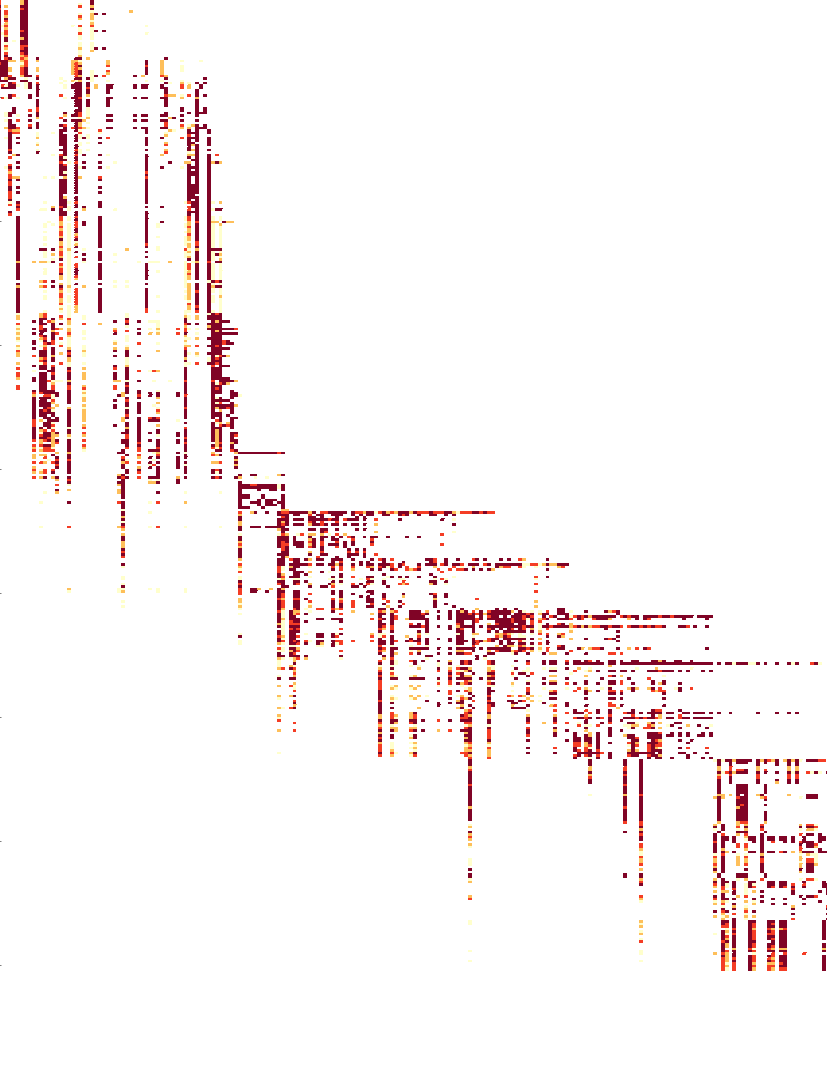
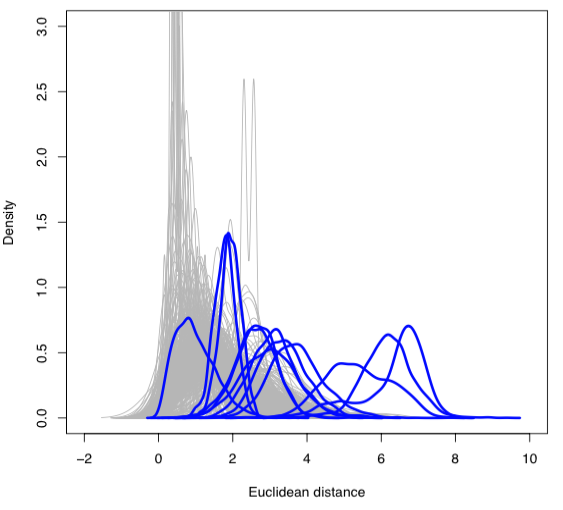
Supplementary Materials

Figure S1. Raw H3N2 measurements: to fill text



Histogram of the Euclidean distance of $\mu$ from the parent clusters for the A/H3N2 analysis with $\kappa=0.05$.}

Macintosh HD:Users:charles:Documents:research:antigenic:GenoPheno:antigenic-clustering:manuscript:figures:lineart:swapIandMuNeighbor.pdf

\caption{\textbf{Proposal 4 - Swap $I\_i$ and $\mu\_i$ with a neighbor}

In this $T$, node 10 is chosen to perform the swap-with-neighbor proposal. In this case, with a neighborhood step-size of 2, the set of candidates are all the nodes within the orange neighborhood minus node 10.

