**Figure 4 – Source data 3**

*Gene Ontology (GO) enrichment analysis of genes showing strain-specific response to starvation.* Significantly enriched functions are shown. Go enrichment analysis was performed on data obtained by the analysis shown in Figure 4 – Figure supplement 1, *i.e.* on genes showing exclusive or significantly higher change in their expression rate in one of the strains. (FDR: false discovery rate)

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Genes showing significant enrichment among strain-specifically upregulated ones in *wt*** | | | | | | | | |
|  | ***Neurospora crassa* (REF)** | **Upload** | | | |  | | |
| **#** | **#** | **Expected** | | **Fold Enrichment** | **+/-** | **Raw p value** | **FDR** |
| Unclassified | 4789 | 295 | 200.24 | | 1.47 | + | 1.41E-20 | 3.09E-17 |
| **Genes showing significant enrichment among strain-specifically upregulated ones in *∆wc-1*** | | | | | | | | |
|  | ***Neurospora crassa* (REF)** | **Upload** | | | |  | | |
| **#** | **#** | **Expected** | | **Fold Enrichment** | **+/-** | **Raw P value** | **FDR** |
| Unclassified | 4789 | 332 | 256.19 | | 1.30 | + | 1.03E-10 | 5.03E-0 |
|  | | | | | | | | |
| Alpha-amino acid catabolic process | 36 | 10 | 1.93 | | 5.19 | + | 8.14E-05 | 6.75E-03 |
| Cellular amino acid catabolic process | 48 | 12 | 2.57 | | 4.67 | + | 3.88E-05 | 3.55E-03 |
| L-phenylalanine catabolic process | 4 | 4 | 0.21 | | 18.69 | + | 3.91E-04 | 2.45E-02 |
|  | | | | | | | | |
| Organic acid catabolic process | 83 | 14 | 4.44 | | 3.15 | + | 3.64E-04 | 2.42E-02 |
| Carboxylic acid catabolic process | 79 | 14 | 4.23 | | 3.31 | + | 2.32E-04 | 1.67E-02 |
|  | | | | | | | | |
| Erythrose 4-phosphate/phosphoenolpyruvate family amino acid catabolic process | 4 | 4 | 0.21 | | 18.69 | + | 3.91E-04 | 2.49E-02 |
|  | | | | | | | | |
| Eisosome assembly | 5 | 4 | 0.27 | | 14.95 | + | 6.75E-04 | 3.90E-02 |
|  |  |  |  | |  |  |  |  |
| **Genes showing significant enrichment among strain-specifically downregulated ones in *wt*** | | | | | | | | |
|  | ***Neurospora crassa* (REF)** | **Upload** | | | |  | | |
| **#** | **#** | | **Expected** | **Fold Enrichment** | **+/-** | **Raw P value** | **FDR** |
| Small molecule biosynthetic process | 293 | 18 | | 6.64 | 2.71 | + | 1.85E-04 | 4.07E-02 |
| Small molecule metabolic process | 696 | 33 | | 15.76 | 2.09 | + | 6.91E-05 | 2.33E-02 |
|  | | | | | | | | |
| Cellular amino acid metabolic process | 209 | 18 | 4.73 | | 3.80 | + | 2.75E-06 | 1.73E-03 |
| Alpha-amino acid metabolic process | 134 | 13 | 3.03 | | 4.28 | + | 2.20E-05 | 1.07E-02 |
|  | | | | | | | | |
| Cellular amino acid biosynthetic process | 100 | 11 | | 2.26 | 4.86 | + | 3.32E-05 | 1.46E-02 |
| Alpha-amino acid biosynthetic process | 81 | 9 | | 1.83 | 4.91 | + | 1.62E-04 | 3.75E-02 |
|  | | | | | | | | |
| Organic acid metabolic process | 380 | 26 | 8.61 | | 3.02 | + | 1.01E-06 | 1.48E-03 |
| Oxoacid metabolic process | 369 | 25 | 8.36 | | 2.99 | + | 1.97E-06 | 1.73E-03 |
| Carboxylic acid metabolic process | 358 | 24 | 8.11 | | 2.96 | + | 3.80E-06 | 2.08E-03 |
|  | | | | | | | | |
| Organic acid biosynthetic process | 156 | 13 | | 3.53 | 3.68 | + | 9.45E-05 | 2.96E-02 |
|  |  |  | |  |  |  |  |  |
| **Genes showing significant enrichment among strain-specifically downregulated ones in *∆wc-1*** | | | | | | | | |
|  | ***Neurospora crassa* (REF)** | **Upload** | | | |  | | |
| **#** | **#** | | **Expected** | **Fold Enrichment** | **+/-** | **Raw P value** | **FDR** |
| Monocarboxylic acid biosynthetic process | 40 | 7 | | 0.70 | 9.99 | + | 1.40E-05 | 6.15E-02 |
| Fatty acid biosynthetic process | 27 | 6 | | 0.47 | 12.68 | + | 1.80E-05 | 2.64E-02 |