

Supplementary Figures

Computational Prediction of RNA–RNA Interactions between Small RNA Tracks from *Betacoronavirus* Nonstructural Protein 3 and Neurotrophin Genes during Infection of an Epithelial Lung Cancer Cell Line: Potential Role of Novel Small Regulatory RNA

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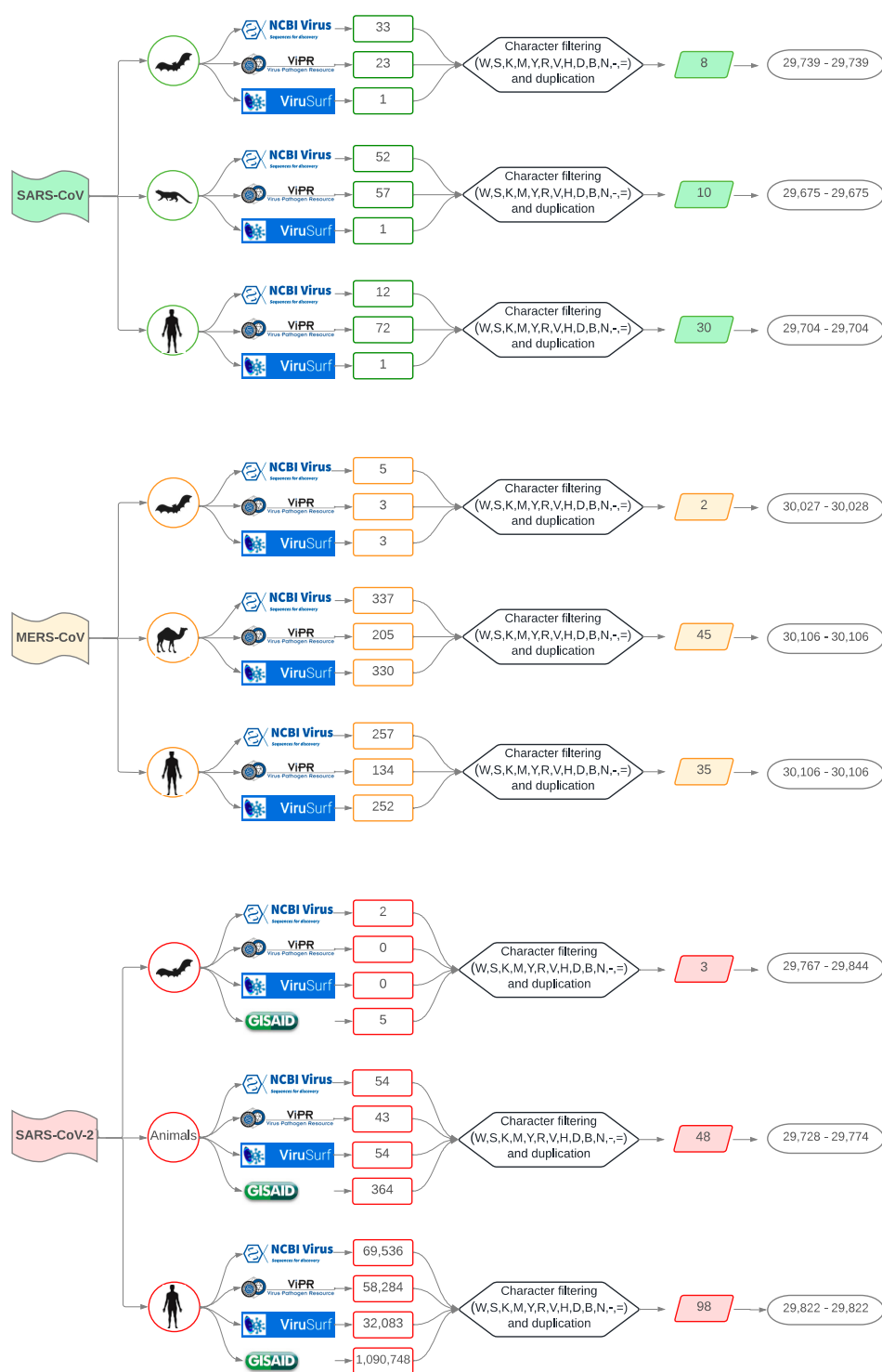


Figure S1. Flowchart showing approach to data collection, curation process and range of sequence lengths for the three *Beta-CoVs* used in the study by [39].

