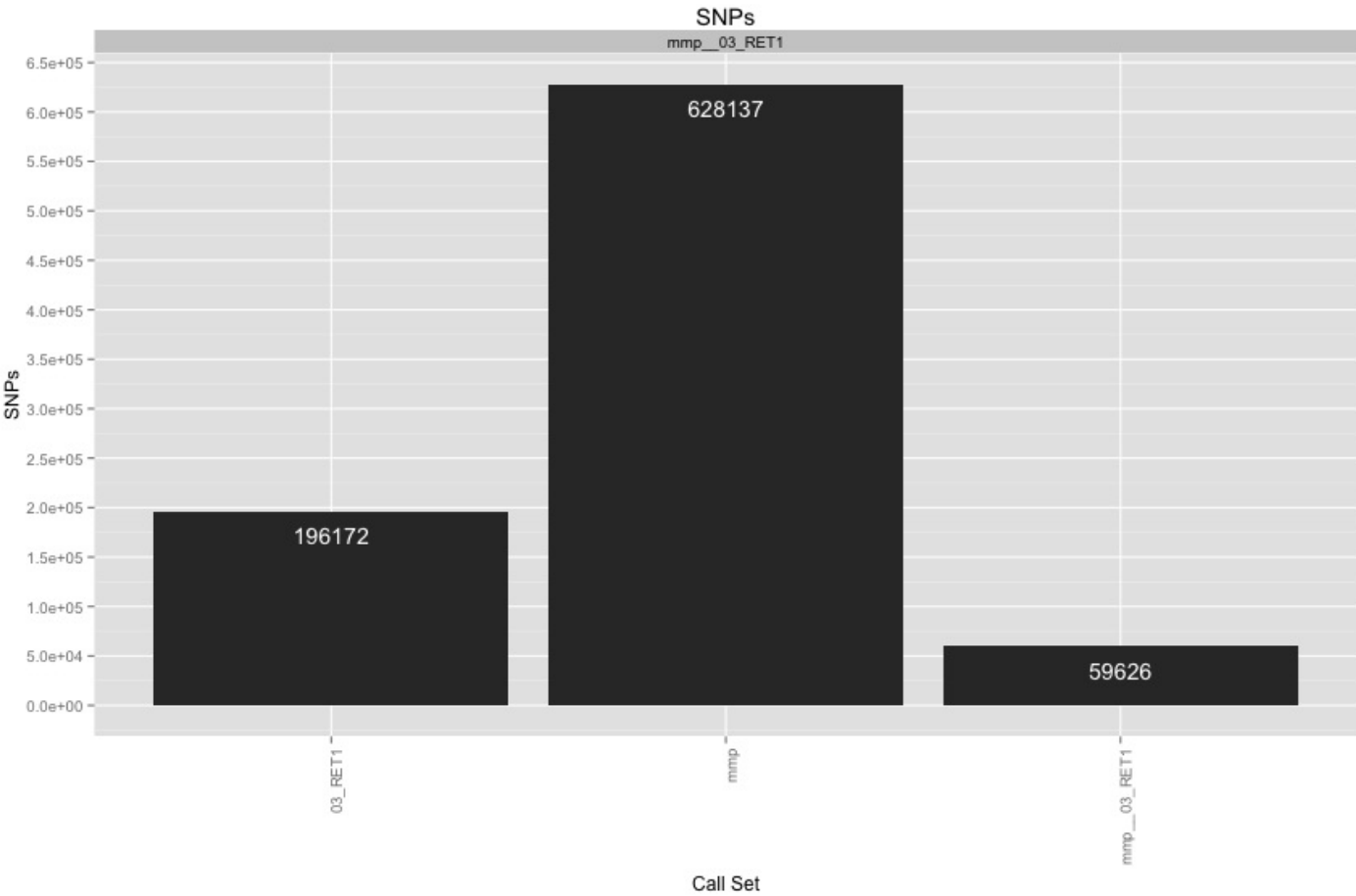


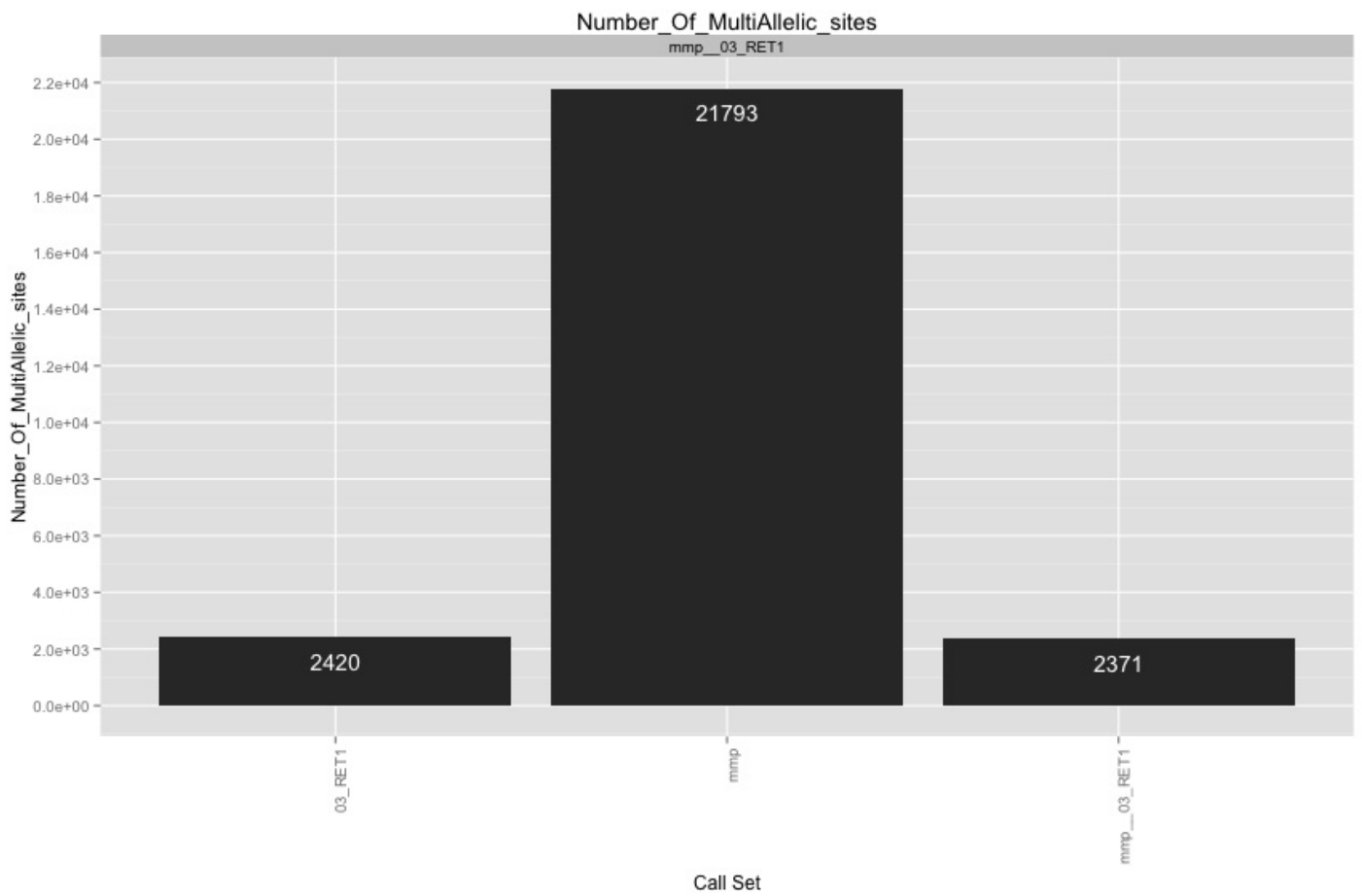
