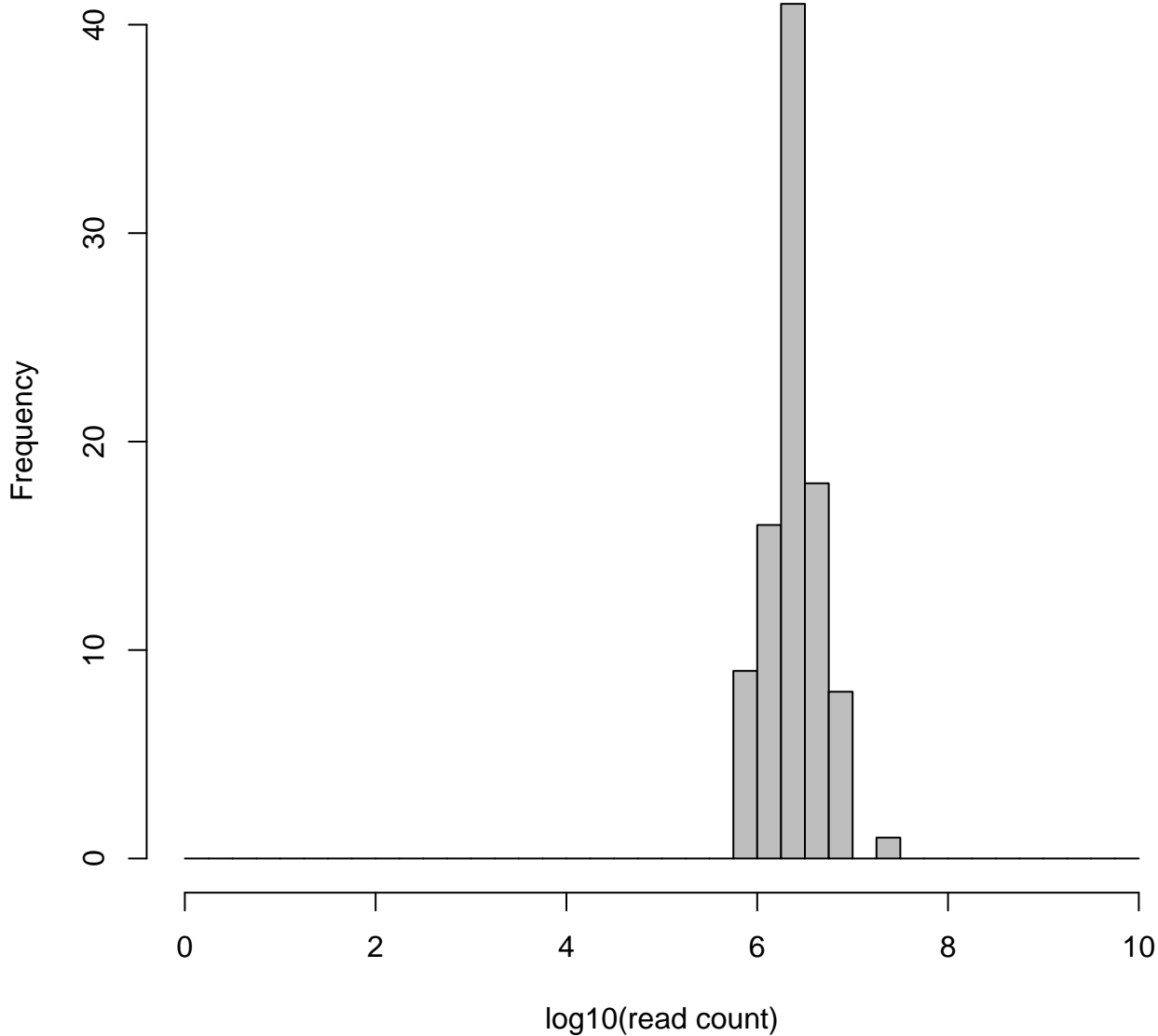
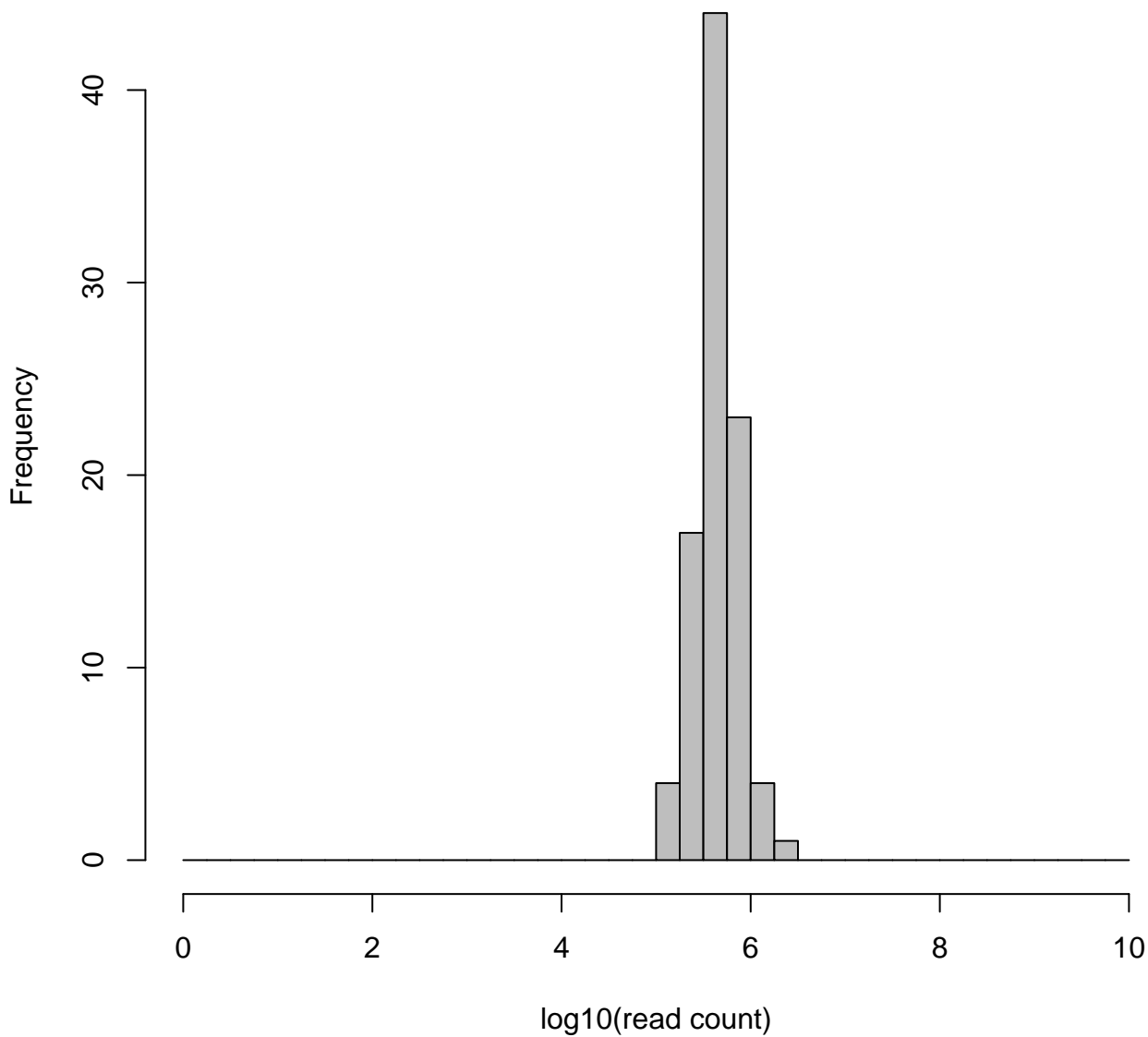


