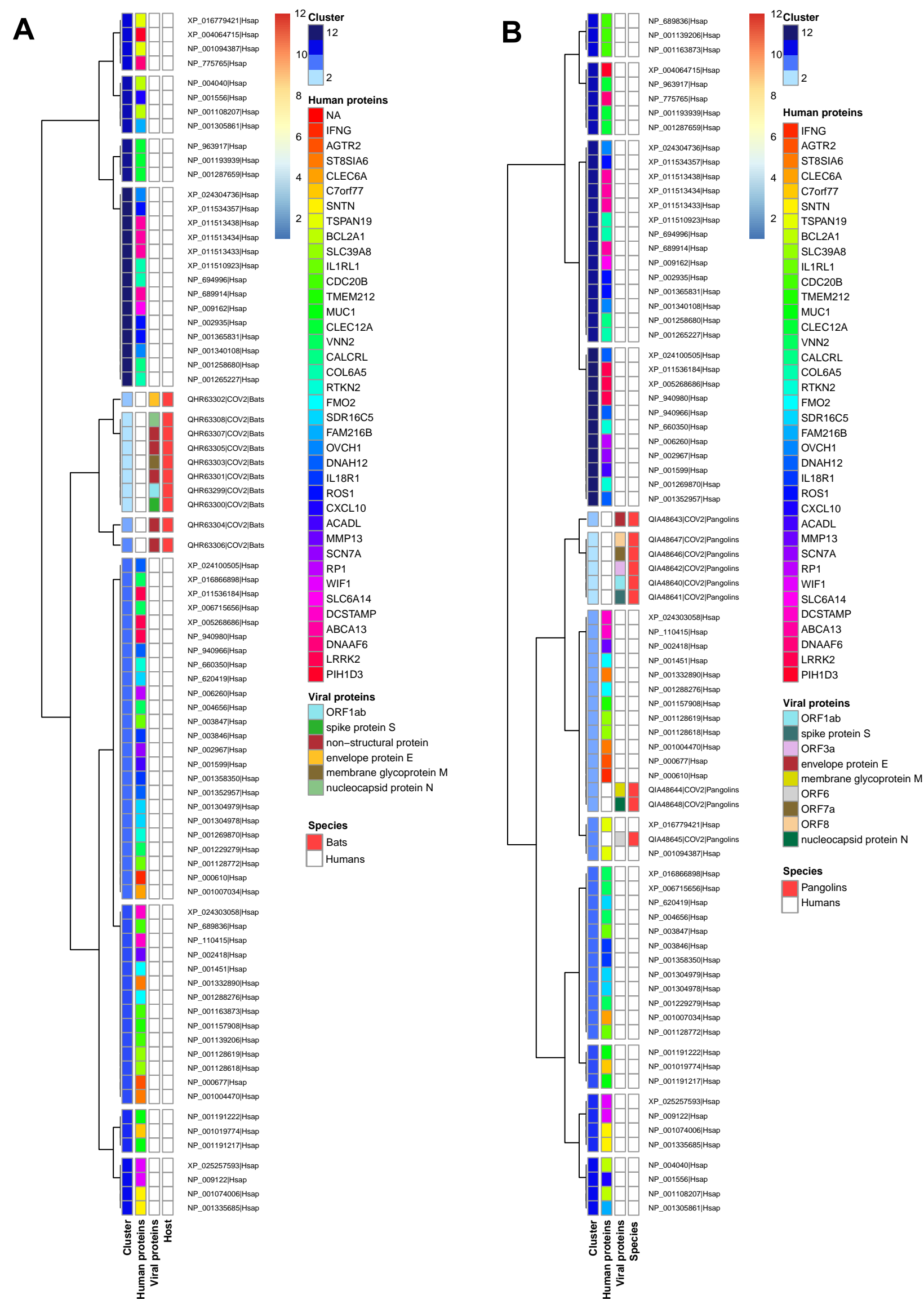


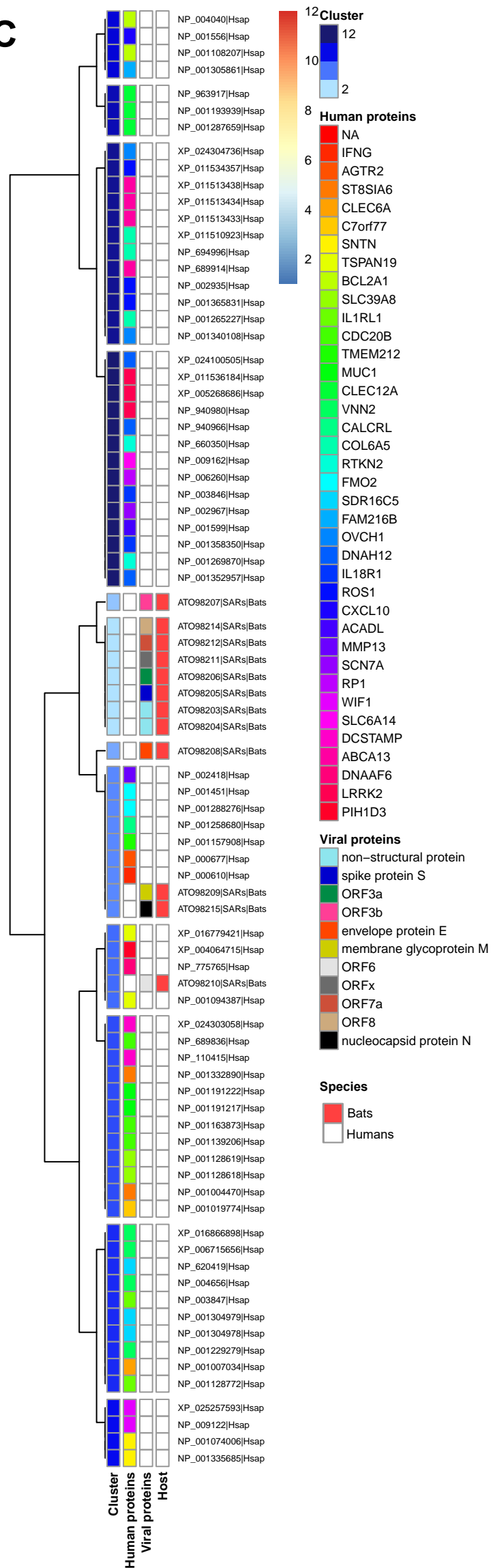
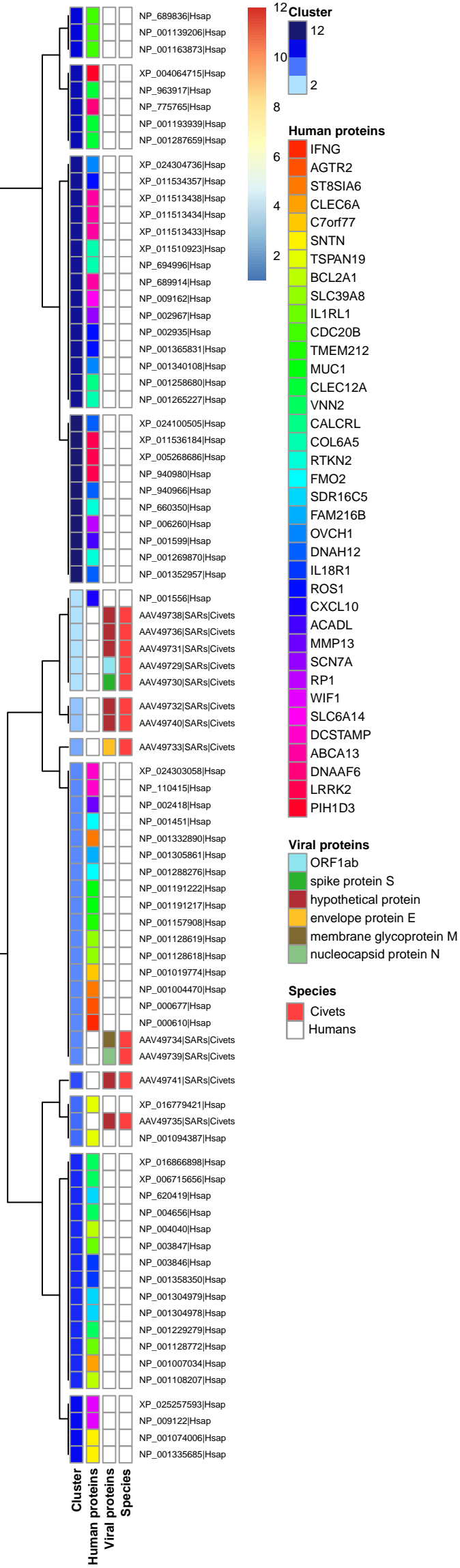
Molecular Features Similarities Between SARS-CoV-2, SARS, MERS and Key Human Genes Could Favour The Viral Infections and Trigger Collateral Effects