Macintosh HD:Users:charles:Documents:research:antigenic:GenoPheno:antigenic-clustering:manuscript:figures:lineart:walkAndBalance.pdf

\caption{\textbf{Proposal 5 - Performs a random walk on an active $\mu\_i$ and balance other active $\mu$'s.}

In this antigenic map, $\mu\_{10}$ is now changed by $\delta$, which causes the antigenic location of viruses in the orange cluster to change.

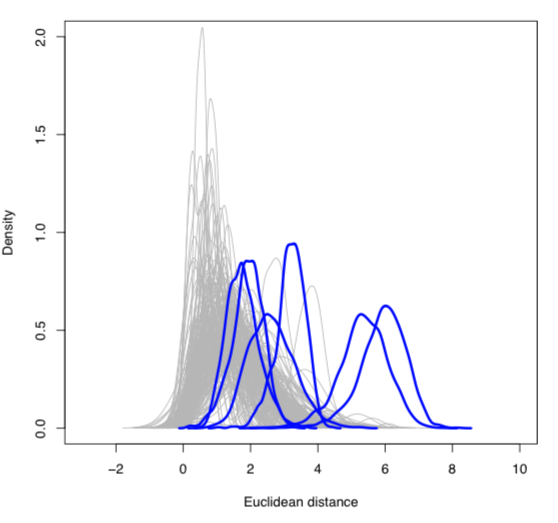
To retain the absolute location of viruses in other clusters, $\mu\_{17}$ and $\mu\_{34}$ are adjusted by subtracting $\delta$. [typo? $\mu\_{17} - \delta$, not +].

Macintosh HD:Users:charles:Documents:research:antigenic:GenoPheno:antigenic-clustering:manuscript:figures:lineart:swapAndFlipNeighbor.pdf

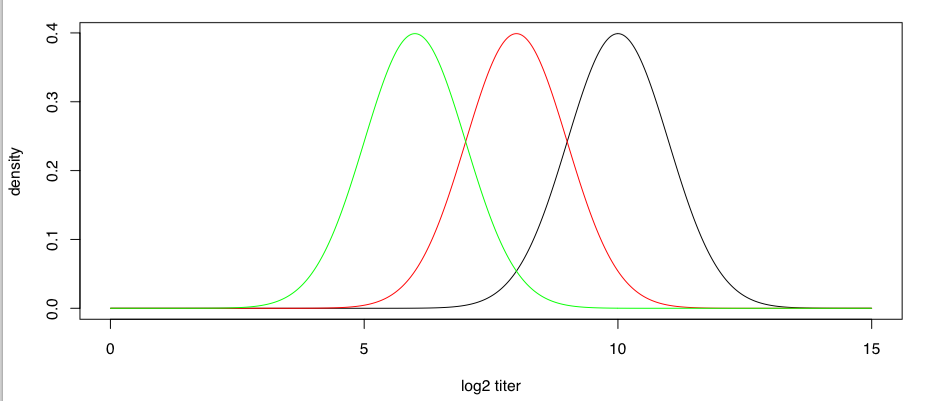
\caption{\textbf{ The candidate of nodes to be flipped in Proposal 7 - Swap with a neighbor and flip another neighbor.}

In the second operation that flips the indicator status of another neighbor, the list of nodes to consider include neighbors from the original pivot node and the neighbors of the newly chosen node.

%Taking the union of the two set of nodes allows a node that may be further away to be chosen and also ensures that the log Metropolis-Hasting ratio would be greater than 0 because the backward operation from the new state to the old state would also have a probability greater than 0.



Histogram of the Euclidean distance of $\mu$ from the parent clusters for the A/H1N1 analysis with $\kappa=0.1$.

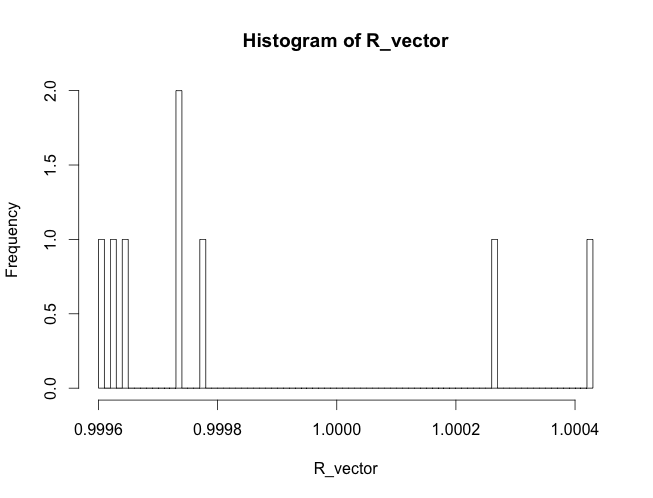


Simulation of log$\_2$ HI titer consists of measurement noises.}

For a virus $i$ and a reference virus for serum $j$ that belongs to the same antigenic cluster, the distribution of measurements follows $N(10, \sigma^2)$. For each antigenic transition between the two viruses, the mean measurement decreases by 2 units.

