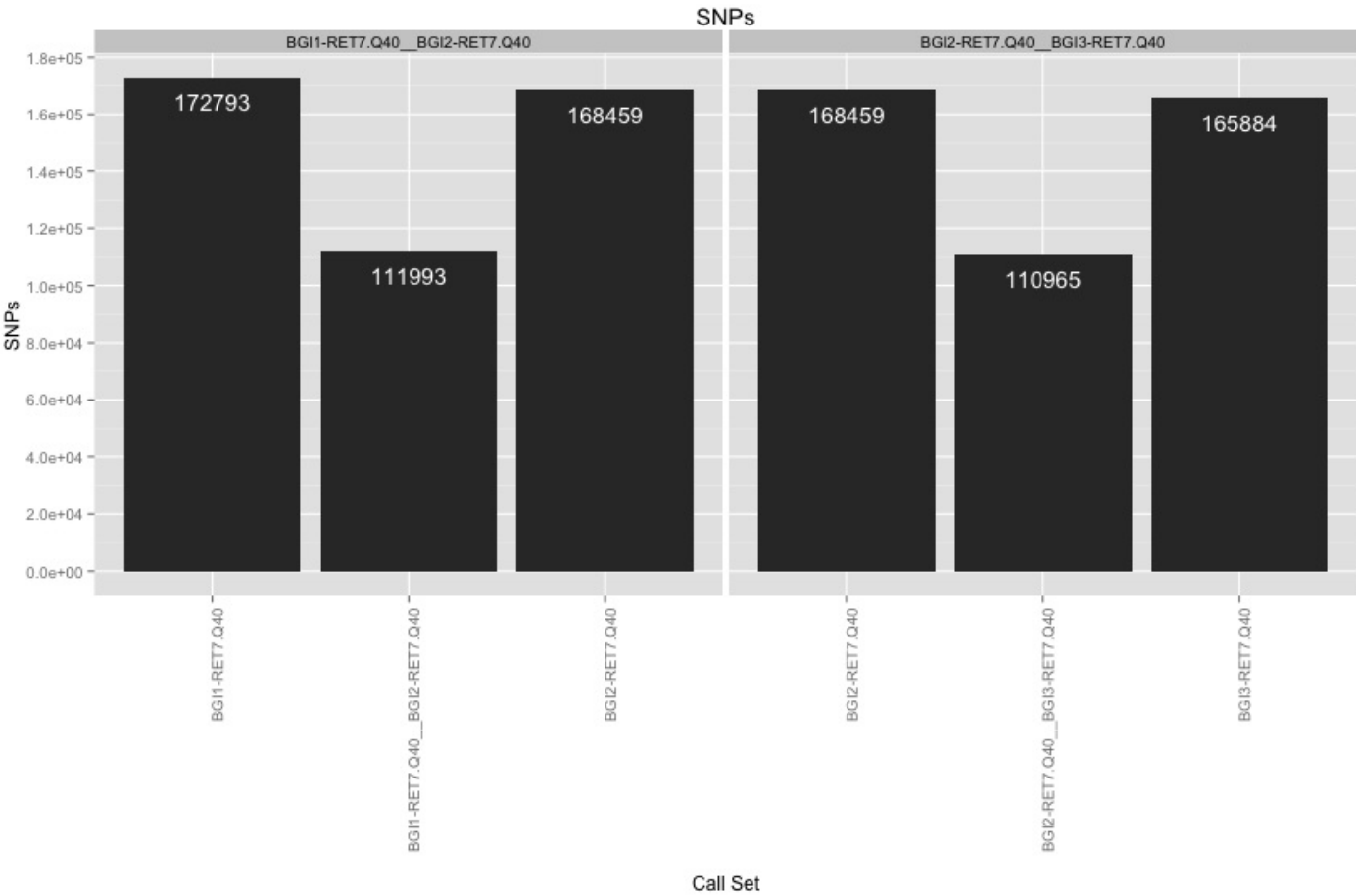