**Supplemental Table 3.** Enrichment of GO terms in ≥ 2-fold up- and down-regulated genes in 2-, 5-, and 8-day old conidia associated with the conidiophore.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **5-day old conidia vs 2 day old conidia** | | **8-day old conidia vs 2 day old conidia** | | **8-day old conidia vs 5 day old conidia** | |
| **Up-regulated genes** | | | | | |
| GO term | Functional annotation | GO term | Functional annotation | GO term | Functional annotation |
| GO:0043169 | cation binding | GO:0003700 | sequence-specific DNA binding transcription factor activity |  |  |
| GO:0003700 | sequence-specific DNA binding transcription factor activity | GO:0001071 | nucleic acid binding transcription factor activity |  |  |
| GO:0001071 | nucleic acid binding transcription factor activity | GO:0000981 | sequence-specific DNA binding RNA polymerase II transcription factor activity |  |  |
| GO:0046872 | metal ion binding | GO:2001141 | regulation of RNA biosynthetic process |  |  |
| GO:0000981 | sequence-specific DNA binding RNA polymerase II transcription factor activity | GO:0051252 | regulation of RNA metabolic process |  |  |
| GO:2001141 | regulation of RNA biosynthetic process | GO:0010556 | regulation of macromolecule biosynthetic process |  |  |
| GO:0051252 | regulation of RNA metabolic process | GO:0006355 | regulation of transcription, DNA-templated |  |  |
| GO:0010556 | regulation of macromolecule biosynthetic process | GO:2000112 | regulation of cellular macromolecule biosynthetic process |  |  |
| GO:0006355 | regulation of transcription, DNA-templated | GO:0010468 | regulation of gene expression |  |  |
| GO:2000112 | regulation of cellular macromolecule biosynthetic process | GO:0009889 | regulation of biosynthetic process |  |  |
| GO:0010468 | regulation of gene expression | GO:0031326 | regulation of cellular biosynthetic process |  |  |
| GO:0009889 | regulation of biosynthetic process | GO:0060255 | regulation of macromolecule metabolic process |  |  |
| GO:0031326 | regulation of cellular biosynthetic process | GO:0051171 | regulation of nitrogen compound metabolic process |  |  |
| GO:0060255 | regulation of macromolecule metabolic process | GO:0019219 | regulation of nucleobase-containing compound metabolic process |  |  |
| GO:0046914 | transition metal ion binding | GO:0080090 | regulation of primary metabolic process |  |  |
| GO:0005634 | nucleus | GO:0031323 | regulation of cellular metabolic process |  |  |
| GO:0051171 | regulation of nitrogen compound metabolic process | GO:0019222 | regulation of metabolic process |  |  |
| GO:0019219 | regulation of nucleobase-containing compound metabolic process | GO:0008270 | zinc ion binding |  |  |
| GO:0008270 | zinc ion binding | GO:0005634 | nucleus |  |  |
| GO:0004601 | peroxidase activity | GO:0046872 | metal ion binding |  |  |
| GO:0016684 | oxidoreductase activity, acting on peroxide as acceptor | GO:0043169 | cation binding |  |  |
| GO:0080090 | regulation of primary metabolic process | GO:0043227 | membrane-bounded organelle |  |  |
| GO:0031323 | regulation of cellular metabolic process | GO:0043231 | intracellular membrane-bounded organelle |  |  |
| GO:0043227 | membrane-bounded organelle | GO:0050794 | regulation of cellular process |  |  |
| GO:0043231 | intracellular membrane-bounded organelle | GO:0050789 | regulation of biological process |  |  |
| GO:0019222 | regulation of metabolic process | GO:0065007 | biological regulation |  |  |
|  |  | GO:0046914 | transition metal ion binding |  |  |

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **5-day old conidia vs 2 day old conidia** | | **8-day old conidia vs 2 day old conidia** | | **8-day old conidia vs 5 day old conidia** | |
| **Down-regulated genes** | | | | | |
