S1 Text. Pheromone genes of Tremellomycetes.

One difference between the Trichosporonales and several Tremellales MAT loci is the presence of only one pheromone precursor gene in the analyzed Trichosporonales MAT loci (Fig 2), whereas more than one pheromone precursor gene is present within the $P/R$ locus in the tetrapolar Tremellales species $C.\ amylolentus$, and $T.\ wingfieldii$ as well as in the bipolar species $C.\ neoformans$ and Cryptococcus gattii [1-4]. In all cases, the pheromone precursor genes can be found in the vicinity of the pheromone receptor gene STE3. The $STE3\alpha$-associated pheromones are slightly shorter in both the Trichosporonales (26-42 amino acids) as well as the Tremellales (38 amino acids) than their $STE3\alpha$-associated counterparts (27-47 in the Trichosporonales, and 39-42 amino acids in the Tremellales) (see Figure below). The predicted Trichosporonales pheromones have the characteristic C-terminal CAAX motif of lipopeptide pheromones, where A is an aliphatic amino acid [5]. However, the Trichosporonales pheromones have a shorter N-terminus compared to the Tremellales pheromones, except for those from the Vanrija species, $C.\ curvatus$ and $C.\ cyanovorans$ (see Figure below).

References

**Figure for Text S1.** Multiple alignment of (putative) pheromones from Tremellomyces. The pheromones associated with the STE3α receptor gene are given on top, pheromones associated with the STE3α receptor gene below. For Tremellales sequences, accession numbers are given after the species abbreviations (C.n., Cryptococcus neoformans; C.g., Cryptococcus gattii; K.h., Kwoniamella heveanensis), Trichosporonales sequences were identified in this study.