/fibrillin conserved domain [IPR006843] (1); FAR1 DNA binding domain [IPR004330] (1); FHY3/FAR1 family [IPR031052] (1) | scaffold_5_mRNA_1357.1 | C_unshiu_00031_mRNA_47.1 | - |
| GF0022362 | 1 | 1 | 0 | Putative U3 small nucleolar RNA-associated protein 7 (2) | protein binding [GO:0005515 molecular_function] (2) | WD40 repeat [IPR001680] (2); WD40-repeat-containing domain [IPR017986] (2); WD40/YVTN repeat-like-containing domain [IPR015943] (2); BING4, C-terminal domain [IPR012952] (2) | scaffold_5_mRNA_1350.1 | C_unshiu_00031_mRNA_52.1 | - |
| GF0022361 | 1 | 1 | 0 | Hypothetical protein (2) | ADP binding [GO:0043531 molecular_function] (2) | NB-ARC [IPR002182] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2) | scaffold_5_mRNA_1344.1 | C_unshiu_00031_mRNA_61.1 | - |
| GF0022360 | 1 | 1 | 0 | Acylsugar acyltransferase 3 (2) | transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (2) | Transferase [IPR003480] (2); Chloramphenicol acetyltransferase-like domain [IPR023213] (1) | scaffold_5_mRNA_1343.1 | C_unshiu_00031_mRNA_62.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0022359 | 1 | 1 | 0 | Hypothetical protein (2) | catalytic activity [GO:0003824 molecular_function] (2); metabolic process [GO:0008152 biological_process] (2); triose-phosphate isomerase activity [GO:0004807 molecular_function] (2) | Triosephosphate isomerase [IPR000652] (2); Aldolase-type TIM barrel [IPR013785] (2) | scaffold_5_mRNA_1342.1 | C_unshiu_00031_mRNA_63.1 | - |
| GF0022358 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_1341.1 | C_unshiu_00031_mRNA_64.1 | - |
| GF0022357 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_1338.1 | C_unshiu_00031_mRNA_65.1 | - |
| GF0022356 | 1 | 1 | 0 | Putative U3 small nucleolar RNA-associated protein 7 (2) | protein binding [GO:0005515 molecular_function] (2); transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (1) | WD40-repeat-containing domain [IPR017986] (2); WD40 repeat [IPR001680] (2); WD40/YVTN repeat-like-containing domain [IPR015943] (2); BING4, C-terminal domain [IPR012952] (2); Transferase [IPR003480] (1) | scaffold_5_mRNA_1337.1 | C_unshiu_00031_mRNA_66.1 | - |
| GF0022355 | 1 | 1 | 0 | Hypothetical protein (2) | | Aspartic peptidase domain [IPR021109] (1) | scaffold_5_mRNA_1334.1 | C_unshiu_00031_mRNA_70.1 | - |
| GF0022354 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (1) | Ribonuclease H-like domain [IPR012337] (1) | scaffold_5_mRNA_1333.1 | C_unshiu_00031_mRNA_71.1 | - |
| GF0022353 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_1331.1 | C_unshiu_00031_mRNA_72.1 | - |
| GF0022352 | 1 | 1 | 0 | SLG-Sc and SLA-Sc genes and Melmoth retrotransposon sequence (1); Hypothetical protein (1) | DNA integration [GO:0015074 biological_process] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | Integrase, catalytic core [IPR001584] (2); Ribonuclease H-like domain [IPR012337] (2); GAG-pre-integrase domain [IPR025724] (1); Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1) | scaffold_5_mRNA_133.1 | C_unshiu_01127_mRNA_1.1 | - |
| GF0022351 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_1326.1 | C_unshiu_00899_mRNA_8.1 | - |
| GF0022350 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_1320.1 | C_unshiu_00797_mRNA_2.1 | - |
| GF0022349 | 1 | 1 | 0 | Hypothetical protein (2) | protein ubiquitination [GO:0016567 biological_process] (2); ubiquitin-protein transferase activity [GO:0004842 molecular_function] (2) | E3 ubiquitin ligase RBR family [IPR031127] (2) | scaffold_5_mRNA_132.1 | C_unshiu_00033_mRNA_34.1 | - |
| GF0022348 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_1316.1 | C_unshiu_00797_mRNA_6.1 | - |
| GF0022347 | 1 | 1 | 0 | Hypothetical protein (2) | | Domain of unknown function DUF4283 [IPR025558] (2) | scaffold_5_mRNA_1314.1 | C_unshiu_00797_mRNA_8.1 | - |
| GF0022346 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_13.1 | C_unshiu_00230_mRNA_34.1 | - |
| GF0022345 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_1294.1 | C_unshiu_00800_mRNA_11.1 | - |
| GF0022344 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_1289.1 | C_unshiu_00868_mRNA_1.1 | - |
| GF0022343 | 1 | 1 | 0 | Hypothetical protein (2) | | Ribokinase-like [IPR029056] (2); Carbohydrate kinase PfkB [IPR011611] (2) | scaffold_5_mRNA_1287.1 | C_unshiu_01520_mRNA_7.1 | - |
| GF0022342 | 1 | 1 | 0 | Hypothetical protein (2) | DNA binding [GO:0003677 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (1) | Zinc finger, BED-type [IPR003656] (2); Zinc finger C2H2-type [IPR013087] (1) | scaffold_5_mRNA_1277.1 | C_unshiu_00899_mRNA_13.1 | - |
| GF0022339 | 1 | 1 | 0 | Hypothetical protein (2) | | Endonuclease/exonuclease/phosphatase [IPR005135] (1) | scaffold_5_mRNA_1264.1 | C_unshiu_00340_mRNA_10.1 | - |
| GF0022338 | 1 | 1 | 0 | BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 (2) | | Leucine-rich repeat domain, L domain-like [IPR032675] (2); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (2) | scaffold_5_mRNA_1249.1 | C_unshiu_01099_mRNA_10.1 | - |
| GF0022337 | 1 | 1 | 0 | Theobromine synthase (2) | methyltransferase activity [GO:0008168 molecular_function] (2) | SAM dependent carboxyl methyltransferase [IPR005299] (2); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (2) | scaffold_5_mRNA_1247.1 | C_unshiu_01099_mRNA_8.1 | - |
| GF0022336 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_1241.1 | C_unshiu_02114_mRNA_6.1 | - |
| GF0022335 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_1240.1 | C_unshiu_02114_mRNA_5.1 | - |
| GF0022334 | 1 | 1 | 0 | Putative disease resistance protein RGA3 (2) | ADP binding [GO:0043531 molecular_function] (2) | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); NB-ARC [IPR002182] (2); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1) | scaffold_5_mRNA_1231.1 | C_unshiu_00803_mRNA_2.1 | - |
| GF0022332 | 1 | 1 | 0 | Hypothetical protein (2) | | Domain of unknown function DUF4371 [IPR025398] (2) | scaffold_5_mRNA_1222.1 | C_unshiu_00097_mRNA_9.1 | - |
| GF0022331 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_5_mRNA_1219.1 | C_unshiu_00468_mRNA_2.1 | - |
| GF0022330 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_1216.1 | C_unshiu_02642_mRNA_1.1 | - |
| GF0022329 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_1206.1 | C_unshiu_01426_mRNA_5.1 | - |
| GF0022327 | 1 | 1 | 0 | Hypothetical protein (2) | ADP binding [GO:0043531 molecular_function] (2) | NB-ARC [IPR002182] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2) | scaffold_5_mRNA_1180.1 | C_unshiu_01092_mRNA_7.1 | - |
| GF0022326 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_1169.1 | C_unshiu_03105_mRNA_1.1 | - |
| GF0022324 | 1 | 1 | 0 | NB-ARC domain disease resistance protein (1); NB-ARC domain-containing disease resistance protein (1) | ADP binding [GO:0043531 molecular_function] (2) | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); NB-ARC [IPR002182] (2); Protein RETICULATA-related [IPR021825] (1) | scaffold_5_mRNA_1161.1 | C_unshiu_00803_mRNA_3.1 | - |
| GF0022323 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_116.1 | C_unshiu_00151_mRNA_4.1 | - |
| GF0022322 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_1154.1 | C_unshiu_01250_mRNA_1.1 | - |
| GF0022320 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_1134.1 | C_unshiu_00699_mRNA_15.1 | - |
| GF0022319 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_1101.1 | C_unshiu_00825_mRNA_7.1 | - |
| GF0022318 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_1100.1 | C_unshiu_00825_mRNA_6.1 | - |
| GF0022317 | 1 | 1 | 0 | Hypothetical protein (2) | 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_110.1 | C_unshiu_00103_mRNA_14.1 | - |
| GF0022316 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_11.1 | C_unshiu_00230_mRNA_33.1 | - |
| GF0022315 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_1097.1 | C_unshiu_00564_mRNA_24.1 | - |
| GF0022314 | 1 | 1 | 0 | Myrcene synthase (1); Hypothetical protein (1) | magnesium ion binding [GO:0000287 molecular_function] (2); terpene synthase activity [GO:0010333 molecular_function] (2); lyase activity [GO:0016829 molecular_function] (2) | Isoprenoid synthase domain [IPR008949] (2); Terpene synthase, metal-binding domain [IPR005630] (2) | scaffold_5_mRNA_1095.1 | C_unshiu_00564_mRNA_21.1 | - |
| GF0022313 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_1094.1 | C_unshiu_00564_mRNA_20.1 | - |
| GF0022312 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_1092.1 | C_unshiu_00564_mRNA_18.1 | - |
| GF0022311 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_1090.1 | C_unshiu_00564_mRNA_16.1 | - |
| GF0022310 | 1 | 1 | 0 | Putative retroelement pol polyprotein (2) | | Gag-polypeptide of LTR copia-type [IPR029472] (2) | scaffold_5_mRNA_1088.1 | C_unshiu_00564_mRNA_14.1 | - |
| GF0022309 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_1087.1 | C_unshiu_00564_mRNA_13.1 | - |
| GF0022308 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_1085.1 | C_unshiu_00564_mRNA_12.1 | - |
| GF0022307 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_1080.1 | C_unshiu_00204_mRNA_19.1 | - |
| GF0022306 | 1 | 1 | 0 | Limonene synthase (2) | terpene synthase activity [GO:0010333 molecular_function] (2); lyase activity [GO:0016829 molecular_function] (2); magnesium ion binding [GO:0000287 molecular_function] (2); metabolic process [GO:0008152 biological_process] (2) | Terpene synthase, N-terminal domain [IPR001906] (2); Terpene synthase, metal-binding domain [IPR005630] (2); Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (2); Isoprenoid synthase domain [IPR008949] (2) | scaffold_5_mRNA_1079.1 | C_unshiu_00204_mRNA_18.1 | - |
| GF0022305 | 1 | 1 | 0 | Putative Tam1 transposon protein TNP2 (2) | | Domain of unknown function DUF4216 [IPR025312] (2); Transposon, En/Spm-like [IPR004242] (2); Probable transposase, Ptta/En/Spm, plant [IPR004252] (1); Transposase-associated domain [IPR029480] (1) | scaffold_5_mRNA_1073.1 | C_unshiu_00204_mRNA_11.1 | - |
| GF0022304 | 1 | 1 | 0 | Hypothetical protein (2) | | Leucine-rich repeat domain, L domain-like [IPR032675] (1) | scaffold_5_mRNA_1070.1 | C_unshiu_00753_mRNA_10.1 | - |
| GF0022303 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_107.1 | C_unshiu_00284_mRNA_6.1 | - |
| GF0022302 | 1 | 1 | 0 | F-box/LRR-repeat protein At3g26922 (2) | protein binding [GO:0005515 molecular_function] (2) | Leucine-rich repeat domain, L domain-like [IPR032675] (2); F-box domain [IPR001810] (2) | scaffold_5_mRNA_1062.1 | C_unshiu_01132_mRNA_11.1 | - |
| GF0022301 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_1058.1 | C_unshiu_01624_mRNA_6.1 | - |
| GF0022300 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_1057.1 | C_unshiu_01624_mRNA_5.1 | - |
| GF0022299 | 1 | 1 | 0 | Hypothetical protein (1); Caffeic acid 3-O-methyltransferase (1) | methyltransferase activity [GO:0008168 molecular_function] (2); O-methyltransferase activity [GO:0008171 molecular_function] (2); protein dimerization activity [GO:0046983 molecular_function] (1) | S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (2); Domain of unknown function DUF4371 [IPR025398] (2); O-methyltransferase COMT-type [IPR016461] (2); O-methyltransferase, family 2 [IPR001077] (2); Plant methyltransferase dimerisation [IPR012967] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1) | scaffold_5_mRNA_1052.1 | C_unshiu_01148_mRNA_5.1 | - |
| GF0022298 | 1 | 1 | 0 | Hypothetical protein (2) | O-methyltransferase activity [GO:0008171 molecular_function] (2); methyltransferase activity [GO:0008168 molecular_function] (1) | S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (2); O-methyltransferase, family 2 [IPR001077] (2); O-methyltransferase COMT-type [IPR016461] (1) | scaffold_5_mRNA_1050.1 | C_unshiu_01148_mRNA_7.1 | - |
| GF0022297 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_1048.1 | C_unshiu_00989_mRNA_10.1 | - |
| GF0022296 | 1 | 1 | 0 | Putative oxidoreductase GLYR1 (2) | phosphogluconate dehydrogenase (decarboxylating) activity [GO:0004616 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2); oxidoreductase activity [GO:0016491 molecular_function] (2); NAD binding [GO:0051287 molecular_function] (2) | 6-phosphogluconate dehydrogenase, domain 2 [IPR013328] (2); 6-phosphogluconate dehydrogenase C-terminal domain-like [IPR008927] (2); 3-hydroxyisobutyrate dehydrogenase, NAD-binding domain [IPR029154] (2); 6-phosphogluconate dehydrogenase, NADP-binding [IPR006115] (2); NAD(P)-binding domain [IPR016040] (2) | scaffold_5_mRNA_1047.1 | C_unshiu_00989_mRNA_9.1 | - |
| GF0022295 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_5_mRNA_1044.1 | C_unshiu_00989_mRNA_6.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0022294 | 1 | 1 | 0 | Hypothetical protein (2) | COPII vesicle coat [GO:0030127 cellular_component] (2); zinc ion binding [GO:0008270 molecular_function] (2); intracellular protein transport [GO:0006886 biological_process] (2); ER to Golgi vesicle-mediated transport [GO:0006888 biological_process] (2) | Zinc finger, Sec23/Sec24-type [IPR006895] (2); von Willebrand factor, type A [IPR002035] (2); Sec23/Sec24, trunk domain [IPR006896] (2); ADF-H/Gelsolin-like domain [IPR029006] (2); Gelsolin-like domain [IPR007123] (2) | scaffold_5_mRNA_1040.1 | C_unshiu_00989_mRNA_2.1 | - |
| GF0022292 | 1 | 1 | 0 | Hypothetical protein (2) | | Gag-polypeptide of LTR copia-type [IPR029472] (1) | scaffold_5_mRNA_1027.1 | C_unshiu_00946_mRNA_8.1 | - |
| GF0022291 | 1 | 1 | 0 | Hypothetical protein (2) | | LOG family [IPR031100] (2) | scaffold_5_mRNA_1025.1 | C_unshiu_00946_mRNA_10.1 | - |
| GF0022290 | 1 | 1 | 0 | Hypothetical protein (2) | | Domain of unknown function DUF4283 [IPR025558] (2) | scaffold_5_mRNA_1024.1 | C_unshiu_00946_mRNA_11.1 | - |
| GF0022289 | 1 | 1 | 0 | Ribonuclease H (2) | nucleic acid binding [GO:0003676 molecular_function] (2); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (2) | Ribonuclease H domain [IPR002156] (2); Ribonuclease H-like domain [IPR012337] (2); TB2/DP1/HVA22-related protein [IPR004345] (1) | scaffold_5_mRNA_1020.1 | C_unshiu_00946_mRNA_14.1 | - |
| GF0022288 | 1 | 1 | 0 | Hypothetical protein (2) | | S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (2) | scaffold_5_mRNA_102.1 | C_unshiu_02888_mRNA_1.1 | - |
| GF0022286 | 1 | 1 | 0 | Hypothetical protein (2) | zinc ion binding [GO:0008270 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | Zinc finger, CCHC-type [IPR001878] (2); Domain of unknown function DUF4283 [IPR025558] (2) | scaffold_5_mRNA_1009.1 | C_unshiu_00083_mRNA_14.1 | - |
| GF0022285 | 1 | 1 | 0 | Hypothetical protein (2) | | Transposon, En/Spm-like [IPR004242] (2); Transposase-associated domain [IPR029480] (2) | scaffold_5_mRNA_1002.1 | C_unshiu_00083_mRNA_17.1 | - |
| GF0022284 | 1 | 1 | 0 | Lysosomal Pro-Xaa carboxypeptidase (2) | proteolysis [GO:0006508 biological_process] (2); serine-type peptidase activity [GO:0008236 molecular_function] (2) | Alpha/Beta hydrolase fold [IPR029058] (2); Peptidase S28 [IPR008758] (2) | scaffold_4_mRNA_999.1 | C_unshiu_01189_mRNA_5.1 | - |
| GF0022283 | 1 | 1 | 0 | Hypothetical protein (2) | serine-type peptidase activity [GO:0008236 molecular_function] (2); proteolysis [GO:0006508 biological_process] (2) | Peptidase S28 [IPR008758] (2) | scaffold_4_mRNA_997.1 | C_unshiu_01189_mRNA_3.1 | - |
| GF0022282 | 1 | 1 | 0 | LRR receptor-like kinase family protein (2) | ATP binding [GO:0005524 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2); protein kinase activity [GO:0004672 molecular_function] (2); protein binding [GO:0005515 molecular_function] (2) | Protein kinase domain [IPR000719] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Protein kinase-like domain [IPR011009] (2); Leucine-rich repeat, typical subtype [IPR003591] (2); Protein kinase, ATP binding site [IPR017441] (2); Tyrosine-protein kinase, active site [IPR008266] (2); Leucine-rich repeat [IPR001611] (2); Concanavalin A-like lectin/glucanase domain [IPR013320] (1) | scaffold_4_mRNA_995.1 | C_unshiu_01189_mRNA_1.1 | - |
| GF0022281 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_984.1 | C_unshiu_00715_mRNA_2.1 | - |
| GF0022280 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (1) | Zinc finger C2H2-type [IPR013087] (1) | scaffold_4_mRNA_983.1 | C_unshiu_00715_mRNA_3.1 | - |
| GF0022279 | 1 | 1 | 0 | LRR receptor-like kinase family protein (2) | ATP binding [GO:0005524 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2); protein kinase activity [GO:0004672 molecular_function] (2); protein binding [GO:0005515 molecular_function] (1) | Protein kinase, ATP binding site [IPR017441] (2); Protein kinase domain [IPR000719] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Protein kinase-like domain [IPR011009] (2); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1) | scaffold_4_mRNA_981.1 | C_unshiu_00715_mRNA_4.1 | - |
| GF0022278 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_980.1 | C_unshiu_00715_mRNA_5.1 | - |
| GF0022277 | 1 | 1 | 0 | Hypothetical leucine rich repeat protein (2) | protein binding [GO:0005515 molecular_function] (2) | Leucine-rich repeat domain, L domain-like [IPR032675] (2); Leucine-rich repeat [IPR001611] (2) | scaffold_4_mRNA_977.1 | C_unshiu_00715_mRNA_8.1 | - |
| GF0022276 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_974.1 | C_unshiu_00715_mRNA_11.1 | - |
| GF0022275 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_973.1 | C_unshiu_00715_mRNA_12.1 | - |
| GF0022274 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_971.1 | C_unshiu_00715_mRNA_14.1 | - |
| GF0022271 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_950.1 | C_unshiu_00013_mRNA_72.1 | - |
| GF0022270 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_943.1 | C_unshiu_00013_mRNA_61.1 | - |
| GF0022269 | 1 | 1 | 0 | Hypothetical protein (2) | | Domain of unknown function DUF1985 [IPR015410] (2) | scaffold_4_mRNA_942.1 | C_unshiu_00013_mRNA_60.1 | - |
| GF0022268 | 1 | 1 | 0 | Hypothetical protein (2) | GTPase activity [GO:0003924 molecular_function] (2); GTP binding [GO:0005525 molecular_function] (2); protein transport [GO:0015031 biological_process] (1); intracellular protein transport [GO:0006886 biological_process] (1); intracellular [GO:0005622 cellular_component] (1); signal transduction [GO:0007165 biological_process] (1); membrane [GO:0016020 cellular_component] (1); nucleocytoplasmic transport [GO:0006913 biological_process] (1); small GTPase mediated signal transduction [GO:0007264 biological_process] (1) | Sigma-54 interaction domain, ATP-binding site 1 [IPR025662] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); Small GTPase superfamily [IPR001806] (2); Small GTP-binding protein domain [IPR005225] (2); Small GTPase superfamily, Rab type [IPR003579] (1); Small GTPase superfamily, ARF type [IPR024156] (1); Ran GTPase [IPR002041] (1); Small GTPase superfamily, Rho type [IPR003578] (1); Small GTPase superfamily, Ras type [IPR020849] (1) | scaffold_4_mRNA_941.1 | C_unshiu_00013_mRNA_59.1 | - |
| GF0022267 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_940.1 | C_unshiu_00013_mRNA_58.1 | - |
| GF0022266 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_938.1 | C_unshiu_00013_mRNA_56.1 | - |
| GF0022265 | 1 | 1 | 0 | Hypothetical protein (2) | | Domain of unknown function DUF4283 [IPR025558] (2) | scaffold_4_mRNA_926.1 | C_unshiu_00013_mRNA_44.1 | - |
| GF0022264 | 1 | 1 | 0 | Putative transporter MCH1 (2) | | Nodulin-like [IPR010658] (2); Major facilitator superfamily domain [IPR020846] (2) | scaffold_4_mRNA_921.1 | C_unshiu_00013_mRNA_41.1 | - |
| GF0022263 | 1 | 1 | 0 | Putative calcium-binding protein CML15 (2) | calcium ion binding [GO:0005509 molecular_function] (2) | EF-hand domain [IPR002048] (2); EF-Hand 1, calcium-binding site [IPR018247] (2); EF-hand domain pair [IPR011992] (2) | scaffold_4_mRNA_92.1 | C_unshiu_00202_mRNA_13.1 | - |
| GF0022262 | 1 | 1 | 0 | Hypothetical protein (2) | | Domain of unknown function DUF4283 [IPR025558] (1) | scaffold_4_mRNA_909.1 | C_unshiu_00013_mRNA_29.1 | - |
| GF0022261 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_900.1 | C_unshiu_00013_mRNA_18.1 | - |
| GF0022260 | 1 | 1 | 0 | Hypothetical protein (2) | proteolysis [GO:0006508 biological_process] (2); cysteine-type peptidase activity [GO:0008234 molecular_function] (2) | Ulp1 protease family, C-terminal catalytic domain [IPR003653] (2) | scaffold_4_mRNA_898.1 | C_unshiu_00013_mRNA_16.1 | - |
| GF0022258 | 1 | 1 | 0 | Hypothetical protein (2) | | Leucine-rich repeat domain, L domain-like [IPR032675] (2) | scaffold_4_mRNA_892.1 | C_unshiu_00013_mRNA_12.1 | - |
| GF0022257 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_887.1 | C_unshiu_00013_mRNA_6.1 | - |
| GF0022256 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_879.1 | C_unshiu_00280_mRNA_31.1 | - |
| GF0022254 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_873.1 | C_unshiu_00280_mRNA_25.1 | - |
| GF0022253 | 1 | 1 | 0 | LRR receptor-like kinase family protein (2) | protein binding [GO:0005515 molecular_function] (2); protein kinase activity [GO:0004672 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2); ATP binding [GO:0005524 molecular_function] (2) | Leucine-rich repeat domain, L domain-like [IPR032675] (2); Protein kinase-like domain [IPR011009] (2); Leucine-rich repeat, typical subtype [IPR003591] (2); Protein kinase domain [IPR000719] (2); Leucine-rich repeat [IPR001611] (2); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (2); Protein kinase, ATP binding site [IPR017441] (2); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1) | scaffold_4_mRNA_871.1 | C_unshiu_00280_mRNA_22.1 | - |
| GF0022252 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_870.1 | C_unshiu_00280_mRNA_21.1 | - |
| GF0022251 | 1 | 1 | 0 | LRR receptor-like kinase family protein (2) | protein binding [GO:0005515 molecular_function] (2); protein kinase activity [GO:0004672 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2); ATP binding [GO:0005524 molecular_function] (2) | Leucine-rich repeat, typical subtype [IPR003591] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Protein kinase-like domain [IPR011009] (2); Protein kinase domain [IPR000719] (2); Leucine-rich repeat [IPR001611] (2); Protein kinase, ATP binding site [IPR017441] (2); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (2); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1) | scaffold_4_mRNA_869.1 | C_unshiu_00280_mRNA_20.1 | - |
| GF0022250 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_866.1 | C_unshiu_03100_mRNA_1.1 | - |
| GF0022249 | 1 | 1 | 0 | Hypothetical protein (2) | cysteine-type peptidase activity [GO:0008234 molecular_function] (2); proteolysis [GO:0006508 biological_process] (2) | Ulp1 protease family, C-terminal catalytic domain [IPR003653] (2); Domain of unknown function DUF1985 [IPR015410] (2) | scaffold_4_mRNA_863.1 | C_unshiu_00258_mRNA_38.1 | - |
| GF0022248 | 1 | 1 | 0 | Hypothetical protein (2) | | MULE transposase domain [IPR018289] (2); Transposase, MuDR, plant [IPR004332] (2) | scaffold_4_mRNA_862.1 | C_unshiu_00258_mRNA_37.1 | - |
| GF0022247 | 1 | 1 | 0 | Hypothetical protein (2) | DNA binding [GO:0003677 molecular_function] (2); protein dimerization activity [GO:0046983 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (1) | Zinc finger, BED-type [IPR003656] (2); HAT, C-terminal dimerisation domain [IPR008906] (2); Zinc finger C2H2-type [IPR013087] (1) | scaffold_4_mRNA_861.1 | C_unshiu_00258_mRNA_35.1 | - |
| GF0022246 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_860.1 | C_unshiu_00258_mRNA_34.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0022245 | 1 | 1 | 0 | Hypothetical protein (2) | | Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (2); LOG family [IPR031100] (2) | scaffold_4_mRNA_845.1 | C_unshiu_00258_mRNA_19.1 | - |
| GF0022244 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_842.1 | C_unshiu_00258_mRNA_15.1 | - |
| GF0022243 | 1 | 1 | 0 | Hypothetical protein (2) | ATP binding [GO:0005524 molecular_function] (2); protein kinase activity [GO:0004672 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2) | Protein kinase-like domain [IPR011009] (2); Protein kinase domain [IPR000719] (2) | scaffold_4_mRNA_841.1 | C_unshiu_00258_mRNA_14.1 | - |
| GF0022242 | 1 | 1 | 0 | Hypothetical protein (2) | cysteine-type peptidase activity [GO:0008234 molecular_function] (2); proteolysis [GO:0006508 biological_process] (2) | Ulp1 protease family, C-terminal catalytic domain [IPR003653] (2) | scaffold_4_mRNA_836.1 | C_unshiu_00258_mRNA_9.1 | - |
| GF0022241 | 1 | 1 | 0 | OTU domain-containing (2) | | OTU domain [IPR003323] (2) | scaffold_4_mRNA_833.1 | C_unshiu_00210_mRNA_2.1 | - |
| GF0022240 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_832.1 | C_unshiu_00210_mRNA_3.1 | - |
| GF0022238 | 1 | 1 | 0 | Hypothetical protein (2) | | GroEL-like equatorial domain [IPR027413] (1) | scaffold_4_mRNA_817.1 | C_unshiu_00210_mRNA_17.1 | - |
| GF0022237 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_807.1 | C_unshiu_01202_mRNA_10.1 | - |
| GF0022236 | 1 | 1 | 0 | Hypothetical protein (2) | | Gag-polypeptide of LTR copia-type [IPR029472] (1) | scaffold_4_mRNA_792.1 | C_unshiu_00607_mRNA_11.1 | - |
| GF0022235 | 1 | 1 | 0 | Caffeic acid O-methyltransferase (1); Caffeic acid 3-O-methyltransferase (1) | O-methyltransferase activity [GO:0008171 molecular_function] (2); methyltransferase activity [GO:0008168 molecular_function] (2) | S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (2); O-methyltransferase, family 2 [IPR001077] (2); O-methyltransferase COMT-type [IPR016461] (2) | scaffold_4_mRNA_785.1 | C_unshiu_00607_mRNA_18.1 | - |
| GF0022234 | 1 | 1 | 0 | Hypothetical protein (2) | cell redox homeostasis [GO:0045454 biological_process] (2) | Thioredoxin-like fold [IPR012336] (2); Thioredoxin domain [IPR013766] (2) | scaffold_4_mRNA_784.1 | C_unshiu_00607_mRNA_19.1 | - |
| GF0022233 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_770.1 | C_unshiu_01214_mRNA_8.1 | - |
| GF0022232 | 1 | 1 | 0 | Lupeol synthase (2) | intramolecular transferase activity [GO:0016866 molecular_function] (2) | Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (2); Squalene cyclase, C-terminal [IPR032696] (2); Terpene synthase, conserved site [IPR002365] (2); Squalene cyclase [IPR018333] (1) | scaffold_4_mRNA_739.1 | C_unshiu_00872_mRNA_10.1 | - |
| GF0022230 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_730.1 | C_unshiu_02901_mRNA_1.1 | - |
| GF0022229 | 1 | 1 | 0 | Hypothetical protein (2) | | MULE transposase domain [IPR018289] (2) | scaffold_4_mRNA_724.1 | C_unshiu_01019_mRNA_17.1 | - |
| GF0022228 | 1 | 1 | 0 | Hypothetical protein (2) | DNA binding [GO:0003677 molecular_function] (2); transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (2); regulation of transcription, DNA-templated [GO:0006355 biological_process] (2) | AP2/ERF domain [IPR001471] (2); DNA-binding domain [IPR016177] (2) | scaffold_4_mRNA_716.1 | C_unshiu_00872_mRNA_4.1 | - |
| GF0022227 | 1 | 1 | 0 | CemA-like proton extrusion protein-related isoform 1 (1); Envelope membrane protein, chloroplastic (1) | integral component of membrane [GO:0016021 cellular_component] (2) | Chloroplast envelope membrane protein, CemA [IPR004282] (2) | scaffold_4_mRNA_712.1 | C_unshiu_00177_mRNA_26.1 | - |
| GF0022226 | 1 | 1 | 0 | Nucleolar protein 56 (1); SAR DNA-binding protein-1 (1) | protein binding [GO:0005515 molecular_function] (1) | Nop domain [IPR002687] (2); NOSIC [IPR012976] (2); NOP5, N-terminal [IPR012974] (2); WD40/YVTN repeat-like-containing domain [IPR015943] (1) | scaffold_4_mRNA_711.1 | C_unshiu_00177_mRNA_25.1 | - |
| GF0022225 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_701.1 | C_unshiu_02892_mRNA_1.1 | - |
| GF0022224 | 1 | 1 | 0 | Leucine-rich repeat protein kinase family protein, putative (1); LRR receptor-like serine/threonine-protein kinase FLS2 (1) | protein binding [GO:0005515 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1) | Leucine-rich repeat, typical subtype [IPR003591] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Protein kinase-like domain [IPR011009] (2); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (2); Leucine-rich repeat [IPR001611] (2); Protein kinase domain [IPR000719] (1); Protein kinase, ATP binding site [IPR017441] (1); Serine/threonine-protein kinase, active site [IPR008271] (1) | scaffold_4_mRNA_699.1 | C_unshiu_00125_mRNA_12.1 | - |
| GF0022223 | 1 | 1 | 0 | GDSL esterase/lipase At5g45670 (1); GDSL-like Lipase/Acylhydrolase superfamily protein, putative isoform 1 (1) | hydrolase activity, acting on ester bonds [GO:0016788 molecular_function] (1) | SGNH hydrolase-type esterase domain [IPR013830] (2); GDSL lipase/esterase [IPR001087] (1) | scaffold_4_mRNA_695.1 | C_unshiu_01102_mRNA_5.1 | - |
| GF0022222 | 1 | 1 | 0 | Hypothetical protein (2) | | SGNH hydrolase-type esterase domain [IPR013830] (1) | scaffold_4_mRNA_693.1 | C_unshiu_00616_mRNA_19.1 | - |
| GF0022221 | 1 | 1 | 0 | GDSL-motif lipase 7 (2) | hydrolase activity, acting on ester bonds [GO:0016788 molecular_function] (2) | GDSL lipase/esterase [IPR001087] (2); SGNH hydrolase-type esterase domain [IPR013830] (2) | scaffold_4_mRNA_689.1 | C_unshiu_00616_mRNA_16.1 | - |
| GF0022218 | 1 | 1 | 0 | Hypothetical protein (1); Leucine-rich repeat protein kinase family protein (1) | protein binding [GO:0005515 molecular_function] (2) | Leucine-rich repeat, typical subtype [IPR003591] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Leucine-rich repeat [IPR001611] (2); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (2) | scaffold_4_mRNA_670.1 | C_unshiu_00892_mRNA_1.1 | - |
| GF0022215 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_645.1 | C_unshiu_01966_mRNA_4.1 | - |
| GF0022214 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_633.1 | C_unshiu_00794_mRNA_3.1 | - |
| GF0022213 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_626.1 | C_unshiu_00794_mRNA_6.4 | - |
| GF0022212 | 1 | 1 | 0 | Hypothetical protein (2) | | Thioredoxin-like fold [IPR012336] (2) | scaffold_4_mRNA_622.1 | C_unshiu_00794_mRNA_8.1 | - |
| GF0022210 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_613.1 | C_unshiu_01014_mRNA_4.1 | - |
| GF0022209 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_612.1 | C_unshiu_01014_mRNA_5.1 | - |
| GF0022208 | 1 | 1 | 0 | Hypothetical protein (2) | | Thioredoxin-like fold [IPR012336] (2) | scaffold_4_mRNA_610.1 | C_unshiu_01014_mRNA_6.1 | - |
| GF0022207 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_609.1 | C_unshiu_01014_mRNA_16.1 | - |
| GF0022206 | 1 | 1 | 0 | Hypothetical protein (2) | | Thioredoxin-like fold [IPR012336] (2) | scaffold_4_mRNA_602.1 | C_unshiu_01014_mRNA_10.1 | - |
| GF0022205 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_600.1 | C_unshiu_02795_mRNA_2.1 | - |
| GF0022204 | 1 | 1 | 0 | SUMO-conjugating enzyme ubc9 (2) | | | scaffold_4_mRNA_59.1 | C_unshiu_00168_mRNA_16.1 | - |
| GF0022203 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_587.1 | C_unshiu_00306_mRNA_11.1 | - |
| GF0022202 | 1 | 1 | 0 | Hypothetical protein (2) | | Domain of unknown function DUF4283 [IPR025558] (2); Zinc knuckle CX2CX4HX4C [IPR025836] (2) | scaffold_4_mRNA_581.1 | C_unshiu_00306_mRNA_17.1 | - |
| GF0022201 | 1 | 1 | 0 | Hypothetical protein (2) | | Protein kinase-like domain [IPR011009] (1) | scaffold_4_mRNA_579.1 | C_unshiu_00306_mRNA_20.1 | - |
| GF0022199 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_565.1 | C_unshiu_00306_mRNA_33.1 | - |
| GF0022198 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_551.1 | C_unshiu_00236_mRNA_20.1 | - |
| GF0022197 | 1 | 1 | 0 | Hypothetical protein (2) | catalytic activity [GO:0003824 molecular_function] (1) | Polymerase/histidinol phosphatase-like [IPR016195] (1) | scaffold_4_mRNA_545.1 | C_unshiu_00236_mRNA_25.1 | - |
| GF0022196 | 1 | 1 | 0 | Mutator-like transposase (2) | | MULE transposase domain [IPR018289] (2); Transposase, MuDR, plant [IPR004332] (2) | scaffold_4_mRNA_534.1 | C_unshiu_00236_mRNA_36.1 | - |
| GF0022195 | 1 | 1 | 0 | Hypothetical protein (2) | | Transposase, MuDR, plant [IPR004332] (2) | scaffold_4_mRNA_523.1 | C_unshiu_00022_mRNA_106.1 | - |
| GF0022194 | 1 | 1 | 0 | Hypothetical protein (2) | | Domain of unknown function DUF1985 [IPR015410] (2) | scaffold_4_mRNA_522.1 | C_unshiu_00022_mRNA_105.1 | - |
| GF0022193 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_519.1 | C_unshiu_00022_mRNA_103.1 | - |
| GF0022192 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_517.1 | C_unshiu_00022_mRNA_101.1 | - |
| GF0022191 | 1 | 1 | 0 | TIGR01456 family HAD hydrolase (2) | | HAD-like domain [IPR023214] (2) | scaffold_4_mRNA_513.1 | C_unshiu_00022_mRNA_97.1 | - |
| GF0022190 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_494.1 | C_unshiu_02521_mRNA_2.1 | - |
| GF0022189 | 1 | 1 | 0 | Receptor-like protein kinase HERK 1 (2) | ATP binding [GO:0005524 molecular_function] (2); protein kinase activity [GO:0004672 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2) | Protein kinase-like domain [IPR011009] (2); Malectin-like carbohydrate-binding domain [IPR024788] (2); Protein kinase domain [IPR000719] (2); Protein kinase, ATP binding site [IPR017441] (2); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1) | scaffold_4_mRNA_487.1 | C_unshiu_00465_mRNA_13.1 | - |
| GF0022186 | 1 | 1 | 0 | Hypothetical protein (2) | cysteine-type peptidase activity [GO:0008234 molecular_function] (2); proteolysis [GO:0006508 biological_process] (2) | Ulp1 protease family, C-terminal catalytic domain [IPR003653] (2) | scaffold_4_mRNA_471.1 | C_unshiu_00342_mRNA_25.1 | - |
| GF0022185 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_457.1 | C_unshiu_00342_mRNA_12.1 | - |
| GF0022184 | 1 | 1 | 0 | Hypothetical protein (2) | | Protein of unknown function DUF674 [IPR007750] (2) | scaffold_4_mRNA_449.1 | C_unshiu_00342_mRNA_5.1 | - |
| GF0022183 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_448.1 | C_unshiu_00342_mRNA_4.1 | - |
| GF0022182 | 1 | 1 | 0 | DUF674 family protein (2) | | Protein of unknown function DUF674 [IPR007750] (2) | scaffold_4_mRNA_447.1 | C_unshiu_00342_mRNA_3.1 | - |
| GF0022181 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_443.1 | C_unshiu_00832_mRNA_2.1 | - |
| GF0022180 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_427.1 | C_unshiu_00832_mRNA_19.1 | - |
| GF0022179 | 1 | 1 | 0 | Nodulin MtN21/EamA-like transporter family protein (2) | membrane [GO:0016020 cellular_component] (2); transmembrane transporter activity [GO:0022857 molecular_function] (2); integral component of membrane [GO:0016021 cellular_component] (2) | WAT1-related protein [IPR030184] (2); EamA domain [IPR000620] (2) | scaffold_4_mRNA_422.1 | C_unshiu_00368_mRNA_14.1 | - |
| GF0022177 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_397.1 | C_unshiu_01865_mRNA_6.1 | - |
| GF0022176 | 1 | 1 | 0 | Putative sugar phosphate/phosphate translocator (2) | ribosome [GO:0005840 cellular_component] (2); structural constituent of ribosome [GO:0003735 molecular_function] (2); translation [GO:0006412 biological_process] (2); intracellular [GO:0005622 cellular_component] (2) | Ribosomal protein L35A [IPR001780] (2); Sugar phosphate transporter domain [IPR004853] (2); Ribosomal protein L35Ae, conserved site [IPR018266] (2); Translation protein, beta-barrel domain [IPR009000] (2) | scaffold_4_mRNA_39.1 | C_unshiu_00168_mRNA_32.1 | - |
| GF0022175 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_385.1 | C_unshiu_00439_mRNA_22.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0022174 | 1 | 1 | 0 | Cysteine/histidine-rich C1 domain protein (2) | intracellular signal transduction [GO:0035556 biological_process] (2); oxidation-reduction process [GO:0055114 biological_process] (1); protein-disulfide reductase activity [GO:0047134 molecular_function] (1) | Protein kinase C-like, phorbol ester/diacylglycerol-binding domain [IPR002219] (2); DC1 [IPR004146] (1); C1-like [IPR011424] (1) | scaffold_4_mRNA_374.1 | C_unshiu_00439_mRNA_10.1 | - |
| GF0022172 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_368.1 | C_unshiu_00439_mRNA_4.1 | - |
| GF0022171 | 1 | 1 | 0 | Hypothetical protein (2) | | X8 domain [IPR012946] (2) | scaffold_4_mRNA_367.1 | C_unshiu_00439_mRNA_3.1 | - |
| GF0022170 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_359.1 | C_unshiu_00979_mRNA_23.1 | - |
| GF0022169 | 1 | 1 | 0 | Thioredoxin H9 (2) | cell redox homeostasis [GO:0045454 biological_process] (2); glycerol ether metabolic process [GO:0006662 biological_process] (2); protein disulfide oxidoreductase activity [GO:0015035 molecular_function] (2) | Thioredoxin-like fold [IPR012336] (2); Thioredoxin domain [IPR013766] (2); Thioredoxin [IPR005746] (2) | scaffold_4_mRNA_346.1 | C_unshiu_00979_mRNA_10.1 | - |
| GF0022168 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_341.1 | C_unshiu_00979_mRNA_5.1 | - |
| GF0022163 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_3263.1 | C_unshiu_00001_mRNA_358.1 | - |
| GF0022161 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_325.1 | C_unshiu_00299_mRNA_34.1 | - |
| GF0022160 | 1 | 1 | 0 | G-type lectin S-receptor-like serine/threonine-protein kinase RLK1 (2) | ATP binding [GO:0005524 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2); protein kinase activity [GO:0004672 molecular_function] (2); protein serine/threonine kinase activity [GO:0004674 molecular_function] (2) | Bulb-type lectin domain [IPR001480] (2); Serine/threonine-protein kinase, active site [IPR008271] (2); Protein kinase, ATP binding site [IPR017441] (2); Protein kinase-like domain [IPR011009] (2); S-receptor-like serine/threonine-protein kinase [IPR024171] (2); Protein kinase domain [IPR000719] (2); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1) | scaffold_4_mRNA_3240.1 | C_unshiu_00001_mRNA_377.1 | - |
| GF0022159 | 1 | 1 | 0 | DEAD-box ATP-dependent RNA helicase (2) | nucleic acid binding [GO:0003676 molecular_function] (2); ATP binding [GO:0005524 molecular_function] (2) | Helicase superfamily 1/2, ATP-binding domain [IPR014001] (2); RNA helicase, DEAD-box type, Q motif [IPR014014] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); ATP-dependent RNA helicase DEAD-box, conserved site [IPR000629] (2); DEAD/DEAH box helicase domain [IPR011545] (2) | scaffold_4_mRNA_324.1 | C_unshiu_00299_mRNA_33.1 | - |
| GF0022158 | 1 | 1 | 0 | Hypothetical protein (1); Putative micronuclear linker histone polyprotein-like (1) | protein binding [GO:0005515 molecular_function] (2); protein-N-terminal asparagine amidohydrolase activity [GO:0008418 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1) | Bromodomain, conserved site [IPR018359] (2); Bromodomain [IPR001487] (2); Protein N-terminal asparagine amidohydrolase [IPR026750] (1); Homeobox domain-like [IPR009057] (1); SANT/Myb domain [IPR001005] (1) | scaffold_4_mRNA_3236.1 | C_unshiu_00001_mRNA_381.1 | - |
| GF0022157 | 1 | 1 | 0 | Homeobox-leucine zipper protein HAT14 (2) | DNA binding [GO:0003677 molecular_function] (2); sequence-specific DNA binding [GO:0043565 molecular_function] (2); regulation of transcription, DNA-templated [GO:0006355 biological_process] (2); transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (2) | Homeobox domain [IPR001356] (2); Leucine zipper, homeobox-associated [IPR003106] (2); Homeodomain-like [IPR009057] (1); Homeobox domain-like [IPR009057] (1) | scaffold_4_mRNA_3233.1 | C_unshiu_00001_mRNA_383.1 | - |
| GF0022156 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_3231.1 | C_unshiu_00001_mRNA_385.1 | - |
| GF0022155 | 1 | 1 | 0 | Non-LTR retroelement reverse transcriptase (1); Hypothetical protein (1) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2); Reverse transcriptase zinc-binding domain [IPR026960] (2); Endonuclease/exonuclease/phosphatase [IPR005135] (2); Vacuolar protein sorting-associated protein 62 [IPR009291] (1) | scaffold_4_mRNA_3218.1 | C_unshiu_00001_mRNA_400.1 | - |
| GF0022154 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_321.1 | C_unshiu_00299_mRNA_30.1 | - |
| GF0022152 | 1 | 1 | 0 | Two-component response regulator ARR3-like protein (2) | phosphorelay signal transduction system [GO:0000160 biological_process] (2) | CheY-like superfamily [IPR011006] (2); Signal transduction response regulator, receiver domain [IPR001789] (2) | scaffold_4_mRNA_320.1 | C_unshiu_00299_mRNA_29.1 | - |
| GF0022151 | 1 | 1 | 0 | Ras-related protein Rab11A (2) | GTP binding [GO:0005525 molecular_function] (2); GTPase activity [GO:0003924 molecular_function] (2); small GTPase mediated signal transduction [GO:0007264 biological_process] (1); nucleocytoplasmic transport [GO:0006913 biological_process] (1); membrane [GO:0016020 cellular_component] (1); signal transduction [GO:0007165 biological_process] (1); intracellular protein transport [GO:0006886 biological_process] (1); intracellular [GO:0005622 cellular_component] (1); protein transport [GO:0015031 biological_process] (1) | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); Small GTPase superfamily [IPR001806] (2); Small GTP-binding protein domain [IPR005225] (2); Small GTPase superfamily, Ras type [IPR020849] (1); Small GTPase superfamily, Rho type [IPR003578] (1); Small GTPase superfamily, ARF type [IPR024156] (1); Small GTPase superfamily, Rab type [IPR003579] (1); Ran GTPase [IPR002041] (1) | scaffold_4_mRNA_3195.1 | C_unshiu_00001_mRNA_317.1 | - |
| GF0022150 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_3193.1 | C_unshiu_00001_mRNA_315.1 | - |
| GF0022149 | 1 | 1 | 0 | Tocopherol O-methyltransferase (1); Sterol methyltransferase-like 3 (1) | methyltransferase activity [GO:0008168 molecular_function] (1); metabolic process [GO:0008152 biological_process] (1); steroid biosynthetic process [GO:0006694 biological_process] (1) | SAM-dependent methyltransferase SMT-type [IPR030384] (1); Methyltransferase type 11 [IPR013216] (1); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); Sterol methyltransferase C-terminal [IPR013705] (1) | scaffold_4_mRNA_3192.2 | C_unshiu_00001_mRNA_314.2 | - |
| GF0022147 | 1 | 1 | 0 | Auxin response factor (2) | regulation of transcription, DNA-templated [GO:0006355 biological_process] (2); response to hormone [GO:0009725 biological_process] (2); nucleus [GO:0005634 cellular_component] (2); DNA binding [GO:0003677 molecular_function] (2) | B3 DNA binding domain [IPR003340] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); DNA-binding pseudobarrel domain [IPR015300] (2); Auxin response factor [IPR010525] (2); Receptor L-domain [IPR000494] (1) | scaffold_4_mRNA_3177.1 | C_unshiu_00001_mRNA_299.1 | - |
| GF0022146 | 1 | 1 | 0 | Disease resistance protein (1); NB-ARC domain disease resistance protein (1) | ADP binding [GO:0043531 molecular_function] (1) | Leucine-rich repeat domain, L domain-like [IPR032675] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1) | scaffold_4_mRNA_3176.1 | C_unshiu_00001_mRNA_298.1 | - |
| GF0022143 | 1 | 1 | 0 | Purple acid phosphatase (2) | acid phosphatase activity [GO:0003993 molecular_function] (2); metal ion binding [GO:0046872 molecular_function] (2); hydrolase activity [GO:0016787 molecular_function] (2) | Purple acid phosphatase-like, N-terminal [IPR008963] (2); Metallo-dependent phosphatase-like [IPR029052] (2); Iron/zinc purple acid phosphatase-like C-terminal domain [IPR025733] (2); Purple acid phosphatase, N-terminal [IPR015914] (2); Calcineurin-like phosphoesterase domain, apaH type [IPR004843] (1); Neocarzinostatin-like [IPR027273] (1); Calcineurin-like phosphoesterase domain, ApaH type [IPR004843] (1) | scaffold_4_mRNA_3144.1 | C_unshiu_00001_mRNA_271.1 | - |
| GF0022142 | 1 | 1 | 0 | Cytochrome P450 (2) | iron ion binding [GO:0005506 molecular_function] (2); heme binding [GO:0020037 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (2) | Cytochrome P450, E-class, group I [IPR002401] (2); Cytochrome P450, conserved site [IPR017972] (2); Cytochrome P450 [IPR001128] (2) | scaffold_4_mRNA_314.1 | C_unshiu_00299_mRNA_23.1 | - |
| GF0022141 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_4_mRNA_3128.1 | C_unshiu_00001_mRNA_252.1 | - |
| GF0022140 | 1 | 1 | 0 | Putative polynucleotide adenylyltransferase family protein-like (1); Polynucleotide adenylyltransferase family protein (1) | | tRNA nucleotidyltransferase/poly(A) polymerase, RNA and SrmB- binding domain [IPR032828] (2) | scaffold_4_mRNA_3122.1 | C_unshiu_00001_mRNA_246.1 | - |
| GF0022138 | 1 | 1 | 0 | Somatic embryogenesis receptor kinase 1 (2) | protein binding [GO:0005515 molecular_function] (2); transmembrane receptor protein kinase activity [GO:0019199 molecular_function] (1) | Leucine-rich repeat domain, L domain-like [IPR032675] (2); Leucine-rich repeat [IPR001611] (2); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (2); Somatic embryogenesis receptor-like kinase [IPR031048] (1) | scaffold_4_mRNA_3109.1 | C_unshiu_00001_mRNA_233.1 | - |
| GF0022137 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_3102.1 | C_unshiu_00001_mRNA_228.1 | - |
| GF0022136 | 1 | 1 | 0 | Hypothetical protein (2) | catalytic activity [GO:0003824 molecular_function] (2) | Alanine racemase/group IV decarboxylase, C-terminal [IPR009006] (2); Orn/DAP/Arg decarboxylase 2, C-terminal [IPR022643] (2) | scaffold_4_mRNA_310.1 | C_unshiu_00299_mRNA_16.1 | - |
| GF0022135 | 1 | 1 | 0 | Hypothetical protein (2) | | Retrotransposon gag domain [IPR005162] (1) | scaffold_4_mRNA_31.1 | C_unshiu_00168_mRNA_38.1 | - |
| GF0022134 | 1 | 1 | 0 | SAUR family protein (2) | response to auxin [GO:0009733 biological_process] (1) | Small auxin-up RNA [IPR003676] (1) | scaffold_4_mRNA_3093.1 | C_unshiu_00001_mRNA_219.1 | - |
| GF0022133 | 1 | 1 | 0 | Hypothetical protein (1); Alpha-1,4 glucan phosphorylase (1) | glycogen phosphorylase activity [GO:0008184 molecular_function] (2); carbohydrate metabolic process [GO:0005975 biological_process] (2) | Glycosyl transferase, family 35 [IPR000811] (2) | scaffold_4_mRNA_3087.1 | C_unshiu_00001_mRNA_212.1 | - |
| GF0022132 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_3084.1 | C_unshiu_00001_mRNA_209.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0022131 | 1 | 1 | 0 | Glycosyltransferase family 61 protein (2) | transferase activity, transferring glycosyl groups [GO:0016757 molecular_function] (2) | Glycosyltransferase 61 [IPR007657] (1); Glycosyltransferase AER61, uncharacterised [IPR007657] (1) | scaffold_4_mRNA_3071.1 | C_unshiu_00001_mRNA_196.1 | - |
| GF0022130 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_3069.1 | C_unshiu_00001_mRNA_194.1 | - |
| GF0022129 | 1 | 1 | 0 | AP2/ERF domain transcription factor (2) | transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (2); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); DNA binding [GO:0003677 molecular_function] (1) | AP2/ERF domain [IPR001471] (1); DNA-binding domain [IPR016177] (1); AP2/ERF transcription factor ERF/PTI6 [IPR017392] (1) | scaffold_4_mRNA_3055.1 | C_unshiu_00001_mRNA_180.1 | - |
| GF0022126 | 1 | 1 | 0 | Phosphate transporter PHO1-like protein (2) | integral component of membrane [GO:0016021 cellular_component] (2) | EXS, C-terminal [IPR004342] (2); SPX domain [IPR004331] (2); PHO1, SPX domain [IPR034092] (1) | scaffold_4_mRNA_3044.1 | C_unshiu_00001_mRNA_168.1 | - |
| GF0022125 | 1 | 1 | 0 | Galactoside 2-alpha-L-fucosyltransferase (2) | cell wall biogenesis [GO:0042546 biological_process] (2); membrane [GO:0016020 cellular_component] (2); galactoside 2-alpha-L-fucosyltransferase activity [GO:0008107 molecular_function] (2) | Xyloglucan fucosyltransferase [IPR004938] (2) | scaffold_4_mRNA_3040.1 | C_unshiu_00001_mRNA_164.1 | - |
| GF0022124 | 1 | 1 | 0 | Expansin (2) | plant-type cell wall organization [GO:0009664 biological_process] (2); extracellular region [GO:0005576 cellular_component] (2) | Expansin/Lol pI [IPR007118] (2); Expansin [IPR002963] (2); Expansin, cellulose-binding-like domain [IPR007117] (2); Expansin/pollen allergen, DPBB domain [IPR007112] (2); RlpA-like protein, double-psi beta-barrel domain [IPR009009] (1); RlpA-like double-psi beta-barrel domain [IPR009009] (1) | scaffold_4_mRNA_304.1 | C_unshiu_00299_mRNA_10.1 | - |
| GF0022122 | 1 | 1 | 0 | Appr-1-p processing enzyme family protein (2) | | Macro domain [IPR002589] (2) | scaffold_4_mRNA_303.1 | C_unshiu_00299_mRNA_9.1 | - |
| GF0022121 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_3009.1 | C_unshiu_00001_mRNA_132.1 | - |
| GF0022120 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_30.1 | C_unshiu_00168_mRNA_39.1 | - |
| GF0022118 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_299.1 | C_unshiu_00299_mRNA_5.1 | - |
| GF0022115 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2); ATP binding [GO:0005524 molecular_function] (2) | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); DEAD/DEAH box helicase domain [IPR011545] (2) | scaffold_4_mRNA_2976.1 | C_unshiu_00001_mRNA_97.1 | - |
| GF0022114 | 1 | 1 | 0 | Hypothetical protein (2) | tRNA (guanine-N2-)-methyltransferase activity [GO:0004809 molecular_function] (2); tRNA processing [GO:0008033 biological_process] (2); RNA binding [GO:0003723 molecular_function] (2) | S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (2); tRNA methyltransferase, Trm1 [IPR002905] (2) | scaffold_4_mRNA_296.1 | C_unshiu_00299_mRNA_2.1 | - |
| GF0022112 | 1 | 1 | 0 | Nitrate transporter 1.7 (2) | transport [GO:0006810 biological_process] (2); membrane [GO:0016020 cellular_component] (2); transporter activity [GO:0005215 molecular_function] (2) | Major facilitator superfamily domain [IPR020846] (2); Proton-dependent oligopeptide transporter family [IPR000109] (2) | scaffold_4_mRNA_2948.1 | C_unshiu_00001_mRNA_70.1 | - |
| GF0022111 | 1 | 1 | 0 | Homoserine dehydrogenase (2) | cellular amino acid metabolic process [GO:0006520 biological_process] (2); oxidation-reduction process [GO:0055114 biological_process] (2) | Homoserine dehydrogenase, catalytic [IPR001342] (2); Glutathione S-transferase, C-terminal-like [IPR010987] (2); NAD(P)-binding domain [IPR016040] (2) | scaffold_4_mRNA_2937.1 | C_unshiu_00001_mRNA_59.1 | - |
| GF0022110 | 1 | 1 | 0 | TIR-NBS-LRR disease resistance protein (2) | protein binding [GO:0005515 molecular_function] (2); ADP binding [GO:0043531 molecular_function] (2); signal transduction [GO:0007165 biological_process] (2) | Leucine-rich repeat domain, L domain-like [IPR032675] (2); Leucine-rich repeat, typical subtype [IPR003591] (2); Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (2); NB-ARC [IPR002182] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); Winged helix-turn-helix DNA-binding domain [IPR011991] (1) | scaffold_4_mRNA_2923.1 | C_unshiu_00001_mRNA_45.1 | - |
| GF0022109 | 1 | 1 | 0 | Hypothetical protein (1); Ribosomal protein S26 (1) | structural constituent of ribosome [GO:0003735 molecular_function] (2); translation [GO:0006412 biological_process] (2); intracellular [GO:0005622 cellular_component] (2); ribosome [GO:0005840 cellular_component] (2) | Ribosomal protein S26e [IPR000892] (2) | scaffold_4_mRNA_292.1 | C_unshiu_01756_mRNA_8.1 | - |
| GF0022108 | 1 | 1 | 0 | Probably inactive leucine-rich repeat receptor-like protein kinase (2) | protein kinase activity [GO:0004672 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2); ATP binding [GO:0005524 molecular_function] (2); protein binding [GO:0005515 molecular_function] (1) | Protein kinase-like domain [IPR011009] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Protein kinase domain [IPR000719] (2); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Leucine-rich repeat [IPR001611] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1) | scaffold_4_mRNA_2918.1 | C_unshiu_00001_mRNA_40.1 | - |
| GF0022107 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_2902.1 | C_unshiu_00001_mRNA_23.1 | - |
| GF0022106 | 1 | 1 | 0 | Putative rnase H family protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (2) | Ribonuclease H domain [IPR002156] (2); Ribonuclease H1, N-terminal [IPR011320] (2); Ribonuclease H-like domain [IPR012337] (2) | scaffold_4_mRNA_2888.1 | C_unshiu_00001_mRNA_6.1 | - |
| GF0022105 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_2880.1 | C_unshiu_00004_mRNA_11.1 | - |
| GF0022104 | 1 | 1 | 0 | Hypothetical protein (2) | transmembrane transporter activity [GO:0022857 molecular_function] (2); membrane [GO:0016020 cellular_component] (2); integral component of membrane [GO:0016021 cellular_component] (2) | WAT1-related protein [IPR030184] (2); EamA domain [IPR000620] (2); Prolamin-like domain [IPR008502] (1) | scaffold_4_mRNA_2875.1 | C_unshiu_00004_mRNA_16.1 | - |
| GF0022103 | 1 | 1 | 0 | Nodulin MtN21/EamA-like transporter family protein (2) | integral component of membrane [GO:0016021 cellular_component] (2); transmembrane transporter activity [GO:0022857 molecular_function] (2); membrane [GO:0016020 cellular_component] (2) | EamA domain [IPR000620] (2); WAT1-related protein [IPR030184] (2) | scaffold_4_mRNA_2871.1 | C_unshiu_00004_mRNA_20.1 | - |
| GF0022102 | 1 | 1 | 0 | Cytochrome P450 82A4 (2) | heme binding [GO:0020037 molecular_function] (2); iron ion binding [GO:0005506 molecular_function] (2); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2) | Cytochrome P450 [IPR001128] (2); Cytochrome P450, conserved site [IPR017972] (2); Cytochrome P450, E-class, group I [IPR002401] (2) | scaffold_4_mRNA_285.1 | C_unshiu_01756_mRNA_4.1 | - |
| GF0022101 | 1 | 1 | 0 | HD domain-containing metal-dependent phosphohydrolase family protein isoform 1 (1); HD domain-containing metal-dependent phosphohydrolase family protein isoform 2 (1) | | HD domain [IPR006674] (2); HD/PDEase domain [IPR003607] (2) | scaffold_4_mRNA_2849.1 | C_unshiu_00004_mRNA_43.1 | - |
| GF0022099 | 1 | 1 | 0 | Glabrous 1 (1); Hypothetical protein (1) | DNA binding [GO:0003677 molecular_function] (2) | SANT/Myb domain [IPR001005] (2); Myb-like domain [IPR017877] (1); Myb domain [IPR017930] (1); Homeobox domain-like [IPR009057] (1); Homeodomain-like [IPR009057] (1) | scaffold_4_mRNA_2840.1 | C_unshiu_00004_mRNA_51.1 | - |
| GF0022098 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_284.1 | C_unshiu_01756_mRNA_3.1 | - |
| GF0022096 | 1 | 1 | 0 | Pyrrolidone-carboxylate peptidase family protein (2) | pyroglutamyl-peptidase activity [GO:0016920 molecular_function] (2); cytosol [GO:0005829 cellular_component] (2); proteolysis [GO:0006508 biological_process] (2) | Peptidase C15, pyroglutamyl peptidase I [IPR000816] (2); Peptidase C15, pyroglutamyl peptidase I-like [IPR016125] (2); Pyroglutamyl peptidase I, Cys active site [IPR033694] (1) | scaffold_4_mRNA_2819.1 | C_unshiu_00004_mRNA_69.2 | - |
| GF0022095 | 1 | 1 | 0 | UDP-N-acetylglucosamine--N-acetylmuramyl-pyrophosphoryl-undecaprenol N-acetylglucosamine transferase isoform 3 (2) | | | scaffold_4_mRNA_2813.1 | C_unshiu_00004_mRNA_77.1 | - |
| GF0022094 | 1 | 1 | 0 | Signal recognition particle receptor subunit beta (2) | GTP binding [GO:0005525 molecular_function] (2); intracellular [GO:0005622 cellular_component] (2); small GTPase mediated signal transduction [GO:0007264 biological_process] (2) | Small GTPase superfamily, ARF type [IPR024156] (2); Signal recognition particle receptor, beta subunit [IPR019009] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2) | scaffold_4_mRNA_2812.1 | C_unshiu_00004_mRNA_78.1 | - |
| GF0022091 | 1 | 1 | 0 | Hypothetical protein (2) | carbon-sulfur lyase activity [GO:0016846 molecular_function] (1); catalytic activity [GO:0003824 molecular_function] (1) | Pyridoxal phosphate-dependent transferase, subdomain 2 [IPR015422] (1); Pyridoxal phosphate-dependent transferase [IPR015424] (1); Alliinase, C-terminal [IPR006948] (1) | scaffold_4_mRNA_2793.1 | C_unshiu_00004_mRNA_95.1 | - |
| GF0022090 | 1 | 1 | 0 | Hypothetical protein (2) | | Protein of unknown function DUF4228, plant [IPR025322] (2) | scaffold_4_mRNA_2791.1 | C_unshiu_00004_mRNA_97.1 | - |
| GF0022089 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_279.1 | C_unshiu_00058_mRNA_74.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0022088 | 1 | 1 | 0 | Hypothetical protein (2) | clathrin adaptor complex [GO:0030131 cellular_component] (2); intracellular protein transport [GO:0006886 biological_process] (2); transport [GO:0006810 biological_process] (2); protein phosphorylation [GO:0006468 biological_process] (2); protein kinase activity [GO:0004672 molecular_function] (2); vesicle-mediated transport [GO:0016192 biological_process] (2); ATP binding [GO:0005524 molecular_function] (2) | Serine/threonine-protein kinase, active site [IPR008271] (2); Protein kinase, ATP binding site [IPR017441] (2); Longin-like domain [IPR011012] (2); Protein kinase-like domain [IPR011009] (2); Clathrin adaptor, mu subunit [IPR001392] (2); Clathrin adaptor, mu subunit, conserved site [IPR018240] (2); AP complex, mu/sigma subunit [IPR022775] (2); Protein kinase domain [IPR000719] (2); Mu homology domain [IPR028565] (2); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1) | scaffold_4_mRNA_2776.1 | C_unshiu_00004_mRNA_114.1 | - |
| GF0022087 | 1 | 1 | 0 | Ribosomal protein S21 family protein (2) | ribosome [GO:0005840 cellular_component] (2); structural constituent of ribosome [GO:0003735 molecular_function] (2); translation [GO:0006412 biological_process] (2) | Ribosomal protein S21 [IPR001911] (2) | scaffold_4_mRNA_2751.1 | C_unshiu_00004_mRNA_140.1 | - |
| GF0022086 | 1 | 1 | 0 | Protein terminal ear1 (2) | nucleic acid binding [GO:0003676 molecular_function] (2); nucleotide binding [GO:0000166 molecular_function] (1) | RNA recognition motif domain [IPR000504] (2); Terminal EAR1-like, RNA recognition motif 3 [IPR034458] (1); Mei2/Mei2-like, C-terminal RNA recognition motif [IPR007201] (1); RNA recognition motif 2 [IPR007201] (1); Nucleotide-binding alpha-beta plait domain [IPR012677] (1) | scaffold_4_mRNA_2729.1 | C_unshiu_00004_mRNA_165.1 | - |
| GF0022084 | 1 | 1 | 0 | E3 ubiquitin-protein ligase mib1 (2) | protein binding [GO:0005515 molecular_function] (2) | Ankyrin repeat [IPR002110] (2); Ankyrin repeat-containing domain [IPR020683] (2) | scaffold_4_mRNA_2686.1 | C_unshiu_00010_mRNA_37.1 | - |
| GF0022083 | 1 | 1 | 0 | Putative F-box protein At1g67623 (2) | protein binding [GO:0005515 molecular_function] (1) | Tetratricopeptide-like helical domain [IPR011990] (1); F-box domain [IPR001810] (1) | scaffold_4_mRNA_2681.1 | C_unshiu_00010_mRNA_41.1 | - |
| GF0022082 | 1 | 1 | 0 | Ribosome silencing factor (2) |  | Protein Iojap/ribosomal silencing factor RsfS [IPR004394] (2) | scaffold_4_mRNA_2680.1 | C_unshiu_00010_mRNA_42.1 | - |
| GF0022081 | 1 | 1 | 0 | Putative mitochondrial chaperone bcs1 (2) | ATP binding [GO:0005524 molecular_function] (1) | AAA+ ATPase domain [IPR003593] (1); AAA-type ATPase, N-terminal domain [IPR025753] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); ATPase, AAA-type, core [IPR003959] (1); ATPase, AAA-type, conserved site [IPR003960] (1) | scaffold_4_mRNA_2670.1 | C_unshiu_00010_mRNA_53.1 | - |
| GF0022078 | 1 | 1 | 0 | Small rubber particle protein (2) |  | Rubber elongation factor [IPR008802] (2) | scaffold_4_mRNA_2639.1 | C_unshiu_00010_mRNA_82.1 | - |
| GF0022077 | 1 | 1 | 0 | Squamosa promoter-binding-like protein 12 (2) | nucleus [GO:0005634 cellular_component] (2); DNA binding [GO:0003677 molecular_function] (2) | Transcription factor, SBP-box [IPR004333] (2) | scaffold_4_mRNA_2627.1 | C_unshiu_00010_mRNA_98.1 | - |
| GF0022076 | 1 | 1 | 0 | Squamosa promoter-binding-like protein 16 (2) | DNA binding [GO:0003677 molecular_function] (2); nucleus [GO:0005634 cellular_component] (2) | Transcription factor, SBP-box [IPR004333] (2) | scaffold_4_mRNA_2610.1 | C_unshiu_00010_mRNA_113.1 | - |
| GF0022075 | 1 | 1 | 0 | AT1G27990 protein (2) |  |  | scaffold_4_mRNA_2603.1 | C_unshiu_00010_mRNA_120.1 | - |
| GF0022074 | 1 | 1 | 0 | NAC domain-containing protein 29 (2) | regulation of transcription, DNA-templated [GO:0006355 biological_process] (2); DNA binding [GO:0003677 molecular_function] (2) | NAC domain [IPR003441] (2) | scaffold_4_mRNA_2584.1 | C_unshiu_00551_mRNA_17.1 | - |
| GF0022072 | 1 | 1 | 0 | Hypothetical protein (2) |  | Protein kinase-like domain [IPR011009] (1) | scaffold_4_mRNA_2552.1 | C_unshiu_00015_mRNA_95.1 | - |
| GF0022071 | 1 | 1 | 0 | Methylesterase (2) |  | Alpha/Beta hydrolase fold [IPR029058] (2); Alpha/beta hydrolase fold-1 [IPR000073] (2) | scaffold_4_mRNA_2546.1 | C_unshiu_00015_mRNA_89.1 | - |
| GF0022070 | 1 | 1 | 0 | Glucosamine/galactosamine-6-phosphate isomerase family protein (2) | carbohydrate metabolic process [GO:0005975 biological_process] (2); 6-phosphogluconolactonase activity [GO:0017057 molecular_function] (2); pentose-phosphate shunt [GO:0006098 biological_process] (2) | 6-phosphogluconolactonase, DevB-type [IPR005900] (2); Glucosamine/galactosamine-6-phosphate isomerase [IPR006148] (2) | scaffold_4_mRNA_2538.2 | C_unshiu_00015_mRNA_81.3 | - |
| GF0022069 | 1 | 1 | 0 | Senescence associated gene 20, putative (2) |  | NTF2-like domain [IPR032710] (2); Wound-induced protein, Wun1 [IPR009798] (2) | scaffold_4_mRNA_253.1 | C_unshiu_00058_mRNA_47.1 | - |
| GF0022068 | 1 | 1 | 0 | Developmental protein SEPALLATA 2 (2) | protein dimerization activity [GO:0046983 molecular_function] (2); nucleus [GO:0005634 cellular_component] (2); DNA binding [GO:0003677 molecular_function] (2); regulation of transcription, DNA-templated [GO:0006355 biological_process] (2); transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (2); RNA polymerase II regulatory region sequence-specific DNA binding [GO:0000977 molecular_function] (1); positive regulation of transcription from RNA polymerase II promoter [GO:0045944 biological_process] (1); MAPK cascade [GO:0000165 biological_process] (1) | Transcription factor, MADS-box [IPR002100] (2); Transcription factor, K-box [IPR002487] (2); MADS MEF2-like [IPR033896] (1) | scaffold_4_mRNA_2524.1 | C_unshiu_00015_mRNA_66.1 | - |
| GF0022067 | 1 | 1 | 0 | Cytochrome P450 734A1 (2) | heme binding [GO:0020037 molecular_function] (2); iron ion binding [GO:0005506 molecular_function] (2); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2) | Cytochrome P450, E-class, group I [IPR002401] (2); Cytochrome P450 [IPR001128] (2); Cytochrome P450, conserved site [IPR017972] (1) | scaffold_4_mRNA_2518.1 | C_unshiu_00015_mRNA_58.1 | - |
| GF0022066 | 1 | 1 | 0 | Cytochrome P450 734A1 (2) | heme binding [GO:0020037 molecular_function] (2); iron ion binding [GO:0005506 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (2) | Cytochrome P450 [IPR001128] (2); Cytochrome P450, E-class, group I [IPR002401] (2); Cytochrome P450, conserved site [IPR017972] (2) | scaffold_4_mRNA_2516.1 | C_unshiu_00015_mRNA_56.1 | - |
| GF0022065 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_4_mRNA_2514.1 | C_unshiu_00015_mRNA_54.1 | - |
| GF0022064 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_4_mRNA_2507.1 | C_unshiu_00023_mRNA_64.1 | - |
| GF0022063 | 1 | 1 | 0 | Putative N-acetyltransferase ycf52 (2) | N-acetyltransferase activity [GO:0008080 molecular_function] (2) | Acyl-CoA N-acyltransferase [IPR016181] (2); GNAT domain [IPR000182] (2) | scaffold_4_mRNA_2478.1 | C_unshiu_00310_mRNA_19.1 | - |
| GF0022062 | 1 | 1 | 0 | Metal-dependent phosphohydrolase (2) |  | HD domain [IPR006674] (2); HD/PDEase domain [IPR003607] (2) | scaffold_4_mRNA_2455.1 | C_unshiu_00535_mRNA_4.1 | - |
| GF0022061 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_4_mRNA_2453.1 | C_unshiu_00535_mRNA_6.1 | - |
| GF0022058 | 1 | 1 | 0 | Allene oxide cyclase (2) | isomerase activity [GO:0016853 molecular_function] (1); chloroplast [GO:0009507 cellular_component] (1) | Allene oxide cyclase [IPR009410] (1) | scaffold_4_mRNA_2415.1 | C_unshiu_00099_mRNA_21.1 | - |
| GF0022055 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_4_mRNA_2369.1 | C_unshiu_00039_mRNA_72.1 | - |
| GF0022054 | 1 | 1 | 0 | Transcription factor MYB1R1 (1); Hypothetical protein (1) | DNA binding [GO:0003677 molecular_function] (2) | Myb domain [IPR017930] (2); Myb domain, plants [IPR006447] (2); SANT/Myb domain [IPR001005] (2); SANT domain [IPR017884] (2); Homeobox domain-like [IPR009057] (1); Homeodomain-like [IPR009057] (1); Armadillo-like helical [IPR011989] (1) | scaffold_4_mRNA_2362.1 | C_unshiu_00039_mRNA_67.1 | - |
| GF0022053 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_4_mRNA_2349.1 | C_unshiu_00039_mRNA_54.1 | - |
| GF0022052 | 1 | 1 | 0 | RRNA 2'-O-methyltransferase fibrillarin (2) | tRNA processing [GO:0008033 biological_process] (2); RNA binding [GO:0003723 molecular_function] (2); rRNA processing [GO:0006364 biological_process] (2); methyltransferase activity [GO:0008168 molecular_function] (2) | Fibrillarin, conserved site [IPR020813] (2); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (2); Fibrillarin [IPR000692] (2) | scaffold_4_mRNA_2321.1 | C_unshiu_00039_mRNA_28.1 | - |
| GF0022049 | 1 | 1 | 0 | Glutathione transferase (2) | protein binding [GO:0005515 molecular_function] (2) | Glutathione S-transferase, N-terminal [IPR004045] (2); Glutathione S-transferase, C-terminal-like [IPR010987] (2); Thioredoxin-like fold [IPR012336] (2); Glutathione S-transferase, C-terminal [IPR004046] (2) | scaffold_4_mRNA_2293.1 | C_unshiu_00460_mRNA_24.1 | - |
| GF0022048 | 1 | 1 | 0 | Hypothetical protein (2) | protein binding [GO:0005515 molecular_function] (2) | Tetratricopeptide-like helical domain [IPR011990] (2); Tetratricopeptide repeat [IPR019734] (2) | scaffold_4_mRNA_2292.1 | C_unshiu_00460_mRNA_21.1 | - |
| GF0022047 | 1 | 1 | 0 | Abscisic acid receptor PYL8 (2) |  | Polyketide cyclase/dehydrase [IPR019587] (2); START-like domain [IPR023393] (2) | scaffold_4_mRNA_229.1 | C_unshiu_00012_mRNA_108.1 | - |
| GF0022046 | 1 | 1 | 0 | Putative ycf19 (2) | membrane [GO:0016020 cellular_component] (2) | CCB3/YggT [IPR003425] (2) | scaffold_4_mRNA_2262.1 | C_unshiu_00349_mRNA_21.1 | - |
| GF0022045 | 1 | 1 | 0 | DUF177 domain protein (2) |  | Protein of unknown function DUF177 [IPR003772] (1); Large ribosomal RNA subunit accumulation protein YceD [IPR003772] (1) | scaffold_4_mRNA_2259.1 | C_unshiu_00349_mRNA_24.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0022044 | 1 | 1 | 0 | Hypothetical protein (2) | ATP binding [GO:0005524 molecular_function] (2) | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); Helicase superfamily 1/2, ATP-binding domain [IPR014001] (2); SNF2-related, N-terminal domain [IPR000330] (2) | scaffold_4_mRNA_225.1 | C_unshiu_00012_mRNA_104.1 | - |
| GF0022043 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_2236.1 | C_unshiu_00130_mRNA_27.1 | - |
| GF0022042 | 1 | 1 | 0 | Transcription initiation factor TFIID subunit 9 (1); Putative transcription initiation factor TFIID subunit 9-like (1) | DNA-templated transcription, initiation [GO:0006352 biological_process] (2); protein heterodimerization activity [GO:0046982 molecular_function] (2) | Histone-fold [IPR009072] (2); Transcription initiation factor TAFII31 [IPR003162] (2) | scaffold_4_mRNA_2229.1 | C_unshiu_00130_mRNA_34.1 | - |
| GF0022041 | 1 | 1 | 0 | Histone-lysine N-methyltransferase SUVR4 (2) | nucleus [GO:0005634 cellular_component] (2); histone lysine methylation [GO:0034968 biological_process] (2); zinc ion binding [GO:0008270 molecular_function] (2); histone-lysine N-methyltransferase activity [GO:0018024 molecular_function] (2) | Pre-SET domain [IPR007728] (2); WIYLD domain [IPR018848] (2); Pre-SET zinc-binding sub-group [IPR003606] (1) | scaffold_4_mRNA_2226.1 | C_unshiu_00130_mRNA_36.1 | - |
| GF0022040 | 1 | 1 | 0 | Cysteine-rich repeat secretory protein 3 (2) | | Gnk2-homologous domain [IPR002902] (2) | scaffold_4_mRNA_2225.1 | C_unshiu_00130_mRNA_37.1 | - |
| GF0022039 | 1 | 1 | 0 | General transcription factor-like zinc finger protein, putative (2) | | | scaffold_4_mRNA_2212.1 | C_unshiu_00130_mRNA_50.1 | - |
| GF0022038 | 1 | 1 | 0 | F-box protein interaction domain protein (2) | protein binding [GO:0005515 molecular_function] (2) | F-box associated domain, type 1 [IPR006527] (2); F-box domain [IPR001810] (2); Quinoprotein amine dehydrogenase, beta chain-like [IPR011044] (1) | scaffold_4_mRNA_2209.1 | C_unshiu_00130_mRNA_52.1 | - |
| GF0022035 | 1 | 1 | 0 | GroES-like zinc-binding dehydrogenase family protein isoform 3 (2) | zinc ion binding [GO:0008270 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2); oxidoreductase activity [GO:0016491 molecular_function] (2) | GroES-like [IPR011032] (2); Alcohol dehydrogenase, zinc-type, conserved site [IPR002328] (2); Alcohol dehydrogenase, N-terminal [IPR013154] (2); NAD(P)-binding domain [IPR016040] (2); Alcohol dehydrogenase superfamily, zinc-type [IPR002085] (1) | scaffold_4_mRNA_2191.1 | C_unshiu_00209_mRNA_37.1 | - |
| GF0022033 | 1 | 1 | 0 | Ferritin (2) | ferric iron binding [GO:0008199 molecular_function] (2); cellular iron ion homeostasis [GO:0006879 biological_process] (2); iron ion transport [GO:0006826 biological_process] (2) | Ferritin [IPR001519] (2); Ferritin/DPS protein domain [IPR008331] (2); Ferritin, conserved site [IPR014034] (2); Ferritin-like superfamily [IPR009078] (2); Ferritin-related [IPR012347] (2); Ferritin-like diiron domain [IPR009040] (1); Ferritin-like diiron domain [IPR009040] (1) | scaffold_4_mRNA_218.1 | C_unshiu_00012_mRNA_97.1 | - |
| GF0022032 | 1 | 1 | 0 | Multiple inositol polyphosphate phosphatase 1 (2) | acid phosphatase activity [GO:0003993 molecular_function] (2); phosphatase activity [GO:0016791 molecular_function] (2) | Histidine phosphatase superfamily, clade-2 [IPR000560] (2); Histidine acid phosphatase, eukaryotic [IPR016274] (2); Histidine phosphatase superfamily [IPR029033] (2) | scaffold_4_mRNA_217.1 | C_unshiu_00012_mRNA_96.1 | - |
| GF0022031 | 1 | 1 | 0 | Cytochrome P450, family 87, subfamily A, polypeptide 6, putative (2) | oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2); heme binding [GO:0020037 molecular_function] (2); iron ion binding [GO:0005506 molecular_function] (2) | Cytochrome P450 [IPR001128] (2); Cytochrome P450, conserved site [IPR017972] (2); Cytochrome P450, E-class, group I [IPR002401] (2) | scaffold_4_mRNA_2158.1 | C_unshiu_00020_mRNA_33.1 | - |
| GF0022030 | 1 | 1 | 0 | Cytochrome P450, family 87, subfamily A, polypeptide 6, putative (2) | heme binding [GO:0020037 molecular_function] (2); iron ion binding [GO:0005506 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (2) | Cytochrome P450, E-class, group I [IPR002401] (2); Cytochrome P450, conserved site [IPR017972] (2); Cytochrome P450 [IPR001128] (2) | scaffold_4_mRNA_2156.1 | C_unshiu_00020_mRNA_31.1 | - |
| GF0022029 | 1 | 1 | 0 | Cytochrome P450, family 87, subfamily A, polypeptide 6, putative (2) | oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2); iron ion binding [GO:0005506 molecular_function] (2); heme binding [GO:0020037 molecular_function] (2) | Cytochrome P450 [IPR001128] (2); Cytochrome P450, conserved site [IPR017972] (2); Cytochrome P450, E-class, group I [IPR002401] (2) | scaffold_4_mRNA_2155.1 | C_unshiu_00020_mRNA_30.1 | - |
| GF0022026 | 1 | 1 | 0 | Putative membrane lipoprotein (2) | | | scaffold_4_mRNA_2139.1 | C_unshiu_00020_mRNA_22.1 | - |
| GF0022025 | 1 | 1 | 0 | Phospholipase C 3 (2) | catalytic activity [GO:0003824 molecular_function] (2); metabolic process [GO:0008152 biological_process] (2); hydrolase activity, acting on ester bonds [GO:0016788 molecular_function] (2) | Phosphoesterase [IPR007312] (2); Alkaline phosphatase-like, alpha/beta/alpha [IPR017849] (1); Alkaline-phosphatase-like, core domain [IPR017850] (1) | scaffold_4_mRNA_2135.1 | C_unshiu_00020_mRNA_19.1 | - |
| GF0022024 | 1 | 1 | 0 | Peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A (2) | | Peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A [IPR021102] (2) | scaffold_4_mRNA_213.1 | C_unshiu_00012_mRNA_93.1 | - |
| GF0022023 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_2128.1 | C_unshiu_00004_mRNA_24.1 | - |
| GF0022021 | 1 | 1 | 0 | Ankyrin repeat RF-like protein, putative (2) | protein binding [GO:0005515 molecular_function] (2) | Ankyrin repeat [IPR002110] (2); Major sperm protein (MSP) domain [IPR000535] (2); PapD-like [IPR008962] (2); Ankyrin repeat-containing domain [IPR020683] (2); Immunoglobulin-like fold [IPR013783] (1) | scaffold_4_mRNA_212.1 | C_unshiu_00012_mRNA_92.1 | - |
| GF0022020 | 1 | 1 | 0 | Hypothetical protein (2) | aspartic-type endopeptidase activity [GO:0004190 molecular_function] (2); proteolysis [GO:0006508 biological_process] (2) | Peptidase family A1 domain [IPR033121] (2); Aspartic peptidase domain [IPR021109] (2); Aspartic peptidase A1 family [IPR001461] (2); Xylanase inhibitor, N-terminal [IPR032861] (1) | scaffold_4_mRNA_2109.1 | C_unshiu_00020_mRNA_7.1 | - |
| GF0022017 | 1 | 1 | 0 | Hypothetical protein (2) | | ELMO domain [IPR006816] (2) | scaffold_4_mRNA_2077.1 | C_unshiu_01238_mRNA_6.1 | - |
| GF0022016 | 1 | 1 | 0 | MatE family protein, expressed (2) | transmembrane transport [GO:0055085 biological_process] (2); drug transmembrane transporter activity [GO:0015238 molecular_function] (2); antiporter activity [GO:0015297 molecular_function] (2); membrane [GO:0016020 cellular_component] (2); drug transmembrane transport [GO:0006855 biological_process] (2) | Multi antimicrobial extrusion protein [IPR002528] (2) | scaffold_4_mRNA_2074.1 | C_unshiu_00700_mRNA_18.1 | - |
| GF0022015 | 1 | 1 | 0 | ELMO domain-containing protein 2 (2) | | ELMO domain [IPR006816] (2) | scaffold_4_mRNA_2071.1 | C_unshiu_00700_mRNA_13.1 | - |
| GF0022014 | 1 | 1 | 0 | Pollen Ole e 1 allergen and extensin family protein (2) | | | scaffold_4_mRNA_207.1 | C_unshiu_00012_mRNA_87.1 | - |
| GF0022013 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_2067.1 | C_unshiu_00700_mRNA_11.1 | - |
| GF0022012 | 1 | 1 | 0 | Hypothetical protein (2) | mRNA splicing, via spliceosome [GO:0000398 biological_process] (2); nucleic acid binding [GO:0003676 molecular_function] (2); RNA binding [GO:0003723 molecular_function] (2); U2AF [GO:0089701 cellular_component] (2); nucleotide binding [GO:0000166 molecular_function] (1) | RNA recognition motif domain, eukaryote [IPR003954] (2); U2 auxiliary factor small subunit [IPR009145] (2); RNA recognition motif domain [IPR000504] (2); Nucleotide-binding alpha-beta plait domain [IPR012677] (1) | scaffold_4_mRNA_2066.1 | C_unshiu_00700_mRNA_9.1 | - |
| GF0022011 | 1 | 1 | 0 | NAC domain-containing protein 67 (1); NAC protein 4 (1) | regulation of transcription, DNA-templated [GO:0006355 biological_process] (2); DNA binding [GO:0003677 molecular_function] (2) | NAC domain [IPR003441] (2) | scaffold_4_mRNA_2061.1 | C_unshiu_00700_mRNA_4.1 | - |
| GF0022010 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_2060.1 | C_unshiu_00700_mRNA_3.1 | - |
| GF0022009 | 1 | 1 | 0 | GDSL esterase/lipase LTL1 (2) | hydrolase activity, acting on ester bonds [GO:0016788 molecular_function] (2) | GDSL lipase/esterase [IPR001087] (2); SGNH hydrolase-type esterase domain [IPR013830] (2) | scaffold_4_mRNA_2046.1 | C_unshiu_00250_mRNA_41.1 | - |
| GF0022008 | 1 | 1 | 0 | Hypothetical protein (2) | | Alpha/Beta hydrolase fold [IPR029058] (2) | scaffold_4_mRNA_2039.1 | C_unshiu_00250_mRNA_33.1 | - |
| GF0022006 | 1 | 1 | 0 | Hypothetical protein (2) | | Domain of unknown function DUF4283 [IPR025558] (2) | scaffold_4_mRNA_2024.1 | C_unshiu_00250_mRNA_13.1 | - |
| GF0022005 | 1 | 1 | 0 | Hypothetical protein (2) | | Zinc knuckle CX2CX4HX4C [IPR025836] (2) | scaffold_4_mRNA_2023.1 | C_unshiu_00250_mRNA_12.1 | - |
| GF0022004 | 1 | 1 | 0 | Hypothetical protein (2) | cysteine-type peptidase activity [GO:0008234 molecular_function] (2); proteolysis [GO:0006508 biological_process] (2) | Ulp1 protease family, C-terminal catalytic domain [IPR003653] (2) | scaffold_4_mRNA_2019.1 | C_unshiu_00250_mRNA_10.1 | - |
