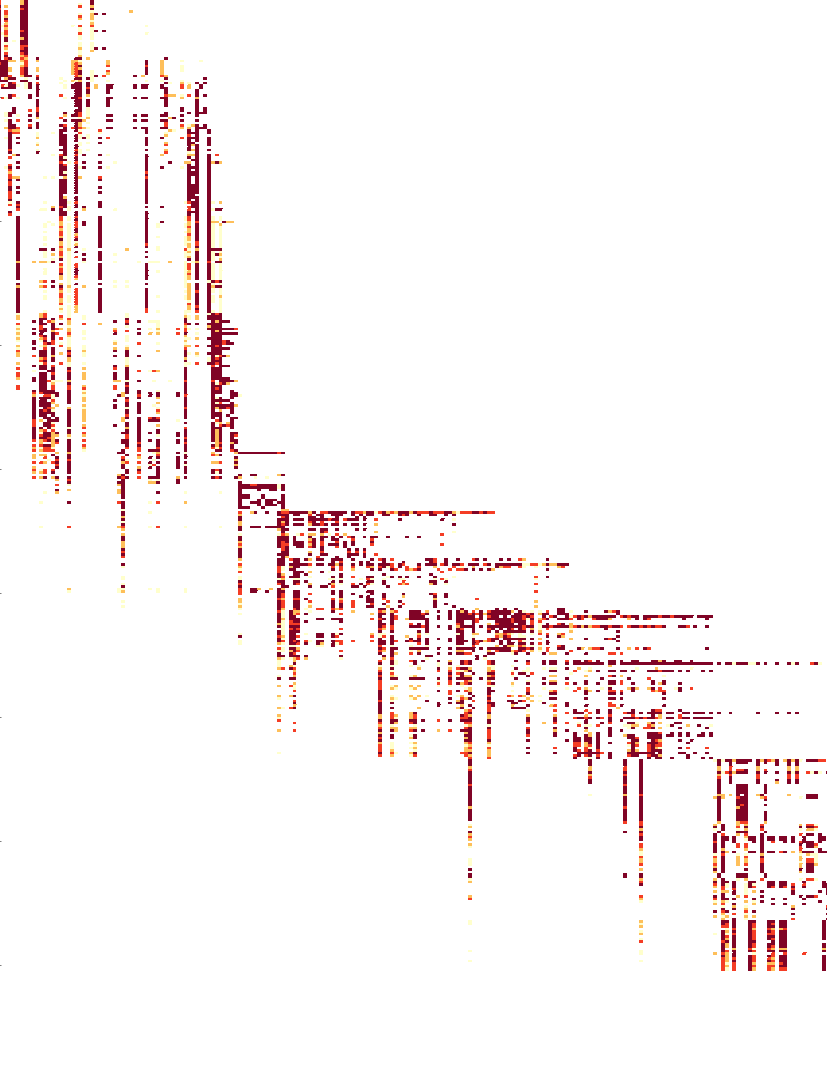
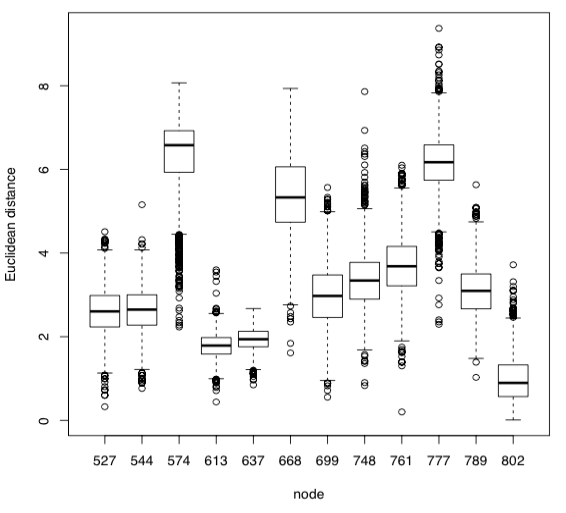
Supplementary Materials

