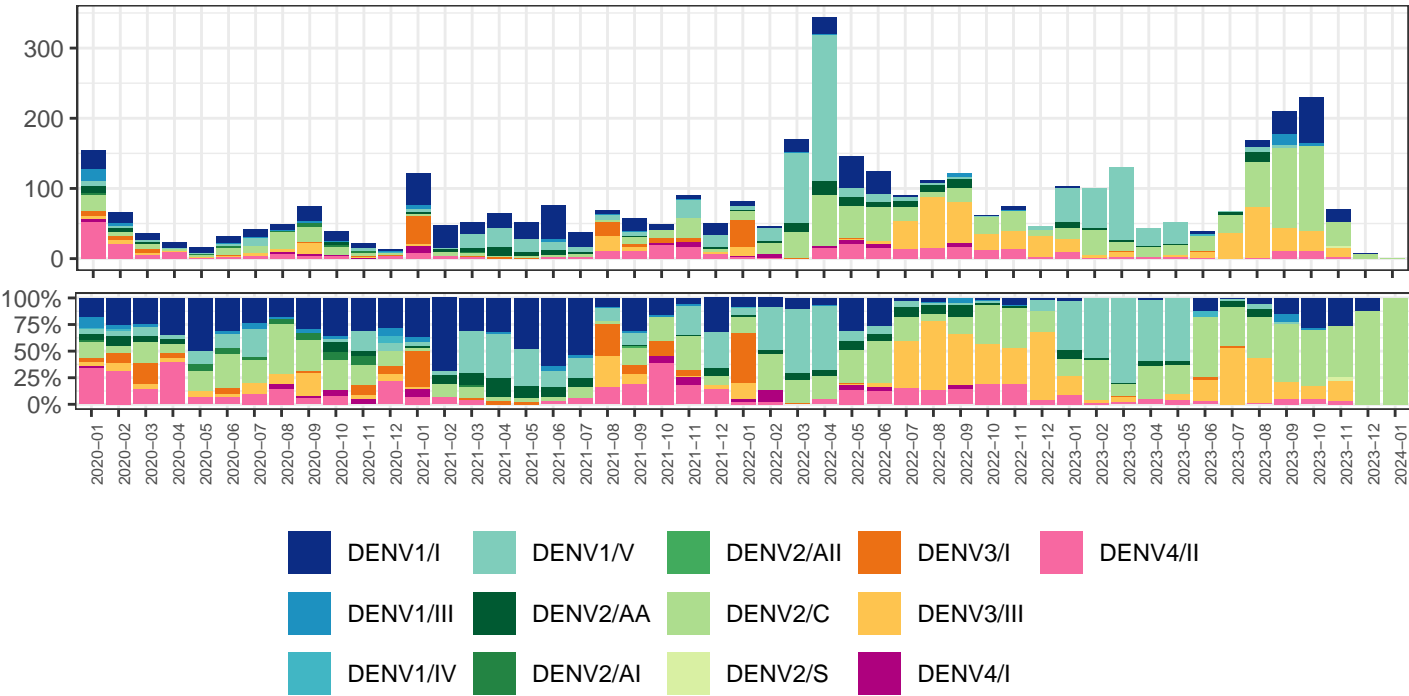
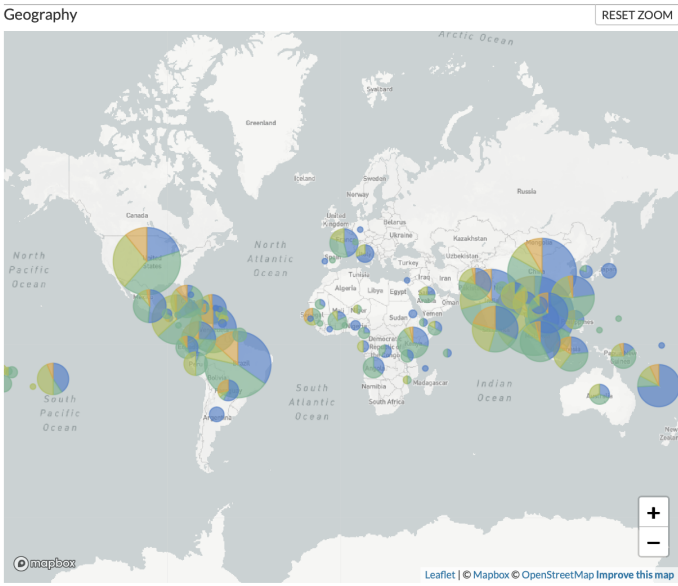
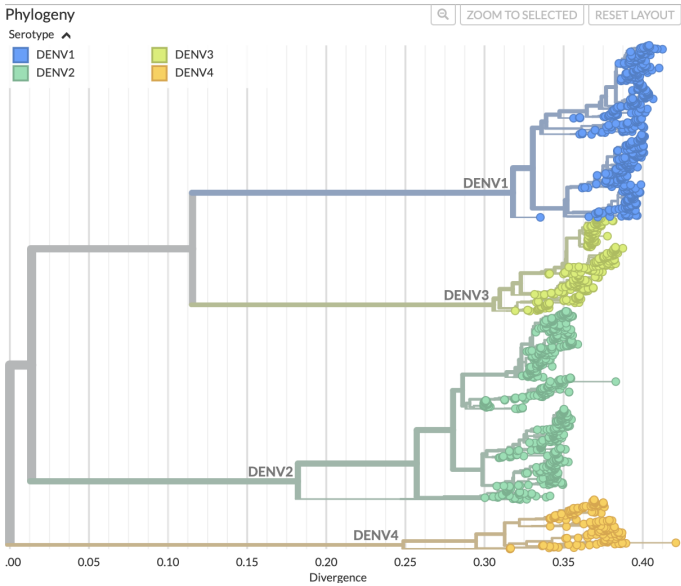


