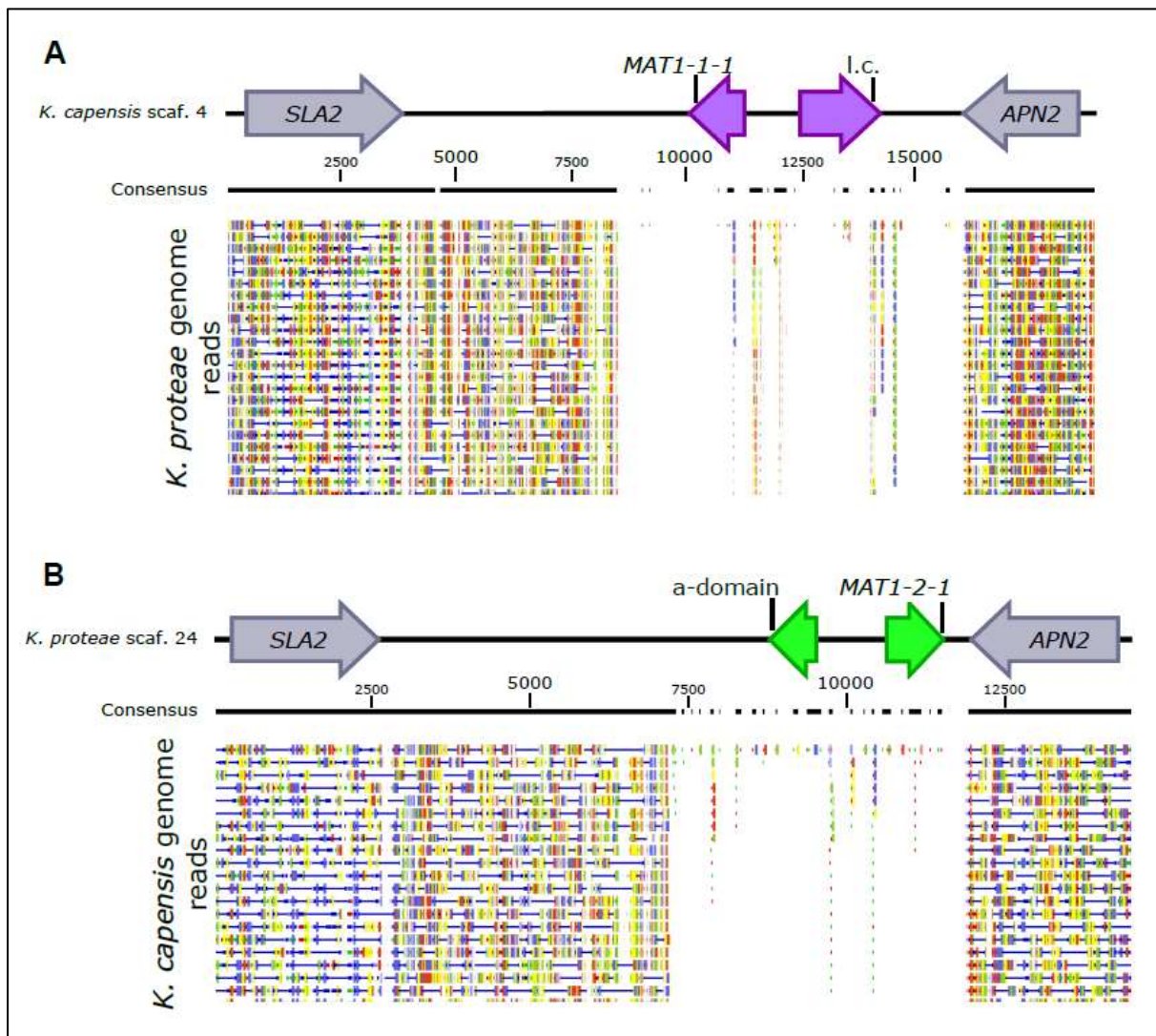**Supplementary figures**

Figure S1. Estimation of *MAT1* idiomorph sizes by read mapping. A) The *MAT1-2* genome reads of *K. proteae* were mapped to the *MAT1-1* idiomorph of *K. capensis* and B) the *MAT1-1* genome reads of *K. capensis* were mapped to the *MAT1-2* genome of *K. proteae*. The consensus sequence represents the consensus according to the read mappings. l.c. = low complexity region protein, a-domain = alpha domain-containing protein.