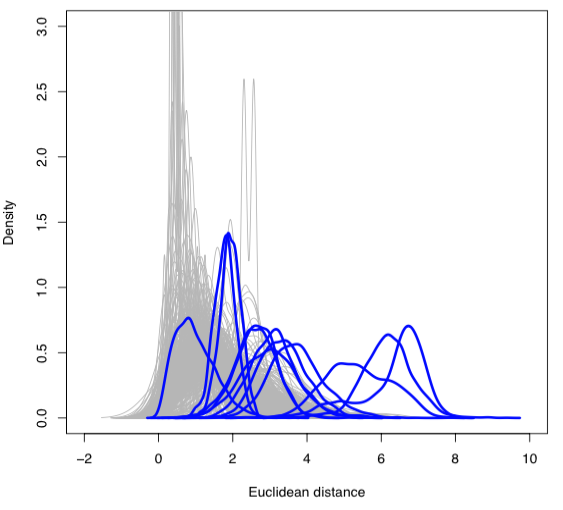
Figure S1. Raw H3N2 measurements: to fill text



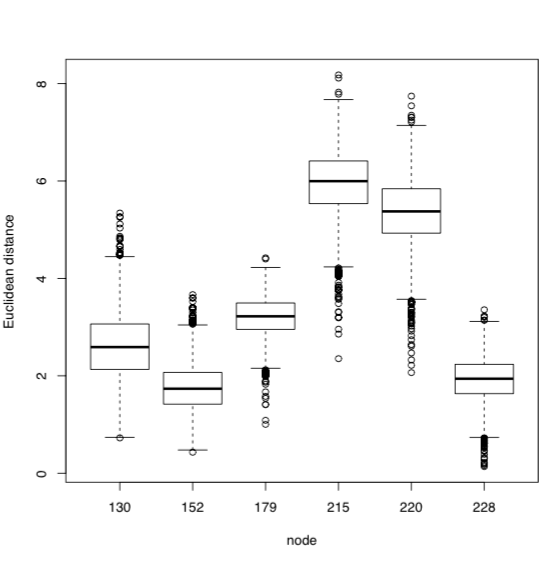
The TX77 sub-heatmap. - A/Bilthoven/2271/1976 and A/Texas/1/1977 are in the middle cluster - upper triangle = $\kappa=0.05$ and higher triangle=$\kappa=0.15



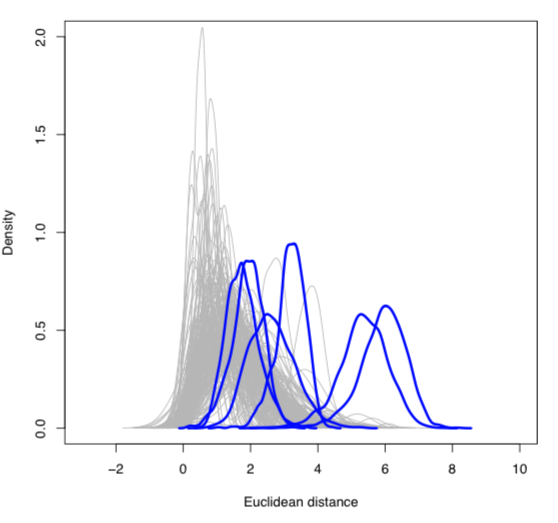
\caption{\textbf{Boxplot of the Euclidean distance of distribution of $\mu\_i$, conditional on $I\_i = 1$, from the parent clusters for the A/H3N2 analysis with $\kappa=0.05$}



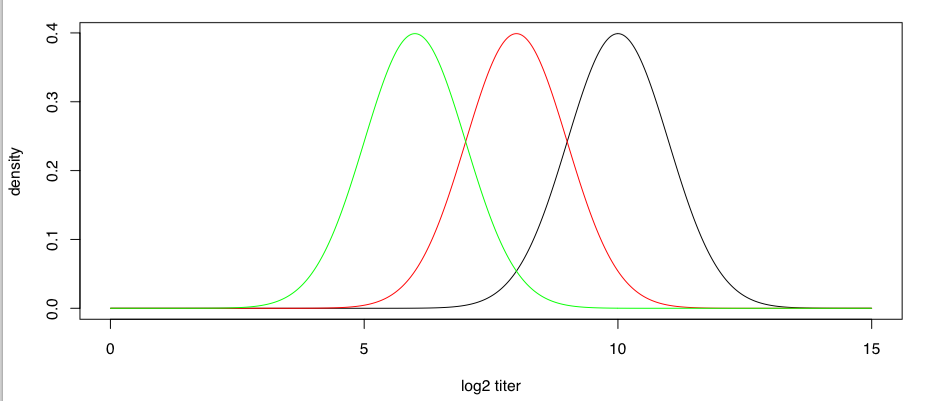
Histogram of the Euclidean distance of $\mu$ from the parent clusters for the A/H3N2 analysis with $\kappa=0.05$.}



