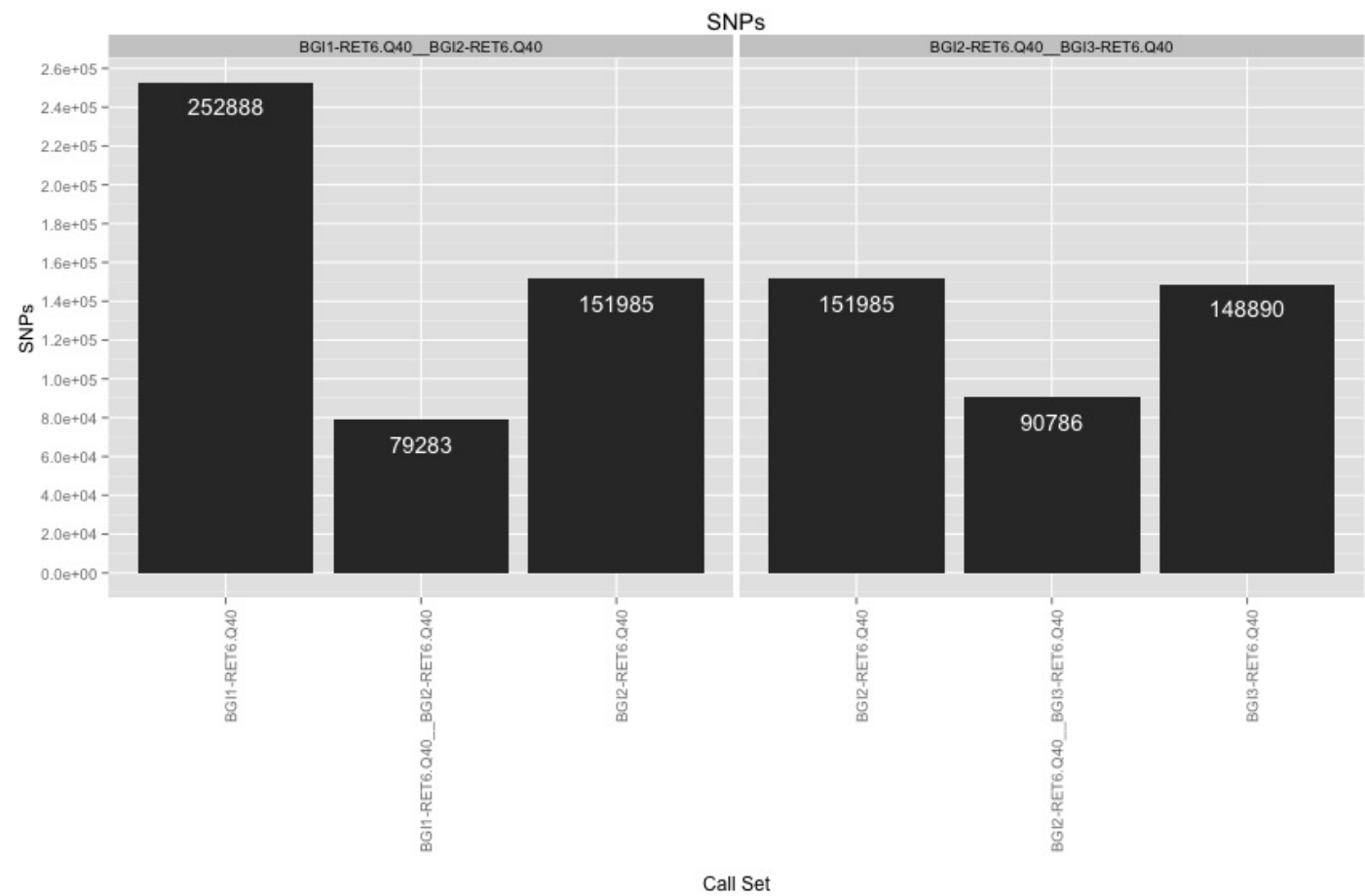


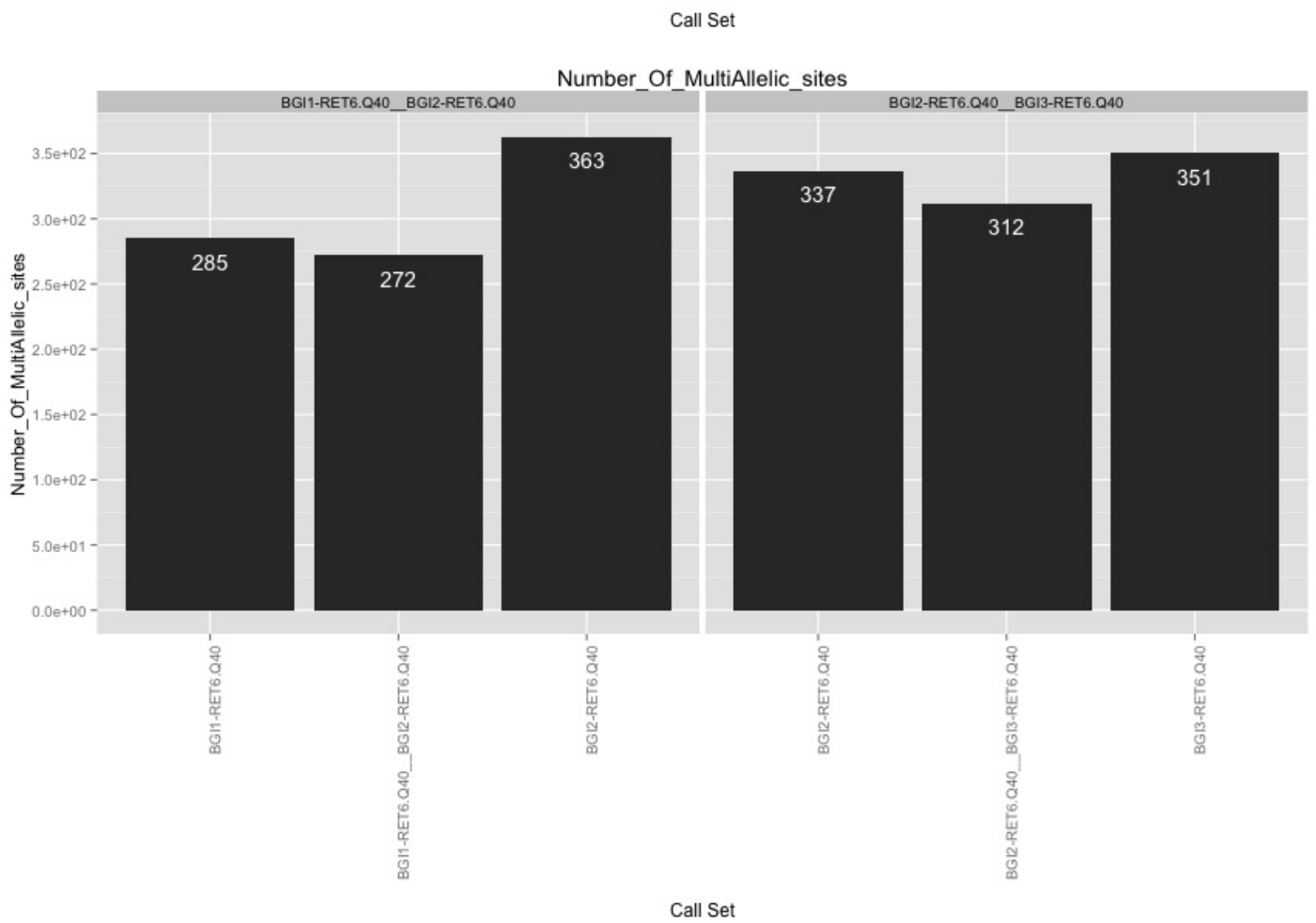
