

Figure S1: Maximum-likelihood phylogenetic tree created from portal vertex protein sequences of members of the subfamily Peduovirinae. Sequences were aligned with Clustal Omega and trees constructed using IQTree v1.6.12 with the LG + G4 substitution model IQTree v1.6.12 with ModelFinder, SH-aLRT test and ultrafast bootstrap (1000 replicates). Enterobacteria phage mEp237 (JQ182730) was used as an outgroup to root the tree. Branch length is proportional to the number of substitutions per site (see scale bar). Members of virus genera are denoted by coloured blocks. An asterisk (*) adjacent to a genus name indicate proposed genera that at the time of writing were yet to be ratified by the International Committee on the Taxonomy of Viruses (100).

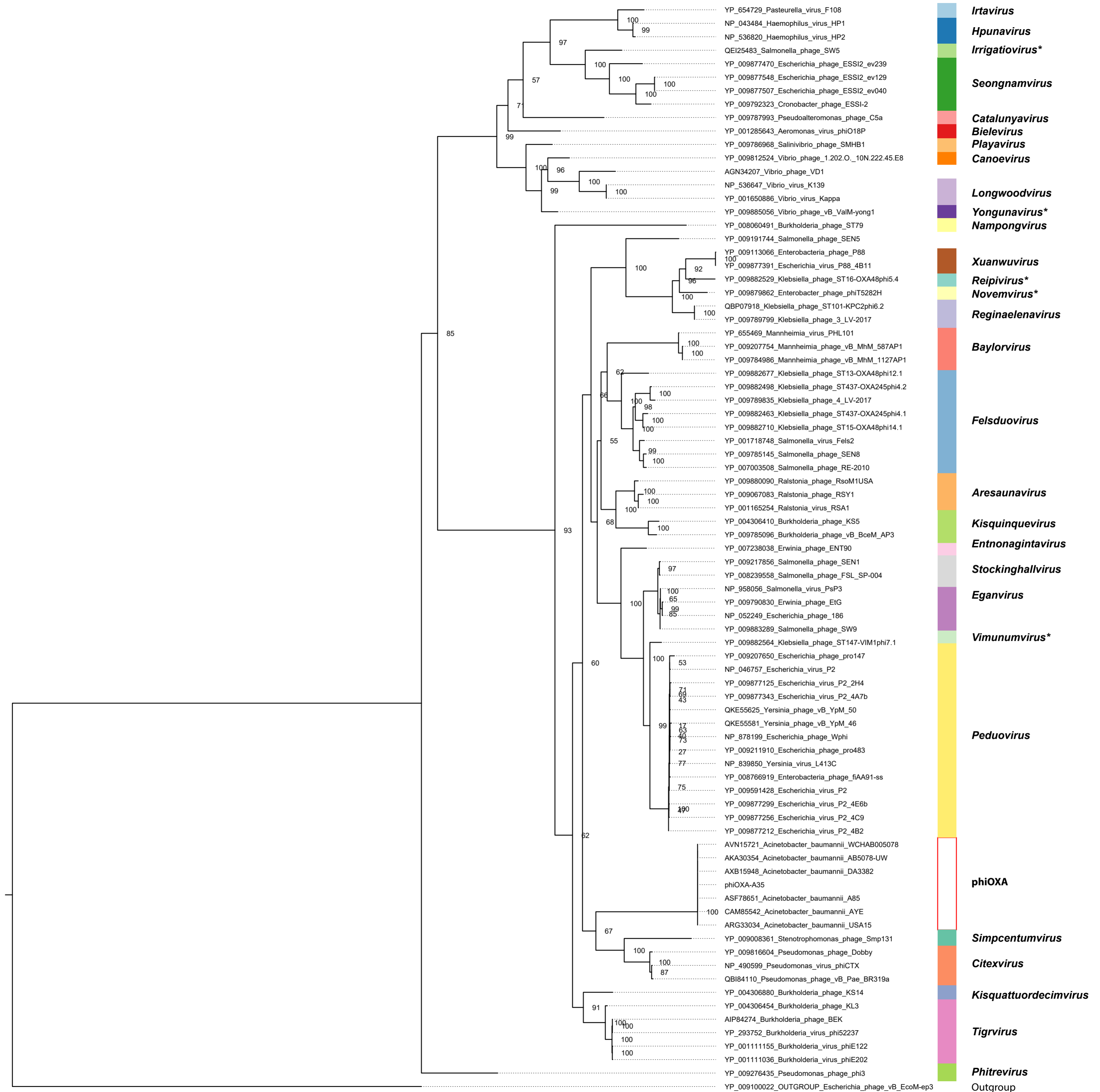


Figure S2: Maximum-likelihood phylogenetic tree created from major capsid protein sequences of members of the subfamily Peduovirinae. Sequences were aligned with Clustal Omega and trees constructed using IQTree v1.6.12 with the WAG + G4 substitution model, SH-aLRT test and ultrafast bootstrap (1000 replicates). Enterobacteria phage mEp237 (JQ182730) was used as an outgroup to root the tree. Branch length is proportional to the number of substitutions per site (see scale bar). Members of virus genera are denoted by coloured blocks. An asterisk (*) adjacent to a genus name indicate proposed genera that at the time of writing were yet to be ratified by the International Committee on the Taxonomy of Viruses (100).

