**Supplemental Table S4. Comparison of GO across species for Set 3 and Set 4.**

**Set 3:** Arabidopsis genes whose orthologs have been associated with the *plant embryo coleoptilar stage* (coleoptilar) of maize in the PO, but which have not been associated with the *plant embryo cotyledonary stage* (cotyledonary) in Arabidopsis.**Set 4:** *G*enes associated with the *plant embryo cotyledonary stage* in Arabidopsis. 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 fro 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 3 – coleoptilar not cotyledonary** | **Set 4 – cotyledonary** |
| GO:0006810 | BP | transport | 2.20e-05 | 2.00e-34 |
| GO:0051704 | BP | multi-organism process | 2.20e-05 | 1.10e-14 |
| GO:0051234 | BP | establishment of localization | 2.40e-05 | 7.40e-38 |
| GO:0051179 | BP | localization | 2.40e-05 | 4.50e-40 |
| GO:0009856 | BP | pollination | 6.20e-05 | --- |
| GO:0009719 | BP | response to endogenous stimulus | 0.00065 | 1.00e-12 |
| GO:0050896 | BP | response to stimulus | 0.008 | 2.00e-75 |
| GO:0016049 | BP | cell growth | 0.022 | 0.00093 |
| GO:0090066 | BP | regulation of anatomical structure size | 0.027 | 0.00051 |
| GO:0008361 | BP | regulation of cell size | 0.027 | 0.00038 |
| GO:0032535 | BP | regulation of cellular component size | 0.027 | 0.00051 |
| GO:0003824 | MF | catalytic activity | 0.00031 | 1.70e-36 |
| GO:0005215 | MF | transporter activity | 0.026 | 3.10e-06 |
| GO:0005576 | CC | extracellular region | 0.03 | --- |
| GO:0009987 | BP | cellular process | --- | 6.70e-165 |
| GO:0044237 | BP | cellular metabolic process | --- | 5.50e-135 |
| GO:0044238 | BP | primary metabolic process | --- | 5.90e-116 |
| GO:0008152 | BP | metabolic process | --- | 2.60e-108 |
| GO:0006807 | BP | nitrogen compound metabolic process | --- | 2.70e-91 |
| GO:0016043 | BP | cellular component organization | --- | 2.70e-86 |
| GO:0006139 | BP | nucleobase, nucleoside, nucleotide and nucleic acid metabolic process | --- | 8.90e-73 |
| GO:0043170 | BP | macromolecule metabolic process | --- | 2.90e-71 |
| GO:0009058 | BP | biosynthetic process | --- | 2.70e-70 |
| GO:0044260 | BP | cellular macromolecule metabolic process | --- | 1.30e-69 |
| GO:0044249 | BP | cellular biosynthetic process | --- | 4.20e-65 |
| GO:0065007 | BP | biological regulation | --- | 1.60e-62 |
| GO:0009628 | BP | response to abiotic stimulus | --- | 6.70e-61 |
| GO:0032501 | BP | multicellular organismal process | --- | 7.60e-60 |
| GO:0032502 | BP | developmental process | --- | 8.90e-60 |
| GO:0007275 | BP | multicellular organismal development | --- | 1.10e-56 |
| GO:0050789 | BP | regulation of biological process | --- | 7.40e-56 |
| GO:0009056 | BP | catabolic process | --- | 3.80e-55 |
| GO:0005975 | BP | carbohydrate metabolic process | --- | 4.20e-50 |
| GO:0048856 | BP | anatomical structure development | --- | 4.20e-50 |
| GO:0009791 | BP | post-embryonic development | --- | 1.20e-49 |