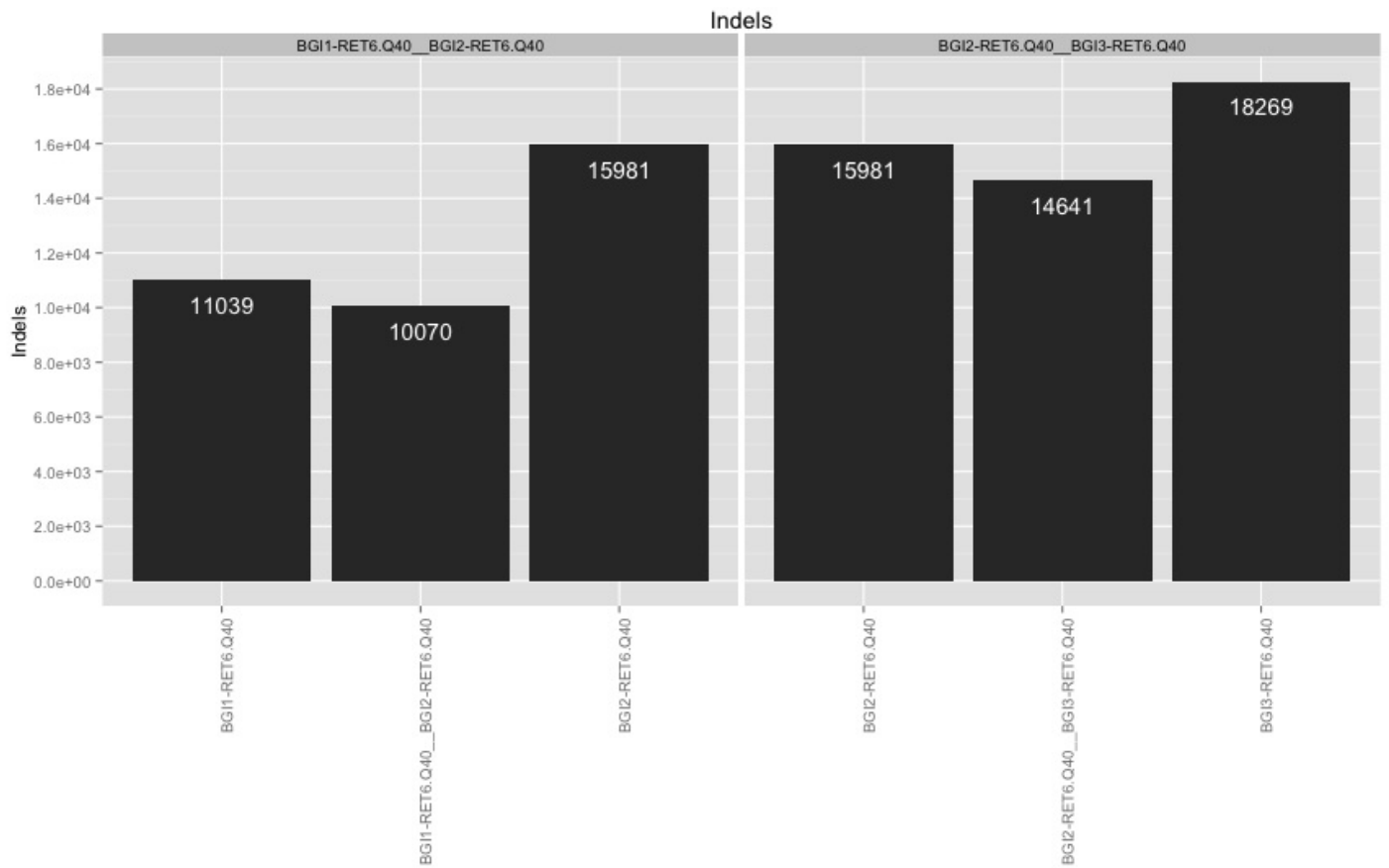
# VCF Compare Script

