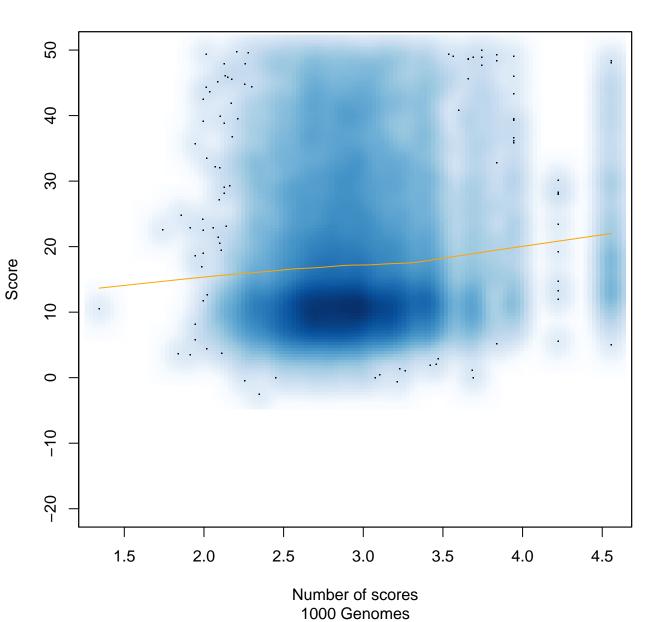
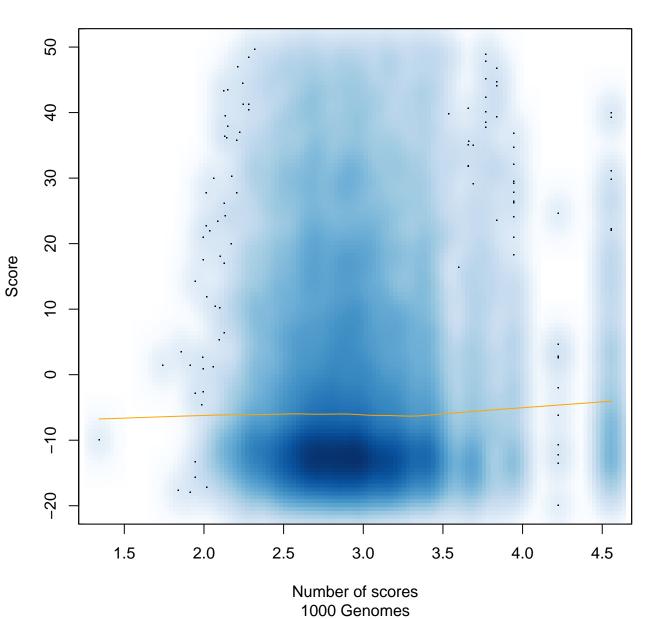
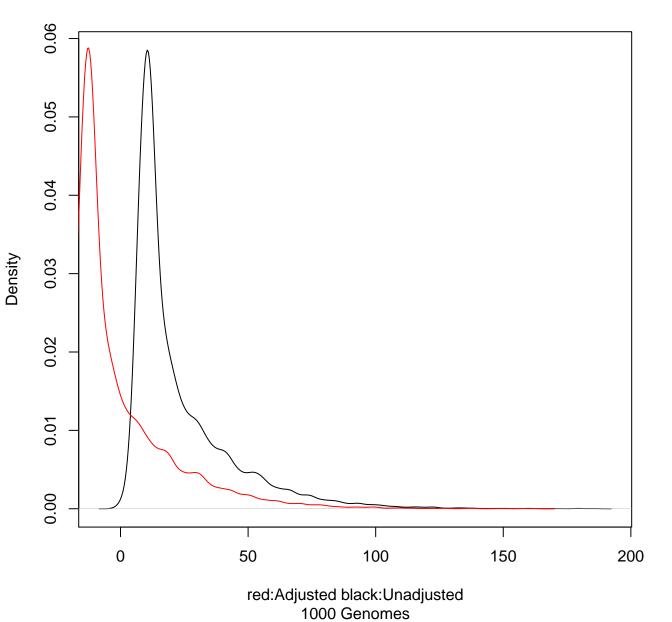
Scores



