

Supplementary Figure 2. Alignment of the YFGNC motif region in clade 1. Biochemically characterized sequences from clade 1 were aligned using MUSCLEv3.8.425 and using default parameters in Geneious v2022.1.1. The region of the YFGNC motif is highlighted using a black box. Colored residues are conserved in at least 50% of the sequences for each given residue position in the alignment.