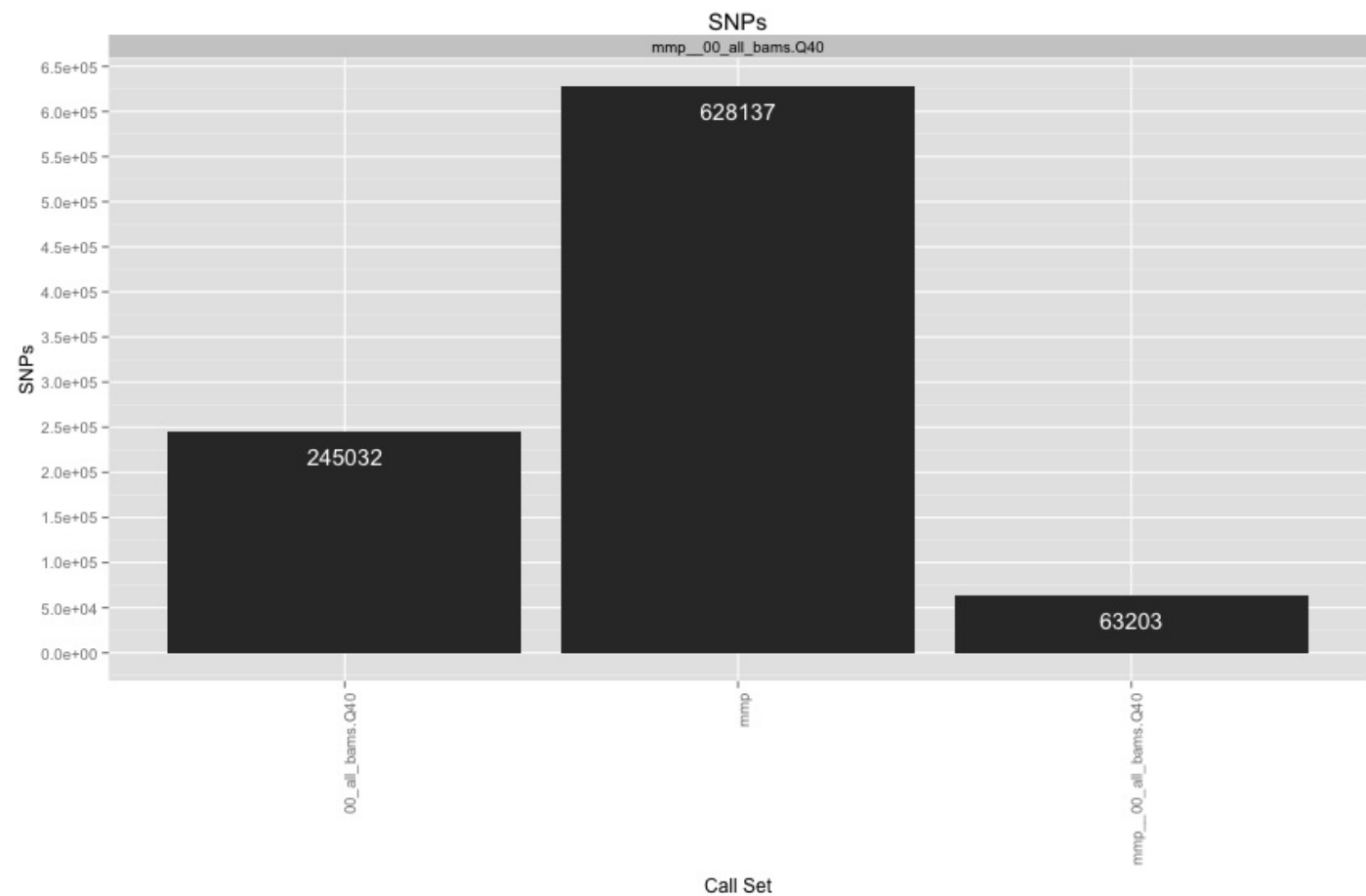


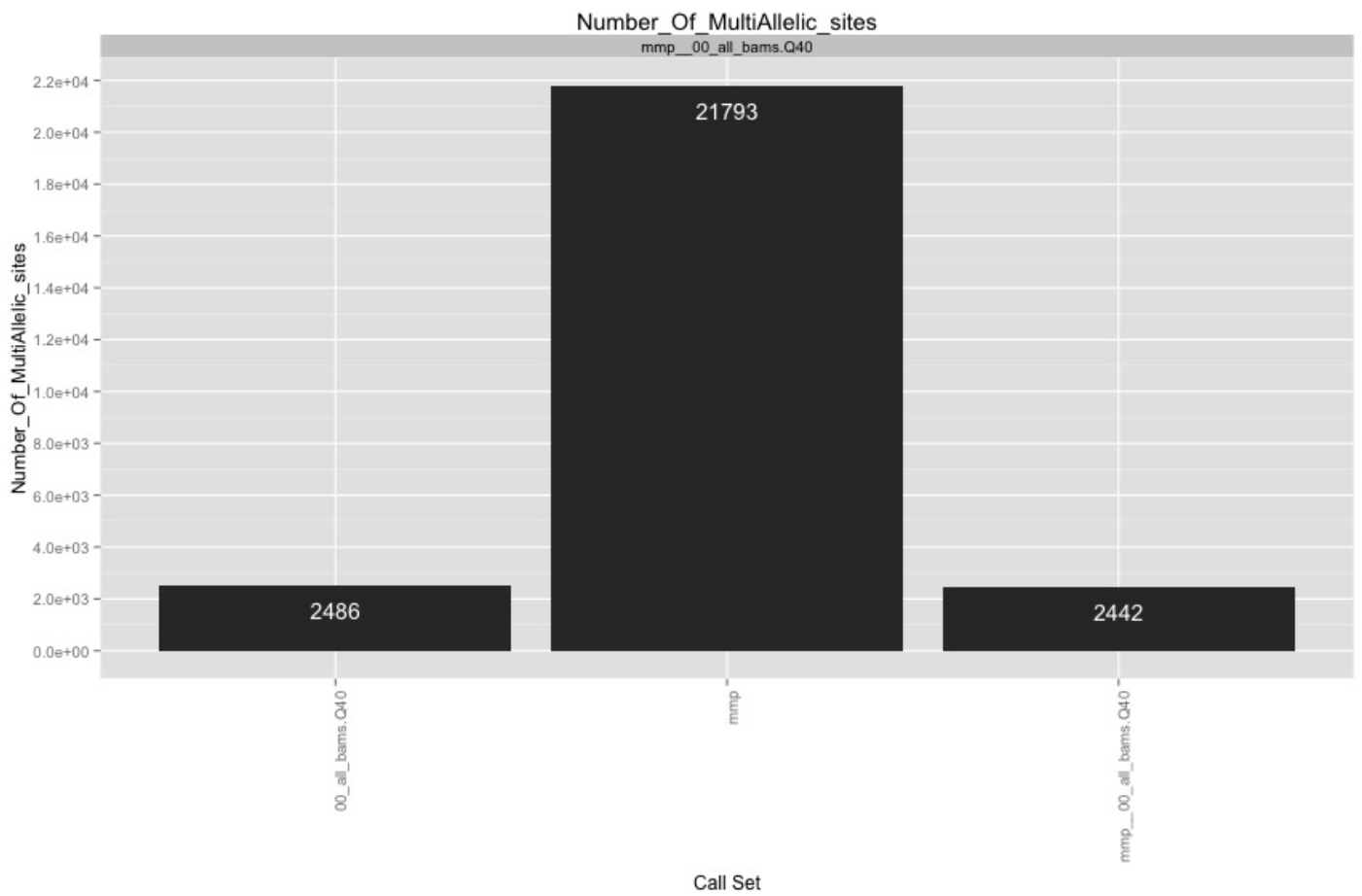
