**Supplemental Table S19. The information of Gene clusters involved in tanshinone pathway**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Input name** | **cluster** | **Gene cluster type** | **Gene ID** | **pHMM hits** | **swiss-prot** |
| group1 | 3 | lignan | evm.model.group1.1580 | n/a | #N/A |
| evm.model.group1.1581 | Dirigent (E=2.9e-37) | Dirigent protein 1 (AtDIR1) |
| evm.model.group1.1582 | Dirigent (E=4.5e-31) | Dirigent protein 15 (AtDIR15) |
| evm.model.group1.1583 | n/a | #N/A |
| evm.model.group1.1584 | Dirigent (E=2.2e-30) | Dirigent protein 23 (AtDIR23) |
| evm.model.group1.1585 | n/a | #N/A |
| evm.model.group1.1586 | polyprenyl\_synt (E=4.3e-21) | Geranylgeranyl pyrophosphate synthase, chloroplastic (GGPP synthase) (GGPS) (EC 2.5.1.-) ((2E,6E)-farnesyl diphosphate synthase) (Dimethylallyltranstransferase) (EC 2.5.1.1) (Farnesyl diphosphate synthase) (Farnesyltranstransferase) (EC 2.5.1.29) (Geranyltranstransferase) (EC 2.5.1.10) |
| evm.model.group1.1587 | n/a | #N/A |
| evm.model.group1.1588 | n/a | Probable glucan endo-1,3-beta-glucosidase A6 (EC 3.2.1.39) ((1->3)-beta-glucan endohydrolase) ((1->3)-beta-glucanase) (Anther-specific protein A6) (Beta-1,3-endoglucanase) (Protein MATERNAL EFFECT EMBRYO ARREST 48) |
| evm.model.group1.1589 | AMP-binding (E=6.9e-48) | Probable acyl-activating enzyme 16, chloroplastic (EC 6.2.1.-) |
| evm.model.group1.1590 | n/a | #N/A |
| evm.model.group1.1591 | n/a | #N/A |
| evm.model.group1.1592 | n/a | #N/A |
| evm.model.group1.1593 | n/a | Uncharacterized protein |
| 5 | putative | evm.model.group1.2774 | n/a | Gag-pol polyprotein |
| evm.model.group1.2775 | DIOX\_N (E=8.4e-08) | Probable 2-oxoglutarate-dependent dioxygenase AOP1 (EC 1.14.11.-) |
| evm.model.group1.2776 | DIOX\_N (E=2e-06) | 2-oxoglutarate-dependent dioxygenase AOP3 (EC 1.14.11.-) |
| evm.model.group1.2777 | 2OG-FeII\_Oxy (E=4.3e-17) | Probable 2-oxoglutarate-dependent dioxygenase AOP1.2 (EC 1.14.11.-) |
| evm.model.group1.2778 | n/a | #N/A |
| evm.model.group1.2779 | n/a | Uncharacterized protein |
| evm.model.group1.2780 | n/a | Uncharacterized protein |
| evm.model.group1.2781 | n/a | Uncharacterized protein |
| evm.model.group1.2782 | n/a | #N/A |
| evm.model.group1.2783 | DIOX\_N (E=7.1e-12) | Probable 2-oxoglutarate-dependent dioxygenase AOP1.2 (EC 1.14.11.-) |
| evm.model.group1.2784 | DIOX\_N (E=1.4e-18) | #N/A |
| 7 | putative | evm.model.group1.3903 | n/a | Outer envelope pore protein 37, chloroplastic (Chloroplastic outer envelope pore protein of 37 kDa) (AtOEP37) |
| evm.model.group1.3904 | n/a | Vacuolar protein sorting-associated protein 20 homolog 2 (AtVPS20-2) (Charged multivesicular body protein 6 homolog 2) (ESCRT-III complex subunit VPS20 homolog 2) |
