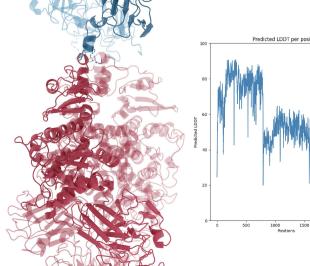
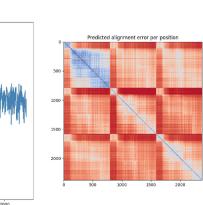


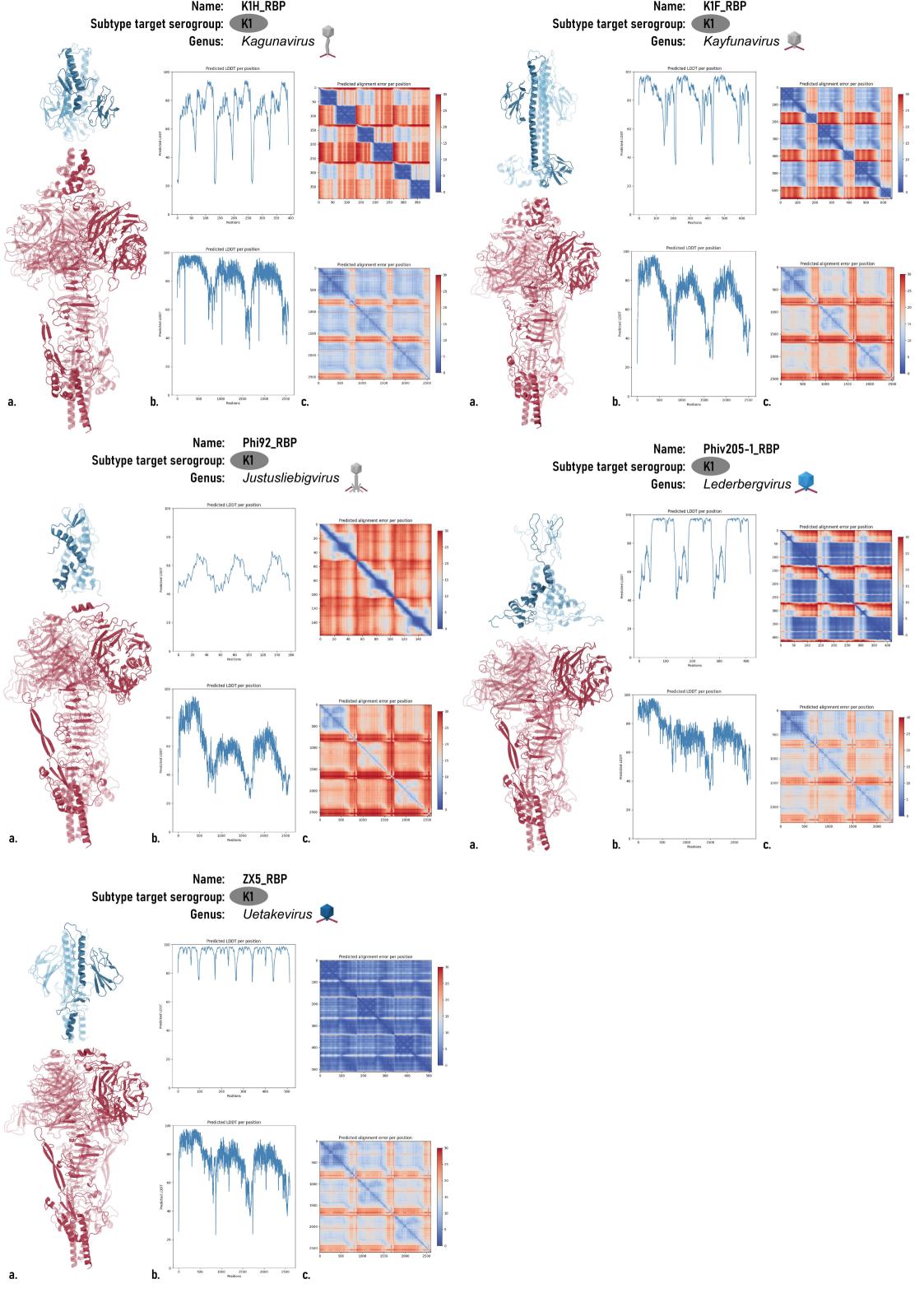
а.



b.



C.



Additional file 4: Figure S4: Predicted quaternary structures of the phage RBPs using AlphaFold2.

RBPs are clustered according to RBP subtype (a) Anchor domain shown in blue and RBD indicated in red, using different shades for each of the three monomers. An asterisk was used to indicate when quaternary structure predictions of RBP domains resulted in erroneous structures. (b) AlphaFold2 predicted LDDT per amino acid position; the upper graph represents the anchor domain and the lower graph the RBD when the structure was predicted separately. (c) AlphaFold2 predicted alignment error per amino acid position; the upper graph represents the anchor domain and the lower graph the structure was predicted separately. (b) AlphaFold2 predicted alignment error per amino acid position; the upper graph represents the anchor domain and the lower graph the RBD when the structure was predicted separately. When quaternary structure predictions of domains were unsuccessful, the tertiary structure was displayed instead.