Boxplot of the Euclidean distance of distribution of $\mu\_i$, conditional on $I\_i = 1$, from the parent clusters for the A/H1N1 analysis with $\kappa=0.1$



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

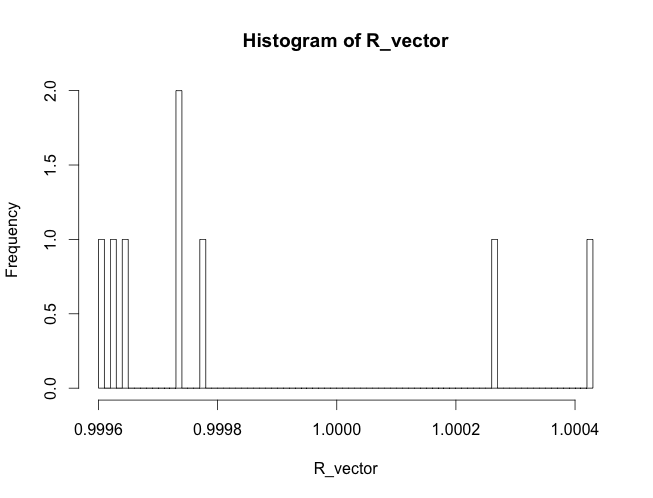


Simulation of log$\_2$ HI titer consists of measurement noises.}

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.

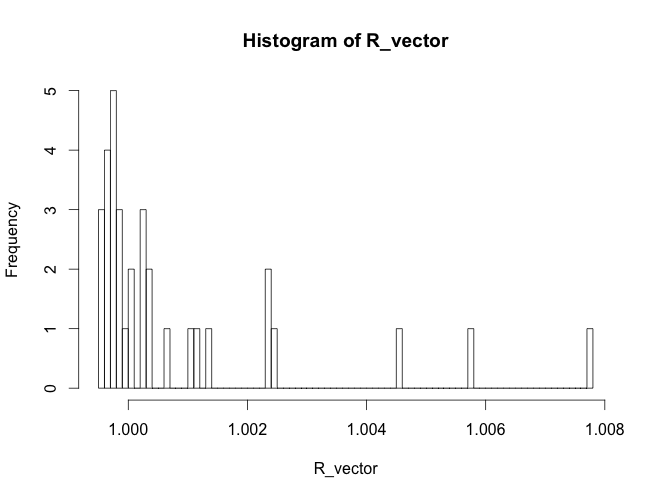
H1N1

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



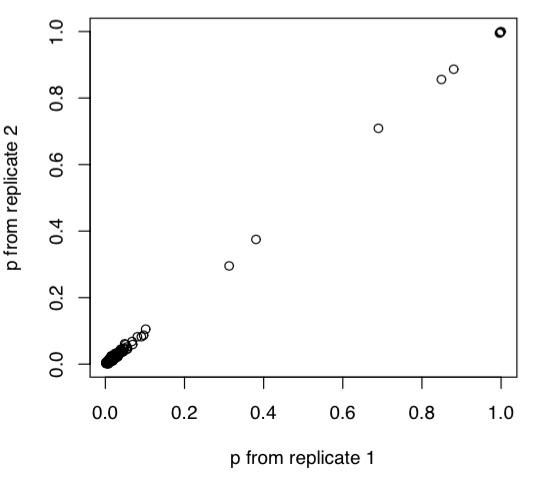
Distribution of Gelman-Rubin statistics of the estimated $p\_i$ on R^2 from 2 replicates for A/H1N1 at $\kappa= 0.1$ .