| evm.model.group1.3905 | Transferase (E=5.9e-58) | Pelargonidin 3-O-(6-caffeoylglucoside) 5-O-(6-O-malonylglucoside) 4'''-malonyltransferase (EC 2.3.1.214) (Anthocyanin 5-O-glucoside-4'''-O-malonyltransferase 2) (Ss5MaT2) |
| evm.model.group1.3906 | Transferase (E=1.3e-15) | Pelargonidin 3-O-(6-caffeoylglucoside) 5-O-(6-O-malonylglucoside) 4'''-malonyltransferase (EC 2.3.1.214) (Anthocyanin 5-O-glucoside-4'''-O-malonyltransferase 2) (Ss5MaT2) |
| evm.model.group1.3907 | n/a | Hydroquinone glucosyltransferase (EC 2.4.1.218) (Arbutin synthase) |
| evm.model.group1.3908 | Transferase (E=3.3e-42) | Pelargonidin 3-O-(6-caffeoylglucoside) 5-O-(6-O-malonylglucoside) 4'''-malonyltransferase (EC 2.3.1.214) (Anthocyanin 5-O-glucoside-4'''-O-malonyltransferase 2) (Ss5MaT2) |
| evm.model.group1.3909 | Transferase (E=3.2e-67) | Pelargonidin 3-O-(6-caffeoylglucoside) 5-O-(6-O-malonylglucoside) 4'''-malonyltransferase (EC 2.3.1.214) (Anthocyanin 5-O-glucoside-4'''-O-malonyltransferase 2) (Ss5MaT2) |
| evm.model.group1.3910 | n/a | Type I inositol polyphosphate 5-phosphatase 12 (At5PTase12) (EC 3.1.3.56) |
| evm.model.group1.3911 | Transferase (E=1.9e-57) | Pelargonidin 3-O-(6-caffeoylglucoside) 5-O-(6-O-malonylglucoside) 4'''-malonyltransferase (EC 2.3.1.214) (Anthocyanin 5-O-glucoside-4'''-O-malonyltransferase 2) (Ss5MaT2) |
| evm.model.group1.3912 | n/a | Probable thiol methyltransferase 2 (EC 2.1.1.9) (Protein HARMLESS TO OZONE LAYER 3) (AtHOL3) |
| evm.model.group1.3913 | Transferase (E=2.7e-65) | Pelargonidin 3-O-(6-caffeoylglucoside) 5-O-(6-O-malonylglucoside) 4'''-malonyltransferase (EC 2.3.1.214) (Anthocyanin 5-O-glucoside-4'''-O-malonyltransferase 2) (Ss5MaT2) |
| evm.model.group1.3914 | Transferase (E=5.3e-17) | Pelargonidin 3-O-(6-caffeoylglucoside) 5-O-(6-O-malonylglucoside) 4'''-malonyltransferase (EC 2.3.1.214) (Anthocyanin 5-O-glucoside-4'''-O-malonyltransferase 2) (Ss5MaT2) |
| evm.model.group1.3915 | TPMT (E=8.6e-10) | Type I inositol polyphosphate 5-phosphatase 12 (At5PTase12) (EC 3.1.3.56) |
| evm.model.group1.3916 | n/a | Polygalacturonase (PG) (EC 3.2.1.15) (Pectinase) |
| evm.model.group1.3917 | n/a | Polygalacturonase (PG) (EC 3.2.1.15) (Pectinase) |
| evm.model.group1.3918 | n/a | Polygalacturonase (PG) (EC 3.2.1.15) (Pectinase) |
| evm.model.group1.3919 | n/a | Polygalacturonase (PG) (EC 3.2.1.15) (Pectinase) |
| evm.model.group1.3920 | Transferase (E=1e-91) | Omega-hydroxypalmitate O-feruloyl transferase (EC 2.3.1.188) (Omega-hydroxyacid hydroxycinnamoyltransferase) (Protein ALIPHATIC SUBERIN FERULOYL TRANSFERASE) |