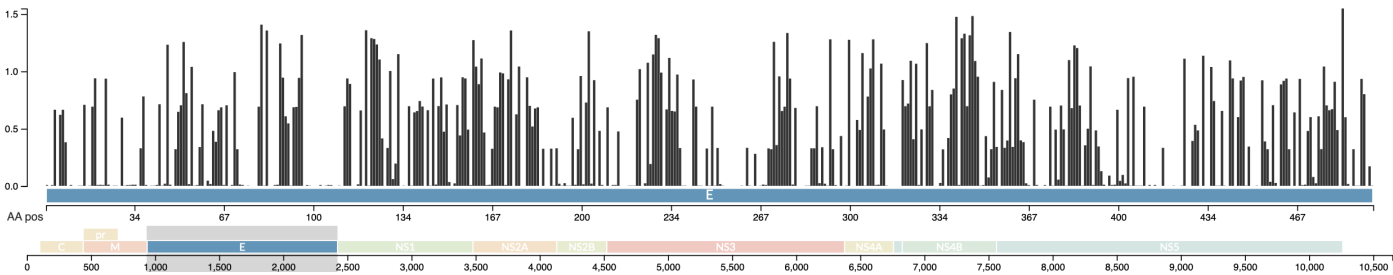
Dengue all (n = 3979)



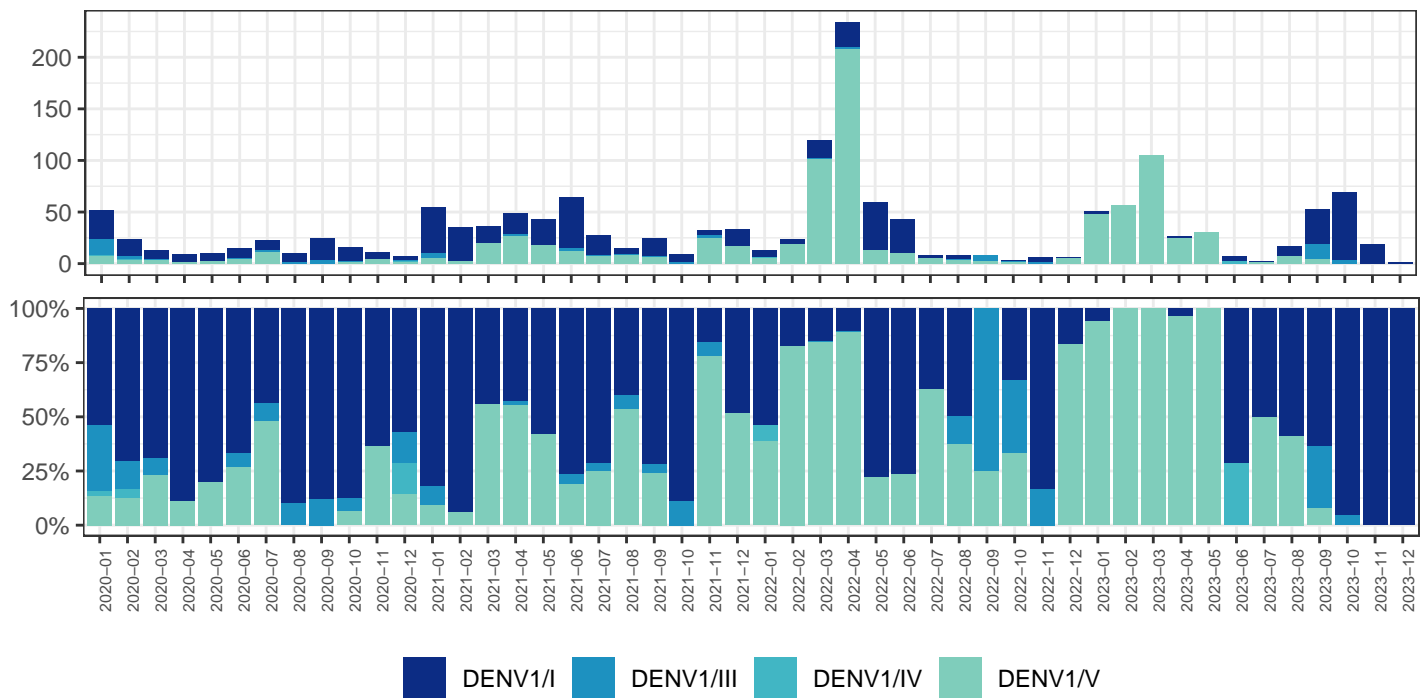
Showing 1957 of 1957 genomes sampled between Jan 1944 and Oct 2023.



