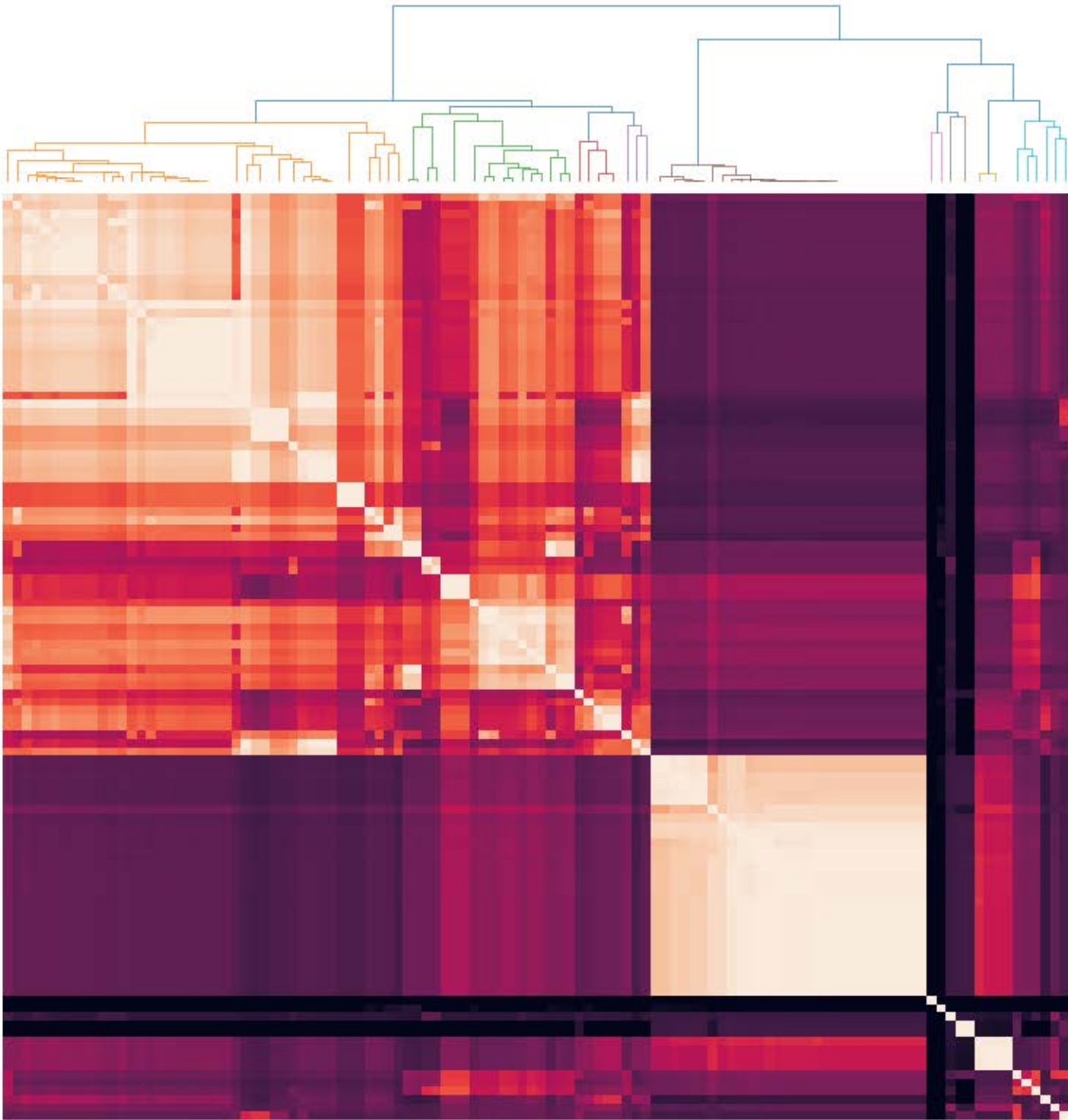
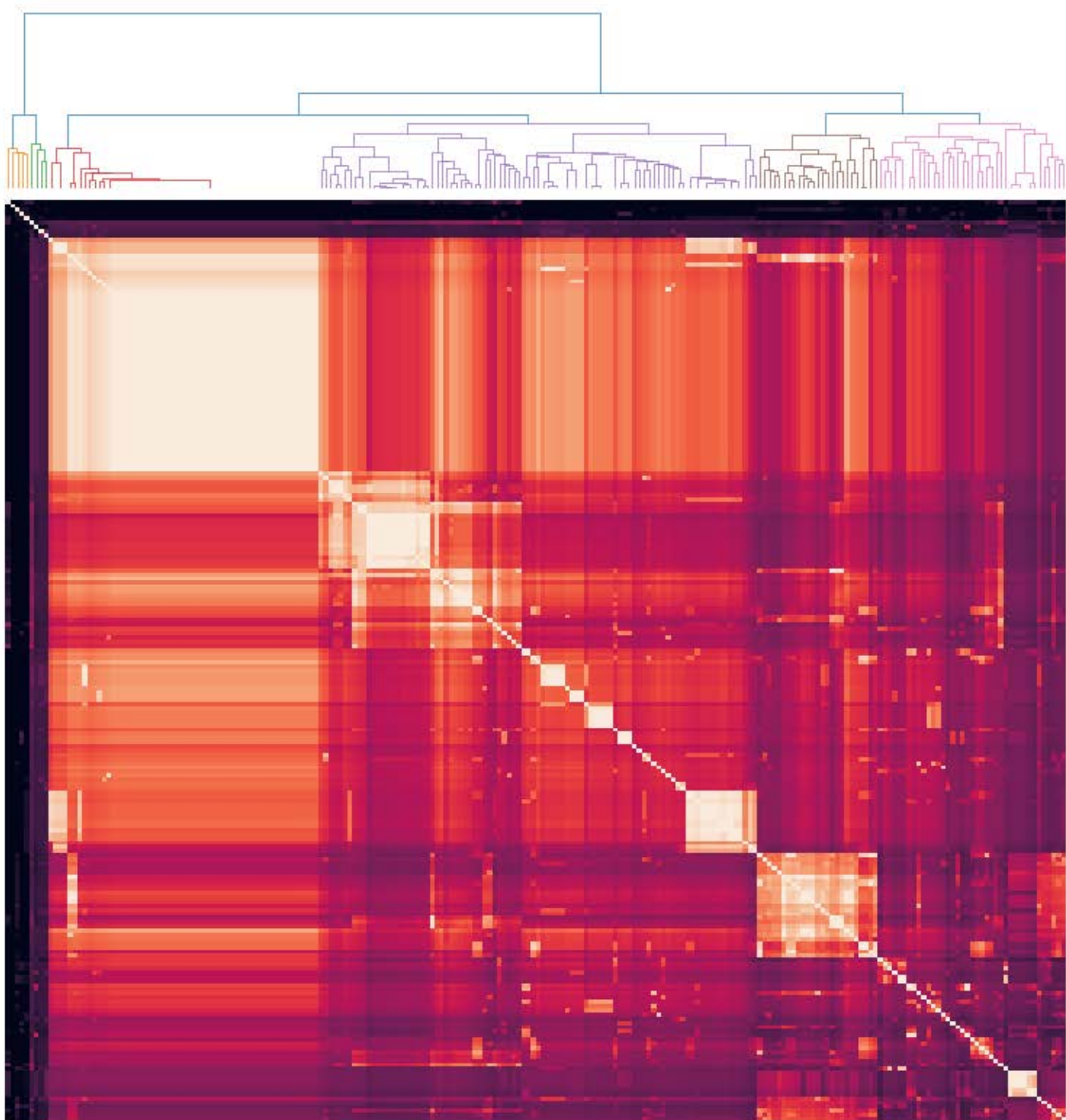


