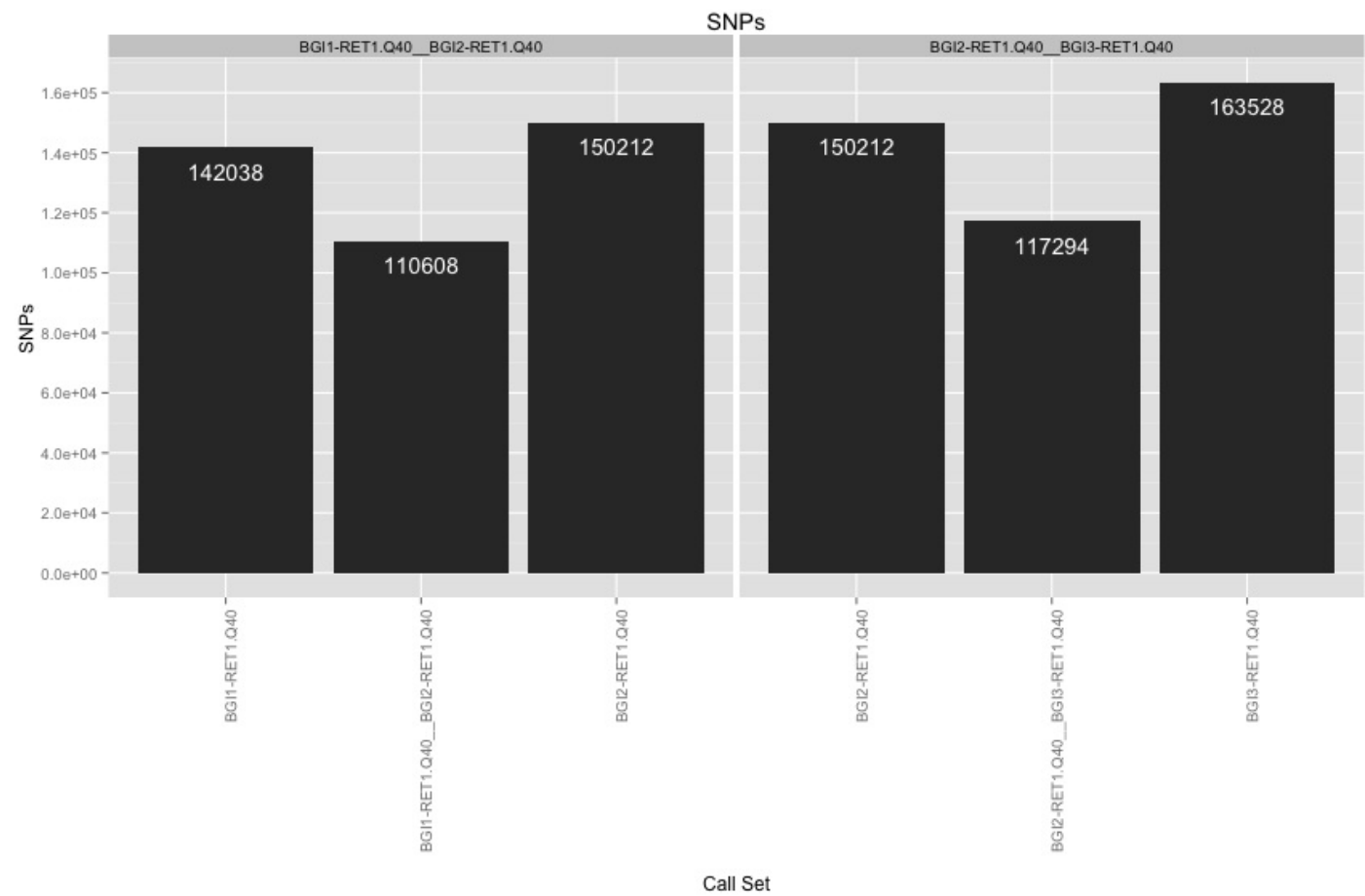