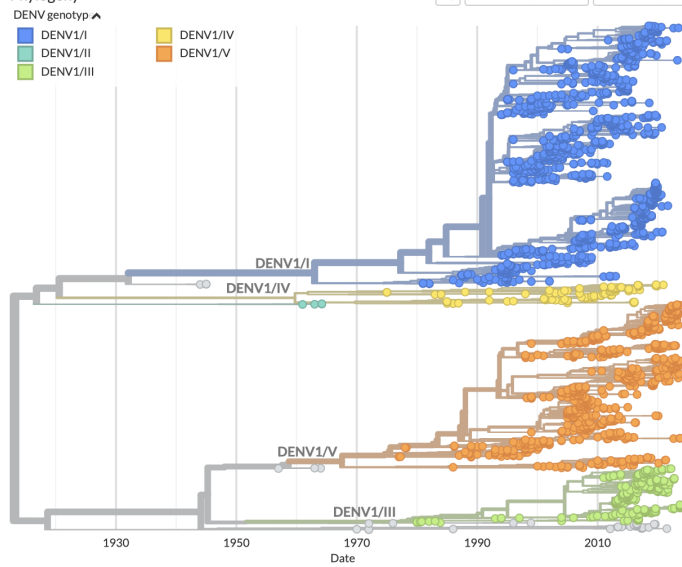
Amino acid diversity of CDS E



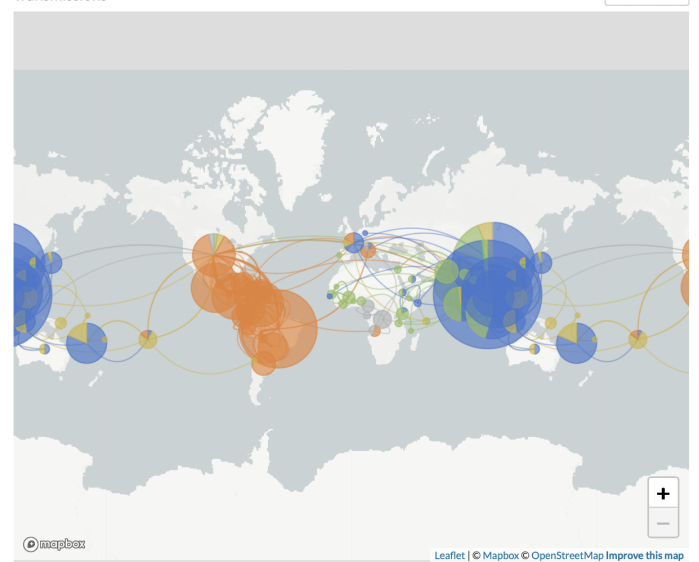
DENV1 (n = 1607)