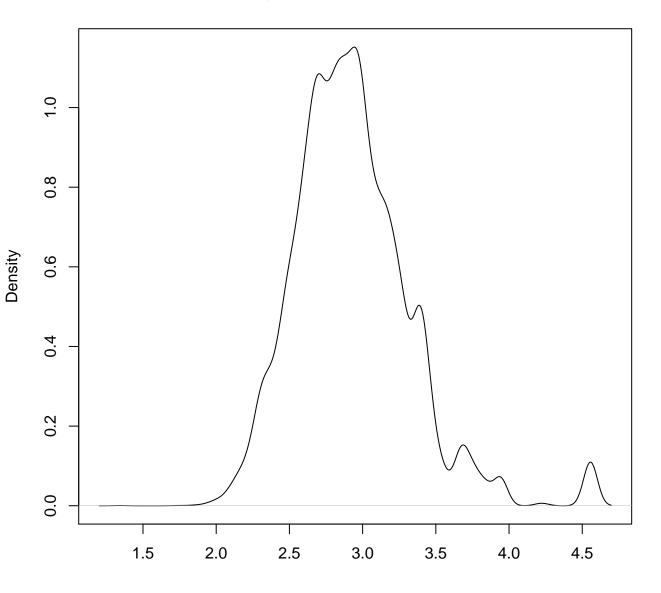
## **Adjusted Scores**



### **Scores distribution**

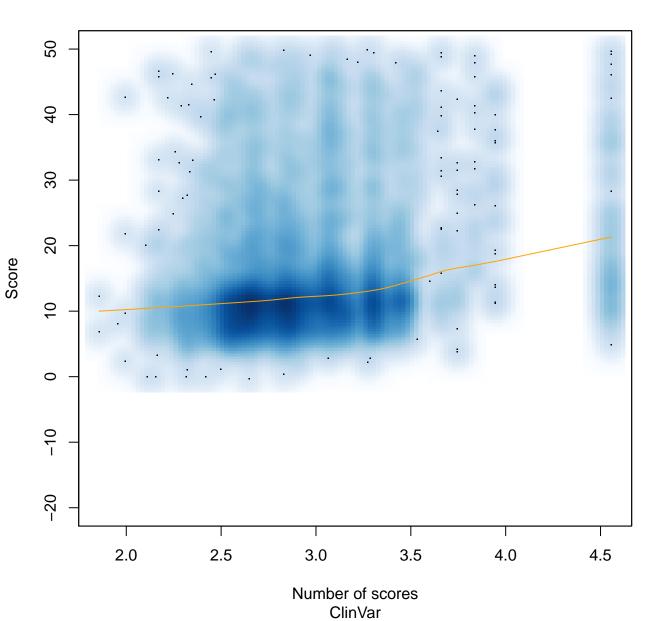


## log10(Number of scores)

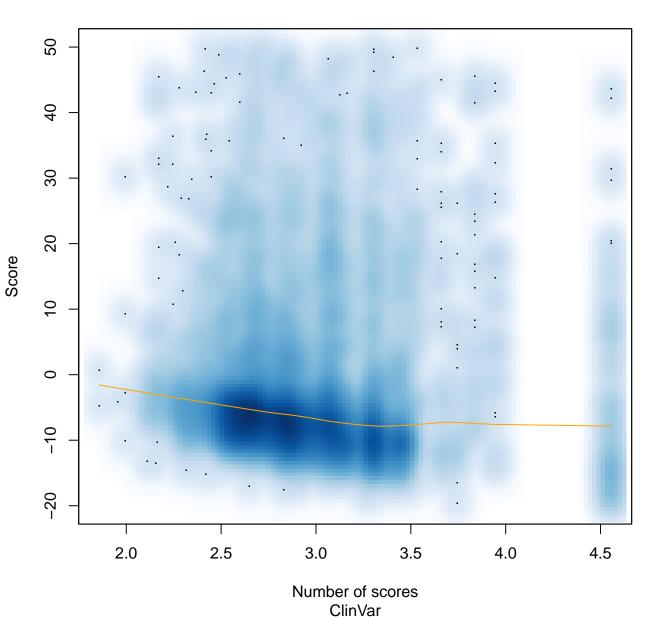


1000 Genomes

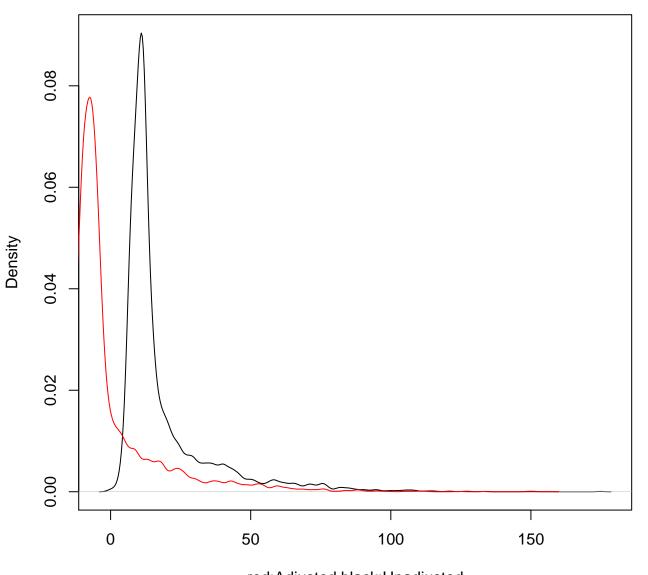
Scores



