Electronic Supplementary Material

Reconciling individual and population levels of porcine reproductive and respiratory syndrome virus evolution

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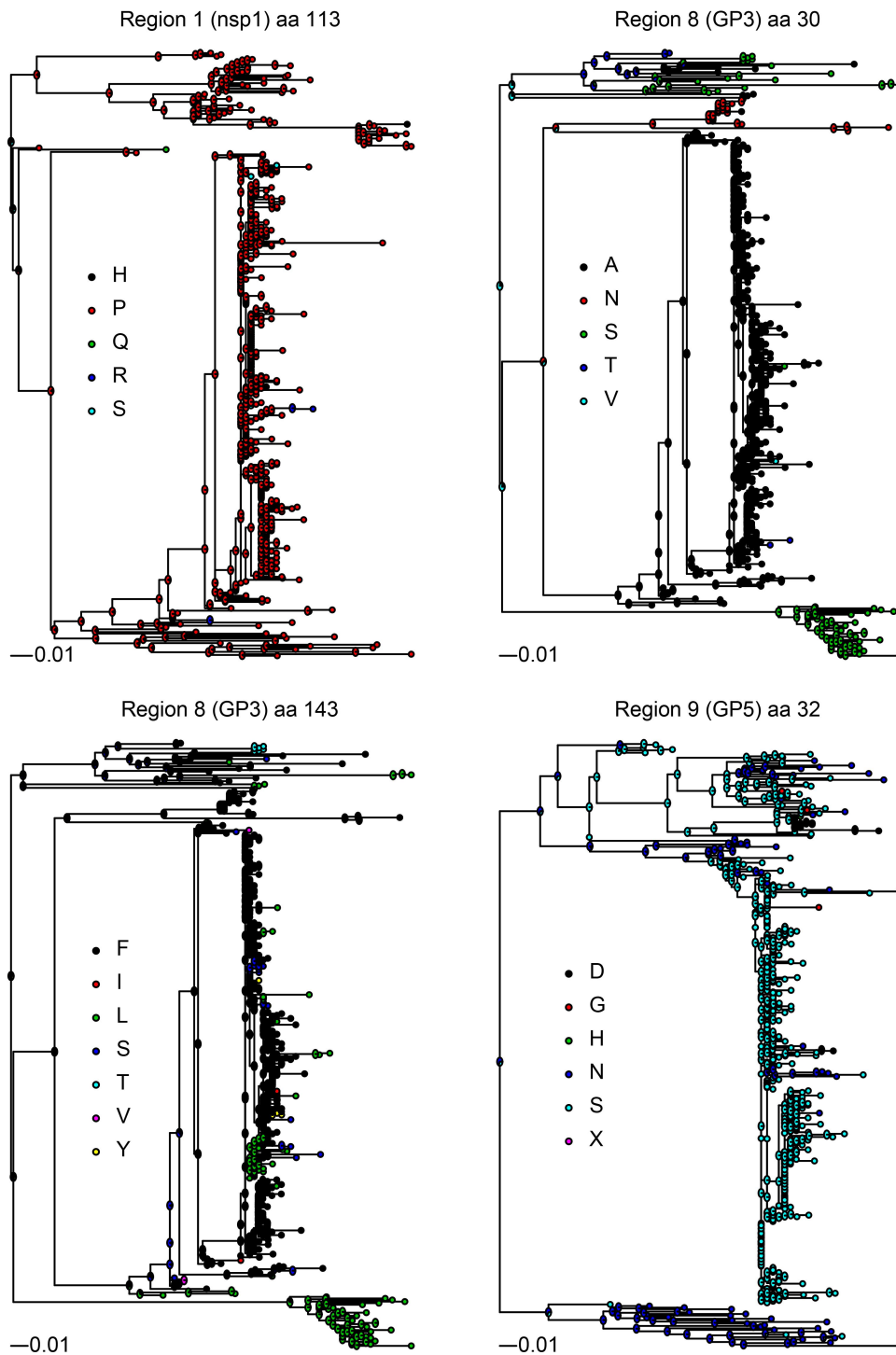
Figure S1. Partition-specific phylogenetic trees reconstructed using the maximum-likelihood method implemented in PhyML. Partitions were defined according to Chen *et al*., 2016. For graphical reasons, only regions for which amino-acid positions were proven under statistically significant diversifying selection in both the current study and in Chen *et al*. (2016) are reported. For each of these positions, the amino acid (named according to IUPAC nomenclature) is represented as a color-coded circle located on the corresponding tree tip (i.e., the sampled viral sequence). Additionally, the results of an amino-acid ancestral-sequence reconstruction are plotted: ancestral nodes (i.e., states) are represented as pie charts whose slices are proportional to the feature (i.e., amino acid) likelihood in the specific ancestral protein.