**Table S6** **GO classification of common expressed genes in shoot formed stage**

|  |  |  |  |
| --- | --- | --- | --- |
| **Catergory** | **Gene Ontology Term** | **The Number****of Genes** | **Corrected P-value\*** |
| biological\_process | GO:0055114 oxidation-reduction process | 229 | 0.0000538 |
| biological\_process | GO:0080090 regulation of primary metabolic process | 189 | 0.00143 |
| biological\_process | GO:0031323 regulation of cellular metabolic process | 192 | 0.00161 |
| biological\_process | GO:0006355 regulation of transcription, DNA-templated | 154 | 0.00183 |
| biological\_process | GO:1903506 regulation of nucleic acid-templated transcription | 154 | 0.00247 |
| biological\_process | GO:2001141 regulation of RNA biosynthetic process | 154 | 0.00266 |
| biological\_process | GO:0051252 regulation of RNA metabolic process | 155 | 0.00376 |
| biological\_process | GO:0060255 regulation of macromolecule metabolic process | 189 | 0.00529 |
| biological\_process | GO:0019219 regulation of nucleobase-containing compound metabolic process | 156 | 0.00919 |
| biological\_process | GO:2000112 regulation of cellular macromolecule biosynthetic process | 161 | 0.01215 |
| biological\_process | GO:0010556 regulation of macromolecule biosynthetic process | 161 | 0.01686 |
| biological\_process | GO:0009889 regulation of biosynthetic process | 162 | 0.01751 |
| biological\_process | GO:0031326 regulation of cellular biosynthetic process | 162 | 0.01751 |
| biological\_process | GO:0006334 nucleosome assembly | 12 | 0.02205 |
| biological\_process | GO:0071365 cellular response to auxin stimulus | 19 | 0.02689 |
| biological\_process | GO:0051171 regulation of nitrogen compound metabolic process | 163 | 0.03012 |
| biological\_process | GO:0009733 response to auxin | 32 | 0.03297 |
| biological\_process | GO:0010468 regulation of gene expression | 162 | 0.05054 |
| cellular\_component | GO:0000786 nucleosome | 21 | 6.99E-08 |
| cellular\_component | GO:0044815 DNA packaging complex | 21 | 0.000000141 |
| cellular\_component | GO:0032993 protein-DNA complex | 22 | 0.000039 |
| cellular\_component | GO:0005576 extracellular region | 68 | 0.00076 |
| cellular\_component | GO:0000785 chromatin | 21 | 0.00292 |
| molecular\_function | GO:0016491 oxidoreductase activity | 251 | 3.83E-08 |
| molecular\_function | GO:0003677 DNA binding | 193 | 0.00000592 |
| molecular\_function | GO:0005506 iron ion binding | 57 | 0.0000555 |
| molecular\_function | GO:0020037 heme binding | 60 | 0.00011 |
| molecular\_function | GO:0003700 transcription factor activity, sequence-specific DNA binding | 78 | 0.00012 |
| molecular\_function | GO:0001071 nucleic acid binding transcription factor activity | 78 | 0.00012 |
| molecular\_function | GO:0004497 monooxygenase activity | 51 | 0.00022 |
| molecular\_function | GO:0046906 tetrapyrrole binding | 63 | 0.00034 |
| molecular\_function | GO:0016701 oxidoreductase activity, acting on single donors with incorporation of molecular oxygen | 21 | 0.00136 |
| molecular\_function | GO:0035251 UDP-glucosyltransferase activity | 28 | 0.00266 |
| molecular\_function | GO:0046982 protein heterodimerization activity | 23 | 0.00413 |
| molecular\_function | GO:0046527 glucosyltransferase activity | 28 | 0.0109 |
|  |  |  |  |
| molecular\_function | GO:0043565 sequence-specific DNA binding | 53 | 0.01593 |
| molecular\_function | GO:0016705 oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen | 51 | 0.01851 |
| molecular\_function | GO:0008289 lipid binding | 31 | 0.03641 |

**\***: Corrected P value of all GO terms are lower than 0.05.