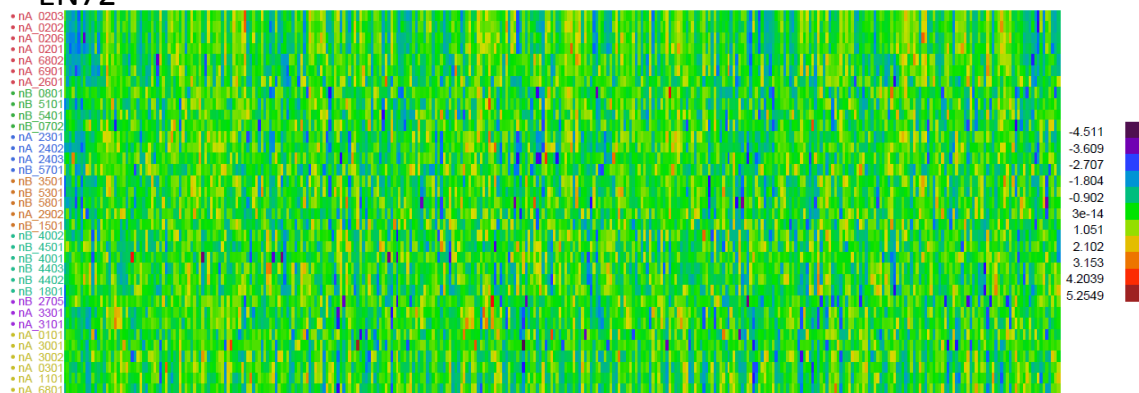


Figure S5: Hierarchical clusters of predicted MHC-I and MHC-II binding to HA1 from additional cluster representative isolates.

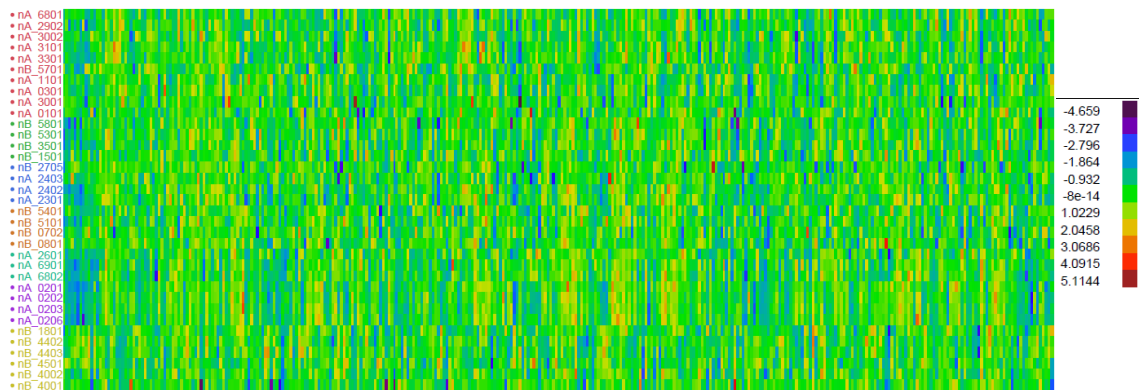
Hierarchical clustering of predicted binding of multiple MHC-I and MHC-II to consecutive peptides in HA1 of each cluster representative virus listed in Table 1 was done by the method of Ward using standardized binding data. The binding data for each HLA was first submitted to principal component analysis and the mean of the first principal component was used as an ordering variable. A comparable plot of binding to HA1 of Influenza A/Bilthoven/16190/68 is shown in Figure 3. The color scale shows the $\ln(\text{ic}_{50})$.