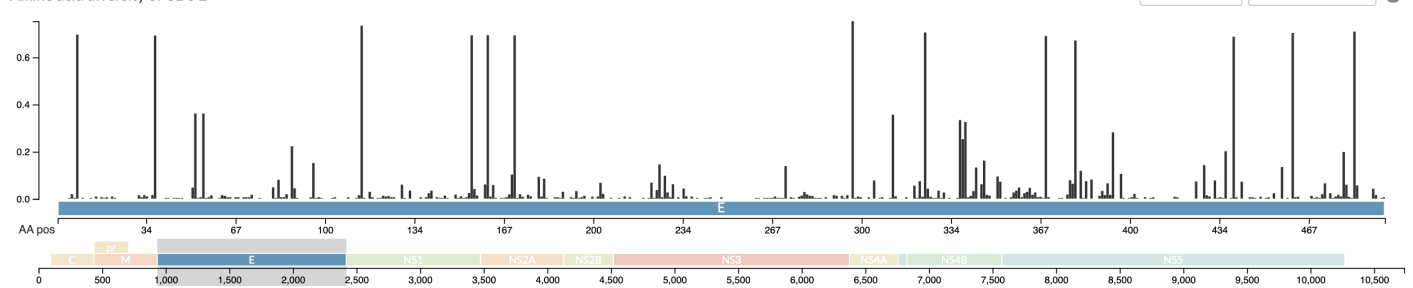
Phylogeny

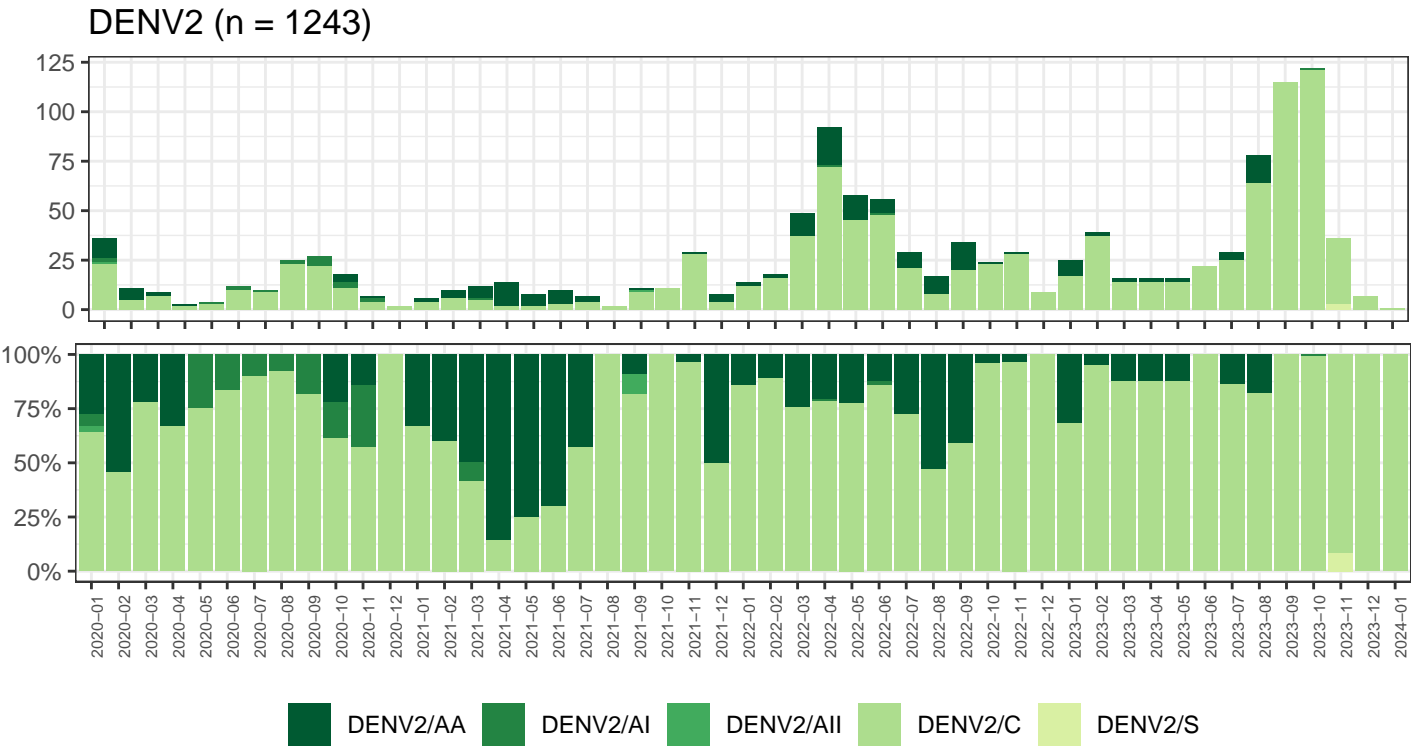