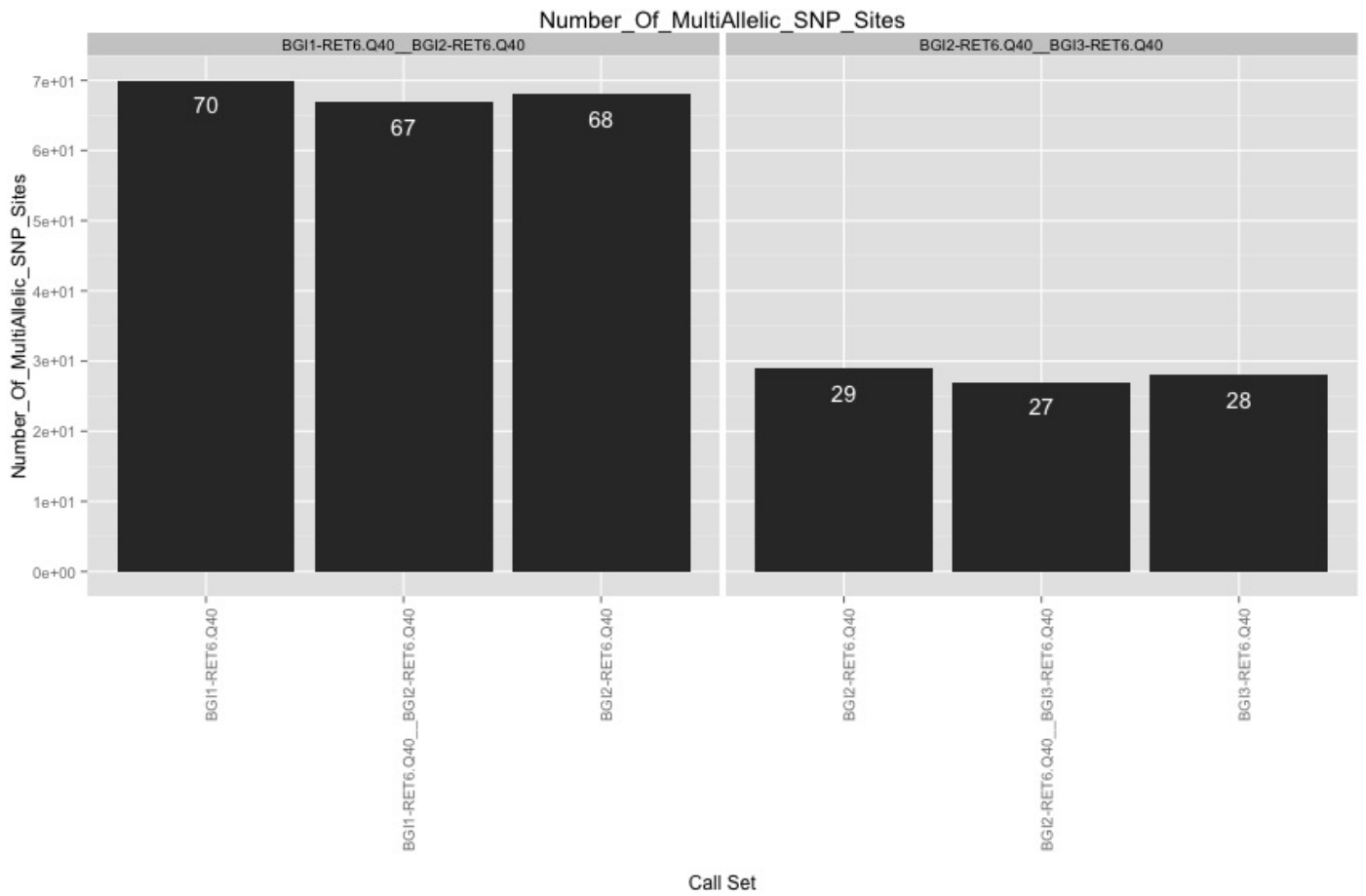
## Files

[1] "BGI1-RET6.txt.Q40.vcf.gz" "BGI2