Supplemental Table 5. Gene Ontology analysis for genes differentially regulated in the *tup1(S649F)* mutant.

A. Genes with log2-fold increase in expression in *tup1(S649F)* **a** vs. WT **a**.

|  |  |  |  |
| --- | --- | --- | --- |
| Gene Ontology Term | Cluster Frequency | Genome Frequency | Corrected p-value |
| Carbohydrate metabolic process | 50 / 359, 13.9% | 282 / 7166, 3.9% | 1.18-12 |
| Oxidation-reduction process | 61 / 359, 17.0% | 466 / 7166, 6.5% | 1.29-09 |
| Transmembrane transport | 57 / 359, 15.7% | 457 / 7166, 6.4% | 5.75-08 |
| Cell wall organization | 37 / 359, 10.3% | 252 / 7166, 3.5% | 2.22-06 |
| Response to drug | 25 /359,7.0% | 134 / 7166 1.9% | 7.83-06 |
| Hydrolase activity | 14 / 359, 3.9% | 49 / 7166, 0.7% | 2.09-05 |
| DNA binding TF activity | 27 / 359, 7.5% | 181 / 7166, 2.5% | 8.49-05 |
| Structural component of cell wall | 12 / 359, 3.9% | 44 / 7166, 0.6% | 0.00032 |
| Cell periphery | 117 / 359, 32.6% | 834 / 7166, 11.6% | 2.27-25 |

B. Genes with log2-fold increase in expression in *tup1(S649F)* vs. WT .

|  |  |  |  |
| --- | --- | --- | --- |
| Gene Ontology Term | Cluster Frequency | Genome Frequency | Corrected p-value |
| Cell periphery | 159 / 561, 28.3% | 834 / 7166, 11.6% | 1.39-27 |
| Carbohydrate metabolic process | 79 / 561, 14.1% | 282 / 7166, 3.9% | 3.45-22 |
| Oxidation-reduction process | 100 / 561, 17.8% | 466 / 7166, 6.5% | 4.96-19 |
| Small molecule metabolic process | 133 / 561, 23.7% | 827 / 7166, 11.5% | 2.09-14 |
| Transmembrane transport | 82 / 561, 14.6% | 457 / 7166, 6.4% | 2.61-10 |
| Cell wall organization | 55 / 561, 9.8% | 252 / 7166, 3.5% | 1.55-09 |
| Organic acid metabolic process | 78 / 561, 13.9% | 448 / 7166, 6.3% | 5.53-09 |
| Response to chemical | 92 / 561, 16.4% | 573 / 7166, 8.0% | 6.38-09 |
| Hydrolase activity | 20 / 561, 3.6% | 49 / 7166, 0.7% | 7.98-08 |
| Cofactor binding | 43 / 561,7.7% | 211 / 7166,2.9% | 1.47-06 |
| Response to drug | 33 / 561,5.9% | 134 / 7166,1.9% | 2.09-06 |
| Sexual reproduction | 42 / 561,7.5% | 233 / 7166,3.3% | 0.00025 |
| Structural component of cell wall | 15 / 561, 2.7% | 44 / 7166, 0.6% | 0.00025 |
| Conjugation with cellular fusion | 26 / 561,4.6% | 117 / 7166,1.6% | 0.001 |
| DNA binding TF activity | 32 / 561, 5.7% | 181 / 7166, 2.5% | 0.00405 |

C. Genes with log2-fold decrease in expression in *tup1(S649F)* **a** vs. WT **a**.

|  |  |  |  |
| --- | --- | --- | --- |
| Gene Ontology Term | Cluster Frequency | Genome Frequency | Corrected p-value |
| Amino acid metabolic process | 8 / 22, 36.4% | 251 / 7166, 3.5% | 6.43-05 |
| Transmembrane transport | 7 / 22, 31.8% | 387 / 7166, 5.4% | 0.00437 |
| Plasma membrane | 4 / 22, 18.2% | 68 / 7166, 0.9% | 0.0024 |

D. Genes with log2-fold decrease in expression in *tup1(S649F)*  vs. WT .

No significant GO terms

E. Genes with log2-fold increase in expression in *tup1(S649F)*  vs. *tup1(S649F)* **a**.

|  |  |  |  |
| --- | --- | --- | --- |
| Gene Ontology Term | Cluster Frequency | Genome Frequency | Corrected p-value |
| Conjugation with cellular fusion | 21 / 121, 17.4% | 117 / 7166, 1.6% | 1.11-13 |
| Small molecule biosynthetic process | 30 / 121,24.8% | 332 / 7166,4.6% | 6.88-12 |
| Amino acid metabolic process | 26 / 121, 21.5% | 249 / 7166, 3.5% | 1.77-11 |
| Response to pheromone | 17 / 121, 14% | 95 / 7166, 1.3% | 1.07-10 |
| Organic acid metabolic process | 30 / 121,24.8% | 466 / 7166,6.2% | 1.56-08 |
| Cell wall | 13 / 121,10.7% | 138 / 7166,1.9% | 4.81-05 |
| Cofactor binding | 15 / 121,12.4% | 211 / 7166,2.9% | 0.00037 |

F. Genes with log2-fold decrease in expression in *tup1(S649F)*  vs. *tup1(S649F)* **a**.

|  |  |  |  |
| --- | --- | --- | --- |
| Gene Ontology Term | Cluster Frequency | Genome Frequency | Corrected p-value |
| Copper ion transport | 3 / 9,33.3% | 18 / 7166,0.3% | 5.42-05 |
| Ferric chelate reductase activity | 2 / 9,22.2% | 7 / 7166,0.1% | 0.00090 |
| Cell periphery | 6 / 9,67% | 824 / 7166,11.5% | 0.00350 |

Categories identified only in *tup1(S649F)*  vs. WT and/or *tup1(S649F)*  vs. *tup1(S649F)* **a**.