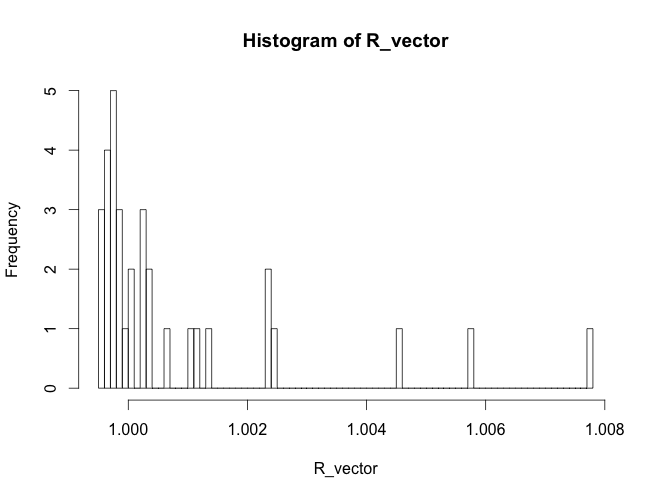
H1N1

/Users/charles/Documents/research/antigenic/GenoPheno/driver/clustering/analysisManuscript2-12-2015/H1N1/concordance/GelmanRubinStat\_2runs\_mds0\_1\_with\_ponGT0\_1\_in\_rep1.png



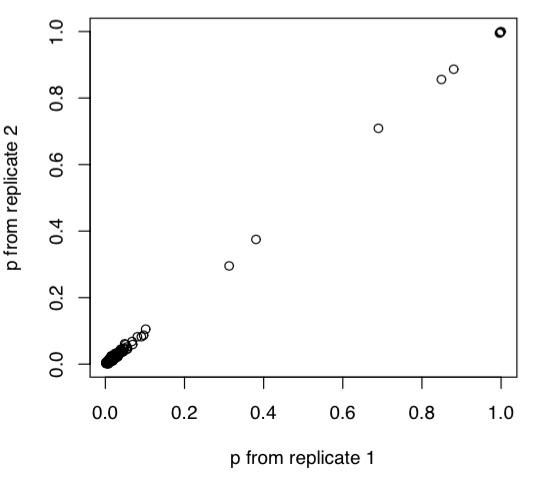
Distribution of Gelman-Rubin statistics of the estimated $p\_i$ on R^2 from 2 replicates for A/H1N1 at $\kappa= 0.1$ .

/Users/charles/Documents/research/antigenic/GenoPheno/driver/clustering/analysisManuscript2-12-2015/H1N1/concordance/GelmanRubinStat\_2runs\_mds0\_3\_with\_ponGT0\_1\_in\_rep1.png