-RET6.txt.Q40.vcf.gz" [3] "BGI3-RET6.txt.Q40.vcf.gz"

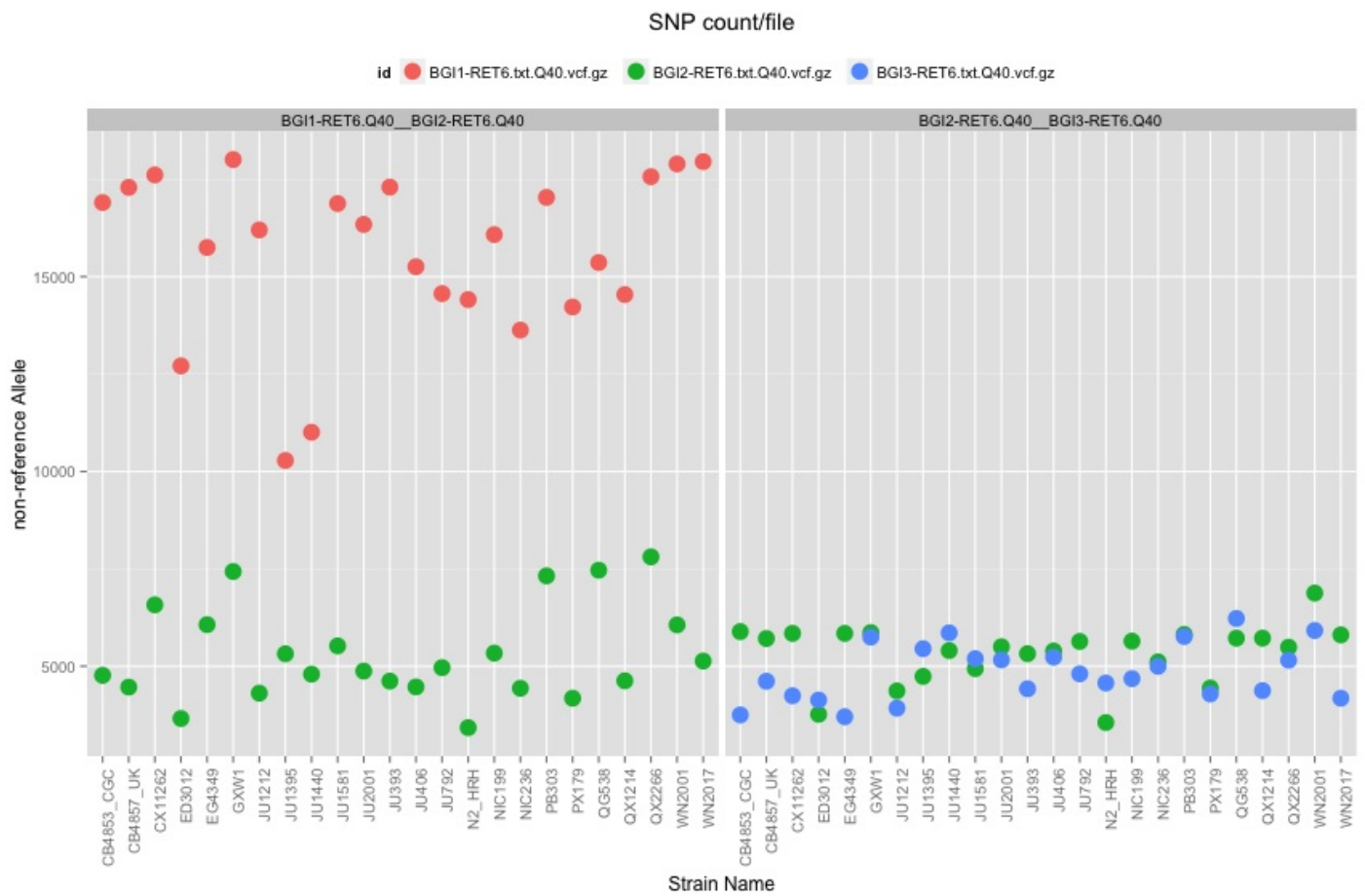