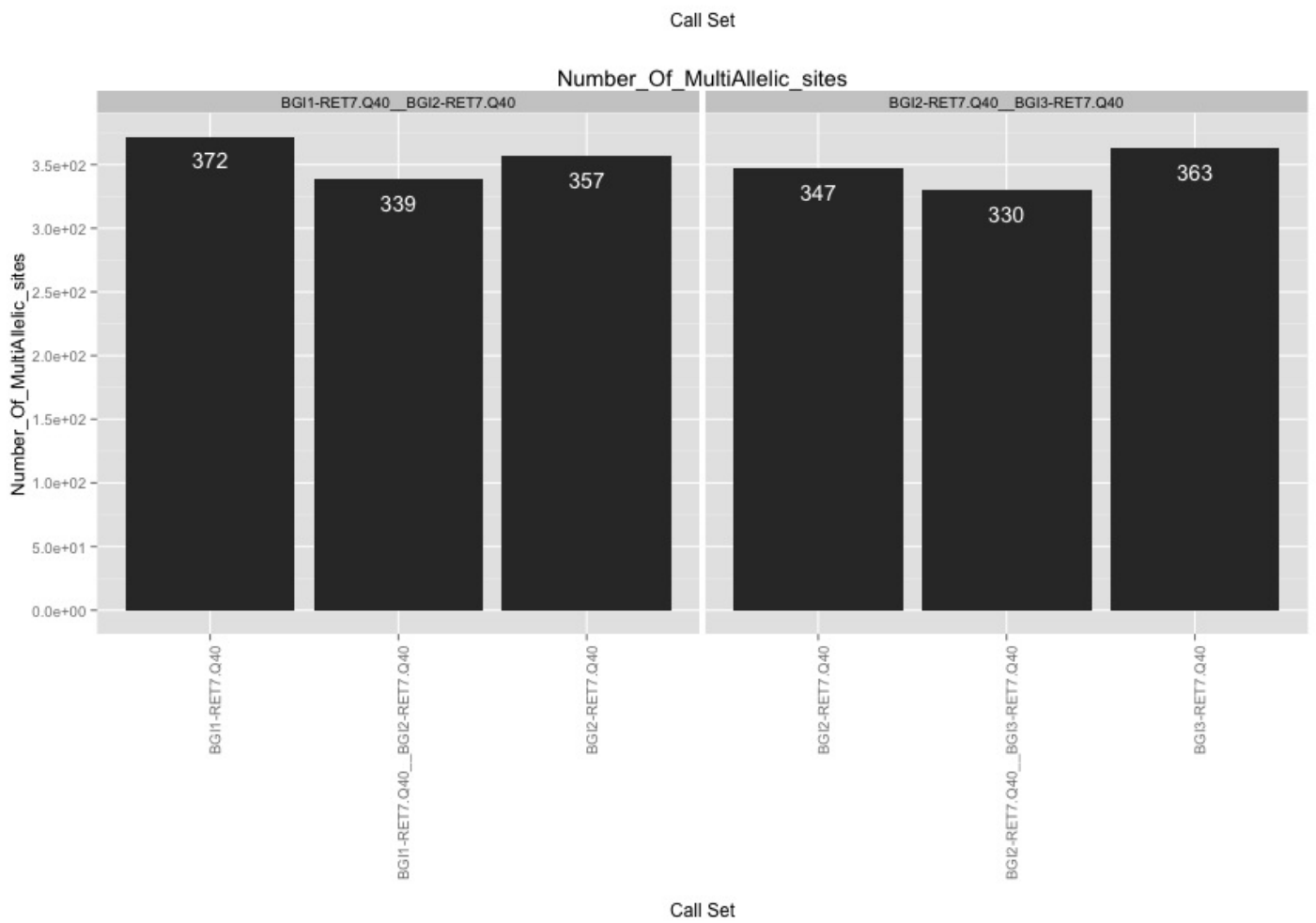