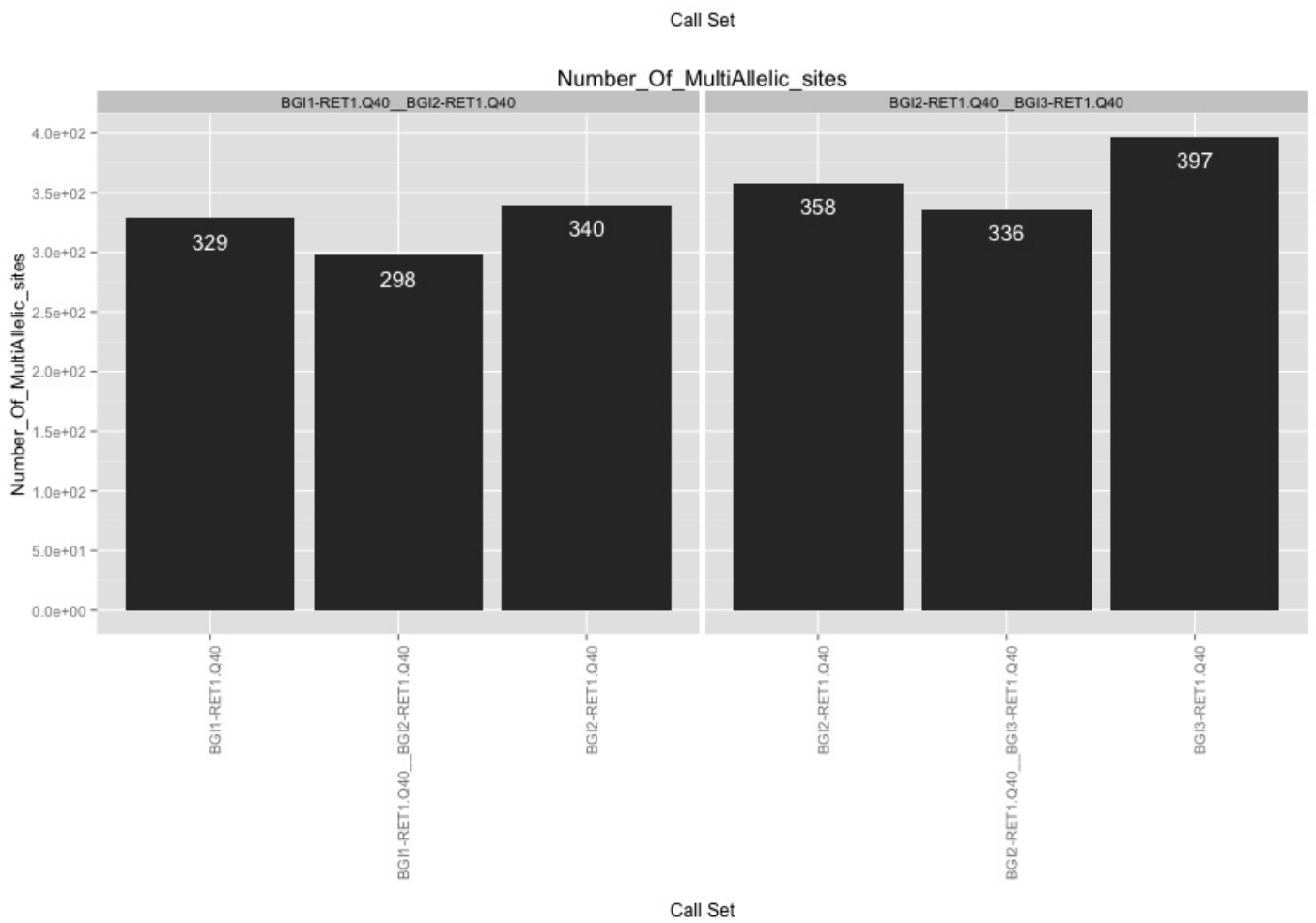