## **Adjusted Scores**

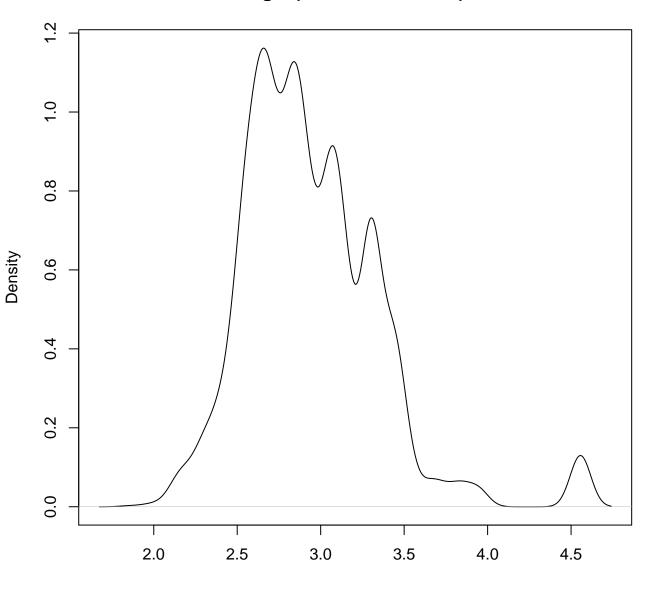


### **Scores distribution**



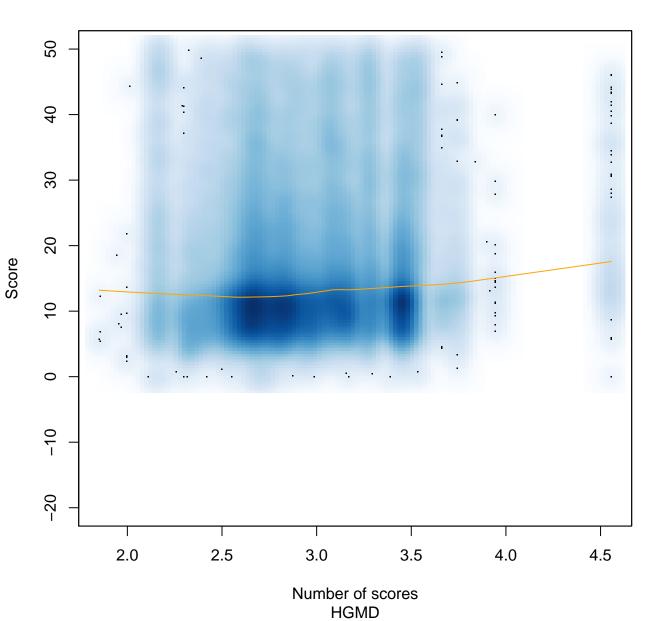
red:Adjusted black:Unadjusted ClinVar

# log10(Number of scores)

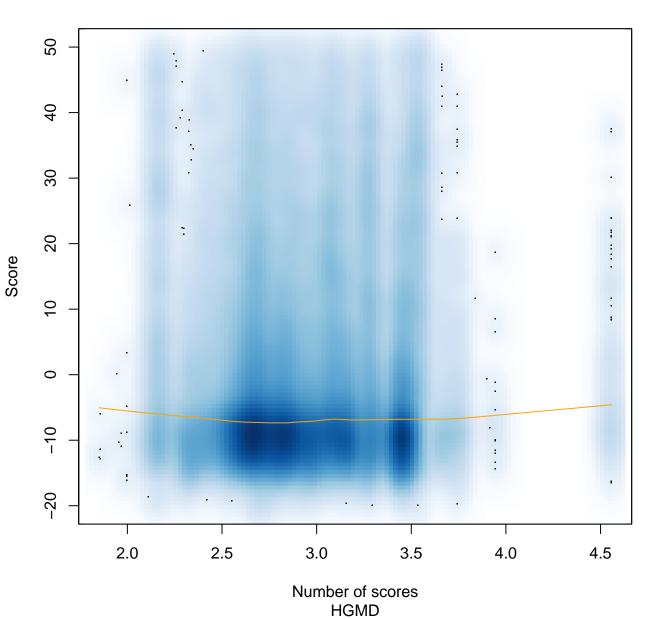


ClinVar

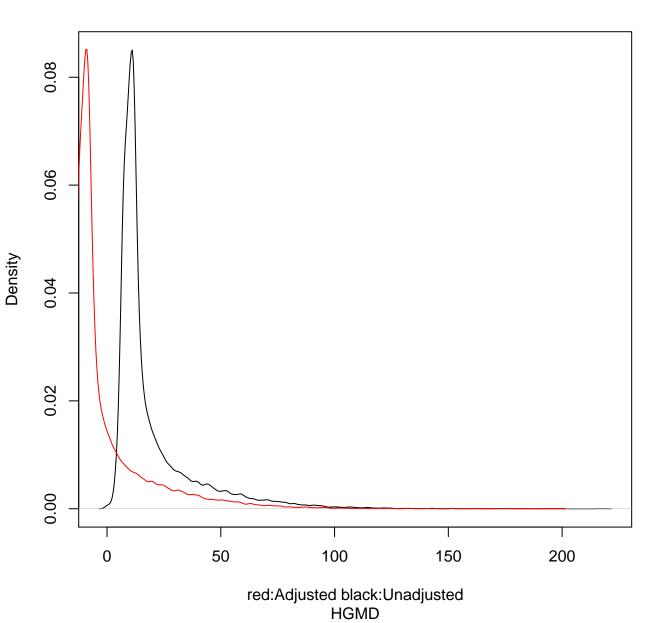