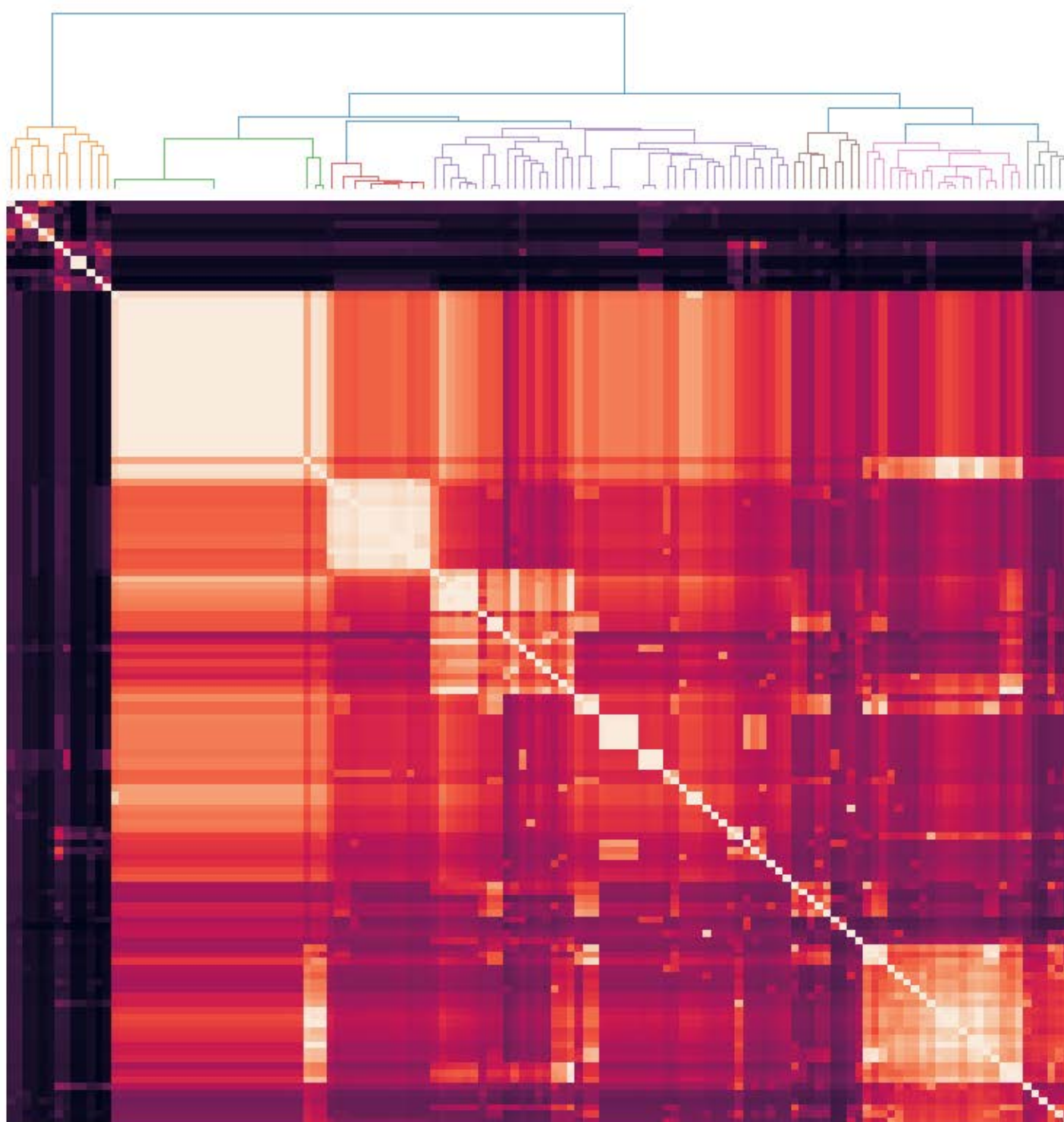
Human coronavirus 229E strains ZDNABERT



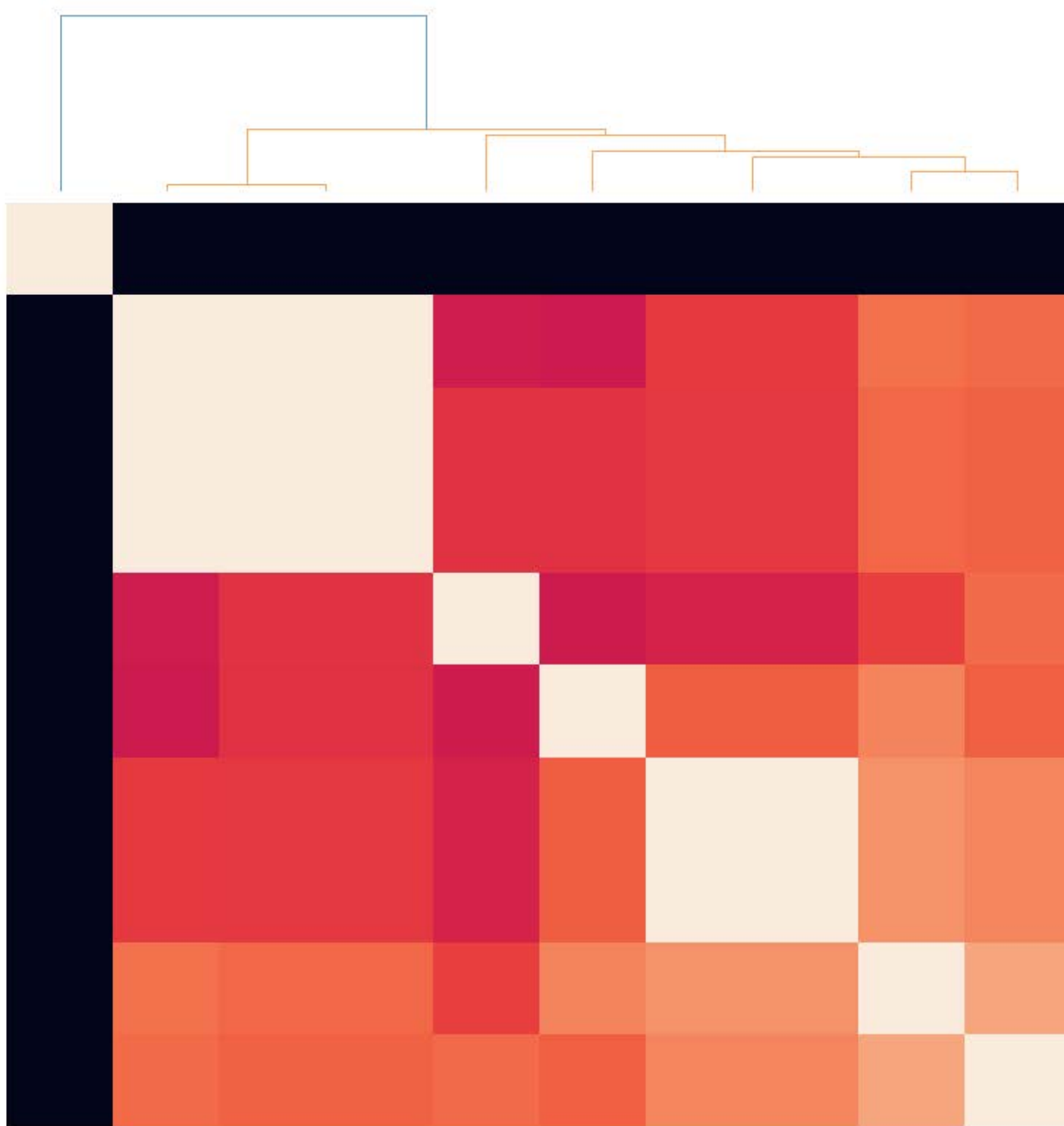
Alphacoronavirus 1



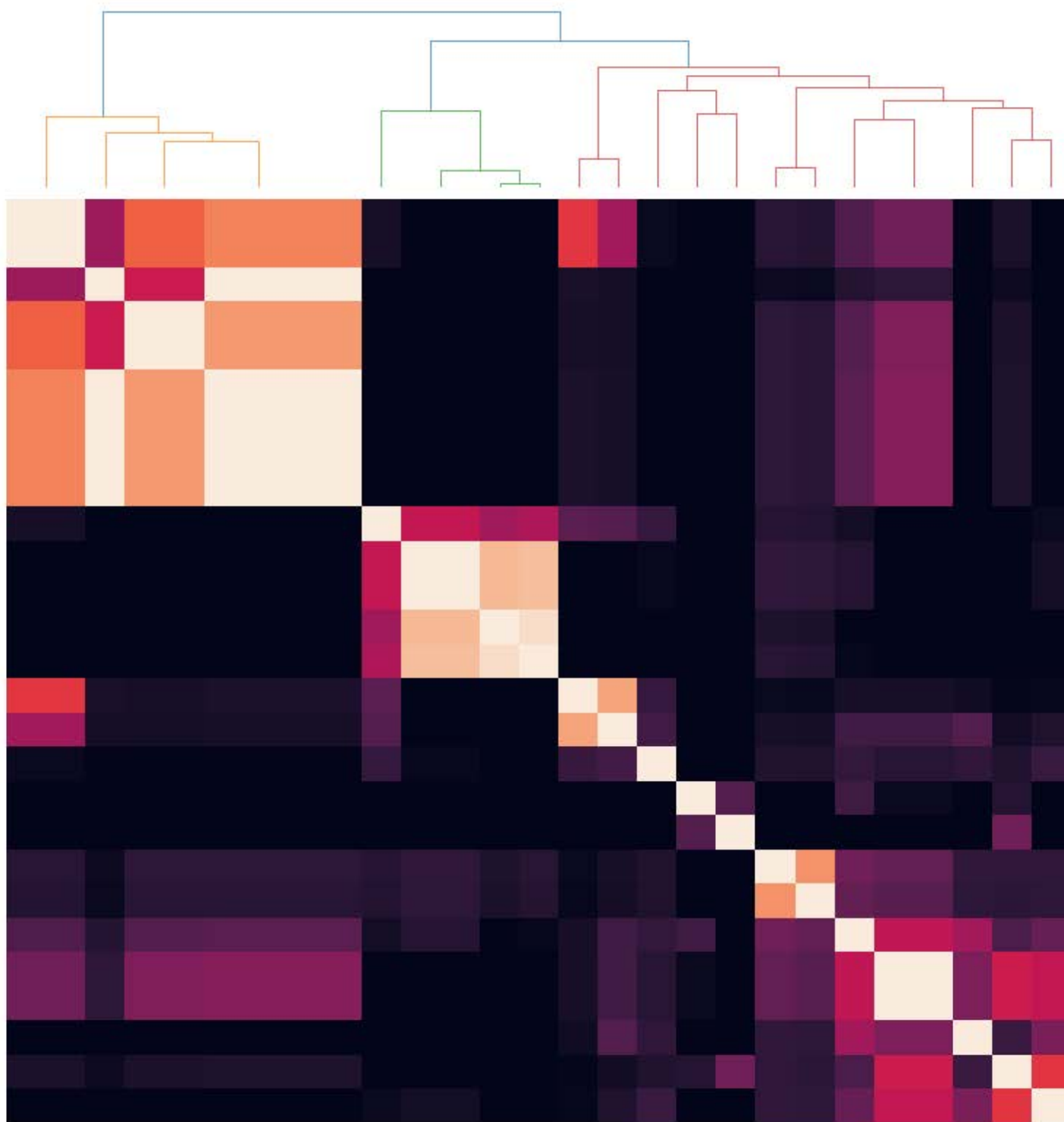
Alphacoronavirus AMALF



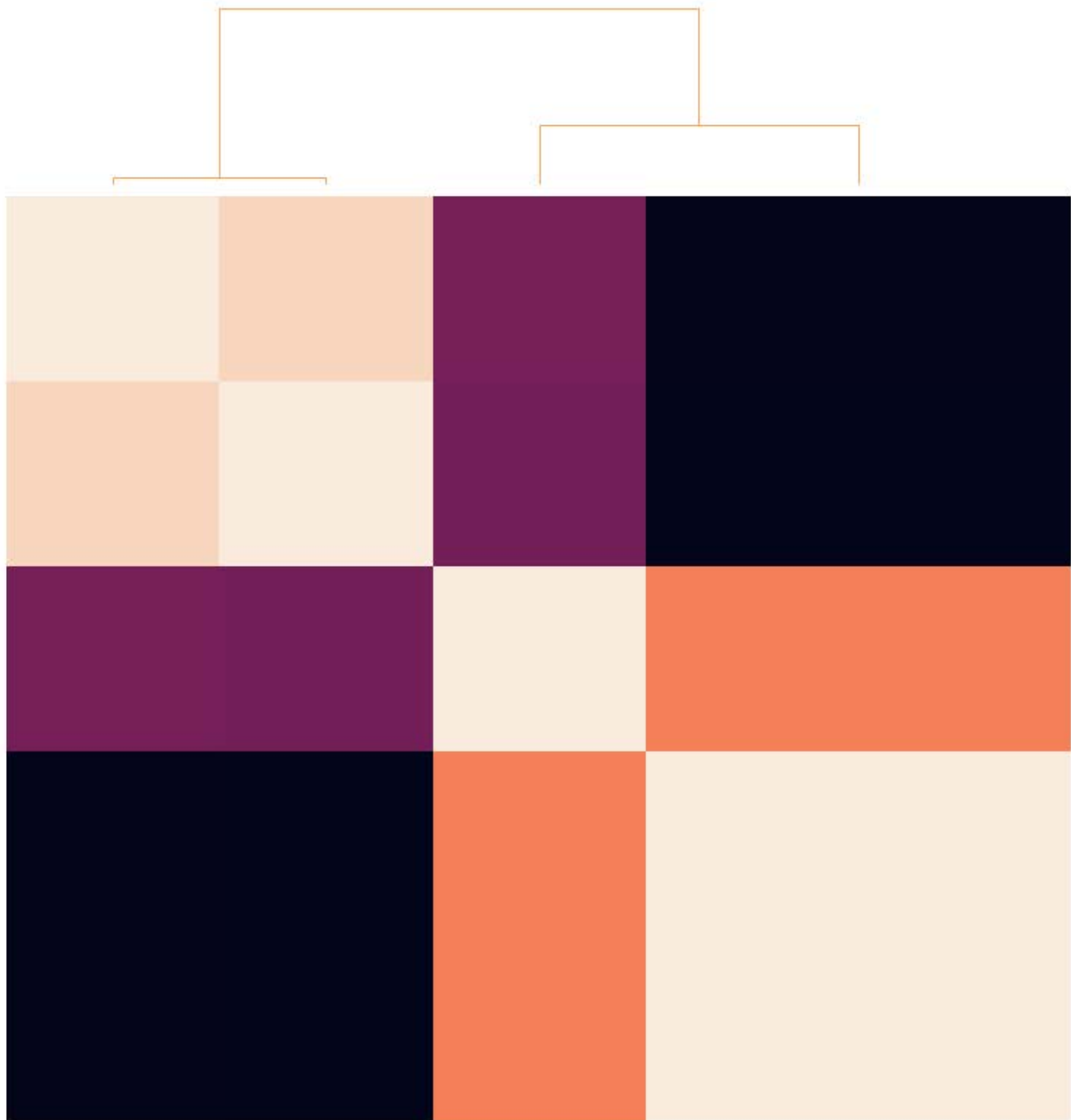
Alphacoronavirus CHB25



