|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Functional Annotation Clustering**  **Current Gene List: down**  **Current Background: *Pisum sativum***  **1428 DAVID IDs**  **108 Cluster(s)** | | | | | |
| Annotation Cluster 1 | | Enrichment Score: 41 | Count | P\_Value | Benjamini |
|  | GOTERM\_MF\_DIRECT | structural constituent of chromatin | 89 | 3.9E-87 | 1.7E-84 |
|  | INTERPRO | Histone-fold | 88 | 1.0E-81 | 1.9E-78 |
|  | GOTERM\_MF\_DIRECT | protein heterodimerization activity | 90 | 2.0E-79 | 4.4E-77 |
|  | GOTERM\_CC\_DIRECT | nucleosome | 89 | 1.4E-71 | 2.2E-69 |
|  | UP\_KW\_CELLULAR\_COMPONENT | Chromosome | 94 | 5.3E-69 | 1.9E-67 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Histone H2A/H2B/H3 | 58 | 6.0E-62 | 3.0E-59 |
|  | INTERPRO | Histone\_H2A/H2B/H3 | 58 | 7.4E-60 | 6.7E-57 |
|  | UP\_KW\_CELLULAR\_COMPONENT | Nucleosome core | 36 | 9.1E-36 | 1.6E-34 |
|  | UP\_KW\_MOLECULAR\_FUNCTION | DNA-binding | 134 | 8.2E-29 | 4.5E-27 |
|  | INTERPRO | Histone\_H3/CENP-A | 23 | 1.8E-26 | 5.4E-24 |
|  | SMART | H3 | 23 | 7.3E-25 | 6.6E-23 |
|  | GOTERM\_MF\_DIRECT | DNA binding | 131 | 5.0E-21 | 7.3E-19 |
|  | UP\_KW\_PTM | Acetylation | 26 | 3.2E-16 | 4.4E-15 |
|  | UP\_KW\_PTM | Phosphoprotein | 50 | 3.3E-15 | 2.3E-14 |
|  | UP\_KW\_CELLULAR\_COMPONENT | Nucleus | 174 | 1.3E-11 | 1.5E-10 |
|  | GOTERM\_CC\_DIRECT | nucleus | 265 | 2.4E-11 | 1.8E-9 |
|  | UP\_KW\_PTM | Methylation | 20 | 2.5E-7 | 8.6E-7 |
| Annotation Cluster 2 | | Enrichment Score: 29.91 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:CENP-T/Histone H4 histone fold | 27 | 1.2E-31 | 3.0E-29 |
|  | GOTERM\_BP\_DIRECT | nucleosome assembly | 46 | 1.8E-31 | 9.0E-29 |
|  | INTERPRO | Histone\_H4\_CS | 27 | 7.1E-31 | 3.2E-28 |
|  | INTERPRO | CENP-T/H4\_C | 27 | 7.1E-31 | 3.2E-28 |
|  | INTERPRO | Histone\_H4 | 27 | 2.2E-30 | 7.8E-28 |
|  | SMART | H4 | 27 | 1.6E-28 | 2.9E-26 |
| Annotation Cluster 3 | | Enrichment Score: 26.65 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:Histone H2A/H2B/H3 | 58 | 6.0E-62 | 3.0E-59 |
|  | INTERPRO | Histone\_H2A/H2B/H3 | 58 | 7.4E-60 | 6.7E-57 |
|  | INTERPRO | Histone\_H2A\_CS | 19 | 3.6E-19 | 9.2E-17 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Histone H2A C-terminal | 20 | 3.9E-18 | 6.6E-16 |
|  | INTERPRO | Histone\_H2A | 20 | 4.5E-18 | 1.0E-15 |
|  | INTERPRO | Histone\_H2A\_C | 20 | 1.4E-17 | 2.8E-15 |
|  | SMART | H2A | 20 | 1.1E-16 | 6.5E-15 |
|  | KEGG\_PATHWAY | ATP-dependent chromatin remodeling | 19 | 1.5E-7 | 1.7E-5 |
| Annotation Cluster 4 | | Enrichment Score: 14.92 | Count | P\_Value | Benjamini |
|  | INTERPRO | HISTONE\_H2B\_site | 15 | 2.9E-16 | 4.3E-14 |
|  | INTERPRO | Histone\_H2B | 15 | 7.2E-16 | 8.6E-14 |
|  | SMART | H2B | 15 | 8.3E-15 | 3.8E-13 |
| Annotation Cluster 5 | | Enrichment Score: 12.53 | Count | P\_Value | Benjamini |
|  | GOTERM\_MF\_DIRECT | oxygen binding | 15 | 1.8E-18 | 2.0E-16 |
|  | GOTERM\_MF\_DIRECT | oxygen carrier activity | 14 | 1.1E-17 | 9.7E-16 |
|  | INTERPRO | Globin-like\_sf | 14 | 7.7E-17 | 1.3E-14 |
|  | INTERPRO | Globin/Proto | 14 | 7.7E-17 | 1.3E-14 |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Nitrogen fixation | 15 | 1.1E-16 | 6.6E-15 |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Oxygen transport | 14 | 1.5E-16 | 6.6E-15 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Globin | 13 | 2.1E-16 | 2.7E-14 |
|  | INTERPRO | Globin | 13 | 4.8E-16 | 6.2E-14 |
|  | INTERPRO | Leghaemoglobin-like | 13 | 4.8E-16 | 6.2E-14 |
|  | UP\_KW\_PTM | Nitration | 13 | 3.2E-14 | 1.5E-13 |
|  | INTERPRO | Leghaemoglobin\_Fe\_BS | 10 | 1.9E-12 | 2.1E-10 |
|  | GOTERM\_BP\_DIRECT | nodulation | 14 | 4.1E-11 | 1.0E-8 |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Nodulation | 14 | 8.7E-11 | 2.5E-9 |
|  | UP\_KW\_LIGAND | Iron | 57 | 5.5E-8 | 1.5E-6 |
|  | GOTERM\_BP\_DIRECT | response to abscisic acid | 13 | 2.6E-6 | 3.2E-4 |
|  | UP\_KW\_LIGAND | Heme | 32 | 1.4E-5 | 1.9E-4 |
|  | GOTERM\_MF\_DIRECT | heme binding | 34 | 2.3E-5 | 1.3E-3 |
| Annotation Cluster 6 | | Enrichment Score: 4.15 | Count | P\_Value | Benjamini |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Cell cycle | 27 | 1.7E-6 | 3.7E-5 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Cyclin C-terminal | 10 | 2.3E-6 | 2.3E-4 |
|  | INTERPRO | Cyclin\_C-dom | 11 | 2.4E-6 | 2.6E-4 |
|  | SMART | Cyclin\_C | 11 | 2.6E-6 | 9.5E-5 |
|  | GOTERM\_BP\_DIRECT | cell division | 22 | 4.2E-6 | 4.1E-4 |
|  | INTERPRO | Cyclins\_cyclin-box | 10 | 1.1E-5 | 1.0E-3 |
|  | INTERPRO | Cyclin\_A/B-like | 8 | 1.8E-5 | 1.5E-3 |
|  | GOTERM\_BP\_DIRECT | regulation of cyclin-dependent protein serine/threonine kinase activity | 11 | 2.6E-5 | 1.8E-3 |
|  | GOTERM\_CC\_DIRECT | cyclin-dependent protein kinase holoenzyme complex | 13 | 3.3E-5 | 1.3E-3 |
|  | INTERPRO | Cyclin | 10 | 6.0E-5 | 4.7E-3 |
|  | GOTERM\_BP\_DIRECT | mitotic cell cycle phase transition | 10 | 7.7E-5 | 3.8E-3 |
|  | INTERPRO | Cyclin-like\_dom | 11 | 1.3E-4 | 9.1E-3 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Cyclin-like | 10 | 1.4E-4 | 9.8E-3 |
|  | PIR\_SUPERFAMILY | Cyclin\_A\_B\_D\_E | 8 | 1.9E-4 | 1.2E-2 |
|  | GOTERM\_MF\_DIRECT | cyclin-dependent protein serine/threonine kinase regulator activity | 10 | 2.1E-4 | 6.2E-3 |
|  | INTERPRO | Cyclin-like\_sf | 12 | 3.8E-4 | 2.1E-2 |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Cell division | 18 | 3.8E-4 | 6.6E-3 |
|  | SMART | CYCLIN | 11 | 5.3E-4 | 1.6E-2 |
|  | INTERPRO | Cyclin\_N | 10 | 6.0E-4 | 3.1E-2 |
|  | UP\_KW\_MOLECULAR\_FUNCTION | Cyclin | 11 | 8.8E-4 | 2.4E-2 |
|  | GOTERM\_CC\_DIRECT | centrosome | 3 | 3.3E-1 | 1.0E0 |
| Annotation Cluster 7 | | Enrichment Score: 3.67 | Count | P\_Value | Benjamini |
|  | GOTERM\_MF\_DIRECT | secondary active sulfate transmembrane transporter activity | 6 | 6.5E-5 | 2.9E-3 |
|  | INTERPRO | S04\_transporter\_CS | 6 | 7.8E-5 | 5.9E-3 |
|  | GOTERM\_MF\_DIRECT | monoatomic anion transmembrane transporter activity | 6 | 1.3E-4 | 4.7E-3 |
|  | UP\_SEQ\_FEATURE | DOMAIN:STAS | 6 | 2.6E-4 | 1.5E-2 |
|  | INTERPRO | STAS\_dom\_sf | 6 | 3.5E-4 | 2.1E-2 |
|  | INTERPRO | STAS\_dom | 6 | 3.5E-4 | 2.1E-2 |
|  | INTERPRO | SLC26A/SulP\_dom | 6 | 4.5E-4 | 2.4E-2 |
|  | INTERPRO | SLC26A/SulP\_fam | 6 | 4.5E-4 | 2.4E-2 |
| Annotation Cluster 8 | | Enrichment Score: 3.06 | Count | P\_Value | Benjamini |
|  | GOTERM\_MF\_DIRECT | double-stranded DNA helicase activity | 6 | 6.2E-6 | 3.9E-4 |
|  | GOTERM\_MF\_DIRECT | forked DNA-dependent helicase activity | 6 | 6.2E-6 | 3.9E-4 |
|  | INTERPRO | MCM\_N | 6 | 7.5E-6 | 7.1E-4 |
|  | INTERPRO | MCM\_CS | 6 | 7.5E-6 | 7.1E-4 |
|  | GOTERM\_BP\_DIRECT | DNA replication | 12 | 1.9E-5 | 1.5E-3 |
|  | GOTERM\_CC\_DIRECT | THO complex | 6 | 3.1E-5 | 1.3E-3 |
|  | GOTERM\_MF\_DIRECT | four-way junction helicase activity | 7 | 4.2E-5 | 2.1E-3 |
|  | KEGG\_PATHWAY | DNA replication | 13 | 1.2E-4 | 3.4E-3 |
|  | INTERPRO | MCM\_lid | 6 | 1.5E-4 | 1.0E-2 |
|  | INTERPRO | MCM\_OB | 6 | 1.5E-4 | 1.0E-2 |
|  | GOTERM\_MF\_DIRECT | single-stranded 3'-5' DNA helicase activity | 6 | 1.7E-4 | 5.8E-3 |
|  | GOTERM\_BP\_DIRECT | mitotic DNA replication initiation | 4 | 3.5E-4 | 1.4E-2 |
|  | GOTERM\_BP\_DIRECT | double-strand break repair via break-induced replication | 7 | 8.0E-4 | 3.1E-2 |
|  | GOTERM\_MF\_DIRECT | single-stranded DNA binding | 12 | 1.2E-3 | 3.1E-2 |
|  | UP\_SEQ\_FEATURE | DOMAIN:MCM | 6 | 1.8E-3 | 7.2E-2 |
|  | SMART | MCM | 6 | 2.4E-3 | 5.4E-2 |
|  | INTERPRO | MCM\_dom | 6 | 2.5E-3 | 9.5E-2 |
|  | INTERPRO | MCM | 6 | 2.5E-3 | 9.5E-2 |
|  | GOTERM\_MF\_DIRECT | chromatin extrusion motor activity | 3 | 2.8E-3 | 5.6E-2 |
|  | GOTERM\_MF\_DIRECT | ATP-dependent H3-H4 histone complex chaperone activity | 3 | 2.8E-3 | 5.6E-2 |
|  | GOTERM\_MF\_DIRECT | cohesin loader activity | 3 | 5.5E-3 | 9.7E-2 |
|  | GOTERM\_MF\_DIRECT | ATP-dependent H2AZ histone chaperone activity | 3 | 5.5E-3 | 9.7E-2 |
|  | GOTERM\_MF\_DIRECT | single-stranded DNA helicase activity | 5 | 5.9E-3 | 1.0E-1 |
|  | GOTERM\_CC\_DIRECT | MCM complex | 6 | 6.0E-3 | 1.4E-1 |
|  | GOTERM\_MF\_DIRECT | DNA clamp loader activity | 4 | 8.1E-2 | 8.1E-1 |
|  | GOTERM\_BP\_DIRECT | DNA strand elongation involved in DNA replication | 3 | 1.9E-1 | 1.0E0 |
|  | UP\_KW\_MOLECULAR\_FUNCTION | Helicase | 11 | 9.7E-1 | 1.0E0 |
|  | INTERPRO | NA-bd\_OB-fold | 12 | 9.8E-1 | 1.0E0 |
| Annotation Cluster 9 | | Enrichment Score: 2.72 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:FLZ-type | 5 | 1.8E-3 | 7.2E-2 |
|  | UP\_SEQ\_FEATURE | ZN\_FING:FLZ-type | 5 | 1.8E-3 | 7.2E-2 |
|  | INTERPRO | Zf-FLZ\_dom | 5 | 2.3E-3 | 9.1E-2 |
| Annotation Cluster 10 | | Enrichment Score: 2.59 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:DUF3700 | 4 | 8.6E-4 | 4.4E-2 |
|  | INTERPRO | TSJT1-like | 4 | 1.1E-3 | 4.9E-2 |
|  | INTERPRO | DUF3700 | 4 | 1.1E-3 | 4.9E-2 |
|  | SMART | DUF3700 | 4 | 1.8E-3 | 4.7E-2 |
|  | INTERPRO | Ntn\_hydrolases\_N | 6 | 6.8E-2 | 1.0E0 |
| Annotation Cluster 11 | | Enrichment Score: 2.24 | Count | P\_Value | Benjamini |
|  | GOTERM\_BP\_DIRECT | starch biosynthetic process | 7 | 6.3E-5 | 3.5E-3 |
|  | INTERPRO | ADP\_Glu\_pyroP\_CS | 5 | 1.9E-4 | 1.2E-2 |
|  | INTERPRO | Trimer\_LpxA-like\_sf | 7 | 2.1E-3 | 8.9E-2 |
|  | INTERPRO | ADP-Glc\_PPase | 5 | 2.3E-3 | 9.1E-2 |
|  | KEGG\_PATHWAY | Starch and sucrose metabolism | 20 | 2.3E-3 | 4.5E-2 |
|  | GOTERM\_MF\_DIRECT | glucose-1-phosphate adenylyltransferase activity | 5 | 2.4E-3 | 5.4E-2 |
|  | KEGG\_PATHWAY | Amino sugar and nucleotide sugar metabolism | 17 | 3.3E-3 | 5.6E-2 |
|  | UP\_KW\_MOLECULAR\_FUNCTION | Allosteric enzyme | 6 | 3.4E-3 | 6.2E-2 |
|  | GOTERM\_BP\_DIRECT | glycogen biosynthetic process | 5 | 5.5E-3 | 1.5E-1 |
|  | KEGG\_PATHWAY | Biosynthesis of nucleotide sugars | 12 | 1.8E-2 | 1.6E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Nucleotidyl transferase | 5 | 3.1E-2 | 5.9E-1 |
|  | INTERPRO | NTP\_transferase\_dom | 5 | 4.9E-2 | 9.1E-1 |
|  | INTERPRO | Nucleotide-diphossugar\_trans | 11 | 9.5E-2 | 1.0E0 |
|  | UP\_KW\_MOLECULAR\_FUNCTION | Nucleotidyltransferase | 5 | 9.7E-1 | 1.0E0 |
| Annotation Cluster 12 | | Enrichment Score: 2 | Count | P\_Value | Benjamini |
|  | GOTERM\_BP\_DIRECT | signal peptide processing | 6 | 1.0E-3 | 3.6E-2 |
|  | GOTERM\_CC\_DIRECT | signal peptidase complex | 4 | 3.9E-3 | 1.2E-1 |
|  | GOTERM\_BP\_DIRECT | protein targeting to ER | 3 | 2.1E-2 | 4.0E-1 |
|  | KEGG\_PATHWAY | Protein export | 6 | 1.2E-1 | 6.9E-1 |
| Annotation Cluster 13 | | Enrichment Score: 1.82 | Count | P\_Value | Benjamini |
|  | INTERPRO | PCO/ADO | 4 | 1.6E-3 | 7.2E-2 |
|  | GOTERM\_BP\_DIRECT | detection of hypoxia | 4 | 1.8E-3 | 5.6E-2 |
|  | GOTERM\_MF\_DIRECT | oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen | 7 | 4.7E-3 | 9.1E-2 |
|  | INTERPRO | RmlC-like\_jellyroll | 8 | 2.0E-1 | 1.0E0 |
|  | INTERPRO | RmlC\_Cupin\_sf | 6 | 2.8E-1 | 1.0E0 |
| Annotation Cluster 14 | | Enrichment Score: 1.82 | Count | P\_Value | Benjamini |
|  | KEGG\_PATHWAY | Porphyrin metabolism | 8 | 7.9E-3 | 8.5E-2 |
|  | GOTERM\_BP\_DIRECT | chlorophyll biosynthetic process | 5 | 1.5E-2 | 3.1E-1 |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Chlorophyll biosynthesis | 4 | 3.0E-2 | 3.2E-1 |
| Annotation Cluster 15 | | Enrichment Score: 1.67 | Count | P\_Value | Benjamini |
|  | GOTERM\_MF\_DIRECT | microtubule binding | 20 | 7.0E-4 | 1.9E-2 |
|  | INTERPRO | Kinesin\_motor\_CS | 8 | 8.1E-4 | 4.0E-2 |
|  | GOTERM\_BP\_DIRECT | microtubule-based movement | 11 | 9.0E-3 | 2.0E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Kinesin motor | 10 | 9.8E-3 | 3.1E-1 |
|  | SMART | KISc | 10 | 1.4E-2 | 2.9E-1 |
|  | INTERPRO | Kinesin\_motor\_dom | 10 | 1.5E-2 | 4.7E-1 |
|  | GOTERM\_BP\_DIRECT | spindle elongation | 4 | 2.1E-2 | 4.0E-1 |
|  | GOTERM\_MF\_DIRECT | microtubule motor activity | 9 | 3.4E-2 | 4.9E-1 |
|  | GOTERM\_CC\_DIRECT | microtubule | 14 | 3.8E-2 | 4.9E-1 |
|  | INTERPRO | Kinesin\_motor\_dom\_sf | 10 | 7.7E-2 | 1.0E0 |
|  | INTERPRO | Kinesin-like\_fam | 6 | 1.3E-1 | 1.0E0 |
|  | UP\_KW\_CELLULAR\_COMPONENT | Microtubule | 12 | 1.6E-1 | 7.2E-1 |
|  | KEGG\_PATHWAY | Motor proteins | 5 | 4.1E-1 | 1.0E0 |
| Annotation Cluster 16 | | Enrichment Score: 1.65 | Count | P\_Value | Benjamini |
|  | GOTERM\_MF\_DIRECT | UDP-glycosyltransferase activity | 14 | 1.6E-3 | 4.0E-2 |
|  | INTERPRO | UDP\_glucos\_trans | 13 | 1.7E-3 | 7.4E-2 |
|  | INTERPRO | UDP\_glycos\_trans\_CS | 9 | 1.5E-2 | 4.8E-1 |
|  | GOTERM\_MF\_DIRECT | UDP-glucosyltransferase activity | 5 | 1.6E-1 | 1.0E0 |
|  | UP\_KW\_MOLECULAR\_FUNCTION | Glycosyltransferase | 15 | 8.3E-1 | 1.0E0 |
| Annotation Cluster 17 | | Enrichment Score: 1.64 | Count | P\_Value | Benjamini |
|  | INTERPRO | HLH\_DNA-bd\_sf | 15 | 4.2E-3 | 1.6E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:BHLH | 14 | 6.3E-3 | 2.1E-1 |
|  | INTERPRO | bHLH\_dom | 14 | 1.1E-2 | 3.6E-1 |
|  | SMART | HLH | 11 | 1.0E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | protein dimerization activity | 23 | 2.2E-1 | 1.0E0 |
| Annotation Cluster 18 | | Enrichment Score: 1.62 | Count | P\_Value | Benjamini |
|  | INTERPRO | UspA | 6 | 7.1E-3 | 2.5E-1 |
|  | INTERPRO | Rossmann-like\_a/b/a\_fold | 11 | 1.6E-2 | 4.9E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:UspA | 4 | 3.4E-2 | 5.9E-1 |
|  | INTERPRO | Universal\_stress\_UspA | 3 | 8.2E-2 | 1.0E0 |
| Annotation Cluster 19 | | Enrichment Score: 1.59 | Count | P\_Value | Benjamini |
|  | GOTERM\_BP\_DIRECT | negative regulation of catalytic activity | 8 | 4.0E-3 | 1.2E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Pectinesterase inhibitor | 9 | 1.5E-2 | 4.0E-1 |
|  | INTERPRO | Pectinesterase\_inhib\_dom | 9 | 3.0E-2 | 6.9E-1 |
|  | INTERPRO | Invertase/methylesterase\_inhib | 9 | 3.4E-2 | 7.5E-1 |
|  | SMART | PMEI | 9 | 3.6E-2 | 6.6E-1 |
|  | GOTERM\_MF\_DIRECT | enzyme inhibitor activity | 9 | 4.7E-2 | 5.8E-1 |
|  | INTERPRO | PME\_Inhibitor | 3 | 7.3E-2 | 1.0E0 |
| Annotation Cluster 20 | | Enrichment Score: 1.59 | Count | P\_Value | Benjamini |
|  | INTERPRO | POT\_fam | 11 | 1.2E-3 | 5.6E-2 |
|  | GOTERM\_MF\_DIRECT | transmembrane transporter activity | 23 | 3.8E-2 | 5.1E-1 |
|  | INTERPRO | MFS\_trans\_sf | 18 | 3.7E-1 | 1.0E0 |
| Annotation Cluster 21 | | Enrichment Score: 1.54 | Count | P\_Value | Benjamini |
|  | UP\_KW\_DOMAIN | Redox-active center | 9 | 6.8E-4 | 6.1E-3 |
|  | GOTERM\_BP\_DIRECT | cell redox homeostasis | 5 | 6.5E-3 | 1.6E-1 |
|  | INTERPRO | Thioredoxin-like\_sf | 17 | 1.1E-2 | 3.6E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Thioredoxin | 8 | 1.8E-2 | 4.3E-1 |
|  | INTERPRO | Thioredoxin\_domain | 8 | 2.5E-2 | 6.2E-1 |
|  | GOTERM\_BP\_DIRECT | response to endoplasmic reticulum stress | 4 | 3.5E-2 | 5.3E-1 |
|  | INTERPRO | PDI\_thioredoxin-like\_dom | 3 | 4.7E-2 | 8.8E-1 |
|  | INTERPRO | Thioredoxin\_CS | 4 | 1.0E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | protein disulfide isomerase activity | 3 | 1.4E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | protein folding | 5 | 9.3E-1 | 1.0E0 |
| Annotation Cluster 22 | | Enrichment Score: 1.47 | Count | P\_Value | Benjamini |
|  | GOTERM\_MF\_DIRECT | channel activity | 5 | 1.5E-2 | 2.2E-1 |
|  | INTERPRO | MIP\_CS | 5 | 2.8E-2 | 6.6E-1 |
|  | INTERPRO | Aquaporin\_transptr | 5 | 3.3E-2 | 7.5E-1 |
|  | INTERPRO | MIP | 5 | 5.6E-2 | 1.0E0 |
|  | INTERPRO | Aquaporin-like | 5 | 5.6E-2 | 1.0E0 |
| Annotation Cluster 23 | | Enrichment Score: 1.46 | Count | P\_Value | Benjamini |
|  | GOTERM\_MF\_DIRECT | glucose-6-phosphate 1-epimerase activity | 4 | 2.1E-3 | 5.0E-2 |
|  | INTERPRO | G6P\_1-epimerase | 3 | 1.9E-2 | 5.7E-1 |
|  | INTERPRO | GH-type\_carb-bd | 4 | 2.2E-2 | 6.0E-1 |
|  | INTERPRO | Gal\_mutarotase\_sf\_dom | 5 | 2.3E-2 | 6.1E-1 |
|  | PIR\_SUPERFAMILY | PHexose\_mutarotase | 3 | 4.2E-2 | 1.0E0 |
|  | INTERPRO | Aldose\_1/G6P\_1-epimerase | 3 | 4.7E-2 | 8.8E-1 |
|  | GOTERM\_MF\_DIRECT | isomerase activity | 4 | 9.9E-2 | 9.0E-1 |
|  | GOTERM\_MF\_DIRECT | carbohydrate binding | 7 | 5.3E-1 | 1.0E0 |
| Annotation Cluster 24 | | Enrichment Score: 1.46 | Count | P\_Value | Benjamini |
|  | INTERPRO | Glyco\_hydro\_18\_chit\_AS | 4 | 5.9E-3 | 2.1E-1 |
|  | GOTERM\_MF\_DIRECT | chitinase activity | 4 | 4.5E-2 | 5.7E-1 |
|  | INTERPRO | Glycosyl\_Hydrlase18\_Chitinase | 3 | 4.7E-2 | 8.8E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:GH18 | 4 | 6.0E-2 | 8.7E-1 |
|  | INTERPRO | Glyco\_hydro18\_cat | 4 | 7.1E-2 | 1.0E0 |
| Annotation Cluster 25 | | Enrichment Score: 1.45 | Count | P\_Value | Benjamini |
|  | INTERPRO | Peptidase\_A22B\_SPP | 3 | 2.5E-2 | 6.2E-1 |
|  | GOTERM\_BP\_DIRECT | membrane protein proteolysis | 3 | 2.7E-2 | 4.5E-1 |
|  | GOTERM\_CC\_DIRECT | lumenal side of endoplasmic reticulum membrane | 3 | 3.5E-2 | 4.9E-1 |
|  | GOTERM\_CC\_DIRECT | cytoplasmic side of endoplasmic reticulum membrane | 3 | 3.5E-2 | 4.9E-1 |
|  | GOTERM\_MF\_DIRECT | aspartic endopeptidase activity, intramembrane cleaving | 3 | 3.6E-2 | 5.0E-1 |
|  | INTERPRO | Preselin/SPP | 3 | 3.9E-2 | 8.0E-1 |
|  | SMART | PSN | 3 | 5.5E-2 | 8.3E-1 |
| Annotation Cluster 26 | | Enrichment Score: 1.32 | Count | P\_Value | Benjamini |
|  | INTERPRO | RlpA-like\_sf | 7 | 2.1E-2 | 5.9E-1 |
|  | INTERPRO | Expan\_Lol\_pI | 6 | 2.5E-2 | 6.2E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Expansin-like EG45 | 6 | 2.8E-2 | 5.7E-1 |
|  | INTERPRO | Expansin | 5 | 3.3E-2 | 7.5E-1 |
|  | INTERPRO | RlpA-like\_DPBB | 6 | 3.4E-2 | 7.5E-1 |
|  | INTERPRO | Expansin/allergen\_DPBB\_dom | 6 | 3.6E-2 | 7.7E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Expansin-like CBD | 5 | 6.3E-2 | 8.9E-1 |
|  | GOTERM\_BP\_DIRECT | anatomical structure morphogenesis | 5 | 7.5E-2 | 8.9E-1 |
|  | INTERPRO | Expansin\_CBD | 5 | 7.7E-2 | 1.0E0 |
|  | INTERPRO | Expansin\_CBD\_sf | 5 | 7.7E-2 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | plant-type cell wall organization | 5 | 9.4E-2 | 8.9E-1 |
|  | SMART | DPBB\_1 | 5 | 1.0E-1 | 1.0E0 |
| Annotation Cluster 27 | | Enrichment Score: 1.29 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:HMA | 8 | 1.6E-2 | 4.0E-1 |
|  | INTERPRO | HMA\_dom | 8 | 2.2E-2 | 6.0E-1 |
|  | INTERPRO | HMA\_dom\_sf | 8 | 2.3E-2 | 6.1E-1 |
|  | UP\_KW\_PTM | Prenylation | 3 | 8.5E-1 | 1.0E0 |
| Annotation Cluster 28 | | Enrichment Score: 1.27 | Count | P\_Value | Benjamini |
|  | GOTERM\_BP\_DIRECT | response to light stimulus | 10 | 1.8E-4 | 7.9E-3 |
|  | INTERPRO | Chloro\_AB-bd\_pln | 5 | 5.8E-3 | 2.1E-1 |
|  | GOTERM\_BP\_DIRECT | photosynthesis, light harvesting in photosystem I | 5 | 6.5E-3 | 1.6E-1 |
|  | INTERPRO | Chloroa\_b-bind | 5 | 1.3E-2 | 4.3E-1 |
|  | KEGG\_PATHWAY | Photosynthesis - antenna proteins | 5 | 1.8E-2 | 1.6E-1 |
|  | GOTERM\_CC\_DIRECT | plastoglobule | 4 | 2.9E-2 | 4.9E-1 |
|  | UP\_KW\_LIGAND | Chromophore | 7 | 3.3E-2 | 2.9E-1 |
|  | GOTERM\_BP\_DIRECT | photosynthesis, light harvesting | 4 | 3.5E-2 | 5.3E-1 |
|  | GOTERM\_CC\_DIRECT | photosystem I | 5 | 1.4E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | chlorophyll binding | 5 | 1.8E-1 | 1.0E0 |
|  | GOTERM\_CC\_DIRECT | chloroplast envelope | 6 | 3.3E-1 | 1.0E0 |
|  | GOTERM\_CC\_DIRECT | photosystem II | 5 | 4.9E-1 | 1.0E0 |
|  | UP\_KW\_CELLULAR\_COMPONENT | Photosystem II | 5 | 5.0E-1 | 1.0E0 |
|  | GOTERM\_CC\_DIRECT | chloroplast thylakoid membrane | 8 | 9.5E-1 | 1.0E0 |
|  | UP\_KW\_CELLULAR\_COMPONENT | Thylakoid | 5 | 9.7E-1 | 1.0E0 |
| Annotation Cluster 29 | | Enrichment Score: 1.25 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:GS catalytic | 3 | 3.5E-2 | 5.9E-1 |
|  | INTERPRO | Gln\_synth\_cat\_dom | 3 | 3.9E-2 | 8.0E-1 |
|  | GOTERM\_MF\_DIRECT | glutamine synthetase activity | 3 | 4.4E-2 | 5.7E-1 |
|  | SMART | Gln-synt\_C | 3 | 5.5E-2 | 8.3E-1 |
|  | INTERPRO | Gln\_synth/guanido\_kin\_cat\_dom | 3 | 1.7E-1 | 1.0E0 |
| Annotation Cluster 30 | | Enrichment Score: 1.11 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:BRCT | 4 | 4.6E-2 | 7.6E-1 |
|  | INTERPRO | BRCT\_dom\_sf | 4 | 6.0E-2 | 1.0E0 |
|  | INTERPRO | BRCT\_dom | 4 | 6.0E-2 | 1.0E0 |
|  | SMART | BRCT | 3 | 2.2E-1 | 1.0E0 |
| Annotation Cluster 31 | | Enrichment Score: 1.11 | Count | P\_Value | Benjamini |
|  | GOTERM\_BP\_DIRECT | mitotic chromosome condensation | 3 | 5.0E-2 | 6.8E-1 |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Mitosis | 7 | 7.1E-2 | 6.9E-1 |
|  | GOTERM\_CC\_DIRECT | condensin complex | 3 | 1.4E-1 | 1.0E0 |
| Annotation Cluster 32 | | Enrichment Score: 1.09 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | TRANSMEM:Helical | 283 | 5.9E-5 | 5.0E-3 |
|  | UP\_KW\_DOMAIN | Transmembrane | 259 | 7.6E-2 | 2.7E-1 |
|  | UP\_KW\_DOMAIN | Transmembrane helix | 166 | 8.6E-1 | 1.0E0 |
|  | GOTERM\_CC\_DIRECT | membrane | 253 | 9.5E-1 | 1.0E0 |
|  | UP\_KW\_CELLULAR\_COMPONENT | Membrane | 307 | 1.0E0 | 1.0E0 |
| Annotation Cluster 33 | | Enrichment Score: 1.08 | Count | P\_Value | Benjamini |
|  | GOTERM\_MF\_DIRECT | carbonate dehydratase activity | 4 | 2.0E-2 | 2.9E-1 |
|  | INTERPRO | Alpha\_CA\_prokaryot-like | 3 | 5.5E-2 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Alpha-carbonic anhydrase | 3 | 5.6E-2 | 8.4E-1 |
