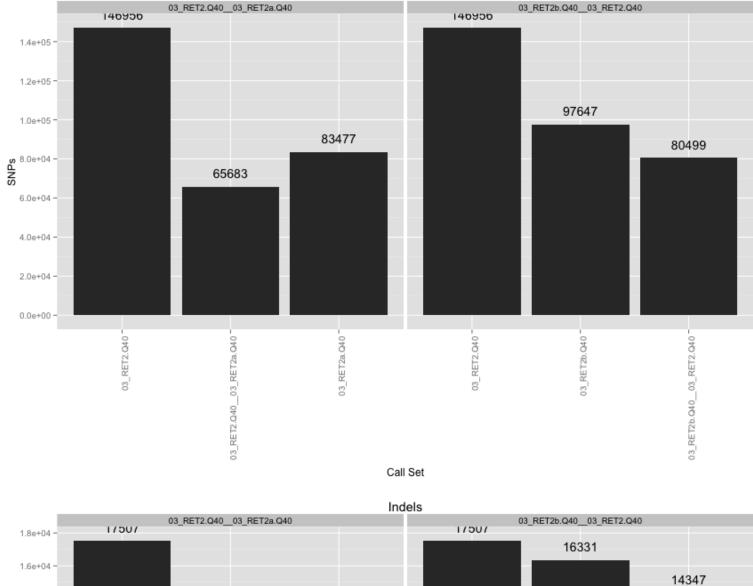
## VCF Compare Script

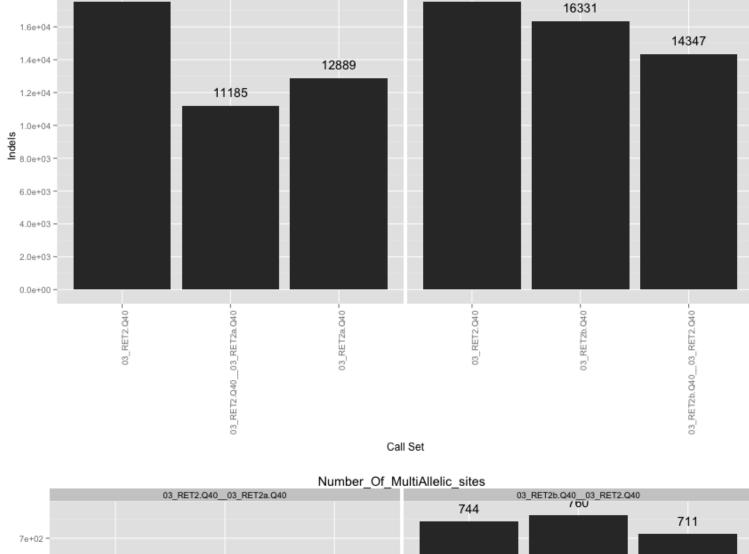
## Files

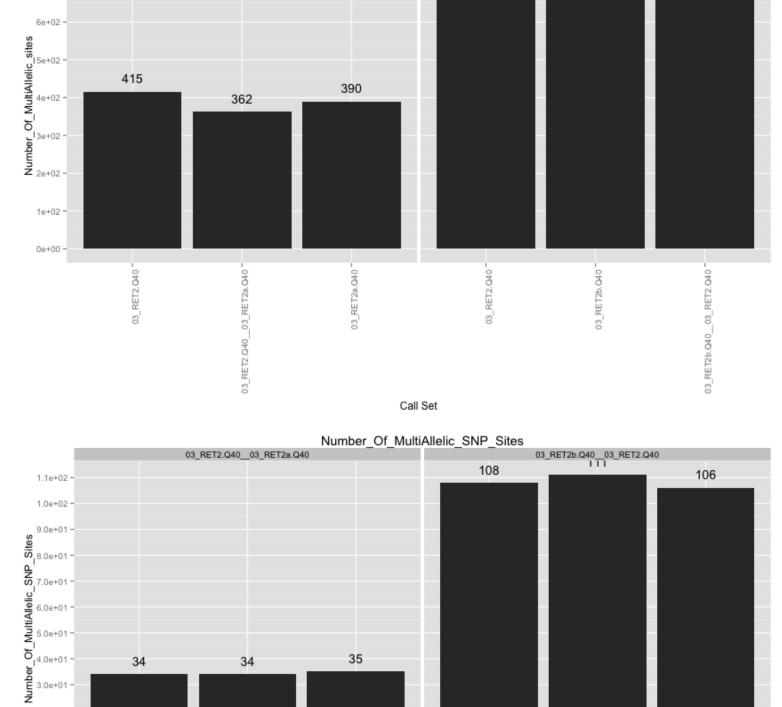
 $[1]\ "03\_RET2b.txt.Q40.vcf.gz"\ "03\_RET2.txt.Q40.vcf.gz"\ [3]\ "03\_RET2a.txt.Q40.vcf.gz"$ 

## Individual VCF Results



SNPs

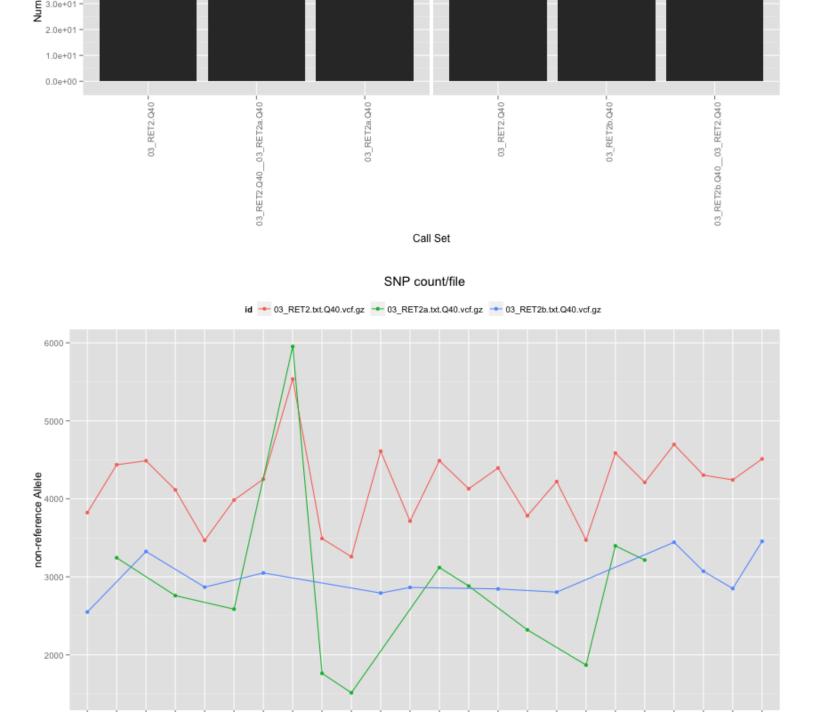




35

34

34



JU1200

Strain Name

SNP count/file

id - 03\_RET2.txt.Q40.vcf.gz - 03\_RET2a.txt.Q40.vcf.gz - 03\_RET2b.txt.Q40.vcf.gz

EG4725

4000 -



## QX1792 -

0.92