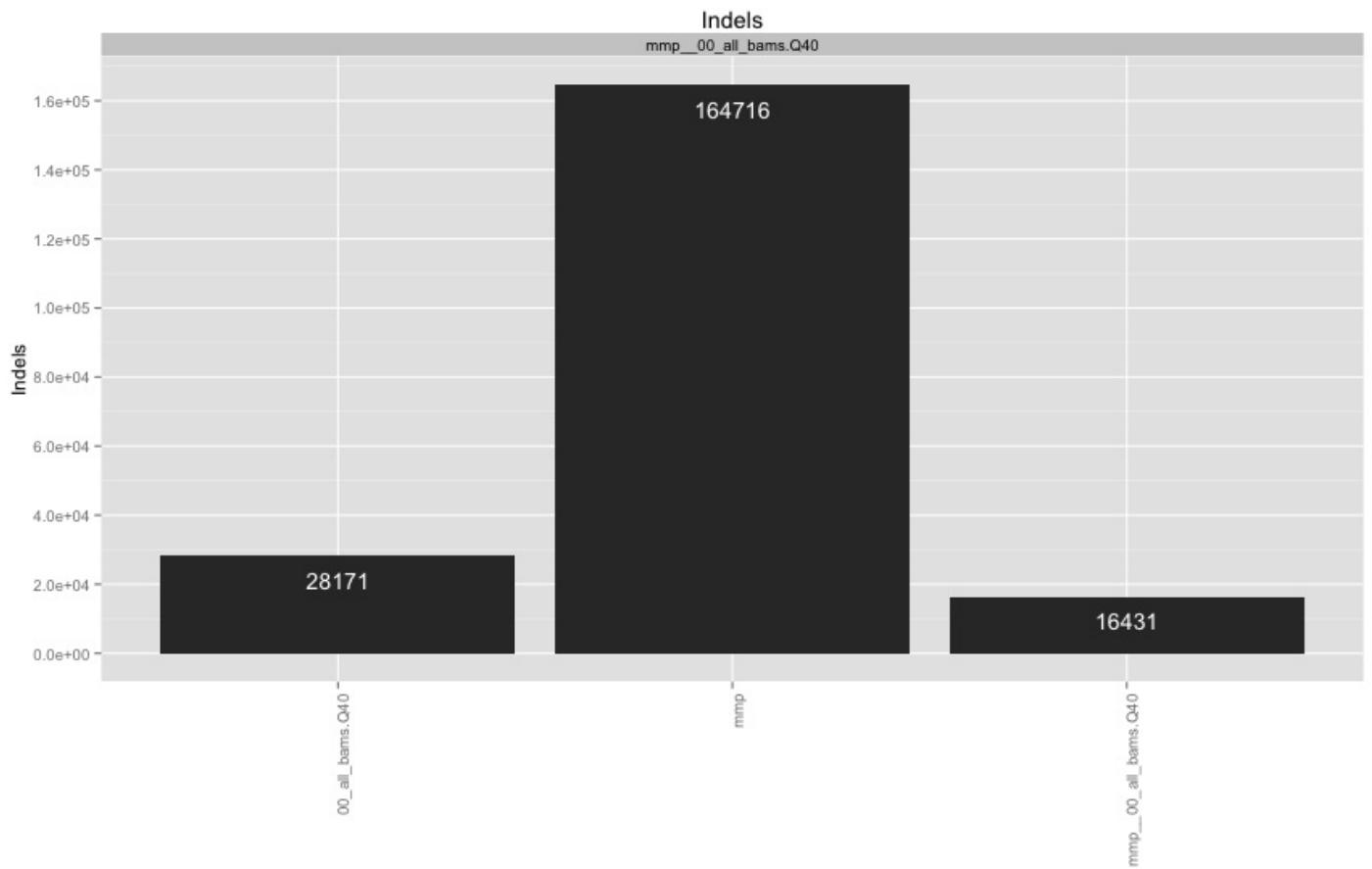
# VCF Compare Script