|  | INTERPRO | CA\_dom | 3 | 6.4E-2 | 1.0E0 |
|  | INTERPRO | Carbonic\_anhydrase\_a-class | 3 | 6.4E-2 | 1.0E0 |
|  | INTERPRO | CA\_dom\_sf | 3 | 6.4E-2 | 1.0E0 |
|  | SMART | Carb\_anhydrase | 3 | 7.6E-2 | 9.4E-1 |
|  | GOTERM\_BP\_DIRECT | one-carbon metabolic process | 3 | 3.6E-1 | 1.0E0 |
|  | GOTERM\_CC\_DIRECT | chloroplast stroma | 8 | 4.8E-1 | 1.0E0 |
| Annotation Cluster 34 | | Enrichment Score: 1.07 | Count | P\_Value | Benjamini |
|  | UP\_KW\_LIGAND | Heme | 32 | 1.4E-5 | 1.9E-4 |
|  | UP\_SEQ\_FEATURE | BINDING:axial binding residue | 21 | 1.9E-2 | 4.4E-1 |
|  | KEGG\_PATHWAY | Brassinosteroid biosynthesis | 4 | 3.2E-2 | 2.5E-1 |
|  | GOTERM\_BP\_DIRECT | brassinosteroid homeostasis | 4 | 6.5E-2 | 8.3E-1 |
|  | GOTERM\_BP\_DIRECT | brassinosteroid biosynthetic process | 4 | 7.1E-2 | 8.7E-1 |
|  | GOTERM\_MF\_DIRECT | oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen | 12 | 2.0E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | iron ion binding | 16 | 2.0E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | sterol metabolic process | 4 | 2.2E-1 | 1.0E0 |
|  | INTERPRO | Cyt\_P450\_E\_grp-I | 11 | 2.3E-1 | 1.0E0 |
|  | INTERPRO | Cyt\_P450 | 11 | 3.1E-1 | 1.0E0 |
|  | INTERPRO | Cyt\_P450\_sf | 11 | 3.2E-1 | 1.0E0 |
|  | INTERPRO | Cyt\_P450\_CS | 9 | 4.1E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | monooxygenase activity | 11 | 4.3E-1 | 1.0E0 |
|  | UP\_KW\_MOLECULAR\_FUNCTION | Monooxygenase | 6 | 8.2E-1 | 1.0E0 |
| Annotation Cluster 35 | | Enrichment Score: 1.05 | Count | P\_Value | Benjamini |
|  | UP\_KW\_DOMAIN | Transit peptide | 20 | 2.7E-2 | 1.6E-1 |
|  | UP\_KW\_CELLULAR\_COMPONENT | Chloroplast | 27 | 8.2E-2 | 5.8E-1 |
|  | UP\_KW\_CELLULAR\_COMPONENT | Plastid | 29 | 1.6E-1 | 7.2E-1 |
|  | GOTERM\_CC\_DIRECT | chloroplast | 37 | 1.7E-1 | 1.0E0 |
| Annotation Cluster 36 | | Enrichment Score: 1.02 | Count | P\_Value | Benjamini |
|  | INTERPRO | Iron\_ascorbate\_oxido\_reductase | 6 | 7.9E-3 | 2.7E-1 |
|  | UP\_KW\_MOLECULAR\_FUNCTION | Dioxygenase | 13 | 1.1E-2 | 1.5E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Fe2OG dioxygenase | 11 | 2.4E-2 | 5.3E-1 |
|  | INTERPRO | Oxoglu/Fe-dep\_dioxygenase\_dom | 11 | 3.6E-2 | 7.7E-1 |
|  | GOTERM\_BP\_DIRECT | gibberellin biosynthetic process | 3 | 1.2E-1 | 1.0E0 |
|  | INTERPRO | IPNS-like\_FE2OG\_OXY | 7 | 2.5E-1 | 1.0E0 |
|  | KEGG\_PATHWAY | Diterpenoid biosynthesis | 3 | 3.3E-1 | 1.0E0 |
|  | INTERPRO | IPNS-like\_sf | 7 | 3.3E-1 | 1.0E0 |
|  | INTERPRO | DIOX\_N | 6 | 3.9E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | dioxygenase activity | 3 | 6.6E-1 | 1.0E0 |
| Annotation Cluster 37 | | Enrichment Score: 1.01 | Count | P\_Value | Benjamini |
|  | INTERPRO | HMG\_box\_dom\_sf | 4 | 5.5E-2 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:HMG box | 3 | 1.0E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DNA\_BIND:HMG box | 3 | 1.0E-1 | 1.0E0 |
|  | INTERPRO | HMG\_box\_dom | 3 | 1.1E-1 | 1.0E0 |
|  | SMART | HMG | 3 | 1.4E-1 | 1.0E0 |
| Annotation Cluster 38 | | Enrichment Score: 0.98 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:X8 | 6 | 2.8E-2 | 5.7E-1 |
|  | INTERPRO | X8 | 6 | 3.8E-2 | 8.0E-1 |
|  | SMART | X8 | 6 | 7.3E-2 | 9.4E-1 |
|  | INTERPRO | Glyco\_hydro\_17 | 5 | 1.9E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | hydrolase activity, hydrolyzing O-glycosyl compounds | 12 | 2.4E-1 | 1.0E0 |
|  | INTERPRO | Glyco\_hydro\_17\_plant | 4 | 3.6E-1 | 1.0E0 |
| Annotation Cluster 39 | | Enrichment Score: 0.95 | Count | P\_Value | Benjamini |
|  | INTERPRO | Pectin\_lyas\_fold | 14 | 2.1E-2 | 5.9E-1 |
|  | INTERPRO | Pectin\_lyase\_fold/virulence | 14 | 2.3E-2 | 6.1E-1 |
|  | INTERPRO | PbH1 | 6 | 4.1E-2 | 8.2E-1 |
|  | SMART | PbH1 | 6 | 7.8E-2 | 9.4E-1 |
|  | GOTERM\_MF\_DIRECT | polygalacturonase activity | 6 | 1.0E-1 | 9.0E-1 |
|  | INTERPRO | Glyco\_hydro\_28 | 5 | 2.2E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | cell wall organization | 12 | 2.4E-1 | 1.0E0 |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Cell wall biogenesis/degradation | 10 | 6.2E-1 | 1.0E0 |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Cell wall biogenesis/degradation | 10 | 6.2E-1 | 1.0E0 |
| Annotation Cluster 40 | | Enrichment Score: 0.91 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:VOC | 3 | 1.1E-1 | 1.0E0 |
|  | INTERPRO | VOC | 3 | 1.2E-1 | 1.0E0 |
|  | INTERPRO | Glyas\_Bleomycin-R\_OHBP\_Dase | 3 | 1.3E-1 | 1.0E0 |
| Annotation Cluster 41 | | Enrichment Score: 0.88 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:Lactate/malate dehydrogenase C-terminal | 3 | 8.2E-2 | 9.7E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Lactate/malate dehydrogenase N-terminal | 3 | 9.1E-2 | 9.8E-1 |
|  | INTERPRO | Lactate/malate\_DH\_C | 3 | 9.2E-2 | 1.0E0 |
|  | INTERPRO | Lactate/malate\_DH\_N | 3 | 1.0E-1 | 1.0E0 |
|  | INTERPRO | Lactate\_DH/Glyco\_Ohase\_4\_C | 3 | 1.3E-1 | 1.0E0 |
|  | UP\_KW\_LIGAND | NAD | 9 | 5.3E-1 | 1.0E0 |
| Annotation Cluster 42 | | Enrichment Score: 0.88 | Count | P\_Value | Benjamini |
|  | UP\_KW\_CELLULAR\_COMPONENT | Cell wall | 26 | 1.6E-2 | 1.4E-1 |
|  | INTERPRO | Pectin\_lyas\_fold | 14 | 2.1E-2 | 5.9E-1 |
|  | INTERPRO | Pectin\_lyase\_fold/virulence | 14 | 2.3E-2 | 6.1E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Pectinesterase catalytic | 4 | 1.8E-1 | 1.0E0 |
|  | KEGG\_PATHWAY | Pentose and glucuronate interconversions | 10 | 1.9E-1 | 7.4E-1 |
|  | INTERPRO | Pectinesterase\_cat | 6 | 2.0E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | pectinesterase activity | 6 | 2.2E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | cell wall modification | 6 | 2.5E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | pectin catabolic process | 5 | 3.4E-1 | 1.0E0 |
|  | INTERPRO | Pectinesterase\_Asp\_AS | 4 | 4.2E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | pectinesterase inhibitor activity | 4 | 4.8E-1 | 1.0E0 |
| Annotation Cluster 43 | | Enrichment Score: 0.87 | Count | P\_Value | Benjamini |
|  | GOTERM\_MF\_DIRECT | procollagen-proline 4-dioxygenase activity | 3 | 8.6E-2 | 8.3E-1 |
|  | INTERPRO | P4HA-like | 3 | 9.2E-2 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | peptidyl-proline hydroxylation to 4-hydroxy-L-proline | 3 | 9.7E-2 | 8.9E-1 |
|  | INTERPRO | Pro\_4\_hyd\_alph\_FE2OG\_OXY | 3 | 1.0E-1 | 1.0E0 |
|  | INTERPRO | Pro\_4\_hyd\_alph | 3 | 1.3E-1 | 1.0E0 |
|  | SMART | P4Hc | 3 | 1.8E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | L-ascorbic acid binding | 3 | 2.3E-1 | 1.0E0 |
|  | KEGG\_PATHWAY | Arginine and proline metabolism | 6 | 2.8E-1 | 8.9E-1 |
| Annotation Cluster 44 | | Enrichment Score: 0.86 | Count | P\_Value | Benjamini |
|  | INTERPRO | MATE\_euk | 5 | 7.2E-2 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | xenobiotic detoxification by transmembrane export across the plasma membrane | 5 | 8.9E-2 | 8.9E-1 |
|  | GOTERM\_MF\_DIRECT | xenobiotic transmembrane transporter activity | 5 | 1.6E-1 | 1.0E0 |
|  | INTERPRO | MATE\_fam | 5 | 1.7E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | antiporter activity | 10 | 2.7E-1 | 1.0E0 |
| Annotation Cluster 45 | | Enrichment Score: 0.84 | Count | P\_Value | Benjamini |
|  | INTERPRO | PLAT/LH2\_dom\_sf | 9 | 2.3E-5 | 1.9E-3 |
|  | GOTERM\_MF\_DIRECT | oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen | 7 | 4.7E-3 | 9.1E-2 |
|  | UP\_SEQ\_FEATURE | DOMAIN:PLAT | 4 | 5.1E-2 | 8.1E-1 |
|  | INTERPRO | PLAT/LH2\_dom | 4 | 6.0E-2 | 1.0E0 |
|  | INTERPRO | LipOase\_Fe\_BS | 3 | 1.7E-1 | 1.0E0 |
|  | INTERPRO | Lipoxygenase\_dom\_3 | 3 | 1.8E-1 | 1.0E0 |
|  | INTERPRO | LipOase\_CS | 3 | 2.4E-1 | 1.0E0 |
|  | INTERPRO | LipOase\_plant | 3 | 2.5E-1 | 1.0E0 |
|  | SMART | LH2 | 3 | 2.5E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Lipoxygenase | 3 | 2.7E-1 | 1.0E0 |
|  | INTERPRO | LipOase\_C | 3 | 3.0E-1 | 1.0E0 |
|  | INTERPRO | LipOase\_C\_sf | 3 | 3.0E-1 | 1.0E0 |
|  | INTERPRO | LipOase | 3 | 3.0E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | fatty acid biosynthetic process | 7 | 3.1E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | oxylipin biosynthetic process | 3 | 3.5E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | lipid oxidation | 3 | 3.5E-1 | 1.0E0 |
|  | KEGG\_PATHWAY | Linoleic acid metabolism | 3 | 3.8E-1 | 1.0E0 |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Fatty acid metabolism | 5 | 5.1E-1 | 1.0E0 |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Fatty acid biosynthesis | 3 | 6.5E-1 | 1.0E0 |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Lipid metabolism | 12 | 6.8E-1 | 1.0E0 |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Lipid biosynthesis | 5 | 7.2E-1 | 1.0E0 |
| Annotation Cluster 46 | | Enrichment Score: 0.83 | Count | P\_Value | Benjamini |
|  | GOTERM\_MF\_DIRECT | cysteine-type endopeptidase inhibitor activity | 4 | 5.0E-2 | 5.9E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Cystatin | 3 | 1.3E-1 | 1.0E0 |
|  | UP\_KW\_MOLECULAR\_FUNCTION | Thiol protease inhibitor | 3 | 1.4E-1 | 1.0E0 |
|  | INTERPRO | Cystatin\_dom | 3 | 1.5E-1 | 1.0E0 |
|  | INTERPRO | Cystatin\_sf | 3 | 1.9E-1 | 1.0E0 |
|  | UP\_KW\_MOLECULAR\_FUNCTION | Protease inhibitor | 3 | 3.9E-1 | 1.0E0 |
| Annotation Cluster 47 | | Enrichment Score: 0.82 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:Rhodanese | 3 | 1.4E-1 | 1.0E0 |
|  | INTERPRO | Rhodanese-like\_dom\_sf | 3 | 1.5E-1 | 1.0E0 |
|  | INTERPRO | Rhodanese-like\_dom | 3 | 1.6E-1 | 1.0E0 |
|  | SMART | RHOD | 3 | 1.7E-1 | 1.0E0 |
| Annotation Cluster 48 | | Enrichment Score: 0.82 | Count | P\_Value | Benjamini |
|  | INTERPRO | CRAL/TRIO\_N\_dom | 4 | 6.5E-2 | 1.0E0 |
|  | INTERPRO | CRAL/TRIO\_N\_dom\_sf | 4 | 9.5E-2 | 1.0E0 |
|  | SMART | CRAL\_TRIO\_N | 4 | 1.0E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:CRAL-TRIO | 4 | 1.9E-1 | 1.0E0 |
|  | INTERPRO | CRAL-TRIO\_dom | 4 | 2.3E-1 | 1.0E0 |
|  | INTERPRO | CRAL-TRIO\_dom\_sf | 4 | 2.4E-1 | 1.0E0 |
|  | SMART | SEC14 | 4 | 3.0E-1 | 1.0E0 |
| Annotation Cluster 49 | | Enrichment Score: 0.81 | Count | P\_Value | Benjamini |
|  | UP\_KW\_LIGAND | Flavoprotein | 11 | 5.7E-2 | 3.8E-1 |
|  | GOTERM\_MF\_DIRECT | FAD binding | 7 | 6.0E-2 | 6.4E-1 |
|  | INTERPRO | Oxid\_FAD\_bind\_N | 4 | 1.5E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:FAD-binding PCMH-type | 4 | 1.7E-1 | 1.0E0 |
|  | UP\_KW\_LIGAND | FAD | 10 | 1.9E-1 | 6.5E-1 |
|  | INTERPRO | FAD-bd\_PCMH | 4 | 1.9E-1 | 1.0E0 |
|  | INTERPRO | FAD-bd\_PCMH\_sub2 | 4 | 1.9E-1 | 1.0E0 |
|  | INTERPRO | FAD-bd\_PCMH-like\_sf | 4 | 2.2E-1 | 1.0E0 |
|  | INTERPRO | FAD-bd\_PCMH\_sub1 | 3 | 3.6E-1 | 1.0E0 |
| Annotation Cluster 50 | | Enrichment Score: 0.78 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:Gnk2-homologous | 4 | 1.5E-1 | 1.0E0 |
|  | INTERPRO | GNK2\_sf | 4 | 1.7E-1 | 1.0E0 |
|  | INTERPRO | GNK2 | 4 | 1.8E-1 | 1.0E0 |
| Annotation Cluster 51 | | Enrichment Score: 0.77 | Count | P\_Value | Benjamini |
|  | INTERPRO | Formin-like\_plant | 3 | 8.2E-2 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | actin nucleation | 3 | 8.7E-2 | 8.9E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:FH2 | 3 | 1.6E-1 | 1.0E0 |
|  | INTERPRO | FH2\_Formin\_sf | 3 | 1.7E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | actin cytoskeleton organization | 3 | 1.8E-1 | 1.0E0 |
|  | INTERPRO | FH2\_Formin | 3 | 1.8E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | actin filament binding | 5 | 6.9E-1 | 1.0E0 |
| Annotation Cluster 52 | | Enrichment Score: 0.75 | Count | P\_Value | Benjamini |
|  | INTERPRO | Iah1-like | 3 | 4.7E-2 | 8.8E-1 |
|  | INTERPRO | SGNH\_hydro\_sf | 8 | 1.0E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | hydrolase activity, acting on ester bonds | 9 | 1.1E-1 | 9.2E-1 |
|  | INTERPRO | GDSL | 7 | 1.6E-1 | 1.0E0 |
|  | INTERPRO | SGNH\_plant\_lipase-like | 4 | 4.9E-1 | 1.0E0 |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Lipid degradation | 3 | 8.6E-1 | 1.0E0 |
| Annotation Cluster 53 | | Enrichment Score: 0.73 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:Calponin-homology (CH) | 3 | 1.3E-1 | 1.0E0 |
|  | INTERPRO | CH\_dom | 3 | 1.5E-1 | 1.0E0 |
|  | INTERPRO | CH\_dom\_sf | 3 | 3.5E-1 | 1.0E0 |
| Annotation Cluster 54 | | Enrichment Score: 0.7 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:N-acetyltransferase | 4 | 1.6E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | acyltransferase activity, transferring groups other than amino-acyl groups | 8 | 1.7E-1 | 1.0E0 |
|  | INTERPRO | GNAT\_dom | 4 | 1.8E-1 | 1.0E0 |
|  | INTERPRO | Acyl\_CoA\_acyltransferase | 4 | 3.1E-1 | 1.0E0 |
| Annotation Cluster 55 | | Enrichment Score: 0.66 | Count | P\_Value | Benjamini |
|  | GOTERM\_BP\_DIRECT | carbohydrate metabolic process | 30 | 3.0E-2 | 4.7E-1 |
|  | GOTERM\_MF\_DIRECT | hydrolase activity, hydrolyzing O-glycosyl compounds | 12 | 2.4E-1 | 1.0E0 |
|  | UP\_KW\_MOLECULAR\_FUNCTION | Glycosidase | 21 | 5.7E-1 | 1.0E0 |
|  | INTERPRO | Glycoside\_hydrolase\_SF | 14 | 5.7E-1 | 1.0E0 |
| Annotation Cluster 56 | | Enrichment Score: 0.65 | Count | P\_Value | Benjamini |
|  | INTERPRO | Glyco\_hydro\_9\_Asp/Glu\_AS | 3 | 3.9E-2 | 8.0E-1 |
|  | INTERPRO | Glyco\_hydro\_9\_His\_AS | 3 | 1.8E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Glycoside hydrolase family 9 | 3 | 2.9E-1 | 1.0E0 |
|  | INTERPRO | 6-hairpin\_glycosidase\_sf | 4 | 3.0E-1 | 1.0E0 |
|  | INTERPRO | Glyco\_hydro\_9 | 3 | 3.5E-1 | 1.0E0 |
|  | INTERPRO | 6hp\_glycosidase-like\_sf | 4 | 3.5E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | cellulose catabolic process | 3 | 3.7E-1 | 1.0E0 |
| Annotation Cluster 57 | | Enrichment Score: 0.63 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:Phytocyanin | 5 | 1.2E-1 | 1.0E0 |
|  | INTERPRO | Phytocyanin-like | 5 | 1.2E-1 | 1.0E0 |
|  | INTERPRO | Phytocyanin\_dom | 5 | 1.4E-1 | 1.0E0 |
|  | INTERPRO | Cupredoxin | 5 | 5.5E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | electron transfer activity | 5 | 5.9E-1 | 1.0E0 |
| Annotation Cluster 58 | | Enrichment Score: 0.63 | Count | P\_Value | Benjamini |
|  | INTERPRO | SWEET | 3 | 1.7E-1 | 1.0E0 |
|  | INTERPRO | SWEET\_rpt | 3 | 1.7E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | sugar transmembrane transporter activity | 3 | 2.9E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | carbohydrate transport | 3 | 3.6E-1 | 1.0E0 |
| Annotation Cluster 59 | | Enrichment Score: 0.62 | Count | P\_Value | Benjamini |
|  | KEGG\_PATHWAY | Mismatch repair | 6 | 9.8E-2 | 6.1E-1 |
|  | KEGG\_PATHWAY | Homologous recombination | 6 | 1.6E-1 | 7.4E-1 |
|  | KEGG\_PATHWAY | Nucleotide excision repair | 4 | 8.5E-1 | 1.0E0 |
| Annotation Cluster 60 | | Enrichment Score: 0.59 | Count | P\_Value | Benjamini |
|  | GOTERM\_BP\_DIRECT | response to symbiotic fungus | 6 | 1.3E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | REGION:VHIID | 3 | 2.0E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | REGION:Leucine repeat II (LRII) | 3 | 2.5E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | MOTIF:VHIID | 3 | 2.7E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | REGION:SAW | 3 | 3.7E-1 | 1.0E0 |
|  | INTERPRO | TF\_GRAS | 3 | 4.0E-1 | 1.0E0 |
| Annotation Cluster 61 | | Enrichment Score: 0.56 | Count | P\_Value | Benjamini |
|  | INTERPRO | AP2/ERF\_ERF\_subfamily | 3 | 1.0E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:AP2/ERF | 6 | 2.6E-1 | 1.0E0 |
|  | INTERPRO | AP2/ERF\_dom | 6 | 3.1E-1 | 1.0E0 |
|  | INTERPRO | AP2/ERF\_dom\_sf | 6 | 3.1E-1 | 1.0E0 |
|  | INTERPRO | DNA-bd\_dom\_sf | 6 | 3.8E-1 | 1.0E0 |
|  | SMART | AP2 | 6 | 4.5E-1 | 1.0E0 |
| Annotation Cluster 62 | | Enrichment Score: 0.55 | Count | P\_Value | Benjamini |
|  | INTERPRO | Plant\_LTP/defense-related | 3 | 1.5E-1 | 1.0E0 |
|  | INTERPRO | Hydrophob\_seed\_dom | 3 | 1.5E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Bifunctional inhibitor/plant lipid transfer protein/seed storage helical | 7 | 2.9E-1 | 1.0E0 |
|  | INTERPRO | Bifunc\_inhib/LTP/seed\_store | 7 | 3.4E-1 | 1.0E0 |
|  | INTERPRO | Bifun\_inhib/LTP/seed\_sf | 7 | 3.8E-1 | 1.0E0 |
|  | SMART | AAI | 5 | 6.4E-1 | 1.0E0 |
| Annotation Cluster 63 | | Enrichment Score: 0.52 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:PHD-type | 7 | 5.4E-2 | 8.3E-1 |
|  | INTERPRO | Znf\_PHD-finger | 5 | 3.6E-1 | 1.0E0 |
|  | INTERPRO | Znf\_PHD | 5 | 4.0E-1 | 1.0E0 |
|  | SMART | PHD | 5 | 5.5E-1 | 1.0E0 |
|  | INTERPRO | Znf\_FYVE\_PHD | 5 | 6.2E-1 | 1.0E0 |
| Annotation Cluster 64 | | Enrichment Score: 0.52 | Count | P\_Value | Benjamini |
|  | GOTERM\_MF\_DIRECT | antiporter activity | 10 | 2.7E-1 | 1.0E0 |
|  | INTERPRO | TPT\_transporter | 4 | 2.9E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Sugar phosphate transporter | 4 | 3.1E-1 | 1.0E0 |
|  | INTERPRO | Sugar\_P\_trans\_dom | 4 | 3.7E-1 | 1.0E0 |
| Annotation Cluster 65 | | Enrichment Score: 0.5 | Count | P\_Value | Benjamini |
|  | GOTERM\_MF\_DIRECT | DNA-binding transcription factor activity | 42 | 5.9E-2 | 6.4E-1 |
|  | GOTERM\_BP\_DIRECT | regulation of DNA-templated transcription | 48 | 3.5E-1 | 1.0E0 |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Transcription regulation | 62 | 6.4E-1 | 1.0E0 |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Transcription | 62 | 7.8E-1 | 1.0E0 |
| Annotation Cluster 66 | | Enrichment Score: 0.49 | Count | P\_Value | Benjamini |
|  | GOTERM\_BP\_DIRECT | response to symbiotic fungus | 6 | 1.3E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:PA | 4 | 1.6E-1 | 1.0E0 |
|  | INTERPRO | Peptidases\_S8\_3 | 5 | 1.7E-1 | 1.0E0 |
|  | INTERPRO | PA\_dom\_sf | 3 | 2.2E-1 | 1.0E0 |
|  | INTERPRO | Peptidase\_S8\_subtilisin-rel | 5 | 2.2E-1 | 1.0E0 |
|  | INTERPRO | PA\_domain | 4 | 2.3E-1 | 1.0E0 |
|  | INTERPRO | S8pro/Inhibitor\_I9\_sf | 5 | 2.9E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | serine-type endopeptidase activity | 10 | 3.5E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Subtilisin-like protease fibronectin type-III | 4 | 3.6E-1 | 1.0E0 |
|  | INTERPRO | Subtilisin-like\_FN3 | 4 | 4.0E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Inhibitor I9 | 4 | 4.1E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Peptidase S8/S53 | 5 | 4.1E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | ACT\_SITE:Charge relay system | 4 | 4.6E-1 | 1.0E0 |
|  | INTERPRO | SBT | 5 | 4.7E-1 | 1.0E0 |
|  | INTERPRO | Peptidase\_S8/S53\_dom | 5 | 4.7E-1 | 1.0E0 |
|  | INTERPRO | S8pro/Inhibitor\_I9 | 4 | 4.7E-1 | 1.0E0 |
|  | INTERPRO | Peptidase\_S8/S53\_dom\_sf | 5 | 6.2E-1 | 1.0E0 |
|  | INTERPRO | Peptidase\_S8\_Ser-AS | 3 | 6.5E-1 | 1.0E0 |
| Annotation Cluster 67 | | Enrichment Score: 0.44 | Count | P\_Value | Benjamini |
|  | INTERPRO | PB1\_dom | 3 | 3.3E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:PB1 | 4 | 3.6E-1 | 1.0E0 |
|  | SMART | PB1 | 3 | 4.0E-1 | 1.0E0 |
| Annotation Cluster 68 | | Enrichment Score: 0.42 | Count | P\_Value | Benjamini |
|  | INTERPRO | MS5/SDI1 | 3 | 1.9E-2 | 5.7E-1 |
|  | INTERPRO | TPR\_rpt | 5 | 6.5E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | REPEAT:TPR | 4 | 6.8E-1 | 1.0E0 |
|  | SMART | TPR | 3 | 9.6E-1 | 1.0E0 |
|  | INTERPRO | TPR-like\_helical\_dom\_sf | 9 | 1.0E0 | 1.0E0 |
| Annotation Cluster 69 | | Enrichment Score: 0.41 | Count | P\_Value | Benjamini |
|  | UP\_KW\_LIGAND | ATP-binding | 67 | 8.2E-2 | 4.4E-1 |
|  | GOTERM\_MF\_DIRECT | ATP binding | 106 | 4.4E-1 | 1.0E0 |
|  | UP\_KW\_LIGAND | Nucleotide-binding | 54 | 6.7E-1 | 1.0E0 |
|  | INTERPRO | P-loop\_NTPase | 50 | 9.3E-1 | 1.0E0 |
| Annotation Cluster 70 | | Enrichment Score: 0.41 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:Enoyl reductase (ER) | 3 | 3.1E-1 | 1.0E0 |
|  | INTERPRO | PKS\_ER | 3 | 3.3E-1 | 1.0E0 |
|  | SMART | PKS\_ER | 3 | 4.2E-1 | 1.0E0 |
|  | INTERPRO | GroES-like\_sf | 4 | 4.4E-1 | 1.0E0 |
|  | INTERPRO | ADH-like\_C | 3 | 4.9E-1 | 1.0E0 |
| Annotation Cluster 71 | | Enrichment Score: 0.4 | Count | P\_Value | Benjamini |
|  | INTERPRO | ABC\_transporter-like\_CS | 8 | 1.2E-1 | 1.0E0 |
|  | GOTERM\_CC\_DIRECT | vacuolar membrane | 8 | 1.4E-1 | 1.0E0 |
|  | INTERPRO | ABCG\_transporters | 3 | 1.6E-1 | 1.0E0 |
|  | INTERPRO | AAA+\_ATPase | 15 | 2.1E-1 | 1.0E0 |
|  | KEGG\_PATHWAY | Folate transport and metabolism | 5 | 2.6E-1 | 8.9E-1 |
|  | INTERPRO | ABCC\_6TM\_D1 | 3 | 2.9E-1 | 1.0E0 |
|  | KEGG\_PATHWAY | ABC transporters | 6 | 3.8E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:ABC transporter | 8 | 4.0E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | ABC-type transporter activity | 8 | 4.0E-1 | 1.0E0 |
|  | INTERPRO | ABCC\_6TM\_D2 | 3 | 4.0E-1 | 1.0E0 |
|  | SMART | AAA | 15 | 4.5E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:ABC transmembrane type-1 | 5 | 4.5E-1 | 1.0E0 |
|  | INTERPRO | ABC\_transporter-like\_ATP-bd | 8 | 4.9E-1 | 1.0E0 |
|  | INTERPRO | ABC1\_TM\_dom | 5 | 5.1E-1 | 1.0E0 |
|  | INTERPRO | ABC1\_TM\_sf | 5 | 6.1E-1 | 1.0E0 |
|  | INTERPRO | ABC\_transporter\_C-like | 3 | 6.1E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | ATP hydrolysis activity | 21 | 6.9E-1 | 1.0E0 |
|  | INTERPRO | ABC2\_TM | 3 | 6.9E-1 | 1.0E0 |