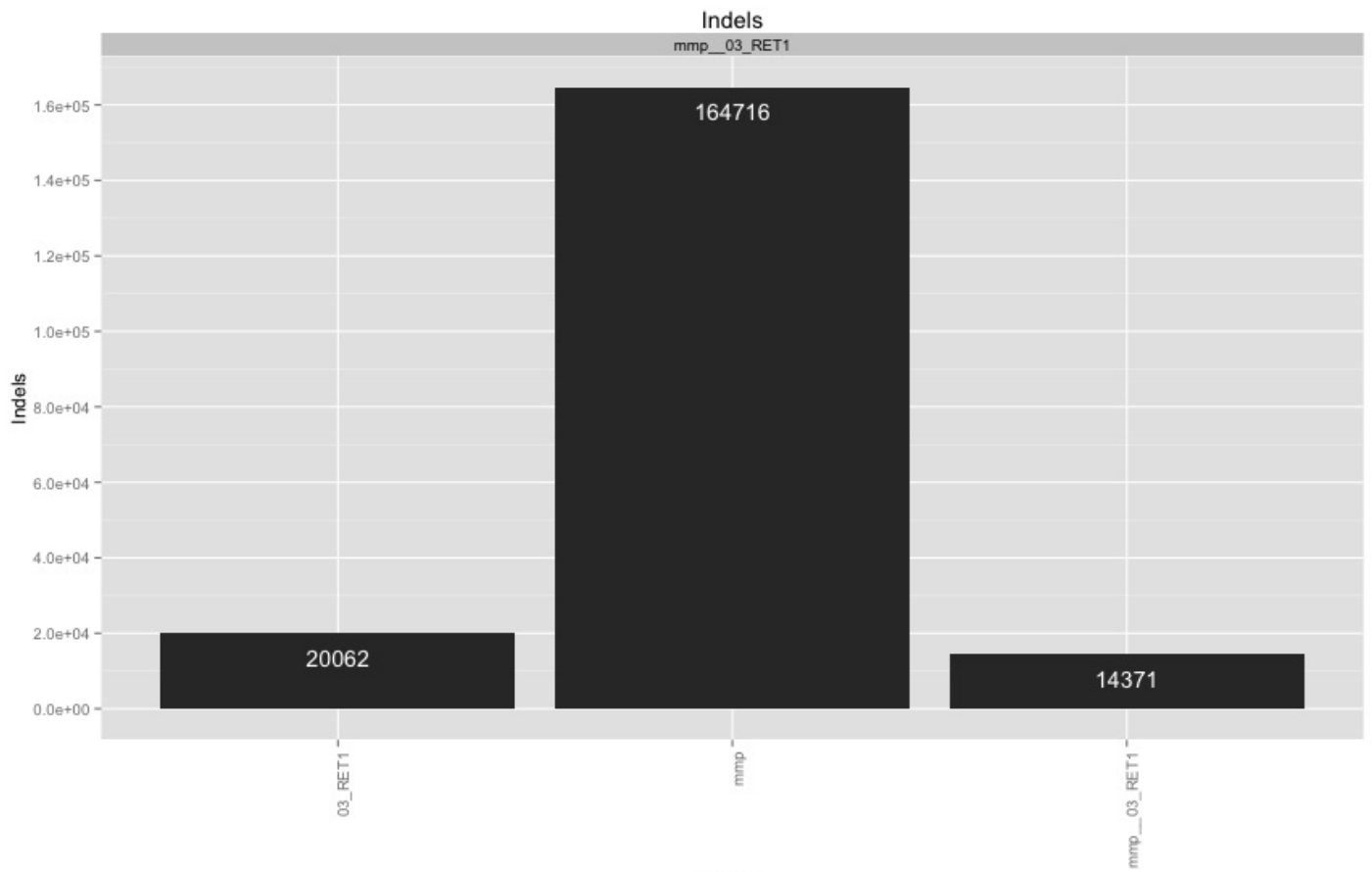
# VCF Compare Script