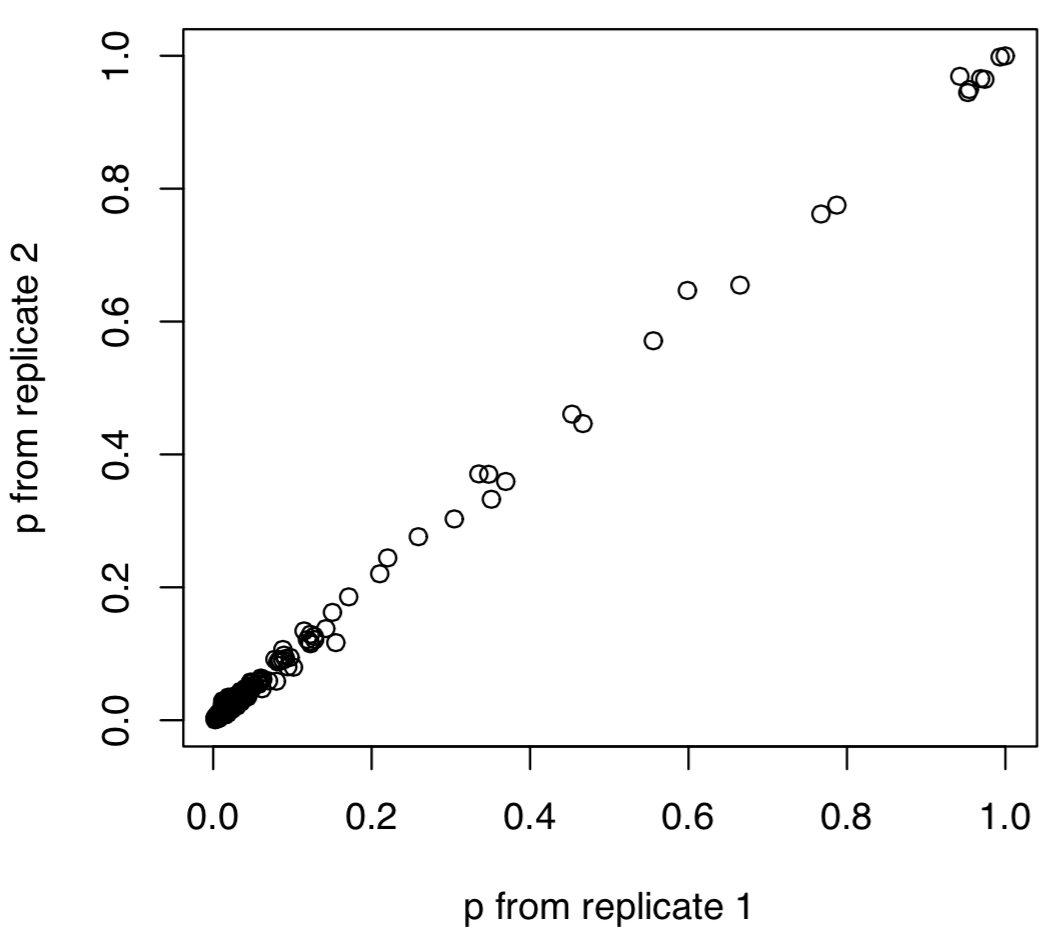
Distribution of Gelman-Rubin statistics of the estimated $p\_i$ on R^2 from 2 replicates for A/H1N1 at $\kappa= 0.3$ .

/Users/charles/Documents/research/antigenic/GenoPheno/driver/clustering/analysisManuscript2-12-2015/H1N1/concordance/H1N1-C3b-mds0\_1-concordance.eps



Scatterplot of the estimated $p\_i$ comparing replicate 1 and 2 for A/H1N1 at $\kappa= 0.1$ ($R^2 = #$).

/Users/charles/Documents/research/antigenic/GenoPheno/driver/clustering/analysisManuscript2-12-2015/H1N1/concordance/H1N1-C3b-mds0\_1Vs0\_3-concordance.eps

