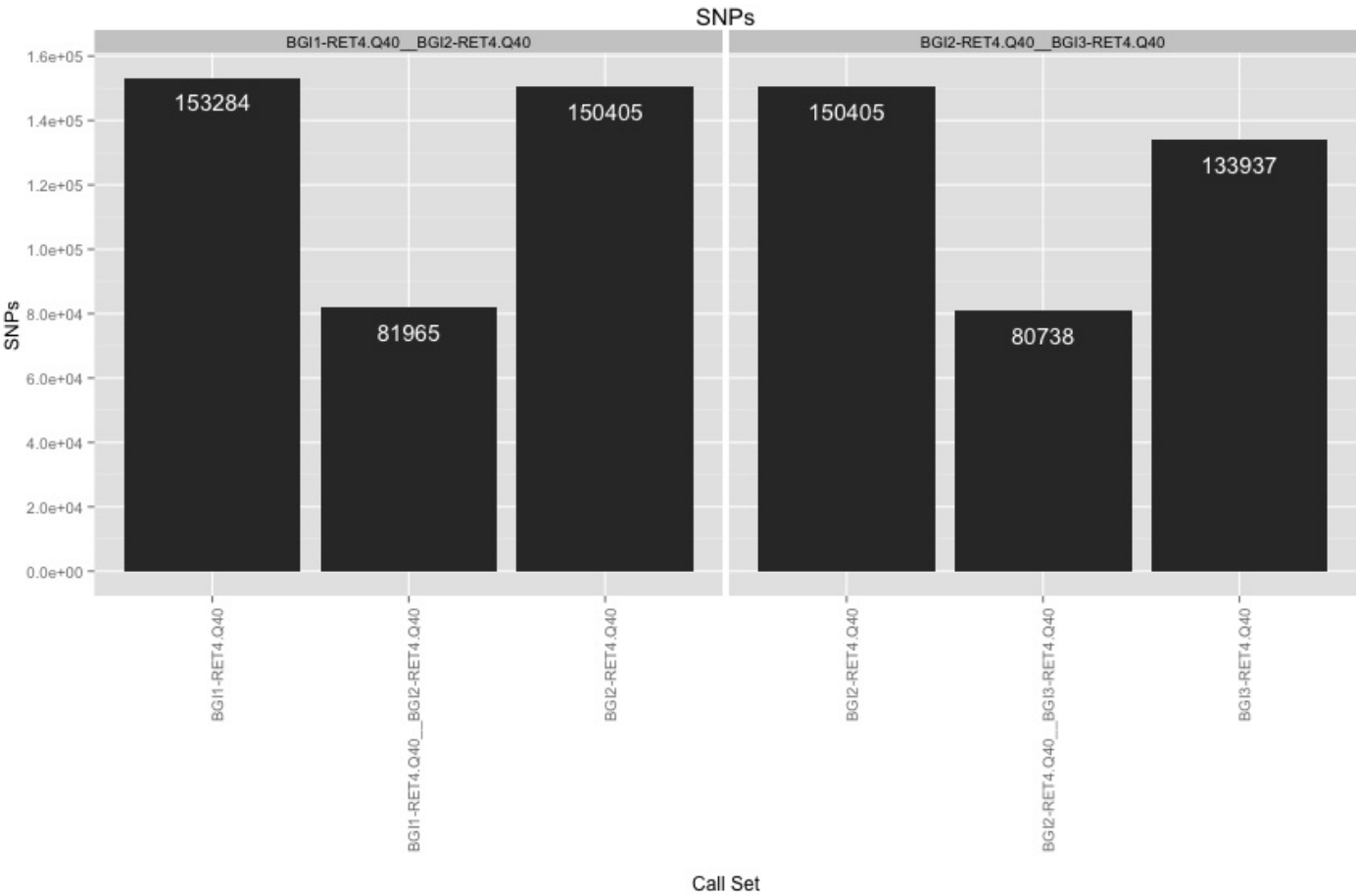