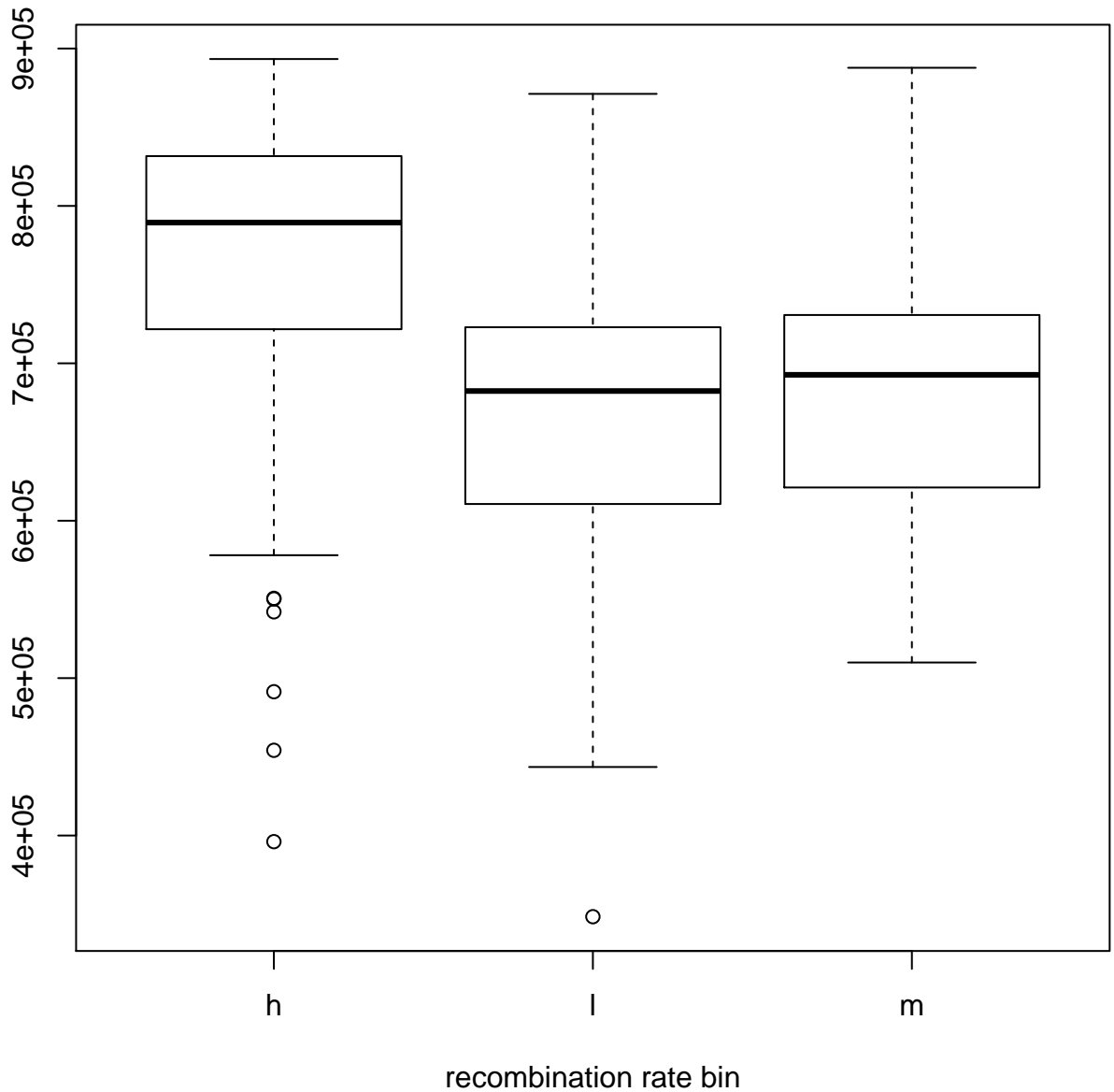
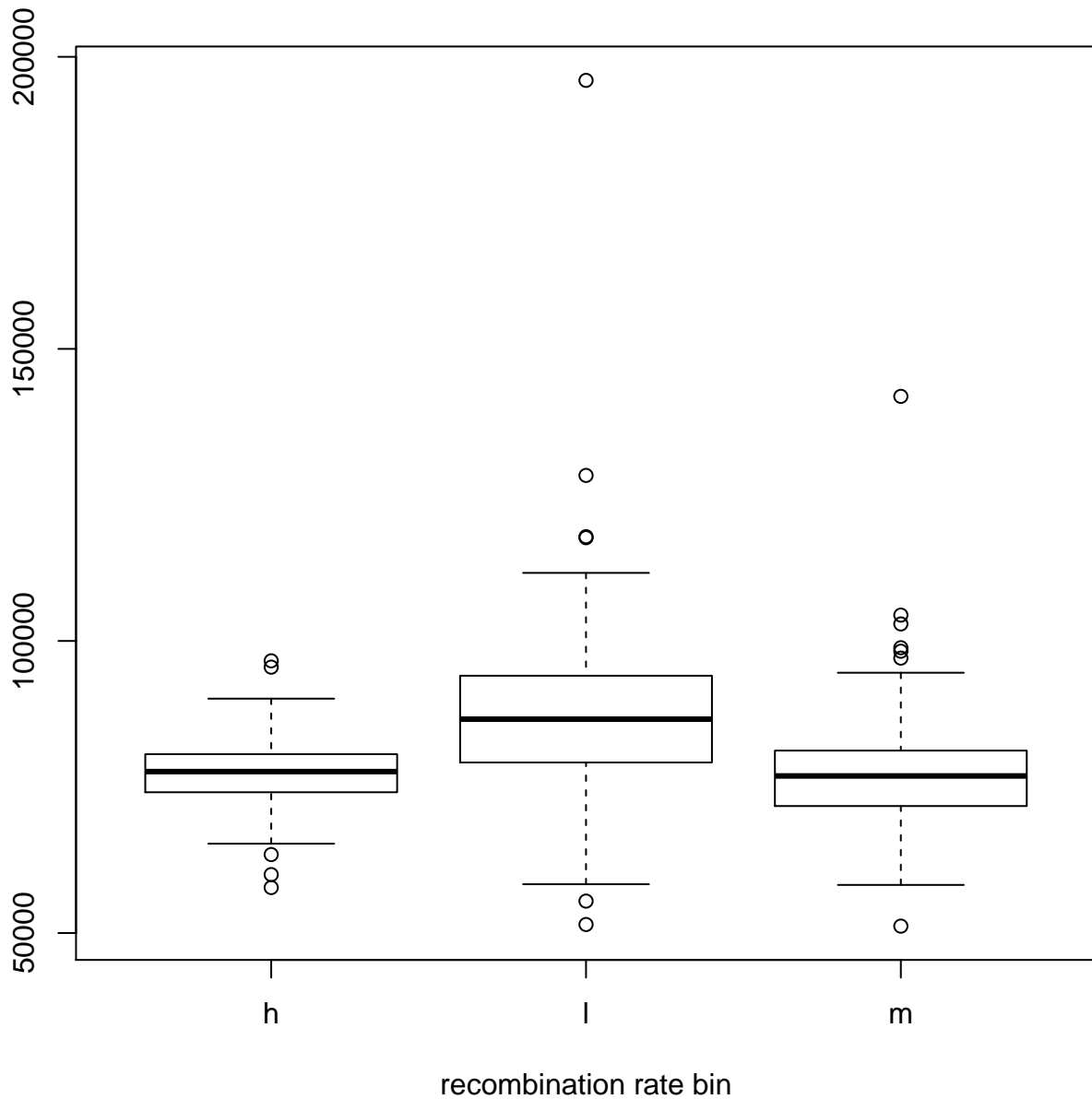


number of good sites



number of biallelic SNPs



proportion of sites polymorphic