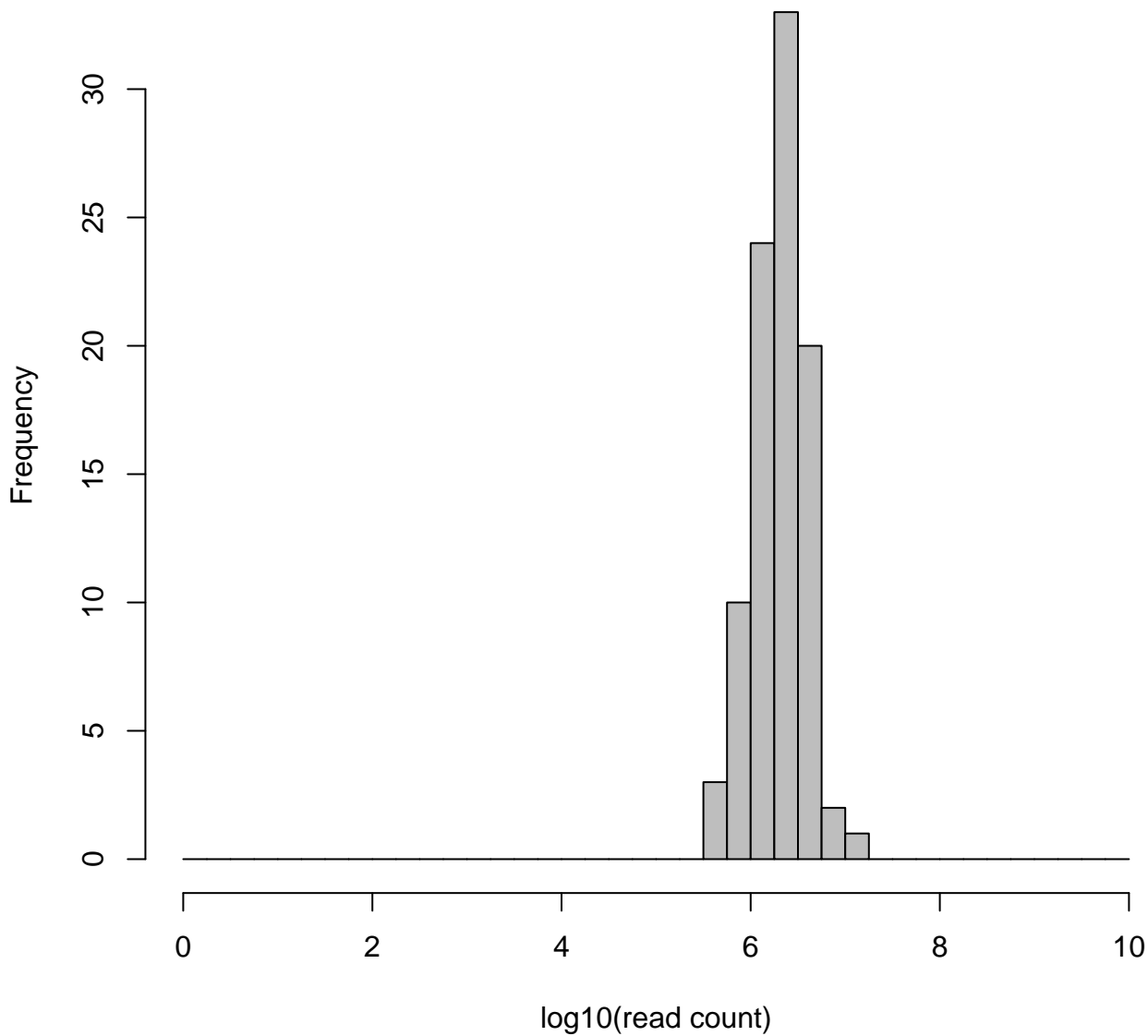
## Read count summary : total clean read