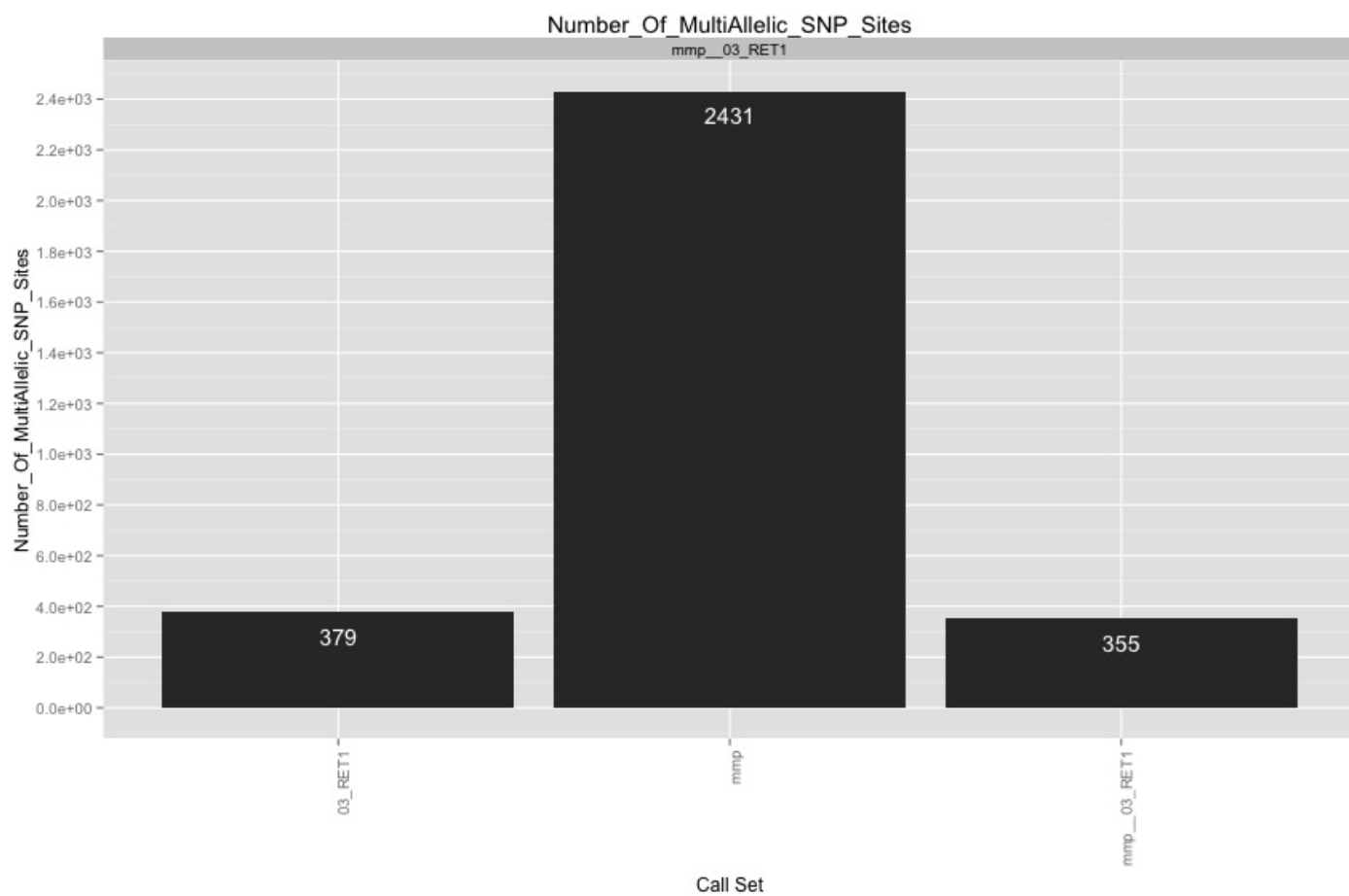
## Files

[1] "mmp.vcf.gz" "03\_RET1.bt.vcf.gz"