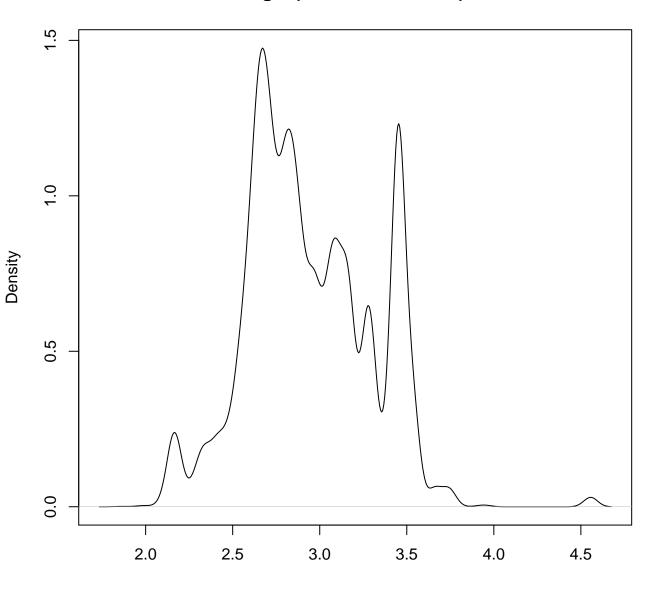
## **Adjusted Scores**



### **Scores distribution**

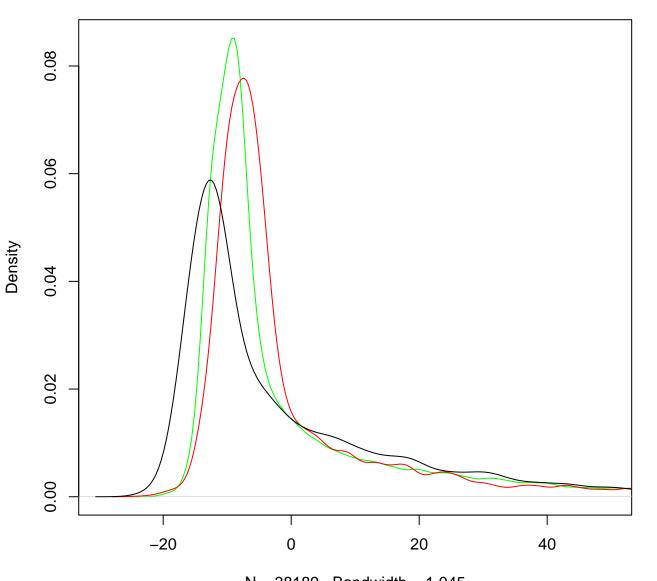


# log10(Number of scores)



HGMD

### Distribution of adjusted log-likelihhods



N = 38189 Bandwidth = 1.045 Black: 1KGenomes, Red: Clinvar, Green: HGMD