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



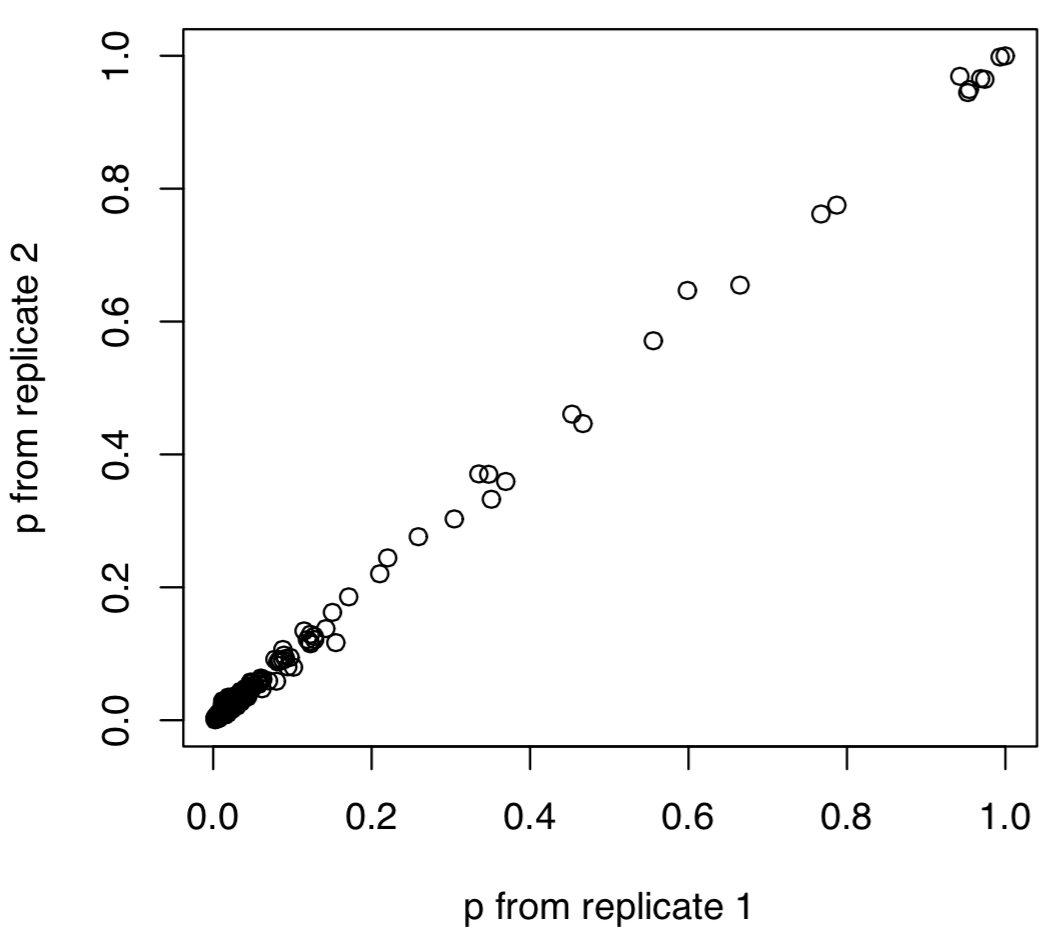
Distribution of Gelman-Rubin statistics of the estimated $p\_i$ on R^2 from 2 replicates for A/H1N1 at $\kappa= 0.3$ .

/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 $\kappa= 0.1$ ($R^2 = #$).