| GF0022003 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_2017.1 | C_unshiu_00250_mRNA_8.1 | - |
| GF0022002 | 1 | 1 | 0 | Hypothetical protein (2) | 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_4_mRNA_1992.1 | C_unshiu_00086_mRNA_28.1 | - |
| GF0022001 | 1 | 1 | 0 | Tetratricopeptide repeat-like superfamily protein, putative (2) | | Pentatricopeptide repeat [IPR002885] (2) | scaffold_4_mRNA_199.1 | C_unshiu_00012_mRNA_78.1 | - |
| GF0022000 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1984.1 | C_unshiu_00086_mRNA_20.1 | - |
| GF0021999 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (1) | Ribonuclease H-like domain [IPR012337] (1) | scaffold_4_mRNA_1982.1 | C_unshiu_00086_mRNA_18.1 | - |
| GF0021998 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_198.1 | C_unshiu_00012_mRNA_77.1 | - |
| GF0021997 | 1 | 1 | 0 | Hypothetical protein (2) | | Transposase, MuDR, plant [IPR004332] (2) | scaffold_4_mRNA_1974.1 | C_unshiu_00086_mRNA_10.1 | - |
| GF0021996 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1953.1 | C_unshiu_01260_mRNA_10.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0021994 | 1 | 1 | 0 | Receptor-like kinase plant (2) | ATP binding [GO:0005524 molecular_function] (2); protein kinase activity [GO:0004672 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2); nucleic acid binding [GO:0003676 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1) | Serine/threonine-protein kinase, active site [IPR008271] (2); Protein kinase, ATP binding site [IPR017441] (2); Protein kinase-like domain [IPR011009] (2); Protein kinase domain [IPR000719] (2); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); HAT, C-terminal dimerisation domain [IPR008906] (1); Ribonuclease H-like domain [IPR012337] (1) | scaffold_4_mRNA_1940.1 | C_unshiu_00296_mRNA_15.1 | - |
| GF0021993 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1939.1 | C_unshiu_00296_mRNA_14.1 | - |
| GF0021992 | 1 | 1 | 0 | Light-harvesting complex II chlorophyll a/b binding protein, n-terminal part (1); Chlorophyll a-b binding protein, chloroplastic (1) | photosynthesis, light harvesting [GO:0009765 biological_process] (2); membrane [GO:0016020 cellular_component] (2) | Chlorophyll A-B binding protein, plant [IPR001344] (2); Chlorophyll a/b binding protein domain [IPR023329] (2); Chlorophyll A-B binding protein [IPR022796] (2); Ribonuclease H1, N-terminal [IPR011320] (1) | scaffold_4_mRNA_1927.1 | C_unshiu_00824_mRNA_2.1 | - |
| GF0021991 | 1 | 1 | 0 | Protein NLP2 (2) | | RWP-RK domain [IPR003035] (2) | scaffold_4_mRNA_1926.1 | C_unshiu_00824_mRNA_3.1 | - |
| GF0021990 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1921.1 | C_unshiu_00835_mRNA_5.1 | - |
| GF0021988 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1908.1 | C_unshiu_00545_mRNA_17.1 | - |
| GF0021987 | 1 | 1 | 0 | Hypothetical protein (2) | DNA binding [GO:0003677 molecular_function] (2) | Zinc finger, BED-type [IPR003656] (2) | scaffold_4_mRNA_1906.1 | C_unshiu_00545_mRNA_15.1 | - |
| GF0021985 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1885.1 | C_unshiu_00665_mRNA_1.1 | - |
| GF0021984 | 1 | 1 | 0 | Hypothetical protein (2) | regulation of transcription, DNA-templated [GO:0006355 biological_process] (1) | FAR1 DNA binding domain [IPR004330] (1); FHY3/FAR1 family [IPR031052] (1) | scaffold_4_mRNA_1884.1 | C_unshiu_00665_mRNA_2.1 | - |
| GF0021982 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1876.1 | C_unshiu_00665_mRNA_10.1 | - |
| GF0021980 | 1 | 1 | 0 | Nonexpressor of pathogenesis-related protein 1 (2) | protein binding [GO:0005515 molecular_function] (2) | Ankyrin repeat [IPR002110] (2); Ankyrin repeat-containing domain [IPR020683] (2); NPR1/NIM1-like, C-terminal [IPR021094] (2); Regulatory protein NPR, central domain [IPR024228] (1) | scaffold_4_mRNA_1870.1 | C_unshiu_02053_mRNA_2.1 | - |
| GF0021979 | 1 | 1 | 0 | Flavone synthase II (2) | heme binding [GO:0020037 molecular_function] (2); iron ion binding [GO:0005506 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (2) | Cytochrome P450, E-class, group I [IPR002401] (2); Cytochrome P450, conserved site [IPR017972] (2); Cytochrome P450 [IPR001128] (2) | scaffold_4_mRNA_1840.1 | C_unshiu_00428_mRNA_3.1 | - |
| GF0021977 | 1 | 1 | 0 | 60S ribosomal protein L6 (2) | structural constituent of ribosome [GO:0003735 molecular_function] (2); translation [GO:0006412 biological_process] (2); intracellular [GO:0005622 cellular_component] (2); ribosome [GO:0005840 cellular_component] (2) | Translation protein SH3-like domain [IPR008991] (2); Ribosomal protein L6, N-terminal [IPR005568] (2); 60S ribosomal protein L6E [IPR000915] (2); Ribosomal protein L2 domain 2 [IPR014722] (2) | scaffold_4_mRNA_1819.1 | C_unshiu_00113_mRNA_46.1 | - |
| GF0021976 | 1 | 1 | 0 | Phosphoribosylanthranilate isomerase (2) | metabolic process [GO:0008152 biological_process] (2); catalytic activity [GO:0003824 molecular_function] (2); tryptophan metabolic process [GO:0006568 biological_process] (2); phosphoribosylanthranilate isomerase activity [GO:0004640 molecular_function] (2) | N-(5'phosphoribosyl) anthranilate isomerase (PRAI) [IPR001240] (2); Aldolase-type TIM barrel [IPR013785] (2); Ribulose-phosphate binding barrel [IPR011060] (2) | scaffold_4_mRNA_181.1 | C_unshiu_00012_mRNA_58.1 | - |
| GF0021975 | 1 | 1 | 0 | Ankyrin repeat family protein (2) | protein binding [GO:0005515 molecular_function] (1) | PGG domain [IPR026961] (2); Ankyrin repeat-containing domain [IPR020683] (2); Ankyrin repeat [IPR002110] (1) | scaffold_4_mRNA_1809.1 | C_unshiu_00113_mRNA_37.1 | - |
| GF0021972 | 1 | 1 | 0 | Non-LTR retroelement reverse transcriptase-like (2) | RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2); Reverse transcriptase zinc-binding domain [IPR026960] (2); Ribonuclease H domain [IPR002156] (2); TB2/DP1/HVA22-related protein [IPR004345] (1); Endonuclease/exonuclease/phosphatase [IPR005135] (1) | scaffold_4_mRNA_18.1 | C_unshiu_00571_mRNA_20.1 | - |
| GF0021971 | 1 | 1 | 0 | Hypothetical protein (2) | | Metacaspase type I, plant [IPR033180] (2); Caspase-like domain [IPR029030] (1) | scaffold_4_mRNA_1795.1 | C_unshiu_00113_mRNA_29.1 | - |
| GF0021970 | 1 | 1 | 0 | Peroxidase 57 (2) | oxidation-reduction process [GO:0055114 biological_process] (2); peroxidase activity [GO:0004601 molecular_function] (2); response to oxidative stress [GO:0006979 biological_process] (2); heme binding [GO:0020037 molecular_function] (2); hydrogen peroxide catabolic process [GO:0042744 biological_process] (1) | Haem peroxidase, plant/fungal/bacterial [IPR002016] (2); Peroxidases heam-ligand binding site [IPR019793] (2); Plant peroxidase [IPR000823] (2); Peroxidase, active site [IPR019794] (2); Haem peroxidase [IPR010255] (2); Secretory peroxidase [IPR033905] (1) | scaffold_4_mRNA_1785.1 | C_unshiu_00113_mRNA_18.1 | - |
| GF0021969 | 1 | 1 | 0 | Pentatricopeptide (2) | zinc ion binding [GO:0008270 molecular_function] (2); protein binding [GO:0005515 molecular_function] (2) | DYW domain [IPR032867] (2); Pentatricopeptide repeat [IPR002885] (2); Tetratricopeptide-like helical domain [IPR011990] (2) | scaffold_4_mRNA_1782.1 | C_unshiu_00113_mRNA_15.1 | - |
| GF0021968 | 1 | 1 | 0 | Hypothetical protein (2) | | Domain of unknown function DUF4283 [IPR025558] (2) | scaffold_4_mRNA_1780.1 | C_unshiu_00113_mRNA_13.1 | - |
| GF0021964 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1743.1 | C_unshiu_00200_mRNA_26.1 | - |
| GF0021963 | 1 | 1 | 0 | Hypothetical protein (2) | transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (2) | Transferase [IPR003480] (2); Chloramphenicol acetyltransferase-like domain [IPR023213] (1) | scaffold_4_mRNA_1741.1 | C_unshiu_00200_mRNA_24.1 | - |
| GF0021962 | 1 | 1 | 0 | Anthocyanin 5-aromatic acyltransferase (2) | transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (2) | Transferase [IPR003480] (2); Chloramphenicol acetyltransferase-like domain [IPR023213] (1) | scaffold_4_mRNA_1739.1 | C_unshiu_00200_mRNA_21.1 | - |
| GF0021961 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1734.1 | C_unshiu_00200_mRNA_13.1 | - |
| GF0021960 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1733.1 | C_unshiu_00200_mRNA_12.1 | - |
| GF0021959 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1727.1 | C_unshiu_00200_mRNA_7.1 | - |
| GF0021957 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1706.1 | C_unshiu_00093_mRNA_4.1 | - |
| GF0021956 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1704.1 | C_unshiu_00357_mRNA_17.1 | - |
| GF0021955 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1700.1 | C_unshiu_00357_mRNA_21.1 | - |
| GF0021954 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1694.1 | C_unshiu_00240_mRNA_27.1 | - |
| GF0021953 | 1 | 1 | 0 | Sterile alpha motif domain-containing family protein (2) | protein binding [GO:0005515 molecular_function] (2) | Sterile alpha motif/pointed domain [IPR013761] (2); Sterile alpha motif domain [IPR001660] (2) | scaffold_4_mRNA_1692.1 | C_unshiu_00240_mRNA_25.1 | - |
| GF0021952 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1689.1 | C_unshiu_00240_mRNA_23.1 | - |
| GF0021951 | 1 | 1 | 0 | DNA replication complex GINS protein PSF3 (2) | | GINS complex, subunit Psf3 [IPR010492] (2); GINS complex [IPR021151] (1); GINS subunit, domain A [IPR021151] (1) | scaffold_4_mRNA_168.1 | C_unshiu_00012_mRNA_45.1 | - |
| GF0021950 | 1 | 1 | 0 | Hypothetical protein (1); Polynucleotidyl transferase, Ribonuclease H fold (1) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_4_mRNA_1679.1 | C_unshiu_00240_mRNA_9.1 | - |
| GF0021949 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1671.1 | C_unshiu_00803_mRNA_5.1 | - |
| GF0021948 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1663.1 | C_unshiu_00240_mRNA_1.1 | - |
| GF0021947 | 1 | 1 | 0 | Hypothetical protein (2) | | Histidine kinase-like ATPase, C-terminal domain [IPR003594] (2) | scaffold_4_mRNA_1654.1 | C_unshiu_01641_mRNA_6.1 | - |
| GF0021946 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1653.1 | C_unshiu_01641_mRNA_5.1 | - |
| GF0021945 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1652.1 | C_unshiu_01641_mRNA_4.1 | - |
| GF0021941 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1619.1 | C_unshiu_00885_mRNA_15.1 | - |
| GF0021940 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1618.1 | C_unshiu_00885_mRNA_14.1 | - |
| GF0021939 | 1 | 1 | 0 | Putative transposable element (1); Hypothetical protein (1) | | Domain of unknown function DUF4216 [IPR025312] (2); Domain of unknown function DUF4218 [IPR025452] (2); Transposon, En/Spm-like [IPR004242] (1) | scaffold_4_mRNA_1615.1 | C_unshiu_02086_mRNA_1.1 | - |
| GF0021938 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1612.1 | C_unshiu_00885_mRNA_6.1 | - |
| GF0021937 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1582.1 | C_unshiu_00461_mRNA_7.1 | - |
| GF0021936 | 1 | 1 | 0 | Hypothetical protein (2) | | GroEL-like apical domain [IPR027409] (2) | scaffold_4_mRNA_1576.1 | C_unshiu_00461_mRNA_1.1 | - |
| GF0021935 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1575.1 | C_unshiu_00895_mRNA_1.1 | - |
| GF0021934 | 1 | 1 | 0 | Hypothetical protein (2) | | Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (2) | scaffold_4_mRNA_1567.1 | C_unshiu_00464_mRNA_3.1 | - |
| GF0021933 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1556.1 | C_unshiu_00847_mRNA_5.1 | - |
| GF0021932 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1555.1 | C_unshiu_00847_mRNA_4.1 | - |
| GF0021931 | 1 | 1 | 0 | DUF1499 family protein (2) | | Protein of unknown function DUF1499 [IPR010865] (2) | scaffold_4_mRNA_1553.1 | C_unshiu_00847_mRNA_2.1 | - |
| GF0021930 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1540.1 | C_unshiu_00365_mRNA_8.1 | - |
| GF0021929 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1535.1 | C_unshiu_00365_mRNA_14.1 | - |
| GF0021927 | 1 | 1 | 0 | Hypothetical protein (2) | | Alpha/Beta hydrolase fold [IPR029058] (2) | scaffold_4_mRNA_1521.1 | C_unshiu_00365_mRNA_27.1 | - |
| GF0021926 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1520.1 | C_unshiu_00738_mRNA_17.1 | - |
| GF0021925 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1518.1 | C_unshiu_00738_mRNA_14.1 | - |
| GF0021924 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_4_mRNA_1517.1 | C_unshiu_00738_mRNA_13.1 | - |
| GF0021923 | 1 | 1 | 0 | Hypothetical protein (2) | | Domain of unknown function DUF4283 [IPR025558] (2) | scaffold_4_mRNA_1514.1 | C_unshiu_00738_mRNA_11.1 | - |
| GF0021922 | 1 | 1 | 0 | Hypothetical protein (2) | protein binding [GO:0005515 molecular_function] (1) | Protein kinase-like domain [IPR011009] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (2); Leucine-rich repeat [IPR001611] (1) | scaffold_4_mRNA_151.1 | C_unshiu_00012_mRNA_27.1 | - |
| GF0021921 | 1 | 1 | 0 | Hypothetical protein (2) | | Retrotransposon gag domain [IPR005162] (2) | scaffold_4_mRNA_1502.1 | C_unshiu_00401_mRNA_4.1 | - |

| **ID** | **Num. in *C. celementine*** | **Num in *C. unshiu*** | **Num in *P.trifoliata*** | **Note** | **GO** | **InterPro** | **Members in *C.clementine*** | **Members in *C.unshiu*** | **Members in *P.trifoliata*** |
|---|---|---|---|---|---|---|---|---|---|
| GF0021920 | 1 | 1 | 0 | Hypothetical protein (1); Phosphoenolpyruvate carboxylase (1) | | Transposase, Tnp1/En/Spm-like [IPR004264] (2) | scaffold_4_mRNA_1501.1 | C_unshiu_00401_mRNA_3.1 | - |
| GF0021919 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1496.1 | C_unshiu_00030_mRNA_60.1 | - |
| GF0021918 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1489.1 | C_unshiu_02540_mRNA_1.1 | - |
| GF0021916 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1486.1 | C_unshiu_00019_mRNA_97.1 | - |
| GF0021915 | 1 | 1 | 0 | Putative invertase inhibitor (2) | enzyme inhibitor activity [GO:0004857 molecular_function] (2) | Pectinesterase inhibitor domain [IPR006501] (2); Pla a 1-like [IPR034088] (1) | scaffold_4_mRNA_1485.1 | C_unshiu_00019_mRNA_96.1 | - |
| GF0021914 | 1 | 1 | 0 | ATP-binding cassette, subfamily F, member 3 (2) | ATPase activity [GO:0016887 molecular_function] (2); ATP binding [GO:0005524 molecular_function] (2) | ABC transporter, conserved site [IPR017871] (2); ABC-transporter extension domain [IPR032781] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); ABC transporter-like [IPR003439] (2); AAA+ ATPase domain [IPR003593] (2) | scaffold_4_mRNA_1481.1 | C_unshiu_00019_mRNA_92.2 | - |
| GF0021913 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1480.1 | C_unshiu_00019_mRNA_91.1 | - |
| GF0021912 | 1 | 1 | 0 | Hypothetical protein (2) | zinc ion binding [GO:0008270 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | Zinc finger, CCHC-type [IPR001878] (2); Zinc knuckle CX2CX4HX4C [IPR025836] (2); Domain of unknown function DUF4283 [IPR025558] (2); Reverse transcriptase zinc-binding domain [IPR026960] (2) | scaffold_4_mRNA_1477.1 | C_unshiu_00019_mRNA_88.1 | - |
| GF0021911 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1473.1 | C_unshiu_00019_mRNA_84.1 | - |
| GF0021910 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1470.1 | C_unshiu_00019_mRNA_83.1 | - |
| GF0021909 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1469.1 | C_unshiu_00019_mRNA_82.1 | - |
| GF0021908 | 1 | 1 | 0 | Hypothetical protein (1); Non-LTR retrolelement reverse transcriptase-like protein (1) | nucleic acid binding [GO:0003676 molecular_function] (2); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (2) | Reverse transcriptase domain [IPR000477] (2); Reverse transcriptase zinc-binding domain [IPR026960] (2); Ribonuclease H-like domain [IPR012337] (2); Ribonuclease H domain [IPR002156] (2) | scaffold_4_mRNA_1468.1 | C_unshiu_00019_mRNA_81.1 | - |
| GF0021907 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1459.1 | C_unshiu_00019_mRNA_72.1 | - |
| GF0021906 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1458.1 | C_unshiu_00019_mRNA_71.1 | - |
| GF0021905 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1444.1 | C_unshiu_00019_mRNA_58.1 | - |
| GF0021904 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1442.1 | C_unshiu_00019_mRNA_56.1 | - |
| GF0021903 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1441.1 | C_unshiu_00019_mRNA_55.1 | - |
| GF0021902 | 1 | 1 | 0 | Hypothetical protein (2) | | Viral movement protein [IPR028919] (2) | scaffold_4_mRNA_1439.1 | C_unshiu_00019_mRNA_53.1 | - |
| GF0021901 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1438.1 | C_unshiu_00019_mRNA_52.1 | - |
| GF0021900 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1435.1 | C_unshiu_00019_mRNA_49.1 | - |
| GF0021899 | 1 | 1 | 0 | Hypothetical protein (2) | | Gag-polypeptide of LTR copia-type [IPR029472] (1) | scaffold_4_mRNA_1434.1 | C_unshiu_00019_mRNA_48.1 | - |
| GF0021898 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1432.1 | C_unshiu_00019_mRNA_46.1 | - |
| GF0021897 | 1 | 1 | 0 | Hypothetical protein (2) | | Leucine-rich repeat domain, L domain-like [IPR032675] (1) | scaffold_4_mRNA_1431.1 | C_unshiu_00019_mRNA_45.1 | - |
| GF0021896 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1430.1 | C_unshiu_00019_mRNA_44.1 | - |
| GF0021895 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1429.1 | C_unshiu_00019_mRNA_43.1 | - |
| GF0021894 | 1 | 1 | 0 | Hypothetical protein (2) | | Leucine-rich repeat domain, L domain-like [IPR032675] (2) | scaffold_4_mRNA_1428.1 | C_unshiu_00019_mRNA_42.1 | - |
| GF0021893 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1427.1 | C_unshiu_00019_mRNA_41.1 | - |
| GF0021892 | 1 | 1 | 0 | NAC transcription factors 48 (2) | regulation of transcription, DNA-templated [GO:0006355 biological_process] (2); DNA binding [GO:0003677 molecular_function] (2) | NAC domain [IPR003441] (2) | scaffold_4_mRNA_1426.1 | C_unshiu_00019_mRNA_40.1 | - |
| GF0021891 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1425.1 | C_unshiu_00019_mRNA_39.1 | - |
| GF0021890 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1423.1 | C_unshiu_00019_mRNA_37.1 | - |
| GF0021889 | 1 | 1 | 0 | Hypothetical protein (2) | regulation of transcription, DNA-templated [GO:0006355 biological_process] (2); DNA binding [GO:0003677 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (1) | NAC domain [IPR003441] (2); Endonuclease/exonuclease/phosphatase [IPR005135] (2); Ribonuclease H-like domain [IPR012337] (1) | scaffold_4_mRNA_1421.1 | C_unshiu_00019_mRNA_35.1 | - |
| GF0021888 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1417.1 | C_unshiu_00019_mRNA_31.1 | - |
| GF0021887 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1413.1 | C_unshiu_00019_mRNA_27.1 | - |
| GF0021886 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1412.1 | C_unshiu_00019_mRNA_26.1 | - |
| GF0021885 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1411.1 | C_unshiu_00019_mRNA_25.1 | - |
| GF0021884 | 1 | 1 | 0 | BED zinc finger,hAT family dimerization domain (2) | DNA binding [GO:0003677 molecular_function] (2); protein dimerization activity [GO:0046983 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | HAT, C-terminal dimerisation domain [IPR008906] (2); Ribonuclease H-like domain [IPR012337] (2); hAT-like transposase, RNase-H fold [IPR025525] (2); Zinc finger, BED-type [IPR003656] (2); Zinc finger C2H2-type [IPR013087] (1) | scaffold_4_mRNA_1410.1 | C_unshiu_00019_mRNA_24.1 | - |
| GF0021883 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1409.1 | C_unshiu_00019_mRNA_22.1 | - |
| GF0021882 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1408.1 | C_unshiu_00019_mRNA_21.1 | - |
| GF0021881 | 1 | 1 | 0 | Inner nuclear membrane Man1 (2) | integral component of nuclear inner membrane [GO:0005639 cellular_component] (2) | Inner nuclear membrane protein MAN1 [IPR018996] (2) | scaffold_4_mRNA_1407.1 | C_unshiu_00019_mRNA_20.1 | - |
| GF0021880 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1404.1 | C_unshiu_00019_mRNA_17.1 | - |
| GF0021879 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2); protein dimerization activity [GO:0046983 molecular_function] (2) | HAT, C-terminal dimerisation domain [IPR008906] (2); Ribonuclease H-like domain [IPR012337] (2) | scaffold_4_mRNA_1403.1 | C_unshiu_00019_mRNA_16.1 | - |
| GF0021878 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1398.1 | C_unshiu_00019_mRNA_10.1 | - |
| GF0021877 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1390.1 | C_unshiu_00061_mRNA_62.1 | - |
| GF0021875 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1379.1 | C_unshiu_00513_mRNA_4.1 | - |
| GF0021874 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1378.1 | C_unshiu_00513_mRNA_5.1 | - |
| GF0021873 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1376.1 | C_unshiu_00204_mRNA_10.1 | - |
| GF0021872 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1370.1 | C_unshiu_02291_mRNA_1.1 | - |
| GF0021871 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1368.1 | C_unshiu_02291_mRNA_3.1 | - |
| GF0021868 | 1 | 1 | 0 | RNA-directed DNA polymerase (Reverse transcriptase) (2) | | Reverse transcriptase domain [IPR000477] (2) | scaffold_4_mRNA_1343.1 | C_unshiu_00483_mRNA_14.1 | - |
| GF0021867 | 1 | 1 | 0 | Hypothetical protein (2) | | ATPase family AAA domain-containing protein 3, domain of unknown function DUF3523 [IPR021911] (2) | scaffold_4_mRNA_134.1 | C_unshiu_00012_mRNA_11.1 | - |
| GF0021866 | 1 | 1 | 0 | Hypothetical protein (2) | protein dimerization activity [GO:0046983 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2); DNA binding [GO:0003677 molecular_function] (2) | hAT-like transposase, RNase-H fold [IPR025525] (2); Ribonuclease H-like domain [IPR012337] (2); HAT, C-terminal dimerisation domain [IPR008906] (2) | scaffold_4_mRNA_1338.1 | C_unshiu_00483_mRNA_10.1 | - |
| GF0021865 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1337.1 | C_unshiu_00483_mRNA_9.1 | - |
| GF0021864 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1332.1 | C_unshiu_00483_mRNA_4.1 | - |
| GF0021863 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1328.1 | C_unshiu_00483_mRNA_2.1 | - |
| GF0021862 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1318.1 | C_unshiu_00028_mRNA_5.1 | - |
| GF0021861 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2); zinc ion binding [GO:0008270 molecular_function] (2) | Zinc finger, CCHC-type [IPR001878] (2) | scaffold_4_mRNA_1313.1 | C_unshiu_00908_mRNA_5.1 | - |
| GF0021860 | 1 | 1 | 0 | Hypothetical protein (2) | | Protein kinase-like domain [IPR011009] (1) | scaffold_4_mRNA_131.1 | C_unshiu_00012_mRNA_8.1 | - |
| GF0021857 | 1 | 1 | 0 | Hypothetical protein (2) | proteolysis [GO:0006508 biological_process] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1) | Aspartic peptidase domain [IPR021109] (1); Aspartic peptidase, active site [IPR001969] (1) | scaffold_4_mRNA_1299.1 | C_unshiu_00271_mRNA_45.1 | - |
| GF0021856 | 1 | 1 | 0 | Retrovirus-related Pol polyprotein from transposon 412 (2) | nucleic acid binding [GO:0003676 molecular_function] (2); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2); Ribonuclease H domain [IPR002156] (2) | scaffold_4_mRNA_1297.1 | C_unshiu_00308_mRNA_19.1 | - |
| GF0021855 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1294.1 | C_unshiu_00735_mRNA_1.1 | - |
| GF0021854 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (1) | Aspartic peptidase domain [IPR021109] (1); Ribonuclease H-like domain [IPR012337] (1) | scaffold_4_mRNA_1292.1 | C_unshiu_00735_mRNA_4.1 | - |
| GF0021853 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1272.1 | C_unshiu_00333_mRNA_10.1 | - |
| GF0021852 | 1 | 1 | 0 | Hypothetical protein (2) | | Protein-tyrosine phosphatase-like [IPR029021] (2); Myotubularin-like phosphatase domain [IPR010569] (2); Myotubularin family [IPR030564] (2) | scaffold_4_mRNA_1263.1 | C_unshiu_02303_mRNA_7.1 | - |
| GF0021851 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1259.1 | C_unshiu_00308_mRNA_24.1 | - |
| GF0021850 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1258.1 | C_unshiu_00308_mRNA_25.1 | - |
| GF0021849 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1256.1 | C_unshiu_00308_mRNA_27.1 | - |
| GF0021848 | 1 | 1 | 0 | Retrotransposon protein, putative, Ty3-gypsy subclass, expressed (2) | | Aspartic peptidase domain [IPR021109] (1) | scaffold_4_mRNA_1255.1 | C_unshiu_00308_mRNA_28.1 | - |
| GF0021847 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1254.1 | C_unshiu_00333_mRNA_7.1 | - |
| GF0021846 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1253.1 | C_unshiu_00333_mRNA_8.1 | - |
| GF0021845 | 1 | 1 | 0 | Hypothetical protein (2) | | Myotubularin-like phosphatase domain [IPR010569] (1); Myotubularin family [IPR030564] (1); Protein-tyrosine phosphatase-like [IPR029021] (1) | scaffold_4_mRNA_1250.1 | C_unshiu_00333_mRNA_9.1 | - |
| GF0021843 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1237.1 | C_unshiu_00809_mRNA_2.1 | - |
| GF0021842 | 1 | 1 | 0 | Hypothetical protein (2) | | Reverse transcriptase domain [IPR000477] (2) | scaffold_4_mRNA_1211.1 | C_unshiu_00140_mRNA_13.1 | - |
| GF0021841 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_121.1 | C_unshiu_00012_mRNA_1.1 | - |
| GF0021840 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1208.1 | C_unshiu_00140_mRNA_16.1 | - |
| GF0021839 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1207.1 | C_unshiu_00140_mRNA_17.1 | - |
| GF0021838 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1192.1 | C_unshiu_00140_mRNA_30.1 | - |
| GF0021837 | 1 | 1 | 0 | RNA-directed DNA polymerase (Reverse transcriptase) (2) | | Reverse transcriptase domain [IPR000477] (2) | scaffold_4_mRNA_1191.1 | C_unshiu_00140_mRNA_31.1 | - |
| GF0021836 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1182.1 | C_unshiu_00532_mRNA_23.1 | - |
| GF0021835 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1181.1 | C_unshiu_00532_mRNA_22.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0021834 | 1 | 1 | 0 | Hypothetical protein (2) | ATP binding [GO:0005524 molecular_function] (2); ATPase activity [GO:0016887 molecular_function] (2); membrane [GO:0016020 cellular_component] (2) | AAA+ ATPase domain [IPR003593] (2); ABC transporter-like [IPR003439] (2); ABC-2 type transporter [IPR013525] (2); ABC-transporter extracellular N-terminal domain [IPR029481] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); Plant PDR ABC transporter associated [IPR013581] (2) | scaffold_4_mRNA_1171.1 | C_unshiu_00532_mRNA_13.1 | - |
| GF0021833 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1170.1 | C_unshiu_00532_mRNA_12.1 | - |
| GF0021832 | 1 | 1 | 0 | Hypothetical protein (2) | | MULE transposase domain [IPR018289] (1) | scaffold_4_mRNA_1167.1 | C_unshiu_00532_mRNA_9.1 | - |
| GF0021831 | 1 | 1 | 0 | Protein kinase G11A (2) | ATP binding [GO:0005524 molecular_function] (2); protein kinase activity [GO:0004672 molecular_function] (2); protein serine/threonine kinase activity [GO:0004674 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2) | Protein kinase domain [IPR000719] (2); Protein kinase-like domain [IPR011009] (2); Serine/threonine-protein kinase, active site [IPR008271] (2); AGC-kinase, C-terminal [IPR000961] (2); Serine/threonine/dual specificity protein kinase, catalytic  domain [IPR002290] (1) | scaffold_4_mRNA_1163.1 | C_unshiu_00532_mRNA_5.1 | - |
| GF0021830 | 1 | 1 | 0 | FOG: Transposon-encoded proteins with TYA, reverse transcriptase, integrase domains in various combinations (1); Hypothetical protein (1) | zinc ion binding [GO:0008270 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | Zinc finger, CCHC-type [IPR001878] (2); Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1) | scaffold_4_mRNA_1160.1 | C_unshiu_00532_mRNA_2.1 | - |
| GF0021829 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1154.1 | C_unshiu_00440_mRNA_19.1 | - |
| GF0021828 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1153.1 | C_unshiu_00440_mRNA_18.1 | - |
| GF0021827 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1152.1 | C_unshiu_00440_mRNA_17.1 | - |
| GF0021826 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_4_mRNA_1151.1 | C_unshiu_00440_mRNA_16.1 | - |
| GF0021825 | 1 | 1 | 0 | Hypothetical protein (2) | DNA binding [GO:0003677 molecular_function] (2) | hAT-like transposase, RNase-H fold [IPR025525] (2) | scaffold_4_mRNA_1150.1 | C_unshiu_00440_mRNA_15.1 | - |
| GF0021824 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1149.1 | C_unshiu_00440_mRNA_14.1 | - |
| GF0021823 | 1 | 1 | 0 | Calmodulin-binding family protein isoform 1 (2) | | | scaffold_4_mRNA_1148.1 | C_unshiu_00440_mRNA_13.1 | - |
| GF0021822 | 1 | 1 | 0 | Unspecific monooxygenase (2) | heme binding [GO:0020037 molecular_function] (2); iron ion binding [GO:0005506 molecular_function] (2); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2) | Cytochrome P450, E-class, group I [IPR002401] (2); Cytochrome P450 [IPR001128] (2) | scaffold_4_mRNA_1142.1 | C_unshiu_00440_mRNA_5.1 | - |
| GF0021821 | 1 | 1 | 0 | Putative retroelement pol polyprotein (1); Hypothetical protein (1) | | | scaffold_4_mRNA_1141.1 | C_unshiu_00440_mRNA_4.1 | - |
| GF0021820 | 1 | 1 | 0 | Hypothetical protein (2) | methyltransferase activity [GO:0008168 molecular_function] (2) | Putative S-adenosyl-L-methionine-dependent methyltransferase [IPR004159] (2); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (2) | scaffold_4_mRNA_1139.1 | C_unshiu_00440_mRNA_2.1 | - |
| GF0021819 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1138.1 | C_unshiu_00440_mRNA_1.1 | - |
| GF0021818 | 1 | 1 | 0 | Hypothetical protein (2) | DNA binding [GO:0003677 molecular_function] (2); regulation of transcription, DNA-templated [GO:0006355 biological_process] (2); transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (2) | AP2/ERF domain [IPR001471] (2); DNA-binding domain [IPR016177] (2) | scaffold_4_mRNA_1136.1 | C_unshiu_00512_mRNA_19.1 | - |
| GF0021817 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1124.1 | C_unshiu_00101_mRNA_2.1 | - |
| GF0021816 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1122.1 | C_unshiu_01133_mRNA_6.1 | - |
| GF0021815 | 1 | 1 | 0 | RNA-directed DNA polymerase (2) | DNA integration [GO:0015074 biological_process] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2); Integrase, catalytic core [IPR001584] (2) | scaffold_4_mRNA_1118.1 | C_unshiu_00929_mRNA_2.1 | - |
| GF0021814 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2); Ribonuclease H domain [IPR002156] (2) | scaffold_4_mRNA_1117.1 | C_unshiu_00929_mRNA_3.1 | - |
| GF0021813 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1116.1 | C_unshiu_00929_mRNA_4.1 | - |
| GF0021812 | 1 | 1 | 0 | LRR receptor-like kinase family protein (2) | protein binding [GO:0005515 molecular_function] (2); protein kinase activity [GO:0004672 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2); ATP binding [GO:0005524 molecular_function] (2) | Protein kinase domain [IPR000719] (2); Leucine-rich repeat, typical subtype [IPR003591] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Protein kinase-like domain [IPR011009] (2); Protein kinase, ATP binding site [IPR017441] (2); Serine/threonine-protein kinase, active site [IPR008271] (2); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (2); Retrotransposon gag domain [IPR005162] (2); Leucine-rich repeat [IPR001611] (2); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Serine/threonine/dual specificity protein kinase, catalytic  domain [IPR002290] (1) | scaffold_4_mRNA_1113.1 | C_unshiu_00929_mRNA_6.1 | - |
| GF0021811 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1102.1 | C_unshiu_00922_mRNA_13.1 | - |
| GF0021810 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_110.1 | C_unshiu_00202_mRNA_32.1 | - |
| GF0021809 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1098.1 | C_unshiu_00725_mRNA_4.1 | - |
| GF0021808 | 1 | 1 | 0 | Putative non-LTR retroelement reverse transcriptase (2) | nucleic acid binding [GO:0003676 molecular_function] (2); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (2) | Reverse transcriptase domain [IPR000477] (2); Ribonuclease H-like domain [IPR012337] (2); Reverse transcriptase zinc-binding domain [IPR026960] (2); Ribonuclease H domain [IPR002156] (2); Endonuclease/exonuclease/phosphatase [IPR005135] (2) | scaffold_4_mRNA_1097.1 | C_unshiu_00725_mRNA_5.1 | - |
| GF0021807 | 1 | 1 | 0 | Hypothetical protein (2) | protein binding [GO:0005515 molecular_function] (1) | Leucine-rich repeat domain, L domain-like [IPR032675] (2); Leucine-rich repeat [IPR001611] (1); Protein kinase-like domain [IPR011009] (1) | scaffold_4_mRNA_1096.1 | C_unshiu_00725_mRNA_8.1 | - |
| GF0021806 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_109.1 | C_unshiu_00202_mRNA_31.1 | - |
| GF0021805 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1084.1 | C_unshiu_00111_mRNA_2.1 | - |
| GF0021804 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1083.1 | C_unshiu_00111_mRNA_3.1 | - |
| GF0021803 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1077.1 | C_unshiu_00111_mRNA_9.1 | - |
| GF0021802 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1074.1 | C_unshiu_00111_mRNA_12.1 | - |
| GF0021801 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1067.1 | C_unshiu_00111_mRNA_19.1 | - |
| GF0021800 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1066.1 | C_unshiu_00111_mRNA_20.1 | - |
| GF0021799 | 1 | 1 | 0 | WD repeat-containing protein 5 (2) | protein binding [GO:0005515 molecular_function] (2) | WD40 repeat [IPR001680] (2); WD40-repeat-containing domain [IPR017986] (2); WD40/YVTN repeat-like-containing domain [IPR015943] (2) | scaffold_4_mRNA_1064.1 | C_unshiu_00111_mRNA_22.1 | - |
| GF0021798 | 1 | 1 | 0 | PIF-like orf1 (1); Hypothetical protein (1) | | Myb/SANT-like domain [IPR024752] (1) | scaffold_4_mRNA_1062.1 | C_unshiu_00111_mRNA_23.1 | - |
| GF0021797 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1060.1 | C_unshiu_00111_mRNA_27.1 | - |
| GF0021796 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1059.1 | C_unshiu_00111_mRNA_28.1 | - |
| GF0021795 | 1 | 1 | 0 | FBD, F-box and leucine rich repeat domain-containing protein (2) | protein binding [GO:0005515 molecular_function] (2) | FBD domain [IPR006566] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); F-box domain [IPR001810] (2) | scaffold_4_mRNA_1058.1 | C_unshiu_00111_mRNA_29.1 | - |
| GF0021794 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1055.1 | C_unshiu_00111_mRNA_33.1 | - |
| GF0021793 | 1 | 1 | 0 | Hypothetical protein (2) | | Transposase, MuDR, plant [IPR004332] (2) | scaffold_4_mRNA_1054.1 | C_unshiu_00111_mRNA_34.1 | - |
| GF0021792 | 1 | 1 | 0 | Putative inorganic polyphosphate/atp-nad kinase (2) | | | scaffold_4_mRNA_1043.1 | C_unshiu_00932_mRNA_4.1 | - |
| GF0021791 | 1 | 1 | 0 | Nepenthesin II (2) | aspartic-type endopeptidase activity [GO:0004190 molecular_function] (2); electron carrier activity [GO:0009055 molecular_function] (2); proteolysis [GO:0006508 biological_process] (2) | Aspartic peptidase, active site [IPR001969] (2); Aspartic peptidase A1 family [IPR001461] (2); Xylanase inhibitor, C-terminal [IPR032799] (2); Xylanase inhibitor, N-terminal [IPR032861] (2); Cupredoxin [IPR008972] (2); Peptidase family A1 domain [IPR033121] (2); Phytocyanin domain [IPR003245] (2); Aspartic peptidase domain [IPR021109] (2); Pepsin-like domain, plant [IPR034161] (1) | scaffold_4_mRNA_1039.1 | C_unshiu_00932_mRNA_9.1 | - |
| GF0021790 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1035.1 | C_unshiu_00932_mRNA_11.1 | - |
| GF0021789 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_103.1 | C_unshiu_00202_mRNA_25.1 | - |
| GF0021788 | 1 | 1 | 0 | Hypothetical protein (2) | aspartic-type endopeptidase activity [GO:0004190 molecular_function] (2); proteolysis [GO:0006508 biological_process] (2) | Aspartic peptidase A1 family [IPR001461] (2); Xylanase inhibitor, C-terminal [IPR032799] (2); Aspartic peptidase domain [IPR021109] (2) | scaffold_4_mRNA_1025.1 | C_unshiu_00059_mRNA_20.1 | - |
| GF0021787 | 1 | 1 | 0 | Putative glycosyltransferase family protein 64 protein C5-like (1); Glycosyltransferase family protein 64 protein C5 (1) | glycosaminoglycan biosynthetic process [GO:0006024 biological_process] (2); heparan sulfate proteoglycan biosynthetic process [GO:0015012 biological_process] (2); integral component of membrane [GO:0016021 cellular_component] (2) | Nucleotide-diphospho-sugar transferases [IPR029044] (2); Glycosyl hydrolase, five-bladed beta-propellor domain [IPR023296] (2); Exostosin , C-terminal [IPR015338] (2) | scaffold_4_mRNA_1021.1 | C_unshiu_00059_mRNA_23.1 | - |
| GF0021786 | 1 | 1 | 0 | Monosacharide transport protein (2) | | | scaffold_4_mRNA_1019.1 | C_unshiu_00059_mRNA_26.1 | - |
| GF0021785 | 1 | 1 | 0 | Hypothetical protein (2) | | Aspartic peptidase domain [IPR021109] (2) | scaffold_4_mRNA_1017.1 | C_unshiu_00059_mRNA_28.1 | - |
| GF0021784 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1016.1 | C_unshiu_00059_mRNA_29.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0021783 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_4_mRNA_1012.1 | C_unshiu_00059_mRNA_33.1 | - |
| GF0021781 | 1 | 1 | 0 | Hypothetical protein (1); Serine carboxypeptidase S28 family protein (1) | proteolysis [GO:0006508 biological_process] (2); serine-type peptidase activity [GO:0008236 molecular_function] (2) | Peptidase S28 [IPR008758] (2) | scaffold_4_mRNA_1006.1 | C_unshiu_00059_mRNA_38.1 | - |
| GF0021780 | 1 | 1 | 0 | Hypothetical protein (2) | zinc ion binding [GO:0008270 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | Matrin/U1-C-like, C2H2-type zinc finger [IPR003604] (1); Zinc finger C2H2-type [IPR013087] (1); Zinc finger, U1-type [IPR003604] (1); Zinc finger, C2H2-like [IPR015880] (1) | scaffold_4_mRNA_1000.1 | C_unshiu_01189_mRNA_6.1 | - |
| GF0021779 | 1 | 1 | 0 | Pre-mRNA-splicing factor ATP-dependent RNA helicase (2) | helicase activity [GO:0004386 molecular_function] (2); ATP-dependent helicase activity [GO:0008026 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2); ATP binding [GO:0005524 molecular_function] (2) | Helicase-associated domain [IPR007502] (2); Helicase, C-terminal [IPR001650] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); DNA/RNA helicase, ATP-dependent, DEAH-box type, conserved site [IPR002464] (2); Helicase superfamily 1/2, ATP-binding domain [IPR014001] (2) | scaffold_3_mRNA_990.1 | C_unshiu_00199_mRNA_16.1 | - |
| GF0021778 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_988.1 | C_unshiu_00199_mRNA_19.1 | - |
| GF0021776 | 1 | 1 | 0 | DNA-directed RNA polymerase D subunit 1-like protein (2) | | Protein of unknown function DUF3223 [IPR021602] (2) | scaffold_3_mRNA_977.1 | C_unshiu_00199_mRNA_27.1 | - |
| GF0021770 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_930.1 | C_unshiu_00587_mRNA_2.1 | - |
| GF0021769 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_925.1 | C_unshiu_00345_mRNA_9.1 | - |
| GF0021768 | 1 | 1 | 0 | Subtilisin-like serine endopeptidase family protein (1); Subtilisin-like serine endopeptidase family protein, putative (1) | serine-type endopeptidase activity [GO:0004252 molecular_function] (2); proteolysis [GO:0006508 biological_process] (2) | Peptidase S8/S53 domain [IPR000209] (2); Peptidase S8, subtilisin-related [IPR015500] (2); Peptidase S8 propeptide/proteinase inhibitor I9 [IPR010259] (2); Peptidase S8, subtilisin, Ser-active site [IPR023828] (2); Cucumisin-like catalytic domain [IPR034197] (1) | scaffold_3_mRNA_908.1 | C_unshiu_01872_mRNA_3.1 | - |
| GF0021767 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_883.1 | C_unshiu_00956_mRNA_4.1 | - |
| GF0021765 | 1 | 1 | 0 | Putative sugar phosphate/phosphate translocator (2) | | Sugar phosphate transporter domain [IPR004853] (2) | scaffold_3_mRNA_874.1 | C_unshiu_00412_mRNA_29.1 | - |
| GF0021764 | 1 | 1 | 0 | Hypothetical protein (2) | protein serine/threonine phosphatase activity [GO:0004722 molecular_function] (2); protein dephosphorylation [GO:0006470 biological_process] (2); catalytic activity [GO:0003824 molecular_function] (2) | Protein phosphatase 2C family [IPR015655] (2); PPM-type phosphatase domain [IPR001932] (2) | scaffold_3_mRNA_84.1 | C_unshiu_00850_mRNA_16.1 | - |
| GF0021762 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1) | Ribonuclease H-like domain [IPR012337] (2); Ribonuclease H domain [IPR002156] (1) | scaffold_3_mRNA_833.1 | C_unshiu_01147_mRNA_13.1 | - |
| GF0021760 | 1 | 1 | 0 | MRNAadenosine methylase isoform 1 (2) | nucleobase-containing compound metabolic process [GO:0006139 biological_process] (2); methyltransferase activity [GO:0008168 molecular_function] (2) | MT-A70-like [IPR007757] (2); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (2) | scaffold_3_mRNA_83.1 | C_unshiu_00850_mRNA_17.1 | - |
| GF0021759 | 1 | 1 | 0 | UPF0551 protein C8orf38 (2) | transferase activity [GO:0016740 molecular_function] (2); biosynthetic process [GO:0009058 biological_process] (2) | Squalene/phytoene synthase [IPR002060] (2); Isoprenoid synthase domain [IPR008949] (2) | scaffold_3_mRNA_818.1 | C_unshiu_00159_mRNA_42.1 | - |
| GF0021756 | 1 | 1 | 0 | Phosphoenolpyruvate carboxylase family protein (2) | catalytic activity [GO:0003824 molecular_function] (2) | Pyruvate/Phosphoenolpyruvate kinase-like domain [IPR015813] (2); HpcH/HpaI aldolase/citrate lyase domain [IPR005000] (2) | scaffold_3_mRNA_80.1 | C_unshiu_01206_mRNA_1.1 | - |
| GF0021752 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_785.1 | C_unshiu_00179_mRNA_24.1 | - |
| GF0021751 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_780.1 | C_unshiu_00179_mRNA_19.1 | - |
| GF0021750 | 1 | 1 | 0 | Glucuronosyltransferase PGSIP8 (2) | | Nucleotide-diphospho-sugar transferases [IPR029044] (2) | scaffold_3_mRNA_767.1 | C_unshiu_01746_mRNA_10.1 | - |
| GF0021749 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_763.1 | C_unshiu_01746_mRNA_7.1 | - |
| GF0021748 | 1 | 1 | 0 | ATP-dependent caseinolytic protease/crotonase family protein isoform 2 (2) | hydro-lyase activity [GO:0016836 molecular_function] (1); 3-hydroxyisobutyryl-CoA hydrolase activity [GO:0003860 molecular_function] (1) | ClpP/crotonase-like domain [IPR029045] (2); Enoyl-CoA hydratase/isomerase, HIBYL-CoA-H type [IPR032259] (2) | scaffold_3_mRNA_750.1 | C_unshiu_02184_mRNA_3.1 | - |
| GF0021744 | 1 | 1 | 0 | Hypothetical protein (2) | palmitoyl hydrolase activity [GO:0098599 molecular_function] (2) | Palmitoyl protein thioesterase [IPR002472] (2); Alpha/Beta hydrolase fold [IPR029058] (2) | scaffold_3_mRNA_722.1 | C_unshiu_00442_mRNA_9.1 | - |
| GF0021743 | 1 | 1 | 0 | Ethylene responsive element binding factor, putative (2) | DNA binding [GO:0003677 molecular_function] (2); transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (2); regulation of transcription, DNA-templated [GO:0006355 biological_process] (2) | DNA-binding domain [IPR016177] (2); AP2/ERF domain [IPR001471] (2) | scaffold_3_mRNA_718.1 | C_unshiu_00795_mRNA_3.1 | - |
| GF0021742 | 1 | 1 | 0 | G-type lectin S-receptor-like serine/threonine-protein kinase RLK1 (2) | protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1) | Bulb-type lectin domain [IPR001480] (2); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Protein kinase, ATP binding site [IPR017441] (1) | scaffold_3_mRNA_712.1 | C_unshiu_00795_mRNA_9.1 | - |
| GF0021741 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_699.1 | C_unshiu_00795_mRNA_11.1 | - |
| GF0021740 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_687.1 | C_unshiu_01638_mRNA_5.1 | - |
| GF0021738 | 1 | 1 | 0 | Transcription factor IIIB 90 kDa subunit (2) | | | scaffold_3_mRNA_669.1 | C_unshiu_00628_mRNA_5.1 | - |
| GF0021737 | 1 | 1 | 0 | Expansin-like B1 (2) | extracellular region [GO:0005576 cellular_component] (2) | Expansin/pollen allergen, DPBB domain [IPR007112] (2); Expansin/Lol pI [IPR007118] (2); Expansin, cellulose-binding-like domain [IPR007117] (2); RlpA-like double-psi beta-barrel domain [IPR009009] (1); RlpA-like protein, double-psi beta-barrel domain [IPR009009] (1) | scaffold_3_mRNA_664.1 | C_unshiu_01811_mRNA_3.1 | - |
| GF0021735 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_657.1 | C_unshiu_00768_mRNA_12.1 | - |
| GF0021734 | 1 | 1 | 0 | Subtilisin-like serine protease (2) | serine-type endopeptidase activity [GO:0004252 molecular_function] (2); proteolysis [GO:0006508 biological_process] (2) | Peptidase S8, subtilisin, Asp-active site [IPR023827] (2); Peptidase S8, subtilisin-related [IPR015500] (2); Peptidase S8/S53 domain [IPR000209] (2); Peptidase S8 propeptide/proteinase inhibitor I9 [IPR010259] (2); Cucumisin-like catalytic domain [IPR034197] (1); Peptidase S8, subtilisin, Ser-active site [IPR023828] (1) | scaffold_3_mRNA_656.1 | C_unshiu_00768_mRNA_11.1 | - |
| GF0021732 | 1 | 1 | 0 | Putative vacuolar sorting-associated protein 13B (1); Hypothetical protein (1) | | Vacuolar protein sorting-associated protein 62 [IPR009291] (2); Vacuolar protein sorting-associated protein 13 [IPR026847] (2); PH domain-like [IPR011993] (2); Vacuolar protein sorting-associated protein 13, SHR-binding domain [IPR009543] (2); Pleckstrin homology domain [IPR001849] (2); VPS13, repeated coiled region [IPR031642] (2); Vacuolar protein sorting-associated protein 13, second N-terminal domain [IPR031646] (1); Vacuolar protein sorting-associated protein 13, N-terminal domain [IPR026854] (1) | scaffold_3_mRNA_633.1 | C_unshiu_00128_mRNA_2.1 | - |
| GF0021731 | 1 | 1 | 0 | Putative vacuolar sorting-associated protein 13A (2) | | Vacuolar protein sorting-associated protein 13, second N-terminal domain [IPR031646] (2); Vacuolar protein sorting-associated protein 13 [IPR026847] (2); Vacuolar protein sorting-associated protein 13, N-terminal domain [IPR026854] (2) | scaffold_3_mRNA_632.1 | C_unshiu_02656_mRNA_1.1 | - |
| GF0021729 | 1 | 1 | 0 | Heavy metal transport/detoxification superfamily protein (2) | metal ion binding [GO:0046872 molecular_function] (2); metal ion transport [GO:0030001 biological_process] (2) | Heavy metal-associated domain, HMA [IPR006121] (2) | scaffold_3_mRNA_6269.1 | C_unshiu_00971_mRNA_8.1 | - |
| GF0021728 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_6265.1 | C_unshiu_00971_mRNA_4.1 | - |
| GF0021723 | 1 | 1 | 0 | Hypothetical protein (1); Protein WAX2 (1) | iron ion binding [GO:0005506 molecular_function] (2); oxidoreductase activity [GO:0016491 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2); fatty acid biosynthetic process [GO:0006633 biological_process] (1); lipid biosynthetic process [GO:0008610 biological_process] (1) | Fatty acid hydroxylase [IPR006694] (2); Uncharacterised domain Wax2, C-terminal [IPR021940] (2) | scaffold_3_mRNA_6255.2 | C_unshiu_00206_mRNA_42.1 | - |
| GF0021722 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_6234.1 | C_unshiu_00206_mRNA_22.1 | - |
| GF0021719 | 1 | 1 | 0 | Blue copper protein (2) | electron carrier activity [GO:0009055 molecular_function] (2) | Phytocyanin domain [IPR003245] (2); Cupredoxin [IPR008972] (2) | scaffold_3_mRNA_6219.1 | C_unshiu_00206_mRNA_6.1 | - |
| GF0021718 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_3_mRNA_6206.1 | C_unshiu_00014_mRNA_107.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0021717 | 1 | 1 | 0 | Hypothetical protein (2) | metal ion binding [GO:0046872 molecular_function] (2); nucleotide binding [GO:0000166 molecular_function] (2); integral component of membrane [GO:0016021 cellular_component] (1) | P-type ATPase, cytoplasmic domain N [IPR023299] (2); Uncharacterised protein family UPF0565 [IPR018881] (2); Cation-transporting P-type ATPase, N-terminal [IPR004014] (2); P-type ATPase, A domain [IPR008250] (2); P-type ATPase, transmembrane domain [IPR023298] (1); P-type ATPase [IPR001757] (1) | scaffold_3_mRNA_6202.1 | C_unshiu_00014_mRNA_103.1 | - |
| GF0021716 | 1 | 1 | 0 | 2-hydroxymuconic semialdehyde hydrolase (2) | | Alpha/Beta hydrolase fold [IPR029058] (2); Alpha/beta hydrolase fold-1 [IPR000073] (2) | scaffold_3_mRNA_62.1 | C_unshiu_00838_mRNA_7.1 | - |
| GF0021715 | 1 | 1 | 0 | Malate dehydrogenase (2) | carbohydrate metabolic process [GO:0005975 biological_process] (2); catalytic activity [GO:0003824 molecular_function] (2); malate dehydrogenase activity [GO:0016615 molecular_function] (2); oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor [GO:0016616 molecular_function] (2); L-malate dehydrogenase activity [GO:0030060 molecular_function] (2); malate metabolic process [GO:0006108 biological_process] (2); oxidation-reduction process [GO:0055114 biological_process] (2); oxidoreductase activity [GO:0016491 molecular_function] (2); carboxylic acid metabolic process [GO:0019752 biological_process] (2) | Lactate/malate dehydrogenase, N-terminal [IPR001236] (2); Malate dehydrogenase, active site [IPR001252] (2); Malate dehydrogenase, NAD-dependent, cytosolic [IPR011274] (2); Lactate dehydrogenase/glycoside hydrolase, family 4, C-terminal [IPR015955] (2); Malate dehydrogenase, type 2 [IPR010945] (2); Lactate/malate dehydrogenase, C-terminal [IPR022383] (2); L-lactate/malate dehydrogenase [IPR001557] (2); NAD(P)-binding domain [IPR016040] (2) | scaffold_3_mRNA_6175.1 | C_unshiu_00014_mRNA_77.1 | - |
| GF0021713 | 1 | 1 | 0 | Putative crossover junction endodeoxyribonuclease (2) | rRNA processing [GO:0006364 biological_process] (2); nucleobase-containing compound metabolic process [GO:0006139 biological_process] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2); Putative pre-16S rRNA nuclease [IPR005227] (2); YqgF/RNase H-like domain [IPR006641] (2) | scaffold_3_mRNA_6154.1 | C_unshiu_00014_mRNA_61.1 | - |
| GF0021712 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_6152.1 | C_unshiu_00014_mRNA_58.1 | - |
| GF0021711 | 1 | 1 | 0 | Cytochrome P450 (2) | | | scaffold_3_mRNA_6151.2 | C_unshiu_00014_mRNA_57.2 | - |
| GF0021709 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_6134.1 | C_unshiu_00014_mRNA_42.1 | - |
| GF0021708 | 1 | 1 | 0 | SAUR family protein (2) | response to auxin [GO:0009733 biological_process] (2) | Small auxin-up RNA [IPR003676] (2) | scaffold_3_mRNA_6133.1 | C_unshiu_00014_mRNA_41.1 | - |
| GF0021707 | 1 | 1 | 0 | Hypothetical protein (2) | pectinesterase activity [GO:0030599 molecular_function] (2); cell wall [GO:0005618 cellular_component] (2); cell wall modification [GO:0042545 biological_process] (2); enzyme inhibitor activity [GO:0004857 molecular_function] (1) | Pectinesterase, catalytic [IPR000070] (2); Pectin lyase fold [IPR012334] (2); Pectin lyase fold/virulence factor [IPR011050] (2); Pectinesterase inhibitor domain [IPR006501] (1) | scaffold_3_mRNA_6130.1 | C_unshiu_00014_mRNA_38.1 | - |
| GF0021706 | 1 | 1 | 0 | Methionyl aminopeptidase (2) | proteolysis [GO:0006508 biological_process] (2); aminopeptidase activity [GO:0004177 molecular_function] (2); metalloexopeptidase activity [GO:0008235 molecular_function] (2) | Peptidase M24A, methionine aminopeptidase, subfamily 1 [IPR002467] (2); MYND-like zinc finger, mRNA-binding [IPR031615] (2); Peptidase M24, methionine aminopeptidase [IPR001714] (2); Peptidase M24 [IPR000994] (1); Peptidase M24, structural domain [IPR000994] (1) | scaffold_3_mRNA_6129.1 | C_unshiu_00014_mRNA_37.1 | - |
| GF0021705 | 1 | 1 | 0 | Hypothetical protein (1); Meiotic recombination protein DMC1 homolog (1) | ATP binding [GO:0005524 molecular_function] (2); DNA binding [GO:0003677 molecular_function] (2); DNA repair [GO:0006281 biological_process] (2); DNA-dependent ATPase activity [GO:0008094 molecular_function] (2) | DNA recombination and repair protein RecA-like, ATP-binding domain [IPR020588] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); DNA recombination and repair protein Rad51, C-terminal [IPR013632] (1); DNA recombination and repair protein Rad51-like, C-terminal [IPR013632] (1) | scaffold_3_mRNA_6120.1 | C_unshiu_00014_mRNA_28.1 | - |
| GF0021704 | 1 | 1 | 0 | Glutathione S-transferase zeta class (2) | catalytic activity [GO:0003824 molecular_function] (2); protein binding [GO:0005515 molecular_function] (2); aromatic amino acid family metabolic process [GO:0009072 biological_process] (2); cytoplasm [GO:0005737 cellular_component] (2) | Thioredoxin-like fold [IPR012336] (2); Glutathione S-transferase, N-terminal [IPR004045] (2); Glutathione S-transferase, C-terminal-like [IPR010987] (2); Glutathione S-transferases, class Zeta [IPR005955] (1); Glutathione S-transferases, class Zeta , N-terminal [IPR034333] (1); Glutathione S-transferases, class Zeta , C-terminal [IPR034330] (1); Maleylacetoacetate isomerase [IPR005955] (1) | scaffold_3_mRNA_6107.1 | C_unshiu_00014_mRNA_16.1 | - |
| GF0021702 | 1 | 1 | 0 | Putative calcium-binding protein CML25 (2) | calcium ion binding [GO:0005509 molecular_function] (2) | EF-Hand 1, calcium-binding site [IPR018247] (2); EF-hand domain [IPR002048] (2); EF-hand domain pair [IPR011992] (2) | scaffold_3_mRNA_6094.1 | C_unshiu_00126_mRNA_49.1 | - |
| GF0021693 | 1 | 1 | 0 | Hypothetical protein (2) | DNA binding [GO:0003677 molecular_function] (1); nucleus [GO:0005634 cellular_component] (1) | Methyl-CpG DNA binding [IPR001739] (1); DNA-binding domain [IPR016177] (1) | scaffold_3_mRNA_6032.1 | C_unshiu_00018_mRNA_116.1 | - |
| GF0021690 | 1 | 1 | 0 | Adenosine deaminases,RNA binding,RNA binding,adenosine deaminases, putative isoform 2 (2) | adenosine deaminase activity [GO:0004000 molecular_function] (2); RNA binding [GO:0003723 molecular_function] (2); RNA processing [GO:0006396 biological_process] (2) | Adenosine deaminase/editase [IPR002466] (2) | scaffold_3_mRNA_6010.1 | C_unshiu_00018_mRNA_99.1 | - |
| GF0021689 | 1 | 1 | 0 | Ripening related protein family (2) | | | scaffold_3_mRNA_6003.1 | C_unshiu_00018_mRNA_92.1 | - |
| GF0021688 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_6.1 | C_unshiu_01604_mRNA_6.1 | - |
| GF0021686 | 1 | 1 | 0 | Cysteine synthase (2) | cyanide metabolic process [GO:0019499 biological_process] (2); mitochondrion [GO:0005739 cellular_component] (2); L-3-cyanoalanine synthase activity [GO:0050017 molecular_function] (2); cysteine biosynthetic process from serine [GO:0006535 biological_process] (2); cysteine synthase activity [GO:0004124 molecular_function] (2) | Cysteine synthase CysK [IPR005859] (2); L-3-cyanoalanine synthase, mitochondrial [IPR031111] (2); Cysteine synthase/cystathionine beta-synthase, pyridoxal-phosphate attachment site [IPR001216] (2); Tryptophan synthase beta subunit-like PLP-dependent enzyme [IPR001926] (2); Cysteine synthase [IPR005856] (2) | scaffold_3_mRNA_5969.1 | C_unshiu_00018_mRNA_60.1 | - |
| GF0021685 | 1 | 1 | 0 | ATP-dependent helicase BRM (2) | ATP binding [GO:0005524 molecular_function] (2); nucleus [GO:0005634 cellular_component] (2); DNA-dependent ATPase activity [GO:0008094 molecular_function] (2); regulation of gene expression, epigenetic [GO:0040029 biological_process] (2); ATP-dependent chromatin remodeling [GO:0043044 biological_process] (2); regulation of transcription, DNA-templated [GO:0006355 biological_process] (2); protein binding [GO:0005515 molecular_function] (1) | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); BRAHMA (BRM) ATPase [IPR031056] (2); Glutamine-Leucine-Glutamine, QLQ [IPR014978] (2); Helicase superfamily 1/2, ATP-binding domain [IPR014001] (2); SNF2-related, N-terminal domain [IPR000330] (2); Helicase, C-terminal [IPR001650] (2); Bromodomain [IPR001487] (1) | scaffold_3_mRNA_5968.1 | C_unshiu_00018_mRNA_59.1 | - |
| GF0021684 | 1 | 1 | 0 | Ubiquitin-conjugating enzyme E2 5 (2) | | Ubiquitin-conjugating enzyme, active site [IPR023313] (2); Ubiquitin-conjugating enzyme/RWD-like [IPR016135] (2); Ubiquitin-conjugating enzyme E2 [IPR000608] (2) | scaffold_3_mRNA_5967.1 | C_unshiu_00018_mRNA_58.1 | - |
| GF0021683 | 1 | 1 | 0 | AT-rich interactive domain-containing protein 1 (2) | DNA binding [GO:0003677 molecular_function] (2) | ARID DNA-binding domain [IPR001606] (2); ELM2 domain [IPR000949] (1) | scaffold_3_mRNA_5966.1 | C_unshiu_00018_mRNA_57.1 | - |
| GF0021678 | 1 | 1 | 0 | Reticulon-like protein B8 (2) | | Reticulon [IPR003388] (2) | scaffold_3_mRNA_5927.1 | C_unshiu_00018_mRNA_19.1 | - |
| GF0021677 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_5923.1 | C_unshiu_00018_mRNA_15.1 | - |
| GF0021676 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_5914.1 | C_unshiu_00026_mRNA_40.1 | - |
| GF0021675 | 1 | 1 | 0 | BTB/POZ domain-containing protein POB1 (2) | protein binding [GO:0005515 molecular_function] (2) | TRAF-like [IPR008974] (2); BTB/POZ domain [IPR000210] (2); BTB/Kelch-associated [IPR011705] (2); SKP1/BTB/POZ domain [IPR011333] (2) | scaffold_3_mRNA_5909.1 | C_unshiu_00026_mRNA_43.1 | - |
| GF0021673 | 1 | 1 | 0 | Arabinogalactan protein 20 (2) | | Arabinogalactan peptide, AGP [IPR009424] (2) | scaffold_3_mRNA_5901.1 | C_unshiu_00026_mRNA_51.1 | - |
| GF0021670 | 1 | 1 | 0 | Kinase superfamily protein, putative isoform 1 (1); Kinase superfamily protein, putative isoform 2 (1) | ATP binding [GO:0005524 molecular_function] (2); protein kinase activity [GO:0004672 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2) | Protein kinase-like domain [IPR011009] (2); Protein kinase domain [IPR000719] (2); Serine/threonine-protein kinase, active site [IPR008271] (2); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1) | scaffold_3_mRNA_589.1 | C_unshiu_01817_mRNA_6.1 | - |
| GF0021669 | 1 | 1 | 0 | Poly(A) RNA polymerase cid14 (2) | | | scaffold_3_mRNA_5884.1 | C_unshiu_00026_mRNA_66.1 | - |
| GF0021668 | 1 | 1 | 0 | DUF1442 family protein (2) | | Protein of unknown function DUF1442 [IPR009902] (2); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (2) | scaffold_3_mRNA_5871.1 | C_unshiu_00026_mRNA_80.1 | - |
| GF0021667 | 1 | 1 | 0 | Hypothetical protein (2) | oxidation-reduction process [GO:0055114 biological_process] (2); UDP-N-acetylmuramate dehydrogenase activity [GO:0008762 molecular_function] (2) | UDP-N-acetylenolpyruvoylglucosamine reductase, C-terminal [IPR011601] (2) | scaffold_3_mRNA_5866.1 | C_unshiu_00026_mRNA_87.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0021666 | 1 | 1 | 0 | Molybdenum cofactor biosynthesis protein C (2) | Mo-molybdopterin cofactor biosynthetic process [GO:0006777 biological_process] (2) | Molybdopterin cofactor biosynthesis C (MoaC) domain [IPR002820] (2); Molybdenum cofactor biosynthesis C [IPR023045] (2); Molybdenum cofactor biosynthesis C, bacterial-type [IPR023046] (1) | scaffold_3_mRNA_5865.1 | C_unshiu_00026_mRNA_88.2 | - |
| GF0021665 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_5858.1 | C_unshiu_00261_mRNA_20.1 | - |
| GF0021663 | 1 | 1 | 0 | Krueppel-like factor 17 (2) | | | scaffold_3_mRNA_5853.1 | C_unshiu_00261_mRNA_15.1 | - |
| GF0021660 | 1 | 1 | 0 | Spotted leaf protein, putative (2) | protein ubiquitination [GO:0016567 biological_process] (2); ubiquitin-protein transferase activity [GO:0004842 molecular_function] (2); protein binding [GO:0005515 molecular_function] (2); binding [GO:0005488 molecular_function] (2) | Armadillo-type fold [IPR016024] (2); Armadillo [IPR000225] (2); U box domain [IPR003613] (2); Armadillo-like helical [IPR011989] (2); Zinc finger, RING/FYVE/PHD-type [IPR013083] (2); Powdery mildew resistance protein, RPW8 domain [IPR008808] (1) | scaffold_3_mRNA_5838.1 | C_unshiu_00978_mRNA_2.1 | - |
| GF0021659 | 1 | 1 | 0 | Translation initiation factor IF-2 (2) | | Protein of unknown function DUF4079 [IPR025067] (2) | scaffold_3_mRNA_5833.1 | C_unshiu_00978_mRNA_7.1 | - |
| GF0021658 | 1 | 1 | 0 | Isoflavone reductase family protein (2) | | | scaffold_3_mRNA_5832.1 | C_unshiu_00978_mRNA_8.1 | - |
| GF0021657 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_5827.1 | C_unshiu_01669_mRNA_2.1 | - |
| GF0021656 | 1 | 1 | 0 | Hypothetical protein (1); D-arabinono-1,4-lactone oxidase family protein (1) | oxidation-reduction process [GO:0055114 biological_process] (2); D-arabinono-1,4-lactone oxidase activity [GO:0003885 molecular_function] (2); membrane [GO:0016020 cellular_component] (2); protein binding [GO:0005515 molecular_function] (1) | D-arabinono-1,4-lactone oxidase [IPR007173] (2); L-gulonolactone oxidase, plant [IPR010030] (2); IQ motif, EF-hand binding site [IPR000048] (1) | scaffold_3_mRNA_5811.1 | C_unshiu_00023_mRNA_95.1 | - |
| GF0021655 | 1 | 1 | 0 | DELLA protein (1); DELLA protein RGL3 (1) | | Transcription factor GRAS [IPR005202] (2) | scaffold_3_mRNA_580.1 | C_unshiu_00318_mRNA_5.1 | - |
| GF0021653 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_5782.1 | C_unshiu_00023_mRNA_69.1 | - |
| GF0021652 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_578.1 | C_unshiu_00318_mRNA_7.1 | - |
| GF0021650 | 1 | 1 | 0 | Nodulin MtN21 family protein (2) | integral component of membrane [GO:0016021 cellular_component] (2); membrane [GO:0016020 cellular_component] (2); transmembrane transporter activity [GO:0022857 molecular_function] (2) | WAT1-related protein [IPR030184] (2); EamA domain [IPR000620] (2) | scaffold_3_mRNA_5772.1 | C_unshiu_00023_mRNA_56.1 | - |
| GF0021649 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_5741.1 | C_unshiu_00023_mRNA_24.1 | - |
| GF0021646 | 1 | 1 | 0 | ABC transporter B family member 4 (1); ABC transporter B family member 11 (1) | ATP binding [GO:0005524 molecular_function] (2); transmembrane transport [GO:0055085 biological_process] (2); ATPase activity, coupled to transmembrane movement of substances [GO:0042626 molecular_function] (2); transport [GO:0006810 biological_process] (2); integral component of membrane [GO:0016021 cellular_component] (2); ATPase activity [GO:0016887 molecular_function] (2); transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (1) | ABC transporter, conserved site [IPR017871] (2); AAA+ ATPase domain [IPR003593] (2); ABC transporter type 1, transmembrane domain [IPR011527] (2); ABC transporter-like [IPR003439] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); Transferase [IPR003480] (1); Chloramphenicol acetyltransferase-like domain [IPR023213] (1) | scaffold_3_mRNA_5728.1 | C_unshiu_00023_mRNA_11.1 | - |
| GF0021642 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_5705.1 | C_unshiu_01229_mRNA_1.1 | - |
| GF0021640 | 1 | 1 | 0 | Hypothetical protein (2) | DNA binding [GO:0003677 molecular_function] (2) | B3 DNA binding domain [IPR003340] (2); DNA-binding pseudobarrel domain [IPR015300] (2) | scaffold_3_mRNA_5702.1 | C_unshiu_00053_mRNA_67.1 | - |
| GF0021637 | 1 | 1 | 0 | Hemopexin (1); Non-LTR reverse transcriptase (1) | | Endonuclease/exonuclease/phosphatase [IPR005135] (2) | scaffold_3_mRNA_5670.1 | C_unshiu_00060_mRNA_14.1 | - |
| GF0021636 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_5664.1 | C_unshiu_00053_mRNA_33.1 | - |
| GF0021635 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_5663.1 | C_unshiu_00053_mRNA_32.1 | - |
| GF0021634 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_5660.1 | C_unshiu_00053_mRNA_29.1 | - |
| GF0021632 | 1 | 1 | 0 | Hypothetical protein (2) | heme binding [GO:0020037 molecular_function] (2) | Cytochrome c-552/DMSO reductase-like, haem-binding domain [IPR019020] (2) | scaffold_3_mRNA_5659.1 | C_unshiu_00053_mRNA_28.1 | - |
| GF0021631 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_5658.1 | C_unshiu_00053_mRNA_27.1 | - |
| GF0021630 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_5654.1 | C_unshiu_00053_mRNA_23.1 | - |
| GF0021629 | 1 | 1 | 0 | ATP-dependent Clp protease, proteolytic subunit ClpP (2) | proteolysis [GO:0006508 biological_process] (2); serine-type endopeptidase activity [GO:0004252 molecular_function] (2) | Clp protease proteolytic subunit /Translocation-enhancing protein TepA [IPR023562] (2); ClpP, Ser active site [IPR018215] (2); ClpP/crotonase-like domain [IPR029045] (2); ATP-dependent Clp protease proteolytic subunit [IPR001907] (2); ClpP, histidine active site [IPR033135] (2) | scaffold_3_mRNA_5647.1 | C_unshiu_00053_mRNA_17.1 | - |
| GF0021626 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_5621.1 | C_unshiu_00291_mRNA_22.1 | - |
| GF0021625 | 1 | 1 | 0 | DNA-(apurinic or apyrimidinic site) lyase (2) | nuclease activity [GO:0004518 molecular_function] (2); DNA repair [GO:0006281 biological_process] (2) | AP endonuclease 1 [IPR004808] (2); Endonuclease/exonuclease/phosphatase [IPR005135] (2) | scaffold_3_mRNA_562.1 | C_unshiu_00318_mRNA_21.1 | - |
| GF0021622 | 1 | 1 | 0 | Cellulose synthase (1); Hypothetical protein (1) | cellulose biosynthetic process [GO:0030244 biological_process] (1); membrane [GO:0016020 cellular_component] (1); cellulose synthase (UDP-forming) activity [GO:0016760 molecular_function] (1) | Zinc finger, RING/FYVE/PHD-type [IPR013083] (2); Nucleotide-diphospho-sugar transferases [IPR029044] (1); Cellulose synthase [IPR005150] (1) | scaffold_3_mRNA_5592.1 | C_unshiu_00139_mRNA_1.1 | - |
| GF0021621 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_5587.1 | C_unshiu_00007_mRNA_24.1 | - |
| GF0021620 | 1 | 1 | 0 | DUF789 family protein (2) | | Protein of unknown function DUF789 [IPR008507] (2) | scaffold_3_mRNA_5586.1 | C_unshiu_00139_mRNA_6.1 | - |
| GF0021617 | 1 | 1 | 0 | Hypothetical protein (1); Putative proline-rich receptor-like protein kinase PERK11 (1) | ATP binding [GO:0005524 molecular_function] (2); protein kinase activity [GO:0004672 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2); polygalacturonase activity [GO:0004650 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1) | Protein kinase domain [IPR000719] (2); Protein kinase-like domain [IPR011009] (2); Pectin lyase fold [IPR012334] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Pectin lyase fold/virulence factor [IPR011050] (1); Rossmann-like alpha/beta/alpha sandwich fold [IPR014729] (1); Glycoside hydrolase, family 28 [IPR000743] (1) | scaffold_3_mRNA_5573.1 | C_unshiu_00139_mRNA_15.1 | - |
| GF0021614 | 1 | 1 | 0 | Hypothetical protein (2) | catalytic activity [GO:0003824 molecular_function] (2); transaminase activity [GO:0008483 molecular_function] (1); pyridoxal phosphate binding [GO:0030170 molecular_function] (1) | Pyridoxal phosphate-dependent transferase, major region, subdomain 2 [IPR015422] (1); Aminotransferase class-III [IPR005814] (1); Pyridoxal phosphate-dependent transferase, subdomain 2 [IPR015422] (1) | scaffold_3_mRNA_5565.1 | C_unshiu_00662_mRNA_1.1 | - |
| GF0021613 | 1 | 1 | 0 | Ribosomal L22e family protein (2) | structural constituent of ribosome [GO:0003735 molecular_function] (2); translation [GO:0006412 biological_process] (2); intracellular [GO:0005622 cellular_component] (2); ribosome [GO:0005840 cellular_component] (2) | Ribosomal protein L22e [IPR002671] (2) | scaffold_3_mRNA_5546.1 | C_unshiu_00662_mRNA_24.1 | - |
| GF0021608 | 1 | 1 | 0 | Cullin 1 (2) | ubiquitin-dependent protein catabolic process [GO:0006511 biological_process] (2); ubiquitin protein ligase binding [GO:0031625 molecular_function] (2); cullin-RING ubiquitin ligase complex [GO:0031461 cellular_component] (2) | Cullin homology [IPR016158] (2); Cullin, N-terminal [IPR001373] (2); Cullin protein, neddylation domain [IPR019559] (2); Cullin repeat-like-containing domain [IPR016159] (2); Winged helix-turn-helix DNA-binding domain [IPR011991] (2); Cullin, conserved site [IPR016157] (2) | scaffold_3_mRNA_5495.1 | C_unshiu_00546_mRNA_2.1 | - |
| GF0021607 | 1 | 1 | 0 | DUF1713 domain protein (2) | | Domain of unknown function DUF1713, mitochondria [IPR013177] (1); Domain of unknown function DUF1713 [IPR013177] (1) | scaffold_3_mRNA_549.1 | C_unshiu_00849_mRNA_18.1 | - |
| GF0021605 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_5487.1 | C_unshiu_00546_mRNA_9.1 | - |
| GF0021604 | 1 | 1 | 0 | Hypothetical protein (2) | cell redox homeostasis [GO:0045454 biological_process] (2); electron carrier activity [GO:0009055 molecular_function] (2); protein disulfide oxidoreductase activity [GO:0015035 molecular_function] (2) | Glutaredoxin subgroup [IPR014025] (2); Thioredoxin-like fold [IPR012336] (2); Glutaredoxin [IPR002109] (2); Glutaredoxin-like, plant II [IPR011905] (2) | scaffold_3_mRNA_5483.1 | C_unshiu_00546_mRNA_13.1 | - |
| GF0021602 | 1 | 1 | 0 | Hypothetical protein (2) | regulation of transcription, DNA-templated [GO:0006355 biological_process] (2) | FHY3/FAR1 family [IPR031052] (2); FAR1 DNA binding domain [IPR004330] (2) | scaffold_3_mRNA_5468.1 | C_unshiu_00251_mRNA_17.1 | - |
| GF0021601 | 1 | 1 | 0 | Hypothetical protein (2) | | Serine endopeptidase DegP2 [IPR015724] (1) | scaffold_3_mRNA_5467.1 | C_unshiu_00817_mRNA_8.1 | - |
| GF0021595 | 1 | 1 | 0 | Sugar transporter ERD6-like 16 (1); Sugar transporter ERD6-like 7 (1) | transmembrane transport [GO:0055085 biological_process] (2); integral component of membrane [GO:0016021 cellular_component] (2); transmembrane transporter activity [GO:0022857 molecular_function] (2); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1) | Major facilitator, sugar transporter-like [IPR005828] (2); Major facilitator superfamily domain [IPR020846] (2); Protein kinase-like domain [IPR011009] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1) | scaffold_3_mRNA_5434.1 | C_unshiu_00069_mRNA_21.1 | - |
| GF0021590 | 1 | 1 | 0 | PALE CRESS protein (PAC) (2) | plastid [GO:0009536 cellular_component] (1); leaf development [GO:0048366 biological_process] (1); chloroplast organization [GO:0009658 biological_process] (1); chloroplast mRNA processing [GO:0010239 biological_process] (1) | Protein PALE CRESS [IPR034563] (1) | scaffold_3_mRNA_5401.1 | C_unshiu_00069_mRNA_52.1 | - |

| **ID** | **Num. in *C. celementine*** | **Num in *C. unshiu*** | **Num in *P.trifoliata*** | **Note** | **GO** | **InterPro** | **Members in *C.clementine*** | **Members in *C.unshiu*** | **Members in *P.trifoliata*** |
|---|---|---|---|---|---|---|---|---|---|
| GF0021587 | 1 | 1 | 0 | Glutathione peroxidase (2) | oxidation-reduction process [GO:0055114 biological_process] (2); response to oxidative stress [GO:0006979 biological_process] (2); glutathione peroxidase activity [GO:0004602 molecular_function] (2) | Glutathione peroxidase active site [IPR029759] (2); Glutathione peroxidase [IPR000889] (2); Thioredoxin-like fold [IPR012336] (2); Glutathione peroxidase conserved site [IPR029760] (2) | scaffold_3_mRNA_5395.2 | C_unshiu_00069_mRNA_57.1 | - |
| GF0021586 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_5384.1 | C_unshiu_00069_mRNA_68.1 | - |
| GF0021585 | 1 | 1 | 0 | Hypothetical protein (2) | proteolysis [GO:0006508 biological_process] (2); cysteine-type peptidase activity [GO:0008234 molecular_function] (2) | Ulp1 protease family, C-terminal catalytic domain [IPR003653] (2) | scaffold_3_mRNA_5382.1 | C_unshiu_00069_mRNA_70.1 | - |
| GF0021584 | 1 | 1 | 0 | WD repeat-containing protein 82 (2) | protein binding [GO:0005515 molecular_function] (2) | WD40 repeat [IPR001680] (2); WD40-repeat-containing domain [IPR017986] (2); G-protein beta WD-40 repeat [IPR020472] (2); WD40/YVTN repeat-like-containing domain [IPR015943] (1) | scaffold_3_mRNA_5379.1 | C_unshiu_00069_mRNA_73.1 | - |
| GF0021583 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_5372.1 | C_unshiu_01525_mRNA_3.1 | - |
| GF0021580 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_5354.1 | C_unshiu_02585_mRNA_1.1 | - |
| GF0021574 | 1 | 1 | 0 | Homocysteine S-methyltransferase 3 (2) | | Homocysteine-binding domain [IPR003726] (2) | scaffold_3_mRNA_5317.1 | C_unshiu_00330_mRNA_33.1 | - |
| GF0021570 | 1 | 1 | 0 | Pentatricopeptide repeat-containing family protein (1); Pentatricopeptide (PPR) repeat protein (1) | protein binding [GO:0005515 molecular_function] (2); zinc ion binding [GO:0008270 molecular_function] (2) | Tetratricopeptide-like helical domain [IPR011990] (2); Pentatricopeptide repeat [IPR002885] (2); DYW domain [IPR032867] (2) | scaffold_3_mRNA_5296.1 | C_unshiu_00217_mRNA_20.1 | - |
| GF0021567 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_5258.1 | C_unshiu_00869_mRNA_6.1 | - |
| GF0021563 | 1 | 1 | 0 | LOB domain-containing protein 16 (2) | | Lateral organ boundaries, LOB [IPR004883] (2) | scaffold_3_mRNA_5237.1 | C_unshiu_00742_mRNA_6.1 | - |
| GF0021561 | 1 | 1 | 0 | Alkyl transferase (2) | transferase activity, transferring alkyl or aryl (other than methyl) groups [GO:0016765 molecular_function] (2) | Decaprenyl diphosphate synthase-like [IPR001441] (2); Di-trans-poly-cis-decaprenylcistransferase-like, conserved site [IPR018520] (1) | scaffold_3_mRNA_5225.1 | C_unshiu_00411_mRNA_20.1 | - |
| GF0021558 | 1 | 1 | 0 | Ethylene-responsive transcription factor ERF098 (2) | regulation of transcription, DNA-templated [GO:0006355 biological_process] (2); transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (2); DNA binding [GO:0003677 molecular_function] (2) | AP2/ERF domain [IPR001471] (2); DNA-binding domain [IPR016177] (2) | scaffold_3_mRNA_5217.1 | C_unshiu_00411_mRNA_18.1 | - |
| GF0021555 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_5184.1 | C_unshiu_00820_mRNA_10.1 | - |
| GF0021553 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_5173.1 | C_unshiu_00659_mRNA_6.1 | - |
| GF0021551 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_5143.1 | C_unshiu_00152_mRNA_28.1 | - |
| GF0021550 | 1 | 1 | 0 | Hypothetical protein (2) | | Vacuolar protein sorting-associated protein 62 [IPR009291] (2) | scaffold_3_mRNA_5140.1 | C_unshiu_00216_mRNA_27.1 | - |
| GF0021548 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_51.1 | C_unshiu_00916_mRNA_14.1 | - |
| GF0021547 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_5096.1 | C_unshiu_00400_mRNA_7.1 | - |
| GF0021546 | 1 | 1 | 0 | Pectate lyase (2) | | AmbAllergen [IPR018082] (2); Pectin lyase fold [IPR012334] (2); Pectate lyase/Amb allergen [IPR002022] (2); Pectin lyase fold/virulence factor [IPR011050] (2) | scaffold_3_mRNA_5087.1 | C_unshiu_00400_mRNA_16.1 | - |
| GF0021545 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_5085.1 | C_unshiu_00400_mRNA_18.1 | - |
| GF0021544 | 1 | 1 | 0 | Adenine nucleotide alpha hydrolases-like superfamily protein, putative (2) | response to stress [GO:0006950 biological_process] (2) | UspA [IPR006016] (2); Rossmann-like alpha/beta/alpha sandwich fold [IPR014729] (2) | scaffold_3_mRNA_507.1 | C_unshiu_00120_mRNA_18.1 | - |
| GF0021543 | 1 | 1 | 0 | E3 ubiquitin-protein ligase PRT1-like protein (1); E3 ubiquitin-protein ligase PRT1 (1) | protein binding [GO:0005515 molecular_function] (2); zinc ion binding [GO:0008270 molecular_function] (2) | Zinc finger, ZZ-type [IPR000433] (2); Zinc finger, RING-type, conserved site [IPR017907] (2); Zinc finger, RING-type [IPR001841] (2); Zinc finger, RING/FYVE/PHD-type [IPR013083] (2); RING-type zinc-finger, LisH dimerisation motif [IPR027370] (1) | scaffold_3_mRNA_5060.1 | C_unshiu_00322_mRNA_41.1 | - |
| GF0021542 | 1 | 1 | 0 | Cytochrome b5 (2) | heme binding [GO:0020037 molecular_function] (2) | Cytochrome b5, heme-binding site [IPR018506] (2); Cytochrome b5-like heme/steroid binding domain [IPR001199] (2) | scaffold_3_mRNA_5054.1 | C_unshiu_00322_mRNA_33.1 | - |
| GF0021541 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_3_mRNA_5046.1 | C_unshiu_00322_mRNA_23.1 | - |
| GF0021538 | 1 | 1 | 0 | Stigma-specific Stig1 family protein, putative (2) | | Stigma-specific protein Stig1 [IPR006969] (2) | scaffold_3_mRNA_5035.1 | C_unshiu_00322_mRNA_14.1 | - |
| GF0021536 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_5028.1 | C_unshiu_00322_mRNA_6.1 | - |