Transmissions

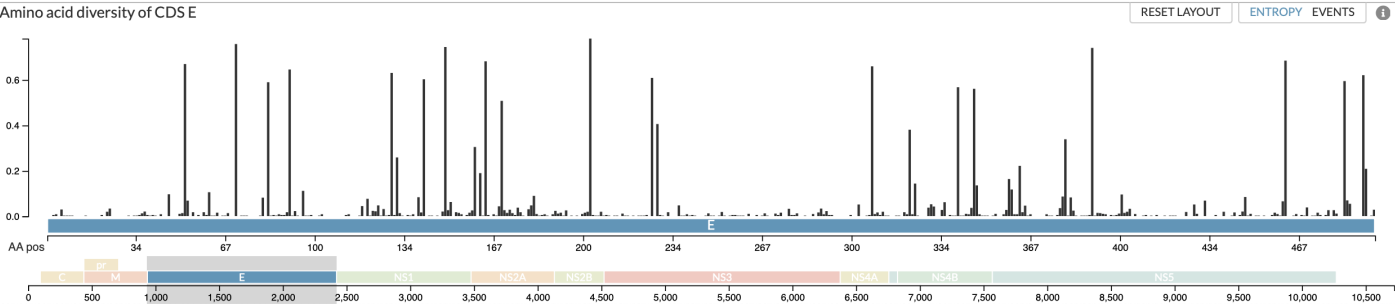
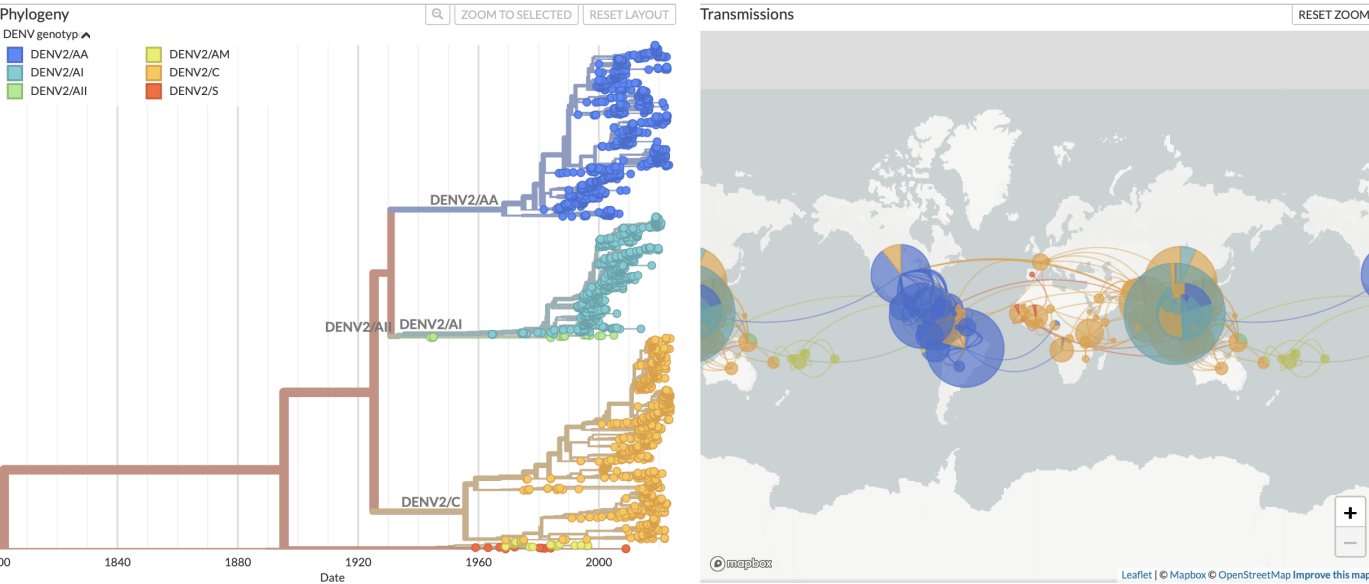