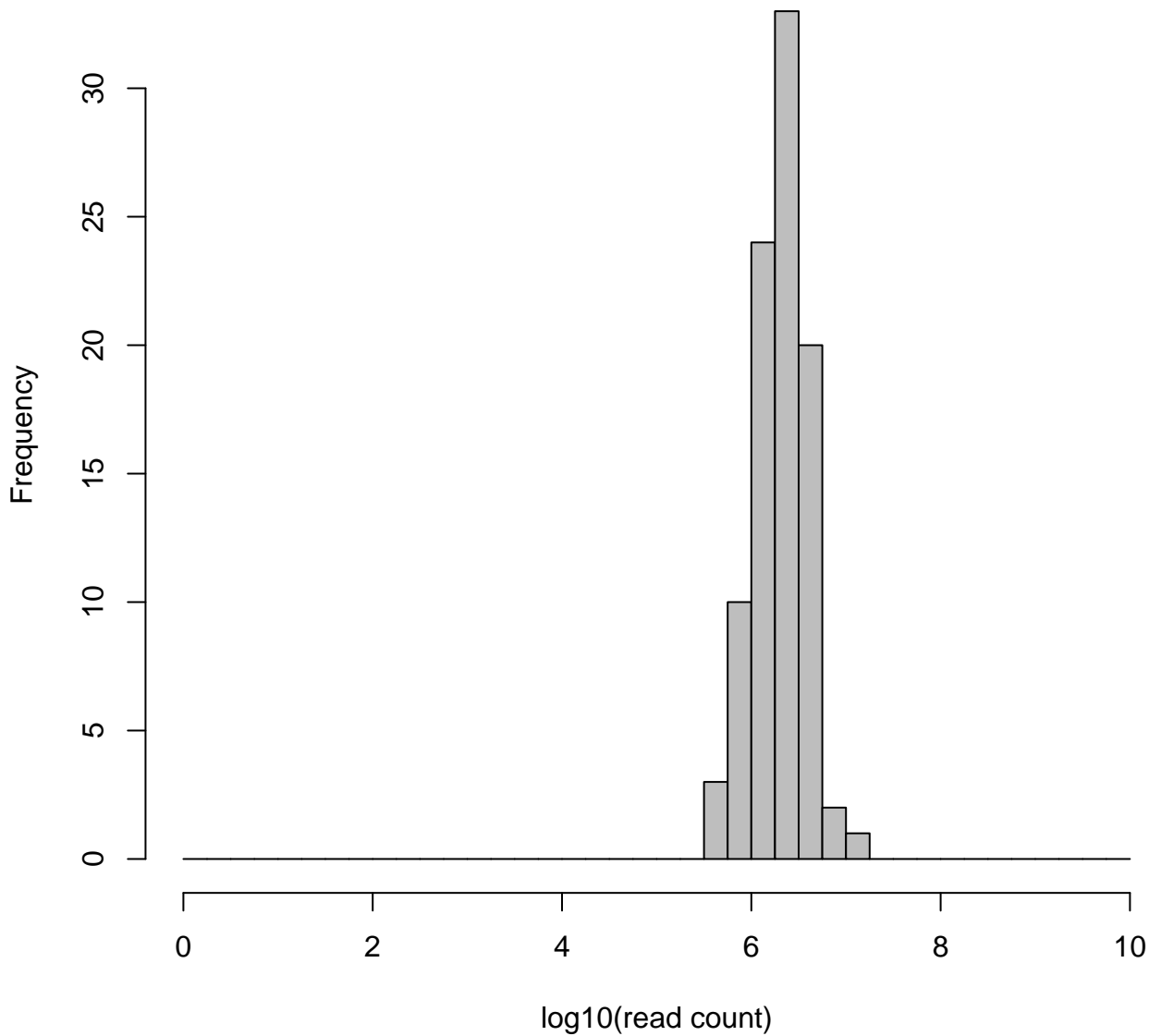
## Read count summary : unique sequence



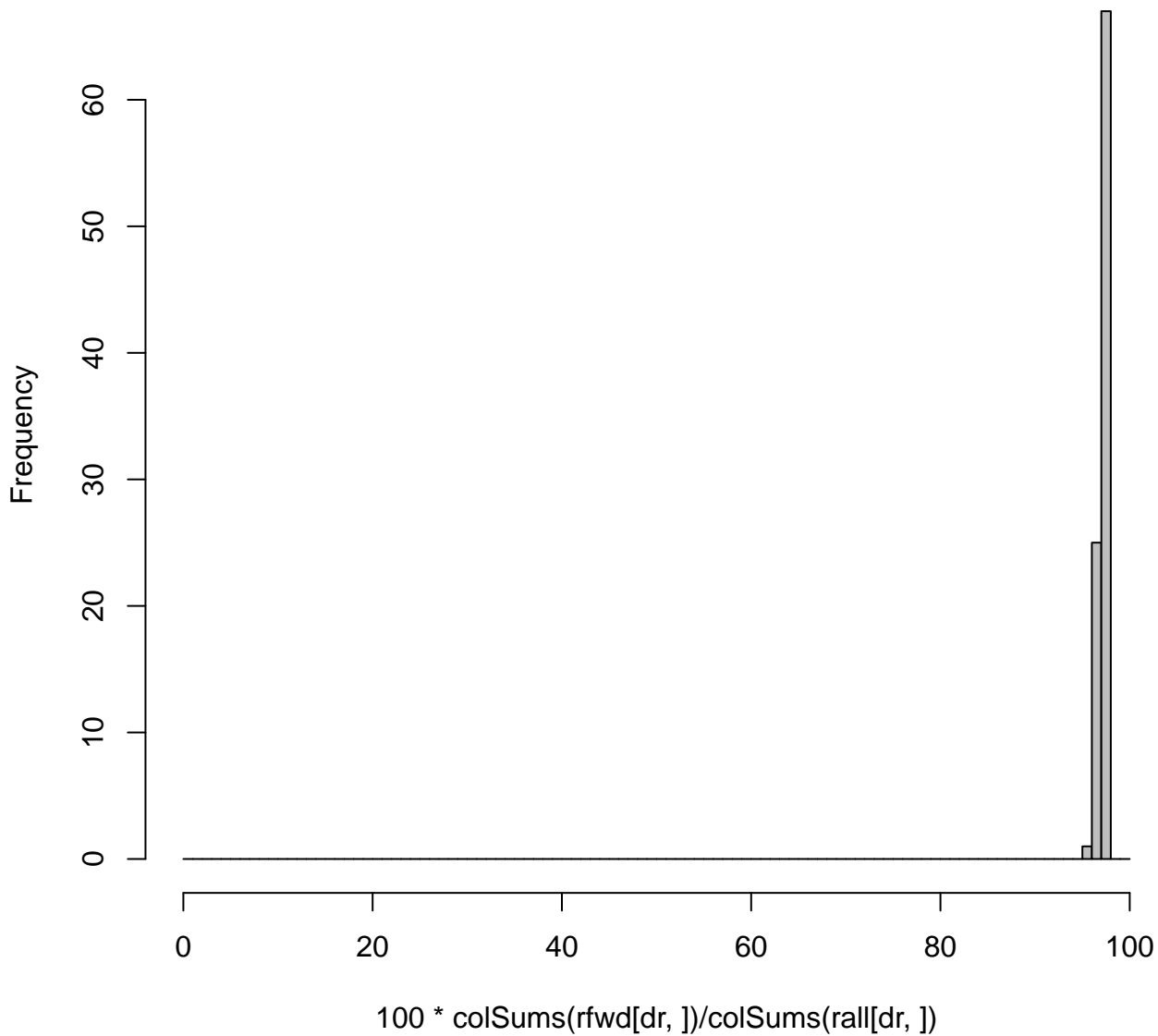
# Read count summary : mapped read

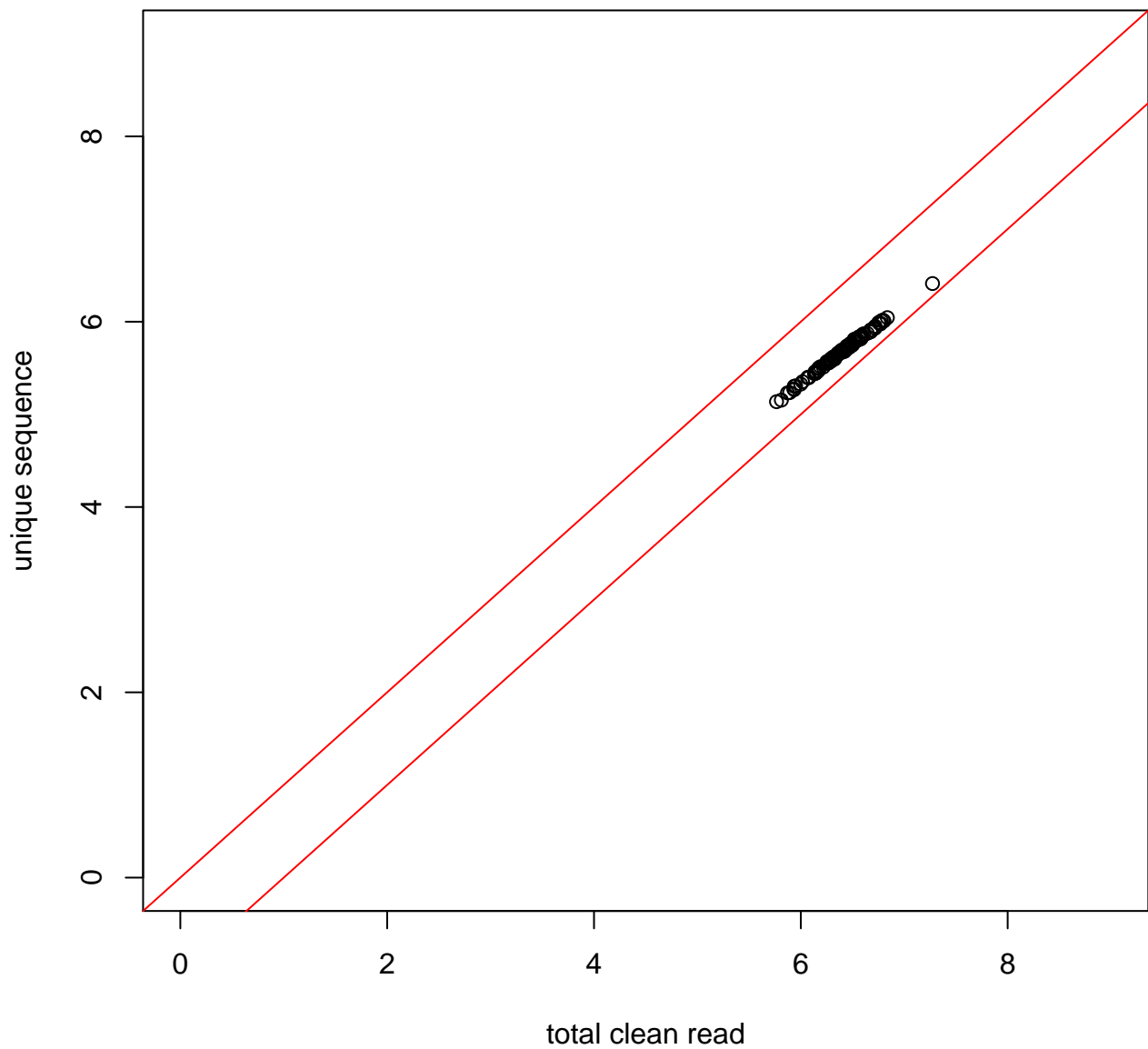


