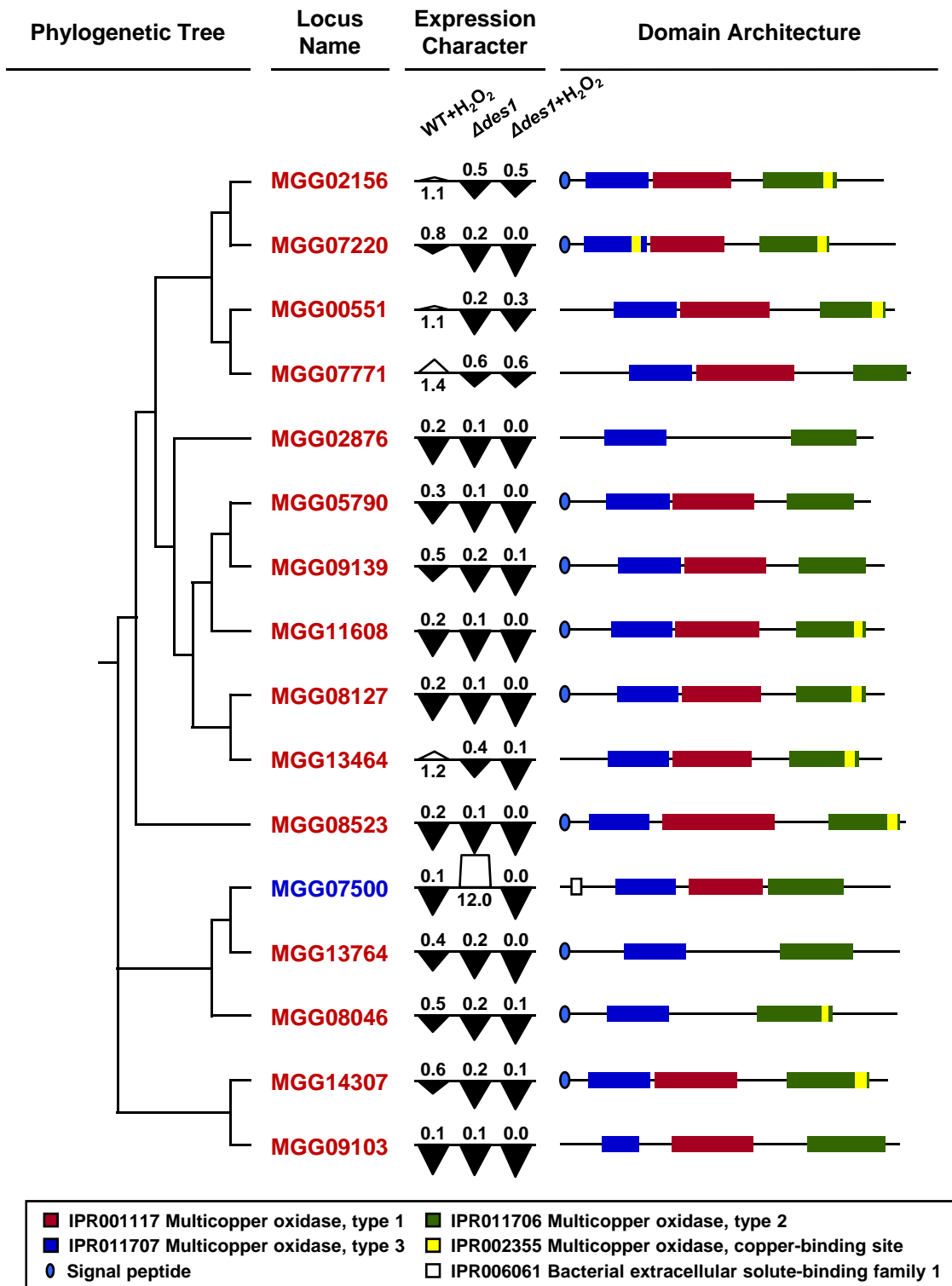


**Figure S8**



**Figure S8. Expression profiles of *M. oryzae* putative laccase-encoding genes in the  $\Delta des1$  mutant.**

A combination of the phylogenetic tree, expression characteristics, and domain architecture of 16 putative laccases in the *M. oryzae* genome were displayed. The phylogenetic tree was generated by ClustalW sequence alignment with 1000 bootstrappings. The transcript levels of the putative laccase-encoding genes in the oxidative condition and/or in the  $\Delta des1$  mutant are indicated. Relative abundance of transcript compared with standard condition (wild type, normal condition) is displayed as a white triangle (up-regulated) or an inverted black triangle (down-regulated). Triangles indicating more than 2.0 (fold change) are displayed as trapezoids by cutting the top of the triangle. Fold changes of the standard condition (1.0) are not shown. Up-regulated genes in the  $\Delta des1$  mutant (more than 1.5 fold) were indicated in blue, and down-regulated genes in the  $\Delta des1$  mutant (less than 0.6 fold) were indicated in red. The InterPro terms and signal peptides are indicated (see legend).