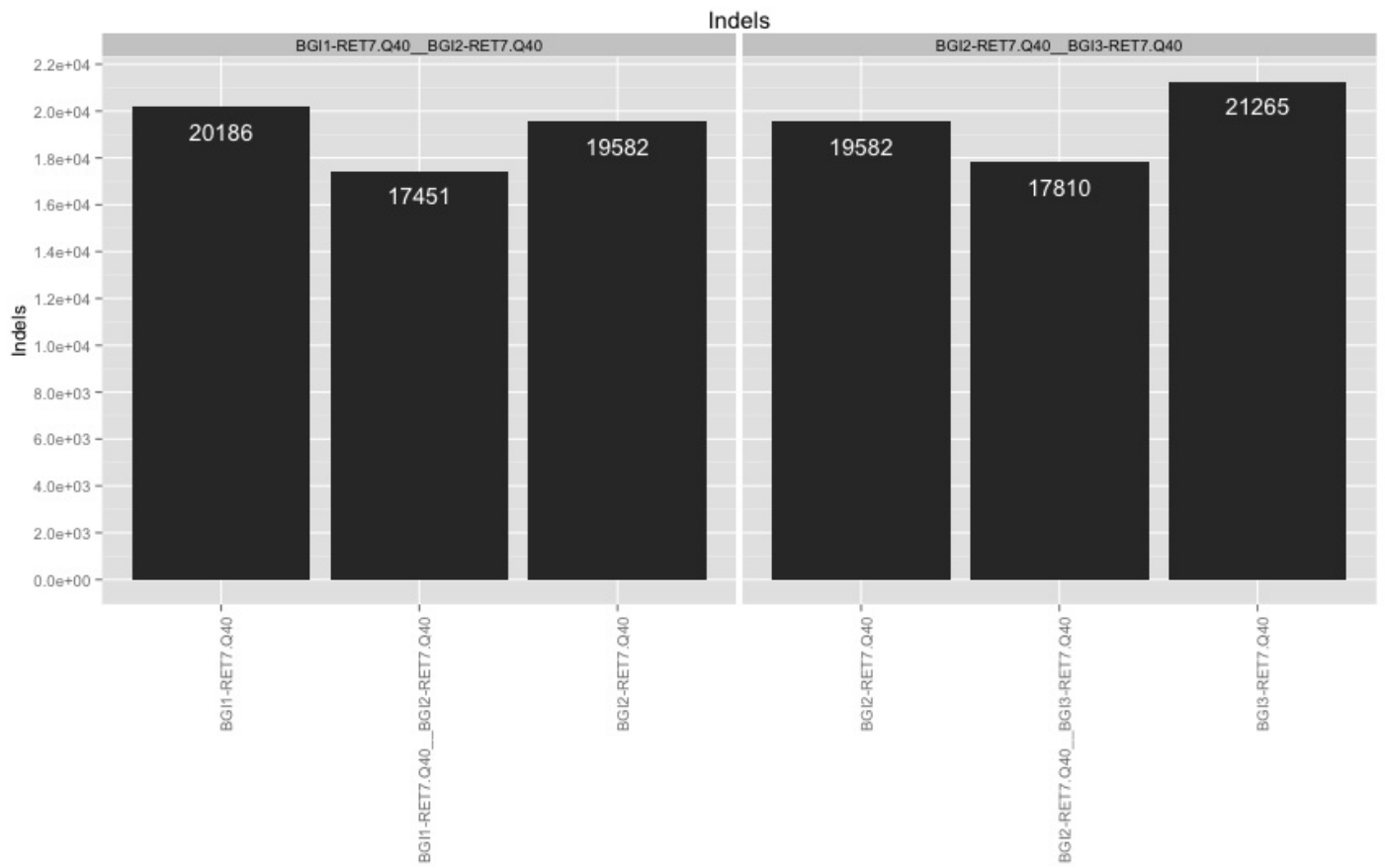# VCF Compare Script