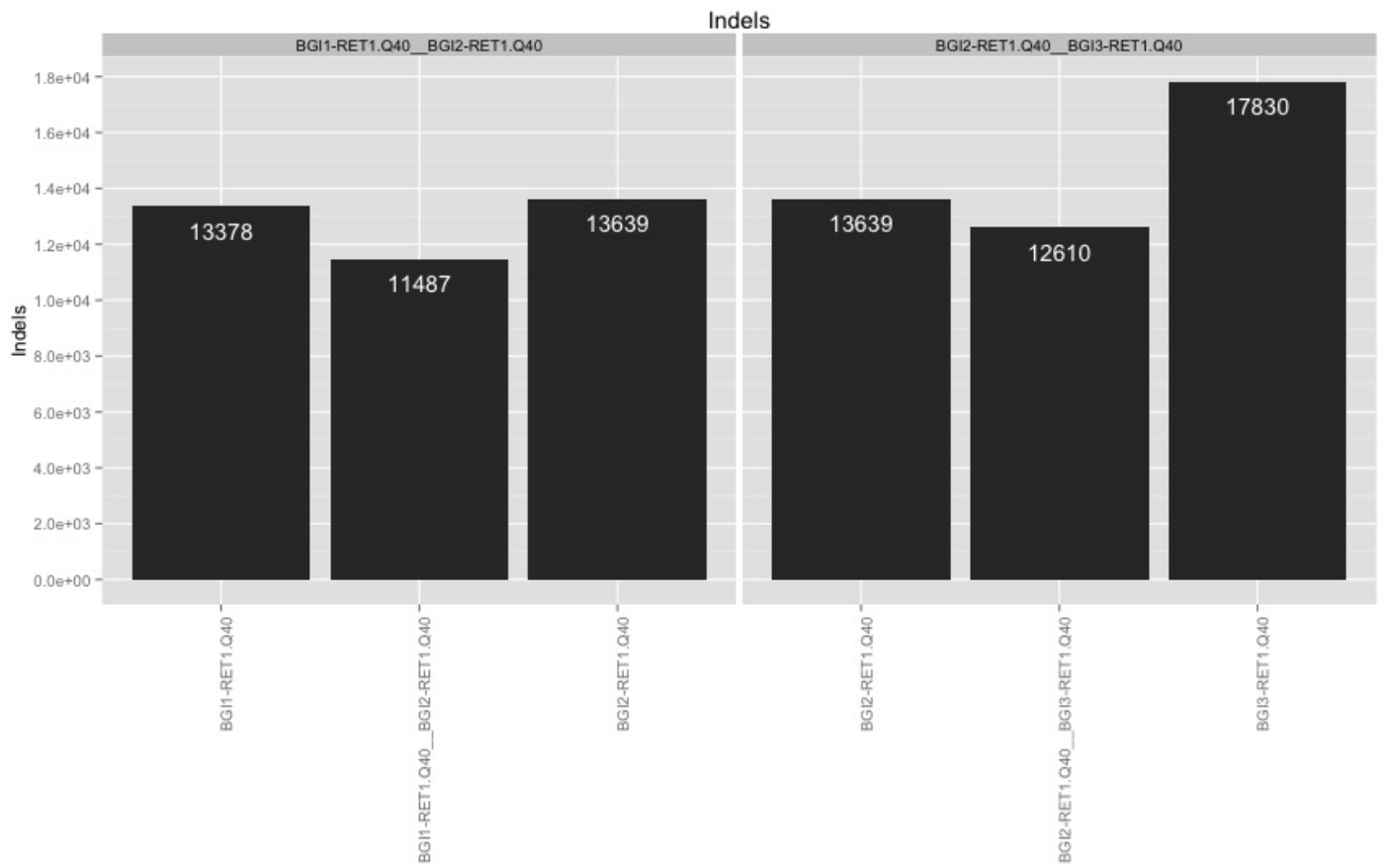# VCF Compare Script

