**Table S5. Transcripts of proteins involved in catabolic processes.**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **PaNo** | **Annotation at the *P. anserina* genome database** | **FC (grisea/wt)** | **Tpm (wt)** | **Tpm (grisea)** | **P value** |
| Pa\_1\_15110 | Putative glucokinase | 3.13 | 129.83 | 406.96 | 0.000 |
| Pa\_6\_10000 | Putative mitochondrial precursor of 2-methylcitrate synthase | 0.08 | 41.82 | 3.23 | 0.000 |
| Pa\_2\_12390 | Putative aconitate hydratase, mitochondrial precursor | 3.09 | 20.42 | 63.20 | 0.000 |
| Pa\_1\_19320 | Putative mitochondrial fumarate hydratase precursor | 4.33 | 167.29 | 724.15 | 0.000 |

PaNo: accession number in the *P. anserina* genome database as found by the blast search. FC: the difference of expression comparing grisea mutant strain to wild type (fold change). Tpm: the number of transcript molecules normalized as tags per million. P value: the significance level of differential expression comparing the *Podospora* grisea mutant strain to the wild type.