MHC-I

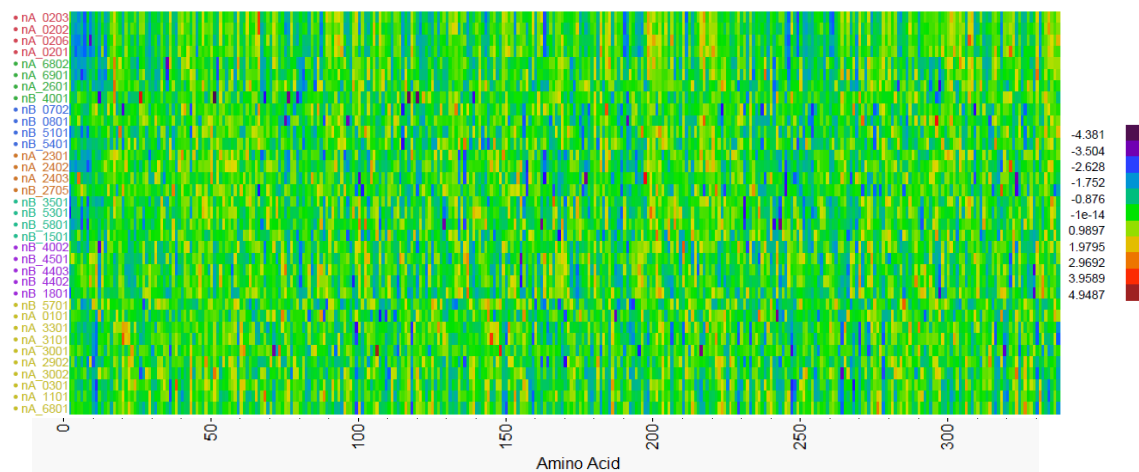
EN72



VI75

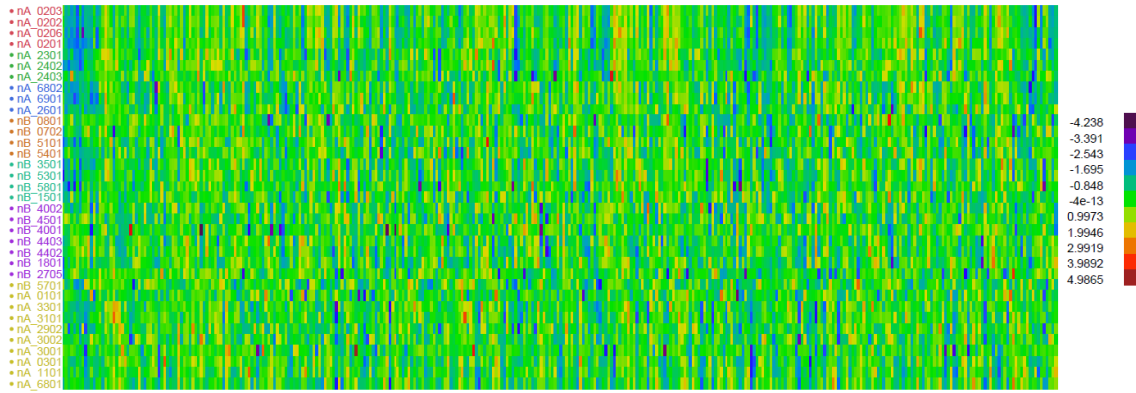


SI87

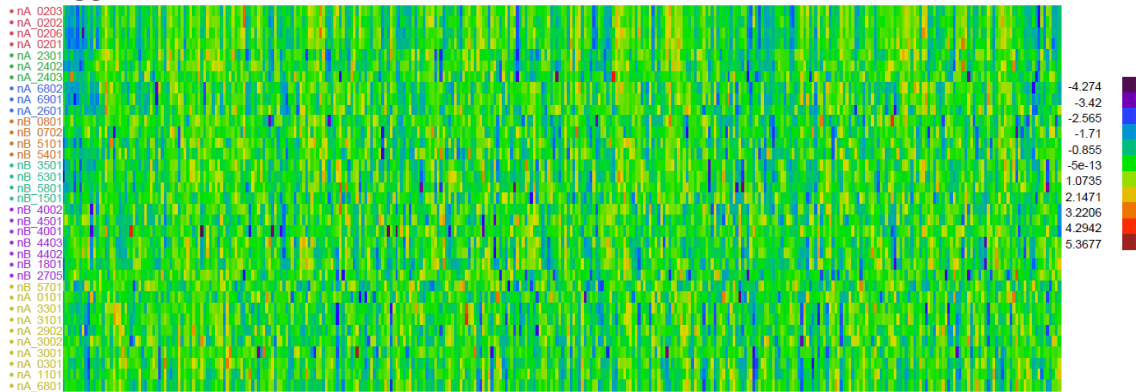


MHC-I

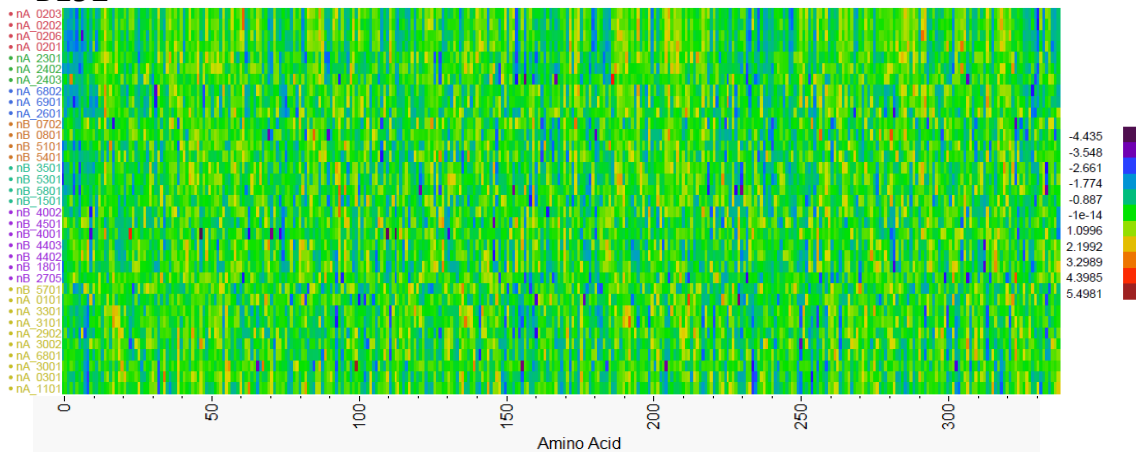
BK79



BE89

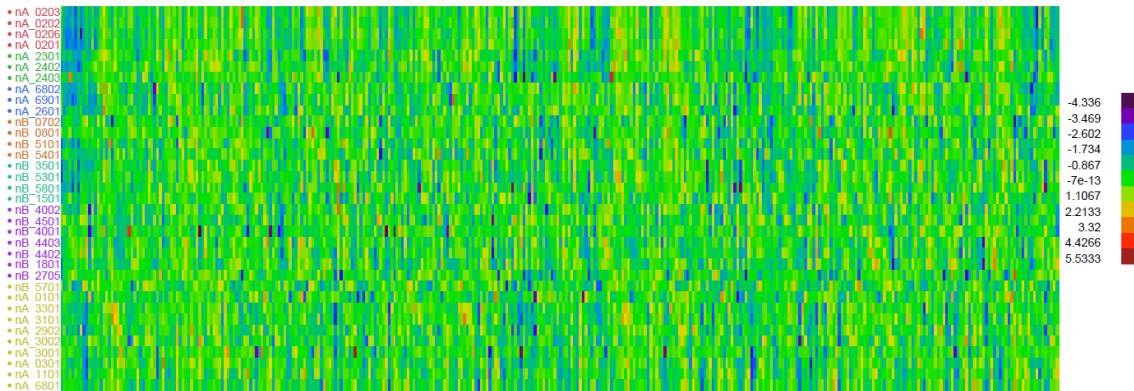