| GO term | Functional annotation | GO term | Functional annotation | GO term | Functional annotation |
| GO:0005840 | ribosome | GO:0005198 | structural molecule activity | GO:0005198 | structural molecule activity |
| GO:0005198 | structural molecule activity | GO:0005840 | ribosome | GO:0032991 | macromolecular complex |
| GO:0003735 | structural constituent of ribosome | GO:0032991 | macromolecular complex | GO:0043232 | intracellular non-membrane-bounded organelle |
| GO:0006412 | translation | GO:0003735 | structural constituent of ribosome | GO:0043228 | non-membrane-bounded organelle |
| GO:0030529 | ribonucleoprotein complex | GO:0044444 | cytoplasmic part | GO:0005840 | ribosome |
| GO:0043232 | intracellular non-membrane-bounded organelle | GO:0006412 | translation | GO:0003735 | structural constituent of ribosome |
| GO:0043228 | non-membrane-bounded organelle | GO:0043232 | intracellular non-membrane-bounded organelle | GO:0030529 | ribonucleoprotein complex |
| GO:0044444 | cytoplasmic part | GO:0043228 | non-membrane-bounded organelle | GO:0006412 | translation |
| GO:0032991 | macromolecular complex | GO:0030529 | ribonucleoprotein complex | GO:0044444 | cytoplasmic part |
| GO:0005622 | intracellular | GO:0005622 | intracellular | GO:0044237 | cellular metabolic process |
| GO:0044267 | cellular protein metabolic process | GO:0044267 | cellular protein metabolic process | GO:0044464 | cell part |
| GO:0019538 | protein metabolic process | GO:0019538 | protein metabolic process | GO:0044424 | intracellular part |
| GO:0004298 | threonine-type endopeptidase activity | GO:0043234 | protein complex | GO:0009987 | cellular process |
| GO:0070003 | threonine-type peptidase activity | GO:0044464 | cell part | GO:0005622 | intracellular |
| GO:0005839 | proteasome core complex | GO:0044424 | intracellular part | GO:0044281 | small molecule metabolic process |
| GO:0044249 | cellular biosynthetic process | GO:0004298 | threonine-type endopeptidase activity | GO:0016043 | cellular component organization |
| GO:0008152 | metabolic process | GO:0070003 | threonine-type peptidase activity | GO:0006996 | organelle organization |
| GO:0034645 | cellular macromolecule biosynthetic process | GO:0044237 | cellular metabolic process | GO:0071840 | cellular component organization or biogenesis |
| GO:1901576 | organic substance biosynthetic process | GO:0005839 | proteasome core complex | GO:0006082 | organic acid metabolic process |
| GO:0009059 | macromolecule biosynthetic process | GO:0044238 | primary metabolic process | GO:0071704 | organic substance metabolic process |
| GO:0009058 | biosynthetic process | GO:0008152 | metabolic process | GO:0044267 | cellular protein metabolic process |
| GO:0044464 | cell part | GO:0071704 | organic substance metabolic process | GO:0034645 | cellular macromolecule biosynthetic process |
| GO:0044723 | single-organism carbohydrate metabolic process | GO:0044249 | cellular biosynthetic process | GO:0009069 | serine family amino acid metabolic process |
| GO:0071704 | organic substance metabolic process | GO:1901576 | organic substance biosynthetic process | GO:1901564 | organonitrogen compound metabolic process |
| GO:0044424 | intracellular part | GO:0034645 | cellular macromolecule biosynthetic process | GO:1902589 | single-organism organelle organization |
| GO:0044238 | primary metabolic process | GO:0044723 | single-organism carbohydrate metabolic process | GO:0019752 | carboxylic acid metabolic process |
| GO:0044237 | cellular metabolic process | GO:0009141 | nucleoside triphosphate metabolic process | GO:0043436 | oxoacid metabolic process |
| GO:0019773 | proteasome core complex, alpha-subunit complex | GO:0009059 | macromolecule biosynthetic process | GO:0009071 | serine family amino acid catabolic process |
