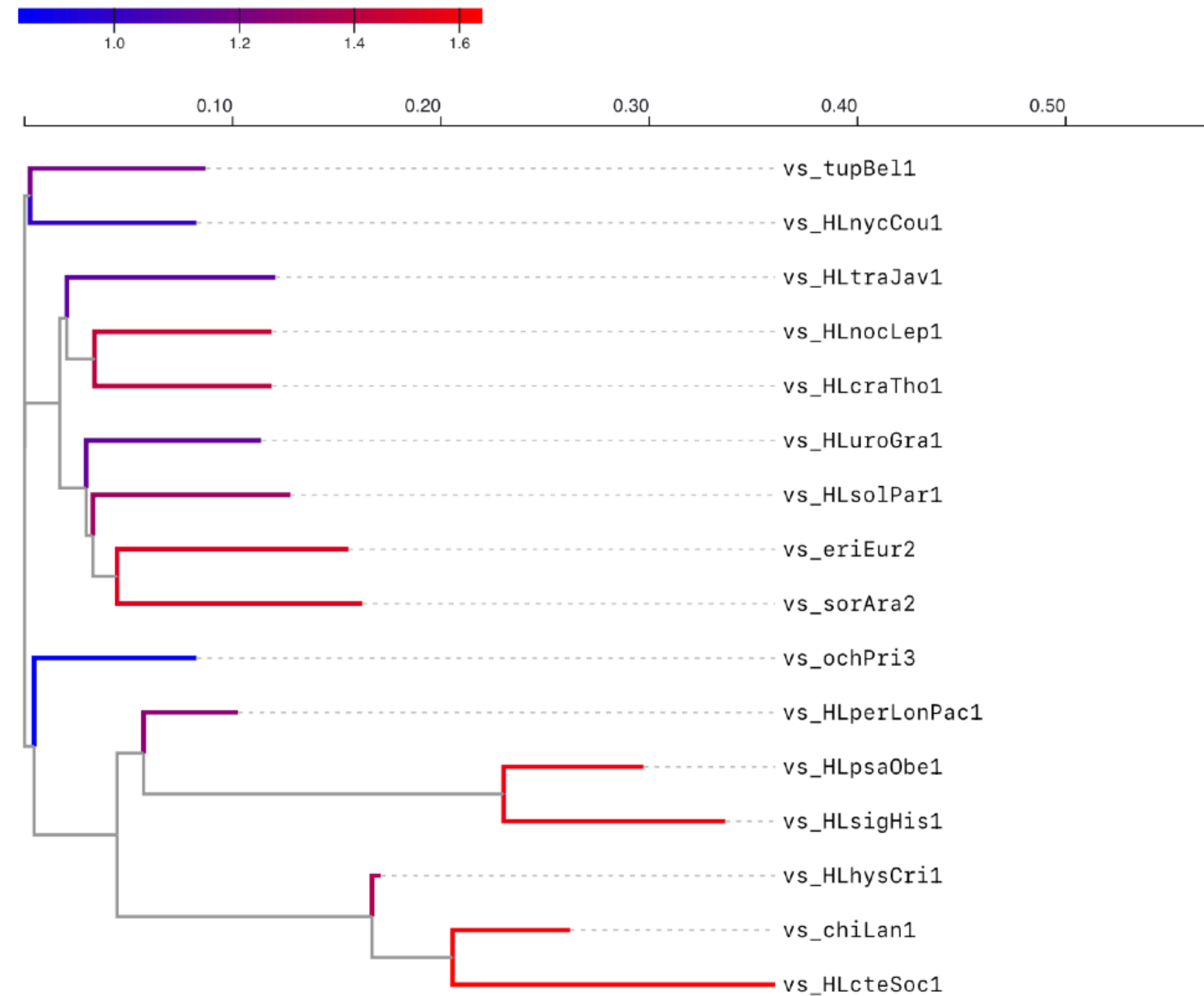


- BUSTED-E can annotate each input alignment with what it identifies as potentially erroneous codon positions (specific sequence, specific column)
- These can be further filtered (e.g. replaced with ‘- - -’) for downstream analyses with other tools
- The stringency of filtering is tunable

- Which species/genomes tend to have the most “putative” errors?



16-taxon Zoonomia tree  
Codons filtered / 1000 codons