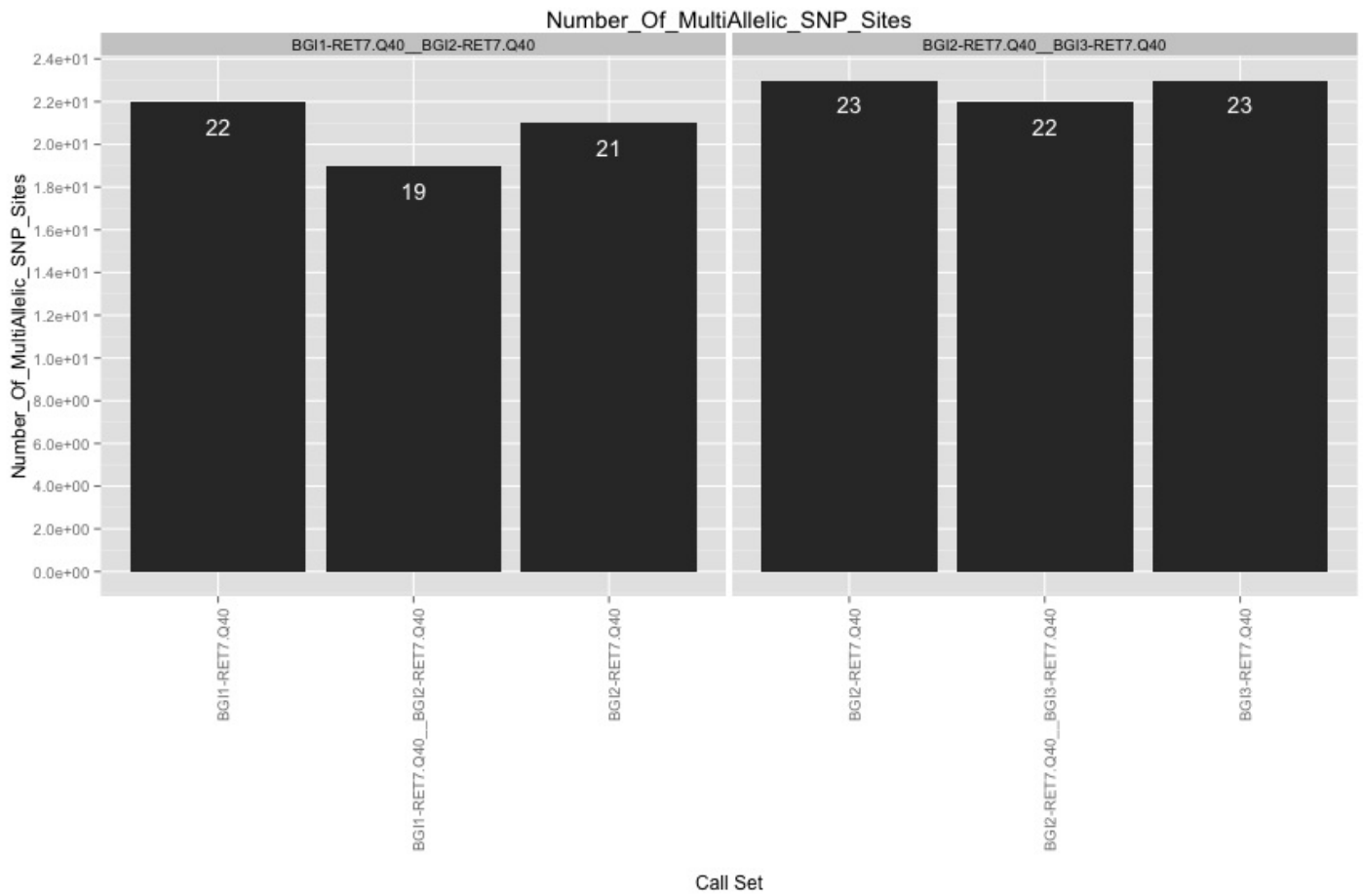
Files