Authors: Lucas L. Maldonado*; Andrea Mendoza Bertelli and Laura Kamenetzky

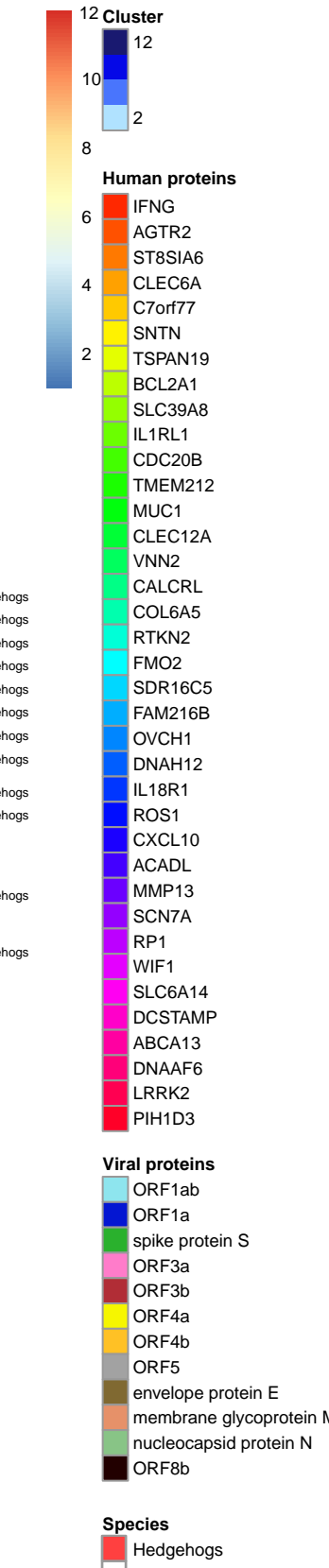
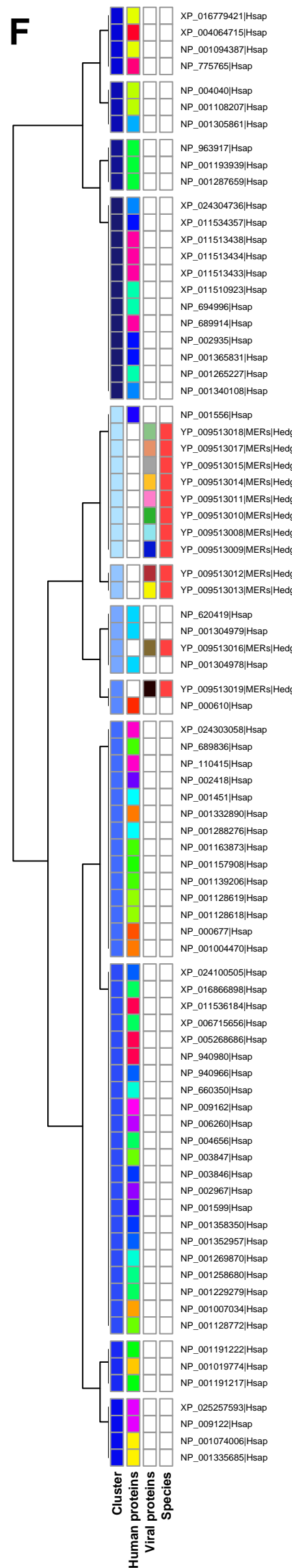
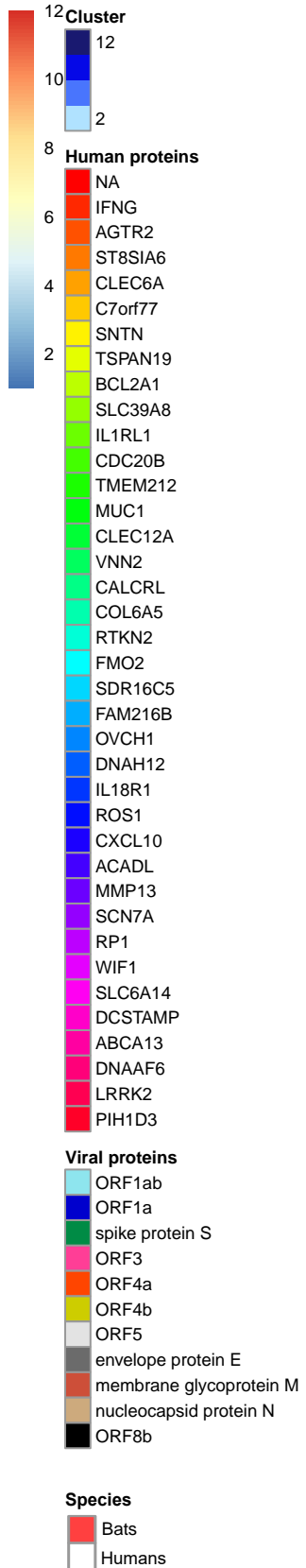
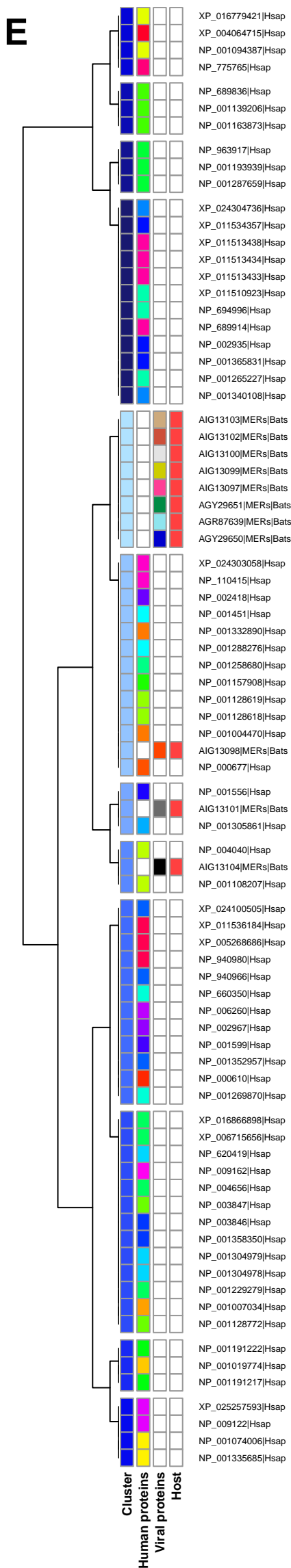


