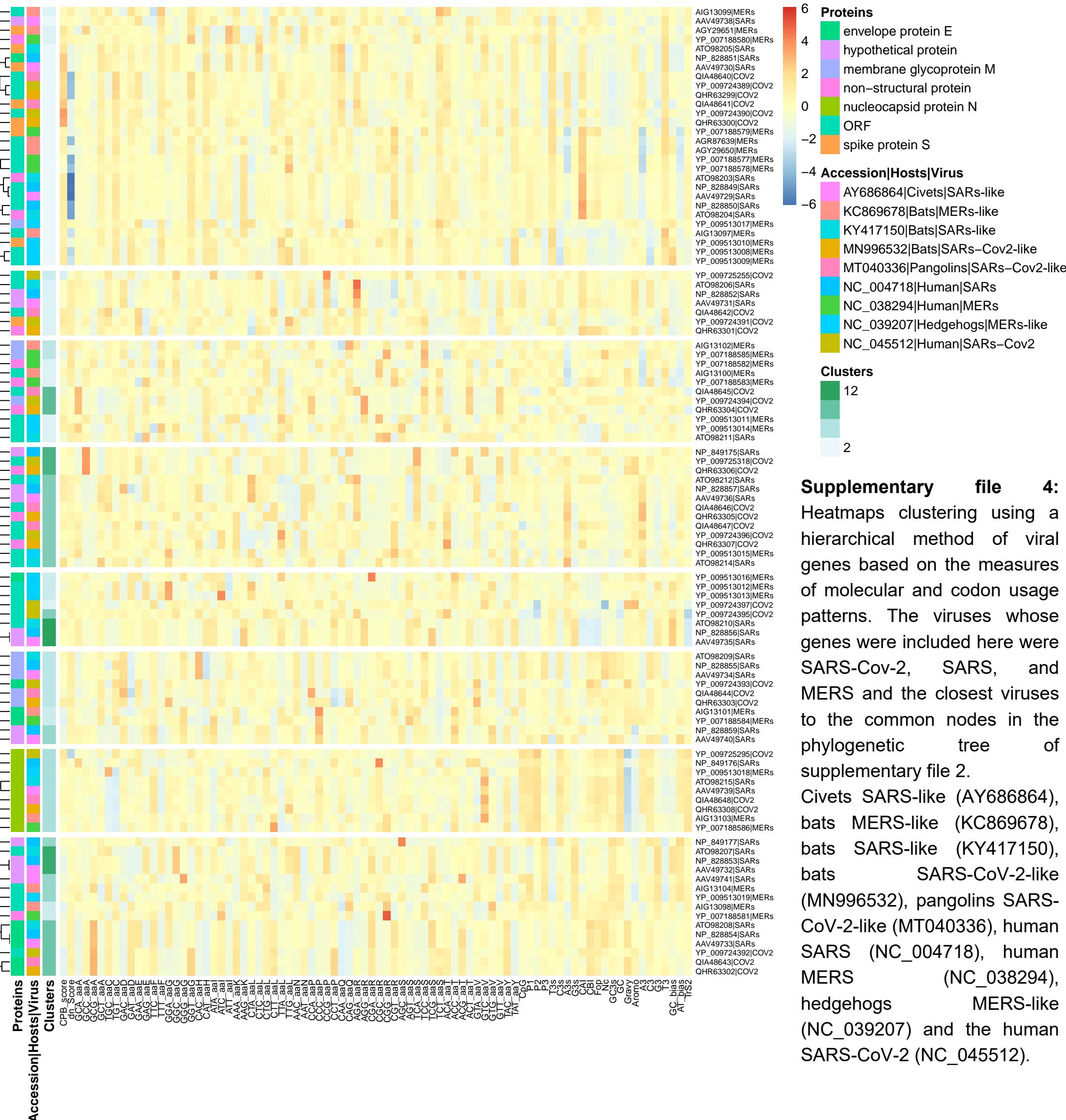


Molecular Features Similarities Between SARS-CoV-2, SARS, MERS and Key Human Genes Could Favour The Viral Infections and Trigger Collateral Effects

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Supplementary file 4:
Heatmaps clustering using a hierarchical method of viral genes based on the measures of molecular and codon usage patterns. The viruses whose genes were included here were SARS-CoV-2, SARS, and MERS and the closest viruses to the common nodes in the phylogenetic tree of supplementary file 2.
Civets SARS-like (AY686864), bats MERS-like (KC869678), bats SARS-like (KY417150), bats SARS-CoV-2-like (MN996532), pangolins SARS-CoV-2-like (MT040336), human SARS (NC_004718), human MERS (NC_038294), hedgehogs MERS-like (NC_039207) and the human SARS-CoV-2 (NC_045512).