Amino acid diversity of CDS E

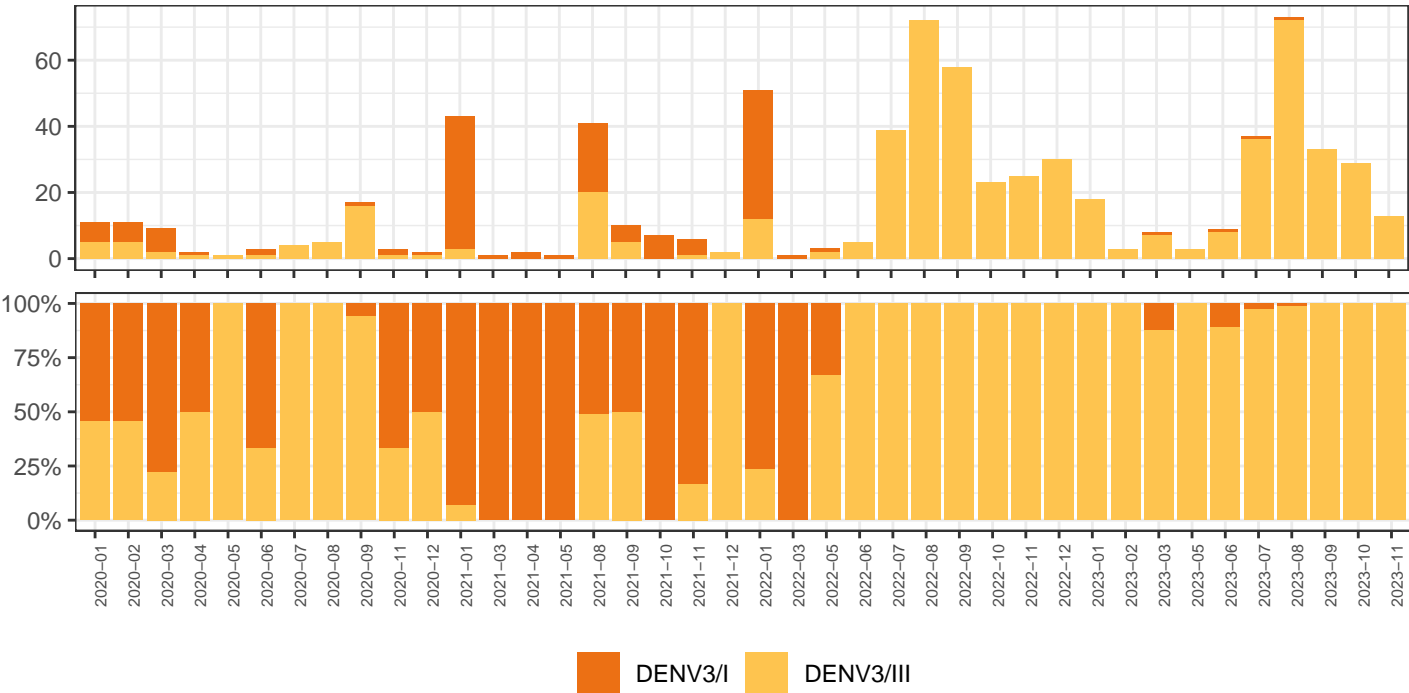




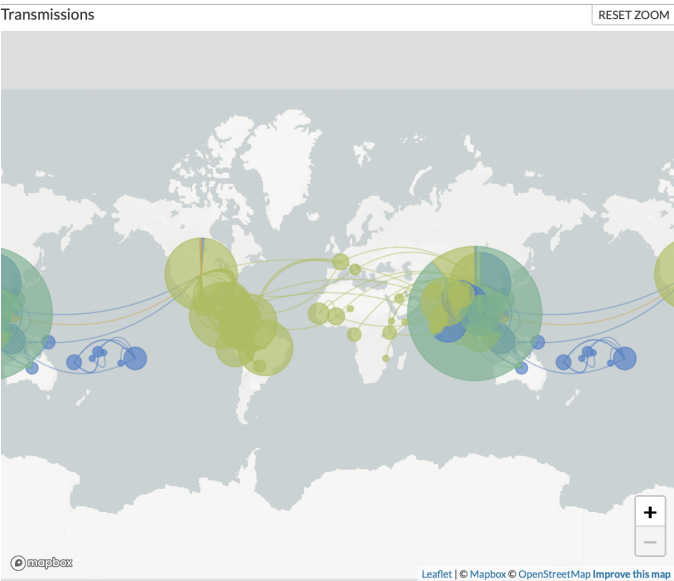
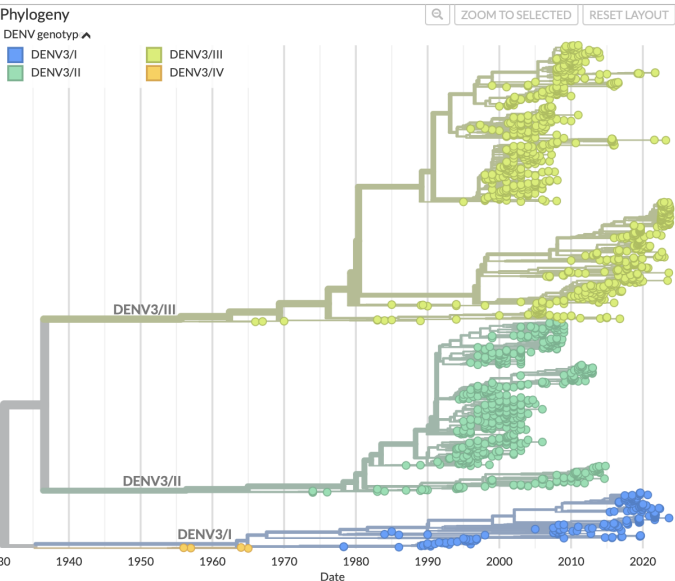
Showing 2752 of 2752 genomes sampled between Jan 1944 and Oct 2023.