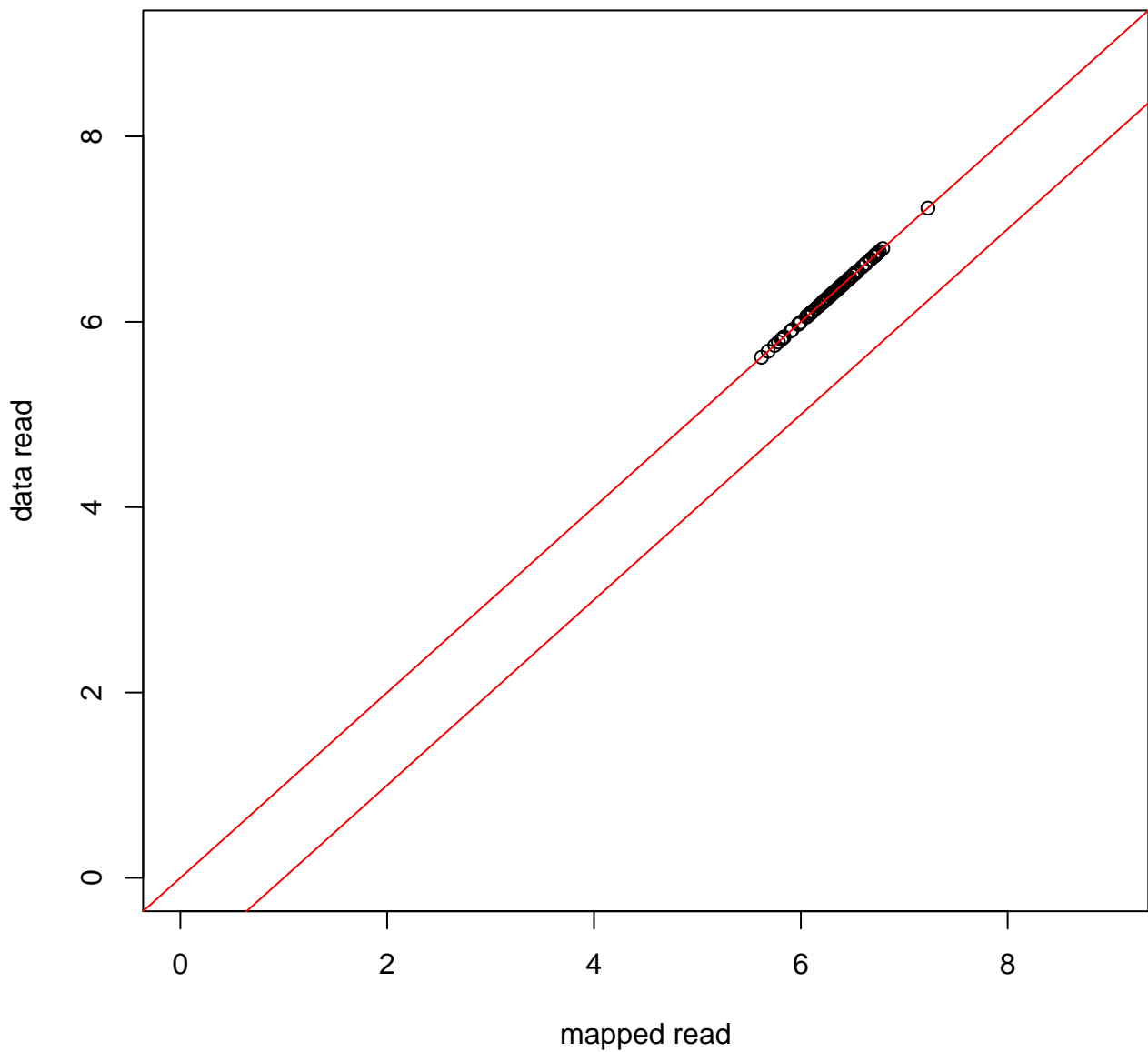
## Read count summary : data read



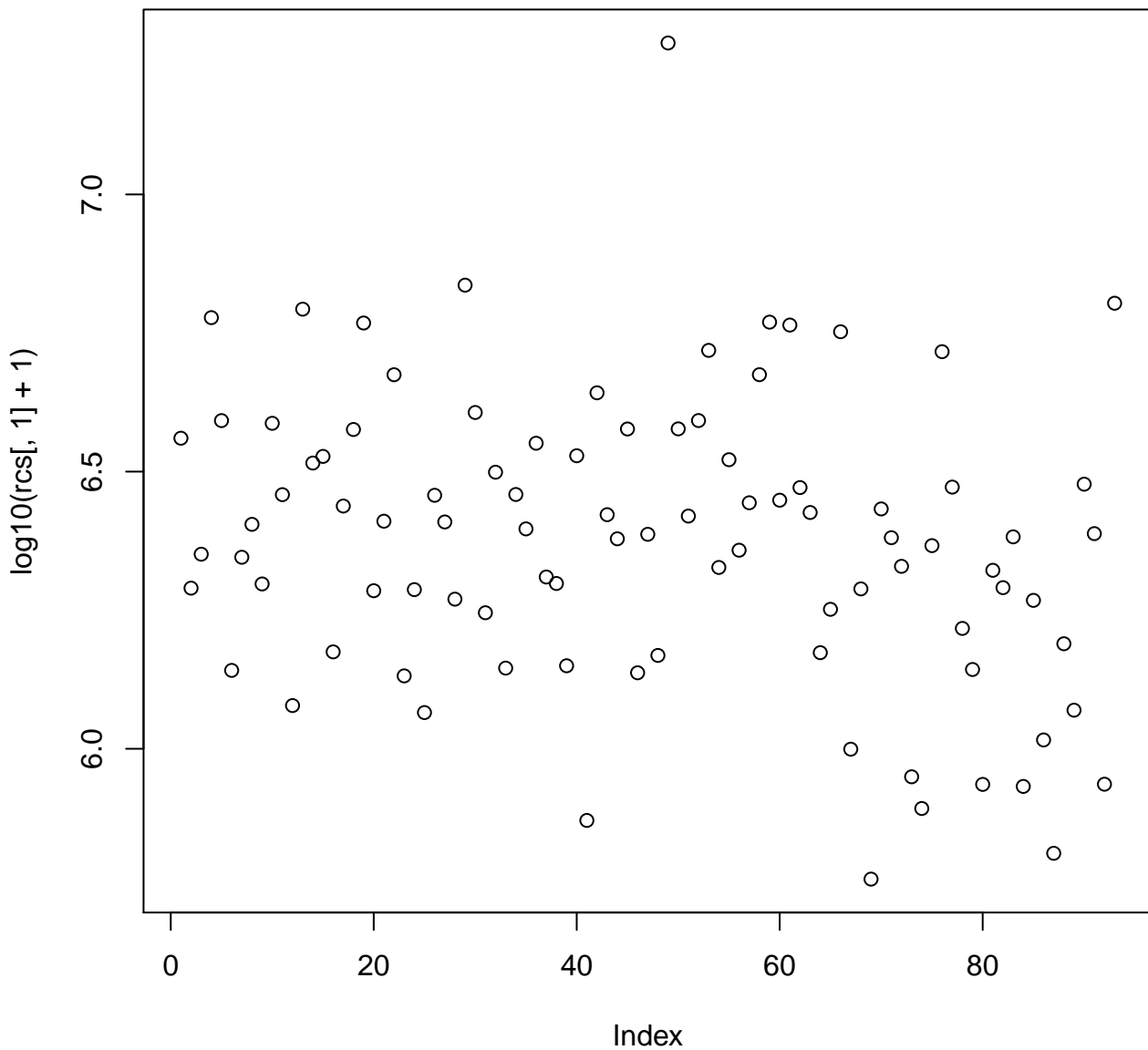
## Read count summary : strand specificity