|  | GOTERM\_CC\_DIRECT | plant-type vacuole | 3 | 9.9E-1 | 1.0E0 |
|  | UP\_KW\_MOLECULAR\_FUNCTION | Translocase | 4 | 1.0E0 | 1.0E0 |
| Annotation Cluster 72 | | Enrichment Score: 0.4 | Count | P\_Value | Benjamini |
|  | INTERPRO | Dirigent | 3 | 3.0E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | phenylpropanoid biosynthetic process | 3 | 3.1E-1 | 1.0E0 |
|  | INTERPRO | Allene\_oxi\_cyc\_Dirigent | 3 | 3.5E-1 | 1.0E0 |
|  | UP\_KW\_CELLULAR\_COMPONENT | Apoplast | 8 | 8.0E-1 | 1.0E0 |
| Annotation Cluster 73 | | Enrichment Score: 0.39 | Count | P\_Value | Benjamini |
|  | KEGG\_PATHWAY | Isoquinoline alkaloid biosynthesis | 3 | 1.8E-1 | 7.4E-1 |
|  | KEGG\_PATHWAY | Phenylalanine metabolism | 3 | 4.8E-1 | 1.0E0 |
|  | KEGG\_PATHWAY | Tropane, piperidine and pyridine alkaloid biosynthesis | 3 | 5.5E-1 | 1.0E0 |
|  | KEGG\_PATHWAY | Tyrosine metabolism | 3 | 5.9E-1 | 1.0E0 |
| Annotation Cluster 74 | | Enrichment Score: 0.36 | Count | P\_Value | Benjamini |
|  | GOTERM\_BP\_DIRECT | hydrogen peroxide catabolic process | 7 | 1.9E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | response to oxidative stress | 8 | 2.4E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | SITE:Transition state stabilizer | 6 | 2.9E-1 | 1.0E0 |
|  | INTERPRO | Secretory\_peroxidase | 5 | 3.9E-1 | 1.0E0 |
|  | INTERPRO | Peroxidases\_heam-ligand\_BS | 5 | 4.2E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Plant heme peroxidase family profile | 5 | 4.3E-1 | 1.0E0 |
|  | INTERPRO | Peroxidase\_pln | 5 | 4.4E-1 | 1.0E0 |
|  | INTERPRO | Peroxidases\_AS | 4 | 4.7E-1 | 1.0E0 |
|  | INTERPRO | Haem\_peroxidase | 5 | 4.8E-1 | 1.0E0 |
|  | INTERPRO | Haem\_peroxidase\_sf | 5 | 5.2E-1 | 1.0E0 |
|  | KEGG\_PATHWAY | Phenylpropanoid biosynthesis | 9 | 5.7E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | peroxidase activity | 5 | 6.5E-1 | 1.0E0 |
|  | UP\_KW\_MOLECULAR\_FUNCTION | Peroxidase | 6 | 7.0E-1 | 1.0E0 |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Hydrogen peroxide | 4 | 7.1E-1 | 1.0E0 |
| Annotation Cluster 75 | | Enrichment Score: 0.35 | Count | P\_Value | Benjamini |
|  | GOTERM\_MF\_DIRECT | pyridoxal phosphate binding | 6 | 2.5E-1 | 1.0E0 |
|  | UP\_KW\_LIGAND | Pyridoxal phosphate | 5 | 2.5E-1 | 7.6E-1 |
|  | INTERPRO | PyrdxlP-dep\_Trfase\_major | 5 | 5.9E-1 | 1.0E0 |
|  | INTERPRO | PyrdxlP-dep\_Trfase\_small | 4 | 6.1E-1 | 1.0E0 |
|  | INTERPRO | PyrdxlP-dep\_Trfase | 4 | 7.8E-1 | 1.0E0 |
| Annotation Cluster 76 | | Enrichment Score: 0.34 | Count | P\_Value | Benjamini |
|  | INTERPRO | Oligpept\_transpt | 3 | 3.3E-1 | 1.0E0 |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Peptide transport | 3 | 4.2E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | oligopeptide transmembrane transporter activity | 3 | 5.4E-1 | 1.0E0 |
|  | INTERPRO | OPT | 3 | 5.6E-1 | 1.0E0 |
| Annotation Cluster 77 | | Enrichment Score: 0.31 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:GST N-terminal | 4 | 3.4E-1 | 1.0E0 |
|  | INTERPRO | GST\_C\_Tau | 3 | 3.7E-1 | 1.0E0 |
|  | INTERPRO | Omega/Tau-like | 3 | 3.8E-1 | 1.0E0 |
|  | INTERPRO | Glutathione\_S-Trfase\_N | 4 | 3.9E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:GST C-terminal | 3 | 5.1E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | glutathione metabolic process | 3 | 5.3E-1 | 1.0E0 |
|  | INTERPRO | Glutathione-S-Trfase\_C-like | 3 | 5.5E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | glutathione transferase activity | 3 | 5.7E-1 | 1.0E0 |
|  | KEGG\_PATHWAY | Glutathione metabolism | 5 | 6.5E-1 | 1.0E0 |
|  | INTERPRO | Glutathione-S-Trfase\_C\_sf | 3 | 7.1E-1 | 1.0E0 |
| Annotation Cluster 78 | | Enrichment Score: 0.31 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | REPEAT:Solcar | 4 | 4.1E-1 | 1.0E0 |
|  | INTERPRO | Mit\_carrier | 3 | 4.4E-1 | 1.0E0 |
|  | INTERPRO | Mitochondrial\_sb/sol\_carrier | 4 | 5.5E-1 | 1.0E0 |
|  | INTERPRO | Mt\_carrier\_dom\_sf | 4 | 5.9E-1 | 1.0E0 |
| Annotation Cluster 79 | | Enrichment Score: 0.31 | Count | P\_Value | Benjamini |
|  | GOTERM\_MF\_DIRECT | protein phosphatase 1 binding | 3 | 1.6E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:PGG | 3 | 3.8E-1 | 1.0E0 |
|  | INTERPRO | PGG\_dom | 3 | 4.2E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | REPEAT:ANK | 6 | 4.4E-1 | 1.0E0 |
|  | INTERPRO | Ankyrin\_rpt | 6 | 5.8E-1 | 1.0E0 |
|  | INTERPRO | Ankyrin\_rpt-contain\_sf | 6 | 6.5E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | protein phosphatase regulator activity | 3 | 6.7E-1 | 1.0E0 |
|  | UP\_KW\_DOMAIN | ANK repeat | 3 | 7.5E-1 | 1.0E0 |
|  | SMART | ANK | 5 | 7.8E-1 | 1.0E0 |
| Annotation Cluster 80 | | Enrichment Score: 0.3 | Count | P\_Value | Benjamini |
|  | INTERPRO | LRR\_N\_plant-typ | 15 | 3.4E-2 | 7.6E-1 |
|  | GOTERM\_BP\_DIRECT | protein phosphorylation | 38 | 2.2E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Protein kinase | 40 | 2.3E-1 | 1.0E0 |
|  | INTERPRO | Leu-rich\_rpt | 20 | 3.5E-1 | 1.0E0 |
|  | INTERPRO | Prot\_kinase\_dom | 40 | 3.8E-1 | 1.0E0 |
|  | UP\_KW\_DOMAIN | Leucine-rich repeat | 18 | 3.9E-1 | 9.9E-1 |
|  | GOTERM\_MF\_DIRECT | protein kinase activity | 30 | 4.0E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | ATP binding | 106 | 4.4E-1 | 1.0E0 |
|  | INTERPRO | Kinase-like\_dom\_sf | 42 | 5.2E-1 | 1.0E0 |
|  | INTERPRO | Ser-Thr/Tyr\_kinase\_cat\_dom | 15 | 6.5E-1 | 1.0E0 |
|  | INTERPRO | Leu-rich\_rpt\_typical-subtyp | 7 | 6.6E-1 | 1.0E0 |
|  | SMART | LRR\_TYP | 7 | 8.2E-1 | 1.0E0 |
|  | INTERPRO | LRR\_dom\_sf | 25 | 8.5E-1 | 1.0E0 |
|  | INTERPRO | Ser/Thr\_kinase\_AS | 23 | 8.7E-1 | 1.0E0 |
|  | INTERPRO | Protein\_kinase\_ATP\_BS | 18 | 8.9E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | protein serine/threonine kinase activity | 18 | 9.3E-1 | 1.0E0 |
|  | SMART | S\_TKc | 24 | 9.7E-1 | 1.0E0 |
|  | UP\_KW\_MOLECULAR\_FUNCTION | Serine/threonine-protein kinase | 15 | 9.9E-1 | 1.0E0 |
|  | UP\_KW\_MOLECULAR\_FUNCTION | Kinase | 36 | 1.0E0 | 1.0E0 |
| Annotation Cluster 81 | | Enrichment Score: 0.27 | Count | P\_Value | Benjamini |
|  | GOTERM\_BP\_DIRECT | amino acid transport | 7 | 2.2E-1 | 1.0E0 |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Amino-acid transport | 7 | 4.4E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Amino acid transporter transmembrane | 5 | 5.3E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | symporter activity | 6 | 5.6E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | auxin-activated signaling pathway | 9 | 5.7E-1 | 1.0E0 |
|  | INTERPRO | AA\_transpt\_TM | 5 | 6.2E-1 | 1.0E0 |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Auxin signaling pathway | 5 | 7.4E-1 | 1.0E0 |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Symport | 4 | 9.5E-1 | 1.0E0 |
| Annotation Cluster 82 | | Enrichment Score: 0.25 | Count | P\_Value | Benjamini |
|  | INTERPRO | C2CH-3rd\_BIRD-IDD | 3 | 2.5E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:C2H2-type | 6 | 4.9E-1 | 1.0E0 |
|  | INTERPRO | Znf\_C2H2\_type | 6 | 6.9E-1 | 1.0E0 |
|  | SMART | ZnF\_C2H2 | 3 | 7.3E-1 | 1.0E0 |
|  | INTERPRO | Znf\_C2H2\_sf | 6 | 8.7E-1 | 1.0E0 |
| Annotation Cluster 83 | | Enrichment Score: 0.24 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:EamA | 4 | 5.5E-1 | 1.0E0 |
|  | INTERPRO | EamA\_dom | 4 | 5.9E-1 | 1.0E0 |
|  | INTERPRO | WAT1-related | 4 | 6.0E-1 | 1.0E0 |
| Annotation Cluster 84 | | Enrichment Score: 0.23 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:H15 | 3 | 4.7E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | S-adenosylmethionine-dependent methyltransferase activity | 12 | 4.7E-1 | 1.0E0 |
|  | SMART | H15 | 3 | 4.9E-1 | 1.0E0 |
|  | INTERPRO | Histone\_H1/H5\_H15 | 3 | 5.0E-1 | 1.0E0 |
|  | INTERPRO | WH\_DNA-bd\_sf | 8 | 7.8E-1 | 1.0E0 |
|  | INTERPRO | WH-like\_DNA-bd\_sf | 7 | 9.6E-1 | 1.0E0 |
| Annotation Cluster 85 | | Enrichment Score: 0.23 | Count | P\_Value | Benjamini |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | ER-Golgi transport | 5 | 2.6E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | vesicle-mediated transport | 5 | 7.5E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | intracellular protein transport | 6 | 7.9E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | endoplasmic reticulum to Golgi vesicle-mediated transport | 3 | 8.2E-1 | 1.0E0 |
| Annotation Cluster 86 | | Enrichment Score: 0.2 | Count | P\_Value | Benjamini |
|  | GOTERM\_MF\_DIRECT | serine-type endopeptidase activity | 10 | 3.5E-1 | 1.0E0 |
|  | UP\_KW\_MOLECULAR\_FUNCTION | Serine protease | 4 | 4.5E-1 | 1.0E0 |
|  | UP\_KW\_MOLECULAR\_FUNCTION | Protease | 12 | 1.0E0 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | proteolysis | 22 | 1.0E0 | 1.0E0 |
| Annotation Cluster 87 | | Enrichment Score: 0.2 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:SET | 3 | 5.8E-1 | 1.0E0 |
|  | INTERPRO | SET\_dom | 3 | 6.1E-1 | 1.0E0 |
|  | INTERPRO | SET\_dom\_sf | 3 | 7.3E-1 | 1.0E0 |
| Annotation Cluster 88 | | Enrichment Score: 0.19 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:AB hydrolase-1 | 4 | 5.3E-1 | 1.0E0 |
|  | INTERPRO | AB\_hydrolase\_1 | 4 | 6.6E-1 | 1.0E0 |
|  | INTERPRO | AB\_hydrolase\_fold | 12 | 7.4E-1 | 1.0E0 |
| Annotation Cluster 89 | | Enrichment Score: 0.19 | Count | P\_Value | Benjamini |
|  | GOTERM\_BP\_DIRECT | methylation | 11 | 3.5E-1 | 1.0E0 |
|  | INTERPRO | SAM-dependent\_MTases\_sf | 10 | 7.6E-1 | 1.0E0 |
|  | UP\_KW\_LIGAND | S-adenosyl-L-methionine | 5 | 8.0E-1 | 1.0E0 |
|  | UP\_KW\_MOLECULAR\_FUNCTION | Methyltransferase | 8 | 8.2E-1 | 1.0E0 |
| Annotation Cluster 90 | | Enrichment Score: 0.18 | Count | P\_Value | Benjamini |
|  | INTERPRO | Aspartic\_peptidase\_A1 | 3 | 5.2E-1 | 1.0E0 |
|  | INTERPRO | TAXi\_C | 3 | 5.2E-1 | 1.0E0 |
|  | INTERPRO | TAXi\_N | 3 | 5.3E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Peptidase A1 | 3 | 5.8E-1 | 1.0E0 |
|  | INTERPRO | PEPTIDASE\_A1 | 3 | 6.1E-1 | 1.0E0 |
|  | INTERPRO | Peptidase\_aspartic\_dom\_sf | 3 | 1.0E0 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | aspartic-type endopeptidase activity | 5 | 1.0E0 | 1.0E0 |
| Annotation Cluster 91 | | Enrichment Score: 0.18 | Count | P\_Value | Benjamini |
|  | INTERPRO | AMP-binding\_CS | 3 | 5.7E-1 | 1.0E0 |
|  | INTERPRO | AMP-dep\_synth/lig\_dom | 3 | 7.0E-1 | 1.0E0 |
|  | INTERPRO | ANL\_N\_sf | 3 | 7.2E-1 | 1.0E0 |
| Annotation Cluster 92 | | Enrichment Score: 0.17 | Count | P\_Value | Benjamini |
|  | INTERPRO | Ser\_caboxypep\_ser\_AS | 3 | 4.4E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | serine-type carboxypeptidase activity | 3 | 7.0E-1 | 1.0E0 |
|  | INTERPRO | Peptidase\_S10 | 3 | 7.0E-1 | 1.0E0 |
|  | GOTERM\_CC\_DIRECT | vacuole | 5 | 9.4E-1 | 1.0E0 |
| Annotation Cluster 93 | | Enrichment Score: 0.17 | Count | P\_Value | Benjamini |
|  | INTERPRO | MFS | 4 | 3.5E-1 | 1.0E0 |
|  | GOTERM\_CC\_DIRECT | plant-type vacuole membrane | 4 | 7.7E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Major facilitator superfamily (MFS) profile | 6 | 8.6E-1 | 1.0E0 |
|  | INTERPRO | MFS\_dom | 6 | 9.0E-1 | 1.0E0 |
| Annotation Cluster 94 | | Enrichment Score: 0.15 | Count | P\_Value | Benjamini |
|  | UP\_KW\_LIGAND | 4Fe-4S | 3 | 6.3E-1 | 1.0E0 |
|  | UP\_KW\_LIGAND | Iron-sulfur | 4 | 7.3E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | 4 iron, 4 sulfur cluster binding | 3 | 7.5E-1 | 1.0E0 |
| Annotation Cluster 95 | | Enrichment Score: 0.15 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:Myb-like | 10 | 5.0E-1 | 1.0E0 |
|  | INTERPRO | Myb\_dom\_plants | 4 | 5.6E-1 | 1.0E0 |
|  | INTERPRO | SANT/Myb | 12 | 6.0E-1 | 1.0E0 |
|  | INTERPRO | Homeodomain-like\_sf | 13 | 8.3E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:HTH myb-type | 7 | 8.4E-1 | 1.0E0 |
|  | INTERPRO | Myb\_dom | 7 | 8.8E-1 | 1.0E0 |
|  | SMART | SANT | 8 | 9.1E-1 | 1.0E0 |
| Annotation Cluster 96 | | Enrichment Score: 0.14 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:Homeobox | 4 | 6.3E-1 | 1.0E0 |
|  | INTERPRO | HD | 4 | 6.7E-1 | 1.0E0 |
|  | SMART | HOX | 4 | 7.9E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DNA\_BIND:Homeobox | 3 | 7.9E-1 | 1.0E0 |
| Annotation Cluster 97 | | Enrichment Score: 0.13 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:RING-type | 15 | 5.7E-1 | 1.0E0 |
|  | INTERPRO | Znf\_RING | 15 | 6.7E-1 | 1.0E0 |
|  | INTERPRO | Znf\_RING\_CS | 5 | 7.1E-1 | 1.0E0 |
|  | INTERPRO | Znf\_RING/FYVE/PHD | 22 | 7.9E-1 | 1.0E0 |
|  | SMART | RING | 12 | 8.4E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | ubiquitin-protein transferase activity | 5 | 8.8E-1 | 1.0E0 |
| Annotation Cluster 98 | | Enrichment Score: 0.13 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | REPEAT:ARM | 3 | 5.0E-1 | 1.0E0 |
|  | INTERPRO | Armadillo | 3 | 7.9E-1 | 1.0E0 |
|  | SMART | ARM | 3 | 8.1E-1 | 1.0E0 |
|  | INTERPRO | ARM-like | 9 | 9.7E-1 | 1.0E0 |
| Annotation Cluster 99 | | Enrichment Score: 0.12 | Count | P\_Value | Benjamini |
|  | INTERPRO | ATPase\_AAA\_CS | 3 | 6.6E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:AAA+ ATPase | 4 | 7.7E-1 | 1.0E0 |
|  | INTERPRO | ATPase\_AAA\_core | 4 | 8.5E-1 | 1.0E0 |
| Annotation Cluster 100 | | Enrichment Score: 0.11 | Count | P\_Value | Benjamini |
|  | INTERPRO | SNF2/RAD54-like\_C | 3 | 5.5E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | ATP-dependent chromatin remodeler activity | 3 | 5.6E-1 | 1.0E0 |
|  | INTERPRO | SNF2\_N | 3 | 7.0E-1 | 1.0E0 |
|  | INTERPRO | SNF2-like\_sf | 3 | 7.2E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | hydrolase activity | 15 | 7.4E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Helicase ATP-binding | 6 | 7.5E-1 | 1.0E0 |
|  | INTERPRO | Helicase\_ATP-bd | 6 | 8.0E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Helicase C-terminal | 6 | 8.1E-1 | 1.0E0 |
|  | SMART | DEXDc | 6 | 8.3E-1 | 1.0E0 |
|  | INTERPRO | Helicase\_C-like | 6 | 8.5E-1 | 1.0E0 |
|  | SMART | HELICc | 6 | 9.2E-1 | 1.0E0 |
|  | INTERPRO | DEAD/DEAH\_box\_helicase\_dom | 3 | 9.4E-1 | 1.0E0 |
|  | UP\_KW\_MOLECULAR\_FUNCTION | Helicase | 11 | 9.7E-1 | 1.0E0 |
| Annotation Cluster 101 | | Enrichment Score: 0.08 | Count | P\_Value | Benjamini |
|  | GOTERM\_CC\_DIRECT | side of membrane | 4 | 6.6E-1 | 1.0E0 |
|  | UP\_KW\_PTM | GPI-anchor | 4 | 8.8E-1 | 1.0E0 |
|  | UP\_KW\_PTM | Lipoprotein | 7 | 9.9E-1 | 1.0E0 |
| Annotation Cluster 102 | | Enrichment Score: 0.06 | Count | P\_Value | Benjamini |
|  | INTERPRO | F-box\_AtFBL13-like | 3 | 6.1E-1 | 1.0E0 |
|  | INTERPRO | F-box\_dom | 8 | 9.2E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:F-box | 7 | 9.3E-1 | 1.0E0 |
|  | INTERPRO | F-box-like\_dom\_sf | 8 | 9.6E-1 | 1.0E0 |
|  | SMART | FBOX | 3 | 9.9E-1 | 1.0E0 |
| Annotation Cluster 103 | | Enrichment Score: 0.02 | Count | P\_Value | Benjamini |
|  | INTERPRO | G-protein\_beta\_WD-40\_rep | 3 | 8.4E-1 | 1.0E0 |
|  | INTERPRO | WD40\_repeat\_CS | 3 | 9.7E-1 | 1.0E0 |
|  | INTERPRO | WD40\_rpt | 6 | 9.8E-1 | 1.0E0 |
|  | INTERPRO | WD40/YVTN\_repeat-like\_dom\_sf | 7 | 9.9E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | REPEAT:WD | 4 | 9.9E-1 | 1.0E0 |
|  | SMART | WD40 | 6 | 1.0E0 | 1.0E0 |
|  | INTERPRO | WD40\_repeat\_dom\_sf | 5 | 1.0E0 | 1.0E0 |
| Annotation Cluster 104 | | Enrichment Score: 0.01 | Count | P\_Value | Benjamini |
|  | SMART | EFh | 3 | 9.6E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:EF-hand | 3 | 9.6E-1 | 1.0E0 |
|  | INTERPRO | EF\_hand\_dom | 3 | 9.7E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | calcium ion binding | 5 | 9.8E-1 | 1.0E0 |
|  | INTERPRO | EF-hand-dom\_pair | 3 | 9.9E-1 | 1.0E0 |
| Annotation Cluster 105 | | Enrichment Score: 0.01 | Count | P\_Value | Benjamini |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Stress response | 4 | 9.4E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | unfolded protein binding | 4 | 9.9E-1 | 1.0E0 |
|  | KEGG\_PATHWAY | Protein processing in endoplasmic reticulum | 6 | 1.0E0 | 1.0E0 |
| Annotation Cluster 106 | | Enrichment Score: 0 | Count | P\_Value | Benjamini |
|  | GOTERM\_CC\_DIRECT | cytosolic small ribosomal subunit | 3 | 9.7E-1 | 1.0E0 |
|  | UP\_KW\_MOLECULAR\_FUNCTION | Ribosomal protein | 4 | 9.8E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | structural constituent of ribosome | 8 | 1.0E0 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | translation | 8 | 1.0E0 | 1.0E0 |
|  | GOTERM\_CC\_DIRECT | ribosome | 7 | 1.0E0 | 1.0E0 |
|  | UP\_KW\_MOLECULAR\_FUNCTION | Ribonucleoprotein | 6 | 1.0E0 | 1.0E0 |
|  | KEGG\_PATHWAY | Ribosome | 7 | 1.0E0 | 1.0E0 |
| Annotation Cluster 107 | | Enrichment Score: 0 | Count | P\_Value | Benjamini |
|  | INTERPRO | RBD\_domain\_sf | 6 | 1.0E0 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:RRM | 4 | 1.0E0 | 1.0E0 |
|  | INTERPRO | RRM\_dom | 4 | 1.0E0 | 1.0E0 |
|  | INTERPRO | Nucleotide-bd\_a/b\_plait\_sf | 4 | 1.0E0 | 1.0E0 |
|  | SMART | RRM | 4 | 1.0E0 | 1.0E0 |
| Annotation Cluster 108 | | Enrichment Score: 0 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | REPEAT:PPR | 4 | 1.0E0 | 1.0E0 |
|  | INTERPRO | TPR-like\_helical\_dom\_sf | 9 | 1.0E0 | 1.0E0 |
|  | INTERPRO | Pentatricopeptide\_rpt | 4 | 1.0E0 | 1.0E0 |

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| **Functional Annotation Clustering**  **Current Gene List: up**  **Current Background: *Pisum sativum***  **2924 DAVID IDs**  **197 Cluster(s)** | | | | | |
| Annotation Cluster 1 | | Enrichment Score: 33.07 | Count | P\_Value | Benjamini |
|  | GOTERM\_BP\_DIRECT | protein phosphorylation | 224 | 4.7E-60 | 2.5E-57 |
|  | INTERPRO | Ser/Thr\_kinase\_AS | 190 | 5.0E-51 | 9.7E-48 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Protein kinase | 217 | 7.0E-51 | 1.9E-48 |
|  | INTERPRO | Prot\_kinase\_dom | 217 | 1.2E-45 | 1.2E-42 |
|  | GOTERM\_MF\_DIRECT | protein kinase activity | 180 | 1.1E-44 | 5.1E-42 |
|  | INTERPRO | Protein\_kinase\_ATP\_BS | 152 | 5.0E-40 | 3.2E-37 |
|  | INTERPRO | Kinase-like\_dom\_sf | 220 | 1.1E-39 | 5.2E-37 |
|  | SMART | S\_TKc | 180 | 9.8E-37 | 1.7E-34 |
|  | GOTERM\_MF\_DIRECT | protein serine/threonine kinase activity | 145 | 9.3E-33 | 1.4E-30 |
|  | INTERPRO | Ser-Thr/Tyr\_kinase\_cat\_dom | 91 | 3.9E-20 | 7.5E-18 |
|  | UP\_KW\_MOLECULAR\_FUNCTION | Kinase | 193 | 1.3E-17 | 8.6E-16 |
|  | GOTERM\_MF\_DIRECT | ATP binding | 322 | 3.9E-14 | 1.8E-12 |
|  | UP\_KW\_MOLECULAR\_FUNCTION | Serine/threonine-protein kinase | 101 | 1.8E-12 | 6.1E-11 |
|  | UP\_KW\_MOLECULAR\_FUNCTION | Transferase | 339 | 3.1E-7 | 6.3E-6 |
| Annotation Cluster 2 | | Enrichment Score: 29.62 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | TRANSMEM:Helical | 811 | 5.8E-66 | 3.1E-63 |
|  | UP\_KW\_DOMAIN | Transmembrane | 800 | 1.3E-40 | 2.7E-39 |
|  | GOTERM\_CC\_DIRECT | membrane | 698 | 2.5E-19 | 1.4E-17 |
|  | UP\_KW\_DOMAIN | Transmembrane helix | 560 | 1.3E-18 | 9.0E-18 |
|  | UP\_KW\_CELLULAR\_COMPONENT | Membrane | 873 | 3.0E-7 | 2.8E-6 |
| Annotation Cluster 3 | | Enrichment Score: 25.72 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:WRKY | 45 | 4.0E-29 | 7.1E-27 |
|  | INTERPRO | WRKY\_dom | 45 | 8.3E-28 | 3.2E-25 |
|  | INTERPRO | WRKY\_dom\_sf | 45 | 2.6E-27 | 8.4E-25 |
|  | INTERPRO | WRKY\_plant | 44 | 3.4E-27 | 9.4E-25 |
|  | SMART | WRKY | 44 | 1.1E-23 | 9.4E-22 |
|  | GOTERM\_MF\_DIRECT | sequence-specific DNA binding | 77 | 1.4E-23 | 1.3E-21 |
| Annotation Cluster 4 | | Enrichment Score: 15.34 | Count | P\_Value | Benjamini |
|  | GOTERM\_BP\_DIRECT | defense response | 98 | 9.7E-32 | 2.6E-29 |
|  | GOTERM\_MF\_DIRECT | ADP binding | 71 | 4.6E-25 | 5.4E-23 |
|  | INTERPRO | Apaf\_helical | 60 | 8.7E-24 | 2.1E-21 |
|  | INTERPRO | NB-ARC | 61 | 4.3E-23 | 9.1E-21 |
|  | GOTERM\_BP\_DIRECT | defense response to other organism | 54 | 1.3E-22 | 1.8E-20 |
|  | UP\_SEQ\_FEATURE | DOMAIN:NB-ARC | 47 | 3.8E-19 | 4.0E-17 |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Plant defense | 76 | 7.4E-19 | 6.6E-17 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Disease resistance N-terminal | 24 | 3.7E-11 | 2.0E-9 |
|  | INTERPRO | RX-like\_CC | 17 | 9.4E-11 | 5.5E-9 |
|  | INTERPRO | Rx\_N | 24 | 1.6E-10 | 9.1E-9 |
|  | INTERPRO | WH-like\_DNA-bd\_sf | 45 | 1.4E-5 | 2.8E-4 |
|  | GOTERM\_BP\_DIRECT | response to other organism | 17 | 1.5E-5 | 3.6E-4 |
|  | INTERPRO | P-loop\_NTPase | 125 | 4.3E-1 | 1.0E0 |
| Annotation Cluster 5 | | Enrichment Score: 14.67 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | BINDING:axial binding residue | 83 | 2.9E-22 | 3.8E-20 |
|  | INTERPRO | Cyt\_P450 | 62 | 8.9E-19 | 1.3E-16 |
|  | INTERPRO | Cyt\_P450\_sf | 62 | 1.6E-18 | 2.2E-16 |
|  | INTERPRO | Cyt\_P450\_E\_grp-I | 58 | 6.2E-18 | 7.9E-16 |
|  | UP\_KW\_LIGAND | Iron | 125 | 7.4E-18 | 2.6E-16 |
|  | UP\_KW\_LIGAND | Heme | 81 | 1.7E-17 | 3.0E-16 |
|  | GOTERM\_MF\_DIRECT | heme binding | 84 | 2.7E-16 | 1.8E-14 |
|  | GOTERM\_MF\_DIRECT | oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen | 58 | 4.0E-16 | 2.4E-14 |
|  | INTERPRO | Cyt\_P450\_CS | 52 | 2.5E-15 | 2.4E-13 |
|  | GOTERM\_MF\_DIRECT | monooxygenase activity | 59 | 1.7E-14 | 9.0E-13 |
|  | GOTERM\_MF\_DIRECT | iron ion binding | 66 | 3.8E-13 | 1.6E-11 |
|  | UP\_KW\_MOLECULAR\_FUNCTION | Oxidoreductase | 137 | 4.4E-7 | 6.3E-6 |