| GO:0005975 | carbohydrate metabolic process | GO:0044260 | cellular macromolecule metabolic process | GO:0005815 | microtubule organizing center |
| GO:0043170 | macromolecule metabolic process | GO:0009058 | biosynthetic process | GO:0006546 | glycine catabolic process |
| GO:0044260 | cellular macromolecule metabolic process | GO:0043170 | macromolecule metabolic process | GO:0008152 | metabolic process |
| GO:0004129 | cytochrome-c oxidase activity | GO:0009205 | purine ribonucleoside triphosphate metabolic process | GO:0000922 | spindle pole |
| GO:0016675 | oxidoreductase activity, acting on a heme group of donors | GO:0009199 | ribonucleoside triphosphate metabolic process | GO:0005575 | cellular\_component |
| GO:0016676 | oxidoreductase activity, acting on a heme group of donors, oxygen as acceptor | GO:0009144 | purine nucleoside triphosphate metabolic process | GO:0044238 | primary metabolic process |
| GO:0015002 | heme-copper terminal oxidase activity | GO:0044281 | small molecule metabolic process | GO:0008150 | biological\_process |
| GO:0043226 | organelle | GO:0006091 | generation of precursor metabolites and energy | GO:0009059 | macromolecule biosynthetic process |
| GO:0043229 | intracellular organelle | GO:0019637 | organophosphate metabolic process | GO:1901576 | organic substance biosynthetic process |
| GO:0051603 | proteolysis involved in cellular protein catabolic process | GO:0009119 | ribonucleoside metabolic process | GO:0006520 | cellular amino acid metabolic process |
| GO:0044262 | cellular carbohydrate metabolic process | GO:0044422 | organelle part | GO:0044260 | cellular macromolecule metabolic process |
| GO:0016491 | oxidoreductase activity | GO:0044446 | intracellular organelle part | GO:0044249 | cellular biosynthetic process |
| GO:0005199 | structural constituent of cell wall | GO:0009123 | nucleoside monophosphate metabolic process | GO:0007017 | microtubule-based process |
| GO:0009277 | fungal-type cell wall | GO:0009117 | nucleotide metabolic process | GO:1901565 | organonitrogen compound catabolic process |
| GO:0016832 | aldehyde-lyase activity | GO:0006753 | nucleoside phosphate metabolic process | GO:0043234 | protein complex |
| GO:0015078 | hydrogen ion transmembrane transporter activity | GO:0009259 | ribonucleotide metabolic process | GO:0044430 | cytoskeletal part |
| GO:0003674 | molecular\_function | GO:0019693 | ribose phosphate metabolic process | GO:0044699 | single-organism process |
| GO:0043234 | protein complex | GO:0015078 | hydrogen ion transmembrane transporter activity | GO:0044710 | single-organism metabolic process |
| GO:0016861 | intramolecular oxidoreductase activity, interconverting aldoses and ketoses | GO:0044429 | mitochondrial part | GO:1901265 | nucleoside phosphate binding |
| GO:0004175 | endopeptidase activity | GO:0042278 | purine nucleoside metabolic process | GO:0000166 | nucleotide binding |
| GO:0016051 | carbohydrate biosynthetic process | GO:0046128 | purine ribonucleoside metabolic process | GO:0036094 | small molecule binding |
| GO:0034637 | cellular carbohydrate biosynthetic process | GO:0004129 | cytochrome-c oxidase activity | GO:0006544 | glycine metabolic process |
| GO:0009055 | electron carrier activity | GO:0030120 | vesicle coat | GO:0043226 | organelle |
| GO:0003824 | catalytic activity | GO:0016675 | oxidoreductase activity, acting on a heme group of donors | GO:0043229 | intracellular organelle |
| GO:0005618 | cell wall | GO:0019773 | proteasome core complex, alpha-subunit complex | GO:0043170 | macromolecule metabolic process |
| GO:0030312 | external encapsulating structure | GO:0044433 | cytoplasmic vesicle part | GO:0044712 | single-organism catabolic process |