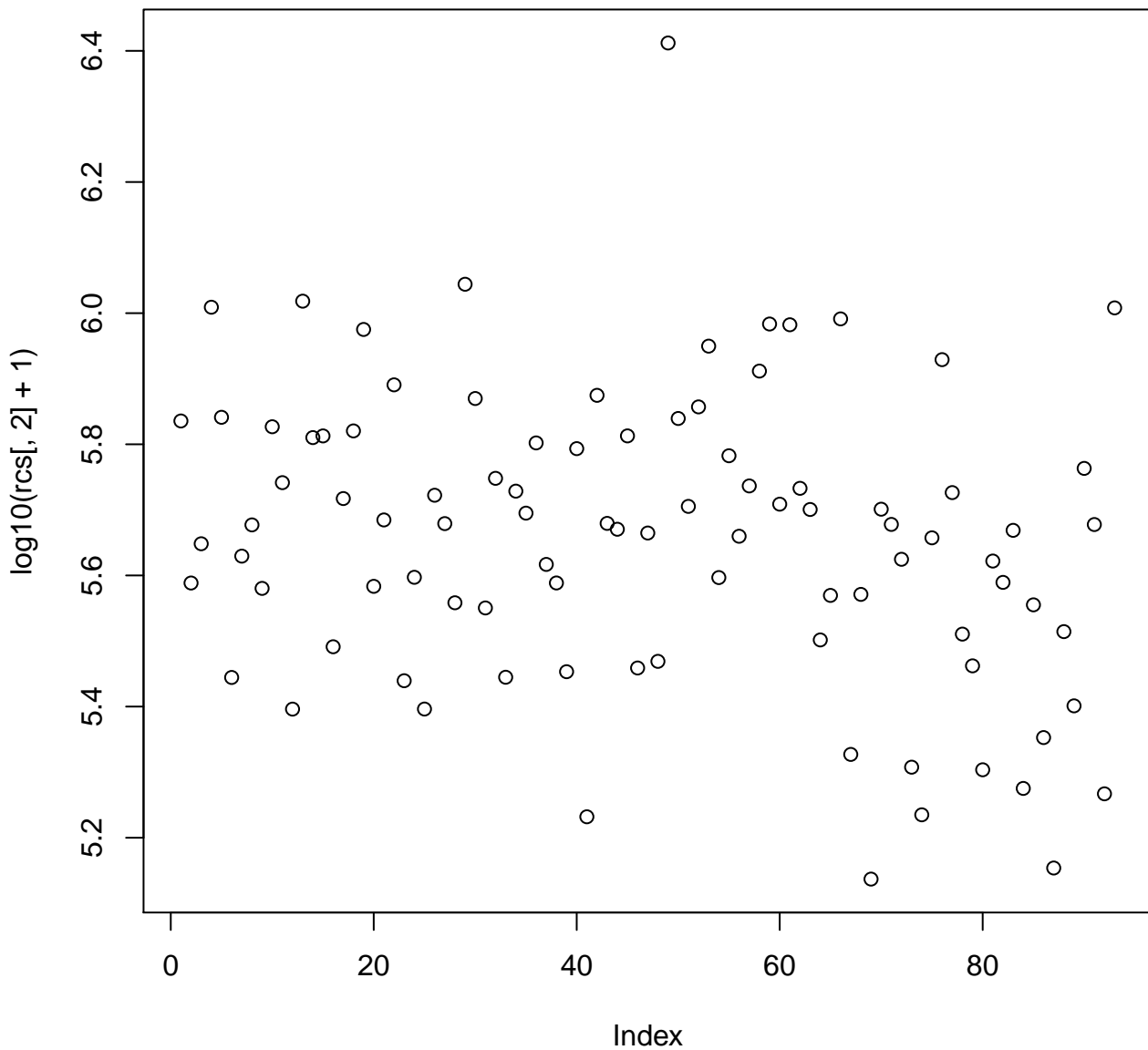


# total clean read

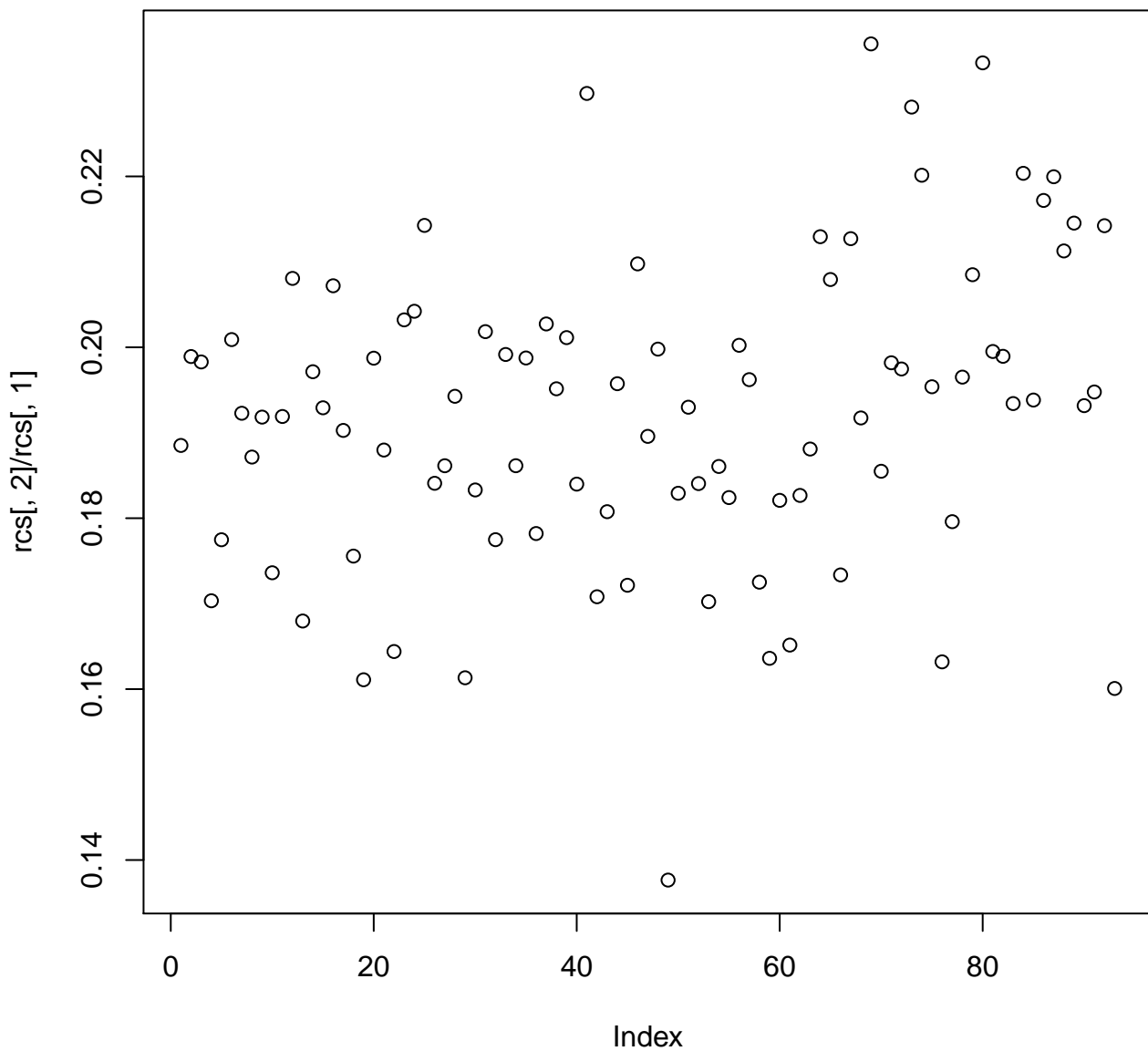




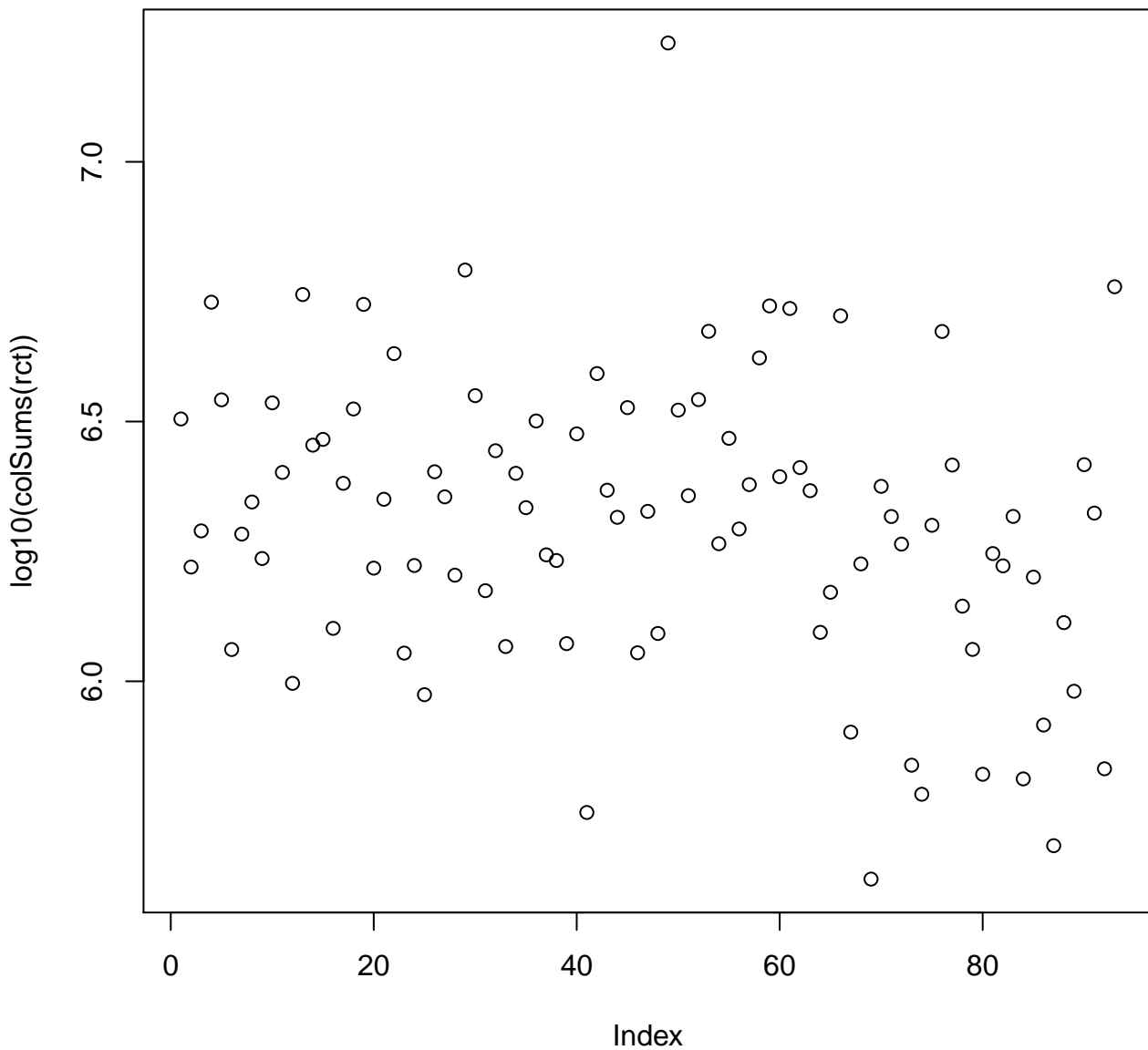
