**Supplemental Table S3. Comparison of GO enrichment analysis for Set 1 versus Set 2 genes in Arabidopsis*.***

**Set 1:** Genes associated to *plant embryo globular stage* (*globular*) but not *mature plant embryo stage* (*mature*)*.*

**Set 2:** Genes associated to *mature plant embryo stage* (*mature*) but not *plant embryo globular stage* (*globular*).

GO Branches: BP = *biological process*, MF = *molecular function*, and CC = *cellular component*. FDR is the False Discovery Rate of (Benjamini & Yekutieli, 2001). Any reported value is significant at P=0.05 when corrected for multiple tests. Colors correspond to FDR values, with red most significant and dark gray non-significant.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **GO Information** | | | **FDR** | |
| **Term ID** | **Branch** | **Term label** | **Set 1 -**  **globular not mature** | **Set 2 -**  **mature not globular** |
|
| GO:0051704 | BP | multi-organism process | 2.30e-18 | --- |
| GO:0009856 | BP | pollination | 8.10e-17 | --- |
| GO:0050896 | BP | response to stimulus | 1.80e-08 | 0.0058 |
| GO:0006810 | BP | transport | 3.00e-07 | --- |
| GO:0051234 | BP | establishment of localization | 1.20e-06 | --- |
| GO:0016049 | BP | cell growth | 1.30e-06 | --- |
| GO:0008361 | BP | regulation of cell size | 1.60e-06 | --- |
| GO:0051179 | BP | localization | 1.80e-06 | --- |
| GO:0090066 | BP | regulation of anatomical structure size | 2.10e-06 | --- |
| GO:0032535 | BP | regulation of cellular component size | 2.10e-06 | --- |
| GO:0009719 | BP | response to endogenous stimulus | 3.20e-06 | --- |
| GO:0006950 | BP | response to stress | 5.40e-06 | --- |
| GO:0009607 | BP | response to biotic stimulus | 7.20e-06 | --- |
| GO:0040007 | BP | growth | 1.60e-05 | --- |
| GO:0019748 | BP | secondary metabolic process | 1.70e-05 | --- |
| GO:0022414 | BP | reproductive process | 2.80e-05 | 0.0017 |
| GO:0000003 | BP | reproduction | 3.20e-05 | 0.0018 |
| GO:0016265 | BP | death | 4.50e-05 | --- |
| GO:0008219 | BP | cell death | 4.50e-05 | --- |
| GO:0030154 | BP | cell differentiation | 5.80e-05 | --- |
| GO:0048869 | BP | cellular developmental process | 0.00017 | --- |
| GO:0003006 | BP | reproductive developmental process | 0.00023 | 0.0085 |
| GO:0065007 | BP | biological regulation | 0.00034 | 3.80e-06 |
| GO:0065008 | BP | regulation of biological quality | 0.00064 | --- |
| GO:0032502 | BP | developmental process | 0.0027 | 0.005 |
| GO:0007165 | BP | signal transduction | 0.0044 | 0.0009 |
| GO:0006519 | BP | cellular amino acid and derivative metabolic process | 0.0044 | --- |
| GO:0007275 | BP | multicellular organismal development | 0.009 | 0.0021 |
| GO:0009653 | BP | anatomical structure morphogenesis | 0.01 | 0.0017 |
| GO:0048856 | BP | anatomical structure development | 0.015 | 0.00097 |
| GO:0050794 | BP | regulation of cellular process | 0.015 | 1.70e-06 |
| GO:0009605 | BP | response to external stimulus | 0.015 | --- |
| GO:0032501 | BP | multicellular organismal process | 0.017 | 0.00059 |
| GO:0008152 | BP | metabolic process | 0.027 | --- |
| GO:0006629 | BP | lipid metabolic process | 0.039 | --- |
| GO:0003824 | MF | catalytic activity | 6.10e-09 | --- |
| GO:0016787 | MF | hydrolase activity | 1.60e-06 | --- |
| GO:0005215 | MF | transporter activity | 3.90e-06 | --- |
| GO:0003700 | MF | transcription factor activity | 4.80e-05 | 9.50e-06 |
| GO:0030528 | MF | transcription regulator activity | 0.00016 | 7.20e-06 |
| GO:0016788 | MF | hydrolase activity, acting on ester bonds | 0.00025 | --- |
| GO:0030234 | MF | enzyme regulator activity | 0.0012 | --- |
| GO:0005576 | CC | extracellular region | 1.20e-17 | --- |
| GO:0030312 | CC | external encapsulating structure | 0.00015 | --- |
| GO:0005618 | CC | cell wall | 0.00015 | --- |
| GO:0005886 | CC | plasma membrane | 0.0011 | --- |
| GO:0050789 | BP | regulation of biological process | --- | 1.70e-06 |
| GO:0019222 | BP | regulation of metabolic process | --- | 3.80e-06 |
| GO:0009908 | BP | flower development | --- | 3.80e-06 |
| GO:0060255 | BP | regulation of macromolecule metabolic process | --- | 3.50e-05 |
| GO:0006350 | BP | transcription | --- | 6.50e-05 |
| GO:0010468 | BP | regulation of gene expression | --- | 0.00012 |
| GO:0006259 | BP | DNA metabolic process | --- | 0.00051 |
| GO:0048608 | BP | reproductive structure development | --- | 0.0017 |
| GO:0009875 | BP | pollen-pistil interaction | --- | 0.005 |
| GO:0009791 | BP | post-embryonic development | --- |  |
| GO:0006139 | BP | nucleobase, nucleoside, nucleotide and nucleic acid metabolic process | --- |  |
| GO:0007049 | BP | cell cycle | --- |  |
| GO:0003677 | MF | DNA binding | --- |  |
| GO:0016301 | MF | kinase activity | --- |  |
| GO:0016772 | MF | transferase activity, transferring phosphorus-containing groups | --- |  |
| GO:0005634 | CC | nucleus | --- |  |