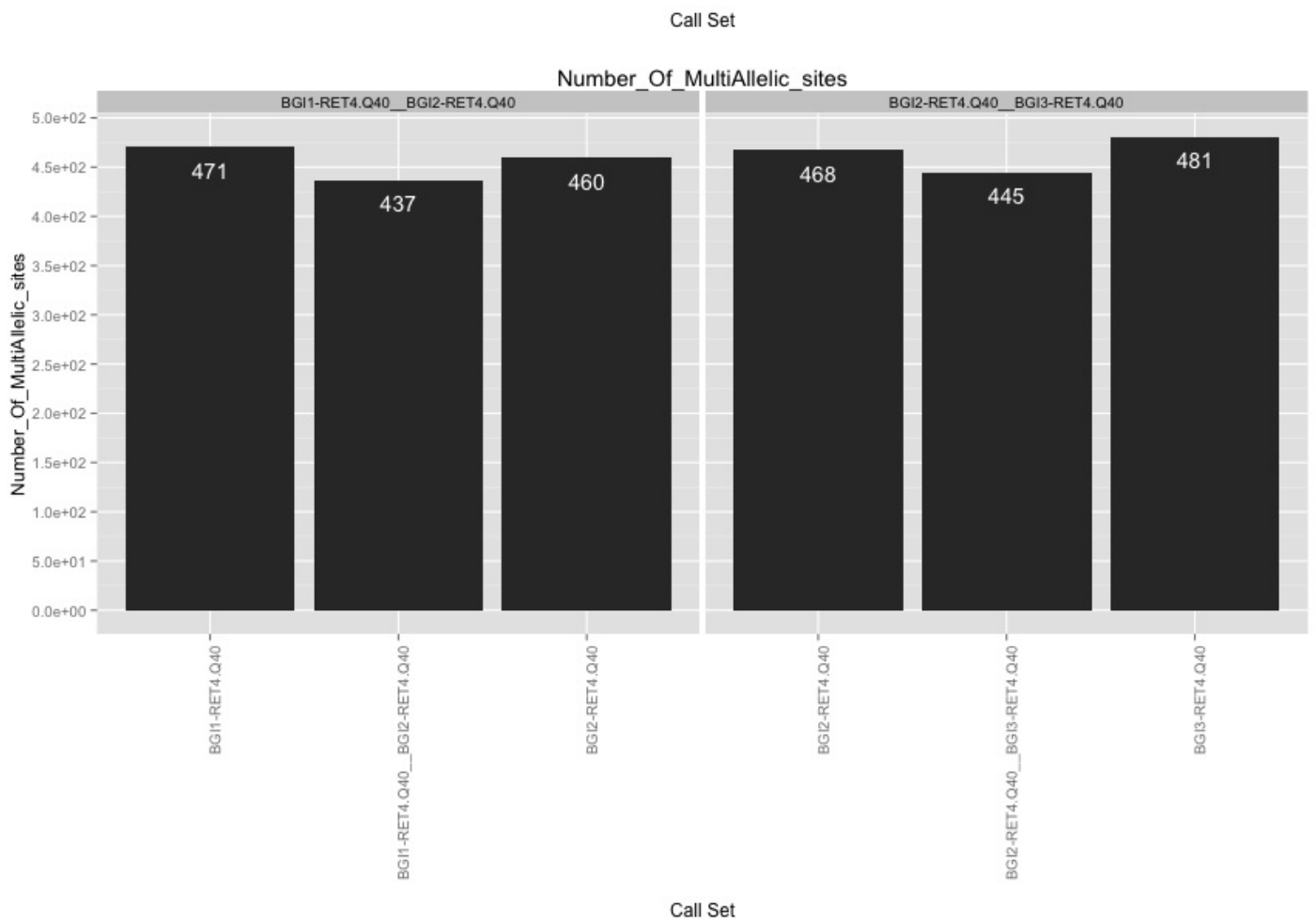