BE92

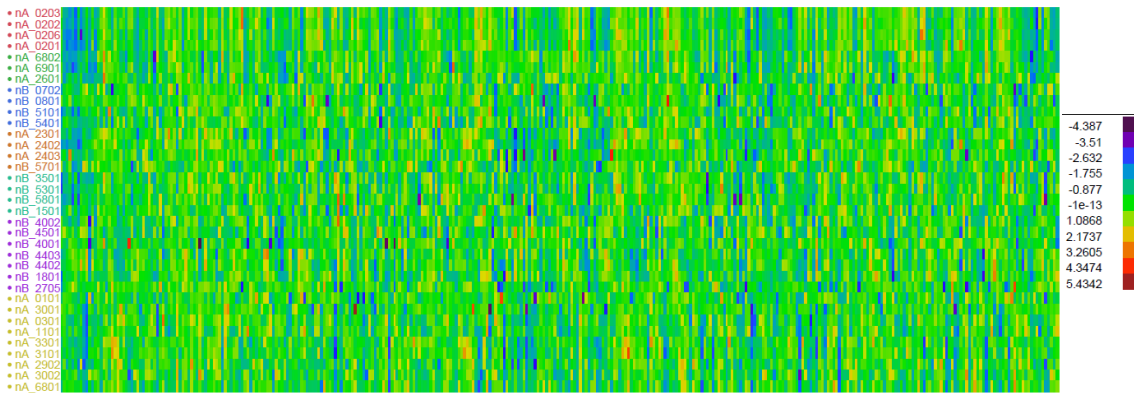


MHC-I

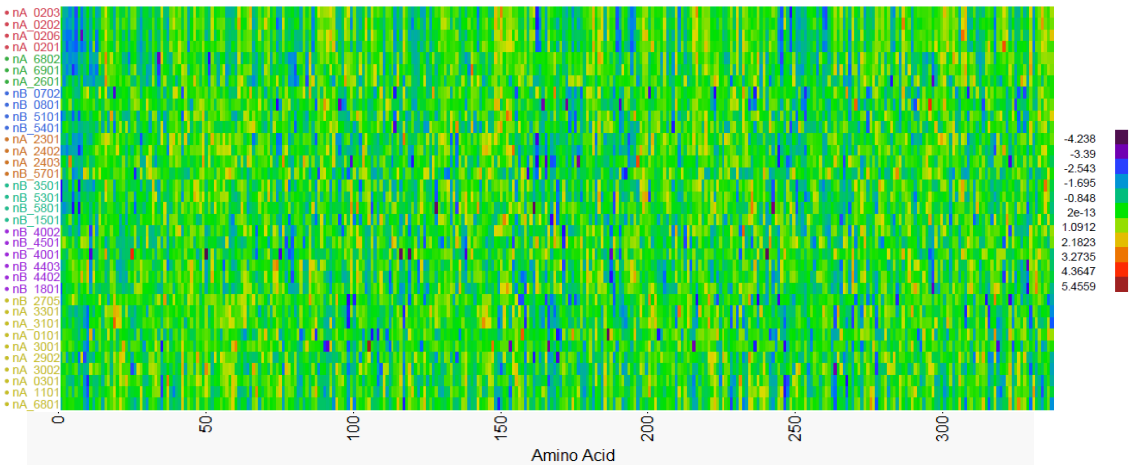
WU95



SY97

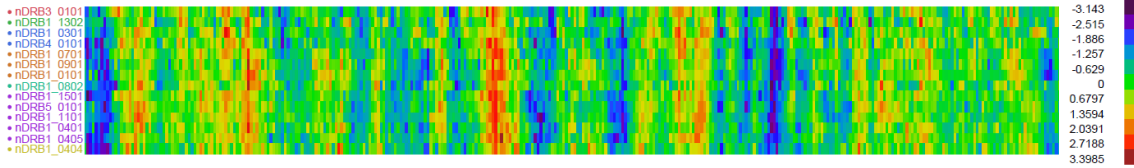


FU02

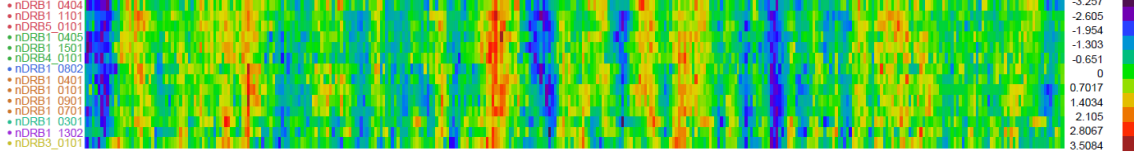


EN72