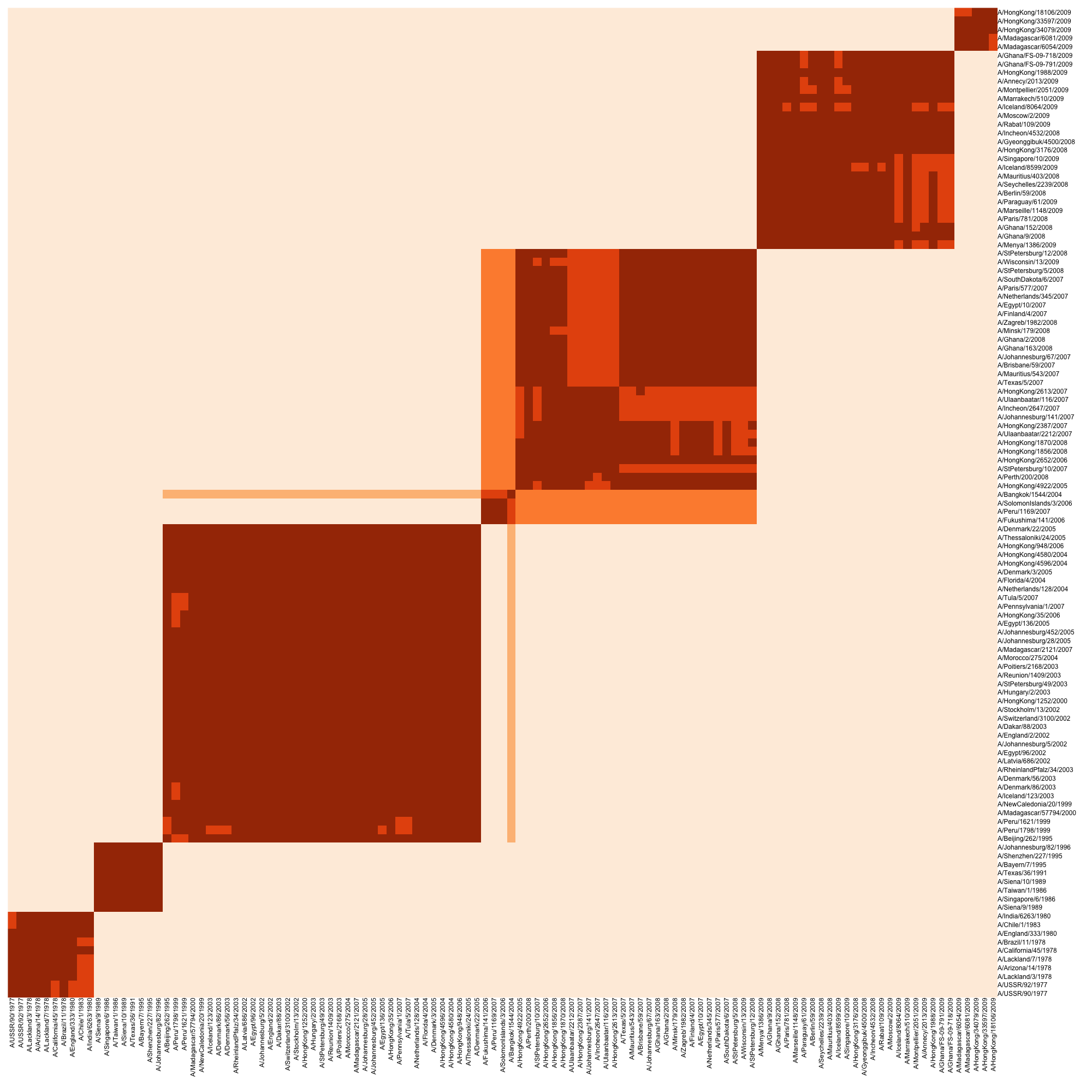


Scatterplot of the estimated $p\_i$ comparing replicate 1 and 2 for A/H1N1 at $\kappa= 0.3$ ($R^2 = #$).

Probably have an aggregated.

E.g. Comping the results from the MCC tree vs. Tree 2.

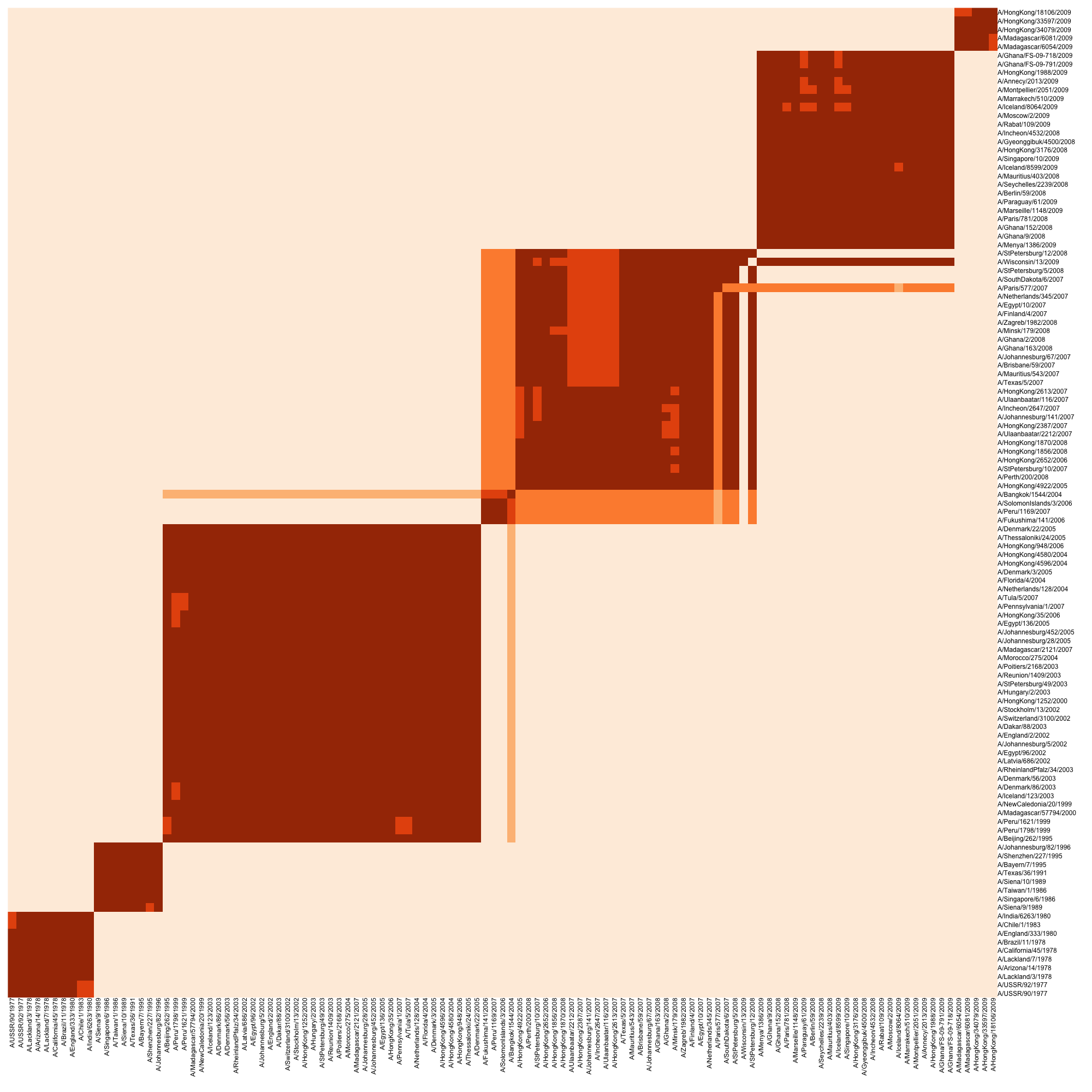
/Users/charles/Documents/research/antigenic/GenoPheno/driver/clustering/analysisManuscript1-21-2015/H1N1/heatmap/H1N1-C3b-mds0\_1\_vsS2-ordered.png