| evm.model.group1.3921 | n/a | 2-alkenal reductase (NADP(+)-dependent) (EC 1.3.1.102) (Alkenal double bound reductase) (Allylic alcohol dehydrogenase 1) (allyl-ADH1) (Flavin-free double bond reductase) (NtDBR) (Pulegone reductase) (NtRed-1) |
| evm.model.group1.3922 | Transferase (E=1.6e-65) | Fatty alcohol:caffeoyl-CoA acyltransferase (EC 2.3.1.-) (Fatty alcohol:caffeoyl-CoA caffeoyl transferase) |
| evm.model.group1.3923 | n/a | Fatty acyl-CoA reductase 2 (EC 1.2.1.84) (Fatty acid reductase 2) (Male sterility protein 2) |
| evm.model.group1.3924 | p450 (E=1.3e-73) | CYP71D373 |
| evm.model.group1.3925 | n/a | V-type proton ATPase subunit D (V-ATPase subunit D) (Vacuolar H(+)-ATPase subunit D) (Vacuolar proton pump subunit D) |
| 11 | putative | evm.model.group1.9736 | Transferase (E=4e-69) | Uncharacterized acetyltransferase At3g50280 (EC 2.3.1.-) |
| evm.model.group1.9737 | n/a | #N/A |
| evm.model.group1.9738 | AMP-binding (E=1.5e-20) | Long-chain-fatty-acid--AMP ligase FadD26 (FAAL) (EC 6.2.1.-) (Acyl-AMP synthetase) |
| evm.model.group1.9739 | AMP-binding (E=1.7e-46) | Long-chain-fatty-acid--AMP ligase FadD26 (FAAL) (EC 6.2.1.-) (Acyl-AMP synthetase) |
| evm.model.group1.9740 | n/a | #N/A |
| evm.model.group1.9741 | Transferase (E=4.1e-81) | Uncharacterized acetyltransferase At3g50280 (EC 2.3.1.-) |
| evm.model.group1.9742 | n/a | #N/A |
| evm.model.group1.9743 | Transferase (E=5.4e-59) | Uncharacterized acetyltransferase At3g50280 (EC 2.3.1.-) |
| evm.model.group1.9744 | n/a | #N/A |
| evm.model.group1.9745 | p450 (E=2.6e-100) | 3,9-dihydroxypterocarpan 6A-monooxygenase (EC 1.14.14.93) (Cytochrome P450 93A1) (Dihydroxypterocarpan 6a-hydroxylase) (D6aH) |
| evm.model.group1.9746 | n/a | Protein POLYCHOME (Protein UV-B-INSENSITIVE 4) |
| evm.model.group1.9747 | n/a | Transcription factor bHLH130 (Basic helix-loop-helix protein 130) (AtbHLH130) (bHLH 130) (Transcription factor EN 69) (bHLH transcription factor bHLH130) |
| group2 | 13 | saccharide | evm.model.group2.430 | UDPGT\_2 (E=1e-89) | UDP-glycosyltransferase 74E2 (EC 2.4.1.-) |
| evm.model.group2.431 | n/a | #N/A |
| evm.model.group2.432 | UDPGT\_2 (E=1.9e-19) | UDP-glycosyltransferase 74F2 (EC 2.4.1.-) (AtSGT1) (Salicylic acid glucosyltransferase 1) |
| evm.model.group2.433 | UDPGT\_2 (E=1.1e-18) | UDP-glycosyltransferase 74F2 (EC 2.4.1.-) (AtSGT1) (Salicylic acid glucosyltransferase 1) |
| evm.model.group2.434 | UDPGT\_2 (E=7.2e-20) | UDP-glycosyltransferase 74F2 (EC 2.4.1.-) (AtSGT1) (Salicylic acid glucosyltransferase 1) |
| evm.model.group2.435 | n/a | Uncharacterized protein |
| evm.model.group2.436 | n/a | Probable sarcosine oxidase (EC 1.5.3.1) |
| evm.model.group2.437 | n/a | Serine/arginine-rich splicing factor RSZ21A (RS-containing zinc finger protein 21A) (Os-RSZ21a) (Os-RSZp21a) |
