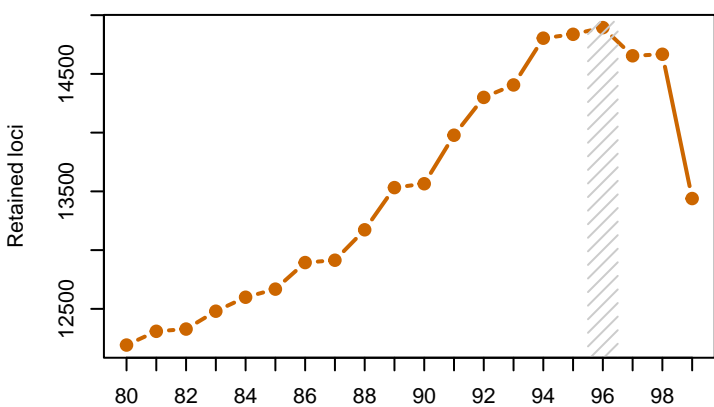
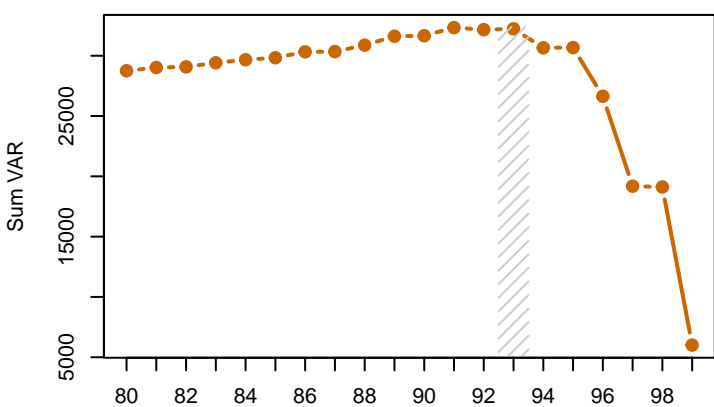


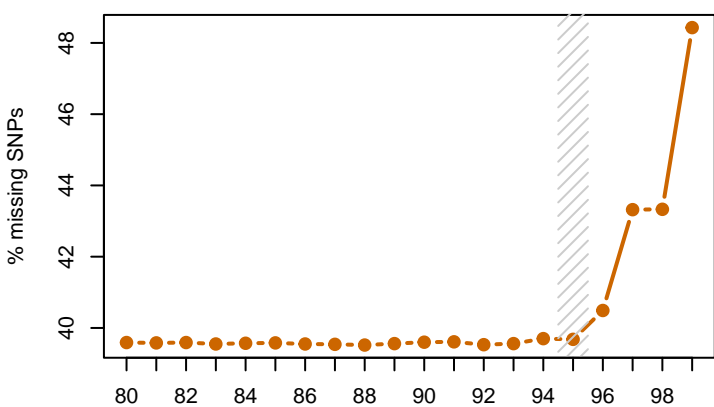
Retained loci across samples



Number of variable sites across samples



Percentage of missing SNPs across samples



Number of new polymorphic sites

