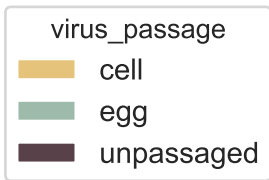


prevalence of mutation

0.30
0.25
0.20
0.15
0.10
0.05
0.00



HA1A138S
HA1H156Q
HA1H156R
HA1T160K
HA1G186V
HA1L194P
HA1T203I
HA1S219F
HA1S219Y
HA1D225G

HA1 mutation