| GF0021531 | 1 | 1 | 0 | Polyribonucleotide nucleotidyltransferase (2) | RNA binding [GO:0003723 molecular_function] (2); polyribonucleotide nucleotidyltransferase activity [GO:0004654 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2); mRNA catabolic process [GO:0006402 biological_process] (2); RNA processing [GO:0006396 biological_process] (1); 3'-5'-exoribonuclease activity [GO:0000175 molecular_function] (1) | K Homology domain, type 1 [IPR004088] (2); PNPase/RNase PH domain [IPR027408] (2); Ribosomal protein S5 domain 2-type fold [IPR020568] (2); Exoribonuclease, phosphorolytic domain 1 [IPR001247] (2); Nucleic acid-binding, OB-fold [IPR012340] (2); S1 domain [IPR003029] (2); Exoribonuclease, phosphorolytic domain 2 [IPR015847] (2); K Homology domain [IPR004087] (2); RNA-binding domain, S1 [IPR022967] (2); Polyribonucleotide nucleotidyltransferase [IPR012162] (2); Polyribonucleotide nucleotidyltransferase, RNA-binding domain [IPR015848] (1) | scaffold_3_mRNA_4990.1 | C_unshiu_00247_mRNA_7.1 | - |
| GF0021529 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_4962.1 | C_unshiu_01337_mRNA_6.1 | - |
| GF0021524 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_4903.1 | C_unshiu_01914_mRNA_4.1 | - |
| GF0021523 | 1 | 1 | 0 | Hypothetical protein (2) | | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); Helicase superfamily 1/2, ATP-binding domain [IPR014001] (1) | scaffold_3_mRNA_4896.1 | C_unshiu_00194_mRNA_43.1 | - |
| GF0021522 | 1 | 1 | 0 | Small basic intrinsic protein 1 (2) | transporter activity [GO:0005215 molecular_function] (2); membrane [GO:0016020 cellular_component] (2); transport [GO:0006810 biological_process] (2) | Major intrinsic protein [IPR000425] (2); Aquaporin-like [IPR023271] (2); Aquaporin transporter [IPR034294] (1) | scaffold_3_mRNA_4883.1 | C_unshiu_00735_mRNA_12.1 | - |
| GF0021521 | 1 | 1 | 0 | Dna-directed rna polymerase subunit alpha (2) | | | scaffold_3_mRNA_4877.1 | C_unshiu_01780_mRNA_2.1 | - |
| GF0021517 | 1 | 1 | 0 | Germin-like protein subfamily 1 member 7 (2) | nutrient reservoir activity [GO:0045735 molecular_function] (2); manganese ion binding [GO:0030145 molecular_function] (2) | RmlC-like cupin domain [IPR011051] (2); Germin [IPR001929] (2); RmlC-like jelly roll fold [IPR014710] (2); Cupin 1 [IPR006045] (2); Germin, manganese binding site [IPR019780] (2) | scaffold_3_mRNA_4850.1 | C_unshiu_02024_mRNA_6.1 | - |
| GF0021516 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_4845.1 | C_unshiu_02024_mRNA_3.1 | - |
| GF0021514 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_4832.1 | C_unshiu_00256_mRNA_26.1 | - |
| GF0021513 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_4825.1 | C_unshiu_01527_mRNA_4.1 | - |
| GF0021512 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_4824.1 | C_unshiu_00491_mRNA_20.1 | - |
| GF0021511 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_4823.1 | C_unshiu_00491_mRNA_21.1 | - |
| GF0021510 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_4822.1 | C_unshiu_00491_mRNA_22.1 | - |
| GF0021508 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_48.1 | C_unshiu_01237_mRNA_8.1 | - |
| GF0021507 | 1 | 1 | 0 | Cytochrome P450 83B1 (2) | oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2); heme binding [GO:0020037 molecular_function] (2); iron ion binding [GO:0005506 molecular_function] (2) | Cytochrome P450 [IPR001128] (2); Cytochrome P450, E-class, group I [IPR002401] (2); Cytochrome P450, conserved site [IPR017972] (2) | scaffold_3_mRNA_4779.1 | C_unshiu_00566_mRNA_3.1 | - |
| GF0021503 | 1 | 1 | 0 | DUF313 domain protein (1); Hypothetical protein (1) | | DNA-binding pseudobarrel domain [IPR015300] (2); B3 domain-containing protein [IPR005508] (2) | scaffold_3_mRNA_4709.1 | C_unshiu_00727_mRNA_5.1 | - |
| GF0021502 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_4656.1 | C_unshiu_00862_mRNA_5.1 | - |
| GF0021501 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_4642.1 | C_unshiu_02772_mRNA_3.1 | - |
| GF0021499 | 1 | 1 | 0 | Putative serine/threonine-protein kinase GCN2 (1); Histidyl tRNA synthetase (1) | cytoplasm [GO:0005737 cellular_component] (1) | Anticodon-binding [IPR004154] (2); Histidine-tRNA ligase/ATP phosphoribosyltransferase regulatory subunit [IPR004516] (1); Protein kinase-like domain [IPR011009] (1); Histidyl tRNA synthetase-related domain [IPR024435] (1) | scaffold_3_mRNA_4619.1 | C_unshiu_00680_mRNA_11.1 | - |
| GF0021498 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_4610.1 | C_unshiu_00680_mRNA_18.1 | - |
| GF0021497 | 1 | 1 | 0 | Zinc finger BED domain-containing protein RICESLEEPER 2 (1); BED zinc finger,hAT family dimerization domain isoform 1 (1) | nucleic acid binding [GO:0003676 molecular_function] (2); protein dimerization activity [GO:0046983 molecular_function] (2); DNA binding [GO:0003677 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2); hAT-like transposase, RNase-H fold [IPR025525] (2); Zinc finger, BED-type [IPR003656] (2); HAT, C-terminal dimerisation domain [IPR008906] (2); Zinc finger, RING/FYVE/PHD-type [IPR013083] (1); Zinc finger C2H2-type [IPR013087] (1) | scaffold_3_mRNA_4605.1 | C_unshiu_00680_mRNA_17.1 | - |
| GF0021496 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_4594.1 | C_unshiu_00552_mRNA_4.1 | - |
| GF0021494 | 1 | 1 | 0 | Hypothetical protein (2) | zinc ion binding [GO:0008270 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1) | Domain of unknown function DUF4283 [IPR025558] (2); Zinc knuckle CX2CX4HX4C [IPR025836] (1); Zinc finger, CCHC-type [IPR001878] (1); CCT domain [IPR010402] (1) | scaffold_3_mRNA_4579.1 | C_unshiu_00575_mRNA_9.1 | - |
| GF0021493 | 1 | 1 | 0 | Hypothetical protein (2) | RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2); Ribonuclease H domain [IPR002156] (2) | scaffold_3_mRNA_4574.1 | C_unshiu_01878_mRNA_5.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0021492 | 1 | 1 | 0 | Hypothetical protein (2) | | Reverse transcriptase domain [IPR000477] (2) | scaffold_3_mRNA_4573.1 | C_unshiu_01878_mRNA_4.1 | - |
| GF0021491 | 1 | 1 | 0 | Isoprene synthase (2) | magnesium ion binding [GO:0000287 molecular_function] (2); terpene synthase activity [GO:0010333 molecular_function] (2); lyase activity [GO:0016829 molecular_function] (2); metabolic process [GO:0008152 biological_process] (2) | Terpene synthase, metal-binding domain [IPR005630] (2); Terpene synthase, N-terminal domain [IPR001906] (2); Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (2); Isoprenoid synthase domain [IPR008949] (2) | scaffold_3_mRNA_4572.1 | C_unshiu_00523_mRNA_7.1 | - |
| GF0021490 | 1 | 1 | 0 | E3 ubiquitin-protein ligase RGLG2 (2) | protein binding [GO:0005515 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1) | Copine [IPR010734] (2); von Willebrand factor, type A [IPR002035] (2); Zinc finger, RING/FYVE/PHD-type [IPR013083] (1); Zinc finger, RING-type [IPR001841] (1) | scaffold_3_mRNA_4562.1 | C_unshiu_00523_mRNA_16.1 | - |
| GF0021487 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2); protein dimerization activity [GO:0046983 molecular_function] (2); DNA binding [GO:0003677 molecular_function] (1) | Ribonuclease H-like domain [IPR012337] (2); HAT, C-terminal dimerisation domain [IPR008906] (2); Zinc finger, BED-type [IPR003656] (1) | scaffold_3_mRNA_4538.1 | C_unshiu_00522_mRNA_7.1 | - |
| GF0021485 | 1 | 1 | 0 | Hypothetical protein (2) | DNA binding [GO:0003677 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (1) | Zinc finger, BED-type [IPR003656] (2); Zinc finger C2H2-type [IPR013087] (1) | scaffold_3_mRNA_4519.1 | C_unshiu_00502_mRNA_10.1 | - |
| GF0021484 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_4516.1 | C_unshiu_00912_mRNA_19.1 | - |
| GF0021483 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_4511.1 | C_unshiu_00502_mRNA_15.1 | - |
| GF0021481 | 1 | 1 | 0 | Hypothetical protein (2) | protein dimerization activity [GO:0046983 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (1) | HAT, C-terminal dimerisation domain [IPR008906] (2); Ribonuclease H-like domain [IPR012337] (1) | scaffold_3_mRNA_4504.1 | C_unshiu_00502_mRNA_20.1 | - |
| GF0021480 | 1 | 1 | 0 | C6HC-type zinc finger RING/U-box protein (2) | protein ubiquitination [GO:0016567 biological_process] (2); ubiquitin-protein transferase activity [GO:0004842 molecular_function] (2) | IBR domain [IPR002867] (2); Zinc finger, RING/FYVE/PHD-type [IPR013083] (2); Zinc finger, RING-type, conserved site [IPR017907] (2); E3 ubiquitin ligase RBR family [IPR031127] (2) | scaffold_3_mRNA_4487.1 | C_unshiu_00471_mRNA_18.1 | - |
| GF0021474 | 1 | 1 | 0 | Polygalacturonase 1 beta-like protein 1 (2) | | BURP domain [IPR004873] (2) | scaffold_3_mRNA_442.1 | C_unshiu_00092_mRNA_57.1 | - |
| GF0021473 | 1 | 1 | 0 | Chitinase (2) | chitin catabolic process [GO:0006032 biological_process] (2); carbohydrate metabolic process [GO:0005975 biological_process] (2); chitinase activity [GO:0004568 molecular_function] (2); cell wall macromolecule catabolic process [GO:0016998 biological_process] (2) | Glycoside hydrolase, family 19, catalytic [IPR000726] (2); Lysozyme-like domain [IPR023346] (2); Glycoside hydrolase, family 19 [IPR016283] (2) | scaffold_3_mRNA_4415.1 | C_unshiu_00054_mRNA_11.1 | - |
| GF0021471 | 1 | 1 | 0 | Class IV chitinase (2) | cell wall macromolecule catabolic process [GO:0016998 biological_process] (2); chitin catabolic process [GO:0006032 biological_process] (2); chitin binding [GO:0008061 molecular_function] (2); chitinase activity [GO:0004568 molecular_function] (2); carbohydrate metabolic process [GO:0005975 biological_process] (2) | Chitin-binding, type 1 [IPR001002] (2); Glycoside hydrolase, family 19, catalytic [IPR000726] (2); Lysozyme-like domain [IPR023346] (2); Glycoside hydrolase, family 19 [IPR016283] (2) | scaffold_3_mRNA_4410.1 | C_unshiu_00054_mRNA_15.1 | - |
| GF0021469 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_4396.1 | C_unshiu_02214_mRNA_1.1 | - |
| GF0021468 | 1 | 1 | 0 | Hypothetical protein (2) | DNA binding [GO:0003677 molecular_function] (2) | Myb-like domain [IPR017877] (2); Homeodomain-like [IPR009057] (1); Homeobox domain-like [IPR009057] (1) | scaffold_3_mRNA_4392.1 | C_unshiu_00054_mRNA_31.1 | - |
| GF0021466 | 1 | 1 | 0 | Hypothetical protein (2) | 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_3_mRNA_4385.1 | C_unshiu_00054_mRNA_38.1 | - |
| GF0021465 | 1 | 1 | 0 | Hypothetical protein (2) | protein kinase activity [GO:0004672 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2); ATP binding [GO:0005524 molecular_function] (2) | Protein kinase domain [IPR000719] (2); Protein kinase-like domain [IPR011009] (2) | scaffold_3_mRNA_4382.1 | C_unshiu_00054_mRNA_40.1 | - |
| GF0021463 | 1 | 1 | 0 | Hypothetical protein (1); Probable protein phosphatase 2C 11 (1) | protein serine/threonine phosphatase activity [GO:0004722 molecular_function] (2); protein dephosphorylation [GO:0006470 biological_process] (2); cation binding [GO:0043169 molecular_function] (2); catalytic activity [GO:0003824 molecular_function] (2) | PPM-type phosphatase, divalent cation binding [IPR000222] (2); Protein phosphatase 2C family [IPR015655] (2); PPM-type phosphatase domain [IPR001932] (2) | scaffold_3_mRNA_4352.1 | C_unshiu_02225_mRNA_3.1 | - |
| GF0021462 | 1 | 1 | 0 | Hypothetical protein (2) | | Protein of unknown function DUF247, plant [IPR004158] (2) | scaffold_3_mRNA_4345.1 | C_unshiu_00528_mRNA_23.1 | - |
| GF0021461 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (1) | Ribonuclease H-like domain [IPR012337] (1) | scaffold_3_mRNA_4339.1 | C_unshiu_01712_mRNA_4.1 | - |
| GF0021460 | 1 | 1 | 0 | Hypothetical protein (2) | protein binding [GO:0005515 molecular_function] (2) | C2 domain [IPR000008] (2); Domain of unknown function DUF4782 [IPR031968] (1); VASt domain [IPR031968] (1) | scaffold_3_mRNA_4333.1 | C_unshiu_00528_mRNA_6.1 | - |
| GF0021459 | 1 | 1 | 0 | Transcription elongation factor s-II, putative (2) | transcription, DNA-templated [GO:0006351 biological_process] (2); nucleus [GO:0005634 cellular_component] (2); zinc ion binding [GO:0008270 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1) | Transcription factor IIS, N-terminal [IPR017923] (2); Transcription elongation factor S-II, central domain [IPR003618] (2); Transcription elongation factor, TFIIS/CRSP70, N-terminal, sub-type [IPR003617] (2); Transcription elongation factor S-IIM [IPR017890] (1) | scaffold_3_mRNA_4326.1 | C_unshiu_01481_mRNA_5.1 | - |
| GF0021458 | 1 | 1 | 0 | F-box/RNI-like superfamily protein isoform 1 (1); F-box/RNI-like superfamily protein isoform 2 (1) | protein binding [GO:0005515 molecular_function] (2) | F-box domain [IPR001810] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2) | scaffold_3_mRNA_4324.1 | C_unshiu_00528_mRNA_2.1 | - |
| GF0021457 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_4323.1 | C_unshiu_01481_mRNA_2.1 | - |
| GF0021456 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_4320.1 | C_unshiu_00902_mRNA_9.1 | - |
| GF0021455 | 1 | 1 | 0 | Hypothetical protein (2) | | Leucine-rich repeat domain, L domain-like [IPR032675] (2) | scaffold_3_mRNA_4318.1 | C_unshiu_00902_mRNA_5.1 | - |
| GF0021453 | 1 | 1 | 0 | Trafficking protein particle complex subunit 2 (2) | transport [GO:0006810 biological_process] (2); intracellular [GO:0005622 cellular_component] (2); ER to Golgi vesicle-mediated transport [GO:0006888 biological_process] (2) | Longin-like domain [IPR011012] (2); Trafficking protein particle complex subunit 2 [IPR006722] (2) | scaffold_3_mRNA_4310.1 | C_unshiu_00712_mRNA_6.1 | - |
| GF0021452 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_4308.1 | C_unshiu_01667_mRNA_3.1 | - |
| GF0021450 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_4305.1 | C_unshiu_00631_mRNA_8.1 | - |
| GF0021449 | 1 | 1 | 0 | Hypothetical protein (2) | binding [GO:0005488 molecular_function] (1) | Armadillo-like helical [IPR011989] (1); Armadillo-type fold [IPR016024] (1) | scaffold_3_mRNA_4297.1 | C_unshiu_00712_mRNA_8.1 | - |
| GF0021448 | 1 | 1 | 0 | Putative Zea mays retrotransposon Opie-2 (1); SLG-Sc and SLA-Sc genes and Melmoth retrotransposon sequence (1) | | Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1) | scaffold_3_mRNA_4292.1 | C_unshiu_01158_mRNA_2.1 | - |
| GF0021447 | 1 | 1 | 0 | Hypothetical protein (2) | | Retrotransposon gag domain [IPR005162] (2) | scaffold_3_mRNA_4286.1 | C_unshiu_01093_mRNA_6.1 | - |
| GF0021446 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_4278.1 | C_unshiu_00518_mRNA_10.1 | - |
| GF0021445 | 1 | 1 | 0 | Hypothetical protein (2) | ATP binding [GO:0005524 molecular_function] (1) | Malectin [IPR021720] (2); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase, ATP binding site [IPR017441] (1) | scaffold_3_mRNA_4272.1 | C_unshiu_00180_mRNA_5.1 | - |
| GF0021444 | 1 | 1 | 0 | Hypothetical protein (2) | transcription coactivator activity [GO:0003713 molecular_function] (2); regulation of transcription, DNA-templated [GO:0006355 biological_process] (2) | Associate of Myc 1 [IPR026060] (2) | scaffold_3_mRNA_4248.1 | C_unshiu_00174_mRNA_3.1 | - |
| GF0021442 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_4232.1 | C_unshiu_00672_mRNA_17.1 | - |
| GF0021440 | 1 | 1 | 0 | RNA-directed DNA polymerase (Reverse transcriptase) (2) | | Reverse transcriptase domain [IPR000477] (2); Endonuclease/exonuclease/phosphatase [IPR005135] (1) | scaffold_3_mRNA_4216.1 | C_unshiu_00232_mRNA_20.1 | - |
| GF0021439 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_4211.1 | C_unshiu_01551_mRNA_6.1 | - |
| GF0021437 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_4198.1 | C_unshiu_00514_mRNA_2.1 | - |
| GF0021435 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_4193.1 | C_unshiu_01953_mRNA_3.1 | - |
| GF0021434 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_4179.1 | C_unshiu_00392_mRNA_8.1 | - |
| GF0021433 | 1 | 1 | 0 | Hypothetical protein (2) | | Domain of unknown function DUF4283 [IPR025558] (2); Reverse transcriptase domain [IPR000477] (1) | scaffold_3_mRNA_4175.1 | C_unshiu_00392_mRNA_3.1 | - |
| GF0021432 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_4172.1 | C_unshiu_00669_mRNA_15.1 | - |
| GF0021430 | 1 | 1 | 0 | Hypothetical protein (2) | | Zinc knuckle CX2CX4HX4C [IPR025836] (2) | scaffold_3_mRNA_4139.1 | C_unshiu_00080_mRNA_14.1 | - |
| GF0021429 | 1 | 1 | 0 | Similarity to non-LTR retroelement reverse transcriptase (2) | | | scaffold_3_mRNA_4138.1 | C_unshiu_00080_mRNA_12.1 | - |
| GF0021428 | 1 | 1 | 0 | Endoribonuclease (2) | | Diphthine--ammonia ligase/Uncharacterised protein MJ0570 [IPR030662] (2); Diphthamide synthase domain [IPR002761] (2); YjgF/YER057c/UK114 family [IPR006175] (2); Rossmann-like alpha/beta/alpha sandwich fold [IPR014729] (2); Endoribonuclease L-PSP/chorismate mutase-like [IPR013813] (2) | scaffold_3_mRNA_4134.1 | C_unshiu_00080_mRNA_8.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0021427 | 1 | 1 | 0 | Hypothetical protein (2) | proteolysis [GO:0006508 biological_process] (2); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (2) | Aspartic peptidase domain [IPR021109] (2); Aspartic peptidase, active site [IPR001969] (2) | scaffold_3_mRNA_4131.1 | C_unshiu_00080_mRNA_5.1 | - |
| GF0021426 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_4124.1 | C_unshiu_00767_mRNA_6.1 | - |
| GF0021425 | 1 | 1 | 0 | Cysteine-rich RLK 29 isoform 1 (2) | protein kinase activity [GO:0004672 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2); ATP binding [GO:0005524 molecular_function] (2) | Protein kinase-like domain [IPR011009] (2); Protein kinase domain [IPR000719] (2); Serine/threonine-protein kinase, active site [IPR008271] (2); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1) | scaffold_3_mRNA_4123.1 | C_unshiu_00767_mRNA_7.1 | - |
| GF0021423 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_4118.1 | C_unshiu_00767_mRNA_12.1 | - |
| GF0021421 | 1 | 1 | 0 | Copper-binding periplasmic protein (2) | | | scaffold_3_mRNA_4101.1 | C_unshiu_01155_mRNA_2.1 | - |
| GF0021420 | 1 | 1 | 0 | Zinc finger protein-related isoform 1 (2) | zinc ion binding [GO:0008270 molecular_function] (2); protein binding [GO:0005515 molecular_function] (2) | Zinc finger, RING-type [IPR001841] (2); Zinc finger, CHY-type [IPR008913] (2); Haemerythrin-like [IPR012312] (2); Zinc finger, CTCHY-type [IPR017921] (2); Zinc finger, RING/FYVE/PHD-type [IPR013083] (2); Rubredoxin-type fold [IPR004039] (1) | scaffold_3_mRNA_4100.1 | C_unshiu_01155_mRNA_3.1 | - |
| GF0021419 | 1 | 1 | 0 | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase familyprotein (2) | acetylglucosaminyltransferase activity [GO:0008375 molecular_function] (2); membrane [GO:0016020 cellular_component] (2) | Glycosyl transferase, family 14 [IPR003406] (2) | scaffold_3_mRNA_4098.1 | C_unshiu_01155_mRNA_6.1 | - |
| GF0021418 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_4087.1 | C_unshiu_01457_mRNA_3.1 | - |
| GF0021416 | 1 | 1 | 0 | Sesquiterpene synthase (2) | metabolic process [GO:0008152 biological_process] (2); lyase activity [GO:0016829 molecular_function] (2); terpene synthase activity [GO:0010333 molecular_function] (2); magnesium ion binding [GO:0000287 molecular_function] (2) | Isoprenoid synthase domain [IPR008949] (2); Terpene synthase, metal-binding domain [IPR005630] (2); Terpene synthase, N-terminal domain [IPR001906] (2); Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (2) | scaffold_3_mRNA_4076.1 | C_unshiu_01640_mRNA_2.1 | - |
| GF0021415 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_4073.1 | C_unshiu_01640_mRNA_5.1 | - |
| GF0021414 | 1 | 1 | 0 | Uncharacterized mitochondrial protein AtMg00310 (2) | | | scaffold_3_mRNA_4070.1 | C_unshiu_00563_mRNA_20.1 | - |
| GF0021412 | 1 | 1 | 0 | Leucine-rich repeat protein kinase family protein (1); Receptor like protein 33 (1) | protein binding [GO:0005515 molecular_function] (2) | Leucine-rich repeat domain, L domain-like [IPR032675] (2); Leucine-rich repeat [IPR001611] (2); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (2); Leucine-rich repeat, typical subtype [IPR003591] (1) | scaffold_3_mRNA_4048.1 | C_unshiu_01491_mRNA_2.1 | - |
| GF0021411 | 1 | 1 | 0 | Hypothetical protein (2) | | Class I glutamine amidotransferase-like [IPR029062] (2); DJ-1/PfpI [IPR002818] (2) | scaffold_3_mRNA_4047.1 | C_unshiu_01491_mRNA_3.1 | - |
| GF0021410 | 1 | 1 | 0 | Hypothetical protein (2) | | Protein kinase-like domain [IPR011009] (2) | scaffold_3_mRNA_4036.1 | C_unshiu_02077_mRNA_4.1 | - |
| GF0021409 | 1 | 1 | 0 | Hypothetical protein (1); Class I glutamine amidotransferase-like superfamily protein isoform 2 (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) | Class I glutamine amidotransferase-like [IPR029062] (2); Ribosomal protein L9, N-terminal [IPR020070] (2); Ribosomal protein L9/RNase H1, N-terminal [IPR009027] (2); DJ-1/PfpI [IPR002818] (2); Ribosomal protein L9 [IPR000244] (1) | scaffold_3_mRNA_4021.1 | C_unshiu_02049_mRNA_5.1 | - |
| GF0021406 | 1 | 1 | 0 | RNA-directed DNA polymerase , related (2) | | Reverse transcriptase domain [IPR000477] (2) | scaffold_3_mRNA_4.1 | C_unshiu_01604_mRNA_4.1 | - |
| GF0021405 | 1 | 1 | 0 | Epidermis-specific secreted glycoprotein EP1 (2) | | Bulb-type lectin domain [IPR001480] (2) | scaffold_3_mRNA_3966.1 | C_unshiu_02596_mRNA_2.1 | - |
| GF0021404 | 1 | 1 | 0 | Alpha-N-acetylglucosaminidase family / NAGLU family isoform 1 (2) | | Alpha-N-acetylglucosaminidase, N-terminal [IPR024240] (2); Alpha-N-acetylglucosaminidase, tim-barrel domain [IPR024733] (2); Alpha-N-acetylglucosaminidase, C-terminal [IPR024732] (2); Alpha-N-acetylglucosaminidase [IPR007781] (2) | scaffold_3_mRNA_396.1 | C_unshiu_00092_mRNA_23.1 | - |
| GF0021401 | 1 | 1 | 0 | Glycosyl transferase family 1 family protein (1); UDP-Glycosyltransferase superfamily protein isoform 3 (1) | | Glycosyl transferase, family 1 [IPR001296] (2) | scaffold_3_mRNA_3942.1 | C_unshiu_00769_mRNA_1.1 | - |
| GF0021400 | 1 | 1 | 0 | Hypothetical protein (2) | | Glycosyl transferase, family 1 [IPR001296] (2) | scaffold_3_mRNA_3932.1 | C_unshiu_01431_mRNA_1.1 | - |
| GF0021399 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_3921.1 | C_unshiu_01537_mRNA_8.1 | - |
| GF0021397 | 1 | 1 | 0 | Hypothetical protein (1); Anaphase-promoting complex subunit 6 (1) | protein binding [GO:0005515 molecular_function] (2); cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1) | Tetratricopeptide-like helical domain [IPR011990] (2); Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1) | scaffold_3_mRNA_3912.1 | C_unshiu_01537_mRNA_5.1 | - |
| GF0021396 | 1 | 1 | 0 | Ankyrin repeat protein, putative (2) | protein binding [GO:0005515 molecular_function] (2) | Ankyrin repeat-containing domain [IPR020683] (2); Ankyrin repeat [IPR002110] (2) | scaffold_3_mRNA_3911.1 | C_unshiu_02956_mRNA_3.1 | - |
| GF0021395 | 1 | 1 | 0 | Hypothetical protein (2) | | Powdery mildew resistance protein, RPW8 domain [IPR008808] (2) | scaffold_3_mRNA_3899.1 | C_unshiu_00438_mRNA_15.1 | - |
| GF0021394 | 1 | 1 | 0 | Hypothetical protein (2) | | Powdery mildew resistance protein, RPW8 domain [IPR008808] (2) | scaffold_3_mRNA_3898.1 | C_unshiu_00438_mRNA_14.1 | - |
| GF0021393 | 1 | 1 | 0 | Hypothetical protein (2) | | Powdery mildew resistance protein, RPW8 domain [IPR008808] (1) | scaffold_3_mRNA_3894.1 | C_unshiu_00438_mRNA_8.1 | - |
| GF0021392 | 1 | 1 | 0 | Pentatricopeptide repeat-containing protein, mitochondrial (1); Pentatricopeptide (PPR) repeat protein (1) | | Pentatricopeptide repeat [IPR002885] (2) | scaffold_3_mRNA_3892.1 | C_unshiu_00438_mRNA_11.1 | - |
| GF0021391 | 1 | 1 | 0 | Pentatricopeptide repeat-containing protein, mitochondrial (1); Pentatricopeptide repeat (PPR) superfamily protein, putative isoform 2 (1) | | Pentatricopeptide repeat [IPR002885] (2) | scaffold_3_mRNA_3890.1 | C_unshiu_00438_mRNA_6.1 | - |
| GF0021389 | 1 | 1 | 0 | Hypothetical protein (2) | | SGNH hydrolase-type esterase domain [IPR013830] (1) | scaffold_3_mRNA_3883.1 | C_unshiu_00072_mRNA_34.1 | - |
| GF0021388 | 1 | 1 | 0 | Mutator-like transposase (2) | | Transposase, MuDR, plant [IPR004332] (2); MULE transposase domain [IPR018289] (2) | scaffold_3_mRNA_3865.1 | C_unshiu_01504_mRNA_5.1 | - |
| GF0021387 | 1 | 1 | 0 | Hypothetical protein (2) | DNA binding [GO:0003677 molecular_function] (1) | Myb domain [IPR017930] (2); Homeodomain-like [IPR009057] (1) | scaffold_3_mRNA_3857.1 | C_unshiu_01069_mRNA_4.1 | - |
| GF0021386 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_3855.1 | C_unshiu_01557_mRNA_2.1 | - |
| GF0021384 | 1 | 1 | 0 | HAT dimerisation (1); Hypothetical protein (1) | protein dimerization activity [GO:0046983 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2); HAT, C-terminal dimerisation domain [IPR008906] (2) | scaffold_3_mRNA_3842.1 | C_unshiu_00995_mRNA_15.1 | - |
| GF0021383 | 1 | 1 | 0 | Hypothetical protein (2) | protein binding [GO:0005515 molecular_function] (2) | Leucine-rich repeat [IPR001611] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2) | scaffold_3_mRNA_3827.1 | C_unshiu_00534_mRNA_12.1 | - |
| GF0021380 | 1 | 1 | 0 | Glycerol kinase (2) | carbohydrate metabolic process [GO:0005975 biological_process] (2); phosphotransferase activity, alcohol group as acceptor [GO:0016773 molecular_function] (2) | Carbohydrate kinase, FGGY, C-terminal [IPR018485] (2); Carbohydrate kinase, FGGY, N-terminal [IPR018484] (2) | scaffold_3_mRNA_3822.1 | C_unshiu_01142_mRNA_8.1 | - |
| GF0021379 | 1 | 1 | 0 | Miraculin (1); Kunitz trypsin inhibitor (1) | endopeptidase inhibitor activity [GO:0004866 molecular_function] (2) | Proteinase inhibitor I3, Kunitz legume [IPR002160] (2); Kunitz inhibitor ST1-like [IPR011065] (2) | scaffold_3_mRNA_3820.1 | C_unshiu_01142_mRNA_10.1 | - |
| GF0021377 | 1 | 1 | 0 | Hypothetical protein (2) | | Translation protein SH3-like domain [IPR008991] (1); Ribosomal protein L2 domain 2 [IPR014722] (1) | scaffold_3_mRNA_3803.1 | C_unshiu_00688_mRNA_16.1 | - |
| GF0021376 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_380.1 | C_unshiu_00092_mRNA_6.1 | - |
| GF0021374 | 1 | 1 | 0 | Gamma-glutamyl hydrolase 2 (2) | glutamine metabolic process [GO:0006541 biological_process] (2); omega peptidase activity [GO:0008242 molecular_function] (2); hydrolase activity [GO:0016787 molecular_function] (2); catalytic activity [GO:0003824 molecular_function] (2) | Class I glutamine amidotransferase-like [IPR029062] (2); Peptidase C26 [IPR011697] (2); Peptidase C26, gamma-glutamyl hydrolase [IPR015527] (2) | scaffold_3_mRNA_3771.1 | C_unshiu_00836_mRNA_8.1 | - |
| GF0021373 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2); nucleotide binding [GO:0000166 molecular_function] (1) | RNA recognition motif domain [IPR000504] (2); Nucleotide-binding alpha-beta plait domain [IPR012677] (1) | scaffold_3_mRNA_3766.1 | C_unshiu_00730_mRNA_4.1 | - |
| GF0021372 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_3_mRNA_3752.1 | C_unshiu_00174_mRNA_19.1 | - |
| GF0021371 | 1 | 1 | 0 | Protein trichome birefringence-like 38 (2) | | Trichome birefringence-like family [IPR029962] (2); PMR5 N-terminal domain [IPR025846] (2); PC-Esterase [IPR026057] (2) | scaffold_3_mRNA_3746.1 | C_unshiu_00705_mRNA_8.1 | - |
| GF0021370 | 1 | 1 | 0 | Protein trichome birefringence-like 38 (1); Trichome birefringence-like protein (1) | | PC-Esterase [IPR026057] (2); Trichome birefringence-like family [IPR029962] (2); PMR5 N-terminal domain [IPR025846] (2) | scaffold_3_mRNA_3744.1 | C_unshiu_00705_mRNA_12.1 | - |
| GF0021368 | 1 | 1 | 0 | Hypothetical protein (1); Putative pentatricopeptide repeat-containing protein, mitochondrial (1) | | Pentatricopeptide repeat [IPR002885] (1) | scaffold_3_mRNA_3720.1 | C_unshiu_01331_mRNA_5.1 | - |
| GF0021367 | 1 | 1 | 0 | Hypothetical protein (2) | | 5-formyltetrahydrofolate cyclo-ligase [IPR002698] (2); 5-formyltetrahydrofolate cyclo-ligase-like domain [IPR024185] (1) | scaffold_3_mRNA_372.1 | C_unshiu_01592_mRNA_5.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0021366 | 1 | 1 | 0 | Hypothetical protein (2) |  | Domain of unknown function DUF4283 [IPR025558] (2) | scaffold_3_mRNA_3716.1 | C_unshiu_02398_mRNA_2.1 | - |
| GF0021365 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_3_mRNA_3713.1 | C_unshiu_02398_mRNA_1.1 | - |
| GF0021364 | 1 | 1 | 0 | Zinc finger (B-box type) family protein (2) | intracellular [GO:0005622 cellular_component] (2); zinc ion binding [GO:0008270 molecular_function] (2) | B-box-type zinc finger [IPR000315] (2); Zinc finger, RING/FYVE/PHD-type [IPR013083] (1) | scaffold_3_mRNA_3711.1 | C_unshiu_01558_mRNA_6.1 | - |
| GF0021363 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_3_mRNA_3704.1 | C_unshiu_02189_mRNA_1.1 | - |
| GF0021362 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_3_mRNA_3700.1 | C_unshiu_00759_mRNA_11.1 | - |
| GF0021361 | 1 | 1 | 0 | Structural maintenance of chromosomes domain protein (2) |  |  | scaffold_3_mRNA_3695.1 | C_unshiu_00759_mRNA_5.1 | - |
| GF0021360 | 1 | 1 | 0 | Hypothetical protein (2) | protein dimerization activity [GO:0046983 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2); HAT, C-terminal dimerisation domain [IPR008906] (2) | scaffold_3_mRNA_3677.1 | C_unshiu_01154_mRNA_3.1 | - |
| GF0021359 | 1 | 1 | 0 | Senescence-related gene 1 (2) | oxidoreductase activity [GO:0016491 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2) | Oxoglutarate/iron-dependent dioxygenase [IPR005123] (2); Non-haem dioxygenase N-terminal domain [IPR026992] (2); Isopenicillin N synthase-like [IPR027443] (2) | scaffold_3_mRNA_3674.1 | C_unshiu_00612_mRNA_10.1 | - |
| GF0021358 | 1 | 1 | 0 | Retrotransposon protein, putative, Ty3-gypsy subclass (1); Hypothetical protein (1) | RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H domain [IPR002156] (2); Ribonuclease H-like domain [IPR012337] (2) | scaffold_3_mRNA_3672.1 | C_unshiu_00612_mRNA_14.1 | - |
| GF0021357 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_3_mRNA_3670.1 | C_unshiu_02344_mRNA_1.1 | - |
| GF0021356 | 1 | 1 | 0 | Calcium and calcium/calmodulin-dependent serine/threonine-protein kinase (2) |  |  | scaffold_3_mRNA_3666.1 | C_unshiu_02152_mRNA_4.1 | - |
| GF0021354 | 1 | 1 | 0 | Hypothetical protein (1); FAR1 DNA-binding domain protein (1) | regulation of transcription, DNA-templated [GO:0006355 biological_process] (2) | FAR1 DNA binding domain [IPR004330] (2); FHY3/FAR1 family [IPR031052] (2) | scaffold_3_mRNA_3653.1 | C_unshiu_01660_mRNA_4.1 | - |
| GF0021353 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_3_mRNA_3650.1 | C_unshiu_00501_mRNA_16.1 | - |
| GF0021351 | 1 | 1 | 0 | Secologanin synthase (2) | oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2); heme binding [GO:0020037 molecular_function] (2); iron ion binding [GO:0005506 molecular_function] (2) | Cytochrome P450 [IPR001128] (2); Cytochrome P450, conserved site [IPR017972] (2); Cytochrome P450, E-class, group I [IPR002401] (2) | scaffold_3_mRNA_3636.1 | C_unshiu_00016_mRNA_2.1 | - |
| GF0021350 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_3_mRNA_3631.1 | C_unshiu_01049_mRNA_4.1 | - |
| GF0021349 | 1 | 1 | 0 | Secologanin synthase (2) | iron ion binding [GO:0005506 molecular_function] (2); heme binding [GO:0020037 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (2) | Cytochrome P450, conserved site [IPR017972] (2); Cytochrome P450, E-class, group I [IPR002401] (2); Cytochrome P450 [IPR001128] (2) | scaffold_3_mRNA_3629.1 | C_unshiu_01049_mRNA_6.1 | - |
| GF0021348 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_3_mRNA_3626.1 | C_unshiu_00784_mRNA_10.1 | - |
| GF0021347 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_3_mRNA_3624.1 | C_unshiu_01685_mRNA_1.1 | - |
| GF0021346 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_3_mRNA_3617.1 | C_unshiu_00393_mRNA_15.1 | - |
| GF0021345 | 1 | 1 | 0 | Heat stress transcription factor B-4b, putative (2) |  |  | scaffold_3_mRNA_3608.1 | C_unshiu_00175_mRNA_17.1 | - |
| GF0021344 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_3_mRNA_3605.1 | C_unshiu_02554_mRNA_2.1 | - |
| GF0021342 | 1 | 1 | 0 | Hypothetical protein (1); Putative isoaspartyl peptidase/L-asparaginase 2 (1) | hydrolase activity [GO:0016787 molecular_function] (2) | Nucleophile aminohydrolases, N-terminal [IPR029055] (2); Peptidase T2, asparaginase 2 [IPR000246] (2) | scaffold_3_mRNA_3591.1 | C_unshiu_01705_mRNA_4.1 | - |
| GF0021340 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_3_mRNA_3560.1 | C_unshiu_00972_mRNA_4.1 | - |
| GF0021339 | 1 | 1 | 0 | Oxalate oxidase 2 (2) | manganese ion binding [GO:0030145 molecular_function] (2); nutrient reservoir activity [GO:0045735 molecular_function] (2) | RmlC-like cupin domain [IPR011051] (2); Cupin 1 [IPR006045] (2); RmlC-like jelly roll fold [IPR014710] (2); Germin [IPR001929] (2) | scaffold_3_mRNA_356.1 | C_unshiu_00509_mRNA_20.1 | - |
| GF0021338 | 1 | 1 | 0 | Heavy metal transport/detoxification superfamily protein (2) |  |  | scaffold_3_mRNA_3559.1 | C_unshiu_00972_mRNA_3.1 | - |
| GF0021337 | 1 | 1 | 0 | RNA polymerase II C-terminal domain phosphatase-like 4 (2) |  | FCP1 homology domain [IPR004274] (2); BRCT domain [IPR001357] (2); HAD-like domain [IPR023214] (2) | scaffold_3_mRNA_355.1 | C_unshiu_00509_mRNA_19.1 | - |
| GF0021336 | 1 | 1 | 0 | Hypothetical protein (2) |  | Retrotransposon gag domain [IPR005162] (2) | scaffold_3_mRNA_3545.1 | C_unshiu_00996_mRNA_7.1 | - |
| GF0021335 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_3_mRNA_3544.1 | C_unshiu_00996_mRNA_8.1 | - |
| GF0021333 | 1 | 1 | 0 | Hypothetical protein (2) | DNA binding [GO:0003677 molecular_function] (1); DNA polymerase processivity factor activity [GO:0030337 molecular_function] (1); regulation of DNA replication [GO:0006275 biological_process] (1) | Proliferating cell nuclear antigen, PCNA, C-terminal [IPR022649] (1); Proliferating cell nuclear antigen, PCNA [IPR000730] (1) | scaffold_3_mRNA_354.1 | C_unshiu_00509_mRNA_18.1 | - |
| GF0021332 | 1 | 1 | 0 | Putative calcium-binding protein CML15 (2) | calcium ion binding [GO:0005509 molecular_function] (2); protein binding [GO:0005515 molecular_function] (1) | EF-hand domain [IPR002048] (2); EF-Hand 1, calcium-binding site [IPR018247] (2); EF-hand domain pair [IPR011992] (2); Sterile alpha motif domain [IPR001660] (1) | scaffold_3_mRNA_3539.1 | C_unshiu_00549_mRNA_14.1 | - |
| GF0021331 | 1 | 1 | 0 | Putative ribonuclease H protein (1); Similarity to non-LTR retroelement reverse transcriptase (1) | nucleic acid binding [GO:0003676 molecular_function] (1) | Reverse transcriptase zinc-binding domain [IPR026960] (2); Ribonuclease H-like domain [IPR012337] (1) | scaffold_3_mRNA_3519.1 | C_unshiu_00931_mRNA_2.1 | - |
| GF0021330 | 1 | 1 | 0 | AT4G38180 protein (1); Protein FAR1-RELATED SEQUENCE 5 (1) | zinc ion binding [GO:0008270 molecular_function] (2); regulation of transcription, DNA-templated [GO:0006355 biological_process] (2); protein binding [GO:0005515 molecular_function] (1) | FHY3/FAR1 family [IPR031052] (2); Zinc finger, SWIM-type [IPR007527] (2); Zinc finger, PMZ-type [IPR006564] (2); FAR1 DNA binding domain [IPR004330] (1); Glutathione S-transferase, N-terminal [IPR004045] (1); Glutathione S-transferase, C-terminal-like [IPR010987] (1); Thioredoxin-like fold [IPR012336] (1); MULE transposase domain [IPR018289] (1) | scaffold_3_mRNA_3513.1 | C_unshiu_00050_mRNA_4.1 | - |
| GF0021329 | 1 | 1 | 0 | Hypothetical protein (2) | DNA integration [GO:0015074 biological_process] (2); nucleic acid binding [GO:0003676 molecular_function] (2); protein binding [GO:0005515 molecular_function] (1) | Integrase, catalytic core [IPR001584] (2); Ribonuclease H-like domain [IPR012337] (2); Glutathione S-transferase, N-terminal [IPR004045] (1); Thioredoxin-like fold [IPR012336] (1) | scaffold_3_mRNA_3507.1 | C_unshiu_00267_mRNA_11.1 | - |
| GF0021328 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_3_mRNA_3506.1 | C_unshiu_00267_mRNA_12.1 | - |
| GF0021327 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_3_mRNA_3492.1 | C_unshiu_01387_mRNA_2.1 | - |
| GF0021326 | 1 | 1 | 0 | Hypothetical protein (2) |  | Histone deacetylase domain [IPR023801] (2); Histone deacetylase superfamily [IPR000286] (1) | scaffold_3_mRNA_3491.1 | C_unshiu_01092_mRNA_5.1 | - |
| GF0021325 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_3_mRNA_3483.1 | C_unshiu_00381_mRNA_11.1 | - |
| GF0021323 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_3_mRNA_3453.1 | C_unshiu_01409_mRNA_8.1 | - |
| GF0021322 | 1 | 1 | 0 | TMV resistance protein N (1); Disease resistance protein (TIR-NBS-LRR class) (1) | ADP binding [GO:0043531 molecular_function] (2); protein binding [GO:0005515 molecular_function] (2); signal transduction [GO:0007165 biological_process] (1) | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); NB-ARC [IPR002182] (2); Leucine-rich repeat [IPR001611] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1) | scaffold_3_mRNA_3444.1 | C_unshiu_01158_mRNA_19.1 | - |
| GF0021321 | 1 | 1 | 0 | Disease resistance protein (TIR-NBS-LRR class) (1); TMV resistance protein N (1) | signal transduction [GO:0007165 biological_process] (2); protein binding [GO:0005515 molecular_function] (2) | Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (2) | scaffold_3_mRNA_3443.1 | C_unshiu_01698_mRNA_1.1 | - |
| GF0021320 | 1 | 1 | 0 | Hypothetical protein (2) | N-acetyltransferase activity [GO:0008080 molecular_function] (2) | Acyl-CoA N-acyltransferase [IPR016181] (2); GNAT domain [IPR000182] (2) | scaffold_3_mRNA_3442.1 | C_unshiu_01158_mRNA_20.1 | - |
| GF0021319 | 1 | 1 | 0 | Protein SUPPRESSOR OF npr1-1, CONSTITUTIVE 1 (2) | ADP binding [GO:0043531 molecular_function] (2); protein binding [GO:0005515 molecular_function] (2) | Leucine-rich repeat [IPR001611] (2); NB-ARC [IPR002182] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Leucine-rich repeat, typical subtype [IPR003591] (1) | scaffold_3_mRNA_3421.1 | C_unshiu_02501_mRNA_1.1 | - |
| GF0021318 | 1 | 1 | 0 | DnaJ homolog subfamily B member 4 (2) | protein folding [GO:0006457 biological_process] (2); unfolded protein binding [GO:0051082 molecular_function] (2) | Chaperone DnaJ, C-terminal [IPR002939] (2); DnaJ domain, conserved site [IPR018253] (2); HSP40/DnaJ peptide-binding [IPR008971] (2); DnaJ domain [IPR001623] (2) | scaffold_3_mRNA_341.1 | C_unshiu_00509_mRNA_5.1 | - |
| GF0021317 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_3_mRNA_3403.1 | C_unshiu_00200_mRNA_34.1 | - |
| GF0021316 | 1 | 1 | 0 | Beta-hexosaminidase subunit B2 (2) | carbohydrate metabolic process [GO:0005975 biological_process] (2); beta-N-acetylhexosaminidase activity [GO:0004563 molecular_function] (2); hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (2) | Glycoside hydrolase family 20, catalytic domain [IPR015883] (2); Glycoside hydrolase superfamily [IPR017853] (2); Beta-hexosaminidase [IPR025705] (2); Chitobiase/beta-hexosaminidase domain 2-like [IPR029018] (2); Beta-hexosaminidase, eukaryotic type, N-terminal [IPR029019] (2); Glycoside hydrolase, catalytic domain [IPR013781] (1) | scaffold_3_mRNA_3388.1 | C_unshiu_00476_mRNA_5.1 | - |
| GF0021315 | 1 | 1 | 0 | Putative fertility restorer homologue (2) | protein binding [GO:0005515 molecular_function] (1) | Pentatricopeptide repeat [IPR002885] (2); Tetratricopeptide-like helical domain [IPR011990] (1); Pentacotripeptide-repeat region of PROPR [IPR033443] (1) | scaffold_3_mRNA_3387.1 | C_unshiu_00476_mRNA_6.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0021314 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_3386.1 | C_unshiu_00476_mRNA_7.1 | - |
| GF0021313 | 1 | 1 | 0 | Proton-dependent oligopeptide transport family protein (1); Nitrate transporter 1.7 (1) | transporter activity [GO:0005215 molecular_function] (2); transport [GO:0006810 biological_process] (2); membrane [GO:0016020 cellular_component] (2) | Major facilitator superfamily domain [IPR020846] (2); Proton-dependent oligopeptide transporter family [IPR000109] (2) | scaffold_3_mRNA_338.1 | C_unshiu_00509_mRNA_1.1 | - |
| GF0021312 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_3361.1 | C_unshiu_00482_mRNA_4.1 | - |
| GF0021311 | 1 | 1 | 0 | Hypothetical protein (2) | | BRCT domain [IPR001357] (2) | scaffold_3_mRNA_335.1 | C_unshiu_00123_mRNA_14.1 | - |
| GF0021310 | 1 | 1 | 0 | Hypothetical protein (2) | | Cobalamin (vitamin B12) biosynthesis CobW-like, C-terminal [IPR011629] (1) | scaffold_3_mRNA_3342.1 | C_unshiu_01398_mRNA_6.1 | - |
| GF0021309 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_3341.1 | C_unshiu_00631_mRNA_13.1 | - |
| GF0021308 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_3333.1 | C_unshiu_01054_mRNA_3.1 | - |
| GF0021307 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_3332.1 | C_unshiu_01157_mRNA_3.1 | - |
| GF0021306 | 1 | 1 | 0 | Hypothetical protein (1); Retrotransposon protein, putative, unclassified (1) | | Aspartic peptidase domain [IPR021109] (1) | scaffold_3_mRNA_3328.1 | C_unshiu_01157_mRNA_1.1 | - |
| GF0021305 | 1 | 1 | 0 | Potato DNA for copia-like transposable element (1); Hypothetical protein (1) | | | scaffold_3_mRNA_3320.1 | C_unshiu_00423_mRNA_7.1 | - |
| GF0021304 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_3313.1 | C_unshiu_02231_mRNA_2.1 | - |
| GF0021303 | 1 | 1 | 0 | RNA-directed DNA polymerase (Reverse transcriptase) (2) | | Reverse transcriptase domain [IPR000477] (2) | scaffold_3_mRNA_3312.1 | C_unshiu_02070_mRNA_1.1 | - |
| GF0021302 | 1 | 1 | 0 | Hypothetical protein (2) | | NAD(P)-binding domain [IPR016040] (1) | scaffold_3_mRNA_3310.1 | C_unshiu_02070_mRNA_3.1 | - |
| GF0021301 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_3309.1 | C_unshiu_02070_mRNA_5.1 | - |
| GF0021300 | 1 | 1 | 0 | Putative glutamyl endopeptidase, chloroplastic (2) | proteolysis [GO:0006508 biological_process] (2); serine-type peptidase activity [GO:0008236 molecular_function] (2); protein binding [GO:0005515 molecular_function] (1) | Alpha/Beta hydrolase fold [IPR029058] (2); Peptidase S9, prolyl oligopeptidase, catalytic domain [IPR001375] (2); WD40/YVTN repeat-like-containing domain [IPR015943] (1) | scaffold_3_mRNA_3292.1 | C_unshiu_00308_mRNA_32.2 | - |
| GF0021299 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_3291.1 | C_unshiu_00194_mRNA_29.1 | - |
| GF0021297 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_3282.1 | C_unshiu_00236_mRNA_8.1 | - |
| GF0021295 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_3268.1 | C_unshiu_00645_mRNA_4.1 | - |
| GF0021293 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_3257.1 | C_unshiu_00167_mRNA_23.1 | - |
| GF0021292 | 1 | 1 | 0 | Embryonic abundant protein-like (2) | methyltransferase activity [GO:0008168 molecular_function] (2); metabolic process [GO:0008152 biological_process] (2) | Methyltransferase type 11 [IPR013216] (2); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (2) | scaffold_3_mRNA_3249.1 | C_unshiu_00167_mRNA_16.1 | - |
| GF0021291 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_3248.1 | C_unshiu_00167_mRNA_15.1 | - |
| GF0021290 | 1 | 1 | 0 | Hypothetical protein (2) | | Arabidopsis retrotransposon Orf1 [IPR004312] (2) | scaffold_3_mRNA_3245.1 | C_unshiu_00167_mRNA_11.1 | - |
| GF0021289 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_3244.1 | C_unshiu_00167_mRNA_10.1 | - |
| GF0021288 | 1 | 1 | 0 | Embryo-abundant protein EMB (2) | | | scaffold_3_mRNA_3243.1 | C_unshiu_00167_mRNA_9.1 | - |
| GF0021287 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_3238.1 | C_unshiu_00167_mRNA_3.1 | - |
| GF0021286 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_3236.1 | C_unshiu_01436_mRNA_2.1 | - |
| GF0021285 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_3229.1 | C_unshiu_02216_mRNA_2.1 | - |
| GF0021284 | 1 | 1 | 0 | Cytokinin riboside 5'-monophosphate phosphoribohydrolase (2) | | | scaffold_3_mRNA_3223.1 | C_unshiu_00246_mRNA_35.1 | - |
| GF0021283 | 1 | 1 | 0 | Hypothetical protein (2) | | Transposase-associated domain [IPR029480] (1) | scaffold_3_mRNA_3219.1 | C_unshiu_00056_mRNA_78.1 | - |
| GF0021282 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_3214.1 | C_unshiu_00104_mRNA_38.1 | - |
| GF0021281 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_3208.1 | C_unshiu_01399_mRNA_6.1 | - |
| GF0021278 | 1 | 1 | 0 | Hypothetical protein (2) | polygalacturonase activity [GO:0004650 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1) | Pectin lyase fold/virulence factor [IPR011050] (2); Pectin lyase fold [IPR012334] (2); Glycoside hydrolase, family 28 [IPR000743] (1); Pectate lyase superfamily protein [IPR024535] (1) | scaffold_3_mRNA_3196.1 | C_unshiu_02157_mRNA_3.1 | - |
| GF0021277 | 1 | 1 | 0 | Galacturan 1,4-alpha-galacturonidase (2) | polygalacturonase activity [GO:0004650 molecular_function] (2); carbohydrate metabolic process [GO:0005975 biological_process] (2) | Pectin lyase fold/virulence factor [IPR011050] (2); Pectin lyase fold [IPR012334] (2); Glycoside hydrolase, family 28 [IPR000743] (2); Pectate lyase superfamily protein [IPR024535] (1) | scaffold_3_mRNA_3191.1 | C_unshiu_01406_mRNA_4.1 | - |
| GF0021275 | 1 | 1 | 0 | Polygalacturonase (2) | carbohydrate metabolic process [GO:0005975 biological_process] (2); polygalacturonase activity [GO:0004650 molecular_function] (2) | Pectin lyase fold/virulence factor [IPR011050] (2); Pectin lyase fold [IPR012334] (2); Glycoside hydrolase, family 28 [IPR000743] (2) | scaffold_3_mRNA_3165.1 | C_unshiu_00324_mRNA_4.1 | - |
| GF0021273 | 1 | 1 | 0 | Polygalacturonase (2) | polygalacturonase activity [GO:0004650 molecular_function] (2); carbohydrate metabolic process [GO:0005975 biological_process] (2) | Glycoside hydrolase, family 28 [IPR000743] (2); Pectin lyase fold/virulence factor [IPR011050] (2); Pectin lyase fold [IPR012334] (2) | scaffold_3_mRNA_3161.1 | C_unshiu_02580_mRNA_2.1 | - |
| GF0021269 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_3129.1 | C_unshiu_01084_mRNA_7.1 | - |
| GF0021265 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_3115.1 | C_unshiu_00950_mRNA_11.1 | - |
| GF0021264 | 1 | 1 | 0 | Thioredoxin superfamily protein, putative (1); Thioredoxin superfamily protein isoform 1 (1) | | | scaffold_3_mRNA_3114.1 | C_unshiu_00950_mRNA_12.1 | - |
| GF0021263 | 1 | 1 | 0 | F-box/FBD/LRR-repeat protein At5g22660 (2) | protein binding [GO:0005515 molecular_function] (2) | Leucine-rich repeat domain, L domain-like [IPR032675] (2); F-box domain [IPR001810] (2); FBD domain [IPR006566] (2) | scaffold_3_mRNA_3113.1 | C_unshiu_00950_mRNA_13.1 | - |
| GF0021262 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_3112.1 | C_unshiu_00950_mRNA_14.1 | - |
| GF0021261 | 1 | 1 | 0 | F-box/FBD/LRR-repeat protein At5g22660 (2) | protein binding [GO:0005515 molecular_function] (2); poly(ADP-ribose) glycohydrolase activity [GO:0004649 molecular_function] (2); carbohydrate metabolic process [GO:0005975 biological_process] (2) | F-box domain [IPR001810] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Poly(ADP-ribose) glycohydrolase [IPR007724] (2); FBD domain [IPR006566] (2) | scaffold_3_mRNA_3111.1 | C_unshiu_00950_mRNA_15.1 | - |
| GF0021260 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_3100.1 | C_unshiu_00278_mRNA_5.1 | - |
| GF0021258 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_3093.1 | C_unshiu_00609_mRNA_8.1 | - |
| GF0021257 | 1 | 1 | 0 | Hypothetical protein (2) | | Leucine-rich repeat domain, L domain-like [IPR032675] (1) | scaffold_3_mRNA_3087.1 | C_unshiu_01332_mRNA_1.1 | - |
| GF0021256 | 1 | 1 | 0 | Hypothetical protein (1); 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_3_mRNA_3085.1 | C_unshiu_01722_mRNA_2.1 | - |
| GF0021254 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_3068.1 | C_unshiu_00117_mRNA_1.1 | - |
| GF0021253 | 1 | 1 | 0 | Hypothetical protein (2) | | Leucine-rich repeat domain, L domain-like [IPR032675] (2); Receptor L-domain [IPR000494] (1) | scaffold_3_mRNA_3065.1 | C_unshiu_00117_mRNA_4.1 | - |
| GF0021252 | 1 | 1 | 0 | Hypothetical protein (2) | RNA binding [GO:0003723 molecular_function] (1); mRNA splicing, via spliceosome [GO:0000398 biological_process] (1); U2AF [GO:0089701 cellular_component] (1) | U2 auxiliary factor small subunit [IPR009145] (1) | scaffold_3_mRNA_3064.1 | C_unshiu_00117_mRNA_5.1 | - |
| GF0021251 | 1 | 1 | 0 | Putative disease resistance protein (2) | | Leucine-rich repeat domain, L domain-like [IPR032675] (2) | scaffold_3_mRNA_3049.1 | C_unshiu_00212_mRNA_14.1 | - |
| GF0021250 | 1 | 1 | 0 | Disease resistance N'-like protein (1); LRR and NB-ARC domains-containing disease resistance protein, putative (1) | ADP binding [GO:0043531 molecular_function] (2) | NB-ARC [IPR002182] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Winged helix-turn-helix DNA-binding domain [IPR011991] (1) | scaffold_3_mRNA_3048.1 | C_unshiu_00212_mRNA_13.1 | - |
| GF0021249 | 1 | 1 | 0 | Hypothetical protein (2) | integral component of membrane [GO:0016021 cellular_component] (2); defense response [GO:0006952 biological_process] (2) | Mlo-related protein [IPR004326] (2) | scaffold_3_mRNA_3047.1 | C_unshiu_00212_mRNA_12.1 | - |
| GF0021248 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_3046.1 | C_unshiu_00212_mRNA_11.1 | - |
| GF0021247 | 1 | 1 | 0 | Nucleic acid-binding isoform 1 (2) | tRNA binding [GO:0000049 molecular_function] (2) | tRNA-binding domain [IPR002547] (2); Nucleic acid-binding, OB-fold [IPR012340] (2) | scaffold_3_mRNA_3037.1 | C_unshiu_00286_mRNA_24.1 | - |
| GF0021246 | 1 | 1 | 0 | Ankyrin repeat family protein (1); Hypothetical protein (1) | protein binding [GO:0005515 molecular_function] (2) | Ankyrin repeat-containing domain [IPR020683] (2); Ankyrin repeat [IPR002110] (2) | scaffold_3_mRNA_3026.1 | C_unshiu_00113_mRNA_41.1 | - |
| GF0021244 | 1 | 1 | 0 | Hypothetical protein (2) | catalytic activity [GO:0003824 molecular_function] (2); metabolic process [GO:0008152 biological_process] (2); regulation of transcription from RNA polymerase II promoter [GO:0006357 biological_process] (1); NuA4 histone acetyltransferase complex [GO:0035267 cellular_component] (1); Piccolo NuA4 histone acetyltransferase complex [GO:0032777 cellular_component] (1) | Enhancer of polycomb-like, N-terminal [IPR019542] (2); Alkaline phosphatase-like, alpha/beta/alpha [IPR017849] (2); Alkaline-phosphatase-like, core domain [IPR017850] (2); Type I phosphodiesterase/nucleotide pyrophosphatase/phosphate transferase [IPR002591] (1); Enhancer of polycomb protein [IPR024943] (1) | scaffold_3_mRNA_3017.1 | C_unshiu_01657_mRNA_6.1 | - |
| GF0021243 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_3014.1 | C_unshiu_00383_mRNA_18.1 | - |
| GF0021241 | 1 | 1 | 0 | Hypothetical protein (2) | | Domain of unknown function DUF4283 [IPR025558] (2) | scaffold_3_mRNA_2988.1 | C_unshiu_01094_mRNA_1.1 | - |
| GF0021240 | 1 | 1 | 0 | Peptide chain release factor-like protein (2) | | | scaffold_3_mRNA_2985.1 | C_unshiu_01437_mRNA_7.1 | - |
| GF0021239 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_2983.1 | C_unshiu_02389_mRNA_3.1 | - |
| GF0021237 | 1 | 1 | 0 | Hypothetical protein (2) | translation release factor activity [GO:0003747 molecular_function] (2); translational termination [GO:0006415 biological_process] (2) | Peptide chain release factor class I/class II [IPR000352] (2); Double-stranded RNA-binding domain [IPR014720] (1) | scaffold_3_mRNA_2970.1 | C_unshiu_00575_mRNA_2.1 | - |
| GF0021235 | 1 | 1 | 0 | Hypothetical protein (2) | signal transduction [GO:0007165 biological_process] (2); protein binding [GO:0005515 molecular_function] (2) | Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (2); Leucine-rich repeat 3 [IPR011713] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2) | scaffold_3_mRNA_2969.1 | C_unshiu_00575_mRNA_1.1 | - |
| GF0021234 | 1 | 1 | 0 | Putative Peptide chain release factor (1); Putative class I peptide chain release factor-like (1) | translation release factor activity [GO:0003747 molecular_function] (2); translational termination [GO:0006415 biological_process] (2) | Peptide chain release factor class I/class II [IPR000352] (2); Alpha/Beta hydrolase fold [IPR029058] (2); Double-stranded RNA-binding domain [IPR014720] (1) | scaffold_3_mRNA_2967.1 | C_unshiu_02982_mRNA_2.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0021233 | 1 | 1 | 0 | Hypothetical protein (2) | phosphogluconate dehydrogenase (decarboxylating) activity [GO:0004616 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2) | NAD(P)-binding domain [IPR016040] (2); 6-phosphogluconate dehydrogenase [IPR006183] (2); 6-phosphogluconate dehydrogenase, NADP-binding [IPR006115] (2) | scaffold_3_mRNA_2939.1 | C_unshiu_01437_mRNA_5.1 | - |
| GF0021232 | 1 | 1 | 0 | Hypothetical protein (1); Peptide chain release factor 2 (1) | translational termination [GO:0006415 biological_process] (2); translation release factor activity [GO:0003747 molecular_function] (2) | Peptide chain release factor class I/class II [IPR000352] (2); Double-stranded RNA-binding domain [IPR014720] (1) | scaffold_3_mRNA_2933.1 | C_unshiu_00231_mRNA_25.1 | - |
| GF0021231 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_2932.1 | C_unshiu_00199_mRNA_20.1 | - |
| GF0021230 | 1 | 1 | 0 | AT-hook motif nuclear localized protein 1 (2) | DNA binding [GO:0003677 molecular_function] (2) | AT hook, DNA-binding motif [IPR017956] (2); PPC domain [IPR005175] (2) | scaffold_3_mRNA_293.1 | C_unshiu_01105_mRNA_2.1 | - |
| GF0021229 | 1 | 1 | 0 | Hypothetical protein (2) | protein binding [GO:0005515 molecular_function] (2); signal transduction [GO:0007165 biological_process] (2) | Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (2) | scaffold_3_mRNA_2927.1 | C_unshiu_01001_mRNA_7.1 | - |
| GF0021228 | 1 | 1 | 0 | Monosacharide transport protein (2) | | | scaffold_3_mRNA_2921.1 | C_unshiu_03103_mRNA_1.1 | - |
| GF0021226 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_2918.1 | C_unshiu_01031_mRNA_13.1 | - |
| GF0021225 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (1) | Ribonuclease H-like domain [IPR012337] (1) | scaffold_3_mRNA_2914.1 | C_unshiu_01031_mRNA_9.1 | - |
| GF0021224 | 1 | 1 | 0 | Hypothetical protein (2) | | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2) | scaffold_3_mRNA_2913.1 | C_unshiu_01031_mRNA_8.1 | - |
| GF0021223 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_291.1 | C_unshiu_01144_mRNA_5.1 | - |
| GF0021222 | 1 | 1 | 0 | Retroelement pol polyprotein-like (2) | | | scaffold_3_mRNA_2909.1 | C_unshiu_01031_mRNA_1.1 | - |
| GF0021221 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_2904.1 | C_unshiu_01094_mRNA_15.1 | - |
| GF0021220 | 1 | 1 | 0 | Hypothetical protein (2) | protein binding [GO:0005515 molecular_function] (2) | Leucine-rich repeat [IPR001611] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2) | scaffold_3_mRNA_2903.1 | C_unshiu_01094_mRNA_14.1 | - |
| GF0021219 | 1 | 1 | 0 | Hypothetical protein (2) | trehalose biosynthetic process [GO:0005992 biological_process] (2); catalytic activity [GO:0003824 molecular_function] (2) | Trehalose-phosphatase [IPR003337] (2); HAD-like domain [IPR023214] (2) | scaffold_3_mRNA_29.1 | C_unshiu_00399_mRNA_9.1 | - |
| GF0021218 | 1 | 1 | 0 | Putative TIR-NBS class resistance protein (1); Hypothetical protein (1) | signal transduction [GO:0007165 biological_process] (1); protein binding [GO:0005515 molecular_function] (1) | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1) | scaffold_3_mRNA_2897.1 | C_unshiu_01094_mRNA_8.1 | - |
| GF0021215 | 1 | 1 | 0 | Conserved hypothetical plastid protein Ycf45 (2) | ATP binding [GO:0005524 molecular_function] (2) | AAA+ ATPase domain [IPR003593] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); ATPase, AAA-type, core [IPR003959] (2) | scaffold_3_mRNA_2874.1 | C_unshiu_00582_mRNA_26.1 | - |
| GF0021214 | 1 | 1 | 0 | Actin-depolymerizing factor 2 (2) | actin binding [GO:0003779 molecular_function] (2); actin filament depolymerization [GO:0030042 biological_process] (2); intracellular [GO:0005622 cellular_component] (2); actin cytoskeleton [GO:0015629 cellular_component] (2) | ADF-H/Gelsolin-like domain [IPR029006] (2); Actin-depolymerising factor homology domain [IPR002108] (2); ADF/Cofilin/Destrin [IPR017904] (1); ADF/Cofilin [IPR017904] (1) | scaffold_3_mRNA_287.1 | C_unshiu_01144_mRNA_9.1 | - |
| GF0021213 | 1 | 1 | 0 | Hypothetical protein (2) | ubiquitin-dependent protein catabolic process [GO:0006511 biological_process] (1); multicellular organismal development [GO:0007275 biological_process] (1); nucleus [GO:0005634 cellular_component] (1) | E3 ubiquitin-protein ligase SIN-like [IPR004162] (1) | scaffold_3_mRNA_2856.1 | C_unshiu_00518_mRNA_15.1 | - |
| GF0021212 | 1 | 1 | 0 | TMV resistance protein N (2) | signal transduction [GO:0007165 biological_process] (2); ADP binding [GO:0043531 molecular_function] (2); protein binding [GO:0005515 molecular_function] (2) | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); AAA+ ATPase domain [IPR003593] (2); NB-ARC [IPR002182] (2); Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (2); Leucine-rich repeat 3 [IPR011713] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Winged helix-turn-helix DNA-binding domain [IPR011991] (2) | scaffold_3_mRNA_2855.1 | C_unshiu_00518_mRNA_14.1 | - |
| GF0021211 | 1 | 1 | 0 | Hypothetical protein (2) | protein binding [GO:0005515 molecular_function] (2); phosphoric ester hydrolase activity [GO:0042578 molecular_function] (2) | SAC domain [IPR002013] (2); WW domain [IPR001202] (2) | scaffold_3_mRNA_2854.1 | C_unshiu_00518_mRNA_13.1 | - |
| GF0021210 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_2853.1 | C_unshiu_00518_mRNA_12.1 | - |
| GF0021207 | 1 | 1 | 0 | Hypothetical protein (2) | | Histone-binding protein RBBP4, N-terminal [IPR022052] (2) | scaffold_3_mRNA_2834.1 | C_unshiu_01977_mRNA_3.1 | - |
| GF0021206 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_2832.1 | C_unshiu_00596_mRNA_9.1 | - |
| GF0021205 | 1 | 1 | 0 | F-box protein SKIP23 (2) | | Domain unknown function DUF295 [IPR005174] (2) | scaffold_3_mRNA_2831.1 | C_unshiu_00596_mRNA_10.1 | - |
| GF0021203 | 1 | 1 | 0 | Hypothetical protein (2) | | Transposase, MuDR, plant [IPR004332] (2); MULE transposase domain [IPR018289] (2) | scaffold_3_mRNA_2823.1 | C_unshiu_02456_mRNA_4.1 | - |
| GF0021201 | 1 | 1 | 0 | Hypothetical protein (2) | zinc ion binding [GO:0008270 molecular_function] (1) | Transposase, MuDR, plant [IPR004332] (2); Zinc finger, PMZ-type [IPR006564] (1); Zinc finger, SWIM-type [IPR007527] (1) | scaffold_3_mRNA_2806.1 | C_unshiu_00097_mRNA_1.1 | - |
| GF0021199 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_2802.1 | C_unshiu_01224_mRNA_5.1 | - |
| GF0021198 | 1 | 1 | 0 | Hypothetical protein (2) | | GAG-pre-integrase domain [IPR025724] (1) | scaffold_3_mRNA_2801.1 | C_unshiu_00181_mRNA_31.1 | - |
| GF0021196 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_2789.1 | C_unshiu_00739_mRNA_13.1 | - |
| GF0021195 | 1 | 1 | 0 | Hypothetical protein (2) | signal transduction [GO:0007165 biological_process] (2); protein binding [GO:0005515 molecular_function] (2) | Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (2) | scaffold_3_mRNA_2771.1 | C_unshiu_00313_mRNA_6.1 | - |
| GF0021194 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_2768.1 | C_unshiu_00313_mRNA_3.1 | - |
| GF0021193 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_2766.1 | C_unshiu_00441_mRNA_1.1 | - |
| GF0021191 | 1 | 1 | 0 | Hypothetical protein (2) | proteolysis [GO:0006508 biological_process] (2); cysteine-type peptidase activity [GO:0008234 molecular_function] (2) | Domain of unknown function DUF1985 [IPR015410] (2); Ulp1 protease family, C-terminal catalytic domain [IPR003653] (2) | scaffold_3_mRNA_2758.1 | C_unshiu_02474_mRNA_2.1 | - |
| GF0021190 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_3_mRNA_2755.1 | C_unshiu_02707_mRNA_3.1 | - |
| GF0021189 | 1 | 1 | 0 | Gag protease polyprotein, putative (2) | | Retrotransposon gag domain [IPR005162] (2) | scaffold_3_mRNA_2751.1 | C_unshiu_00723_mRNA_10.1 | - |
| GF0021188 | 1 | 1 | 0 | Tubulin beta-9 chain (1); Tubulin beta-7 chain (1) | microtubule-based process [GO:0007017 biological_process] (2); GTP binding [GO:0005525 molecular_function] (2); structural constituent of cytoskeleton [GO:0005200 molecular_function] (2); microtubule [GO:0005874 cellular_component] (2); GTPase activity [GO:0003924 molecular_function] (2) | Beta tubulin [IPR002453] (2); Tubulin, conserved site [IPR017975] (2); Tubulin/FtsZ, GTPase domain [IPR003008] (2); Beta tubulin, autoregulation binding site [IPR013838] (2); Tubulin [IPR000217] (2); Tubulin, C-terminal [IPR023123] (1) | scaffold_3_mRNA_275.1 | C_unshiu_01325_mRNA_6.1 | - |
| GF0021187 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_2747.1 | C_unshiu_01266_mRNA_5.1 | - |
| GF0021186 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_2746.1 | C_unshiu_00948_mRNA_2.1 | - |
| GF0021185 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_2745.1 | C_unshiu_01266_mRNA_6.1 | - |
| GF0021184 | 1 | 1 | 0 | Suppressor of npr1-1, constitutive 1-like protein (1); Disease resistance protein (TIR-NBS-LRR class) (1) | signal transduction [GO:0007165 biological_process] (2); protein binding [GO:0005515 molecular_function] (2); ADP binding [GO:0043531 molecular_function] (1) | Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1) | scaffold_3_mRNA_2740.1 | C_unshiu_02202_mRNA_3.1 | - |
| GF0021183 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_2738.1 | C_unshiu_02202_mRNA_2.1 | - |
| GF0021180 | 1 | 1 | 0 | Protein SUPPRESSOR OF npr1-1, CONSTITUTIVE 1 (2) | protein binding [GO:0005515 molecular_function] (2); ADP binding [GO:0043531 molecular_function] (1) | Leucine-rich repeat 3 [IPR011713] (2); Leucine-rich repeat, typical subtype [IPR003591] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Leucine-rich repeat [IPR001611] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1) | scaffold_3_mRNA_2727.1 | C_unshiu_00931_mRNA_6.1 | - |
| GF0021179 | 1 | 1 | 0 | Disease resistance protein (TIR-NBS-LRR class) (2) | signal transduction [GO:0007165 biological_process] (2); ADP binding [GO:0043531 molecular_function] (2); protein binding [GO:0005515 molecular_function] (2) | NB-ARC [IPR002182] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (2); Repeat of unknown function XGLTT [IPR008164] (1); Leucine-rich repeat [IPR001611] (1); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Leucine-rich repeat 3 [IPR011713] (1) | scaffold_3_mRNA_2723.1 | C_unshiu_02362_mRNA_3.1 | - |
| GF0021178 | 1 | 1 | 0 | Hypothetical protein (2) | | Endonuclease/exonuclease/phosphatase [IPR005135] (2) | scaffold_3_mRNA_2719.1 | C_unshiu_01276_mRNA_2.1 | - |
| GF0021177 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_2714.1 | C_unshiu_01276_mRNA_8.1 | - |
| GF0021176 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_2703.1 | C_unshiu_01030_mRNA_3.1 | - |
| GF0021175 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (1) | Retrotransposon gag domain [IPR005162] (2); Aspartic peptidase domain [IPR021109] (2); Ribonuclease H-like domain [IPR012337] (1) | scaffold_3_mRNA_2702.1 | C_unshiu_01030_mRNA_4.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0021174 | 1 | 1 | 0 | Disease resistance protein (TIR-NBS-LRR class) (2) | ADP binding [GO:0043531 molecular_function] (2); signal transduction [GO:0007165 biological_process] (1); protein binding [GO:0005515 molecular_function] (1) | NB-ARC [IPR002182] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); Leucine-rich repeat, typical subtype [IPR003591] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1) | scaffold_3_mRNA_2697.1 | C_unshiu_01466_mRNA_5.1 | - |
| GF0021173 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_2695.1 | C_unshiu_02537_mRNA_2.1 | - |
| GF0021172 | 1 | 1 | 0 | Hypothetical protein (2) | | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2) | scaffold_3_mRNA_2693.1 | C_unshiu_01034_mRNA_16.1 | - |
| GF0021171 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_2690.1 | C_unshiu_01233_mRNA_3.1 | - |
| GF0021170 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_269.1 | C_unshiu_03068_mRNA_2.1 | - |
| GF0021169 | 1 | 1 | 0 | Hypothetical protein (2) | | Arabidopsis retrotransposon Orf1 [IPR004312] (2) | scaffold_3_mRNA_2686.1 | C_unshiu_00637_mRNA_10.1 | - |
| GF0021168 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_2683.1 | C_unshiu_00272_mRNA_16.1 | - |
| GF0021166 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_2672.1 | C_unshiu_01663_mRNA_1.1 | - |
| GF0021165 | 1 | 1 | 0 | Caffeic acid O-methyltransferase (2) | O-methyltransferase activity [GO:0008171 molecular_function] (2); methyltransferase activity [GO:0008168 molecular_function] (1) | S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (2); Winged helix-turn-helix DNA-binding domain [IPR011991] (2); O-methyltransferase, family 2 [IPR001077] (2); O-methyltransferase COMT-type [IPR016461] (1) | scaffold_3_mRNA_2668.1 | C_unshiu_01111_mRNA_1.1 | - |
| GF0021164 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_2666.1 | C_unshiu_01979_mRNA_1.1 | - |
| GF0021163 | 1 | 1 | 0 | Cysteine-rich RLK (RECEPTOR-like protein kinase) 8 (2) | | Gag-polypeptide of LTR copia-type [IPR029472] (2); Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1) | scaffold_3_mRNA_2665.1 | C_unshiu_01979_mRNA_2.1 | - |
| GF0021162 | 1 | 1 | 0 | Hypothetical protein (1); LRR receptor-like kinase family protein (1) | ATP binding [GO:0005524 molecular_function] (2); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1) | Protein kinase, ATP binding site [IPR017441] (2); Protein kinase-like domain [IPR011009] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Protein kinase domain [IPR000719] (1) | scaffold_3_mRNA_2663.1 | C_unshiu_01979_mRNA_5.1 | - |
| GF0021161 | 1 | 1 | 0 | Egg cell-secreted protein 1.4 (2) | | Prolamin-like domain [IPR008502] (2) | scaffold_3_mRNA_2654.1 | C_unshiu_00828_mRNA_11.1 | - |
| GF0021160 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_2649.1 | C_unshiu_00828_mRNA_7.1 | - |
| GF0021159 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_2641.1 | C_unshiu_00708_mRNA_7.1 | - |
| GF0021158 | 1 | 1 | 0 | Hypothetical protein (2) | diacylglycerol O-acyltransferase activity [GO:0004144 molecular_function] (2) | O-acyltransferase WSD1, C-terminal [IPR009721] (2) | scaffold_3_mRNA_2636.1 | C_unshiu_00031_mRNA_7.1 | - |
| GF0021157 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (1) | Reverse transcriptase zinc-binding domain [IPR026960] (2); Ribonuclease H-like domain [IPR012337] (1) | scaffold_3_mRNA_2626.1 | C_unshiu_00717_mRNA_6.1 | - |
| GF0021156 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_2625.1 | C_unshiu_00717_mRNA_7.1 | - |
| GF0021155 | 1 | 1 | 0 | Hypothetical protein (2) | protein binding [GO:0005515 molecular_function] (2); signal transduction [GO:0007165 biological_process] (1) | Leucine-rich repeat [IPR001611] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Domain of unknown function DUF4371 [IPR025398] (1); Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (1); Leucine-rich repeat, typical subtype [IPR003591] (1) | scaffold_3_mRNA_2621.1 | C_unshiu_00717_mRNA_10.1 | - |
| GF0021154 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_2617.1 | C_unshiu_00717_mRNA_12.1 | - |
| GF0021153 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_2616.1 | C_unshiu_00717_mRNA_13.1 | - |
| GF0021152 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_2609.1 | C_unshiu_01012_mRNA_6.1 | - |
| GF0021150 | 1 | 1 | 0 | TMV resistance N (2) | | Leucine-rich repeat domain, L domain-like [IPR032675] (2) | scaffold_3_mRNA_2602.1 | C_unshiu_01012_mRNA_4.1 | - |
| GF0021149 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_2590.1 | C_unshiu_02326_mRNA_4.1 | - |
| GF0021148 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_2583.1 | C_unshiu_00015_mRNA_107.1 | - |
| GF0021146 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_2578.1 | C_unshiu_00015_mRNA_114.1 | - |
| GF0021145 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_2577.1 | C_unshiu_00015_mRNA_115.1 | - |
| GF0021144 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_2576.1 | C_unshiu_00015_mRNA_116.1 | - |
| GF0021143 | 1 | 1 | 0 | Hypothetical protein (2) | protein binding [GO:0005515 molecular_function] (2) | PDZ domain [IPR001478] (2); Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1) | scaffold_3_mRNA_2575.1 | C_unshiu_00602_mRNA_3.1 | - |
| GF0021142 | 1 | 1 | 0 | Hypothetical protein (1); Phosphoribosylaminoimidazole carboxylase, chloroplastic (1) | 'de novo' IMP biosynthetic process [GO:0006189 biological_process] (2) | Phosphoribosylaminoimidazole carboxylase PurE domain [IPR000031] (1); PurE domain [IPR000031] (1) | scaffold_3_mRNA_2574.1 | C_unshiu_00602_mRNA_4.1 | - |
| GF0021141 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_2562.1 | C_unshiu_00959_mRNA_3.1 | - |
| GF0021140 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_2561.1 | C_unshiu_00959_mRNA_2.1 | - |
| GF0021139 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_2542.1 | C_unshiu_00692_mRNA_6.1 | - |
| GF0021138 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_2541.1 | C_unshiu_00692_mRNA_5.1 | - |
| GF0021137 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_2540.1 | C_unshiu_00621_mRNA_11.1 | - |
| GF0021136 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_2539.1 | C_unshiu_00621_mRNA_12.1 | - |
| GF0021135 | 1 | 1 | 0 | Hypothetical protein (1); Serine/threonine-protein kinase PBS1 (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_2537.1 | C_unshiu_00621_mRNA_13.1 | - |
| GF0021132 | 1 | 1 | 0 | Hypothetical protein (2) | | Endonuclease/exonuclease/phosphatase [IPR005135] (2) | scaffold_3_mRNA_2526.1 | C_unshiu_00617_mRNA_14.1 | - |
| GF0021131 | 1 | 1 | 0 | Hypothetical protein (2) | transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); DNA binding [GO:0003677 molecular_function] (1) | AP2/ERF domain [IPR001471] (1); DNA-binding domain [IPR016177] (1) | scaffold_3_mRNA_25.1 | C_unshiu_00399_mRNA_13.1 | - |
| GF0021130 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_2499.1 | C_unshiu_02644_mRNA_2.1 | - |
| GF0021129 | 1 | 1 | 0 | Zinc knuckle family protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2); zinc ion binding [GO:0008270 molecular_function] (2) | Zinc finger, CCHC-type [IPR001878] (2) | scaffold_3_mRNA_2498.1 | C_unshiu_02644_mRNA_1.1 | - |
| GF0021128 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_2494.1 | C_unshiu_00534_mRNA_18.1 | - |
| GF0021127 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_2489.1 | C_unshiu_02548_mRNA_2.1 | - |
| GF0021126 | 1 | 1 | 0 | Caffeic acid 3-O-methyltransferase (1); Caffeic acid O-methyltransferase (1) | protein dimerization activity [GO:0046983 molecular_function] (2); methyltransferase activity [GO:0008168 molecular_function] (2); O-methyltransferase activity [GO:0008171 molecular_function] (1) | Plant methyltransferase dimerisation [IPR012967] (2); O-methyltransferase COMT-type [IPR016461] (2); Winged helix-turn-helix DNA-binding domain [IPR011991] (2); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (1); O-methyltransferase, family 2 [IPR001077] (1) | scaffold_3_mRNA_2480.1 | C_unshiu_02205_mRNA_2.1 | - |
| GF0021125 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_2476.1 | C_unshiu_01285_mRNA_1.1 | - |
| GF0021124 | 1 | 1 | 0 | RING-H2 finger B1A (2) | zinc ion binding [GO:0008270 molecular_function] (2); protein binding [GO:0005515 molecular_function] (2) | Zinc finger, RING-type [IPR001841] (2); Zinc finger, RING/FYVE/PHD-type [IPR013083] (2); Zinc finger, RING-H2-type [IPR024766] (1) | scaffold_3_mRNA_247.2 | C_unshiu_00343_mRNA_19.2 | - |
| GF0021123 | 1 | 1 | 0 | Retrotransposon protein, putative, Ty1-copia subclass (2) | nucleic acid binding [GO:0003676 molecular_function] (1); DNA integration [GO:0015074 biological_process] (1); zinc ion binding [GO:0008270 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_3_mRNA_2457.1 | C_unshiu_02085_mRNA_2.1 | - |
| GF0021122 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_2451.1 | C_unshiu_01600_mRNA_5.1 | - |
| GF0021121 | 1 | 1 | 0 | Protein AIG1 (2) | GTP binding [GO:0005525 molecular_function] (2) | AIG1-type guanine nucleotide-binding (G) domain [IPR006703] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1) | scaffold_3_mRNA_2429.1 | C_unshiu_02127_mRNA_2.1 | - |
| GF0021120 | 1 | 1 | 0 | Retrotransposon protein, putative, Ty3-gypsy subclass (2) | nucleic acid binding [GO:0003676 molecular_function] (2); DNA integration [GO:0015074 biological_process] (2) | Integrase, catalytic core [IPR001584] (2); Ribonuclease H-like domain [IPR012337] (2) | scaffold_3_mRNA_2428.1 | C_unshiu_02127_mRNA_3.1 | - |
| GF0021119 | 1 | 1 | 0 | Hypothetical protein (2) | GTP binding [GO:0005525 molecular_function] (1) | AIG1-type guanine nucleotide-binding (G) domain [IPR006703] (1) | scaffold_3_mRNA_2427.1 | C_unshiu_02127_mRNA_4.1 | - |
| GF0021118 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_2426.1 | C_unshiu_02127_mRNA_5.1 | - |
| GF0021117 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_2423.1 | C_unshiu_00373_mRNA_21.1 | - |
| GF0021116 | 1 | 1 | 0 | Protein AIG1 (2) | GTP binding [GO:0005525 molecular_function] (2) | AIG1-type guanine nucleotide-binding (G) domain [IPR006703] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2) | scaffold_3_mRNA_2422.1 | C_unshiu_00373_mRNA_22.1 | - |
| GF0021115 | 1 | 1 | 0 | Protein AIG1 (2) | GTP binding [GO:0005525 molecular_function] (2) | AIG1-type guanine nucleotide-binding (G) domain [IPR006703] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1) | scaffold_3_mRNA_2421.1 | C_unshiu_00373_mRNA_23.1 | - |
| GF0021114 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_2419.1 | C_unshiu_00373_mRNA_25.1 | - |
| GF0021113 | 1 | 1 | 0 | Hypothetical protein (1); Retrotransposon protein, putative, Ty3-gypsy subclass (1) | | Aspartic peptidase domain [IPR021109] (1); Retroviral aspartyl protease [IPR013242] (1) | scaffold_3_mRNA_2417.1 | C_unshiu_00491_mRNA_17.1 | - |
| GF0021112 | 1 | 1 | 0 | Protein AIG1 (2) | GTP binding [GO:0005525 molecular_function] (2) | AIG1-type guanine nucleotide-binding (G) domain [IPR006703] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); LOG family [IPR031100] (1) | scaffold_3_mRNA_2409.1 | C_unshiu_00964_mRNA_12.1 | - |
| GF0021110 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_2398.1 | C_unshiu_00329_mRNA_3.1 | - |
| GF0021108 | 1 | 1 | 0 | Hypothetical protein (2) | GTP binding [GO:0005525 molecular_function] (2) | AIG1-type guanine nucleotide-binding (G) domain [IPR006703] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2) | scaffold_3_mRNA_2384.1 | C_unshiu_01164_mRNA_1.1 | - |
| GF0021107 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_2379.1 | C_unshiu_00373_mRNA_3.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0021106 | 1 | 1 | 0 | Hypothetical protein (2) | GTP binding [GO:0005525 molecular_function] (1) | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); AIG1-type guanine nucleotide-binding (G) domain [IPR006703] (1) | scaffold_3_mRNA_2378.1 | C_unshiu_00373_mRNA_4.1 | - |
| GF0021105 | 1 | 1 | 0 | Protein AIG1 (2) | GTP binding [GO:0005525 molecular_function] (2) | AIG1-type guanine nucleotide-binding (G) domain [IPR006703] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2) | scaffold_3_mRNA_2377.1 | C_unshiu_00373_mRNA_6.1 | - |
| GF0021104 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_3_mRNA_2376.1 | C_unshiu_00373_mRNA_7.1 | - |
| GF0021103 | 1 | 1 | 0 | AIG1 domain-containing protein (2) | GTP binding [GO:0005525 molecular_function] (2) | AIG1-type guanine nucleotide-binding (G) domain [IPR006703] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2) | scaffold_3_mRNA_2375.1 | C_unshiu_00373_mRNA_8.1 | - |
| GF0021102 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_3_mRNA_2369.1 | C_unshiu_00373_mRNA_14.1 | - |
| GF0021101 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_3_mRNA_2351.1 | C_unshiu_00625_mRNA_7.1 | - |