| evm.model.group2.438 | Glycos\_transf\_2 (E=4e-10) | Probable xyloglucan glycosyltransferase 8 (EC 2.4.1.-) (Cellulose synthase-like protein C8) (AtCslC8) |
| evm.model.group2.439 | n/a | Fasciclin-like arabinogalactan protein 14 |
| evm.model.group2.440 | p450 (E=2.2e-107) | Ferruginol synthase (EC 1.14.13.190) (Cytochrome P450 76AH1) |
| evm.model.group2.441 | n/a | #N/A |
| evm.model.group2.442 | p450 (E=1.4e-62) | Premnaspirodiene oxygenase (HPO) (EC 1.14.14.151) (Cytochrome P450 71D55) |
| evm.model.group2.443 | n/a | Formin-like protein 13 (AtFH13) |
| 16 | saccharide | evm.model.group2.1129 | n/a | Phosphoribosylglycinamide formyltransferase, chloroplastic (EC 2.1.2.2) (5'-phosphoribosylglycinamide transformylase) (GAR transformylase) (GART) |
| evm.model.group2.1130 | n/a | Peroxiredoxin-2E, chloroplastic (EC 1.11.1.15) (Peroxiredoxin IIE) (Thioredoxin peroxidase 2E) |
| evm.model.group2.1131 | Glycos\_transf\_2 (E=3.7e-10) | Glucomannan 4-beta-mannosyltransferase 9 (EC 2.4.1.32) (Cellulose synthase-like protein A9) (AtCslA9) (Glucomannan synthase) (Mannan synthase 9) (Protein RESISTANT TO AGROBACTERIUM TRANSFORMATION 4) |
| evm.model.group2.1132 | p450 (E=3.3e-62) | Geraniol 8-hydroxylase (EC 1.14.14.83) (Cytochrome P450 76B6) (Geraniol 10-hydroxylase) (CrG10H) |
| evm.model.group2.1133 | p450 (E=5.1e-30) | Iridoid oxidase (CrIO) (EC 1.14.14.161) (Cytochrome P450 76A26) (CrCYP76A26) |
| evm.model.group2.1134 | n/a | Uncharacterized protein |
| evm.model.group2.1135 | n/a | #N/A |
| 18 | saccharide | evm.model.group2.1759 | n/a | Protein DETOXIFICATION 33 (AtDTX33) (Multidrug and toxic compound extrusion protein 33) (MATE protein 33) |
| evm.model.group2.1760 | n/a | 4-hydroxy-3-methylbut-2-enyl diphosphate reductase, chloroplastic (EC 1.17.7.4) (Protein CHLOROPLAST BIOGENESIS 6) |
| evm.model.group2.1761 | n/a | 4-hydroxy-3-methylbut-2-enyl diphosphate reductase, chloroplastic (EC 1.17.7.4) (Protein CHLOROPLAST BIOGENESIS 6) |
| evm.model.group2.1762 | n/a | Protein TIC 62, chloroplastic (Translocon at the inner envelope membrane of chloroplasts 62) (AtTIC62) |
| evm.model.group2.1763 | Methyltransf\_11 (E=2.2e-06) | EEF1A lysine methyltransferase 4 (EC 2.1.1.-) |
| evm.model.group2.1764 | n/a | 4-hydroxy-3-methylbut-2-enyl diphosphate reductase |
| evm.model.group2.1765 | n/a | Small subunit ribosomal protein S29 |
| evm.model.group2.1766 | n/a | Protein trichome birefringence-like 16 |
| evm.model.group2.1767 | n/a | #N/A |
| evm.model.group2.1768 | n/a | Uncharacterized protein |
| evm.model.group2.1769 | Epimerase (E=9e-06) | Protein HIGH CHLOROPHYLL FLUORESCENCE PHENOTYPE 173, chloroplastic |