## Individual VCF Results





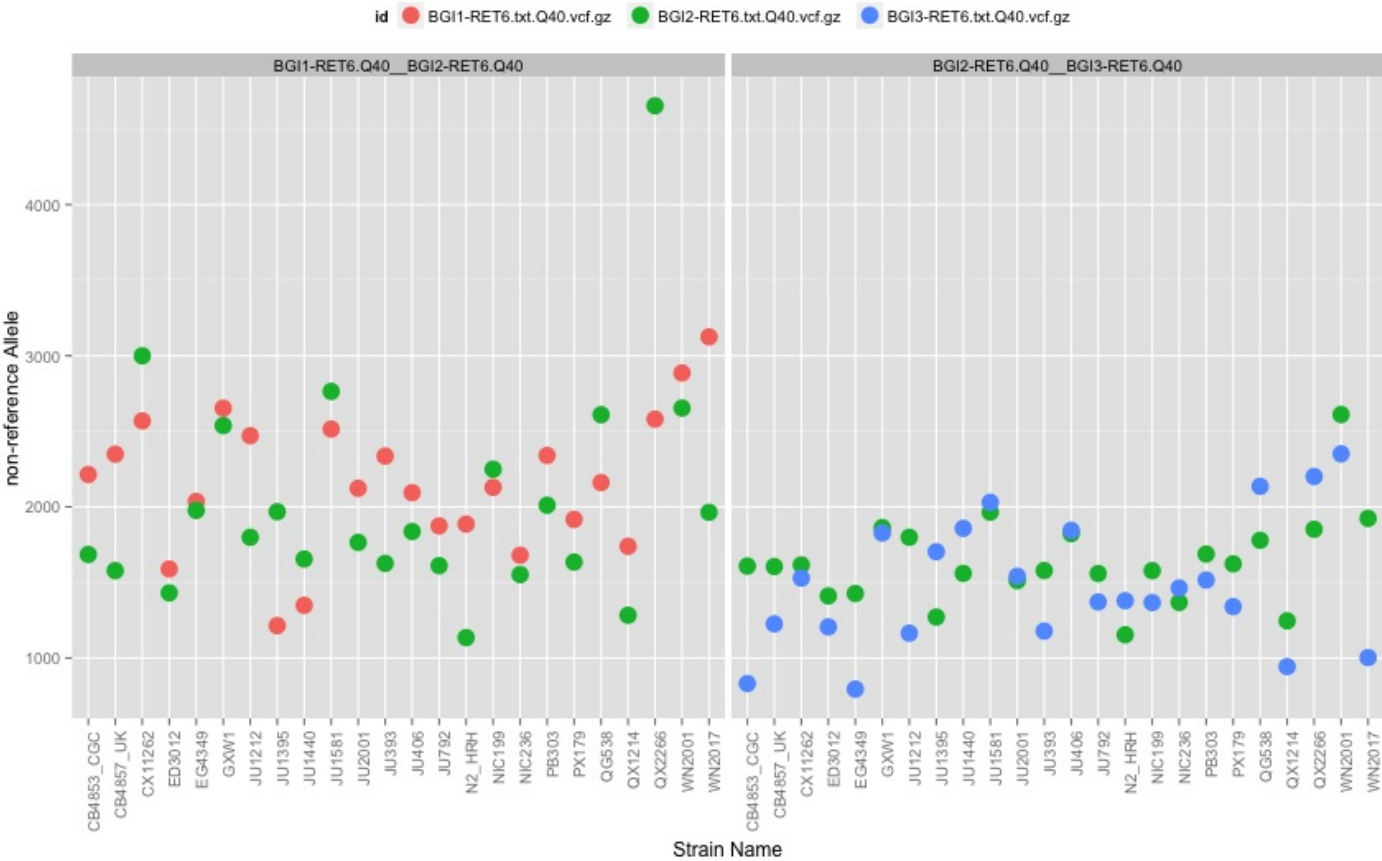