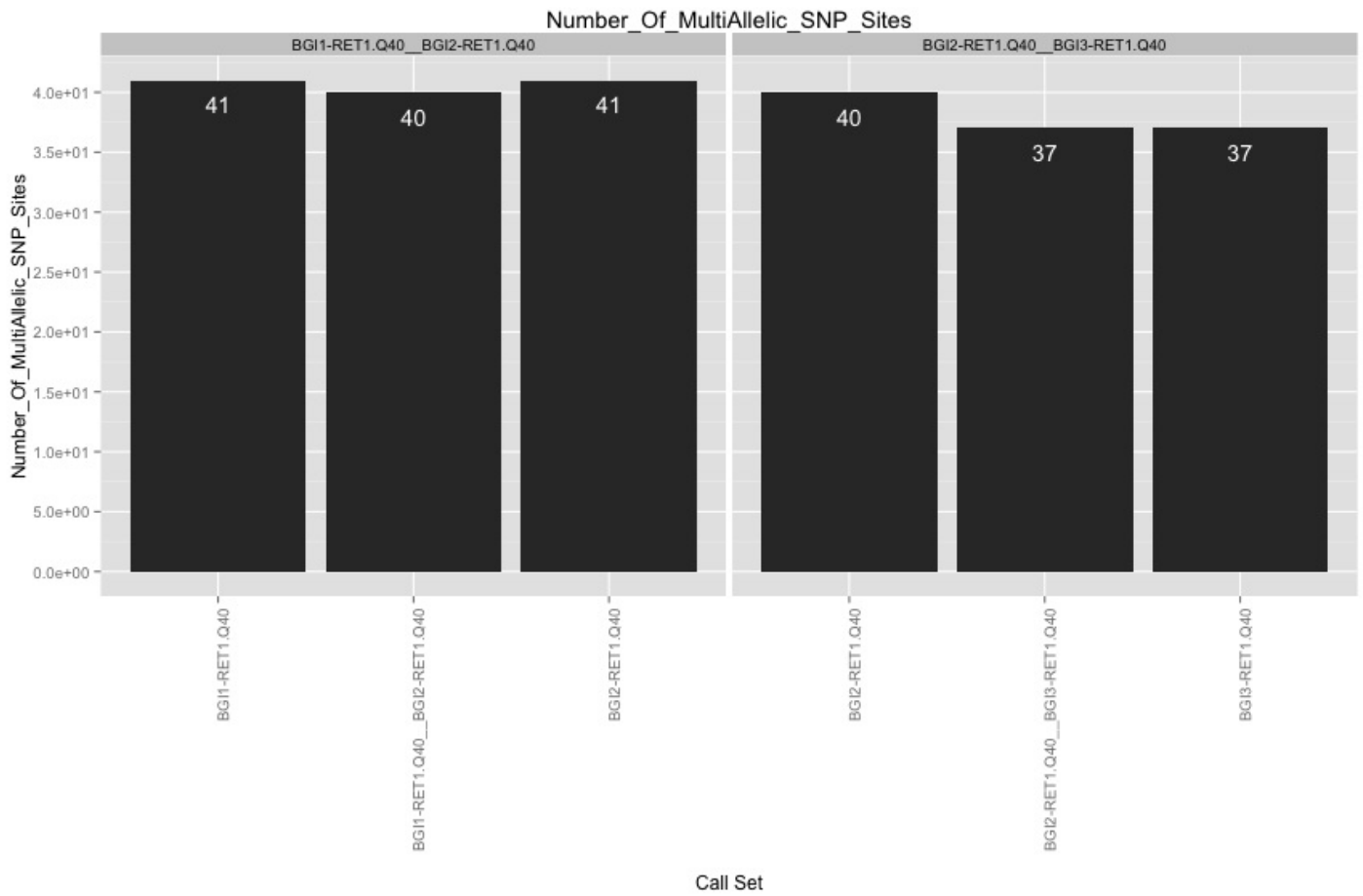## Files

[1] "BGI1-RET1.txt.Q40.vcf.gz" "BGI2-RET1.txt.Q40.vcf.gz" [3] "BGI3-RET1.txt.Q40.vcf.gz"