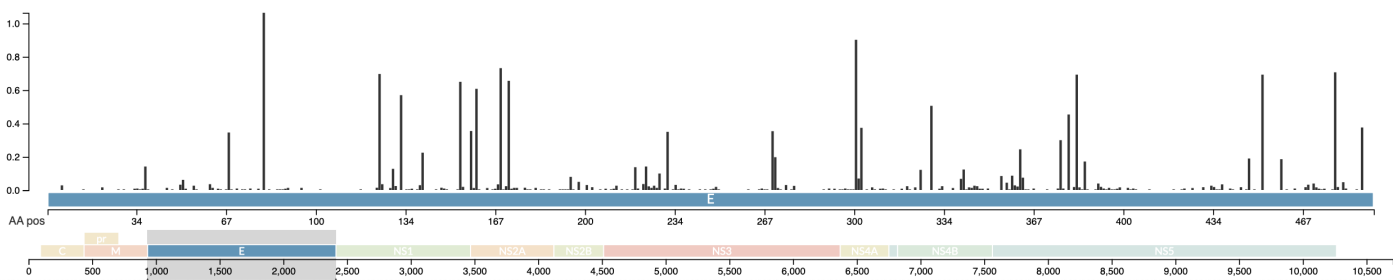
DENV3 (n = 714)