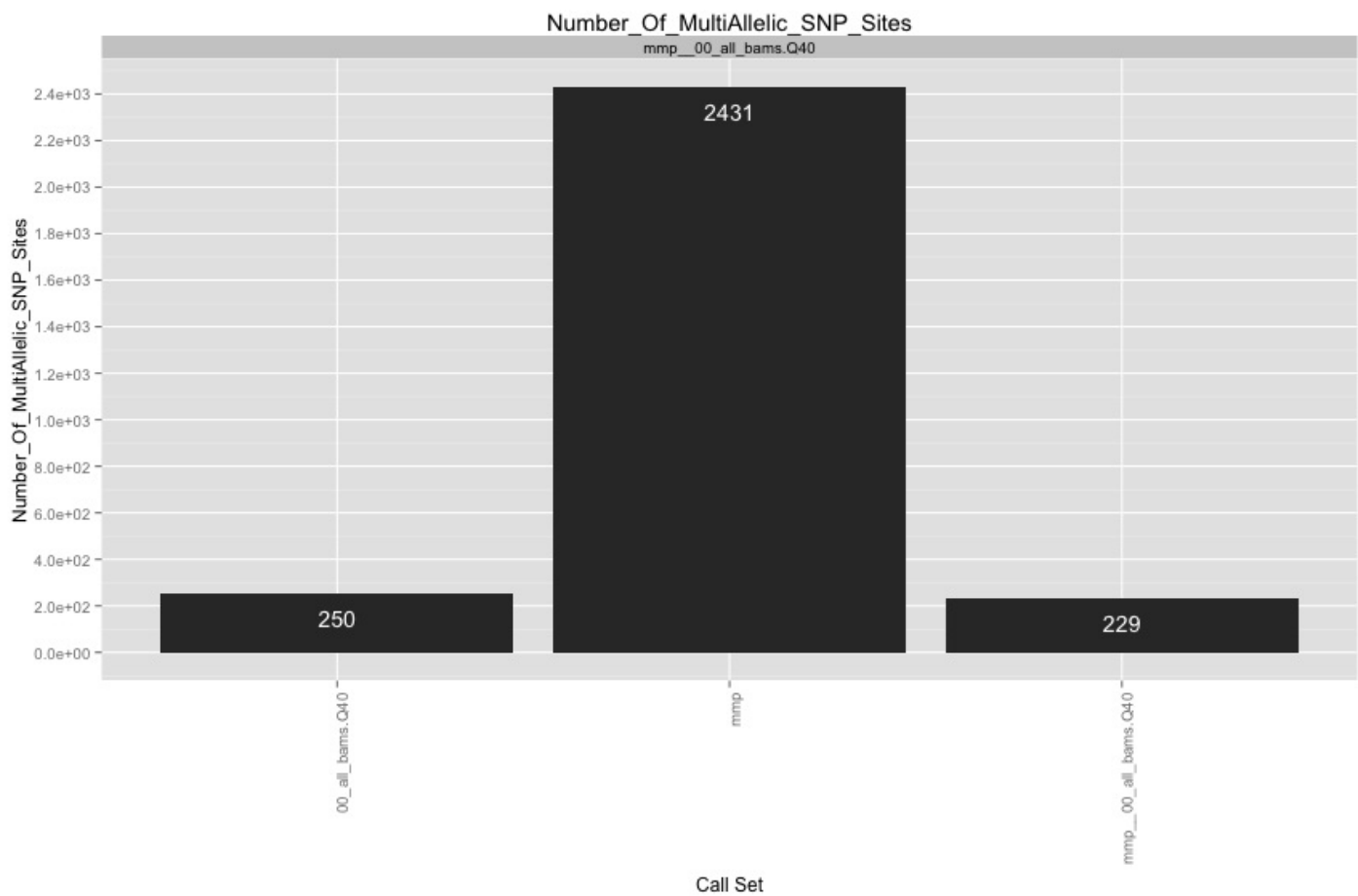
## Files

[1] "mmp.vcf.gz" "00a//bams.txt.Q40.vcf.gz"