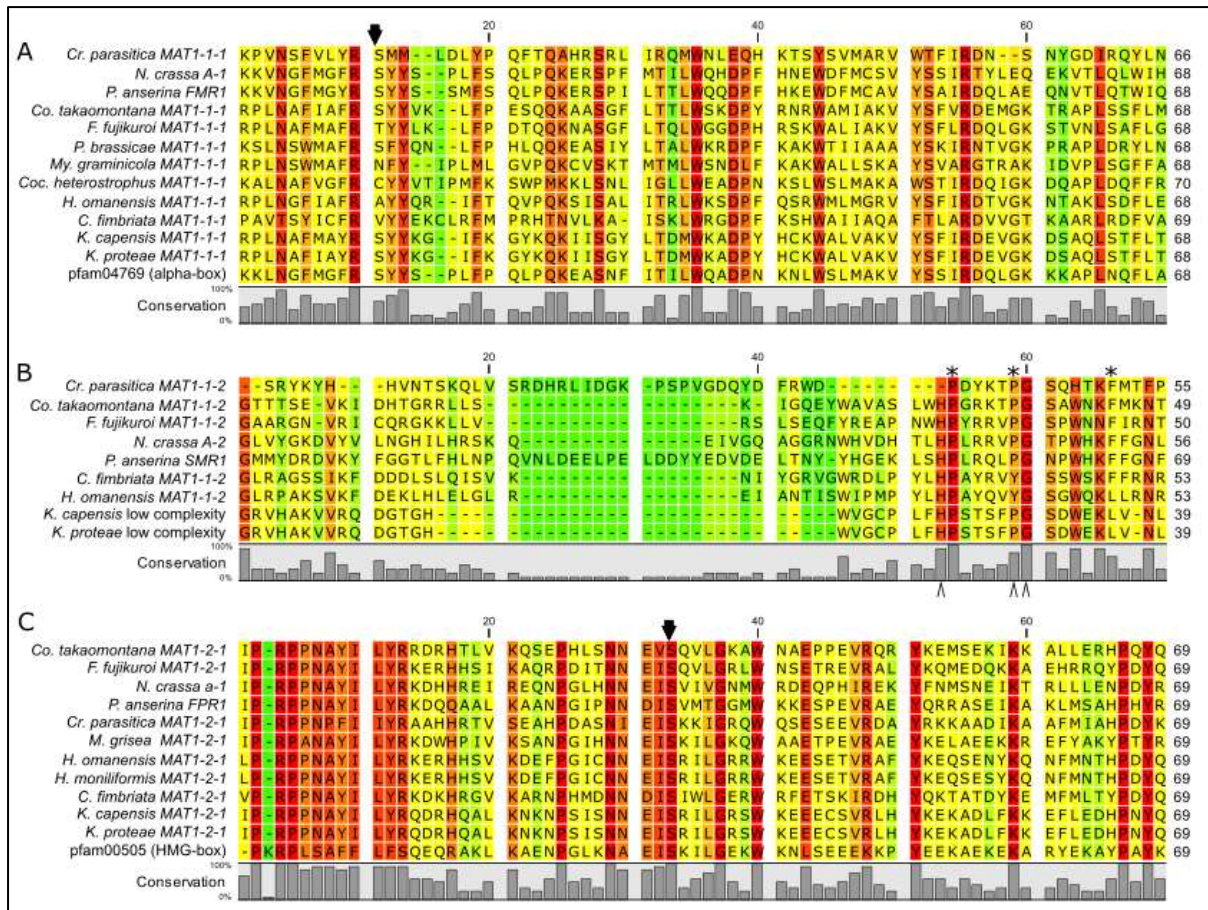
Figure S2. Alignment of *Knoxdaviesia MAT1* proteins to those of other Sordariomycetes. A) Alpha domain of *MAT1-1-1,* B) proposed PPF (*) and HPG (^) domains of *MAT1-1-2* and C) HMG-box domain of *MAT1-2-1*. As for Fig. 2, the conservation of residues is illustrated with a spectrum from green to red, with green representing < 30%, yellow < 65%, orange < 100% and red 100% amino acid identity. Conserved intron positions are indicated with black arrows. GenBank accession numbers are given in the text.
