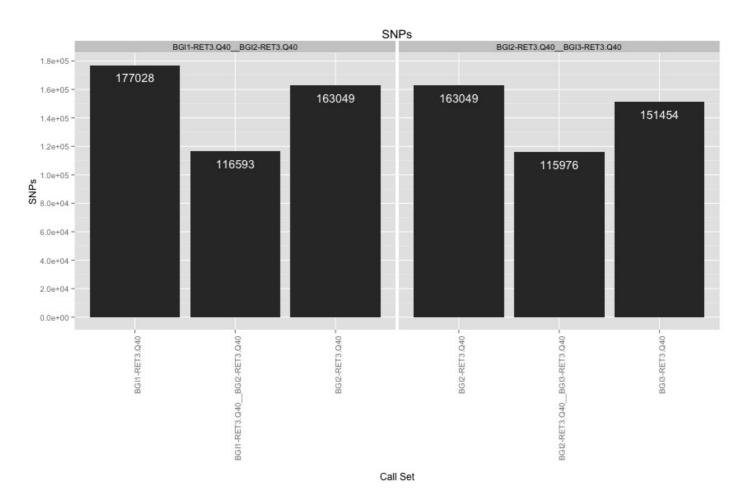
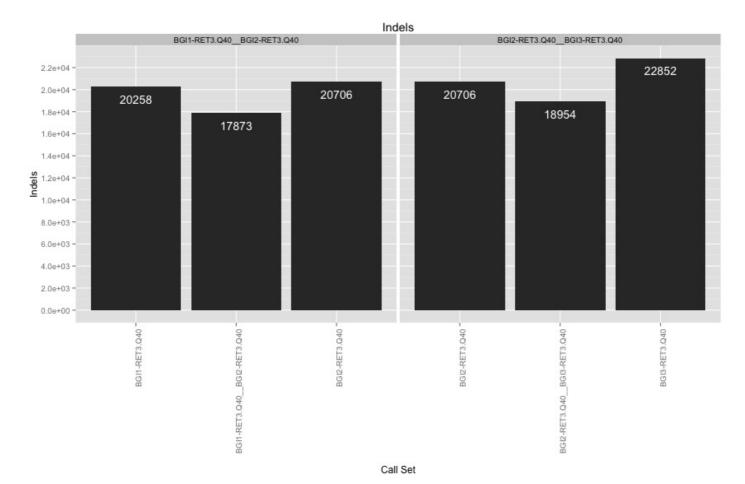
VCF Compare Script

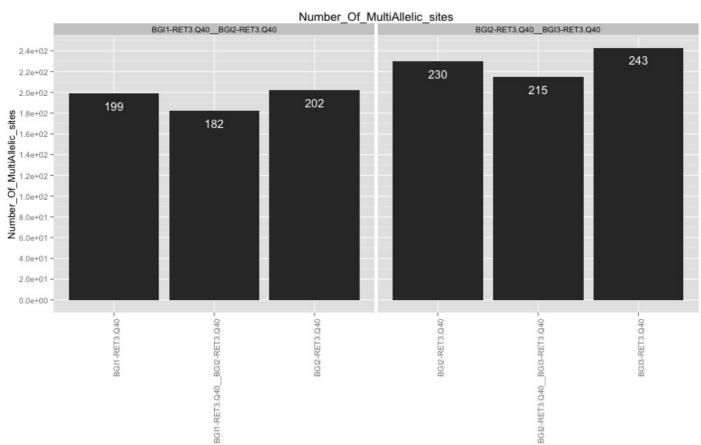
Files

[1] "BGI1-RET3.txt.Q40.vcf.gz" "BGI2-RET3.txt.Q40.vcf.gz" [3] "BGI3-RET3.txt.Q40.vcf.gz"