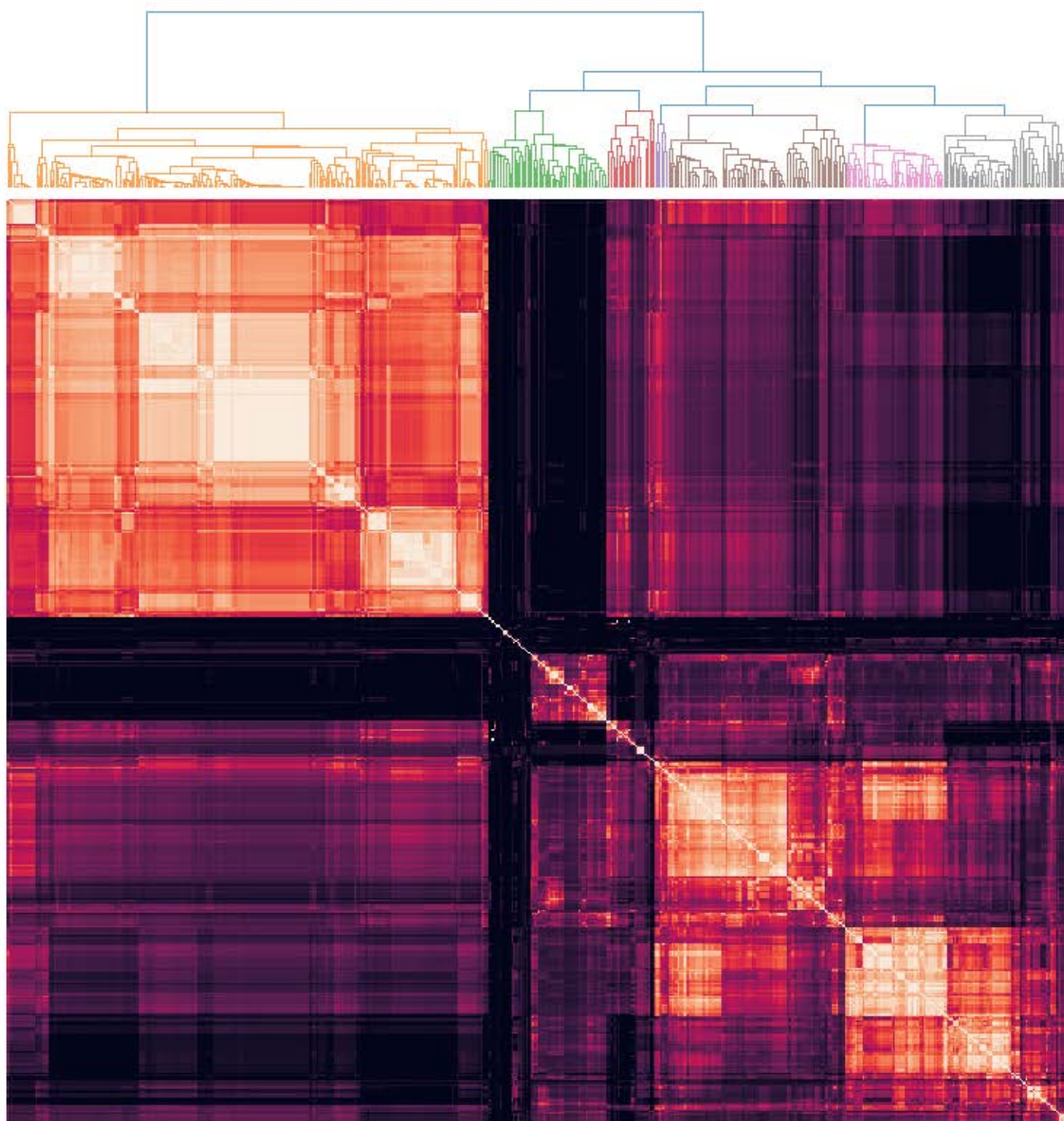
Bat coronavirus HKU10



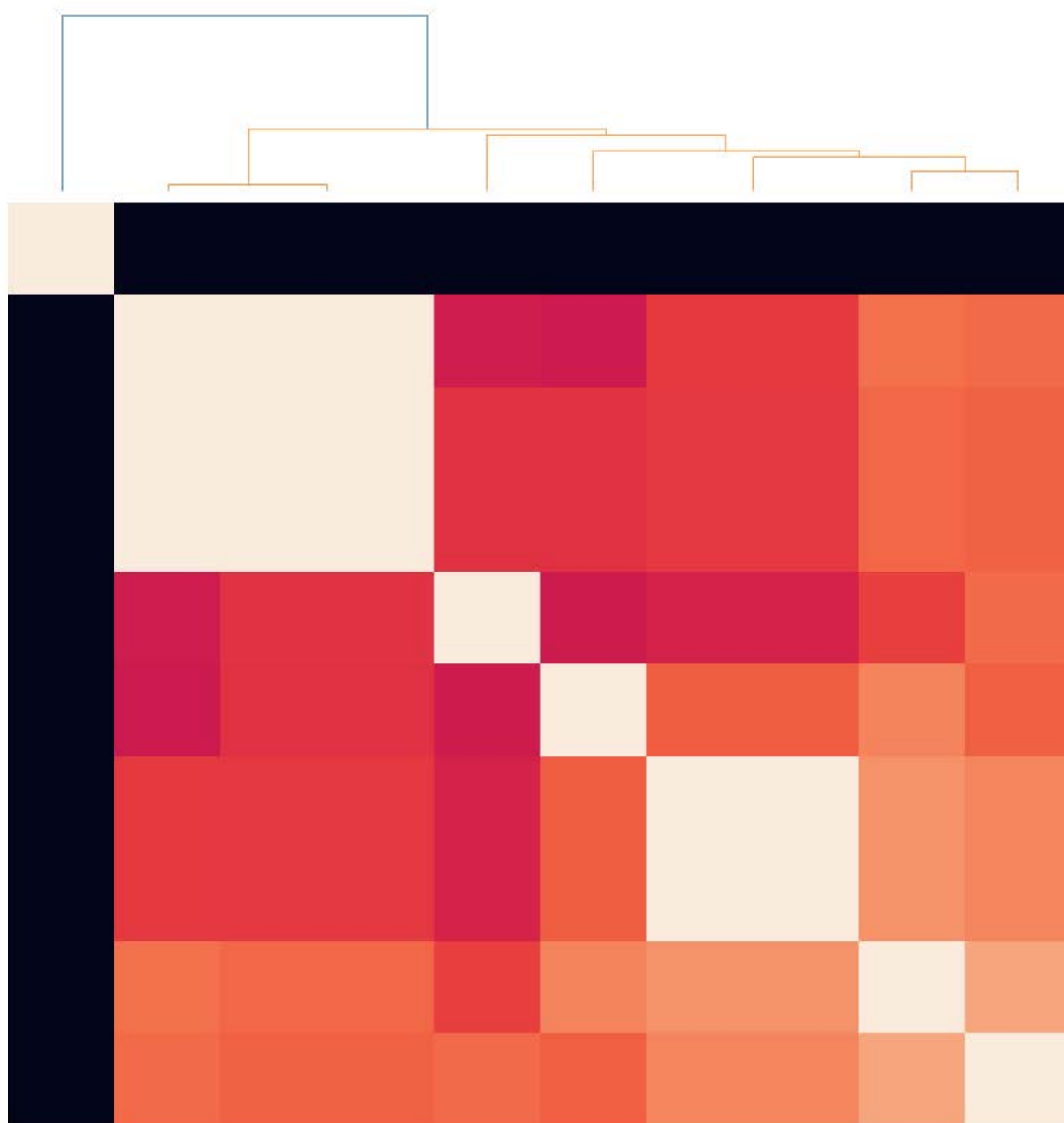
Beluga whale coronavirus SW1



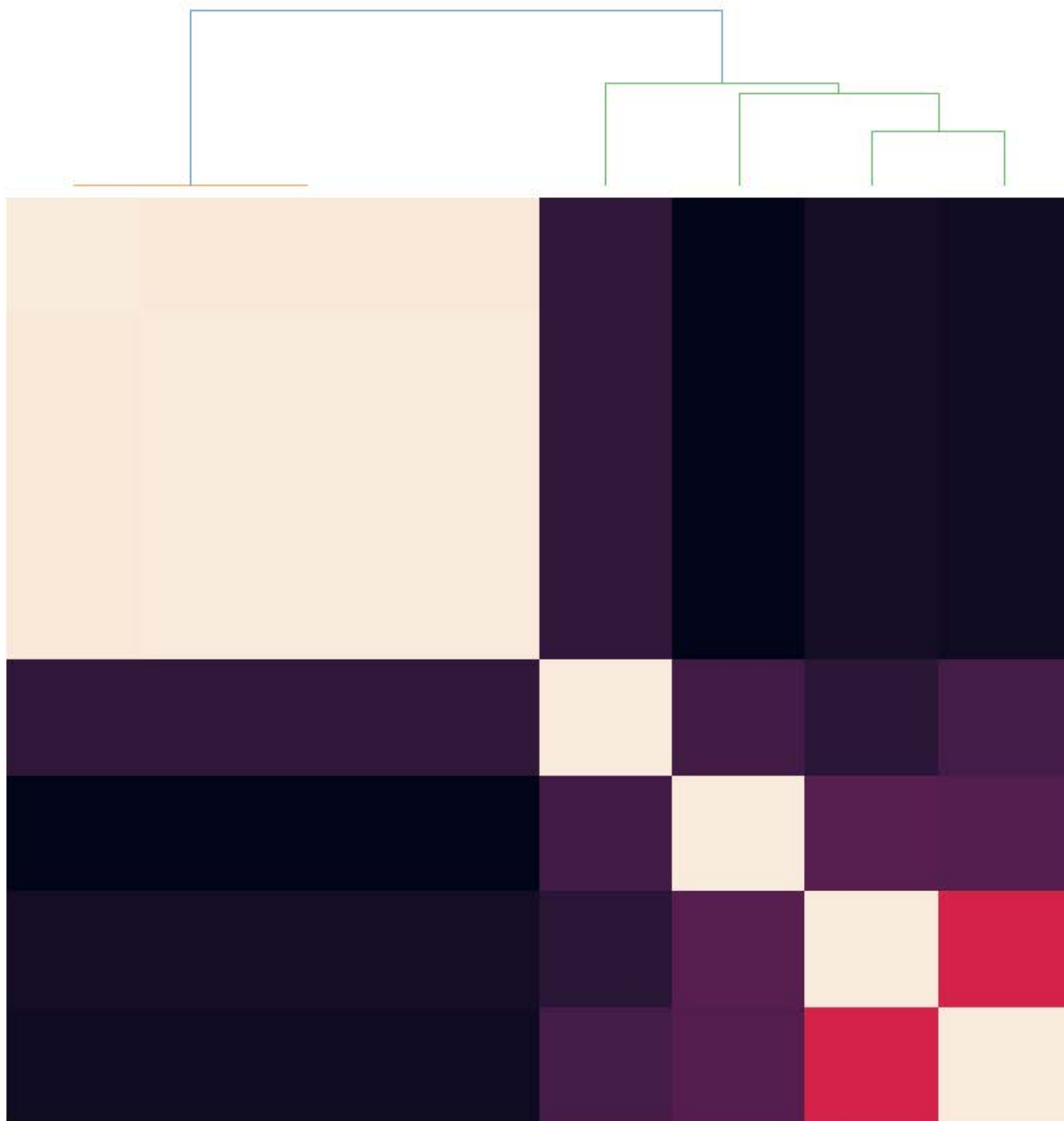
Betacoronavirus 1



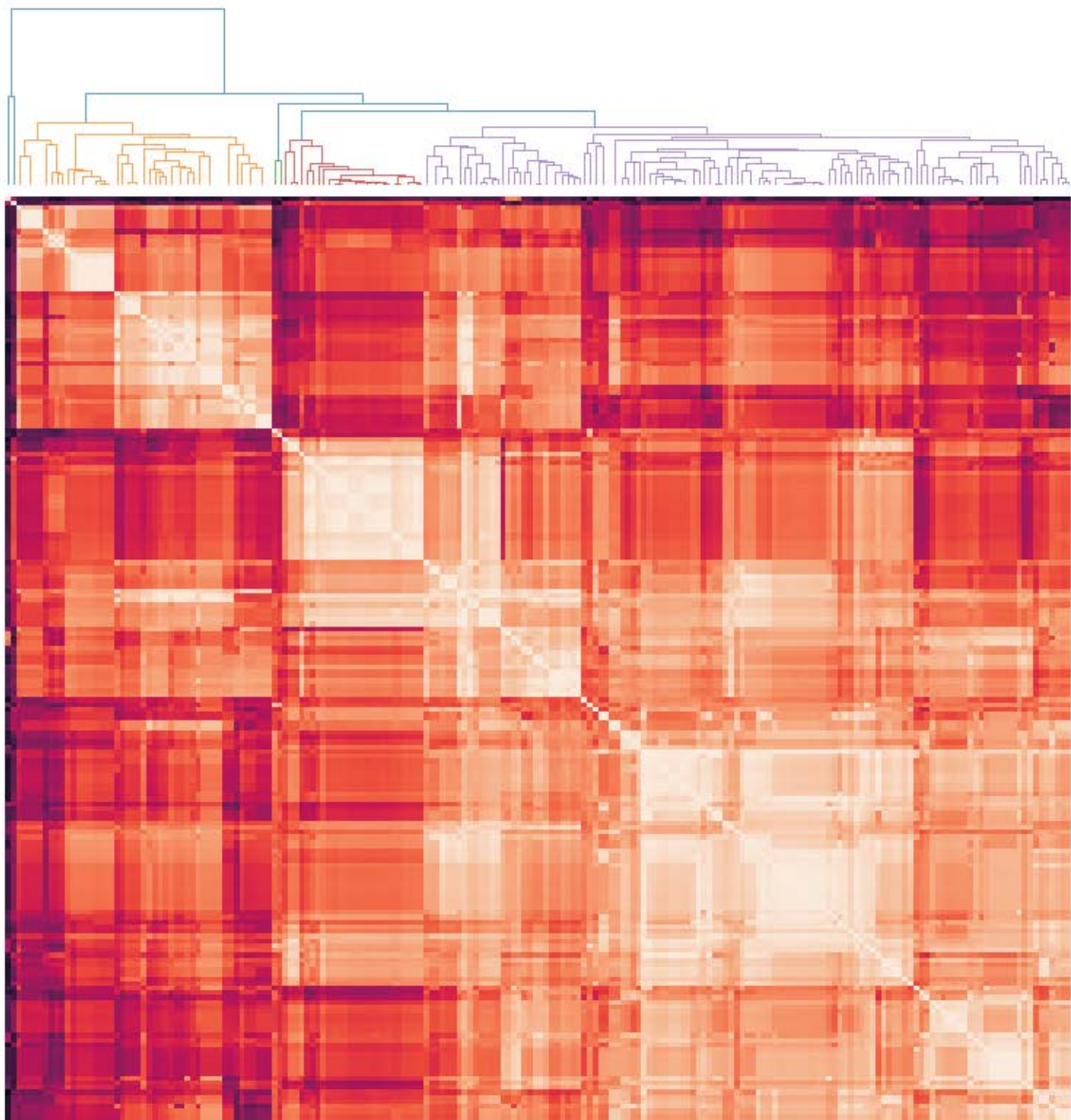
Bulbul coronavirus HKU11



