



**S7 Fig. Structural mapping of phylogenetic ‘trunk’ amino acid substitutions on Victoria-lineage and Yamagata-lineage HA trimers.** HA1 units are in darker grey while HA2 are white-grey, with the RBS shown in pink. (A) Victoria-lineage virus B/Brisbane/60/2008 (PDB: 4FQM), (B) Yamagata-lineage virus B/Yamanashi/166/98 (PDB: 4M40) and (C) rotated Yamagata-lineage virus B/Yamanashi/166/98. On the front-facing selected HA1 monomer (darkest grey), trunk mutations are labeled with residue number and coloured by location: in antigenic epitope (orange) or other (blue), while they are shown in black on the other two monomers for simplicity.