## Number of SNPs/Strain



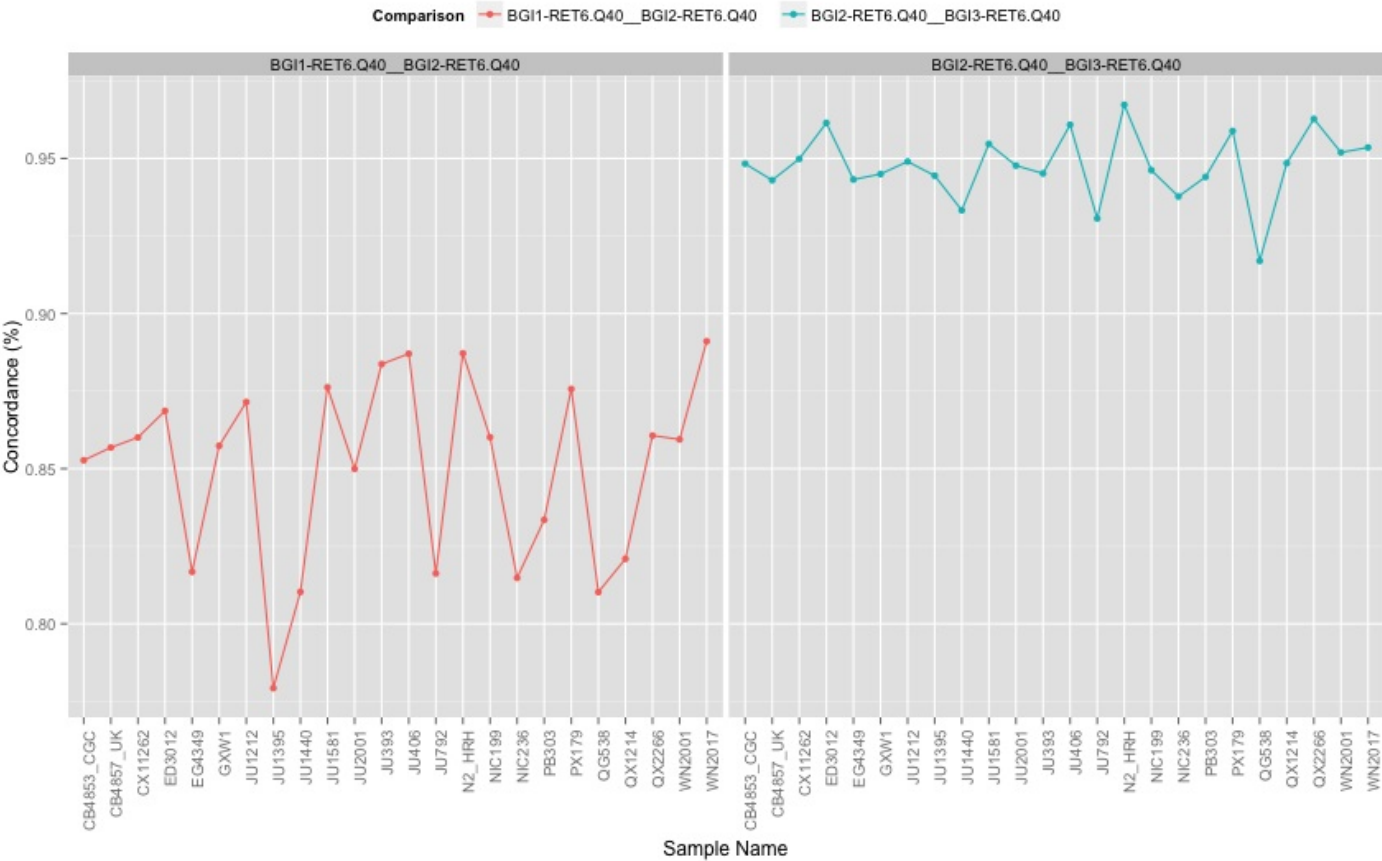