|  | UP\_KW\_MOLECULAR\_FUNCTION | Monooxygenase | 31 | 7.0E-5 | 5.9E-4 |
| Annotation Cluster 6 | | Enrichment Score: 14.58 | Count | P\_Value | Benjamini |
|  | GOTERM\_MF\_DIRECT | DNA-binding transcription factor activity | 192 | 1.5E-41 | 3.6E-39 |
|  | GOTERM\_BP\_DIRECT | regulation of DNA-templated transcription | 201 | 1.7E-26 | 3.1E-24 |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Transcription regulation | 247 | 4.5E-17 | 2.0E-15 |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Transcription | 249 | 7.0E-15 | 2.1E-13 |
|  | UP\_KW\_MOLECULAR\_FUNCTION | DNA-binding | 140 | 6.0E-5 | 5.8E-4 |
|  | GOTERM\_CC\_DIRECT | nucleus | 371 | 1.9E-1 | 1.0E0 |
|  | UP\_KW\_CELLULAR\_COMPONENT | Nucleus | 197 | 9.9E-1 | 1.0E0 |
| Annotation Cluster 7 | | Enrichment Score: 14.47 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:NAC | 33 | 7.0E-16 | 5.2E-14 |
|  | INTERPRO | NAC-dom | 33 | 7.4E-15 | 6.5E-13 |
|  | INTERPRO | NAC\_dom\_sf | 33 | 7.4E-15 | 6.5E-13 |
| Annotation Cluster 8 | | Enrichment Score: 14.38 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:Bulb-type lectin | 28 | 1.2E-17 | 1.0E-15 |
|  | INTERPRO | Bulb-type\_lectin\_dom\_sf | 29 | 1.8E-17 | 2.1E-15 |
|  | INTERPRO | Bulb-type\_lectin\_dom | 29 | 1.8E-17 | 2.1E-15 |
|  | INTERPRO | SRK-like\_kinase | 26 | 7.2E-17 | 7.8E-15 |
|  | SMART | B\_lectin | 28 | 2.0E-15 | 1.1E-13 |
|  | GOTERM\_BP\_DIRECT | recognition of pollen | 26 | 3.8E-15 | 4.1E-13 |
|  | INTERPRO | S\_locus\_glycoprot\_dom | 24 | 1.4E-14 | 1.1E-12 |
|  | INTERPRO | Pan\_app | 24 | 6.4E-14 | 5.2E-12 |
|  | PIR\_SUPERFAMILY | SRK | 26 | 1.3E-13 | 7.0E-12 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Apple | 22 | 6.7E-13 | 4.0E-11 |
|  | SMART | PAN\_AP | 19 | 4.5E-11 | 1.7E-9 |
| Annotation Cluster 9 | | Enrichment Score: 12.7 | Count | P\_Value | Benjamini |
|  | INTERPRO | LRR\_dom\_sf | 135 | 7.3E-19 | 1.2E-16 |
|  | UP\_KW\_DOMAIN | Leucine-rich repeat | 92 | 3.0E-16 | 1.5E-15 |
|  | INTERPRO | Leu-rich\_rpt\_typical-subtyp | 46 | 1.2E-12 | 8.3E-11 |
|  | INTERPRO | LRR\_N\_plant-typ | 50 | 9.5E-12 | 6.1E-10 |
|  | INTERPRO | Leu-rich\_rpt | 79 | 3.6E-11 | 2.2E-9 |
|  | SMART | LRR\_TYP | 46 | 6.7E-10 | 1.9E-8 |
| Annotation Cluster 10 | | Enrichment Score: 11.32 | Count | P\_Value | Benjamini |
|  | GOTERM\_MF\_DIRECT | polysaccharide binding | 29 | 3.0E-20 | 2.4E-18 |
|  | INTERPRO | WAK\_GUB | 27 | 6.2E-19 | 1.1E-16 |
|  | INTERPRO | WAK\_assoc\_C | 12 | 1.0E-8 | 4.5E-7 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Wall-associated receptor kinase galacturonan-binding | 10 | 3.7E-7 | 9.3E-6 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Wall-associated receptor kinase C-terminal | 7 | 3.7E-5 | 5.3E-4 |
| Annotation Cluster 11 | | Enrichment Score: 11.25 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:AP2/ERF | 34 | 3.5E-14 | 2.3E-12 |
|  | INTERPRO | AP2/ERF\_dom | 34 | 2.7E-13 | 2.0E-11 |
|  | INTERPRO | AP2/ERF\_dom\_sf | 34 | 2.7E-13 | 2.0E-11 |
|  | INTERPRO | DNA-bd\_dom\_sf | 34 | 5.7E-12 | 3.8E-10 |
|  | SMART | AP2 | 34 | 5.0E-11 | 1.7E-9 |
|  | GOTERM\_BP\_DIRECT | ethylene-activated signaling pathway | 21 | 4.5E-8 | 2.7E-6 |
| Annotation Cluster 12 | | Enrichment Score: 8.6 | Count | P\_Value | Benjamini |
|  | INTERPRO | FLA\_A | 16 | 1.4E-15 | 1.4E-13 |
|  | GOTERM\_BP\_DIRECT | plant-type secondary cell wall biogenesis | 18 | 7.6E-12 | 6.8E-10 |
|  | GOTERM\_CC\_DIRECT | side of membrane | 28 | 1.0E-10 | 3.9E-9 |
|  | UP\_SEQ\_FEATURE | DOMAIN:FAS1 | 16 | 6.8E-10 | 3.0E-8 |
|  | INTERPRO | FAS1\_domain | 16 | 1.9E-9 | 9.0E-8 |
|  | INTERPRO | FAS1\_dom\_sf | 16 | 1.9E-9 | 9.0E-8 |
|  | SMART | FAS1 | 15 | 2.1E-8 | 4.8E-7 |
|  | UP\_KW\_PTM | GPI-anchor | 28 | 5.5E-6 | 3.9E-5 |
|  | UP\_KW\_PTM | Lipoprotein | 43 | 1.4E-2 | 6.5E-2 |
| Annotation Cluster 13 | | Enrichment Score: 7.17 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:Gnk2-homologous | 16 | 4.0E-8 | 1.3E-6 |
|  | INTERPRO | GNK2\_sf | 16 | 7.4E-8 | 2.8E-6 |
|  | INTERPRO | GNK2 | 16 | 1.0E-7 | 3.6E-6 |
| Annotation Cluster 14 | | Enrichment Score: 6.89 | Count | P\_Value | Benjamini |
|  | INTERPRO | Disease\_R\_plants | 31 | 1.7E-11 | 1.1E-9 |
|  | UP\_SEQ\_FEATURE | DOMAIN:TIR | 25 | 1.4E-10 | 6.7E-9 |
|  | INTERPRO | TIR\_dom | 25 | 6.2E-10 | 3.3E-8 |
|  | INTERPRO | Toll\_tir\_struct\_dom\_sf | 25 | 1.1E-9 | 5.5E-8 |
|  | SMART | TIR | 25 | 2.2E-8 | 4.8E-7 |
|  | GOTERM\_BP\_DIRECT | signal transduction | 41 | 5.6E-6 | 1.5E-4 |
|  | GOTERM\_MF\_DIRECT | S-adenosylmethionine-dependent methyltransferase activity | 34 | 9.5E-3 | 9.3E-2 |
|  | INTERPRO | WH\_DNA-bd\_sf | 27 | 4.2E-2 | 2.4E-1 |
| Annotation Cluster 15 | | Enrichment Score: 6.56 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:GST C-terminal | 19 | 4.7E-9 | 1.8E-7 |
|  | INTERPRO | Glutathione-S-Trfase\_C-like | 19 | 1.5E-8 | 6.2E-7 |
|  | INTERPRO | GST\_C\_Tau | 16 | 1.7E-8 | 6.9E-7 |
|  | UP\_SEQ\_FEATURE | DOMAIN:GST N-terminal | 20 | 2.2E-8 | 7.9E-7 |
|  | INTERPRO | Omega/Tau-like | 16 | 2.5E-8 | 1.0E-6 |
|  | GOTERM\_MF\_DIRECT | glutathione transferase activity | 19 | 3.9E-8 | 1.1E-6 |
|  | GOTERM\_BP\_DIRECT | glutathione metabolic process | 18 | 5.5E-8 | 3.0E-6 |
|  | INTERPRO | Glutathione\_S-Trfase\_N | 20 | 9.2E-8 | 3.3E-6 |
|  | INTERPRO | GST\_C | 14 | 1.0E-6 | 2.8E-5 |
|  | INTERPRO | Glutathione-S-Trfase\_C\_sf | 19 | 2.2E-6 | 5.3E-5 |
|  | KEGG\_PATHWAY | Glutathione metabolism | 22 | 2.2E-5 | 3.2E-4 |
|  | INTERPRO | Thioredoxin-like\_sf | 37 | 2.6E-5 | 4.8E-4 |
|  | INTERPRO | Glutathione\_S-Trfase | 11 | 2.7E-4 | 3.7E-3 |
| Annotation Cluster 16 | | Enrichment Score: 6.33 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:Sieve element occlusion C-terminal | 8 | 1.1E-7 | 3.2E-6 |
|  | INTERPRO | SEO\_C | 8 | 1.8E-7 | 5.8E-6 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Sieve element occlusion N-terminal | 8 | 3.4E-7 | 9.0E-6 |
|  | INTERPRO | SEO\_N | 8 | 5.6E-7 | 1.7E-5 |
|  | INTERPRO | SEOA | 8 | 1.5E-6 | 3.8E-5 |
|  | GOTERM\_BP\_DIRECT | phloem development | 8 | 2.0E-6 | 6.3E-5 |
| Annotation Cluster 17 | | Enrichment Score: 6.07 | Count | P\_Value | Benjamini |
|  | INTERPRO | Cupredoxin | 29 | 5.7E-9 | 2.7E-7 |
|  | INTERPRO | Laccase | 12 | 1.0E-8 | 4.5E-7 |
|  | GOTERM\_MF\_DIRECT | hydroquinone:oxygen oxidoreductase activity | 12 | 1.4E-8 | 4.2E-7 |
|  | INTERPRO | CuRO\_1\_LCC | 12 | 3.8E-8 | 1.5E-6 |
|  | INTERPRO | CuRO\_2\_LCC | 12 | 6.9E-8 | 2.6E-6 |
|  | GOTERM\_BP\_DIRECT | lignin catabolic process | 12 | 1.1E-7 | 4.9E-6 |
|  | INTERPRO | CuRO\_3\_LCC | 11 | 1.6E-7 | 5.3E-6 |
|  | INTERPRO | Cu\_oxidase\_CS | 11 | 8.3E-7 | 2.4E-5 |
|  | INTERPRO | Cu\_oxidase\_Cu\_BS | 11 | 1.3E-6 | 3.6E-5 |
|  | INTERPRO | Cu-oxidase\_C | 14 | 1.9E-6 | 4.9E-5 |
|  | INTERPRO | Cu-oxidase\_fam | 14 | 4.6E-6 | 1.1E-4 |
|  | INTERPRO | Cu-oxidase-like\_N | 14 | 4.6E-6 | 1.1E-4 |
|  | INTERPRO | Cu-oxidase\_2nd | 14 | 1.3E-5 | 2.5E-4 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Plastocyanin-like | 14 | 1.5E-5 | 2.5E-4 |
|  | UP\_KW\_LIGAND | Copper | 15 | 2.9E-4 | 2.0E-3 |
|  | GOTERM\_MF\_DIRECT | copper ion binding | 14 | 9.1E-4 | 1.2E-2 |
| Annotation Cluster 18 | | Enrichment Score: 5.68 | Count | P\_Value | Benjamini |
|  | INTERPRO | EGF-like\_dom | 13 | 2.0E-7 | 6.3E-6 |
|  | UP\_SEQ\_FEATURE | DOMAIN:EGF-like | 11 | 3.7E-6 | 6.6E-5 |
|  | UP\_KW\_DOMAIN | EGF-like domain | 12 | 1.3E-5 | 5.0E-5 |
| Annotation Cluster 19 | | Enrichment Score: 5.64 | Count | P\_Value | Benjamini |
|  | GOTERM\_CC\_DIRECT | apoplast | 47 | 3.4E-10 | 9.6E-9 |
|  | UP\_KW\_CELLULAR\_COMPONENT | Apoplast | 47 | 7.8E-9 | 2.2E-7 |
|  | GOTERM\_CC\_DIRECT | cell wall | 27 | 1.5E-3 | 2.0E-2 |
|  | UP\_KW\_CELLULAR\_COMPONENT | Secreted | 100 | 6.8E-3 | 4.8E-2 |
| Annotation Cluster 20 | | Enrichment Score: 5.55 | Count | P\_Value | Benjamini |
|  | INTERPRO | Homeodomain-like\_sf | 65 | 4.0E-8 | 1.5E-6 |
|  | UP\_SEQ\_FEATURE | DOMAIN:HTH myb-type | 43 | 6.0E-8 | 1.9E-6 |
|  | INTERPRO | Myb\_dom | 43 | 4.3E-7 | 1.3E-5 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Myb-like | 42 | 4.9E-7 | 1.1E-5 |
|  | INTERPRO | SANT/Myb | 48 | 6.4E-6 | 1.4E-4 |
|  | INTERPRO | Myb\_TF\_plants | 14 | 3.0E-4 | 3.9E-3 |
|  | SMART | SANT | 38 | 1.4E-3 | 1.5E-2 |
| Annotation Cluster 21 | | Enrichment Score: 5.39 | Count | P\_Value | Benjamini |
|  | INTERPRO | CCT\_CS | 10 | 1.4E-8 | 5.9E-7 |
|  | GOTERM\_BP\_DIRECT | regulation of jasmonic acid mediated signaling pathway | 12 | 1.1E-7 | 4.9E-6 |
|  | GOTERM\_BP\_DIRECT | response to wounding | 12 | 1.3E-6 | 4.2E-5 |
|  | INTERPRO | TIFY/JAZ | 10 | 2.1E-6 | 5.2E-5 |
|  | GOTERM\_BP\_DIRECT | regulation of defense response | 10 | 3.1E-6 | 8.7E-5 |
|  | INTERPRO | Tify\_dom | 10 | 1.9E-5 | 3.5E-4 |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Jasmonic acid signaling pathway | 10 | 3.6E-5 | 5.4E-4 |
|  | SMART | TIFY | 10 | 9.2E-5 | 1.3E-3 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Tify | 10 | 4.0E-4 | 4.6E-3 |
| Annotation Cluster 22 | | Enrichment Score: 5.05 | Count | P\_Value | Benjamini |
|  | INTERPRO | HMA\_dom\_sf | 25 | 1.8E-9 | 8.9E-8 |
|  | UP\_SEQ\_FEATURE | DOMAIN:HMA | 24 | 1.8E-9 | 7.4E-8 |
|  | INTERPRO | HMA\_dom | 24 | 7.3E-9 | 3.4E-7 |
|  | INTERPRO | HIPP | 7 | 3.8E-4 | 4.8E-3 |
|  | UP\_KW\_PTM | Prenylation | 13 | 7.7E-2 | 2.2E-1 |
|  | UP\_KW\_PTM | Methylation | 12 | 6.9E-1 | 1.0E0 |
| Annotation Cluster 23 | | Enrichment Score: 4.85 | Count | P\_Value | Benjamini |
|  | INTERPRO | NDR1-like | 17 | 4.4E-7 | 1.3E-5 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Late embryogenesis abundant protein LEA-2 subgroup | 11 | 7.5E-5 | 1.0E-3 |
|  | INTERPRO | LEA\_2 | 12 | 8.5E-5 | 1.4E-3 |
| Annotation Cluster 24 | | Enrichment Score: 4.84 | Count | P\_Value | Benjamini |
|  | GOTERM\_MF\_DIRECT | calcium ion binding | 49 | 5.7E-10 | 2.2E-8 |
|  | UP\_KW\_LIGAND | Calcium | 61 | 4.2E-8 | 4.9E-7 |
|  | INTERPRO | EF\_hand\_pair\_protein\_CML-like | 11 | 1.6E-7 | 5.3E-6 |
|  | INTERPRO | EF\_Hand\_1\_Ca\_BS | 24 | 3.2E-4 | 4.2E-3 |
|  | INTERPRO | EF-hand-dom\_pair | 27 | 4.7E-4 | 5.7E-3 |
|  | UP\_SEQ\_FEATURE | DOMAIN:EF-hand | 23 | 6.9E-4 | 7.3E-3 |
|  | INTERPRO | EF\_hand\_dom | 23 | 1.8E-3 | 1.9E-2 |
|  | SMART | EFh | 21 | 2.5E-3 | 2.1E-2 |
| Annotation Cluster 25 | | Enrichment Score: 4.72 | Count | P\_Value | Benjamini |
|  | GOTERM\_MF\_DIRECT | symporter activity | 33 | 1.1E-8 | 3.6E-7 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Amino acid transporter transmembrane | 25 | 8.2E-7 | 1.8E-5 |
|  | GOTERM\_BP\_DIRECT | amino acid transport | 25 | 2.6E-6 | 7.8E-5 |
|  | INTERPRO | AA\_transpt\_TM | 25 | 5.9E-6 | 1.3E-4 |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Symport | 34 | 1.1E-5 | 2.0E-4 |
|  | GOTERM\_BP\_DIRECT | auxin-activated signaling pathway | 35 | 8.3E-5 | 1.7E-3 |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Auxin signaling pathway | 27 | 1.6E-4 | 2.1E-3 |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Amino-acid transport | 25 | 2.5E-3 | 2.4E-2 |
|  | GOTERM\_CC\_DIRECT | endomembrane system | 64 | 7.0E-3 | 8.5E-2 |
| Annotation Cluster 26 | | Enrichment Score: 4.45 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:BHLH | 32 | 1.2E-6 | 2.5E-5 |
|  | INTERPRO | HLH\_DNA-bd\_sf | 32 | 4.8E-6 | 1.1E-4 |
|  | INTERPRO | bHLH\_dom | 32 | 5.4E-6 | 1.2E-4 |
|  | SMART | HLH | 29 | 1.3E-4 | 1.7E-3 |
|  | GOTERM\_MF\_DIRECT | protein dimerization activity | 53 | 1.5E-2 | 1.4E-1 |
| Annotation Cluster 27 | | Enrichment Score: 4.4 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:Cathepsin propeptide inhibitor | 18 | 1.3E-7 | 3.6E-6 |
|  | GOTERM\_MF\_DIRECT | cysteine-type endopeptidase activity | 24 | 1.4E-7 | 3.7E-6 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Peptidase C1A papain C-terminal | 18 | 4.4E-7 | 1.1E-5 |
|  | INTERPRO | Peptidase\_C1A\_papain-like | 18 | 4.8E-7 | 1.4E-5 |
|  | INTERPRO | Prot\_inhib\_I29 | 18 | 4.8E-7 | 1.4E-5 |
|  | INTERPRO | Pept\_his\_AS | 17 | 9.5E-7 | 2.7E-5 |
|  | INTERPRO | Peptidase\_C1A | 18 | 1.2E-6 | 3.3E-5 |
|  | GOTERM\_CC\_DIRECT | lysosome | 20 | 1.3E-6 | 2.9E-5 |
|  | INTERPRO | Peptidase\_C1A\_C | 18 | 1.9E-6 | 4.9E-5 |
|  | SMART | Inhibitor\_I29 | 18 | 5.6E-6 | 1.1E-4 |
|  | INTERPRO | Pept\_cys\_AS | 16 | 9.7E-6 | 1.9E-4 |
|  | SMART | Pept\_C1 | 18 | 1.7E-5 | 3.0E-4 |
|  | GOTERM\_BP\_DIRECT | proteolysis involved in protein catabolic process | 20 | 5.2E-5 | 1.1E-3 |
|  | INTERPRO | Pept\_asp\_AS | 13 | 6.5E-5 | 1.1E-3 |
|  | GOTERM\_CC\_DIRECT | extracellular space | 23 | 1.4E-4 | 2.6E-3 |
|  | UP\_KW\_MOLECULAR\_FUNCTION | Protease | 52 | 8.8E-1 | 1.0E0 |
|  | UP\_KW\_MOLECULAR\_FUNCTION | Thiol protease | 20 | 9.8E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | cysteine-type peptidase activity | 19 | 1.0E0 | 1.0E0 |
|  | INTERPRO | Papain-like\_cys\_pep\_sf | 22 | 1.0E0 | 1.0E0 |
| Annotation Cluster 28 | | Enrichment Score: 4.31 | Count | P\_Value | Benjamini |
|  | GOTERM\_MF\_DIRECT | phenylalanine ammonia-lyase activity | 9 | 1.1E-8 | 3.6E-7 |
|  | INTERPRO | Aromatic\_Lyase | 9 | 1.4E-7 | 4.9E-6 |
|  | GOTERM\_BP\_DIRECT | phenylpropanoid metabolic process | 8 | 2.5E-7 | 9.5E-6 |
|  | GOTERM\_MF\_DIRECT | ammonia-lyase activity | 7 | 1.7E-6 | 4.1E-5 |
|  | INTERPRO | Phe\_NH3-lyase | 7 | 2.1E-6 | 5.2E-5 |
|  | INTERPRO | Phe/His\_NH3-lyase\_AS | 7 | 2.1E-6 | 5.2E-5 |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Phenylalanine catabolism | 9 | 5.0E-6 | 1.1E-4 |
|  | GOTERM\_BP\_DIRECT | L-phenylalanine catabolic process | 9 | 7.4E-6 | 1.9E-4 |
|  | INTERPRO | Phe\_NH3-lyase\_shielding\_dom\_sf | 6 | 2.4E-5 | 4.5E-4 |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Phenylpropanoid metabolism | 5 | 3.6E-4 | 4.0E-3 |
|  | KEGG\_PATHWAY | Phenylalanine metabolism | 10 | 1.5E-3 | 1.4E-2 |
|  | INTERPRO | Fumarase/histidase\_N | 8 | 1.5E-3 | 1.7E-2 |
|  | INTERPRO | L-Aspartase-like | 9 | 8.8E-3 | 7.2E-2 |
|  | UP\_SEQ\_FEATURE | CROSSLNK:5-imidazolinone (Ala-Gly) | 3 | 1.1E-2 | 7.3E-2 |
|  | GOTERM\_BP\_DIRECT | cinnamic acid biosynthetic process | 3 | 1.4E-2 | 1.5E-1 |
|  | UP\_SEQ\_FEATURE | ACT\_SITE:Proton donor/acceptor | 4 | 3.5E-1 | 1.0E0 |
| Annotation Cluster 29 | | Enrichment Score: 4.26 | Count | P\_Value | Benjamini |
|  | INTERPRO | Cupredoxin | 29 | 5.7E-9 | 2.7E-7 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Phytocyanin | 15 | 2.4E-5 | 3.8E-4 |
|  | INTERPRO | Phytocyanin\_dom | 15 | 5.3E-5 | 9.1E-4 |
|  | INTERPRO | Phytocyanin-like | 14 | 1.1E-4 | 1.6E-3 |
|  | INTERPRO | ENL\_dom | 6 | 1.5E-3 | 1.7E-2 |
|  | GOTERM\_MF\_DIRECT | electron transfer activity | 16 | 2.4E-2 | 1.8E-1 |
| Annotation Cluster 30 | | Enrichment Score: 4.16 | Count | P\_Value | Benjamini |
|  | INTERPRO | Chalcone/stilbene\_synthase\_AS | 10 | 8.5E-8 | 3.1E-6 |
|  | GOTERM\_MF\_DIRECT | naringenin-chalcone synthase activity | 7 | 1.7E-6 | 4.1E-5 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Chalcone/stilbene synthase N-terminal | 10 | 3.0E-6 | 5.9E-5 |
|  | INTERPRO | Chalcone/stilbene\_synt\_N | 10 | 5.5E-6 | 1.2E-4 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Chalcone/stilbene synthase C-terminal | 10 | 7.1E-6 | 1.2E-4 |
|  | KEGG\_PATHWAY | Flavonoid biosynthesis | 18 | 7.4E-6 | 1.2E-4 |
|  | INTERPRO | Polyketide\_synthase\_type-III | 10 | 8.6E-6 | 1.8E-4 |
|  | GOTERM\_BP\_DIRECT | polyketide biosynthetic process | 10 | 1.2E-5 | 3.0E-4 |
|  | INTERPRO | Chalcone/stilbene\_synt\_C | 10 | 1.3E-5 | 2.5E-4 |
|  | PIR\_SUPERFAMILY | PKS\_III | 9 | 3.1E-4 | 4.1E-3 |
|  | UP\_SEQ\_FEATURE | ACT\_SITE:Acyl-thioester intermediate | 8 | 3.4E-4 | 4.1E-3 |
|  | INTERPRO | Thiolase-like | 14 | 4.0E-4 | 5.0E-3 |
|  | GOTERM\_BP\_DIRECT | flavonoid biosynthetic process | 10 | 7.8E-4 | 1.4E-2 |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Flavonoid biosynthesis | 10 | 2.7E-3 | 2.4E-2 |
|  | KEGG\_PATHWAY | Circadian rhythm - plant | 12 | 3.8E-3 | 3.1E-2 |
|  | KEGG\_PATHWAY | Tropane, piperidine and pyridine alkaloid biosynthesis | 10 | 4.0E-3 | 3.1E-2 |
|  | UP\_KW\_MOLECULAR\_FUNCTION | Acyltransferase | 19 | 8.7E-2 | 4.2E-1 |
| Annotation Cluster 31 | | Enrichment Score: 4.01 | Count | P\_Value | Benjamini |
|  | INTERPRO | C2\_dom | 22 | 1.8E-5 | 3.4E-4 |
|  | UP\_SEQ\_FEATURE | DOMAIN:C2 | 20 | 5.3E-5 | 7.6E-4 |
|  | INTERPRO | C2\_domain\_sf | 22 | 2.3E-4 | 3.3E-3 |
|  | SMART | C2 | 19 | 4.3E-4 | 5.3E-3 |
| Annotation Cluster 32 | | Enrichment Score: 3.95 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:Fungal lipase-type | 10 | 7.4E-5 | 1.0E-3 |
|  | GOTERM\_MF\_DIRECT | phospholipase A1 activity | 6 | 1.1E-4 | 2.1E-3 |
|  | INTERPRO | Fungal\_lipase-type | 10 | 1.7E-4 | 2.5E-3 |
| Annotation Cluster 33 | | Enrichment Score: 3.94 | Count | P\_Value | Benjamini |
|  | INTERPRO | Homeobox\_CS | 16 | 1.0E-7 | 3.6E-6 |
|  | GOTERM\_MF\_DIRECT | DNA-binding transcription factor activity, RNA polymerase II-specific | 48 | 2.6E-5 | 5.5E-4 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Homeobox | 20 | 2.8E-5 | 4.3E-4 |
|  | INTERPRO | HD | 20 | 7.5E-5 | 1.2E-3 |
|  | INTERPRO | Leu\_zip\_homeo | 9 | 2.6E-4 | 3.6E-3 |
|  | UP\_SEQ\_FEATURE | DNA\_BIND:Homeobox | 16 | 8.7E-4 | 8.8E-3 |
|  | SMART | HOX | 20 | 9.2E-4 | 1.1E-2 |
|  | INTERPRO | HD-ZIP\_Homeobox\_LZ\_Class\_II | 6 | 1.1E-3 | 1.2E-2 |
|  | SMART | HALZ | 6 | 2.6E-3 | 2.1E-2 |
| Annotation Cluster 34 | | Enrichment Score: 3.73 | Count | P\_Value | Benjamini |
|  | INTERPRO | SLSG/EP1 | 7 | 6.0E-6 | 1.3E-4 |
|  | PIR\_SUPERFAMILY | SLG | 7 | 5.1E-5 | 1.4E-3 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Serine-threonine/tyrosine-protein kinase catalytic | 4 | 2.0E-2 | 1.2E-1 |
| Annotation Cluster 35 | | Enrichment Score: 3.69 | Count | P\_Value | Benjamini |
|  | INTERPRO | DIOX\_N | 23 | 3.5E-5 | 6.3E-4 |
|  | INTERPRO | Plant\_2OG-oxidoreductases | 15 | 4.4E-5 | 7.6E-4 |
|  | UP\_KW\_LIGAND | Vitamin C | 15 | 4.8E-5 | 4.2E-4 |
|  | INTERPRO | IPNS-like\_FE2OG\_OXY | 23 | 5.7E-5 | 9.7E-4 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Fe2OG dioxygenase | 24 | 1.5E-4 | 1.8E-3 |
|  | INTERPRO | IPNS-like\_sf | 23 | 2.6E-4 | 3.6E-3 |
|  | INTERPRO | Oxoglu/Fe-dep\_dioxygenase\_dom | 24 | 4.2E-4 | 5.2E-3 |
|  | GOTERM\_MF\_DIRECT | dioxygenase activity | 10 | 4.4E-2 | 2.8E-1 |
| Annotation Cluster 36 | | Enrichment Score: 3.15 | Count | P\_Value | Benjamini |
|  | INTERPRO | DC1 | 6 | 1.3E-4 | 1.9E-3 |
|  | INTERPRO | C1-like\_sf | 6 | 6.8E-4 | 8.1E-3 |
|  | UP\_SEQ\_FEATURE | DOMAIN:DC1 | 4 | 4.1E-3 | 3.1E-2 |
| Annotation Cluster 37 | | Enrichment Score: 3.13 | Count | P\_Value | Benjamini |
|  | KEGG\_PATHWAY | ABC transporters | 27 | 2.8E-9 | 8.1E-8 |
|  | INTERPRO | ABCG\_PDR\_2 | 10 | 6.9E-7 | 2.0E-5 |
|  | INTERPRO | ABCG\_dom | 15 | 1.3E-6 | 3.5E-5 |
|  | INTERPRO | ABC2\_TM | 18 | 5.4E-6 | 1.2E-4 |
|  | GOTERM\_MF\_DIRECT | ABC-type transporter activity | 31 | 8.5E-6 | 1.9E-4 |
|  | INTERPRO | PDR\_assoc | 10 | 1.3E-5 | 2.5E-4 |
|  | UP\_SEQ\_FEATURE | DOMAIN:ABC transporter | 30 | 1.8E-5 | 2.9E-4 |
|  | INTERPRO | AAA+\_ATPase | 43 | 7.5E-5 | 1.2E-3 |
|  | INTERPRO | ABC\_transporter-like\_ATP-bd | 30 | 9.6E-5 | 1.5E-3 |
|  | INTERPRO | ABC\_trans\_N | 7 | 2.5E-4 | 3.5E-3 |
|  | INTERPRO | ABCG\_PDR\_1 | 6 | 6.8E-4 | 8.1E-3 |
|  | INTERPRO | ABC\_transporter-like\_CS | 19 | 2.2E-3 | 2.3E-2 |
|  | GOTERM\_MF\_DIRECT | ATP hydrolysis activity | 65 | 3.7E-3 | 4.1E-2 |
|  | SMART | AAA | 43 | 3.8E-3 | 2.9E-2 |
|  | KEGG\_PATHWAY | Folate transport and metabolism | 10 | 3.7E-2 | 2.4E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:ABC transmembrane type-1 | 12 | 9.8E-2 | 4.1E-1 |
|  | INTERPRO | ABC1\_TM\_dom | 12 | 1.4E-1 | 5.8E-1 |
|  | GOTERM\_MF\_DIRECT | ABC-type oligopeptide transporter activity | 4 | 1.5E-1 | 6.4E-1 |
|  | GOTERM\_BP\_DIRECT | oligopeptide export from mitochondrion | 4 | 1.6E-1 | 8.7E-1 |
|  | INTERPRO | ABC1\_TM\_sf | 12 | 2.5E-1 | 8.4E-1 |
|  | INTERPRO | Type\_1\_exporter | 4 | 5.7E-1 | 1.0E0 |
|  | GOTERM\_CC\_DIRECT | mitochondrial inner membrane | 10 | 9.5E-1 | 1.0E0 |
| Annotation Cluster 38 | | Enrichment Score: 3.11 | Count | P\_Value | Benjamini |
|  | INTERPRO | MADS-box/MEF2\_TF | 13 | 1.2E-4 | 1.8E-3 |
|  | UP\_SEQ\_FEATURE | DOMAIN:MADS-box | 14 | 1.4E-4 | 1.8E-3 |
|  | GOTERM\_MF\_DIRECT | RNA polymerase II cis-regulatory region sequence-specific DNA binding | 34 | 1.7E-4 | 3.1E-3 |
|  | INTERPRO | TF\_MADSbox | 14 | 3.0E-4 | 3.9E-3 |
|  | INTERPRO | TF\_MADSbox\_sf | 14 | 3.0E-4 | 3.9E-3 |
|  | INTERPRO | MADS\_MEF2-like | 12 | 3.0E-4 | 3.9E-3 |
|  | UP\_SEQ\_FEATURE | DOMAIN:K-box | 11 | 4.9E-4 | 5.3E-3 |
|  | INTERPRO | TF\_Kbox | 11 | 8.7E-4 | 1.0E-2 |
|  | GOTERM\_MF\_DIRECT | RNA polymerase II transcription regulatory region sequence-specific DNA binding | 15 | 9.9E-4 | 1.3E-2 |
|  | SMART | MADS | 14 | 1.9E-3 | 1.8E-2 |
|  | GOTERM\_BP\_DIRECT | positive regulation of transcription by RNA polymerase II | 14 | 9.3E-1 | 1.0E0 |
| Annotation Cluster 39 | | Enrichment Score: 2.89 | Count | P\_Value | Benjamini |
|  | GOTERM\_BP\_DIRECT | plant-type hypersensitive response | 6 | 3.0E-4 | 6.0E-3 |
|  | GOTERM\_BP\_DIRECT | regulation of salicylic acid mediated signaling pathway | 6 | 8.4E-4 | 1.4E-2 |