Supplementary file 7: Control clustering based on the molecular features and codon usage patterns using the viral genes of the viruses coming from their animal hosts (bats, pangolins, civets and hedgehogs) and the 70 overexpressed human genes of lungs tissue that grouped with the viral genes of the humans SARS-CoV-2, SARS and MERS using a hierarchical method and bootstrapping.

A). gene clustering of the bat virus SARs-CoV-2-like (MN996532) and 70 overexpressed human genes of lungs tissue. B). gene clustering of the pangolin virus SARS-CoV-2-like (MT040336) and 70 overexpressed human genes of lungs tissue. C). gene clustering of the bat virus SARS-like (KY417150) and 70 overexpressed human genes of lungs tissue. D). gene clustering of the civets virus SARS-like (AY686864) and 70 overexpressed human genes of lungs tissue. E). gene clustering of the bat virus MERs-like (KC869678) and 70 overexpressed human genes of lungs tissue. F). gene clustering of the hedgehogs virus MERS-like (NC_039207) and 70 overexpressed human genes of lungs tissue. G.i). Overexpressed human genes of lung tissues that grouped with SARS-CoV-2, SARS and MERS of humans and animals. Significant differences of groups and counts of human genes are showed according to human and animal hosts in colour or black. The differences observed were statistically tested using the chi-square test. G.ii). Gene clustering of SARS-CoV-2 and under-expressed human genes in lung tissues. G.iii). Gene clustering of SARS and under-expressed human genes in lung tissues. G.iv). Gene clustering of MERS and under-expressed human genes in lung tissues.

