**Table S2. Selected genes of *P. anserina* and their expression level comparing grisea mutant strain to the wild type.**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **PaNo** | **Annotation in the *P. anserina* genome database/ Protein description** | **FC (grisea/WT)** | **Tpm (wt)** | **Tpm (grisea)** | **P value** |
| *Pa\_1\_16400* | Putative copper transport protein/ *PaCtr1*, target gene of GRISEA | 0.10 | 85.70 | 8.56 | 0.000 |
| *Pa\_4\_4770* | Low-affinity copper transport protein encoded by the ctr2 gene/ *PaCtr2*, target gene of Grisea encoding a high affinity copper transporter | 0.06 | 15.14 | 0.98 | 0.000 |
| *Pa\_3\_10440* | Copper transporter encoded by the Pactr3 gene/ *PaCtr3*, target gene of GRISEA, encoding high affinity copper transporter | < 0.04 | 1.41 | < 0.05 | 0.001 |
| *Pa\_1\_4220* | Putative protein of unknown function/ low affinity copper transporter | 1.49 | 91.73 | 136.22 | 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. ‘Protein description’ entries indicate conclusions from the current transcriptome and qRT-PCR analysis.