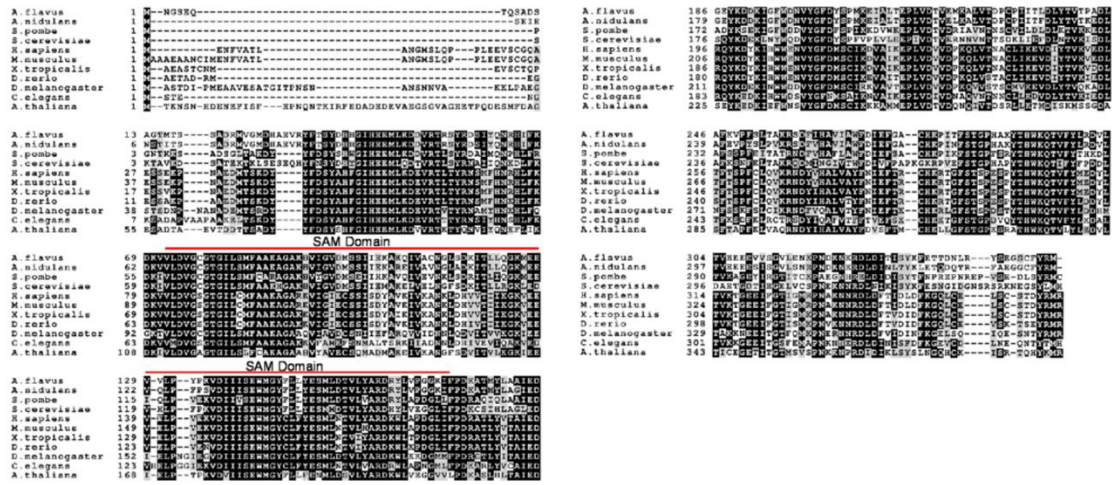


**S1 Fig. Multiple sequence alignment and phylogenetic analysis of RmtA and other homologs in model organisms.** (A) Sequences aligned using Muscle (<http://www.ebi.ac.uk/Tools/msa/muscle/>). Alignment was visualized with BoxShade v3.21 ([http://ch.embnnet.org/software/BOX\\_form.html](http://ch.embnnet.org/software/BOX_form.html)). (B) Phylogenetic tree of RmtA homologs from model organisms. Phylogenetic trees constructed using MEGA v6.0. Trees were generated with Maximum-Likelihood model with a bootstrap value of 1000.

**A**



**B**