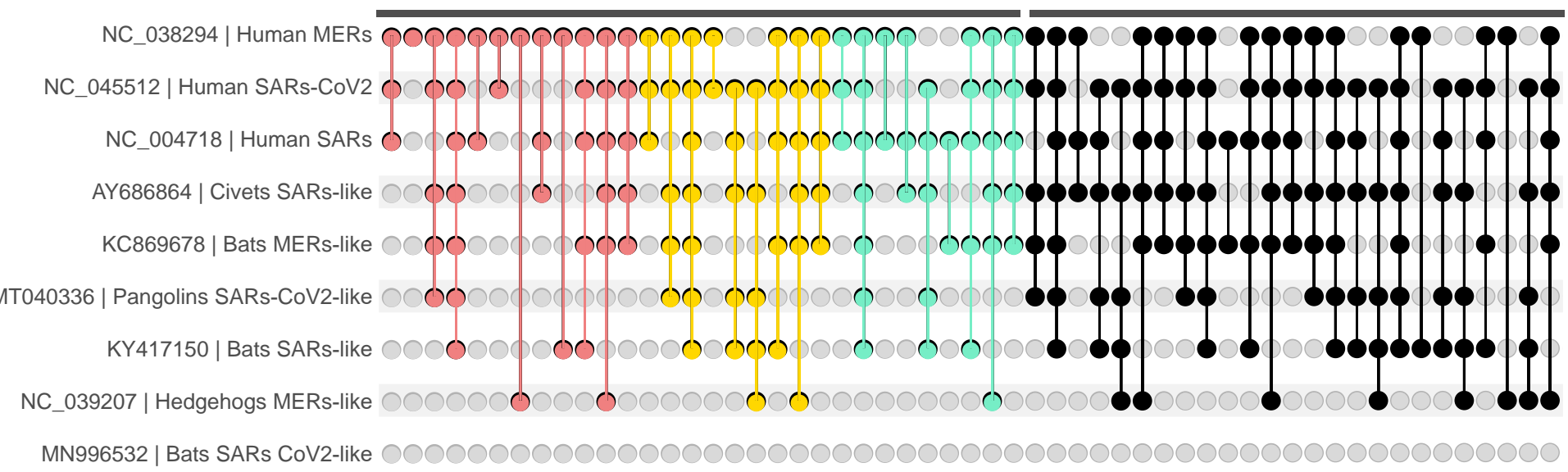
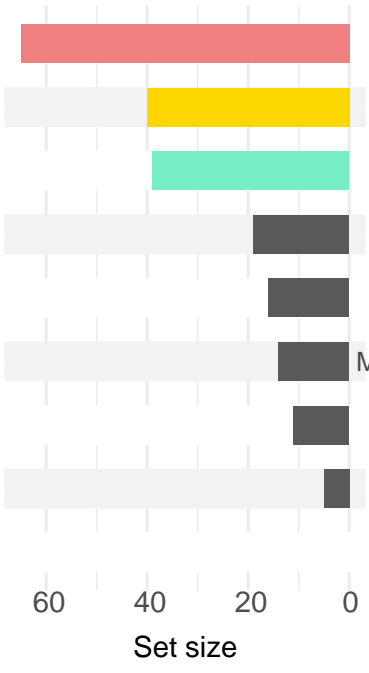
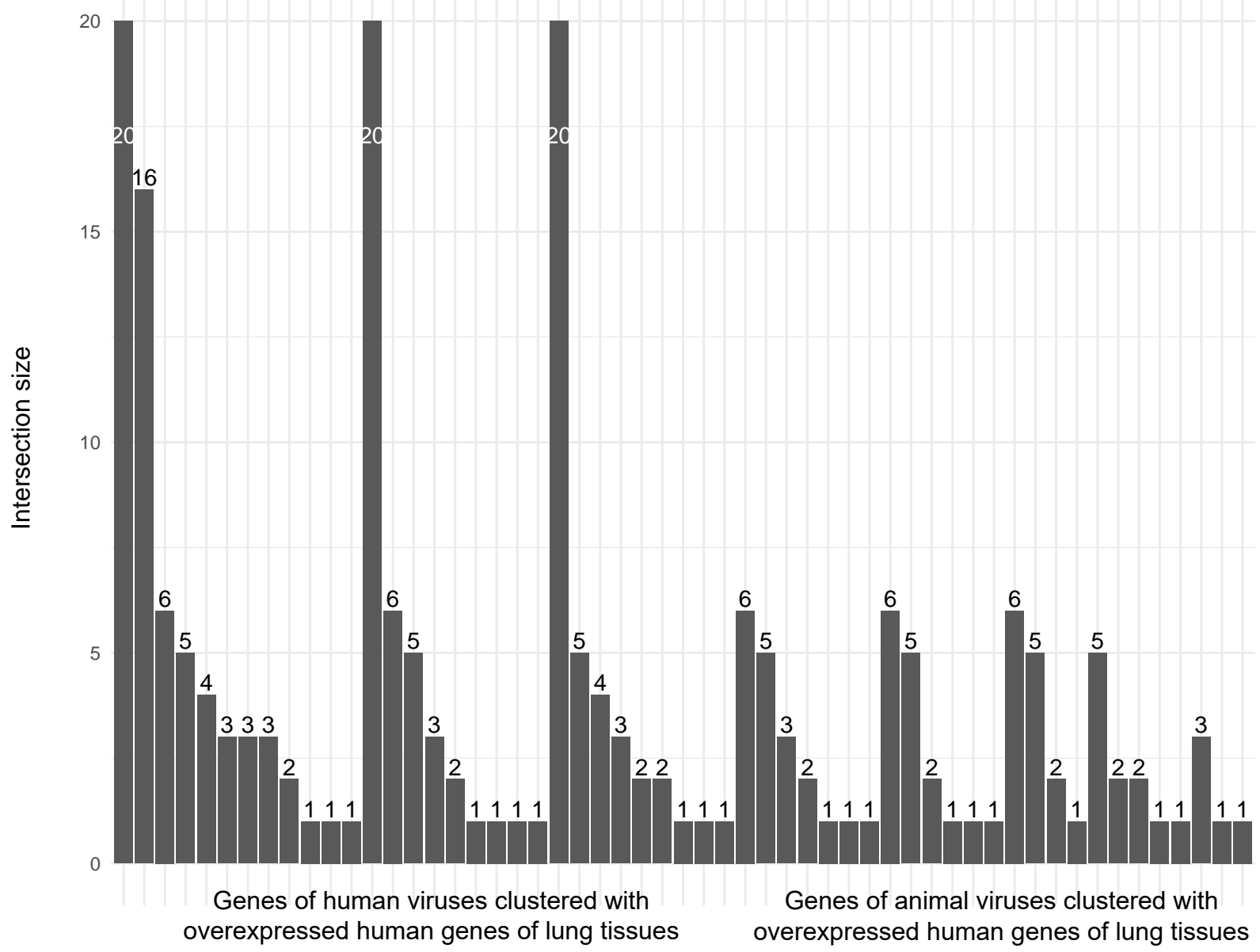
C**D**