| GO:0006950 | BP | response to stress | --- | 1.70e-49 |
| GO:0043412 | BP | macromolecule modification | --- | 3.70e-48 |
| GO:0050794 | BP | regulation of cellular process | --- | 3.90e-40 |
| GO:0006464 | BP | protein modification process | --- | 7.40e-39 |
| GO:0048608 | BP | reproductive structure development | --- | 4.60e-37 |
| GO:0003006 | BP | reproductive developmental process | --- | 1.10e-30 |
| GO:0009607 | BP | response to biotic stimulus | --- | 2.60e-30 |
| GO:0000003 | BP | reproduction | --- | 5.00e-30 |
| GO:0022414 | BP | reproductive process | --- | 7.10e-30 |
| GO:0006629 | BP | lipid metabolic process | --- | 3.10e-29 |
| GO:0007049 | BP | cell cycle | --- | 1.80e-27 |
| GO:0019222 | BP | regulation of metabolic process | --- | 6.90e-27 |
| GO:0019538 | BP | protein metabolic process | --- | 7.80e-27 |
| GO:0044267 | BP | cellular protein metabolic process | --- | 2.20e-25 |
| GO:0006091 | BP | generation of precursor metabolites and energy | --- | 3.00e-24 |
| GO:0006519 | BP | cellular amino acid and derivative metabolic process | --- | 1.20e-23 |
| GO:0009653 | BP | anatomical structure morphogenesis | --- | 1.90e-21 |
| GO:0009908 | BP | flower development | --- | 2.20e-21 |
| GO:0006259 | BP | DNA metabolic process | --- | 2.50e-21 |
| GO:0060255 | BP | regulation of macromolecule metabolic process | --- | 1.90e-19 |
| GO:0019748 | BP | secondary metabolic process | --- | 1.90e-19 |
| GO:0015979 | BP | photosynthesis | --- | 5.80e-19 |
| GO:0009059 | BP | macromolecule biosynthetic process | --- | 1.00e-18 |
| GO:0065008 | BP | regulation of biological quality | --- | 1.40e-17 |
| GO:0006350 | BP | transcription | --- | 2.00e-17 |
| GO:0034645 | BP | cellular macromolecule biosynthetic process | --- | 5.40e-17 |
| GO:0010468 | BP | regulation of gene expression | --- | 6.40e-16 |
| GO:0009790 | BP | embryonic development |  | 5.50e-14 |
| GO:0040029 | BP | regulation of gene expression, epigenetic |  | 6.80e-14 |
| GO:0048869 | BP | cellular developmental process |  | 7.70e-14 |
| GO:0007165 | BP | signal transduction |  | 1.10e-12 |
| GO:0009605 | BP | response to external stimulus |  | 1.40e-10 |
| GO:0010467 | BP | gene expression |  | 2.00e-10 |
| GO:0042592 | BP | homeostatic process |  | 9.90e-10 |
| GO:0030154 | BP | cell differentiation |  | 6.00e-09 |
| GO:0016265 | BP | death |  | 7.00e-09 |
| GO:0008219 | BP | cell death |  | 7.00e-09 |
| GO:0040007 | BP | growth |  | 1.10e-08 |
| GO:0009606 | BP | tropism |  | 1.90e-06 |
| GO:0019725 | BP | cellular homeostasis |  | 2.20e-06 |
| GO:0007154 | BP | cell communication |  | 0.00053 |
| GO:0005515 | MF | protein binding |  | 4.70e-39 |
| GO:0005488 | MF | binding |  | 2.00e-29 |
| GO:0000166 | MF | nucleotide binding |  | 2.20e-22 |
| GO:0016740 | MF | transferase activity |  | 2.10e-13 |
| GO:0016787 | MF | hydrolase activity |  | 2.30e-11 |
| GO:0016817 | MF | hydrolase activity, acting on acid anhydrides |  | 2.50e-09 |