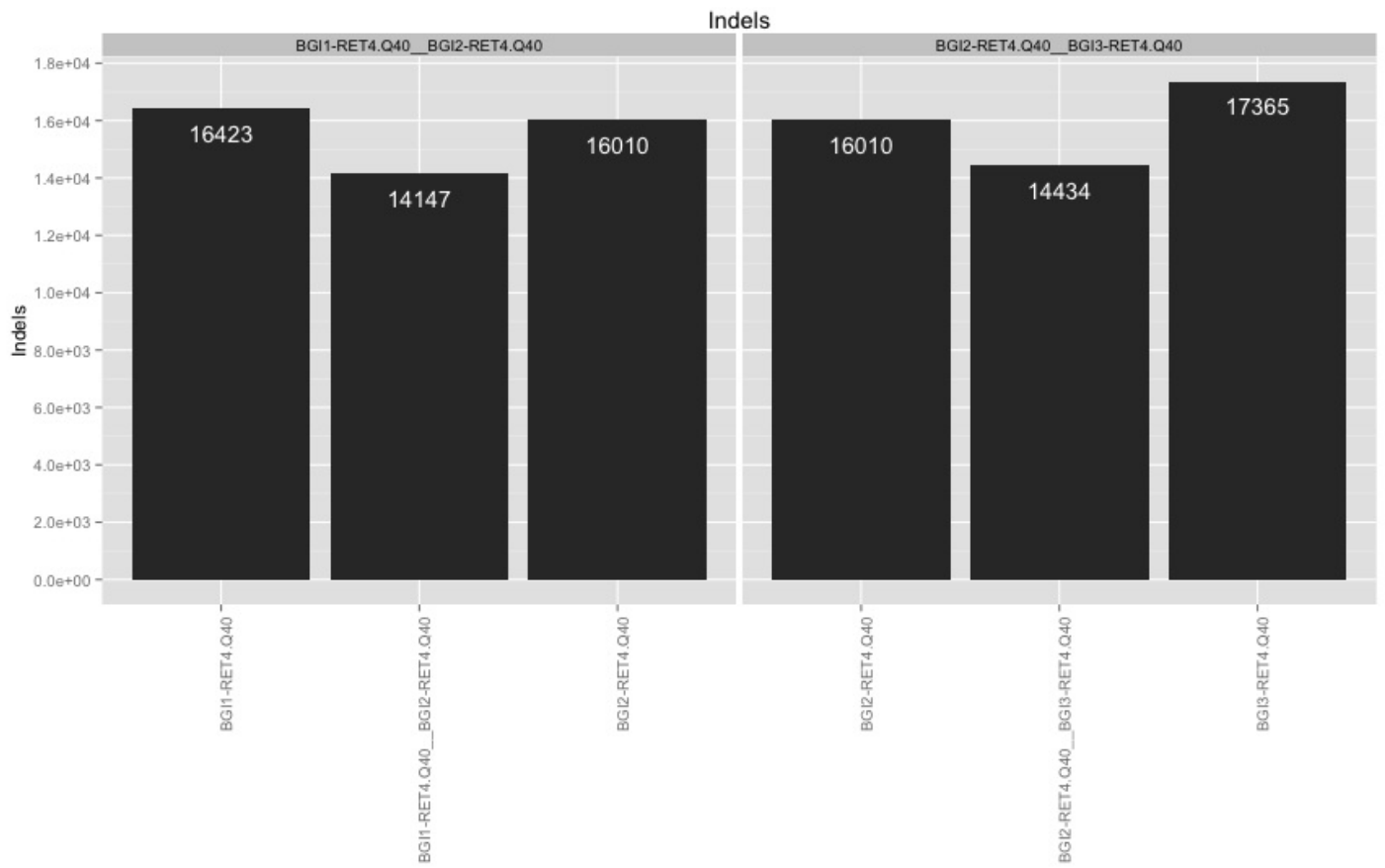# VCF Compare Script