| evm.model.group2.1770 | UDPGT\_2 (E=5.5e-30) | 7-deoxyloganetin glucosyltransferase (EC 2.4.1.324) (Genipin glucosyltransferase) (UDP-glucose glucosyltransferase 2) (GjUGT2) (UDP-glycosyltransferase 85A24) |
| evm.model.group2.1771 | p450 (E=1.6e-24) | Beta-amyrin 28-monooxygenase (EC 1.14.14.126) (Beta-amyrin 28-oxidase) (Cytochrome P450 716A17) (VvCYP716A17) |
| evm.model.group2.1772 | n/a | #N/A |
| evm.model.group2.1773 | n/a | Fasciclin-like arabinogalactan protein 1 |
| evm.model.group2.1774 | n/a | #N/A |
| evm.model.group2.1775 | n/a | Endoglucanase (EC 3.2.1.4) (Abscission cellulase) (Endo-1,4-beta-glucanase) |
| evm.model.group2.1776 | n/a | WRKY transcription factor 22 (WRKY DNA-binding protein 22) |
| evm.model.group2.1777 | n/a | #N/A |
| evm.model.group2.1778 | Methyltransf\_7 (E=2.2e-23) | Salicylate carboxymethyltransferase (EC 2.1.1.274) (S-adenosyl-L-methionine:salicylate acid carboxylmethyltransferase) (CbSAMT) (Salicylate O-methyltransferase) |
| evm.model.group2.1779 | n/a | #N/A |
| evm.model.group2.1780 | n/a | #N/A |
| evm.model.group2.1781 | n/a | Meiotic recombination protein SPO11-2 (AtSPO11-2) (EC 5.6.2.2) |
| evm.model.group2.1782 | n/a | gag\_pre-integrs domain-containing protein (Fragment) |
| evm.model.group2.1783 | Aminotran\_1\_2 (E=1.2e-23) | 1-aminocyclopropane-1-carboxylate synthase (ACC synthase) (EC 4.4.1.14) (S-adenosyl-L-methionine methylthioadenosine-lyase) |
| group4 | 23 | polyketide | evm.model.group4.88 | n/a | #N/A |
| evm.model.group4.89 | Epimerase (E=3.9e-08) | Phenylcoumaran benzylic ether reductase TP7 (NtPCBER) (EC 1.23.1.-) (Protein TOBACCO PETAL 7) |
| evm.model.group4.90 | n/a | Cycloeucalenol cycloisomerase (EC 5.5.1.9) (Cycloeucalenol--obtusifoliol isomerase) (Cyclopropyl sterol isomerase) |
| evm.model.group4.91 | Epimerase (E=1.4e-06) | Isoflavone reductase-like protein (Pollen allergen Ole e 12) (allergen Ole e 12) |
| evm.model.group4.92 | n/a | CBS domain-containing protein CBSX3, mitochondrial |
| evm.model.group4.93 | n/a | Pentatricopeptide repeat-containing protein At1g19525 |
| evm.model.group4.94 | n/a | Protein RADIALIS-like 6 (AtRL6) (Protein RAD-like 6) (Protein RADIALIS-LIKE SANT/MYB 3) (Protein RSM3) |
| evm.model.group4.95 | AMP-binding (E=7e-69) | Putative fatty-acid--CoA ligase fadD25 (EC 6.2.1.-) (Acyl-CoA synthetase) |
| evm.model.group4.96 | n/a | Sugar transporter ERD6-like 6 |
| evm.model.group4.97 | Chal\_sti\_synt\_C (E=1.3e-09) | 3-ketoacyl-CoA synthase 4 (KCS-4) (EC 2.3.1.199) (Very long-chain fatty acid condensing enzyme 4) (VLCFA condensing enzyme 4) |
| evm.model.group4.98 | n/a | Protein RADIALIS-like 6 (AtRL6) (Protein RAD-like 6) (Protein RADIALIS-LIKE SANT/MYB 3) (Protein RSM3) |