[1] "BGI1-RET7.txt.Q40.vcf.gz" "BGI2-RET7.txt.Q40.vcf.gz" [3] "BGI3-RET7.txt.Q40.vcf.gz"

Individual VCF Results

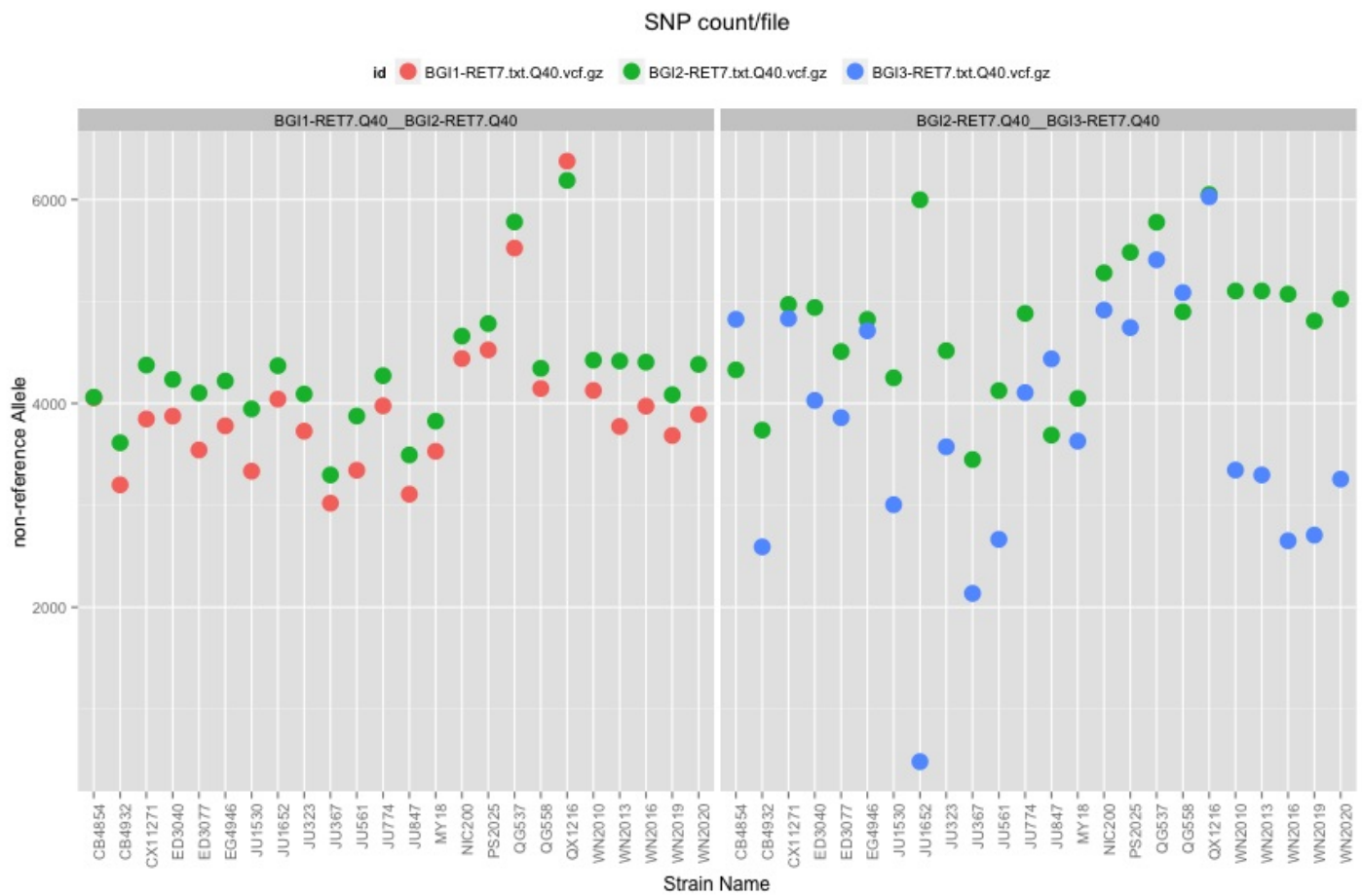# Indels

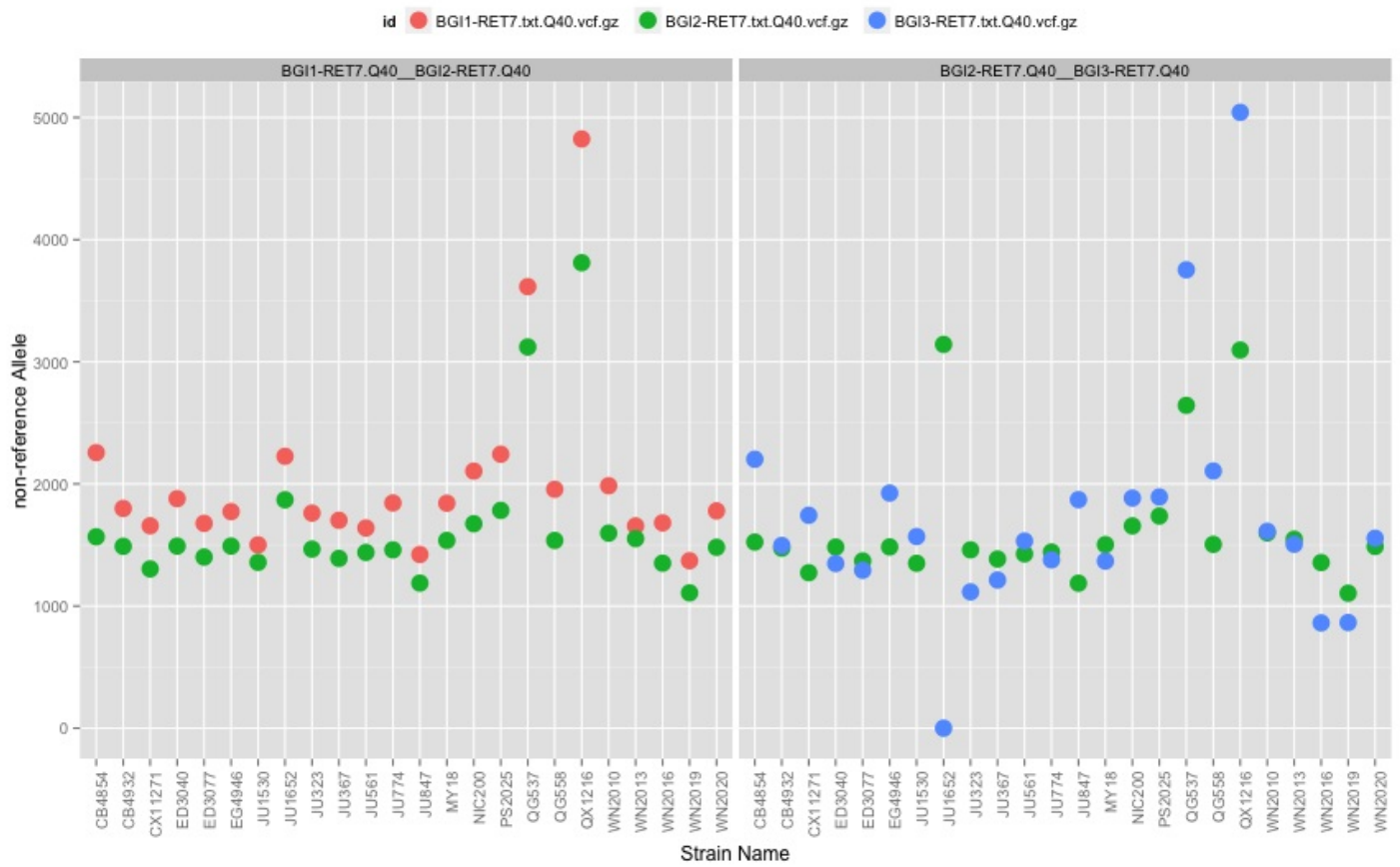| BGI1-RET7.Q40__BGI2-RET7.Q40 | BGI2-RET7.Q40__BGI3-RET7.Q40 |