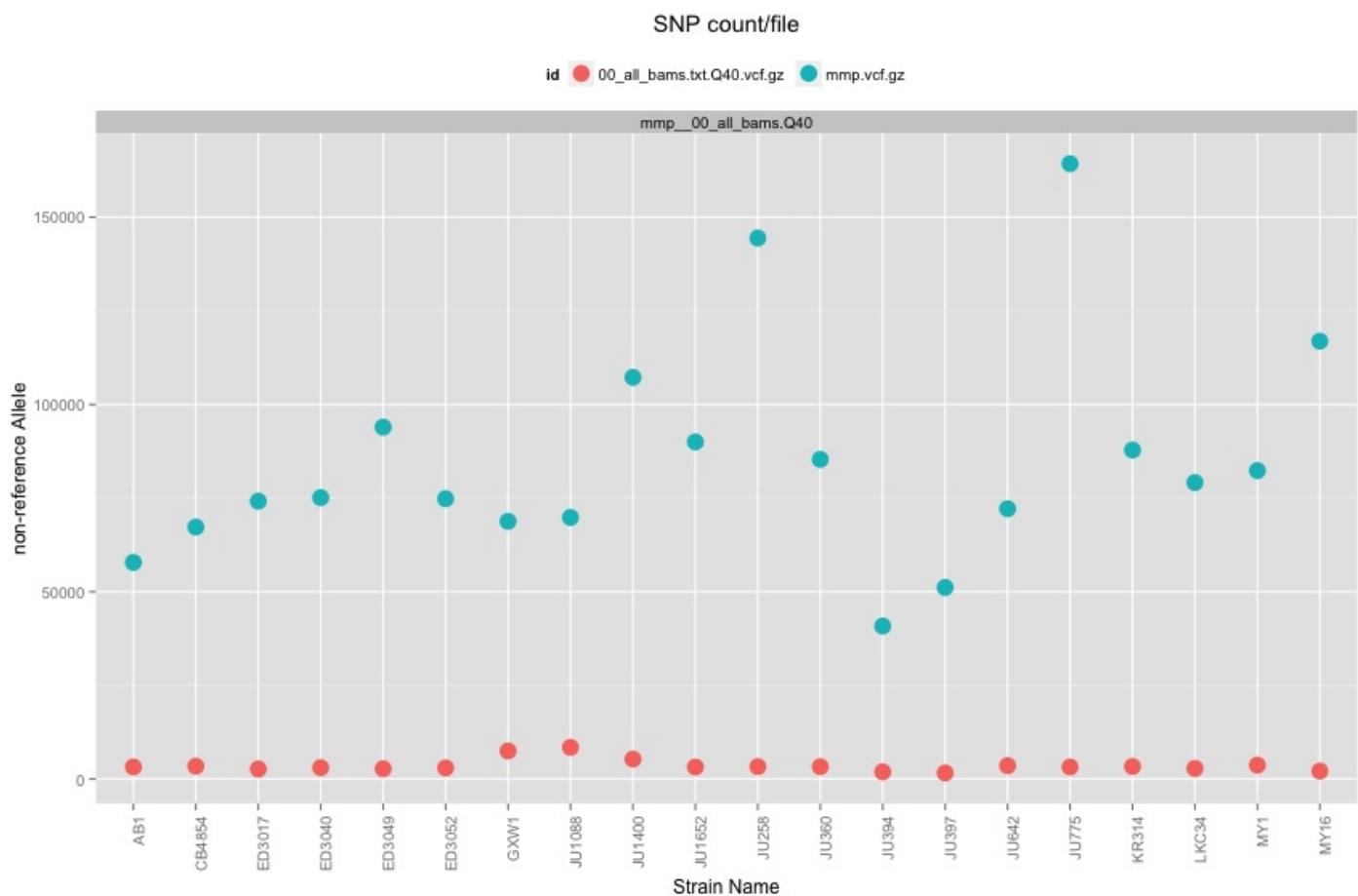
## Individual VCF Results