| GF0021100 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_3_mRNA_2348.1 | C_unshiu_00625_mRNA_10.1 | - |
| GF0021099 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_3_mRNA_2346.1 | C_unshiu_00625_mRNA_13.1 | - |
| GF0021098 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_3_mRNA_2345.1 | C_unshiu_00625_mRNA_14.1 | - |
| GF0021097 | 1 | 1 | 0 | Phenylcoumaran benzylic ether reductase-like protein (2) |  | NmrA-like domain [IPR008030] (2); NAD(P)-binding domain [IPR016040] (1) | scaffold_3_mRNA_2343.1 | C_unshiu_00625_mRNA_16.1 | - |
| GF0021096 | 1 | 1 | 0 | Cytokinin riboside 5'-monophosphate phosphoribohydrolase (2) |  | LOG family [IPR031100] (2) | scaffold_3_mRNA_2340.1 | C_unshiu_00625_mRNA_19.1 | - |
| GF0021095 | 1 | 1 | 0 | Phenylcoumaran benzylic ether reductase (2) |  | NmrA-like domain [IPR008030] (2); NAD(P)-binding domain [IPR016040] (2) | scaffold_3_mRNA_2334.1 | C_unshiu_01141_mRNA_2.1 | - |
| GF0021094 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_3_mRNA_2333.1 | C_unshiu_01141_mRNA_3.1 | - |
| GF0021093 | 1 | 1 | 0 | Hypothetical protein (2) | DNA binding [GO:0003677 molecular_function] (2) | Zinc finger, BED-type [IPR003656] (2) | scaffold_3_mRNA_2332.1 | C_unshiu_01141_mRNA_5.1 | - |
| GF0021092 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_3_mRNA_2330.1 | C_unshiu_01853_mRNA_1.1 | - |
| GF0021091 | 1 | 1 | 0 | Hypothetical protein (2) |  | Reverse transcriptase domain [IPR000477] (2) | scaffold_3_mRNA_2327.1 | C_unshiu_01853_mRNA_5.1 | - |
| GF0021090 | 1 | 1 | 0 | Isoflavone reductase (1); Isoflavone reductase homolog 1 (1) |  | NAD(P)-binding domain [IPR016040] (2); NmrA-like domain [IPR008030] (2) | scaffold_3_mRNA_2322.1 | C_unshiu_02472_mRNA_3.1 | - |
| GF0021089 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_3_mRNA_2321.1 | C_unshiu_02472_mRNA_2.1 | - |
| GF0021088 | 1 | 1 | 0 | Hypothetical protein (2) | protein dimerization activity [GO:0046983 molecular_function] (1) | HAT, C-terminal dimerisation domain [IPR008906] (1) | scaffold_3_mRNA_2320.1 | C_unshiu_00446_mRNA_17.1 | - |
| GF0021087 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_3_mRNA_2319.1 | C_unshiu_02156_mRNA_2.1 | - |
| GF0021084 | 1 | 1 | 0 | D-isomer specific 2-hydroxyacid dehydrogenase family protein isoform 2 (2) | oxidation-reduction process [GO:0055114 biological_process] (2); NAD binding [GO:0051287 molecular_function] (2) | NAD(P)-binding domain [IPR016040] (2); D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding domain [IPR006140] (2) | scaffold_3_mRNA_2312.1 | C_unshiu_00410_mRNA_25.1 | - |
| GF0021083 | 1 | 1 | 0 | Hypothetical protein (2) | ATP binding [GO:0005524 molecular_function] (2); protein kinase activity [GO:0004672 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2) | Protein kinase-like domain [IPR011009] (2); Protein kinase domain [IPR000719] (2) | scaffold_3_mRNA_2309.1 | C_unshiu_00410_mRNA_28.1 | - |
| GF0021081 | 1 | 1 | 0 | Putative non-LTR retroelement reverse transcriptase (2) |  | Endonuclease/exonuclease/phosphatase [IPR005135] (2); Reverse transcriptase domain [IPR000477] (2) | scaffold_3_mRNA_2300.1 | C_unshiu_00453_mRNA_18.1 | - |
| GF0021080 | 1 | 1 | 0 | Ribonuclease H (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_3_mRNA_2275.1 | C_unshiu_00618_mRNA_4.1 | - |
| GF0021079 | 1 | 1 | 0 | RNA-directed DNA polymerase ; Ribonuclease H, putative (1); Hypothetical protein (1) |  | Endonuclease/exonuclease/phosphatase [IPR005135] (2) | scaffold_3_mRNA_2271.1 | C_unshiu_00618_mRNA_15.1 | - |
| GF0021075 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_3_mRNA_2258.1 | C_unshiu_00345_mRNA_19.1 | - |
| GF0021074 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_3_mRNA_2248.1 | C_unshiu_00902_mRNA_10.1 | - |
| GF0021073 | 1 | 1 | 0 | Putative retroelement pol polyprotein (2) |  |  | scaffold_3_mRNA_2245.1 | C_unshiu_00189_mRNA_10.1 | - |
| GF0021071 | 1 | 1 | 0 | Hypothetical protein (1); AC transposase, putative, expressed (1) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_3_mRNA_2235.1 | C_unshiu_00417_mRNA_6.1 | - |
| GF0021070 | 1 | 1 | 0 | BED zinc finger,hAT family dimerization domain (2) | protein dimerization activity [GO:0046983 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2); HAT, C-terminal dimerisation domain [IPR008906] (2) | scaffold_3_mRNA_2234.1 | C_unshiu_00417_mRNA_5.1 | - |
| GF0021068 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_3_mRNA_2218.1 | C_unshiu_02035_mRNA_1.1 | - |
| GF0021067 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_3_mRNA_2212.1 | C_unshiu_00417_mRNA_19.1 | - |
| GF0021066 | 1 | 1 | 0 | Kunitz trypsin inhibitor (2) | endopeptidase inhibitor activity [GO:0004866 molecular_function] (2) | Proteinase inhibitor I3, Kunitz legume [IPR002160] (2); Kunitz inhibitor ST1-like [IPR011065] (2) | scaffold_3_mRNA_2209.1 | C_unshiu_00765_mRNA_9.1 | - |
| GF0021065 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_3_mRNA_2206.1 | C_unshiu_00765_mRNA_5.1 | - |
| GF0021064 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_3_mRNA_2204.1 | C_unshiu_00765_mRNA_3.1 | - |
| GF0021062 | 1 | 1 | 0 | Succinyl-CoA ligase [GDP-forming] subunit alpha, mitochondrial (2) | cofactor binding [GO:0048037 molecular_function] (2); catalytic activity [GO:0003824 molecular_function] (2); metabolic process [GO:0008152 biological_process] (2) | Succinyl-CoA ligase, alpha subunit [IPR005810] (2); CoA-binding [IPR003781] (2); ATP-citrate lyase/succinyl-CoA ligase [IPR005811] (2); NAD(P)-binding domain [IPR016040] (2); Succinyl-CoA synthetase-like [IPR016102] (2); ATP-citrate lyase/succinyl-CoA ligase, active site [IPR017440] (1); ATP-citrate lyase/succinyl-CoA ligase, conserved site [IPR033847] (1) | scaffold_3_mRNA_2183.1 | C_unshiu_00297_mRNA_7.1 | - |
| GF0021058 | 1 | 1 | 0 | Hypothetical protein (2) |  | MULE transposase domain [IPR018289] (2) | scaffold_3_mRNA_2164.1 | C_unshiu_00297_mRNA_14.1 | - |
| GF0021054 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_3_mRNA_2147.1 | C_unshiu_02179_mRNA_2.1 | - |
| GF0021053 | 1 | 1 | 0 | Hypothetical protein (2) | nucleosome [GO:0000786 cellular_component] (2); DNA binding [GO:0003677 molecular_function] (2); protein heterodimerization activity [GO:0046982 molecular_function] (2) | Histone H2B [IPR000558] (2); Histone-fold [IPR009072] (2) | scaffold_3_mRNA_2142.1 | C_unshiu_00721_mRNA_9.1 | - |
| GF0021052 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_3_mRNA_2139.1 | C_unshiu_00669_mRNA_1.1 | - |
| GF0021051 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_3_mRNA_2135.1 | C_unshiu_00938_mRNA_1.1 | - |
| GF0021050 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_3_mRNA_2116.1 | C_unshiu_00837_mRNA_3.1 | - |
| GF0021049 | 1 | 1 | 0 | Endoglucanase (2) | catalytic activity [GO:0003824 molecular_function] (2); carbohydrate metabolic process [GO:0005975 biological_process] (2); hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (2) | Six-hairpin glycosidase-like [IPR008928] (2); Glycoside hydrolase family 9 [IPR001701] (2); Glycosyl hydrolases family 9, Asp/Glu active sites [IPR033126] (1); Six-hairpin glycosidase [IPR012341] (1) | scaffold_3_mRNA_210.1 | C_unshiu_00223_mRNA_23.1 | - |
| GF0021048 | 1 | 1 | 0 | Hypothetical protein (1); RNA-directed DNA polymerase (Reverse transcriptase) (1) |  | Reverse transcriptase domain [IPR000477] (2) | scaffold_3_mRNA_2091.1 | C_unshiu_00224_mRNA_5.1 | - |
| GF0021047 | 1 | 1 | 0 | TMV resistance N (2) |  | Leucine-rich repeat 3 [IPR011713] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2) | scaffold_3_mRNA_2089.1 | C_unshiu_00493_mRNA_10.1 | - |
| GF0021046 | 1 | 1 | 0 | Hypothetical protein (1); Disease resistance protein (TIR-NBS-LRR class) (1) | ADP binding [GO:0043531 molecular_function] (1) | Leucine-rich repeat domain, L domain-like [IPR032675] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1) | scaffold_3_mRNA_2086.1 | C_unshiu_00493_mRNA_8.1 | - |
| GF0021044 | 1 | 1 | 0 | Verticillium wilt resistance-like protein (2) | protein binding [GO:0005515 molecular_function] (2) | Leucine-rich repeat domain, L domain-like [IPR032675] (2); Leucine-rich repeat, typical subtype [IPR003591] (2); Leucine-rich repeat [IPR001611] (2); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (2) | scaffold_3_mRNA_2065.1 | C_unshiu_00356_mRNA_7.1 | - |
| GF0021041 | 1 | 1 | 0 | Hypothetical protein (2) |  | Malectin-like carbohydrate-binding domain [IPR024788] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (1) | scaffold_3_mRNA_2048.1 | C_unshiu_01252_mRNA_1.1 | - |
| GF0021040 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_3_mRNA_2035.1 | C_unshiu_00101_mRNA_11.1 | - |
| GF0021039 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_3_mRNA_2029.1 | C_unshiu_00101_mRNA_6.1 | - |
| GF0021036 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_3_mRNA_2007.1 | C_unshiu_00841_mRNA_7.1 | - |
| GF0021035 | 1 | 1 | 0 | Retrotransposon gag protein, putative (1); Hypothetical protein (1) |  | Retrotransposon gag domain [IPR005162] (2); Retroviral aspartyl protease [IPR013242] (1); Aspartic peptidase domain [IPR021109] (1) | scaffold_3_mRNA_2002.1 | C_unshiu_00350_mRNA_33.1 | - |
| GF0021034 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_3_mRNA_2000.1 | C_unshiu_01489_mRNA_7.1 | - |
| GF0021033 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_3_mRNA_1992.1 | C_unshiu_01100_mRNA_10.1 | - |
| GF0021032 | 1 | 1 | 0 | Hypothetical protein (2) |  | Retrotransposon gag domain [IPR005162] (2) | scaffold_3_mRNA_1981.1 | C_unshiu_01100_mRNA_22.1 | - |
| GF0021031 | 1 | 1 | 0 | Transposon protein, putative, unclassified, expressed (2) | regulation of transcription, DNA-templated [GO:0006355 biological_process] (2) | FAR1 DNA binding domain [IPR004330] (2); FHY3/FAR1 family [IPR031052] (2); MULE transposase domain [IPR018289] (2) | scaffold_3_mRNA_1977.1 | C_unshiu_00674_mRNA_13.1 | - |
| GF0021030 | 1 | 1 | 0 | CAAX amino terminal protease family protein (2) | membrane [GO:0016020 cellular_component] (2) | CAAX amino terminal protease [IPR003675] (2) | scaffold_3_mRNA_197.1 | C_unshiu_00541_mRNA_18.1 | - |
| GF0021029 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_3_mRNA_1963.1 | C_unshiu_01943_mRNA_2.1 | - |
| GF0021028 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_3_mRNA_1960.1 | C_unshiu_02795_mRNA_1.1 | - |
| GF0021027 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_3_mRNA_1957.1 | C_unshiu_01530_mRNA_8.1 | - |
| GF0021026 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_3_mRNA_1955.1 | C_unshiu_02770_mRNA_2.1 | - |
| GF0021025 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_3_mRNA_1953.1 | C_unshiu_02770_mRNA_6.1 | - |
| GF0021024 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_3_mRNA_1940.1 | C_unshiu_01409_mRNA_2.1 | - |
| GF0021023 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_3_mRNA_1915.1 | C_unshiu_02323_mRNA_3.1 | - |
| GF0021022 | 1 | 1 | 0 | Cation/H(+) antiporter 15 (2) | solute:proton antiporter activity [GO:0015299 molecular_function] (2); transmembrane transport [GO:0055085 biological_process] (2); integral component of membrane [GO:0016021 cellular_component] (2); cation transport [GO:0006812 biological_process] (2) | Cation/H+ exchanger [IPR006153] (2); Rossmann-like alpha/beta/alpha sandwich fold [IPR014729] (1) | scaffold_3_mRNA_191.1 | C_unshiu_00541_mRNA_10.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0021020 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1898.1 | C_unshiu_00366_mRNA_2.1 | - |
| GF0021018 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1887.1 | C_unshiu_02614_mRNA_8.1 | - |
| GF0021017 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1881.1 | C_unshiu_00050_mRNA_20.1 | - |
| GF0021016 | 1 | 1 | 0 | Integrase (2) | nucleic acid binding [GO:0003676 molecular_function] (2); DNA integration [GO:0015074 biological_process] (2) | Ribonuclease H-like domain [IPR012337] (2); Integrase, catalytic core [IPR001584] (2); Retrotransposon gag domain [IPR005162] (1) | scaffold_3_mRNA_1876.1 | C_unshiu_00164_mRNA_31.1 | - |
| GF0021014 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1852.1 | C_unshiu_01432_mRNA_5.1 | - |
| GF0021013 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1851.1 | C_unshiu_01432_mRNA_6.1 | - |
| GF0021012 | 1 | 1 | 0 | Hypothetical protein (2) | | Reverse transcriptase domain [IPR000477] (2) | scaffold_3_mRNA_1848.1 | C_unshiu_00104_mRNA_31.1 | - |
| GF0021011 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1844.1 | C_unshiu_01432_mRNA_11.1 | - |
| GF0021010 | 1 | 1 | 0 | ABC transporter C family member 10 (2) | transmembrane transport [GO:0055085 biological_process] (2); ATP binding [GO:0005524 molecular_function] (2); ATPase activity, coupled to transmembrane movement of substances [GO:0042626 molecular_function] (2); transport [GO:0006810 biological_process] (2); ATPase activity [GO:0016887 molecular_function] (2); integral component of membrane [GO:0016021 cellular_component] (2) | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); ABC transporter-like [IPR003439] (2); ABC transporter type 1, transmembrane domain [IPR011527] (2); AAA+ ATPase domain [IPR003593] (2); ABC transporter, conserved site [IPR017871] (2) | scaffold_3_mRNA_184.1 | C_unshiu_00541_mRNA_4.1 | - |
| GF0021009 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1839.1 | C_unshiu_01029_mRNA_8.1 | - |
| GF0021008 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1826.1 | C_unshiu_00280_mRNA_9.1 | - |
| GF0021007 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1812.1 | C_unshiu_01671_mRNA_5.1 | - |
| GF0021005 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1806.1 | C_unshiu_01666_mRNA_10.1 | - |
| GF0021004 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_18.1 | C_unshiu_00852_mRNA_14.1 | - |
| GF0021003 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1797.1 | C_unshiu_01424_mRNA_4.1 | - |
| GF0021002 | 1 | 1 | 0 | RNA-directed DNA polymerase (1); Hypothetical protein (1) | | Reverse transcriptase domain [IPR000477] (1) | scaffold_3_mRNA_1789.1 | C_unshiu_00579_mRNA_16.1 | - |
| GF0021001 | 1 | 1 | 0 | Ribonuclease P/MRP protein subunit POP5 (2) | ribonuclease activity [GO:0004540 molecular_function] (2); tRNA processing [GO:0008033 biological_process] (2); ribonuclease P activity [GO:0004526 molecular_function] (1); RNA metabolic process [GO:0016070 biological_process] (1) | Ribonuclease P/MRP protein subunit [IPR002759] (2); Ribonuclease P/MRP protein subunit Pop5 [IPR016819] (1) | scaffold_3_mRNA_1771.1 | C_unshiu_00463_mRNA_6.1 | - |
| GF0021000 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1770.1 | C_unshiu_00463_mRNA_7.1 | - |
| GF0020999 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1766.1 | C_unshiu_00463_mRNA_10.1 | - |
| GF0020998 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_3_mRNA_1763.1 | C_unshiu_00463_mRNA_13.1 | - |
| GF0020997 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (1) | Ribonuclease H-like domain [IPR012337] (1) | scaffold_3_mRNA_1762.1 | C_unshiu_00463_mRNA_15.1 | - |
| GF0020996 | 1 | 1 | 0 | Hypothetical protein (2) | | Zinc knuckle CX2CX4HX4C [IPR025836] (2) | scaffold_3_mRNA_1761.1 | C_unshiu_00463_mRNA_16.1 | - |
| GF0020995 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1754.1 | C_unshiu_00323_mRNA_23.1 | - |
| GF0020994 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1740.1 | C_unshiu_00948_mRNA_11.1 | - |
| GF0020993 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1737.1 | C_unshiu_00948_mRNA_10.1 | - |
| GF0020992 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1719.1 | C_unshiu_01797_mRNA_4.1 | - |
| GF0020991 | 1 | 1 | 0 | IAA-amino acid hydrolase ILR1-like 4 (1); IAA-amino acid hydrolase ILR1-like 8 (1) | metabolic process [GO:0008152 biological_process] (1); hydrolase activity [GO:0016787 molecular_function] (1) | Peptidase M20, dimerisation domain [IPR011650] (1); Peptidase M20 [IPR002933] (1) | scaffold_3_mRNA_1713.1 | C_unshiu_01859_mRNA_4.1 | - |
| GF0020990 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1711.1 | C_unshiu_00542_mRNA_10.1 | - |
| GF0020988 | 1 | 1 | 0 | Ta11 non-LTR retroelement protein-like (2) | | Domain of unknown function DUF4283 [IPR025558] (2); Zinc knuckle CX2CX4HX4C [IPR025836] (2) | scaffold_3_mRNA_1708.1 | C_unshiu_01834_mRNA_4.1 | - |
| GF0020987 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1707.1 | C_unshiu_01834_mRNA_3.1 | - |
| GF0020985 | 1 | 1 | 0 | Peroxidase 5 (1); Hypothetical protein (1) | heme binding [GO:0020037 molecular_function] (2); response to oxidative stress [GO:0006979 biological_process] (2); peroxidase activity [GO:0004601 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2) | Haem peroxidase [IPR010255] (2); Plant peroxidase [IPR000823] (2); Haem peroxidase, plant/fungal/bacterial [IPR002016] (2) | scaffold_3_mRNA_1698.1 | C_unshiu_00542_mRNA_5.1 | - |
| GF0020984 | 1 | 1 | 0 | Nascent polypeptide-associated complex subunit alpha-like protein (2) | | Nascent polypeptide-associated complex NAC domain [IPR002715] (2); Nascent polypeptide-associated complex subunit alpha [IPR016641] (2) | scaffold_3_mRNA_1697.1 | C_unshiu_00542_mRNA_3.1 | - |
| GF0020983 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_169.1 | C_unshiu_00609_mRNA_5.1 | - |
| GF0020982 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1688.1 | C_unshiu_01224_mRNA_7.1 | - |
| GF0020981 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1686.1 | C_unshiu_01224_mRNA_9.1 | - |
| GF0020980 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1683.1 | C_unshiu_02726_mRNA_1.1 | - |
| GF0020979 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1681.1 | C_unshiu_01253_mRNA_2.1 | - |
| GF0020977 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1664.1 | C_unshiu_00564_mRNA_4.1 | - |
| GF0020976 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1653.1 | C_unshiu_00180_mRNA_31.1 | - |
| GF0020975 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_165.1 | C_unshiu_00609_mRNA_10.1 | - |
| GF0020974 | 1 | 1 | 0 | Hypothetical protein (2) | zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1) | Endonuclease/exonuclease/phosphatase [IPR005135] (2); Zinc finger, CCHC-type [IPR001878] (1); Zinc knuckle CX2CX4HX4C [IPR025836] (1); Ribonuclease H-like domain [IPR012337] (1) | scaffold_3_mRNA_1648.1 | C_unshiu_00431_mRNA_10.1 | - |
| GF0020973 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1628.1 | C_unshiu_02854_mRNA_2.1 | - |
| GF0020971 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1624.1 | C_unshiu_00392_mRNA_14.1 | - |
| GF0020970 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1619.1 | C_unshiu_00793_mRNA_13.1 | - |
| GF0020969 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1618.1 | C_unshiu_00793_mRNA_12.1 | - |
| GF0020968 | 1 | 1 | 0 | Hypothetical protein (2) | regulation of transcription, DNA-templated [GO:0006355 biological_process] (2) | FHY3/FAR1 family [IPR031052] (2); FAR1 DNA binding domain [IPR004330] (2); MULE transposase domain [IPR018289] (1) | scaffold_3_mRNA_1614.1 | C_unshiu_00793_mRNA_5.1 | - |
| GF0020967 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1612.1 | C_unshiu_00793_mRNA_3.1 | - |
| GF0020966 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1609.1 | C_unshiu_02958_mRNA_4.1 | - |
| GF0020965 | 1 | 1 | 0 | Phenazine biosynthesis PhzC/PhzF family protein (2) | biosynthetic process [GO:0009058 biological_process] (2); catalytic activity [GO:0003824 molecular_function] (2) | Phenazine biosynthesis PhzF protein [IPR003719] (2) | scaffold_3_mRNA_1606.1 | C_unshiu_00069_mRNA_66.1 | - |
| GF0020962 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1592.2 | C_unshiu_01627_mRNA_4.1 | - |
| GF0020961 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1586.1 | C_unshiu_00264_mRNA_13.1 | - |
| GF0020960 | 1 | 1 | 0 | Acetolactate synthase small subunit (1); Hypothetical protein (1) | proteolysis [GO:0006508 biological_process] (2); amino acid binding [GO:0016597 molecular_function] (2); serine-type endopeptidase activity [GO:0004252 molecular_function] (2); branched-chain amino acid biosynthetic process [GO:0009082 biological_process] (2); acetolactate synthase activity [GO:0003984 molecular_function] (2); metabolic process [GO:0008152 biological_process] (2); pyridoxal phosphate binding [GO:0030170 molecular_function] (2); catalytic activity [GO:0003824 molecular_function] (1) | Acetolactate synthase, small subunit [IPR004789] (2); Peptidase S1C [IPR001940] (2); Cys/Met metabolism, pyridoxal phosphate-dependent enzyme [IPR000277] (2); Peptidase S1, PA clan [IPR009003] (2); ACT domain [IPR002912] (2); Pyridoxal phosphate-dependent transferase, major region, subdomain 1 [IPR015421] (1); Pyridoxal phosphate-dependent transferase [IPR015424] (1) | scaffold_3_mRNA_1579.1 | C_unshiu_01812_mRNA_2.1 | - |
| GF0020959 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1572.1 | C_unshiu_00772_mRNA_6.1 | - |
| GF0020958 | 1 | 1 | 0 | Phospholipase A2 family protein (1); Phospholipase A2 (1) | calcium ion binding [GO:0005509 molecular_function] (2); phospholipase A2 activity [GO:0004623 molecular_function] (2); lipid catabolic process [GO:0016042 biological_process] (2); phospholipid metabolic process [GO:0006644 biological_process] (1); arachidonic acid secretion [GO:0050482 biological_process] (1) | Phospholipase A2 [IPR001211] (2); Phospholipase A2 domain [IPR016090] (2); Phospholipase A2, histidine active site [IPR033113] (2) | scaffold_3_mRNA_1567.1 | C_unshiu_00480_mRNA_18.1 | - |
| GF0020956 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1551.1 | C_unshiu_00935_mRNA_4.1 | - |
| GF0020954 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1535.1 | C_unshiu_02518_mRNA_4.1 | - |
| GF0020951 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1484.1 | C_unshiu_01286_mRNA_4.1 | - |
| GF0020950 | 1 | 1 | 0 | Hypothetical protein (2) | | Haem oxygenase-like, multi-helical [IPR016084] (1) | scaffold_3_mRNA_1479.1 | C_unshiu_00936_mRNA_5.1 | - |
| GF0020949 | 1 | 1 | 0 | Hypothetical protein (2) | | Transposase, MuDR, plant [IPR004332] (2) | scaffold_3_mRNA_1471.1 | C_unshiu_03075_mRNA_1.1 | - |
| GF0020948 | 1 | 1 | 0 | Glycoside hydrolase family 28 protein (2) | polygalacturonase activity [GO:0004650 molecular_function] (2); carbohydrate metabolic process [GO:0005975 biological_process] (2) | Parallel beta-helix repeat [IPR006626] (2); Glycoside hydrolase, family 28 [IPR000743] (2); Pectin lyase fold [IPR012334] (2); Pectin lyase fold/virulence factor [IPR011050] (2) | scaffold_3_mRNA_147.1 | C_unshiu_00609_mRNA_25.1 | - |
| GF0020947 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1466.1 | C_unshiu_01915_mRNA_3.1 | - |
| GF0020945 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1446.1 | C_unshiu_00195_mRNA_11.1 | - |
| GF0020944 | 1 | 1 | 0 | Hypothetical protein (2) | histone binding [GO:0042393 molecular_function] (2) | SRA-YDG [IPR003105] (2); PUA-like domain [IPR015947] (2) | scaffold_3_mRNA_1422.1 | C_unshiu_01257_mRNA_7.1 | - |
| GF0020942 | 1 | 1 | 0 | Transcription factor bHLH25 (1); Hypothetical protein (1) | protein dimerization activity [GO:0046983 molecular_function] (2) | Myc-type, basic helix-loop-helix (bHLH) domain [IPR011598] (2) | scaffold_3_mRNA_1402.1 | C_unshiu_01216_mRNA_3.1 | - |
| GF0020940 | 1 | 1 | 0 | Hypothetical protein (2) | | Isoprenoid synthase domain [IPR008949] (1); Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (1) | scaffold_3_mRNA_1362.1 | C_unshiu_00164_mRNA_46.1 | - |
| GF0020939 | 1 | 1 | 0 | Hypothetical protein (2) | | Retrotransposon gag domain [IPR005162] (2) | scaffold_3_mRNA_1355.1 | C_unshiu_02396_mRNA_1.1 | - |
| GF0020938 | 1 | 1 | 0 | Hypothetical protein (2) | | Chromo domain-like [IPR016197] (1); Chromo domain [IPR023780] (1) | scaffold_3_mRNA_1336.1 | C_unshiu_00752_mRNA_4.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0020937 | 1 | 1 | 0 | Hypothetical protein (2) | | Protein-only RNase P, C-terminal [IPR031595] (1); Pentacotripeptide-repeat region of PROPR [IPR033443] (1) | scaffold_3_mRNA_1335.1 | C_unshiu_00752_mRNA_2.1 | - |
| GF0020936 | 1 | 1 | 0 | Hypothetical protein (2) | | High mobility group box domain [IPR009071] (2) | scaffold_3_mRNA_1334.1 | C_unshiu_00968_mRNA_8.1 | - |
| GF0020935 | 1 | 1 | 0 | Hypothetical protein (2) | fatty-acyl-CoA reductase (alcohol-forming) activity [GO:0080019 molecular_function] (2) | Fatty acyl-CoA reductase [IPR026055] (2) | scaffold_3_mRNA_1332.1 | C_unshiu_00381_mRNA_5.1 | - |
| GF0020933 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1320.1 | C_unshiu_00149_mRNA_28.1 | - |
| GF0020930 | 1 | 1 | 0 | Hypothetical protein (2) | | Domain of unknown function DUF1985 [IPR015410] (2) | scaffold_3_mRNA_1312.1 | C_unshiu_00149_mRNA_20.1 | - |
| GF0020927 | 1 | 1 | 0 | Transposase (2) | | Domain of unknown function DUF4216 [IPR025312] (2); Domain of unknown function DUF4218 [IPR025452] (2) | scaffold_3_mRNA_1299.1 | C_unshiu_00157_mRNA_17.1 | - |
| GF0020926 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1297.1 | C_unshiu_02014_mRNA_2.1 | - |
| GF0020925 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1283.1 | C_unshiu_01468_mRNA_3.1 | - |
| GF0020923 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1271.1 | C_unshiu_01165_mRNA_5.1 | - |
| GF0020922 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1268.1 | C_unshiu_01165_mRNA_2.1 | - |
| GF0020921 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1260.1 | C_unshiu_00227_mRNA_4.1 | - |
| GF0020920 | 1 | 1 | 0 | Putative PIFa transposase (2) | | Harbinger transposase-derived nuclease domain [IPR027806] (2); Myb/SANT-like domain [IPR024752] (2) | scaffold_3_mRNA_1259.1 | C_unshiu_00227_mRNA_5.1 | - |
| GF0020919 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (1) | Ribonuclease H-like domain [IPR012337] (1) | scaffold_3_mRNA_1236.1 | C_unshiu_02212_mRNA_3.1 | - |
| GF0020918 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1224.1 | C_unshiu_01714_mRNA_4.1 | - |
| GF0020915 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1200.1 | C_unshiu_00695_mRNA_1.1 | - |
| GF0020914 | 1 | 1 | 0 | Hypothetical protein (2) | zinc ion binding [GO:0008270 molecular_function] (2) | Zinc finger, PMZ-type [IPR006564] (2); Zinc finger, SWIM-type [IPR007527] (1) | scaffold_3_mRNA_1197.1 | C_unshiu_00695_mRNA_2.1 | - |
| GF0020913 | 1 | 1 | 0 | Ethylene-responsive transcription factor (2) | transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (2); regulation of transcription, DNA-templated [GO:0006355 biological_process] (2); DNA binding [GO:0003677 molecular_function] (2) | DNA-binding domain [IPR016177] (2); AP2/ERF domain [IPR001471] (2); AP2/ERF transcription factor ERF/PTI6 [IPR017392] (1) | scaffold_3_mRNA_1195.1 | C_unshiu_00695_mRNA_3.1 | - |
| GF0020912 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1181.1 | C_unshiu_00843_mRNA_10.1 | - |
| GF0020911 | 1 | 1 | 0 | Hypothetical protein (2) | | Mitochondrial carrier domain [IPR023395] (2); Mitochondrial substrate/solute carrier [IPR018108] (2) | scaffold_3_mRNA_1175.1 | C_unshiu_00843_mRNA_5.1 | - |
| GF0020908 | 1 | 1 | 0 | Hypothetical protein (2) | oxidation-reduction process [GO:0055114 biological_process] (2); oxidoreductase activity [GO:0016491 molecular_function] (2) | Oxoglutarate/iron-dependent dioxygenase [IPR005123] (2); Isopenicillin N synthase-like [IPR027443] (2) | scaffold_3_mRNA_1167.1 | C_unshiu_00580_mRNA_23.1 | - |
| GF0020907 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1162.1 | C_unshiu_00580_mRNA_16.1 | - |
| GF0020906 | 1 | 1 | 0 | Protein BREAKING OF ASYMMETRY IN THE STOMATAL LINEAGE (2) | | | scaffold_3_mRNA_1147.1 | C_unshiu_00580_mRNA_2.1 | - |
| GF0020905 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1143.1 | C_unshiu_02363_mRNA_3.1 | - |
| GF0020902 | 1 | 1 | 0 | DUF4283 domain protein (2) | | Domain of unknown function DUF4283 [IPR025558] (2) | scaffold_3_mRNA_1137.1 | C_unshiu_00154_mRNA_3.1 | - |
| GF0020901 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2); zinc ion binding [GO:0008270 molecular_function] (2) | Zinc finger, CCHC-type [IPR001878] (2); Zinc knuckle CX2CX4HX4C [IPR025836] (2) | scaffold_3_mRNA_1136.1 | C_unshiu_00154_mRNA_4.1 | - |
| GF0020898 | 1 | 1 | 0 | RNA-binding (RRM/RBD/RNP motif) family protein (1); Hypothetical protein (1) | nucleic acid binding [GO:0003676 molecular_function] (2); nucleotide binding [GO:0000166 molecular_function] (1) | RNA recognition motif domain [IPR000504] (2); Nucleotide-binding alpha-beta plait domain [IPR012677] (1) | scaffold_3_mRNA_1100.1 | C_unshiu_01729_mRNA_1.1 | - |
| GF0020897 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1086.1 | C_unshiu_00331_mRNA_13.1 | - |
| GF0020896 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_3_mRNA_1083.1 | C_unshiu_00331_mRNA_10.1 | - |
| GF0020895 | 1 | 1 | 0 | PLASMODESMATA CALLOSE-BINDING PROTEIN 3 (2) | | X8 domain [IPR012946] (2) | scaffold_3_mRNA_1081.1 | C_unshiu_00331_mRNA_8.1 | - |
| GF0020894 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1076.1 | C_unshiu_00331_mRNA_4.1 | - |
| GF0020893 | 1 | 1 | 0 | Hypothetical protein (2) | | Rossmann-like alpha/beta/alpha sandwich fold [IPR014729] (2); Cysteinyl-tRNA synthetase/mycothiol ligase [IPR024909] (2); tRNA synthetases class I, catalytic domain [IPR032678] (2) | scaffold_3_mRNA_1052.1 | C_unshiu_00030_mRNA_87.1 | - |
| GF0020891 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_3_mRNA_1038.1 | C_unshiu_00030_mRNA_75.1 | - |
| GF0020890 | 1 | 1 | 0 | Beta-amylase, family GH14 (1); Chloroplast beta-amylase 3 (1) | polysaccharide catabolic process [GO:0000272 biological_process] (2); beta-amylase activity [GO:0016161 molecular_function] (2); carbohydrate metabolic process [GO:0005975 biological_process] (1) | Glycoside hydrolase, family 14 [IPR001554] (2); Glycoside hydrolase superfamily [IPR017853] (2); Glycoside hydrolase, catalytic domain [IPR013781] (1) | scaffold_3_mRNA_103.1 | C_unshiu_00503_mRNA_28.1 | - |
| GF0020889 | 1 | 1 | 0 | Hypothetical protein (1); RNA-directed DNA polymerase (Reverse transcriptase) (1) | | Reverse transcriptase domain [IPR000477] (2) | scaffold_2_mRNA_999.1 | C_unshiu_00514_mRNA_7.1 | - |
| GF0020888 | 1 | 1 | 0 | Hypothetical protein (2) | | Transcription factor BREVIS RADIX, N-terminal domain [IPR027988] (2) | scaffold_2_mRNA_998.1 | C_unshiu_00514_mRNA_8.1 | - |
| GF0020887 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_994.1 | C_unshiu_00514_mRNA_18.1 | - |
| GF0020886 | 1 | 1 | 0 | Hypothetical protein (2) | | Transcription factor BREVIS RADIX, N-terminal domain [IPR027988] (1) | scaffold_2_mRNA_993.1 | C_unshiu_00514_mRNA_19.1 | - |
| GF0020883 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_986.1 | C_unshiu_00894_mRNA_7.1 | - |
| GF0020881 | 1 | 1 | 0 | Hypothetical protein (2) | | Protein kinase-like domain [IPR011009] (2) | scaffold_2_mRNA_981.1 | C_unshiu_00729_mRNA_5.1 | - |
| GF0020880 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_980.1 | C_unshiu_00444_mRNA_19.1 | - |
| GF0020879 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_97.1 | C_unshiu_00652_mRNA_12.1 | - |
| GF0020878 | 1 | 1 | 0 | Hypothetical protein (1); Ribonuclease H (1) | nucleic acid binding [GO:0003676 molecular_function] (2) | Reverse transcriptase zinc-binding domain [IPR026960] (2); Ribonuclease H-like domain [IPR012337] (2); Bifunctional inhibitor/plant lipid transfer protein/seed storage helical domain [IPR016140] (1) | scaffold_2_mRNA_968.1 | C_unshiu_00960_mRNA_15.1 | - |
| GF0020877 | 1 | 1 | 0 | Hypothetical protein (2) | protein binding [GO:0005515 molecular_function] (2) | Ubiquitin-related domain [IPR029071] (2); Ubiquitin domain [IPR000626] (2) | scaffold_2_mRNA_965.1 | C_unshiu_00960_mRNA_11.1 | - |
| GF0020875 | 1 | 1 | 0 | Hypothetical protein (2) | 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); Ribonuclease H-like domain [IPR012337] (1) | scaffold_2_mRNA_961.1 | C_unshiu_00960_mRNA_6.1 | - |
| GF0020874 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_96.1 | C_unshiu_00652_mRNA_13.1 | - |
| GF0020872 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_940.1 | C_unshiu_00569_mRNA_12.1 | - |
| GF0020871 | 1 | 1 | 0 | Verticillium wilt resistance-like protein (2) | protein binding [GO:0005515 molecular_function] (2) | Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (2); Leucine-rich repeat [IPR001611] (2); Leucine-rich repeat, typical subtype [IPR003591] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2) | scaffold_2_mRNA_928.1 | C_unshiu_00162_mRNA_1.1 | - |
| GF0020870 | 1 | 1 | 0 | Non-LTR retroelement reverse transcriptase-like, putative (2) | nucleic acid binding [GO:0003676 molecular_function] (2); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2); Ribonuclease H domain [IPR002156] (2); TB2/DP1/HVA22-related protein [IPR004345] (1) | scaffold_2_mRNA_912.1 | C_unshiu_00162_mRNA_14.1 | - |
| GF0020869 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_901.1 | C_unshiu_00162_mRNA_24.1 | - |
| GF0020866 | 1 | 1 | 0 | Photosystem II 5 kDa protein, chloroplastic (2) | | | scaffold_2_mRNA_876.1 | C_unshiu_00072_mRNA_9.1 | - |
| GF0020865 | 1 | 1 | 0 | Zinc finger CCCH domain-containing protein 24 (2) | protein binding [GO:0005515 molecular_function] (1) | Ankyrin repeat-containing domain [IPR020683] (1); Ankyrin repeat [IPR002110] (1) | scaffold_2_mRNA_867.1 | C_unshiu_00072_mRNA_19.1 | - |
| GF0020864 | 1 | 1 | 0 | Aldehyde dehydrogenase (2) | metabolic process [GO:0008152 biological_process] (2); oxidation-reduction process [GO:0055114 biological_process] (2); oxidoreductase activity [GO:0016491 molecular_function] (2); cellular aldehyde metabolic process [GO:0006081 biological_process] (1); oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor [GO:0016620 molecular_function] (1); aldehyde dehydrogenase [NAD(P)+] activity [GO:0004030 molecular_function] (1) | Aldehyde dehydrogenase domain [IPR015590] (2); Aldehyde/histidinol dehydrogenase [IPR016161] (2); Aldehyde dehydrogenase N-terminal domain [IPR016162] (2); Aldehyde dehydrogenase NAD(P)-dependent [IPR012394] (1); Aldehyde dehydrogenase, C-terminal [IPR016163] (1) | scaffold_2_mRNA_858.1 | C_unshiu_00072_mRNA_29.1 | - |
| GF0020863 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_852.1 | C_unshiu_00072_mRNA_38.1 | - |
| GF0020862 | 1 | 1 | 0 | F-box protein SKIP23 (2) | protein binding [GO:0005515 molecular_function] (1) | Domain unknown function DUF295 [IPR005174] (2); Kelch-type beta propeller [IPR015915] (1); Galactose oxidase, beta-propeller [IPR015916] (1); Galactose oxidase/kelch, beta-propeller [IPR011043] (1) | scaffold_2_mRNA_851.1 | C_unshiu_00072_mRNA_41.1 | - |
| GF0020860 | 1 | 1 | 0 | Outer envelope protein 80, chloroplastic (2) | outer membrane [GO:0019867 cellular_component] (2) | Bacterial surface antigen (D15) [IPR000184] (2) | scaffold_2_mRNA_845.1 | C_unshiu_00072_mRNA_50.1 | - |
| GF0020858 | 1 | 1 | 0 | Sucrose phosphate phosphatase (2) | sucrose-phosphate phosphatase activity [GO:0050307 molecular_function] (2); magnesium ion binding [GO:0000287 molecular_function] (2); sucrose biosynthetic process [GO:0005986 biological_process] (2) | Sucrose phosphatase, plant/cyanobacteria [IPR012847] (2); HAD-like domain [IPR023214] (2); HAD-superfamily hydrolase, subfamily IIB [IPR006379] (2); NTF2-like domain [IPR032710] (2); Sucrose-phosphatase, N-terminal [IPR006380] (1); Sucrose-6-phosphate phosphohydrolase, C-terminal [IPR013679] (1); Sucrose-phosphatase, C-terminal [IPR013679] (1); Sucrose-phosphate synthase [IPR006380] (1) | scaffold_2_mRNA_81.1 | C_unshiu_00062_mRNA_44.1 | - |
| GF0020856 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_805.1 | C_unshiu_00171_mRNA_5.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0020855 | 1 | 1 | 0 | DUF247 domain protein (1); UPF0481 protein (1) | | Protein of unknown function DUF247, plant [IPR004158] (2) | scaffold_2_mRNA_801.1 | C_unshiu_00550_mRNA_15.1 | - |
| GF0020854 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_797.1 | C_unshiu_00550_mRNA_11.1 | - |
| GF0020853 | 1 | 1 | 0 | DUF594 family protein (2) | | Protein of unknown function DUF594 [IPR007658] (2); Domain of unknown function DUF4220 [IPR025315] (2) | scaffold_2_mRNA_788.1 | C_unshiu_00550_mRNA_1.1 | - |
| GF0020852 | 1 | 1 | 0 | Hypothetical protein (2) | | Protein of unknown function DUF594 [IPR007658] (2) | scaffold_2_mRNA_787.1 | C_unshiu_00260_mRNA_39.1 | - |
| GF0020851 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_783.1 | C_unshiu_00260_mRNA_35.1 | - |
| GF0020850 | 1 | 1 | 0 | Transcription factor bHLH130 (1); Transcription factor bHLH122 (1) | protein dimerization activity [GO:0046983 molecular_function] (2) | Myc-type, basic helix-loop-helix (bHLH) domain [IPR011598] (2) | scaffold_2_mRNA_775.1 | C_unshiu_00260_mRNA_28.1 | - |
| GF0020849 | 1 | 1 | 0 | Flavonoid 3'-monooxygenase (2) | oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2); heme binding [GO:0020037 molecular_function] (2); iron ion binding [GO:0005506 molecular_function] (2) | Cytochrome P450, E-class, group I [IPR002401] (2); Cytochrome P450, conserved site [IPR017972] (2); Cytochrome P450 [IPR001128] (2) | scaffold_2_mRNA_772.1 | C_unshiu_00260_mRNA_23.1 | - |
| GF0020847 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_761.1 | C_unshiu_00260_mRNA_15.1 | - |
| GF0020846 | 1 | 1 | 0 | Cysteine protease (1); Hypothetical protein (1) | biosynthetic process [GO:0009058 biological_process] (2); cysteine-type peptidase activity [GO:0008234 molecular_function] (2); transferase activity [GO:0016740 molecular_function] (2); proteolysis [GO:0006508 biological_process] (2); farnesyl-diphosphate farnesyltransferase activity [GO:0004310 molecular_function] (1); transferase activity, transferring alkyl or aryl (other than methyl) groups [GO:0016765 molecular_function] (1); ergosterol biosynthetic process [GO:0006696 biological_process] (1); squalene synthase activity [GO:0051996 molecular_function] (1) | Isoprenoid synthase domain [IPR008949] (2); Cysteine peptidase, histidine active site [IPR025660] (2); Cysteine peptidase, cysteine active site [IPR000169] (2); Squalene/phytoene synthase [IPR002060] (2); Peptidase C1A [IPR013128] (2); Cathepsin propeptide inhibitor domain (I29) [IPR013201] (2); Cysteine peptidase, asparagine active site [IPR025661] (2); Peptidase C1A, papain C-terminal [IPR000668] (2); Trans-Isoprenyl Diphosphate Synthases, head-to-head [IPR033904] (1); Squalene/phytoene synthase, conserved site [IPR019845] (1) | scaffold_2_mRNA_76.1 | C_unshiu_00213_mRNA_28.1 | - |
| GF0020845 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_759.1 | C_unshiu_00260_mRNA_14.1 | - |
| GF0020844 | 1 | 1 | 0 | UDP-glucose flavonoid 3-O-glucosyltransferase 7 (2) | metabolic process [GO:0008152 biological_process] (2); transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (2) | UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (2) | scaffold_2_mRNA_751.1 | C_unshiu_00260_mRNA_6.1 | - |
| GF0020843 | 1 | 1 | 0 | Phytoene synthase (2) | transferase activity, transferring alkyl or aryl (other than methyl) groups [GO:0016765 molecular_function] (2); biosynthetic process [GO:0009058 biological_process] (2); transferase activity [GO:0016740 molecular_function] (2); farnesyl-diphosphate farnesyltransferase activity [GO:0004310 molecular_function] (1); squalene synthase activity [GO:0051996 molecular_function] (1); ergosterol biosynthetic process [GO:0006696 biological_process] (1) | Squalene/phytoene synthase, conserved site [IPR019845] (2); Squalene/phytoene synthase [IPR002060] (2); Isoprenoid synthase domain [IPR008949] (2); Trans-Isoprenyl Diphosphate Synthases, head-to-head [IPR033904] (1) | scaffold_2_mRNA_75.1 | C_unshiu_00213_mRNA_29.1 | - |
| GF0020842 | 1 | 1 | 0 | UDP-glucose flavonoid 3-O-glucosyltransferase 7 (2) | metabolic process [GO:0008152 biological_process] (2); transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (2) | UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (2) | scaffold_2_mRNA_743.1 | C_unshiu_00260_mRNA_5.1 | - |
| GF0020841 | 1 | 1 | 0 | Histidine-containing phosphotransfer protein 4 (2) | phosphorelay signal transduction system [GO:0000160 biological_process] (2); signal transducer activity [GO:0004871 molecular_function] (2) | Signal transduction histidine kinase, phosphotransfer (Hpt) domain [IPR008207] (2) | scaffold_2_mRNA_738.1 | C_unshiu_00028_mRNA_25.1 | - |
| GF0020837 | 1 | 1 | 0 | Lipoxygenase (2) | oxidoreductase activity [GO:0016491 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2); oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen [GO:0016702 molecular_function] (2); metal ion binding [GO:0046872 molecular_function] (2); protein binding [GO:0005515 molecular_function] (2) | Lipoxygenase, plant [IPR001246] (2); Lipoxygenase, domain 3 [IPR027433] (2); PLAT/LH2 domain [IPR001024] (2); Lipoxygenase [IPR000907] (2); Lipoxygenase, conserved site [IPR020834] (2); Lipoxygenase, iron binding site [IPR020833] (2); Lipoxygenase, C-terminal [IPR013819] (2) | scaffold_2_mRNA_708.1 | C_unshiu_00076_mRNA_52.1 | - |
| GF0020836 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_705.1 | C_unshiu_00871_mRNA_11.1 | - |
| GF0020834 | 1 | 1 | 0 | Putative lipoxygenase 5 (2) | protein binding [GO:0005515 molecular_function] (2); metal ion binding [GO:0046872 molecular_function] (2); oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen [GO:0016702 molecular_function] (2); oxidoreductase activity [GO:0016491 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2) | Lipoxygenase, C-terminal [IPR013819] (2); Lipoxygenase [IPR000907] (2); PLAT/LH2 domain [IPR001024] (2); Lipoxygenase, plant [IPR001246] (2) | scaffold_2_mRNA_701.1 | C_unshiu_00076_mRNA_47.1 | - |
| GF0020833 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_697.1 | C_unshiu_00076_mRNA_44.1 | - |
| GF0020832 | 1 | 1 | 0 | Lipoxygenase (2) | metal ion binding [GO:0046872 molecular_function] (2); protein binding [GO:0005515 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2); oxidoreductase activity [GO:0016491 molecular_function] (2); oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen [GO:0016702 molecular_function] (2) | Lipoxygenase, conserved site [IPR020834] (2); Lipoxygenase, C-terminal [IPR013819] (2); Lipoxygenase, iron binding site [IPR020833] (2); Lipoxygenase, plant [IPR001246] (2); PLAT/LH2 domain [IPR001024] (2); Lipoxygenase, domain 3 [IPR027433] (2); Lipoxygenase [IPR000907] (2) | scaffold_2_mRNA_695.1 | C_unshiu_00076_mRNA_42.1 | - |
| GF0020831 | 1 | 1 | 0 | Retrotransposon protein, putative, Ty1-copia subclass (2) | zinc ion binding [GO:0008270 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | Zinc finger, CCHC-type [IPR001878] (2) | scaffold_2_mRNA_692.1 | C_unshiu_00636_mRNA_10.1 | - |
| GF0020829 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_684.1 | C_unshiu_00076_mRNA_37.1 | - |
| GF0020828 | 1 | 1 | 0 | Acetyl-coenzyme A synthetase (2) | metabolic process [GO:0008152 biological_process] (2); catalytic activity [GO:0003824 molecular_function] (2) | AMP-binding, conserved site [IPR020845] (2); AMP-dependent synthetase/ligase [IPR000873] (2) | scaffold_2_mRNA_68.2 | C_unshiu_00213_mRNA_38.1 | - |
| GF0020827 | 1 | 1 | 0 | G-type lectin S-receptor-like serine/threonine-protein kinase RLK1 (2) | protein phosphorylation [GO:0006468 biological_process] (2); protein serine/threonine kinase activity [GO:0004674 molecular_function] (2); protein kinase activity [GO:0004672 molecular_function] (2); ATP binding [GO:0005524 molecular_function] (2); recognition of pollen [GO:0048544 biological_process] (1) | Bulb-type lectin domain [IPR001480] (2); Protein kinase, ATP binding site [IPR017441] (2); Serine/threonine-protein kinase, active site [IPR008271] (2); Protein kinase-like domain [IPR011009] (2); S-receptor-like serine/threonine-protein kinase [IPR024171] (2); Protein kinase domain [IPR000719] (2); S-locus glycoprotein domain [IPR000858] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1) | scaffold_2_mRNA_678.1 | C_unshiu_00076_mRNA_31.1 | - |
| GF0020826 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_667.1 | C_unshiu_00076_mRNA_20.1 | - |
| GF0020824 | 1 | 1 | 0 | Hypothetical protein (2) | magnesium ion binding [GO:0000287 molecular_function] (2); lyase activity [GO:0016829 molecular_function] (2); terpene synthase activity [GO:0010333 molecular_function] (2); metabolic process [GO:0008152 biological_process] (1) | Isoprenoid synthase domain [IPR008949] (2); Terpene synthase, metal-binding domain [IPR005630] (2); Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (2); Terpene synthase, N-terminal domain [IPR001906] (1) | scaffold_2_mRNA_650.1 | C_unshiu_00076_mRNA_11.1 | - |
| GF0020823 | 1 | 1 | 0 | Hypothetical protein (2) | | Domain of unknown function DUF4283 [IPR025558] (2) | scaffold_2_mRNA_612.1 | C_unshiu_00029_mRNA_29.1 | - |
| GF0020822 | 1 | 1 | 0 | Hypothetical protein (2) | | Endonuclease/exonuclease/phosphatase [IPR005135] (2) | scaffold_2_mRNA_611.1 | C_unshiu_00029_mRNA_30.1 | - |
| GF0020820 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_61.1 | C_unshiu_00109_mRNA_60.1 | - |
| GF0020819 | 1 | 1 | 0 | Hypothetical protein (2) | ATP binding [GO:0005524 molecular_function] (2); formate-tetrahydrofolate ligase activity [GO:0004329 molecular_function] (2); folic acid-containing compound biosynthetic process [GO:0009396 biological_process] (2) | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); Formate-tetrahydrofolate ligase, FTHFS [IPR000559] (2) | scaffold_2_mRNA_607.1 | C_unshiu_00029_mRNA_36.1 | - |
| GF0020818 | 1 | 1 | 0 | 10-formyltetrahydrofolate synthetase family protein (2) | ATP binding [GO:0005524 molecular_function] (2); formate-tetrahydrofolate ligase activity [GO:0004329 molecular_function] (2); folic acid-containing compound biosynthetic process [GO:0009396 biological_process] (2) | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); Formate-tetrahydrofolate ligase, FTHFS [IPR000559] (2) | scaffold_2_mRNA_606.1 | C_unshiu_00029_mRNA_37.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0020816 | 1 | 1 | 0 | Cyclin dependent protein kinase homolog (1); Hypothetical protein (1) | ATP binding [GO:0005524 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2); protein kinase activity [GO:0004672 molecular_function] (2) | Protein kinase-like domain [IPR011009] (2); Protein kinase domain [IPR000719] (2); Pentatricopeptide repeat [IPR002885] (2); Serine/threonine-protein kinase, active site [IPR008271] (2); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1) | scaffold_2_mRNA_576.1 | C_unshiu_00029_mRNA_59.1 | - |
| GF0020815 | 1 | 1 | 0 | Disease resistance response protein 206 (2) | | Plant disease resistance response protein [IPR004265] (2) | scaffold_2_mRNA_571.1 | C_unshiu_00754_mRNA_8.1 | - |
| GF0020814 | 1 | 1 | 0 | Cytochrome P450 monooxygenase CYP83A1 (2) | heme binding [GO:0020037 molecular_function] (2); iron ion binding [GO:0005506 molecular_function] (2); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2) | Cytochrome P450 [IPR001128] (2); Cytochrome P450, E-class, group I [IPR002401] (2) | scaffold_2_mRNA_545.1 | C_unshiu_00213_mRNA_7.1 | - |
| GF0020813 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_544.1 | C_unshiu_00213_mRNA_8.1 | - |
| GF0020812 | 1 | 1 | 0 | Serine/threonine-protein phosphatase PP2A-1 catalytic subunit (1); Serine/threonine-protein phosphatase PP2A catalytic subunit (1) | hydrolase activity [GO:0016787 molecular_function] (2) | Serine/threonine-specific protein phosphatase/bis(5-nucleosyl)-tetraphosphatase [IPR006186] (2); Metallo-dependent phosphatase-like [IPR029052] (2); Calcineurin-like phosphoesterase domain, ApaH type [IPR004843] (1); Calcineurin-like phosphoesterase domain, apaH type [IPR004843] (1) | scaffold_2_mRNA_531.1 | C_unshiu_00213_mRNA_22.2 | - |
| GF0020811 | 1 | 1 | 0 | Vignain (2) | cysteine-type peptidase activity [GO:0008234 molecular_function] (2); proteolysis [GO:0006508 biological_process] (2) | Cathepsin propeptide inhibitor domain (I29) [IPR013201] (2); Peptidase C1A, papain C-terminal [IPR000668] (2); Cysteine peptidase, asparagine active site [IPR025661] (2); Cysteine peptidase, histidine active site [IPR025660] (2); Peptidase C1A [IPR013128] (2) | scaffold_2_mRNA_529.1 | C_unshiu_00213_mRNA_24.1 | - |
| GF0020810 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_525.1 | C_unshiu_00062_mRNA_41.1 | - |
| GF0020809 | 1 | 1 | 0 | Hypothetical protein (2) | cysteine-type peptidase activity [GO:0008234 molecular_function] (2); phosphotransferase activity, alcohol group as acceptor [GO:0016773 molecular_function] (2); proteolysis [GO:0006508 biological_process] (2) | Ulp1 protease family, C-terminal catalytic domain [IPR003653] (2); Carbohydrate/puine kinase, PfkB, conserved site [IPR002173] (2); Carbohydrate kinase PfkB [IPR011611] (2); Ribokinase-like [IPR029056] (2) | scaffold_2_mRNA_520.1 | C_unshiu_00062_mRNA_35.1 | - |
| GF0020808 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_519.1 | C_unshiu_00062_mRNA_33.1 | - |
| GF0020807 | 1 | 1 | 0 | Hypothetical protein (2) | | Leucine-rich repeat domain, L domain-like [IPR032675] (2) | scaffold_2_mRNA_518.1 | C_unshiu_00062_mRNA_32.1 | - |
| GF0020806 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_516.1 | C_unshiu_00062_mRNA_30.1 | - |
| GF0020805 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_515.1 | C_unshiu_00062_mRNA_29.1 | - |
| GF0020804 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_513.1 | C_unshiu_00062_mRNA_27.1 | - |
| GF0020803 | 1 | 1 | 0 | Cytokinin riboside 5'-monophosphate phosphoribohydrolase (2) | | LOG family [IPR031100] (2); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (2) | scaffold_2_mRNA_51.1 | C_unshiu_00109_mRNA_49.1 | - |
| GF0020802 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_508.1 | C_unshiu_00062_mRNA_22.1 | - |
| GF0020801 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_507.1 | C_unshiu_00062_mRNA_21.1 | - |
| GF0020800 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_505.1 | C_unshiu_00062_mRNA_19.1 | - |
| GF0020799 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_498.1 | C_unshiu_02524_mRNA_1.1 | - |
| GF0020798 | 1 | 1 | 0 | Hypothetical protein (2) | DNA binding [GO:0003677 molecular_function] (2); regulation of transcription, DNA-templated [GO:0006355 biological_process] (2) | NAC domain [IPR003441] (2) | scaffold_2_mRNA_493.1 | C_unshiu_00992_mRNA_3.1 | - |
| GF0020797 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_489.1 | C_unshiu_00992_mRNA_7.1 | - |
| GF0020795 | 1 | 1 | 0 | DUF2431 domain protein (2) | | Domain of unknown function DUF2431 [IPR019446] (2) | scaffold_2_mRNA_4716.1 | C_unshiu_00077_mRNA_73.1 | - |
| GF0020794 | 1 | 1 | 0 | Hypothetical protein (2) | sulfotransferase activity [GO:0008146 molecular_function] (2) | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); Sulfotransferase domain [IPR000863] (2) | scaffold_2_mRNA_471.1 | C_unshiu_00061_mRNA_15.1 | - |
| GF0020793 | 1 | 1 | 0 | Pentatricopeptide (1); Hypothetical protein (1) | protein binding [GO:0005515 molecular_function] (2); zinc ion binding [GO:0008270 molecular_function] (1) | Pentatricopeptide repeat [IPR002885] (2); Tetratricopeptide-like helical domain [IPR011990] (2); DYW domain [IPR032867] (1) | scaffold_2_mRNA_4708.1 | C_unshiu_00077_mRNA_65.1 | - |
| GF0020792 | 1 | 1 | 0 | Pectinesterase inhibitor (2) | enzyme inhibitor activity [GO:0004857 molecular_function] (2) | Pectinesterase inhibitor domain [IPR006501] (2) | scaffold_2_mRNA_4705.1 | C_unshiu_00077_mRNA_63.1 | - |
| GF0020791 | 1 | 1 | 0 | SnRNA-activating protein complex subunit 3 isoform 3 (2) | | snRNA-activating protein complex, subunit 3 [IPR022042] (2) | scaffold_2_mRNA_4701.1 | C_unshiu_00077_mRNA_59.1 | - |
| GF0020790 | 1 | 1 | 0 | Metal ion binding protein (2) | metal ion transport [GO:0030001 biological_process] (2); metal ion binding [GO:0046872 molecular_function] (2) | Heavy metal-associated domain, HMA [IPR006121] (2) | scaffold_2_mRNA_4676.1 | C_unshiu_00077_mRNA_34.1 | - |
| GF0020789 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_4673.1 | C_unshiu_00077_mRNA_31.1 | - |
| GF0020788 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_467.1 | C_unshiu_00061_mRNA_11.1 | - |
| GF0020786 | 1 | 1 | 0 | CASP-like protein 2B1 (2) | | Domain of unknown function DUF588 [IPR006702] (2); Casparian strip membrane protein [IPR006459] (2) | scaffold_2_mRNA_4658.1 | C_unshiu_00077_mRNA_18.1 | - |
| GF0020785 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_465.1 | C_unshiu_00061_mRNA_9.1 | - |
| GF0020784 | 1 | 1 | 0 | Inositol monophosphatase (2) | phosphatidylinositol phosphorylation [GO:0046854 biological_process] (2); inositol phosphate dephosphorylation [GO:0046855 biological_process] (1); inositol monophosphate 1-phosphatase activity [GO:0008934 molecular_function] (1) | Inositol monophosphatase, metal-binding site [IPR020583] (2); Inositol monophosphatase, conserved site [IPR020550] (2); Inositol monophosphatase, Lithium-sensitive [IPR020552] (1); Inositol monophosphatase-like [IPR000760] (1); Inositol monophosphatase [IPR033942] (1); Inositol monophosphatase [IPR000760] (1) | scaffold_2_mRNA_4646.1 | C_unshiu_00077_mRNA_6.2 | - |
| GF0020783 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_4638.1 | C_unshiu_00337_mRNA_45.1 | - |
| GF0020782 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_4631.1 | C_unshiu_00337_mRNA_40.1 | - |
| GF0020781 | 1 | 1 | 0 | Hypothetical protein (2) | protein binding [GO:0005515 molecular_function] (2) | F-box domain [IPR001810] (2) | scaffold_2_mRNA_463.1 | C_unshiu_00061_mRNA_7.1 | - |
| GF0020780 | 1 | 1 | 0 | Serine/threonine-protein kinase HT1 (2) | ATP binding [GO:0005524 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2); protein kinase activity [GO:0004672 molecular_function] (2); protein serine/threonine kinase activity [GO:0004674 molecular_function] (1) | Protein kinase domain [IPR000719] (2); Protein kinase-like domain [IPR011009] (2); Serine/threonine-protein kinase, active site [IPR008271] (2); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Serine/threonine-protein kinase HT1, plant [IPR015783] (1) | scaffold_2_mRNA_4617.1 | C_unshiu_00337_mRNA_26.1 | - |
| GF0020778 | 1 | 1 | 0 | BAH and coiled-coil domain-containing 1 (2) | chromatin binding [GO:0003682 molecular_function] (2); protein binding [GO:0005515 molecular_function] (2); zinc ion binding [GO:0008270 molecular_function] (2) | Bromo adjacent homology (BAH) domain [IPR001025] (2); Zinc finger, FYVE/PHD-type [IPR011011] (2); Zinc finger, RING/FYVE/PHD-type [IPR013083] (2); Zinc finger, PHD-type, conserved site [IPR019786] (2); Zinc finger, PHD-type [IPR001965] (2); Zinc finger, PHD-finger [IPR019787] (2) | scaffold_2_mRNA_4593.1 | C_unshiu_00337_mRNA_3.1 | - |
| GF0020775 | 1 | 1 | 0 | Hypothetical protein (2) | | Transposase, MuDR, plant [IPR004332] (2) | scaffold_2_mRNA_459.1 | C_unshiu_00061_mRNA_3.1 | - |
| GF0020773 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_4579.1 | C_unshiu_00048_mRNA_1.1 | - |
| GF0020772 | 1 | 1 | 0 | Pectate lyase (2) | | Pectin lyase fold/virulence factor [IPR011050] (2); Pectin lyase fold [IPR012334] (2); Pectate lyase/Amb allergen [IPR002022] (2); AmbAllergen [IPR018082] (2) | scaffold_2_mRNA_4578.1 | C_unshiu_00048_mRNA_2.1 | - |
| GF0020771 | 1 | 1 | 0 | Peroxisomal membrane protein PMP22 (2) | integral component of membrane [GO:0016021 cellular_component] (2) | Mpv17/PMP22 [IPR007248] (2) | scaffold_2_mRNA_4570.1 | C_unshiu_00048_mRNA_10.1 | - |
| GF0020770 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_4566.1 | C_unshiu_00048_mRNA_14.1 | - |
| GF0020769 | 1 | 1 | 0 | Autophagy-related protein 8C (2) | | Ubiquitin-related domain [IPR029071] (2); Autophagy protein Atg8 ubiquitin-like [IPR004241] (2) | scaffold_2_mRNA_4552.2 | C_unshiu_00048_mRNA_29.2 | - |
| GF0020768 | 1 | 1 | 0 | Senescence regulator (2) | | Senescence regulator S40 [IPR007608] (2) | scaffold_2_mRNA_4550.1 | C_unshiu_00048_mRNA_31.1 | - |
| GF0020767 | 1 | 1 | 0 | ATP synthase F1, gamma subunit (2) | ATP synthesis coupled proton transport [GO:0015986 biological_process] (2); proton-transporting ATP synthase activity, rotational mechanism [GO:0046933 molecular_function] (2); proton-transporting ATP synthase complex, catalytic core F(1) [GO:0045261 cellular_component] (2); proton-transporting ATPase activity, rotational mechanism [GO:0046961 molecular_function] (1) | ATP synthase, F1 complex, gamma subunit conserved site [IPR023632] (1); ATPase, F1 complex, gamma subunit domain [IPR023633] (1); ATPase, F1 complex, gamma subunit conserved site [IPR023632] (1); ATP synthase, F1 complex, gamma subunit [IPR000131] (1); ATPase, F1 complex, gamma subunit [IPR000131] (1) | scaffold_2_mRNA_4548.1 | C_unshiu_00048_mRNA_33.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0020765 | 1 | 1 | 0 | Protein DETOXIFICATION 36 (1); Protein TRANSPARENT TESTA 12 (1) | transmembrane transport [GO:0055085 biological_process] (2); drug transmembrane transporter activity [GO:0015238 molecular_function] (2); antiporter activity [GO:0015297 molecular_function] (2); membrane [GO:0016020 cellular_component] (2); drug transmembrane transport [GO:0006855 biological_process] (2); oxidoreductase activity [GO:0016491 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); FMN binding [GO:0010181 molecular_function] (1); catalytic activity [GO:0003824 molecular_function] (1) | Multi antimicrobial extrusion protein [IPR002528] (2); Alpha-hydroxy acid dehydrogenase, FMN-dependent [IPR012133] (1); FMN-dependent alpha-hydroxy acid dehydrogenase, active site [IPR008259] (1); Aldolase-type TIM barrel [IPR013785] (1); FMN-dependent dehydrogenase [IPR000262] (1) | scaffold_2_mRNA_4538.1 | C_unshiu_00048_mRNA_42.1 | - |
| GF0020764 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2); metal ion binding [GO:0046872 molecular_function] (1) | Zinc finger, double-stranded RNA binding [IPR022755] (2); Zinc finger C2H2-type/integrase DNA-binding domain [IPR013087] (1); Zinc finger, C2H2-like [IPR015880] (1); Zinc finger, C2H2 [IPR007087] (1); Zinc finger C2H2-type [IPR013087] (1) | scaffold_2_mRNA_4533.1 | C_unshiu_00048_mRNA_49.1 | - |
| GF0020761 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_2_mRNA_452.1 | C_unshiu_01757_mRNA_6.1 | - |
| GF0020760 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_2_mRNA_4512.1 | C_unshiu_00107_mRNA_27.1 | - |
| GF0020759 | 1 | 1 | 0 | Dopamine beta-monooxygenase, putative (1); Eukaryotic cytochrome b561 protein (1) | integral component of membrane [GO:0016021 cellular_component] (1) | Cytochrome b561/ferric reductase transmembrane [IPR006593] (2); Cytochrome b561 domain [IPR004877] (1) | scaffold_2_mRNA_4505.1 | C_unshiu_00048_mRNA_70.1 | - |
| GF0020758 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_2_mRNA_4504.1 | C_unshiu_00048_mRNA_71.1 | - |
| GF0020757 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_2_mRNA_4500.1 | C_unshiu_00048_mRNA_75.1 | - |
| GF0020756 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_2_mRNA_450.1 | C_unshiu_01757_mRNA_8.1 | - |
| GF0020755 | 1 | 1 | 0 | NAD(P)-binding Rossmann-fold superfamily protein isoform 2 (1); 3-beta hydroxysteroid dehydrogenase/isomerase (1) |  | NAD(P)-binding domain [IPR016040] (2) | scaffold_2_mRNA_4499.1 | C_unshiu_00048_mRNA_76.1 | - |
| GF0020754 | 1 | 1 | 0 | Hypothetical protein (2) | protein dimerization activity [GO:0046983 molecular_function] (2); DNA binding [GO:0003677 molecular_function] (2) | Transcription factor, MADS-box [IPR002100] (2) | scaffold_2_mRNA_4492.1 | C_unshiu_00048_mRNA_81.1 | - |
| GF0020752 | 1 | 1 | 0 | Glycosyl hydrolase family protein (2) | hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (2); carbohydrate metabolic process [GO:0005975 biological_process] (2) | Glycoside hydrolase family 3 C-terminal domain [IPR002772] (2); Glycoside hydrolase, family 3, N-terminal [IPR001764] (2); Fibronectin type III-like domain [IPR026891] (2); Glycoside hydrolase superfamily [IPR017853] (2); Immunoglobulin-like fold [IPR013783] (1); Glycoside hydrolase family 3 [IPR026892] (1) | scaffold_2_mRNA_4486.1 | C_unshiu_00048_mRNA_86.1 | - |
| GF0020751 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_2_mRNA_4484.1 | C_unshiu_00048_mRNA_88.1 | - |
| GF0020750 | 1 | 1 | 0 | Hypothetical protein (2) |  | Glycosyl transferase, family 1 [IPR001296] (2) | scaffold_2_mRNA_4482.1 | C_unshiu_00048_mRNA_91.1 | - |
| GF0020749 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_2_mRNA_448.1 | C_unshiu_00244_mRNA_17.1 | - |
| GF0020748 | 1 | 1 | 0 | RNA recognition motif 2 in plant MEI2-like protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2); nucleotide binding [GO:0000166 molecular_function] (1) | RNA recognition motif domain [IPR000504] (2); MEI2-like, RNA recognition motif 1 [IPR034453] (1); RNA recognition motif 2 [IPR007201] (1); MEI2-like, RNA recognition motif 3 [IPR034454] (1); Nucleotide-binding alpha-beta plait domain [IPR012677] (1); Mei2/Mei2-like, C-terminal RNA recognition motif [IPR007201] (1) | scaffold_2_mRNA_4462.1 | C_unshiu_00074_mRNA_33.1 | - |
| GF0020747 | 1 | 1 | 0 | Hypothetical protein (2) |  | Aspartic peptidase domain [IPR021109] (1) | scaffold_2_mRNA_446.1 | C_unshiu_00244_mRNA_21.1 | - |
| GF0020746 | 1 | 1 | 0 | Bidirectional sugar transporter SWEET2 (2) | integral component of membrane [GO:0016021 cellular_component] (2) | SWEET sugar transporter [IPR004316] (2) | scaffold_2_mRNA_4450.1 | C_unshiu_00002_mRNA_8.1 | - |
| GF0020745 | 1 | 1 | 0 | Protein transporter Sec61 subunit alpha isoform 2 (2) | protein transport [GO:0015031 biological_process] (2); protein retention in ER lumen [GO:0006621 biological_process] (2); integral component of membrane [GO:0016021 cellular_component] (2); ER retention sequence binding [GO:0046923 molecular_function] (2); membrane [GO:0016020 cellular_component] (2) | SecY conserved site [IPR030659] (2); SecY/SEC61-alpha family [IPR002208] (2); Translocon Sec61/SecY, plug domain [IPR019561] (2); ER lumen protein retaining receptor [IPR000133] (2); SecY subunit domain [IPR023201] (2) | scaffold_2_mRNA_4421.1 | C_unshiu_00002_mRNA_37.1 | - |
| GF0020744 | 1 | 1 | 0 | Cellulose synthase (2) | membrane [GO:0016020 cellular_component] (2); cellulose synthase (UDP-forming) activity [GO:0016760 molecular_function] (2); cellulose biosynthetic process [GO:0030244 biological_process] (2) | Nucleotide-diphospho-sugar transferases [IPR029044] (2); Zinc finger, RING/FYVE/PHD-type [IPR013083] (2); Cellulose synthase, RING-type zinc finger [IPR027934] (2); Cellulose synthase [IPR005150] (2) | scaffold_2_mRNA_4408.1 | C_unshiu_00002_mRNA_50.1 | - |
| GF0020741 | 1 | 1 | 0 | Tig (2) |  | Conserved hypothetical protein CHP02058 [IPR011719] (2); Tubulin/FtsZ, 2-layer sandwich domain [IPR018316] (2) | scaffold_2_mRNA_4368.2 | C_unshiu_00002_mRNA_88.1 | - |
| GF0020738 | 1 | 1 | 0 | Hypothetical protein (2) | protein binding [GO:0005515 molecular_function] (1) | Pentatricopeptide repeat [IPR002885] (2); Tetratricopeptide-like helical domain [IPR011990] (1) | scaffold_2_mRNA_4361.1 | C_unshiu_00002_mRNA_93.1 | - |
| GF0020737 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_2_mRNA_435.1 | C_unshiu_00244_mRNA_34.1 | - |
| GF0020736 | 1 | 1 | 0 | ATP synthase mitochondrial F1 complex assembly factor 1 (2) | mitochondrion [GO:0005739 cellular_component] (2); protein complex assembly [GO:0006461 biological_process] (2) | ATP11 [IPR010591] (2) | scaffold_2_mRNA_4347.1 | C_unshiu_00002_mRNA_107.1 | - |
| GF0020735 | 1 | 1 | 0 | Ethylene-responsive transcription factor ERF091 (2) | regulation of transcription, DNA-templated [GO:0006355 biological_process] (2); transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (2); DNA binding [GO:0003677 molecular_function] (2) | DNA-binding domain [IPR016177] (2); AP2/ERF domain [IPR001471] (2) | scaffold_2_mRNA_4340.1 | C_unshiu_00002_mRNA_114.1 | - |
| GF0020734 | 1 | 1 | 0 | Eugenol O-methyltransferase (1); O-methyltransferase ZRP4 (1) | O-methyltransferase activity [GO:0008171 molecular_function] (2); protein dimerization activity [GO:0046983 molecular_function] (2); methyltransferase activity [GO:0008168 molecular_function] (2) | Winged helix-turn-helix DNA-binding domain [IPR011991] (2); O-methyltransferase, family 2 [IPR001077] (2); O-methyltransferase COMT-type [IPR016461] (2); Protein of unknown function DUF599 [IPR006747] (2); Plant methyltransferase dimerisation [IPR012967] (2); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (2) | scaffold_2_mRNA_4325.1 | C_unshiu_00002_mRNA_127.1 | - |
| GF0020733 | 1 | 1 | 0 | MLO protein homolog 1 (2) | integral component of membrane [GO:0016021 cellular_component] (2); defense response [GO:0006952 biological_process] (2) | Mlo-related protein [IPR004326] (2) | scaffold_2_mRNA_4323.1 | C_unshiu_00002_mRNA_129.1 | - |
| GF0020729 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_2_mRNA_4283.1 | C_unshiu_00310_mRNA_30.1 | - |
| GF0020728 | 1 | 1 | 0 | 50S ribosomal protein L21, mitochondrial (2) | structural constituent of ribosome [GO:0003735 molecular_function] (2); intracellular [GO:0005622 cellular_component] (2); translation [GO:0006412 biological_process] (2); ribosome [GO:0005840 cellular_component] (2); RNA binding [GO:0003723 molecular_function] (2) | Ribosomal protein L21 [IPR001787] (2); Ribosomal protein L21, conserved site [IPR018258] (2); Ribosomal protein L21-like [IPR028909] (2) | scaffold_2_mRNA_4276.1 | C_unshiu_00002_mRNA_174.1 | - |
| GF0020727 | 1 | 1 | 0 | Stem-specific protein TSJT1 (2) |  | Domain of unknown function DUF3700 [IPR024286] (2); Nucleophile aminohydrolases, N-terminal [IPR029055] (2) | scaffold_2_mRNA_4259.1 | C_unshiu_00002_mRNA_192.1 | - |
| GF0020725 | 1 | 1 | 0 | Serine/threonine-protein kinase receptor (2) | protein phosphorylation [GO:0006468 biological_process] (2); protein kinase activity [GO:0004672 molecular_function] (2); ATP binding [GO:0005524 molecular_function] (2) | Protein kinase domain [IPR000719] (2); Protein kinase-like domain [IPR011009] (2); Serine/threonine-protein kinase, active site [IPR008271] (2); Protein kinase, ATP binding site [IPR017441] (2); Concanavalin A-like lectin/glucanase domain [IPR013320] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1) | scaffold_2_mRNA_4245.1 | C_unshiu_00002_mRNA_206.1 | - |
| GF0020722 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_2_mRNA_4218.1 | C_unshiu_00153_mRNA_13.1 | - |
| GF0020721 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_2_mRNA_421.1 | C_unshiu_00526_mRNA_4.1 | - |
| GF0020719 | 1 | 1 | 0 | Nuclease S1 (2) | hydrolase activity, acting on ester bonds [GO:0016788 molecular_function] (2); endonuclease activity [GO:0004519 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2); DNA catabolic process [GO:0006308 biological_process] (2) | Phospholipase C/P1 nuclease domain [IPR008947] (2); S1/P1 nuclease [IPR003154] (2) | scaffold_2_mRNA_4203.1 | C_unshiu_00153_mRNA_24.1 | - |
| GF0020718 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_2_mRNA_420.1 | C_unshiu_00526_mRNA_2.1 | - |
| GF0020717 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_2_mRNA_419.1 | C_unshiu_00526_mRNA_1.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0020716 | 1 | 1 | 0 | F-box protein SKIP27 (2) | protein binding [GO:0005515 molecular_function] (2) | F-box domain [IPR001810] (2) | scaffold_2_mRNA_4185.1 | C_unshiu_00153_mRNA_41.1 | - |
| GF0020715 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_4178.1 | C_unshiu_00153_mRNA_45.1 | - |
| GF0020714 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_416.1 | C_unshiu_00692_mRNA_3.1 | - |
| GF0020713 | 1 | 1 | 0 | B-box type zinc finger protein (2) | intracellular [GO:0005622 cellular_component] (2); zinc ion binding [GO:0008270 molecular_function] (2) | B-box-type zinc finger [IPR000315] (2) | scaffold_2_mRNA_4157.1 | C_unshiu_00070_mRNA_51.2 | - |
| GF0020712 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_412.1 | C_unshiu_01377_mRNA_3.1 | - |
| GF0020711 | 1 | 1 | 0 | Ubiquitin family protein (1); Polyubiquitin (1) | protein binding [GO:0005515 molecular_function] (2) | Ubiquitin-related domain [IPR029071] (2); Ubiquitin [IPR019956] (2); Ubiquitin conserved site [IPR019954] (2); Ubiquitin domain [IPR000626] (2) | scaffold_2_mRNA_4112.1 | C_unshiu_00027_mRNA_4.1 | - |
| GF0020710 | 1 | 1 | 0 | Thiazole biosynthetic enzyme (2) | thiamine biosynthetic process [GO:0009228 biological_process] (2); oxidation-reduction process [GO:0055114 biological_process] (2); oxidoreductase activity [GO:0016491 molecular_function] (2); response to stress [GO:0006950 biological_process] (2) | Thiamine thiazole synthase [IPR027495] (2); Thiazole biosynthetic enzyme Thi4 family [IPR002922] (2); FAD/NAD(P)-binding domain [IPR023753] (2) | scaffold_2_mRNA_4109.1 | C_unshiu_00027_mRNA_7.1 | - |
| GF0020709 | 1 | 1 | 0 | Probable dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 3B (1); Probable dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 3A (1) | | Oligosaccharyl transferase complex, subunit OST3/OST6 [IPR021149] (2) | scaffold_2_mRNA_4107.1 | C_unshiu_00027_mRNA_9.1 | - |
| GF0020708 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (1) | Ribonuclease H-like domain [IPR012337] (1) | scaffold_2_mRNA_410.1 | C_unshiu_01377_mRNA_2.1 | - |
| GF0020706 | 1 | 1 | 0 | Tobamovirus multiplication 1 (2) | | Domain of unknown function DUF1084 [IPR009457] (2) | scaffold_2_mRNA_4088.1 | C_unshiu_00027_mRNA_30.1 | - |
| GF0020702 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_406.1 | C_unshiu_01190_mRNA_2.1 | - |
| GF0020701 | 1 | 1 | 0 | CBL-interacting serine/threonine-protein kinase 9 (2) | signal transduction [GO:0007165 biological_process] (2); ATP binding [GO:0005524 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2); protein kinase activity [GO:0004672 molecular_function] (2) | Protein kinase domain [IPR000719] (2); NAF domain [IPR004041] (2); NAF/FISL domain [IPR018451] (2); Protein kinase-like domain [IPR011009] (2); Protein kinase, ATP binding site [IPR017441] (2); Serine/threonine-protein kinase, active site [IPR008271] (2); KA1 domain/Ssp2, C-terminal [IPR028375] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1) | scaffold_2_mRNA_4053.3 | C_unshiu_00027_mRNA_66.3 | - |
| GF0020699 | 1 | 1 | 0 | Hypothetical protein (2) | | Leucine-rich repeat domain, L domain-like [IPR032675] (1) | scaffold_2_mRNA_4018.1 | C_unshiu_00091_mRNA_52.1 | - |
| GF0020696 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_400.1 | C_unshiu_00246_mRNA_2.1 | - |
| GF0020695 | 1 | 1 | 0 | Putative oxidoreductase GLYR1 (2) | 3-hydroxyisobutyrate dehydrogenase activity [GO:0008442 molecular_function] (2); NAD binding [GO:0051287 molecular_function] (2); oxidoreductase activity [GO:0016491 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2); phosphogluconate dehydrogenase (decarboxylating) activity [GO:0004616 molecular_function] (2) | 3-hydroxyisobutyrate dehydrogenase-related, conserved site [IPR002204] (2); 3-hydroxyisobutyrate dehydrogenase [IPR011548] (2); NAD(P)-binding domain [IPR016040] (2); 6-phosphogluconate dehydrogenase, NADP-binding [IPR006115] (2); 3-hydroxyisobutyrate dehydrogenase, NAD-binding domain [IPR029154] (2); 6-phosphogluconate dehydrogenase C-terminal domain-like [IPR008927] (2); 6-phosphogluconate dehydrogenase, domain 2 [IPR013328] (2) | scaffold_2_mRNA_3993.1 | C_unshiu_00091_mRNA_25.1 | - |
| GF0020694 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_3985.1 | C_unshiu_00091_mRNA_17.1 | - |
| GF0020693 | 1 | 1 | 0 | FAD-binding Berberine family protein (2) | oxidation-reduction process [GO:0055114 biological_process] (2); oxidoreductase activity [GO:0016491 molecular_function] (2); flavin adenine dinucleotide binding [GO:0050660 molecular_function] (2); catalytic activity [GO:0003824 molecular_function] (2); oxidoreductase activity, acting on CH-OH group of donors [GO:0016614 molecular_function] (2) | FAD-binding, type 2, subdomain 1 [IPR016167] (2); CO dehydrogenase flavoprotein-like, FAD-binding, subdomain 2 [IPR016169] (2); FAD linked oxidase, N-terminal [IPR006094] (2); FAD-binding, type 2 [IPR016166] (2); Berberine/berberine-like [IPR012951] (2) | scaffold_2_mRNA_3968.1 | C_unshiu_00143_mRNA_8.1 | - |
| GF0020692 | 1 | 1 | 0 | Toprim domain-containing protein isoform 1 (1); Toprim domain-containing protein (1) | ATP binding [GO:0005524 molecular_function] (2); DNA helicase activity [GO:0003678 molecular_function] (2); DNA replication [GO:0006260 biological_process] (2); 5'-3' DNA helicase activity [GO:0043139 molecular_function] (1); single-stranded DNA binding [GO:0003697 molecular_function] (1) | DNA helicase, DnaB-like, C-terminal [IPR007694] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); Toprim domain [IPR006171] (1); Archaeal primase DnaG/twinkle, TOPRIM domain [IPR034154] (1); TOPRIM domain [IPR006171] (1); Twinkle-like protein [IPR027032] (1) | scaffold_2_mRNA_3961.1 | C_unshiu_00143_mRNA_12.1 | - |
| GF0020691 | 1 | 1 | 0 | Receptor-like serine/threonine-protein kinase ALE2 (2) | ATP binding [GO:0005524 molecular_function] (2); protein kinase activity [GO:0004672 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2); protein binding [GO:0005515 molecular_function] (2) | Leucine-rich repeat [IPR001611] (2); Protein kinase-like domain [IPR011009] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Protein kinase domain [IPR000719] (2); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1) | scaffold_2_mRNA_3959.1 | C_unshiu_00143_mRNA_14.1 | - |
| GF0020688 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_395.1 | C_unshiu_00246_mRNA_6.1 | - |
| GF0020687 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_3942.1 | C_unshiu_00143_mRNA_27.1 | - |
| GF0020686 | 1 | 1 | 0 | Charged multivesicular body protein 2a (1); Charged multivesicular body protein 2b-B, putative (1) | vacuolar transport [GO:0007034 biological_process] (2) | Snf7 family [IPR005024] (2); Zinc finger, LSD1-type [IPR005735] (1) | scaffold_2_mRNA_3941.1 | C_unshiu_00143_mRNA_28.1 | - |
| GF0020685 | 1 | 1 | 0 | Hypothetical protein (1); Putative retroelement pol polyprotein (1) | | | scaffold_2_mRNA_3919.1 | C_unshiu_00143_mRNA_49.1 | - |
| GF0020684 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_3911.1 | C_unshiu_00125_mRNA_60.1 | - |
| GF0020683 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_3903.1 | C_unshiu_00125_mRNA_50.1 | - |
| GF0020682 | 1 | 1 | 0 | Hypothetical protein (1); Monosacharide transport protein (1) | | | scaffold_2_mRNA_3882.1 | C_unshiu_00125_mRNA_29.1 | - |
| GF0020681 | 1 | 1 | 0 | TMV resistance protein N (1); Putative TIR-NBS type R protein 4 (1) | protein binding [GO:0005515 molecular_function] (2); ADP binding [GO:0043531 molecular_function] (2); signal transduction [GO:0007165 biological_process] (2) | Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (2); Winged helix-turn-helix DNA-binding domain [IPR011991] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); NB-ARC [IPR002182] (2) | scaffold_2_mRNA_3868.1 | C_unshiu_02276_mRNA_3.1 | - |
| GF0020680 | 1 | 1 | 0 | Hypothetical protein (2) | carbohydrate binding [GO:0030246 molecular_function] (1); catalytic activity [GO:0003824 molecular_function] (1); carbohydrate metabolic process [GO:0005975 biological_process] (1) | Galactose mutarotase-like domain [IPR011013] (1); Galactose mutarotase, N-terminal barrel [IPR031727] (1) | scaffold_2_mRNA_3867.1 | C_unshiu_02276_mRNA_4.1 | - |
| GF0020679 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_2_mRNA_3865.1 | C_unshiu_02276_mRNA_5.1 | - |