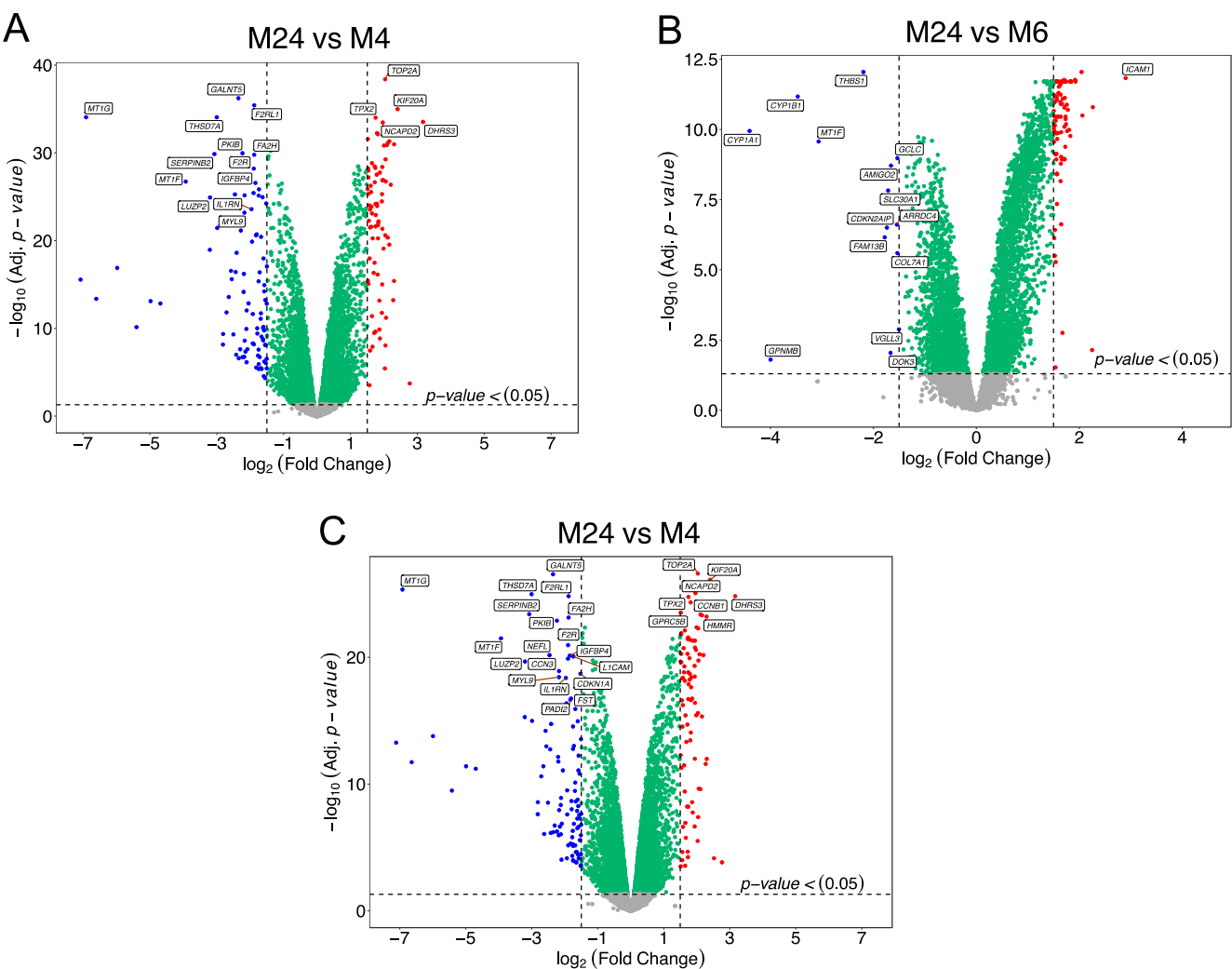


Figure S2. Volcano plots showing the differential expression profiling of mock cultures of Calu-3 cells infected with *Beta-CoVs* between the final and initial time (MM). Vertical lines denote an absolute value of $|\log_2\text{FC}| > 1.5$ versus $-\log_{10}(\text{Adj. } p\text{-value}) < 0.05$ in (A) SARS-CoV; (B) MERS-CoV; and (C) SARS-CoV-2. Upregulated DEGs are shown as red dots and downregulated DEGs as blue dots.