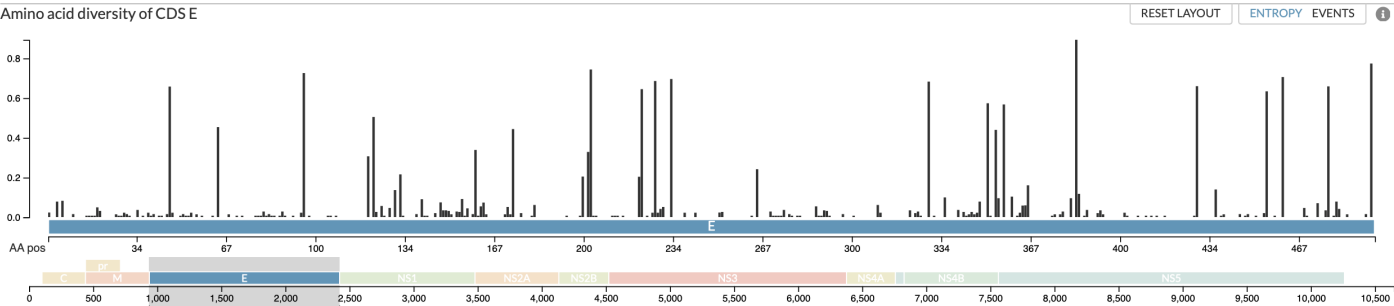
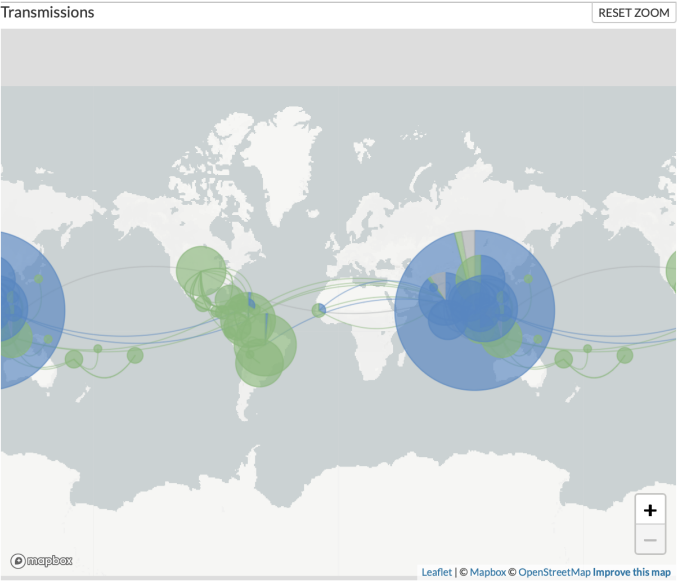
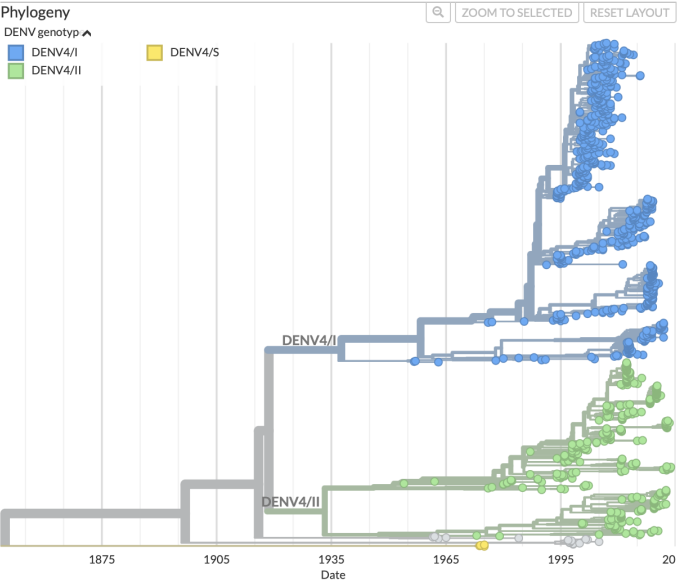
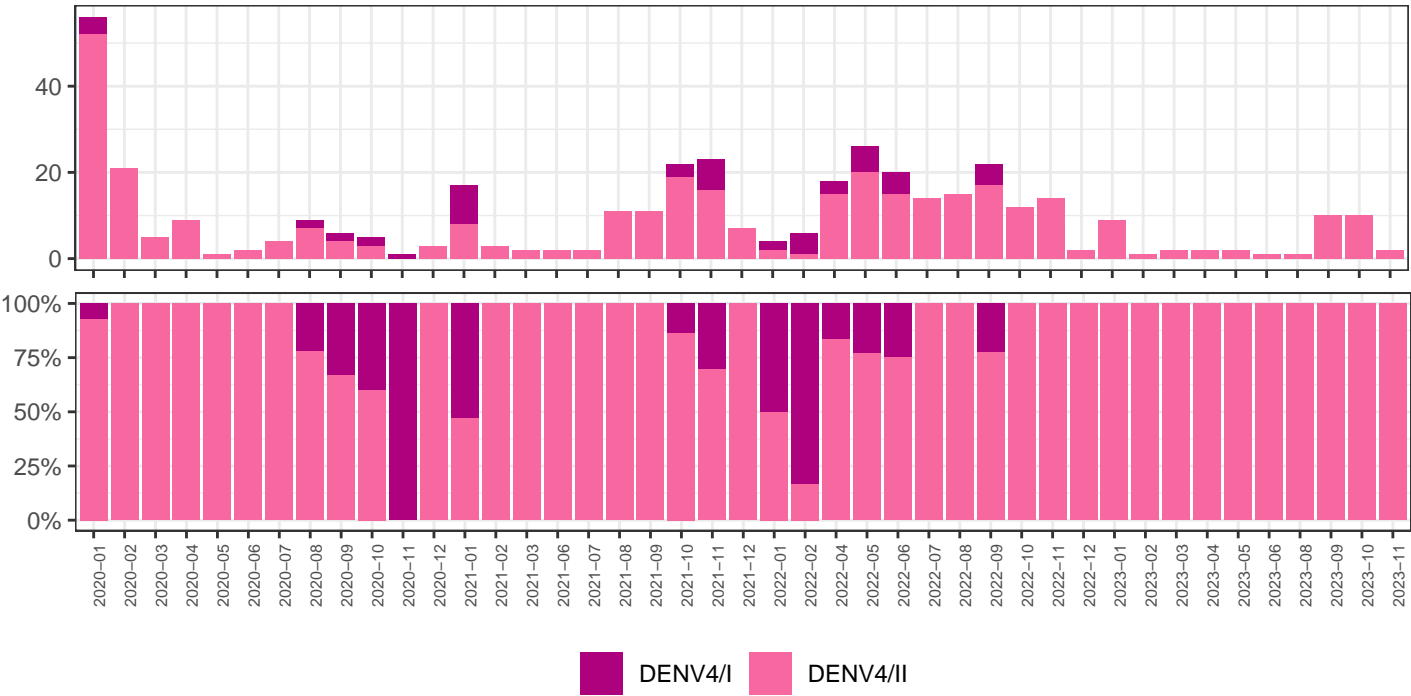
Showing 1675 of 1675 genomes sampled between Jan 1956 and Oct 2023.



Amino acid diversity of CDS E



DENV4 (n = 415)



Methods: Data Processing