Individual VCF Results

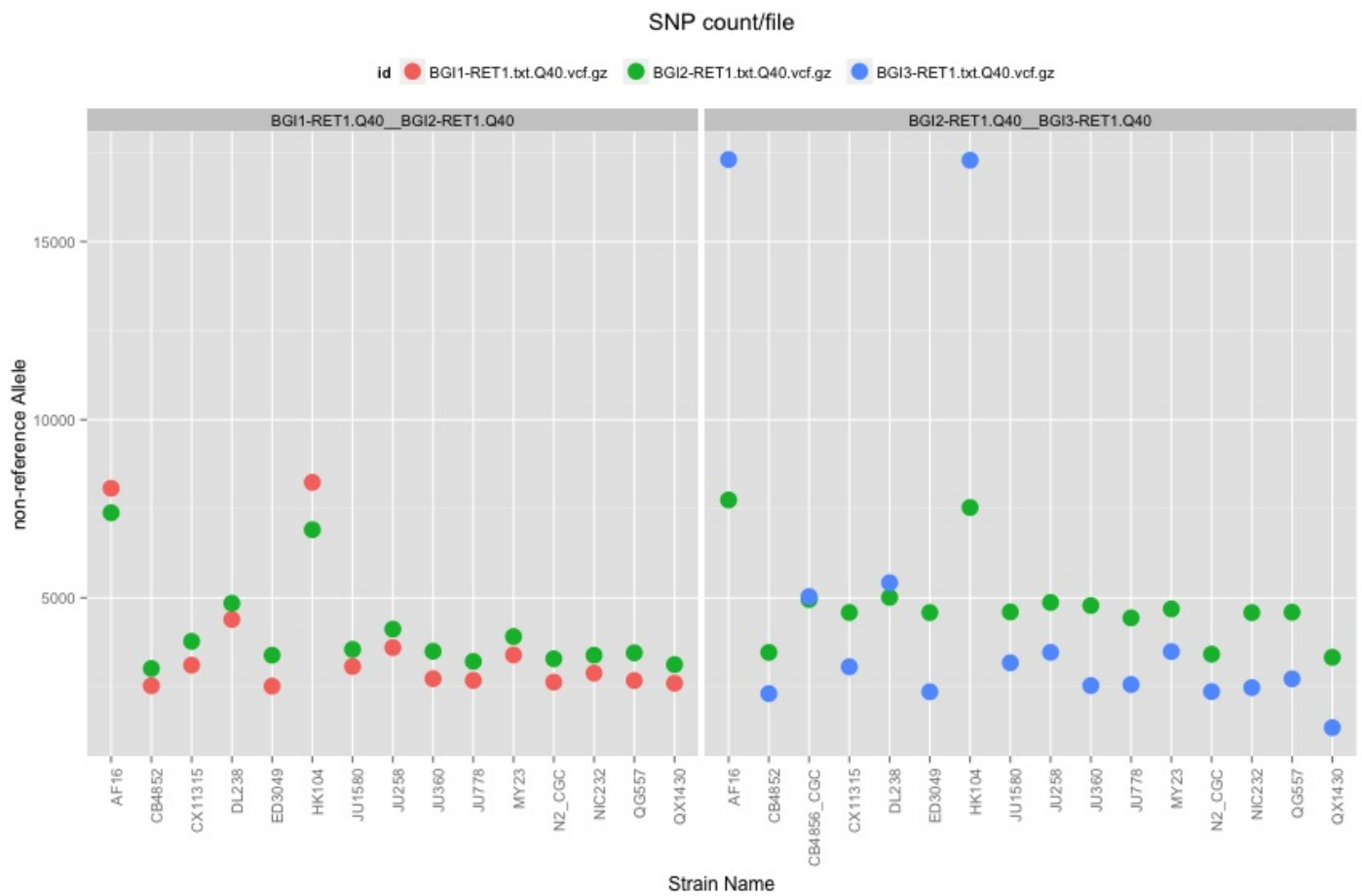