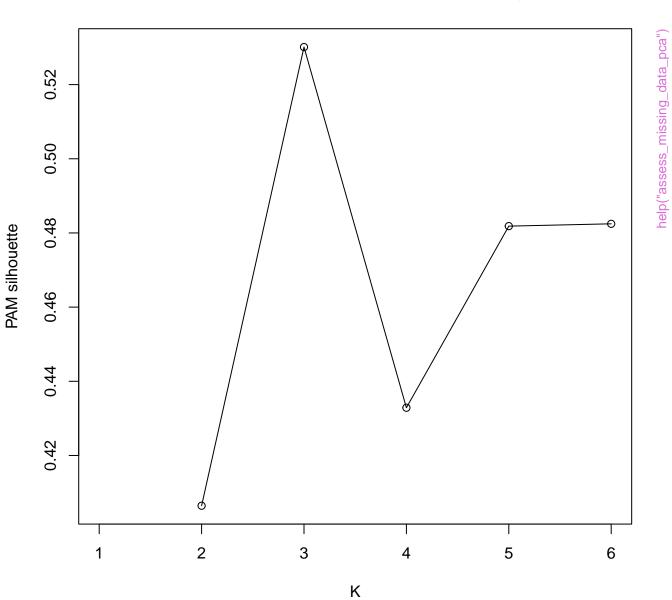
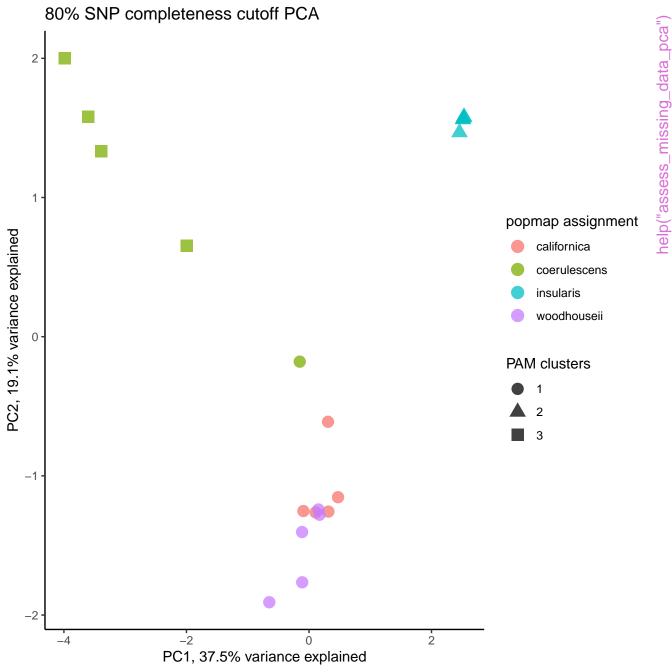
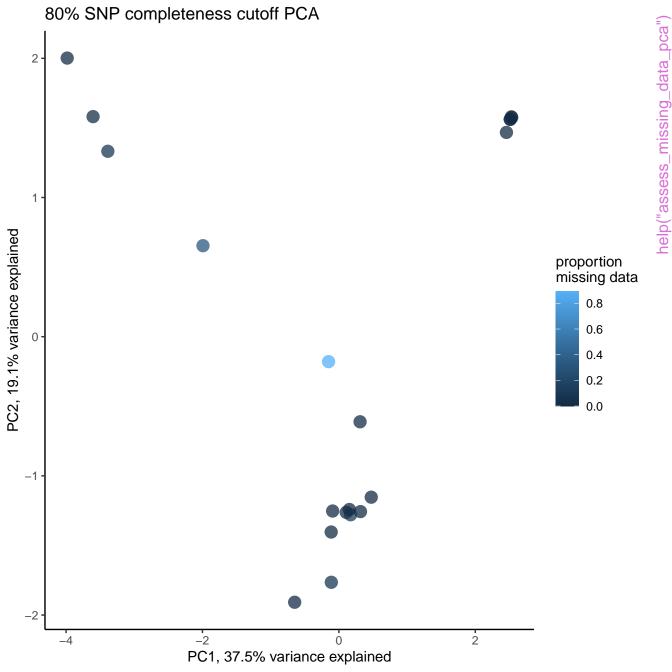
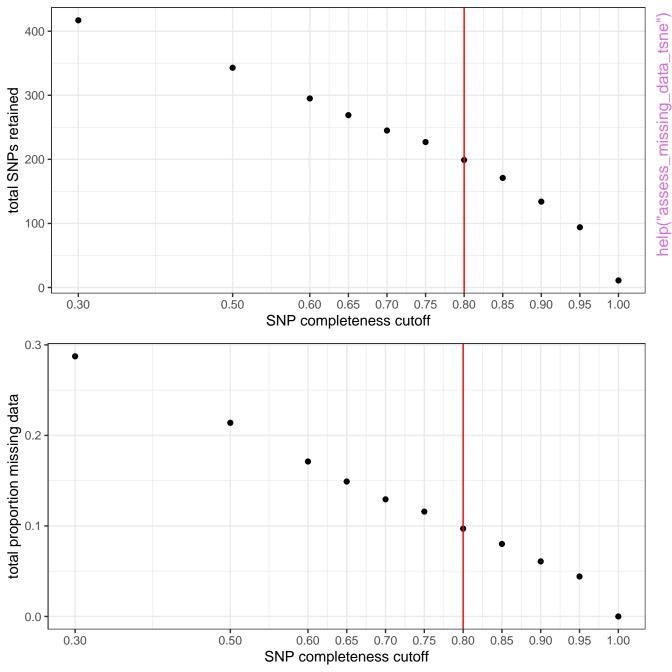


