



**FIGURE S5** Alignment of *C. orbiculare* CoHex1, CoWsc, and CoPex4 with homologs of other ascomycete fungi. (A) Amino acid sequence of *C. orbiculare* CoHex1 (N4UJ9) was aligned with *N. crassa* Hex1 (P87252) *A. oryzae* AoHex (I8TQ26), and *M. oryzae* MgHex (Q2KGA0) using the Clustal W program. (B) Amino acid sequence of *C. orbiculare* CoWsc (N4VZG1) was aligned with *N. crassa* Wsc (U9W802) using the Clustal W program. (C) Alignment of *C. orbiculare* CoPex4 with *S. cerevisiae* Pex4. Amino acid sequence of *C. orbiculare* CoPex4 (N4W4I0) was aligned with *C. graminicola* Pex4 (E3Q679), *C. higginsianum* Pex4 (H1UZJ1) and *S. cerevisiae* Pex4 (C7GYG2) using the Clustal W program. Shading of residues represents percentage amino acid conservation: black, 100%; dark grey, 75%; light grey, 50%.