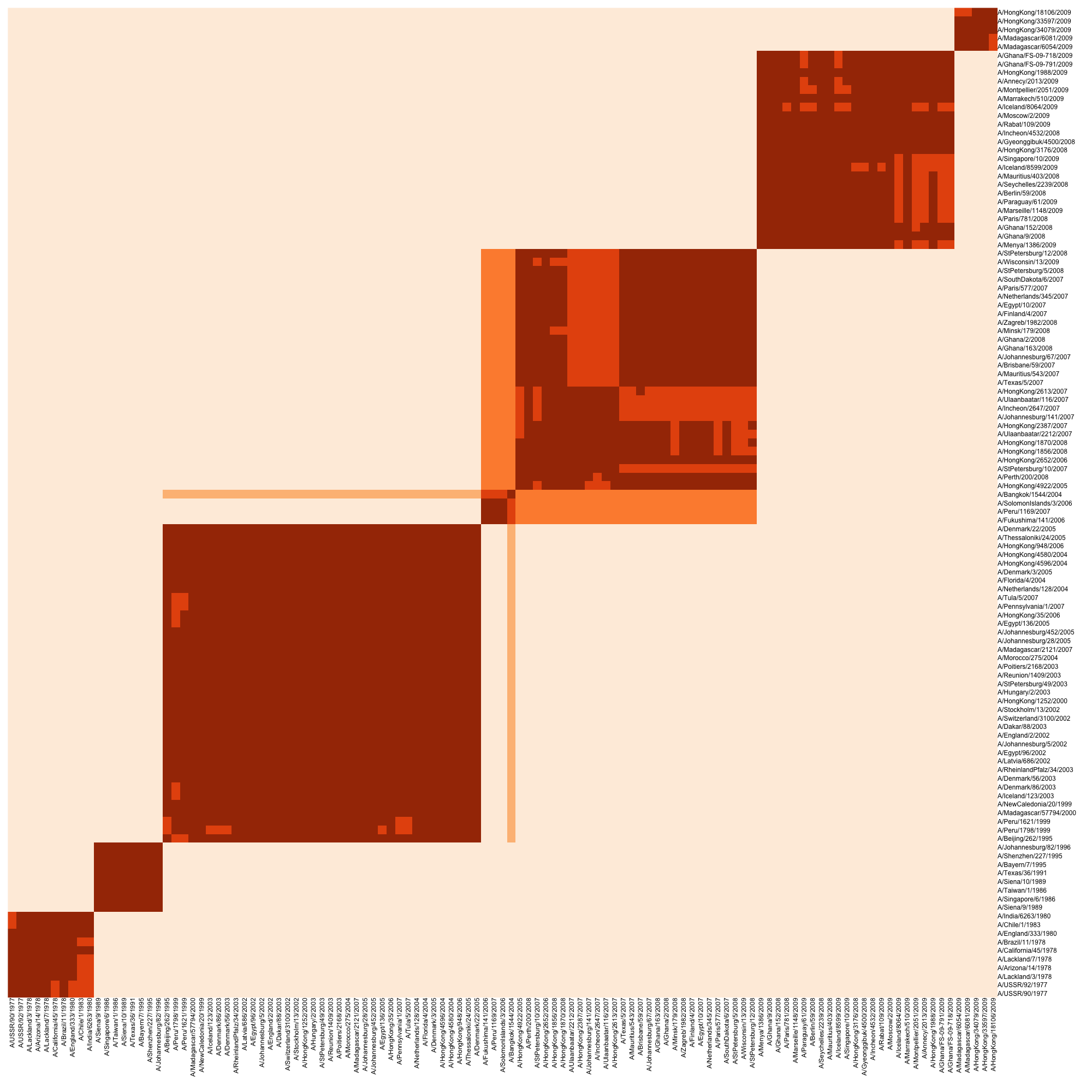
/Users/charles/Documents/research/antigenic/GenoPheno/driver/clustering/analysisManuscript2-12-2015/H1N1/concordance/H1N1-C3b-mds0\_1Vs0\_3-concordance.eps



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

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

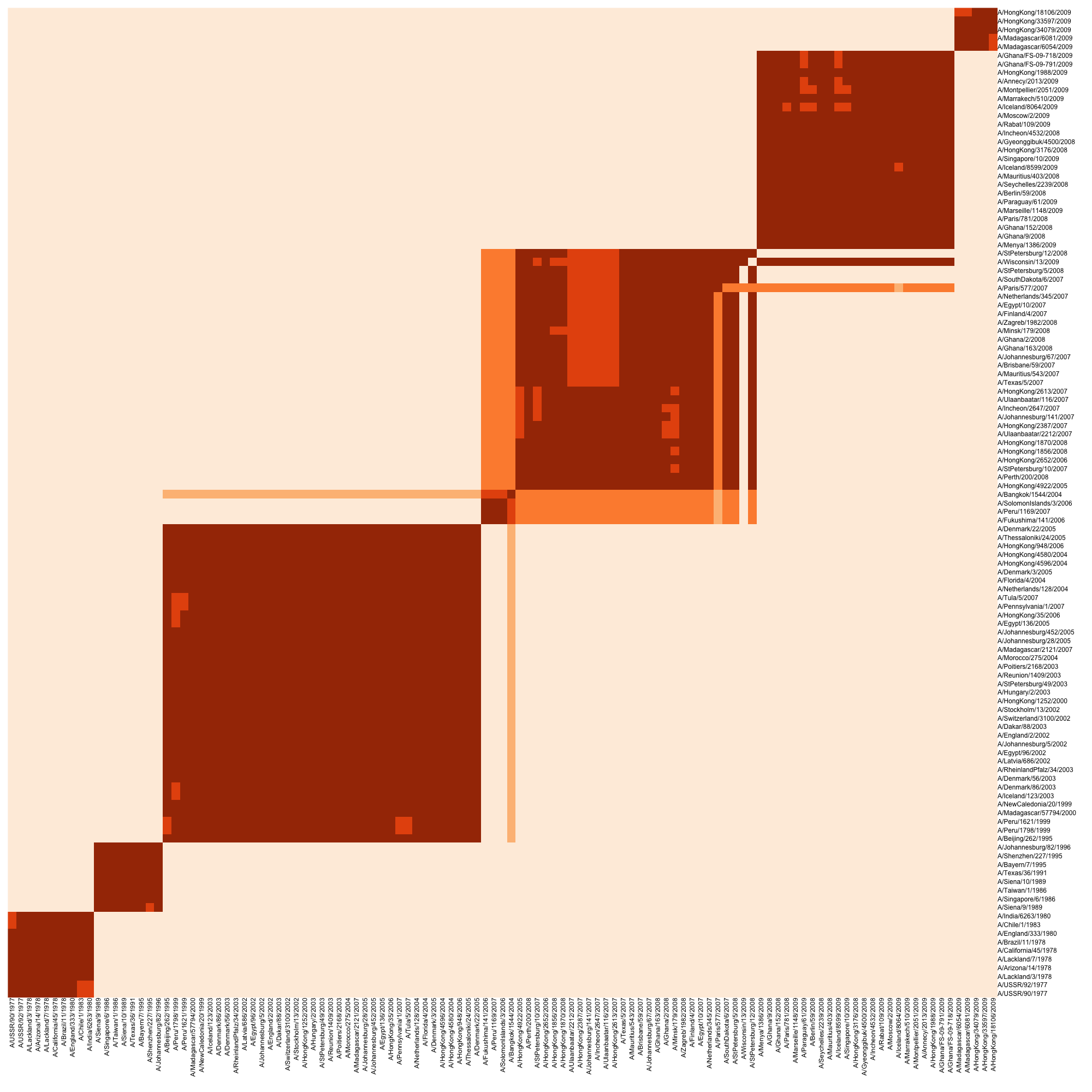
/Users/charles/Documents/research/antigenic/GenoPheno/driver/clustering/analysisManuscript1-21-2015/H1N1/heatmap/H1N1-C3b-mds0\_1\_vsS2-ordered.png