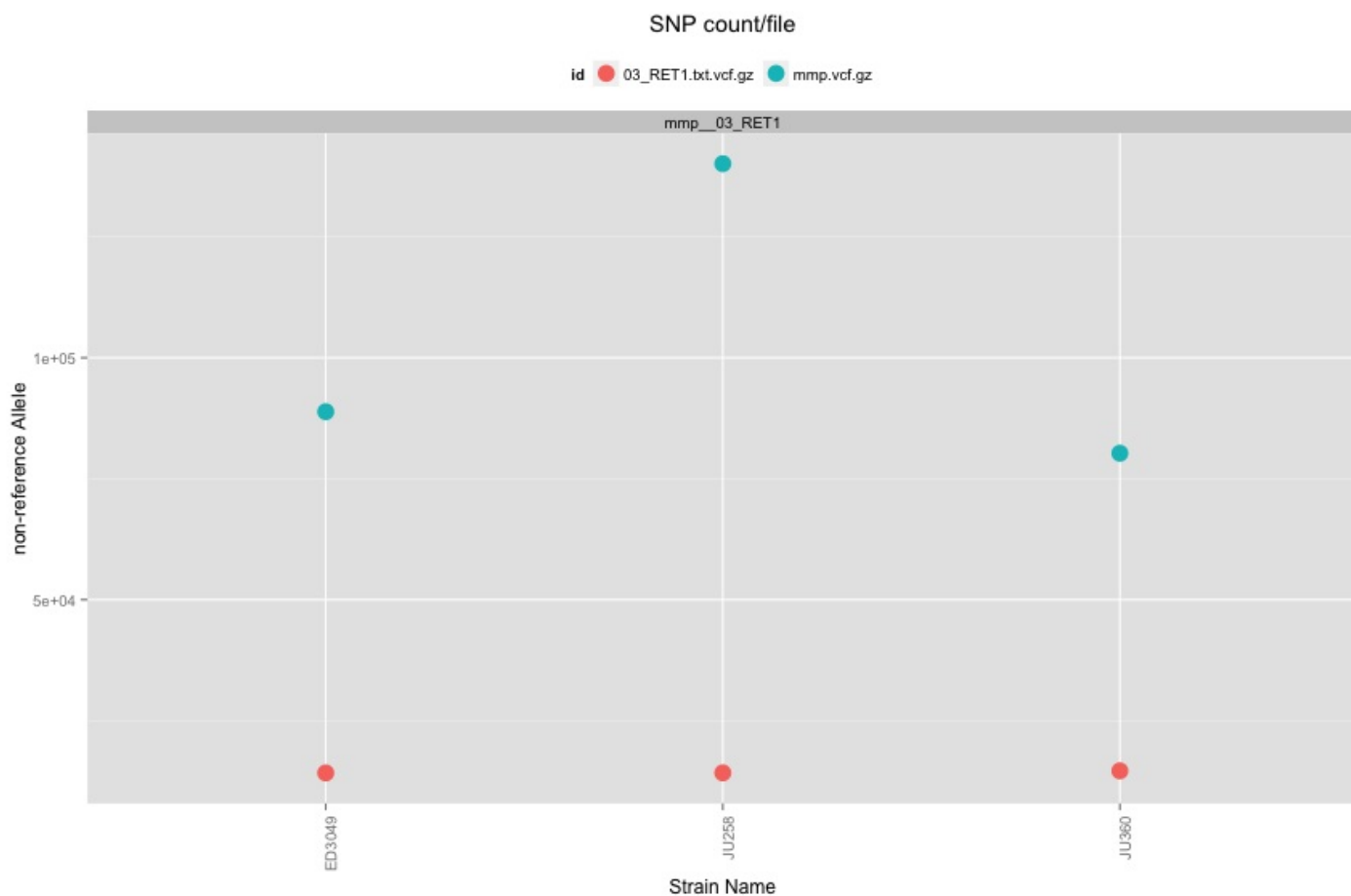
## Individual VCF Results