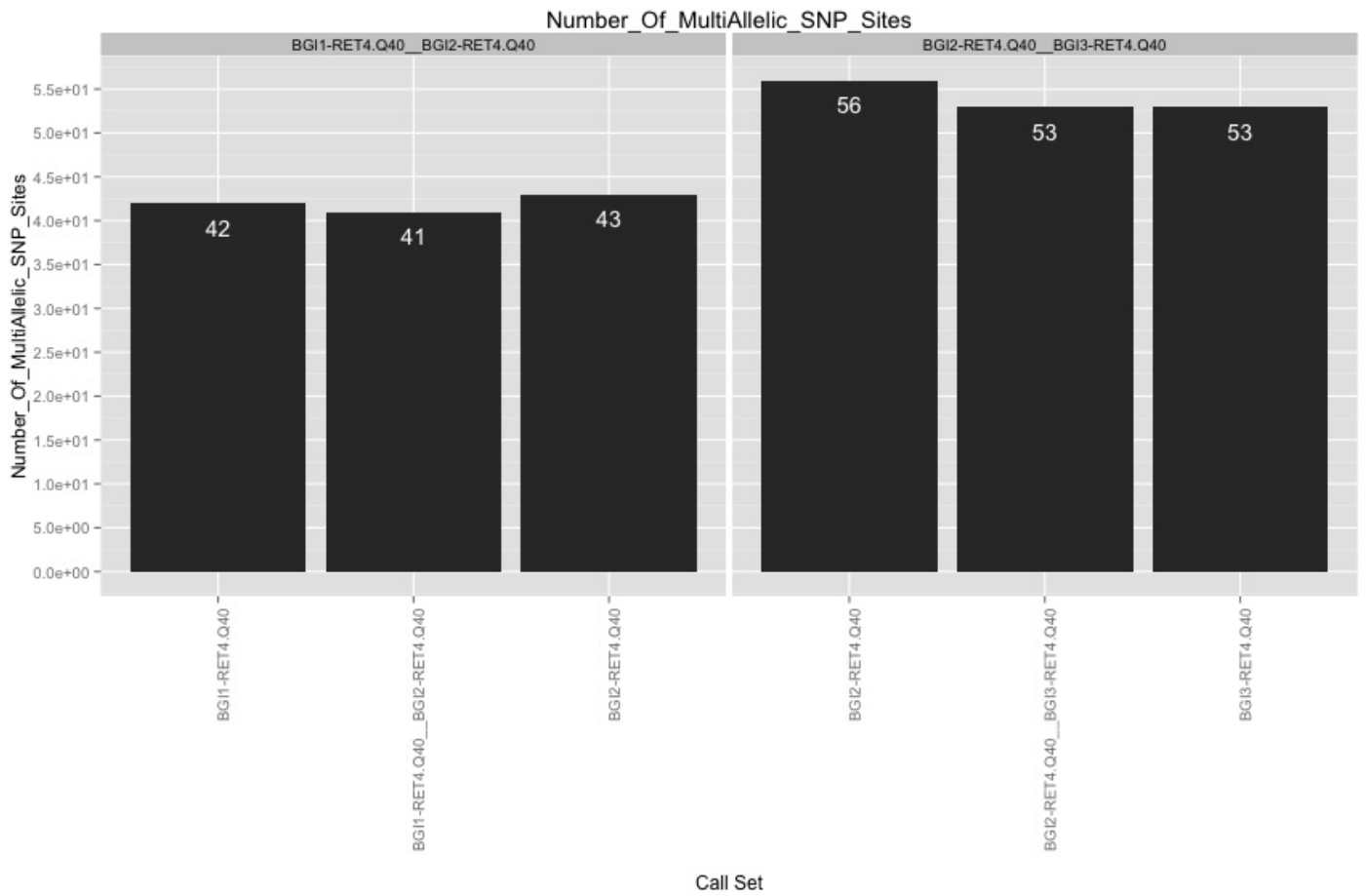
Files