(very similar here)

Between MCC tree (upper triangle) and Tree 3 (lower triangle)

Users/charles/Documents/research/antigenic/GenoPheno/driver/clustering/analysisManuscript1-21-2015/H1N1/heatmap/H1N1-C3b-mds0\_1\_vsS3-ordered.png

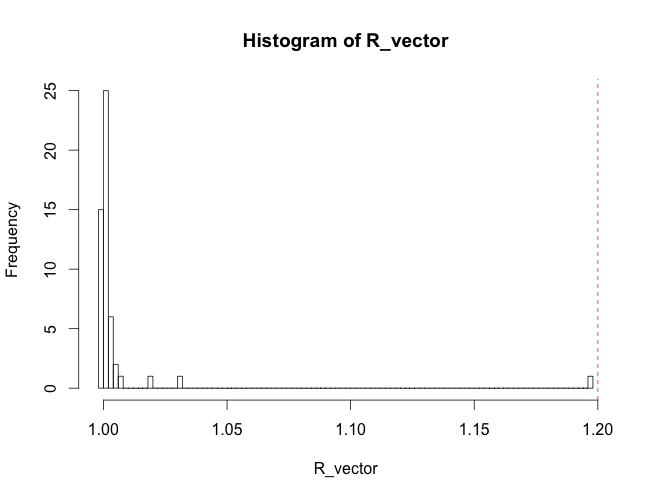


see the dropbox folder for more..

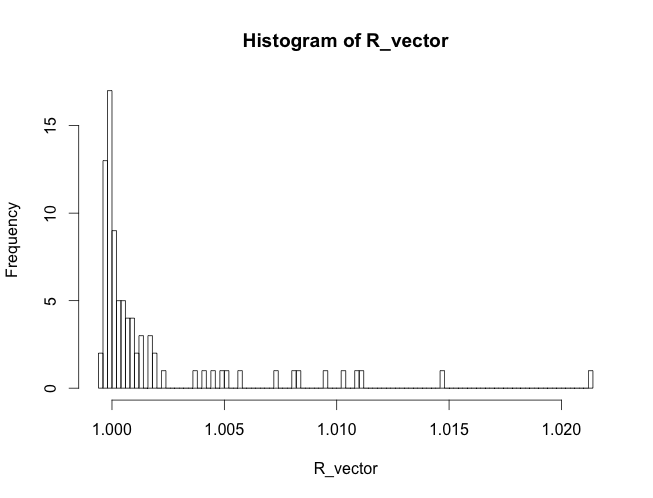
H3N2

MCMC convergence diagnostics:

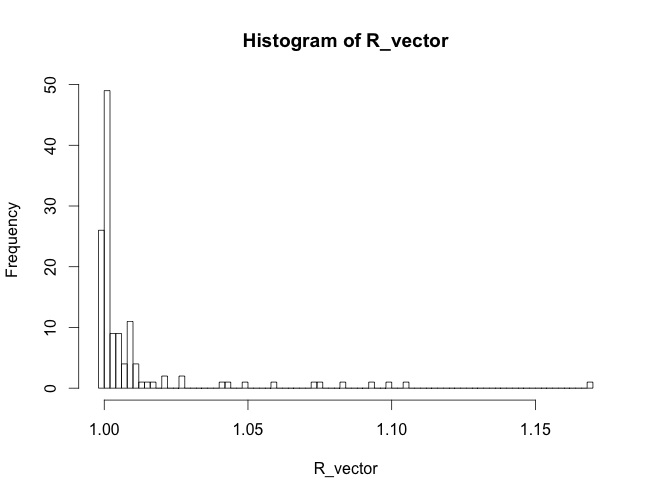
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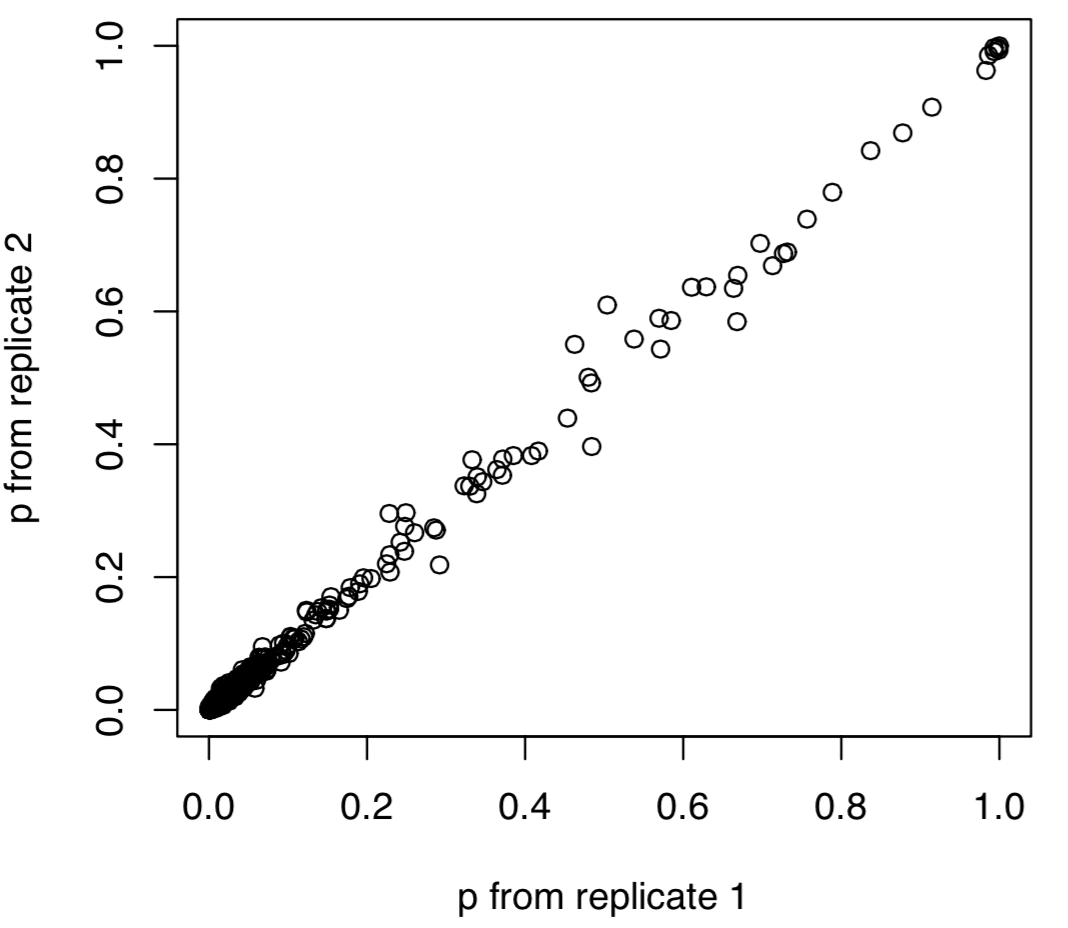
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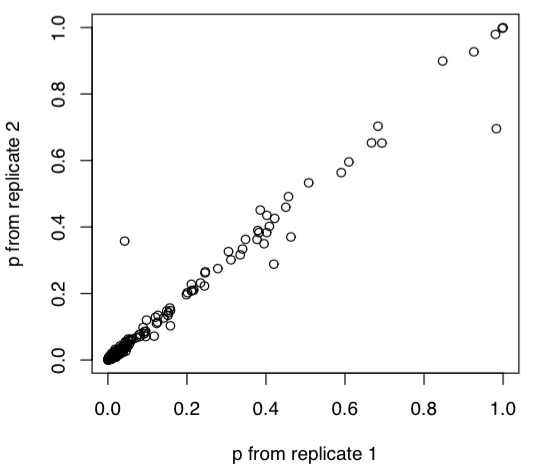
/Users/charles/Documents/research/antigenic/GenoPheno/driver/clustering/analysisManuscript2-12-2015/H3N2/concordance/GelmanRubinStat\_mds0\_15\_with\_ponGT0\_1\_in\_rep1.png



