S3 File. DNA and protein alignments built to determine intron landscapes.

Alignments were performed using Muscle as described in the materials and methods section. Exonic sequences from *Passalora* species were aligned to the previous DNA alignment using Muscle and new alignment was manually edited in GeneDoc. All names are as described in Figure 3 and S4 File.

DNA alignments: introns are highlighted in yellow. Four-level shade indicates nucleotide conservation over 90%, 80%, 60%, and under 60%. In D, two-level shade indicates nucleotide conservation over and lower than 65%. In B, insertion of a single nucleotide in the sequence of *Lentfl* makes it a pseudogene.

Protein alignments: positions of RSIs, previously identified ILEs and novel ILEs are indicated in yellow, orange and red, respectively. For novel ILEs, the position is indicated within the sequence of the two most closely related fungal species. Numbers indicate phase 0, 1 or 2. Numbering of intron positions in Figure 3 corresponds to the position in the corresponding alignment below, minus the number of upstream intron positions. Four-level shade indicates amino acid identity of 100%, over 80%, over 60%, and under 60%.
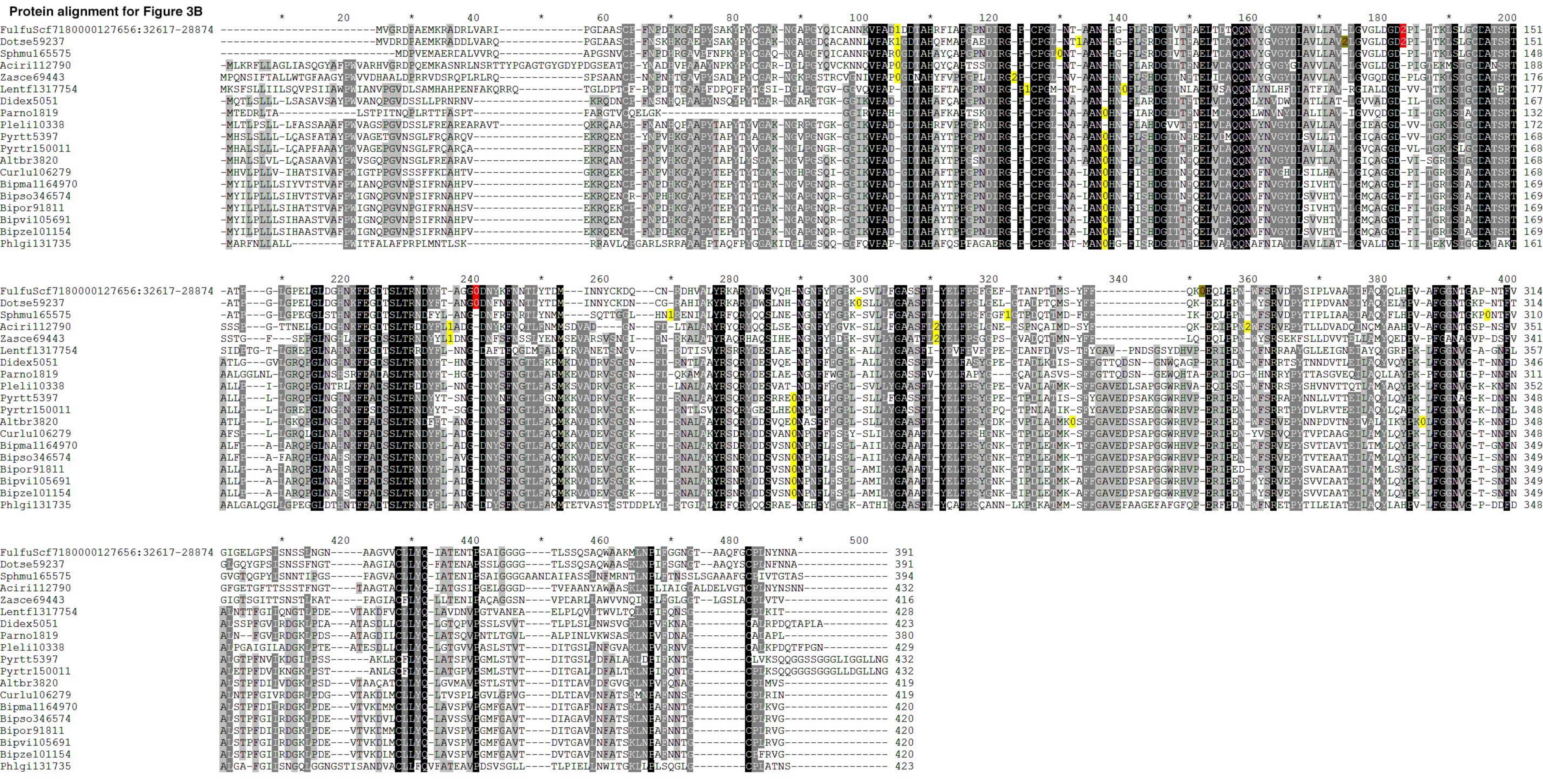
DNA alignment for Figure 3A

Protein alignment for Figure 3A

DNA alignment for Figure 3B

Protein alignment for Figure 3B

DNA alignment for Figure 3C

Protein alignment for Figure 3C

DNA alignment for Figure 3D

Protein alignment for Figure 3D