## Singletons

Singletons

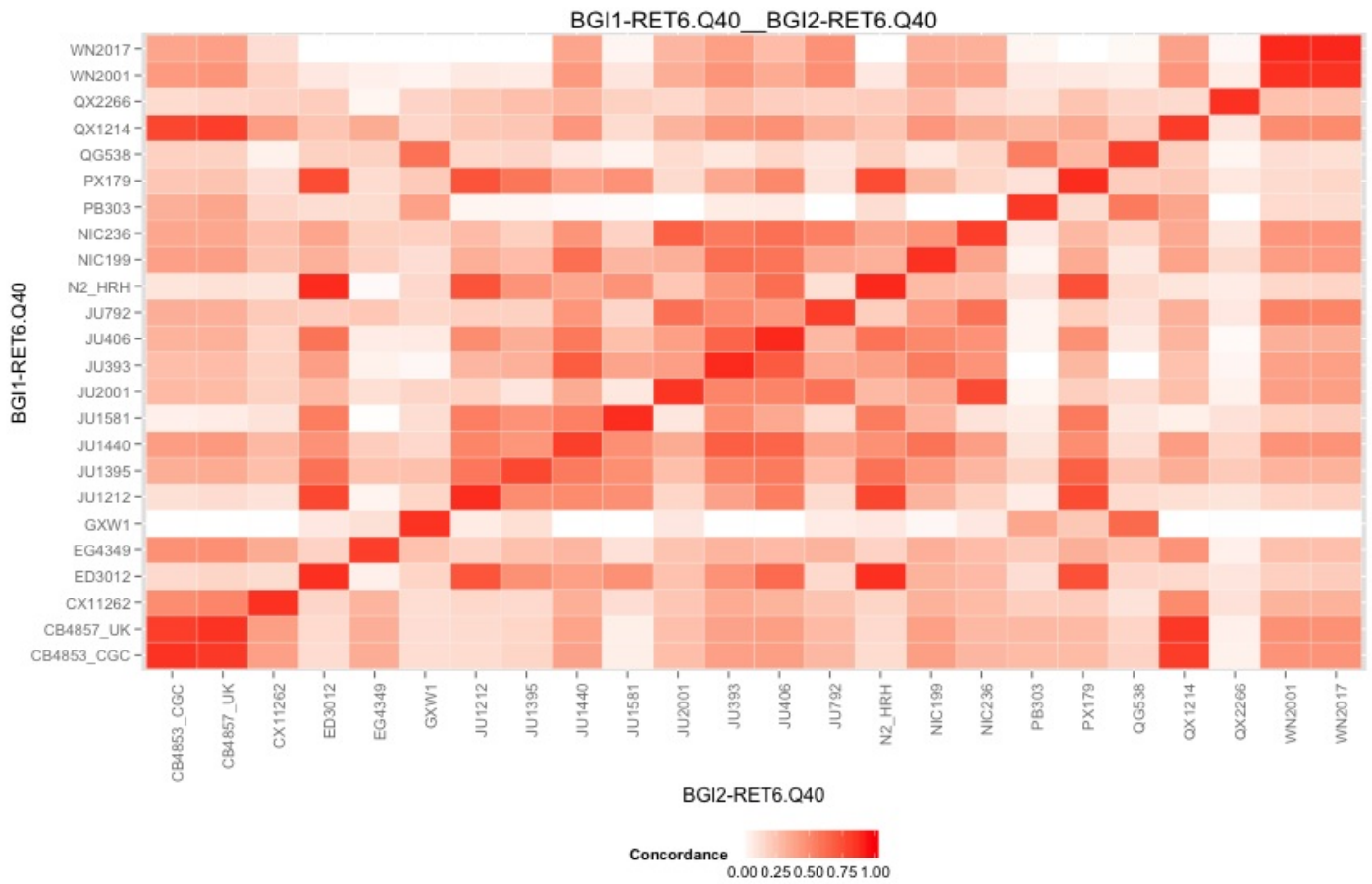


Ind. Sample Concordance

Concordance by Strain



Pairwise Concordance



[[2]]