[1] "BGI1-RET4.txt.Q40.vcf.gz" "BGI2-RET4.txt.Q40.vcf.gz" [3] "BGI3-RET4.txt.Q40.vcf.gz"

Individual VCF Results

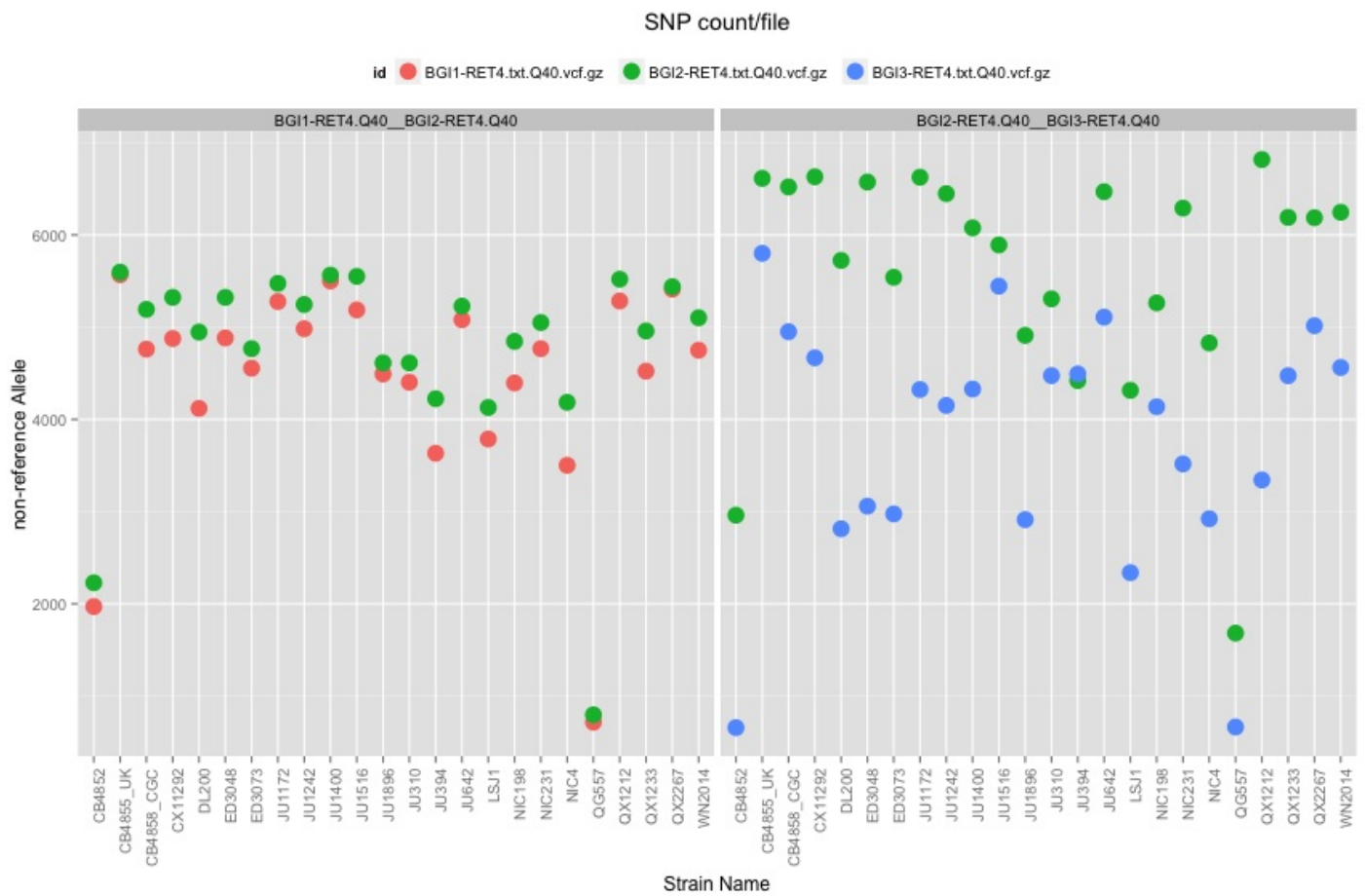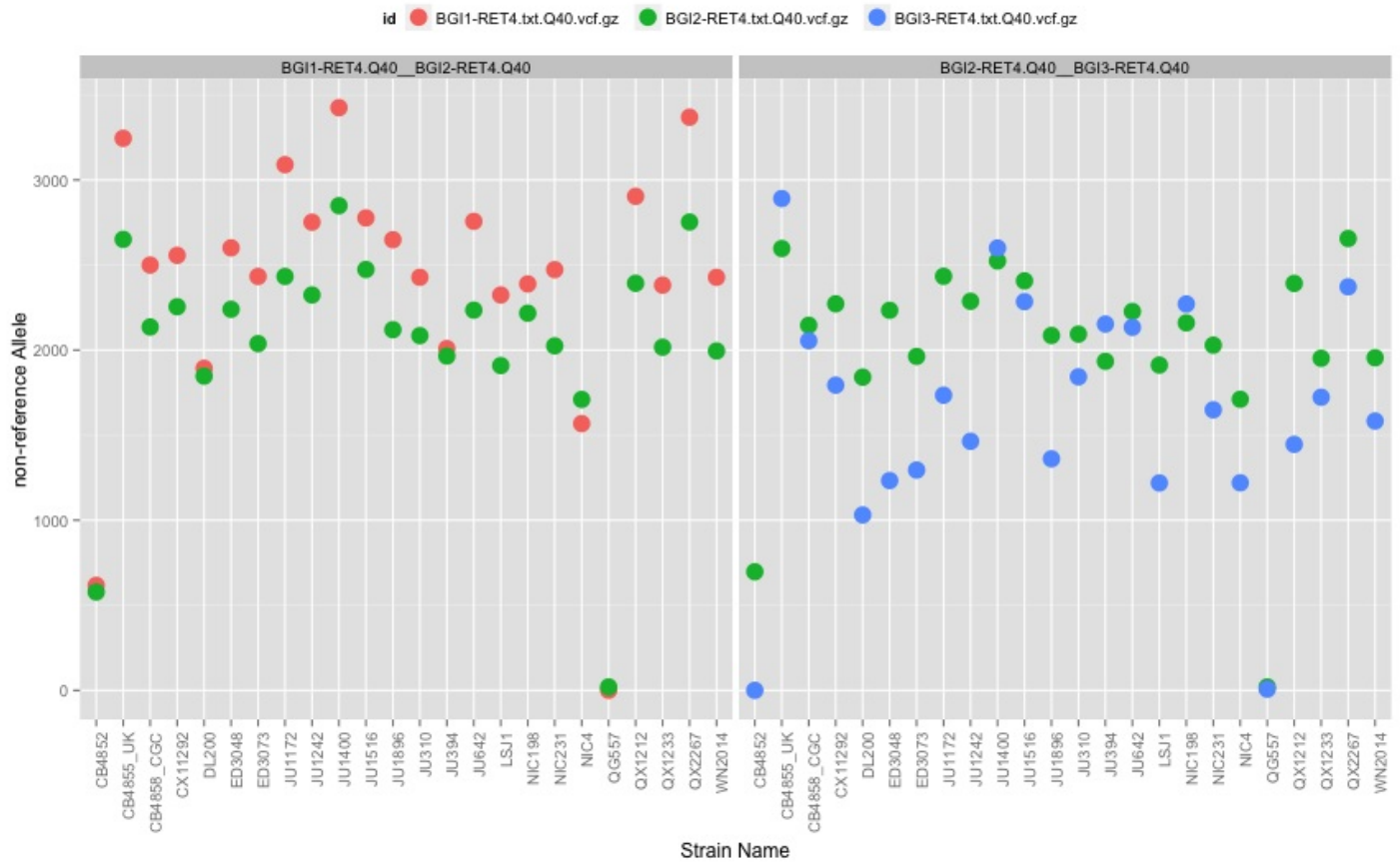# Indels

