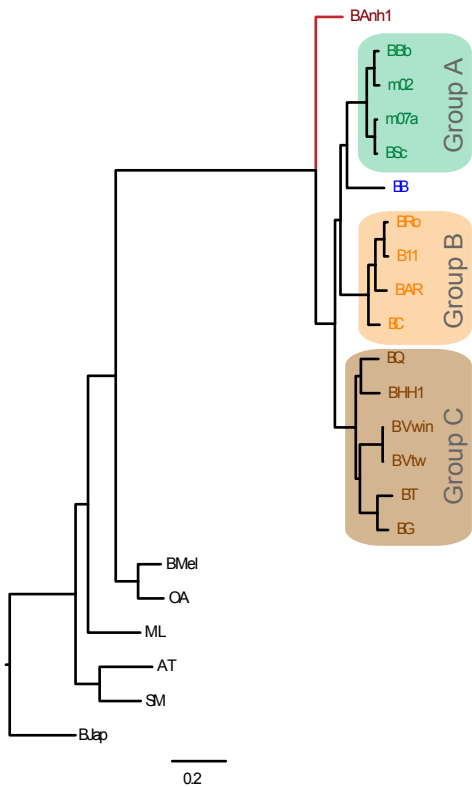
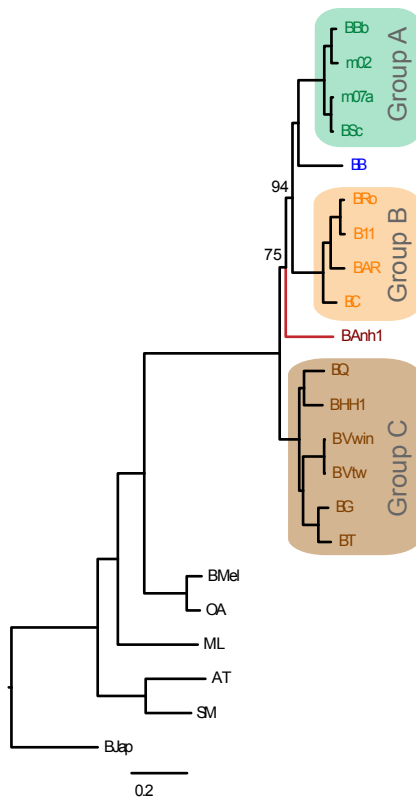


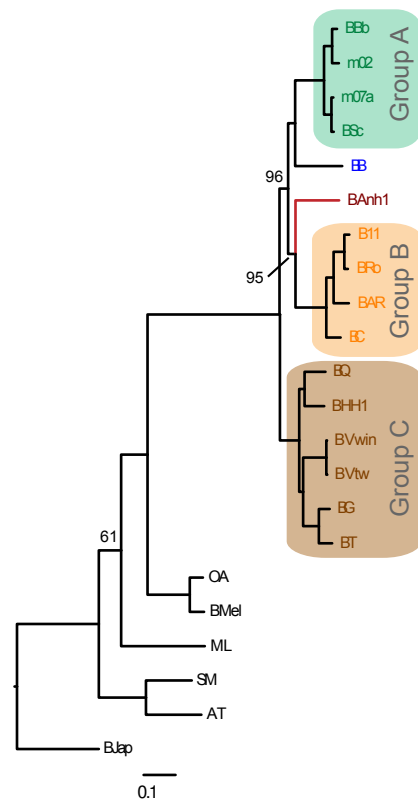
A



B



C



## Datasets

## Best tree picked by RAxML for each of the alignments

Nucleotide	Full concatenation All divergence level concatenations	none	none
Amino acid	15-20% divergence level 20-25% divergence level	Full concatenation	5-10% divergence level 10-15% divergence level
Nucleotide without 3rd codon position	15-20% divergence level 20-25% divergence level	Full concatenation 10-15% divergence level	5-10% divergence level