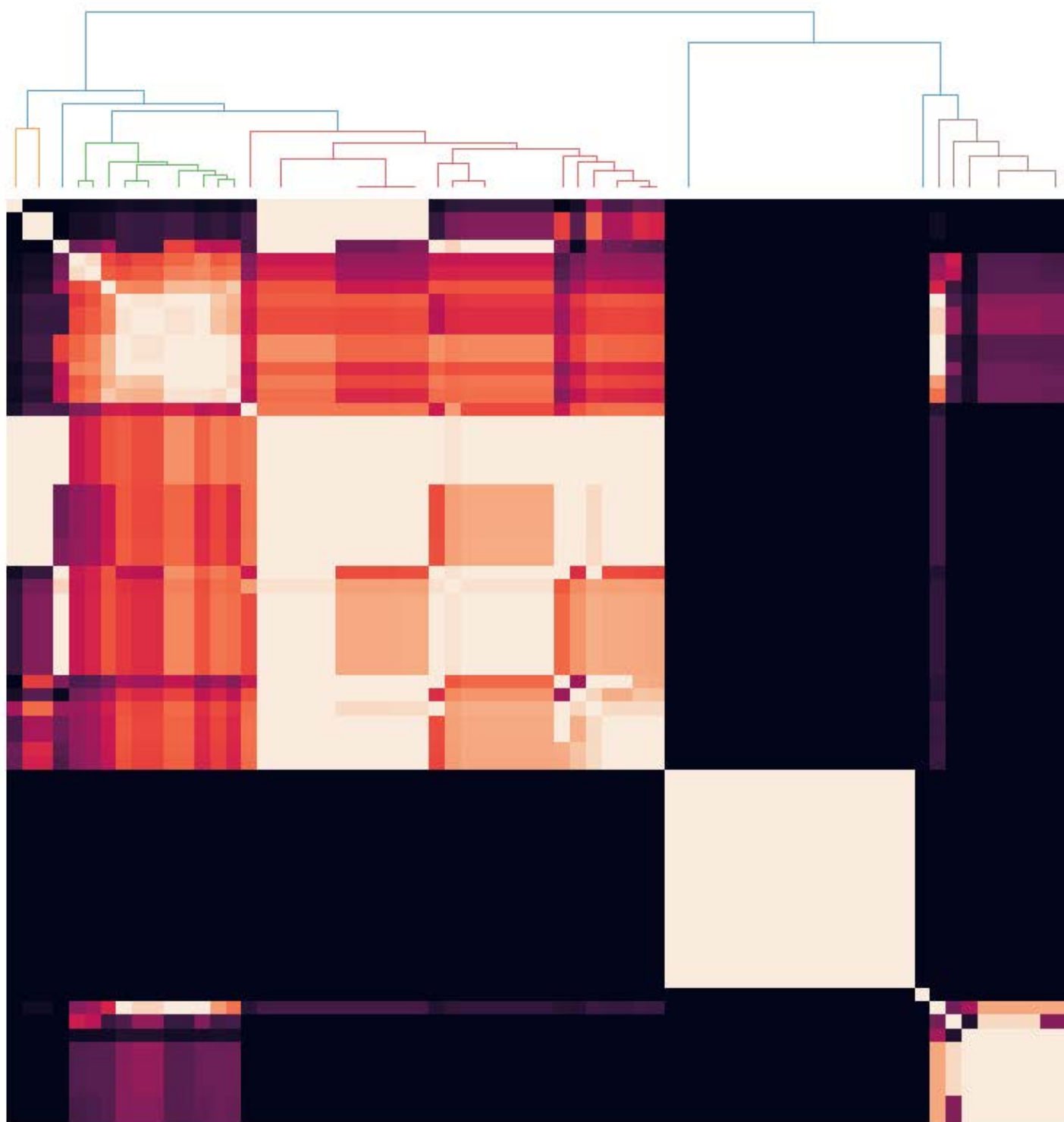
China Rattus coronavirus HKU24



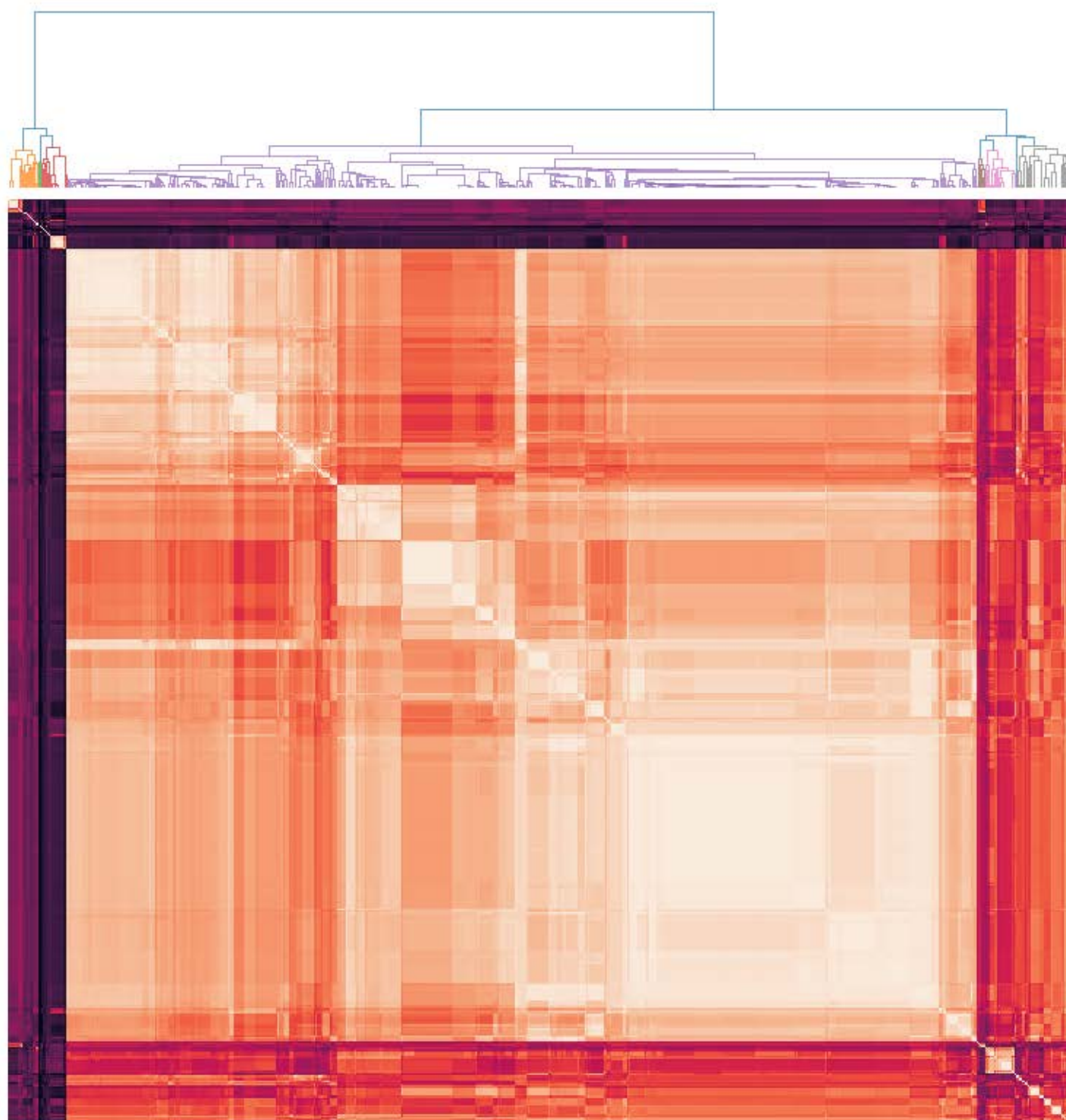
Coronavirus HKU15



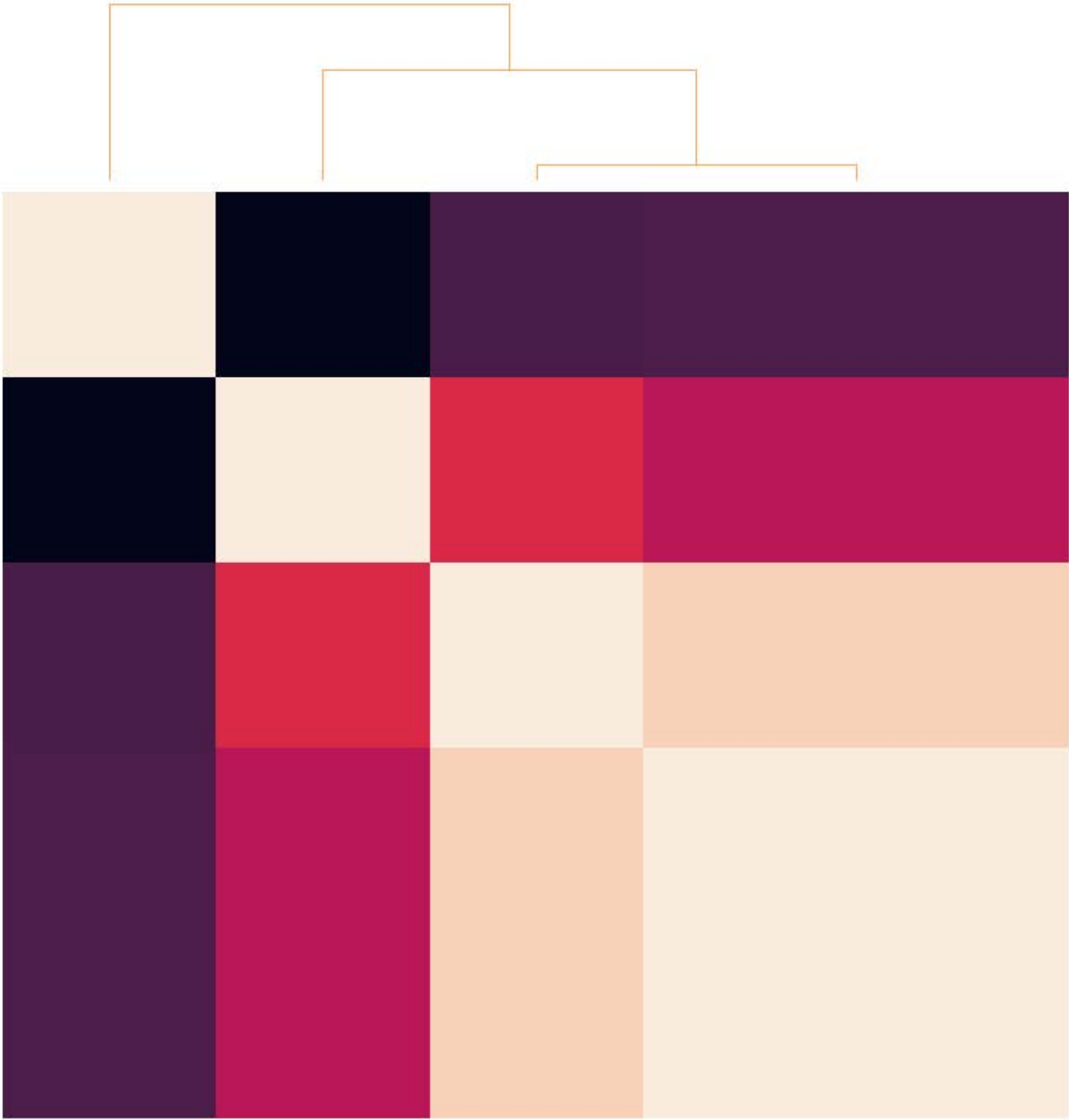
Human coronavirus HKU1 strains ZDNABERT



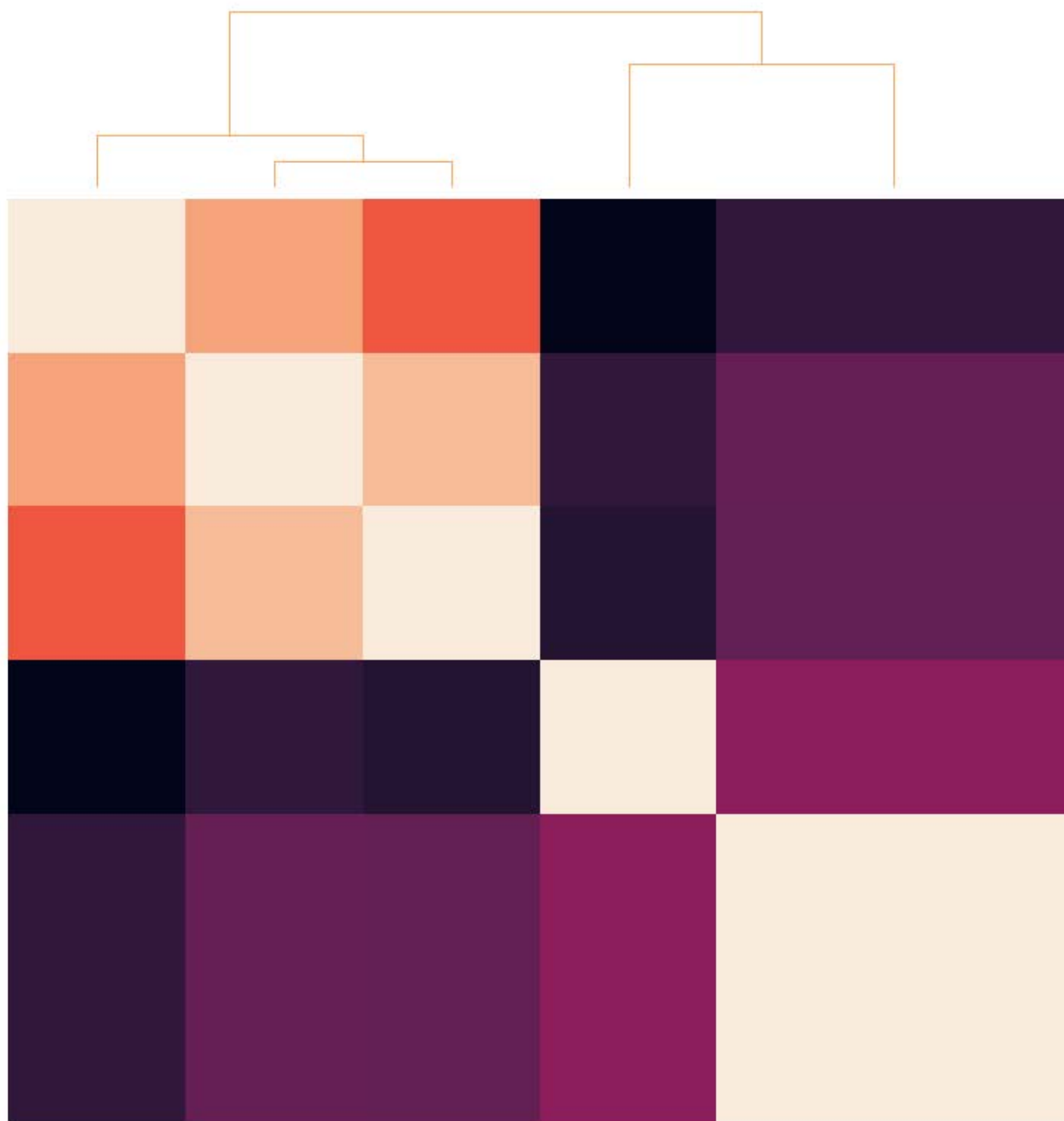
MERS strains ZDNABERT



