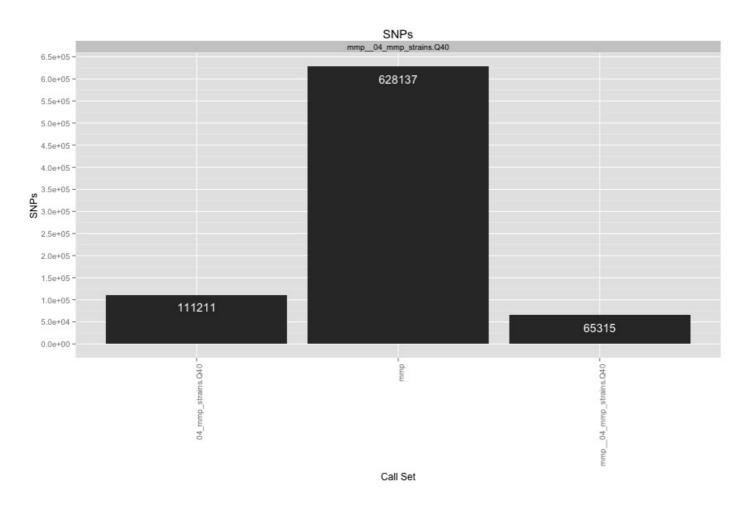
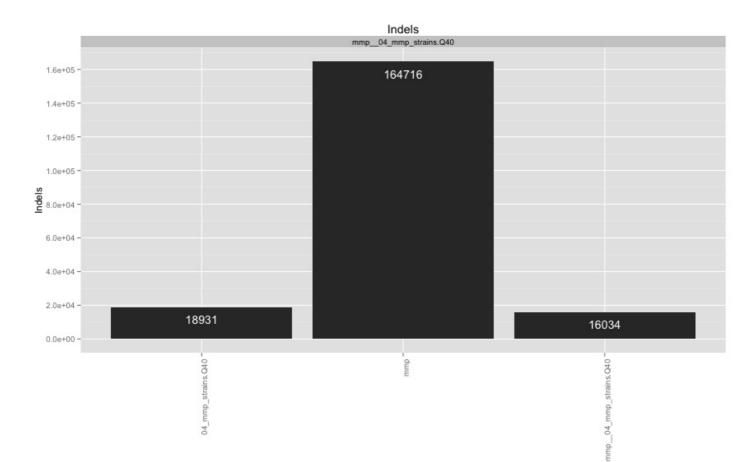
# **VCF Compare Script**

## Files

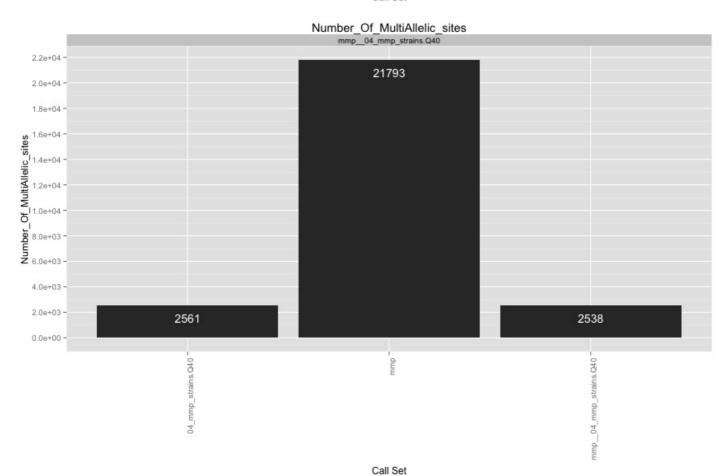
[1] "mmp.vcf.gz" "04mmpstrains.txt.Q40.vcf.gz"

