



**Figure S4. Multiple alignment of the potential GH5 family protein sequence identified from *D. v. virgifera* with four fungal GH5 proteins (A) and the maximum-likelihood phylogeny including other known GH5 family proteins (B).** The potential amino acid residues for the catalytic nucleophile and catalytic proton donor are highlighted with magenta and green in the alignment, respectively (based on Larsson *et al.* 2006, *J Mol Biol* 357: 1500). Coleopteran proteins included in the phylogeny are found in Table S5. The *D. v. virgifera* sequence is shown in red. The GH5 protein sequences are classified into subfamilies according to Aspeborg *et al.* (2012, *BMC Evol Biol* 12: 186). Bacterial, plant, fungal, and nematode sequences are indicated by brown, green, cyan, and grey. The numbers at internal branches show the bootstrap values (%) for the maximum-likelihood and neighbor-joining phylogenies in this order. Only bootstrap values higher than 70% are shown.