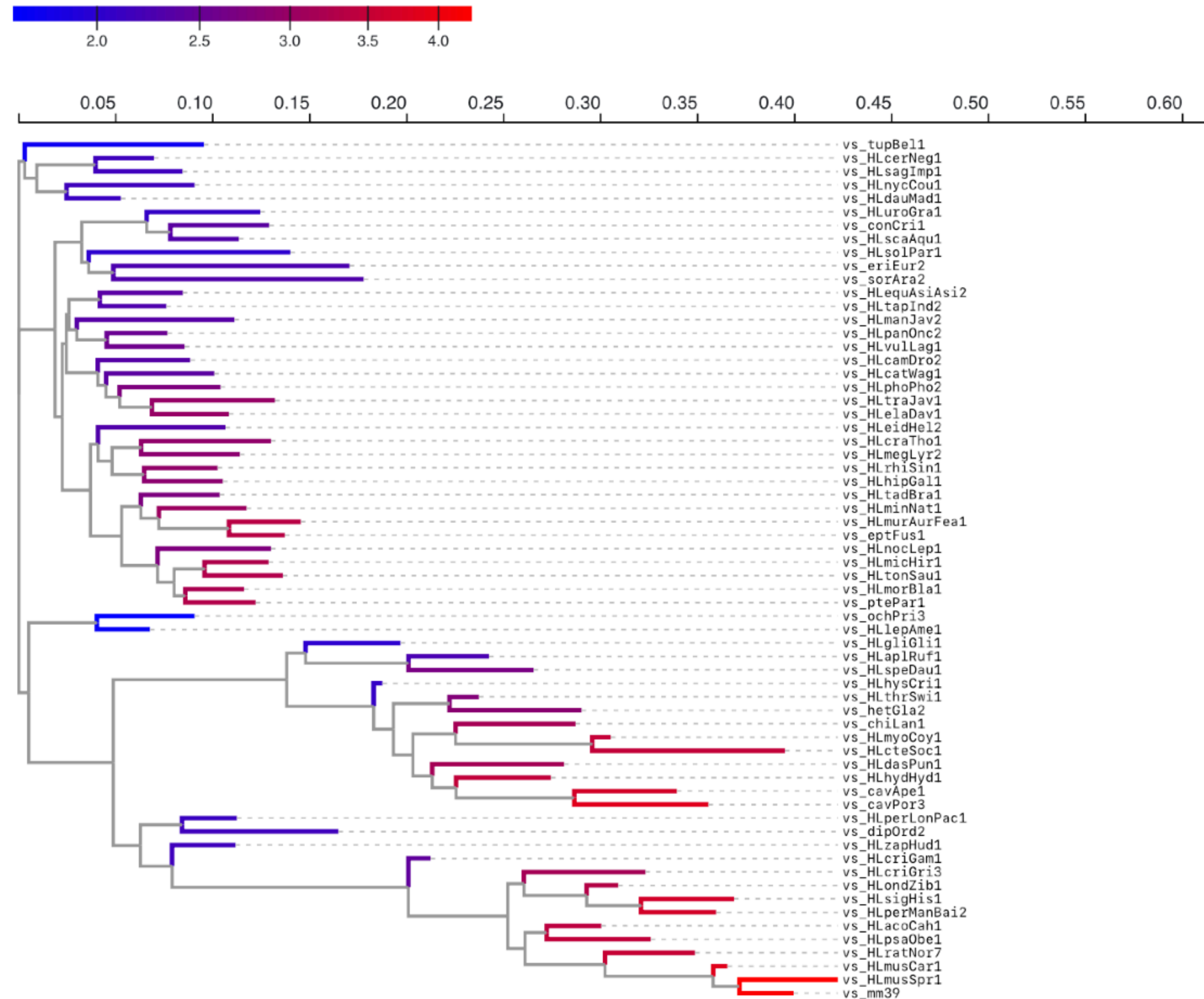
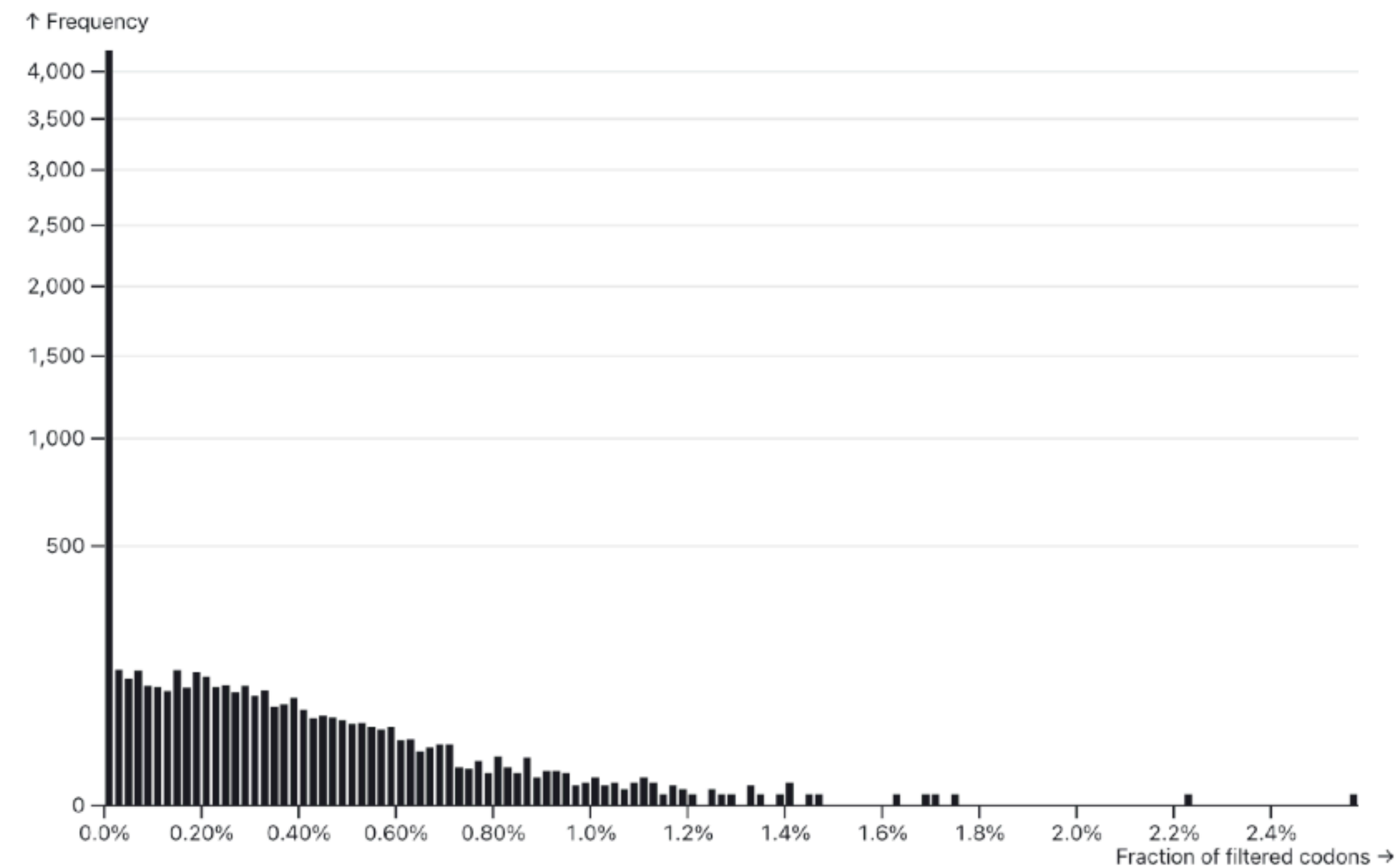
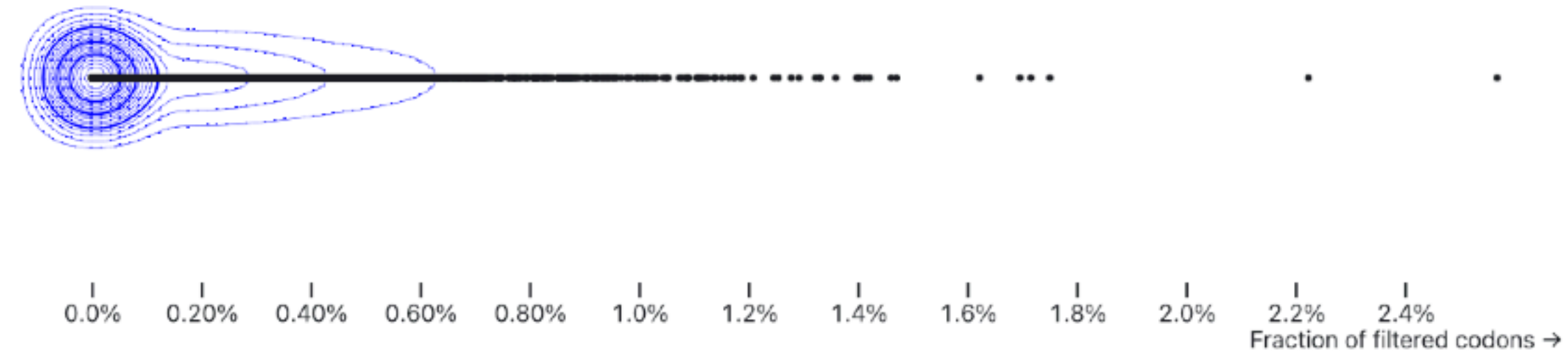


- Which species/genomes tend to have the most “putative” errors?



- The distribution of per MSA filtered codon counts

Fractions of filtered sites (of the entire alignment character count, seqs x codons)



16-taxon Zoonomia tree  
Codons filtered / 1000 codons