| GO:0016818 | MF | hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides |  | 2.70e-09 |
| GO:0016462 | MF | pyrophosphatase activity |  | 3.90e-09 |
| GO:0016772 | MF | transferase activity, transferring phosphorus-containing groups |  | 2.70e-08 |
| GO:0017111 | MF | nucleoside-triphosphatase activity |  | 3.00e-08 |
| GO:0005198 | MF | structural molecule activity |  | 1.70e-06 |
| GO:0016301 | MF | kinase activity |  | 1.50e-05 |
| GO:0003677 | MF | DNA binding |  | 0.00012 |
| GO:0016788 | MF | hydrolase activity, acting on ester bonds |  | 0.008 |
| GO:0003774 | MF | motor activity |  | 0.015 |
| GO:0004518 | MF | nuclease activity |  | 0.02 |
| GO:0008135 | MF | translation factor activity, nucleic acid binding |  | 0.047 |
| GO:0044464 | CC | cell part |  | 2.30e-170 |
| GO:0005623 | CC | cell |  | 2.30e-170 |
| GO:0005622 | CC | intracellular |  | 5.70e-124 |
| GO:0044424 | CC | intracellular part |  | 2.90e-122 |
| GO:0044446 | CC | intracellular organelle part |  | 6.00e-94 |
| GO:0044422 | CC | organelle part |  | 6.00e-94 |
| GO:0043229 | CC | intracellular organelle |  | 4.60e-89 |
| GO:0043226 | CC | organelle |  | 4.80e-89 |
| GO:0005737 | CC | cytoplasm |  | 2.90e-88 |
| GO:0044444 | CC | cytoplasmic part |  | 1.30e-84 |
| GO:0043227 | CC | membrane-bounded organelle |  | 4.80e-84 |
| GO:0043231 | CC | intracellular membrane-bounded organelle |  | 8.60e-84 |
| GO:0016020 | CC | membrane |  | 2.60e-60 |
| GO:0009536 | CC | plastid |  | 2.60e-56 |
| GO:0005829 | CC | cytosol |  | 1.90e-46 |
| GO:0005886 | CC | plasma membrane |  | 4.80e-33 |
| GO:0031975 | CC | envelope |  | 6.30e-30 |
| GO:0031967 | CC | organelle envelope |  | 6.30e-30 |
| GO:0032991 | CC | macromolecular complex |  | 6.70e-29 |
| GO:0009579 | CC | thylakoid |  | 1.40e-19 |
| GO:0043232 | CC | intracellular non-membrane-bounded organelle |  | 9.70e-19 |
| GO:0043228 | CC | non-membrane-bounded organelle |  | 9.70e-19 |
| GO:0005773 | CC | vacuole |  | 6.50e-18 |
| GO:0031974 | CC | membrane-enclosed lumen |  | 6.30e-17 |
| GO:0043233 | CC | organelle lumen |  | 1.20e-16 |
| GO:0070013 | CC | intracellular organelle lumen |  | 1.20e-16 |
| GO:0005794 | CC | Golgi apparatus |  | 1.90e-16 |
| GO:0044428 | CC | nuclear part |  | 4.60e-16 |
| GO:0005634 | CC | nucleus |  | 3.40e-15 |
| GO:0031981 | CC | nuclear lumen |  | 2.70e-12 |
| GO:0005783 | CC | endoplasmic reticulum |  | 1.80e-11 |
| GO:0005768 | CC | endosome |  | 3.30e-09 |
| GO:0005730 | CC | nucleolus |  | 4.70e-09 |
| GO:0005840 | CC | ribosome |  | 5.10e-07 |
| GO:0012505 | CC | endomembrane system |  | 7.50e-07 |
| GO:0005777 | CC | peroxisome |  | 1.60e-05 |
| GO:0042579 | CC | microbody |  | 1.60e-05 |
| GO:0030529 | CC | ribonucleoprotein complex |  | 4.60e-05 |
| GO:0005654 | CC | nucleoplasm |  | 0.00015 |
| GO:0030312 | CC | external encapsulating structure |  | 0.0017 |
| GO:0005635 | CC | nuclear envelope |  | 0.002 |
| GO:0005618 | CC | cell wall |  | 0.002 |
| GO:0005856 | CC | cytoskeleton |  | 0.0021 |