| GF0020678 | 1 | 1 | 0 | Hypothetical protein (2) | protein dimerization activity [GO:0046983 molecular_function] (2); DNA binding [GO:0003677 molecular_function] (2) | Transcription factor, MADS-box [IPR002100] (2) | scaffold_2_mRNA_3859.1 | C_unshiu_00185_mRNA_13.1 | - |
| GF0020677 | 1 | 1 | 0 | Hypothetical protein (2) | | Leucine-rich repeat domain, L domain-like [IPR032675] (1) | scaffold_2_mRNA_3857.1 | C_unshiu_00185_mRNA_14.1 | - |
| GF0020676 | 1 | 1 | 0 | Hypothetical protein (2) | | Domain of unknown function DUF239 [IPR004314] (1); Neprosin [IPR004314] (1) | scaffold_2_mRNA_3853.1 | C_unshiu_00185_mRNA_18.1 | - |
| GF0020675 | 1 | 1 | 0 | Hypothetical protein (2) | | Ribosomal protein S25 [IPR004977] (2) | scaffold_2_mRNA_385.1 | C_unshiu_00246_mRNA_16.1 | - |
| GF0020674 | 1 | 1 | 0 | 14 kDa zinc-binding protein (2) | catalytic activity [GO:0003824 molecular_function] (2) | HIT-like domain [IPR011146] (2); Histidine triad (HIT) protein [IPR001310] (2); Histidine triad, conserved site [IPR019808] (2) | scaffold_2_mRNA_3843.1 | C_unshiu_00185_mRNA_29.1 | - |
| GF0020673 | 1 | 1 | 0 | Verticillium wilt resistance-like protein (2) | protein binding [GO:0005515 molecular_function] (2) | Leucine-rich repeat domain, L domain-like [IPR032675] (2); Leucine-rich repeat, typical subtype [IPR003591] (2); Leucine-rich repeat [IPR001611] (2) | scaffold_2_mRNA_3841.1 | C_unshiu_00185_mRNA_31.1 | - |
| GF0020672 | 1 | 1 | 0 | Receptor like protein 33 (2) | protein binding [GO:0005515 molecular_function] (2) | Leucine-rich repeat, typical subtype [IPR003591] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Leucine-rich repeat [IPR001611] (2) | scaffold_2_mRNA_3836.1 | C_unshiu_00185_mRNA_35.1 | - |
| GF0020671 | 1 | 1 | 0 | Hypothetical protein (2) | RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2); Ribonuclease H domain [IPR002156] (2) | scaffold_2_mRNA_3834.1 | C_unshiu_02643_mRNA_3.1 | - |
| GF0020670 | 1 | 1 | 0 | Monosacharide transport protein (2) | | | scaffold_2_mRNA_3832.1 | C_unshiu_00185_mRNA_39.1 | - |
| GF0020668 | 1 | 1 | 0 | Phospholipase, patatin family (2) | metabolic process [GO:0008152 biological_process] (2); lipid metabolic process [GO:0006629 biological_process] (2) | Acyl transferase/acyl hydrolase/lysophospholipase [IPR016035] (2); Patatin-like phospholipase domain [IPR002641] (1); Patatin/Phospholipase A2-related [IPR002641] (1) | scaffold_2_mRNA_3826.1 | C_unshiu_00185_mRNA_45.1 | - |
| GF0020667 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_3824.1 | C_unshiu_00185_mRNA_46.1 | - |
| GF0020666 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_3823.1 | C_unshiu_00185_mRNA_47.1 | - |
| GF0020665 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_3822.1 | C_unshiu_00185_mRNA_48.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0020664 | 1 | 1 | 0 | Hypothetical protein (2) | protein binding [GO:0005515 molecular_function] (2) | Ankyrin repeat [IPR002110] (2); PGG domain [IPR026961] (2); Ankyrin repeat-containing domain [IPR020683] (2) | scaffold_2_mRNA_3821.1 | C_unshiu_00185_mRNA_49.1 | - |
| GF0020663 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_3819.1 | C_unshiu_00185_mRNA_51.1 | - |
| GF0020662 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_3813.1 | C_unshiu_00073_mRNA_65.1 | - |
| GF0020660 | 1 | 1 | 0 | Urease accessory protein D (2) | nickel cation binding [GO:0016151 molecular_function] (2); nitrogen compound metabolic process [GO:0006807 biological_process] (2) | Urease accessory protein UreD [IPR002669] (2) | scaffold_2_mRNA_3805.1 | C_unshiu_00073_mRNA_57.1 | - |
| GF0020659 | 1 | 1 | 0 | Putative 54S ribosomal protein L12, mitochondrial-like (2) | structural constituent of ribosome [GO:0003735 molecular_function] (2); intracellular [GO:0005622 cellular_component] (2); translation [GO:0006412 biological_process] (2); ribosome [GO:0005840 cellular_component] (2) | Ribosomal protein L7/L12 [IPR000206] (2); Ribosomal protein L7/L12, C-terminal/adaptor protein ClpS-like [IPR014719] (2); Ribosomal protein L7/L12, C-terminal [IPR013823] (2) | scaffold_2_mRNA_3804.1 | C_unshiu_00073_mRNA_56.1 | - |
| GF0020658 | 1 | 1 | 0 | Poly(A) polymerase 1 isoform 1 (2) | nucleotidyltransferase activity [GO:0016779 molecular_function] (2); RNA 3'-end processing [GO:0031123 biological_process] (2); nucleus [GO:0005634 cellular_component] (2); RNA binding [GO:0003723 molecular_function] (2); polynucleotide adenylyltransferase activity [GO:0004652 molecular_function] (2); RNA polyadenylation [GO:0043631 biological_process] (2) | Poly(A) polymerase, RNA-binding domain [IPR007010] (2); Polymerase, nucleotidyl transferase domain [IPR002934] (2); Poly(A) polymerase, central domain [IPR007012] (2); Poly(A) polymerase [IPR014492] (2); Nucleotidyltransferase, class I, C-terminal-like [IPR011068] (2) | scaffold_2_mRNA_3801.1 | C_unshiu_00073_mRNA_53.1 | - |
| GF0020657 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (1) | Ribonuclease H-like domain [IPR012337] (1) | scaffold_2_mRNA_3762.1 | C_unshiu_00073_mRNA_13.1 | - |
| GF0020656 | 1 | 1 | 0 | LOB domain-containing protein 6 (2) | | Lateral organ boundaries, LOB [IPR004883] (2) | scaffold_2_mRNA_3731.1 | C_unshiu_00035_mRNA_11.1 | - |
| GF0020655 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_373.1 | C_unshiu_00246_mRNA_28.1 | - |
| GF0020654 | 1 | 1 | 0 | Hypothetical protein (2) | catalytic activity [GO:0003824 molecular_function] (2); carbohydrate metabolic process [GO:0005975 biological_process] (2); hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (2) | Glycoside hydrolase superfamily [IPR017853] (2); Aldolase-type TIM barrel [IPR013785] (2); Glycoside hydrolase, family 27 [IPR002241] (2); Glycoside hydrolase family 27/36, conserved site [IPR000111] (1) | scaffold_2_mRNA_3721.1 | C_unshiu_00022_mRNA_80.1 | - |
| GF0020653 | 1 | 1 | 0 | WD repeat-containing protein 26 (2) | protein binding [GO:0005515 molecular_function] (2) | WD40-repeat-containing domain [IPR017986] (2); WD40 repeat [IPR001680] (2); WD40 repeat, conserved site [IPR019775] (2); WD40/YVTN repeat-like-containing domain [IPR015943] (2); G-protein beta WD-40 repeat [IPR020472] (2); CTLH, C-terminal LisH motif [IPR006595] (2); LIS1 homology motif [IPR006594] (2); Six-bladed beta-propeller, TolB-like [IPR011042] (1) | scaffold_2_mRNA_3720.2 | C_unshiu_00022_mRNA_79.1 | - |
| GF0020652 | 1 | 1 | 0 | Retrotransposon protein, putative, Ty1-copia subclass (2) | zinc ion binding [GO:0008270 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | Zinc finger, CCHC-type [IPR001878] (2); Ribonuclease H-like domain [IPR012337] (1) | scaffold_2_mRNA_372.1 | C_unshiu_00246_mRNA_29.1 | - |
| GF0020651 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_3702.1 | C_unshiu_00022_mRNA_61.1 | - |
| GF0020650 | 1 | 1 | 0 | Hypothetical protein (2) | | Rossmann-like alpha/beta/alpha sandwich fold [IPR014729] (2) | scaffold_2_mRNA_3690.1 | C_unshiu_00022_mRNA_49.1 | - |
| GF0020649 | 1 | 1 | 0 | Hypothetical protein (2) | | Gag-polypeptide of LTR copia-type [IPR029472] (1) | scaffold_2_mRNA_369.1 | C_unshiu_00834_mRNA_6.1 | - |
| GF0020648 | 1 | 1 | 0 | Kinase superfamily protein (2) | polysaccharide binding [GO:0030247 molecular_function] (2) | Wall-associated receptor kinase, galacturonan-binding domain [IPR025287] (2); Wall-associated receptor kinase, C-terminal [IPR032872] (2) | scaffold_2_mRNA_3668.1 | C_unshiu_00022_mRNA_27.1 | - |
| GF0020647 | 1 | 1 | 0 | Probable protein phosphatase 2C 15 (2) | catalytic activity [GO:0003824 molecular_function] (2); protein dephosphorylation [GO:0006470 biological_process] (2); protein serine/threonine phosphatase activity [GO:0004722 molecular_function] (2) | Protein phosphatase 2C family [IPR015655] (2); PPM-type phosphatase domain [IPR001932] (2) | scaffold_2_mRNA_3664.1 | C_unshiu_00022_mRNA_21.1 | - |
| GF0020645 | 1 | 1 | 0 | Auxin-responsive protein IAA12 (2) | regulation of transcription, DNA-templated [GO:0006355 biological_process] (2); protein binding [GO:0005515 molecular_function] (2); nucleus [GO:0005634 cellular_component] (2) | AUX/IAA protein [IPR003311] (2); PB1 domain [IPR000270] (2); AUX/IAA domain [IPR033389] (1) | scaffold_2_mRNA_3648.1 | C_unshiu_00022_mRNA_4.1 | - |
| GF0020639 | 1 | 1 | 0 | RING/U-box superfamily protein, putative isoform 4 (1); Hypothetical protein (1) | polysaccharide binding [GO:0030247 molecular_function] (1) | Wall-associated receptor kinase, galacturonan-binding domain [IPR025287] (1) | scaffold_2_mRNA_3631.1 | C_unshiu_00965_mRNA_8.1 | - |
| GF0020638 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_362.1 | C_unshiu_00672_mRNA_7.1 | - |
| GF0020636 | 1 | 1 | 0 | Hypothetical protein (2) | | Zinc knuckle CX2CX4HX4C [IPR025836] (2) | scaffold_2_mRNA_361.1 | C_unshiu_00672_mRNA_6.1 | - |
| GF0020634 | 1 | 1 | 0 | E3 ubiquitin-protein ligase RHA2A (2) | zinc ion binding [GO:0008270 molecular_function] (2); protein binding [GO:0005515 molecular_function] (2) | Zinc finger, RING/FYVE/PHD-type [IPR013083] (2); Zinc finger, RING-type [IPR001841] (2) | scaffold_2_mRNA_3586.1 | C_unshiu_00064_mRNA_58.1 | - |
| GF0020633 | 1 | 1 | 0 | Hypothetical protein (2) | ATP binding [GO:0005524 molecular_function] (2); protein kinase activity [GO:0004672 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2) | Protein kinase, ATP binding site [IPR017441] (2); Protein kinase domain [IPR000719] (2); Protein kinase-like domain [IPR011009] (2); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1) | scaffold_2_mRNA_3582.1 | C_unshiu_00064_mRNA_54.1 | - |
| GF0020632 | 1 | 1 | 0 | Farnesylated protein 2 (2) | metal ion binding [GO:0046872 molecular_function] (2); metal ion transport [GO:0030001 biological_process] (2) | Heavy metal-associated domain, HMA [IPR006121] (2) | scaffold_2_mRNA_3551.1 | C_unshiu_00064_mRNA_19.1 | - |
| GF0020631 | 1 | 1 | 0 | Bilirubin oxidase (2) | oxidation-reduction process [GO:0055114 biological_process] (2); oxidoreductase activity [GO:0016491 molecular_function] (2); copper ion binding [GO:0005507 molecular_function] (2); DNA binding [GO:0003677 molecular_function] (2) | SANT/Myb domain [IPR001005] (2); Multicopper oxidase, type 3 [IPR011707] (2); Multicopper oxidase, type 1 [IPR001117] (2); Myb-like domain [IPR017877] (2); Multicopper oxidase, type 2 [IPR011706] (2); Cupredoxin [IPR008972] (2); Homeodomain-like [IPR009057] (1); Homeobox domain-like [IPR009057] (1) | scaffold_2_mRNA_3548.1 | C_unshiu_00064_mRNA_16.1 | - |
| GF0020630 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_3545.1 | C_unshiu_00064_mRNA_13.1 | - |
| GF0020629 | 1 | 1 | 0 | Proton myo-inositol cotransporter (2) | transporter activity [GO:0005215 molecular_function] (2); transmembrane transport [GO:0055085 biological_process] (2); integral component of membrane [GO:0016021 cellular_component] (2); substrate-specific transmembrane transporter activity [GO:0022891 molecular_function] (2); membrane [GO:0016020 cellular_component] (2); transmembrane transporter activity [GO:0022857 molecular_function] (2) | Sugar/inositol transporter [IPR003663] (2); Major facilitator, sugar transporter-like [IPR005828] (2); Major facilitator superfamily domain [IPR020846] (2); Sugar transporter, conserved site [IPR005829] (2) | scaffold_2_mRNA_354.1 | C_unshiu_00111_mRNA_44.1 | - |
| GF0020628 | 1 | 1 | 0 | Cytokinin riboside 5'-monophosphate phosphoribohydrolase (2) | | | scaffold_2_mRNA_353.1 | C_unshiu_00111_mRNA_43.1 | - |
| GF0020626 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_352.1 | C_unshiu_00111_mRNA_41.1 | - |
| GF0020625 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_3513.1 | C_unshiu_00017_mRNA_98.1 | - |
| GF0020624 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_3512.1 | C_unshiu_00017_mRNA_97.1 | - |
| GF0020623 | 1 | 1 | 0 | Protein BCCIP homolog (2) | | BCP1 family [IPR025602] (2) | scaffold_2_mRNA_3503.1 | C_unshiu_00017_mRNA_88.1 | - |
| GF0020622 | 1 | 1 | 0 | Hypothetical protein (2) | oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2); iron ion binding [GO:0005506 molecular_function] (2); heme binding [GO:0020037 molecular_function] (2) | Cytochrome P450 [IPR001128] (2) | scaffold_2_mRNA_3488.1 | C_unshiu_00017_mRNA_75.1 | - |
| GF0020621 | 1 | 1 | 0 | Hypothetical protein (2) | DNA binding [GO:0003677 molecular_function] (1) | Myb-like domain [IPR017877] (2); Homeodomain-like [IPR009057] (1) | scaffold_2_mRNA_3483.1 | C_unshiu_00017_mRNA_70.1 | - |
| GF0020620 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_3480.1 | C_unshiu_00017_mRNA_68.1 | - |
| GF0020619 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_348.1 | C_unshiu_01893_mRNA_14.1 | - |
| GF0020618 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_346.1 | C_unshiu_01893_mRNA_12.1 | - |
| GF0020617 | 1 | 1 | 0 | Hypothetical protein (2) | | Cullin protein, neddylation domain [IPR019559] (2); Winged helix-turn-helix DNA-binding domain [IPR011991] (2) | scaffold_2_mRNA_3459.1 | C_unshiu_00017_mRNA_47.1 | - |
| GF0020616 | 1 | 1 | 0 | Protein FAR1-RELATED SEQUENCE 9 (1); Transposon protein, putative, unclassified, expressed (1) | regulation of transcription, DNA-templated [GO:0006355 biological_process] (2); zinc ion binding [GO:0008270 molecular_function] (1) | MULE transposase domain [IPR018289] (2); FHY3/FAR1 family [IPR031052] (2); Zinc finger, PMZ-type [IPR006564] (1); Zinc finger, SWIM-type [IPR007527] (1) | scaffold_2_mRNA_3457.1 | C_unshiu_01323_mRNA_1.1 | - |
| GF0020615 | 1 | 1 | 0 | 1-aminocyclopropane-1-carboxylate oxidase homolog 12 (1); 1-aminocyclopropane-1-carboxylate oxidase like 12 (1) | oxidation-reduction process [GO:0055114 biological_process] (2); oxidoreductase activity [GO:0016491 molecular_function] (2) | Isopenicillin N synthase-like [IPR027443] (2); Non-haem dioxygenase N-terminal domain [IPR026992] (2); Oxoglutarate/iron-dependent dioxygenase [IPR005123] (2) | scaffold_2_mRNA_3454.1 | C_unshiu_00017_mRNA_46.1 | - |
| GF0020614 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_344.1 | C_unshiu_01893_mRNA_10.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0020610 | 1 | 1 | 0 | Hypothetical protein (2) | 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) | Peptidase A2A, retrovirus, catalytic [IPR001995] (1); Zinc finger, CCHC-type [IPR001878] (1) | scaffold_2_mRNA_342.1 | C_unshiu_01893_mRNA_7.1 | - |
| GF0020609 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_3417.1 | C_unshiu_00276_mRNA_20.1 | - |
| GF0020608 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_341.1 | C_unshiu_01893_mRNA_6.1 | - |
| GF0020607 | 1 | 1 | 0 | Monosacharide transport protein (1); Hypothetical protein (1) | | | scaffold_2_mRNA_3405.1 | C_unshiu_00262_mRNA_32.1 | - |
| GF0020605 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_340.1 | C_unshiu_01893_mRNA_4.1 | - |
| GF0020604 | 1 | 1 | 0 | Hypothetical protein (1); RING-H2 finger protein ATL29 (1) | protein binding [GO:0005515 molecular_function] (2); zinc ion binding [GO:0008270 molecular_function] (2); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1) | Zinc finger, RING-type [IPR001841] (2); Zinc finger, RING/FYVE/PHD-type [IPR013083] (2); Peptidase A2A, retrovirus, catalytic [IPR001995] (1) | scaffold_2_mRNA_338.1 | C_unshiu_01305_mRNA_1.1 | - |
| GF0020603 | 1 | 1 | 0 | Cyclin J18 (2) | | Cyclin, N-terminal [IPR006671] (2); Cyclin-like [IPR013763] (2) | scaffold_2_mRNA_3377.1 | C_unshiu_00262_mRNA_10.1 | - |
| GF0020602 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_3372.1 | C_unshiu_00262_mRNA_4.1 | - |
| GF0020601 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_3370.1 | C_unshiu_00262_mRNA_2.1 | - |
| GF0020600 | 1 | 1 | 0 | Mavicyanin (2) | electron carrier activity [GO:0009055 molecular_function] (2) | Cupredoxin [IPR008972] (2); Phytocyanin domain [IPR003245] (2); Blue (type 1) copper protein, binding site [IPR028871] (2) | scaffold_2_mRNA_3369.1 | C_unshiu_00262_mRNA_1.1 | - |
| GF0020599 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_3359.1 | C_unshiu_00197_mRNA_26.1 | - |
| GF0020598 | 1 | 1 | 0 | Hypothetical protein (1); Retrovirus-related Pol polyprotein from transposon 412 (1) | nucleic acid binding [GO:0003676 molecular_function] (2); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (2) | Ribonuclease H domain [IPR002156] (2); Ribonuclease H-like domain [IPR012337] (2) | scaffold_2_mRNA_3349.1 | C_unshiu_00401_mRNA_8.1 | - |
| GF0020597 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_3345.1 | C_unshiu_00300_mRNA_27.1 | - |
| GF0020596 | 1 | 1 | 0 | Protein NRT1/ PTR FAMILY 8.3 (2) | oligopeptide transport [GO:0006857 biological_process] (2); transporter activity [GO:0005215 molecular_function] (2); transport [GO:0006810 biological_process] (2); membrane [GO:0016020 cellular_component] (2) | PTR2 family proton/oligopeptide symporter, conserved site [IPR018456] (2); Proton-dependent oligopeptide transporter family [IPR000109] (2); Major facilitator superfamily domain [IPR020846] (2) | scaffold_2_mRNA_3336.1 | C_unshiu_00401_mRNA_21.1 | - |
| GF0020595 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_332.1 | C_unshiu_00565_mRNA_21.1 | - |
| GF0020594 | 1 | 1 | 0 | Nucleus, subunit A, putative isoform 2 (1); Hypothetical protein (1) | integral component of membrane [GO:0016021 cellular_component] (2); regulation of transcription, DNA-templated [GO:0006355 biological_process] (2); nucleus [GO:0005634 cellular_component] (2) | RNA polymerase II transcription factor SIII, subunit A [IPR010684] (2) | scaffold_2_mRNA_3317.1 | C_unshiu_00259_mRNA_27.1 | - |
| GF0020591 | 1 | 1 | 0 | Transcription factor IBH1 (2) | protein dimerization activity [GO:0046983 molecular_function] (1) | Myc-type, basic helix-loop-helix (bHLH) domain [IPR011598] (1) | scaffold_2_mRNA_3297.1 | C_unshiu_00259_mRNA_3.1 | - |
| GF0020590 | 1 | 1 | 0 | Hypothetical protein (2) | DNA binding [GO:0003677 molecular_function] (2); nucleus [GO:0005634 cellular_component] (2); regulation of transcription, DNA-templated [GO:0006355 biological_process] (2) | GC-rich sequence DNA-binding factor domain [IPR022783] (2) | scaffold_2_mRNA_3296.1 | C_unshiu_00259_mRNA_2.1 | - |
| GF0020589 | 1 | 1 | 0 | Hypothetical protein (1); Cysteine-rich RLK (RECEPTOR-like protein kinase) 8 (1) | | Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1) | scaffold_2_mRNA_3293.1 | C_unshiu_00864_mRNA_24.1 | - |
| GF0020588 | 1 | 1 | 0 | CXE carboxylesterase (2) | hydrolase activity [GO:0016787 molecular_function] (2); metabolic process [GO:0008152 biological_process] (2) | Alpha/beta hydrolase fold-3 [IPR013094] (2); Alpha/Beta hydrolase fold [IPR029058] (2) | scaffold_2_mRNA_3290.1 | C_unshiu_00864_mRNA_21.1 | - |
| GF0020587 | 1 | 1 | 0 | Hypothetical protein (2) | | Protein of unknown function DUF538 [IPR007493] (2) | scaffold_2_mRNA_3283.1 | C_unshiu_01310_mRNA_2.1 | - |
| GF0020585 | 1 | 1 | 0 | Ferredoxin (2) | electron carrier activity [GO:0009055 molecular_function] (2); iron-sulfur cluster binding [GO:0051536 molecular_function] (2) | 2Fe-2S ferredoxin-type iron-sulfur binding domain [IPR001041] (2); Beta-grasp domain [IPR012675] (2) | scaffold_2_mRNA_3272.1 | C_unshiu_00141_mRNA_58.1 | - |
| GF0020584 | 1 | 1 | 0 | Maternal effect embryo arrest protein (2) | | | scaffold_2_mRNA_3264.1 | C_unshiu_00141_mRNA_49.1 | - |
| GF0020583 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_3263.1 | C_unshiu_00141_mRNA_48.1 | - |
| GF0020582 | 1 | 1 | 0 | Hypothetical protein (2) | regulation of transcription, DNA-templated [GO:0006355 biological_process] (1) | FHY3/FAR1 family [IPR031052] (1) | scaffold_2_mRNA_3258.1 | C_unshiu_00141_mRNA_43.1 | - |
| GF0020581 | 1 | 1 | 0 | Hypothetical protein (1); Zinc ion binding,nucleic acid binding-like protein (1) | zinc ion binding [GO:0008270 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | Domain of unknown function DUF4283 [IPR025558] (2); Zinc knuckle CX2CX4HX4C [IPR025836] (2); Zinc finger, CCHC-type [IPR001878] (2) | scaffold_2_mRNA_3250.1 | C_unshiu_00141_mRNA_38.1 | - |
| GF0020580 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_3249.1 | C_unshiu_00141_mRNA_37.1 | - |
| GF0020579 | 1 | 1 | 0 | Hypothetical protein (2) | | Gnk2-homologous domain [IPR002902] (2) | scaffold_2_mRNA_3245.1 | C_unshiu_00141_mRNA_33.1 | - |
| GF0020578 | 1 | 1 | 0 | CDNA clone:J013024E12, full insert sequence (1); Glutamate receptor 2.1 (1) | membrane [GO:0016020 cellular_component] (1); ionotropic glutamate receptor activity [GO:0004970 molecular_function] (1) | Periplasmic binding protein-like I [IPR028082] (2); Receptor, ligand binding region [IPR001828] (2); Ionotropic glutamate receptor [IPR001320] (1) | scaffold_2_mRNA_3243.1 | C_unshiu_00141_mRNA_31.1 | - |
| GF0020577 | 1 | 1 | 0 | Ubiquitin-like-conjugating enzyme ATG10 (2) | | Autophagy-related protein 3 [IPR007135] (2) | scaffold_2_mRNA_3234.1 | C_unshiu_00141_mRNA_20.1 | - |
| GF0020576 | 1 | 1 | 0 | UDP-glycosyltransferase 74E2 (2) | transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (2); metabolic process [GO:0008152 biological_process] (2) | UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (2) | scaffold_2_mRNA_3229.1 | C_unshiu_00141_mRNA_15.1 | - |
| GF0020575 | 1 | 1 | 0 | Ribonuclease H (2) | nucleic acid binding [GO:0003676 molecular_function] (2); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2); Ribonuclease H domain [IPR002156] (2); TB2/DP1/HVA22-related protein [IPR004345] (1) | scaffold_2_mRNA_3225.1 | C_unshiu_00389_mRNA_15.1 | - |
| GF0020574 | 1 | 1 | 0 | Hypothetical protein (2) | zinc ion binding [GO:0008270 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | Domain of unknown function DUF4283 [IPR025558] (2); Zinc knuckle CX2CX4HX4C [IPR025836] (2); Zinc finger, CCHC-type [IPR001878] (2) | scaffold_2_mRNA_3223.1 | C_unshiu_00141_mRNA_9.1 | - |
| GF0020573 | 1 | 1 | 0 | UDP-glycosyltransferase 74F2 (2) | transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (2); metabolic process [GO:0008152 biological_process] (2) | UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (2) | scaffold_2_mRNA_3222.1 | C_unshiu_00141_mRNA_8.1 | - |
| GF0020572 | 1 | 1 | 0 | UDP-glycosyltransferase 74E2 (2) | metabolic process [GO:0008152 biological_process] (2); transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (2) | UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (2) | scaffold_2_mRNA_3219.1 | C_unshiu_00141_mRNA_6.1 | - |
| GF0020569 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_3176.1 | C_unshiu_01154_mRNA_1.1 | - |
| GF0020567 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_3167.1 | C_unshiu_00187_mRNA_29.1 | - |
| GF0020566 | 1 | 1 | 0 | Pre-mRNA-splicing factor ATP-dependent RNA helicase (2) | helicase activity [GO:0004386 molecular_function] (2) | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); Helicase superfamily 1/2, ATP-binding domain [IPR014001] (2); Helicase-associated domain [IPR007502] (2); Helicase, C-terminal [IPR001650] (2) | scaffold_2_mRNA_3160.1 | C_unshiu_01154_mRNA_10.1 | - |
| GF0020565 | 1 | 1 | 0 | Hypothetical protein (2) | | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2) | scaffold_2_mRNA_3159.1 | C_unshiu_01154_mRNA_11.1 | - |
| GF0020564 | 1 | 1 | 0 | Hypothetical protein (2) | | Zinc finger, RING/FYVE/PHD-type [IPR013083] (1) | scaffold_2_mRNA_3157.1 | C_unshiu_00472_mRNA_2.1 | - |
| GF0020563 | 1 | 1 | 0 | Hypothetical protein (2) | nuclear-transcribed mRNA catabolic process, nonsense-mediated decay [GO:0000184 biological_process] (1); helicase activity [GO:0004386 molecular_function] (1); metal ion binding [GO:0046872 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1); DNA binding [GO:0003677 molecular_function] (1); cytoplasm [GO:0005737 cellular_component] (1) | RNA helicase UPF1, UPF2-interacting domain [IPR018999] (1); Zinc finger, CCCH-type [IPR000571] (1) | scaffold_2_mRNA_3156.1 | C_unshiu_00472_mRNA_3.1 | - |
| GF0020562 | 1 | 1 | 0 | Essential protein Yae1, putative isoform 3 (2) | | | scaffold_2_mRNA_3154.1 | C_unshiu_00472_mRNA_6.1 | - |
| GF0020560 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_3146.1 | C_unshiu_00472_mRNA_14.1 | - |
| GF0020558 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (2) | Ribonuclease H domain [IPR002156] (2); Ribonuclease H-like domain [IPR012337] (2) | scaffold_2_mRNA_3141.1 | C_unshiu_00136_mRNA_52.1 | - |
| GF0020557 | 1 | 1 | 0 | Hypothetical protein (2) | serine-type endopeptidase activity [GO:0004252 molecular_function] (2); proteolysis [GO:0006508 biological_process] (2) | Peptidase S8/S53 domain [IPR000209] (2); Peptidase S8, subtilisin-related [IPR015500] (1) | scaffold_2_mRNA_3140.1 | C_unshiu_00136_mRNA_51.1 | - |
| GF0020556 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_3138.1 | C_unshiu_00136_mRNA_49.1 | - |
| GF0020555 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_3136.1 | C_unshiu_00136_mRNA_47.1 | - |
| GF0020554 | 1 | 1 | 0 | Hypothetical protein (2) | | MULE transposase domain [IPR018289] (2) | scaffold_2_mRNA_3134.1 | C_unshiu_00136_mRNA_45.1 | - |
| GF0020553 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_3130.1 | C_unshiu_00136_mRNA_41.1 | - |
| GF0020552 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_3129.1 | C_unshiu_00136_mRNA_40.1 | - |
| GF0020551 | 1 | 1 | 0 | Period circadian protein, putative isoform 1 (2) | | | scaffold_2_mRNA_3126.1 | C_unshiu_00136_mRNA_33.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0020550 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_3123.1 | C_unshiu_00136_mRNA_31.1 | - |
| GF0020549 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_3106.1 | C_unshiu_00136_mRNA_12.1 | - |
| GF0020548 | 1 | 1 | 0 | Epithiospecifier protein (2) | protein binding [GO:0005515 molecular_function] (2) | Kelch-type beta propeller [IPR015915] (2); Kelch repeat type 1 [IPR006652] (2) | scaffold_2_mRNA_3101.1 | C_unshiu_00136_mRNA_7.1 | - |
| GF0020547 | 1 | 1 | 0 | Hypothetical protein (2) | oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2); iron ion binding [GO:0005506 molecular_function] (2); heme binding [GO:0020037 molecular_function] (2) | Cytochrome P450 [IPR001128] (2) | scaffold_2_mRNA_31.1 | C_unshiu_00109_mRNA_30.1 | - |
| GF0020546 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_3097.1 | C_unshiu_00136_mRNA_3.1 | - |
| GF0020545 | 1 | 1 | 0 | Hypothetical protein (2) | zinc ion binding [GO:0008270 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | Zinc finger, CCHC-type [IPR001878] (2); Zinc knuckle CX2CX4HX4C [IPR025836] (2) | scaffold_2_mRNA_308.1 | C_unshiu_00392_mRNA_27.1 | - |
| GF0020544 | 1 | 1 | 0 | Putative leucine-rich repeat disease resistance protein (1); Verticillium wilt resistance-like protein (1) | protein binding [GO:0005515 molecular_function] (2) | Leucine-rich repeat domain, L domain-like [IPR032675] (2); Leucine-rich repeat, typical subtype [IPR003591] (2); Leucine-rich repeat [IPR001611] (2); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1) | scaffold_2_mRNA_3070.1 | C_unshiu_00863_mRNA_11.1 | - |
| GF0020543 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_3065.1 | C_unshiu_00863_mRNA_3.1 | - |
| GF0020542 | 1 | 1 | 0 | Leucine-rich repeat receptor-like serine/threonine-protein kinase BAM2 (2) | protein binding [GO:0005515 molecular_function] (2) | Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (2); Leucine-rich repeat [IPR001611] (2); Leucine-rich repeat, typical subtype [IPR003591] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2) | scaffold_2_mRNA_3063.1 | C_unshiu_00081_mRNA_69.1 | - |
| GF0020540 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_305.1 | C_unshiu_00392_mRNA_22.1 | - |
| GF0020539 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_304.1 | C_unshiu_00392_mRNA_21.1 | - |
| GF0020538 | 1 | 1 | 0 | Receptor like protein 33 (2) | protein binding [GO:0005515 molecular_function] (2) | Leucine-rich repeat domain, L domain-like [IPR032675] (2); Leucine-rich repeat, typical subtype [IPR003591] (2); Leucine-rich repeat [IPR001611] (2) | scaffold_2_mRNA_3037.1 | C_unshiu_00081_mRNA_67.1 | - |
| GF0020536 | 1 | 1 | 0 | Hypothetical protein (2) | | Leucine-rich repeat domain, L domain-like [IPR032675] (1) | scaffold_2_mRNA_3027.1 | C_unshiu_00081_mRNA_57.1 | - |
| GF0020535 | 1 | 1 | 0 | Downward leaf curling protein (2) | protein binding [GO:0005515 molecular_function] (2) | Sterile alpha motif domain [IPR001660] (2); Sterile alpha motif/pointed domain [IPR013761] (2) | scaffold_2_mRNA_3023.1 | C_unshiu_00081_mRNA_53.2 | - |
| GF0020534 | 1 | 1 | 0 | Nup133/Nup155-like nucleoporin (2) | protein binding [GO:0005515 molecular_function] (2) | WD40/YVTN repeat-like-containing domain [IPR015943] (2); Nucleoporin, Nup133/Nup155-like, N-terminal [IPR014908] (2); Nucleoporin, Nup133/Nup155-like, C-terminal [IPR007187] (1) | scaffold_2_mRNA_3022.1 | C_unshiu_00081_mRNA_52.1 | - |
| GF0020533 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_302.1 | C_unshiu_00392_mRNA_20.1 | - |
| GF0020532 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_3017.1 | C_unshiu_00081_mRNA_47.1 | - |
| GF0020531 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_301.1 | C_unshiu_00392_mRNA_19.1 | - |
| GF0020530 | 1 | 1 | 0 | DGCR14 protein (2) | | Nuclear protein DGCR14 [IPR019148] (2) | scaffold_2_mRNA_3009.1 | C_unshiu_00081_mRNA_39.1 | - |
| GF0020529 | 1 | 1 | 0 | Putative serine/threonine-protein kinase WNK11 (2) | protein phosphorylation [GO:0006468 biological_process] (2); protein kinase activity [GO:0004672 molecular_function] (2); ATP binding [GO:0005524 molecular_function] (2) | Protein kinase domain [IPR000719] (2); Protein kinase-like domain [IPR011009] (2) | scaffold_2_mRNA_3008.1 | C_unshiu_00081_mRNA_38.1 | - |
| GF0020528 | 1 | 1 | 0 | Hypothetical protein (2) | integral component of membrane [GO:0016021 cellular_component] (1) | Cytochrome b561 domain [IPR004877] (1); Cytochrome b561/ferric reductase transmembrane [IPR006593] (1) | scaffold_2_mRNA_3001.1 | C_unshiu_00081_mRNA_27.1 | - |
| GF0020527 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_300.1 | C_unshiu_00361_mRNA_5.1 | - |
| GF0020526 | 1 | 1 | 0 | Hypothetical protein (2) | protein binding [GO:0005515 molecular_function] (2) | F-box domain [IPR001810] (2) | scaffold_2_mRNA_2989.1 | C_unshiu_00081_mRNA_17.1 | - |
| GF0020525 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2981.1 | C_unshiu_00081_mRNA_9.1 | - |
| GF0020524 | 1 | 1 | 0 | Hypothetical protein (2) | regulation of transcription, DNA-templated [GO:0006355 biological_process] (1) | FHY3/FAR1 family [IPR031052] (1) | scaffold_2_mRNA_2980.1 | C_unshiu_00081_mRNA_8.1 | - |
| GF0020523 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_298.1 | C_unshiu_00392_mRNA_18.1 | - |
| GF0020522 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2976.1 | C_unshiu_00081_mRNA_4.1 | - |
| GF0020521 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2975.1 | C_unshiu_00081_mRNA_3.1 | - |
| GF0020520 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2973.1 | C_unshiu_00081_mRNA_2.1 | - |
| GF0020518 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2956.1 | C_unshiu_00283_mRNA_13.1 | - |
| GF0020517 | 1 | 1 | 0 | Hypothetical protein (2) | | Gag-polypeptide of LTR copia-type [IPR029472] (1) | scaffold_2_mRNA_2955.1 | C_unshiu_00283_mRNA_15.1 | - |
| GF0020516 | 1 | 1 | 0 | Hypothetical protein (2) | | Glycine rich protein [IPR010800] (2) | scaffold_2_mRNA_2952.1 | C_unshiu_00283_mRNA_17.1 | - |
| GF0020514 | 1 | 1 | 0 | Hypothetical protein (2) | | Domain of unknown function DUF4283 [IPR025558] (2) | scaffold_2_mRNA_2931.1 | C_unshiu_00172_mRNA_5.1 | - |
| GF0020513 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2930.1 | C_unshiu_00172_mRNA_6.1 | - |
| GF0020512 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2); protein dimerization activity [GO:0046983 molecular_function] (2) | HAT, C-terminal dimerisation domain [IPR008906] (2); Ribonuclease H-like domain [IPR012337] (2) | scaffold_2_mRNA_293.1 | C_unshiu_01129_mRNA_3.1 | - |
| GF0020511 | 1 | 1 | 0 | Polynucleotidyl transferase, Ribonuclease H fold (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_2_mRNA_2929.1 | C_unshiu_00172_mRNA_7.1 | - |
| GF0020510 | 1 | 1 | 0 | Hypothetical protein (2) | lipid metabolic process [GO:0006629 biological_process] (2) | Partial AB-hydrolase lipase domain [IPR006693] (2); Alpha/Beta hydrolase fold [IPR029058] (1) | scaffold_2_mRNA_2926.1 | C_unshiu_00172_mRNA_10.1 | - |
| GF0020509 | 1 | 1 | 0 | Zinc finger CCCH domain-containing protein 32 (2) | metal ion binding [GO:0046872 molecular_function] (2) | Zinc finger, CCCH-type [IPR000571] (2) | scaffold_2_mRNA_2922.1 | C_unshiu_00172_mRNA_14.1 | - |
| GF0020508 | 1 | 1 | 0 | Ribonuclease H protein, putative (1); Non-LTR retroelement reverse transcriptase-like protein (1) | | Reverse transcriptase domain [IPR000477] (1) | scaffold_2_mRNA_2920.1 | C_unshiu_00172_mRNA_16.1 | - |
| GF0020507 | 1 | 1 | 0 | Hypothetical protein (2) | zinc ion binding [GO:0008270 molecular_function] (2) | Zinc finger, SWIM-type [IPR007527] (2); Zinc finger, PMZ-type [IPR006564] (2) | scaffold_2_mRNA_2918.1 | C_unshiu_00172_mRNA_18.1 | - |
| GF0020506 | 1 | 1 | 0 | Hypothetical protein (2) | | MULE transposase domain [IPR018289] (2) | scaffold_2_mRNA_2917.1 | C_unshiu_00172_mRNA_19.1 | - |
| GF0020505 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2915.1 | C_unshiu_00172_mRNA_21.1 | - |
| GF0020504 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2889.1 | C_unshiu_00958_mRNA_4.1 | - |
| GF0020503 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2880.1 | C_unshiu_00958_mRNA_12.1 | - |
| GF0020501 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_287.1 | C_unshiu_01129_mRNA_7.1 | - |
| GF0020500 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (1) | Ribonuclease H-like domain [IPR012337] (1) | scaffold_2_mRNA_2868.1 | C_unshiu_00249_mRNA_46.1 | - |
| GF0020499 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2859.1 | C_unshiu_00722_mRNA_9.1 | - |
| GF0020498 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2855.1 | C_unshiu_00722_mRNA_5.1 | - |
| GF0020497 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Domain of unknown function DUF4371 [IPR025398] (2); Ribonuclease H-like domain [IPR012337] (2) | scaffold_2_mRNA_2841.1 | C_unshiu_00593_mRNA_15.1 | - |
| GF0020496 | 1 | 1 | 0 | Hypothetical protein (2) | zinc ion binding [GO:0008270 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | Zinc finger, CCHC-type [IPR001878] (2) | scaffold_2_mRNA_2830.1 | C_unshiu_00300_mRNA_25.1 | - |
| GF0020495 | 1 | 1 | 0 | Hypothetical protein (2) | nutrient reservoir activity [GO:0045735 molecular_function] (2); manganese ion binding [GO:0030145 molecular_function] (2) | Cupin 1 [IPR006045] (2); Germin [IPR001929] (2); RmlC-like jelly roll fold [IPR014710] (2); RmlC-like cupin domain [IPR011051] (2) | scaffold_2_mRNA_2829.1 | C_unshiu_00300_mRNA_26.1 | - |
| GF0020494 | 1 | 1 | 0 | Hypothetical protein (2) | membrane [GO:0016020 cellular_component] (2); galactosyltransferase activity [GO:0008378 molecular_function] (2); protein glycosylation [GO:0006486 biological_process] (2); zinc ion binding [GO:0008270 molecular_function] (1) | Glycosyl transferase, family 31 [IPR002659] (2); Domain of unknown function DUF4094 [IPR025298] (2); Zinc finger, DHHC-type, palmitoyltransferase [IPR001594] (1); Palmitoyltransferase, DHHC domain [IPR001594] (1) | scaffold_2_mRNA_2809.1 | C_unshiu_00893_mRNA_10.1 | - |
| GF0020493 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2803.1 | C_unshiu_00893_mRNA_4.1 | - |
| GF0020492 | 1 | 1 | 0 | High mobility group (HMG)-box protein (2) | | High mobility group box domain [IPR009071] (2) | scaffold_2_mRNA_2796.1 | C_unshiu_01554_mRNA_3.1 | - |
| GF0020490 | 1 | 1 | 0 | Hypothetical protein (2) | | Domain of unknown function DUF4283 [IPR025558] (2) | scaffold_2_mRNA_2794.1 | C_unshiu_01098_mRNA_9.1 | - |
| GF0020488 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_279.1 | C_unshiu_00228_mRNA_44.1 | - |
| GF0020487 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_278.1 | C_unshiu_00228_mRNA_43.1 | - |
| GF0020486 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2773.1 | C_unshiu_00029_mRNA_86.1 | - |
| GF0020485 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2772.1 | C_unshiu_00029_mRNA_85.1 | - |
| GF0020484 | 1 | 1 | 0 | Hypothetical protein (2) | | Domain of unknown function DUF1985 [IPR015410] (2) | scaffold_2_mRNA_2771.1 | C_unshiu_00029_mRNA_84.1 | - |
| GF0020483 | 1 | 1 | 0 | Hypothetical protein (2) | | Probable transposase, Ptta/En/Spm, plant [IPR004252] (2) | scaffold_2_mRNA_2770.1 | C_unshiu_00029_mRNA_83.1 | - |
| GF0020482 | 1 | 1 | 0 | Retrotransposon gag protein, , putative (2) | | Chromo domain [IPR023780] (2); Chromo domain-like [IPR016197] (2) | scaffold_2_mRNA_277.1 | C_unshiu_00228_mRNA_42.1 | - |
| GF0020481 | 1 | 1 | 0 | Hypothetical protein (2) | U4/U6 x U5 tri-snRNP complex [GO:0046540 cellular_component] (1); spliceosomal tri-snRNP complex assembly [GO:0000244 biological_process] (1); mRNA splicing, via spliceosome [GO:0000398 biological_process] (1) | Nop domain [IPR002687] (2); U4/U6 small nuclear ribonucleoprotein Prp31 [IPR027105] (1) | scaffold_2_mRNA_2767.1 | C_unshiu_00029_mRNA_80.1 | - |
| GF0020480 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_276.1 | C_unshiu_00228_mRNA_41.1 | - |
| GF0020479 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2757.1 | C_unshiu_00029_mRNA_65.1 | - |
| GF0020476 | 1 | 1 | 0 | Transposon protein, putative, Pong sub-class (2) | hydrolase activity, acting on ester bonds [GO:0016788 molecular_function] (2) | Harbinger transposase-derived protein [IPR006912] (2) | scaffold_2_mRNA_2743.1 | C_unshiu_00354_mRNA_5.1 | - |
| GF0020475 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_274.1 | C_unshiu_00228_mRNA_39.1 | - |
| GF0020474 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2729.1 | C_unshiu_00699_mRNA_2.1 | - |
| GF0020473 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2723.1 | C_unshiu_00699_mRNA_11.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0020472 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2722.1 | C_unshiu_00607_mRNA_14.1 | - |
| GF0020470 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_271.1 | C_unshiu_00228_mRNA_30.1 | - |
| GF0020469 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_270.1 | C_unshiu_00228_mRNA_29.1 | - |
| GF0020466 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2687.1 | C_unshiu_00642_mRNA_4.1 | - |
| GF0020465 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2685.1 | C_unshiu_00642_mRNA_2.1 | - |
| GF0020464 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2681.1 | C_unshiu_01288_mRNA_8.1 | - |
| GF0020463 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_268.1 | C_unshiu_00228_mRNA_28.1 | - |
| GF0020461 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2668.1 | C_unshiu_00178_mRNA_24.1 | - |
| GF0020460 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2664.1 | C_unshiu_01138_mRNA_5.1 | - |
| GF0020459 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2662.1 | C_unshiu_01138_mRNA_7.1 | - |
| GF0020458 | 1 | 1 | 0 | Putative CAI-1 autoinducer sensor kinase/phosphatase cqsS-like (1); CAI-1 autoinducer sensor kinase/phosphatase cqsS isoform 2 (1) | | Harbinger transposase-derived nuclease domain [IPR027806] (2) | scaffold_2_mRNA_2658.1 | C_unshiu_00081_mRNA_72.1 | - |
| GF0020457 | 1 | 1 | 0 | Hypothetical protein (2) | ATP binding [GO:0005524 molecular_function] (2) | Chaperonin Cpn60/TCP-1 family [IPR002423] (2); GroEL-like equatorial domain [IPR027413] (2) | scaffold_2_mRNA_2650.1 | C_unshiu_00417_mRNA_4.1 | - |
| GF0020456 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2648.1 | C_unshiu_00198_mRNA_6.1 | - |
| GF0020454 | 1 | 1 | 0 | Retrotransposon gag protein (1); Hypothetical protein (1) | | | scaffold_2_mRNA_263.1 | C_unshiu_00228_mRNA_25.1 | - |
| GF0020453 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2624.1 | C_unshiu_00498_mRNA_25.1 | - |
| GF0020452 | 1 | 1 | 0 | Hypothetical protein (1); Chaperone protein DnaK (1) | | Heat shock protein 70 family [IPR013126] (2); Heat shock protein 70, conserved site [IPR018181] (2); Protein of unknown function DUF604 [IPR006740] (1) | scaffold_2_mRNA_2615.1 | C_unshiu_01832_mRNA_3.1 | - |
| GF0020451 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2606.1 | C_unshiu_02067_mRNA_3.1 | - |
| GF0020450 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2604.1 | C_unshiu_02067_mRNA_1.1 | - |
| GF0020449 | 1 | 1 | 0 | Hypothetical protein (2) | protein kinase activity [GO:0004672 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2); ATP binding [GO:0005524 molecular_function] (2); protein tyrosine kinase activity [GO:0004713 molecular_function] (1) | Protein kinase, ATP binding site [IPR017441] (2); Protein kinase-like domain [IPR011009] (2); Protein kinase domain [IPR000719] (2); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); Tyrosine-protein kinase, catalytic domain [IPR020635] (1) | scaffold_2_mRNA_26.1 | C_unshiu_00109_mRNA_23.1 | - |
| GF0020448 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_2_mRNA_2598.1 | C_unshiu_01444_mRNA_9.1 | - |
| GF0020447 | 1 | 1 | 0 | Hypothetical protein (2) | | Metallo-beta-lactamase [IPR001279] (2) | scaffold_2_mRNA_2596.1 | C_unshiu_01444_mRNA_6.1 | - |
| GF0020446 | 1 | 1 | 0 | Monosacharide transport protein (1); Hypothetical protein (1) | | Reverse transcriptase domain [IPR000477] (2) | scaffold_2_mRNA_2590.1 | C_unshiu_00531_mRNA_18.1 | - |
| GF0020445 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_259.1 | C_unshiu_00228_mRNA_22.1 | - |
| GF0020444 | 1 | 1 | 0 | Hypothetical protein (2) | | Aspartic peptidase domain [IPR021109] (1) | scaffold_2_mRNA_2589.1 | C_unshiu_00531_mRNA_19.1 | - |
| GF0020443 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2588.1 | C_unshiu_00531_mRNA_20.1 | - |
| GF0020441 | 1 | 1 | 0 | Hypothetical protein (2) | | Protein of unknown function wound-induced [IPR022251] (2) | scaffold_2_mRNA_2562.1 | C_unshiu_00265_mRNA_14.1 | - |
| GF0020440 | 1 | 1 | 0 | Hypothetical protein (2) | 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_2555.1 | C_unshiu_00467_mRNA_9.1 | - |
| GF0020439 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2554.1 | C_unshiu_00579_mRNA_2.1 | - |
| GF0020438 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2553.1 | C_unshiu_00579_mRNA_1.1 | - |
| GF0020437 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_255.1 | C_unshiu_00228_mRNA_20.1 | - |
| GF0020432 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2515.1 | C_unshiu_00939_mRNA_5.1 | - |
| GF0020431 | 1 | 1 | 0 | Cyclic nucleotide-gated ion channel, putative (1); Cyclic nucleotide-gated ion channel 1 (1) | protein binding [GO:0005515 molecular_function] (2) | Cyclic nucleotide-binding domain [IPR000595] (2); IQ motif, EF-hand binding site [IPR000048] (2); Cyclic nucleotide-binding-like [IPR018490] (2); RmlC-like jelly roll fold [IPR014710] (2) | scaffold_2_mRNA_2513.1 | C_unshiu_02654_mRNA_1.1 | - |
| GF0020430 | 1 | 1 | 0 | Retrotransposon gag protein (2) | | Retrotransposon gag domain [IPR005162] (2) | scaffold_2_mRNA_2512.1 | C_unshiu_02654_mRNA_2.1 | - |
| GF0020429 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2506.1 | C_unshiu_00724_mRNA_14.1 | - |
| GF0020428 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_250.1 | C_unshiu_00228_mRNA_17.1 | - |
| GF0020426 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2495.1 | C_unshiu_00724_mRNA_5.1 | - |
| GF0020425 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_249.1 | C_unshiu_00228_mRNA_16.1 | - |
| GF0020424 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2484.1 | C_unshiu_00565_mRNA_1.1 | - |
| GF0020422 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2480.1 | C_unshiu_00565_mRNA_3.1 | - |
| GF0020421 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_248.1 | C_unshiu_00228_mRNA_15.1 | - |
| GF0020420 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2477.1 | C_unshiu_00565_mRNA_5.1 | - |
| GF0020419 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2475.1 | C_unshiu_00565_mRNA_7.1 | - |
| GF0020418 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2474.1 | C_unshiu_00565_mRNA_8.1 | - |
| GF0020417 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2470.1 | C_unshiu_00565_mRNA_16.1 | - |
| GF0020416 | 1 | 1 | 0 | Hypothetical protein (2) | 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_246.1 | C_unshiu_00228_mRNA_13.1 | - |
| GF0020415 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2455.1 | C_unshiu_01407_mRNA_5.1 | - |
| GF0020414 | 1 | 1 | 0 | Hypothetical protein (2) | | Viral movement protein [IPR028919] (2) | scaffold_2_mRNA_2454.1 | C_unshiu_01407_mRNA_4.1 | - |
| GF0020413 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_245.1 | C_unshiu_00228_mRNA_12.1 | - |
| GF0020412 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2449.1 | C_unshiu_00128_mRNA_9.1 | - |
| GF0020411 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2447.1 | C_unshiu_00128_mRNA_11.1 | - |
| GF0020410 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2443.1 | C_unshiu_00239_mRNA_29.1 | - |
| GF0020409 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2428.1 | C_unshiu_00128_mRNA_28.1 | - |
| GF0020408 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2422.1 | C_unshiu_01182_mRNA_13.1 | - |
| GF0020407 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2420.1 | C_unshiu_01182_mRNA_14.1 | - |
| GF0020406 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2417.1 | C_unshiu_00160_mRNA_4.1 | - |
| GF0020405 | 1 | 1 | 0 | Hypothetical protein (2) | aspartic-type endopeptidase activity [GO:0004190 molecular_function] (2); zinc ion binding [GO:0008270 molecular_function] (2); proteolysis [GO:0006508 biological_process] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | Zinc finger, CCHC-type [IPR001878] (2); Reverse transcriptase domain [IPR000477] (2); Peptidase A2A, retrovirus, catalytic [IPR001995] (2) | scaffold_2_mRNA_2416.1 | C_unshiu_00160_mRNA_5.1 | - |
| GF0020404 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2415.1 | C_unshiu_00160_mRNA_6.1 | - |
| GF0020403 | 1 | 1 | 0 | Hypothetical protein (2) | | Reverse transcriptase domain [IPR000477] (2) | scaffold_2_mRNA_2413.1 | C_unshiu_00160_mRNA_8.1 | - |
| GF0020402 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2412.1 | C_unshiu_00160_mRNA_9.1 | - |
| GF0020401 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2411.1 | C_unshiu_00160_mRNA_10.1 | - |
| GF0020400 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2408.1 | C_unshiu_00317_mRNA_25.1 | - |
| GF0020399 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2406.1 | C_unshiu_01845_mRNA_13.1 | - |
| GF0020398 | 1 | 1 | 0 | Hypothetical protein (2) | | Viral movement protein [IPR028919] (2) | scaffold_2_mRNA_2405.1 | C_unshiu_01845_mRNA_12.1 | - |
| GF0020397 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2403.1 | C_unshiu_01845_mRNA_10.1 | - |
| GF0020396 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2402.1 | C_unshiu_01845_mRNA_9.1 | - |
| GF0020395 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2401.1 | C_unshiu_01845_mRNA_8.1 | - |
| GF0020394 | 1 | 1 | 0 | Hypothetical protein (2) | | Reverse transcriptase domain [IPR000477] (2) | scaffold_2_mRNA_2400.1 | C_unshiu_01845_mRNA_7.1 | - |
| GF0020393 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_24.1 | C_unshiu_00109_mRNA_21.1 | - |
| GF0020392 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2399.1 | C_unshiu_01845_mRNA_6.1 | - |
| GF0020391 | 1 | 1 | 0 | Hypothetical protein (2) | | Viral movement protein [IPR028919] (2); Reverse transcriptase domain [IPR000477] (2) | scaffold_2_mRNA_2398.1 | C_unshiu_01845_mRNA_5.1 | - |
| GF0020390 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2397.1 | C_unshiu_01845_mRNA_3.1 | - |
| GF0020389 | 1 | 1 | 0 | Hypothetical protein (2) | | Reverse transcriptase domain [IPR000477] (2) | scaffold_2_mRNA_2396.1 | C_unshiu_01845_mRNA_2.1 | - |
| GF0020388 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2390.1 | C_unshiu_02734_mRNA_2.1 | - |
| GF0020387 | 1 | 1 | 0 | Hypothetical protein (2) | 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_239.1 | C_unshiu_00228_mRNA_6.1 | - |
| GF0020386 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2); zinc ion binding [GO:0008270 molecular_function] (2) | Zinc finger, CCHC-type [IPR001878] (2) | scaffold_2_mRNA_2388.1 | C_unshiu_00678_mRNA_2.1 | - |
| GF0020385 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2387.1 | C_unshiu_00655_mRNA_15.1 | - |
| GF0020384 | 1 | 1 | 0 | Hypothetical protein (2) | | Uncharacterised protein family UPF0274 [IPR007451] (1) | scaffold_2_mRNA_2383.1 | C_unshiu_00655_mRNA_5.1 | - |
| GF0020383 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2382.1 | C_unshiu_00655_mRNA_4.1 | - |
| GF0020382 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2374.1 | C_unshiu_01129_mRNA_1.1 | - |
| GF0020381 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_237.1 | C_unshiu_00228_mRNA_5.1 | - |
| GF0020380 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2366.1 | C_unshiu_00261_mRNA_26.1 | - |
| GF0020379 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2359.1 | C_unshiu_00261_mRNA_30.1 | - |
| GF0020378 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2356.1 | C_unshiu_00261_mRNA_29.1 | - |
| GF0020377 | 1 | 1 | 0 | Hypothetical protein (2) | | Viral movement protein [IPR028919] (1) | scaffold_2_mRNA_235.1 | C_unshiu_00228_mRNA_4.1 | - |
| GF0020376 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2347.1 | C_unshiu_01397_mRNA_4.1 | - |
| GF0020375 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2346.1 | C_unshiu_01397_mRNA_5.1 | - |
| GF0020374 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_234.1 | C_unshiu_00228_mRNA_3.1 | - |
| GF0020373 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2339.1 | C_unshiu_01759_mRNA_5.1 | - |
| GF0020372 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2337.1 | C_unshiu_01759_mRNA_7.1 | - |
| GF0020371 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2336.1 | C_unshiu_01759_mRNA_8.1 | - |
| GF0020370 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2325.1 | C_unshiu_00160_mRNA_3.1 | - |
| GF0020369 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2318.1 | C_unshiu_00474_mRNA_9.1 | - |
| GF0020368 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2317.1 | C_unshiu_00474_mRNA_7.1 | - |
| GF0020367 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2314.1 | C_unshiu_00065_mRNA_70.1 | - |
| GF0020366 | 1 | 1 | 0 | Hypothetical protein (2) | | Reverse transcriptase domain [IPR000477] (1) | scaffold_2_mRNA_2311.1 | C_unshiu_00065_mRNA_68.1 | - |
| GF0020365 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2310.1 | C_unshiu_00065_mRNA_67.1 | - |
| GF0020364 | 1 | 1 | 0 | Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1); Hypothetical protein (1) | | | scaffold_2_mRNA_2308.1 | C_unshiu_00065_mRNA_64.1 | - |
| GF0020363 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2307.1 | C_unshiu_00065_mRNA_63.1 | - |
| GF0020362 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2306.1 | C_unshiu_00640_mRNA_16.1 | - |
| GF0020361 | 1 | 1 | 0 | Retrotransposon protein, putative, Ty3-gypsy subclass (2) | | | scaffold_2_mRNA_2298.1 | C_unshiu_00074_mRNA_42.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0020360 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2297.1 | C_unshiu_00074_mRNA_43.1 | - |
| GF0020359 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2296.1 | C_unshiu_01585_mRNA_1.1 | - |
| GF0020358 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2295.1 | C_unshiu_01585_mRNA_2.1 | - |
| GF0020357 | 1 | 1 | 0 | Hypothetical protein (2) | | Viral movement protein [IPR028919] (2) | scaffold_2_mRNA_2290.1 | C_unshiu_01585_mRNA_5.1 | - |
| GF0020356 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_228.1 | C_unshiu_02996_mRNA_2.1 | - |
| GF0020355 | 1 | 1 | 0 | Retrotransposon protein, putative, Ty1-copia subclass (2) | zinc ion binding [GO:0008270 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | Zinc finger, CCHC-type [IPR001878] (2) | scaffold_2_mRNA_2259.1 | C_unshiu_01017_mRNA_6.1 | - |
| GF0020354 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2258.1 | C_unshiu_01017_mRNA_5.1 | - |
| GF0020353 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2256.1 | C_unshiu_01017_mRNA_3.1 | - |
| GF0020351 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2250.1 | C_unshiu_00934_mRNA_1.1 | - |
| GF0020350 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_225.1 | C_unshiu_01199_mRNA_6.1 | - |
| GF0020349 | 1 | 1 | 0 | Cytokinin riboside 5'-monophosphate phosphoribohydrolase (2) | | Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (2); LOG family [IPR031100] (2) | scaffold_2_mRNA_2249.1 | C_unshiu_00934_mRNA_2.1 | - |
| GF0020348 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2248.1 | C_unshiu_00934_mRNA_3.1 | - |
| GF0020347 | 1 | 1 | 0 | Hypothetical protein (2) | zinc ion binding [GO:0008270 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | Zinc finger, CCHC-type [IPR001878] (2); Reverse transcriptase domain [IPR000477] (2) | scaffold_2_mRNA_2241.1 | C_unshiu_00520_mRNA_7.1 | - |
| GF0020346 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2240.1 | C_unshiu_00520_mRNA_8.1 | - |
| GF0020345 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_224.1 | C_unshiu_01199_mRNA_7.1 | - |
| GF0020344 | 1 | 1 | 0 | RNA-directed DNA polymerase (Reverse transcriptase) (1); Hypothetical protein (1) | | Reverse transcriptase domain [IPR000477] (2) | scaffold_2_mRNA_2239.1 | C_unshiu_00520_mRNA_9.1 | - |
| GF0020343 | 1 | 1 | 0 | Hypothetical protein (2) | | Viral movement protein [IPR028919] (2) | scaffold_2_mRNA_2237.1 | C_unshiu_00520_mRNA_12.1 | - |
| GF0020342 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2234.1 | C_unshiu_00520_mRNA_15.1 | - |
| GF0020341 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_223.1 | C_unshiu_01199_mRNA_8.1 | - |
| GF0020337 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2206.1 | C_unshiu_00683_mRNA_2.1 | - |
| GF0020336 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2201.1 | C_unshiu_02309_mRNA_1.1 | - |
| GF0020335 | 1 | 1 | 0 | Orcinol O-methyltransferase (1); Hypothetical protein (1) | O-methyltransferase activity [GO:0008171 molecular_function] (2); methyltransferase activity [GO:0008168 molecular_function] (2); protein dimerization activity [GO:0046983 molecular_function] (1) | O-methyltransferase, family 2 [IPR001077] (2); Winged helix-turn-helix DNA-binding domain [IPR011991] (2); O-methyltransferase COMT-type [IPR016461] (2); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (2); Plant methyltransferase dimerisation [IPR012967] (1) | scaffold_2_mRNA_2194.1 | C_unshiu_00683_mRNA_7.1 | - |
| GF0020334 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2193.1 | C_unshiu_00683_mRNA_8.1 | - |
| GF0020333 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2178.1 | C_unshiu_01134_mRNA_4.1 | - |
| GF0020331 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2159.1 | C_unshiu_00593_mRNA_13.1 | - |
| GF0020330 | 1 | 1 | 0 | BED zinc finger,hAT family dimerization domain isoform 1 (2) | nucleic acid binding [GO:0003676 molecular_function] (2); protein dimerization activity [GO:0046983 molecular_function] (2); DNA binding [GO:0003677 molecular_function] (2) | Zinc finger, BED-type [IPR003656] (2); hAT-like transposase, RNase-H fold [IPR025525] (2); Ribonuclease H-like domain [IPR012337] (2); HAT, C-terminal dimerisation domain [IPR008906] (2); Zinc finger C2H2-type [IPR013087] (1) | scaffold_2_mRNA_2156.1 | C_unshiu_02468_mRNA_1.1 | - |
| GF0020329 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2150.1 | C_unshiu_00823_mRNA_6.1 | - |
| GF0020328 | 1 | 1 | 0 | Cytokinin riboside 5'-monophosphate phosphoribohydrolase (2) | | Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (2); LOG family [IPR031100] (2) | scaffold_2_mRNA_2149.1 | C_unshiu_01925_mRNA_2.1 | - |
| GF0020326 | 1 | 1 | 0 | Contains similarity to reverse trancriptase , related (2) | | Reverse transcriptase zinc-binding domain [IPR026960] (2) | scaffold_2_mRNA_2145.1 | C_unshiu_01305_mRNA_4.1 | - |
| GF0020325 | 1 | 1 | 0 | CDNA clone:002-110-H12, full insert sequence (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_2_mRNA_2144.1 | C_unshiu_01305_mRNA_3.1 | - |
| GF0020324 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2143.1 | C_unshiu_01305_mRNA_2.1 | - |
| GF0020323 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2129.1 | C_unshiu_00878_mRNA_1.1 | - |
| GF0020322 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2127.1 | C_unshiu_01360_mRNA_7.1 | - |
| GF0020320 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2105.1 | C_unshiu_01496_mRNA_3.1 | - |
| GF0020319 | 1 | 1 | 0 | LRR receptor-like kinase family protein (1); Hypothetical protein (1) | protein binding [GO:0005515 molecular_function] (2); protein kinase activity [GO:0004672 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2); ATP binding [GO:0005524 molecular_function] (2) | Protein kinase, ATP binding site [IPR017441] (2); Leucine-rich repeat [IPR001611] (2); Protein kinase domain [IPR000719] (2); Leucine-rich repeat, typical subtype [IPR003591] (2); Protein kinase-like domain [IPR011009] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Armadillo [IPR000225] (2); WD40 repeat, conserved site [IPR019775] (1); WD40 repeat [IPR001680] (1); WD40-repeat-containing domain [IPR017986] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1) | scaffold_2_mRNA_21.1 | C_unshiu_00109_mRNA_18.1 | - |
| GF0020318 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2095.1 | C_unshiu_00658_mRNA_6.1 | - |
| GF0020317 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2089.1 | C_unshiu_00658_mRNA_12.1 | - |
| GF0020316 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2087.1 | C_unshiu_00658_mRNA_14.1 | - |
| GF0020315 | 1 | 1 | 0 | Hypothetical protein (2) | | Retrotransposon gag domain [IPR005162] (2) | scaffold_2_mRNA_2080.1 | C_unshiu_01028_mRNA_5.1 | - |
| GF0020314 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2076.1 | C_unshiu_00610_mRNA_9.1 | - |
| GF0020312 | 1 | 1 | 0 | Hypothetical protein (2) | | NAD(P)-binding domain [IPR016040] (1); NmrA-like domain [IPR008030] (1) | scaffold_2_mRNA_2065.1 | C_unshiu_01013_mRNA_5.1 | - |
| GF0020311 | 1 | 1 | 0 | Putative non-LTR reverse transcriptase (1); Putative pol polyprotein (1) | | | scaffold_2_mRNA_2063.1 | C_unshiu_00044_mRNA_73.1 | - |
| GF0020310 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2055.1 | C_unshiu_00909_mRNA_3.1 | - |
| GF0020309 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2046.1 | C_unshiu_01300_mRNA_2.1 | - |
| GF0020308 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2040.1 | C_unshiu_00915_mRNA_17.1 | - |
| GF0020307 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2039.1 | C_unshiu_00915_mRNA_18.1 | - |
| GF0020306 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2038.1 | C_unshiu_00915_mRNA_19.1 | - |
| GF0020305 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2034.1 | C_unshiu_01201_mRNA_2.1 | - |
| GF0020302 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2024.1 | C_unshiu_00533_mRNA_1.1 | - |
| GF0020301 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2022.1 | C_unshiu_00533_mRNA_3.1 | - |
| GF0020300 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2021.1 | C_unshiu_00533_mRNA_4.1 | - |
| GF0020299 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_2_mRNA_2014.1 | C_unshiu_00059_mRNA_11.1 | - |
| GF0020298 | 1 | 1 | 0 | Hypothetical protein (2) | | Retrotransposon gag domain [IPR005162] (2) | scaffold_2_mRNA_2012.1 | C_unshiu_00533_mRNA_12.1 | - |
| GF0020297 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_2011.1 | C_unshiu_00533_mRNA_13.1 | - |
| GF0020296 | 1 | 1 | 0 | Hypothetical protein (2) | 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_2006.1 | C_unshiu_01875_mRNA_1.1 | - |
| GF0020295 | 1 | 1 | 0 | Transmembrane E3 ubiquitin-protein ligase 1 (1); Hypothetical protein (1) | zinc ion binding [GO:0008270 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1) | Zinc finger, RING-type [IPR001841] (1); Zinc finger, RING-CH-type [IPR011016] (1); Zinc finger, RING/FYVE/PHD-type [IPR013083] (1) | scaffold_2_mRNA_2005.1 | C_unshiu_01875_mRNA_3.1 | - |
| GF0020292 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_200.1 | C_unshiu_00464_mRNA_7.1 | - |
| GF0020291 | 1 | 1 | 0 | Hypothetical protein (2) | protein binding [GO:0005515 molecular_function] (2) | Leucine-rich repeat [IPR001611] (2); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2) | scaffold_2_mRNA_20.1 | C_unshiu_00109_mRNA_17.1 | - |
| GF0020290 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_199.1 | C_unshiu_00464_mRNA_6.1 | - |
| GF0020289 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1988.1 | C_unshiu_00231_mRNA_39.1 | - |
| GF0020288 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1981.1 | C_unshiu_00030_mRNA_15.1 | - |
| GF0020287 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1974.1 | C_unshiu_00030_mRNA_20.1 | - |
| GF0020286 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1973.1 | C_unshiu_00030_mRNA_21.1 | - |
| GF0020285 | 1 | 1 | 0 | Retrotransposon protein, putative, Ty1-copia subclass (2) | | | scaffold_2_mRNA_1972.1 | C_unshiu_00030_mRNA_22.1 | - |
| GF0020284 | 1 | 1 | 0 | Nicotianamine aminotransferase A (2) | pyridoxal phosphate binding [GO:0030170 molecular_function] (2); cellular amino acid metabolic process [GO:0006520 biological_process] (2); catalytic activity [GO:0003824 molecular_function] (2); biosynthetic process [GO:0009058 biological_process] (2); transaminase activity [GO:0008483 molecular_function] (2) | Pyridoxal phosphate-dependent transferase, major region, subdomain 1 [IPR015421] (2); Aminotransferase, class I/classII [IPR004839] (2); Pyridoxal phosphate-dependent transferase [IPR015424] (2); Tyrosine/nicotianamine aminotransferase [IPR005958] (2); Pyridoxal phosphate-dependent transferase, subdomain 2 [IPR015422] (1); Pyridoxal phosphate-dependent transferase, major region, subdomain 2 [IPR015422] (1) | scaffold_2_mRNA_1969.1 | C_unshiu_00030_mRNA_24.1 | - |
| GF0020283 | 1 | 1 | 0 | Hypothetical protein (1); Ribonuclease H protein (1) | nucleic acid binding [GO:0003676 molecular_function] (2); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (2) | Ribonuclease H domain [IPR002156] (2); Ribonuclease H-like domain [IPR012337] (2); TB2/DP1/HVA22-related protein [IPR004345] (1) | scaffold_2_mRNA_1967.1 | C_unshiu_00030_mRNA_26.1 | - |
| GF0020282 | 1 | 1 | 0 | Hypothetical protein (2) | transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (2); metabolic process [GO:0008152 biological_process] (2) | UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (2) | scaffold_2_mRNA_1960.1 | C_unshiu_00030_mRNA_33.1 | - |
| GF0020281 | 1 | 1 | 0 | Nicotianamine aminotransferase A (1); Tyrosine transaminase (1) | catalytic activity [GO:0003824 molecular_function] (2); biosynthetic process [GO:0009058 biological_process] (2); pyridoxal phosphate binding [GO:0030170 molecular_function] (2) | Pyridoxal phosphate-dependent transferase, major region, subdomain 1 [IPR015421] (2); Aminotransferase, class I/classII [IPR004839] (2); Pyridoxal phosphate-dependent transferase [IPR015424] (2); Pyridoxal phosphate-dependent transferase, subdomain 2 [IPR015422] (1); Pyridoxal phosphate-dependent transferase, major region, subdomain 2 [IPR015422] (1) | scaffold_2_mRNA_1955.1 | C_unshiu_00030_mRNA_37.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0020280 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1946.1 | C_unshiu_00030_mRNA_47.1 | - |
| GF0020279 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1941.1 | C_unshiu_00030_mRNA_51.1 | - |
| GF0020278 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1940.1 | C_unshiu_00030_mRNA_52.1 | - |
| GF0020277 | 1 | 1 | 0 | Hypothetical protein (2) | | LOG family [IPR031100] (1) | scaffold_2_mRNA_194.1 | C_unshiu_00478_mRNA_17.1 | - |
| GF0020276 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1939.1 | C_unshiu_00030_mRNA_53.1 | - |
| GF0020275 | 1 | 1 | 0 | Hypothetical protein (2) | 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_2_mRNA_1938.1 | C_unshiu_00030_mRNA_54.1 | - |
| GF0020274 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1925.1 | C_unshiu_00804_mRNA_2.1 | - |
| GF0020273 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1924.1 | C_unshiu_00804_mRNA_3.1 | - |
| GF0020272 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1921.1 | C_unshiu_00804_mRNA_5.1 | - |
| GF0020271 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1918.1 | C_unshiu_00804_mRNA_7.1 | - |
| GF0020270 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1917.1 | C_unshiu_00804_mRNA_8.1 | - |
| GF0020269 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1916.1 | C_unshiu_00804_mRNA_9.1 | - |
| GF0020268 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1913.1 | C_unshiu_00804_mRNA_11.1 | - |
| GF0020267 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1912.1 | C_unshiu_00804_mRNA_12.1 | - |
| GF0020264 | 1 | 1 | 0 | Hypothetical protein (2) | | Prefoldin alpha-like [IPR004127] (2); Prefoldin [IPR009053] (1) | scaffold_2_mRNA_1897.1 | C_unshiu_01608_mRNA_1.1 | - |
| GF0020263 | 1 | 1 | 0 | Hypothetical protein (2) | zinc ion binding [GO:0008270 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | Zinc finger, CCHC-type [IPR001878] (2) | scaffold_2_mRNA_1896.1 | C_unshiu_00906_mRNA_3.1 | - |
| GF0020262 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1895.1 | C_unshiu_01352_mRNA_5.1 | - |
| GF0020261 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1893.1 | C_unshiu_02033_mRNA_4.1 | - |
| GF0020260 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1889.1 | C_unshiu_01390_mRNA_4.1 | - |
| GF0020259 | 1 | 1 | 0 | Hypothetical protein (2) | DNA binding [GO:0003677 molecular_function] (2); transcription, DNA-templated [GO:0006351 biological_process] (2); DNA-directed RNA polymerase activity [GO:0003899 molecular_function] (1); DNA-directed 5'-3' RNA polymerase activity [GO:0003899 molecular_function] (1) | RNA polymerase Rpb1, domain 5 [IPR007081] (2) | scaffold_2_mRNA_1888.1 | C_unshiu_01390_mRNA_5.1 | - |
| GF0020258 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1886.1 | C_unshiu_01390_mRNA_7.1 | - |
| GF0020257 | 1 | 1 | 0 | Hypothetical protein (2) | zinc ion binding [GO:0008270 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | Zinc finger, CCHC-type [IPR001878] (2) | scaffold_2_mRNA_1885.1 | C_unshiu_02183_mRNA_3.1 | - |
| GF0020256 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1877.1 | C_unshiu_00543_mRNA_6.1 | - |
| GF0020255 | 1 | 1 | 0 | Hypothetical protein (2) | | Transposon, En/Spm-like [IPR004242] (2) | scaffold_2_mRNA_1876.1 | C_unshiu_00543_mRNA_7.1 | - |
| GF0020254 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1873.1 | C_unshiu_00543_mRNA_9.1 | - |
| GF0020252 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1864.1 | C_unshiu_00856_mRNA_2.1 | - |
| GF0020251 | 1 | 1 | 0 | Hypothetical protein (2) | | MULE transposase domain [IPR018289] (1) | scaffold_2_mRNA_1856.1 | C_unshiu_01560_mRNA_5.1 | - |
| GF0020250 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_185.1 | C_unshiu_01376_mRNA_5.1 | - |
| GF0020249 | 1 | 1 | 0 | MYB family protein (2) | DNA binding [GO:0003677 molecular_function] (2) | Homeobox domain-like [IPR009057] (1); Homeodomain-like [IPR009057] (1); Myb-like domain [IPR017877] (1) | scaffold_2_mRNA_1849.1 | C_unshiu_00114_mRNA_32.1 | - |
| GF0020248 | 1 | 1 | 0 | Hypothetical protein (2) | DNA binding [GO:0003677 molecular_function] (2) | hAT-like transposase, RNase-H fold [IPR025525] (2) | scaffold_2_mRNA_1840.1 | C_unshiu_00114_mRNA_40.1 | - |
| GF0020247 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1837.1 | C_unshiu_00114_mRNA_42.1 | - |
| GF0020246 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1832.1 | C_unshiu_01906_mRNA_4.1 | - |
| GF0020243 | 1 | 1 | 0 | Putative non-LTR retrolelement reverse transcriptase (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_2_mRNA_1827.1 | C_unshiu_00349_mRNA_27.1 | - |
| GF0020242 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1823.1 | C_unshiu_01464_mRNA_1.1 | - |
| GF0020241 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1822.1 | C_unshiu_01464_mRNA_2.1 | - |
| GF0020240 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1821.1 | C_unshiu_01464_mRNA_3.1 | - |
| GF0020239 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1819.1 | C_unshiu_01464_mRNA_5.1 | - |
| GF0020238 | 1 | 1 | 0 | Glyceraldehyde-3-phosphate dehydrogenase 1, cytosolic (2) | oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor [GO:0016620 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2) | Glyceraldehyde 3-phosphate dehydrogenase, catalytic domain [IPR020829] (2); Glyceraldehyde 3-phosphate dehydrogenase, NAD(P) binding domain [IPR020828] (2); NAD(P)-binding domain [IPR016040] (2); Glyceraldehyde 3-phosphate dehydrogenase, active site [IPR020830] (2); Glyceraldehyde/Erythrose phosphate dehydrogenase family [IPR020831] (2) | scaffold_2_mRNA_1814.1 | C_unshiu_00767_mRNA_4.1 | - |
| GF0020237 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1808.1 | C_unshiu_00466_mRNA_10.1 | - |
| GF0020236 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1803.1 | C_unshiu_00466_mRNA_5.1 | - |
| GF0020235 | 1 | 1 | 0 | Hypothetical protein (2) | ATP binding [GO:0005524 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2); protein serine/threonine kinase activity [GO:0004674 molecular_function] (2); protein kinase activity [GO:0004672 molecular_function] (2) | S-locus receptor kinase, C-terminal [IPR021820] (2); Bulb-type lectin domain [IPR001480] (2); Protein kinase domain [IPR000719] (2); Protein kinase-like domain [IPR011009] (2); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); Serine/threonine/dual specificity protein kinase, catalytic  domain [IPR002290] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1) | scaffold_2_mRNA_1794.1 | C_unshiu_01820_mRNA_1.1 | - |
| GF0020233 | 1 | 1 | 0 | Mitochondrial transcription termination factor family protein, putative (1); Hypothetical protein (1) | mitochondrion [GO:0005739 cellular_component] (1); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1); double-stranded DNA binding [GO:0003690 molecular_function] (1) | Mitochodrial transcription termination factor [IPR003690] (1) | scaffold_2_mRNA_1772.1 | C_unshiu_01458_mRNA_3.1 | - |
| GF0020232 | 1 | 1 | 0 | Myosin-H heavy chain (2) | | EEIG1/EHBP1 N-terminal domain [IPR019448] (2) | scaffold_2_mRNA_1769.1 | C_unshiu_01458_mRNA_7.1 | - |
| GF0020231 | 1 | 1 | 0 | UPF0481 protein (2) | | Protein of unknown function DUF247, plant [IPR004158] (2) | scaffold_2_mRNA_1767.1 | C_unshiu_01738_mRNA_5.1 | - |
| GF0020229 | 1 | 1 | 0 | Monosacharide transport protein (2) | | | scaffold_2_mRNA_1743.1 | C_unshiu_01178_mRNA_6.1 | - |
| GF0020228 | 1 | 1 | 0 | LRR receptor-like serine/threonine-protein kinase ERL2 (1); Leucine-rich repeat receptor-like protein kinase PXL1 (1) | protein binding [GO:0005515 molecular_function] (2) | Leucine-rich repeat [IPR001611] (2); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Leucine-rich repeat, typical subtype [IPR003591] (2) | scaffold_2_mRNA_1740.1 | C_unshiu_01178_mRNA_8.1 | - |
| GF0020227 | 1 | 1 | 0 | Hypothetical protein (2) | | Leucine-rich repeat domain, L domain-like [IPR032675] (2); Nucleotide-diphospho-sugar transferase [IPR005069] (2) | scaffold_2_mRNA_1733.1 | C_unshiu_01421_mRNA_2.1 | - |
| GF0020226 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1729.1 | C_unshiu_01869_mRNA_1.1 | - |
| GF0020225 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1726.1 | C_unshiu_01421_mRNA_6.1 | - |
| GF0020224 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1716.1 | C_unshiu_01990_mRNA_5.1 | - |
| GF0020223 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1705.1 | C_unshiu_01629_mRNA_11.1 | - |
| GF0020222 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1702.1 | C_unshiu_01629_mRNA_8.1 | - |
| GF0020221 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1700.1 | C_unshiu_01629_mRNA_6.1 | - |
| GF0020220 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1692.1 | C_unshiu_00125_mRNA_10.1 | - |
| GF0020219 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1680.1 | C_unshiu_01058_mRNA_4.1 | - |
| GF0020218 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1678.1 | C_unshiu_01058_mRNA_2.1 | - |
| GF0020217 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1677.1 | C_unshiu_01058_mRNA_1.1 | - |
| GF0020216 | 1 | 1 | 0 | Hypothetical protein (2) | regulation of transcription, DNA-templated [GO:0006355 biological_process] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | Carlavirus nucleic acid-binding protein [IPR002568] (2) | scaffold_2_mRNA_1640.1 | C_unshiu_00744_mRNA_13.1 | - |
| GF0020214 | 1 | 1 | 0 | Hypothetical protein (2) | cysteine-type peptidase activity [GO:0008234 molecular_function] (2); proteolysis [GO:0006508 biological_process] (2) | Ulp1 protease family, C-terminal catalytic domain [IPR003653] (2) | scaffold_2_mRNA_1634.1 | C_unshiu_01700_mRNA_9.1 | - |
| GF0020213 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1609.1 | C_unshiu_02477_mRNA_4.1 | - |
| GF0020212 | 1 | 1 | 0 | Hypothetical protein (2) | | Retrotransposon gag domain [IPR005162] (2) | scaffold_2_mRNA_1608.1 | C_unshiu_00636_mRNA_14.1 | - |
| GF0020211 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1607.1 | C_unshiu_00636_mRNA_13.1 | - |
| GF0020209 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_156.1 | C_unshiu_01201_mRNA_9.1 | - |
| GF0020208 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_2_mRNA_1555.1 | C_unshiu_00026_mRNA_8.1 | - |
| GF0020205 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_155.1 | C_unshiu_01201_mRNA_8.1 | - |
| GF0020203 | 1 | 1 | 0 | Histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH4 (2) | histone lysine methylation [GO:0034968 biological_process] (2); nucleus [GO:0005634 cellular_component] (2); zinc ion binding [GO:0008270 molecular_function] (2); histone-lysine N-methyltransferase activity [GO:0018024 molecular_function] (2); protein binding [GO:0005515 molecular_function] (2) | Pre-SET domain [IPR007728] (2); SET domain [IPR001214] (2); Post-SET domain [IPR003616] (2) | scaffold_2_mRNA_1546.1 | C_unshiu_00026_mRNA_12.1 | - |
| GF0020202 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_154.1 | C_unshiu_01201_mRNA_7.1 | - |
| GF0020201 | 1 | 1 | 0 | Aminopeptidase (2) | | Protein of unknown function DUF3754 [IPR022227] (2) | scaffold_2_mRNA_1536.1 | C_unshiu_00026_mRNA_22.1 | - |
| GF0020199 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_153.1 | C_unshiu_01201_mRNA_6.1 | - |
| GF0020198 | 1 | 1 | 0 | Hypothetical protein (2) | structural constituent of ribosome [GO:0003735 molecular_function] (2); intracellular [GO:0005622 cellular_component] (2); translation [GO:0006412 biological_process] (2); ribosome [GO:0005840 cellular_component] (2) | Ribosomal protein S27e, zinc-binding domain [IPR023407] (2); Ribosomal protein S27e [IPR000592] (2); Zinc-binding ribosomal protein [IPR011332] (2) | scaffold_2_mRNA_1518.1 | C_unshiu_00653_mRNA_12.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0020196 | 1 | 1 | 0 | Hypothetical protein (2) | ATP binding [GO:0005524 molecular_function] (2); nucleotide binding [GO:0000166 molecular_function] (2); RNA binding [GO:0003723 molecular_function] (2); tRNA aminoacylation for protein translation [GO:0006418 biological_process] (2); cytoplasm [GO:0005737 cellular_component] (2); tyrosyl-tRNA aminoacylation [GO:0006437 biological_process] (2); aminoacyl-tRNA ligase activity [GO:0004812 molecular_function] (2); tyrosine-tRNA ligase activity [GO:0004831 molecular_function] (2) | Tyrosine-tRNA ligase, bacterial-type, type 1 [IPR024107] (2); Rossmann-like alpha/beta/alpha sandwich fold [IPR014729] (2); Tyrosine-tRNA ligase [IPR002307] (2); Aminoacyl-tRNA synthetase, class Ic [IPR002305] (2); RNA-binding S4 domain [IPR002942] (2); Aminoacyl-tRNA synthetase, class I, conserved site [IPR001412] (2); Tyrosine-tRNA ligase, bacterial-type [IPR024088] (2) | scaffold_2_mRNA_1498.1 | C_unshiu_00957_mRNA_10.1 | - |
