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| --- | --- | --- | --- | --- | --- |
| Gene ID | Group(s) | Log2FC | Regulated | GO annotation | KEGG annotation |
| Unigene31564\_All | HLvsLL/HLvsML | -2.66633258/ -2.92618536 | Down/Down | NA | egr:104421208/3e-14/omega-hydroxypalmitate O-feruloyl transferase; K15400 omega-hydroxypalmitate O-feruloyl transferase [EC:2.3.1.188] |
| Unigene18001\_All | HLvsLL/HLvsML | -2.15245172/ -1.97822422 | Down/Down | NA | mtr:MTR\_8g096530/5e-28/omega-hydroxypalmitate O-feruloyl transferase; K15400 omega-hydroxypalmitate O-feruloyl transferase [EC:2.3.1.188] |
| CL1709.Contig9\_All | HLvsML | -3.265573297 | Down | NA | jcu:105635402/9e-94/vinorine synthase-like; K13065 shikimate O-hydroxycinnamoyltransferase [EC:2.3.1.133] |
| CL10633.Contig6\_All | MLvsLL | 2.313843715 | Up | NA | vra:106769199/5e-51/flavonol synthase/flavanone 3-hydroxylase-like; K05278 flavonol synthase [EC:1.14.11.23] |
| CL9672.Contig4\_All | HLvsLL | -1.542934946 | Down | NA | fve:101296827/5e-41/flavonol synthase/flavanone 3-hydroxylase-like; K05278 flavonol synthase [EC:1.14.11.23] |
| CL10633.Contig3\_All | MLvsLL | 2.571737817 | Up | NA | pda:103696959/2e-65/leucoanthocyanidin dioxygenase-like; K05277 leucoanthocyanidin dioxygenase [EC:1.14.11.19] |
| CL3969.Contig2\_All | HLvsLL | -1.846834147 | Down | NA | vvi:100233142/1e-156/LDOX, ANS; leucoanthocyanidin dioxygenase; K05277 leucoanthocyanidin dioxygenase [EC:1.14.11.19] |
| Unigene15127\_All | HLvsLL/HLvsML | -3.03051123/ -2.50293348 | Down/Down | NA | mtr:MTR\_7g086000/5e-09/transferase family protein; K13065 shikimate O-hydroxycinnamoyltransferase [EC:2.3.1.133] |
| Unigene18529\_All | HLvsLL | -3.76674 | Down  | biological\_process:GO:0009813//flavonoid biosynthetic process;GO:0052696//flavonoid glucuronidation;cellular\_component:GO:0043231//intracellular membrane-bounded organelle;molecular\_function:GO:0080043//quercetin 3-O-glucosyltransferase activity;GO:0080044//quercetin 7-O-glucosyltransferase activity; | egr:104456188/3e-55/UDP-glycosyltransferase 74F2-like; K13691 pathogen-inducible salicylic acid glucosyltransferase [EC:2.4.1.-] |
| Unigene62812\_All | MLvsLL | 6.465383158 | Up | NA | cam:101510753/2e-58/phenolic glucoside malonyltransferase 1-like; K13264 isoflavone 7-O-glucoside-6''-O-malonyltransferase [EC:2.3.1.115] |
| CL285.Contig2\_All | HLvsML | -2.925180781 | Down | NA | mdm:103439955/6e-20/caffeic acid 3-O-methyltransferase; K13066 caffeic acid 3-O-methyltransferase [EC:2.1.1.68] |
| CL10851.Contig1\_All | MLvsLL | 6.53575614 | Up | NA | spen:107014577/0.0/shikimate O-hydroxycinnamoyltransferase; K13065 shikimate O-hydroxycinnamoyltransferase [EC:2.3.1.133] |
| CL18920.Contig24\_All | HLvsLL | 4.460283 | Up | biological\_process:GO:0009813//flavonoid biosynthetic process;GO:0052696//flavonoid glucuronidation; cellular\_component:GO:0043231//intracellular membrane-bounded organelle; molecular\_function:GO:0080043//quercetin 3-O-glucosyltransferase activity; GO:0080044//quercetin 7-O-glucosyltransferase activity; | vra:106769098/1e-33/UDP-glycosyltransferase 83A1-like; K04628 ceramide galactosyltransferase [EC:2.4.1.47] |