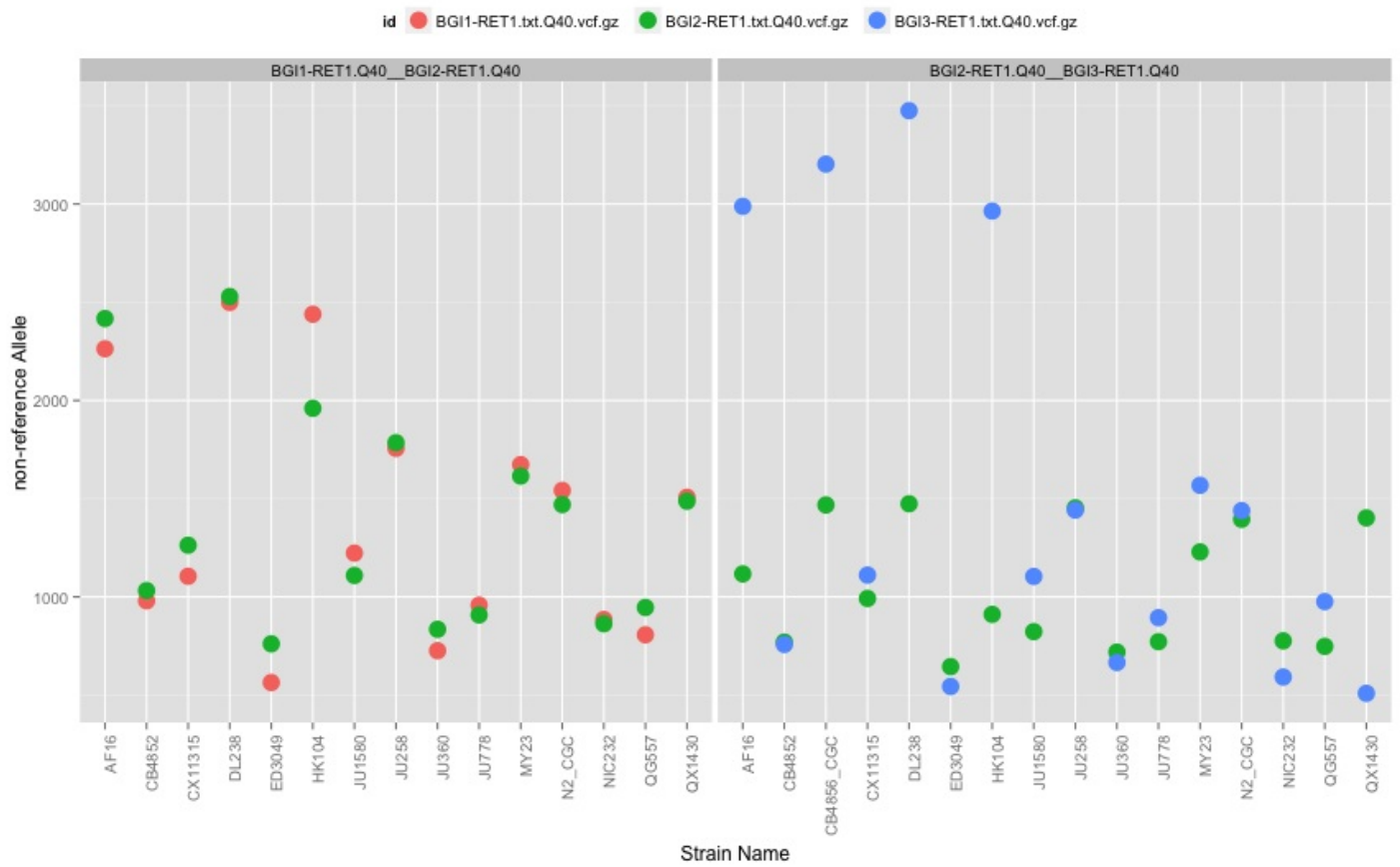## Indels