| GO:0019751 | polyol metabolic process | GO:0016676 | oxidoreductase activity, acting on a heme group of donors, oxygen as acceptor | GO:0019538 | protein metabolic process |
| GO:0016853 | isomerase activity | GO:0015002 | heme-copper terminal oxidase activity | GO:0007010 | cytoskeleton organization |
| GO:0015077 | monovalent inorganic cation transmembrane transporter activity | GO:0009161 | ribonucleoside monophosphate metabolic process | GO:0044422 | organelle part |
| GO:0006486 | protein glycosylation | GO:0009124 | nucleoside monophosphate biosynthetic process | GO:0044446 | intracellular organelle part |
| GO:0043413 | macromolecule glycosylation | GO:0046034 | ATP metabolic process | GO:0009058 | biosynthetic process |
| GO:0044710 | single-organism metabolic process | GO:0009206 | purine ribonucleoside triphosphate biosynthetic process | GO:0046907 | intracellular transport |
| GO:0008150 | biological\_process | GO:0009145 | purine nucleoside triphosphate biosynthetic process | GO:0035639 | purine ribonucleoside triphosphate binding |
| GO:0016860 | intramolecular oxidoreductase activity | GO:0009201 | ribonucleoside triphosphate biosynthetic process | GO:0032550 | purine ribonucleoside binding |
| GO:0008233 | peptidase activity | GO:0009142 | nucleoside triphosphate biosynthetic process | GO:0032549 | ribonucleoside binding |
| GO:0006414 | translational elongation | GO:0006520 | cellular amino acid metabolic process | GO:0032555 | purine ribonucleotide binding |
|  |  | GO:0009150 | purine ribonucleotide metabolic process | GO:0001883 | purine nucleoside binding |
|  |  | GO:0009055 | electron carrier activity | GO:0001882 | nucleoside binding |
|  |  | GO:1901564 | organonitrogen compound metabolic process | GO:0005524 | ATP binding |
|  |  | GO:0046907 | intracellular transport | GO:0044763 | single-organism cellular process |
|  |  | GO:0051649 | establishment of localization in cell | GO:0051649 | establishment of localization in cell |
|  |  | GO:0006082 | organic acid metabolic process | GO:0032559 | adenyl ribonucleotide binding |
|  |  | GO:0006418 | tRNA aminoacylation for protein translation | GO:0044282 | small molecule catabolic process |
|  |  | GO:1901659 | glycosyl compound biosynthetic process | GO:0006807 | nitrogen compound metabolic process |
|  |  | GO:0042455 | ribonucleoside biosynthetic process | GO:0032553 | ribonucleotide binding |
|  |  | GO:0009163 | nucleoside biosynthetic process | GO:0097367 | carbohydrate derivative binding |
|  |  | GO:0044710 | single-organism metabolic process | GO:0017076 | purine nucleotide binding |
|  |  | GO:0006163 | purine nucleotide metabolic process | GO:1901606 | alpha-amino acid catabolic process |
|  |  | GO:0051603 | proteolysis involved in cellular protein catabolic process | GO:1901136 | carbohydrate derivative catabolic process |
|  |  | GO:0019752 | carboxylic acid metabolic process | GO:0030554 | adenyl nucleotide binding |
|  |  | GO:0043436 | oxoacid metabolic process | GO:1901605 | alpha-amino acid metabolic process |
|  |  | GO:0009167 | purine ribonucleoside monophosphate metabolic process | GO:0009063 | cellular amino acid catabolic process |
|  |  | GO:0009126 | purine nucleoside monophosphate metabolic process | GO:0000226 | microtubule cytoskeleton organization |
|  |  | GO:0004812 | aminoacyl-tRNA ligase activity | GO:0008092 | cytoskeletal protein binding |
|  |  | GO:0043039 | tRNA aminoacylation | GO:0022402 | cell cycle process |
|  |  | GO:0043038 | amino acid activation | GO:0009203 | ribonucleoside triphosphate catabolic process |
|  |  | GO:0003674 | molecular\_function | GO:0009207 | purine ribonucleoside triphosphate catabolic process |
|  |  | GO:0044455 | mitochondrial membrane part | GO:0005199 | structural constituent of cell wall |