(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

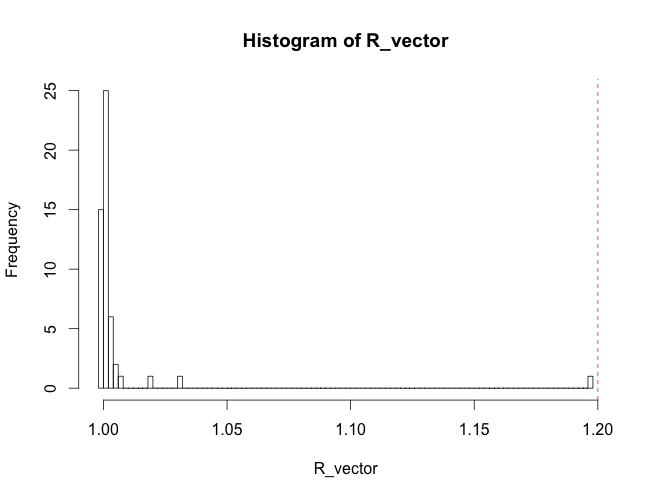


see the dropbox folder for more..

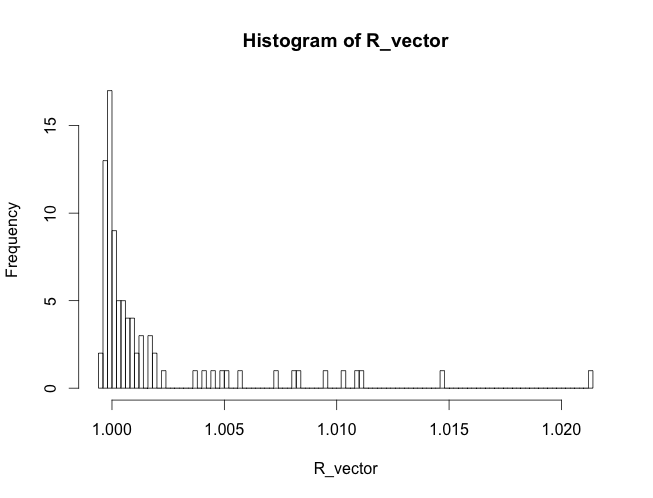
H3N2

MCMC convergence diagnostics:

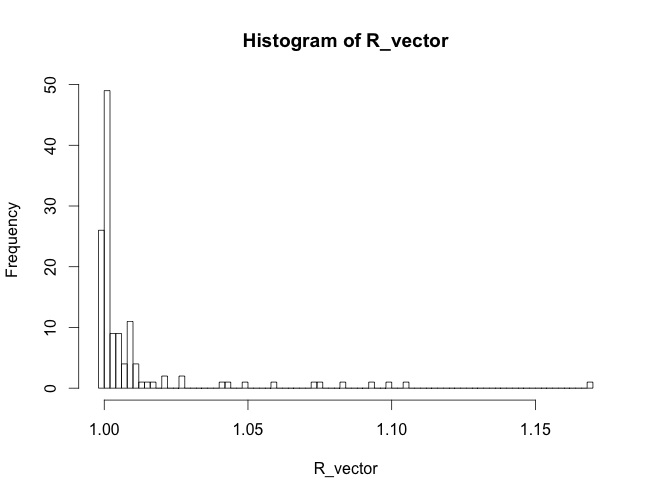
/Users/charles/Documents/research/antigenic/GenoPheno/driver/clustering/analysisManuscript2-12-2015/H3N2/concordance/GelmanRubinStat\_mds0\_1\_with\_ponGT0\_1\_in\_rep1.png



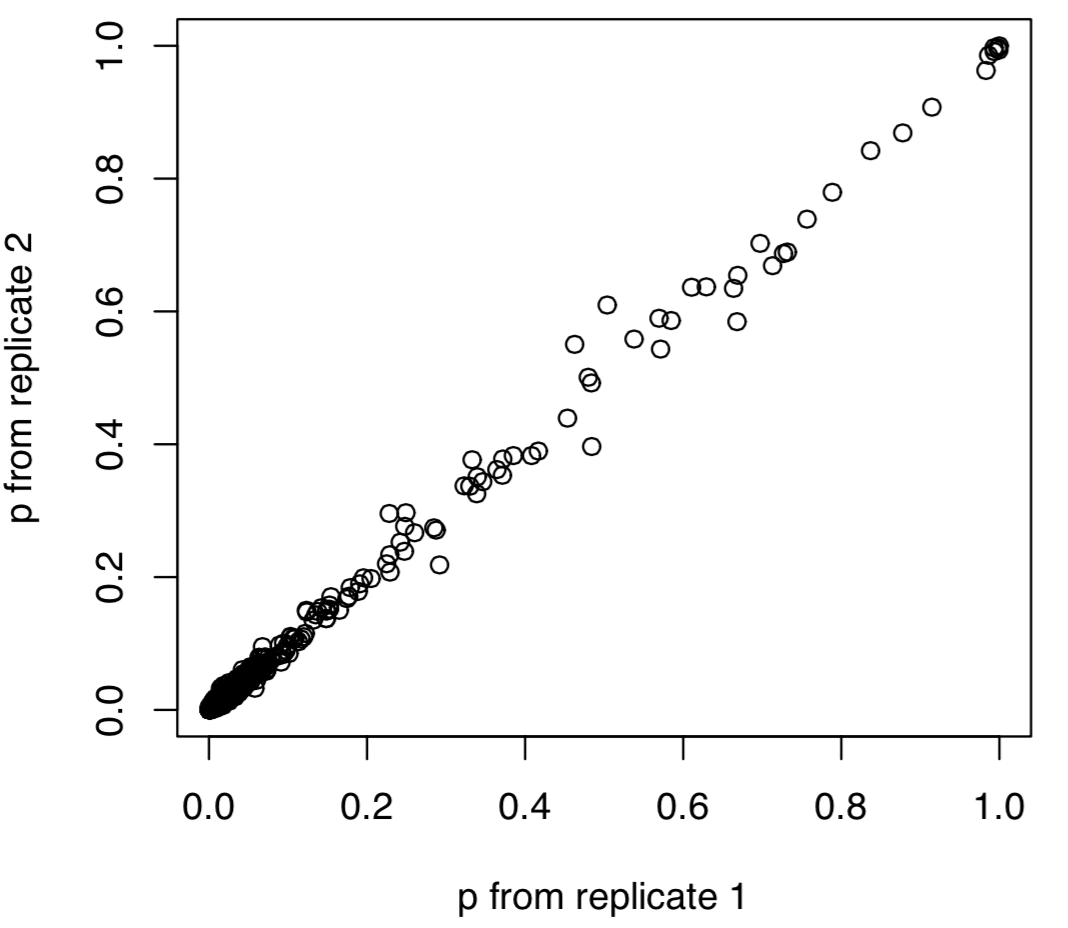
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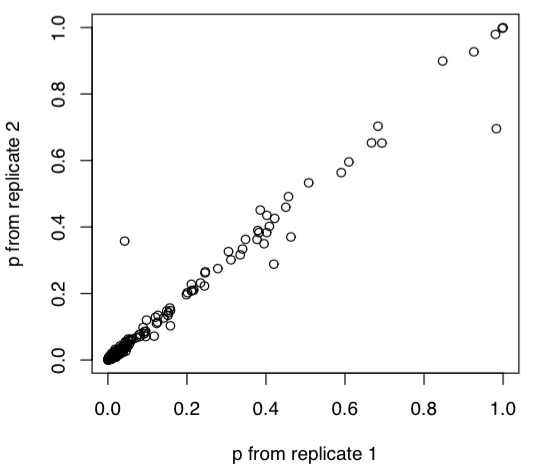
/Users/charles/Documents/research/antigenic/GenoPheno/driver/clustering/analysisManuscript2-12-2015/H3N2/concordance/GelmanRubinStat\_mds0\_15\_with\_ponGT0\_1\_in\_rep1.png