# unique sequence



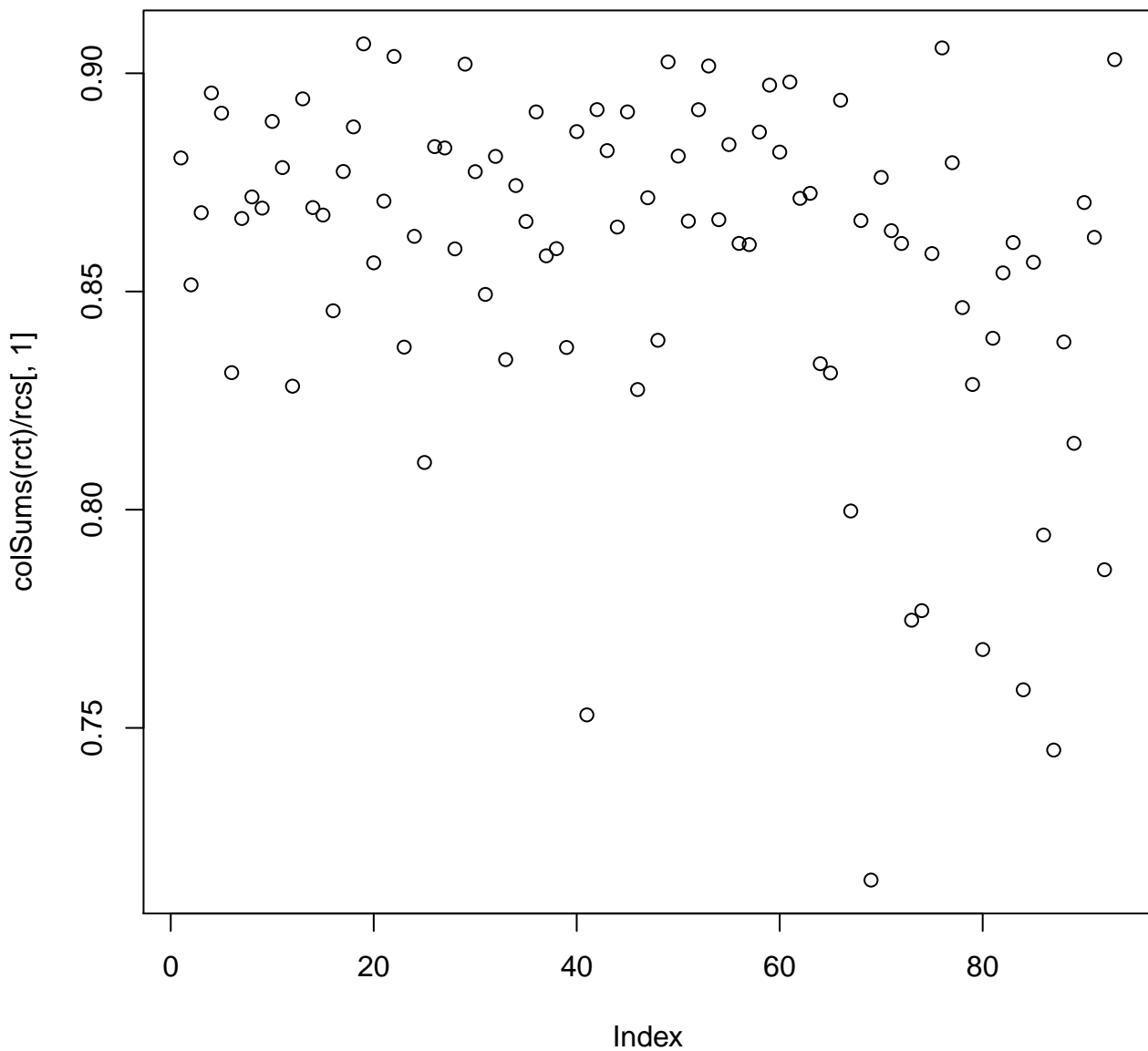
**unique sequence / total clean read**



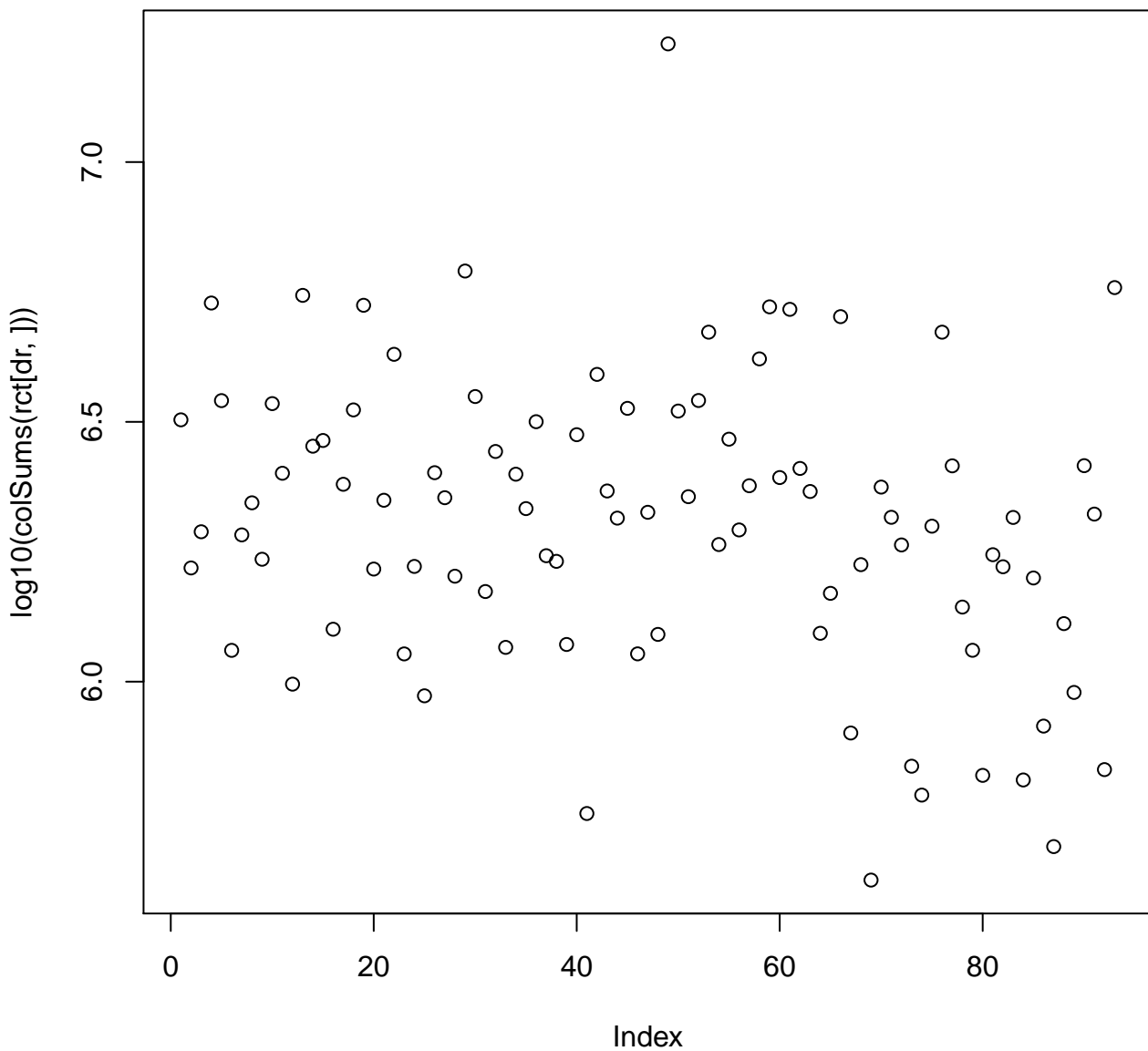
# mapped read



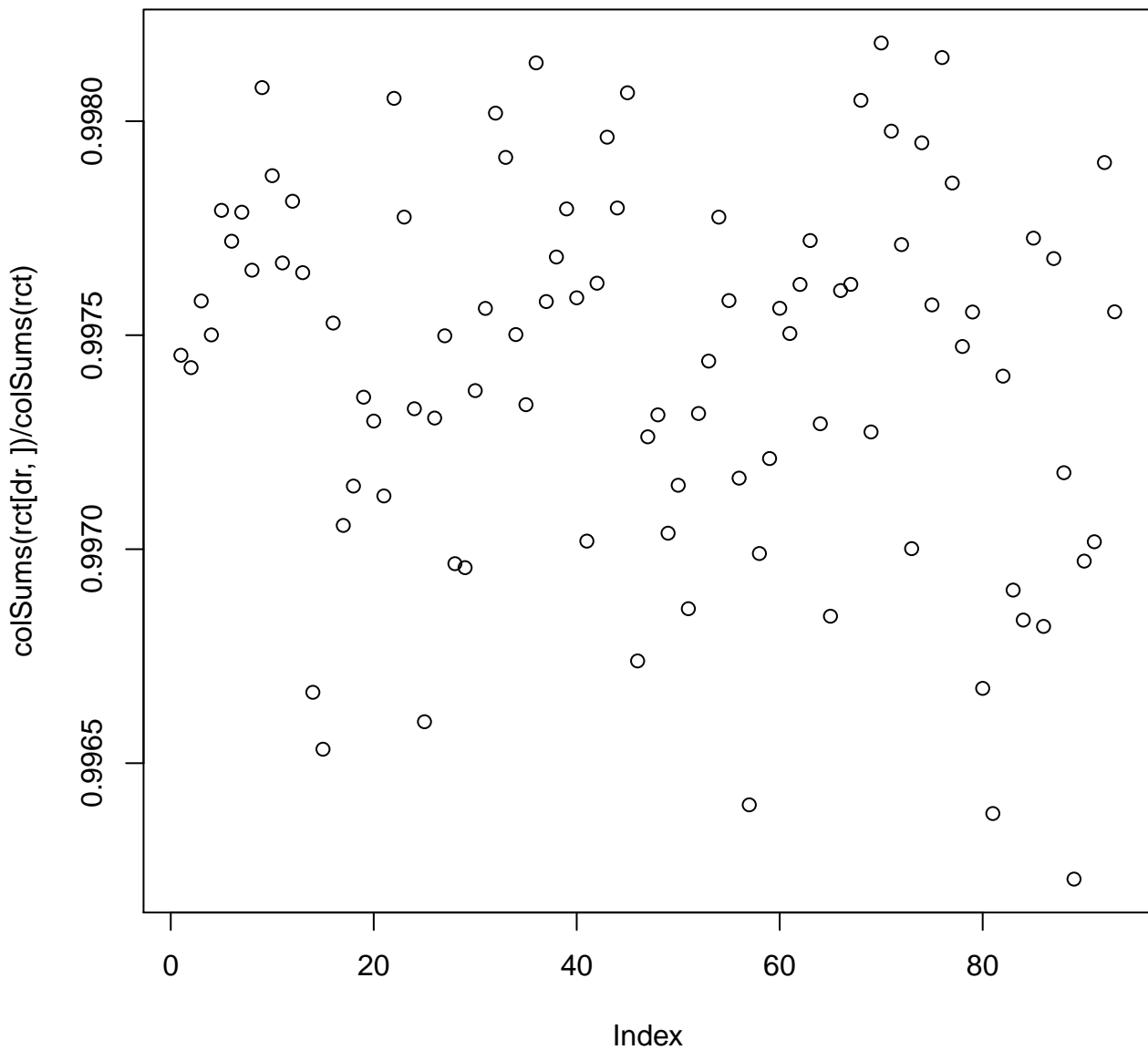
