Figure S6: Predicted high affinity MHC-II binding peptides gained, lost and conserved in HA1 in transitions between temporal clusters of H3N2.

For cluster representative viruses shown in Table 1 the scoring system shown in Table 2 was used to assign a categorical classification to predicted high affinity peptides according to whether they were new (-2), showed enhanced binding of an existing high binder (-1), conserved (0), showed reduced binding but were still high affinity (+1), or lost their status as predicted high affinity binders (+2). The plots show the aggregate number of each class of change in the HA1 protein associated with the transitions between clusters (HK68 to EN77, HK68 to FU02 etc) for 14 different MHC-II.

DRB1*01:01

DRB1*03:01

DRB1*04:01

DRB1*04:04

DRB1*04:05

DRB1*07:01

DRB1*08:02

DRB1*09:01

DRB1*11:01

DRB1*13:02

DRB1*15:01

DRB3*01:01

DRB4*01:01

DRB5*01:01