H.i). under-expressed human genes of lung tissues that grouped with SARS-CoV-2, SARS and MERS of humans and animals. Significant differences of groups and counts of human genes are showed according to human and animal hosts in colour or black. The differences observed were statistically tested using the chi-square test. H.ii). gene clustering of the bat virus SARs-CoV-2-like (MN996532) and 66 under-expressed human genes of lungs tissue. H.iii). gene clustering of the pangolin virus SARS-CoV-2-like (MT040336) and 66 under-expressed human genes of lungs tissue. H.iv). gene clustering of the bat virus SARS-like (KY417150) and 66 under-expressed human genes of lungs tissue. H.v). gene clustering of the civets virus SARS-like (AY686864) and 66 under-expressed human genes of lungs tissue. H.vi). gene clustering of the bat virus MERs-like (KC869678) and 66 under-expressed human genes of lungs tissue. H.vii). gene clustering of the hedgehogs virus MERS-like (NC_039207) and 66 under-expressed human genes of lungs tissue.



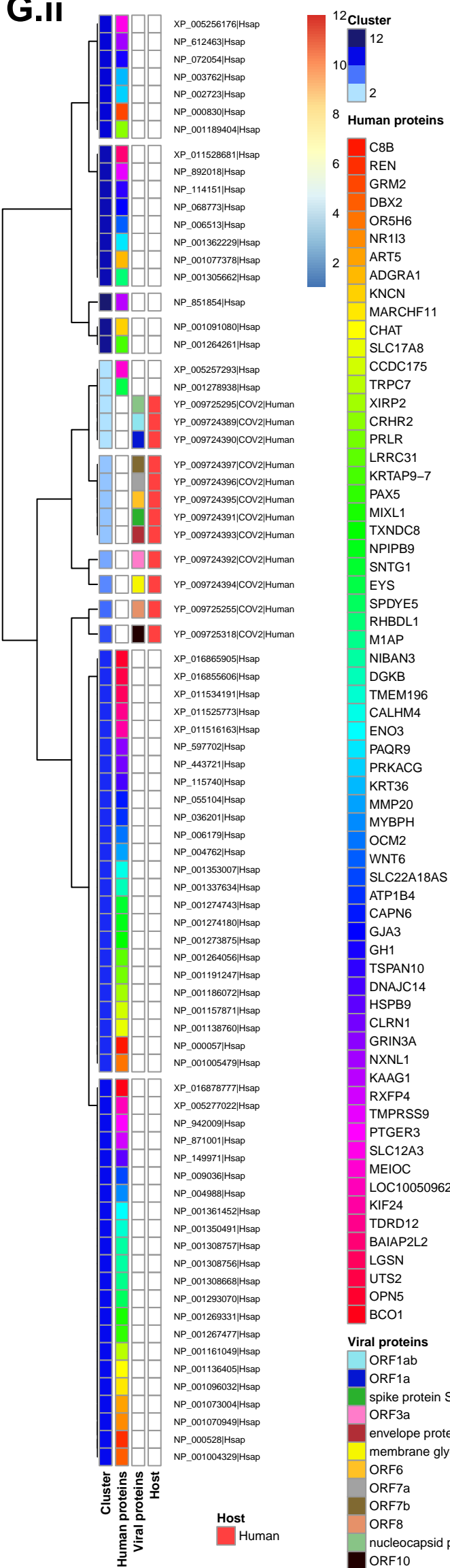
G.i

Overexpressed human genes of lung tissues that grouped with SARS-CoV-2, SARS and MERS of humans and animals. Significant differences of groups and counts of human genes are showed according to human and animal hosts in color or black. The differences observed were statistically tested using the chi-square test:

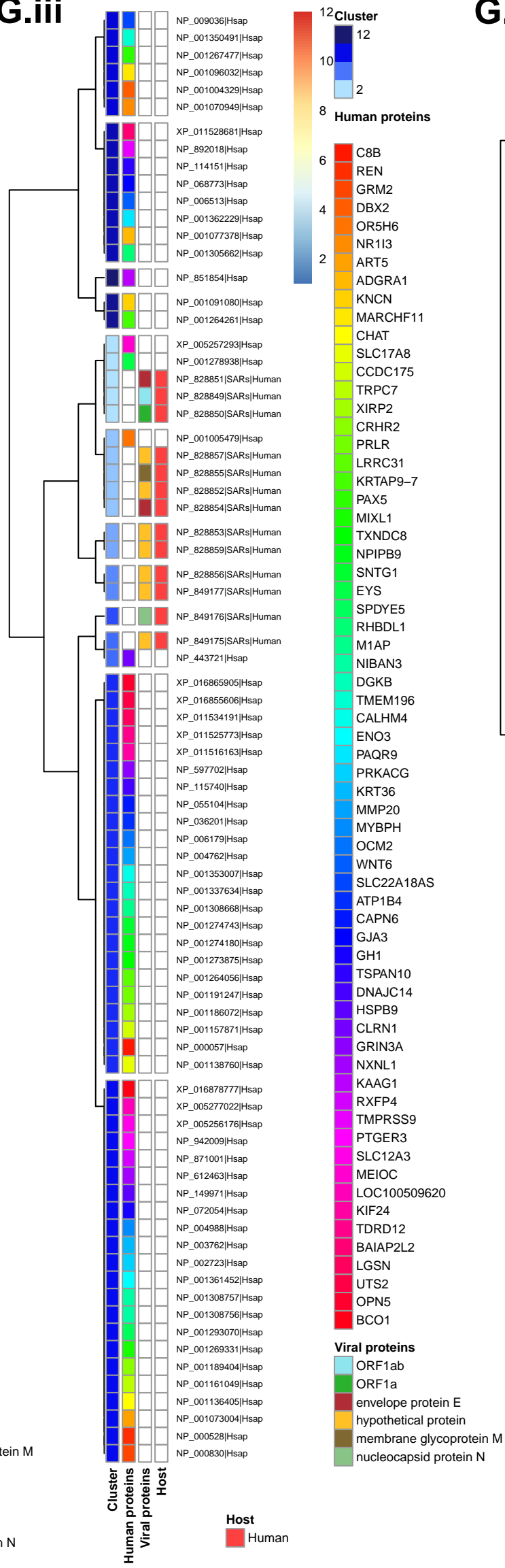


Human SARS-CoV-2 vs animal SARS-CoV-2-like (p-value = $1.039e^{-15}$). Human SARS vs animal SARS-like (p-value = $2.35e^{-12}$). Human MERS vs animal MERS-like (p-value = $6.5e^{-13}$). Differences among all the groups (p-value = $2.9e^{-09}$). Chi-square test - Kruskal-Wallis rank sum test and corrected FDR