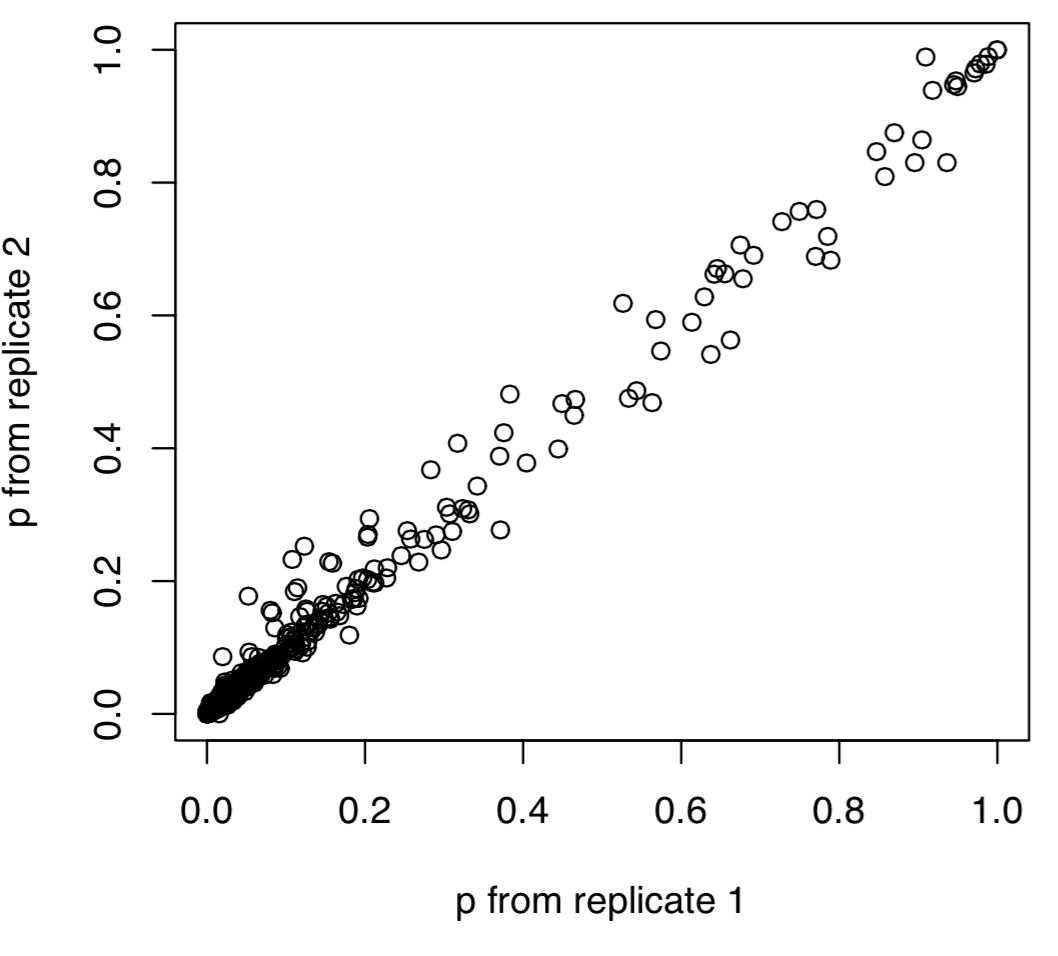
/Users/charles/Documents/research/antigenic/GenoPheno/driver/clustering/analysisManuscript2-12-2015/H3N2/concordance/H3N2-C3b-mds0\_05-concordance.eps



/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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see dropbox for other samples