mapped read / total clean read



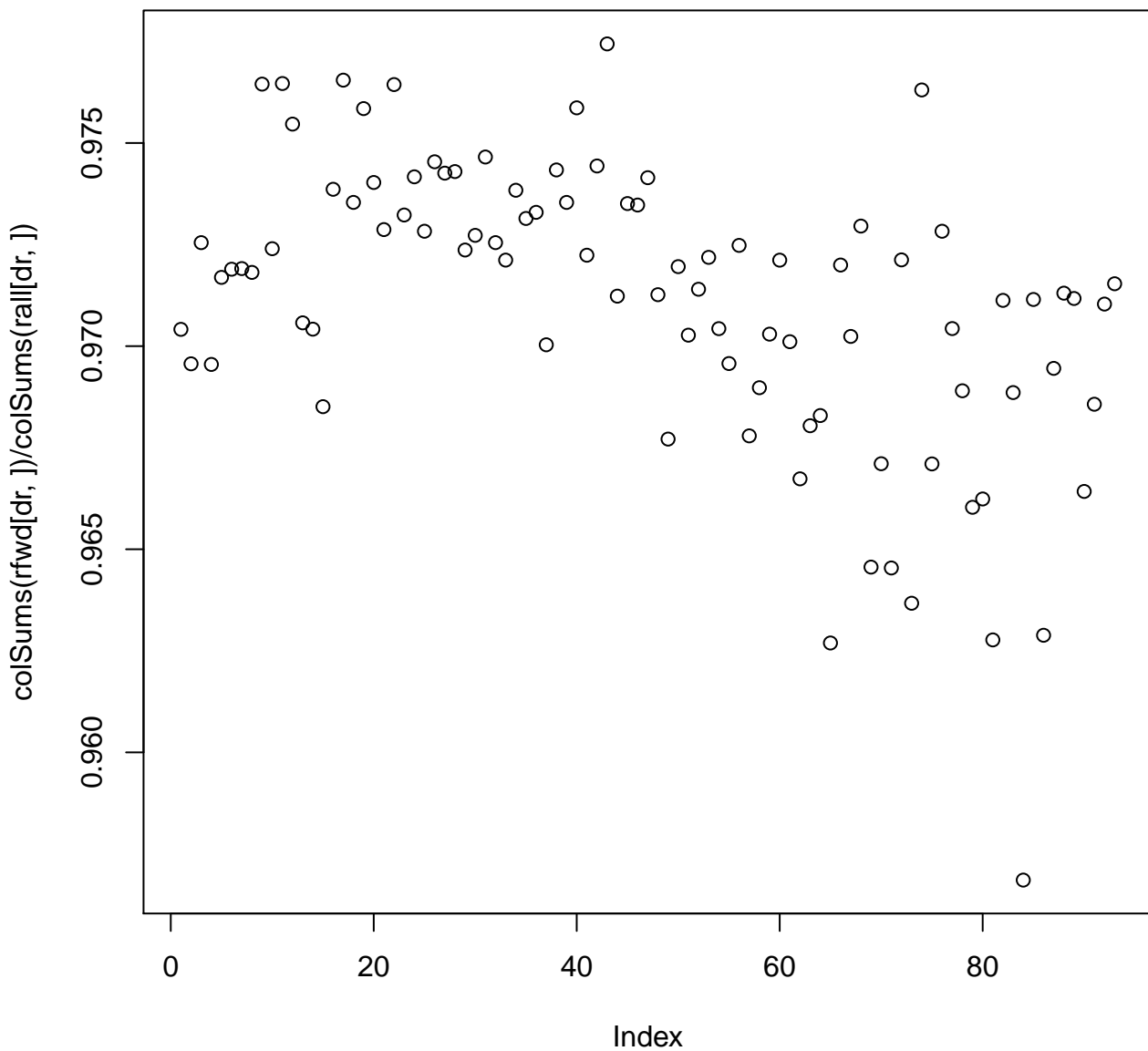
# data read



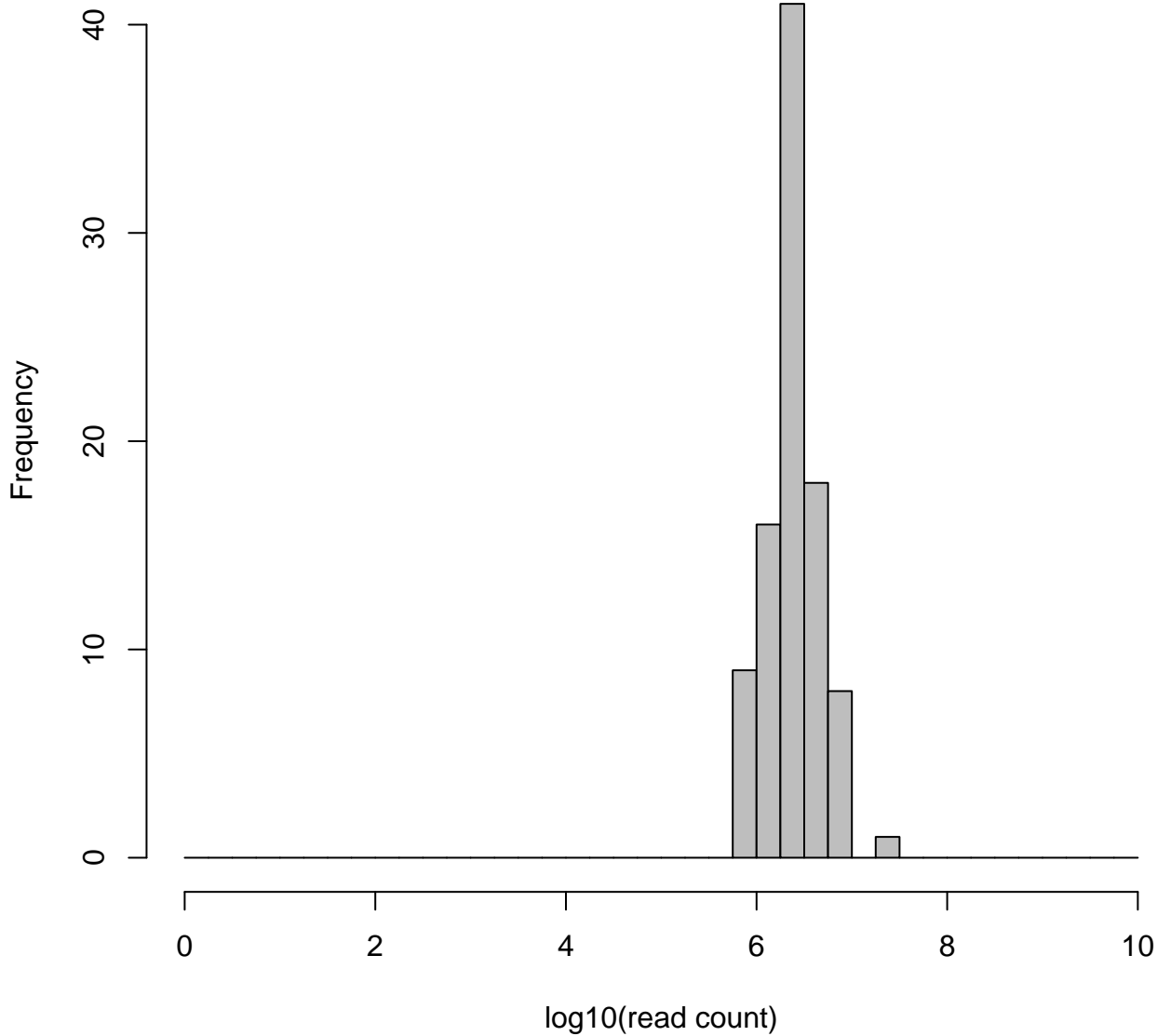
