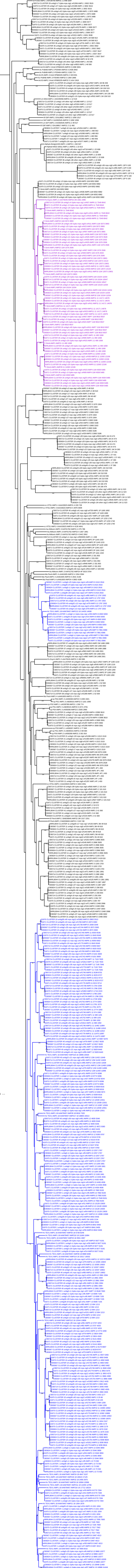


**Supplemental Figure 6. Phylogeny of acetylation (A) domains across *S. infantum* strains. Maximum likelihood phylogeny created in RAxML using the best-fit amino acid substitution model RTREV + F and an automatically optimized number of bootstrap replicates. A domains belonging to the cyclosporin cluster are color coded purple while A domains involved in biosynthesis of peptidobiotics are color coded blue.**



Tree Scale: 0.1