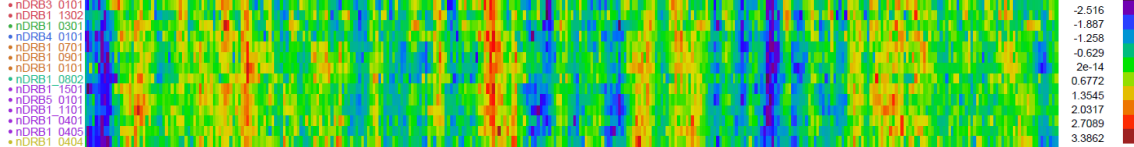
MHC-II



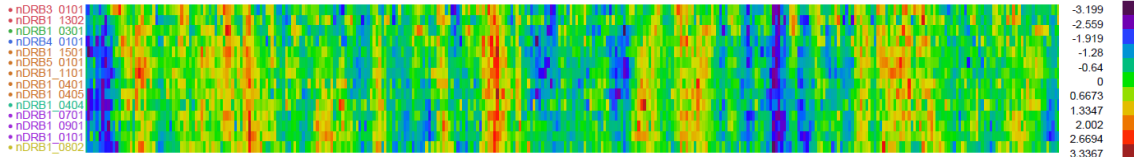
V175



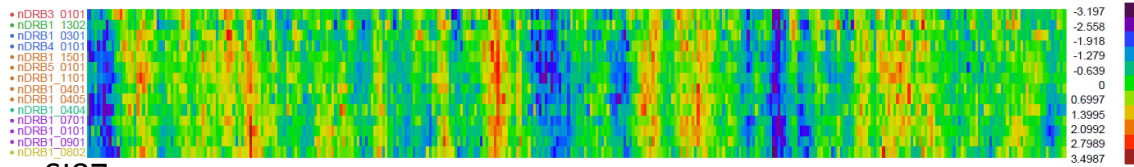
BK79



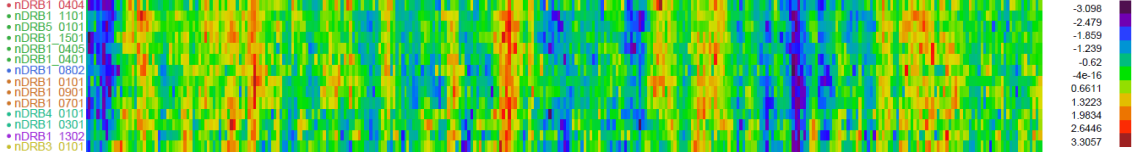
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