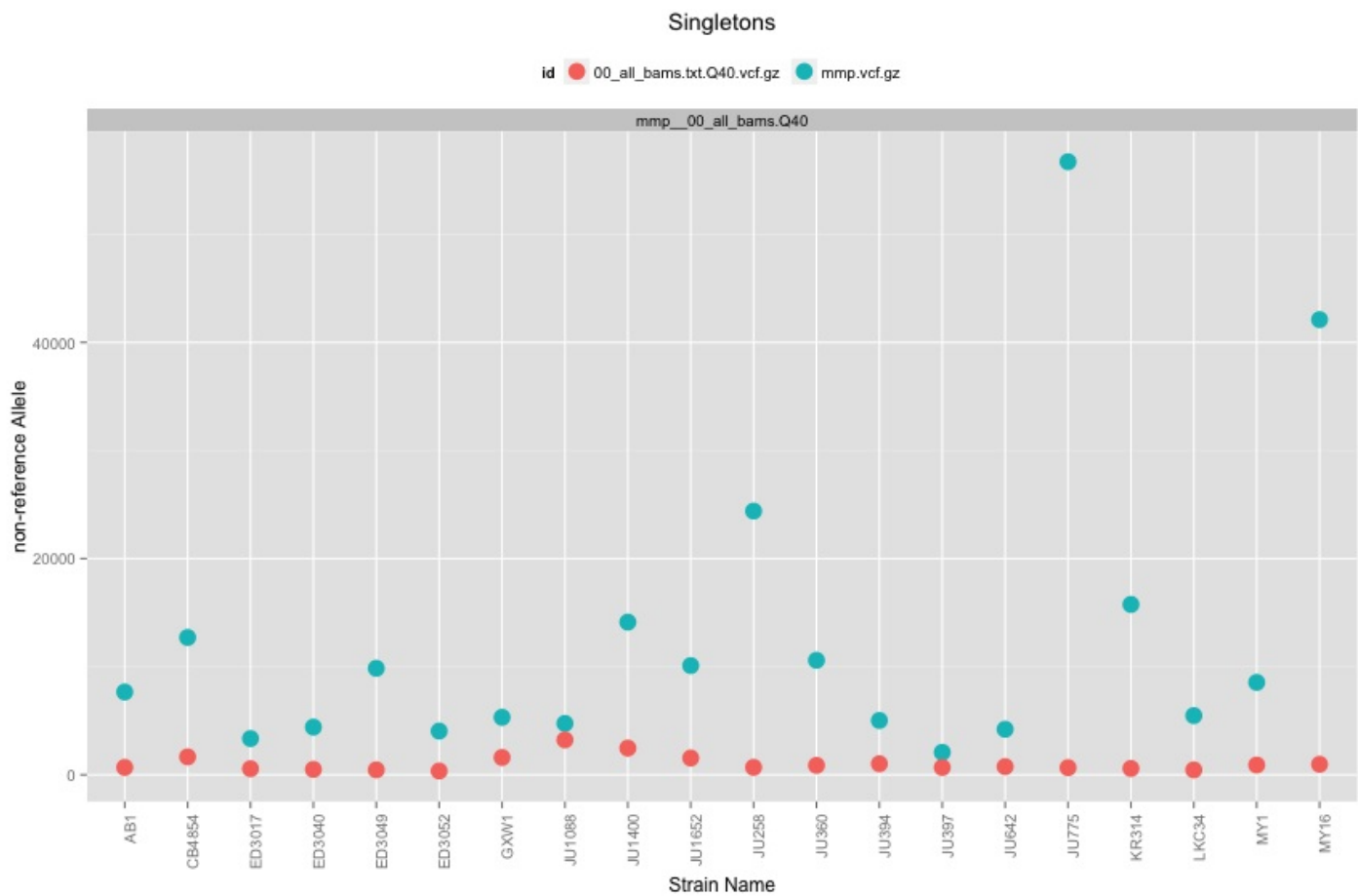




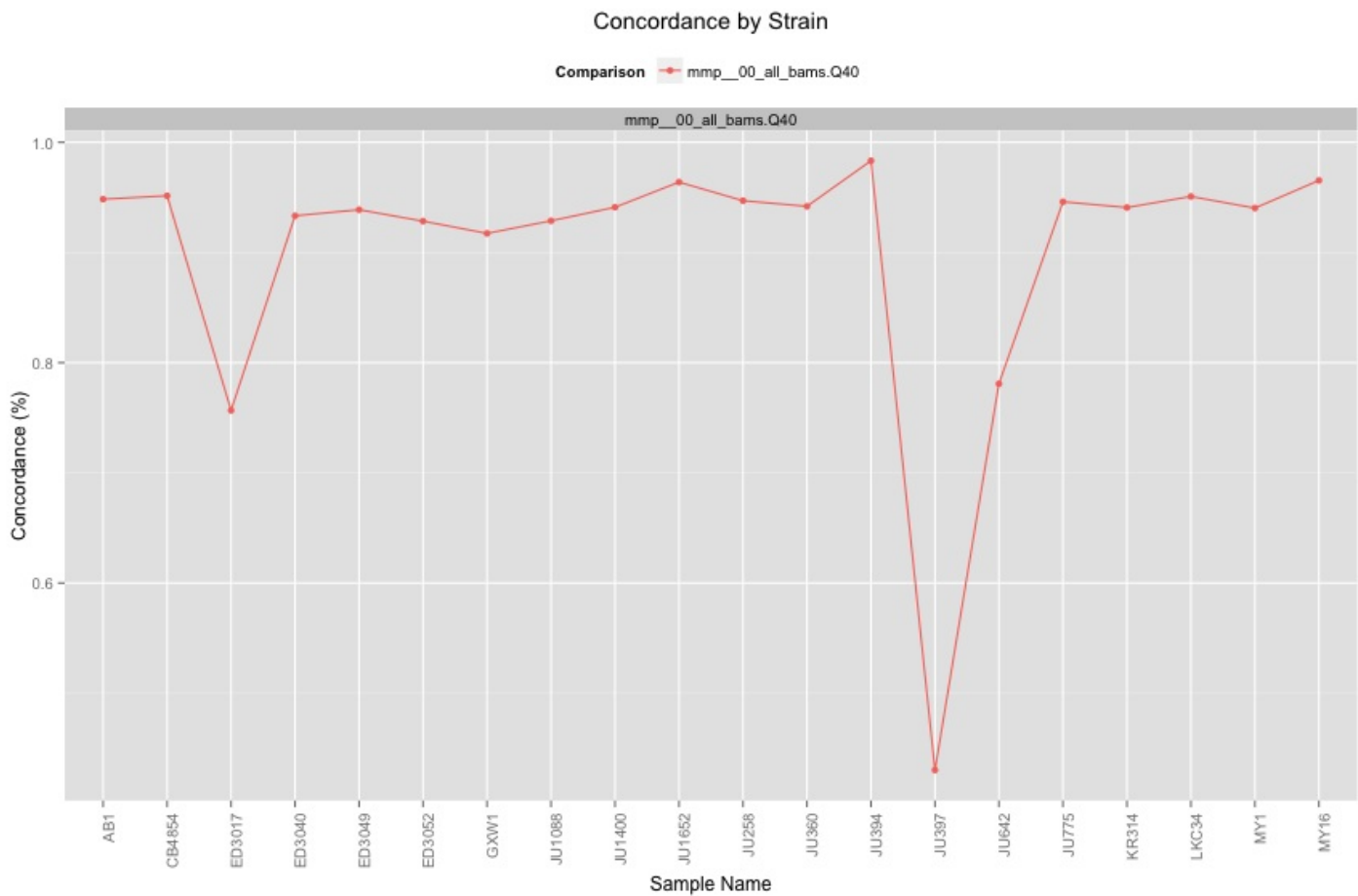