|  |  | GO:0009156 | ribonucleoside monophosphate biosynthetic process | GO:0046130 | purine ribonucleoside catabolic process |
|  |  | GO:0016832 | aldehyde-lyase activity | GO:0009143 | nucleoside triphosphate catabolic process |
|  |  | GO:0008150 | biological\_process | GO:1901069 | guanosine-containing compound catabolic process |
|  |  | GO:0072521 | purine-containing compound metabolic process | GO:0009277 | fungal-type cell wall |
|  |  | GO:0015077 | monovalent inorganic cation transmembrane transporter activity | GO:0006184 | GTP catabolic process |
|  |  | GO:0016876 | ligase activity, forming aminoacyl-tRNA and related compounds | GO:0051258 | protein polymerization |
|  |  | GO:0005575 | cellular\_component | GO:0009146 | purine nucleoside triphosphate catabolic process |
|  |  | GO:0016875 | ligase activity, forming carbon-oxygen bonds | GO:0044427 | chromosomal part |
|  |  | GO:0009260 | ribonucleotide biosynthetic process | GO:0006152 | purine nucleoside catabolic process |
|  |  | GO:0015986 | ATP synthesis coupled proton transport |  |  |
|  |  | GO:0046390 | ribose phosphate biosynthetic process |  |  |
|  |  | GO:0006754 | ATP biosynthetic process |  |  |
|  |  | GO:0005975 | carbohydrate metabolic process |  |  |
|  |  | GO:0015985 | energy coupled proton transport, down electrochemical gradient |  |  |
|  |  | GO:0009987 | cellular process |  |  |
|  |  | GO:0006399 | tRNA metabolic process |  |  |
|  |  | GO:0090407 | organophosphate biosynthetic process |  |  |
|  |  | GO:1902582 | single-organism intracellular transport |  |  |
|  |  | GO:1901137 | carbohydrate derivative biosynthetic process |  |  |
|  |  | GO:0016861 | intramolecular oxidoreductase activity, interconverting aldoses and ketoses |  |  |
|  |  | GO:0046129 | purine ribonucleoside biosynthetic process |  |  |
|  |  | GO:0042451 | purine nucleoside biosynthetic process |  |  |
|  |  | GO:1901135 | carbohydrate derivative metabolic process |  |  |
|  |  | GO:0015992 | proton transport |  |  |
|  |  | GO:0006818 | hydrogen transport |  |  |
|  |  | GO:0044262 | cellular carbohydrate metabolic process |  |  |
|  |  | GO:1902600 | hydrogen ion transmembrane transport |  |  |
|  |  | GO:0005996 | monosaccharide metabolic process |  |  |
|  |  | GO:0009127 | purine nucleoside monophosphate biosynthetic process |  |  |
|  |  | GO:0009168 | purine ribonucleoside monophosphate biosynthetic process |  |  |
|  |  | GO:0030117 | membrane coat |  |  |
|  |  | GO:0009152 | purine ribonucleotide biosynthetic process |  |  |
|  |  | GO:1901575 | organic substance catabolic process |  |  |
|  |  | GO:0006096 | glycolytic process |  |  |
|  |  | GO:0005199 | structural constituent of cell wall |  |  |
|  |  | GO:0022900 | electron transport chain |  |  |
|  |  | GO:0009277 | fungal-type cell wall |  |  |
|  |  | GO:0034660 | ncRNA metabolic process |  |  |
|  |  | GO:0016209 | antioxidant activity |  |  |
|  |  | GO:0045184 | establishment of protein localization |  |  |
|  |  | GO:0006886 | intracellular protein transport |  |  |
|  |  | GO:0044724 | single-organism carbohydrate catabolic process |  |  |
|  |  | GO:0019318 | hexose metabolic process |  |  |
|  |  | GO:0043226 | organelle |  |  |
|  |  | GO:0043229 | intracellular organelle |  |  |
|  |  | GO:0006164 | purine nucleotide biosynthetic process |  |  |
|  |  | GO:1902589 | single-organism organelle organization |  |  |
|  |  | GO:0044712 | single-organism catabolic process |  |  |
|  |  | GO:0003824 | catalytic activity |  |  |
|  |  | GO:0009056 | catabolic process |  |  |
|  |  | GO:0004175 | endopeptidase activity |  |  |
|  |  | GO:0016051 | carbohydrate biosynthetic process |  |  |
|  |  | GO:0015031 | protein transport |  |  |