| GF0020195 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1489.1 | C_unshiu_00999_mRNA_2.1 | - |
| GF0020193 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_148.1 | C_unshiu_00174_mRNA_32.1 | - |
| GF0020192 | 1 | 1 | 0 | Pentatricopeptide repeat-containing protein, mitochondrial (2) | protein binding [GO:0005515 molecular_function] (1) | Pentatricopeptide repeat [IPR002885] (2); Tetratricopeptide-like helical domain [IPR011990] (1) | scaffold_2_mRNA_1479.1 | C_unshiu_00999_mRNA_10.1 | - |
| GF0020191 | 1 | 1 | 0 | Hypothetical protein (2) | zinc ion binding [GO:0008270 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | Zinc finger, CCHC-type [IPR001878] (2) | scaffold_2_mRNA_147.1 | C_unshiu_00174_mRNA_31.1 | - |
| GF0020190 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1460.1 | C_unshiu_00016_mRNA_6.1 | - |
| GF0020186 | 1 | 1 | 0 | Phospholipase A1 (2) | lipid metabolic process [GO:0006629 biological_process] (2); phosphatidylcholine 1-acylhydrolase activity [GO:0008970 molecular_function] (1) | Fungal lipase-like domain [IPR002921] (2); Alpha/Beta hydrolase fold [IPR029058] (2); Phospholipase A1-II [IPR033556] (1) | scaffold_2_mRNA_1451.1 | C_unshiu_00184_mRNA_16.1 | - |
| GF0020185 | 1 | 1 | 0 | Hypothetical protein (2) | | Reverse transcriptase domain [IPR000477] (2) | scaffold_2_mRNA_145.1 | C_unshiu_00174_mRNA_28.1 | - |
| GF0020184 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (1) | Ribonuclease H-like domain [IPR012337] (1) | scaffold_2_mRNA_1448.1 | C_unshiu_00184_mRNA_18.1 | - |
| GF0020182 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_144.1 | C_unshiu_00174_mRNA_27.1 | - |
| GF0020181 | 1 | 1 | 0 | Cytokinin riboside 5'-monophosphate phosphoribohydrolase (2) | | LOG family [IPR031100] (2); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (2) | scaffold_2_mRNA_143.1 | C_unshiu_00174_mRNA_25.1 | - |
| GF0020180 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_142.1 | C_unshiu_00174_mRNA_24.1 | - |
| GF0020179 | 1 | 1 | 0 | Hypothetical protein (2) | drug transmembrane transport [GO:0006855 biological_process] (2); antiporter activity [GO:0015297 molecular_function] (2); drug transmembrane transporter activity [GO:0015238 molecular_function] (2); membrane [GO:0016020 cellular_component] (2); transmembrane transport [GO:0055085 biological_process] (2) | Multi antimicrobial extrusion protein [IPR002528] (2) | scaffold_2_mRNA_1413.1 | C_unshiu_00184_mRNA_38.1 | - |
| GF0020178 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1411.1 | C_unshiu_00176_mRNA_19.1 | - |
| GF0020177 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_141.1 | C_unshiu_00174_mRNA_23.1 | - |
| GF0020176 | 1 | 1 | 0 | Verticillium wilt disease resistance protein (1); Verticillium wilt resistance-like protein (1) | protein binding [GO:0005515 molecular_function] (2) | Leucine-rich repeat [IPR001611] (2); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Leucine-rich repeat, typical subtype [IPR003591] (2) | scaffold_2_mRNA_1408.1 | C_unshiu_00176_mRNA_21.1 | - |
| GF0020175 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1400.1 | C_unshiu_00176_mRNA_28.1 | - |
| GF0020174 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_140.1 | C_unshiu_01119_mRNA_10.1 | - |
| GF0020173 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1394.1 | C_unshiu_00176_mRNA_31.1 | - |
| GF0020172 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1392.1 | C_unshiu_00068_mRNA_32.1 | - |
| GF0020171 | 1 | 1 | 0 | Phospholipase A1-II 7 (1); Hypothetical protein (1) | phosphatidylcholine 1-acylhydrolase activity [GO:0008970 molecular_function] (1); lipid metabolic process [GO:0006629 biological_process] (1) | Fungal lipase-like domain [IPR002921] (1); Alpha/Beta hydrolase fold [IPR029058] (1); Phospholipase A1-II [IPR033556] (1) | scaffold_2_mRNA_1387.1 | C_unshiu_00176_mRNA_34.1 | - |
| GF0020170 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1378.1 | C_unshiu_00859_mRNA_2.1 | - |
| GF0020169 | 1 | 1 | 0 | Carbohydrate-binding X8 domain protein (2) | | X8 domain [IPR012946] (2) | scaffold_2_mRNA_1371.1 | C_unshiu_00176_mRNA_47.1 | - |
| GF0020167 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1345.1 | C_unshiu_00107_mRNA_9.1 | - |
| GF0020166 | 1 | 1 | 0 | Hypothetical protein (2) | | Domain of unknown function DUF4283 [IPR025558] (2) | scaffold_2_mRNA_133.1 | C_unshiu_00691_mRNA_14.1 | - |
| GF0020165 | 1 | 1 | 0 | DnaJ like subfamily B member 13 (2) | unfolded protein binding [GO:0051082 molecular_function] (2); protein folding [GO:0006457 biological_process] (2) | HSP40/DnaJ peptide-binding [IPR008971] (2); Chaperone DnaJ, C-terminal [IPR002939] (2) | scaffold_2_mRNA_1323.1 | C_unshiu_00403_mRNA_11.1 | - |
| GF0020164 | 1 | 1 | 0 | Hypothetical protein (2) | | WHIM2 domain [IPR028941] (2); WHIM1 domain [IPR028942] (1); WHIM3 domain [IPR028935] (1) | scaffold_2_mRNA_1322.1 | C_unshiu_00403_mRNA_10.1 | - |
| GF0020163 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1317.1 | C_unshiu_00403_mRNA_4.1 | - |
| GF0020162 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_130.1 | C_unshiu_00799_mRNA_12.1 | - |
| GF0020161 | 1 | 1 | 0 | Glycerol-3-phosphate dehydrogenase [NAD(+)] GPDHC1, cytosolic (2) | oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor [GO:0016616 molecular_function] (2); NAD binding [GO:0051287 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2); oxidoreductase activity [GO:0016491 molecular_function] (2); glycerol-3-phosphate dehydrogenase [NAD+] activity [GO:0004367 molecular_function] (2); glycerol-3-phosphate catabolic process [GO:0046168 biological_process] (2); glycerol-3-phosphate dehydrogenase complex [GO:0009331 cellular_component] (2); protein homodimerization activity [GO:0042803 molecular_function] (2); glycerol-3-phosphate metabolic process [GO:0006072 biological_process] (2); carbohydrate metabolic process [GO:0005975 biological_process] (2) | Glycerol-3-phosphate dehydrogenase, NAD-dependent, N-terminal [IPR011128] (2); Glycerol-3-phosphate dehydrogenase, NAD-dependent, C-terminal [IPR006109] (2); NAD(P)-binding domain [IPR016040] (2); Glycerol-3-phosphate dehydrogenase, NAD-dependent [IPR006168] (2); 6-phosphogluconate dehydrogenase C-terminal domain-like [IPR008927] (2); 6-phosphogluconate dehydrogenase, domain 2 [IPR013328] (2); Glycerol-3-phosphate dehydrogenase, NAD-dependent, eukaryotic [IPR017751] (2) | scaffold_2_mRNA_1292.1 | C_unshiu_00055_mRNA_53.1 | - |
| GF0020160 | 1 | 1 | 0 | Hypothetical protein (2) | | Sieve element occlusion, N-terminal [IPR027942] (2) | scaffold_2_mRNA_1287.1 | C_unshiu_00055_mRNA_56.1 | - |
| GF0020158 | 1 | 1 | 0 | Polynucleotidyl transferase, Ribonuclease H fold (2) | nucleic acid binding [GO:0003676 molecular_function] (2); nucleotide binding [GO:0000166 molecular_function] (1) | Ribonuclease H-like domain [IPR012337] (2); Reverse transcriptase zinc-binding domain [IPR026960] (2); RNA recognition motif domain [IPR000504] (2); Nucleotide-binding alpha-beta plait domain [IPR012677] (1) | scaffold_2_mRNA_1282.1 | C_unshiu_01160_mRNA_11.1 | - |
| GF0020157 | 1 | 1 | 0 | Hypothetical protein (1); Non-LTR retroelement reverse transcriptase-like (1) | nucleic acid binding [GO:0003676 molecular_function] (1) | Reverse transcriptase zinc-binding domain [IPR026960] (2); Ribonuclease H-like domain [IPR012337] (1) | scaffold_2_mRNA_1279.1 | C_unshiu_01160_mRNA_8.1 | - |
| GF0020156 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_127.1 | C_unshiu_00799_mRNA_10.1 | - |
| GF0020155 | 1 | 1 | 0 | E3 ubiquitin-protein ligase RGLG2 (2) | zinc ion binding [GO:0008270 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1) | von Willebrand factor, type A [IPR002035] (2); Copine [IPR010734] (2); Zinc finger, RING-type [IPR001841] (1); Zinc finger, RING/FYVE/PHD-type [IPR013083] (1) | scaffold_2_mRNA_1269.1 | C_unshiu_00052_mRNA_11.2 | - |
| GF0020154 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1243.1 | C_unshiu_00049_mRNA_21.1 | - |
| GF0020153 | 1 | 1 | 0 | Hypothetical protein (2) | protein binding [GO:0005515 molecular_function] (1) | Pentatricopeptide repeat [IPR002885] (2); Tetratricopeptide-like helical domain [IPR011990] (1) | scaffold_2_mRNA_1242.1 | C_unshiu_00049_mRNA_22.1 | - |
| GF0020152 | 1 | 1 | 0 | Myb-related protein Myb4 (2) | DNA binding [GO:0003677 molecular_function] (2) | SANT/Myb domain [IPR001005] (2); Myb domain [IPR017930] (2); Homeodomain-like [IPR009057] (1); Homeobox domain-like [IPR009057] (1) | scaffold_2_mRNA_1232.1 | C_unshiu_00049_mRNA_42.1 | - |
| GF0020151 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_123.1 | C_unshiu_00799_mRNA_7.1 | - |
| GF0020150 | 1 | 1 | 0 | Dual specificity mitogen-activated protein kinase kinase 1 (2) | ATP binding [GO:0005524 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2); protein kinase activity [GO:0004672 molecular_function] (2) | Protein kinase-like domain [IPR011009] (2); Nuclear transport factor 2, eukaryote [IPR018222] (2); Protein kinase domain [IPR000719] (2); Protein kinase, ATP binding site [IPR017441] (2); NTF2-like domain [IPR032710] (2); Serine/threonine-protein kinase, active site [IPR008271] (2); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1) | scaffold_2_mRNA_1224.1 | C_unshiu_00049_mRNA_51.1 | - |
| GF0020149 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_122.1 | C_unshiu_00799_mRNA_6.1 | - |
| GF0020147 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1210.1 | C_unshiu_00049_mRNA_66.1 | - |
| GF0020146 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_121.1 | C_unshiu_00799_mRNA_5.1 | - |
| GF0020145 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1195.1 | C_unshiu_00049_mRNA_76.1 | - |
| GF0020144 | 1 | 1 | 0 | Glutaredoxin (2) | cell redox homeostasis [GO:0045454 biological_process] (2); electron carrier activity [GO:0009055 molecular_function] (2); protein disulfide oxidoreductase activity [GO:0015035 molecular_function] (2) | Thioredoxin-like fold [IPR012336] (2); Glutaredoxin, eukaryotic/virial [IPR011899] (2); Glutaredoxin [IPR002109] (2); Glutaredoxin active site [IPR011767] (2); Glutaredoxin subgroup [IPR014025] (2) | scaffold_2_mRNA_1193.1 | C_unshiu_00049_mRNA_78.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0020143 | 1 | 1 | 0 | Glycogen synthase kinase-3 MsK-3 (2) | protein phosphorylation [GO:0006468 biological_process] (2); protein kinase activity [GO:0004672 molecular_function] (2); ATP binding [GO:0005524 molecular_function] (2) | Protein kinase domain [IPR000719] (2); Protein kinase-like domain [IPR011009] (2); Serine/threonine-protein kinase, active site [IPR008271] (2); Protein kinase, ATP binding site [IPR017441] (2); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1) | scaffold_2_mRNA_1182.1 | C_unshiu_00067_mRNA_7.1 | - |
| GF0020142 | 1 | 1 | 0 | Hypothetical protein (2) | 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_118.1 | C_unshiu_00188_mRNA_27.1 | - |
| GF0020140 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1163.1 | C_unshiu_00067_mRNA_26.1 | - |
| GF0020138 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_114.1 | C_unshiu_00456_mRNA_18.1 | - |
| GF0020137 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1139.1 | C_unshiu_00044_mRNA_24.1 | - |
| GF0020136 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1134.1 | C_unshiu_00067_mRNA_56.1 | - |
| GF0020135 | 1 | 1 | 0 | Ubiquitin-conjugating enzyme E2 5 (2) | | Ubiquitin-conjugating enzyme/RWD-like [IPR016135] (2); Ubiquitin-conjugating enzyme, active site [IPR023313] (2); Ubiquitin-conjugating enzyme E2 [IPR000608] (2) | scaffold_2_mRNA_1129.1 | C_unshiu_00189_mRNA_51.1 | - |
| GF0020134 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1124.1 | C_unshiu_00189_mRNA_46.1 | - |
| GF0020133 | 1 | 1 | 0 | Protease Do-like 9 (2) | protein binding [GO:0005515 molecular_function] (2); serine-type endopeptidase activity [GO:0004252 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1) | Peptidase S1, PA clan [IPR009003] (2); PDZ domain [IPR001478] (2); Peptidase S1C [IPR001940] (1) | scaffold_2_mRNA_1120.1 | C_unshiu_00189_mRNA_40.1 | - |
| GF0020132 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_112.1 | C_unshiu_00456_mRNA_17.1 | - |
| GF0020131 | 1 | 1 | 0 | Nodulin MtN21/EamA-like transporter family protein (2) | integral component of membrane [GO:0016021 cellular_component] (2); membrane [GO:0016020 cellular_component] (2); transmembrane transporter activity [GO:0022857 molecular_function] (2) | EamA domain [IPR000620] (2); WAT1-related protein [IPR030184] (2) | scaffold_2_mRNA_1119.1 | C_unshiu_00189_mRNA_39.1 | - |
| GF0020129 | 1 | 1 | 0 | Trichome birefringence-like 26 (2) | | Altered xyloglucan 4-like [IPR029975] (2); PC-Esterase [IPR026057] (2); PMR5 N-terminal domain [IPR025846] (2); Trichome birefringence-like family [IPR029962] (2) | scaffold_2_mRNA_1110.1 | C_unshiu_00189_mRNA_30.1 | - |
| GF0020128 | 1 | 1 | 0 | Hypothetical protein (2) | | Domain of unknown function DUF4283 [IPR025558] (2) | scaffold_2_mRNA_11.1 | C_unshiu_00109_mRNA_9.1 | - |
| GF0020127 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_109.1 | C_unshiu_00652_mRNA_1.1 | - |
| GF0020126 | 1 | 1 | 0 | Carboxypeptidase (2) | proteolysis [GO:0006508 biological_process] (2); serine-type carboxypeptidase activity [GO:0004185 molecular_function] (2) | Peptidase S10, serine carboxypeptidase [IPR001563] (2); Alpha/Beta hydrolase fold [IPR029058] (2) | scaffold_2_mRNA_1087.1 | C_unshiu_00494_mRNA_13.1 | - |
| GF0020125 | 1 | 1 | 0 | F-box protein SKIP23 (2) | protein binding [GO:0005515 molecular_function] (2) | F-box domain [IPR001810] (2); Domain unknown function DUF295 [IPR005174] (2); Kelch-type beta propeller [IPR015915] (1) | scaffold_2_mRNA_1086.1 | C_unshiu_00494_mRNA_12.1 | - |
| GF0020123 | 1 | 1 | 0 | Nse1 non-SMC component of SMC5-6 complex family protein (2) | Smc5-Smc6 complex [GO:0030915 cellular_component] (2); DNA repair [GO:0006281 biological_process] (2) | Non-structural maintenance of chromosomes element 1 [IPR011513] (2); Zinc finger, RING-like [IPR014857] (1); Zinc finger, RING/FYVE/PHD-type [IPR013083] (1) | scaffold_2_mRNA_1069.1 | C_unshiu_00235_mRNA_6.1 | - |
| GF0020122 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1061.1 | C_unshiu_00235_mRNA_17.1 | - |
| GF0020121 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1051.1 | C_unshiu_00235_mRNA_26.1 | - |
| GF0020120 | 1 | 1 | 0 | Hypothetical protein (2) | protein binding [GO:0005515 molecular_function] (1) | Pentatricopeptide repeat [IPR002885] (2); Tetratricopeptide-like helical domain [IPR011990] (1) | scaffold_2_mRNA_1050.1 | C_unshiu_00235_mRNA_27.1 | - |
| GF0020119 | 1 | 1 | 0 | Transcription factor bHLH36 (2) | protein dimerization activity [GO:0046983 molecular_function] (2); DNA binding [GO:0003677 molecular_function] (2) | Myc-type, basic helix-loop-helix (bHLH) domain [IPR011598] (2); Achaete-scute transcription factor-related [IPR015660] (2) | scaffold_2_mRNA_1049.1 | C_unshiu_00235_mRNA_28.1 | - |
| GF0020118 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1047.1 | C_unshiu_00235_mRNA_30.1 | - |
| GF0020116 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_102.1 | C_unshiu_00652_mRNA_6.1 | - |
| GF0020115 | 1 | 1 | 0 | Hyp O-arabinosyltransferase homolog (2) | | | scaffold_2_mRNA_1015.1 | C_unshiu_00050_mRNA_51.1 | - |
| GF0020114 | 1 | 1 | 0 | AT-hook motif nuclear-localized protein 17 (2) | | PPC domain [IPR005175] (2); AT-hook motif nuclear-localised protein [IPR014476] (2) | scaffold_2_mRNA_1014.1 | C_unshiu_00050_mRNA_52.1 | - |
| GF0020113 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_1013.1 | C_unshiu_00050_mRNA_53.1 | - |
| GF0020112 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_2_mRNA_101.1 | C_unshiu_00652_mRNA_7.1 | - |
| GF0020111 | 1 | 1 | 0 | Hypothetical protein (1); Alcohol acyltransferase (1) | transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (2) | Transferase [IPR003480] (2); Chloramphenicol acetyltransferase-like domain [IPR023213] (1) | scaffold_2_mRNA_1000.1 | C_unshiu_00514_mRNA_6.1 | - |
| GF0020110 | 1 | 1 | 0 | Profilin (2) | actin binding [GO:0003779 molecular_function] (2) | Profilin conserved site [IPR027310] (2); Profilin [IPR005455] (2) | scaffold_1_mRNA_986.1 | C_unshiu_00191_mRNA_24.1 | - |
| GF0020109 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_982.1 | C_unshiu_00191_mRNA_28.1 | - |
| GF0020108 | 1 | 1 | 0 | Aspartic proteinase nepenthesin-2 (2) | aspartic-type endopeptidase activity [GO:0004190 molecular_function] (2); proteolysis [GO:0006508 biological_process] (2) | Aspartic peptidase domain [IPR021109] (2); Peptidase family A1 domain [IPR033121] (2); Aspartic peptidase A1 family [IPR001461] (2); Xylanase inhibitor, C-terminal [IPR032799] (2) | scaffold_1_mRNA_98.1 | C_unshiu_00129_mRNA_5.1 | - |
| GF0020107 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_972.1 | C_unshiu_00973_mRNA_11.1 | - |
| GF0020106 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_969.1 | C_unshiu_00973_mRNA_8.1 | - |
| GF0020105 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_964.1 | C_unshiu_00973_mRNA_3.1 | - |
| GF0020103 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_949.1 | C_unshiu_00516_mRNA_5.1 | - |
| GF0020102 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_944.1 | C_unshiu_00055_mRNA_29.1 | - |
| GF0020101 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_943.1 | C_unshiu_00055_mRNA_30.1 | - |
| GF0020100 | 1 | 1 | 0 | Hypothetical protein (2) | protein dimerization activity [GO:0046983 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2); DNA binding [GO:0003677 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2); Zinc finger, BED-type [IPR003656] (2); HAT, C-terminal dimerisation domain [IPR008906] (2); GH3 family [IPR004993] (2) | scaffold_1_mRNA_941.1 | C_unshiu_00055_mRNA_32.1 | - |
| GF0020098 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_937.1 | C_unshiu_00055_mRNA_34.1 | - |
| GF0020097 | 1 | 1 | 0 | Hypothetical protein (2) | | MULE transposase domain [IPR018289] (2) | scaffold_1_mRNA_936.1 | C_unshiu_00055_mRNA_35.1 | - |
| GF0020095 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_933.1 | C_unshiu_00055_mRNA_36.1 | - |
| GF0020094 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_927.1 | C_unshiu_00119_mRNA_23.1 | - |
| GF0020093 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_910.1 | C_unshiu_00068_mRNA_57.1 | - |
| GF0020092 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_907.1 | C_unshiu_00068_mRNA_54.1 | - |
| GF0020091 | 1 | 1 | 0 | Hypothetical protein (2) | | Domain of unknown function DUF4283 [IPR025558] (2) | scaffold_1_mRNA_903.1 | C_unshiu_00068_mRNA_50.1 | - |
| GF0020090 | 1 | 1 | 0 | Hypothetical protein (2) | protein dimerization activity [GO:0046983 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | HAT, C-terminal dimerisation domain [IPR008906] (2); Ribonuclease H-like domain [IPR012337] (2) | scaffold_1_mRNA_901.1 | C_unshiu_00068_mRNA_47.1 | - |
| GF0020089 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_896.1 | C_unshiu_00068_mRNA_43.1 | - |
| GF0020088 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_895.1 | C_unshiu_00068_mRNA_42.1 | - |
| GF0020087 | 1 | 1 | 0 | Hypothetical protein (2) | | Domain of unknown function DUF4283 [IPR025558] (2) | scaffold_1_mRNA_894.1 | C_unshiu_00068_mRNA_41.1 | - |
| GF0020086 | 1 | 1 | 0 | Novel interactor of JAZ long variant (2) | signal transduction [GO:0007165 biological_process] (2) | Ninja family [IPR031307] (2); Jas TPL-binding domain [IPR032308] (2) | scaffold_1_mRNA_888.1 | C_unshiu_00068_mRNA_36.1 | - |
| GF0020085 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_868.1 | C_unshiu_00354_mRNA_6.1 | - |
| GF0020084 | 1 | 1 | 0 | Hypothetical protein (2) | protein dimerization activity [GO:0046983 molecular_function] (2) | HAT, C-terminal dimerisation domain [IPR008906] (2) | scaffold_1_mRNA_867.1 | C_unshiu_00068_mRNA_15.1 | - |
| GF0020083 | 1 | 1 | 0 | Hypothetical protein (2) | DNA binding [GO:0003677 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (1) | Zinc finger, BED-type [IPR003656] (2); Zinc finger C2H2-type [IPR013087] (1) | scaffold_1_mRNA_866.1 | C_unshiu_00068_mRNA_14.1 | - |
| GF0020082 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_1_mRNA_865.1 | C_unshiu_00068_mRNA_13.1 | - |
| GF0020081 | 1 | 1 | 0 | Hypothetical protein (2) | lyase activity [GO:0016829 molecular_function] (2); terpene synthase activity [GO:0010333 molecular_function] (2); metabolic process [GO:0008152 biological_process] (2) | Terpene synthase, N-terminal domain [IPR001906] (2); Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (2) | scaffold_1_mRNA_864.1 | C_unshiu_00068_mRNA_12.1 | - |
| GF0020080 | 1 | 1 | 0 | Putative non-LTR retroelement reverse transcriptase (1); Ribonuclease H-like superfamily protein (1) | nucleic acid binding [GO:0003676 molecular_function] (2) | Reverse transcriptase zinc-binding domain [IPR026960] (2); Ribonuclease H-like domain [IPR012337] (2) | scaffold_1_mRNA_860.1 | C_unshiu_00331_mRNA_12.1 | - |
| GF0020079 | 1 | 1 | 0 | NAD(P)-binding Rossmann-fold superfamily protein isoform 2 (2) | coenzyme binding [GO:0050662 molecular_function] (1); catalytic activity [GO:0003824 molecular_function] (1) | NAD(P)-binding domain [IPR016040] (2); NAD-dependent epimerase/dehydratase, N-terminal domain [IPR001509] (1) | scaffold_1_mRNA_86.1 | C_unshiu_00129_mRNA_16.1 | - |
| GF0020078 | 1 | 1 | 0 | Polynucleotidyl transferase, Ribonuclease H fold (1); Ribonuclease H (1) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_1_mRNA_857.1 | C_unshiu_00068_mRNA_6.1 | - |
| GF0020077 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_84.1 | C_unshiu_00129_mRNA_19.1 | - |
| GF0020075 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_834.1 | C_unshiu_00600_mRNA_6.1 | - |
| GF0020074 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_832.1 | C_unshiu_00600_mRNA_4.1 | - |
| GF0020073 | 1 | 1 | 0 | Hypothetical protein (2) | intracellular protein transport [GO:0006886 biological_process] (2); binding [GO:0005488 molecular_function] (2); vesicle-mediated transport [GO:0016192 biological_process] (2); membrane coat [GO:0030117 cellular_component] (2) | Armadillo-like helical [IPR011989] (2); Armadillo-type fold [IPR016024] (2); Clathrin/coatomer adaptor, adaptin-like, N-terminal [IPR002553] (2) | scaffold_1_mRNA_831.1 | C_unshiu_00600_mRNA_3.1 | - |
| GF0020072 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_827.1 | C_unshiu_00075_mRNA_59.1 | - |
| GF0020071 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_826.1 | C_unshiu_00075_mRNA_58.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0020070 | 1 | 1 | 0 | Ras-related protein Rab7 (2) | GTP binding [GO:0005525 molecular_function] (2); GTPase activity [GO:0003924 molecular_function] (2); signal transduction [GO:0007165 biological_process] (1); intracellular [GO:0005622 cellular_component] (1); intracellular protein transport [GO:0006886 biological_process] (1); nucleocytoplasmic transport [GO:0006913 biological_process] (1); small GTPase mediated signal transduction [GO:0007264 biological_process] (1); membrane [GO:0016020 cellular_component] (1); protein transport [GO:0015031 biological_process] (1) | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); Small GTPase superfamily [IPR001806] (2); Small GTP-binding protein domain [IPR005225] (2); Small GTPase superfamily, Ras type [IPR020849] (1); Small GTPase superfamily, Rab type [IPR003579] (1); Ran GTPase [IPR002041] (1); Small GTPase superfamily, Rho type [IPR003578] (1) | scaffold_1_mRNA_813.1 | C_unshiu_00075_mRNA_45.1 | - |
| GF0020069 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_809.1 | C_unshiu_00075_mRNA_29.1 | - |
| GF0020068 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_805.1 | C_unshiu_00075_mRNA_24.1 | - |
| GF0020067 | 1 | 1 | 0 | Putative xyloglucan glycosyltransferase 5 (2) | | Nucleotide-diphospho-sugar transferases [IPR029044] (2) | scaffold_1_mRNA_78.1 | C_unshiu_00129_mRNA_26.1 | - |
| GF0020066 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_775.1 | C_unshiu_00075_mRNA_8.1 | - |
| GF0020065 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_767.1 | C_unshiu_01122_mRNA_13.1 | - |
| GF0020064 | 1 | 1 | 0 | Hypothetical protein (2) | magnesium ion binding [GO:0000287 molecular_function] (2); terpene synthase activity [GO:0010333 molecular_function] (2); lyase activity [GO:0016829 molecular_function] (2) | Terpene synthase, metal-binding domain [IPR005630] (2); Isoprenoid synthase domain [IPR008949] (2) | scaffold_1_mRNA_766.1 | C_unshiu_01122_mRNA_8.1 | - |
| GF0020062 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_764.1 | C_unshiu_01122_mRNA_10.1 | - |
| GF0020060 | 1 | 1 | 0 | General transcription factor IIH subunit 4 (2) | ATP-dependent DNA helicase activity [GO:0004003 molecular_function] (2); nucleus [GO:0005634 cellular_component] (2); core TFIIH complex [GO:0000439 cellular_component] (2); nucleotide-excision repair [GO:0006289 biological_process] (2) | Transcription factor TFIIH subunit p52/Tfb2 [IPR004598] (2) | scaffold_1_mRNA_756.1 | C_unshiu_01122_mRNA_5.1 | - |
| GF0020059 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_753.1 | C_unshiu_00947_mRNA_6.1 | - |
| GF0020058 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_748.1 | C_unshiu_00947_mRNA_1.1 | - |
| GF0020055 | 1 | 1 | 0 | CBS domain-containing protein CBSX5 (2) | | | scaffold_1_mRNA_743.1 | C_unshiu_01381_mRNA_3.1 | - |
| GF0020054 | 1 | 1 | 0 | Hypothetical protein (1); Protein FAR1-RELATED SEQUENCE 5 (1) | nucleic acid binding [GO:0003676 molecular_function] (2); zinc ion binding [GO:0008270 molecular_function] (2); regulation of transcription, DNA-templated [GO:0006355 biological_process] (2); 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) | MULE transposase domain [IPR018289] (2); Zinc finger, PMZ-type [IPR006564] (2); Zinc finger, SWIM-type [IPR007527] (2); FHY3/FAR1 family [IPR031052] (2); Zinc finger, CCHC-type [IPR001878] (2); Cytochrome P450 [IPR001128] (1); FAR1 DNA binding domain [IPR004330] (1) | scaffold_1_mRNA_742.1 | C_unshiu_00178_mRNA_37.1 | - |
| GF0020053 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_741.1 | C_unshiu_02595_mRNA_1.1 | - |
| GF0020052 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2); zinc ion binding [GO:0008270 molecular_function] (2) | Zinc finger, CCHC-type [IPR001878] (2) | scaffold_1_mRNA_740.1 | C_unshiu_01381_mRNA_4.1 | - |
| GF0020051 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_1_mRNA_734.1 | C_unshiu_00148_mRNA_40.1 | - |
| GF0020049 | 1 | 1 | 0 | Hypothetical protein (2) | DNA binding [GO:0003677 molecular_function] (2); sequence-specific DNA binding [GO:0043565 molecular_function] (2) | Lambda repressor-like, DNA-binding domain [IPR010982] (2); Cro/C1-type helix-turn-helix domain [IPR001387] (2) | scaffold_1_mRNA_718.1 | C_unshiu_00148_mRNA_27.1 | - |
| GF0020048 | 1 | 1 | 0 | Hypothetical protein (1); DNA mismatch repair protein Msh6-2 (1) | mismatch repair [GO:0006298 biological_process] (2); mismatched DNA binding [GO:0030983 molecular_function] (2); ATP binding [GO:0005524 molecular_function] (2) | DNA mismatch repair protein MutS, N-terminal [IPR016151] (2); DNA mismatch repair protein MutS-like, N-terminal [IPR007695] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); DNA mismatch repair protein MutS, connector domain [IPR007860] (1); DNA mismatch repair protein MutS, core [IPR007696] (1); DNA mismatch repair protein MutS, C-terminal [IPR000432] (1) | scaffold_1_mRNA_716.1 | C_unshiu_00148_mRNA_25.1 | - |
| GF0020044 | 1 | 1 | 0 | Putative sulfate transporter 3.4 (2) | membrane [GO:0016020 cellular_component] (2); secondary active sulfate transmembrane transporter activity [GO:0008271 molecular_function] (2); sulfate transport [GO:0008272 biological_process] (2); integral component of membrane [GO:0016021 cellular_component] (2); transmembrane transport [GO:0055085 biological_process] (2); sulfate transmembrane transporter activity [GO:0015116 molecular_function] (2); sulfate transmembrane transport [GO:1902358 biological_process] (2) | Sulfate transporter 3.4 [IPR030317] (2); SLC26A/SulP transporter [IPR001902] (2); STAS domain [IPR002645] (2); SLC26A/SulP transporter domain [IPR011547] (2); Sulphate anion transporter, conserved site [IPR018045] (2) | scaffold_1_mRNA_711.1 | C_unshiu_00242_mRNA_6.1 | - |
| GF0020043 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_710.1 | C_unshiu_00242_mRNA_4.1 | - |
| GF0020042 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_684.1 | C_unshiu_00016_mRNA_61.1 | - |
| GF0020041 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_683.1 | C_unshiu_00016_mRNA_62.1 | - |
| GF0020040 | 1 | 1 | 0 | Protease inhibitor/seed storage/lipid transfer protein family protein (2) | | Bifunctional inhibitor/plant lipid transfer protein/seed storage helical domain [IPR016140] (2) | scaffold_1_mRNA_680.1 | C_unshiu_00016_mRNA_64.1 | - |
| GF0020038 | 1 | 1 | 0 | DUF2921 family protein (1); Hypothetical protein (1) | | Protein of unknown function DUF2921 [IPR021319] (2) | scaffold_1_mRNA_665.1 | C_unshiu_00016_mRNA_81.1 | - |
| GF0020037 | 1 | 1 | 0 | RNA-binding motif protein, X-linked 2 (2) | nucleic acid binding [GO:0003676 molecular_function] (2); nucleotide binding [GO:0000166 molecular_function] (1) | RNA recognition motif domain [IPR000504] (2); Nucleotide-binding alpha-beta plait domain [IPR012677] (1) | scaffold_1_mRNA_663.1 | C_unshiu_00016_mRNA_83.1 | - |
| GF0020035 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_632.1 | C_unshiu_00039_mRNA_14.1 | - |
| GF0020033 | 1 | 1 | 0 | Zinc finger (Ran-binding) family protein (2) | zinc ion binding [GO:0008270 molecular_function] (2) | Zinc finger, RanBP2-type [IPR001876] (2) | scaffold_1_mRNA_626.1 | C_unshiu_00547_mRNA_6.1 | - |
| GF0020032 | 1 | 1 | 0 | NADH-cytochrome b5 reductase (2) | oxidoreductase activity [GO:0016491 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2) | Flavoprotein pyridine nucleotide cytochrome reductase [IPR001709] (2); Riboflavin synthase-like beta-barrel [IPR017938] (2); NADH:cytochrome b5 reductase (CBR) [IPR001834] (2); Oxidoreductase FAD/NAD(P)-binding [IPR001433] (2); Ferredoxin reductase-type FAD-binding domain [IPR017927] (2); Oxidoreductase, FAD-binding domain [IPR008333] (2) | scaffold_1_mRNA_622.1 | C_unshiu_00547_mRNA_9.1 | - |
| GF0020031 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_6.1 | C_unshiu_00144_mRNA_39.1 | - |
| GF0020030 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_599.1 | C_unshiu_00203_mRNA_39.1 | - |
| GF0020029 | 1 | 1 | 0 | Putative chaperon P13.9 (2) | unfolded protein binding [GO:0051082 molecular_function] (2); heat shock protein binding [GO:0031072 molecular_function] (2) | Heat shock protein DnaJ, cysteine-rich domain [IPR001305] (2) | scaffold_1_mRNA_593.1 | C_unshiu_00203_mRNA_31.1 | - |
| GF0020028 | 1 | 1 | 0 | Hypothetical protein (2) | structural constituent of ribosome [GO:0003735 molecular_function] (2); translation [GO:0006412 biological_process] (2); intracellular [GO:0005622 cellular_component] (2); ribosome [GO:0005840 cellular_component] (2) | Ribosomal protein L36 [IPR000473] (2) | scaffold_1_mRNA_583.1 | C_unshiu_00203_mRNA_21.1 | - |
| GF0020027 | 1 | 1 | 0 | Hypothetical protein (2) | | Protein of unknown function DUF247, plant [IPR004158] (2) | scaffold_1_mRNA_580.1 | C_unshiu_00203_mRNA_18.1 | - |
| GF0020026 | 1 | 1 | 0 | RNA 2'-phosphotransferase isoform 1 (2) | tRNA splicing, via endonucleolytic cleavage and ligation [GO:0006388 biological_process] (2); transferase activity, transferring phosphorus-containing groups [GO:0016772 molecular_function] (2) | Phosphotransferase KptA/Tpt1 [IPR002745] (2) | scaffold_1_mRNA_573.1 | C_unshiu_00203_mRNA_9.1 | - |
| GF0020023 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_537.1 | C_unshiu_00572_mRNA_2.1 | - |
| GF0020022 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_536.1 | C_unshiu_00572_mRNA_3.1 | - |
| GF0020021 | 1 | 1 | 0 | Hypothetical protein (2) | protein phosphorylation [GO:0006468 biological_process] (2); protein kinase activity [GO:0004672 molecular_function] (2) | Protein kinase-like domain [IPR011009] (2); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1) | scaffold_1_mRNA_535.1 | C_unshiu_00572_mRNA_4.1 | - |
| GF0020020 | 1 | 1 | 0 | Hypothetical protein (2) | | Leucine-rich repeat domain, L domain-like [IPR032675] (2) | scaffold_1_mRNA_533.1 | C_unshiu_00572_mRNA_6.1 | - |
| GF0020019 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_532.1 | C_unshiu_00572_mRNA_8.1 | - |
| GF0020018 | 1 | 1 | 0 | Lectin (2) | carbohydrate binding [GO:0030246 molecular_function] (2) | Concanavalin A-like lectin/glucanase domain [IPR013320] (2); Legume lectin domain [IPR001220] (2); Legume lectin [IPR016363] (1); Lectin [IPR016363] (1) | scaffold_1_mRNA_521.1 | C_unshiu_00572_mRNA_19.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0020017 | 1 | 1 | 0 | Putative ycf36 (1); Hypothetical protein (1) | | Uncharacterised protein family Ycf36 [IPR009631] (2); Protein of unknown function DUF778 [IPR008496] (1) | scaffold_1_mRNA_505.1 | C_unshiu_00055_mRNA_4.1 | - |
| GF0020016 | 1 | 1 | 0 | Calcineurin B-like protein 10 (2) | calcium ion binding [GO:0005509 molecular_function] (2) | EF-hand domain pair [IPR011992] (2); EF-Hand 1, calcium-binding site [IPR018247] (2); EF-hand domain [IPR002048] (2) | scaffold_1_mRNA_502.1 | C_unshiu_00055_mRNA_6.1 | - |
| GF0020012 | 1 | 1 | 0 | NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial (2) | oxidation-reduction process [GO:0055114 biological_process] (2); iron-sulfur cluster binding [GO:0051536 molecular_function] (2) | NADH:ubiquinone oxidoreductase-like, 20kDa subunit [IPR006137] (2) | scaffold_1_mRNA_493.1 | C_unshiu_00055_mRNA_17.1 | - |
| GF0020011 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_491.1 | C_unshiu_00055_mRNA_19.1 | - |
| GF0020010 | 1 | 1 | 0 | DUF1764 domain protein (2) | | Protein of unknown function DUF1764, eukaryotic [IPR013885] (2) | scaffold_1_mRNA_487.1 | C_unshiu_00055_mRNA_24.1 | - |
| GF0020006 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_459.1 | C_unshiu_00006_mRNA_25.1 | - |
| GF0020005 | 1 | 1 | 0 | Poly(A) polymerase 1 isoform 1 (2) | nucleus [GO:0005634 cellular_component] (2); RNA binding [GO:0003723 molecular_function] (2); nucleotidyltransferase activity [GO:0016779 molecular_function] (2); RNA 3'-end processing [GO:0031123 biological_process] (2); RNA polyadenylation [GO:0043631 biological_process] (2); polynucleotide adenylyltransferase activity [GO:0004652 molecular_function] (2) | Poly(A) polymerase [IPR014492] (2); Nucleotidyltransferase, class I, C-terminal-like [IPR011068] (2); Poly(A) polymerase, RNA-binding domain [IPR007010] (2); Polymerase, nucleotidyl transferase domain [IPR002934] (2); Poly(A) polymerase, central domain [IPR007012] (2) | scaffold_1_mRNA_456.1 | C_unshiu_00006_mRNA_28.1 | - |
| GF0020004 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_455.1 | C_unshiu_00006_mRNA_29.1 | - |
| GF0020003 | 1 | 1 | 0 | Hypothetical protein (2) | rRNA processing [GO:0006364 biological_process] (2); metalloendopeptidase activity [GO:0004222 molecular_function] (2) | Endoribonuclease YbeY [IPR002036] (2); Metalloprotease catalytic domain, predicted [IPR023091] (2) | scaffold_1_mRNA_454.1 | C_unshiu_00006_mRNA_32.1 | - |
| GF0020002 | 1 | 1 | 0 | Receptor-like protein kinase HSL1 (2) | protein phosphorylation [GO:0006468 biological_process] (2); protein kinase activity [GO:0004672 molecular_function] (2); ATP binding [GO:0005524 molecular_function] (2) | Protein kinase domain [IPR000719] (2); Leucine-rich repeat, typical subtype [IPR003591] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Protein kinase-like domain [IPR011009] (2); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (2); Protein kinase, ATP binding site [IPR017441] (2); Serine/threonine-protein kinase, active site [IPR008271] (2); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1) | scaffold_1_mRNA_452.1 | C_unshiu_00006_mRNA_34.1 | - |
| GF0020001 | 1 | 1 | 0 | 60S ribosomal protein L36 (2) | ribosome [GO:0005840 cellular_component] (2); structural constituent of ribosome [GO:0003735 molecular_function] (2); intracellular [GO:0005622 cellular_component] (2); translation [GO:0006412 biological_process] (2) | Ribosomal protein L36e [IPR000509] (2) | scaffold_1_mRNA_439.1 | C_unshiu_00006_mRNA_51.1 | - |
| GF0020000 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_433.1 | C_unshiu_00006_mRNA_57.1 | - |
| GF0019999 | 1 | 1 | 0 | Hypothetical protein (2) | defense response [GO:0006952 biological_process] (1) | NONRESPONDING TO OXYLIPINS 2 [IPR033252] (1) | scaffold_1_mRNA_426.1 | C_unshiu_00006_mRNA_63.1 | - |
| GF0019998 | 1 | 1 | 0 | Peptidyl-tRNA hydrolase II (PTH2) family protein (2) | aminoacyl-tRNA hydrolase activity [GO:0004045 molecular_function] (2) | Peptidyl-tRNA hydrolase II domain [IPR023476] (2); Peptidyl-tRNA hydrolase, PTH2 [IPR002833] (2) | scaffold_1_mRNA_425.1 | C_unshiu_00006_mRNA_64.1 | - |
| GF0019997 | 1 | 1 | 0 | SWIM zinc finger protein/MAP kinase kinase kinase (Mapkkk), putative (1); SWIM zinc finger family protein / mitogen-activated protein kinase kinase kinase-related, putative (1) | zinc ion binding [GO:0008270 molecular_function] (2); protein binding [GO:0005515 molecular_function] (2) | Zinc finger, SWIM-type [IPR007527] (2); Zinc finger, RING/FYVE/PHD-type [IPR013083] (2); Zinc finger, RING-type [IPR001841] (2) | scaffold_1_mRNA_424.1 | C_unshiu_00006_mRNA_65.1 | - |
| GF0019996 | 1 | 1 | 0 | SGNH hydrolase-type esterase superfamily protein, putative (2) | hydrolase activity, acting on ester bonds [GO:0016788 molecular_function] (2) | SGNH hydrolase-type esterase domain [IPR013830] (2); GDSL lipase/esterase [IPR001087] (2) | scaffold_1_mRNA_423.1 | C_unshiu_00006_mRNA_67.1 | - |
| GF0019995 | 1 | 1 | 0 | Chromosome condensation regulator RCC1 repeat protein (2) | | Regulator of chromosome condensation 1/beta-lactamase-inhibitor protein II [IPR009091] (2); Regulator of chromosome condensation, RCC1 [IPR000408] (2) | scaffold_1_mRNA_422.1 | C_unshiu_00006_mRNA_68.1 | - |
| GF0019994 | 1 | 1 | 0 | Nuclear pore complex protein Nup85 (2) | | Nucleoporin Nup85-like [IPR011502] (2) | scaffold_1_mRNA_421.1 | C_unshiu_00006_mRNA_69.1 | - |
| GF0019993 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_42.1 | C_unshiu_00003_mRNA_153.1 | - |
| GF0019992 | 1 | 1 | 0 | Hypothetical protein (2) | protein binding [GO:0005515 molecular_function] (2) | Ankyrin repeat-containing domain [IPR020683] (2); Ankyrin repeat [IPR002110] (2); PGG domain [IPR026961] (1) | scaffold_1_mRNA_408.1 | C_unshiu_00006_mRNA_86.1 | - |
| GF0019991 | 1 | 1 | 0 | Hypothetical protein (2) | | Ankyrin repeat-containing domain [IPR020683] (2) | scaffold_1_mRNA_405.1 | C_unshiu_00006_mRNA_88.1 | - |
| GF0019989 | 1 | 1 | 0 | Hypothetical protein (2) | tocopherol cyclase activity [GO:0009976 molecular_function] (2) | Tocopherol cyclase [IPR025893] (2) | scaffold_1_mRNA_395.1 | C_unshiu_00006_mRNA_97.1 | - |
| GF0019988 | 1 | 1 | 0 | Putative hydrolase YtaP (2) | proteolysis [GO:0006508 biological_process] (1); serine-type peptidase activity [GO:0008236 molecular_function] (1) | Alpha/Beta hydrolase fold [IPR029058] (2); Alpha/beta hydrolase fold-5 [IPR029059] (1); Peptidase S9, prolyl oligopeptidase, catalytic domain [IPR001375] (1) | scaffold_1_mRNA_388.1 | C_unshiu_00006_mRNA_103.1 | - |
| GF0019987 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_386.2 | C_unshiu_00006_mRNA_105.1 | - |
| GF0019986 | 1 | 1 | 0 | Putative VHS/GAT domain containing family protein (2) | intracellular [GO:0005622 cellular_component] (2); intracellular protein transport [GO:0006886 biological_process] (2) | GAT domain [IPR004152] (2); ENTH/VHS [IPR008942] (2); VHS domain [IPR002014] (2); VHS subgroup [IPR018205] (1) | scaffold_1_mRNA_385.1 | C_unshiu_00006_mRNA_106.1 | - |
| GF0019985 | 1 | 1 | 0 | Hypothetical protein (2) | integral component of membrane [GO:0016021 cellular_component] (2) | Mpv17/PMP22 [IPR007248] (2) | scaffold_1_mRNA_371.1 | C_unshiu_00006_mRNA_121.1 | - |
| GF0019984 | 1 | 1 | 0 | Hypothetical protein (2) | heme binding [GO:0020037 molecular_function] (2); iron ion binding [GO:0005506 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (2) | Cytochrome P450 [IPR001128] (2); Cytochrome P450, conserved site [IPR017972] (2) | scaffold_1_mRNA_37.1 | C_unshiu_00003_mRNA_147.1 | - |
| GF0019983 | 1 | 1 | 0 | Hypothetical protein (1); Leucine-rich repeat extensin-like protein 7 (1) | protein binding [GO:0005515 molecular_function] (2) | Leucine-rich repeat domain, L domain-like [IPR032675] (2); Leucine-rich repeat [IPR001611] (2); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (1) | scaffold_1_mRNA_3601.1 | C_unshiu_01269_mRNA_5.1 | - |
| GF0019982 | 1 | 1 | 0 | Hypothetical protein (1); Zinc finger CCCH domain-containing protein 16 (1) | metal ion binding [GO:0046872 molecular_function] (2) | Zinc finger, CCCH-type [IPR000571] (2) | scaffold_1_mRNA_3600.1 | C_unshiu_01269_mRNA_6.1 | - |
| GF0019981 | 1 | 1 | 0 | Hypothetical protein (2) | protein kinase activity [GO:0004672 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2); ATP binding [GO:0005524 molecular_function] (2) | Protein kinase-like domain [IPR011009] (2); Protein kinase domain [IPR000719] (2) | scaffold_1_mRNA_3599.1 | C_unshiu_01269_mRNA_7.1 | - |
| GF0019979 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_3592.1 | C_unshiu_00591_mRNA_12.1 | - |
| GF0019978 | 1 | 1 | 0 | Zinc/RING finger 3 (2) | protein binding [GO:0005515 molecular_function] (2); zinc ion binding [GO:0008270 molecular_function] (2) | Zinc finger, RING/FYVE/PHD-type [IPR013083] (2); Zinc finger, RING-type [IPR001841] (2) | scaffold_1_mRNA_3586.1 | C_unshiu_00591_mRNA_19.1 | - |
| GF0019968 | 1 | 1 | 0 | Low temperature and salt responsive protein family isoform 1 (2) | integral component of membrane [GO:0016021 cellular_component] (2) | Proteolipid membrane potential modulator [IPR000612] (2) | scaffold_1_mRNA_3513.1 | C_unshiu_01195_mRNA_3.1 | - |
| GF0019966 | 1 | 1 | 0 | Hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyltransferase (1); Hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyl transferase (1) | transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (2) | Transferase [IPR003480] (2); Chloramphenicol acetyltransferase-like domain [IPR023213] (1) | scaffold_1_mRNA_3507.1 | C_unshiu_01195_mRNA_8.1 | - |
| GF0019963 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (1); protein binding [GO:0005515 molecular_function] (1) | Kelch-type beta propeller [IPR015915] (1); Ribonuclease H-like domain [IPR012337] (1) | scaffold_1_mRNA_3494.1 | C_unshiu_01447_mRNA_7.1 | - |
| GF0019962 | 1 | 1 | 0 | Hypothetical protein (1); Pentatricopeptide repeat-containing family protein (1) | protein binding [GO:0005515 molecular_function] (2) | Zinc finger, RING/FYVE/PHD-type [IPR013083] (2); Pentatricopeptide repeat [IPR002885] (2); Tetratricopeptide-like helical domain [IPR011990] (2) | scaffold_1_mRNA_3487.1 | C_unshiu_00562_mRNA_3.1 | - |
| GF0019960 | 1 | 1 | 0 | Hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyl transferase (2) | transferase activity, transferring acyl groups other than amino-acyl groups [GO:0016747 molecular_function] (2) | Transferase [IPR003480] (2); Chloramphenicol acetyltransferase-like domain [IPR023213] (1) | scaffold_1_mRNA_3461.1 | C_unshiu_00348_mRNA_4.1 | - |
| GF0019959 | 1 | 1 | 0 | Tetratricopeptide repeat protein 1 (2) | protein binding [GO:0005515 molecular_function] (2) | Tetratricopeptide-like helical domain [IPR011990] (2); Tetratricopeptide repeat-containing domain [IPR013026] (2); Tetratricopeptide repeat [IPR019734] (2); Tetratricopeptide repeat 1 [IPR001440] (1) | scaffold_1_mRNA_3460.1 | C_unshiu_00348_mRNA_5.1 | - |
| GF0019957 | 1 | 1 | 0 | Cinnamoyl-CoA reductase 1 (2) | coenzyme binding [GO:0050662 molecular_function] (2); catalytic activity [GO:0003824 molecular_function] (2) | NAD(P)-binding domain [IPR016040] (2); NAD-dependent epimerase/dehydratase, N-terminal domain [IPR001509] (1); NAD-dependent epimerase/dehydratase [IPR001509] (1) | scaffold_1_mRNA_3457.1 | C_unshiu_01142_mRNA_1.1 | - |
| GF0019951 | 1 | 1 | 0 | Putative blight-associated protein p12 (2) | | Expansin/pollen allergen, DPBB domain [IPR007112] (2); RlpA-like protein, double-psi beta-barrel domain [IPR009009] (1); RlpA-like double-psi beta-barrel domain [IPR009009] (1) | scaffold_1_mRNA_3431.1 | C_unshiu_00348_mRNA_30.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0019950 | 1 | 1 | 0 | Cytochrome P450 (1); Cytochrome P450, family 81, subfamily D, polypeptide 8, putative (1) | oxidation-reduction process [GO:0055114 biological_process] (2); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (2); heme binding [GO:0020037 molecular_function] (2); iron ion binding [GO:0005506 molecular_function] (2) | Cytochrome P450, conserved site [IPR017972] (2); Cytochrome P450, E-class, group I [IPR002401] (2); Cytochrome P450 [IPR001128] (2) | scaffold_1_mRNA_3415.1 | C_unshiu_00237_mRNA_15.1 | - |
| GF0019947 | 1 | 1 | 0 | DUF1795-like photosystem II reaction center PsbP family protein (2) | photosystem II oxygen evolving complex [GO:0009654 cellular_component] (1); photosystem II [GO:0009523 cellular_component] (1); photosynthesis [GO:0015979 biological_process] (1); calcium ion binding [GO:0005509 molecular_function] (1); extrinsic component of membrane [GO:0019898 cellular_component] (1) | Mog1/PsbP, alpha/beta/alpha sandwich [IPR016123] (2); PsbP family [IPR002683] (1) | scaffold_1_mRNA_339.1 | C_unshiu_00833_mRNA_4.1 | - |
| GF0019946 | 1 | 1 | 0 | Hypothetical protein (2) | carbohydrate metabolic process [GO:0005975 biological_process] (2); hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (2) | Concanavalin A-like lectin/glucanase domain [IPR013320] (2); Glycoside hydrolase family 16 [IPR000757] (2) | scaffold_1_mRNA_3384.1 | C_unshiu_02081_mRNA_6.1 | - |
| GF0019945 | 1 | 1 | 0 | CTC-interacting domain 5, putative isoform 1 (2) | protein binding [GO:0005515 molecular_function] (2) | UBA-like [IPR009060] (2); Ubiquitin system component Cue [IPR003892] (2) | scaffold_1_mRNA_338.1 | C_unshiu_00833_mRNA_5.1 | - |
| GF0019943 | 1 | 1 | 0 | Hypothetical protein (1); Probable xyloglucan endotransglucosylase/hydrolase protein 23 (1) | apoplast [GO:0048046 cellular_component] (2); cellular glucan metabolic process [GO:0006073 biological_process] (2); hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (2); cell wall [GO:0005618 cellular_component] (2); carbohydrate metabolic process [GO:0005975 biological_process] (2); xyloglucan:xyloglucosyl transferase activity [GO:0016762 molecular_function] (2) | Glycoside hydrolase family 16 [IPR000757] (2); Nucleotide-diphospho-sugar transferase [IPR005069] (2); Xyloglucan endo-transglycosylase, C-terminal [IPR010713] (2); Glycoside hydrolase, family 16, active site [IPR008263] (2); Concanavalin A-like lectin/glucanase domain [IPR013320] (2) | scaffold_1_mRNA_3375.1 | C_unshiu_02828_mRNA_3.1 | - |
| GF0019941 | 1 | 1 | 0 | Hypothetical protein (2) |  | DNA-binding pseudobarrel domain [IPR015300] (1) | scaffold_1_mRNA_3357.1 | C_unshiu_00347_mRNA_30.1 | - |
| GF0019940 | 1 | 1 | 0 | Hypothetical protein (2) |  | Pre-mRNA splicing Prp18-interacting factor [IPR021715] (2) | scaffold_1_mRNA_3355.1 | C_unshiu_00347_mRNA_29.1 | - |
| GF0019937 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_1_mRNA_3350.1 | C_unshiu_00347_mRNA_26.1 | - |
| GF0019936 | 1 | 1 | 0 | Replication protein A 32 kDa subunit (2) | DNA replication [GO:0006260 biological_process] (2); DNA recombination [GO:0006310 biological_process] (2); DNA repair [GO:0006281 biological_process] (2); DNA binding [GO:0003677 molecular_function] (2); nucleus [GO:0005634 cellular_component] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | OB-fold nucleic acid binding domain, AA-tRNA synthetase-type [IPR004365] (2); Replication factor A protein 2 [IPR014646] (2); Replication protein A, C-terminal [IPR014892] (2); Winged helix-turn-helix DNA-binding domain [IPR011991] (2); Nucleic acid-binding, OB-fold [IPR012340] (2) | scaffold_1_mRNA_3342.2 | C_unshiu_00347_mRNA_18.2 | - |
| GF0019935 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_1_mRNA_3339.1 | C_unshiu_00347_mRNA_15.1 | - |
| GF0019933 | 1 | 1 | 0 | Homogentisate phytyltransferase (2) | integral component of membrane [GO:0016021 cellular_component] (2); prenyltransferase activity [GO:0004659 molecular_function] (1); transferase activity, transferring alkyl or aryl (other than methyl) groups [GO:0016765 molecular_function] (1) | UbiA prenyltransferase family [IPR000537] (2) | scaffold_1_mRNA_3329.2 | C_unshiu_00347_mRNA_6.1 | - |
| GF0019932 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_1_mRNA_3325.1 | C_unshiu_00347_mRNA_3.1 | - |
| GF0019930 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_1_mRNA_3316.1 | C_unshiu_00105_mRNA_10.1 | - |
| GF0019929 | 1 | 1 | 0 | Pentatricopeptide repeat-containing protein, putative isoform 2 (1); Pentatricopeptide repeat-containing protein, mitochondrial (1) | serine-type endopeptidase activity [GO:0004252 molecular_function] (2); proteolysis [GO:0006508 biological_process] (2) | Peptidase S8/S53 domain [IPR000209] (2); Pentatricopeptide repeat [IPR002885] (2) | scaffold_1_mRNA_3304.1 | C_unshiu_00105_mRNA_21.1 | - |
| GF0019927 | 1 | 1 | 0 | Pentatricopeptide (2) | protein binding [GO:0005515 molecular_function] (1) | Pentatricopeptide repeat [IPR002885] (2); Tetratricopeptide-like helical domain [IPR011990] (1) | scaffold_1_mRNA_3295.1 | C_unshiu_00105_mRNA_30.1 | - |
| GF0019924 | 1 | 1 | 0 | Mitotic-spindle organizing protein 1B (2) | gamma-tubulin complex localization [GO:0033566 biological_process] (1); gamma-tubulin ring complex [GO:0008274 cellular_component] (1) | Mitotic-spindle organizing protein 1 [IPR022214] (1); Protein of unknown function DUF3743 [IPR022214] (1) | scaffold_1_mRNA_3285.1 | C_unshiu_00105_mRNA_38.1 | - |
| GF0019923 | 1 | 1 | 0 | Hypothetical protein (2) | ATPase activity, coupled to transmembrane movement of substances [GO:0042626 molecular_function] (2); transmembrane transport [GO:0055085 biological_process] (2); ATP binding [GO:0005524 molecular_function] (2); integral component of membrane [GO:0016021 cellular_component] (2); transport [GO:0006810 biological_process] (2) | ABC transporter type 1, transmembrane domain [IPR011527] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1) | scaffold_1_mRNA_3277.1 | C_unshiu_00105_mRNA_46.1 | - |
| GF0019922 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_1_mRNA_3260.1 | C_unshiu_00131_mRNA_24.1 | - |
| GF0019921 | 1 | 1 | 0 | UPF0414 transmembrane protein C20orf30 like (2) |  | Protein of unknown function DUF872, transmembrane [IPR008590] (2) | scaffold_1_mRNA_3252.1 | C_unshiu_00131_mRNA_32.1 | - |
| GF0019919 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_1_mRNA_323.1 | C_unshiu_00309_mRNA_9.1 | - |
| GF0019918 | 1 | 1 | 0 | Hypothetical protein (2) | binding [GO:0005488 molecular_function] (2); protein binding [GO:0005515 molecular_function] (1); microtubule [GO:0005874 cellular_component] (1) | Armadillo-like helical [IPR011989] (2); Armadillo-type fold [IPR016024] (2); HEAT repeat associated with sister chromatid cohesion protein [IPR026003] (1); HEAT repeat [IPR000357] (1); MT-associated protein TORTIFOLIA1/SPIRAL2-like [IPR033337] (1) | scaffold_1_mRNA_3226.1 | C_unshiu_00131_mRNA_58.1 | - |
| GF0019917 | 1 | 1 | 0 | Squalene monooxygenase (2) | squalene monooxygenase activity [GO:0004506 molecular_function] (2); integral component of membrane [GO:0016021 cellular_component] (2); oxidoreductase activity [GO:0016491 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2); flavin adenine dinucleotide binding [GO:0050660 molecular_function] (2) | FAD/NAD(P)-binding domain [IPR023753] (2); Squalene epoxidase [IPR013698] (2) | scaffold_1_mRNA_3225.1 | C_unshiu_00583_mRNA_16.1 | - |
| GF0019913 | 1 | 1 | 0 | Organic cation/carnitine transporter 7 (2) | transmembrane transport [GO:0055085 biological_process] (2); transmembrane transporter activity [GO:0022857 molecular_function] (2); integral component of membrane [GO:0016021 cellular_component] (2) | Major facilitator,  sugar transporter-like [IPR005828] (2); Major facilitator superfamily domain [IPR020846] (2) | scaffold_1_mRNA_3204.1 | C_unshiu_00315_mRNA_15.1 | - |
| GF0019912 | 1 | 1 | 0 | Synaptic vesicle 2-related protein (2) | transmembrane transporter activity [GO:0022857 molecular_function] (2); integral component of membrane [GO:0016021 cellular_component] (2); transmembrane transport [GO:0055085 biological_process] (2) | Major facilitator,  sugar transporter-like [IPR005828] (2); Major facilitator superfamily domain [IPR020846] (2) | scaffold_1_mRNA_3202.1 | C_unshiu_00315_mRNA_13.1 | - |
| GF0019909 | 1 | 1 | 0 | Glucosidase II beta subunit-like protein (2) |  | Mannose-6-phosphate receptor binding domain [IPR009011] (2); Glucosidase II beta subunit-like [IPR012913] (2) | scaffold_1_mRNA_3197.1 | C_unshiu_00066_mRNA_3.1 | - |
| GF0019908 | 1 | 1 | 0 | Hypothetical protein (2) |  | Leucine-rich repeat domain, L domain-like [IPR032675] (2) | scaffold_1_mRNA_3194.1 | C_unshiu_00066_mRNA_6.1 | - |
| GF0019900 | 1 | 1 | 0 | Chloroplast photosystem II subunit X (2) | membrane [GO:0016020 cellular_component] (2); photosynthesis [GO:0015979 biological_process] (2); photosystem II [GO:0009523 cellular_component] (2) | Photosystem II PsbX [IPR009518] (2) | scaffold_1_mRNA_3093.1 | C_unshiu_00498_mRNA_13.1 | - |
| GF0019896 | 1 | 1 | 0 | Pentatricopeptide repeat-containing family protein (2) | protein binding [GO:0005515 molecular_function] (2) | Pentatricopeptide repeat [IPR002885] (2); Tetratricopeptide-like helical domain [IPR011990] (2) | scaffold_1_mRNA_3059.1 | C_unshiu_00150_mRNA_30.1 | - |
| GF0019895 | 1 | 1 | 0 | Putative nucleoredoxin 1 (2) | oxidation-reduction process [GO:0055114 biological_process] (1); protein-disulfide reductase activity [GO:0047134 molecular_function] (1); cell redox homeostasis [GO:0045454 biological_process] (1) | Thioredoxin-like fold [IPR012336] (2); DC1 [IPR004146] (1); C1-like [IPR011424] (1); Thioredoxin domain [IPR013766] (1); Ricin B, lectin domain [IPR000772] (1) | scaffold_1_mRNA_3056.1 | C_unshiu_00150_mRNA_27.1 | - |
| GF0019894 | 1 | 1 | 0 | Hypothetical protein (2) | oxidation-reduction process [GO:0055114 biological_process] (2); oxidoreductase activity [GO:0016491 molecular_function] (2) | FAD/NAD(P)-binding domain [IPR023753] (2) | scaffold_1_mRNA_304.1 | C_unshiu_01113_mRNA_12.1 | - |
| GF0019893 | 1 | 1 | 0 | Monofunctional lysine-ketoglutarate reductase 1 (2) |  | Alanine dehydrogenase/pyridine nucleotide transhydrogenase, N-terminal [IPR007886] (2); Alanine dehydrogenase/pyridine nucleotide transhydrogenase, NAD(H)-binding domain [IPR007698] (2) | scaffold_1_mRNA_3033.1 | C_unshiu_00150_mRNA_2.1 | - |
| GF0019892 | 1 | 1 | 0 | Invertase/pectin methylesterase inhibitor family protein (1); Pectinesterase inhibitor (1) | enzyme inhibitor activity [GO:0004857 molecular_function] (2); negative regulation of catalytic activity [GO:0043086 biological_process] (1); pectinesterase inhibitor activity [GO:0046910 molecular_function] (1) | Pectinesterase inhibitor domain [IPR006501] (2); Pectinesterase inhibitor, plant [IPR034086] (1) | scaffold_1_mRNA_3031.1 | C_unshiu_02111_mRNA_1.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0019891 | 1 | 1 | 0 | Monooxygenase family protein (2) | oxidoreductase activity [GO:0016491 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2) | FAD/NAD(P)-binding domain [IPR023753] (2) | scaffold_1_mRNA_302.1 | C_unshiu_01113_mRNA_11.1 | - |
| GF0019890 | 1 | 1 | 0 | Kinesin-like protein NACK2 (2) | microtubule binding [GO:0008017 molecular_function] (2); microtubule motor activity [GO:0003777 molecular_function] (2); microtubule-based movement [GO:0007018 biological_process] (2); ATP binding [GO:0005524 molecular_function] (2) | Kinesin motor domain, conserved site [IPR019821] (2); Kinesin motor domain [IPR001752] (2); NPK1-activating kinesin-like protein, C-terminal [IPR021881] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); Kinesin-like protein [IPR027640] (1) | scaffold_1_mRNA_3013.1 | C_unshiu_00341_mRNA_13.1 | - |
| GF0019889 | 1 | 1 | 0 | Sucrose synthase (2) | sucrose metabolic process [GO:0005985 biological_process] (2); sucrose synthase activity [GO:0016157 molecular_function] (2) | Sucrose synthase, plant/cyanobacteria [IPR012820] (2); Glycosyl transferase, family 1 [IPR001296] (2); Sucrose synthase [IPR000368] (2) | scaffold_1_mRNA_3012.4 | C_unshiu_00341_mRNA_12.3 | - |
| GF0019888 | 1 | 1 | 0 | DnaJ like subfamily C member 28 (1); Hypothetical protein (1) |  | DnaJ homologue, subfamily C, member 28, conserved domain [IPR018961] (1) | scaffold_1_mRNA_3011.1 | C_unshiu_00341_mRNA_11.1 | - |
| GF0019887 | 1 | 1 | 0 | Hypothetical protein (1); Mitochondrial ferredoxin 2 (1) |  | Beta-grasp domain [IPR012675] (1) | scaffold_1_mRNA_3005.1 | C_unshiu_00341_mRNA_6.1 | - |
| GF0019885 | 1 | 1 | 0 | 20 kDa chaperonin, chloroplastic (2) | cytoplasm [GO:0005737 cellular_component] (2); ATP binding [GO:0005524 molecular_function] (2); positive regulation of superoxide dismutase activity [GO:1901671 biological_process] (2); transition metal ion binding [GO:0046914 molecular_function] (2); protein folding [GO:0006457 biological_process] (2) | GroES chaperonin family [IPR020818] (2); GroES-like [IPR011032] (2); Chaperonin GroES, conserved site [IPR018369] (2); Chaperonin Cpn20 [IPR017416] (2) | scaffold_1_mRNA_2995.1 | C_unshiu_00047_mRNA_91.1 | - |
| GF0019884 | 1 | 1 | 0 | Ethylene-responsive transcription factor ERF018 (2) | DNA binding [GO:0003677 molecular_function] (2); transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (2); regulation of transcription, DNA-templated [GO:0006355 biological_process] (2) | DNA-binding domain [IPR016177] (2); AP2/ERF domain [IPR001471] (2) | scaffold_1_mRNA_2994.1 | C_unshiu_00047_mRNA_90.1 | - |
| GF0019883 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_1_mRNA_297.1 | C_unshiu_01113_mRNA_3.1 | - |
| GF0019882 | 1 | 1 | 0 | Subtilisin-like serine protease (2) | proteolysis [GO:0006508 biological_process] (2); serine-type endopeptidase activity [GO:0004252 molecular_function] (2) | PA domain [IPR003137] (2); Peptidase S8/S53 domain [IPR000209] (2); Peptidase S8, subtilisin-related [IPR015500] (2); Peptidase S8 propeptide/proteinase inhibitor I9 [IPR010259] (1); Cucumisin-like catalytic domain [IPR034197] (1); Protease propeptides/proteinase inhibitor I9 [IPR009020] (1) | scaffold_1_mRNA_2967.1 | C_unshiu_00047_mRNA_62.1 | - |
| GF0019881 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_1_mRNA_296.1 | C_unshiu_01113_mRNA_4.1 | - |
| GF0019880 | 1 | 1 | 0 | Hypothetical protein (1); Rho guanine nucleotide exchange factor 7, putative (1) |  |  | scaffold_1_mRNA_2958.1 | C_unshiu_00047_mRNA_52.1 | - |
| GF0019879 | 1 | 1 | 0 | OBP3-responsive gene 4 isoform 2 (2) |  |  | scaffold_1_mRNA_2957.1 | C_unshiu_00047_mRNA_51.1 | - |
| GF0019878 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_1_mRNA_295.1 | C_unshiu_01113_mRNA_5.1 | - |
| GF0019875 | 1 | 1 | 0 | NB-ARC domain disease resistance protein (1); NB-ARC domain-containing disease resistance protein (1) | ADP binding [GO:0043531 molecular_function] (2) | NB-ARC [IPR002182] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (1) | scaffold_1_mRNA_2933.1 | C_unshiu_00047_mRNA_27.1 | - |
| GF0019874 | 1 | 1 | 0 | Hypothetical protein (2) | transmembrane transport [GO:0055085 biological_process] (2); integral component of membrane [GO:0016021 cellular_component] (2); calcium ion transport [GO:0006816 biological_process] (1); calcium:proton antiporter activity [GO:0015369 molecular_function] (1) | Sodium/calcium exchanger membrane region [IPR004837] (2); Amino acid transporter, transmembrane domain [IPR013057] (2); Calcium/proton exchanger CAX [IPR004798] (1) | scaffold_1_mRNA_2926.1 | C_unshiu_00047_mRNA_18.1 | - |
| GF0019873 | 1 | 1 | 0 | Hypothetical protein (2) | serine-type endopeptidase activity [GO:0004252 molecular_function] (2); proteolysis [GO:0006508 biological_process] (2) | Peptidase S8/S53 domain [IPR000209] (2); Peptidase S8, subtilisin, Ser-active site [IPR023828] (2); Peptidase S8, subtilisin-related [IPR015500] (1) | scaffold_1_mRNA_2917.1 | C_unshiu_00047_mRNA_9.1 | - |
| GF0019872 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_1_mRNA_2911.1 | C_unshiu_01542_mRNA_6.1 | - |
| GF0019870 | 1 | 1 | 0 | Non-LTR reverse transcriptase (1); Hypothetical protein (1) |  | Endonuclease/exonuclease/phosphatase [IPR005135] (2) | scaffold_1_mRNA_2909.1 | C_unshiu_01542_mRNA_2.1 | - |
| GF0019869 | 1 | 1 | 0 | DUF2431 domain protein (1); Hypothetical protein (1) |  | Domain of unknown function DUF2431 [IPR019446] (2); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (2) | scaffold_1_mRNA_2907.1 | C_unshiu_00934_mRNA_13.1 | - |
| GF0019868 | 1 | 1 | 0 | Hypothetical protein (2) |  | Domain of unknown function DUF2431 [IPR019446] (2) | scaffold_1_mRNA_2905.1 | C_unshiu_00133_mRNA_65.1 | - |
| GF0019867 | 1 | 1 | 0 | Hypothetical protein (1); DUF2431 domain protein (1) |  | Domain of unknown function DUF2431 [IPR019446] (2); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (2) | scaffold_1_mRNA_2904.1 | C_unshiu_01511_mRNA_15.1 | - |
| GF0019865 | 1 | 1 | 0 | Uridine kinase (2) | kinase activity [GO:0016301 molecular_function] (2); metabolic process [GO:0008152 biological_process] (2); ATP binding [GO:0005524 molecular_function] (2); uridine kinase activity [GO:0004849 molecular_function] (1); nucleoside metabolic process [GO:0009116 biological_process] (1); UMP salvage [GO:0044206 biological_process] (1) | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); Phosphoribulokinase/uridine kinase [IPR006083] (2); Uridine kinase-like [IPR000764] (2); Phosphoribosyltransferase-like [IPR029057] (2); Uridine kinase-like protein, plant [IPR029930] (1); Phosphoribosyltransferase domain [IPR000836] (1) | scaffold_1_mRNA_2885.1 | C_unshiu_00080_mRNA_49.1 | - |
| GF0019852 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_1_mRNA_2808.1 | C_unshiu_00681_mRNA_12.1 | - |
| GF0019851 | 1 | 1 | 0 | Bromo adjacent-like domain protein (2) | chromatin binding [GO:0003682 molecular_function] (2) | Agenet domain, plant type [IPR014002] (2); Agenet-like domain [IPR008395] (2); Bromo adjacent homology (BAH) domain [IPR001025] (2); WLM domain [IPR013536] (2) | scaffold_1_mRNA_2807.1 | C_unshiu_00681_mRNA_13.1 | - |
| GF0019850 | 1 | 1 | 0 | Cytochrome P450 (2) | heme binding [GO:0020037 molecular_function] (2); iron ion binding [GO:0005506 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (2) | Cytochrome P450 [IPR001128] (2) | scaffold_1_mRNA_2800.1 | C_unshiu_01231_mRNA_1.1 | - |
| GF0019849 | 1 | 1 | 0 | Cytochrome P450 (2) | iron ion binding [GO:0005506 molecular_function] (2); heme binding [GO:0020037 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (2) | Cytochrome P450 [IPR001128] (2); Cytochrome P450, E-class, group I [IPR002401] (2) | scaffold_1_mRNA_2798.1 | C_unshiu_00681_mRNA_21.1 | - |
| GF0019848 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_1_mRNA_2796.1 | C_unshiu_00554_mRNA_18.1 | - |
| GF0019847 | 1 | 1 | 0 | Cytochrome P450 (2) | oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2); heme binding [GO:0020037 molecular_function] (2); iron ion binding [GO:0005506 molecular_function] (2) | Cytochrome P450, E-class, group I [IPR002401] (2); Cytochrome P450, conserved site [IPR017972] (2); Cytochrome P450 [IPR001128] (2) | scaffold_1_mRNA_2792.1 | C_unshiu_00554_mRNA_14.1 | - |
| GF0019845 | 1 | 1 | 0 | Boron transporter-like protein (2) | anion transport [GO:0006820 biological_process] (2); membrane [GO:0016020 cellular_component] (2); inorganic anion exchanger activity [GO:0005452 molecular_function] (2); integral component of membrane [GO:0016021 cellular_component] (2) | Bicarbonate transporter, eukaryotic [IPR003020] (2); Bicarbonate transporter, C-terminal [IPR011531] (2) | scaffold_1_mRNA_278.1 | C_unshiu_00553_mRNA_17.1 | - |
| GF0019843 | 1 | 1 | 0 | Hypothetical protein (2) | metal ion binding [GO:0046872 molecular_function] (2); metal ion transport [GO:0030001 biological_process] (2) | Heavy metal-associated domain, HMA [IPR006121] (2) | scaffold_1_mRNA_2778.1 | C_unshiu_00554_mRNA_5.1 | - |
| GF0019842 | 1 | 1 | 0 | Hypothetical protein (2) |  |  | scaffold_1_mRNA_2769.1 | C_unshiu_01429_mRNA_5.1 | - |
| GF0019840 | 1 | 1 | 0 | Deoxyuridine 5'-triphosphate nucleotidohydrolase family protein (1); Putative deoxyuridine 5'-triphosphate nucleotidohydrolase-like (1) | dUTP metabolic process [GO:0046080 biological_process] (2); hydrolase activity [GO:0016787 molecular_function] (1); dUTP diphosphatase activity [GO:0004170 molecular_function] (1) | dUTPase-like [IPR029054] (2); Deoxyuridine triphosphate nucleotidohydrolase [IPR008181] (1); dUTPase, trimeric [IPR033704] (1); Deoxyuridine triphosphate nucleotidohydrolase/Deoxycytidine triphosphate deaminase [IPR008180] (1) | scaffold_1_mRNA_2767.1 | C_unshiu_01429_mRNA_7.1 | - |
| GF0019839 | 1 | 1 | 0 | V-type proton ATPase subunit e (2) | proton-transporting V-type ATPase, V0 domain [GO:0033179 cellular_component] (2); hydrogen ion transmembrane transporter activity [GO:0015078 molecular_function] (2); ATP hydrolysis coupled proton transport [GO:0015991 biological_process] (2) | ATPase, V0 complex, subunit e1/e2 [IPR008389] (2) | scaffold_1_mRNA_2739.1 | C_unshiu_00103_mRNA_58.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0019838 | 1 | 1 | 0 | Transcription initiation factor TFIID subunit 6 (2) | protein heterodimerization activity [GO:0046982 molecular_function] (2); nucleus [GO:0005634 cellular_component] (2); binding [GO:0005488 molecular_function] (2); regulation of sequence-specific DNA binding transcription factor activity [GO:0051090 biological_process] (2); DNA-templated transcription, initiation [GO:0006352 biological_process] (2) | Armadillo-type fold [IPR016024] (2); TAF6, C-terminal HEAT repeat domain [IPR011442] (2); TATA box binding protein associated factor (TAF) [IPR004823] (2); Armadillo-like helical [IPR011989] (2); Histone-fold [IPR009072] (2) | scaffold_1_mRNA_2737.1 | C_unshiu_00103_mRNA_56.1 | - |
| GF0019836 | 1 | 1 | 0 | Hypothetical protein (2) | protein binding [GO:0005515 molecular_function] (1) | F-box domain [IPR001810] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1) | scaffold_1_mRNA_2710.1 | C_unshiu_00103_mRNA_26.1 | - |
| GF0019834 | 1 | 1 | 0 | Hypothetical protein (2) | regulation of transcription, DNA-templated [GO:0006355 biological_process] (1) | FHY3/FAR1 family [IPR031052] (1) | scaffold_1_mRNA_2690.1 | C_unshiu_02382_mRNA_5.1 | - |
| GF0019831 | 1 | 1 | 0 | Calcium-dependent protein kinase 21 (2) | ATP binding [GO:0005524 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2); protein kinase activity [GO:0004672 molecular_function] (2); calcium ion binding [GO:0005509 molecular_function] (1) | Serine/threonine-protein kinase, active site [IPR008271] (2); Protein kinase domain [IPR000719] (2); Protein kinase-like domain [IPR011009] (2); Protein kinase, ATP binding site [IPR017441] (1); EF-hand domain [IPR002048] (1); Serine/threonine/dual specificity protein kinase, catalytic  domain [IPR002290] (1); EF-Hand 1, calcium-binding site [IPR018247] (1); EF-hand domain pair [IPR011992] (1) | scaffold_1_mRNA_2654.1 | C_unshiu_00062_mRNA_1.1 | - |
| GF0019830 | 1 | 1 | 0 | Calcium-dependent protein kinase 21 (1); Calcium-dependent protein kinase 29 (1) | protein kinase activity [GO:0004672 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2); ATP binding [GO:0005524 molecular_function] (2); calcium ion binding [GO:0005509 molecular_function] (1) | Protein kinase-like domain [IPR011009] (2); Protein kinase domain [IPR000719] (2); EF-hand domain pair [IPR011992] (1); EF-Hand 1, calcium-binding site [IPR018247] (1); EF-hand domain [IPR002048] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Protein kinase, ATP binding site [IPR017441] (1) | scaffold_1_mRNA_2649.1 | C_unshiu_02583_mRNA_1.1 | - |
| GF0019828 | 1 | 1 | 0 | Ankyrin repeat family protein, putative (2) | protein binding [GO:0005515 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2); protein kinase activity [GO:0004672 molecular_function] (2); ATP binding [GO:0005524 molecular_function] (2) | Protein kinase domain [IPR000719] (2); Ankyrin repeat [IPR002110] (2); Protein kinase-like domain [IPR011009] (2); Serine/threonine-protein kinase, active site [IPR008271] (2); Protein kinase, ATP binding site [IPR017441] (2); PGG domain [IPR026961] (2); Ankyrin repeat-containing domain [IPR020683] (2); Serine/threonine/dual specificity protein kinase, catalytic  domain [IPR002290] (1) | scaffold_1_mRNA_2635.1 | C_unshiu_00277_mRNA_8.1 | - |
| GF0019827 | 1 | 1 | 0 | Hypothetical protein (1); Calmodulin-domain protein kinase 9 isoform 3 (1) | calcium ion binding [GO:0005509 molecular_function] (2); ATP binding [GO:0005524 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1) | EF-Hand 1, calcium-binding site [IPR018247] (2); EF-hand domain [IPR002048] (2); EF-hand domain pair [IPR011992] (2); Serine/threonine-protein kinase, active site [IPR008271] (1); Serine/threonine/dual specificity protein kinase, catalytic  domain [IPR002290] (1); Protein kinase-like domain [IPR011009] (1); Protein kinase domain [IPR000719] (1) | scaffold_1_mRNA_2631.1 | C_unshiu_00277_mRNA_12.1 | - |
| GF0019826 | 1 | 1 | 0 | RING/U-box superfamily protein, putative isoform 1 (1); RING-H2 finger protein ATL1Q (1) | protein binding [GO:0005515 molecular_function] (2); zinc ion binding [GO:0008270 molecular_function] (2) | Zinc finger, RING-type [IPR001841] (2); Zinc finger, RING/FYVE/PHD-type [IPR013083] (2); RidA family [IPR006056] (1); YjgF/YER057c/UK114 family [IPR006175] (1); RidA, conserved site [IPR019897] (1); Endoribonuclease L-PSP/chorismate mutase-like [IPR013813] (1) | scaffold_1_mRNA_2627.1 | C_unshiu_01352_mRNA_1.1 | - |
| GF0019824 | 1 | 1 | 0 | Polyadenylate-binding protein RBP47C (1); Hypothetical protein (1) | nucleic acid binding [GO:0003676 molecular_function] (2); nucleotide binding [GO:0000166 molecular_function] (1); ADP binding [GO:0043531 molecular_function] (1) | RNA recognition motif domain [IPR000504] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); Nucleotide-binding alpha-beta plait domain [IPR012677] (1); NB-ARC [IPR002182] (1) | scaffold_1_mRNA_2611.1 | C_unshiu_00998_mRNA_7.1 | - |
| GF0019823 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_260.1 | C_unshiu_00553_mRNA_4.1 | - |
| GF0019822 | 1 | 1 | 0 | Proteasome subunit beta type (2) | threonine-type endopeptidase activity [GO:0004298 molecular_function] (2); endopeptidase activity [GO:0004175 molecular_function] (2); proteasome core complex [GO:0005839 cellular_component] (2); proteolysis involved in cellular protein catabolic process [GO:0051603 biological_process] (2) | Proteasome beta-type subunit, conserved site [IPR016050] (2); Proteasome B-type subunit [IPR023333] (2); Peptidase T1A, proteasome beta-subunit [IPR000243] (2); Nucleophile aminohydrolases, N-terminal [IPR029055] (2); Proteasome, subunit alpha/beta [IPR001353] (2) | scaffold_1_mRNA_26.1 | C_unshiu_00003_mRNA_138.1 | - |
| GF0019821 | 1 | 1 | 0 | Cytochrome P450 716B1 (2) | oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2); iron ion binding [GO:0005506 molecular_function] (2); heme binding [GO:0020037 molecular_function] (2); monooxygenase activity [GO:0004497 molecular_function] (1) | Cytochrome P450, B-class [IPR002397] (2); Cytochrome P450, conserved site [IPR017972] (2); Cytochrome P450 [IPR001128] (2) | scaffold_1_mRNA_2595.1 | C_unshiu_00595_mRNA_9.1 | - |
| GF0019820 | 1 | 1 | 0 | Aminotransferase-like, plant mobile domain family protein (1); C globular stage, putative (1) | | Aminotransferase-like, plant mobile domain [IPR019557] (2); Protein of unknown function DUF716 (TMEM45) [IPR006904] (2) | scaffold_1_mRNA_2584.1 | C_unshiu_00017_mRNA_22.1 | - |
| GF0019819 | 1 | 1 | 0 | Hypothetical protein (2) | | Leucine-rich repeat domain, L domain-like [IPR032675] (1) | scaffold_1_mRNA_2578.1 | C_unshiu_00017_mRNA_30.1 | - |
| GF0019818 | 1 | 1 | 0 | F-box/LRR-repeat protein At3g58900 (1); Hypothetical protein (1) | protein binding [GO:0005515 molecular_function] (1) | Leucine-rich repeat domain, L domain-like [IPR032675] (2); F-box domain [IPR001810] (1) | scaffold_1_mRNA_2577.1 | C_unshiu_00017_mRNA_31.1 | - |
| GF0019817 | 1 | 1 | 0 | LRR receptor-like kinase family protein (1); LRR receptor-like serine/threonine-protein kinase GSO1 (1) | protein binding [GO:0005515 molecular_function] (2) | Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (2); Leucine-rich repeat [IPR001611] (2); Leucine-rich repeat, typical subtype [IPR003591] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2) | scaffold_1_mRNA_2573.1 | C_unshiu_02856_mRNA_2.1 | - |
| GF0019815 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_2571.1 | C_unshiu_02856_mRNA_3.1 | - |
| GF0019814 | 1 | 1 | 0 | Protein FAR1-RELATED SEQUENCE 5 (2) | regulation of transcription, DNA-templated [GO:0006355 biological_process] (2); zinc ion binding [GO:0008270 molecular_function] (2) | FAR1 DNA binding domain [IPR004330] (2); FHY3/FAR1 family [IPR031052] (2); Zinc finger, SWIM-type [IPR007527] (2); MULE transposase domain [IPR018289] (2) | scaffold_1_mRNA_2566.1 | C_unshiu_01265_mRNA_7.1 | - |
| GF0019813 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_2562.1 | C_unshiu_01265_mRNA_2.1 | - |
| GF0019812 | 1 | 1 | 0 | Hypothetical protein (2) | | Aminotransferase-like, plant mobile domain [IPR019557] (2); Protein of unknown function DUF716 (TMEM45) [IPR006904] (2) | scaffold_1_mRNA_2558.1 | C_unshiu_03061_mRNA_1.1 | - |
| GF0019811 | 1 | 1 | 0 | FBD, F-box and leucine rich repeat domain-containing protein (2) | protein binding [GO:0005515 molecular_function] (2) | Leucine-rich repeat 2 [IPR013101] (2); F-box domain [IPR001810] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); FBD domain [IPR006566] (1) | scaffold_1_mRNA_2554.1 | C_unshiu_02130_mRNA_1.1 | - |
| GF0019810 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_2551.1 | C_unshiu_00036_mRNA_51.1 | - |
| GF0019809 | 1 | 1 | 0 | Serine/threonine-protein kinase PBS1 (2) | protein phosphorylation [GO:0006468 biological_process] (2); protein kinase activity [GO:0004672 molecular_function] (2); ATP binding [GO:0005524 molecular_function] (2) | Serine/threonine-protein kinase, active site [IPR008271] (2); Protein kinase, ATP binding site [IPR017441] (2); Protein kinase-like domain [IPR011009] (2); Protein kinase domain [IPR000719] (2); Concanavalin A-like lectin/glucanase domain [IPR013320] (1) | scaffold_1_mRNA_2550.1 | C_unshiu_00036_mRNA_52.1 | - |
| GF0019808 | 1 | 1 | 0 | Hypothetical protein (2) | | Protein of unknown function DUF4666 [IPR031421] (2) | scaffold_1_mRNA_255.1 | C_unshiu_00749_mRNA_12.1 | - |
| GF0019807 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_2547.1 | C_unshiu_00576_mRNA_15.1 | - |