BGI1-RET4.Q40__BGI2-RET4.Q40	BGI2-RET4.Q40__BGI3-RET4.Q40

Number_Of_MultiAllelic_sites

BGI1-RET4.Q40__BGI2-RET4.Q40	BGI2-RET4.Q40__BGI3-RET4.Q40

Number_Of_MultiAllelic_SNP_Sites
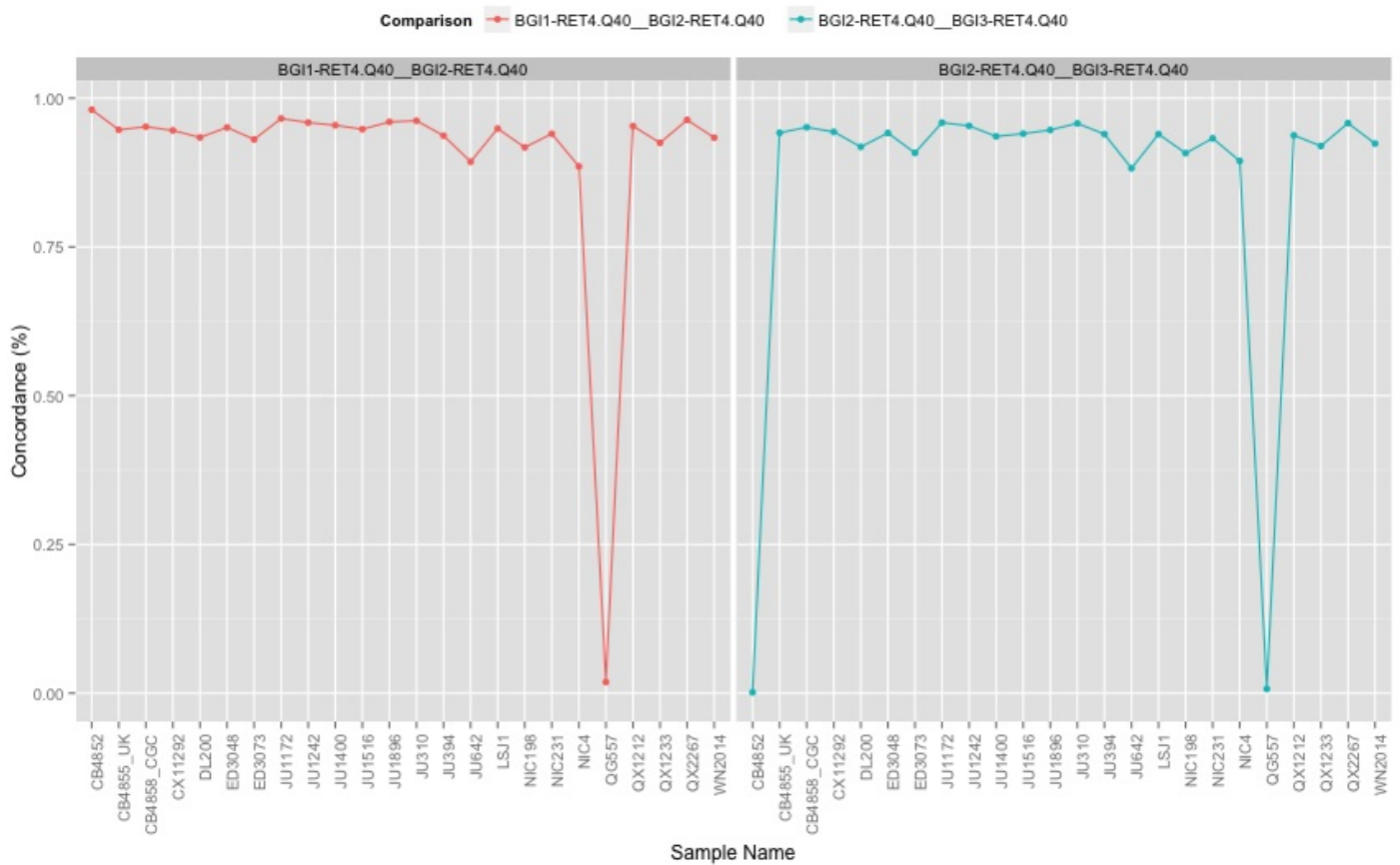
Number of SNPs/Strain