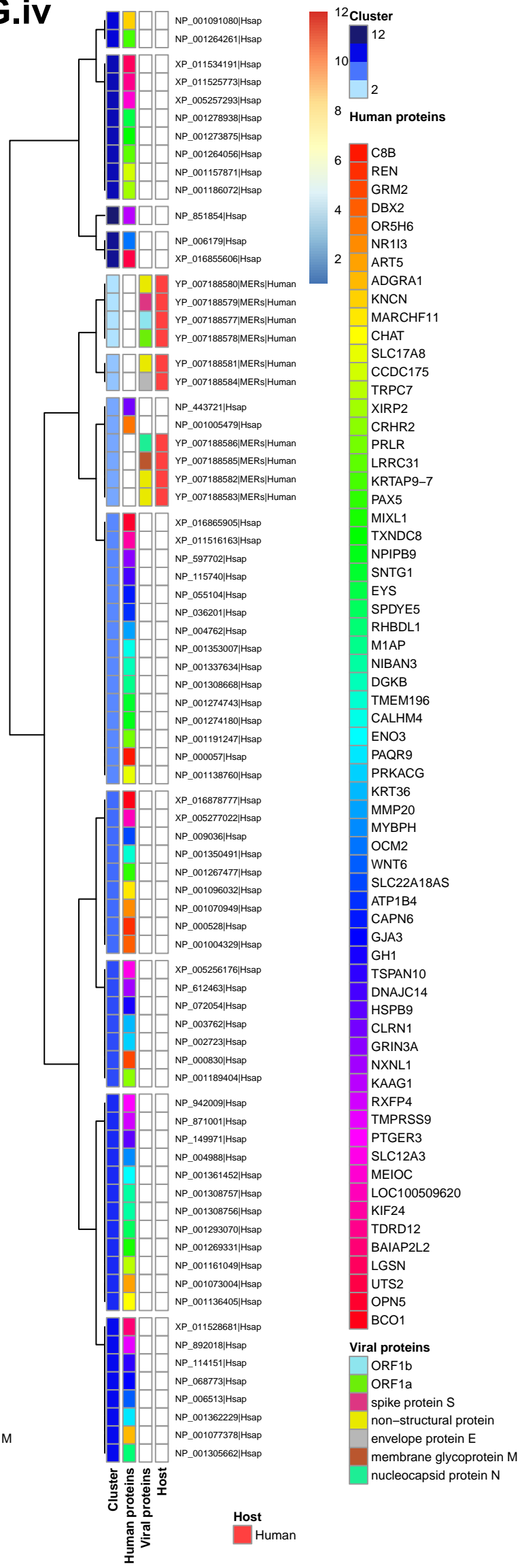
G.ii



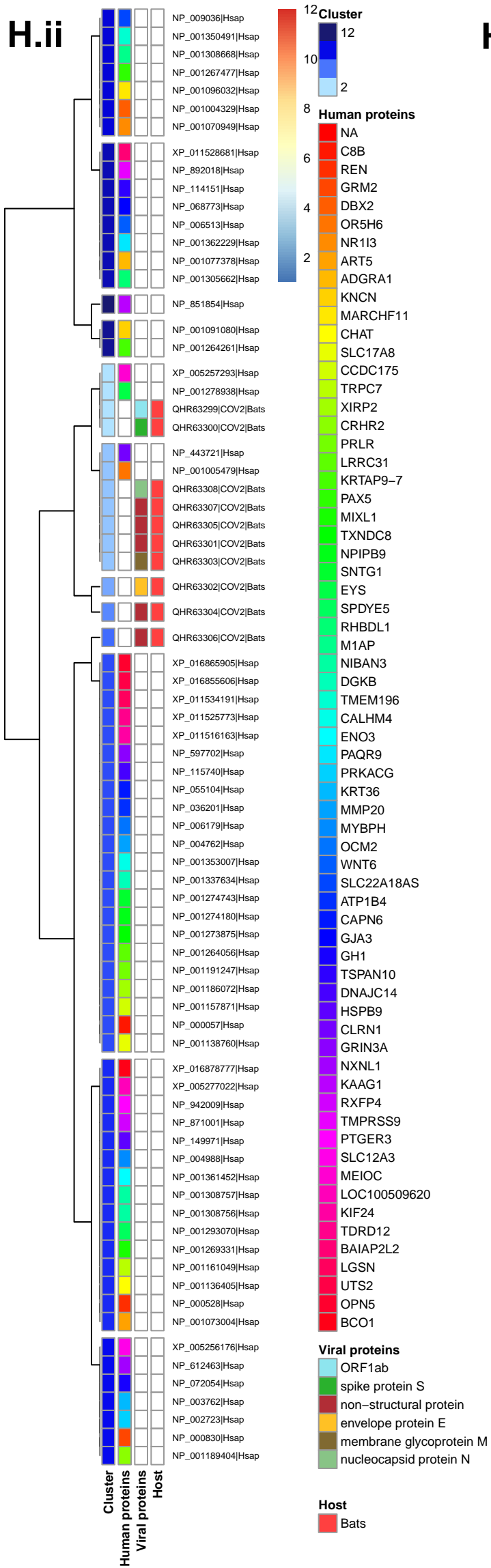
G.iii



G.iv



H.ii



H.iii