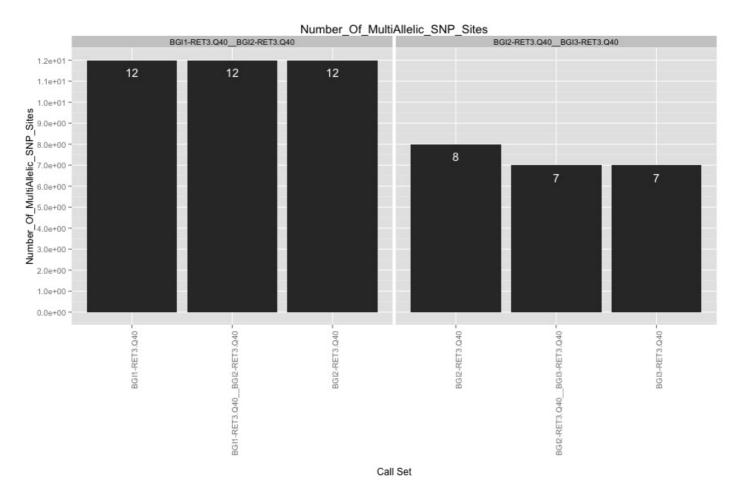
Individual VCF Results



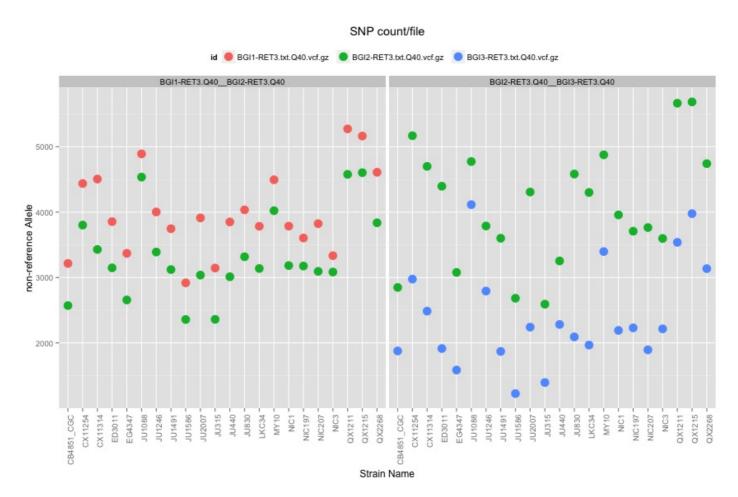




Call Set

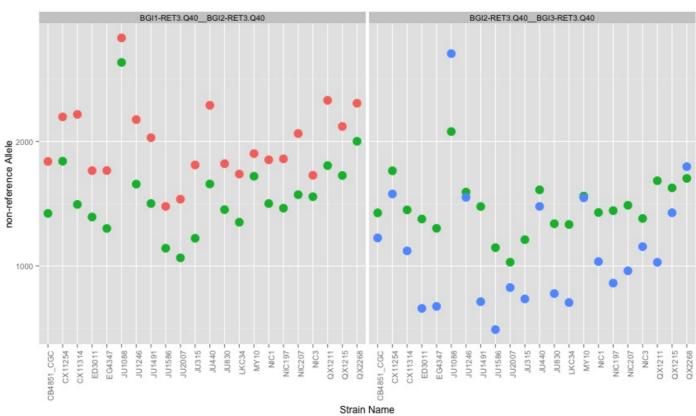


Number of SNPs/Strain



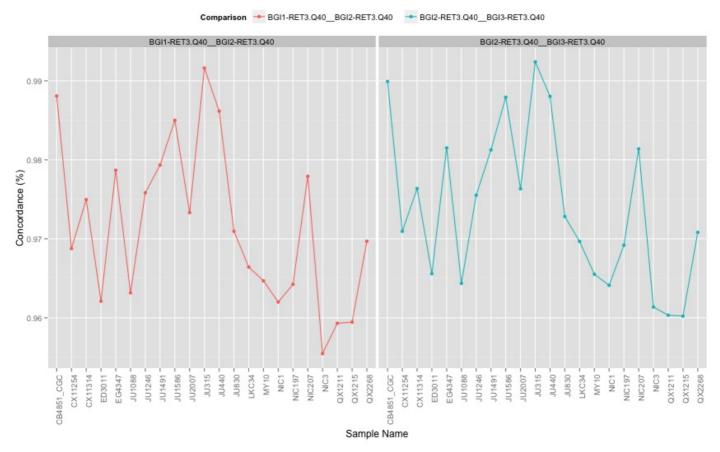
Singletons



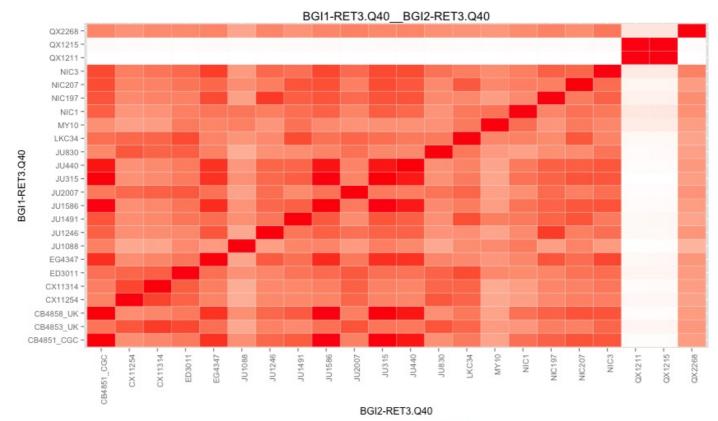


Ind. Sample Concordance



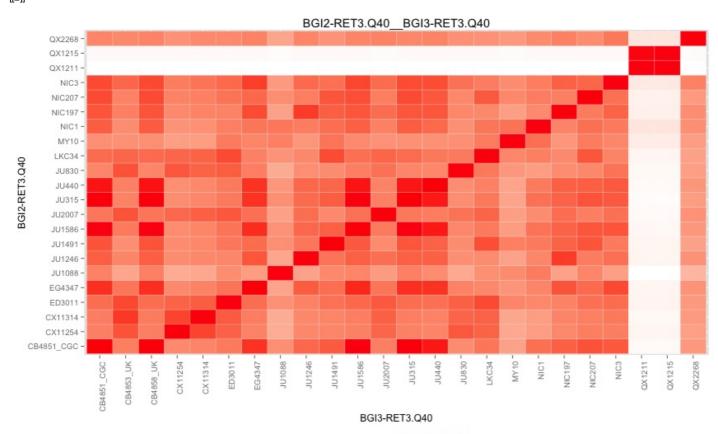


Pairwise Concordance



Concordance 0.00 0.25 0.50 0.75 1.00

[[2]]



Concordance 0.00 0.25 0.50 0.75 1.00