|  |  | GO:0016853 | isomerase activity |  |  |
|  |  | GO:0046039 | GTP metabolic process |  |  |
|  |  | GO:0006220 | pyrimidine nucleotide metabolic process |  |  |
|  |  | GO:1901293 | nucleoside phosphate biosynthetic process |  |  |
|  |  | GO:0044430 | cytoskeletal part |  |  |
|  |  | GO:0009165 | nucleotide biosynthetic process |  |  |
|  |  | GO:0055086 | nucleobase-containing small molecule metabolic process |  |  |
|  |  | GO:1901657 | glycosyl compound metabolic process |  |  |
|  |  | GO:0009116 | nucleoside metabolic process |  |  |
|  |  | GO:0016651 | oxidoreductase activity, acting on NAD(P)H |  |  |
|  |  | GO:0031090 | organelle membrane |  |  |
|  |  | GO:0072522 | purine-containing compound biosynthetic process |  |  |
|  |  | GO:0007010 | cytoskeleton organization |  |  |
|  |  | GO:0019866 | organelle inner membrane |  |  |
|  |  | GO:0072686 | mitotic spindle |  |  |
|  |  | GO:0016192 | vesicle-mediated transport |  |  |
|  |  | GO:0005819 | spindle |  |  |
|  |  | GO:1901068 | guanosine-containing compound metabolic process |  |  |
|  |  | GO:0005743 | mitochondrial inner membrane |  |  |
|  |  | GO:0005737 | cytoplasm |  |  |
|  |  | GO:0016860 | intramolecular oxidoreductase activity |  |  |
|  |  | GO:0071840 | cellular component organization or biogenesis |  |  |
|  |  | GO:0008233 | peptidase activity |  |  |
|  |  | GO:1902494 | catalytic complex |  |  |
|  |  | GO:0006486 | protein glycosylation |  |  |
|  |  | GO:0043413 | macromolecule glycosylation |  |  |
|  |  | GO:0016482 | cytoplasmic transport |  |  |
|  |  | GO:0015672 | monovalent inorganic cation transport |  |  |
|  |  | GO:0022890 | inorganic cation transmembrane transporter activity |  |  |
|  |  | GO:0016874 | ligase activity |  |  |
|  |  | GO:0044275 | cellular carbohydrate catabolic process |  |  |
|  |  | GO:0005739 | mitochondrion |  |  |
|  |  | GO:0070011 | peptidase activity, acting on L-amino acid peptides |  |  |
|  |  | GO:0044711 | single-organism biosynthetic process |  |  |
|  |  | GO:0003678 | DNA helicase activity |  |  |
|  |  | GO:0016043 | cellular component organization |  |  |
|  |  | GO:0005618 | cell wall |  |  |
|  |  | GO:0030312 | external encapsulating structure |  |  |
|  |  | GO:0045735 | nutrient reservoir activity |  |  |
|  |  | GO:0019751 | polyol metabolic process |  |  |
|  |  | GO:1901136 | carbohydrate derivative catabolic process |  |  |
|  |  | GO:0006760 | folic acid-containing compound metabolic process |  |  |
|  |  | GO:0030029 | actin filament-based process |  |  |
|  |  | GO:0000940 | condensed chromosome outer kinetochore |  |  |
|  |  | GO:0030036 | actin cytoskeleton organization |  |  |
|  |  | GO:0009203 | ribonucleoside triphosphate catabolic process |  |  |
|  |  | GO:0000942 | condensed nuclear chromosome outer kinetochore |  |  |
|  |  | GO:0009207 | purine ribonucleoside triphosphate catabolic process |  |  |
|  |  | GO:0009071 | serine family amino acid catabolic process |  |  |
|  |  | GO:0042729 | DASH complex |  |  |
|  |  | GO:0046130 | purine ribonucleoside catabolic process |  |  |
|  |  | GO:0009143 | nucleoside triphosphate catabolic process |  |  |
|  |  | GO:1901069 | guanosine-containing compound catabolic process |  |  |
|  |  | GO:0006546 | glycine catabolic process |  |  |
|  |  | GO:0006184 | GTP catabolic process |  |  |
|  |  | GO:0008716 | D-alanine-D-alanine ligase activity |  |  |
|  |  | GO:0051258 | protein polymerization |  |  |
|  |  | GO:0009146 | purine nucleoside triphosphate catabolic process |  |  |
|  |  | GO:0045263 | proton-transporting ATP synthase complex, coupling factor F(o) |  |  |
|  |  | GO:0006152 | purine nucleoside catabolic process |  |  |
|  |  | GO:0006006 | glucose metabolic process |  |  |
|  |  | GO:0016491 | oxidoreductase activity |  |  |