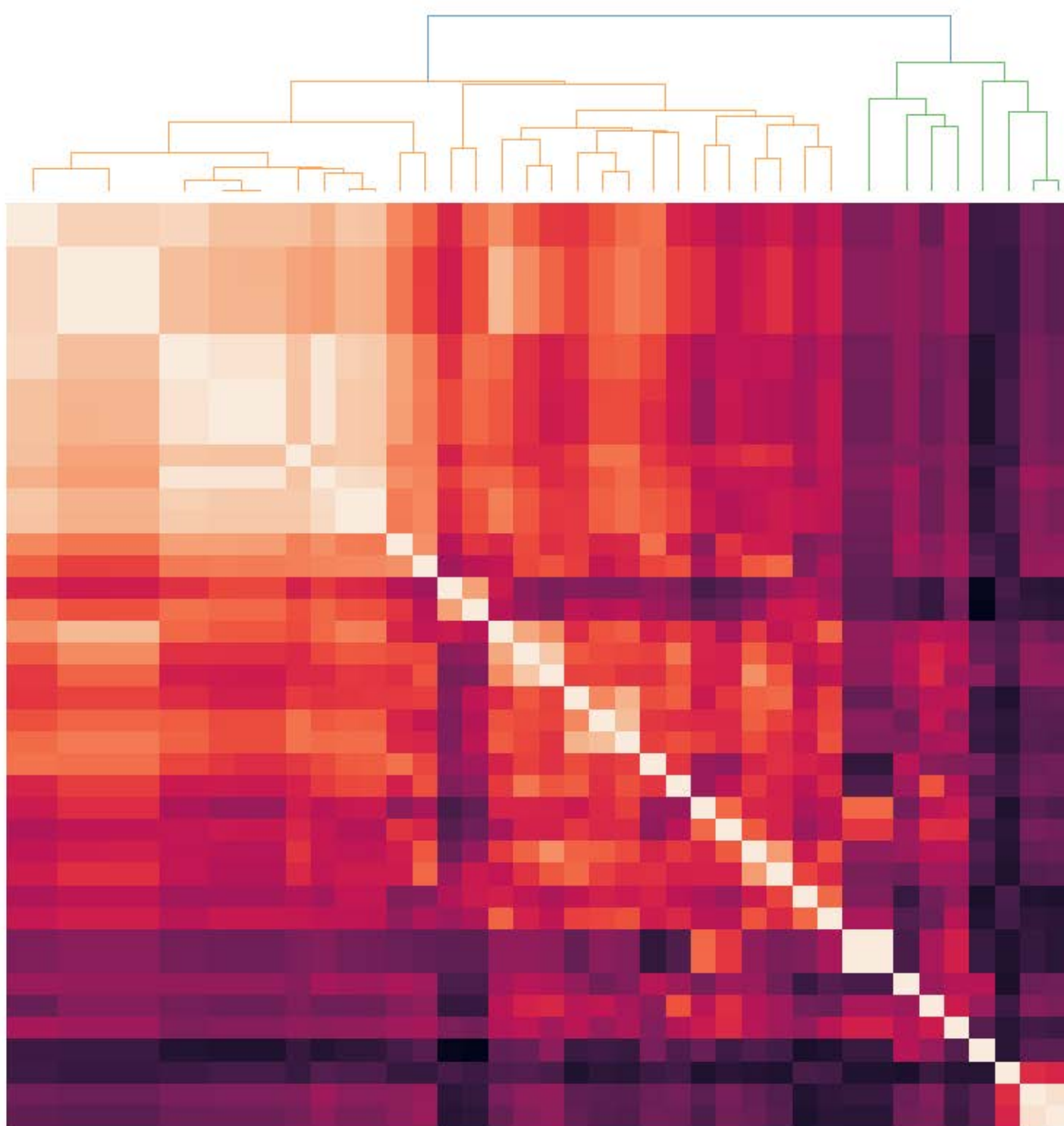
Miniopterus bat coronavirus 1



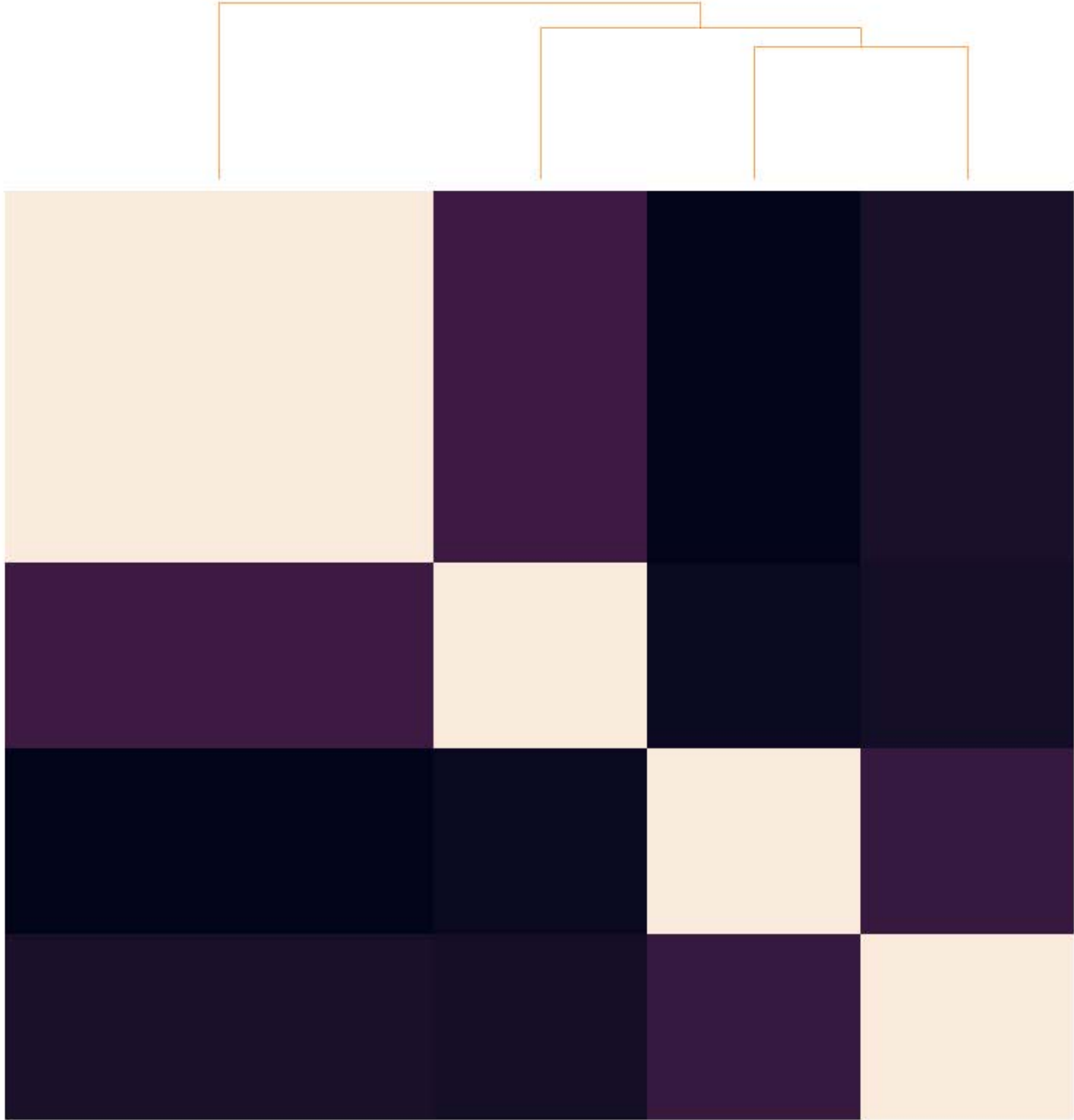
Miniopterus bat coronavirus HKU8



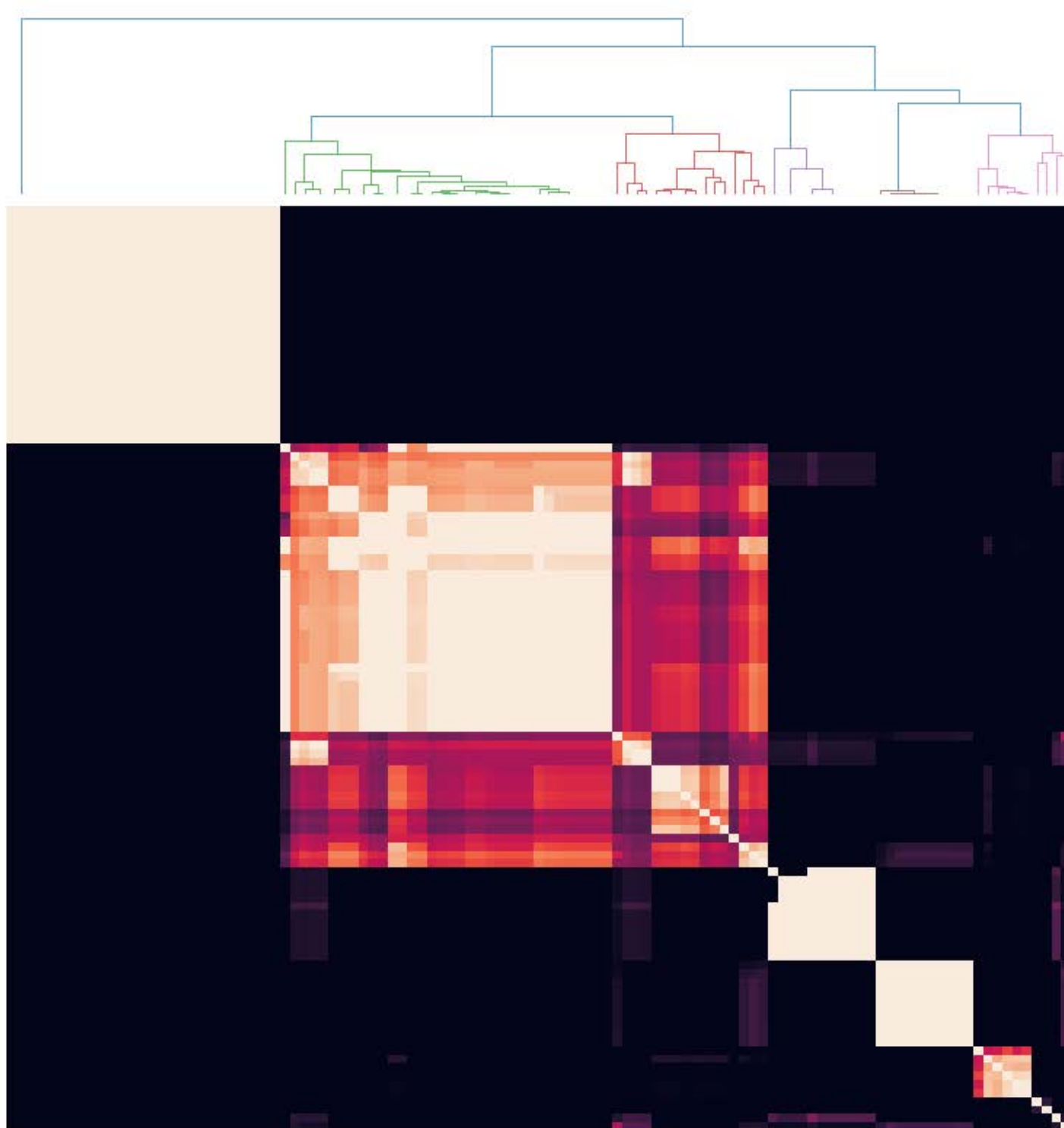
Murine coronavirus



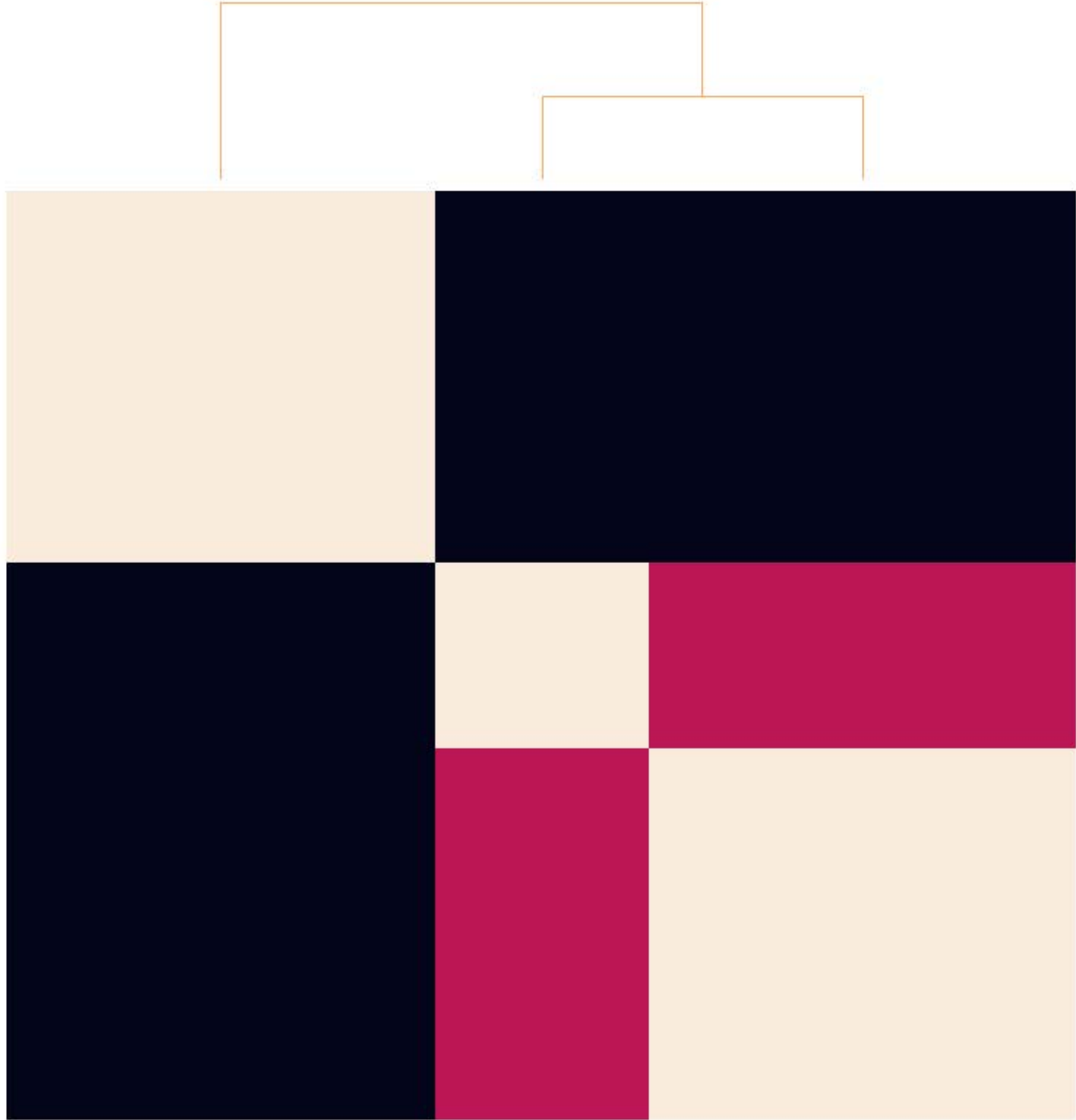