## Number of SNPs/Strain



## Singletons



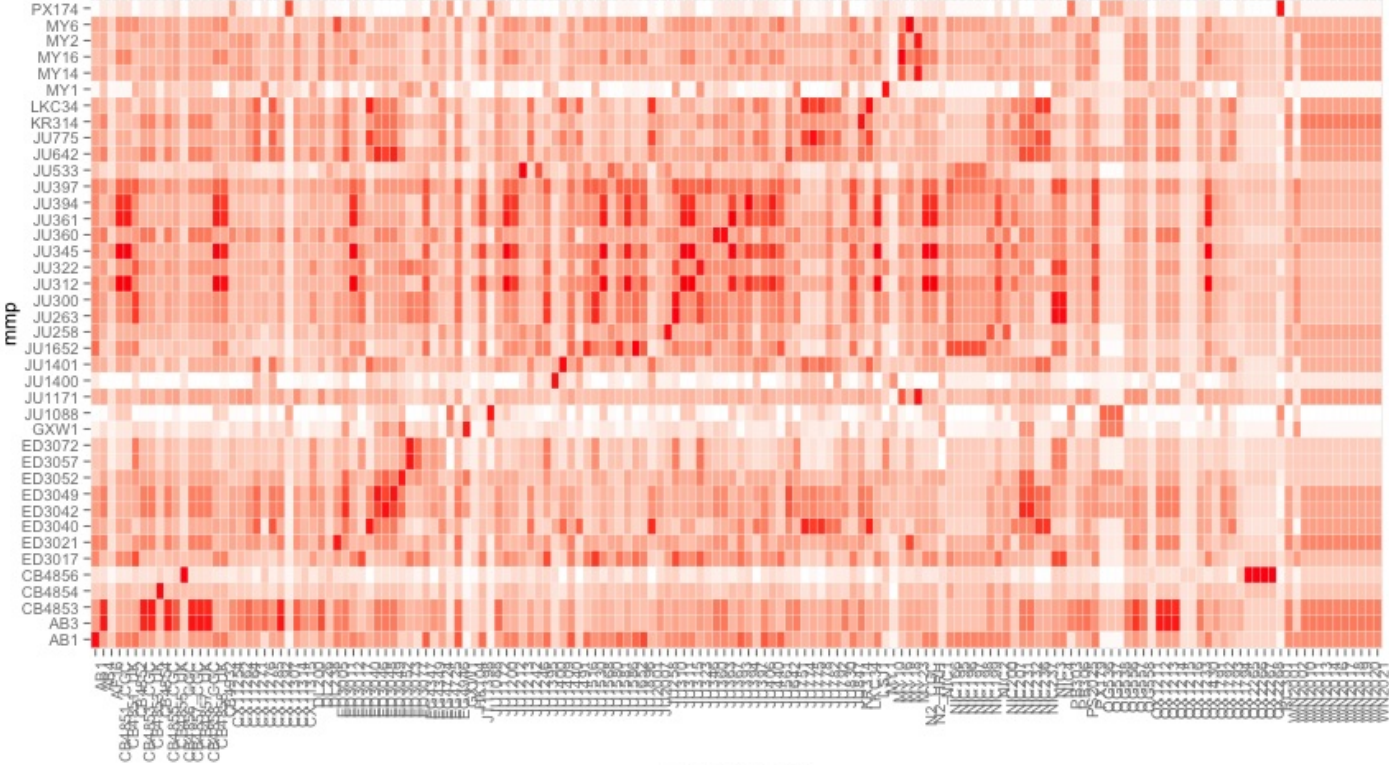
Ind. Sample Concordance



Pairwise Concordance

[[1]]

mmp\_00\_all\_bams.Q40



00\_all\_bams.Q40

Concordance 0.00 0.25 0.50 0.75 1.00