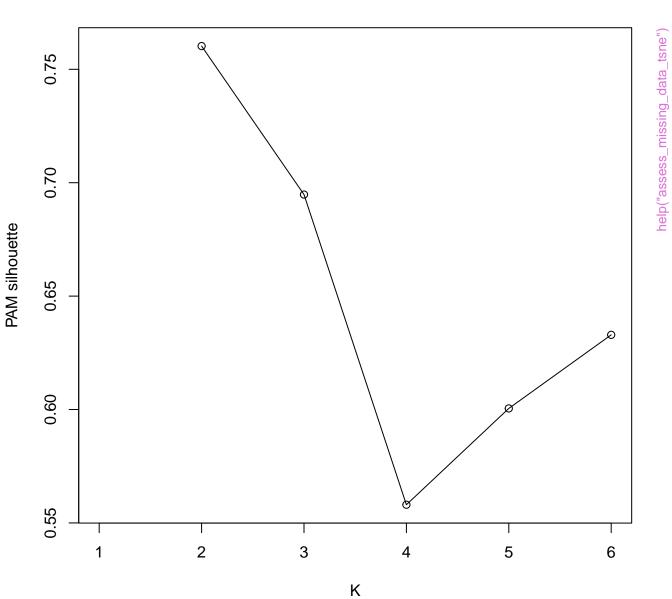
## 80% SNP completeness cutoff PAM clustering results