|  | UP\_SEQ\_FEATURE | DOMAIN:MACPF | 5 | 1.4E-3 | 1.3E-2 |
|  | INTERPRO | CAD1/NSL1-like | 5 | 1.9E-3 | 2.0E-2 |
|  | INTERPRO | MACPF | 5 | 1.9E-3 | 2.0E-2 |
|  | SMART | MACPF | 5 | 3.9E-3 | 2.9E-2 |
| Annotation Cluster 40 | | Enrichment Score: 2.84 | Count | P\_Value | Benjamini |
|  | INTERPRO | ConA-like\_dom\_sf | 25 | 7.7E-6 | 1.6E-4 |
|  | INTERPRO | GH16\_AS | 11 | 8.4E-5 | 1.3E-3 |
|  | UP\_SEQ\_FEATURE | ACT\_SITE:Nucleophile | 30 | 1.0E-4 | 1.4E-3 |
|  | GOTERM\_MF\_DIRECT | xyloglucan:xyloglucosyl transferase activity | 13 | 3.2E-4 | 4.5E-3 |
|  | INTERPRO | XTH | 13 | 3.6E-4 | 4.6E-3 |
|  | INTERPRO | XET\_C | 13 | 3.6E-4 | 4.6E-3 |
|  | UP\_SEQ\_FEATURE | ACT\_SITE:Proton donor | 24 | 4.6E-4 | 5.2E-3 |
|  | UP\_SEQ\_FEATURE | DOMAIN:GH16 | 13 | 4.8E-4 | 5.3E-3 |
|  | GOTERM\_BP\_DIRECT | cell wall biogenesis | 14 | 5.3E-4 | 9.9E-3 |
|  | INTERPRO | Beta-glucanase/XTH | 13 | 9.2E-4 | 1.1E-2 |
|  | INTERPRO | GH16 | 13 | 9.2E-4 | 1.1E-2 |
|  | GOTERM\_MF\_DIRECT | hydrolase activity, hydrolyzing O-glycosyl compounds | 33 | 1.0E-3 | 1.3E-2 |
|  | UP\_SEQ\_FEATURE | CARBOHYD:N-linked (GlcNAc...) asparagine | 13 | 1.1E-3 | 1.1E-2 |
|  | GOTERM\_BP\_DIRECT | xyloglucan metabolic process | 13 | 1.4E-3 | 2.0E-2 |
|  | GOTERM\_CC\_DIRECT | cell wall | 27 | 1.5E-3 | 2.0E-2 |
|  | PIR\_SUPERFAMILY | XET | 13 | 8.1E-3 | 7.1E-2 |
|  | GOTERM\_BP\_DIRECT | cell wall organization | 29 | 1.3E-2 | 1.5E-1 |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Cell wall biogenesis/degradation | 29 | 1.8E-1 | 1.0E0 |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Cell wall biogenesis/degradation | 29 | 1.8E-1 | 1.0E0 |
|  | UP\_KW\_CELLULAR\_COMPONENT | Cell wall | 27 | 9.2E-1 | 1.0E0 |
| Annotation Cluster 41 | | Enrichment Score: 2.73 | Count | P\_Value | Benjamini |
|  | GOTERM\_MF\_DIRECT | inositol-polyphosphate 5-phosphatase activity | 7 | 2.1E-4 | 3.6E-3 |
|  | INTERPRO | IP5P\_plant | 7 | 2.5E-4 | 3.5E-3 |
|  | GOTERM\_MF\_DIRECT | phosphatidylinositol-3,4,5-trisphosphate 5-phosphatase activity | 7 | 3.2E-4 | 4.5E-3 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Inositol polyphosphate-related phosphatase | 7 | 3.7E-4 | 4.4E-3 |
|  | INTERPRO | IPPc | 7 | 7.9E-4 | 9.3E-3 |
|  | GOTERM\_MF\_DIRECT | phosphatidylinositol-4,5-bisphosphate 5-phosphatase activity | 7 | 1.2E-3 | 1.5E-2 |
|  | SMART | IPPc | 7 | 2.2E-3 | 2.0E-2 |
|  | GOTERM\_BP\_DIRECT | phosphatidylinositol dephosphorylation | 7 | 2.1E-2 | 2.1E-1 |
|  | INTERPRO | Endo/exonu/phosph\_ase\_sf | 8 | 9.6E-1 | 1.0E0 |
| Annotation Cluster 42 | | Enrichment Score: 2.67 | Count | P\_Value | Benjamini |
|  | GOTERM\_BP\_DIRECT | regulation of salicylic acid biosynthetic process | 6 | 5.2E-4 | 9.9E-3 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Calmodulin binding protein C-terminal | 5 | 2.2E-3 | 1.9E-2 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Calmodulin binding protein central | 5 | 2.2E-3 | 1.9E-2 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Calmodulin binding protein-like N-terminal | 5 | 2.2E-3 | 1.9E-2 |
|  | INTERPRO | CBP60 | 5 | 2.9E-3 | 2.9E-2 |
|  | INTERPRO | Calmod\_bind\_C | 5 | 2.9E-3 | 2.9E-2 |
|  | INTERPRO | Calmod\_bind\_M | 5 | 2.9E-3 | 2.9E-2 |
|  | INTERPRO | Calmodulin\_bind\_N | 5 | 2.9E-3 | 2.9E-2 |
| Annotation Cluster 43 | | Enrichment Score: 2.57 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:SHSP | 12 | 1.3E-4 | 1.7E-3 |
|  | INTERPRO | A-crystallin/Hsp20\_dom | 12 | 3.6E-4 | 4.6E-3 |
|  | INTERPRO | HSP20-like\_chaperone | 12 | 4.4E-3 | 4.1E-2 |
|  | GOTERM\_BP\_DIRECT | cellular response to heat | 7 | 2.5E-1 | 1.0E0 |
| Annotation Cluster 44 | | Enrichment Score: 2.5 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:Alpha/beta hydrolase fold-3 | 8 | 2.4E-3 | 2.0E-2 |
|  | INTERPRO | AB\_hydrolase\_3 | 8 | 3.6E-3 | 3.4E-2 |
|  | INTERPRO | Carboxylest/Gibb\_receptor | 8 | 3.6E-3 | 3.4E-2 |
| Annotation Cluster 45 | | Enrichment Score: 2.47 | Count | P\_Value | Benjamini |
|  | KEGG\_PATHWAY | Phenylpropanoid biosynthesis | 41 | 1.4E-9 | 5.3E-8 |
|  | GOTERM\_MF\_DIRECT | peroxidase activity | 21 | 9.2E-4 | 1.2E-2 |
|  | UP\_SEQ\_FEATURE | ACT\_SITE:Proton acceptor | 36 | 1.9E-3 | 1.8E-2 |
|  | UP\_SEQ\_FEATURE | SITE:Transition state stabilizer | 17 | 2.9E-3 | 2.3E-2 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Plant heme peroxidase family profile | 16 | 3.4E-3 | 2.6E-2 |
|  | INTERPRO | Haem\_peroxidase\_sf | 17 | 4.6E-3 | 4.2E-2 |
|  | INTERPRO | Secretory\_peroxidase | 15 | 5.7E-3 | 5.1E-2 |
|  | INTERPRO | Haem\_peroxidase | 16 | 6.6E-3 | 5.7E-2 |
|  | GOTERM\_BP\_DIRECT | hydrogen peroxide catabolic process | 17 | 7.0E-3 | 9.0E-2 |
|  | INTERPRO | Peroxidase\_pln | 15 | 9.6E-3 | 7.7E-2 |
|  | INTERPRO | Peroxidases\_heam-ligand\_BS | 14 | 1.7E-2 | 1.3E-1 |
|  | GOTERM\_BP\_DIRECT | response to oxidative stress | 19 | 1.7E-2 | 1.9E-1 |
|  | UP\_KW\_MOLECULAR\_FUNCTION | Peroxidase | 20 | 3.4E-2 | 2.0E-1 |
|  | INTERPRO | Peroxidases\_AS | 11 | 3.6E-2 | 2.1E-1 |
|  | GOTERM\_CC\_DIRECT | plant-type cell wall | 10 | 5.4E-2 | 5.5E-1 |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Hydrogen peroxide | 15 | 6.1E-2 | 4.9E-1 |
| Annotation Cluster 46 | | Enrichment Score: 2.36 | Count | P\_Value | Benjamini |
|  | GOTERM\_BP\_DIRECT | jasmonic acid biosynthetic process | 7 | 3.8E-5 | 8.6E-4 |
|  | INTERPRO | Allene\_oxi\_cyc\_Dirigent | 9 | 3.0E-3 | 3.0E-2 |
|  | GOTERM\_MF\_DIRECT | allene-oxide cyclase activity | 3 | 2.3E-2 | 1.7E-1 |
|  | INTERPRO | Allene\_ox\_cyc | 3 | 2.4E-2 | 1.6E-1 |
|  | INTERPRO | Allene\_oxi\_cyc\_sf | 3 | 2.4E-2 | 1.6E-1 |
| Annotation Cluster 47 | | Enrichment Score: 2.35 | Count | P\_Value | Benjamini |
|  | INTERPRO | Mitochondrial\_chaperone\_BCS1 | 9 | 1.4E-5 | 2.8E-4 |
|  | INTERPRO | AAA\_N\_dom | 8 | 9.3E-5 | 1.5E-3 |
|  | INTERPRO | ATPase\_AAA\_CS | 9 | 9.2E-2 | 4.3E-1 |
|  | INTERPRO | ATPase\_AAA\_core | 15 | 1.1E-1 | 4.8E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:AAA+ ATPase | 13 | 1.3E-1 | 5.1E-1 |
| Annotation Cluster 48 | | Enrichment Score: 2.35 | Count | P\_Value | Benjamini |
|  | INTERPRO | Powdery\_mildew-R\_dom | 5 | 1.1E-3 | 1.2E-2 |
|  | UP\_SEQ\_FEATURE | DOMAIN:RPW8 | 4 | 6.8E-3 | 4.7E-2 |
|  | GOTERM\_BP\_DIRECT | defense response to fungus | 11 | 1.2E-2 | 1.5E-1 |
| Annotation Cluster 49 | | Enrichment Score: 2.34 | Count | P\_Value | Benjamini |
|  | INTERPRO | AMP-binding\_CS | 14 | 1.1E-4 | 1.6E-3 |
|  | INTERPRO | AMP-dep\_synth/lig\_dom | 14 | 1.2E-3 | 1.4E-2 |
|  | UP\_SEQ\_FEATURE | DOMAIN:AMP-dependent synthetase/ligase | 13 | 1.3E-3 | 1.2E-2 |
|  | INTERPRO | ANL\_N\_sf | 14 | 1.8E-3 | 1.9E-2 |
|  | UP\_SEQ\_FEATURE | DOMAIN:AMP-binding enzyme C-terminal | 9 | 3.2E-3 | 2.5E-2 |
|  | INTERPRO | AMP-bd\_C\_sf | 10 | 4.5E-3 | 4.2E-2 |
|  | INTERPRO | AMP-bd\_C | 9 | 4.9E-3 | 4.5E-2 |
|  | GOTERM\_MF\_DIRECT | CoA-ligase activity | 5 | 4.9E-2 | 3.0E-1 |
|  | UP\_KW\_MOLECULAR\_FUNCTION | Ligase | 15 | 8.8E-1 | 1.0E0 |
| Annotation Cluster 50 | | Enrichment Score: 2.24 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:Cytochrome b561 | 7 | 7.4E-4 | 7.6E-3 |
|  | INTERPRO | Cyt\_b561/ferric\_Rdtase\_TM | 7 | 1.5E-3 | 1.6E-2 |
|  | SMART | B561 | 7 | 1.6E-3 | 1.6E-2 |
|  | UP\_SEQ\_FEATURE | DOMAIN:DOMON | 5 | 2.2E-3 | 1.9E-2 |
|  | INTERPRO | DOMON\_domain | 5 | 2.9E-3 | 2.9E-2 |
|  | INTERPRO | UCP037471 | 4 | 5.0E-3 | 4.5E-2 |
|  | INTERPRO | AIR12\_DOMON | 4 | 8.3E-3 | 6.9E-2 |
|  | PIR\_SUPERFAMILY | UCP037471 | 4 | 1.5E-2 | 1.1E-1 |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Electron transport | 8 | 9.5E-1 | 1.0E0 |
| Annotation Cluster 51 | | Enrichment Score: 2.21 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | REGION:SAW | 10 | 1.1E-3 | 1.1E-2 |
|  | INTERPRO | TF\_GRAS | 10 | 1.8E-3 | 1.9E-2 |
|  | UP\_SEQ\_FEATURE | REGION:Leucine repeat II (LRII) | 8 | 2.9E-3 | 2.3E-2 |
|  | UP\_SEQ\_FEATURE | MOTIF:VHIID | 7 | 1.7E-2 | 1.0E-1 |
|  | GOTERM\_BP\_DIRECT | response to symbiotic fungus | 12 | 2.4E-2 | 2.3E-1 |
|  | UP\_SEQ\_FEATURE | REGION:VHIID | 6 | 2.7E-2 | 1.4E-1 |
| Annotation Cluster 52 | | Enrichment Score: 2.18 | Count | P\_Value | Benjamini |
|  | UP\_KW\_MOLECULAR\_FUNCTION | Ligand-gated ion channel | 11 | 5.1E-5 | 5.7E-4 |
|  | GOTERM\_MF\_DIRECT | monoatomic ion channel activity | 7 | 3.2E-4 | 4.5E-3 |
|  | INTERPRO | Ion\_trans\_dom | 9 | 3.5E-4 | 4.5E-3 |
|  | INTERPRO | cNMP-bd\_dom | 10 | 6.9E-4 | 8.2E-3 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Cyclic nucleotide-binding | 9 | 1.6E-3 | 1.5E-2 |
|  | INTERPRO | cNMP-bd\_dom\_sf | 9 | 2.5E-3 | 2.6E-2 |
|  | UP\_KW\_MOLECULAR\_FUNCTION | Ion channel | 19 | 2.8E-3 | 2.1E-2 |
|  | INTERPRO | RmlC-like\_jellyroll | 20 | 4.4E-3 | 4.1E-2 |
|  | GOTERM\_BP\_DIRECT | monoatomic ion transport | 6 | 6.1E-2 | 4.7E-1 |
|  | GOTERM\_MF\_DIRECT | voltage-gated potassium channel activity | 4 | 6.7E-2 | 3.8E-1 |
|  | GOTERM\_BP\_DIRECT | monoatomic ion transmembrane transport | 6 | 6.8E-2 | 5.1E-1 |
|  | INTERPRO | K\_chnl\_volt-dep\_EAG/ELK/ERG | 4 | 7.3E-2 | 3.6E-1 |
|  | SMART | cNMP | 6 | 9.2E-2 | 4.0E-1 |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Ion transport | 26 | 9.9E-1 | 1.0E0 |
| Annotation Cluster 53 | | Enrichment Score: 2.15 | Count | P\_Value | Benjamini |
|  | INTERPRO | Aspartic\_peptidase\_A1 | 15 | 8.0E-6 | 1.7E-4 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Peptidase A1 | 15 | 2.8E-5 | 4.3E-4 |
|  | INTERPRO | PEPTIDASE\_A1 | 15 | 6.3E-5 | 1.1E-3 |
|  | INTERPRO | TAXi\_C | 11 | 2.6E-3 | 2.7E-2 |
|  | INTERPRO | TAXi\_N | 11 | 3.0E-3 | 3.0E-2 |
|  | INTERPRO | Pepsin-like\_plant | 6 | 1.9E-2 | 1.3E-1 |
|  | UP\_KW\_MOLECULAR\_FUNCTION | Aspartyl protease | 6 | 1.4E-1 | 6.4E-1 |
|  | INTERPRO | Aspartic\_peptidase\_AS | 11 | 1.0E0 | 1.0E0 |
|  | INTERPRO | Peptidase\_aspartic\_dom\_sf | 15 | 1.0E0 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | aspartic-type endopeptidase activity | 17 | 1.0E0 | 1.0E0 |
| Annotation Cluster 54 | | Enrichment Score: 2.11 | Count | P\_Value | Benjamini |
|  | GOTERM\_BP\_DIRECT | endoplasmic reticulum to cytosol auxin transport | 6 | 2.7E-3 | 3.9E-2 |
|  | INTERPRO | PILS1/3/4/5/7 | 5 | 4.4E-3 | 4.1E-2 |
|  | INTERPRO | Mem\_transp\_PIN-like | 6 | 4.0E-2 | 2.3E-1 |
| Annotation Cluster 55 | | Enrichment Score: 2.1 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:U-box | 16 | 3.2E-6 | 6.0E-5 |
|  | INTERPRO | PUB22/23/24-like | 8 | 6.8E-6 | 1.4E-4 |
|  | INTERPRO | Ubox\_domain | 16 | 9.7E-6 | 1.9E-4 |
|  | INTERPRO | RING-Ubox\_PUB | 12 | 6.7E-5 | 1.1E-3 |
|  | SMART | Ubox | 16 | 8.0E-5 | 1.3E-3 |
|  | GOTERM\_BP\_DIRECT | protein ubiquitination | 41 | 1.8E-2 | 1.9E-1 |
|  | UP\_SEQ\_FEATURE | REPEAT:ARM | 6 | 2.6E-1 | 8.4E-1 |
|  | INTERPRO | U-box\_domain\_protein | 3 | 3.6E-1 | 1.0E0 |
|  | INTERPRO | Armadillo | 8 | 4.0E-1 | 1.0E0 |
|  | SMART | ARM | 6 | 7.6E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | ubiquitin protein ligase activity | 16 | 9.8E-1 | 1.0E0 |
|  | INTERPRO | ARM-like | 17 | 1.0E0 | 1.0E0 |
|  | INTERPRO | ARM-type\_fold | 18 | 1.0E0 | 1.0E0 |
| Annotation Cluster 56 | | Enrichment Score: 2.06 | Count | P\_Value | Benjamini |
|  | INTERPRO | Myb\_CC\_LHEQLE | 6 | 5.3E-3 | 4.8E-2 |
|  | UP\_SEQ\_FEATURE | DOMAIN:MYB-CC type transcription factor LHEQLE-containing | 4 | 6.8E-3 | 4.7E-2 |
|  | INTERPRO | PHR1-like | 7 | 9.0E-3 | 7.3E-2 |
|  | INTERPRO | Myb\_dom\_plants | 13 | 1.7E-2 | 1.2E-1 |
| Annotation Cluster 57 | | Enrichment Score: 2.04 | Count | P\_Value | Benjamini |
|  | INTERPRO | Thaumatin | 8 | 2.4E-3 | 2.5E-2 |
|  | INTERPRO | Osmotin/thaumatin-like\_sf | 8 | 2.4E-3 | 2.5E-2 |
|  | SMART | THN | 8 | 7.3E-3 | 5.1E-2 |
|  | INTERPRO | Thaumatin\_CS | 5 | 3.4E-2 | 2.0E-1 |
|  | PIR\_SUPERFAMILY | Thaumatin | 6 | 4.6E-2 | 2.4E-1 |
| Annotation Cluster 58 | | Enrichment Score: 1.94 | Count | P\_Value | Benjamini |
|  | GOTERM\_BP\_DIRECT | cutin biosynthetic process | 9 | 5.0E-7 | 1.8E-5 |
|  | GOTERM\_MF\_DIRECT | glycerol-3-phosphate 2-O-acyltransferase activity | 5 | 1.6E-3 | 1.9E-2 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Phospholipid/glycerol acyltransferase | 5 | 7.3E-2 | 3.3E-1 |
|  | GOTERM\_MF\_DIRECT | phosphatase activity | 10 | 7.5E-2 | 4.1E-1 |
|  | INTERPRO | Plipid/glycerol\_acylTrfase | 5 | 9.0E-2 | 4.3E-1 |
|  | SMART | PlsC | 5 | 1.3E-1 | 5.3E-1 |
|  | KEGG\_PATHWAY | Glycerolipid metabolism | 9 | 5.4E-1 | 1.0E0 |
| Annotation Cluster 59 | | Enrichment Score: 1.9 | Count | P\_Value | Benjamini |
|  | INTERPRO | Copine\_C | 6 | 4.2E-4 | 5.2E-3 |
|  | INTERPRO | VWF\_A | 8 | 4.3E-3 | 4.1E-2 |
|  | SMART | VWA | 8 | 7.3E-3 | 5.1E-2 |
|  | INTERPRO | E3\_ligase/Copine\_domain | 4 | 1.3E-2 | 9.6E-2 |
|  | INTERPRO | vWFA\_dom\_sf | 8 | 5.0E-2 | 2.7E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:VWFA | 3 | 4.4E-1 | 1.0E0 |
| Annotation Cluster 60 | | Enrichment Score: 1.84 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:VQ | 6 | 9.7E-3 | 6.5E-2 |
|  | INTERPRO | VQ | 6 | 1.3E-2 | 9.8E-2 |
|  | INTERPRO | VQ\_8/17/18/20/21/25 | 3 | 2.4E-2 | 1.6E-1 |
| Annotation Cluster 61 | | Enrichment Score: 1.79 | Count | P\_Value | Benjamini |
|  | INTERPRO | Lipoxy\_PLAT/LH2 | 6 | 3.0E-3 | 3.0E-2 |
|  | INTERPRO | LipOase\_Fe\_BS | 7 | 3.2E-3 | 3.1E-2 |
|  | GOTERM\_BP\_DIRECT | oxylipin biosynthetic process | 9 | 3.4E-3 | 4.8E-2 |
|  | INTERPRO | Lipoxygenase\_dom\_3 | 7 | 4.0E-3 | 3.8E-2 |
|  | UP\_SEQ\_FEATURE | DOMAIN:PLAT | 7 | 6.4E-3 | 4.7E-2 |
|  | INTERPRO | PLAT/LH2\_dom | 7 | 9.0E-3 | 7.3E-2 |
|  | INTERPRO | LipOase\_CS | 7 | 1.1E-2 | 8.5E-2 |
|  | GOTERM\_BP\_DIRECT | lipid oxidation | 8 | 1.3E-2 | 1.5E-1 |
|  | INTERPRO | LipOase\_plant | 7 | 1.3E-2 | 9.6E-2 |
|  | SMART | LH2 | 7 | 1.3E-2 | 8.4E-2 |
|  | GOTERM\_MF\_DIRECT | oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen | 9 | 1.5E-2 | 1.4E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Lipoxygenase | 7 | 1.7E-2 | 1.0E-1 |
|  | INTERPRO | LipOase\_C | 7 | 2.3E-2 | 1.6E-1 |
|  | INTERPRO | LipOase | 7 | 2.3E-2 | 1.6E-1 |
|  | INTERPRO | LipOase\_C\_sf | 7 | 2.3E-2 | 1.6E-1 |
|  | KEGG\_PATHWAY | Linoleic acid metabolism | 7 | 2.4E-2 | 1.6E-1 |
|  | INTERPRO | PLAT/LH2\_dom\_sf | 7 | 3.8E-2 | 2.2E-1 |
|  | GOTERM\_BP\_DIRECT | fatty acid biosynthetic process | 16 | 5.6E-2 | 4.6E-1 |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Fatty acid metabolism | 13 | 1.9E-1 | 1.0E0 |
|  | UP\_KW\_MOLECULAR\_FUNCTION | Dioxygenase | 14 | 3.9E-1 | 1.0E0 |
| Annotation Cluster 62 | | Enrichment Score: 1.78 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:FAD-binding PCMH-type | 10 | 2.0E-3 | 1.8E-2 |
|  | INTERPRO | FAD-bd\_PCMH | 10 | 3.4E-3 | 3.2E-2 |
|  | INTERPRO | FAD-bd\_PCMH\_sub2 | 10 | 3.4E-3 | 3.2E-2 |
|  | INTERPRO | FAD-bd\_PCMH-like\_sf | 10 | 5.2E-3 | 4.7E-2 |
|  | INTERPRO | Oxid\_FAD\_bind\_N | 9 | 5.8E-3 | 5.1E-2 |
|  | INTERPRO | FAD-linked\_Oxidoreductases\_BP | 6 | 6.8E-3 | 5.8E-2 |
|  | GOTERM\_MF\_DIRECT | FAD binding | 13 | 1.2E-2 | 1.2E-1 |
|  | UP\_KW\_LIGAND | Flavoprotein | 21 | 1.8E-2 | 7.1E-2 |
|  | GOTERM\_MF\_DIRECT | cytokinin dehydrogenase activity | 4 | 2.3E-2 | 1.7E-1 |
|  | INTERPRO | Cytok\_DH\_C\_sf | 4 | 2.5E-2 | 1.6E-1 |
|  | INTERPRO | Cytokinin\_DH\_FAD/cytokin-bd | 4 | 2.5E-2 | 1.6E-1 |
|  | GOTERM\_BP\_DIRECT | cytokinin metabolic process | 4 | 2.8E-2 | 2.6E-1 |
|  | INTERPRO | Oxy\_OxRdtase\_FAD\_BS | 4 | 3.2E-2 | 2.0E-1 |
|  | INTERPRO | FAD-linked\_Oxase-like\_C | 4 | 4.1E-2 | 2.3E-1 |
|  | INTERPRO | FAD-bd\_PCMH\_sub1 | 7 | 4.2E-2 | 2.4E-1 |
|  | UP\_KW\_LIGAND | FAD | 20 | 9.0E-2 | 3.2E-1 |
|  | KEGG\_PATHWAY | Zeatin biosynthesis | 5 | 3.0E-1 | 1.0E0 |
| Annotation Cluster 63 | | Enrichment Score: 1.75 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:Glycolipid transfer protein | 4 | 1.5E-2 | 9.4E-2 |
|  | GOTERM\_MF\_DIRECT | ceramide 1-phosphate binding | 4 | 1.7E-2 | 1.4E-1 |
|  | GOTERM\_MF\_DIRECT | ceramide 1-phosphate transfer activity | 4 | 1.7E-2 | 1.4E-1 |
|  | INTERPRO | Glycolipid\_transfer\_prot\_dom | 4 | 1.8E-2 | 1.3E-1 |
|  | INTERPRO | GLTP\_sf | 4 | 1.8E-2 | 1.3E-1 |
|  | GOTERM\_BP\_DIRECT | intermembrane lipid transfer | 4 | 2.0E-2 | 2.1E-1 |
|  | GOTERM\_BP\_DIRECT | ceramide transport | 4 | 2.0E-2 | 2.1E-1 |
| Annotation Cluster 64 | | Enrichment Score: 1.69 | Count | P\_Value | Benjamini |
|  | GOTERM\_BP\_DIRECT | plant-type primary cell wall biogenesis | 9 | 1.2E-3 | 2.0E-2 |
|  | INTERPRO | CES\_Znf\_RING | 5 | 6.2E-3 | 5.4E-2 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Cellulose synthase RING-type zinc finger | 4 | 6.8E-3 | 4.7E-2 |
|  | GOTERM\_MF\_DIRECT | cellulose synthase (UDP-forming) activity | 9 | 7.3E-3 | 7.4E-2 |
|  | INTERPRO | Cellulose\_synth | 9 | 7.7E-3 | 6.5E-2 |
|  | INTERPRO | Nucleotide-diphossugar\_trans | 21 | 3.2E-2 | 2.0E-1 |
|  | GOTERM\_BP\_DIRECT | cellulose biosynthetic process | 9 | 4.6E-2 | 3.9E-1 |
|  | GOTERM\_CC\_DIRECT | trans-Golgi network | 12 | 3.1E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | mannan synthase activity | 3 | 5.0E-1 | 1.0E0 |
| Annotation Cluster 65 | | Enrichment Score: 1.68 | Count | P\_Value | Benjamini |
|  | GOTERM\_MF\_DIRECT | calmodulin binding | 28 | 3.7E-5 | 7.6E-4 |
|  | UP\_KW\_MOLECULAR\_FUNCTION | Calmodulin-binding | 18 | 1.9E-2 | 1.3E-1 |
|  | INTERPRO | IQ\_motif\_EF-hand-BS | 10 | 5.6E-2 | 2.9E-1 |
|  | SMART | IQ | 9 | 8.8E-2 | 3.9E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:DUF4005 | 4 | 1.4E-1 | 5.2E-1 |
|  | INTERPRO | DUF4005 | 4 | 1.6E-1 | 6.4E-1 |
| Annotation Cluster 66 | | Enrichment Score: 1.66 | Count | P\_Value | Benjamini |
|  | INTERPRO | WAK-like | 5 | 1.9E-3 | 2.0E-2 |
|  | INTERPRO | EGF-like\_Ca-bd\_dom | 4 | 2.5E-2 | 1.6E-1 |
|  | SMART | EGF\_CA | 4 | 4.2E-2 | 2.3E-1 |
|  | INTERPRO | EGF\_Ca-bd\_CS | 3 | 1.2E-1 | 5.1E-1 |
| Annotation Cluster 67 | | Enrichment Score: 1.62 | Count | P\_Value | Benjamini |
|  | GOTERM\_MF\_DIRECT | signaling receptor activity | 11 | 2.6E-4 | 4.1E-3 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Bet v I/Major latex protein | 9 | 5.0E-3 | 3.7E-2 |
|  | INTERPRO | Bet\_v\_I/MLP | 9 | 7.7E-3 | 6.5E-2 |
|  | INTERPRO | START-like\_dom\_sf | 15 | 1.2E-2 | 9.5E-2 |
|  | INTERPRO | Plant\_def-hormone\_signal | 7 | 1.3E-2 | 9.6E-2 |
|  | GOTERM\_MF\_DIRECT | protein phosphatase inhibitor activity | 8 | 2.1E-2 | 1.7E-1 |
|  | GOTERM\_MF\_DIRECT | abscisic acid binding | 7 | 2.3E-2 | 1.7E-1 |
|  | UP\_KW\_MOLECULAR\_FUNCTION | Pathogenesis-related protein | 7 | 7.9E-2 | 4.1E-1 |
|  | INTERPRO | MLP-like | 4 | 1.1E-1 | 5.1E-1 |
|  | GOTERM\_BP\_DIRECT | abscisic acid-activated signaling pathway | 7 | 1.1E-1 | 7.4E-1 |
|  | INTERPRO | Bet\_v\_I\_allergen | 4 | 1.8E-1 | 6.9E-1 |
|  | SMART | Bet\_v\_1 | 4 | 2.6E-1 | 9.3E-1 |
| Annotation Cluster 68 | | Enrichment Score: 1.61 | Count | P\_Value | Benjamini |
|  | INTERPRO | AA/rel\_permease1 | 6 | 1.1E-2 | 8.4E-2 |
|  | PIR\_SUPERFAMILY | AA\_transporter | 6 | 2.5E-2 | 1.5E-1 |
|  | GOTERM\_MF\_DIRECT | polyamine transmembrane transporter activity | 3 | 3.6E-2 | 2.4E-1 |
|  | INTERPRO | RMV1-like | 3 | 3.8E-2 | 2.3E-1 |
| Annotation Cluster 69 | | Enrichment Score: 1.59 | Count | P\_Value | Benjamini |
|  | KEGG\_PATHWAY | Cutin, suberine and wax biosynthesis | 11 | 5.4E-4 | 5.2E-3 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Fatty acyl-CoA reductase C-terminal | 4 | 1.5E-2 | 9.4E-2 |
|  | INTERPRO | FAR\_C | 4 | 1.8E-2 | 1.3E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Thioester reductase (TE) | 4 | 2.7E-2 | 1.4E-1 |
|  | GOTERM\_MF\_DIRECT | alcohol-forming very long-chain fatty acyl-CoA reductase activity | 4 | 3.0E-2 | 2.1E-1 |
|  | INTERPRO | FAR | 4 | 3.2E-2 | 2.0E-1 |
|  | INTERPRO | Far\_NAD-bd | 4 | 3.2E-2 | 2.0E-1 |
|  | GOTERM\_BP\_DIRECT | long-chain fatty-acyl-CoA metabolic process | 4 | 3.6E-2 | 3.3E-1 |
|  | GOTERM\_BP\_DIRECT | suberin biosynthetic process | 4 | 4.6E-2 | 3.9E-1 |
|  | KEGG\_PATHWAY | Peroxisome | 8 | 6.9E-1 | 1.0E0 |
| Annotation Cluster 70 | | Enrichment Score: 1.58 | Count | P\_Value | Benjamini |
|  | INTERPRO | Allene\_oxi\_cyc\_Dirigent | 9 | 3.0E-3 | 3.0E-2 |
|  | INTERPRO | Dirigent | 6 | 7.2E-2 | 3.6E-1 |
|  | GOTERM\_BP\_DIRECT | phenylpropanoid biosynthetic process | 6 | 8.4E-2 | 5.8E-1 |
| Annotation Cluster 71 | | Enrichment Score: 1.57 | Count | P\_Value | Benjamini |
|  | GOTERM\_BP\_DIRECT | cutin biosynthetic process | 9 | 5.0E-7 | 1.8E-5 |
|  | GOTERM\_BP\_DIRECT | wax biosynthetic process | 4 | 1.3E-3 | 2.0E-2 |
|  | INTERPRO | LC-FACS\_euk | 4 | 8.3E-3 | 6.9E-2 |
|  | KEGG\_PATHWAY | Fatty acid degradation | 10 | 1.1E-1 | 5.5E-1 |
|  | GOTERM\_MF\_DIRECT | long-chain fatty acid-CoA ligase activity | 4 | 1.2E-1 | 5.9E-1 |
|  | KEGG\_PATHWAY | Fatty acid biosynthesis | 6 | 4.3E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | fatty acid metabolic process | 5 | 5.5E-1 | 1.0E0 |
|  | KEGG\_PATHWAY | Peroxisome | 8 | 6.9E-1 | 1.0E0 |
|  | KEGG\_PATHWAY | Fatty acid metabolism | 6 | 7.6E-1 | 1.0E0 |
| Annotation Cluster 72 | | Enrichment Score: 1.51 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:NAD-dependent epimerase/dehydratase | 9 | 1.2E-2 | 8.1E-2 |