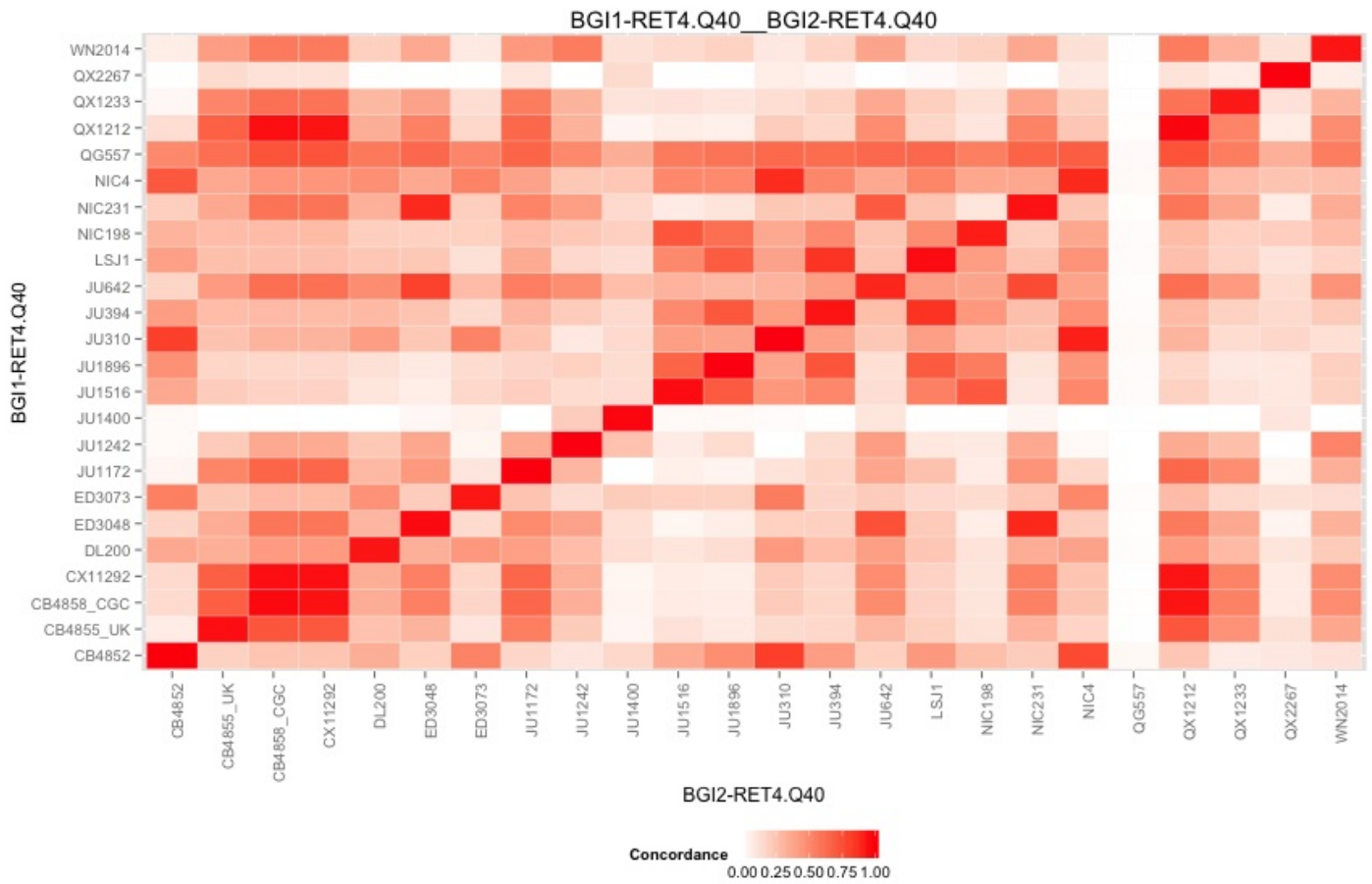

SNP count/file

Singletons

Singletons

Ind. Sample Concordance

Concordance by Strain

Pairwise Concordance

[[1]]

BGI1-RET4.Q40__BGI2-RET4.Q40

[[2]]

BGI2-RET4.Q40__BGI3-RET4.Q40