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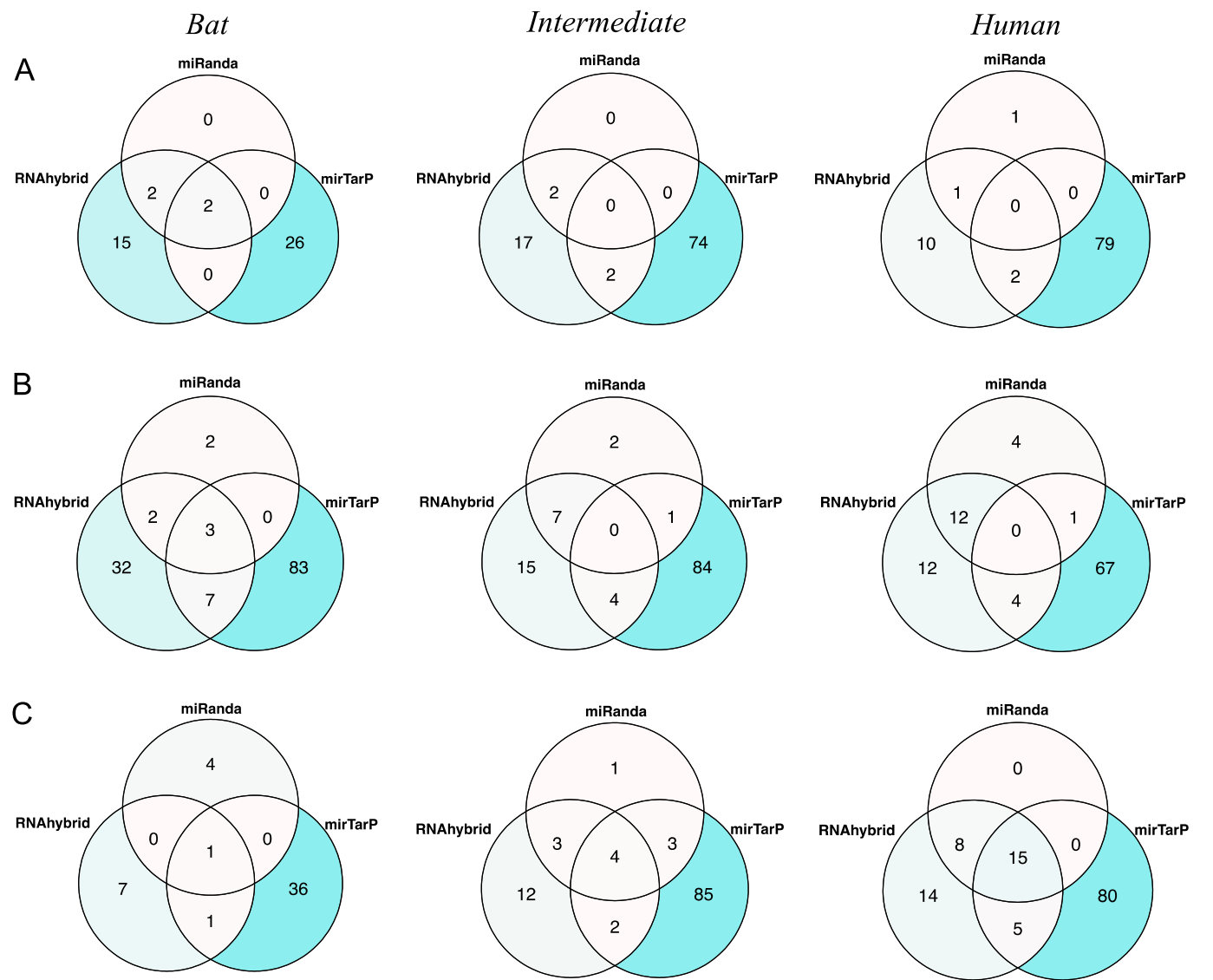


Figure S3. Potential common miRNAs:virusRNAs pairings predicted by RNAhybrid, miRanda and mirTarP in *Beta-CoVs*. **(A)** There are 2 interaction pairs in SARS-CoV; **(B)** 3 in MERS-CoV; and **(C)** 20 in SARS-CoV-2. Venn diagrams sections are colored based on the number of pairing predictions.

