Database mining and transcriptional analysis of genes encoding inulin-modifying enzymes of Aspergillus niger

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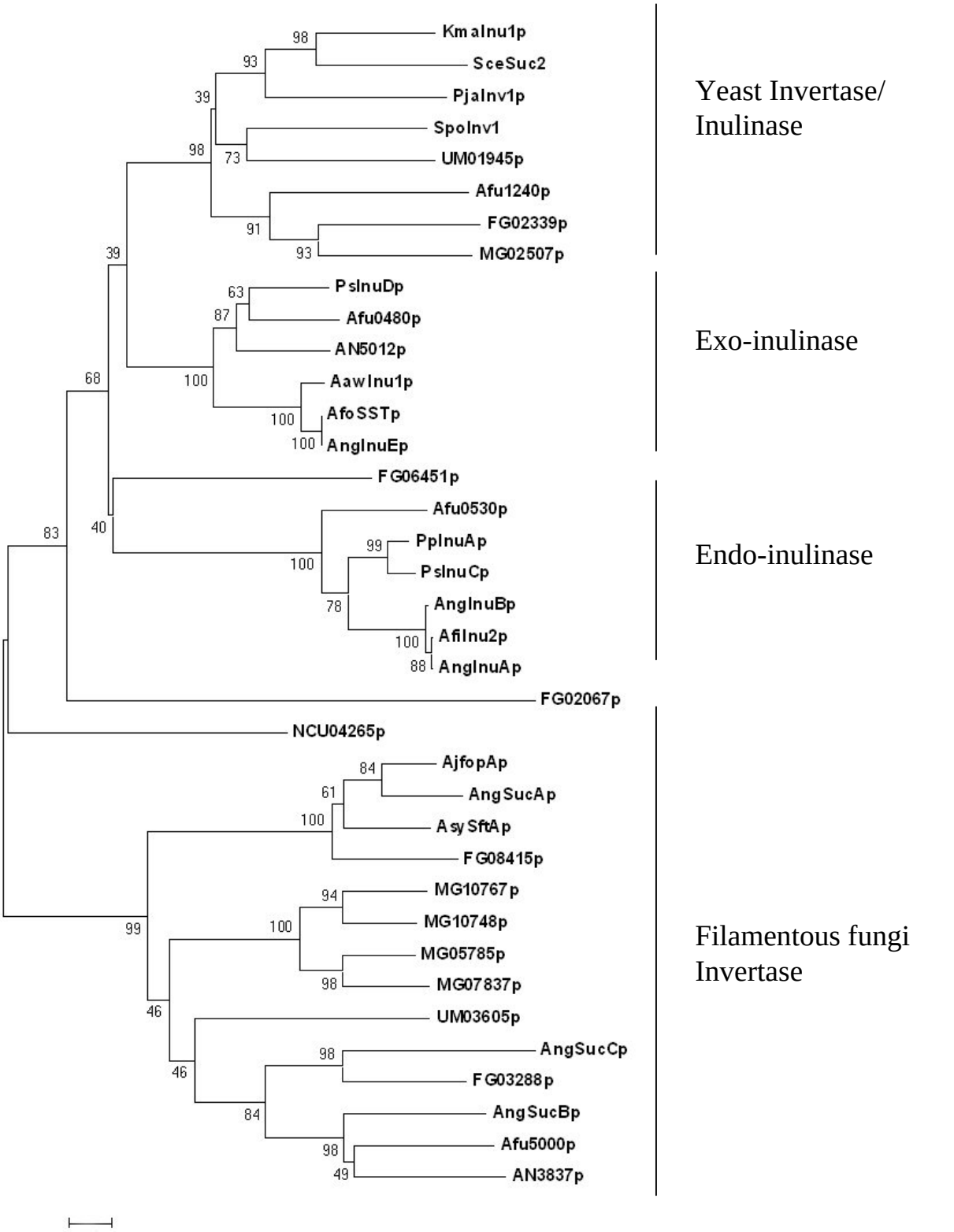

Supplementary Fig. S1. Neighbour-joining tree of GH32 family members identified in the genomes of *A. niger*, *A. nidulans*, *A. fumigatus*, *N. crassa*, *G. zeae*, *M. grisea* and *U. maydis*, together with functionally described GH32 family members from filamentous fungi and yeasts. If the fungal protein has a highest blastp hit with a bacterial GH32 enzyme, this enzyme was included in the tree. BmeFruA, *Bacillus megaterium* FruA (AAM19071); BsuSacC, *Bacillus subtilus* SacC (CAA29137); BmaCft, *Bacillus macerans* Cft (Q9F0I5). Proteins predicted to lack an N-terminal signal sequence were considered as intracellular enzymes and indicated by the grey background. Accession numbers of the proteins are listed in Tables 1 and 2 of the main paper. Bootstrap values are indicated at the node of each branch. The tree was created with Mega 3.1 using default settings for gap and extension penalties. Bar indicates 10% amino acid sequence difference.