|  | INTERPRO | Epimerase\_deHydtase | 9 | 1.8E-2 | 1.3E-1 |
|  | INTERPRO | NAD(P)\_dehydrat-like | 7 | 2.0E-2 | 1.4E-1 |
|  | GOTERM\_MF\_DIRECT | oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor | 10 | 2.0E-1 | 7.5E-1 |
| Annotation Cluster 73 | | Enrichment Score: 1.47 | Count | P\_Value | Benjamini |
|  | INTERPRO | Solute-binding\_3/MltF\_N | 4 | 1.3E-2 | 9.6E-2 |
|  | INTERPRO | Iontropic\_Glu\_rcpt\_pln | 4 | 2.5E-2 | 1.6E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Ionotropic glutamate receptor C-terminal | 4 | 2.7E-2 | 1.4E-1 |
|  | GOTERM\_MF\_DIRECT | ligand-gated monoatomic ion channel activity | 4 | 3.0E-2 | 2.1E-1 |
|  | INTERPRO | Iontro\_rcpt\_C | 4 | 3.2E-2 | 2.0E-1 |
|  | INTERPRO | ANF\_lig-bd\_rcpt | 4 | 3.2E-2 | 2.0E-1 |
|  | INTERPRO | Peripla\_BP\_I | 4 | 4.1E-2 | 2.3E-1 |
|  | INTERPRO | Ionotropic\_Glu\_rcpt | 4 | 5.1E-2 | 2.7E-1 |
|  | SMART | PBPe | 4 | 5.4E-2 | 2.8E-1 |
|  | PIR\_SUPERFAMILY | Iontro\_Glu-like\_rcpt\_pln | 4 | 6.5E-2 | 2.9E-1 |
| Annotation Cluster 74 | | Enrichment Score: 1.46 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:Iron/zinc purple acid phosphatase-like C-terminal | 5 | 8.8E-3 | 6.0E-2 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Purple acid phosphatase N-terminal | 5 | 1.4E-2 | 9.4E-2 |
|  | INTERPRO | MPP\_PAP | 5 | 2.3E-2 | 1.6E-1 |
|  | INTERPRO | Purple\_acid\_PPase\_C\_dom | 5 | 2.3E-2 | 1.6E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Calcineurin-like phosphoesterase | 7 | 2.4E-2 | 1.4E-1 |
|  | GOTERM\_MF\_DIRECT | acid phosphatase activity | 7 | 2.9E-2 | 2.1E-1 |
|  | INTERPRO | Purple\_acid\_Pase\_N | 5 | 3.4E-2 | 2.0E-1 |
|  | INTERPRO | Purple\_acid\_Pase-like\_N | 5 | 3.4E-2 | 2.0E-1 |
|  | INTERPRO | PPA-like | 4 | 4.1E-2 | 2.3E-1 |
|  | INTERPRO | Calcineurin-like\_PHP\_ApaH | 8 | 1.6E-1 | 6.3E-1 |
|  | INTERPRO | Metallo-depent\_PP-like | 8 | 2.7E-1 | 9.0E-1 |
| Annotation Cluster 75 | | Enrichment Score: 1.45 | Count | P\_Value | Benjamini |
|  | INTERPRO | PLipase\_D\_pln | 5 | 4.4E-3 | 4.1E-2 |
|  | GOTERM\_BP\_DIRECT | phosphatidylcholine metabolic process | 5 | 5.2E-3 | 7.0E-2 |
|  | INTERPRO | PLipase\_D\_C | 5 | 1.5E-2 | 1.1E-1 |
|  | PIR\_SUPERFAMILY | PLD\_plant | 5 | 1.7E-2 | 1.1E-1 |
|  | KEGG\_PATHWAY | Ether lipid metabolism | 7 | 2.0E-2 | 1.4E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:PLD phosphodiesterase | 5 | 2.2E-2 | 1.3E-1 |
|  | INTERPRO | PLipase\_D/transphosphatidylase | 5 | 2.8E-2 | 1.8E-1 |
|  | GOTERM\_BP\_DIRECT | phospholipid catabolic process | 7 | 3.2E-2 | 2.9E-1 |
|  | SMART | PLDc | 5 | 5.3E-2 | 2.8E-1 |
|  | KEGG\_PATHWAY | Glycerophospholipid metabolism | 15 | 9.5E-2 | 5.2E-1 |
|  | INTERPRO | PLipase\_D\_fam | 5 | 1.2E-1 | 5.3E-1 |
|  | GOTERM\_MF\_DIRECT | phospholipase D activity | 5 | 1.3E-1 | 6.1E-1 |
|  | KEGG\_PATHWAY | Endocytosis | 12 | 8.5E-1 | 1.0E0 |
| Annotation Cluster 76 | | Enrichment Score: 1.44 | Count | P\_Value | Benjamini |
|  | GOTERM\_MF\_DIRECT | phosphatidylinositol-4,5-bisphosphate binding | 10 | 3.1E-3 | 3.6E-2 |
|  | INTERPRO | Exo70 | 6 | 1.1E-2 | 8.4E-2 |
|  | GOTERM\_BP\_DIRECT | exocytosis | 11 | 1.4E-2 | 1.5E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Exocyst complex subunit Exo70 C-terminal | 5 | 3.2E-2 | 1.7E-1 |
|  | INTERPRO | Exo70\_C | 5 | 4.0E-2 | 2.3E-1 |
|  | GOTERM\_CC\_DIRECT | exocyst | 8 | 6.3E-2 | 5.8E-1 |
|  | INTERPRO | Cullin\_repeat-like\_dom\_sf | 6 | 1.8E-1 | 6.9E-1 |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Exocytosis | 5 | 4.4E-1 | 1.0E0 |
| Annotation Cluster 77 | | Enrichment Score: 1.44 | Count | P\_Value | Benjamini |
|  | INTERPRO | KN\_HD | 6 | 1.9E-2 | 1.3E-1 |
|  | INTERPRO | TALE\_homeobox | 6 | 1.9E-2 | 1.3E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:ELK | 4 | 2.0E-2 | 1.2E-1 |
|  | UP\_SEQ\_FEATURE | DNA\_BIND:Homeobox; TALE-type | 4 | 2.0E-2 | 1.2E-1 |
|  | INTERPRO | ELK\_dom | 4 | 2.5E-2 | 1.6E-1 |
|  | INTERPRO | KNOX1 | 4 | 4.1E-2 | 2.3E-1 |
|  | INTERPRO | KNOX2 | 4 | 4.1E-2 | 2.3E-1 |
|  | SMART | KNOX1 | 4 | 6.8E-2 | 3.3E-1 |
|  | SMART | KNOX2 | 4 | 6.8E-2 | 3.3E-1 |
|  | SMART | ELK | 3 | 1.6E-1 | 6.5E-1 |
| Annotation Cluster 78 | | Enrichment Score: 1.41 | Count | P\_Value | Benjamini |
|  | INTERPRO | RmlC-like\_jellyroll | 20 | 4.4E-3 | 4.1E-2 |
|  | INTERPRO | Germin | 8 | 8.5E-3 | 7.0E-2 |
|  | INTERPRO | Germin\_Mn-BS | 8 | 8.5E-3 | 7.0E-2 |
|  | GOTERM\_MF\_DIRECT | manganese ion binding | 9 | 4.8E-2 | 3.0E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Cupin type-1 | 10 | 5.4E-2 | 2.6E-1 |
|  | INTERPRO | Cupin\_1 | 10 | 9.9E-2 | 4.5E-1 |
|  | INTERPRO | RmlC\_Cupin\_sf | 11 | 1.9E-1 | 7.1E-1 |
|  | SMART | Cupin\_1 | 9 | 3.4E-1 | 1.0E0 |
| Annotation Cluster 79 | | Enrichment Score: 1.41 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:PI-PLC Y-box | 4 | 6.8E-3 | 4.7E-2 |
|  | GOTERM\_MF\_DIRECT | phosphatidylinositol phospholipase C activity | 4 | 7.6E-3 | 7.6E-2 |
|  | INTERPRO | PLipase\_C\_Pinositol-sp\_Y | 4 | 8.3E-3 | 6.9E-2 |
|  | INTERPRO | PI-PLC\_fam | 4 | 8.3E-3 | 6.9E-2 |
|  | GOTERM\_BP\_DIRECT | release of sequestered calcium ion into cytosol | 4 | 9.5E-3 | 1.2E-1 |
|  | INTERPRO | PLipase\_C\_PInositol-sp\_X\_dom | 4 | 1.3E-2 | 9.6E-2 |
|  | SMART | PLCYc | 4 | 1.5E-2 | 9.0E-2 |
|  | SMART | PLCXc | 4 | 2.2E-2 | 1.3E-1 |
|  | GOTERM\_BP\_DIRECT | phosphatidylinositol-mediated signaling | 4 | 4.6E-2 | 3.9E-1 |
|  | GOTERM\_BP\_DIRECT | lipid catabolic process | 9 | 1.8E-1 | 9.8E-1 |
|  | KEGG\_PATHWAY | Phosphatidylinositol signaling system | 8 | 2.9E-1 | 1.0E0 |
|  | UP\_KW\_MOLECULAR\_FUNCTION | Transducer | 4 | 3.5E-1 | 1.0E0 |
|  | INTERPRO | PLC-like\_Pdiesterase\_TIM-brl | 4 | 3.9E-1 | 1.0E0 |
|  | KEGG\_PATHWAY | Inositol phosphate metabolism | 7 | 4.4E-1 | 1.0E0 |
| Annotation Cluster 80 | | Enrichment Score: 1.36 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:EamA | 12 | 3.2E-2 | 1.7E-1 |
|  | INTERPRO | EamA\_dom | 12 | 5.0E-2 | 2.7E-1 |
|  | INTERPRO | WAT1-related | 12 | 5.3E-2 | 2.9E-1 |
| Annotation Cluster 81 | | Enrichment Score: 1.35 | Count | P\_Value | Benjamini |
|  | INTERPRO | Thioredoxin\_H-type-like | 5 | 6.2E-3 | 5.4E-2 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Thioredoxin | 11 | 4.7E-2 | 2.4E-1 |
|  | INTERPRO | Thioredoxin\_domain | 11 | 7.0E-2 | 3.5E-1 |
|  | INTERPRO | Thioredoxin\_CS | 5 | 2.0E-1 | 7.3E-1 |
| Annotation Cluster 82 | | Enrichment Score: 1.34 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:GH18 | 6 | 3.5E-2 | 1.8E-1 |
|  | INTERPRO | Glyco\_hydro18\_cat | 6 | 4.6E-2 | 2.5E-1 |
|  | INTERPRO | Chitinase-like | 4 | 6.1E-2 | 3.1E-1 |
| Annotation Cluster 83 | | Enrichment Score: 1.34 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:Trichome birefringence-like N-terminal | 9 | 2.8E-2 | 1.5E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Trichome birefringence-like C-terminal | 9 | 3.3E-2 | 1.7E-1 |
|  | INTERPRO | TBL | 9 | 3.7E-2 | 2.2E-1 |
|  | INTERPRO | TBL\_N | 9 | 4.0E-2 | 2.3E-1 |
|  | GOTERM\_MF\_DIRECT | O-acetyltransferase activity | 9 | 4.1E-2 | 2.7E-1 |
|  | INTERPRO | TBL\_C | 9 | 4.8E-2 | 2.6E-1 |
|  | UP\_KW\_DOMAIN | Signal-anchor | 19 | 1.7E-1 | 4.9E-1 |
| Annotation Cluster 84 | | Enrichment Score: 1.33 | Count | P\_Value | Benjamini |
|  | INTERPRO | Prot\_inh\_Kunz-lg | 4 | 4.1E-2 | 2.3E-1 |
|  | INTERPRO | Kunitz\_inhibitor\_STI-like\_sf | 4 | 4.1E-2 | 2.3E-1 |
|  | GOTERM\_MF\_DIRECT | endopeptidase inhibitor activity | 5 | 4.2E-2 | 2.8E-1 |
|  | SMART | STI | 4 | 6.8E-2 | 3.3E-1 |
| Annotation Cluster 85 | | Enrichment Score: 1.31 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:NADH:flavin oxidoreductase/NADH oxidase N-terminal | 5 | 4.8E-3 | 3.6E-2 |
|  | INTERPRO | Oye-like | 5 | 6.2E-3 | 5.4E-2 |
|  | INTERPRO | OxRdtase\_FMN\_N | 5 | 6.2E-3 | 5.4E-2 |
|  | GOTERM\_MF\_DIRECT | FMN binding | 6 | 1.9E-1 | 7.5E-1 |
|  | UP\_KW\_LIGAND | FMN | 5 | 4.3E-1 | 1.0E0 |
|  | INTERPRO | Aldolase\_TIM | 8 | 9.3E-1 | 1.0E0 |
| Annotation Cluster 86 | | Enrichment Score: 1.28 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:Saposin B-type | 4 | 2.0E-2 | 1.2E-1 |
|  | INTERPRO | SapB\_1 | 4 | 2.5E-2 | 1.6E-1 |
|  | INTERPRO | SapB\_2 | 4 | 2.5E-2 | 1.6E-1 |
|  | INTERPRO | SaposinB\_dom | 4 | 2.5E-2 | 1.6E-1 |
|  | INTERPRO | Saposin-like | 4 | 2.5E-2 | 1.6E-1 |
|  | UP\_KW\_PTM | Zymogen | 6 | 1.4E-1 | 3.4E-1 |
|  | INTERPRO | Aspartic\_peptidase\_AS | 11 | 1.0E0 | 1.0E0 |
| Annotation Cluster 87 | | Enrichment Score: 1.28 | Count | P\_Value | Benjamini |
|  | INTERPRO | FAD-bd\_8 | 5 | 1.5E-2 | 1.1E-1 |
|  | INTERPRO | Fe\_red\_NAD-bd\_6 | 5 | 4.0E-2 | 2.3E-1 |
|  | INTERPRO | Cyt\_b245\_heavy\_chain | 4 | 4.1E-2 | 2.3E-1 |
|  | INTERPRO | RBOH/FRE | 5 | 4.7E-2 | 2.6E-1 |
|  | INTERPRO | Fe3\_Rdtase\_TM\_dom | 4 | 5.1E-2 | 2.7E-1 |
|  | INTERPRO | FNR\_nucleotide-bd | 6 | 6.5E-2 | 3.2E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:FAD-binding FR-type | 5 | 6.5E-2 | 2.9E-1 |
|  | GOTERM\_MF\_DIRECT | NAD(P)H oxidase H2O2-forming activity | 4 | 6.7E-2 | 3.8E-1 |
|  | INTERPRO | Riboflavin\_synthase-like\_b-brl | 6 | 7.2E-2 | 3.6E-1 |
|  | INTERPRO | FAD-bd\_FR\_type | 5 | 8.0E-2 | 3.8E-1 |
|  | INTERPRO | NADPH\_Ox | 3 | 9.4E-2 | 4.4E-1 |
| Annotation Cluster 88 | | Enrichment Score: 1.28 | Count | P\_Value | Benjamini |
|  | UP\_KW\_LIGAND | Lectin | 9 | 2.2E-3 | 9.6E-3 |
|  | INTERPRO | Legume\_lectin\_dom | 7 | 1.7E-2 | 1.3E-1 |
|  | INTERPRO | L-type\_Lectin-RKs | 4 | 1.4E-1 | 5.8E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Legume lectin | 3 | 2.6E-1 | 8.4E-1 |
|  | INTERPRO | Leguminous\_Lectin | 3 | 2.9E-1 | 9.2E-1 |
| Annotation Cluster 89 | | Enrichment Score: 1.27 | Count | P\_Value | Benjamini |
|  | GOTERM\_MF\_DIRECT | hydrolase activity, hydrolyzing O-glycosyl compounds | 33 | 1.0E-3 | 1.3E-2 |
|  | INTERPRO | Glycoside\_hydrolase\_SF | 36 | 8.2E-2 | 3.9E-1 |
|  | GOTERM\_BP\_DIRECT | carbohydrate metabolic process | 49 | 1.7E-1 | 9.5E-1 |
|  | UP\_KW\_MOLECULAR\_FUNCTION | Glycosidase | 43 | 5.4E-1 | 1.0E0 |
| Annotation Cluster 90 | | Enrichment Score: 1.23 | Count | P\_Value | Benjamini |
|  | INTERPRO | DDP-like\_NUDIX | 5 | 6.2E-3 | 5.4E-2 |
|  | INTERPRO | NUDIX\_hydrolase\_CS | 8 | 9.9E-3 | 7.9E-2 |
|  | GOTERM\_MF\_DIRECT | pyrophosphatase activity | 5 | 2.1E-2 | 1.7E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Nudix hydrolase | 8 | 2.2E-2 | 1.3E-1 |
|  | INTERPRO | NUDIX\_hydrolase\_dom | 8 | 3.1E-2 | 2.0E-1 |
|  | INTERPRO | NUDIX\_hydrolase-like\_dom\_sf | 8 | 5.0E-2 | 2.7E-1 |
|  | INTERPRO | Nudix\_hydrolase6-like | 3 | 5.5E-2 | 2.9E-1 |
|  | INTERPRO | Pre-Nudix | 3 | 5.5E-2 | 2.9E-1 |
|  | GOTERM\_MF\_DIRECT | ADP-ribose diphosphatase activity | 3 | 2.0E-1 | 7.5E-1 |
|  | GOTERM\_MF\_DIRECT | NADH pyrophosphatase activity | 3 | 2.0E-1 | 7.5E-1 |
|  | KEGG\_PATHWAY | Purine metabolism | 9 | 4.8E-1 | 1.0E0 |
|  | KEGG\_PATHWAY | Nicotinate and nicotinamide metabolism | 3 | 7.2E-1 | 1.0E0 |
| Annotation Cluster 91 | | Enrichment Score: 1.21 | Count | P\_Value | Benjamini |
|  | INTERPRO | MIP\_CS | 7 | 3.0E-2 | 1.9E-1 |
|  | INTERPRO | Aquaporin\_transptr | 7 | 3.8E-2 | 2.2E-1 |
|  | INTERPRO | MIP | 7 | 7.5E-2 | 3.6E-1 |
|  | INTERPRO | Aquaporin-like | 7 | 7.5E-2 | 3.6E-1 |
|  | GOTERM\_MF\_DIRECT | channel activity | 5 | 1.3E-1 | 6.1E-1 |
| Annotation Cluster 92 | | Enrichment Score: 1.2 | Count | P\_Value | Benjamini |
|  | SMART | ZnF\_C2H2 | 12 | 1.7E-2 | 9.9E-2 |
|  | UP\_SEQ\_FEATURE | DOMAIN:C2H2-type | 17 | 2.9E-2 | 1.5E-1 |
|  | INTERPRO | Znf\_C2H2\_type | 18 | 9.0E-2 | 4.3E-1 |
|  | INTERPRO | Znf\_C2H2\_sf | 18 | 3.8E-1 | 1.0E0 |
| Annotation Cluster 93 | | Enrichment Score: 1.15 | Count | P\_Value | Benjamini |
|  | INTERPRO | LOR | 5 | 3.4E-2 | 2.0E-1 |
|  | INTERPRO | LOR\_sf | 5 | 3.4E-2 | 2.0E-1 |
|  | INTERPRO | Tubby-like\_C | 5 | 3.2E-1 | 1.0E0 |
| Annotation Cluster 94 | | Enrichment Score: 1.13 | Count | P\_Value | Benjamini |
|  | GOTERM\_MF\_DIRECT | protein serine/threonine phosphatase activity | 15 | 3.0E-2 | 2.1E-1 |
|  | GOTERM\_BP\_DIRECT | protein dephosphorylation | 15 | 4.6E-2 | 3.9E-1 |
|  | INTERPRO | PP2C\_BS | 7 | 6.3E-2 | 3.2E-1 |
|  | INTERPRO | PP2C | 11 | 6.6E-2 | 3.3E-1 |
|  | GOTERM\_MF\_DIRECT | cation binding | 7 | 6.7E-2 | 3.8E-1 |
|  | INTERPRO | PPM-type-like\_dom\_sf | 12 | 8.0E-2 | 3.8E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:PPM-type phosphatase | 11 | 8.0E-2 | 3.5E-1 |
|  | INTERPRO | PPM-type\_phosphatase-like\_dom | 11 | 1.2E-1 | 5.1E-1 |
|  | SMART | PP2Cc | 11 | 2.3E-1 | 8.7E-1 |
| Annotation Cluster 95 | | Enrichment Score: 1.1 | Count | P\_Value | Benjamini |
|  | GOTERM\_MF\_DIRECT | lipase activity | 7 | 1.1E-2 | 1.0E-1 |
|  | INTERPRO | MAG\_DAG\_Lipase | 4 | 5.1E-2 | 2.7E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Serine aminopeptidase S33 | 4 | 2.5E-1 | 8.1E-1 |
|  | INTERPRO | Hydrolase\_4 | 4 | 2.8E-1 | 9.2E-1 |
| Annotation Cluster 96 | | Enrichment Score: 1.09 | Count | P\_Value | Benjamini |
|  | INTERPRO | Carbonic\_anhydrase\_CS | 3 | 5.5E-2 | 2.9E-1 |
|  | INTERPRO | Carbonic\_anhydrase | 3 | 5.5E-2 | 2.9E-1 |
|  | INTERPRO | Carbonic\_anhydrase\_sf | 3 | 5.5E-2 | 2.9E-1 |
|  | INTERPRO | Beta\_CA\_cladeB | 3 | 5.5E-2 | 2.9E-1 |
|  | GOTERM\_BP\_DIRECT | carbon utilization | 3 | 6.0E-2 | 4.7E-1 |
|  | SMART | Pro\_CA | 3 | 7.9E-2 | 3.6E-1 |
|  | GOTERM\_MF\_DIRECT | carbonate dehydratase activity | 4 | 1.2E-1 | 5.9E-1 |
|  | KEGG\_PATHWAY | Nitrogen metabolism | 5 | 3.5E-1 | 1.0E0 |
| Annotation Cluster 97 | | Enrichment Score: 1.09 | Count | P\_Value | Benjamini |
|  | INTERPRO | Alpha\_amylase | 3 | 2.4E-2 | 1.6E-1 |
|  | INTERPRO | A-amylase\_pln | 3 | 2.4E-2 | 1.6E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Alpha-amylase C-terminal beta-sheet | 3 | 4.8E-2 | 2.4E-1 |
|  | PIR\_SUPERFAMILY | Alph-amls\_plant | 3 | 5.0E-2 | 2.4E-1 |
|  | GOTERM\_MF\_DIRECT | alpha-amylase activity | 3 | 5.2E-2 | 3.1E-1 |
|  | INTERPRO | A-amylase\_bs\_C | 3 | 5.5E-2 | 2.9E-1 |
|  | SMART | Alpha-amyl\_C2 | 3 | 7.9E-2 | 3.6E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Glycosyl hydrolase family 13 catalytic | 3 | 1.7E-1 | 6.1E-1 |
|  | INTERPRO | Glyco\_hydro\_13\_cat\_dom | 3 | 1.9E-1 | 6.9E-1 |
|  | SMART | Aamy | 3 | 2.5E-1 | 9.2E-1 |
|  | INTERPRO | Glyco\_hydro\_b | 4 | 4.1E-1 | 1.0E0 |
| Annotation Cluster 98 | | Enrichment Score: 1.06 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:Extensin | 4 | 2.7E-2 | 1.4E-1 |
|  | INTERPRO | Extensin\_dom | 4 | 3.2E-2 | 2.0E-1 |
|  | GOTERM\_MF\_DIRECT | structural constituent of cell wall | 4 | 9.2E-2 | 4.9E-1 |
|  | GOTERM\_BP\_DIRECT | plant-type cell wall organization | 4 | 7.1E-1 | 1.0E0 |
| Annotation Cluster 99 | | Enrichment Score: 1.03 | Count | P\_Value | Benjamini |
|  | INTERPRO | UspA | 7 | 3.8E-2 | 2.2E-1 |
|  | INTERPRO | U-box\_ubiquitin\_ligases | 5 | 4.7E-2 | 2.6E-1 |
|  | INTERPRO | Rossmann-like\_a/b/a\_fold | 11 | 4.6E-1 | 1.0E0 |
| Annotation Cluster 100 | | Enrichment Score: 1.02 | Count | P\_Value | Benjamini |
|  | INTERPRO | SWEET | 5 | 6.2E-2 | 3.1E-1 |
|  | INTERPRO | SWEET\_rpt | 5 | 6.2E-2 | 3.1E-1 |
|  | GOTERM\_BP\_DIRECT | carbohydrate transport | 6 | 1.2E-1 | 7.7E-1 |
|  | GOTERM\_MF\_DIRECT | sugar transmembrane transporter activity | 5 | 1.8E-1 | 7.3E-1 |
| Annotation Cluster 101 | | Enrichment Score: 1.01 | Count | P\_Value | Benjamini |
|  | INTERPRO | POT\_fam | 12 | 6.0E-2 | 3.1E-1 |
|  | GOTERM\_BP\_DIRECT | dipeptide transport | 4 | 8.1E-2 | 5.7E-1 |
|  | GOTERM\_MF\_DIRECT | dipeptide transmembrane transporter activity | 4 | 1.0E-1 | 5.5E-1 |
|  | INTERPRO | NRT1/PTR | 4 | 1.1E-1 | 5.1E-1 |
|  | GOTERM\_MF\_DIRECT | tripeptide transmembrane transporter activity | 4 | 1.5E-1 | 6.4E-1 |
| Annotation Cluster 102 | | Enrichment Score: 1.01 | Count | P\_Value | Benjamini |
|  | INTERPRO | PEBP-like\_sf | 4 | 6.1E-2 | 3.1E-1 |
|  | INTERPRO | PEBP | 4 | 6.1E-2 | 3.1E-1 |
|  | INTERPRO | Phosphatidylethanolamine-bd\_CS | 3 | 1.2E-1 | 5.1E-1 |
|  | INTERPRO | PEBP\_euk | 3 | 2.1E-1 | 7.6E-1 |
| Annotation Cluster 103 | | Enrichment Score: 1.01 | Count | P\_Value | Benjamini |
|  | GOTERM\_BP\_DIRECT | positive regulation of growth | 5 | 6.2E-2 | 4.7E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:DUF3475 | 4 | 9.6E-2 | 4.0E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:DUF668 | 4 | 1.1E-1 | 4.5E-1 |
|  | INTERPRO | DUF3475 | 4 | 1.1E-1 | 5.1E-1 |
|  | INTERPRO | DUF668 | 4 | 1.3E-1 | 5.4E-1 |
| Annotation Cluster 104 | | Enrichment Score: 1 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:Ammonium transporter AmtB-like | 3 | 8.3E-2 | 3.6E-1 |
|  | INTERPRO | Ammonium/urea\_transptr | 3 | 9.4E-2 | 4.4E-1 |
|  | INTERPRO | Ammonium\_transpt\_CS | 3 | 9.4E-2 | 4.4E-1 |
|  | INTERPRO | NH4\_transpt\_AmtB-like\_dom | 3 | 9.4E-2 | 4.4E-1 |
|  | GOTERM\_MF\_DIRECT | ammonium channel activity | 3 | 1.1E-1 | 5.7E-1 |
|  | GOTERM\_BP\_DIRECT | ammonium transmembrane transport | 3 | 1.3E-1 | 7.7E-1 |
| Annotation Cluster 105 | | Enrichment Score: 0.99 | Count | P\_Value | Benjamini |
|  | INTERPRO | Sugar\_transporter\_CS | 12 | 3.3E-2 | 2.0E-1 |
|  | INTERPRO | MFS\_trans\_sf | 43 | 3.9E-2 | 2.3E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Major facilitator superfamily (MFS) profile | 23 | 5.0E-2 | 2.4E-1 |
|  | INTERPRO | MFS\_dom | 23 | 9.3E-2 | 4.4E-1 |
|  | INTERPRO | Myo-inositol\_Transporter | 4 | 9.9E-2 | 4.5E-1 |
|  | GOTERM\_MF\_DIRECT | myo-inositol:proton symporter activity | 3 | 2.0E-1 | 7.5E-1 |
|  | INTERPRO | Sugar/inositol\_transpt | 9 | 2.3E-1 | 8.2E-1 |
|  | INTERPRO | MFS\_sugar\_transport-like | 17 | 4.4E-1 | 1.0E0 |
| Annotation Cluster 106 | | Enrichment Score: 0.96 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:Glycoside hydrolase family 5 | 4 | 9.6E-2 | 4.0E-1 |
|  | INTERPRO | Glyco\_hydro\_5 | 4 | 1.1E-1 | 5.1E-1 |
|  | GOTERM\_BP\_DIRECT | polysaccharide catabolic process | 7 | 1.2E-1 | 7.7E-1 |
| Annotation Cluster 107 | | Enrichment Score: 0.94 | Count | P\_Value | Benjamini |
|  | KEGG\_PATHWAY | Stilbenoid, diarylheptanoid and gingerol biosynthesis | 5 | 9.1E-2 | 5.2E-1 |
|  | INTERPRO | Cation-dep\_OMT | 3 | 1.2E-1 | 5.1E-1 |
|  | INTERPRO | SAM\_O-MeTrfase | 3 | 1.2E-1 | 5.1E-1 |
|  | GOTERM\_MF\_DIRECT | O-methyltransferase activity | 8 | 1.4E-1 | 6.1E-1 |
| Annotation Cluster 108 | | Enrichment Score: 0.94 | Count | P\_Value | Benjamini |
|  | INTERPRO | MOT1/MOT2 | 3 | 9.4E-2 | 4.4E-1 |
|  | GOTERM\_BP\_DIRECT | molybdate ion transport | 3 | 1.0E-1 | 6.8E-1 |
|  | GOTERM\_MF\_DIRECT | molybdate ion transmembrane transporter activity | 3 | 1.5E-1 | 6.6E-1 |
| Annotation Cluster 109 | | Enrichment Score: 0.94 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | MOTIF:DGA/G | 4 | 6.1E-2 | 2.8E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:PNPLA | 4 | 9.6E-2 | 4.0E-1 |
|  | INTERPRO | PNPLA\_dom | 4 | 1.1E-1 | 5.1E-1 |
|  | INTERPRO | Acyl\_Trfase/lysoPLipase | 4 | 1.4E-1 | 5.8E-1 |
|  | UP\_SEQ\_FEATURE | MOTIF:GXSXG | 3 | 2.1E-1 | 7.2E-1 |
| Annotation Cluster 110 | | Enrichment Score: 0.92 | Count | P\_Value | Benjamini |
|  | GOTERM\_MF\_DIRECT | ATP hydrolysis activity | 65 | 3.7E-3 | 4.1E-2 |
|  | UP\_KW\_LIGAND | ATP-binding | 122 | 5.1E-1 | 1.0E0 |
|  | UP\_KW\_LIGAND | Nucleotide-binding | 107 | 9.2E-1 | 1.0E0 |
| Annotation Cluster 111 | | Enrichment Score: 0.91 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:Pleckstrin-like plant | 3 | 6.5E-2 | 2.9E-1 |
|  | INTERPRO | PH\_pln | 3 | 7.4E-2 | 3.6E-1 |
|  | INTERPRO | VAB | 3 | 1.4E-1 | 5.7E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:VAN3-binding protein-like auxin canalisation | 3 | 1.9E-1 | 6.7E-1 |
|  | INTERPRO | VAN3-bd-like\_auxin\_canal | 3 | 2.1E-1 | 7.6E-1 |
| Annotation Cluster 112 | | Enrichment Score: 0.88 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:ACT | 6 | 8.2E-2 | 3.6E-1 |
|  | INTERPRO | ACR1-12 | 4 | 9.9E-2 | 4.5E-1 |
|  | INTERPRO | ACT\_dom | 6 | 1.0E-1 | 4.8E-1 |
|  | INTERPRO | ACT-like\_dom\_sf | 6 | 1.3E-1 | 5.6E-1 |
|  | GOTERM\_MF\_DIRECT | amino acid binding | 4 | 3.4E-1 | 1.0E0 |
| Annotation Cluster 113 | | Enrichment Score: 0.85 | Count | P\_Value | Benjamini |
|  | GOTERM\_BP\_DIRECT | response to light stimulus | 9 | 5.9E-2 | 4.7E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:ALOG | 4 | 6.1E-2 | 2.8E-1 |
|  | INTERPRO | ALOG\_dom | 4 | 7.3E-2 | 3.6E-1 |
|  | INTERPRO | ALOG | 4 | 7.3E-2 | 3.6E-1 |
|  | GOTERM\_BP\_DIRECT | mRNA transcription | 4 | 8.1E-2 | 5.7E-1 |
|  | UP\_KW\_MOLECULAR\_FUNCTION | Developmental protein | 6 | 8.4E-1 | 1.0E0 |
|  | UP\_KW\_MOLECULAR\_FUNCTION | Developmental protein | 6 | 8.4E-1 | 1.0E0 |
| Annotation Cluster 114 | | Enrichment Score: 0.82 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:Dof-type | 5 | 1.3E-1 | 5.1E-1 |
|  | INTERPRO | Dof | 5 | 1.6E-1 | 6.4E-1 |
|  | INTERPRO | Znf\_Dof | 5 | 1.6E-1 | 6.4E-1 |
| Annotation Cluster 115 | | Enrichment Score: 0.81 | Count | P\_Value | Benjamini |
|  | INTERPRO | Ser\_caboxypep\_ser\_AS | 7 | 8.2E-2 | 3.9E-1 |
|  | INTERPRO | Peptidase\_S10 | 9 | 1.2E-1 | 5.4E-1 |
|  | GOTERM\_MF\_DIRECT | serine-type carboxypeptidase activity | 9 | 1.3E-1 | 6.0E-1 |