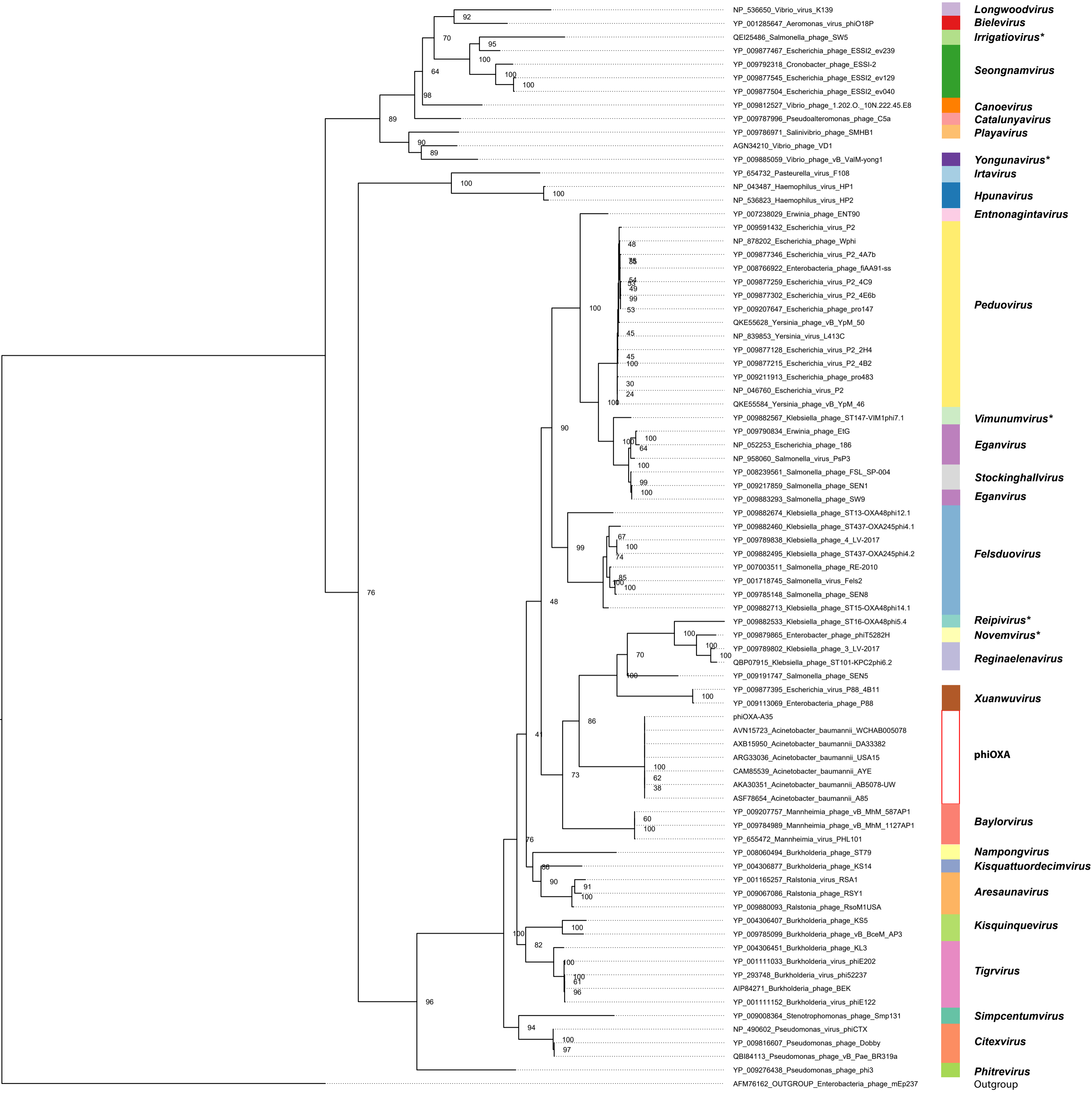
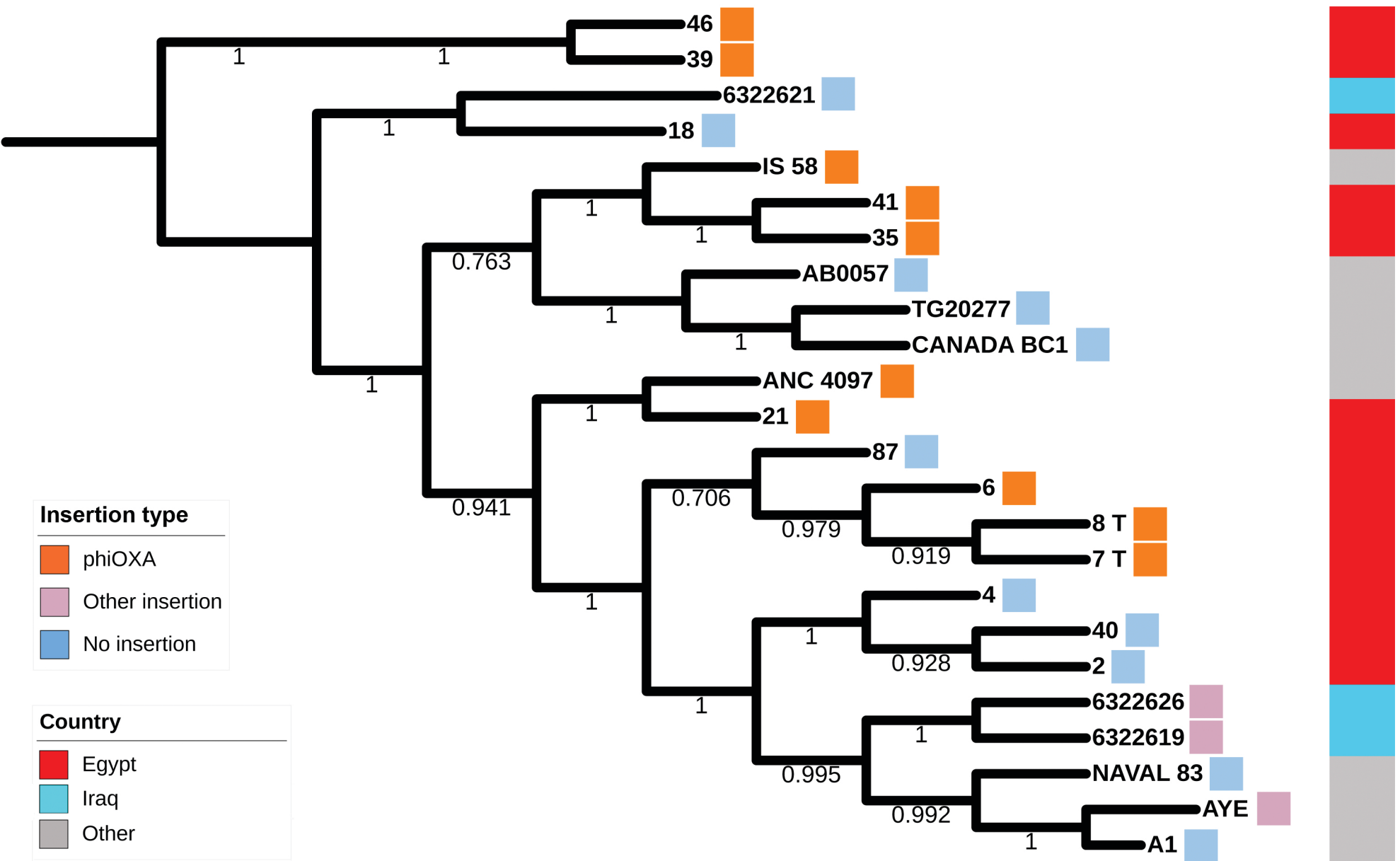


Figure S3: Distribution of different inserted elements at the tRNA-Leu site in CC^{PAS}1 isolates. The tree is the same as that shown in Figure 1, retaining only those leaves representing CC^{PAS}1 isolates. Leaves are annotated with the type of insertion found at tRNA-Leu: orange indicates phiOXA, pale blue indicates no insertion, and pale pink indicates an insertion other than phiOXA is present. In the case of strain AYE the insertion is bacteriophage RPHR (2) which is identical to phiOXA except for the *ISAbal-oxa23* insertion (see Figure 4), and in isolates 6322619 and 6322626 this represents the insertion of an unrelated uncharacterised element.

Tree scale: 0.001



References

1. Van Zyl L, Lueder M, Bishop-Lilly K, Turner D, Adriaenssens E, et al. Create five new genera and 29 species in the subfamily *Peduvirinae* 2019.002D; 2019. <https://ictv.global/ICTV/proposals/2020>
2. Vallenet D, Nordmann P, Barbe V, Poirel L, Mangenot S, et al. Comparative analysis of *Acinetobacters*: three genomes for three lifestyles. *PLoS One* 2008;3:e1805. 10.1371/journal.pone.0001805