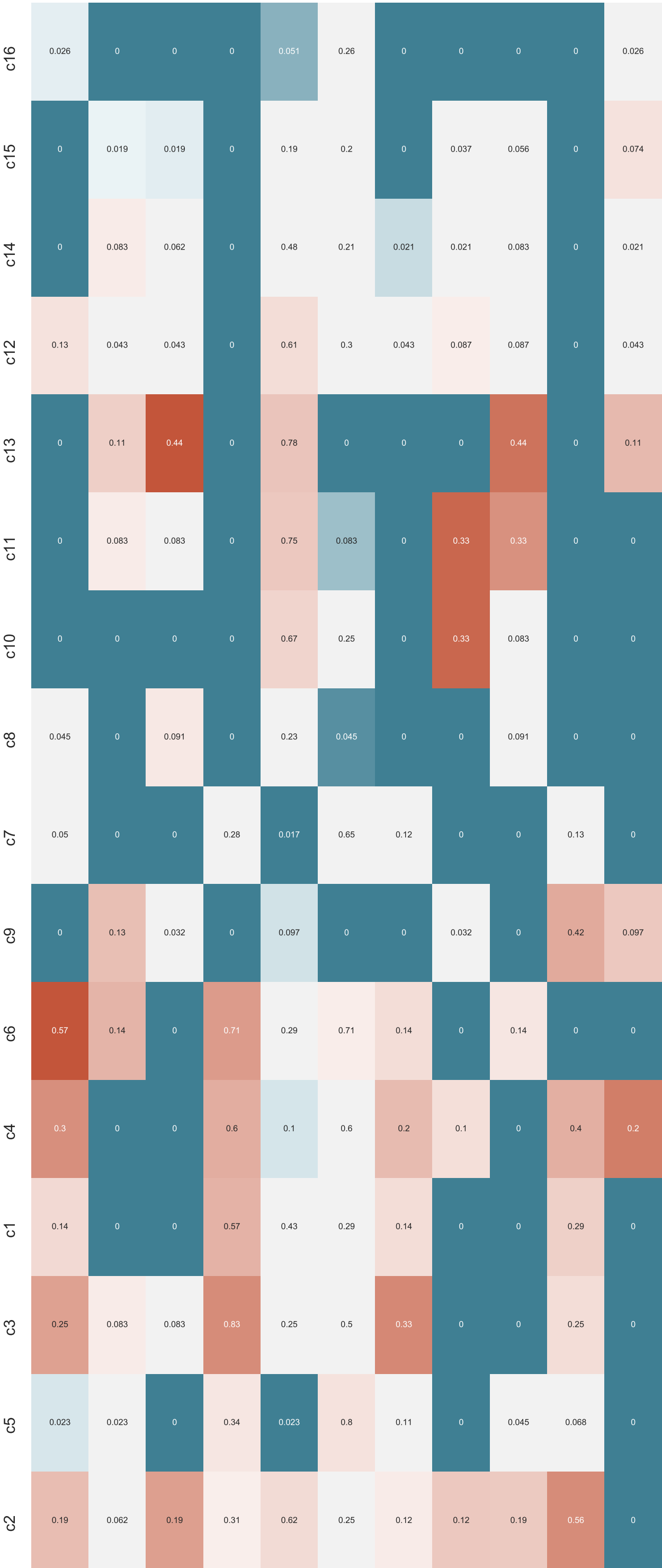


Clade



3.0

1.5

0.0

-1.5

-3.0

log2 enrichment

HA1 mutation
(overall frequency in egg-passaged viruses)