| GF0019806 | 1 | 1 | 0 | Serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit A (1); Ankyrin repeat family protein, putative (1) | protein binding [GO:0005515 molecular_function] (2) | Ankyrin repeat-containing domain [IPR020683] (2); Ankyrin repeat [IPR002110] (2) | scaffold_1_mRNA_2541.1 | C_unshiu_02076_mRNA_3.1 | - |
| GF0019805 | 1 | 1 | 0 | Ankyrin repeat protein (2) | protein binding [GO:0005515 molecular_function] (1) | PGG domain [IPR026961] (2); Ankyrin repeat-containing domain [IPR020683] (2); Ankyrin repeat [IPR002110] (1) | scaffold_1_mRNA_2540.1 | C_unshiu_02122_mRNA_1.1 | - |
| GF0019804 | 1 | 1 | 0 | Hypothetical protein (2) | | Protein of unknown function DUF4666 [IPR031421] (2) | scaffold_1_mRNA_254.1 | C_unshiu_00749_mRNA_11.1 | - |
| GF0019803 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_2519.1 | C_unshiu_00142_mRNA_8.1 | - |
| GF0019801 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_2500.1 | C_unshiu_00157_mRNA_2.1 | - |
| GF0019800 | 1 | 1 | 0 | Cation transport protein chaC (2) | glutathione catabolic process [GO:0006751 biological_process] (1); gamma-glutamylcyclotransferase activity [GO:0003839 molecular_function] (1) | Gamma-glutamyl cyclotransferase-like [IPR013024] (1); Glutathione-specific gamma-glutamylcyclotransferase [IPR006840] (1); ChaC-like protein [IPR006840] (1); Butirosin biosynthesis, BtrG-like [IPR013024] (1) | scaffold_1_mRNA_25.2 | C_unshiu_00003_mRNA_137.2 | - |
| GF0019799 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_2499.1 | C_unshiu_00157_mRNA_7.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0019798 | 1 | 1 | 0 | E3 ubiquitin-protein ligase RBBP6 (1); Hypothetical protein (1) | nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1) | Zinc finger, CCHC-type [IPR001878] (1); Retrotransposon gag domain [IPR005162] (1) | scaffold_1_mRNA_2498.1 | C_unshiu_01430_mRNA_1.1 | - |
| GF0019797 | 1 | 1 | 0 | Disease resistance family protein / LRR family protein, putative (2) | protein binding [GO:0005515 molecular_function] (2) | Leucine-rich repeat [IPR001611] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2) | scaffold_1_mRNA_2494.1 | C_unshiu_00487_mRNA_23.1 | - |
| GF0019796 | 1 | 1 | 0 | Disease resistance family protein / LRR family protein, putative (2) | protein binding [GO:0005515 molecular_function] (2) | Leucine-rich repeat, typical subtype [IPR003591] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Leucine-rich repeat [IPR001611] (2); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (2) | scaffold_1_mRNA_2492.1 | C_unshiu_00487_mRNA_21.1 | - |
| GF0019795 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_2490.1 | C_unshiu_00487_mRNA_19.1 | - |
| GF0019793 | 1 | 1 | 0 | Lambda class glutathione S-transferase (1); Glutathione S-transferase L3 (1) | protein binding [GO:0005515 molecular_function] (1) | Glutathione S-transferase, C-terminal-like [IPR010987] (2); Ubiquitin domain [IPR000626] (1); Ubiquitin-related domain [IPR029071] (1); Ubiquitin [IPR019956] (1) | scaffold_1_mRNA_2473.1 | C_unshiu_00395_mRNA_15.1 | - |
| GF0019792 | 1 | 1 | 0 | Non-race specific disease resistance 1 (2) | | | scaffold_1_mRNA_2471.1 | C_unshiu_00395_mRNA_13.1 | - |
| GF0019791 | 1 | 1 | 0 | ABC transporter B family member 15 (2) | transport [GO:0006810 biological_process] (2); integral component of membrane [GO:0016021 cellular_component] (2); ATPase activity [GO:0016887 molecular_function] (2); ATP binding [GO:0005524 molecular_function] (2); transmembrane transport [GO:0055085 biological_process] (2); ATPase activity, coupled to transmembrane movement of substances [GO:0042626 molecular_function] (2) | ABC transporter, conserved site [IPR017871] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); AAA+ ATPase domain [IPR003593] (2); ABC transporter-like [IPR003439] (2); ABC transporter type 1, transmembrane domain [IPR011527] (2) | scaffold_1_mRNA_2470.1 | C_unshiu_00395_mRNA_12.1 | - |
| GF0019790 | 1 | 1 | 0 | Hypothetical protein (2) | drug transmembrane transporter activity [GO:0015238 molecular_function] (2); antiporter activity [GO:0015297 molecular_function] (2); membrane [GO:0016020 cellular_component] (2); drug transmembrane transport [GO:0006855 biological_process] (2); transmembrane transport [GO:0055085 biological_process] (2) | Multi antimicrobial extrusion protein [IPR002528] (2) | scaffold_1_mRNA_2464.1 | C_unshiu_00395_mRNA_6.1 | - |
| GF0019788 | 1 | 1 | 0 | Hypothetical protein (2) | | Ataxin-2, C-terminal [IPR009818] (2) | scaffold_1_mRNA_2447.1 | C_unshiu_00626_mRNA_13.1 | - |
| GF0019786 | 1 | 1 | 0 | Terpenoid synthase (1); Delta-cadinene synthase isozyme A (1) | lyase activity [GO:0016829 molecular_function] (2); terpene synthase activity [GO:0010333 molecular_function] (2); magnesium ion binding [GO:0000287 molecular_function] (2) | Isoprenoid synthase domain [IPR008949] (2); Terpene synthase, metal-binding domain [IPR005630] (2) | scaffold_1_mRNA_2439.1 | C_unshiu_01516_mRNA_1.1 | - |
| GF0019785 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_2436.1 | C_unshiu_01516_mRNA_6.1 | - |
| GF0019784 | 1 | 1 | 0 | Delta-cadinene synthase isozyme XC14 (1); (+)-delta-cadinene synthase isozyme A (1) | lyase activity [GO:0016829 molecular_function] (2); terpene synthase activity [GO:0010333 molecular_function] (2); metabolic process [GO:0008152 biological_process] (2) | Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (2); Terpene synthase, N-terminal domain [IPR001906] (2) | scaffold_1_mRNA_2419.1 | C_unshiu_01090_mRNA_5.1 | - |
| GF0019781 | 1 | 1 | 0 | Sesquiterpene synthase (2) | magnesium ion binding [GO:0000287 molecular_function] (2); terpene synthase activity [GO:0010333 molecular_function] (2); lyase activity [GO:0016829 molecular_function] (2); metabolic process [GO:0008152 biological_process] (2) | Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (2); Terpene synthase, N-terminal domain [IPR001906] (2); Terpene synthase, metal-binding domain [IPR005630] (2); Isoprenoid synthase domain [IPR008949] (2) | scaffold_1_mRNA_2409.1 | C_unshiu_01090_mRNA_13.1 | - |
| GF0019780 | 1 | 1 | 0 | Hypothetical protein (2) | DNA binding [GO:0003677 molecular_function] (1) | Myb-like domain [IPR017877] (2); Homeodomain-like [IPR009057] (1) | scaffold_1_mRNA_24.1 | C_unshiu_00003_mRNA_136.1 | - |
| GF0019779 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_2396.1 | C_unshiu_00743_mRNA_10.1 | - |
| GF0019778 | 1 | 1 | 0 | Sesquiterpene synthase (2) | metabolic process [GO:0008152 biological_process] (2); terpene synthase activity [GO:0010333 molecular_function] (2); lyase activity [GO:0016829 molecular_function] (2); magnesium ion binding [GO:0000287 molecular_function] (2) | Isoprenoid synthase domain [IPR008949] (2); Terpene synthase, metal-binding domain [IPR005630] (2); Terpene synthase, N-terminal domain [IPR001906] (2); Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (2) | scaffold_1_mRNA_2395.1 | C_unshiu_00743_mRNA_11.1 | - |
| GF0019777 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_2393.1 | C_unshiu_01083_mRNA_6.1 | - |
| GF0019776 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_2392.1 | C_unshiu_01083_mRNA_5.1 | - |
| GF0019775 | 1 | 1 | 0 | Hypothetical protein (2) | 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_2389.1 | C_unshiu_02083_mRNA_4.1 | - |
| GF0019774 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (1) | Endonuclease/exonuclease/phosphatase [IPR005135] (2); Ribonuclease H-like domain [IPR012337] (1) | scaffold_1_mRNA_2381.1 | C_unshiu_00174_mRNA_5.1 | - |
| GF0019772 | 1 | 1 | 0 | Hypothetical protein (1); FAR1 DNA-binding domain protein (1) | zinc ion binding [GO:0008270 molecular_function] (2); regulation of transcription, DNA-templated [GO:0006355 biological_process] (2) | Zinc finger, SWIM-type [IPR007527] (2); FHY3/FAR1 family [IPR031052] (2); FAR1 DNA binding domain [IPR004330] (2) | scaffold_1_mRNA_2371.1 | C_unshiu_00132_mRNA_17.1 | - |
| GF0019771 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_2358.1 | C_unshiu_01256_mRNA_1.1 | - |
| GF0019770 | 1 | 1 | 0 | Hypothetical protein (2) | | Retrotransposon gag domain [IPR005162] (2) | scaffold_1_mRNA_2353.1 | C_unshiu_02834_mRNA_2.1 | - |
| GF0019769 | 1 | 1 | 0 | Monosacharide transport protein (2) | | | scaffold_1_mRNA_2351.1 | C_unshiu_02834_mRNA_5.1 | - |
| GF0019768 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_2350.1 | C_unshiu_02834_mRNA_6.1 | - |
| GF0019767 | 1 | 1 | 0 | Hypothetical protein (2) | ATP binding [GO:0005524 molecular_function] (2); protein kinase activity [GO:0004672 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2) | Protein kinase-like domain [IPR011009] (2); Protein kinase domain [IPR000719] (2); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); Serine/threonine-protein kinase, active site [IPR008271] (1) | scaffold_1_mRNA_2345.1 | C_unshiu_00462_mRNA_17.1 | - |
| GF0019766 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_2344.1 | C_unshiu_00462_mRNA_16.1 | - |
| GF0019765 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_2343.1 | C_unshiu_00462_mRNA_15.1 | - |
| GF0019764 | 1 | 1 | 0 | Cysteine-rich RLK (Receptor-like kinase) protein (2) | ATP binding [GO:0005524 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2); protein serine/threonine kinase activity [GO:0004674 molecular_function] (2); protein kinase activity [GO:0004672 molecular_function] (2) | S-locus receptor kinase, C-terminal [IPR021820] (2); Serine/threonine-protein kinase, active site [IPR008271] (2); Protein kinase, ATP binding site [IPR017441] (2); Protein kinase-like domain [IPR011009] (2); Protein kinase domain [IPR000719] (2); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1) | scaffold_1_mRNA_2342.1 | C_unshiu_00462_mRNA_14.1 | - |
| GF0019763 | 1 | 1 | 0 | Hypothetical protein (2) | | Retrotransposon gag domain [IPR005162] (2) | scaffold_1_mRNA_2340.1 | C_unshiu_00462_mRNA_13.1 | - |
| GF0019762 | 1 | 1 | 0 | S-locus lectin kinase family protein (2) | recognition of pollen [GO:0048544 biological_process] (2) | Bulb-type lectin domain [IPR001480] (2); PAN/Apple domain [IPR003609] (2); S-locus glycoprotein domain [IPR000858] (2); Protein kinase-like domain [IPR011009] (1) | scaffold_1_mRNA_2338.1 | C_unshiu_00210_mRNA_29.1 | - |
| GF0019761 | 1 | 1 | 0 | Cysteine-rich RLK (Receptor-like kinase) protein (2) | ATP binding [GO:0005524 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2); protein kinase activity [GO:0004672 molecular_function] (2) | Serine/threonine-protein kinase, active site [IPR008271] (2); Protein kinase domain [IPR000719] (2); Protein kinase-like domain [IPR011009] (2); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1) | scaffold_1_mRNA_2332.1 | C_unshiu_01720_mRNA_3.1 | - |
| GF0019758 | 1 | 1 | 0 | S-locus lectin protein kinase family protein, putative (1); Hypothetical protein (1) | | Bulb-type lectin domain [IPR001480] (2) | scaffold_1_mRNA_2308.1 | C_unshiu_00386_mRNA_23.1 | - |
| GF0019756 | 1 | 1 | 0 | S-locus lectin kinase family protein (2) | recognition of pollen [GO:0048544 biological_process] (2); protein binding [GO:0005515 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1); ATP binding [GO:0005524 molecular_function] (1); protein tyrosine kinase activity [GO:0004713 molecular_function] (1) | Protein kinase-like domain [IPR011009] (2); Bulb-type lectin domain [IPR001480] (2); PAN/Apple domain [IPR003609] (2); EGF-like domain [IPR000742] (2); S-locus glycoprotein domain [IPR000858] (2); Tyrosine-protein kinase, catalytic domain [IPR020635] (1); Protein kinase domain [IPR000719] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1) | scaffold_1_mRNA_2289.1 | C_unshiu_00210_mRNA_28.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0019755 | 1 | 1 | 0 | G-type lectin S-receptor-like serine/threonine-protein kinase (2) | protein kinase activity [GO:0004672 molecular_function] (2); recognition of pollen [GO:0048544 biological_process] (2); protein phosphorylation [GO:0006468 biological_process] (2); ATP binding [GO:0005524 molecular_function] (2) | Protein kinase domain [IPR000719] (2); Protein kinase-like domain [IPR011009] (2); S-locus glycoprotein domain [IPR000858] (2); Serine/threonine-protein kinase, active site [IPR008271] (2); Bulb-type lectin domain [IPR001480] (2); PAN/Apple domain [IPR003609] (2); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1) | scaffold_1_mRNA_2284.1 | C_unshiu_00210_mRNA_34.1 | - |
| GF0019754 | 1 | 1 | 0 | Retrotransposon protein, putative, unclassified (2) | | Retrotransposon gag domain [IPR005162] (2); Retroviral aspartyl protease [IPR013242] (2); Aspartic peptidase domain [IPR021109] (1) | scaffold_1_mRNA_2283.1 | C_unshiu_00210_mRNA_35.1 | - |
| GF0019751 | 1 | 1 | 0 | G-type lectin S-receptor-like serine/threonine-protein kinase (2) | ATP binding [GO:0005524 molecular_function] (2); protein kinase activity [GO:0004672 molecular_function] (2); recognition of pollen [GO:0048544 biological_process] (2); protein phosphorylation [GO:0006468 biological_process] (2); protein serine/threonine kinase activity [GO:0004674 molecular_function] (1) | PAN/Apple domain [IPR003609] (2); Bulb-type lectin domain [IPR001480] (2); Serine/threonine-protein kinase, active site [IPR008271] (2); S-locus glycoprotein domain [IPR000858] (2); Protein kinase-like domain [IPR011009] (2); Protein kinase domain [IPR000719] (2); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); S-receptor-like serine/threonine-protein kinase [IPR024171] (1); Concanavalin A-like lectin/glucanase domain [IPR013320] (1) | scaffold_1_mRNA_2270.1 | C_unshiu_01771_mRNA_4.1 | - |
| GF0019749 | 1 | 1 | 0 | Hypothetical protein (1); RNA-directed DNA polymerase (Reverse transcriptase), Ribonuclease H (1) | | Reverse transcriptase domain [IPR000477] (1) | scaffold_1_mRNA_2267.1 | C_unshiu_00274_mRNA_33.1 | - |
| GF0019748 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_2262.1 | C_unshiu_00274_mRNA_29.1 | - |
| GF0019746 | 1 | 1 | 0 | Hypothetical protein (2) | calcium ion binding [GO:0005509 molecular_function] (2) | EF-hand domain [IPR002048] (2); EF-Hand 1, calcium-binding site [IPR018247] (2); EF-hand domain pair [IPR011992] (2); Protein kinase-like domain [IPR011009] (1) | scaffold_1_mRNA_2248.1 | C_unshiu_00274_mRNA_18.1 | - |
| GF0019745 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_2247.1 | C_unshiu_00274_mRNA_17.1 | - |
| GF0019744 | 1 | 1 | 0 | Hypothetical protein (2) | | Zinc knuckle CX2CX4HX4C [IPR025836] (2); Domain of unknown function DUF4283 [IPR025558] (2) | scaffold_1_mRNA_2245.1 | C_unshiu_00274_mRNA_14.1 | - |
| GF0019743 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_2240.1 | C_unshiu_00274_mRNA_9.1 | - |
| GF0019742 | 1 | 1 | 0 | Hypothetical protein (2) | | Reverse transcriptase domain [IPR000477] (2) | scaffold_1_mRNA_2236.1 | C_unshiu_00274_mRNA_6.1 | - |
| GF0019741 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_2235.1 | C_unshiu_00274_mRNA_5.1 | - |
| GF0019740 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_2234.1 | C_unshiu_00274_mRNA_4.1 | - |
| GF0019739 | 1 | 1 | 0 | Non-LTR retroelement reverse transcriptase-like protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (2) | Ribonuclease H domain [IPR002156] (2); Ribonuclease H-like domain [IPR012337] (2); Reverse transcriptase zinc-binding domain [IPR026960] (2) | scaffold_1_mRNA_2230.1 | C_unshiu_00369_mRNA_44.1 | - |
| GF0019738 | 1 | 1 | 0 | S-locus lectin kinase family protein, putative (1); S-locus lectin protein kinase family protein isoform 4 (1) | recognition of pollen [GO:0048544 biological_process] (2); ATP binding [GO:0005524 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1) | S-locus glycoprotein domain [IPR000858] (2); Bulb-type lectin domain [IPR001480] (2); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase domain [IPR000719] (1); Protein kinase-like domain [IPR011009] (1) | scaffold_1_mRNA_2229.1 | C_unshiu_00369_mRNA_42.1 | - |
| GF0019737 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_2194.1 | C_unshiu_00137_mRNA_29.1 | - |
| GF0019735 | 1 | 1 | 0 | Hypothetical protein (1); FBD-associated F-box protein At4g10400 (1) | protein binding [GO:0005515 molecular_function] (1) | FBD domain [IPR006566] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); F-box domain [IPR001810] (1) | scaffold_1_mRNA_2178.1 | C_unshiu_00137_mRNA_39.1 | - |
| GF0019734 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2); Ribonuclease H domain [IPR002156] (2) | scaffold_1_mRNA_2170.1 | C_unshiu_00137_mRNA_48.1 | - |
| GF0019733 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_2157.1 | C_unshiu_00993_mRNA_8.1 | - |
| GF0019731 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (1) | Ribonuclease H-like domain [IPR012337] (1) | scaffold_1_mRNA_2152.1 | C_unshiu_00822_mRNA_8.1 | - |
| GF0019730 | 1 | 1 | 0 | F-box and associated interaction domains-containing protein (1); Hypothetical protein (1) | protein binding [GO:0005515 molecular_function] (2) | F-box domain [IPR001810] (2); WD40/YVTN repeat-like-containing domain [IPR015943] (1) | scaffold_1_mRNA_2150.1 | C_unshiu_01676_mRNA_4.1 | - |
| GF0019729 | 1 | 1 | 0 | Hypothetical protein (1); Ubiquitin carboxyl-terminal hydrolase 12 (1) | protein binding [GO:0005515 molecular_function] (2) | TRAF-like [IPR008974] (2); MATH/TRAF domain [IPR002083] (2) | scaffold_1_mRNA_2119.1 | C_unshiu_00187_mRNA_33.1 | - |
| GF0019728 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_2102.1 | C_unshiu_00187_mRNA_18.1 | - |
| GF0019727 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_2096.1 | C_unshiu_00187_mRNA_11.1 | - |
| GF0019726 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_2093.1 | C_unshiu_00187_mRNA_8.1 | - |
| GF0019725 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_2087.1 | C_unshiu_00429_mRNA_23.1 | - |
| GF0019724 | 1 | 1 | 0 | DNase I superfamily protein, putative (1); Hypothetical protein (1) | | Endonuclease/exonuclease/phosphatase [IPR005135] (1) | scaffold_1_mRNA_2084.1 | C_unshiu_00087_mRNA_18.1 | - |
| GF0019723 | 1 | 1 | 0 | Hypothetical protein (2) | protein binding [GO:0005515 molecular_function] (2); zinc ion binding [GO:0008270 molecular_function] (2) | Zinc finger, RING-type [IPR001841] (2); Zinc finger, RING/FYVE/PHD-type [IPR013083] (2) | scaffold_1_mRNA_2059.1 | C_unshiu_00044_mRNA_20.1 | - |
| GF0019722 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_2058.1 | C_unshiu_00044_mRNA_21.1 | - |
| GF0019721 | 1 | 1 | 0 | Hypothetical protein (2) | | Leucine-rich repeat domain, L domain-like [IPR032675] (2) | scaffold_1_mRNA_2052.1 | C_unshiu_00044_mRNA_26.1 | - |
| GF0019720 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_2049.1 | C_unshiu_00044_mRNA_28.1 | - |
| GF0019719 | 1 | 1 | 0 | Hypothetical protein (2) | ADP binding [GO:0043531 molecular_function] (2) | NB-ARC [IPR002182] (2); AAA+ ATPase domain [IPR003593] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Winged helix-turn-helix DNA-binding domain [IPR011991] (1) | scaffold_1_mRNA_2048.1 | C_unshiu_00044_mRNA_30.1 | - |
| GF0019717 | 1 | 1 | 0 | Serine/threonine-protein kinase isoform 2 (2) | ATP binding [GO:0005524 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2); protein kinase activity [GO:0004672 molecular_function] (2) | Protein kinase-like domain [IPR011009] (2); Protein kinase domain [IPR000719] (2); Serine/threonine-protein kinase, active site [IPR008271] (2); Protein kinase, ATP binding site [IPR017441] (2); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1) | scaffold_1_mRNA_2038.1 | C_unshiu_00044_mRNA_46.1 | - |
| GF0019716 | 1 | 1 | 0 | Legume lectin family protein (2) | carbohydrate binding [GO:0030246 molecular_function] (2) | Legume lectin domain [IPR001220] (2); Concanavalin A-like lectin/glucanase domain [IPR013320] (2); Lectin [IPR016363] (1); Legume lectin [IPR016363] (1) | scaffold_1_mRNA_2037.1 | C_unshiu_00044_mRNA_48.1 | - |
| GF0019715 | 1 | 1 | 0 | Early nodulin-like protein 2 (2) | electron carrier activity [GO:0009055 molecular_function] (2) | Cupredoxin [IPR008972] (2); Phytocyanin domain [IPR003245] (2) | scaffold_1_mRNA_2022.1 | C_unshiu_00044_mRNA_62.1 | - |
| GF0019711 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_2010.1 | C_unshiu_00247_mRNA_35.1 | - |
| GF0019710 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1995.1 | C_unshiu_00035_mRNA_48.1 | - |
| GF0019708 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1986.1 | C_unshiu_00035_mRNA_60.1 | - |
| GF0019707 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1985.1 | C_unshiu_00035_mRNA_61.1 | - |
| GF0019706 | 1 | 1 | 0 | Hypothetical protein (2) | | Leucine-rich repeat domain, L domain-like [IPR032675] (1) | scaffold_1_mRNA_1984.1 | C_unshiu_00035_mRNA_62.1 | - |
| GF0019704 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1970.1 | C_unshiu_00035_mRNA_75.1 | - |
| GF0019703 | 1 | 1 | 0 | Glycoside hydrolase family 79 amino-terminal domain protein (2) | membrane [GO:0016020 cellular_component] (2); hydrolase activity, acting on glycosyl bonds [GO:0016798 molecular_function] (2); carbohydrate metabolic process [GO:0005975 biological_process] (1) | Glycoside hydrolase superfamily [IPR017853] (2); Glycoside hydrolase, family 79 [IPR005199] (2); Glycoside hydrolase, catalytic domain [IPR013781] (1) | scaffold_1_mRNA_197.1 | C_unshiu_00005_mRNA_97.1 | - |
| GF0019702 | 1 | 1 | 0 | NBS-LRR class resistance protein Fy1-Ry1 (2) | ADP binding [GO:0043531 molecular_function] (2) | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); NB-ARC [IPR002182] (2); Winged helix-turn-helix DNA-binding domain [IPR011991] (1) | scaffold_1_mRNA_1968.1 | C_unshiu_00035_mRNA_77.1 | - |
| GF0019701 | 1 | 1 | 0 | Putative disease resistance protein (2) | ADP binding [GO:0043531 molecular_function] (2) | NB-ARC [IPR002182] (2); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); Winged helix-turn-helix DNA-binding domain [IPR011991] (1) | scaffold_1_mRNA_1967.1 | C_unshiu_00035_mRNA_78.1 | - |
| GF0019700 | 1 | 1 | 0 | Hypothetical protein (2) | | Leucine-rich repeat domain, L domain-like [IPR032675] (1) | scaffold_1_mRNA_1964.1 | C_unshiu_00468_mRNA_13.1 | - |
| GF0019699 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1958.1 | C_unshiu_00035_mRNA_84.1 | - |
| GF0019698 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1956.1 | C_unshiu_00035_mRNA_87.1 | - |
| GF0019697 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1955.1 | C_unshiu_00035_mRNA_88.1 | - |
| GF0019696 | 1 | 1 | 0 | Hypothetical protein (2) | | Probable transposase, Ptta/En/Spm, plant [IPR004252] (2) | scaffold_1_mRNA_1949.1 | C_unshiu_00035_mRNA_94.1 | - |
| GF0019695 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1936.1 | C_unshiu_00452_mRNA_3.1 | - |
| GF0019694 | 1 | 1 | 0 | Hypothetical protein (2) | | Leucine-rich repeat domain, L domain-like [IPR032675] (2) | scaffold_1_mRNA_1931.1 | C_unshiu_00452_mRNA_12.1 | - |
| GF0019693 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1929.1 | C_unshiu_00452_mRNA_14.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0019692 | 1 | 1 | 0 | Hypothetical protein (2) | ADP binding [GO:0043531 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (1); DNA integration [GO:0015074 biological_process] (1) | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (2); NB-ARC [IPR002182] (2); Integrase, catalytic core [IPR001584] (1); Ribonuclease H-like domain [IPR012337] (1) | scaffold_1_mRNA_1926.1 | C_unshiu_00452_mRNA_17.1 | - |
| GF0019691 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1925.1 | C_unshiu_00452_mRNA_18.1 | - |
| GF0019690 | 1 | 1 | 0 | Hypothetical protein (2) | | Harbinger transposase-derived nuclease domain [IPR027806] (2) | scaffold_1_mRNA_1917.1 | C_unshiu_00452_mRNA_23.1 | - |
| GF0019689 | 1 | 1 | 0 | Cytokinin riboside 5'-monophosphate phosphoribohydrolase (2) | | LOG family [IPR031100] (2); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (2) | scaffold_1_mRNA_1914.1 | C_unshiu_00452_mRNA_25.1 | - |
| GF0019688 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_191.1 | C_unshiu_00852_mRNA_13.1 | - |
| GF0019687 | 1 | 1 | 0 | NO APICAL MERISTEM (2) | regulation of transcription, DNA-templated [GO:0006355 biological_process] (2); phosphotransferase activity, alcohol group as acceptor [GO:0016773 molecular_function] (2); DNA binding [GO:0003677 molecular_function] (2) | NAC domain [IPR003441] (2); Carbohydrate/puine kinase, PfkB, conserved site [IPR002173] (2) | scaffold_1_mRNA_1909.1 | C_unshiu_00282_mRNA_2.1 | - |
| GF0019686 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1906.1 | C_unshiu_00282_mRNA_5.1 | - |
| GF0019684 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1894.1 | C_unshiu_00282_mRNA_17.1 | - |
| GF0019683 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1885.1 | C_unshiu_00108_mRNA_31.1 | - |
| GF0019682 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1877.1 | C_unshiu_00108_mRNA_20.1 | - |
| GF0019680 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1856.1 | C_unshiu_01727_mRNA_4.1 | - |
| GF0019679 | 1 | 1 | 0 | Hypothetical protein (2) | | Trichome birefringence-like family [IPR029962] (2); PMR5 N-terminal domain [IPR025846] (2); PC-Esterase [IPR026057] (2) | scaffold_1_mRNA_1836.1 | C_unshiu_00288_mRNA_3.1 | - |
| GF0019678 | 1 | 1 | 0 | Ferrochelatase (2) | | PC-Esterase [IPR026057] (2); Trichome birefringence-like family [IPR029962] (2) | scaffold_1_mRNA_1834.1 | C_unshiu_00288_mRNA_5.1 | - |
| GF0019677 | 1 | 1 | 0 | Lipid transfer protein 2 (2) | lipid binding [GO:0008289 molecular_function] (2); lipid transport [GO:0006869 biological_process] (2) | Plant lipid transfer protein/Par allergen [IPR000528] (2); Bifunctional inhibitor/plant lipid transfer protein/seed storage helical domain [IPR016140] (2) | scaffold_1_mRNA_1818.1 | C_unshiu_01700_mRNA_5.1 | - |
| GF0019676 | 1 | 1 | 0 | Hypothetical protein (2) | | Domain of unknown function DUF1985 [IPR015410] (2) | scaffold_1_mRNA_1815.1 | C_unshiu_01700_mRNA_8.1 | - |
| GF0019675 | 1 | 1 | 0 | Hypothetical protein (2) | | Transposase, MuDR, plant [IPR004332] (2) | scaffold_1_mRNA_1814.1 | C_unshiu_01700_mRNA_10.1 | - |
| GF0019673 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1810.1 | C_unshiu_00426_mRNA_19.1 | - |
| GF0019671 | 1 | 1 | 0 | Hypothetical protein (2) | proteolysis [GO:0006508 biological_process] (2); cysteine-type peptidase activity [GO:0008234 molecular_function] (2) | Ulp1 protease family, C-terminal catalytic domain [IPR003653] (2) | scaffold_1_mRNA_1806.1 | C_unshiu_00426_mRNA_22.1 | - |
| GF0019670 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1799.1 | C_unshiu_00426_mRNA_25.1 | - |
| GF0019669 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1798.1 | C_unshiu_00426_mRNA_26.1 | - |
| GF0019668 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1792.1 | C_unshiu_01098_mRNA_5.1 | - |
| GF0019667 | 1 | 1 | 0 | Hypothetical protein (2) | | Domain of unknown function DUF4219 [IPR025314] (2) | scaffold_1_mRNA_1790.1 | C_unshiu_01098_mRNA_3.1 | - |
| GF0019666 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1780.1 | C_unshiu_00694_mRNA_4.1 | - |
| GF0019665 | 1 | 1 | 0 | Hypothetical protein (2) | | Domain of unknown function DUF4371 [IPR025398] (2) | scaffold_1_mRNA_1777.1 | C_unshiu_00694_mRNA_8.1 | - |
| GF0019664 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1771.1 | C_unshiu_00694_mRNA_14.1 | - |
| GF0019663 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1770.1 | C_unshiu_02477_mRNA_3.1 | - |
| GF0019662 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1769.1 | C_unshiu_00022_mRNA_31.1 | - |
| GF0019661 | 1 | 1 | 0 | Hypothetical protein (2) | | Transposase, MuDR, plant [IPR004332] (2) | scaffold_1_mRNA_1762.1 | C_unshiu_00944_mRNA_4.1 | - |
| GF0019660 | 1 | 1 | 0 | Caffeic acid 3-O-methyltransferase (1); Caffeate O-methyltransferase (1) | O-methyltransferase activity [GO:0008171 molecular_function] (2); methyltransferase activity [GO:0008168 molecular_function] (2) | Winged helix-turn-helix DNA-binding domain [IPR011991] (2); O-methyltransferase, family 2 [IPR001077] (2); O-methyltransferase COMT-type [IPR016461] (2); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (2) | scaffold_1_mRNA_1761.1 | C_unshiu_00944_mRNA_3.1 | - |
| GF0019659 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1758.1 | C_unshiu_00770_mRNA_2.1 | - |
| GF0019658 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1757.1 | C_unshiu_01217_mRNA_3.1 | - |
| GF0019657 | 1 | 1 | 0 | Hypothetical protein (2) | oxidoreductase activity [GO:0016491 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2) | Peptidase S24/S26A/S26B/S26C [IPR015927] (2); Aldo/keto reductase [IPR020471] (2); Aldo/keto reductase, conserved site [IPR018170] (2); NADP-dependent oxidoreductase domain [IPR023210] (2); Aldo/keto reductase/potassium channel subunit beta [IPR001395] (1) | scaffold_1_mRNA_1753.1 | C_unshiu_01217_mRNA_5.1 | - |
| GF0019656 | 1 | 1 | 0 | Hypothetical protein (2) | oxidation-reduction process [GO:0055114 biological_process] (2); oxidoreductase activity [GO:0016491 molecular_function] (2) | Aldo/keto reductase, conserved site [IPR018170] (2); NADP-dependent oxidoreductase domain [IPR023210] (2); Aldo/keto reductase/potassium channel subunit beta [IPR001395] (1); Aldo/keto reductase [IPR020471] (1) | scaffold_1_mRNA_1752.1 | C_unshiu_01217_mRNA_6.1 | - |
| GF0019655 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1750.1 | C_unshiu_01217_mRNA_8.1 | - |
| GF0019654 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1740.1 | C_unshiu_00455_mRNA_22.1 | - |
| GF0019653 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1739.1 | C_unshiu_00455_mRNA_20.1 | - |
| GF0019652 | 1 | 1 | 0 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (2) | iron ion binding [GO:0005506 molecular_function] (2); L-ascorbic acid binding [GO:0031418 molecular_function] (2); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (2); oxidoreductase activity [GO:0016491 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2) | Prolyl 4-hydroxylase, alpha subunit [IPR006620] (2); Oxoglutarate/iron-dependent dioxygenase [IPR005123] (2) | scaffold_1_mRNA_1736.1 | C_unshiu_00455_mRNA_16.1 | - |
| GF0019651 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1732.1 | C_unshiu_00455_mRNA_11.1 | - |
| GF0019650 | 1 | 1 | 0 | Hypothetical protein (2) | | Leucine-rich repeat domain, L domain-like [IPR032675] (2) | scaffold_1_mRNA_1731.1 | C_unshiu_00455_mRNA_10.1 | - |
| GF0019648 | 1 | 1 | 0 | G-type lectin S-receptor-like serine/threonine-protein kinase (2) | recognition of pollen [GO:0048544 biological_process] (2); protein phosphorylation [GO:0006468 biological_process] (2); protein kinase activity [GO:0004672 molecular_function] (2); ATP binding [GO:0005524 molecular_function] (2) | PAN/Apple domain [IPR003609] (2); S-locus glycoprotein domain [IPR000858] (2); Serine/threonine-protein kinase, active site [IPR008271] (2); Protein kinase-like domain [IPR011009] (2); Protein kinase domain [IPR000719] (2); Bulb-type lectin domain [IPR001480] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1) | scaffold_1_mRNA_1720.1 | C_unshiu_00071_mRNA_41.1 | - |
| GF0019647 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1716.1 | C_unshiu_00071_mRNA_37.1 | - |
| GF0019646 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1714.1 | C_unshiu_00071_mRNA_35.1 | - |
| GF0019645 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1713.1 | C_unshiu_00071_mRNA_34.1 | - |
| GF0019644 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_1_mRNA_1712.1 | C_unshiu_00071_mRNA_33.1 | - |
| GF0019643 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1707.1 | C_unshiu_00071_mRNA_28.1 | - |
| GF0019642 | 1 | 1 | 0 | Pre-mRNA-splicing factor SPF27 (2) | mRNA processing [GO:0006397 biological_process] (2) | Pre-mRNA-splicing factor SPF27 [IPR008409] (2) | scaffold_1_mRNA_1705.1 | C_unshiu_00071_mRNA_26.1 | - |
| GF0019641 | 1 | 1 | 0 | Putative AC9 transposase (1); Putative hAT family dimerisation domain containing protein (1) | protein dimerization activity [GO:0046983 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2); DNA binding [GO:0003677 molecular_function] (2) | HAT, C-terminal dimerisation domain [IPR008906] (2); Ribonuclease H-like domain [IPR012337] (2); hAT-like transposase, RNase-H fold [IPR025525] (2) | scaffold_1_mRNA_1702.1 | C_unshiu_00071_mRNA_24.1 | - |
| GF0019640 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1701.1 | C_unshiu_00071_mRNA_23.1 | - |
| GF0019638 | 1 | 1 | 0 | Hypothetical protein (2) | | Transposase-associated domain [IPR029480] (2) | scaffold_1_mRNA_1693.1 | C_unshiu_00071_mRNA_14.1 | - |
| GF0019637 | 1 | 1 | 0 | 66 kDa stress protein (2) | protein binding [GO:0005515 molecular_function] (2) | WD40-repeat-containing domain [IPR017986] (2); WD40 repeat [IPR001680] (2); WD40 repeat, conserved site [IPR019775] (2); WD40/YVTN repeat-like-containing domain [IPR015943] (2) | scaffold_1_mRNA_1689.1 | C_unshiu_00071_mRNA_10.1 | - |
| GF0019636 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1684.1 | C_unshiu_00071_mRNA_4.1 | - |
| GF0019635 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1673.1 | C_unshiu_00097_mRNA_45.1 | - |
| GF0019634 | 1 | 1 | 0 | Hypothetical protein (1); Pentatricopeptide repeat-containing protein, mitochondrial (1) | protein binding [GO:0005515 molecular_function] (2) | Tetratricopeptide-like helical domain [IPR011990] (2); Pentatricopeptide repeat [IPR002885] (2); Expansin/pollen allergen, DPBB domain [IPR007112] (1); RlpA-like protein, double-psi beta-barrel domain [IPR009009] (1) | scaffold_1_mRNA_1670.1 | C_unshiu_00097_mRNA_47.1 | - |
| GF0019632 | 1 | 1 | 0 | Hypothetical protein (2) | | Retrotransposon gag domain [IPR005162] (2) | scaffold_1_mRNA_1667.1 | C_unshiu_02271_mRNA_2.1 | - |
| GF0019631 | 1 | 1 | 0 | Transposable element Ac (2) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_1_mRNA_1663.1 | C_unshiu_02806_mRNA_2.1 | - |
| GF0019630 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1653.1 | C_unshiu_00750_mRNA_4.1 | - |
| GF0019628 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1644.1 | C_unshiu_00462_mRNA_5.1 | - |
| GF0019627 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1643.1 | C_unshiu_00462_mRNA_6.1 | - |
| GF0019626 | 1 | 1 | 0 | Hypothetical protein (2) | trehalose biosynthetic process [GO:0005992 biological_process] (2); catalytic activity [GO:0003824 molecular_function] (2) | Trehalose-phosphatase [IPR003337] (2); HAD-like domain [IPR023214] (1) | scaffold_1_mRNA_164.1 | C_unshiu_00005_mRNA_65.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0019625 | 1 | 1 | 0 | Hypothetical protein (2) | DNA binding [GO:0003677 molecular_function] (1); protein dimerization activity [GO:0046983 molecular_function] (1) | Transcription factor, MADS-box [IPR002100] (1) | scaffold_1_mRNA_1632.1 | C_unshiu_00667_mRNA_3.1 | - |
| GF0019624 | 1 | 1 | 0 | Hypothetical protein (2) | transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (2); glycolipid biosynthetic process [GO:0009247 biological_process] (2) | Diacylglycerol glucosyltransferase, N-terminal [IPR009695] (2) | scaffold_1_mRNA_163.1 | C_unshiu_00005_mRNA_64.1 | - |
| GF0019623 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1628.1 | C_unshiu_00667_mRNA_9.1 | - |
| GF0019622 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1627.1 | C_unshiu_00667_mRNA_10.1 | - |
| GF0019621 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1625.1 | C_unshiu_00667_mRNA_13.1 | - |
| GF0019620 | 1 | 1 | 0 | Putative non-LTR retroelement reverse transcriptase (1); Hypothetical protein (1) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2); Domain of unknown function DUF4283 [IPR025558] (2); Reverse transcriptase domain [IPR000477] (2); Zinc knuckle CX2CX4HX4C [IPR025836] (2); Reverse transcriptase zinc-binding domain [IPR026960] (1) | scaffold_1_mRNA_1623.1 | C_unshiu_00667_mRNA_15.1 | - |
| GF0019619 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1621.1 | C_unshiu_00910_mRNA_1.1 | - |
| GF0019618 | 1 | 1 | 0 | Hypothetical protein (2) | carbohydrate metabolic process [GO:0005975 biological_process] (1) | Glycoside hydrolase, catalytic domain [IPR013781] (1) | scaffold_1_mRNA_1617.1 | C_unshiu_00910_mRNA_3.1 | - |
| GF0019617 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1613.1 | C_unshiu_00910_mRNA_8.1 | - |
| GF0019616 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1612.1 | C_unshiu_00910_mRNA_9.1 | - |
| GF0019614 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1585.1 | C_unshiu_00469_mRNA_12.1 | - |
| GF0019611 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1578.1 | C_unshiu_00598_mRNA_11.1 | - |
| GF0019610 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1573.1 | C_unshiu_00598_mRNA_6.1 | - |
| GF0019609 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1568.1 | C_unshiu_01470_mRNA_1.1 | - |
| GF0019608 | 1 | 1 | 0 | Putative isoaspartyl peptidase/L-asparaginase 2 (1); Hypothetical protein (1) | hydrolase activity [GO:0016787 molecular_function] (2) | Peptidase T2, asparaginase 2 [IPR000246] (2); Nucleophile aminohydrolases, N-terminal [IPR029055] (2); Pre-mRNA-splicing factor 19 [IPR013915] (2) | scaffold_1_mRNA_1567.1 | C_unshiu_01470_mRNA_2.1 | - |
| GF0019607 | 1 | 1 | 0 | Hypothetical protein (2) | vesicle-mediated transport [GO:0016192 biological_process] (2); vesicle docking involved in exocytosis [GO:0006904 biological_process] (2) | Sec1-like protein [IPR001619] (2); Sec1-like, domain 2 [IPR027482] (1) | scaffold_1_mRNA_1560.1 | C_unshiu_02288_mRNA_2.1 | - |
| GF0019606 | 1 | 1 | 0 | Aldose 1-epimerase (2) | isomerase activity [GO:0016853 molecular_function] (2); carbohydrate metabolic process [GO:0005975 biological_process] (2); catalytic activity [GO:0003824 molecular_function] (2); hexose metabolic process [GO:0019318 biological_process] (2); carbohydrate binding [GO:0030246 molecular_function] (2) | Aldose 1-/Glucose-6-phosphate 1-epimerase [IPR008183] (2); Galactose mutarotase-like domain [IPR011013] (2); Aldose 1-epimerase [IPR015443] (2); Glycoside hydrolase-type carbohydrate-binding, subgroup [IPR014718] (1); Glycoside hydrolase-type carbohydrate-binding [IPR014718] (1) | scaffold_1_mRNA_1552.1 | C_unshiu_00604_mRNA_7.1 | - |
| GF0019605 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1551.1 | C_unshiu_00604_mRNA_8.1 | - |
| GF0019604 | 1 | 1 | 0 | Hypothetical protein (2) | | Transposase, MuDR, plant [IPR004332] (2) | scaffold_1_mRNA_1546.1 | C_unshiu_00604_mRNA_11.1 | - |
| GF0019602 | 1 | 1 | 0 | Hypothetical protein (2) | phosphogluconate dehydrogenase (decarboxylating) activity [GO:0004616 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2) | NAD(P)-binding domain [IPR016040] (2); 6-phosphogluconate dehydrogenase, NADP-binding [IPR006115] (2) | scaffold_1_mRNA_1541.1 | C_unshiu_00450_mRNA_16.1 | - |
| GF0019601 | 1 | 1 | 0 | Hypothetical protein (2) | DNA binding [GO:0003677 molecular_function] (2) | Zinc finger, BED-type [IPR003656] (2) | scaffold_1_mRNA_1538.1 | C_unshiu_00450_mRNA_13.1 | - |
| GF0019600 | 1 | 1 | 0 | Hypothetical protein (2) | proteolysis [GO:0006508 biological_process] (2); cysteine-type peptidase activity [GO:0008234 molecular_function] (2) | Ulp1 protease family, C-terminal catalytic domain [IPR003653] (2) | scaffold_1_mRNA_1536.1 | C_unshiu_00450_mRNA_12.1 | - |
| GF0019599 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1531.1 | C_unshiu_00450_mRNA_6.1 | - |
| GF0019597 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1507.1 | C_unshiu_00756_mRNA_8.1 | - |
| GF0019596 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1505.1 | C_unshiu_00756_mRNA_7.1 | - |
| GF0019595 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1493.1 | C_unshiu_01400_mRNA_3.1 | - |
| GF0019594 | 1 | 1 | 0 | Outer arm dynein light chain 1 protein (2) | protein binding [GO:0005515 molecular_function] (2) | Leucine-rich repeat domain, L domain-like [IPR032675] (2); Leucine-rich repeat [IPR001611] (2); Leucine rich repeat 4 [IPR025875] (1) | scaffold_1_mRNA_1491.1 | C_unshiu_00145_mRNA_72.1 | - |
| GF0019593 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1490.1 | C_unshiu_00145_mRNA_71.1 | - |
| GF0019592 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1484.1 | C_unshiu_00145_mRNA_64.1 | - |
| GF0019591 | 1 | 1 | 0 | Hypothetical protein (2) | zinc ion binding [GO:0008270 molecular_function] (2); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2); proteolysis [GO:0006508 biological_process] (2) | Peptidase A2A, retrovirus, catalytic [IPR001995] (2); Reverse transcriptase domain [IPR000477] (2); Retropepsins [IPR018061] (2); Zinc finger, CCHC-type [IPR001878] (2); Aspartic peptidase domain [IPR021109] (2) | scaffold_1_mRNA_1477.1 | C_unshiu_00145_mRNA_57.1 | - |
| GF0019590 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1475.1 | C_unshiu_00145_mRNA_55.1 | - |
| GF0019589 | 1 | 1 | 0 | Hypothetical protein (2) | | Transposon, En/Spm-like [IPR004242] (2) | scaffold_1_mRNA_1468.1 | C_unshiu_02111_mRNA_4.1 | - |
| GF0019588 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1467.1 | C_unshiu_00470_mRNA_31.1 | - |
| GF0019587 | 1 | 1 | 0 | Hypothetical protein (2) | one-carbon metabolic process [GO:0006730 biological_process] (1); adenosylhomocysteinase activity [GO:0004013 molecular_function] (1) | NAD(P)-binding domain [IPR016040] (2); S-adenosyl-L-homocysteine hydrolase, NAD binding domain [IPR015878] (2); Adenosylhomocysteinase [IPR000043] (1); Adenosylhomocysteinase-like [IPR000043] (1) | scaffold_1_mRNA_1466.1 | C_unshiu_00470_mRNA_30.1 | - |
| GF0019586 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1460.1 | C_unshiu_00470_mRNA_28.1 | - |
| GF0019585 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1458.1 | C_unshiu_00470_mRNA_26.1 | - |
| GF0019584 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1456.1 | C_unshiu_00470_mRNA_22.1 | - |
| GF0019583 | 1 | 1 | 0 | Hypothetical protein (2) | | Aspartic peptidase domain [IPR021109] (1) | scaffold_1_mRNA_1451.1 | C_unshiu_00470_mRNA_17.1 | - |
| GF0019582 | 1 | 1 | 0 | ARM repeat superfamily protein isoform 1 (2) | binding [GO:0005488 molecular_function] (2); protein binding [GO:0005515 molecular_function] (2) | Armadillo-like helical [IPR011989] (2); Armadillo [IPR000225] (2); Armadillo-type fold [IPR016024] (2) | scaffold_1_mRNA_145.1 | C_unshiu_00005_mRNA_48.1 | - |
| GF0019581 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1448.1 | C_unshiu_01388_mRNA_4.1 | - |
| GF0019580 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1444.1 | C_unshiu_00470_mRNA_11.1 | - |
| GF0019579 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1443.1 | C_unshiu_00470_mRNA_10.1 | - |
| GF0019578 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1433.1 | C_unshiu_00864_mRNA_11.1 | - |
| GF0019577 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1432.1 | C_unshiu_00864_mRNA_13.1 | - |
| GF0019576 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1428.1 | C_unshiu_00393_mRNA_10.1 | - |
| GF0019575 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1426.1 | C_unshiu_00393_mRNA_7.1 | - |
| GF0019574 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1425.1 | C_unshiu_00393_mRNA_6.1 | - |
| GF0019573 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1423.1 | C_unshiu_00393_mRNA_4.1 | - |
| GF0019571 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1414.1 | C_unshiu_02293_mRNA_4.1 | - |
| GF0019570 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1405.1 | C_unshiu_00138_mRNA_41.1 | - |
| GF0019569 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1404.1 | C_unshiu_01933_mRNA_10.1 | - |
| GF0019568 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1403.1 | C_unshiu_01933_mRNA_9.1 | - |
| GF0019567 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1402.1 | C_unshiu_01933_mRNA_8.1 | - |
| GF0019566 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1396.1 | C_unshiu_00816_mRNA_2.1 | - |
| GF0019565 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1395.1 | C_unshiu_00816_mRNA_3.1 | - |
| GF0019564 | 1 | 1 | 0 | Hypothetical protein (2) | structural constituent of cell wall [GO:0005199 molecular_function] (1) | Pistil-specific extensin-like protein [IPR003882] (1) | scaffold_1_mRNA_1383.1 | C_unshiu_00816_mRNA_10.1 | - |
| GF0019563 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1368.1 | C_unshiu_00128_mRNA_48.1 | - |
| GF0019561 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1356.1 | C_unshiu_00796_mRNA_4.1 | - |
| GF0019560 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1345.1 | C_unshiu_00360_mRNA_18.1 | - |
| GF0019559 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1330.1 | C_unshiu_01540_mRNA_6.1 | - |
| GF0019558 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1322.1 | C_unshiu_00156_mRNA_23.1 | - |
| GF0019557 | 1 | 1 | 0 | Integral membrane protein (2) | | Protein of unknown function DUF2838 [IPR021261] (2) | scaffold_1_mRNA_1320.1 | C_unshiu_00156_mRNA_20.1 | - |
| GF0019556 | 1 | 1 | 0 | Hypothetical protein (2) | | Protein of unknown function DUF241, plant [IPR004320] (2) | scaffold_1_mRNA_1316.1 | C_unshiu_00156_mRNA_15.1 | - |
| GF0019555 | 1 | 1 | 0 | Hypothetical protein (2) | | Domain of unknown function DUF4219 [IPR025314] (2) | scaffold_1_mRNA_1312.1 | C_unshiu_00270_mRNA_17.1 | - |
| GF0019554 | 1 | 1 | 0 | Putative ribonuclease H protein (2) | | Reverse transcriptase zinc-binding domain [IPR026960] (2) | scaffold_1_mRNA_1306.1 | C_unshiu_00270_mRNA_13.1 | - |
| GF0019553 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1305.1 | C_unshiu_00270_mRNA_12.1 | - |
| GF0019552 | 1 | 1 | 0 | Putative RNA-directed DNA polymerase (Reverse transcriptase) (1); Hypothetical protein (1) | | Reverse transcriptase domain [IPR000477] (2) | scaffold_1_mRNA_1304.1 | C_unshiu_00270_mRNA_10.1 | - |
| GF0019550 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1288.1 | C_unshiu_00364_mRNA_9.1 | - |
| GF0019549 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1281.1 | C_unshiu_00364_mRNA_18.1 | - |
| GF0019548 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1279.1 | C_unshiu_00201_mRNA_27.1 | - |
| GF0019547 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1278.1 | C_unshiu_00201_mRNA_26.1 | - |
| GF0019546 | 1 | 1 | 0 | Serine/threonine-protein kinase CBK1 (2) | protein serine/threonine kinase activity [GO:0004674 molecular_function] (2); protein kinase activity [GO:0004672 molecular_function] (2); protein phosphorylation [GO:0006468 biological_process] (2); ATP binding [GO:0005524 molecular_function] (2) | AGC-kinase, C-terminal [IPR000961] (2); Protein kinase, ATP binding site [IPR017441] (2); Serine/threonine-protein kinase, active site [IPR008271] (2); Protein kinase-like domain [IPR011009] (2); Protein kinase domain [IPR000719] (2); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1) | scaffold_1_mRNA_1277.1 | C_unshiu_00201_mRNA_25.1 | - |
| GF0019545 | 1 | 1 | 0 | Putative nuclease HARBI1 (2) | | Harbinger transposase-derived nuclease domain [IPR027806] (2) | scaffold_1_mRNA_1276.1 | C_unshiu_00201_mRNA_24.1 | - |
| GF0019544 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1267.1 | C_unshiu_00368_mRNA_17.1 | - |
| GF0019543 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1266.1 | C_unshiu_00368_mRNA_16.1 | - |
| GF0019542 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1261.1 | C_unshiu_00242_mRNA_22.1 | - |
| GF0019541 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1259.1 | C_unshiu_00242_mRNA_20.1 | - |
| GF0019540 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1258.1 | C_unshiu_00242_mRNA_19.1 | - |
| GF0019539 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1243.1 | C_unshiu_00398_mRNA_19.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0019538 | 1 | 1 | 0 | RNA-directed DNA polymerase ; Ribonuclease H, putative (2) | | Endonuclease/exonuclease/phosphatase [IPR005135] (2) | scaffold_1_mRNA_1234.1 | C_unshiu_00055_mRNA_9.1 | - |
| GF0019537 | 1 | 1 | 0 | Hypothetical protein (2) | zinc ion binding [GO:0008270 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | Zinc knuckle CX2CX4HX4C [IPR025836] (2); Zinc finger, CCHC-type [IPR001878] (2); Domain of unknown function DUF4283 [IPR025558] (2) | scaffold_1_mRNA_1233.1 | C_unshiu_00398_mRNA_9.1 | - |
| GF0019536 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1232.1 | C_unshiu_00398_mRNA_8.1 | - |
| GF0019535 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1227.1 | C_unshiu_00177_mRNA_12.1 | - |
| GF0019533 | 1 | 1 | 0 | Mitochondrial transcription termination factor family protein, putative isoform 2 (2) | double-stranded DNA binding [GO:0003690 molecular_function] (2); regulation of transcription, DNA-templated [GO:0006355 biological_process] (2); mitochondrion [GO:0005739 cellular_component] (1) | Mitochondrial transcription termination factor [IPR003690] (1); Transcription termination factor, mitochondrial/chloroplastic [IPR003690] (1) | scaffold_1_mRNA_1219.1 | C_unshiu_00613_mRNA_2.1 | - |
| GF0019532 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1218.1 | C_unshiu_00613_mRNA_3.1 | - |
| GF0019531 | 1 | 1 | 0 | Cytokinin riboside 5'-monophosphate phosphoribohydrolase (1); Hypothetical protein (1) | | LOG family [IPR031100] (1) | scaffold_1_mRNA_1215.1 | C_unshiu_00613_mRNA_5.1 | - |
| GF0019530 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1214.1 | C_unshiu_00613_mRNA_6.1 | - |
| GF0019529 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1213.1 | C_unshiu_00613_mRNA_7.1 | - |
| GF0019528 | 1 | 1 | 0 | Retrovirus-related pol polyprotein from transposon tnt 1-94 (1); Hypothetical protein (1) | | GAG-pre-integrase domain [IPR025724] (1) | scaffold_1_mRNA_1210.1 | C_unshiu_00613_mRNA_13.1 | - |
| GF0019526 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1200.1 | C_unshiu_00270_mRNA_22.1 | - |
| GF0019525 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1192.1 | C_unshiu_00909_mRNA_9.1 | - |
| GF0019524 | 1 | 1 | 0 | Hypothetical protein (2) | zinc ion binding [GO:0008270 molecular_function] (2); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2); proteolysis [GO:0006508 biological_process] (2); oxidoreductase activity, acting on CH-OH group of donors [GO:0016614 molecular_function] (1); cytokinin metabolic process [GO:0009690 biological_process] (1); catalytic activity [GO:0003824 molecular_function] (1); cytokinin dehydrogenase activity [GO:0019139 molecular_function] (1); oxidation-reduction process [GO:0055114 biological_process] (1); flavin adenine dinucleotide binding [GO:0050660 molecular_function] (1) | Aspartic peptidase domain [IPR021109] (2); Zinc finger, CCHC-type [IPR001878] (2); Aspartic peptidase, active site [IPR001969] (2); Peptidase A2A, retrovirus, catalytic [IPR001995] (2); Vanillyl-alcohol oxidase/Cytokinin dehydrogenase C-terminal domain [IPR016170] (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); Retropepsins [IPR018061] (1); Cytokinin dehydrogenase 1, FAD/cytokinin binding domain [IPR015345] (1); FAD-linked oxidase-like, C-terminal [IPR016164] (1) | scaffold_1_mRNA_1191.1 | C_unshiu_00909_mRNA_8.1 | - |
| GF0019523 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1180.1 | C_unshiu_00039_mRNA_31.1 | - |
| GF0019522 | 1 | 1 | 0 | Shikimate kinase (2) | integral component of membrane [GO:0016021 cellular_component] (2); transport [GO:0006810 biological_process] (2) | Folate-biopterin transporter [IPR004324] (2); Major facilitator superfamily domain [IPR020846] (2) | scaffold_1_mRNA_118.1 | C_unshiu_00005_mRNA_20.1 | - |
| GF0019521 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1175.1 | C_unshiu_00385_mRNA_10.1 | - |
| GF0019520 | 1 | 1 | 0 | Pol polyprotein (1); Hypothetical protein (1) | | | scaffold_1_mRNA_1174.1 | C_unshiu_00385_mRNA_9.1 | - |
| GF0019519 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1173.1 | C_unshiu_00385_mRNA_8.1 | - |
| GF0019518 | 1 | 1 | 0 | Hypothetical protein (2) | | DnaJ domain [IPR001623] (2); DnaJ domain, conserved site [IPR018253] (2) | scaffold_1_mRNA_1172.1 | C_unshiu_00385_mRNA_7.1 | - |
| GF0019517 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1169.1 | C_unshiu_00385_mRNA_4.1 | - |
| GF0019516 | 1 | 1 | 0 | Hypothetical protein (2) | | Aspartic peptidase domain [IPR021109] (1) | scaffold_1_mRNA_1166.1 | C_unshiu_00867_mRNA_14.1 | - |
| GF0019515 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1163.1 | C_unshiu_00867_mRNA_16.1 | - |
| GF0019514 | 1 | 1 | 0 | Hypothetical protein (2) | | Aspartic peptidase domain [IPR021109] (1) | scaffold_1_mRNA_1162.1 | C_unshiu_00867_mRNA_15.1 | - |
| GF0019513 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1161.1 | C_unshiu_02478_mRNA_2.1 | - |
| GF0019512 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1160.1 | C_unshiu_00867_mRNA_13.1 | - |
| GF0019511 | 1 | 1 | 0 | Similarity to non-LTR retroelement reverse transcriptase (2) | | | scaffold_1_mRNA_1159.1 | C_unshiu_00867_mRNA_12.1 | - |
| GF0019510 | 1 | 1 | 0 | Hypothetical protein (2) | | Retrotransposon gag domain [IPR005162] (2) | scaffold_1_mRNA_1156.1 | C_unshiu_00867_mRNA_8.1 | - |
| GF0019509 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1155.1 | C_unshiu_00867_mRNA_7.1 | - |
| GF0019508 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1145.1 | C_unshiu_00687_mRNA_1.1 | - |
| GF0019507 | 1 | 1 | 0 | Hypothetical protein (2) | zinc ion binding [GO:0008270 molecular_function] (2) | Zinc finger, SWIM-type [IPR007527] (2); Zinc finger, PMZ-type [IPR006564] (2); MULE transposase domain [IPR018289] (1) | scaffold_1_mRNA_1140.1 | C_unshiu_00191_mRNA_6.1 | - |
| GF0019506 | 1 | 1 | 0 | Cytochrome P450 76AD1-like protein (2) | oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2); iron ion binding [GO:0005506 molecular_function] (2); heme binding [GO:0020037 molecular_function] (2) | Cytochrome P450 [IPR001128] (2); Cytochrome P450, conserved site [IPR017972] (2); Cytochrome P450, E-class, group I [IPR002401] (2) | scaffold_1_mRNA_1136.1 | C_unshiu_00191_mRNA_10.1 | - |
| GF0019505 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1131.1 | C_unshiu_00191_mRNA_14.1 | - |
| GF0019504 | 1 | 1 | 0 | Retrotransposon protein, putative, Ty1-copia subclass (2) | nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1) | GAG-pre-integrase domain [IPR025724] (2); Zinc finger, CCHC-type [IPR001878] (1); Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1) | scaffold_1_mRNA_1128.1 | C_unshiu_00191_mRNA_17.1 | - |
| GF0019503 | 1 | 1 | 0 | Hypothetical protein (2) | oxidation-reduction process [GO:0055114 biological_process] (1); oxidoreductase activity [GO:0016491 molecular_function] (1) | Oxidoreductase FAD/NAD(P)-binding [IPR001433] (1) | scaffold_1_mRNA_1123.1 | C_unshiu_01200_mRNA_4.1 | - |
| GF0019502 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1122.1 | C_unshiu_01200_mRNA_5.1 | - |
| GF0019501 | 1 | 1 | 0 | Hypothetical protein (2) | peptide biosynthetic process [GO:0043043 biological_process] (2); cytoplasm [GO:0005737 cellular_component] (2) | Translation elongation factor P/YeiP, conserved site [IPR013852] (2); Elongation factor P, C-terminal [IPR015365] (2); Nucleic acid-binding, OB-fold [IPR012340] (2) | scaffold_1_mRNA_1119.1 | C_unshiu_01200_mRNA_8.1 | - |
| GF0019500 | 1 | 1 | 0 | Hypothetical protein (2) | | Harbinger transposase-derived nuclease domain [IPR027806] (2) | scaffold_1_mRNA_1118.1 | C_unshiu_01200_mRNA_9.1 | - |
| GF0019499 | 1 | 1 | 0 | Hypothetical protein (2) | | Zinc knuckle CX2CX4HX4C [IPR025836] (2) | scaffold_1_mRNA_1105.1 | C_unshiu_00087_mRNA_12.1 | - |
| GF0019498 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1102.1 | C_unshiu_00087_mRNA_14.1 | - |
| GF0019497 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1100.1 | C_unshiu_00087_mRNA_15.1 | - |
| GF0019496 | 1 | 1 | 0 | Non-LTR retroelement reverse transcriptase-like (1); Non-LTR retroelement reverse transcriptase (1) | nucleic acid binding [GO:0003676 molecular_function] (2) | Reverse transcriptase zinc-binding domain [IPR026960] (2); Ribonuclease H-like domain [IPR012337] (2) | scaffold_1_mRNA_1094.1 | C_unshiu_00087_mRNA_19.1 | - |
| GF0019495 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1083.1 | C_unshiu_00198_mRNA_21.1 | - |
| GF0019494 | 1 | 1 | 0 | Transposon protein, putative, Mutator sub-class (2) | DNA binding [GO:0003677 molecular_function] (2); transposition, DNA-mediated [GO:0006313 biological_process] (2); transposase activity [GO:0004803 molecular_function] (2) | MULE transposase domain [IPR018289] (2); Transposase, mutator type [IPR001207] (2); Transposase, MuDR, plant [IPR004332] (2) | scaffold_1_mRNA_1080.1 | C_unshiu_00198_mRNA_17.1 | - |
| GF0019493 | 1 | 1 | 0 | Effector of transcription2, putative (2) | | GIY-YIG nuclease superfamily [IPR000305] (1) | scaffold_1_mRNA_1067.1 | C_unshiu_00156_mRNA_11.1 | - |
| GF0019492 | 1 | 1 | 0 | Serine acetyltransferase (2) | cytoplasm [GO:0005737 cellular_component] (2); cysteine biosynthetic process from serine [GO:0006535 biological_process] (2); serine O-acetyltransferase activity [GO:0009001 molecular_function] (2); transferase activity [GO:0016740 molecular_function] (2) | Hexapeptide repeat [IPR001451] (2); Serine acetyltransferase, N-terminal [IPR010493] (2); Hexapeptide transferase, conserved site [IPR018357] (2); Trimeric LpxA-like [IPR011004] (2); Serine O-acetyltransferase [IPR005881] (2) | scaffold_1_mRNA_1066.1 | C_unshiu_00156_mRNA_10.1 | - |
| GF0019491 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1060.1 | C_unshiu_00156_mRNA_3.1 | - |
| GF0019490 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1056.1 | C_unshiu_00579_mRNA_7.1 | - |
| GF0019489 | 1 | 1 | 0 | Hypothetical protein (2) | | Plant self-incompatibility S1 [IPR010264] (2) | scaffold_1_mRNA_1045.1 | C_unshiu_00296_mRNA_4.1 | - |
| GF0019487 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1029.1 | C_unshiu_00942_mRNA_3.1 | - |
| GF0019486 | 1 | 1 | 0 | Hypothetical protein (2) | nucleic acid binding [GO:0003676 molecular_function] (2); protein dimerization activity [GO:0046983 molecular_function] (2) | HAT, C-terminal dimerisation domain [IPR008906] (2); Ribonuclease H-like domain [IPR012337] (2) | scaffold_1_mRNA_1022.1 | C_unshiu_00584_mRNA_12.1 | - |
| GF0019485 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1013.1 | C_unshiu_00584_mRNA_31.1 | - |
| GF0019484 | 1 | 1 | 0 | Aspartic proteinase nepenthesin-1 (2) | aspartic-type endopeptidase activity [GO:0004190 molecular_function] (2); proteolysis [GO:0006508 biological_process] (2) | Aspartic peptidase domain [IPR021109] (2); Peptidase family A1 domain [IPR033121] (2); Xylanase inhibitor, N-terminal [IPR032861] (2); Xylanase inhibitor, C-terminal [IPR032799] (2); Aspartic peptidase A1 family [IPR001461] (2); CND41-like [IPR033873] (1) | scaffold_1_mRNA_101.1 | C_unshiu_00129_mRNA_1.1 | - |
| GF0019483 | 1 | 1 | 0 | Myo-inositol oxygenase 2 isoform 2 (1); Hypothetical protein (1) | cytoplasm [GO:0005737 cellular_component] (2); oxidation-reduction process [GO:0055114 biological_process] (2); inositol catabolic process [GO:0019310 biological_process] (2); inositol oxygenase activity [GO:0050113 molecular_function] (2); iron ion binding [GO:0005506 molecular_function] (2) | Inositol oxygenase [IPR007828] (2) | scaffold_1_mRNA_1007.1 | C_unshiu_00032_mRNA_5.1 | - |
| GF0019482 | 1 | 1 | 0 | Hypothetical protein (2) | | | scaffold_1_mRNA_1006.1 | C_unshiu_00032_mRNA_4.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0018835 | 1 | 2 | 0 | Cyclic nucleotide-gated ion channel 1 (3) |  | Cyclic nucleotide-binding domain [IPR000595] (3); RmlC-like jelly roll fold [IPR014710] (3); Cyclic nucleotide-binding-like [IPR018490] (3) | scaffold_9_mRNA_3703.1 | C_unshiu_00740_mRNA_6.1,C_unshiu_00740_mRNA_9.1 | - |
| GF0018605 | 1 | 2 | 0 | Hypothetical protein (3) |  | Viral movement protein [IPR028919] (3) | scaffold_9_mRNA_3352.1 | C_unshiu_00017_mRNA_59.1,C_unshiu_01110_mRNA_2.1 | - |
| GF0018511 | 1 | 2 | 0 | Hypothetical protein (3) |  |  | scaffold_9_mRNA_3128.1 | C_unshiu_00577_mRNA_1.1,C_unshiu_02129_mRNA_3.1 | - |
| GF0018445 | 1 | 2 | 0 | Ozone-responsive stress related protein (2); Hypothetical protein (1) |  | Protein of unknown function DUF1138 [IPR009515] (3) | scaffold_9_mRNA_2993.1 | C_unshiu_00574_mRNA_14.1,C_unshiu_00574_mRNA_3.1 | - |
| GF0018443 | 1 | 2 | 0 | DUF642 family protein (3) |  | Galactose-binding domain-like [IPR008979] (3); Domain of unknown function DUF642 [IPR006946] (3) | scaffold_9_mRNA_2989.1 | C_unshiu_01689_mRNA_3.1,C_unshiu_02440_mRNA_2.1 | - |
| GF0018427 | 1 | 2 | 0 | CDP-diacylglycerol--inositol 3-phosphatidyltransferase (3) | phospholipid biosynthetic process [GO:0008654 biological_process] (3); membrane [GO:0016020 cellular_component] (3); phosphotransferase activity, for other substituted phosphate groups [GO:0016780 molecular_function] (3) | CDP-diacylglycerol-inositol 3-phosphatidyltransferase, eukaryote [IPR014387] (3); CDP-alcohol phosphatidyltransferase [IPR000462] (3) | scaffold_9_mRNA_2905.1 | C_unshiu_00132_mRNA_7.1,C_unshiu_02260_mRNA_1.1 | - |
| GF0018392 | 1 | 2 | 0 | MuDR family transposase isoform 1 (2); Putative muDR family transposase-like (1) | DNA binding [GO:0003677 molecular_function] (3); transposase activity [GO:0004803 molecular_function] (3); transposition, DNA-mediated [GO:0006313 biological_process] (3); zinc ion binding [GO:0008270 molecular_function] (1) | MULE transposase domain [IPR018289] (3); Transposase, MuDR, plant [IPR004332] (3); Transposase, mutator type [IPR001207] (3); Zinc finger, SWIM-type [IPR007527] (1); Zinc finger, BED-type [IPR003656] (1); Zinc finger, PMZ-type [IPR006564] (1) | scaffold_9_mRNA_2778.1 | C_unshiu_01023_mRNA_1.1,C_unshiu_01118_mRNA_1.1 | - |
| GF0018373 | 1 | 2 | 0 | Zinc knuckle family protein (3) | zinc ion binding [GO:0008270 molecular_function] (3); nucleic acid binding [GO:0003676 molecular_function] (3) | Zinc finger, CCHC-type [IPR001878] (3) | scaffold_9_mRNA_2717.1 | C_unshiu_00292_mRNA_34.1,C_unshiu_00324_mRNA_8.1 | - |
| GF0018309 | 1 | 2 | 0 | Cytochrome P450 (3) | iron ion binding [GO:0005506 molecular_function] (3); heme binding [GO:0020037 molecular_function] (3); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (3); oxidation-reduction process [GO:0055114 biological_process] (3) | Cytochrome P450, conserved site [IPR017972] (3); Cytochrome P450, E-class, group I [IPR002401] (3); Cytochrome P450 [IPR001128] (3) | scaffold_9_mRNA_2521.1 | C_unshiu_00345_mRNA_14.1,C_unshiu_01737_mRNA_5.1 | - |
| GF0018307 | 1 | 2 | 0 | Hypothetical protein (3) |  |  | scaffold_9_mRNA_2506.1 | C_unshiu_00755_mRNA_7.1,C_unshiu_01500_mRNA_2.1 | - |
| GF0018295 | 1 | 2 | 0 | Hypothetical protein (3) |  |  | scaffold_9_mRNA_2456.1 | C_unshiu_00011_mRNA_74.1,C_unshiu_02904_mRNA_4.1 | - |
| GF0018282 | 1 | 2 | 0 | Hypothetical protein (3) |  |  | scaffold_9_mRNA_2394.1 | C_unshiu_01098_mRNA_4.1,C_unshiu_01106_mRNA_11.1 | - |
| GF0018204 | 1 | 2 | 0 | Hypothetical protein (3) |  |  | scaffold_9_mRNA_2043.1 | C_unshiu_00385_mRNA_11.1,C_unshiu_01691_mRNA_3.1 | - |
| GF0018109 | 1 | 2 | 0 | Hypothetical protein (3) |  |  | scaffold_9_mRNA_1758.1 | C_unshiu_00106_mRNA_24.1,C_unshiu_00629_mRNA_9.1 | - |
| GF0018095 | 1 | 2 | 0 | Hypothetical protein (2); Ta11 non-LTR retroelement protein-like (1) |  | Domain of unknown function DUF4283 [IPR025558] (3); Zinc knuckle CX2CX4HX4C [IPR025836] (1) | scaffold_9_mRNA_1700.1 | C_unshiu_00032_mRNA_42.1,C_unshiu_00211_mRNA_14.1 | - |
| GF0018085 | 1 | 2 | 0 | Hypothetical protein (2); Far-red impaired responsive 1-like protein (1) | regulation of transcription, DNA-templated [GO:0006355 biological_process] (3) | FAR1 DNA binding domain [IPR004330] (3); FHY3/FAR1 family [IPR031052] (3); MULE transposase domain [IPR018289] (2) | scaffold_9_mRNA_1669.1 | C_unshiu_00294_mRNA_12.1,C_unshiu_01009_mRNA_9.1 | - |
| GF0018077 | 1 | 2 | 0 | Transposon protein, putative, unclassified (2); FOG: Transposon-encoded proteins with TYA, reverse transcriptase, integrase domains in various combinations (1) | nucleic acid binding [GO:0003676 molecular_function] (3); zinc ion binding [GO:0008270 molecular_function] (3) | Zinc finger, CCHC-type [IPR001878] (3) | scaffold_9_mRNA_1622.1 | C_unshiu_00586_mRNA_4.1,C_unshiu_01107_mRNA_11.1 | - |
| GF0018067 | 1 | 2 | 0 | UBX domain protein (3) | protein binding [GO:0005515 molecular_function] (3) | UBA-like [IPR009060] (3); UAS [IPR006577] (3); Thioredoxin-like fold [IPR012336] (3); UBX domain [IPR001012] (2); Ubiquitin-related domain [IPR029071] (2); UBX domain-containing protein 2/7 [IPR017346] (2) | scaffold_9_mRNA_1582.1 | C_unshiu_01176_mRNA_7.1,C_unshiu_02187_mRNA_2.1 | - |
| GF0018057 | 1 | 2 | 0 | Hypothetical protein (3) |  | MULE transposase domain [IPR018289] (3) | scaffold_9_mRNA_1511.1 | C_unshiu_00122_mRNA_19.1,C_unshiu_01258_mRNA_9.1 | - |
| GF0018052 | 1 | 2 | 0 | Hypothetical protein (2); Monosacharide transport protein (1) |  |  | scaffold_9_mRNA_1505.1 | C_unshiu_00028_mRNA_46.1,C_unshiu_00414_mRNA_16.1 | - |
| GF0018036 | 1 | 2 | 0 | Putative methyltransferase PMT20 (3) | methyltransferase activity [GO:0008168 molecular_function] (3) | Putative S-adenosyl-L-methionine-dependent methyltransferase [IPR004159] (3); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (3) | scaffold_9_mRNA_1459.1 | C_unshiu_00131_mRNA_9.2,C_unshiu_00351_mRNA_8.2 | - |
| GF0018011 | 1 | 2 | 0 | Hypothetical protein (3) | protein kinase activity [GO:0004672 molecular_function] (3); protein phosphorylation [GO:0006468 biological_process] (3); ATP binding [GO:0005524 molecular_function] (3) | Protein kinase-like domain [IPR011009] (3); Protein kinase domain [IPR000719] (3); Protein kinase, ATP binding site [IPR017441] (3); Serine/threonine-protein kinase, active site [IPR008271] (3); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (2); Serine/threonine/dual specificity protein kinase, catalytic  domain [IPR002290] (2); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1) | scaffold_9_mRNA_1363.1 | C_unshiu_00057_mRNA_6.1,C_unshiu_00344_mRNA_29.1 | - |
| GF0018010 | 1 | 2 | 0 | Hypothetical protein (3) | protein binding [GO:0005515 molecular_function] (3) | PB1 domain [IPR000270] (3) | scaffold_9_mRNA_1362.1 | C_unshiu_00057_mRNA_7.1,C_unshiu_00344_mRNA_30.1 | - |
| GF0017888 | 1 | 2 | 0 | Hypothetical protein (3) |  |  | scaffold_8_mRNA_953.1 | C_unshiu_00203_mRNA_4.1,C_unshiu_02725_mRNA_4.1 | - |
| GF0017883 | 1 | 2 | 0 | Pentatricopeptide (PPR) repeat protein (3) | protein binding [GO:0005515 molecular_function] (2) | Pentatricopeptide repeat [IPR002885] (3); Tetratricopeptide-like helical domain [IPR011990] (2) | scaffold_8_mRNA_946.1 | C_unshiu_01262_mRNA_1.1,C_unshiu_01415_mRNA_3.1 | - |
| GF0017849 | 1 | 2 | 0 | Hypothetical protein (3) | calmodulin binding [GO:0005516 molecular_function] (3) | Calcium-transporting P-type ATPase, N-terminal autoinhibitory domain [IPR024750] (3) | scaffold_8_mRNA_877.1 | C_unshiu_01185_mRNA_5.1,C_unshiu_02065_mRNA_4.1 | - |
| GF0017822 | 1 | 2 | 0 | Pectinesterase 31 (3) | cell wall modification [GO:0042545 biological_process] (3); cell wall [GO:0005618 cellular_component] (3); pectinesterase activity [GO:0030599 molecular_function] (3) | Pectin lyase fold/virulence factor [IPR011050] (3); Pectinesterase, catalytic [IPR000070] (3); Pectin lyase fold [IPR012334] (3) | scaffold_8_mRNA_796.1 | C_unshiu_01962_mRNA_1.1,C_unshiu_02198_mRNA_1.1 | - |
| GF0017803 | 1 | 2 | 0 | Hypothetical protein (3) |  |  | scaffold_8_mRNA_758.1 | C_unshiu_00085_mRNA_5.1,C_unshiu_02763_mRNA_1.1 | - |
| GF0017791 | 1 | 2 | 0 | DUF241 domain protein (3) |  | Protein of unknown function DUF241, plant [IPR004320] (3) | scaffold_8_mRNA_72.1 | C_unshiu_00041_mRNA_14.1,C_unshiu_00041_mRNA_16.1 | - |
| GF0017668 | 1 | 2 | 0 | Plant basic secretory protein (BSP) family protein (2); Hypothetical protein (1) |  | Uncharacterised protein family, basic secretory protein [IPR007541] (3) | scaffold_8_mRNA_398.1 | C_unshiu_00363_mRNA_9.1,C_unshiu_02320_mRNA_3.1 | - |
| GF0017431 | 1 | 2 | 0 | ATP synthase subunit epsilon (3) |  |  | scaffold_8_mRNA_2981.1 | C_unshiu_00375_mRNA_17.1,C_unshiu_00571_mRNA_5.1 | - |
| GF0017430 | 1 | 2 | 0 | Palmitoyltransferase (2); Hypothetical protein (1) | zinc ion binding [GO:0008270 molecular_function] (2) | Zinc finger, DHHC-type, palmitoyltransferase [IPR001594] (2); Palmitoyltransferase, DHHC domain [IPR001594] (1) | scaffold_8_mRNA_2978.1 | C_unshiu_00375_mRNA_20.1,C_unshiu_00571_mRNA_8.1 | - |
| GF0017218 | 1 | 2 | 0 | Hypothetical protein (3) | 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_2576.1 | C_unshiu_00320_mRNA_24.1,C_unshiu_01839_mRNA_1.1 | - |
| GF0017200 | 1 | 2 | 0 | Nucleic acid binding / zinc ion binding protein (2); Hypothetical protein (1) | nucleic acid binding [GO:0003676 molecular_function] (1); zinc ion binding [GO:0008270 molecular_function] (1) | Zinc knuckle CX2CX4HX4C [IPR025836] (3); Domain of unknown function DUF4283 [IPR025558] (3); Zinc finger, CCHC-type [IPR001878] (1) | scaffold_8_mRNA_2543.1 | C_unshiu_00055_mRNA_8.1,C_unshiu_02387_mRNA_1.1 | - |
| GF0017148 | 1 | 2 | 0 | Hypothetical protein (3) |  |  | scaffold_8_mRNA_2380.1 | C_unshiu_00479_mRNA_17.1,C_unshiu_00894_mRNA_1.1 | - |
| GF0017080 | 1 | 2 | 0 | Putative metal tolerance protein 4-like (3) | transmembrane transport [GO:0055085 biological_process] (3); integral component of membrane [GO:0016021 cellular_component] (3); cation transmembrane transporter activity [GO:0008324 molecular_function] (3); cation transport [GO:0006812 biological_process] (3) | Cation efflux protein [IPR002524] (3); Cation efflux protein transmembrane domain [IPR027469] (2) | scaffold_8_mRNA_2197.1 | C_unshiu_00413_mRNA_19.1,C_unshiu_01166_mRNA_3.1 | - |
| GF0017059 | 1 | 2 | 0 | Ribosomal protein L15 (3) | protein binding [GO:0005515 molecular_function] (1) | Pentatricopeptide repeat [IPR002885] (3); Tetratricopeptide-like helical domain [IPR011990] (1) | scaffold_8_mRNA_2134.1 | C_unshiu_00693_mRNA_11.1,C_unshiu_00940_mRNA_1.1 | - |
| GF0017037 | 1 | 2 | 0 | Hypothetical protein (3) |  |  | scaffold_8_mRNA_2003.1 | C_unshiu_00360_mRNA_4.1,C_unshiu_01649_mRNA_1.1 | - |
| GF0017033 | 1 | 2 | 0 | Hypothetical protein (2); Retrotransposon protein, putative, Ty3-gypsy subclass (1) | DNA integration [GO:0015074 biological_process] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2); Integrase, catalytic core [IPR001584] (2); Aspartic peptidase domain [IPR021109] (1) | scaffold_8_mRNA_1993.1 | C_unshiu_00087_mRNA_24.1,C_unshiu_01302_mRNA_6.1 | - |
| GF0017029 | 1 | 2 | 0 | Hypothetical protein (3) | aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1) | Aspartic peptidase, active site [IPR001969] (1); Retropepsins [IPR018061] (1); Aspartic peptidase domain [IPR021109] (1) | scaffold_8_mRNA_1984.1 | C_unshiu_00222_mRNA_6.1,C_unshiu_00527_mRNA_26.1 | - |
| GF0017026 | 1 | 2 | 0 | Hypothetical protein (3) |  |  | scaffold_8_mRNA_1973.1 | C_unshiu_00811_mRNA_4.1,C_unshiu_02435_mRNA_2.1 | - |
| GF0016998 | 1 | 2 | 0 | Hypothetical protein (3) | proteolysis [GO:0006508 biological_process] (1); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (1) | Aspartic peptidase domain [IPR021109] (3); Aspartic peptidase, active site [IPR001969] (1) | scaffold_8_mRNA_1821.1 | C_unshiu_01216_mRNA_5.1,C_unshiu_01419_mRNA_5.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0016973 | 1 | 2 | 0 | Hypothetical protein (3) |  | Domain of unknown function DUF4219 [IPR025314] (3) | scaffold_8_mRNA_1746.1 | C_unshiu_00100_mRNA_39.1,C_unshiu_00213_mRNA_57.1 | - |
| GF0016952 | 1 | 2 | 0 | BED zinc finger,hAT family dimerization domain (2); Transposable element Ac (1) | protein dimerization activity [GO:0046983 molecular_function] (3); nucleic acid binding [GO:0003676 molecular_function] (3); DNA binding [GO:0003677 molecular_function] (1) | HAT, C-terminal dimerisation domain [IPR008906] (3); Ribonuclease H-like domain [IPR012337] (3); hAT-like transposase, RNase-H fold [IPR025525] (1) | scaffold_8_mRNA_1678.1 | C_unshiu_00321_mRNA_12.1,C_unshiu_01985_mRNA_1.1 | - |
| GF0016931 | 1 | 2 | 0 | Hypothetical protein (3) |  |  | scaffold_8_mRNA_1505.1 | C_unshiu_00177_mRNA_33.1,C_unshiu_01030_mRNA_15.1 | - |
| GF0016929 | 1 | 2 | 0 | Hydroxyproline-rich glycoprotein family protein, putative (3) |  |  | scaffold_8_mRNA_1502.1 | C_unshiu_00151_mRNA_21.1,C_unshiu_02832_mRNA_2.1 | - |
| GF0016907 | 1 | 2 | 0 | Hypothetical protein (3) |  |  | scaffold_8_mRNA_1381.1 | C_unshiu_00244_mRNA_7.1,C_unshiu_01081_mRNA_1.1 | - |
| GF0016906 | 1 | 2 | 0 | Hypothetical protein (3) |  |  | scaffold_8_mRNA_1365.1 | C_unshiu_00244_mRNA_2.1,C_unshiu_01081_mRNA_5.1 | - |
| GF0016890 | 1 | 2 | 0 | Hypothetical protein (3) |  | HAD-like domain [IPR023214] (3); FCP1 homology domain [IPR004274] (3) | scaffold_8_mRNA_1310.1 | C_unshiu_00859_mRNA_11.1,C_unshiu_01482_mRNA_3.1 | - |
| GF0016882 | 1 | 2 | 0 | Hypothetical protein (3) |  |  | scaffold_8_mRNA_1260.1 | C_unshiu_02026_mRNA_2.1,C_unshiu_02519_mRNA_1.1 | - |
| GF0016872 | 1 | 2 | 0 | Lectin (3) | carbohydrate binding [GO:0030246 molecular_function] (3) | Legume lectin, alpha chain, conserved site [IPR000985] (3); Legume lectin domain [IPR001220] (3); Concanavalin A-like lectin/glucanase domain [IPR013320] (3); Legume lectin [IPR016363] (1); Lectin [IPR016363] (1) | scaffold_8_mRNA_1218.1 | C_unshiu_00694_mRNA_15.1,C_unshiu_00694_mRNA_16.1 | - |
| GF0016869 | 1 | 2 | 0 | Sodium:hydrogen antiporter 1 isoform 1 (3) | transmembrane transport [GO:0055085 biological_process] (3); integral component of membrane [GO:0016021 cellular_component] (3) | Citrate transporter-like domain [IPR004680] (3) | scaffold_8_mRNA_1207.1 | C_unshiu_01085_mRNA_8.1,C_unshiu_02035_mRNA_3.1 | - |
| GF0016864 | 1 | 2 | 0 | Geraniol 10-hydroxylase (1); Bergamotene oxidase (1); TSA: Wollemia nobilis transcribed RNA sequence (1) | oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (3); oxidation-reduction process [GO:0055114 biological_process] (3); iron ion binding [GO:0005506 molecular_function] (3); heme binding [GO:0020037 molecular_function] (3) | Cytochrome P450 [IPR001128] (3); Cytochrome P450, E-class, group I [IPR002401] (1); Reverse transcriptase zinc-binding domain [IPR026960] (1) | scaffold_8_mRNA_1174.1 | C_unshiu_00617_mRNA_16.1,C_unshiu_01730_mRNA_7.1 | - |
| GF0016832 | 1 | 2 | 0 | Auxin-induced protein X10A (2); Auxin-induced protein 10A5 (1) | response to auxin [GO:0009733 biological_process] (3) | Small auxin-up RNA [IPR003676] (3) | scaffold_8_mRNA_1083.1 | C_unshiu_00396_mRNA_28.1,C_unshiu_00649_mRNA_9.1 | - |
| GF0016822 | 1 | 2 | 0 | Auxin-induced protein X10A (3) | response to auxin [GO:0009733 biological_process] (3) | Small auxin-up RNA [IPR003676] (3) | scaffold_8_mRNA_1041.1 | C_unshiu_00649_mRNA_16.1,C_unshiu_01573_mRNA_13.1 | - |
| GF0016818 | 1 | 2 | 0 | Retrotransposon gag protein (2); Hypothetical protein (1) |  | Retrotransposon gag domain [IPR005162] (3) | scaffold_8_mRNA_1035.1 | C_unshiu_00956_mRNA_11.1,C_unshiu_01859_mRNA_3.1 | - |
| GF0016815 | 1 | 2 | 0 | Hypothetical protein (3) |  | PIN domain-like [IPR029060] (2); Phosphoribosyltransferase-like [IPR029057] (1); NYN domain, limkain-b1-type [IPR021139] (1) | scaffold_8_mRNA_1025.1 | C_unshiu_00435_mRNA_3.1,C_unshiu_02125_mRNA_2.1 | - |
| GF0016764 | 1 | 2 | 0 | Hypothetical protein (3) | peptide-methionine (R)-S-oxide reductase activity [GO:0033743 molecular_function] (2); oxidation-reduction process [GO:0055114 biological_process] (2) | Mss4-like [IPR011057] (3); Peptide methionine sulphoxide reductase MrsB [IPR002579] (2) | scaffold_7_mRNA_91.1 | C_unshiu_00488_mRNA_3.1,C_unshiu_01559_mRNA_9.1 | - |
| GF0016751 | 1 | 2 | 0 | Prenylated rab acceptor family protein (3) |  | Prenylated rab acceptor PRA1 [IPR004895] (3) | scaffold_7_mRNA_884.1 | C_unshiu_00437_mRNA_2.1,C_unshiu_00726_mRNA_12.1 | - |