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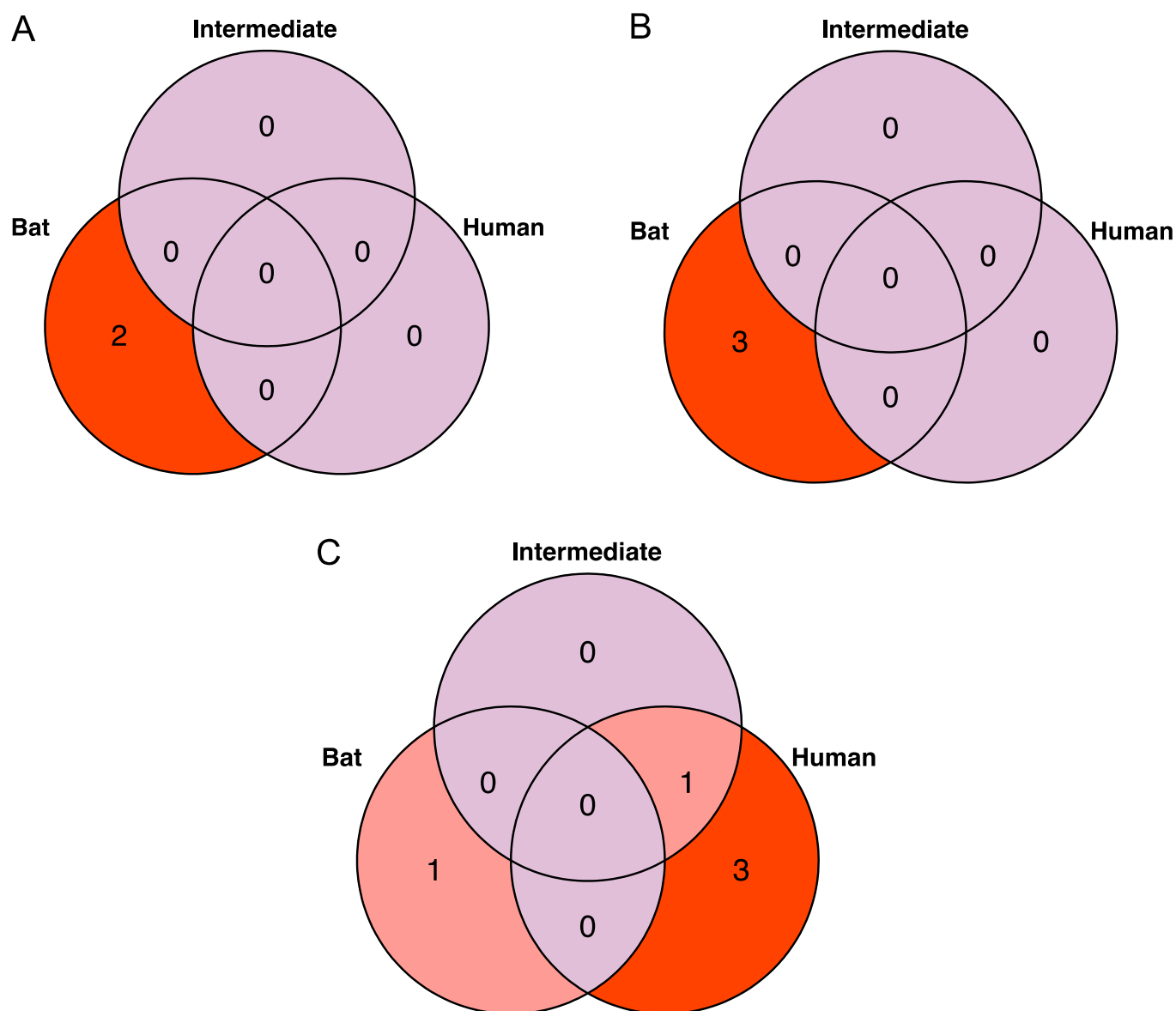


Figure S4. Comparison of vsRNAs encoded by *Beta-CoVs* across hosts of bats, intermediate animals, and humans. Venn diagrams show that 2 vsRNAs in (A) SARS-CoV, and 3 in (B) MERS-CoV are exclusive to bats, while 6 in (C) SARS-CoV-2 are observed in all three hosts, including 1 for bats, 1 for intermediate animals and 4 for humans.

