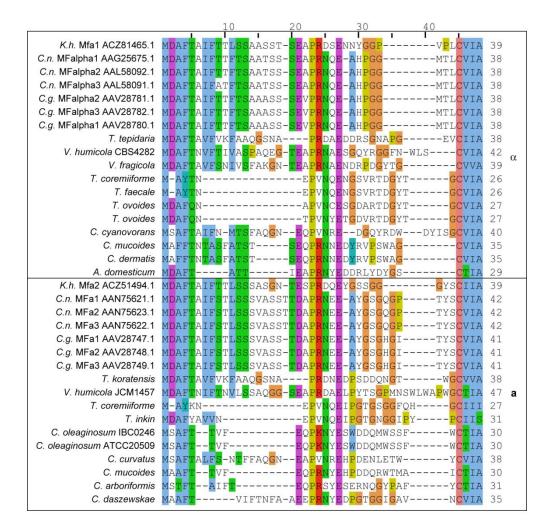
## S1 Text. Pheromone genes of *Tremellomycetes*.

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*a-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

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**Figure for Text S1.** Multiple alignment of (putative) pheromones from *Tremellomyce*tes. The pheromones associated with the *STE3* $\alpha$  receptor gene are given on top, pheromones associated with the *STE3* $\alpha$  receptor gene below. For *Tremellales* sequences, accession numbers are given after the species abbreviations (*C.n.*, *Cryp*tococcus neoformans; C.g., *Cryptococcus gattii*; *K.h.*, *Kwoniella heveanensis*), *Trichosporonales* sequences were identified in this study.