Number_Of_MultiAllelic_sites

| BGI1-RET7.Q40__BGI2-RET7.Q40 | BGI2-RET7.Q40__BGI3-RET7.Q40 |

Number_Of_MultiAllelic_SNP_Sites

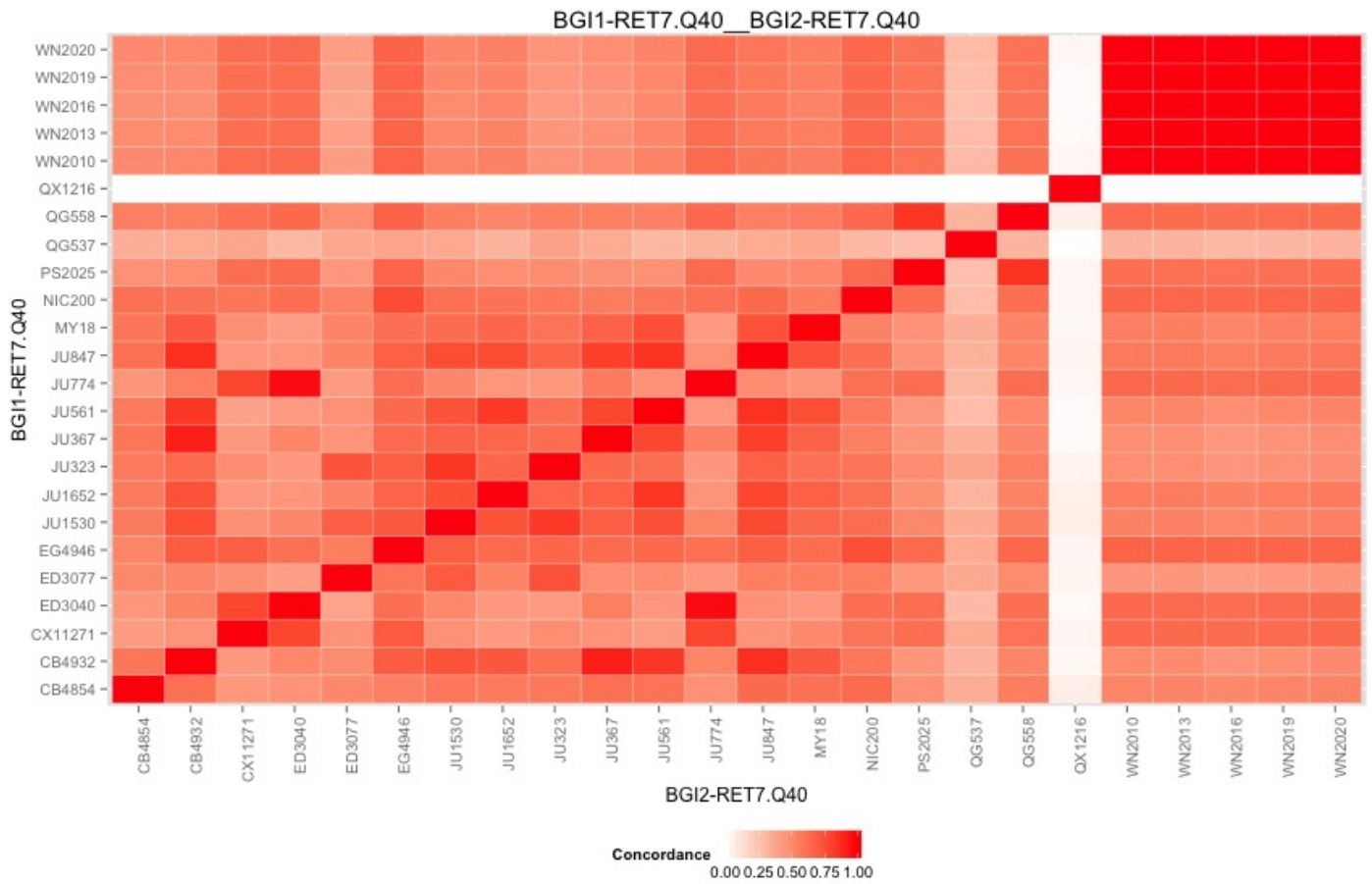## Number of SNPs/Strain

SNP count/file

Singletons

Singletons

Ind. Sample Concordance

Concordance by Strain

Pairwise Concordance

[[1]]

BGI1-RET7.Q40__BGI2-RET7.Q40

Concordance
0.00 0.25 0.50 0.75 1.00

[[2]]

BGI2-RET7.Q40__BGI3-RET7.Q40

Concordance
0.00 0.25 0.50 0.75 1.00