| GF0016658 | 1 | 2 | 0 | Hydroxyproline-rich glycoprotein family protein, putative (3) |  |  | scaffold_7_mRNA_720.1 | C_unshiu_00288_mRNA_25.1,C_unshiu_02333_mRNA_5.1 | - |
| GF0016616 | 1 | 2 | 0 | Protein RMD5 like A (3) | protein binding [GO:0005515 molecular_function] (3); zinc ion binding [GO:0008270 molecular_function] (3) | RING-type zinc-finger, LisH dimerisation motif [IPR027370] (3); CTLH/CRA C-terminal to LisH motif domain [IPR024964] (3); Zinc finger, RING-type [IPR001841] (3); Zinc finger, RING/FYVE/PHD-type [IPR013083] (3); CTLH, C-terminal LisH motif [IPR006595] (3); CRA domain [IPR013144] (3); LIS1 homology motif [IPR006594] (3); Rmd5 [IPR027711] (2) | scaffold_7_mRNA_660.1 | C_unshiu_00764_mRNA_7.1,C_unshiu_02109_mRNA_2.1 | - |
| GF0016568 | 1 | 2 | 0 | Glycosyl hydrolase family 43 protein (3) | hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553 molecular_function] (3); carbohydrate metabolic process [GO:0005975 biological_process] (3) | Glycoside hydrolase, family 43 [IPR006710] (3); Glycosyl hydrolase, five-bladed beta-propellor domain [IPR023296] (3) | scaffold_7_mRNA_598.1 | C_unshiu_00510_mRNA_27.1,C_unshiu_01220_mRNA_12.1 | - |
| GF0016546 | 1 | 2 | 0 | AT4g04660 protein (2); Hypothetical protein (1) | zinc ion binding [GO:0008270 molecular_function] (3); nucleic acid binding [GO:0003676 molecular_function] (3) | Zinc finger, CCHC-type [IPR001878] (3); Zinc knuckle CX2CX4HX4C [IPR025836] (3); Domain of unknown function DUF4283 [IPR025558] (3) | scaffold_7_mRNA_572.1 | C_unshiu_00136_mRNA_36.1,C_unshiu_02688_mRNA_1.1 | - |
| GF0016507 | 1 | 2 | 0 | Polypeptide with an integrase domain (1); Hypothetical protein (1); Potato DNA for copia-like transposable element (1) | nucleic acid binding [GO:0003676 molecular_function] (3); DNA integration [GO:0015074 biological_process] (3) | Ribonuclease H-like domain [IPR012337] (3); Integrase, catalytic core [IPR001584] (3); Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1) | scaffold_7_mRNA_513.1 | C_unshiu_00202_mRNA_2.1,C_unshiu_02229_mRNA_1.1 | - |
| GF0016446 | 1 | 2 | 0 | Reticulon-like protein B13 (3) |  | Reticulon [IPR003388] (3) | scaffold_7_mRNA_408.1 | C_unshiu_01032_mRNA_10.1,C_unshiu_01066_mRNA_7.1 | - |
| GF0016443 | 1 | 2 | 0 | Methyl esterase 1 (3) |  | Alpha/Beta hydrolase fold [IPR029058] (3); Alpha/beta hydrolase fold-1 [IPR000073] (3) | scaffold_7_mRNA_399.1 | C_unshiu_00025_mRNA_93.2,C_unshiu_01066_mRNA_2.2 | - |
| GF0016347 | 1 | 2 | 0 | T-complex protein 1 subunit gamma (2); TCP-1/cpn60 chaperonin family protein (1) | ATP binding [GO:0005524 molecular_function] (3); unfolded protein binding [GO:0051082 molecular_function] (2); protein folding [GO:0006457 biological_process] (2) | GroEL-like equatorial domain [IPR027413] (3); Chaperonin Cpn60/TCP-1 family [IPR002423] (3); GroEL-like apical domain [IPR027409] (2); T-complex protein 1, gamma subunit [IPR012719] (2); Chaperone tailless complex polypeptide 1 (TCP-1) [IPR017998] (2); Chaperonin TCP-1, conserved site [IPR002194] (2); TCP-1-like chaperonin intermediate domain [IPR027410] (1) | scaffold_7_mRNA_2726.1 | C_unshiu_00001_mRNA_404.1,C_unshiu_02885_mRNA_1.1 | - |
| GF0016280 | 1 | 2 | 0 | BZIP transcription factor (2); BZIP transcription factor bZIP124 (1) | regulation of transcription, DNA-templated [GO:0006355 biological_process] (3); sequence-specific DNA binding [GO:0043565 molecular_function] (3); transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (3) | Basic-leucine zipper domain [IPR004827] (3) | scaffold_7_mRNA_256.1 | C_unshiu_00209_mRNA_31.1,C_unshiu_02267_mRNA_2.1 | - |
| GF0016261 | 1 | 2 | 0 | Hypothetical protein (2); Disease resistance protein family, putative (1) | ADP binding [GO:0043531 molecular_function] (1) | Leucine-rich repeat domain, L domain-like [IPR032675] (3); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1); NB-ARC [IPR002182] (1) | scaffold_7_mRNA_2488.1 | C_unshiu_02139_mRNA_1.1,C_unshiu_02824_mRNA_1.1 | - |
| GF0016164 | 1 | 2 | 0 | Hypothetical protein (3) | protein phosphorylation [GO:0006468 biological_process] (2); protein kinase activity [GO:0004672 molecular_function] (2); ATP binding [GO:0005524 molecular_function] (1) | Bulb-type lectin domain [IPR001480] (3); Protein kinase-like domain [IPR011009] (2); Protein kinase domain [IPR000719] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1) | scaffold_7_mRNA_2225.1 | C_unshiu_00414_mRNA_5.1,C_unshiu_00611_mRNA_2.1 | - |
| GF0016162 | 1 | 2 | 0 | Hypothetical protein (3) | 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_2213.1 | C_unshiu_00040_mRNA_78.1,C_unshiu_00611_mRNA_16.1 | - |
| GF0016089 | 1 | 2 | 0 | Polynucleotidyl transferase, ribonuclease H-like superfamily protein (1); Putative non-LTR retroelement reverse transcriptase (1); Hypothetical protein (1) | nucleic acid binding [GO:0003676 molecular_function] (2) | Ribonuclease H-like domain [IPR012337] (2) | scaffold_7_mRNA_2021.1 | C_unshiu_00508_mRNA_3.1,C_unshiu_02073_mRNA_3.1 | - |
| GF0016061 | 1 | 2 | 0 | Hypothetical protein (3) |  |  | scaffold_7_mRNA_1961.1 | C_unshiu_00448_mRNA_22.1,C_unshiu_02045_mRNA_6.1 | - |
| GF0016007 | 1 | 2 | 0 | Hypothetical protein (3) | nucleic acid binding [GO:0003676 molecular_function] (3) | Ribonuclease H-like domain [IPR012337] (3) | scaffold_7_mRNA_1806.1 | C_unshiu_00181_mRNA_23.1,C_unshiu_01698_mRNA_6.1 | - |
| GF0015997 | 1 | 2 | 0 | Hypothetical protein (2); Phytosulfokine receptor (1) | protein binding [GO:0005515 molecular_function] (1) | Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (3); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Leucine-rich repeat [IPR001611] (1); Leucine-rich repeat, typical subtype [IPR003591] (1) | scaffold_7_mRNA_1756.1 | C_unshiu_01401_mRNA_9.1,C_unshiu_02586_mRNA_1.1 | - |
| GF0015957 | 1 | 2 | 0 | S locus F-box protein with the low allelic sequence polymorphism 1-S2 (3) | protein binding [GO:0005515 molecular_function] (3) | F-box associated interaction domain [IPR017451] (3); F-box domain [IPR001810] (3); Kelch-type beta propeller [IPR015915] (1) | scaffold_7_mRNA_157.1 | C_unshiu_00073_mRNA_10.1,C_unshiu_02420_mRNA_2.1 | - |
| GF0015954 | 1 | 2 | 0 | S locus F-box protein with the low allelic sequence polymorphism 1-S2 (2); Class S F-box protein (1) | protein binding [GO:0005515 molecular_function] (3) | Galactose oxidase/kelch, beta-propeller [IPR011043] (3); F-box associated interaction domain [IPR017451] (3); F-box domain [IPR001810] (3); F-box associated domain, type 3 [IPR013187] (3) | scaffold_7_mRNA_156.1 | C_unshiu_00073_mRNA_9.1,C_unshiu_02420_mRNA_1.1 | - |
| GF0015953 | 1 | 2 | 0 | Caffeoyl CoA O-methyltransferase (3) | O-methyltransferase activity [GO:0008171 molecular_function] (3) | O-methyltransferase, family 3 [IPR002935] (3); S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (3) | scaffold_7_mRNA_1558.1 | C_unshiu_01330_mRNA_7.1,C_unshiu_01330_mRNA_8.2 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0015939 | 1 | 2 | 0 | Disease resistance protein RPS2 (3) | ADP binding [GO:0043531 molecular_function] (3); protein binding [GO:0005515 molecular_function] (3) | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (3); Leucine-rich repeat [IPR001611] (3); NB-ARC [IPR002182] (3); Leucine-rich repeat, typical subtype [IPR003591] (3); Leucine-rich repeat domain, L domain-like [IPR032675] (3); Winged helix-turn-helix DNA-binding domain [IPR011991] (1) | scaffold_7_mRNA_1529.1 | C_unshiu_00185_mRNA_4.1,C_unshiu_01149_mRNA_2.1 | - |
| GF0015922 | 1 | 2 | 0 | Hypothetical protein (2); Ribulose bisphosphate carboxylase large chain (1) | carbon fixation [GO:0015977 biological_process] (3); ribulose-bisphosphate carboxylase activity [GO:0016984 molecular_function] (3) | Ribulose bisphosphate carboxylase, large subunit, ferrodoxin-like N-terminal [IPR017443] (3) | scaffold_7_mRNA_1492.1 | C_unshiu_00271_mRNA_3.1,C_unshiu_00271_mRNA_4.1 | - |
| GF0015866 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_7_mRNA_1356.1 | C_unshiu_00595_mRNA_30.1,C_unshiu_01521_mRNA_5.1 | - |
| GF0015864 | 1 | 2 | 0 | To encode a PR protein, Belongs to the plant thionin family with the following members:, putative (3) | | | scaffold_7_mRNA_1351.1 | C_unshiu_00208_mRNA_2.1,C_unshiu_02723_mRNA_1.1 | - |
| GF0015859 | 1 | 2 | 0 | Coatomer beta subunit, putative (3) | protein binding [GO:0005515 molecular_function] (2) | G-protein beta WD-40 repeat [IPR020472] (2); WD40 repeat, conserved site [IPR019775] (2); WD40/YVTN repeat-like-containing domain [IPR015943] (2); WD40-repeat-containing domain [IPR017986] (2); WD40 repeat [IPR001680] (2) | scaffold_7_mRNA_1340.1 | C_unshiu_00208_mRNA_11.1,C_unshiu_03029_mRNA_1.1 | - |
| GF0015698 | 1 | 2 | 0 | DNA-binding storekeeper protein-related transcriptional regulator (2); DNA-binding storekeeper protein-related transcriptional regulator, putative (1) | regulation of transcription, DNA-templated [GO:0006355 biological_process] (1) | Protein of unknown function DUF573 [IPR007592] (2); GLABROUS1 enhancer-binding protein family [IPR007592] (1) | scaffold_6_mRNA_999.1 | C_unshiu_00232_mRNA_1.1,C_unshiu_01104_mRNA_8.1 | - |
| GF0015694 | 1 | 2 | 0 | S-norcoclaurine synthase 2 (3) | defense response [GO:0006952 biological_process] (3); response to biotic stimulus [GO:0009607 biological_process] (3) | Bet v I/Major latex protein [IPR000916] (3); START-like domain [IPR023393] (3); Major latex protein domain [IPR024948] (2) | scaffold_6_mRNA_975.1 | C_unshiu_00232_mRNA_21.1,C_unshiu_02251_mRNA_4.1 | - |
| GF0015689 | 1 | 2 | 0 | Protein TIC 20-v, chloroplastic (3) | | Chloroplast protein import component Tic20 [IPR005691] (3) | scaffold_6_mRNA_944.1 | C_unshiu_00407_mRNA_24.1,C_unshiu_02121_mRNA_4.1 | - |
| GF0015660 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_6_mRNA_830.1 | C_unshiu_00415_mRNA_18.1,C_unshiu_02226_mRNA_3.1 | - |
| GF0015648 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_6_mRNA_77.1 | C_unshiu_00092_mRNA_18.1,C_unshiu_01857_mRNA_6.1 | - |
| GF0015643 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_6_mRNA_745.1 | C_unshiu_01235_mRNA_4.1,C_unshiu_01632_mRNA_2.1 | - |
| GF0015622 | 1 | 2 | 0 | Hypothetical protein (3) | | MULE transposase domain [IPR018289] (3) | scaffold_6_mRNA_640.1 | C_unshiu_00198_mRNA_27.1,C_unshiu_01907_mRNA_3.1 | - |
| GF0015608 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_6_mRNA_477.1 | C_unshiu_00871_mRNA_9.1,C_unshiu_01659_mRNA_7.1 | - |
| GF0015604 | 1 | 2 | 0 | Hypothetical protein (3) | | Reverse transcriptase domain [IPR000477] (3); Paraneoplastic antigen Ma [IPR026523] (1) | scaffold_6_mRNA_427.1 | C_unshiu_00871_mRNA_23.1,C_unshiu_01933_mRNA_11.1 | - |
| GF0015601 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_6_mRNA_402.1 | C_unshiu_01100_mRNA_14.1,C_unshiu_01409_mRNA_3.1 | - |
| GF0015360 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_6_mRNA_287.1 | C_unshiu_00262_mRNA_13.1,C_unshiu_00484_mRNA_23.1 | - |
| GF0015248 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_6_mRNA_271.1 | C_unshiu_00176_mRNA_10.1,C_unshiu_00780_mRNA_7.1 | - |
| GF0015050 | 1 | 2 | 0 | UPF0481 protein (3) | | Protein of unknown function DUF247, plant [IPR004158] (3) | scaffold_6_mRNA_2432.1 | C_unshiu_01263_mRNA_10.1,C_unshiu_01499_mRNA_1.1 | - |
| GF0014816 | 1 | 2 | 0 | Translocase of chloroplast (3) | P-P-bond-hydrolysis-driven protein transmembrane transporter activity [GO:0015450 molecular_function] (3); intracellular protein transport [GO:0006886 biological_process] (3); GTP binding [GO:0005525 molecular_function] (3); chloroplast outer membrane [GO:0009707 cellular_component] (3) | AIG1-type guanine nucleotide-binding (G) domain [IPR006703] (3); Chloroplast protein import component Toc34 [IPR005688] (3); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (3) | scaffold_6_mRNA_2095.1 | C_unshiu_00644_mRNA_7.1,C_unshiu_01587_mRNA_9.1 | - |
| GF0014643 | 1 | 2 | 0 | Protein FAR1-RELATED SEQUENCE 6 (1); Hypothetical protein (1); FAR1 DNA-binding domain protein (1) | regulation of transcription, DNA-templated [GO:0006355 biological_process] (2); zinc ion binding [GO:0008270 molecular_function] (1) | FHY3/FAR1 family [IPR031052] (2); FAR1 DNA binding domain [IPR004330] (2); Zinc finger, SWIM-type [IPR007527] (1); MULE transposase domain [IPR018289] (1); Zinc finger, PMZ-type [IPR006564] (1) | scaffold_6_mRNA_1813.1 | C_unshiu_00332_mRNA_7.1,C_unshiu_01382_mRNA_6.1 | - |
| GF0014633 | 1 | 2 | 0 | Nucleic acid binding / zinc ion binding protein (2); AT4g04660 protein (1) | zinc ion binding [GO:0008270 molecular_function] (2); nucleic acid binding [GO:0003676 molecular_function] (2) | Zinc knuckle CX2CX4HX4C [IPR025836] (3); Domain of unknown function DUF4283 [IPR025558] (3); Zinc finger, CCHC-type [IPR001878] (2) | scaffold_6_mRNA_1794.1 | C_unshiu_00390_mRNA_18.1,C_unshiu_01311_mRNA_4.1 | - |
| GF0014467 | 1 | 2 | 0 | Hypothetical protein (3) | | Domain of unknown function DUF1985 [IPR015410] (1) | scaffold_6_mRNA_1390.1 | C_unshiu_00198_mRNA_31.1,C_unshiu_00219_mRNA_27.1 | - |
| GF0014454 | 1 | 2 | 0 | Caffeic acid 3-O-methyltransferase (2); Caffeic acid O-methyltransferase (1) | methyltransferase activity [GO:0008168 molecular_function] (3); protein dimerization activity [GO:0046983 molecular_function] (3); O-methyltransferase activity [GO:0008171 molecular_function] (3) | S-adenosyl-L-methionine-dependent methyltransferase [IPR029063] (3); Plant methyltransferase dimerisation [IPR012967] (3); O-methyltransferase COMT-type [IPR016461] (3); O-methyltransferase, family 2 [IPR001077] (3); Winged helix-turn-helix DNA-binding domain [IPR011991] (3) | scaffold_6_mRNA_1352.1 | C_unshiu_01123_mRNA_7.1,C_unshiu_01732_mRNA_5.1 | - |
| GF0014446 | 1 | 2 | 0 | LRR receptor-like serine/threonine-protein kinase EFR (2); Hypothetical protein (1) | protein binding [GO:0005515 molecular_function] (1) | Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (3); Leucine-rich repeat domain, L domain-like [IPR032675] (3); Leucine-rich repeat [IPR001611] (1) | scaffold_6_mRNA_134.1 | C_unshiu_00272_mRNA_6.1,C_unshiu_00378_mRNA_10.1 | - |
| GF0014388 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_6_mRNA_1120.1 | C_unshiu_01629_mRNA_17.1,C_unshiu_02021_mRNA_6.1 | - |
| GF0014358 | 1 | 2 | 0 | H( +)-transporting atpase plant/fungi plasma membrane type, putative (1); Plasma membrane ATPase (1); Hypothetical protein (1) | integral component of membrane [GO:0016021 cellular_component] (3); metal ion binding [GO:0046872 molecular_function] (3); nucleotide binding [GO:0000166 molecular_function] (3) | HAD-like domain [IPR023214] (3); P-type ATPase, A domain [IPR008250] (3); P-type ATPase, cytoplasmic domain N [IPR023299] (3); P-type ATPase, transmembrane domain [IPR023298] (3); P-type ATPase [IPR001757] (3); P-type ATPase, phosphorylation site [IPR018303] (3) | scaffold_6_mRNA_1022.1 | C_unshiu_00626_mRNA_2.1,C_unshiu_02317_mRNA_2.1 | - |
| GF0014357 | 1 | 2 | 0 | Transmembrane and coiled-coil domains protein 1 (2); Hypothetical protein (1) | membrane [GO:0016020 cellular_component] (1) | Uncharacterised conserved protein UCP023322, transmembrane eukaryotic [IPR008559] (1) | scaffold_6_mRNA_1014.1 | C_unshiu_00402_mRNA_6.1,C_unshiu_00626_mRNA_4.1 | - |
| GF0014354 | 1 | 2 | 0 | RNA-directed DNA polymerase , related (1); Ribonuclease H protein, putative (1); RNA-directed DNA polymerase (Reverse transcriptase) (1) | | Reverse transcriptase zinc-binding domain [IPR026960] (2) | scaffold_6_mRNA_101.1 | C_unshiu_00187_mRNA_38.1,C_unshiu_00329_mRNA_5.1 | - |
| GF0014344 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_5_mRNA_961.1 | C_unshiu_00408_mRNA_19.1,C_unshiu_00540_mRNA_16.1 | - |
| GF0014318 | 1 | 2 | 0 | Putative non-LTR reverse transcriptase (1); Polynucleotidyl transferase, Ribonuclease H fold (1); RNA-directed DNA polymerase (Reverse transcriptase), Polynucleotidyl transferase, Ribonuclease H fold-like protein (1) | nucleic acid binding [GO:0003676 molecular_function] (2); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1) | Reverse transcriptase zinc-binding domain [IPR026960] (3); Ribonuclease H-like domain [IPR012337] (2); Ribonuclease H domain [IPR002156] (1); Plant disease resistance response protein [IPR004265] (1) | scaffold_5_mRNA_804.1 | C_unshiu_00213_mRNA_4.1,C_unshiu_00583_mRNA_3.1 | - |
| GF0014317 | 1 | 2 | 0 | Zinc knuckle family protein (3) | zinc ion binding [GO:0008270 molecular_function] (3); nucleic acid binding [GO:0003676 molecular_function] (3) | Zinc finger, CCHC-type [IPR001878] (3); Domain of unknown function DUF4219 [IPR025314] (2) | scaffold_5_mRNA_797.1 | C_unshiu_00471_mRNA_28.1,C_unshiu_00583_mRNA_9.1 | - |
| GF0014273 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_5_mRNA_608.1 | C_unshiu_00354_mRNA_12.1,C_unshiu_00354_mRNA_8.1 | - |
| GF0014272 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_5_mRNA_607.1 | C_unshiu_00354_mRNA_11.1,C_unshiu_00354_mRNA_9.1 | - |
| GF0014256 | 1 | 2 | 0 | Hypothetical protein (3) | regulation of transcription, DNA-templated [GO:0006355 biological_process] (3) | FHY3/FAR1 family [IPR031052] (3); MULE transposase domain [IPR018289] (2) | scaffold_5_mRNA_569.1 | C_unshiu_00085_mRNA_50.1,C_unshiu_01109_mRNA_2.1 | - |
| GF0014124 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_5_mRNA_5013.1 | C_unshiu_00009_mRNA_162.1,C_unshiu_00192_mRNA_3.1 | - |
| GF0013990 | 1 | 2 | 0 | Putative carboxylesterase 2 (3) | hydrolase activity [GO:0016787 molecular_function] (3); metabolic process [GO:0008152 biological_process] (3) | Alpha/beta hydrolase fold-3 [IPR013094] (3); Alpha/Beta hydrolase fold [IPR029058] (3) | scaffold_5_mRNA_4792.1 | C_unshiu_00054_mRNA_2.1,C_unshiu_00951_mRNA_14.1 | - |
| GF0013931 | 1 | 2 | 0 | Dienelactone hydrolase-like protein (3) | hydrolase activity [GO:0016787 molecular_function] (3) | Alpha/Beta hydrolase fold [IPR029058] (3); Dienelactone hydrolase [IPR002925] (3) | scaffold_5_mRNA_4694.1 | C_unshiu_01033_mRNA_16.1,C_unshiu_01089_mRNA_19.1 | - |
| GF0013892 | 1 | 2 | 0 | Chaperone DnaJ-domain superfamily protein (3) | | DnaJ domain [IPR001623] (3) | scaffold_5_mRNA_4631.1 | C_unshiu_00495_mRNA_28.1,C_unshiu_00802_mRNA_15.1 | - |
| GF0013866 | 1 | 2 | 0 | UDP-galactose transporter 2 (3) | nucleotide-sugar transport [GO:0015780 biological_process] (3); nucleotide-sugar transmembrane transporter activity [GO:0005338 molecular_function] (3) | Bi-functional UDP-rhamnose/UDP-galactose transporter [IPR031089] (3); Sugar phosphate transporter domain [IPR004853] (3) | scaffold_5_mRNA_4593.1 | C_unshiu_00278_mRNA_38.1,C_unshiu_01416_mRNA_2.1 | - |
| GF0013773 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_5_mRNA_4450.1 | C_unshiu_00238_mRNA_35.1,C_unshiu_00319_mRNA_2.1 | - |
| GF0013715 | 1 | 2 | 0 | Hypothetical protein (3) | | Zinc-ribbon 15 [IPR031493] (3) | scaffold_5_mRNA_4379.1 | C_unshiu_00477_mRNA_23.1,C_unshiu_00552_mRNA_19.1 | - |
| GF0013696 | 1 | 2 | 0 | Hypothetical protein (3) | protein binding [GO:0005515 molecular_function] (1) | Pentatricopeptide repeat [IPR002885] (3); Tetratricopeptide-like helical domain [IPR011990] (1) | scaffold_5_mRNA_435.1 | C_unshiu_00378_mRNA_3.1,C_unshiu_00378_mRNA_33.1 | - |
| GF0013591 | 1 | 2 | 0 | Putative retroelement pol polyprotein (3) | 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_417.1 | C_unshiu_00141_mRNA_5.1,C_unshiu_00617_mRNA_5.1 | - |
| GF0013504 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_5_mRNA_4041.1 | C_unshiu_00022_mRNA_23.1,C_unshiu_00582_mRNA_7.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0013450 | 1 | 2 | 0 | Stearoyl-acyl carrier protein desaturase (3) | fatty acid metabolic process [GO:0006631 biological_process] (3); oxidation-reduction process [GO:0055114 biological_process] (3); acyl-[acyl-carrier-protein] desaturase activity [GO:0045300 molecular_function] (3); oxidoreductase activity [GO:0016491 molecular_function] (2) | Fatty acid desaturase, type 2 [IPR005067] (3); Ferritin-like superfamily [IPR009078] (3); Ribonucleotide reductase-related [IPR012348] (2) | scaffold_5_mRNA_3940.1 | C_unshiu_00447_mRNA_24.1,C_unshiu_02182_mRNA_3.1 | - |
| GF0013449 | 1 | 2 | 0 | Eukaryotic translation initiation factor 5B (2); Translation initiation factor IF-2, putative (1) | GTP binding [GO:0005525 molecular_function] (2); GTPase activity [GO:0003924 molecular_function] (2) | Translation protein, beta-barrel domain [IPR009000] (3); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (3); Translation initiation factor IF- 2, domain 3 [IPR023115] (3); Small GTP-binding protein domain [IPR005225] (2); Transcription factor, GTP-binding domain [IPR000795] (2) | scaffold_5_mRNA_3937.1 | C_unshiu_00447_mRNA_21.1,C_unshiu_02182_mRNA_7.1 | - |
| GF0013329 | 1 | 2 | 0 | Putative retroelement pol polyprotein (2); Hypothetical protein (1) | | | scaffold_5_mRNA_371.1 | C_unshiu_00328_mRNA_5.1,C_unshiu_01324_mRNA_3.1 | - |
| GF0013307 | 1 | 2 | 0 | Hypothetical protein (2); Phosphoprotein phosphatase (1) | ADP binding [GO:0043531 molecular_function] (1) | Leucine-rich repeat domain, L domain-like [IPR032675] (3); NB-ARC [IPR002182] (1); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (1) | scaffold_5_mRNA_3647.1 | C_unshiu_00453_mRNA_21.1,C_unshiu_00453_mRNA_28.1 | - |
| GF0013286 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_5_mRNA_3575.1 | C_unshiu_00244_mRNA_16.1,C_unshiu_00782_mRNA_9.1 | - |
| GF0013264 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_5_mRNA_3447.1 | C_unshiu_01332_mRNA_4.1,C_unshiu_02372_mRNA_3.1 | - |
| GF0013257 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_5_mRNA_3433.1 | C_unshiu_00269_mRNA_21.1,C_unshiu_00344_mRNA_36.1 | - |
| GF0013232 | 1 | 2 | 0 | Ras-related protein Rab11C (1); Hypothetical protein (1); RAB GTPase-like protein B1C (1) | GTP binding [GO:0005525 molecular_function] (3); protein transport [GO:0015031 biological_process] (2); signal transduction [GO:0007165 biological_process] (2); small GTPase mediated signal transduction [GO:0007264 biological_process] (2); membrane [GO:0016020 cellular_component] (2); GTPase activity [GO:0003924 molecular_function] (1); intracellular [GO:0005622 cellular_component] (1) | Small GTPase superfamily [IPR001806] (3); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (3); Small GTPase superfamily, Ras type [IPR020849] (2); Small GTPase superfamily, Rab type [IPR003579] (2); Small GTP-binding protein domain [IPR005225] (1); Small GTPase superfamily, Rho type [IPR003578] (1) | scaffold_5_mRNA_331.1 | C_unshiu_01174_mRNA_6.1,C_unshiu_01207_mRNA_2.1 | - |
| GF0013218 | 1 | 2 | 0 | GTP-binding protein YPTM2 (1); RAB GTPase-like protein B1C (1); Ras-like GTP-binding protein YPT1 (1) | GTP binding [GO:0005525 molecular_function] (3); small GTPase mediated signal transduction [GO:0007264 biological_process] (2); membrane [GO:0016020 cellular_component] (2); signal transduction [GO:0007165 biological_process] (2); protein transport [GO:0015031 biological_process] (2); intracellular [GO:0005622 cellular_component] (1); GTPase activity [GO:0003924 molecular_function] (1) | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (3); Small GTPase superfamily [IPR001806] (3); Small GTPase superfamily, Ras type [IPR020849] (2); Small GTPase superfamily, Rab type [IPR003579] (2); Small GTPase superfamily, Rho type [IPR003578] (1) | scaffold_5_mRNA_328.1 | C_unshiu_00746_mRNA_7.1,C_unshiu_01215_mRNA_14.1 | - |
| GF0013185 | 1 | 2 | 0 | Amino acid permease family protein (1); Hypothetical protein (1); Neutral amino acid transporter (1) | amino acid transmembrane transporter activity [GO:0015171 molecular_function] (3); amino acid transmembrane transport [GO:0003333 biological_process] (3); membrane [GO:0016020 cellular_component] (3); protein binding [GO:0005515 molecular_function] (1) | Amino acid/polyamine transporter I [IPR002293] (3); Arfaptin homology (AH) domain/BAR domain [IPR027267] (1); SH3 domain [IPR001452] (1) | scaffold_5_mRNA_3172.1 | C_unshiu_00809_mRNA_10.1,C_unshiu_00961_mRNA_7.1 | - |
| GF0013182 | 1 | 2 | 0 | LRR receptor-like serine/threonine-protein kinase GSO1 (3) | protein binding [GO:0005515 molecular_function] (3) | Leucine-rich repeat, typical subtype [IPR003591] (3); Leucine-rich repeat domain, L domain-like [IPR032675] (3); Leucine-rich repeat [IPR001611] (3); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (2); SH3 domain [IPR001452] (1) | scaffold_5_mRNA_3122.1 | C_unshiu_00888_mRNA_6.1,C_unshiu_02001_mRNA_5.1 | - |
| GF0013139 | 1 | 2 | 0 | Hypothetical protein (3) | protein binding [GO:0005515 molecular_function] (3) | Ankyrin repeat-containing domain [IPR020683] (3); Ankyrin repeat [IPR002110] (3) | scaffold_5_mRNA_2983.1 | C_unshiu_00016_mRNA_3.1,C_unshiu_00382_mRNA_1.1 | - |
| GF0013039 | 1 | 2 | 0 | Hypothetical protein (3) | | Retrotransposon gag domain [IPR005162] (1) | scaffold_5_mRNA_2441.1 | C_unshiu_01665_mRNA_1.1,C_unshiu_01989_mRNA_1.1 | - |
| GF0012991 | 1 | 2 | 0 | Hypothetical protein (3) | | Transposon, En/Spm-like [IPR004242] (1); Probable transposase, Ptta/En/Spm, plant [IPR004252] (1); Domain of unknown function DUF4216 [IPR025312] (1) | scaffold_5_mRNA_2247.1 | C_unshiu_00258_mRNA_1.1,C_unshiu_01853_mRNA_4.1 | - |
| GF0012988 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_5_mRNA_2224.1 | C_unshiu_00111_mRNA_45.1,C_unshiu_00464_mRNA_15.1 | - |
| GF0012968 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_5_mRNA_2149.1 | C_unshiu_00100_mRNA_30.1,C_unshiu_00419_mRNA_18.1 | - |
| GF0012956 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_5_mRNA_2055.1 | C_unshiu_00871_mRNA_22.1,C_unshiu_00871_mRNA_33.1 | - |
| GF0012926 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_5_mRNA_1937.1 | C_unshiu_00568_mRNA_19.1,C_unshiu_01974_mRNA_2.1 | - |
| GF0012921 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_5_mRNA_1929.1 | C_unshiu_01841_mRNA_2.1,C_unshiu_02592_mRNA_2.1 | - |
| GF0012913 | 1 | 2 | 0 | Hypothetical protein (3) | regulation of transcription, DNA-templated [GO:0006355 biological_process] (3); DNA binding [GO:0003677 molecular_function] (3) | NAC domain [IPR003441] (3) | scaffold_5_mRNA_1880.1 | C_unshiu_00573_mRNA_10.1,C_unshiu_00647_mRNA_10.1 | - |
| GF0012864 | 1 | 2 | 0 | Hypothetical protein (2); Late embryogenesis abundant hydroxyproline-rich glycoprotein, putative (1) | | Late embryogenesis abundant protein, LEA-14 [IPR004864] (3); Immunoglobulin-like fold [IPR013783] (3) | scaffold_5_mRNA_1708.1 | C_unshiu_00202_mRNA_9.1,C_unshiu_01766_mRNA_2.1 | - |
| GF0012844 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_5_mRNA_1583.1 | C_unshiu_00174_mRNA_46.1,C_unshiu_02392_mRNA_2.1 | - |
| GF0012842 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_5_mRNA_1538.1 | C_unshiu_00128_mRNA_16.1,C_unshiu_01666_mRNA_5.1 | - |
| GF0012830 | 1 | 2 | 0 | Peroxidase 2 (3) | peroxidase activity [GO:0004601 molecular_function] (3); oxidation-reduction process [GO:0055114 biological_process] (3); heme binding [GO:0020037 molecular_function] (3); response to oxidative stress [GO:0006979 biological_process] (3); hydrogen peroxide catabolic process [GO:0042744 biological_process] (1) | Haem peroxidase [IPR010255] (3); Peroxidase, active site [IPR019794] (3); Peroxidases heam-ligand binding site [IPR019793] (3); Plant peroxidase [IPR000823] (3); Haem peroxidase, plant/fungal/bacterial [IPR002016] (3); Secretory peroxidase [IPR033905] (1) | scaffold_5_mRNA_1449.2 | C_unshiu_00530_mRNA_2.1,C_unshiu_00678_mRNA_16.1 | - |
| GF0012806 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_5_mRNA_1364.1 | C_unshiu_01675_mRNA_5.1,C_unshiu_01952_mRNA_2.1 | - |
| GF0012781 | 1 | 2 | 0 | Hypothetical protein (3) | | Retrotransposon gag domain [IPR005162] (2) | scaffold_5_mRNA_1262.1 | C_unshiu_00340_mRNA_14.1,C_unshiu_00444_mRNA_10.1 | - |
| GF0012776 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_5_mRNA_1227.1 | C_unshiu_01048_mRNA_3.1,C_unshiu_01401_mRNA_4.1 | - |
| GF0012775 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_5_mRNA_1224.1 | C_unshiu_00160_mRNA_13.1,C_unshiu_00160_mRNA_14.1 | - |
| GF0012768 | 1 | 2 | 0 | NB-ARC domain disease resistance protein (1); NB-ARC domain-containing disease resistance protein (1); LRR and NB-ARC domains-containing disease resistance protein (1) | ADP binding [GO:0043531 molecular_function] (3) | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (3); NB-ARC [IPR002182] (3); Leucine-rich repeat domain, L domain-like [IPR032675] (2) | scaffold_5_mRNA_113.1 | C_unshiu_00019_mRNA_5.1,C_unshiu_00904_mRNA_4.1 | - |
| GF0012759 | 1 | 2 | 0 | Hypothetical protein (3) | terpene synthase activity [GO:0010333 molecular_function] (3); lyase activity [GO:0016829 molecular_function] (3); metabolic process [GO:0008152 biological_process] (3); nucleic acid binding [GO:0003676 molecular_function] (1) | Terpene synthase, N-terminal domain [IPR001906] (3); Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (3); Ribonuclease H-like domain [IPR012337] (1) | scaffold_5_mRNA_1099.1 | C_unshiu_00825_mRNA_5.1,C_unshiu_01139_mRNA_2.1 | - |
| GF0012754 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_5_mRNA_1076.1 | C_unshiu_00240_mRNA_16.1,C_unshiu_00685_mRNA_2.1 | - |
| GF0012747 | 1 | 2 | 0 | Hypothetical protein (2); Putative Ty3-gypsy-like 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_5_mRNA_1053.1 | C_unshiu_01148_mRNA_3.1,C_unshiu_01624_mRNA_1.1 | - |
| GF0012740 | 1 | 2 | 0 | Hypothetical protein (3) | | Gag-polypeptide of LTR copia-type [IPR029472] (2) | scaffold_5_mRNA_1033.1 | C_unshiu_00091_mRNA_10.1,C_unshiu_01351_mRNA_4.1 | - |
| GF0012727 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_4_mRNA_963.1 | C_unshiu_01776_mRNA_3.1,C_unshiu_02475_mRNA_1.1 | - |
| GF0012662 | 1 | 2 | 0 | Transducin wd40 repeat-like superfamily protein (3) | zinc ion binding [GO:0008270 molecular_function] (3); nucleic acid binding [GO:0003676 molecular_function] (3) | Zinc finger, CCHC-type [IPR001878] (3) | scaffold_4_mRNA_847.1 | C_unshiu_00169_mRNA_9.1,C_unshiu_00202_mRNA_5.1 | - |
| GF0012602 | 1 | 2 | 0 | Hypothetical protein (3) | | TB2/DP1/HVA22-related protein [IPR004345] (3); Leucine-rich repeat domain, L domain-like [IPR032675] (1) | scaffold_4_mRNA_664.1 | C_unshiu_01019_mRNA_10.1,C_unshiu_02720_mRNA_2.1 | - |
| GF0012574 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_4_mRNA_571.1 | C_unshiu_00141_mRNA_54.1,C_unshiu_01045_mRNA_12.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0011351 | 1 | 2 | 0 | Hypothetical protein (3) | nucleic acid binding [GO:0003676 molecular_function] (2); zinc ion binding [GO:0008270 molecular_function] (2); regulation of transcription, DNA-templated [GO:0006355 biological_process] (1) | Zinc finger, CCHC-type [IPR001878] (2); FAR1 DNA binding domain [IPR004330] (1); FHY3/FAR1 family [IPR031052] (1); Zinc finger, SWIM-type [IPR007527] (1); Zinc finger, PMZ-type [IPR006564] (1) | scaffold_4_mRNA_1751.1 | C_unshiu_00059_mRNA_57.1,C_unshiu_00416_mRNA_31.1 | - |
| GF0011143 | 1 | 2 | 0 | Hypothetical protein (3) | zinc ion binding [GO:0008270 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1) | Domain of unknown function DUF4283 [IPR025558] (3); Zinc finger, CCHC-type [IPR001878] (1); Zinc knuckle CX2CX4HX4C [IPR025836] (1) | scaffold_4_mRNA_1197.1 | C_unshiu_00140_mRNA_26.1,C_unshiu_00250_mRNA_18.1 | - |
| GF0011129 | 1 | 2 | 0 | Retrotransposon gag protein (3) | | Retrotransposon gag domain [IPR005162] (3) | scaffold_4_mRNA_1161.1 | C_unshiu_00532_mRNA_3.1,C_unshiu_01230_mRNA_4.1 | - |
| GF0011026 | 1 | 2 | 0 | Putative L-type lectin-domain containing receptor kinase S.7 (1); L-type lectin-domain containing receptor kinase IX.1 (1); Clade XV lectin receptor kinase (1) | carbohydrate binding [GO:0030246 molecular_function] (3); protein kinase activity [GO:0004672 molecular_function] (3); protein phosphorylation [GO:0006468 biological_process] (3); ATP binding [GO:0005524 molecular_function] (3); nucleus [GO:0005634 cellular_component] (1); DNA binding [GO:0003677 molecular_function] (1) | Concanavalin A-like lectin/glucanase domain [IPR013320] (3); Protein kinase-like domain [IPR011009] (3); Legume lectin domain [IPR001220] (3); Protein kinase domain [IPR000719] (3); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); KNOX2 [IPR005541] (1); KNOX1 [IPR005540] (1) | scaffold_3_mRNA_902.1 | C_unshiu_00412_mRNA_5.1,C_unshiu_02762_mRNA_1.1 | - |
| GF0010423 | 1 | 2 | 0 | Hypothetical protein (3) | nucleic acid binding [GO:0003676 molecular_function] (3); zinc ion binding [GO:0008270 molecular_function] (3) | Zinc knuckle CX2CX4HX4C [IPR025836] (3); Zinc finger, CCHC-type [IPR001878] (3); Domain of unknown function DUF4283 [IPR025558] (2); Ribonuclease H-like domain [IPR012337] (1) | scaffold_3_mRNA_5723.1 | C_unshiu_00101_mRNA_39.1,C_unshiu_00254_mRNA_8.1 | - |
| GF0010235 | 1 | 2 | 0 | Gibberellin receptor GID1C (3) | hydrolase activity [GO:0016787 molecular_function] (3); metabolic process [GO:0008152 biological_process] (3) | Alpha/Beta hydrolase fold [IPR029058] (3); Lipase, GDXG, putative histidine active site [IPR002168] (3); Lipase, GDXG, putative serine active site [IPR033140] (3); Alpha/beta hydrolase fold-3 [IPR013094] (3) | scaffold_3_mRNA_5443.1 | C_unshiu_00069_mRNA_13.1,C_unshiu_02089_mRNA_3.1 | - |
| GF0010199 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_3_mRNA_5389.1 | C_unshiu_00069_mRNA_63.1,C_unshiu_02801_mRNA_3.1 | - |
| GF0010140 | 1 | 2 | 0 | Sesquiterpene synthase (3) | metabolic process [GO:0008152 biological_process] (3); magnesium ion binding [GO:0000287 molecular_function] (3); terpene synthase activity [GO:0010333 molecular_function] (3); lyase activity [GO:0016829 molecular_function] (3) | Isoprenoid synthase domain [IPR008949] (3); Terpene synthase, N-terminal domain [IPR001906] (3); Terpene synthase, metal-binding domain [IPR005630] (3); Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (3) | scaffold_3_mRNA_530.1 | C_unshiu_00120_mRNA_43.1,C_unshiu_01646_mRNA_2.1 | - |
| GF0009883 | 1 | 2 | 0 | Expansin (3) | plant-type cell wall organization [GO:0009664 biological_process] (3); extracellular region [GO:0005576 cellular_component] (3) | Expansin, cellulose-binding-like domain [IPR007117] (3); Expansin [IPR002963] (3); Expansin/Lol pI [IPR007118] (3); Expansin/pollen allergen, DPBB domain [IPR007112] (3); RlpA-like double-psi beta-barrel domain [IPR009009] (2); RlpA-like protein, double-psi beta-barrel domain [IPR009009] (1) | scaffold_3_mRNA_4899.1 | C_unshiu_00194_mRNA_49.1,C_unshiu_01905_mRNA_3.1 | - |
| GF0009855 | 1 | 2 | 0 | Hypothetical protein (3) | transcription factor activity, sequence-specific DNA binding [GO:0003700 molecular_function] (3); regulation of transcription, DNA-templated [GO:0006355 biological_process] (3); multicellular organismal development [GO:0007275 biological_process] (2); multicellular organism development [GO:0007275 biological_process] (1) | AP2-like ethylene-responsive transcription factor [IPR031112] (3) | scaffold_3_mRNA_4827.1 | C_unshiu_01263_mRNA_2.1,C_unshiu_02352_mRNA_2.1 | - |
| GF0009841 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_3_mRNA_4803.1 | C_unshiu_00076_mRNA_58.1,C_unshiu_00101_mRNA_46.1 | - |
| GF0009825 | 1 | 2 | 0 | Soluble inorganic pyrophosphatase (3) | magnesium ion binding [GO:0000287 molecular_function] (3); cytoplasm [GO:0005737 cellular_component] (3); inorganic diphosphatase activity [GO:0004427 molecular_function] (3); phosphate-containing compound metabolic process [GO:0006796 biological_process] (3) | Inorganic pyrophosphatase [IPR008162] (3) | scaffold_3_mRNA_4776.1 | C_unshiu_00566_mRNA_1.1,C_unshiu_00875_mRNA_12.1 | - |
| GF0009781 | 1 | 2 | 0 | Disease resistance protein (TIR-NBS-LRR class) (2); TMV resistance protein N, putative (1) | signal transduction [GO:0007165 biological_process] (3); ADP binding [GO:0043531 molecular_function] (3); protein binding [GO:0005515 molecular_function] (3) | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (3); NB-ARC [IPR002182] (3); Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (3); Winged helix-turn-helix DNA-binding domain [IPR011991] (3); Leucine-rich repeat domain, L domain-like [IPR032675] (2); Leucine-rich repeat 3 [IPR011713] (1) | scaffold_3_mRNA_4699.1 | C_unshiu_00727_mRNA_15.1,C_unshiu_01868_mRNA_4.1 | - |
| GF0009763 | 1 | 2 | 0 | Hypothetical protein (3) | | Pectin lyase fold [IPR012334] (1) | scaffold_3_mRNA_4646.1 | C_unshiu_00862_mRNA_1.1,C_unshiu_03021_mRNA_1.1 | - |
| GF0009756 | 1 | 2 | 0 | Progesterone 5-beta-reductase (3) | | NAD(P)-binding domain [IPR016040] (3) | scaffold_3_mRNA_4631.1 | C_unshiu_01232_mRNA_5.1,C_unshiu_02232_mRNA_1.1 | - |
| GF0009690 | 1 | 2 | 0 | RING/U-box superfamily protein, putative isoform 3 (3) | ubiquitin-protein transferase activity [GO:0004842 molecular_function] (3); protein ubiquitination [GO:0016567 biological_process] (3) | E3 ubiquitin ligase RBR family [IPR031127] (3); IBR domain [IPR002867] (3) | scaffold_3_mRNA_4434.1 | C_unshiu_01148_mRNA_2.1,C_unshiu_01307_mRNA_1.1 | - |
| GF0009660 | 1 | 2 | 0 | Hypothetical protein (2); NB-ARC domain-containing disease resistance protein (1) | ADP binding [GO:0043531 molecular_function] (3) | NB-ARC [IPR002182] (3); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (3); Winged helix-turn-helix DNA-binding domain [IPR011991] (1) | scaffold_3_mRNA_4334.1 | C_unshiu_00528_mRNA_8.1,C_unshiu_02515_mRNA_2.1 | - |
| GF0009656 | 1 | 2 | 0 | Transcription elongation factor A protein 2 (2); Transcription elongation factor S-II (1) | nucleus [GO:0005634 cellular_component] (3); transcription, DNA-templated [GO:0006351 biological_process] (3); DNA binding [GO:0003677 molecular_function] (2); zinc ion binding [GO:0008270 molecular_function] (2) | Transcription elongation factor S-II, central domain [IPR003618] (3); Transcription elongation factor, TFIIS/CRSP70, N-terminal, sub-type [IPR003617] (3); Transcription factor IIS, N-terminal [IPR017923] (3); Transcription elongation factor S-IIM [IPR017890] (2) | scaffold_3_mRNA_4322.1 | C_unshiu_00151_mRNA_18.1,C_unshiu_01481_mRNA_1.1 | - |
| GF0009637 | 1 | 2 | 0 | LRR receptor-like kinase (3) | ATP binding [GO:0005524 molecular_function] (3); protein kinase activity [GO:0004672 molecular_function] (3); protein phosphorylation [GO:0006468 biological_process] (3); protein binding [GO:0005515 molecular_function] (1) | Protein kinase-like domain [IPR011009] (3); Protein kinase domain [IPR000719] (3); Malectin [IPR021720] (3); Concanavalin A-like lectin/glucanase domain [IPR013320] (2); Protein kinase, ATP binding site [IPR017441] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (1); Leucine-rich repeat [IPR001611] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1) | scaffold_3_mRNA_4267.1 | C_unshiu_00082_mRNA_33.1,C_unshiu_01902_mRNA_2.1 | - |
| GF0009564 | 1 | 2 | 0 | Epidermis-specific secreted glycoprotein EP1 (1); Epidermis-specific secreted EP1-like glycoprotein (1); Hypothetical protein (1) | | Bulb-type lectin domain [IPR001480] (2) | scaffold_3_mRNA_3973.1 | C_unshiu_01045_mRNA_6.1,C_unshiu_01636_mRNA_2.1 | - |
| GF0009533 | 1 | 2 | 0 | Hypothetical protein (3) | zinc ion binding [GO:0008270 molecular_function] (3) | Zinc finger, GRF-type [IPR010666] (3) | scaffold_3_mRNA_3848.1 | C_unshiu_00311_mRNA_7.1,C_unshiu_00945_mRNA_6.1 | - |
| GF0009528 | 1 | 2 | 0 | Cytochrome P450 71A1 (2); Cytochrome P450 (1) | iron ion binding [GO:0005506 molecular_function] (3); heme binding [GO:0020037 molecular_function] (3); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (3); oxidation-reduction process [GO:0055114 biological_process] (3) | Cytochrome P450, E-class, group I [IPR002401] (3); Cytochrome P450, conserved site [IPR017972] (3); Cytochrome P450 [IPR001128] (3) | scaffold_3_mRNA_3843.1 | C_unshiu_00945_mRNA_11.1,C_unshiu_01646_mRNA_3.1 | - |
| GF0009520 | 1 | 2 | 0 | UPF0481 protein (2); DUF247 domain protein (1) | | Protein of unknown function DUF247, plant [IPR004158] (3) | scaffold_3_mRNA_3781.1 | C_unshiu_00188_mRNA_18.1,C_unshiu_01092_mRNA_12.1 | - |
| GF0009502 | 1 | 2 | 0 | Hypothetical protein (3) | nucleic acid binding [GO:0003676 molecular_function] (3) | Ribonuclease H-like domain [IPR012337] (3) | scaffold_3_mRNA_3714.1 | C_unshiu_01558_mRNA_3.1,C_unshiu_02398_mRNA_3.1 | - |
| GF0009497 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_3_mRNA_3708.1 | C_unshiu_01558_mRNA_9.1,C_unshiu_02189_mRNA_2.1 | - |
| GF0009469 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_3_mRNA_3547.1 | C_unshiu_00996_mRNA_5.1,C_unshiu_01344_mRNA_6.1 | - |
| GF0009448 | 1 | 2 | 0 | Hypothetical protein (3) | | Domain of unknown function DUF4219 [IPR025314] (3) | scaffold_3_mRNA_3488.1 | C_unshiu_00156_mRNA_4.1,C_unshiu_00556_mRNA_15.1 | - |
| GF0009441 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_3_mRNA_3450.1 | C_unshiu_00934_mRNA_10.1,C_unshiu_01158_mRNA_16.1 | - |
| GF0009426 | 1 | 2 | 0 | Hypothetical protein (3) | | Galactose-binding domain-like [IPR008979] (1) | scaffold_3_mRNA_3414.1 | C_unshiu_00200_mRNA_32.1,C_unshiu_01452_mRNA_5.1 | - |
| GF0009421 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_3_mRNA_3379.1 | C_unshiu_00688_mRNA_5.1,C_unshiu_00924_mRNA_13.1 | - |
| GF0009420 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_3_mRNA_3377.1 | C_unshiu_00822_mRNA_7.1,C_unshiu_01746_mRNA_5.1 | - |
| GF0009378 | 1 | 2 | 0 | Hypothetical protein (2); Retrotransposon protein, putative, Ty3-gypsy subclass (1) | RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1) | Aspartic peptidase domain [IPR021109] (1); Ribonuclease H-like domain [IPR012337] (1); Reverse transcriptase domain [IPR000477] (1); Ribonuclease H domain [IPR002156] (1) | scaffold_3_mRNA_3207.1 | C_unshiu_00236_mRNA_2.1,C_unshiu_01399_mRNA_5.1 | - |
| GF0009325 | 1 | 2 | 0 | Hypothetical protein (3) | | Leucine-rich repeat 3 [IPR011713] (2); Leucine-rich repeat domain, L domain-like [IPR032675] (2) | scaffold_3_mRNA_2979.1 | C_unshiu_02389_mRNA_1.1,C_unshiu_03143_mRNA_1.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0009321 | 1 | 2 | 0 | Hypothetical protein (3) | | Alpha/Beta hydrolase fold [IPR029058] (3) | scaffold_3_mRNA_2930.1 | C_unshiu_00384_mRNA_3.1,C_unshiu_01094_mRNA_7.1 | - |
| GF0009320 | 1 | 2 | 0 | NB-ARC domain disease resistance protein (2); TIR-NBS-LRR class disease resistance protein (1) | ADP binding [GO:0043531 molecular_function] (3) | Winged helix-turn-helix DNA-binding domain [IPR011991] (3); NB-ARC [IPR002182] (3); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (3); Leucine-rich repeat 3 [IPR011713] (1) | scaffold_3_mRNA_2898.1 | C_unshiu_01094_mRNA_9.1,C_unshiu_03116_mRNA_1.1 | - |
| GF0009257 | 1 | 2 | 0 | TMV resistance protein N (2); Hypothetical protein (1) | signal transduction [GO:0007165 biological_process] (3); protein binding [GO:0005515 molecular_function] (3) | Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (3) | scaffold_3_mRNA_2670.1 | C_unshiu_00272_mRNA_26.1,C_unshiu_01111_mRNA_10.1 | - |
| GF0009255 | 1 | 2 | 0 | Ankyrin repeat family protein, putative (3) | protein binding [GO:0005515 molecular_function] (3); regulation of salicylic acid mediated signaling pathway [GO:2000031 biological_process] (1); regulation of defense response [GO:0031347 biological_process] (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] (3); Ankyrin repeat [IPR002110] (3); Protein accelerated cell death 6 [IPR032846] (1) | scaffold_3_mRNA_2661.1 | C_unshiu_00828_mRNA_12.1,C_unshiu_02556_mRNA_1.1 | - |
| GF0009243 | 1 | 2 | 0 | AT4G00440 protein (3) | | Domain of unknown function DUF4378 [IPR025486] (3); Domain of unknown function DUF3741 [IPR022212] (3) | scaffold_3_mRNA_262.1 | C_unshiu_00534_mRNA_4.1,C_unshiu_01077_mRNA_11.1 | - |
| GF0009232 | 1 | 2 | 0 | LYR family of Fe/S cluster biogenesis protein isoform 1 (3) | | Complex 1 LYR protein [IPR008011] (3); LYR motif-containing protein 2 [IPR026868] (3) | scaffold_3_mRNA_2580.1 | C_unshiu_00015_mRNA_111.1,C_unshiu_00602_mRNA_1.1 | - |
| GF0009200 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_3_mRNA_2497.1 | C_unshiu_00534_mRNA_15.1,C_unshiu_01198_mRNA_7.1 | - |
| GF0009186 | 1 | 2 | 0 | TMV resistance protein N (3) | protein binding [GO:0005515 molecular_function] (3); ADP binding [GO:0043531 molecular_function] (3); signal transduction [GO:0007165 biological_process] (3); ATP binding [GO:0005524 molecular_function] (1); protein kinase activity [GO:0004672 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1) | P-loop containing nucleoside triphosphate hydrolase [IPR027417] (3); NB-ARC [IPR002182] (3); Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (3); Leucine-rich repeat domain, L domain-like [IPR032675] (3); Leucine-rich repeat 3 [IPR011713] (2); Winged helix-turn-helix DNA-binding domain [IPR011991] (2); Protein kinase, ATP binding site [IPR017441] (1); Protein kinase domain [IPR000719] (1); Leucine-rich repeat, typical subtype [IPR003591] (1); Protein kinase-like domain [IPR011009] (1) | scaffold_3_mRNA_2433.1 | C_unshiu_00476_mRNA_12.1,C_unshiu_00956_mRNA_9.1 | - |
| GF0009173 | 1 | 2 | 0 | Protein AIG1 (3) | GTP binding [GO:0005525 molecular_function] (3) | AIG1-type guanine nucleotide-binding (G) domain [IPR006703] (3); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (3) | scaffold_3_mRNA_2372.1 | C_unshiu_00373_mRNA_11.1,C_unshiu_00811_mRNA_5.1 | - |
| GF0009163 | 1 | 2 | 0 | Transcription termination factor family protein (2); Hypothetical protein (1) | double-stranded DNA binding [GO:0003690 molecular_function] (2); regulation of transcription, DNA-templated [GO:0006355 biological_process] (2); mitochondrion [GO:0005739 cellular_component] (2) | Mitochodrial transcription termination factor [IPR003690] (2) | scaffold_3_mRNA_2344.1 | C_unshiu_00625_mRNA_15.1,C_unshiu_01853_mRNA_6.1 | - |
| GF0009145 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_3_mRNA_2295.1 | C_unshiu_00100_mRNA_16.1,C_unshiu_00344_mRNA_22.1 | - |
| GF0009100 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_3_mRNA_2112.1 | C_unshiu_00916_mRNA_13.1,C_unshiu_03049_mRNA_1.1 | - |
| GF0009058 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_3_mRNA_1949.1 | C_unshiu_00100_mRNA_20.1,C_unshiu_01666_mRNA_3.1 | - |
| GF0009024 | 1 | 2 | 0 | Hypothetical protein (2); Polynucleotidyl transferase, ribonuclease H-like superfamily protein (1) | nucleic acid binding [GO:0003676 molecular_function] (3) | Ribonuclease H-like domain [IPR012337] (3) | scaffold_3_mRNA_1742.1 | C_unshiu_00023_mRNA_6.1,C_unshiu_00874_mRNA_3.1 | - |
| GF0009021 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_3_mRNA_1732.1 | C_unshiu_00948_mRNA_12.1,C_unshiu_01788_mRNA_4.1 | - |
| GF0009020 | 1 | 2 | 0 | Hypothetical protein (3) | | Aspartic peptidase domain [IPR021109] (1) | scaffold_3_mRNA_1731.1 | C_unshiu_00588_mRNA_4.1,C_unshiu_01886_mRNA_5.1 | - |
| GF0009014 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_3_mRNA_1712.1 | C_unshiu_00512_mRNA_10.1,C_unshiu_00613_mRNA_10.1 | - |
| GF0009013 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_3_mRNA_1704.1 | C_unshiu_00542_mRNA_7.1,C_unshiu_01834_mRNA_1.1 | - |
| GF0009008 | 1 | 2 | 0 | Mitochondrial substrate carrier family protein B (3) | transmembrane transport [GO:0055085 biological_process] (3) | Mitochondrial substrate/solute carrier [IPR018108] (3); Mitochondrial carrier domain [IPR023395] (3); Mitochondrial carrier protein [IPR002067] (3) | scaffold_3_mRNA_168.1 | C_unshiu_00495_mRNA_15.1,C_unshiu_00609_mRNA_6.1 | - |
| GF0009002 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_3_mRNA_166.1 | C_unshiu_00609_mRNA_7.1,C_unshiu_01000_mRNA_14.1 | - |
| GF0008986 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_3_mRNA_1616.1 | C_unshiu_00793_mRNA_8.1,C_unshiu_02382_mRNA_2.1 | - |
| GF0008955 | 1 | 2 | 0 | Hypothetical protein (3) | polysaccharide binding [GO:0030247 molecular_function] (3) | Wall-associated receptor kinase, galacturonan-binding domain [IPR025287] (3) | scaffold_3_mRNA_1507.1 | C_unshiu_01368_mRNA_5.1,C_unshiu_02518_mRNA_1.1 | - |
| GF0008934 | 1 | 2 | 0 | SFBBbeta protein (2); S locus F-box protein with the low allelic sequence polymorphism 1-S2 (1) | protein binding [GO:0005515 molecular_function] (3) | F-box associated interaction domain [IPR017451] (3); F-box domain [IPR001810] (3); Galactose oxidase/kelch, beta-propeller [IPR011043] (1); F-box associated domain, type 3 [IPR013187] (1) | scaffold_3_mRNA_1448.1 | C_unshiu_00285_mRNA_33.1,C_unshiu_01684_mRNA_2.1 | - |
| GF0008908 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_3_mRNA_1384.1 | C_unshiu_00284_mRNA_26.1,C_unshiu_01612_mRNA_5.1 | - |
| GF0008829 | 1 | 2 | 0 | Hypothetical protein (3) | nucleic acid binding [GO:0003676 molecular_function] (1) | Ribonuclease H-like domain [IPR012337] (1) | scaffold_3_mRNA_1194.1 | C_unshiu_00695_mRNA_4.1,C_unshiu_00948_mRNA_4.1 | - |
| GF0008772 | 1 | 2 | 0 | Presenilin (3) | protein processing [GO:0016485 biological_process] (3); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (3); integral component of membrane [GO:0016021 cellular_component] (3) | Presenilin/signal peptide peptidase [IPR006639] (3); Peptidase A22A, presenilin [IPR001108] (3) | scaffold_3_mRNA_1101.1 | C_unshiu_00154_mRNA_37.1,C_unshiu_01729_mRNA_2.1 | - |
| GF0008762 | 1 | 2 | 0 | Hypothetical protein (3) | DNA binding [GO:0003677 molecular_function] (3); regulation of transcription, DNA-templated [GO:0006355 biological_process] (3) | NAC domain [IPR003441] (3) | scaffold_3_mRNA_1090.1 | C_unshiu_00154_mRNA_48.1,C_unshiu_02011_mRNA_2.1 | - |
| GF0008609 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_2_mRNA_780.1 | C_unshiu_00260_mRNA_20.1,C_unshiu_00260_mRNA_32.1 | - |
| GF0008380 | 1 | 2 | 0 | Hypothetical protein (3) | cysteine-type peptidase activity [GO:0008234 molecular_function] (1); proteolysis [GO:0006508 biological_process] (1) | Domain of unknown function DUF1985 [IPR015410] (2); Ulp1 protease family, C-terminal catalytic domain [IPR003653] (1) | scaffold_2_mRNA_457.1 | C_unshiu_00147_mRNA_4.1,C_unshiu_01757_mRNA_1.1 | - |
| GF0007883 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_2_mRNA_3899.1 | C_unshiu_00125_mRNA_46.1,C_unshiu_00405_mRNA_26.1 | - |
| GF0007409 | 1 | 2 | 0 | Hypothetical protein (3) | | Reverse transcriptase zinc-binding domain [IPR026960] (3) | scaffold_2_mRNA_3051.1 | C_unshiu_00081_mRNA_74.1,C_unshiu_02626_mRNA_2.1 | - |
| GF0007408 | 1 | 2 | 0 | Receptor like protein 6 (1); Verticillium wilt disease resistance protein (1); Leucine-rich repeat, plant specific (1) | protein binding [GO:0005515 molecular_function] (2) | Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (3); Leucine-rich repeat domain, L domain-like [IPR032675] (3); Leucine-rich repeat [IPR001611] (2) | scaffold_2_mRNA_3043.1 | C_unshiu_00081_mRNA_71.1,C_unshiu_01944_mRNA_1.1 | - |
| GF0007315 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_2_mRNA_2851.1 | C_unshiu_00142_mRNA_24.1,C_unshiu_01808_mRNA_5.1 | - |
| GF0007257 | 1 | 2 | 0 | Limonene synthase (3) | metabolic process [GO:0008152 biological_process] (3); terpene synthase activity [GO:0010333 molecular_function] (3); lyase activity [GO:0016829 molecular_function] (3); magnesium ion binding [GO:0000287 molecular_function] (3) | Isoprenoid synthase domain [IPR008949] (3); Terpenoid cyclases/protein prenyltransferase alpha-alpha toroid [IPR008930] (3); Terpene synthase, N-terminal domain [IPR001906] (3); Terpene synthase, metal-binding domain [IPR005630] (3) | scaffold_2_mRNA_2700.1 | C_unshiu_00663_mRNA_11.1,C_unshiu_00663_mRNA_12.1 | - |
| GF0007242 | 1 | 2 | 0 | Chaperonin ATPase (3) | ATP binding [GO:0005524 molecular_function] (3); protein refolding [GO:0042026 biological_process] (2); cytoplasm [GO:0005737 cellular_component] (2) | GroEL-like equatorial domain [IPR027413] (3); GroEL-like apical domain [IPR027409] (3); Chaperonin Cpn60/TCP-1 family [IPR002423] (3); TCP-1-like chaperonin intermediate domain [IPR027410] (2); Chaperonin Cpn60 [IPR001844] (2) | scaffold_2_mRNA_2638.2 | C_unshiu_00833_mRNA_12.1,C_unshiu_02807_mRNA_2.2 | - |
| GF0007231 | 1 | 2 | 0 | Hypothetical protein (3) | | Retrotransposon gag domain [IPR005162] (2) | scaffold_2_mRNA_2570.1 | C_unshiu_00953_mRNA_5.1,C_unshiu_01401_mRNA_6.1 | - |
| GF0007204 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_2_mRNA_2478.1 | C_unshiu_00565_mRNA_4.1,C_unshiu_00836_mRNA_5.1 | - |
| GF0007192 | 1 | 2 | 0 | Protein phosphatase 1 regulatory subunit pprA (3) | protein binding [GO:0005515 molecular_function] (3) | Leucine-rich repeat [IPR001611] (3); Leucine-rich repeat domain, L domain-like [IPR032675] (3); Leucine-rich repeat, typical subtype [IPR003591] (3); Endonuclease/exonuclease/phosphatase [IPR005135] (2) | scaffold_2_mRNA_2342.1 | C_unshiu_01397_mRNA_8.1,C_unshiu_01759_mRNA_1.1 | - |
| GF0007190 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_2_mRNA_2332.1 | C_unshiu_00871_mRNA_15.1,C_unshiu_01759_mRNA_4.1 | - |
| GF0007124 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_2_mRNA_191.1 | C_unshiu_01873_mRNA_9.1,C_unshiu_01925_mRNA_8.1 | - |
| GF0007113 | 1 | 2 | 0 | Hypothetical protein (3) | nucleic acid binding [GO:0003676 molecular_function] (1) | GAG-pre-integrase domain [IPR025724] (2); Ribonuclease H-like domain [IPR012337] (1); Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1) | scaffold_2_mRNA_1882.1 | C_unshiu_00543_mRNA_1.1,C_unshiu_02183_mRNA_5.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0006985 | 1 | 2 | 0 | Nudix hydrolase 17, mitochondrial (3) | hydrolase activity [GO:0016787 molecular_function] (3) | NUDIX hydrolase domain-like [IPR015797] (3); NUDIX hydrolase, conserved site [IPR020084] (3); NUDIX hydrolase domain [IPR000086] (3) | scaffold_2_mRNA_1517.1 | C_unshiu_00653_mRNA_11.1,C_unshiu_02017_mRNA_3.1 | - |
| GF0006896 | 1 | 2 | 0 | Ankyrin repeat family protein, putative (3) | protein binding [GO:0005515 molecular_function] (3); 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] (3); Ankyrin repeat-containing domain [IPR020683] (3); Ankyrin repeat [IPR002110] (3); Protein accelerated cell death 6 [IPR032846] (1) | scaffold_2_mRNA_1304.1 | C_unshiu_00987_mRNA_10.1,C_unshiu_01842_mRNA_1.1 | - |
| GF0006851 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_2_mRNA_1236.1 | C_unshiu_00049_mRNA_33.1,C_unshiu_00049_mRNA_34.1 | - |
| GF0006675 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_1_mRNA_983.1 | C_unshiu_00191_mRNA_27.1,C_unshiu_01414_mRNA_10.1 | - |
| GF0006640 | 1 | 2 | 0 | Hypothetical protein (3) | nucleic acid binding [GO:0003676 molecular_function] (3); protein dimerization activity [GO:0046983 molecular_function] (3) | HAT, C-terminal dimerisation domain [IPR008906] (3); Ribonuclease H-like domain [IPR012337] (3) | scaffold_1_mRNA_911.1 | C_unshiu_00068_mRNA_59.1,C_unshiu_00837_mRNA_12.1 | - |
| GF0006558 | 1 | 2 | 0 | Hypothetical protein (2); Transposon protein, putative, unclassified (1) | protein binding [GO:0005515 molecular_function] (2) | Leucine-rich repeat domain, L domain-like [IPR032675] (3); Leucine-rich repeat [IPR001611] (2); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (2) | scaffold_1_mRNA_706.1 | C_unshiu_00242_mRNA_1.1,C_unshiu_00372_mRNA_3.1 | - |
| GF0006292 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_1_mRNA_3546.1 | C_unshiu_00305_mRNA_1.1,C_unshiu_01994_mRNA_5.1 | - |
| GF0006038 | 1 | 2 | 0 | Cysteine-rich RLK (RECEPTOR-like protein kinase) 8 (2); Pol polyprotein (1) | nucleic acid binding [GO:0003676 molecular_function] (2); zinc ion binding [GO:0008270 molecular_function] (1) | Zinc finger, CCHC-type [IPR001878] (1); GAG-pre-integrase domain [IPR025724] (1); Ribonuclease H-like domain [IPR012337] (1); Reverse transcriptase, RNA-dependent DNA polymerase [IPR013103] (1) | scaffold_1_mRNA_316.1 | C_unshiu_00169_mRNA_11.1,C_unshiu_00193_mRNA_12.1 | - |
| GF0005662 | 1 | 2 | 0 | Plant natriuretic peptide A (3) | | Expansin/pollen allergen, DPBB domain [IPR007112] (3); RlpA-like double-psi beta-barrel domain [IPR009009] (2); RlpA-like protein, double-psi beta-barrel domain [IPR009009] (1) | scaffold_1_mRNA_250.1 | C_unshiu_00553_mRNA_1.1,C_unshiu_00749_mRNA_15.1 | - |
| GF0005630 | 1 | 2 | 0 | Hypothetical protein (3) | | Transposase, MuDR, plant [IPR004332] (1) | scaffold_1_mRNA_239.1 | C_unshiu_01092_mRNA_2.1,C_unshiu_02810_mRNA_2.1 | - |
| GF0005613 | 1 | 2 | 0 | Hypothetical protein (2); Cysteine-rich RLK (Receptor-like kinase) protein (1) | protein serine/threonine kinase activity [GO:0004674 molecular_function] (3); ATP binding [GO:0005524 molecular_function] (1); protein phosphorylation [GO:0006468 biological_process] (1); protein kinase activity [GO:0004672 molecular_function] (1) | S-locus receptor kinase, C-terminal [IPR021820] (3); Protein kinase-like domain [IPR011009] (2); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (1); Serine/threonine-protein kinase, active site [IPR008271] (1); Protein kinase domain [IPR000719] (1) | scaffold_1_mRNA_2312.1 | C_unshiu_00954_mRNA_10.1,C_unshiu_02084_mRNA_6.1 | - |
| GF0005612 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_1_mRNA_2310.1 | C_unshiu_00021_mRNA_12.1,C_unshiu_00688_mRNA_15.1 | - |
| GF0005408 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_1_mRNA_1742.1 | C_unshiu_00097_mRNA_51.1,C_unshiu_00167_mRNA_8.1 | - |
| GF0005359 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_1_mRNA_1599.1 | C_unshiu_00558_mRNA_14.1,C_unshiu_01614_mRNA_4.1 | - |
| GF0005351 | 1 | 2 | 0 | Cytokinin riboside 5'-monophosphate phosphoribohydrolase (3) | | LOG family [IPR031100] (3); Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG [IPR005269] (3) | scaffold_1_mRNA_1561.1 | C_unshiu_01470_mRNA_6.1,C_unshiu_02288_mRNA_3.1 | - |
| GF0005344 | 1 | 2 | 0 | Zinc knuckle family protein (3) | zinc ion binding [GO:0008270 molecular_function] (3); nucleic acid binding [GO:0003676 molecular_function] (3) | Zinc finger, CCHC-type [IPR001878] (3); Domain of unknown function DUF4219 [IPR025314] (2) | scaffold_1_mRNA_1547.1 | C_unshiu_00890_mRNA_2.1,C_unshiu_01153_mRNA_7.1 | - |
| GF0005335 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_1_mRNA_1525.1 | C_unshiu_00031_mRNA_33.1,C_unshiu_00450_mRNA_2.1 | - |
| GF0005190 | 1 | 2 | 0 | Hypothetical protein (3) | | | scaffold_1_mRNA_1028.1 | C_unshiu_00198_mRNA_3.1,C_unshiu_01216_mRNA_9.1 | - |
| GF0005077 | 1 | 3 | 0 | Dienelactone hydrolase family, putative (4) | hydrolase activity [GO:0016787 molecular_function] (4) | Dienelactone hydrolase [IPR002925] (4); Alpha/Beta hydrolase fold [IPR029058] (4) | scaffold_9_mRNA_455.1 | C_unshiu_00097_mRNA_36.1,C_unshiu_01541_mRNA_4.1,C_unshiu_01541_mRNA_9.1 | - |
| GF0005023 | 1 | 3 | 0 | LRR receptor-like kinase family protein (4) | protein binding [GO:0005515 molecular_function] (4); protein kinase activity [GO:0004672 molecular_function] (4); protein phosphorylation [GO:0006468 biological_process] (4); ATP binding [GO:0005524 molecular_function] (4) | Protein kinase domain [IPR000719] (4); Protein kinase-like domain [IPR011009] (4); Leucine-rich repeat domain, L domain-like [IPR032675] (4); Leucine-rich repeat, typical subtype [IPR003591] (4); Leucine-rich repeat-containing N-terminal, plant-type [IPR013210] (4); Serine/threonine-protein kinase, active site [IPR008271] (4); Protein kinase, ATP binding site [IPR017441] (4); Leucine-rich repeat [IPR001611] (4); Concanavalin A-like lectin/glucanase domain [IPR013320] (3); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (3); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1) | scaffold_9_mRNA_2973.1 | C_unshiu_00132_mRNA_13.1,C_unshiu_00345_mRNA_29.1,C_unshiu_01900_mRNA_3.1 | - |
| GF0005020 | 1 | 3 | 0 | Hypothetical protein (2); Systemin receptor SR160, putative (2) | protein kinase activity [GO:0004672 molecular_function] (4); protein phosphorylation [GO:0006468 biological_process] (4); ATP binding [GO:0005524 molecular_function] (4) | Serine/threonine-protein kinase, active site [IPR008271] (4); Protein kinase-like domain [IPR011009] (4); Protein kinase domain [IPR000719] (4); Serine/threonine/dual specificity protein kinase, catalytic domain [IPR002290] (3); Serine-threonine/tyrosine-protein kinase catalytic domain [IPR001245] (1); Serine-threonine/tyrosine-protein kinase, catalytic domain [IPR001245] (1); Leucine-rich repeat domain, L domain-like [IPR032675] (1) | scaffold_9_mRNA_2964.1 | C_unshiu_00095_mRNA_1.1,C_unshiu_01005_mRNA_1.1,C_unshiu_01821_mRNA_4.1 | - |
| GF0005015 | 1 | 3 | 0 | Disease resistance protein (4) | protein binding [GO:0005515 molecular_function] (4); ADP binding [GO:0043531 molecular_function] (4) | Leucine-rich repeat [IPR001611] (4); NB-ARC [IPR002182] (4); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (4); Leucine-rich repeat domain, L domain-like [IPR032675] (4); Winged helix-turn-helix DNA-binding domain [IPR011991] (1); Receptor L-domain [IPR000494] (1) | scaffold_9_mRNA_2906.1 | C_unshiu_00478_mRNA_18.1,C_unshiu_00478_mRNA_19.1,C_unshiu_01777_mRNA_2.1 | - |
| GF0004978 | 1 | 3 | 0 | Hypothetical protein (2); RNA-directed DNA polymerase , related (1); LINE-type retrotransposon LIb DNA, Insertion at the S11 site-like protein (1) | nucleic acid binding [GO:0003676 molecular_function] (2) | Reverse transcriptase domain [IPR000477] (3); Ribonuclease H-like domain [IPR012337] (2); Endonuclease/exonuclease/phosphatase [IPR005135] (1) | scaffold_9_mRNA_2195.1 | C_unshiu_00241_mRNA_21.1,C_unshiu_00936_mRNA_17.1,C_unshiu_01718_mRNA_1.1 | - |
| GF0004976 | 1 | 3 | 0 | Hypothetical protein (3); DUF4283 domain protein (1) | | Domain of unknown function DUF4283 [IPR025558] (3) | scaffold_9_mRNA_2151.1 | C_unshiu_00107_mRNA_44.1,C_unshiu_00107_mRNA_45.1,C_unshiu_00957_mRNA_14.1 | - |
| GF0004969 | 1 | 3 | 0 | Hypothetical protein (4) | | | scaffold_9_mRNA_200.1 | C_unshiu_01104_mRNA_9.1,C_unshiu_01866_mRNA_7.1,C_unshiu_01866_mRNA_9.1 | - |
| GF0004930 | 1 | 3 | 0 | Hypothetical protein (4) | | | scaffold_9_mRNA_1450.1 | C_unshiu_00468_mRNA_5.1,C_unshiu_00776_mRNA_11.1,C_unshiu_01292_mRNA_6.1 | - |
| GF0004913 | 1 | 3 | 0 | Hypothetical protein (4) | | | scaffold_8_mRNA_966.1 | C_unshiu_00094_mRNA_37.1,C_unshiu_00122_mRNA_5.1,C_unshiu_01451_mRNA_4.1 | - |
| GF0004897 | 1 | 3 | 0 | Hypothetical protein (3); Peptidase aspartic, active site (1) | aspartic-type endopeptidase activity [GO:0004190 molecular_function] (2); proteolysis [GO:0006508 biological_process] (2) | Retroviral aspartyl protease [IPR013242] (2); Aspartic peptidase domain [IPR021109] (2); Retrotransposon gag domain [IPR005162] (2); Aspartic peptidase, active site [IPR001969] (2); Chromo domain [IPR023780] (1); Chromo domain-like [IPR016197] (1) | scaffold_8_mRNA_757.1 | C_unshiu_00061_mRNA_59.1,C_unshiu_00766_mRNA_4.1,C_unshiu_01741_mRNA_1.1 | - |
| GF0004808 | 1 | 3 | 0 | Kiwellin (4) | | RlpA-like double-psi beta-barrel domain [IPR009009] (3); RlpA-like protein, double-psi beta-barrel domain [IPR009009] (1) | scaffold_8_mRNA_2743.1 | C_unshiu_00438_mRNA_26.1,C_unshiu_00808_mRNA_14.1,C_unshiu_02581_mRNA_3.1 | - |
| GF0004706 | 1 | 3 | 0 | Hypothetical protein (4) | | | scaffold_8_mRNA_1684.1 | C_unshiu_00373_mRNA_30.1,C_unshiu_01134_mRNA_1.1,C_unshiu_01665_mRNA_6.1 | - |
| GF0004702 | 1 | 3 | 0 | Hypothetical protein (4) | | | scaffold_8_mRNA_1589.1 | C_unshiu_00480_mRNA_13.1,C_unshiu_01336_mRNA_11.1,C_unshiu_01407_mRNA_15.1 | - |
| GF0004680 | 1 | 3 | 0 | Hypothetical protein (2); Ribonuclease H-like superfamily protein (1); Polynucleotidyl transferase, Ribonuclease H fold (1) | nucleic acid binding [GO:0003676 molecular_function] (4); zinc ion binding [GO:0008270 molecular_function] (1) | Reverse transcriptase zinc-binding domain [IPR026960] (4); Ribonuclease H-like domain [IPR012337] (4); Endonuclease/exonuclease/phosphatase [IPR005135] (2); Domain of unknown function DUF4283 [IPR025558] (1); Zinc knuckle CX2CX4HX4C [IPR025836] (1); Zinc finger, CCHC-type [IPR001878] (1) | scaffold_8_mRNA_1295.1 | C_unshiu_00004_mRNA_109.1,C_unshiu_00006_mRNA_120.1,C_unshiu_01309_mRNA_8.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0004665 | 1 | 3 | 0 | BED zinc finger,hAT family dimerization domain (4) | protein dimerization activity [GO:0046983 molecular_function] (4); nucleic acid binding [GO:0003676 molecular_function] (4); DNA binding [GO:0003677 molecular_function] (3) | HAT, C-terminal dimerisation domain [IPR008906] (4); Ribonuclease H-like domain [IPR012337] (4); hAT-like transposase, RNase-H fold [IPR025525] (3) | scaffold_8_mRNA_1112.1 | C_unshiu_00821_mRNA_13.1,C_unshiu_01012_mRNA_7.1,C_unshiu_01215_mRNA_7.1 | - |
| GF0004503 | 1 | 3 | 0 | Hypothetical protein (4) | | | scaffold_7_mRNA_2125.1 | C_unshiu_00274_mRNA_30.1,C_unshiu_00479_mRNA_10.1,C_unshiu_00638_mRNA_8.1 | - |
| GF0004394 | 1 | 3 | 0 | Hypothetical protein (4) | | | scaffold_6_mRNA_63.1 | C_unshiu_00028_mRNA_30.1,C_unshiu_00057_mRNA_38.1,C_unshiu_01792_mRNA_1.1 | - |
| GF0004392 | 1 | 3 | 0 | Hypothetical protein (4) | | | scaffold_6_mRNA_580.1 | C_unshiu_00385_mRNA_1.1,C_unshiu_01145_mRNA_14.1,C_unshiu_01969_mRNA_4.1 | - |
| GF0004386 | 1 | 3 | 0 | Hypothetical protein (4) | | | scaffold_6_mRNA_5.1 | C_unshiu_00635_mRNA_13.1,C_unshiu_01511_mRNA_7.1,C_unshiu_02232_mRNA_3.1 | - |
| GF0004321 | 1 | 3 | 0 | Hypothetical protein (4) | | | scaffold_6_mRNA_206.1 | C_unshiu_00358_mRNA_7.1,C_unshiu_00377_mRNA_10.1,C_unshiu_01568_mRNA_17.1 | - |
| GF0004299 | 1 | 3 | 0 | Hypothetical protein (4) | protein dimerization activity [GO:0046983 molecular_function] (4); nucleic acid binding [GO:0003676 molecular_function] (4) | HAT, C-terminal dimerisation domain [IPR008906] (4); Ribonuclease H-like domain [IPR012337] (4) | scaffold_6_mRNA_1625.1 | C_unshiu_00016_mRNA_39.1,C_unshiu_00102_mRNA_48.1,C_unshiu_00661_mRNA_1.1 | - |
| GF0004192 | 1 | 3 | 0 | Hypothetical protein (2); Putative non-LTR reverse transcriptase (1); Putative non-LTR retroelement reverse transcriptase (1) | nucleic acid binding [GO:0003676 molecular_function] (2) | Reverse transcriptase zinc-binding domain [IPR026960] (4); Ribonuclease H-like domain [IPR012337] (2); Endonuclease/exonuclease/phosphatase [IPR005135] (1) | scaffold_5_mRNA_5121.1 | C_unshiu_00003_mRNA_42.1,C_unshiu_00164_mRNA_34.1,C_unshiu_01461_mRNA_4.1 | - |
| GF0003985 | 1 | 3 | 0 | Hypothetical protein (4) | transferase activity, transferring hexosyl groups [GO:0016758 molecular_function] (4); metabolic process [GO:0008152 biological_process] (4) | UDP-glucuronosyl/UDP-glucosyltransferase [IPR002213] (4) | scaffold_5_mRNA_2789.1 | C_unshiu_00818_mRNA_6.1,C_unshiu_01306_mRNA_8.1,C_unshiu_01408_mRNA_5.1 | - |
| GF0003982 | 1 | 3 | 0 | Disease resistance protein (CC-NBS-LRR class) family protein (4) | ADP binding [GO:0043531 molecular_function] (4) | Leucine-rich repeat domain, L domain-like [IPR032675] (4); P-loop containing nucleoside triphosphate hydrolase [IPR027417] (4); NB-ARC [IPR002182] (4); AAA+ ATPase domain [IPR003593] (2); Winged helix-turn-helix DNA-binding domain [IPR011991] (1) | scaffold_5_mRNA_2640.1 | C_unshiu_00689_mRNA_9.1,C_unshiu_00775_mRNA_13.1,C_unshiu_00991_mRNA_11.1 | - |
| GF0003952 | 1 | 3 | 0 | Hypothetical protein (4) | | Viral movement protein [IPR028919] (4) | scaffold_5_mRNA_2127.1 | C_unshiu_00287_mRNA_5.1,C_unshiu_00374_mRNA_22.1,C_unshiu_01530_mRNA_9.1 | - |
| GF0003947 | 1 | 3 | 0 | Hypothetical protein (4) | cysteine-type peptidase activity [GO:0008234 molecular_function] (3); proteolysis [GO:0006508 biological_process] (3) | Ulp1 protease family, C-terminal catalytic domain [IPR003653] (3) | scaffold_5_mRNA_2021.1 | C_unshiu_00469_mRNA_14.1,C_unshiu_00524_mRNA_18.1,C_unshiu_02936_mRNA_1.1 | - |
| GF0003871 | 1 | 3 | 0 | Hypothetical protein (4) | | | scaffold_5_mRNA_1239.1 | C_unshiu_00776_mRNA_2.1,C_unshiu_01292_mRNA_1.1,C_unshiu_02114_mRNA_4.1 | - |
| GF0003491 | 1 | 3 | 0 | Hypothetical protein (4) | | | scaffold_3_mRNA_4496.1 | C_unshiu_00471_mRNA_8.1,C_unshiu_01119_mRNA_4.1,C_unshiu_01443_mRNA_5.1 | - |
| GF0003470 | 1 | 3 | 0 | Hypothetical protein (4) | | | scaffold_3_mRNA_4276.1 | C_unshiu_00031_mRNA_59.1,C_unshiu_00075_mRNA_60.1,C_unshiu_00191_mRNA_2.1 | - |
| GF0003365 | 1 | 3 | 0 | Hypothetical protein (3); LRR and NB-ARC domain disease resistance protein, putative (1) | ribosome [GO:0005840 cellular_component] (1); structural constituent of ribosome [GO:0003735 molecular_function] (1); translation [GO:0006412 biological_process] (1) | Leucine-rich repeat domain, L domain-like [IPR032675] (4); Ribosomal protein L2, domain 3 [IPR014726] (1); Ribosomal protein L2 domain 2 [IPR014722] (1); Ribosomal protein L2, C-terminal [IPR022669] (1); Translation protein SH3-like domain [IPR008991] (1) | scaffold_3_mRNA_3089.1 | C_unshiu_00117_mRNA_17.1,C_unshiu_01392_mRNA_3.1,C_unshiu_02119_mRNA_5.1 | - |
| GF0003322 | 1 | 3 | 0 | TMV resistance protein N (3); Hypothetical protein (1) | signal transduction [GO:0007165 biological_process] (4); protein binding [GO:0005515 molecular_function] (4) | Toll/interleukin-1 receptor homology (TIR) domain [IPR000157] (4) | scaffold_3_mRNA_2711.1 | C_unshiu_00272_mRNA_17.1,C_unshiu_01276_mRNA_11.1,C_unshiu_02064_mRNA_5.1 | - |
| GF0003318 | 1 | 3 | 0 | Hypothetical protein (4) | | | scaffold_3_mRNA_2643.1 | C_unshiu_00708_mRNA_9.1,C_unshiu_00828_mRNA_1.1,C_unshiu_02315_mRNA_1.1 | - |
| GF0003302 | 1 | 3 | 0 | Hypothetical protein (2); Non-LTR reverse transcriptase (1); Putative non-LTR retroelement reverse transcriptase (1) | nucleic acid binding [GO:0003676 molecular_function] (3); RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (2); zinc ion binding [GO:0008270 molecular_function] (1) | Ribonuclease H-like domain [IPR012337] (2); Ribonuclease H domain [IPR002156] (2); Endonuclease/exonuclease/phosphatase [IPR005135] (2); Domain of unknown function DUF4283 [IPR025558] (1); Zinc knuckle CX2CX4HX4C [IPR025836] (1); Zinc finger, CCHC-type [IPR001878] (1) | scaffold_3_mRNA_2527.1 | C_unshiu_00320_mRNA_15.1,C_unshiu_01148_mRNA_6.1,C_unshiu_01214_mRNA_7.1 | - |
| GF0003224 | 1 | 3 | 0 | Hypothetical protein (4) | | | scaffold_3_mRNA_1480.1 | C_unshiu_00169_mRNA_27.1,C_unshiu_00229_mRNA_43.1,C_unshiu_01764_mRNA_4.1 | - |
| GF0003097 | 1 | 3 | 0 | Non-LTR reverse transcriptase (2); Non-LTR retroelement reverse transcriptase-like protein (1); Hypothetical protein (1) | RNA-DNA hybrid ribonuclease activity [GO:0004523 molecular_function] (1); nucleic acid binding [GO:0003676 molecular_function] (1) | Endonuclease/exonuclease/phosphatase [IPR005135] (4); Reverse transcriptase zinc-binding domain [IPR026960] (2); Nucleotide-diphospho-sugar transferases [IPR029044] (1); Ribonuclease H-like domain [IPR012337] (1); Ribonuclease H domain [IPR002156] (1) | scaffold_2_mRNA_4189.1 | C_unshiu_00401_mRNA_26.1,C_unshiu_01062_mRNA_5.1,C_unshiu_02043_mRNA_2.1 | - |
| GF0003021 | 1 | 3 | 0 | Hypothetical protein (4) | | Domain of unknown function DUF4218 [IPR025452] (1) | scaffold_2_mRNA_2815.1 | C_unshiu_00036_mRNA_79.1,C_unshiu_00059_mRNA_25.1,C_unshiu_00893_mRNA_13.1 | - |
| GF0002984 | 1 | 3 | 0 | Hypothetical protein (4) | | | scaffold_2_mRNA_2200.1 | C_unshiu_00056_mRNA_68.1,C_unshiu_00171_mRNA_3.1,C_unshiu_01030_mRNA_8.1 | - |
| GF0002865 | 1 | 3 | 0 | Hypothetical protein (4) | calcium ion binding [GO:0005509 molecular_function] (4) | EF-hand domain pair [IPR011992] (4); EF-hand domain [IPR002048] (4) | scaffold_1_mRNA_585.1 | C_unshiu_00203_mRNA_23.1,C_unshiu_00488_mRNA_20.1,C_unshiu_00662_mRNA_18.1 | - |
| GF0002857 | 1 | 3 | 0 | Hypothetical protein (4) | | Domain of unknown function DUF1985 [IPR015410] (4) | scaffold_1_mRNA_435.1 | C_unshiu_00001_mRNA_236.1,C_unshiu_00958_mRNA_1.1,C_unshiu_01032_mRNA_8.1 | - |
| GF0002726 | 1 | 3 | 0 | Hypothetical protein (4) | | GDP-fucose protein O-fucosyltransferase [IPR019378] (4) | scaffold_1_mRNA_1619.1 | C_unshiu_00205_mRNA_17.1,C_unshiu_01378_mRNA_2.1,C_unshiu_02317_mRNA_1.1 | - |
| GF0002715 | 1 | 3 | 0 | Hypothetical protein (4) | nucleic acid binding [GO:0003676 molecular_function] (3); zinc ion binding [GO:0008270 molecular_function] (3); proteolysis [GO:0006508 biological_process] (2); aspartic-type endopeptidase activity [GO:0004190 molecular_function] (2) | Zinc finger, CCHC-type [IPR001878] (3); Aspartic peptidase domain [IPR021109] (3); Peptidase A2A, retrovirus, catalytic [IPR001995] (2); Retropepsins [IPR018061] (2) | scaffold_1_mRNA_1499.1 | C_unshiu_00104_mRNA_3.1,C_unshiu_00145_mRNA_32.1,C_unshiu_00198_mRNA_30.1 | - |
| GF0002714 | 1 | 3 | 0 | Hypothetical protein (4) | 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) | Reverse transcriptase domain [IPR000477] (4); Zinc finger, CCHC-type [IPR001878] (1); Aspartic peptidase, active site [IPR001969] (1) | scaffold_1_mRNA_1494.1 | C_unshiu_00239_mRNA_22.1,C_unshiu_00280_mRNA_17.1,C_unshiu_01400_mRNA_4.1 | - |
| GF0002712 | 1 | 3 | 0 | Hypothetical protein (4) | | | scaffold_1_mRNA_1471.1 | C_unshiu_00145_mRNA_50.1,C_unshiu_01649_mRNA_4.1,C_unshiu_01695_mRNA_14.1 | - |
| GF0002708 | 1 | 3 | 0 | Hypothetical protein (4) | | | scaffold_1_mRNA_1391.1 | C_unshiu_00020_mRNA_66.1,C_unshiu_00143_mRNA_2.1,C_unshiu_01687_mRNA_8.1 | - |
| GF0002704 | 1 | 3 | 0 | Hypothetical protein (4) | | | scaffold_1_mRNA_1301.1 | C_unshiu_00106_mRNA_16.1,C_unshiu_00493_mRNA_11.1,C_unshiu_01478_mRNA_9.1 | - |
| GF0002683 | 1 | 3 | 0 | Hypothetical protein (4) | | | scaffold_1_mRNA_1014.1 | C_unshiu_00584_mRNA_22.1,C_unshiu_00584_mRNA_24.1,C_unshiu_00584_mRNA_26.1 | - |
| GF0002519 | 1 | 4 | 0 | Hypothetical protein (5) | | | scaffold_8_mRNA_1590.1 | C_unshiu_00174_mRNA_45.1,C_unshiu_00287_mRNA_3.1,C_unshiu_01407_mRNA_16.1,C_unshiu_01432_mRNA_3.1 | - |
| GF0002412 | 1 | 4 | 0 | Hypothetical protein (5) | | | scaffold_6_mRNA_2940.1 | C_unshiu_00009_mRNA_95.1,C_unshiu_00009_mRNA_96.1,C_unshiu_01212_mRNA_7.1,C_unshiu_02167_mRNA_3.1 | - |
| GF0002394 | 1 | 4 | 0 | Hypothetical protein (5) | | | scaffold_6_mRNA_2090.1 | C_unshiu_00644_mRNA_2.1,C_unshiu_00865_mRNA_1.1,C_unshiu_01587_mRNA_4.1,C_unshiu_02708_mRNA_3.1 | - |
| GF0002256 | 1 | 4 | 0 | Hypothetical protein (5) | | | scaffold_5_mRNA_2496.1 | C_unshiu_00360_mRNA_5.1,C_unshiu_01219_mRNA_9.1,C_unshiu_01338_mRNA_4.1,C_unshiu_02140_mRNA_4.1 | - |
| GF0002094 | 1 | 4 | 0 | Cytochrome P450 83B1 (5) | heme binding [GO:0020037 molecular_function] (5); iron ion binding [GO:0005506 molecular_function] (5); oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705 molecular_function] (5); oxidation-reduction process [GO:0055114 biological_process] (5) | Cytochrome P450 [IPR001128] (5); Cytochrome P450, conserved site [IPR017972] (5); Cytochrome P450, E-class, group I [IPR002401] (5) | scaffold_3_mRNA_4861.1 | C_unshiu_00356_mRNA_15.1,C_unshiu_01363_mRNA_2.1,C_unshiu_02715_mRNA_1.1,C_unshiu_02742_mRNA_1.1 | - |

| ID | Num. in *C. celementine* | Num in *C. unshiu* | Num in *P.trifoliata* | Note | GO | InterPro | Members in *C.clementine* | Members in *C.unshiu* | Members in *P.trifoliata* |
|---|---|---|---|---|---|---|---|---|---|
| GF0002070 | 1 | 4 | 0 | Hypothetical protein (3); Selenoprotein (2) |  | Thioredoxin-like fold [IPR012336] (5); Sep15/SelM redox [IPR014912] (4); Selenoprotein Sep15/SelM [IPR014912] (1) | scaffold_3_mRNA_4346.1 | C_unshiu_00054_mRNA_53.1,C_unshiu_00787_mRNA_15.1,C_unshiu_00787_mRNA_2.1,C_unshiu_00787_mRNA_6.1 | - |
| GF0002061 | 1 | 4 | 0 | Hypothetical protein (3); Monosacharide transport protein (2) |  |  | scaffold_3_mRNA_3939.1 | C_unshiu_00022_mRNA_40.1,C_unshiu_00101_mRNA_44.1,C_unshiu_01265_mRNA_12.1,C_unshiu_02081_mRNA_1.1 | - |
| GF0001759 | 1 | 4 | 0 | Ac-like transposase (4); Hypothetical protein (1) | DNA binding [GO:0003677 molecular_function] (4); nucleic acid binding [GO:0003676 molecular_function] (4) | Ribonuclease H-like domain [IPR012337] (4); hAT-like transposase, RNase-H fold [IPR025525] (4) | scaffold_1_mRNA_1878.1 | C_unshiu_00009_mRNA_98.1,C_unshiu_00697_mRNA_7.1,C_unshiu_01906_mRNA_1.1,C_unshiu_02105_mRNA_3.1 | - |