

Supplemental Figure 2. **Multiple sequence alignments and phylogeny of SIX proteins.**

The phylogeny is inferred from multiple sequence alignments as implemented in MAFFT software (L-INS-i algorithm, 1000 iterations). Tree tips and label colors reflect the pathogen’s host. Hosts are outlined below each tree. The color-coded amino acid sequence alignments shown to the right of the tree. Icons of the hosts/substrates are drawn on top of the consensus tree branches. All variants of protein sequences as identified by BLAST are included. a) SIX1, b) SIX7, c) SIX13.