**S2 Table. Top enriched GO categories of decreased mRNA levels in the Δ*wetA* conidia.**

| GO Category | # of Genes | % of Genes in Category |
|---|---|---|
| **Biological Process** | | |
| metabolic process | 846 | 25.22% |
| biosynthetic process | 298 | 27.41% |
| organic substance biosynthetic process | 280 | 27.78% |
| cellular biosynthetic process | 275 | 28.09% |
| oxidation-reduction process | 235 | 28.87% |
| cellular nitrogen compound biosynthetic process | 209 | 33.07% |
| organonitrogen compound metabolic process | 204 | 30.96% |
| organic cyclic compound biosynthetic process | 161 | 28.75% |
| heterocycle biosynthetic process | 157 | 30.13% |
| organonitrogen compound biosynthetic process | 153 | 31.94% |
| cellular amide metabolic process | 94 | 33.57% |
| amide biosynthetic process | 86 | 33.46% |
| peptide metabolic process | 73 | 33.64% |
| translation | 60 | 38.22% |
| organophosphate metabolic process | 60 | 34.29% |
| cofactor metabolic process | 44 | 35.48% |
| nucleoside phosphate metabolic process | 40 | 40.00% |
| coenzyme metabolic process | 37 | 39.36% |
| pyridine-containing compound metabolic process | 19 | 54.29% |
| pyridine nucleotide metabolic process | 17 | 54.84% |
| nicotinamide nucleotide metabolic process | 17 | 54.84% |
| vitamin metabolic process | 16 | 66.67% |
| cellular modified amino acid metabolic process | 14 | 51.85% |
| cellular modified amino acid biosynthetic process | 13 | 59.09% |
| tetrapyrrole metabolic process | 9 | 69.23% |
| GTP metabolic process | 6 | 100.00% |
| molybdopterin cofactor metabolic process | 6 | 85.71% |
| prosthetic group metabolic process | 6 | 85.71% |
| **Molecular Function** | | |
| oxidoreductase activity | 1095 | 29.59% |
| RNA polymerase II transcription factor activity, sequence-specific DNA binding | 167 | 35.33% |
| structural molecule activity | 115 | 46.96% |
| structural constituent of ribosome | 97 | 54.64% |

| **Cellular Component** | | |
|---|---|---|
| extracellular region | 74 | 29.60% |
| intracellular ribonucleoprotein complex | 53 | 39.85% |
| ribonucleoprotein complex | 53 | 39.85% |
| ribosome | 53 | 54.64% |
| ribosomal subunit | 12 | 63.16% |
| small ribosomal subunit | 8 | 80.00% |