| 26 | saccharide-polyketide | evm.model.group4.3630 | FA\_desaturase\_2 (E=1.2e-83) | Stearoyl-[acyl-carrier-protein] 9-desaturase, chloroplastic (Stearoyl-ACP desaturase) (EC 1.14.19.2) (Acyl-[acyl-carrier-protein] desaturase) (Delta(9) stearoyl-acyl carrier protein desaturase) |
| evm.model.group4.3631 | FA\_desaturase\_2 (E=1.8e-83) | Stearoyl-[acyl-carrier-protein] 9-desaturase, chloroplastic (Stearoyl-ACP desaturase) (EC 1.14.19.2) (Acyl-[acyl-carrier-protein] desaturase) (Delta(9) stearoyl-acyl carrier protein desaturase) |
| evm.model.group4.3632 | n/a | Cysteine synthase, chloroplastic/chromoplastic (EC 2.5.1.47) (At.OAS.7-4) (Beta-substituted Ala synthase 2;1) (ARAth-Bsas2;1) (CSase B) (AtCS-B) (CS-B) (O-acetylserine (thiol)-lyase) (O-acetylserine sulfhydrylase) (OAS-TL B) (cpACS1) |
| evm.model.group4.3633 | adh\_short\_C2 (E=2.2e-07) | (+)-neomenthol dehydrogenase (EC 1.1.1.-) (EC 1.1.1.208) (Menthone:neomenthol reductase) (Short-chain dehydrogenase/reductase 1) (AtSDR1) |
| evm.model.group4.3634 | n/a | Uncharacterized protein |
| evm.model.group4.3635 | n/a | Formin-like protein 1 (OsFH1) |
| evm.model.group4.3636 | UDPGT\_2 (E=2.3e-20) | UDP-glycosyltransferase 74D1 (EC 2.4.1.-) (Jasmonate glucosyltransferase 1) (AtJGT1) |
| evm.model.group4.3637 | n/a | Acetolactate synthase small subunit 2, chloroplastic (Acetohydroxy-acid synthase small subunit) (AHAS) (ALS) |
| evm.model.group4.3638 | n/a | 50S ribosomal protein L2 |
| evm.model.group4.3639 | n/a | 2-alkenal reductase (NADP(+)-dependent) (EC 1.3.1.102) (Alkenal double bound reductase) (Allylic alcohol dehydrogenase 1) (allyl-ADH1) (Flavin-free double bond reductase) (NtDBR) (Pulegone reductase) (NtRed-1) |
| evm.model.group4.3640 | n/a | 2-alkenal reductase (NADP(+)-dependent) (EC 1.3.1.102) (Alkenal double bound reductase) (Allylic alcohol dehydrogenase 1) (allyl-ADH1) (Flavin-free double bond reductase) (NtDBR) (Pulegone reductase) (NtRed-1) |
| evm.model.group4.3641 | n/a | 2-alkenal reductase (NADP(+)-dependent) (EC 1.3.1.102) (Alkenal double bound reductase) (Allylic alcohol dehydrogenase 1) (allyl-ADH1) (Flavin-free double bond reductase) (NtDBR) (Pulegone reductase) (NtRed-1) |
| evm.model.group4.3642 | n/a | Exonuclease V, chloroplastic (Exo V) (EC 3.1.-.-) |
| evm.model.group4.3643 | Chal\_sti\_synt\_C (E=9e-59), Chal\_sti\_synt\_N (E=3.1e-21) | Chalcone synthase (EC 2.3.1.74) (Naringenin-chalcone synthase) |
| evm.model.group4.3644 | Chal\_sti\_synt\_C (E=5.4e-61), Chal\_sti\_synt\_N (E=4.7e-21) | Chalcone synthase (EC 2.3.1.74) (Naringenin-chalcone synthase) |
| evm.model.group4.3645 | n/a | Protein RALF-like 2 |
| evm.model.group4.3646 | Transferase (E=1.1e-92) | Fatty alcohol:caffeoyl-CoA acyltransferase (EC 2.3.1.-) (Fatty alcohol:caffeoyl-CoA caffeoyl transferase) |