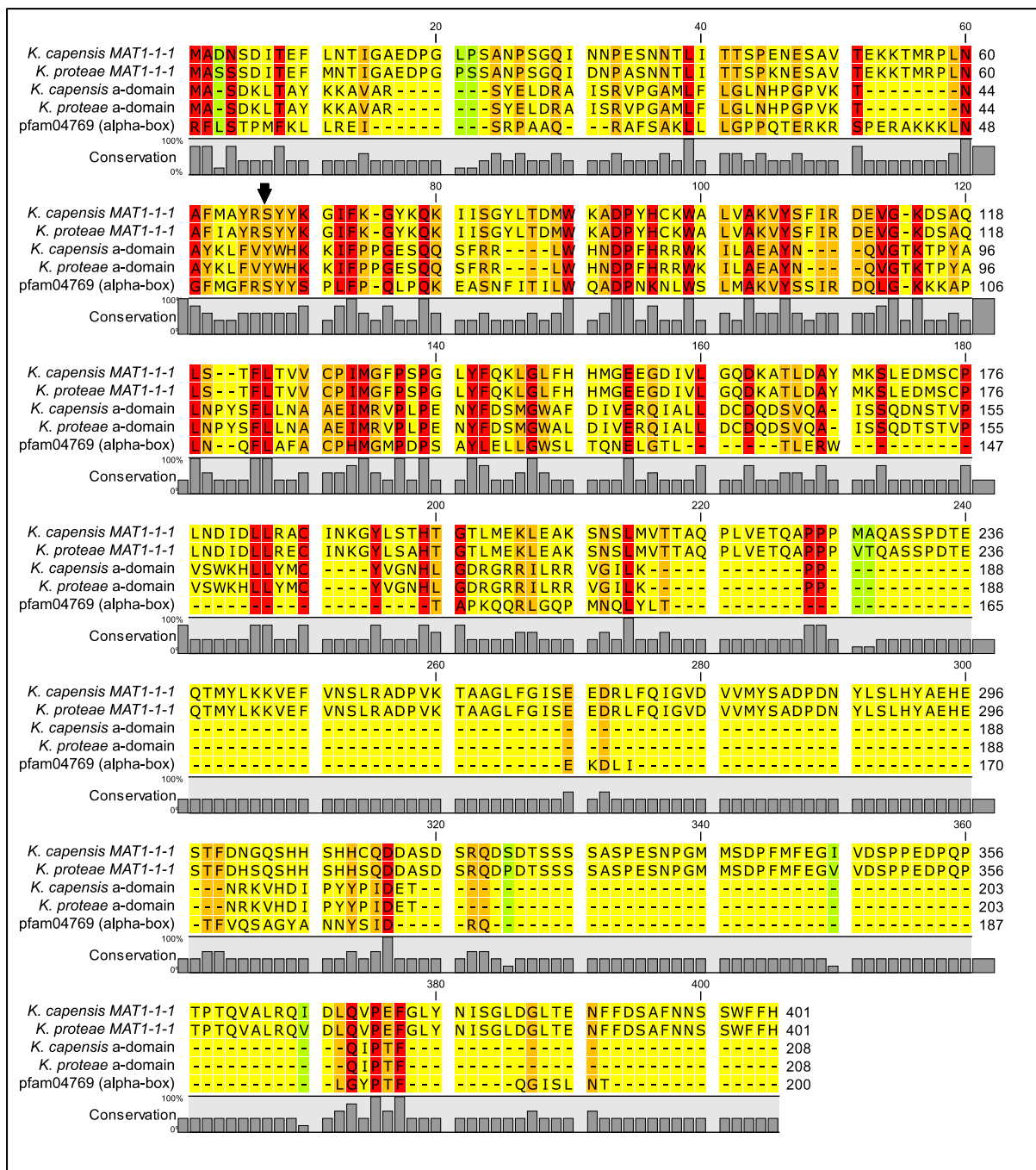
Figure S3. Alignment between *Knoxdaviesia MAT1-1-1* and *MAT1-2-7* (alpha domain-containing) proteins. The consensus MAT alpha 1 sequence (PFAM04769) is included as a reference. Green = 0%, yellow = 40%, orange = 60% and red ≥ 80% amino acid conservation. The conserved intron position is indicated with a black arrow.