| BGI1-RET1.Q40__BGI2-RET1.Q40 | BGI2-RET1.Q40__BGI3-RET1.Q40 |

Bar chart values (top panel, y-axis: Indels):
- BGI1-RET1.Q40: 13378
- BGI1-RET1.Q40__BGI2-RET1.Q40: 11487
- BGI2-RET1.Q40: 13639
- BGI2-RET1.Q40: 13639
- BGI2-RET1.Q40__BGI3-RET1.Q40: 12610
- BGI3-RET1.Q40: 17830

Call Set

Number_Of_MultiAllelic_sites

| BGI1-RET1.Q40__BGI2-RET1.Q40 | BGI2-RET1.Q40__BGI3-RET1.Q40 |

Bar chart values (bottom panel, y-axis: Number_Of_MultiAllelic_sites):
- BGI1-RET1.Q40: 329
- BGI1-RET1.Q40__BGI2-RET1.Q40: 298
- BGI2-RET1.Q40: 340
- BGI2-RET1.Q40: 358
- BGI2-RET1.Q40__BGI3-RET1.Q40: 336
- BGI3-RET1.Q40: 397

Call Set

Number_Of_MultiAllelic_SNP_Sites

Number of SNPs/Strain
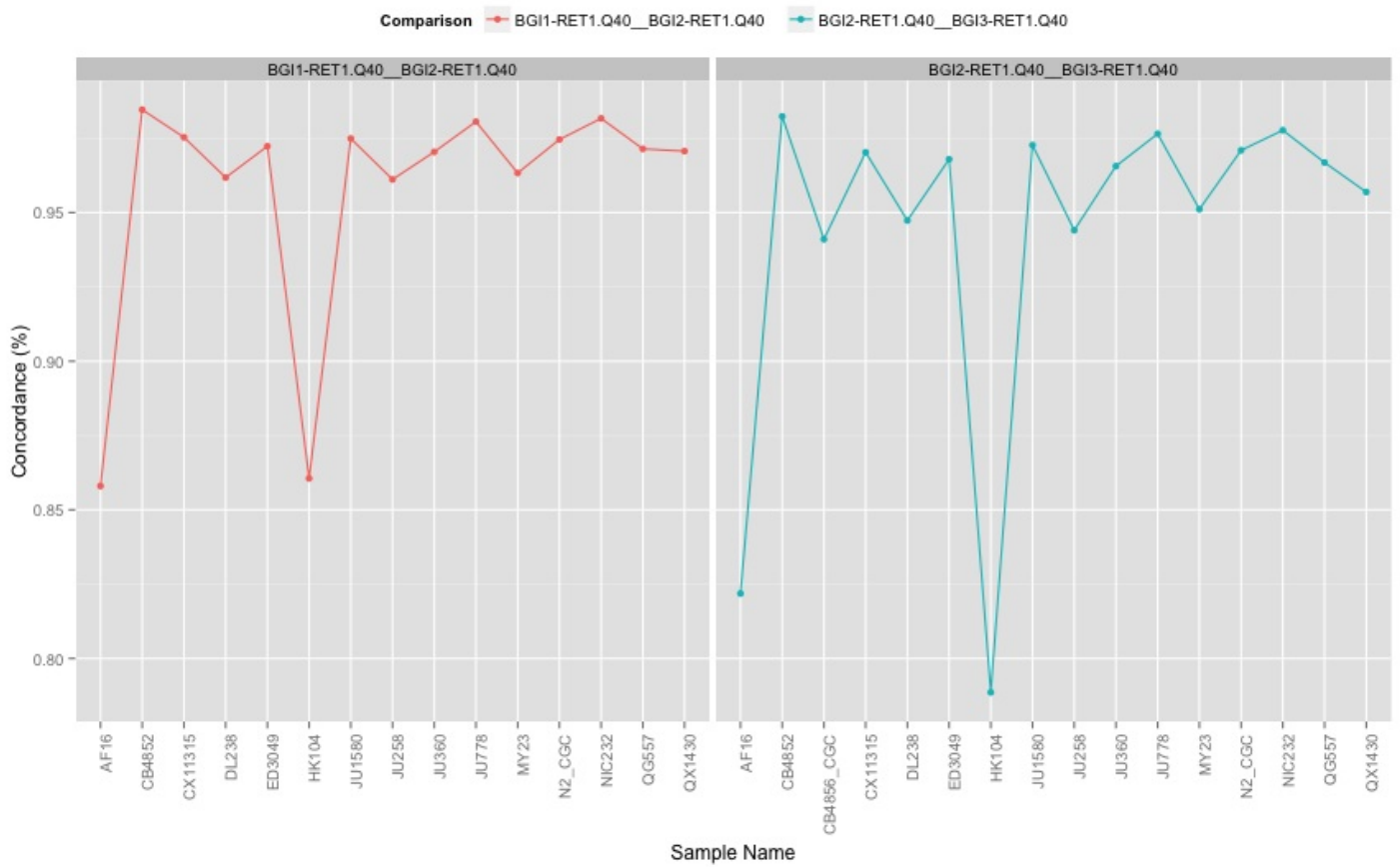

SNP count/file

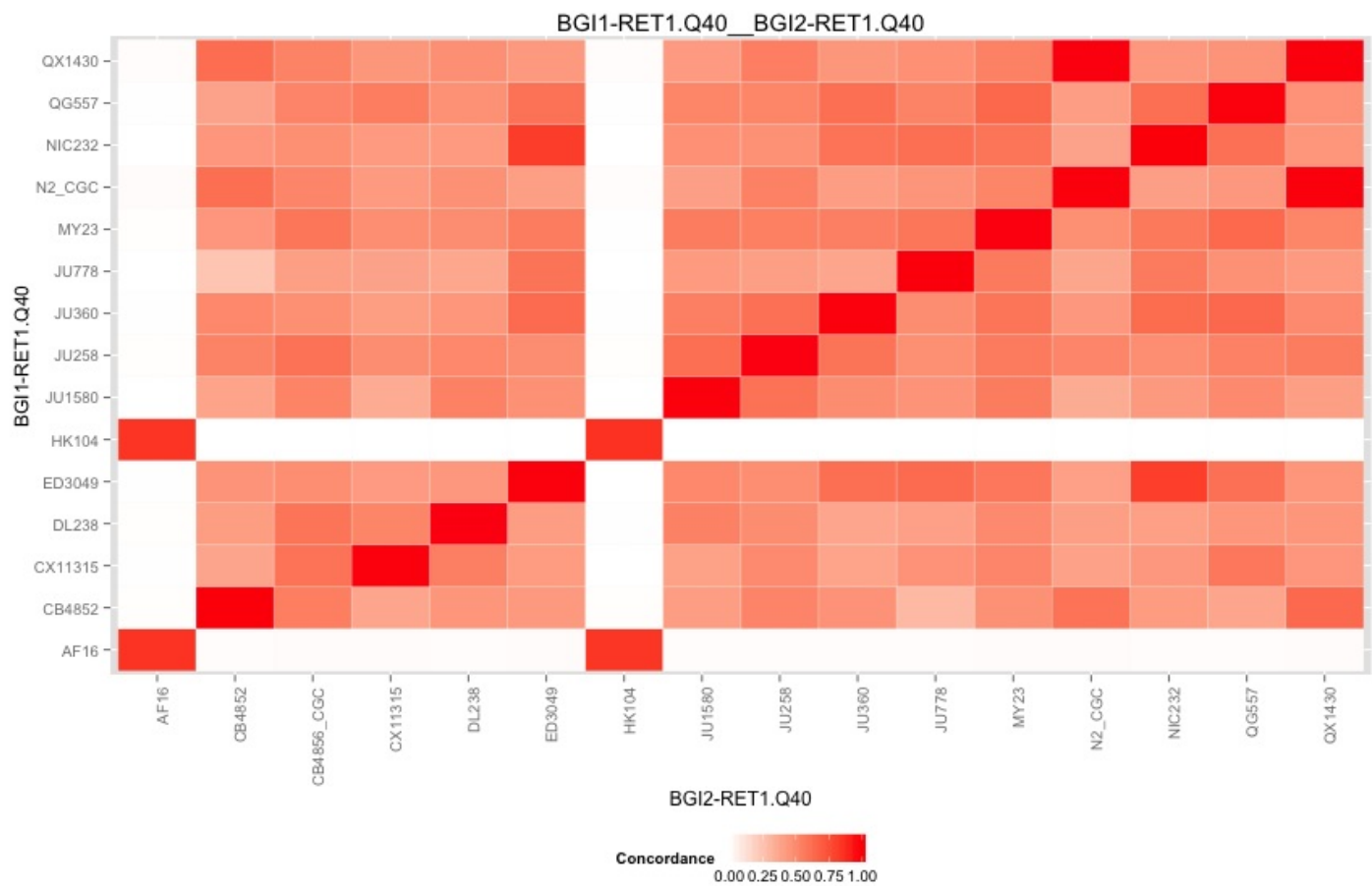## Singletons

Singletons

Ind. Sample Concordance

Concordance by Strain

Pairwise Concordance

[[1]]

BGI1-RET1.Q40__BGI2-RET1.Q40

[[2]]

BGI2-RET1.Q40__BGI3-RET1.Q40