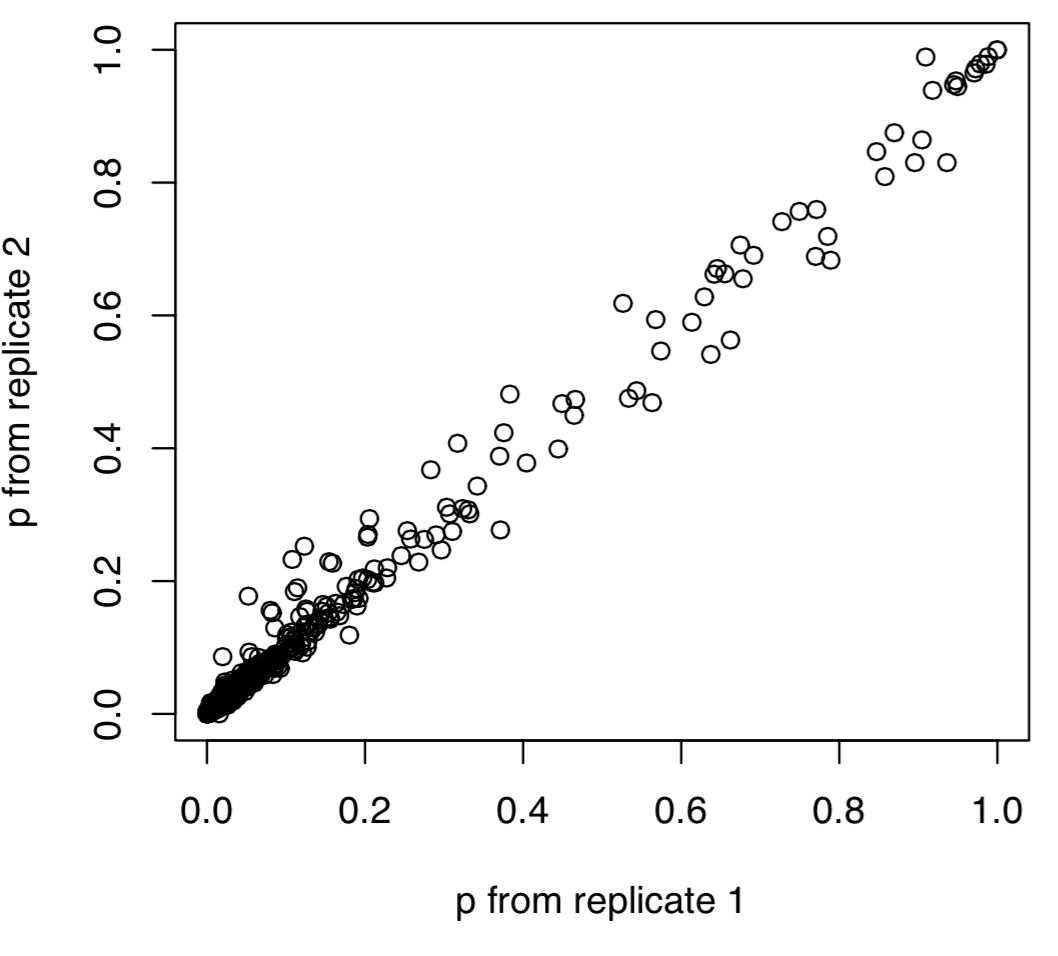
/Users/charles/Documents/research/antigenic/GenoPheno/driver/clustering/analysisManuscript2-12-2015/H3N2/concordance/H3N2-C3b-mds0\_05-concordance.eps



/Users/charles/Documents/research/antigenic/GenoPheno/driver/clustering/analysisManuscript2-12-2015/H3N2/concordance/H3N2-C3b-mds0\_1-concordance.eps



/Users/charles/Documents/research/antigenic/GenoPheno/driver/clustering/analysisManuscript2-12-2015/H3N2/concordance/H3N2-C3b-mds0\_15-concordance.eps



Eg.

/Users/charles/Documents/research/antigenic/GenoPheno/antigenic-clustering/summarizedResults/H3N2/heatmap/H3N2-C3b-mds0\_1\_vsS2-ordered.png

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- 山 pe イ 

see dropbox for other samples