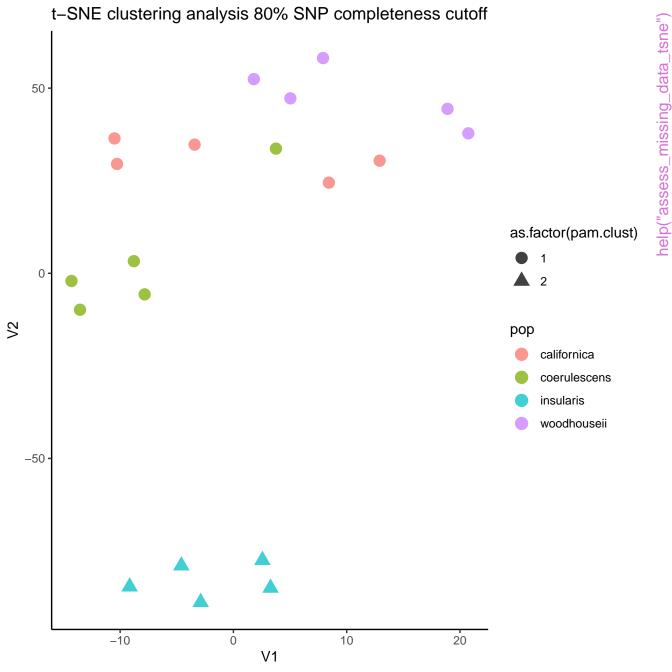


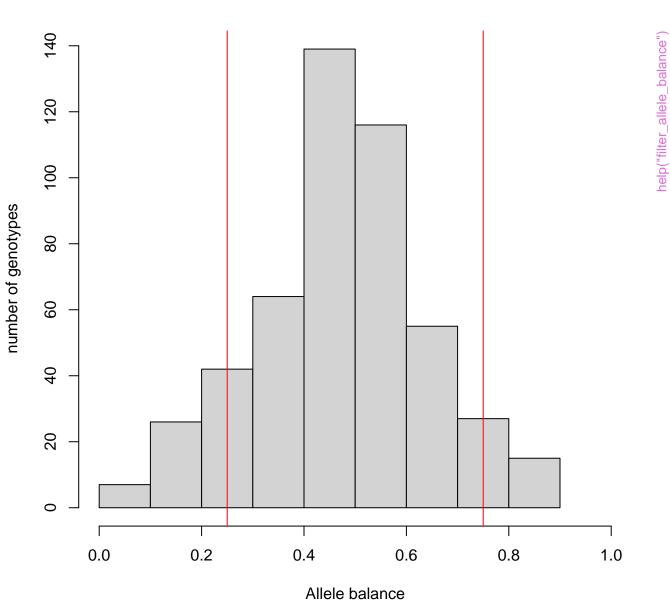




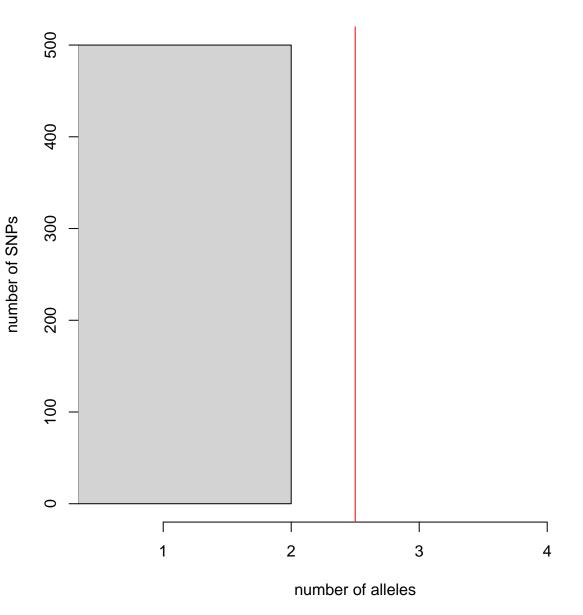




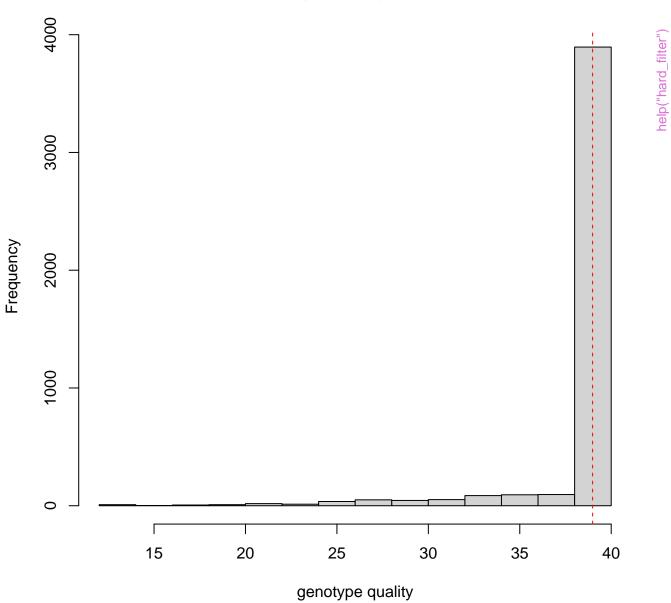




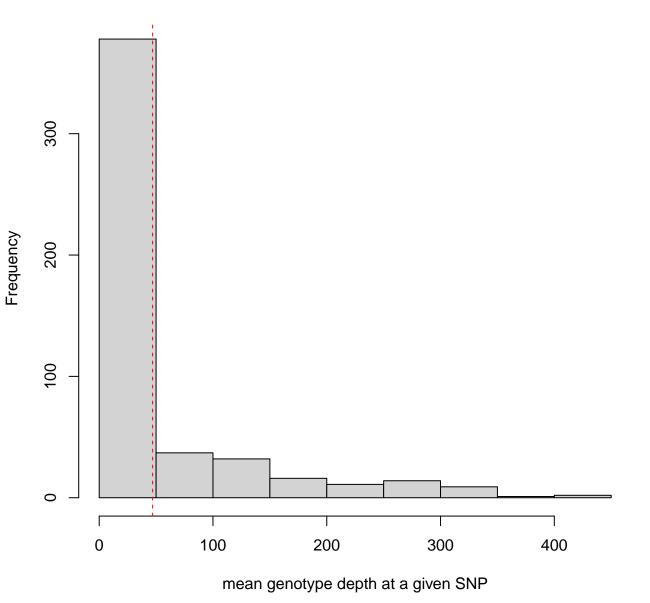