|  | GOTERM\_BP\_DIRECT | secondary metabolic process | 3 | 4.3E-1 | 1.0E0 |
| Annotation Cluster 116 | | Enrichment Score: 0.81 | Count | P\_Value | Benjamini |
|  | INTERPRO | PUP\_plant | 3 | 1.4E-1 | 5.7E-1 |
|  | GOTERM\_MF\_DIRECT | purine nucleoside transmembrane transporter activity | 3 | 1.5E-1 | 6.6E-1 |
|  | GOTERM\_MF\_DIRECT | purine nucleobase transmembrane transporter activity | 3 | 1.8E-1 | 7.2E-1 |
| Annotation Cluster 117 | | Enrichment Score: 0.81 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:Peptidase C14 caspase | 3 | 1.4E-1 | 5.5E-1 |
|  | INTERPRO | Metacaspase | 3 | 1.6E-1 | 6.5E-1 |
|  | INTERPRO | Pept\_C14\_caspase | 3 | 1.6E-1 | 6.5E-1 |
| Annotation Cluster 118 | | Enrichment Score: 0.79 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:DUF547 | 3 | 1.2E-1 | 4.8E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Ternary complex factor MIP1 leucine-zipper | 3 | 1.2E-1 | 4.8E-1 |
|  | INTERPRO | MIP1\_Leuzipper | 3 | 1.9E-1 | 6.9E-1 |
|  | INTERPRO | DUF547 | 3 | 2.4E-1 | 8.3E-1 |
| Annotation Cluster 119 | | Enrichment Score: 0.78 | Count | P\_Value | Benjamini |
|  | INTERPRO | Znf\_RING-CH | 5 | 1.3E-1 | 5.6E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:RING-CH-type | 4 | 1.5E-1 | 5.7E-1 |
|  | SMART | RINGv | 5 | 2.2E-1 | 8.6E-1 |
| Annotation Cluster 120 | | Enrichment Score: 0.76 | Count | P\_Value | Benjamini |
|  | UP\_KW\_DOMAIN | Glutamine amidotransferase | 5 | 2.8E-2 | 9.4E-2 |
|  | INTERPRO | Class\_I\_gatase-like | 3 | 4.3E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | glutamine metabolic process | 3 | 4.3E-1 | 1.0E0 |
| Annotation Cluster 121 | | Enrichment Score: 0.76 | Count | P\_Value | Benjamini |
|  | INTERPRO | P\_typ\_ATPase\_HD\_dom | 10 | 1.4E-2 | 1.0E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Cation-transporting P-type ATPase C-terminal | 5 | 1.8E-2 | 1.1E-1 |
|  | INTERPRO | ATPase\_P-typ\_transduc\_dom\_A\_sf | 11 | 7.0E-2 | 3.5E-1 |
|  | INTERPRO | ATPase\_P-typ\_cation-transptr\_C | 5 | 8.0E-2 | 3.8E-1 |
|  | GOTERM\_MF\_DIRECT | P-type calcium transporter activity | 5 | 1.7E-1 | 7.2E-1 |
|  | INTERPRO | ATPase\_P-typ\_TM\_dom\_sf | 11 | 1.8E-1 | 6.9E-1 |
|  | INTERPRO | ATPase\_P-typ\_P\_site | 10 | 1.9E-1 | 6.9E-1 |
|  | INTERPRO | HAD-like\_sf | 20 | 2.0E-1 | 7.4E-1 |
|  | INTERPRO | HAD\_sf | 21 | 2.0E-1 | 7.4E-1 |
|  | GOTERM\_BP\_DIRECT | calcium ion transmembrane transport | 5 | 2.1E-1 | 1.0E0 |
|  | INTERPRO | ATPase\_P-typ\_cyto\_dom\_N | 11 | 2.6E-1 | 8.8E-1 |
|  | INTERPRO | P\_typ\_ATPase | 10 | 2.6E-1 | 8.8E-1 |
|  | GOTERM\_BP\_DIRECT | intracellular calcium ion homeostasis | 4 | 3.1E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Cation-transporting P-type ATPase N-terminal | 5 | 4.0E-1 | 1.0E0 |
|  | INTERPRO | ATPase\_P-typ\_cation-transptr\_N | 5 | 4.6E-1 | 1.0E0 |
|  | SMART | Cation\_ATPase\_N | 5 | 5.2E-1 | 1.0E0 |
|  | UP\_KW\_MOLECULAR\_FUNCTION | Translocase | 14 | 9.6E-1 | 1.0E0 |
| Annotation Cluster 122 | | Enrichment Score: 0.75 | Count | P\_Value | Benjamini |
|  | INTERPRO | Glyco\_hydro\_32\_AS | 3 | 1.2E-1 | 5.1E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Glycosyl hydrolase family 32 C-terminal | 3 | 1.2E-1 | 4.8E-1 |
|  | INTERPRO | Glyco\_hydro\_32\_C | 3 | 1.4E-1 | 5.7E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Glycosyl hydrolase family 32 N-terminal | 3 | 1.7E-1 | 6.1E-1 |
|  | INTERPRO | Glyco\_hydro\_32\_N | 3 | 1.9E-1 | 6.9E-1 |
|  | INTERPRO | Glyco\_hydro\_32 | 3 | 1.9E-1 | 6.9E-1 |
|  | INTERPRO | Fructan\_Metab\_Enzymes | 3 | 1.9E-1 | 6.9E-1 |
|  | SMART | Glyco\_32 | 3 | 2.5E-1 | 9.2E-1 |
|  | INTERPRO | Glyco\_hydro\_beta-prop\_sf | 3 | 3.1E-1 | 9.9E-1 |
| Annotation Cluster 123 | | Enrichment Score: 0.73 | Count | P\_Value | Benjamini |
|  | INTERPRO | C2B\_MCTP\_PRT\_plant | 3 | 1.2E-1 | 5.1E-1 |
|  | INTERPRO | C2C\_MCTP\_PRT\_plant | 3 | 1.2E-1 | 5.1E-1 |
|  | INTERPRO | MCTP\_C | 3 | 2.6E-1 | 8.8E-1 |
|  | INTERPRO | QUIRKY-like | 3 | 3.4E-1 | 1.0E0 |
| Annotation Cluster 124 | | Enrichment Score: 0.72 | Count | P\_Value | Benjamini |
|  | INTERPRO | Pectinesterase\_Tyr\_AS | 6 | 4.6E-2 | 2.5E-1 |
|  | INTERPRO | Pectinesterase\_Asp\_AS | 10 | 5.2E-2 | 2.8E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Pectinesterase inhibitor | 12 | 6.6E-2 | 3.0E-1 |
|  | GOTERM\_MF\_DIRECT | enzyme inhibitor activity | 14 | 7.1E-2 | 4.0E-1 |
|  | GOTERM\_BP\_DIRECT | pectin catabolic process | 11 | 8.9E-2 | 6.1E-1 |
|  | INTERPRO | Pectinesterase\_inhib\_dom | 12 | 1.3E-1 | 5.4E-1 |
|  | INTERPRO | Invertase/methylesterase\_inhib | 12 | 1.5E-1 | 6.0E-1 |
|  | SMART | PMEI | 12 | 1.7E-1 | 6.7E-1 |
|  | INTERPRO | Pectinesterase\_cat | 10 | 1.9E-1 | 7.1E-1 |
|  | GOTERM\_MF\_DIRECT | pectinesterase activity | 10 | 2.2E-1 | 8.2E-1 |
|  | GOTERM\_BP\_DIRECT | cell wall modification | 10 | 2.8E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | pectinesterase inhibitor activity | 8 | 2.9E-1 | 9.6E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Pectinesterase catalytic | 5 | 3.6E-1 | 1.0E0 |
|  | INTERPRO | Pectin\_lyas\_fold | 12 | 8.4E-1 | 1.0E0 |
|  | INTERPRO | Pectin\_lyase\_fold/virulence | 12 | 8.5E-1 | 1.0E0 |
|  | KEGG\_PATHWAY | Pentose and glucuronate interconversions | 8 | 9.4E-1 | 1.0E0 |
| Annotation Cluster 125 | | Enrichment Score: 0.7 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:PGG | 6 | 1.3E-1 | 5.1E-1 |
|  | INTERPRO | PGG\_dom | 6 | 1.7E-1 | 6.5E-1 |
|  | INTERPRO | Ankyrin\_rpt-contain\_sf | 14 | 3.5E-1 | 1.0E0 |
| Annotation Cluster 126 | | Enrichment Score: 0.68 | Count | P\_Value | Benjamini |
|  | INTERPRO | WIP1/2/3/4/5/6 | 3 | 1.2E-1 | 5.1E-1 |
|  | GOTERM\_BP\_DIRECT | anatomical structure development | 3 | 1.3E-1 | 7.7E-1 |
|  | INTERPRO | C2CH-3rd\_BIRD-IDD | 5 | 1.3E-1 | 5.6E-1 |
|  | GOTERM\_BP\_DIRECT | regulation of gene expression | 3 | 1.0E0 | 1.0E0 |
| Annotation Cluster 127 | | Enrichment Score: 0.67 | Count | P\_Value | Benjamini |
|  | INTERPRO | GLIP1-5/GLL25 | 3 | 1.3E-2 | 9.6E-2 |
|  | INTERPRO | SGNH\_plant\_lipase-like | 9 | 1.7E-1 | 6.6E-1 |
|  | INTERPRO | GDSL\_Est/Lipase | 3 | 4.1E-1 | 1.0E0 |
|  | INTERPRO | SGNH\_hydro\_sf | 10 | 4.3E-1 | 1.0E0 |
|  | INTERPRO | GDSL | 9 | 4.8E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | hydrolase activity, acting on ester bonds | 11 | 5.3E-1 | 1.0E0 |
| Annotation Cluster 128 | | Enrichment Score: 0.66 | Count | P\_Value | Benjamini |
|  | GOTERM\_BP\_DIRECT | response to light stimulus | 9 | 5.9E-2 | 4.7E-1 |
|  | GOTERM\_BP\_DIRECT | gibberellin catabolic process | 3 | 8.0E-2 | 5.7E-1 |
|  | KEGG\_PATHWAY | Diterpenoid biosynthesis | 3 | 6.2E-1 | 1.0E0 |
|  | INTERPRO | Iron\_ascorbate\_oxido\_reductase | 3 | 7.4E-1 | 1.0E0 |
| Annotation Cluster 129 | | Enrichment Score: 0.66 | Count | P\_Value | Benjamini |
|  | INTERPRO | SCF\_F-box\_domain | 3 | 5.5E-2 | 2.9E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:DUF295 | 3 | 3.5E-1 | 1.0E0 |
|  | INTERPRO | DUF295 | 3 | 5.2E-1 | 1.0E0 |
| Annotation Cluster 130 | | Enrichment Score: 0.66 | Count | P\_Value | Benjamini |
|  | GOTERM\_MF\_DIRECT | UDP-glycosyltransferase activity | 16 | 9.8E-2 | 5.2E-1 |
|  | INTERPRO | UDP\_glycos\_trans\_CS | 11 | 1.3E-1 | 5.4E-1 |
|  | INTERPRO | UDP\_glucos\_trans | 14 | 1.3E-1 | 5.4E-1 |
|  | GOTERM\_MF\_DIRECT | UDP-glucosyltransferase activity | 7 | 2.7E-1 | 9.3E-1 |
|  | GOTERM\_MF\_DIRECT | quercetin 3-O-glucosyltransferase activity | 5 | 4.9E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | quercetin 7-O-glucosyltransferase activity | 5 | 4.9E-1 | 1.0E0 |
| Annotation Cluster 131 | | Enrichment Score: 0.66 | Count | P\_Value | Benjamini |
|  | INTERPRO | GlrX-like\_pln\_2 | 4 | 3.2E-2 | 2.0E-1 |
|  | INTERPRO | Glutaredoxin\_subgr | 3 | 1.9E-1 | 6.9E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Glutaredoxin | 4 | 3.0E-1 | 9.1E-1 |
|  | INTERPRO | Glutaredoxin | 4 | 4.3E-1 | 1.0E0 |
|  | UP\_KW\_DOMAIN | Redox-active center | 5 | 6.8E-1 | 1.0E0 |
| Annotation Cluster 132 | | Enrichment Score: 0.65 | Count | P\_Value | Benjamini |
|  | GOTERM\_BP\_DIRECT | extracellular matrix organization | 3 | 1.5E-1 | 8.4E-1 |
|  | GOTERM\_BP\_DIRECT | collagen catabolic process | 3 | 1.5E-1 | 8.4E-1 |
|  | GOTERM\_CC\_DIRECT | extracellular matrix | 3 | 1.7E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | metalloendopeptidase activity | 5 | 6.8E-1 | 1.0E0 |
| Annotation Cluster 133 | | Enrichment Score: 0.64 | Count | P\_Value | Benjamini |
|  | GOTERM\_BP\_DIRECT | nucleoside transmembrane transport | 3 | 1.5E-1 | 8.4E-1 |
|  | PIR\_SUPERFAMILY | ENT | 3 | 2.2E-1 | 8.2E-1 |
|  | INTERPRO | Eqnu\_transpt | 3 | 2.9E-1 | 9.2E-1 |
|  | GOTERM\_MF\_DIRECT | nucleoside transmembrane transporter activity | 3 | 3.0E-1 | 9.6E-1 |
| Annotation Cluster 134 | | Enrichment Score: 0.63 | Count | P\_Value | Benjamini |
|  | GOTERM\_BP\_DIRECT | sucrose metabolic process | 5 | 3.9E-2 | 3.4E-1 |
|  | INTERPRO | Sucrose\_synthase\_pln/cyn | 3 | 1.9E-1 | 6.9E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Sucrose synthase | 3 | 2.1E-1 | 7.2E-1 |
|  | INTERPRO | Sucrose\_synth | 3 | 2.4E-1 | 8.3E-1 |
|  | GOTERM\_MF\_DIRECT | sucrose synthase activity | 3 | 2.5E-1 | 8.7E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Glycosyl transferase family 1 | 3 | 6.4E-1 | 1.0E0 |
|  | INTERPRO | Glyco\_trans\_1 | 3 | 6.8E-1 | 1.0E0 |
| Annotation Cluster 135 | | Enrichment Score: 0.6 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:Beta-ketoacyl-[acyl-carrier-protein] synthase III C-terminal | 4 | 1.7E-1 | 6.1E-1 |
|  | INTERPRO | ACP\_syn\_III\_C | 4 | 1.9E-1 | 7.1E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:FAE | 4 | 2.0E-1 | 6.9E-1 |
|  | INTERPRO | FAE1\_typ3\_polyketide\_synth | 4 | 2.3E-1 | 8.2E-1 |
|  | INTERPRO | 3-ktacl-CoA\_syn | 4 | 2.3E-1 | 8.2E-1 |
|  | PIR\_SUPERFAMILY | 3-ktacl-CoA\_syn | 4 | 3.1E-1 | 9.4E-1 |
|  | KEGG\_PATHWAY | Fatty acid elongation | 4 | 6.2E-1 | 1.0E0 |
| Annotation Cluster 136 | | Enrichment Score: 0.59 | Count | P\_Value | Benjamini |
|  | GOTERM\_MF\_DIRECT | 1-deoxy-D-xylulose-5-phosphate synthase activity | 3 | 7.0E-2 | 3.9E-1 |
|  | INTERPRO | Dxylulose-5-P\_synthase | 3 | 7.4E-2 | 3.6E-1 |
|  | INTERPRO | Transketolase\_C | 3 | 1.4E-1 | 5.7E-1 |
|  | INTERPRO | Transketo\_C/PFOR\_II | 3 | 2.1E-1 | 7.6E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Transketolase-like pyrimidine-binding | 3 | 2.1E-1 | 7.2E-1 |
|  | INTERPRO | Transketolase-like\_Pyr-bd | 3 | 2.4E-1 | 8.3E-1 |
|  | INTERPRO | THDP-binding | 5 | 2.6E-1 | 8.8E-1 |
|  | GOTERM\_BP\_DIRECT | thiamine biosynthetic process | 3 | 2.8E-1 | 1.0E0 |
|  | SMART | Transket\_pyr | 3 | 3.2E-1 | 1.0E0 |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Isoprene biosynthesis | 4 | 3.7E-1 | 1.0E0 |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Thiamine biosynthesis | 3 | 3.9E-1 | 1.0E0 |
|  | UP\_KW\_LIGAND | Thiamine pyrophosphate | 3 | 4.9E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | chlorophyll biosynthetic process | 3 | 6.1E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | terpenoid biosynthetic process | 3 | 7.2E-1 | 1.0E0 |
| Annotation Cluster 137 | | Enrichment Score: 0.56 | Count | P\_Value | Benjamini |
|  | GOTERM\_MF\_DIRECT | malate dehydrogenase (decarboxylating) (NAD+) activity | 4 | 4.7E-2 | 2.9E-1 |
|  | GOTERM\_MF\_DIRECT | NAD binding | 11 | 1.4E-1 | 6.3E-1 |
|  | INTERPRO | Malic\_enzyme\_CS | 3 | 1.6E-1 | 6.5E-1 |
|  | GOTERM\_MF\_DIRECT | malate dehydrogenase (decarboxylating) (NADP+) activity | 3 | 1.8E-1 | 7.2E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Malic enzyme NAD-binding | 3 | 1.9E-1 | 6.7E-1 |
|  | INTERPRO | Malic\_NAD-bd | 3 | 2.1E-1 | 7.6E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Malic enzyme N-terminal | 3 | 2.1E-1 | 7.2E-1 |
|  | GOTERM\_BP\_DIRECT | pyruvate metabolic process | 4 | 2.3E-1 | 1.0E0 |
|  | INTERPRO | Malic\_N\_dom\_sf | 3 | 2.4E-1 | 8.3E-1 |
|  | INTERPRO | Malic\_N\_dom | 3 | 2.4E-1 | 8.3E-1 |
|  | INTERPRO | Malic\_OxRdtase | 3 | 2.6E-1 | 8.8E-1 |
|  | SMART | Malic\_M | 3 | 2.9E-1 | 9.7E-1 |
|  | SMART | malic | 3 | 3.2E-1 | 1.0E0 |
|  | PIR\_SUPERFAMILY | ME | 3 | 3.3E-1 | 9.4E-1 |
|  | GOTERM\_BP\_DIRECT | malate metabolic process | 4 | 3.7E-1 | 1.0E0 |
|  | INTERPRO | Aminoacid\_DH-like\_N\_sf | 3 | 5.0E-1 | 1.0E0 |
|  | KEGG\_PATHWAY | Carbon fixation by Calvin cycle | 6 | 8.3E-1 | 1.0E0 |
|  | KEGG\_PATHWAY | Pyruvate metabolism | 9 | 8.6E-1 | 1.0E0 |
|  | KEGG\_PATHWAY | Carbon metabolism | 14 | 1.0E0 | 1.0E0 |
| Annotation Cluster 138 | | Enrichment Score: 0.52 | Count | P\_Value | Benjamini |
|  | INTERPRO | CASP/CASPL | 4 | 1.8E-1 | 6.9E-1 |
|  | INTERPRO | CASPL | 3 | 2.6E-1 | 8.8E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Casparian strip membrane protein | 4 | 4.0E-1 | 1.0E0 |
|  | INTERPRO | CASP\_dom | 4 | 4.5E-1 | 1.0E0 |
| Annotation Cluster 139 | | Enrichment Score: 0.51 | Count | P\_Value | Benjamini |
|  | INTERPRO | DnaJ\_C/III\_chloroplastic | 4 | 1.3E-2 | 9.6E-2 |
|  | GOTERM\_BP\_DIRECT | chaperone-mediated protein folding | 4 | 1.3E-1 | 7.7E-1 |
|  | INTERPRO | J\_dom\_sf | 8 | 7.9E-1 | 1.0E0 |
|  | INTERPRO | DnaJ\_domain | 7 | 8.3E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:J | 6 | 8.4E-1 | 1.0E0 |
|  | SMART | DnaJ | 6 | 9.3E-1 | 1.0E0 |
| Annotation Cluster 140 | | Enrichment Score: 0.51 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:ABC transmembrane type-1 | 12 | 9.8E-2 | 4.1E-1 |
|  | INTERPRO | ABC1\_TM\_dom | 12 | 1.4E-1 | 5.8E-1 |
|  | INTERPRO | ABC1\_TM\_sf | 12 | 2.5E-1 | 8.4E-1 |
|  | INTERPRO | ABCC\_6TM\_D2 | 5 | 3.2E-1 | 1.0E0 |
|  | GOTERM\_CC\_DIRECT | vacuolar membrane | 11 | 3.3E-1 | 1.0E0 |
|  | INTERPRO | ABCC\_6TM\_D1 | 4 | 3.8E-1 | 1.0E0 |
|  | INTERPRO | ABC\_transporter\_C-like | 5 | 6.2E-1 | 1.0E0 |
|  | GOTERM\_CC\_DIRECT | plant-type vacuole | 6 | 9.9E-1 | 1.0E0 |
| Annotation Cluster 141 | | Enrichment Score: 0.49 | Count | P\_Value | Benjamini |
|  | INTERPRO | Aldo-Keto\_reductase | 3 | 2.6E-1 | 8.8E-1 |
|  | GOTERM\_MF\_DIRECT | aldo-keto reductase (NADPH) activity | 3 | 2.7E-1 | 9.3E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:NADP-dependent oxidoreductase | 5 | 3.3E-1 | 9.5E-1 |
|  | INTERPRO | NADP\_OxRdtase\_dom | 5 | 4.0E-1 | 1.0E0 |
|  | INTERPRO | NADP\_OxRdtase\_dom\_sf | 5 | 4.0E-1 | 1.0E0 |
| Annotation Cluster 142 | | Enrichment Score: 0.48 | Count | P\_Value | Benjamini |
|  | INTERPRO | Znf\_RING/FYVE/PHD | 60 | 1.2E-1 | 5.1E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:RING-type | 36 | 1.6E-1 | 6.0E-1 |
|  | INTERPRO | Znf\_RING | 36 | 2.9E-1 | 9.2E-1 |
|  | SMART | RING | 28 | 7.3E-1 | 1.0E0 |
|  | UP\_KW\_LIGAND | Zinc | 100 | 1.0E0 | 1.0E0 |
| Annotation Cluster 143 | | Enrichment Score: 0.46 | Count | P\_Value | Benjamini |
|  | INTERPRO | X8\_dom\_prot | 4 | 1.6E-1 | 6.4E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:X8 | 6 | 2.7E-1 | 8.4E-1 |
|  | INTERPRO | X8 | 6 | 3.4E-1 | 1.0E0 |
|  | INTERPRO | Glyco\_hydro\_17\_plant | 6 | 4.5E-1 | 1.0E0 |
|  | INTERPRO | Glyco\_hydro\_17 | 6 | 5.0E-1 | 1.0E0 |
|  | SMART | X8 | 6 | 5.1E-1 | 1.0E0 |
| Annotation Cluster 144 | | Enrichment Score: 0.45 | Count | P\_Value | Benjamini |
|  | GOTERM\_MF\_DIRECT | serine-type endopeptidase inhibitor activity | 5 | 1.3E-1 | 6.1E-1 |
|  | UP\_KW\_MOLECULAR\_FUNCTION | Serine protease inhibitor | 3 | 4.1E-1 | 1.0E0 |
|  | UP\_KW\_MOLECULAR\_FUNCTION | Protease inhibitor | 3 | 7.8E-1 | 1.0E0 |
| Annotation Cluster 145 | | Enrichment Score: 0.44 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:VOC | 3 | 3.3E-1 | 9.5E-1 |
|  | INTERPRO | VOC | 3 | 3.6E-1 | 1.0E0 |
|  | INTERPRO | Glyas\_Fos-R\_dOase\_dom | 3 | 3.6E-1 | 1.0E0 |
|  | INTERPRO | Glyas\_Bleomycin-R\_OHBP\_Dase | 3 | 3.9E-1 | 1.0E0 |
| Annotation Cluster 146 | | Enrichment Score: 0.44 | Count | P\_Value | Benjamini |
|  | INTERPRO | Glyco\_hydro\_1\_N\_CS | 7 | 1.7E-1 | 6.5E-1 |
|  | KEGG\_PATHWAY | Biosynthesis of various plant secondary metabolites | 10 | 2.2E-1 | 1.0E0 |
|  | KEGG\_PATHWAY | Cyanoamino acid metabolism | 8 | 4.2E-1 | 1.0E0 |
|  | INTERPRO | Glyco\_hydro\_1\_AS | 3 | 4.6E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | beta-glucosidase activity | 9 | 5.7E-1 | 1.0E0 |
|  | INTERPRO | Glyco\_hydro\_1 | 7 | 5.9E-1 | 1.0E0 |
| Annotation Cluster 147 | | Enrichment Score: 0.43 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:OVATE | 3 | 1.7E-1 | 6.1E-1 |
|  | INTERPRO | Ovate\_C | 3 | 1.9E-1 | 6.9E-1 |
|  | UP\_KW\_MOLECULAR\_FUNCTION | Repressor | 9 | 6.8E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | negative regulation of DNA-templated transcription | 4 | 8.7E-1 | 1.0E0 |
| Annotation Cluster 148 | | Enrichment Score: 0.42 | Count | P\_Value | Benjamini |
|  | INTERPRO | GLABRA2/ANL2/PDF2/ATML1-like | 4 | 1.1E-1 | 5.1E-1 |
|  | SMART | START | 4 | 3.8E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:START | 4 | 4.2E-1 | 1.0E0 |
|  | INTERPRO | START\_lipid-bd\_dom | 4 | 4.8E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | lipid binding | 8 | 9.7E-1 | 1.0E0 |
| Annotation Cluster 149 | | Enrichment Score: 0.4 | Count | P\_Value | Benjamini |
|  | INTERPRO | Ankyrin\_rpt-contain\_sf | 14 | 3.5E-1 | 1.0E0 |
|  | INTERPRO | Ankyrin\_rpt | 13 | 3.7E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | REPEAT:ANK | 11 | 4.0E-1 | 1.0E0 |
|  | SMART | ANK | 13 | 4.3E-1 | 1.0E0 |
|  | UP\_KW\_DOMAIN | ANK repeat | 8 | 4.4E-1 | 9.5E-1 |
| Annotation Cluster 150 | | Enrichment Score: 0.4 | Count | P\_Value | Benjamini |
|  | INTERPRO | Unkempt-like | 4 | 6.1E-2 | 3.1E-1 |
|  | UP\_SEQ\_FEATURE | REPEAT:ANK | 11 | 4.0E-1 | 1.0E0 |
|  | UP\_KW\_DOMAIN | ANK repeat | 8 | 4.4E-1 | 9.5E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:C3H1-type | 6 | 5.9E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | ZN\_FING:C3H1-type | 6 | 5.9E-1 | 1.0E0 |
|  | INTERPRO | Znf\_CCCH | 6 | 6.5E-1 | 1.0E0 |
|  | SMART | ZnF\_C3H1 | 6 | 6.8E-1 | 1.0E0 |
| Annotation Cluster 151 | | Enrichment Score: 0.39 | Count | P\_Value | Benjamini |
|  | GOTERM\_MF\_DIRECT | calcium-dependent phospholipid binding | 5 | 6.4E-2 | 3.8E-1 |
|  | INTERPRO | Annexin | 3 | 3.1E-1 | 9.9E-1 |
|  | GOTERM\_MF\_DIRECT | phosphatidylserine binding | 3 | 3.5E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | response to water deprivation | 5 | 3.7E-1 | 1.0E0 |
|  | INTERPRO | Annexin\_sf | 3 | 4.1E-1 | 1.0E0 |
|  | INTERPRO | Annexin\_repeat | 3 | 4.1E-1 | 1.0E0 |
|  | UP\_KW\_DOMAIN | Annexin | 3 | 4.8E-1 | 9.5E-1 |
|  | SMART | ANX | 3 | 4.9E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | response to cold | 4 | 7.1E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | response to heat | 8 | 7.1E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | response to salt stress | 5 | 9.6E-1 | 1.0E0 |
| Annotation Cluster 152 | | Enrichment Score: 0.38 | Count | P\_Value | Benjamini |
|  | INTERPRO | HAD-SF\_hydro\_IIB | 3 | 3.4E-1 | 1.0E0 |
|  | INTERPRO | Trehalose\_PPase | 3 | 3.4E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | trehalose-phosphatase activity | 3 | 4.6E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | trehalose biosynthetic process | 3 | 5.5E-1 | 1.0E0 |
| Annotation Cluster 153 | | Enrichment Score: 0.37 | Count | P\_Value | Benjamini |
|  | INTERPRO | AUX\_IAA | 4 | 2.5E-1 | 8.5E-1 |
|  | INTERPRO | PB1-like | 6 | 3.7E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:PB1 | 6 | 4.5E-1 | 1.0E0 |
|  | INTERPRO | AUX/IAA\_dom | 4 | 5.0E-1 | 1.0E0 |
|  | UP\_KW\_MOLECULAR\_FUNCTION | Repressor | 9 | 6.8E-1 | 1.0E0 |
| Annotation Cluster 154 | | Enrichment Score: 0.36 | Count | P\_Value | Benjamini |
|  | GOTERM\_BP\_DIRECT | ethylene biosynthetic process | 5 | 7.1E-2 | 5.3E-1 |
|  | INTERPRO | Ethylene\_sulfur-biosynth | 4 | 1.4E-1 | 5.8E-1 |
|  | GOTERM\_MF\_DIRECT | 1-aminocyclopropane-1-carboxylate synthase activity | 3 | 2.0E-1 | 7.5E-1 |
|  | GOTERM\_BP\_DIRECT | fruit ripening | 3 | 2.8E-1 | 1.0E0 |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Ethylene biosynthesis | 3 | 3.9E-1 | 1.0E0 |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Fruit ripening | 3 | 3.9E-1 | 1.0E0 |
|  | INTERPRO | NHTrfase\_class1\_PyrdxlP-BS | 3 | 3.9E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | transaminase activity | 4 | 3.9E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | amino acid metabolic process | 5 | 4.5E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Aminotransferase class I/classII large | 3 | 7.4E-1 | 1.0E0 |
|  | INTERPRO | Aminotransferase\_I/II\_large | 3 | 7.8E-1 | 1.0E0 |
|  | INTERPRO | PyrdxlP-dep\_Trfase\_small | 6 | 7.9E-1 | 1.0E0 |
|  | UP\_KW\_LIGAND | Pyridoxal phosphate | 5 | 8.1E-1 | 1.0E0 |
|  | INTERPRO | PyrdxlP-dep\_Trfase | 7 | 8.5E-1 | 1.0E0 |
|  | INTERPRO | PyrdxlP-dep\_Trfase\_major | 7 | 8.6E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | pyridoxal phosphate binding | 5 | 9.3E-1 | 1.0E0 |
| Annotation Cluster 155 | | Enrichment Score: 0.36 | Count | P\_Value | Benjamini |
|  | INTERPRO | TPT\_transporter | 6 | 3.4E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Sugar phosphate transporter | 6 | 3.7E-1 | 1.0E0 |