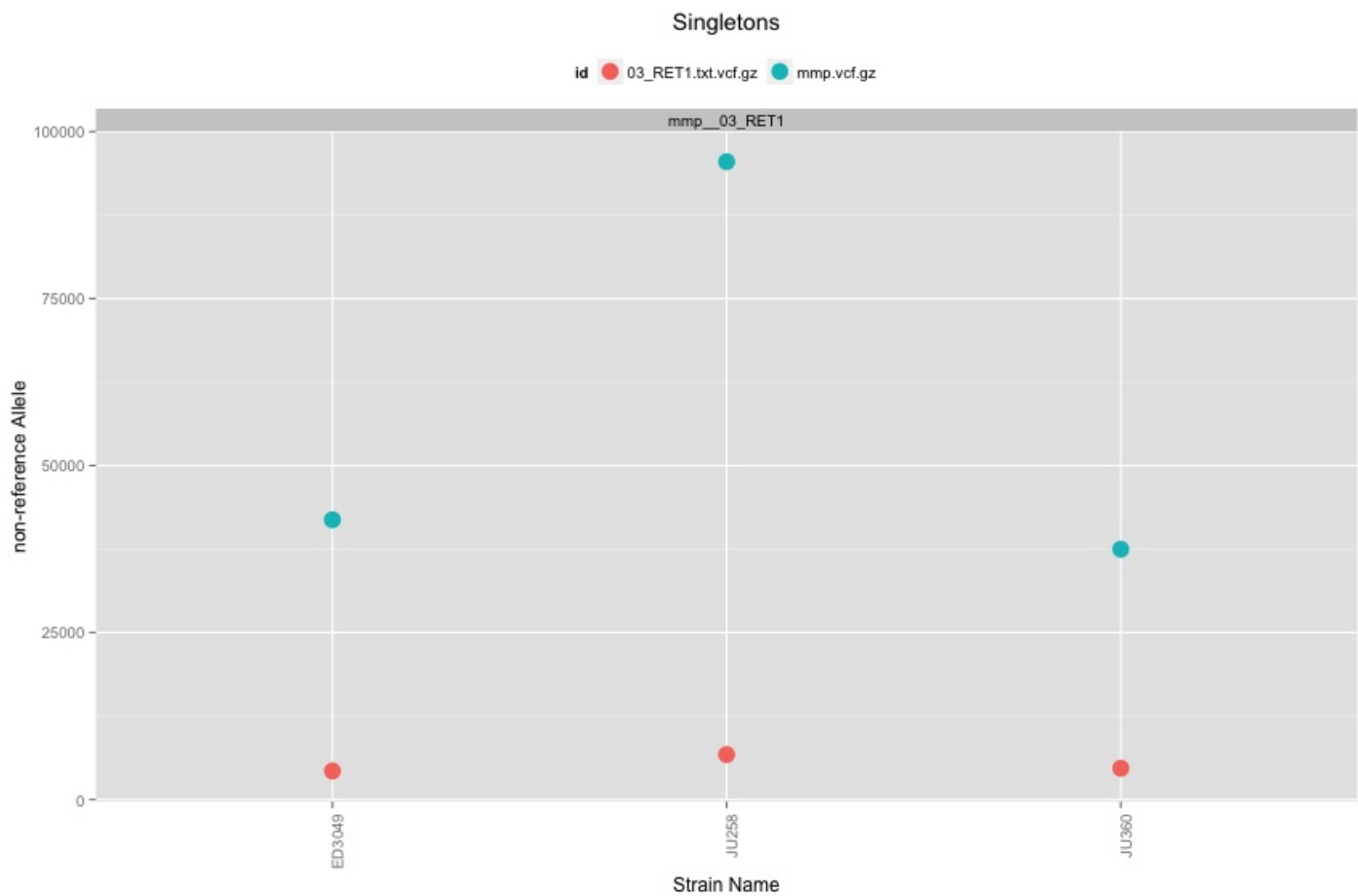




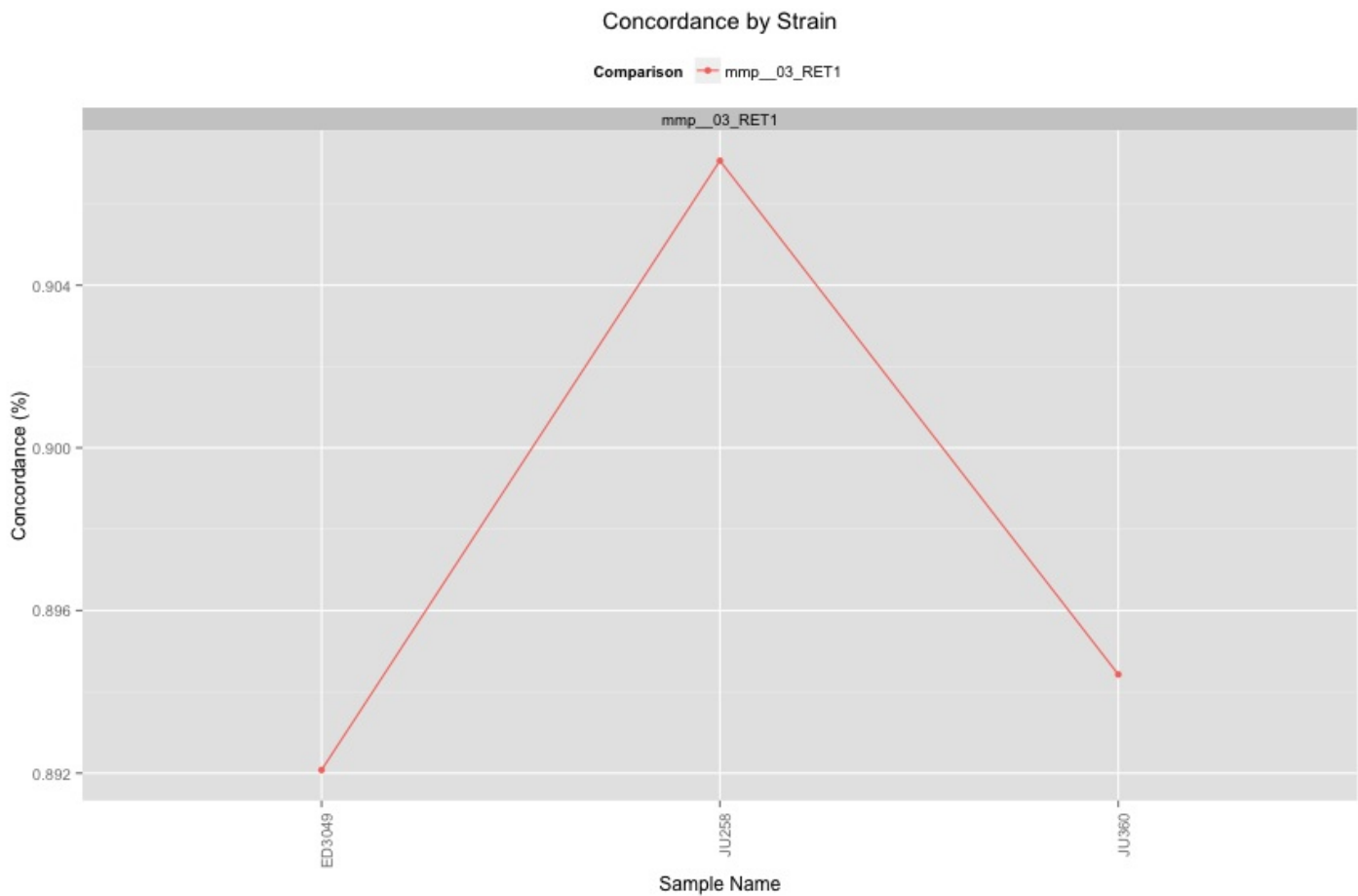
## Number of SNPs/Strain



## Singletons



Ind. Sample Concordance



Pairwise Concordance



```
## Error: subscript out of bounds
```