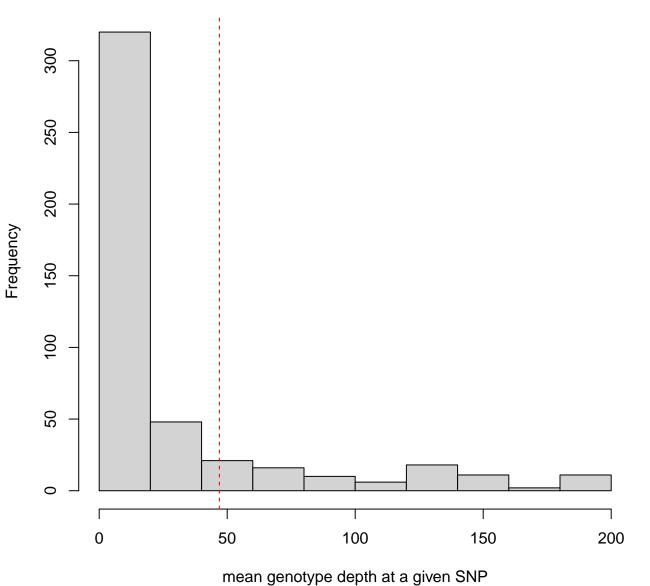
Histogram of gq.matrix



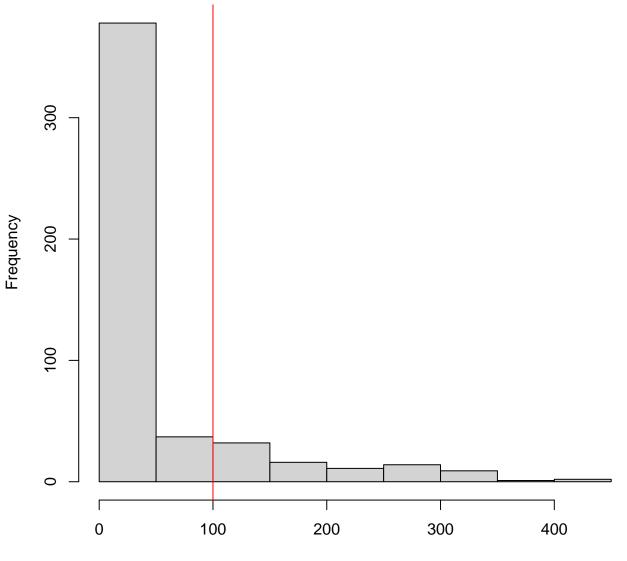
## depth of all called SNPs



## depth of SNPs < 200



## max depth cutoff



mean genotype depth at a given SNP

# folded SFS