Myodes coronavirus 2JL14



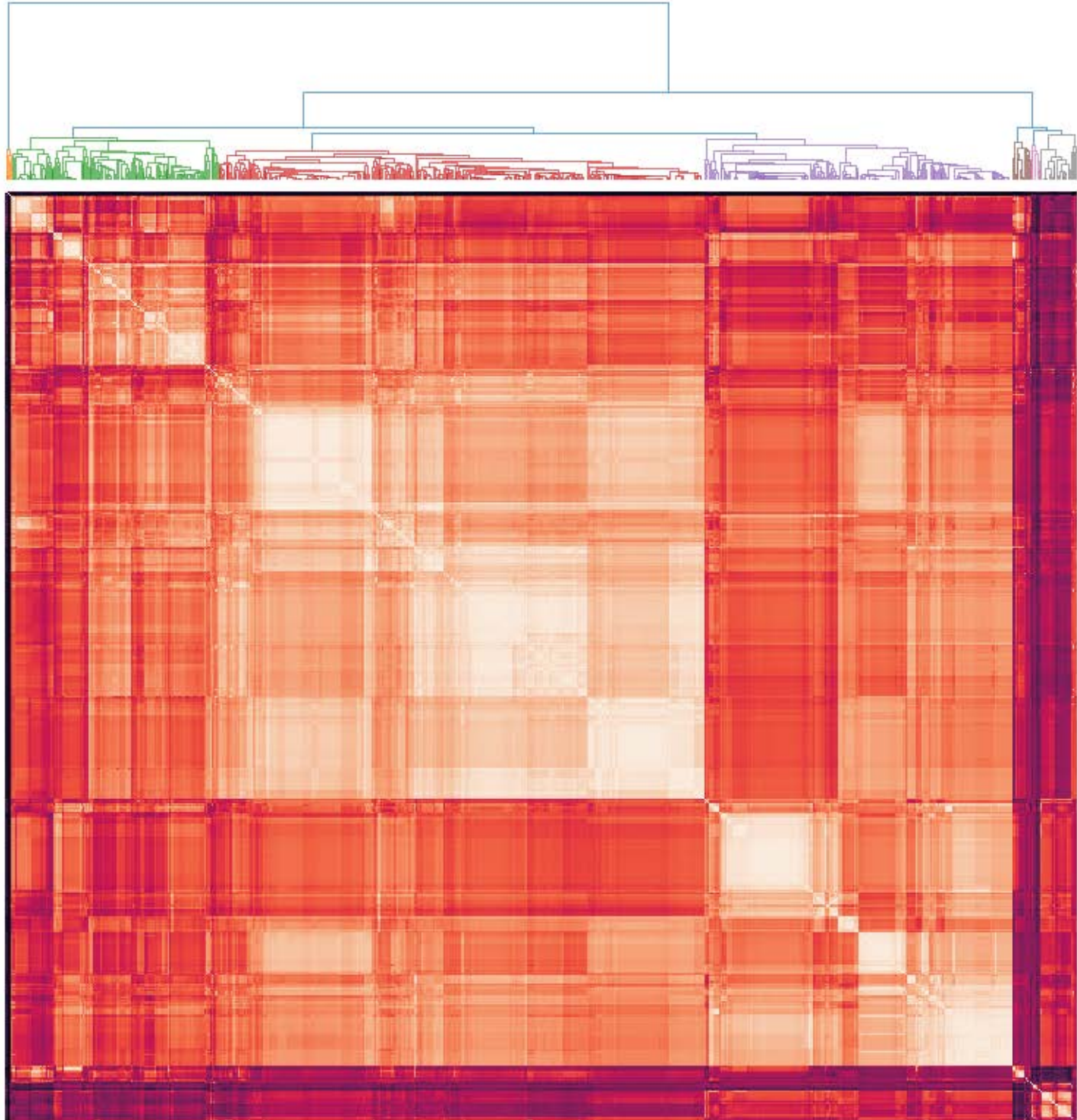
Human coronavirus NL63 strains ZDNABERT



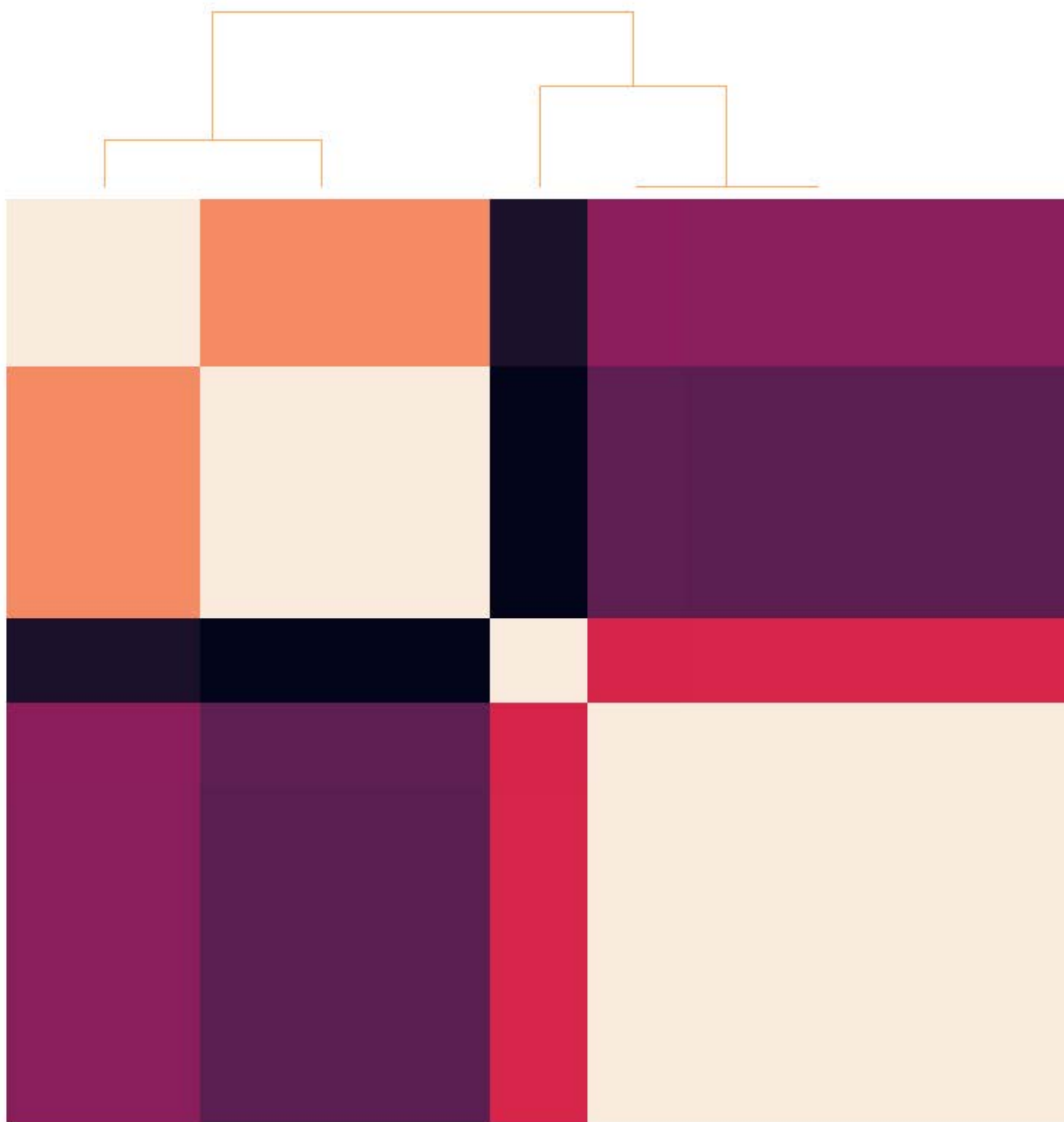
NL63-related bat coronavirus strain BtKYNL63-9b



Porcine epidemic diarrhea virus

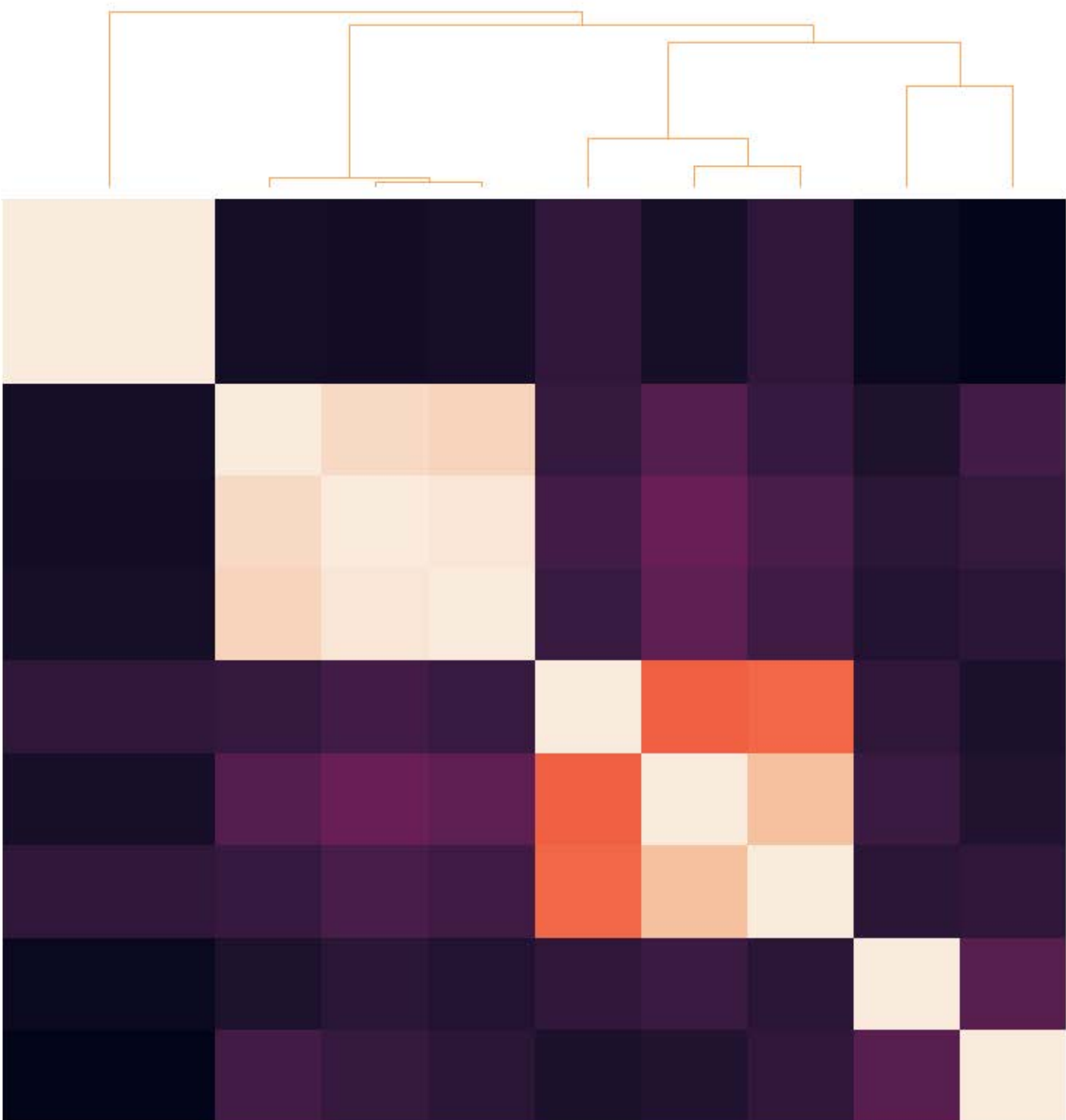


Rhinolophus bat coronavirus HKU2



A heatmap visualization of a 10x10 matrix. The color scale ranges from dark purple (low values) to light yellow (high values). The matrix shows a block-like structure with high values (yellow) concentrated in the top-left and bottom-right corners, and low values (dark purple) in the center. A dendrogram is visible at the top, showing the hierarchical clustering of the rows. The color scale is indicated by a vertical bar on the right side of the heatmap.

Rousettus bat coronavirus HKU9



Tylonycteris bat coronavirus HKU4