|  | INTERPRO | Sugar\_P\_trans\_dom | 6 | 4.6E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | antiporter activity | 15 | 5.9E-1 | 1.0E0 |
| Annotation Cluster 156 | | Enrichment Score: 0.36 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:K+ potassium transporter C-terminal | 3 | 3.3E-1 | 9.5E-1 |
|  | INTERPRO | K\_trans\_C | 3 | 3.6E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:K+ potassium transporter integral membrane | 3 | 4.2E-1 | 1.0E0 |
|  | INTERPRO | K+\_transporter | 3 | 4.6E-1 | 1.0E0 |
|  | INTERPRO | K\_trans\_N | 3 | 4.6E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | potassium ion transmembrane transporter activity | 3 | 4.6E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | potassium ion transmembrane transport | 3 | 6.3E-1 | 1.0E0 |
| Annotation Cluster 157 | | Enrichment Score: 0.34 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:NAF | 3 | 4.4E-1 | 1.0E0 |
|  | INTERPRO | NAF/FISL\_domain | 3 | 4.6E-1 | 1.0E0 |
|  | INTERPRO | NAF\_dom | 3 | 4.8E-1 | 1.0E0 |
| Annotation Cluster 158 | | Enrichment Score: 0.32 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:HSF-type DNA-binding | 5 | 2.5E-1 | 8.1E-1 |
|  | INTERPRO | HSF\_DNA-bd | 5 | 2.9E-1 | 9.2E-1 |
|  | SMART | HSF | 5 | 4.3E-1 | 1.0E0 |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Stress response | 13 | 7.8E-1 | 1.0E0 |
|  | UP\_KW\_PTM | Phosphoprotein | 13 | 1.0E0 | 1.0E0 |
| Annotation Cluster 159 | | Enrichment Score: 0.3 | Count | P\_Value | Benjamini |
|  | GOTERM\_MF\_DIRECT | zinc ion transmembrane transporter activity | 4 | 4.3E-1 | 1.0E0 |
|  | INTERPRO | ZIP | 3 | 5.2E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | zinc ion transmembrane transport | 3 | 5.5E-1 | 1.0E0 |
| Annotation Cluster 160 | | Enrichment Score: 0.3 | Count | P\_Value | Benjamini |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Fatty acid metabolism | 13 | 1.9E-1 | 1.0E0 |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Oxylipin biosynthesis | 3 | 5.5E-1 | 1.0E0 |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Fatty acid biosynthesis | 6 | 6.3E-1 | 1.0E0 |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Lipid biosynthesis | 7 | 9.8E-1 | 1.0E0 |
| Annotation Cluster 161 | | Enrichment Score: 0.29 | Count | P\_Value | Benjamini |
|  | INTERPRO | Sugar/inositol\_transpt | 9 | 2.3E-1 | 8.2E-1 |
|  | INTERPRO | STP/PLT\_plant | 5 | 4.6E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | monosaccharide transmembrane transporter activity | 3 | 7.5E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | monosaccharide transmembrane transport | 3 | 8.8E-1 | 1.0E0 |
| Annotation Cluster 162 | | Enrichment Score: 0.28 | Count | P\_Value | Benjamini |
|  | INTERPRO | Syntaxin\_N | 3 | 2.4E-1 | 8.3E-1 |
|  | SMART | SynN | 3 | 2.9E-1 | 9.7E-1 |
|  | INTERPRO | Syntaxin/epimorphin\_CS | 3 | 3.1E-1 | 9.9E-1 |
|  | INTERPRO | Syntaxin | 3 | 4.1E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:T-SNARE coiled-coil homology | 4 | 4.5E-1 | 1.0E0 |
|  | INTERPRO | T\_SNARE\_dom | 4 | 5.0E-1 | 1.0E0 |
|  | SMART | t\_SNARE | 4 | 5.1E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | vesicle docking | 3 | 5.3E-1 | 1.0E0 |
|  | INTERPRO | SNARE | 3 | 5.4E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | SNAP receptor activity | 4 | 6.3E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | vesicle fusion | 3 | 7.4E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | SNARE binding | 5 | 7.5E-1 | 1.0E0 |
|  | GOTERM\_CC\_DIRECT | SNARE complex | 4 | 7.6E-1 | 1.0E0 |
|  | KEGG\_PATHWAY | SNARE interactions in vesicular transport | 3 | 8.7E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | intracellular protein transport | 7 | 9.9E-1 | 1.0E0 |
| Annotation Cluster 163 | | Enrichment Score: 0.28 | Count | P\_Value | Benjamini |
|  | GOTERM\_MF\_DIRECT | O-methyltransferase activity | 8 | 1.4E-1 | 6.1E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:O-methyltransferase | 5 | 3.6E-1 | 1.0E0 |
|  | INTERPRO | O\_MeTrfase\_dom | 5 | 4.1E-1 | 1.0E0 |
|  | INTERPRO | COMT-like | 5 | 4.1E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Plant methyltransferase dimerisation | 4 | 4.7E-1 | 1.0E0 |
|  | INTERPRO | Plant\_MeTrfase\_dimerisation | 4 | 5.2E-1 | 1.0E0 |
|  | UP\_KW\_LIGAND | S-adenosyl-L-methionine | 12 | 6.3E-1 | 1.0E0 |
|  | PIR\_SUPERFAMILY | O-mtase | 4 | 8.2E-1 | 1.0E0 |
|  | INTERPRO | SAM-dependent\_MTases\_sf | 19 | 8.7E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | methylation | 11 | 9.9E-1 | 1.0E0 |
|  | UP\_KW\_MOLECULAR\_FUNCTION | Methyltransferase | 10 | 1.0E0 | 1.0E0 |
| Annotation Cluster 164 | | Enrichment Score: 0.27 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:GRAM | 3 | 3.5E-1 | 1.0E0 |
|  | INTERPRO | GEM-like | 3 | 3.9E-1 | 1.0E0 |
|  | INTERPRO | GRAM | 3 | 5.2E-1 | 1.0E0 |
|  | SMART | GRAM | 3 | 6.4E-1 | 1.0E0 |
|  | INTERPRO | PH-like\_dom\_sf | 3 | 9.9E-1 | 1.0E0 |
| Annotation Cluster 165 | | Enrichment Score: 0.27 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:MATH | 4 | 4.4E-1 | 1.0E0 |
|  | INTERPRO | MATH/TRAF\_dom | 4 | 5.2E-1 | 1.0E0 |
|  | SMART | MATH | 4 | 5.7E-1 | 1.0E0 |
|  | INTERPRO | TRAF-like | 4 | 6.5E-1 | 1.0E0 |
| Annotation Cluster 166 | | Enrichment Score: 0.25 | Count | P\_Value | Benjamini |
|  | INTERPRO | JINGUBANG-like | 4 | 1.8E-2 | 1.3E-1 |
|  | INTERPRO | G-protein\_beta\_WD-40\_rep | 5 | 9.1E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | REPEAT:WD | 7 | 1.0E0 | 1.0E0 |
|  | INTERPRO | WD40\_rpt | 7 | 1.0E0 | 1.0E0 |
|  | INTERPRO | WD40/YVTN\_repeat-like\_dom\_sf | 9 | 1.0E0 | 1.0E0 |
|  | INTERPRO | WD40\_repeat\_dom\_sf | 7 | 1.0E0 | 1.0E0 |
|  | SMART | WD40 | 7 | 1.0E0 | 1.0E0 |
| Annotation Cluster 167 | | Enrichment Score: 0.25 | Count | P\_Value | Benjamini |
|  | INTERPRO | Ub\_ligase/GEF\_domain | 3 | 4.8E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | REPEAT:RCC1 | 3 | 5.4E-1 | 1.0E0 |
|  | INTERPRO | Reg\_chr\_condens | 3 | 5.8E-1 | 1.0E0 |
|  | INTERPRO | RCC1/BLIP-II | 3 | 6.8E-1 | 1.0E0 |
| Annotation Cluster 168 | | Enrichment Score: 0.22 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:Cation-transporting P-type ATPase N-terminal | 5 | 4.0E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | regulation of intracellular pH | 5 | 4.5E-1 | 1.0E0 |
|  | INTERPRO | ATPase\_P-typ\_cation-transptr\_N | 5 | 4.6E-1 | 1.0E0 |
|  | SMART | Cation\_ATPase\_N | 5 | 5.2E-1 | 1.0E0 |
|  | INTERPRO | P-type\_ATPase\_IIIA | 3 | 7.0E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | proton export across plasma membrane | 3 | 7.2E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | P-type proton-exporting transporter activity | 3 | 7.6E-1 | 1.0E0 |
|  | KEGG\_PATHWAY | Oxidative phosphorylation | 4 | 1.0E0 | 1.0E0 |
| Annotation Cluster 169 | | Enrichment Score: 0.21 | Count | P\_Value | Benjamini |
|  | INTERPRO | CRAL/TRIO\_N\_dom\_sf | 4 | 3.9E-1 | 1.0E0 |
|  | INTERPRO | CRAL/TRIO\_N\_dom | 3 | 5.8E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:CRAL-TRIO | 4 | 6.0E-1 | 1.0E0 |
|  | INTERPRO | CRAL-TRIO\_dom | 4 | 6.7E-1 | 1.0E0 |
|  | INTERPRO | CRAL-TRIO\_dom\_sf | 4 | 6.9E-1 | 1.0E0 |
|  | SMART | CRAL\_TRIO\_N | 3 | 7.0E-1 | 1.0E0 |
|  | SMART | SEC14 | 4 | 7.7E-1 | 1.0E0 |
| Annotation Cluster 170 | | Enrichment Score: 0.2 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:N-acetyltransferase | 4 | 5.5E-1 | 1.0E0 |
|  | INTERPRO | GNAT\_dom | 4 | 5.8E-1 | 1.0E0 |
|  | INTERPRO | Acyl\_CoA\_acyltransferase | 4 | 7.8E-1 | 1.0E0 |
| Annotation Cluster 171 | | Enrichment Score: 0.19 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | REPEAT:Solcar | 6 | 5.2E-1 | 1.0E0 |
|  | INTERPRO | Mit\_carrier | 4 | 6.0E-1 | 1.0E0 |
|  | INTERPRO | Mitochondrial\_sb/sol\_carrier | 6 | 7.1E-1 | 1.0E0 |
|  | INTERPRO | Mt\_carrier\_dom\_sf | 6 | 7.6E-1 | 1.0E0 |
| Annotation Cluster 172 | | Enrichment Score: 0.19 | Count | P\_Value | Benjamini |
|  | INTERPRO | Ald\_DH\_CS\_GLU | 4 | 3.9E-1 | 1.0E0 |
|  | INTERPRO | Ald\_DH\_CS\_CYS | 3 | 4.1E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor | 4 | 5.4E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | aldehyde dehydrogenase (NAD+) activity | 4 | 6.4E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Aldehyde dehydrogenase | 4 | 7.1E-1 | 1.0E0 |
|  | INTERPRO | Ald\_DH\_C | 4 | 7.5E-1 | 1.0E0 |
|  | INTERPRO | Aldehyde\_DH\_dom | 4 | 7.9E-1 | 1.0E0 |
|  | INTERPRO | Ald\_DH\_N | 4 | 9.0E-1 | 1.0E0 |
|  | INTERPRO | Ald\_DH/histidinol\_DH | 4 | 9.2E-1 | 1.0E0 |
| Annotation Cluster 173 | | Enrichment Score: 0.18 | Count | P\_Value | Benjamini |
|  | SMART | BTB | 5 | 5.6E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:BTB | 5 | 6.1E-1 | 1.0E0 |
|  | INTERPRO | BTB/POZ\_dom | 5 | 6.9E-1 | 1.0E0 |
|  | INTERPRO | SKP1/BTB/POZ\_sf | 6 | 8.1E-1 | 1.0E0 |
| Annotation Cluster 174 | | Enrichment Score: 0.17 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:Beta-galactosidase galactose-binding | 3 | 2.4E-1 | 7.8E-1 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Beta-galactosidase beta-sandwich | 3 | 3.5E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Glycoside hydrolase 35 catalytic | 3 | 5.2E-1 | 1.0E0 |
|  | GOTERM\_CC\_DIRECT | vacuole | 13 | 7.7E-1 | 1.0E0 |
|  | INTERPRO | BetaGal\_gal-bd | 5 | 7.9E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | beta-galactosidase activity | 5 | 8.2E-1 | 1.0E0 |
|  | INTERPRO | GHD | 5 | 8.3E-1 | 1.0E0 |
|  | INTERPRO | Gly\_Hdrlase\_35\_cat | 5 | 8.7E-1 | 1.0E0 |
|  | INTERPRO | Glycoside\_Hdrlase\_35 | 5 | 9.1E-1 | 1.0E0 |
|  | INTERPRO | Galactose-bd-like\_sf | 6 | 9.3E-1 | 1.0E0 |
|  | INTERPRO | Glyco\_hydro\_35\_CS | 3 | 9.7E-1 | 1.0E0 |
| Annotation Cluster 175 | | Enrichment Score: 0.16 | Count | P\_Value | Benjamini |
|  | KEGG\_PATHWAY | Arginine and proline metabolism | 7 | 6.0E-1 | 1.0E0 |
|  | KEGG\_PATHWAY | Pantothenate and CoA biosynthesis | 5 | 6.1E-1 | 1.0E0 |
|  | KEGG\_PATHWAY | beta-Alanine metabolism | 4 | 9.0E-1 | 1.0E0 |
| Annotation Cluster 176 | | Enrichment Score: 0.14 | Count | P\_Value | Benjamini |
|  | UP\_KW\_LIGAND | Potassium | 10 | 4.8E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Cation/H+ exchanger transmembrane | 6 | 5.2E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | potassium ion transport | 7 | 6.9E-1 | 1.0E0 |
|  | INTERPRO | Cation/H\_exchanger\_TM | 6 | 7.0E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | regulation of pH | 6 | 7.1E-1 | 1.0E0 |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Potassium transport | 9 | 7.4E-1 | 1.0E0 |
|  | INTERPRO | CPA2\_transporter | 4 | 8.7E-1 | 1.0E0 |
|  | INTERPRO | Na+/solute\_symporter\_sf | 4 | 9.4E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | proton transmembrane transport | 7 | 9.8E-1 | 1.0E0 |
| Annotation Cluster 177 | | Enrichment Score: 0.14 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:PPIase cyclophilin-type | 3 | 6.4E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | protein peptidyl-prolyl isomerization | 3 | 6.8E-1 | 1.0E0 |
|  | INTERPRO | Cyclophilin-type\_PPIase\_dom | 3 | 6.8E-1 | 1.0E0 |
|  | INTERPRO | Cyclophilin-like\_dom\_sf | 3 | 7.0E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | peptidyl-prolyl cis-trans isomerase activity | 3 | 9.3E-1 | 1.0E0 |
| Annotation Cluster 178 | | Enrichment Score: 0.13 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:Subtilisin-like protease fibronectin type-III | 6 | 4.5E-1 | 1.0E0 |
|  | INTERPRO | Subtilisin-like\_FN3 | 6 | 5.1E-1 | 1.0E0 |
|  | INTERPRO | Peptidases\_S8\_3 | 5 | 6.6E-1 | 1.0E0 |
|  | INTERPRO | Peptidase\_S8\_Ser-AS | 5 | 6.7E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Inhibitor I9 | 5 | 7.1E-1 | 1.0E0 |
|  | INTERPRO | Peptidase\_S8\_subtilisin-rel | 5 | 7.4E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | ACT\_SITE:Charge relay system | 5 | 7.7E-1 | 1.0E0 |
|  | INTERPRO | S8pro/Inhibitor\_I9 | 5 | 7.8E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Peptidase S8/S53 | 6 | 8.1E-1 | 1.0E0 |
|  | INTERPRO | S8pro/Inhibitor\_I9\_sf | 5 | 8.2E-1 | 1.0E0 |
|  | INTERPRO | Peptidase\_S8/S53\_dom | 6 | 8.6E-1 | 1.0E0 |
|  | INTERPRO | SBT | 6 | 8.6E-1 | 1.0E0 |
|  | UP\_KW\_MOLECULAR\_FUNCTION | Serine protease | 4 | 9.0E-1 | 1.0E0 |
|  | INTERPRO | Peptidase\_S8/S53\_dom\_sf | 6 | 9.4E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | serine-type endopeptidase activity | 8 | 1.0E0 | 1.0E0 |
| Annotation Cluster 179 | | Enrichment Score: 0.12 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:NPH3 | 3 | 7.0E-1 | 1.0E0 |
|  | INTERPRO | NPH3\_dom | 3 | 7.4E-1 | 1.0E0 |
|  | INTERPRO | NPH3/RPT2-like | 3 | 7.5E-1 | 1.0E0 |
|  | INTERPRO | SKP1/BTB/POZ\_sf | 6 | 8.1E-1 | 1.0E0 |
| Annotation Cluster 180 | | Enrichment Score: 0.12 | Count | P\_Value | Benjamini |
|  | INTERPRO | Plant\_B3\_domain | 3 | 4.8E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:TF-B3 | 6 | 7.8E-1 | 1.0E0 |
|  | INTERPRO | B3\_DNA-bd | 6 | 8.6E-1 | 1.0E0 |
|  | SMART | B3 | 6 | 8.8E-1 | 1.0E0 |
|  | INTERPRO | DNA-bd\_pseudobarrel\_sf | 6 | 9.3E-1 | 1.0E0 |
| Annotation Cluster 181 | | Enrichment Score: 0.11 | Count | P\_Value | Benjamini |
|  | GOTERM\_MF\_DIRECT | calcium-dependent protein serine/threonine kinase activity | 3 | 6.7E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | calcium/calmodulin-dependent protein kinase activity | 3 | 6.7E-1 | 1.0E0 |
|  | INTERPRO | CDPK\_Ser/Thr\_kinases | 3 | 7.3E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | intracellular signal transduction | 7 | 7.8E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | protein autophosphorylation | 3 | 9.1E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | peptidyl-serine phosphorylation | 4 | 9.6E-1 | 1.0E0 |
| Annotation Cluster 182 | | Enrichment Score: 0.11 | Count | P\_Value | Benjamini |
|  | GOTERM\_MF\_DIRECT | misfolded protein binding | 6 | 4.1E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | cellular response to unfolded protein | 5 | 5.7E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | heat shock protein binding | 5 | 5.7E-1 | 1.0E0 |
|  | INTERPRO | HSP70\_peptide-bd\_sf | 5 | 6.1E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | chaperone cofactor-dependent protein refolding | 6 | 7.2E-1 | 1.0E0 |
|  | INTERPRO | HSP70\_C\_sf | 3 | 8.2E-1 | 1.0E0 |
|  | INTERPRO | ATPase\_NBD | 7 | 8.5E-1 | 1.0E0 |
|  | INTERPRO | Hsp\_70\_fam | 5 | 9.1E-1 | 1.0E0 |
|  | INTERPRO | Heat\_shock\_70\_CS | 3 | 9.1E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | protein refolding | 5 | 9.7E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | unfolded protein binding | 8 | 1.0E0 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | ATP-dependent protein folding chaperone | 5 | 1.0E0 | 1.0E0 |
|  | KEGG\_PATHWAY | Protein processing in endoplasmic reticulum | 9 | 1.0E0 | 1.0E0 |
|  | KEGG\_PATHWAY | Spliceosome | 4 | 1.0E0 | 1.0E0 |
| Annotation Cluster 183 | | Enrichment Score: 0.1 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:Exostosin GT47 | 3 | 7.2E-1 | 1.0E0 |
|  | INTERPRO | Exostosin | 3 | 7.7E-1 | 1.0E0 |
|  | INTERPRO | Exostosin\_GT47 | 3 | 7.7E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | protein glycosylation | 5 | 9.1E-1 | 1.0E0 |
| Annotation Cluster 184 | | Enrichment Score: 0.1 | Count | P\_Value | Benjamini |
|  | INTERPRO | FucosylTrfase\_pln | 3 | 6.4E-1 | 1.0E0 |
|  | INTERPRO | GDP-Fuc\_O-FucTrfase | 3 | 7.0E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | fucose metabolic process | 3 | 7.9E-1 | 1.0E0 |
|  | PIR\_SUPERFAMILY | UCP009360 | 3 | 8.1E-1 | 1.0E0 |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Fucose metabolism | 3 | 8.9E-1 | 1.0E0 |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Carbohydrate metabolism | 9 | 9.5E-1 | 1.0E0 |
| Annotation Cluster 185 | | Enrichment Score: 0.07 | Count | P\_Value | Benjamini |
|  | GOTERM\_CC\_DIRECT | photosystem II oxygen evolving complex | 3 | 4.7E-1 | 1.0E0 |
|  | KEGG\_PATHWAY | Photosynthesis | 6 | 8.1E-1 | 1.0E0 |
|  | GOTERM\_CC\_DIRECT | extrinsic component of membrane | 3 | 8.3E-1 | 1.0E0 |
|  | GOTERM\_CC\_DIRECT | photosystem II | 5 | 9.3E-1 | 1.0E0 |
|  | UP\_KW\_CELLULAR\_COMPONENT | Photosystem II | 5 | 9.5E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | photosynthesis | 5 | 9.9E-1 | 1.0E0 |
|  | UP\_KW\_BIOLOGICAL\_PROCESS | Photosynthesis | 4 | 1.0E0 | 1.0E0 |
|  | UP\_KW\_CELLULAR\_COMPONENT | Thylakoid | 6 | 1.0E0 | 1.0E0 |
| Annotation Cluster 186 | | Enrichment Score: 0.06 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:BZIP | 4 | 8.1E-1 | 1.0E0 |
|  | INTERPRO | bZIP\_sf | 4 | 8.5E-1 | 1.0E0 |
|  | INTERPRO | bZIP | 4 | 8.6E-1 | 1.0E0 |
|  | SMART | BRLZ | 4 | 9.3E-1 | 1.0E0 |
| Annotation Cluster 187 | | Enrichment Score: 0.06 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:Expansin-like CBD | 3 | 8.2E-1 | 1.0E0 |
|  | INTERPRO | Expansin\_CBD | 3 | 8.5E-1 | 1.0E0 |
|  | INTERPRO | Expansin\_CBD\_sf | 3 | 8.5E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | anatomical structure morphogenesis | 3 | 8.6E-1 | 1.0E0 |
|  | INTERPRO | Expan\_Lol\_pI | 3 | 8.7E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Expansin-like EG45 | 3 | 8.7E-1 | 1.0E0 |
|  | INTERPRO | RlpA-like\_DPBB | 3 | 8.9E-1 | 1.0E0 |
|  | INTERPRO | Expansin/allergen\_DPBB\_dom | 3 | 9.0E-1 | 1.0E0 |
|  | INTERPRO | RlpA-like\_sf | 3 | 9.4E-1 | 1.0E0 |
| Annotation Cluster 188 | | Enrichment Score: 0.05 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:BURP | 3 | 8.5E-1 | 1.0E0 |
|  | INTERPRO | BURP | 3 | 8.6E-1 | 1.0E0 |
|  | INTERPRO | BURP\_dom | 3 | 8.8E-1 | 1.0E0 |
|  | SMART | BURP | 3 | 9.4E-1 | 1.0E0 |
| Annotation Cluster 189 | | Enrichment Score: 0.02 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:Bifunctional inhibitor/plant lipid transfer protein/seed storage helical | 7 | 9.0E-1 | 1.0E0 |
|  | INTERPRO | Bifunc\_inhib/LTP/seed\_store | 7 | 9.3E-1 | 1.0E0 |
|  | INTERPRO | Bifun\_inhib/LTP/seed\_sf | 7 | 9.5E-1 | 1.0E0 |
|  | INTERPRO | Plant\_nsLTP | 3 | 9.9E-1 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | lipid transport | 5 | 9.9E-1 | 1.0E0 |
|  | SMART | AAI | 3 | 1.0E0 | 1.0E0 |
| Annotation Cluster 190 | | Enrichment Score: 0.02 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | REPEAT:TPR | 5 | 9.3E-1 | 1.0E0 |
|  | UP\_KW\_DOMAIN | TPR repeat | 5 | 9.4E-1 | 1.0E0 |
|  | INTERPRO | TPR\_rpt | 6 | 9.6E-1 | 1.0E0 |
|  | SMART | TPR | 6 | 9.8E-1 | 1.0E0 |
|  | INTERPRO | TPR-like\_helical\_dom\_sf | 8 | 1.0E0 | 1.0E0 |
| Annotation Cluster 191 | | Enrichment Score: 0 | Count | P\_Value | Benjamini |
|  | UP\_KW\_DOMAIN | Transit peptide | 19 | 9.8E-1 | 1.0E0 |
|  | UP\_KW\_CELLULAR\_COMPONENT | Chloroplast | 20 | 1.0E0 | 1.0E0 |
|  | UP\_KW\_CELLULAR\_COMPONENT | Plastid | 21 | 1.0E0 | 1.0E0 |
| Annotation Cluster 192 | | Enrichment Score: 0 | Count | P\_Value | Benjamini |
|  | INTERPRO | Kinesin-like\_fam | 3 | 9.8E-1 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:Kinesin motor | 3 | 1.0E0 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | microtubule motor activity | 3 | 1.0E0 | 1.0E0 |
|  | INTERPRO | Kinesin\_motor\_dom | 3 | 1.0E0 | 1.0E0 |
|  | SMART | KISc | 3 | 1.0E0 | 1.0E0 |
|  | UP\_KW\_MOLECULAR\_FUNCTION | Motor protein | 4 | 1.0E0 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | microtubule binding | 8 | 1.0E0 | 1.0E0 |
|  | GOTERM\_BP\_DIRECT | microtubule-based movement | 3 | 1.0E0 | 1.0E0 |
|  | INTERPRO | Kinesin\_motor\_dom\_sf | 4 | 1.0E0 | 1.0E0 |
| Annotation Cluster 193 | | Enrichment Score: 0 | Count | P\_Value | Benjamini |
|  | UP\_KW\_CELLULAR\_COMPONENT | Cytoskeleton | 6 | 9.9E-1 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | microtubule binding | 8 | 1.0E0 | 1.0E0 |
|  | GOTERM\_CC\_DIRECT | microtubule | 5 | 1.0E0 | 1.0E0 |
|  | UP\_KW\_CELLULAR\_COMPONENT | Microtubule | 5 | 1.0E0 | 1.0E0 |
| Annotation Cluster 194 | | Enrichment Score: 0 | Count | P\_Value | Benjamini |
|  | SMART | RAB | 3 | 1.0E0 | 1.0E0 |
|  | INTERPRO | Small\_GTP-bd | 3 | 1.0E0 | 1.0E0 |
|  | UP\_KW\_LIGAND | GTP-binding | 4 | 1.0E0 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | GTPase activity | 4 | 1.0E0 | 1.0E0 |
|  | GOTERM\_MF\_DIRECT | GTP binding | 5 | 1.0E0 | 1.0E0 |
| Annotation Cluster 195 | | Enrichment Score: 0 | Count | P\_Value | Benjamini |
|  | SMART | FBOX | 6 | 1.0E0 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:F-box | 10 | 1.0E0 | 1.0E0 |
|  | INTERPRO | F-box\_dom | 10 | 1.0E0 | 1.0E0 |
|  | INTERPRO | F-box-like\_dom\_sf | 11 | 1.0E0 | 1.0E0 |
| Annotation Cluster 196 | | Enrichment Score: 0 | Count | P\_Value | Benjamini |
|  | UP\_SEQ\_FEATURE | DOMAIN:RRM | 6 | 1.0E0 | 1.0E0 |
|  | INTERPRO | RRM\_dom | 6 | 1.0E0 | 1.0E0 |
|  | INTERPRO | Nucleotide-bd\_a/b\_plait\_sf | 6 | 1.0E0 | 1.0E0 |
|  | INTERPRO | RBD\_domain\_sf | 6 | 1.0E0 | 1.0E0 |
|  | SMART | RRM | 6 | 1.0E0 | 1.0E0 |
| Annotation Cluster 197 | | Enrichment Score: 0 | Count | P\_Value | Benjamini |
|  | INTERPRO | PolX-like\_BBD | 4 | 1.0E0 | 1.0E0 |
|  | INTERPRO | Znf\_CCHC\_sf | 4 | 1.0E0 | 1.0E0 |
|  | UP\_SEQ\_FEATURE | DOMAIN:CCHC-type | 4 | 1.0E0 | 1.0E0 |
|  | INTERPRO | Znf\_CCHC | 4 | 1.0E0 | 1.0E0 |
|  | SMART | ZnF\_C2HC | 3 | 1.0E0 | 1.0E0 |