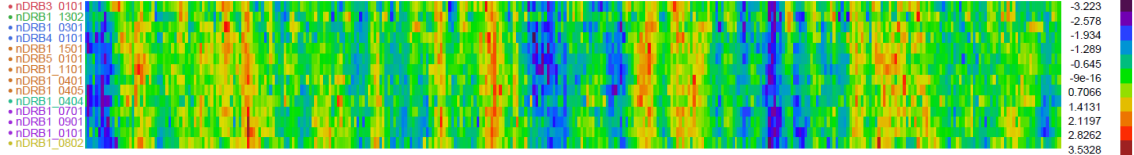
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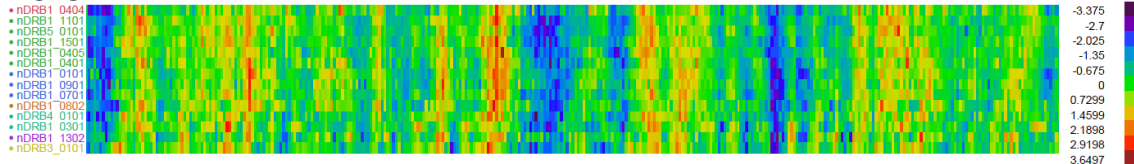
SI87



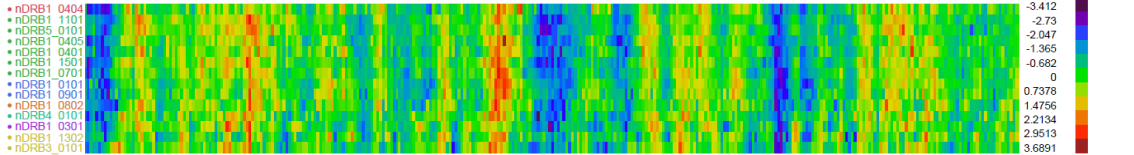
WU95



SY97



FU02



0 50 100 150 200 250 300 Amino Acid