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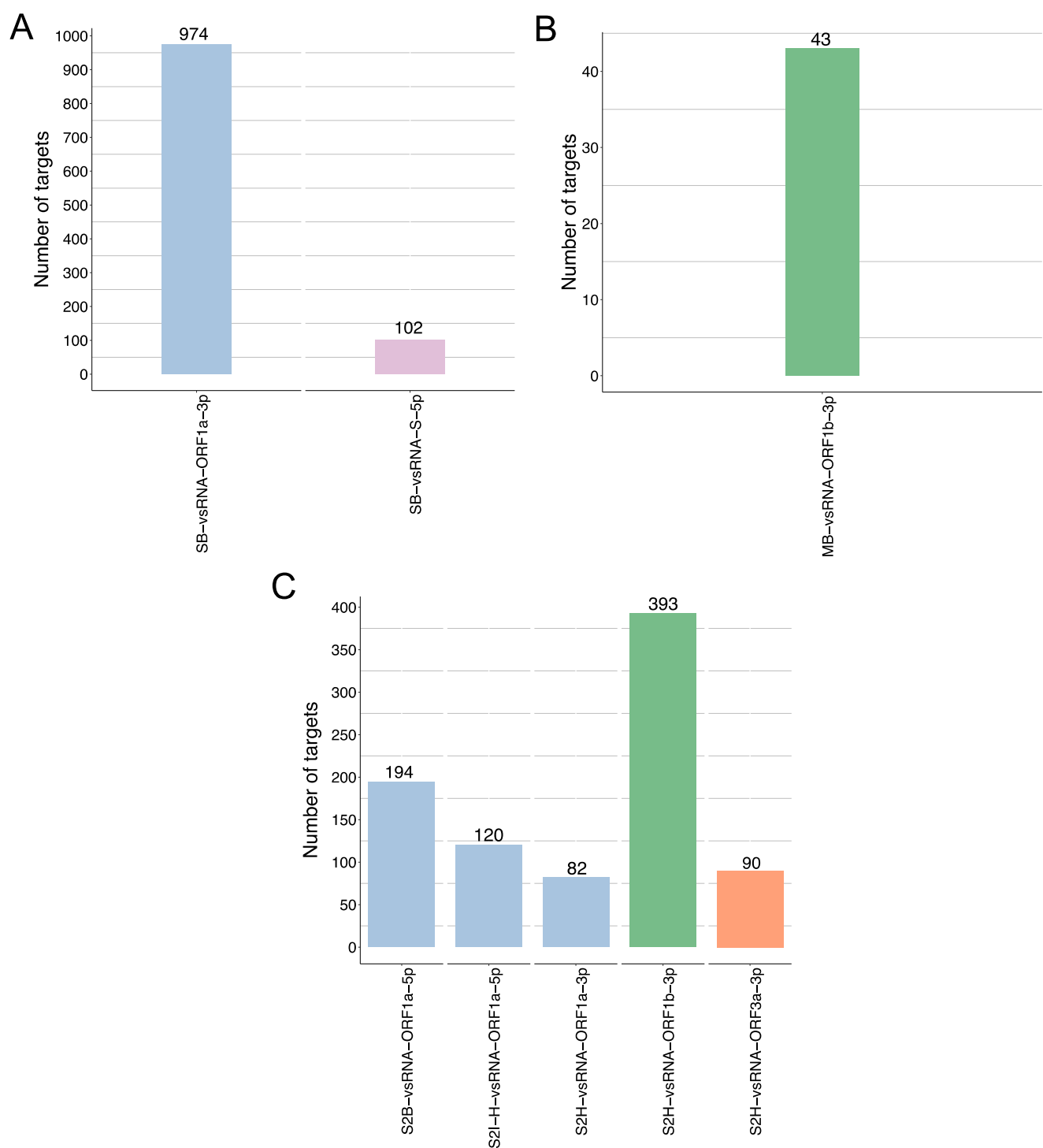


Figure S5. Number of predicted targets in the human genome for each vsRNA candidate in the three *Beta-CoVs*. **(A)** SARS-CoV encoded 2 vsRNAs registering 1076 targets; **(B)** MERS-CoV encoded 1 vsRNA showing 43 targets; and **(C)** SARS-CoV-2 with 5 vsRNAs obtained 879 human genes. Each vsRNA is colored given the detected ORF.