pathogens

Supplementary Materials

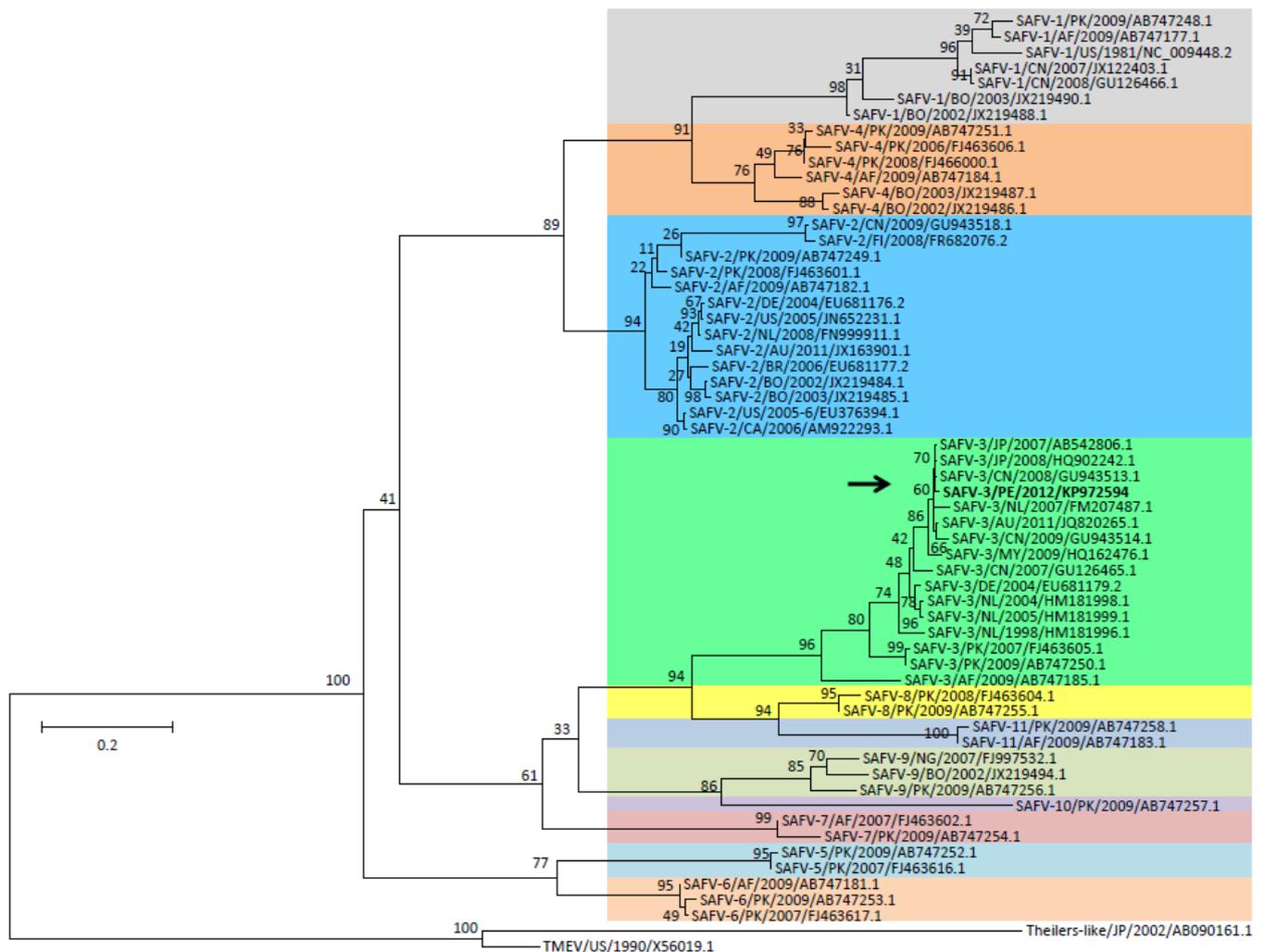# Full Genomic Characterization of a Saffold Virus Isolated in Peru

Figure S1. Phylogenetic analysis of SAFV partial VP1 (B) sequences. Each strain is labeled using standard identifiers, including virus type, country of isolation (using ISO country codes), isolate name (if any), year of isolation and GenBank accession number. Additionally, SAFV1–11 serotypes are color coded for easy viewing. The Peruvian isolate described here is highlighted in bold and with an arrow. The tree was constructed using a total of 53 publicly available complete VP1 sequences covering serotypes 1–11 plus 7 additional partial VP1 sequences. Scale bars represent the number of substitutions per site.