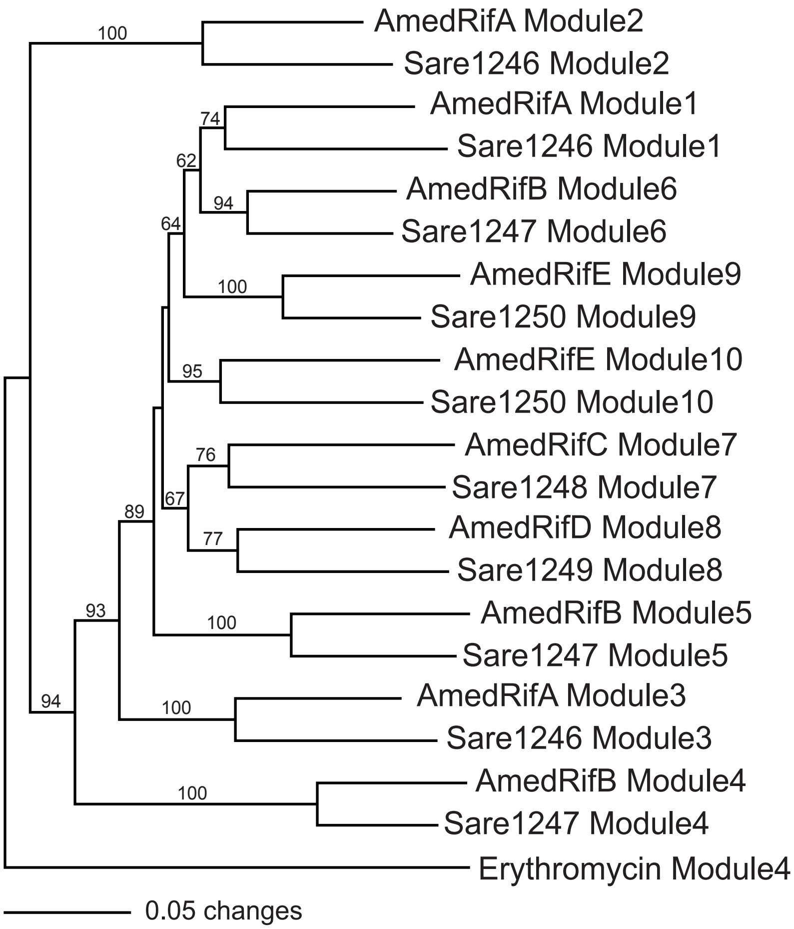

Supplemental Figure 1. Polyketide ketosynthase phylogeny. Neighbor-joining distance tree constructed using the aligned amino acid sequences of the *rif* KS domains from *A. mediterranei* and *S. arenicola*. Bootstrap values (in percent) calculated from 1000 re-samplings are shown at their respective nodes for values greater than or equal to 60%. The KS domain from module 4 of the erythromycin biosynthetic pathway (*Saccharopolyspora erythraea*) was used to position the root.