

S2 Fig. Multiple sequence alignment of *A. flavus* RmtA, RmtB, and RmtC, and phylogenetic analysis of these protein sequences and those of their putative homologs in *A. nidulans*. (A) Sequences alignment of *A. flavus* RmtA, RmtB (EED57275.1), and RmtC (EED50528.1) using Muscle (<http://www.ebi.ac.uk/Tools/msa/muscle/>). Alignment was visualized with BoxShade v3.21 (http://ch.embnet.org/software/BOX_form.html). (B) Phylogenetic tree of RmtA, RmtB, and RmtC from *A. flavus* and *A. nidulans*. Accession numbers for *A. nidulans* RmtB and RmtC sequence are XP_660700.1 and XP_657738.1 respectively. The phylogenetic tree was constructed using MEGA v6.0, and it was generated with Maximum-Likelihood model with a bootstrap value of 1000.