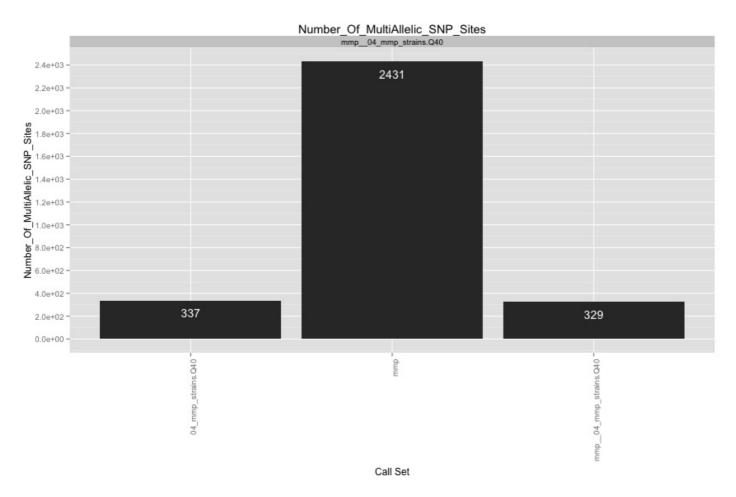
#### **Individual VCF Results**



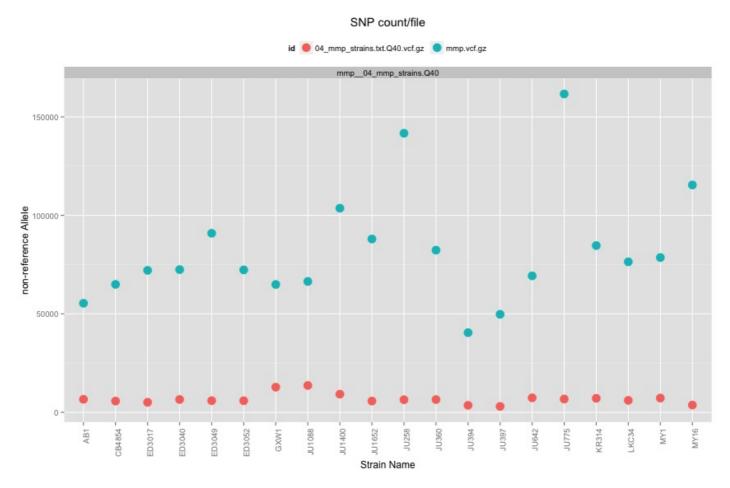






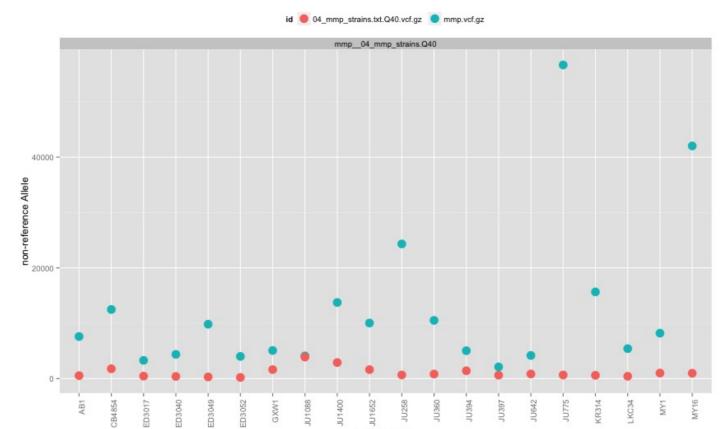


## **Number of SNPs/Strain**



## **Singletons**

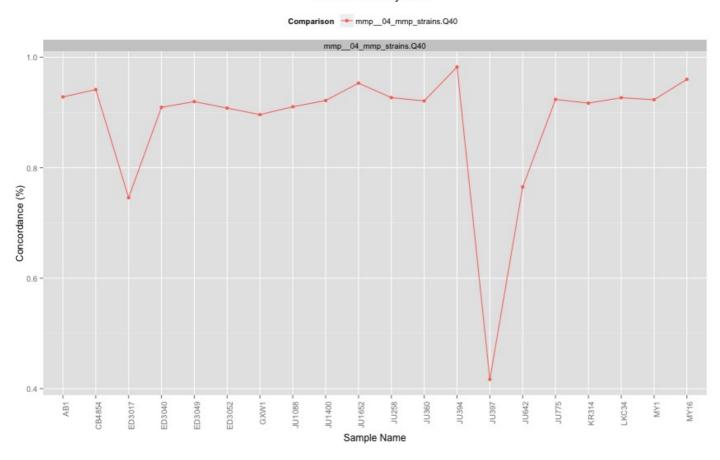




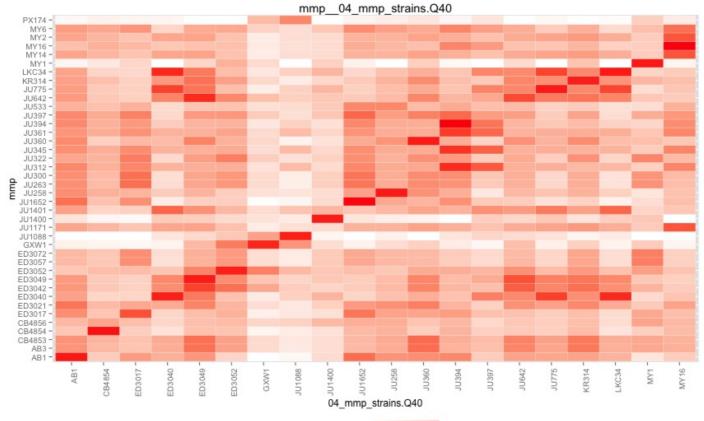
#### Ind. Sample Concordance



Strain Name



#### **Pairwise Concordance**



Concordance 0.00 0.25 0.50 0.75 1.00