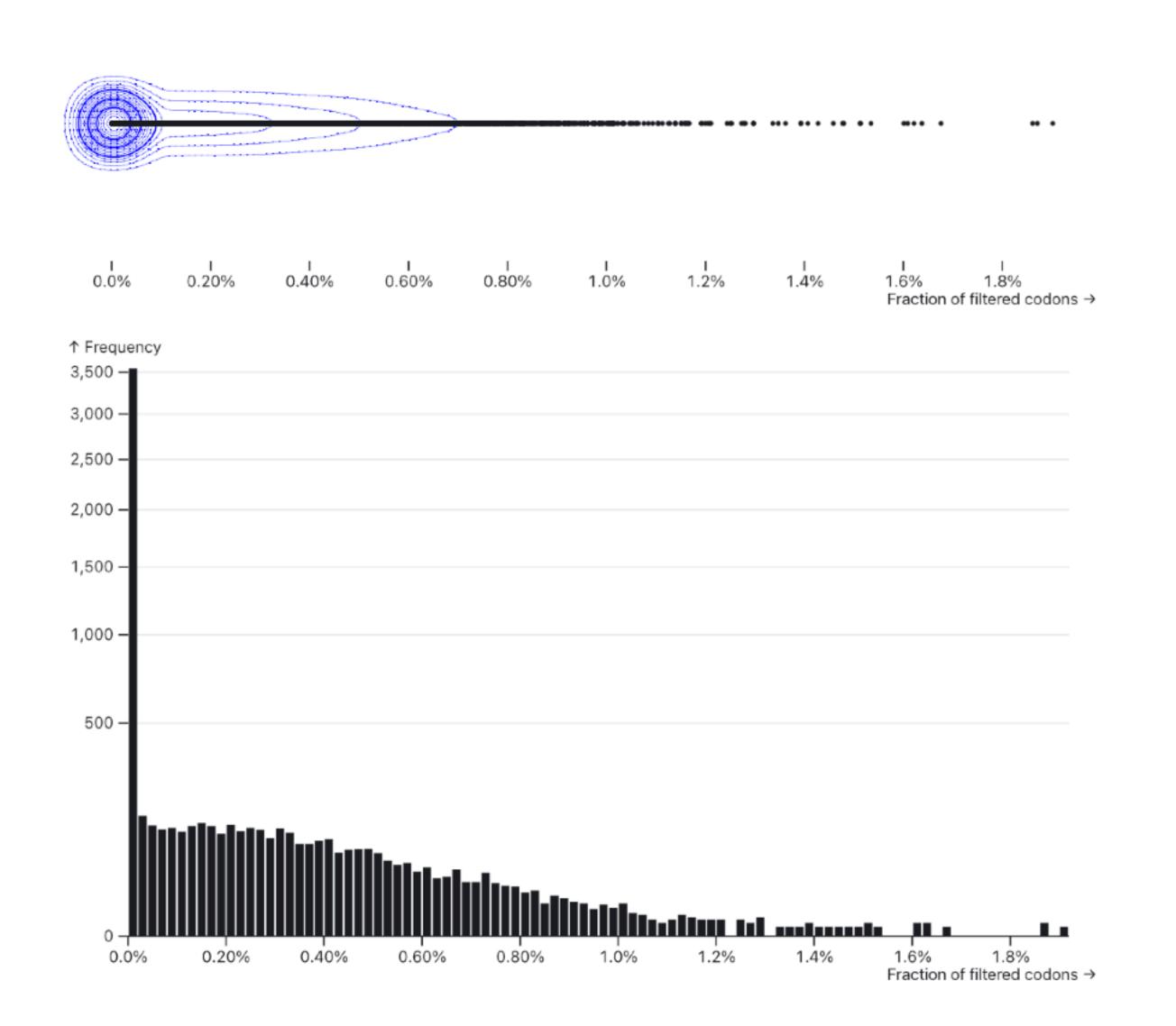
• The distribution of per MSA filtered codon counts

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



• The distribution of per MSA filtered codon counts

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