**data read / mapped read**



# strand specificity

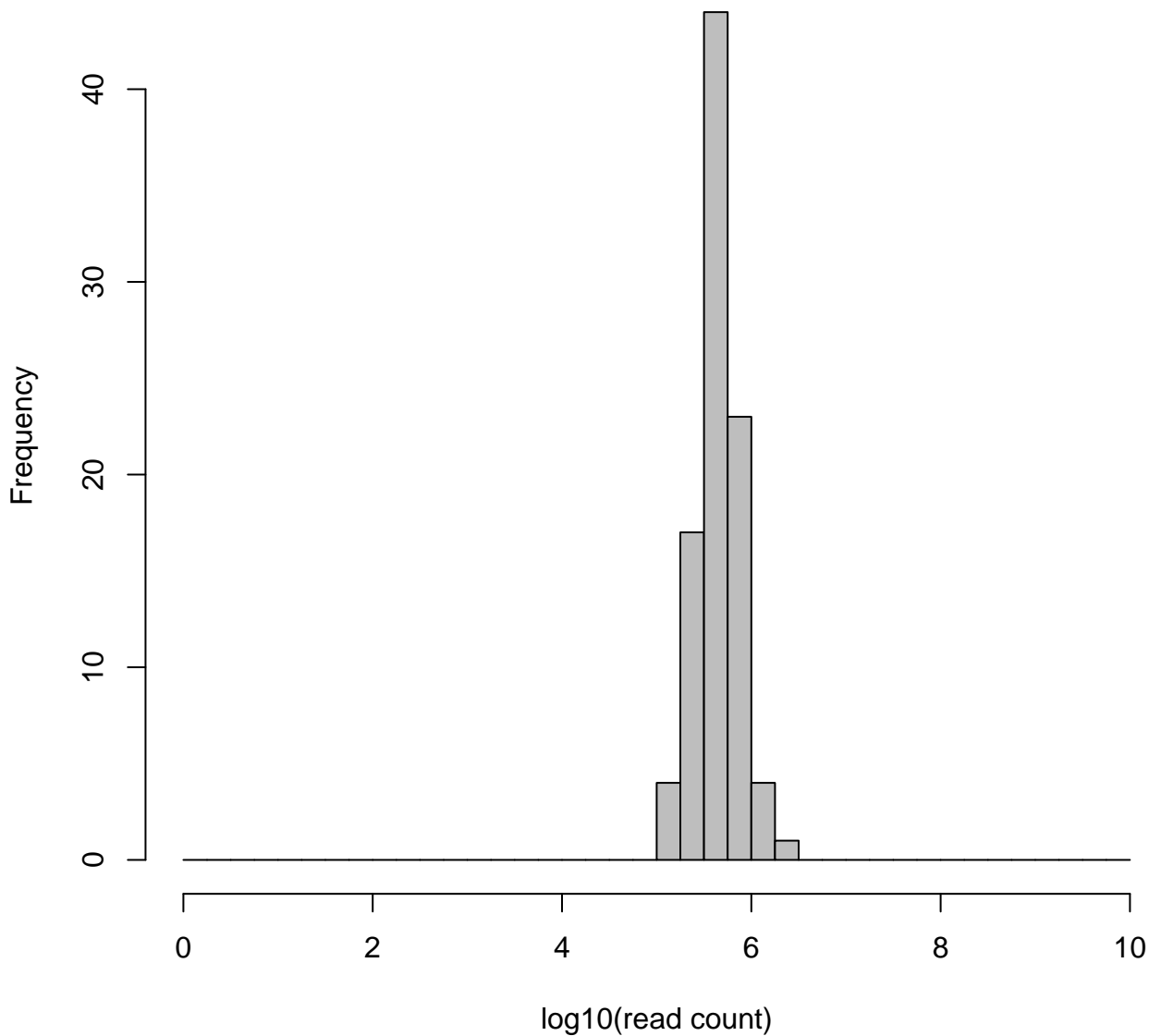


# Read count summary (all) : total clean read

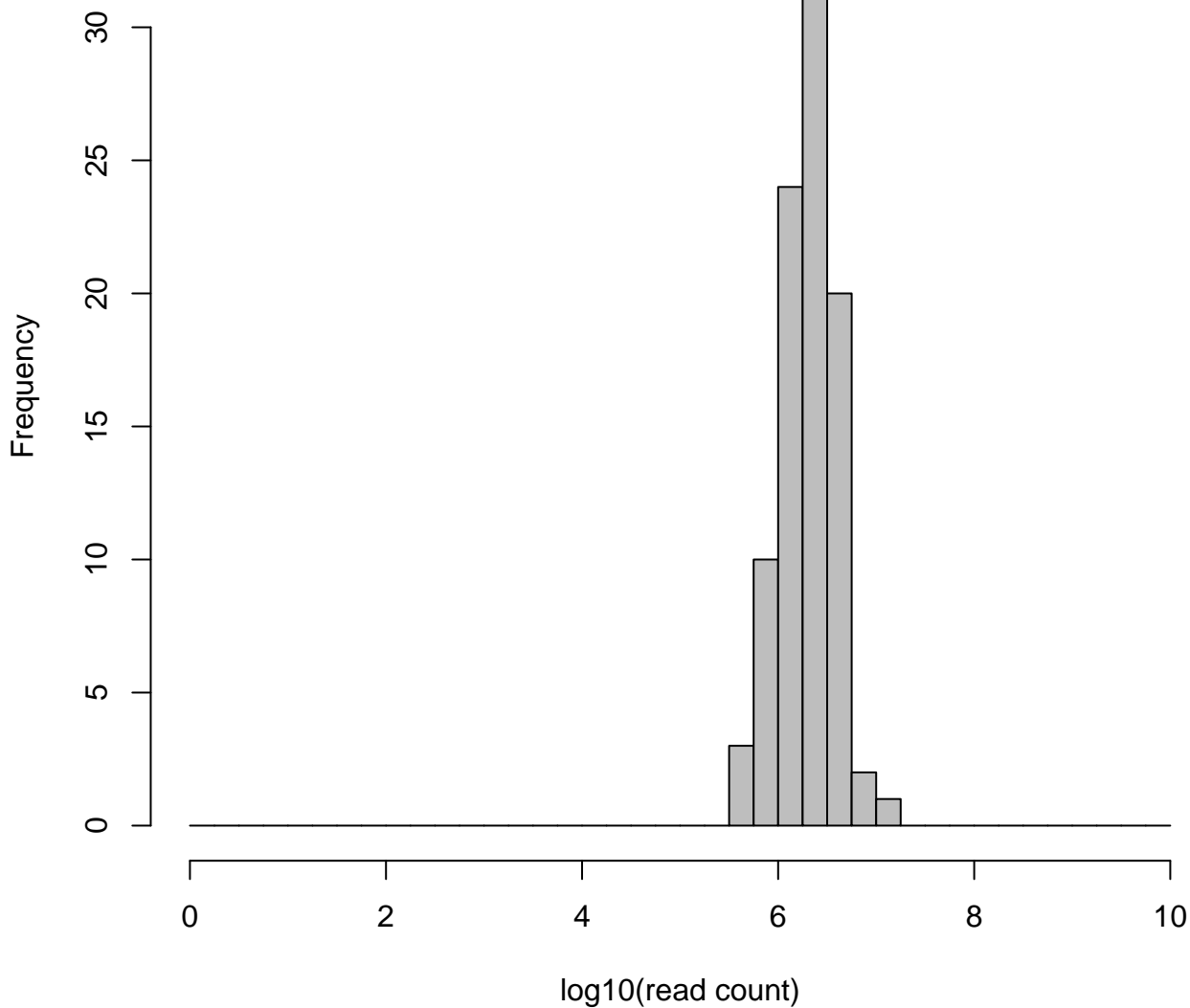




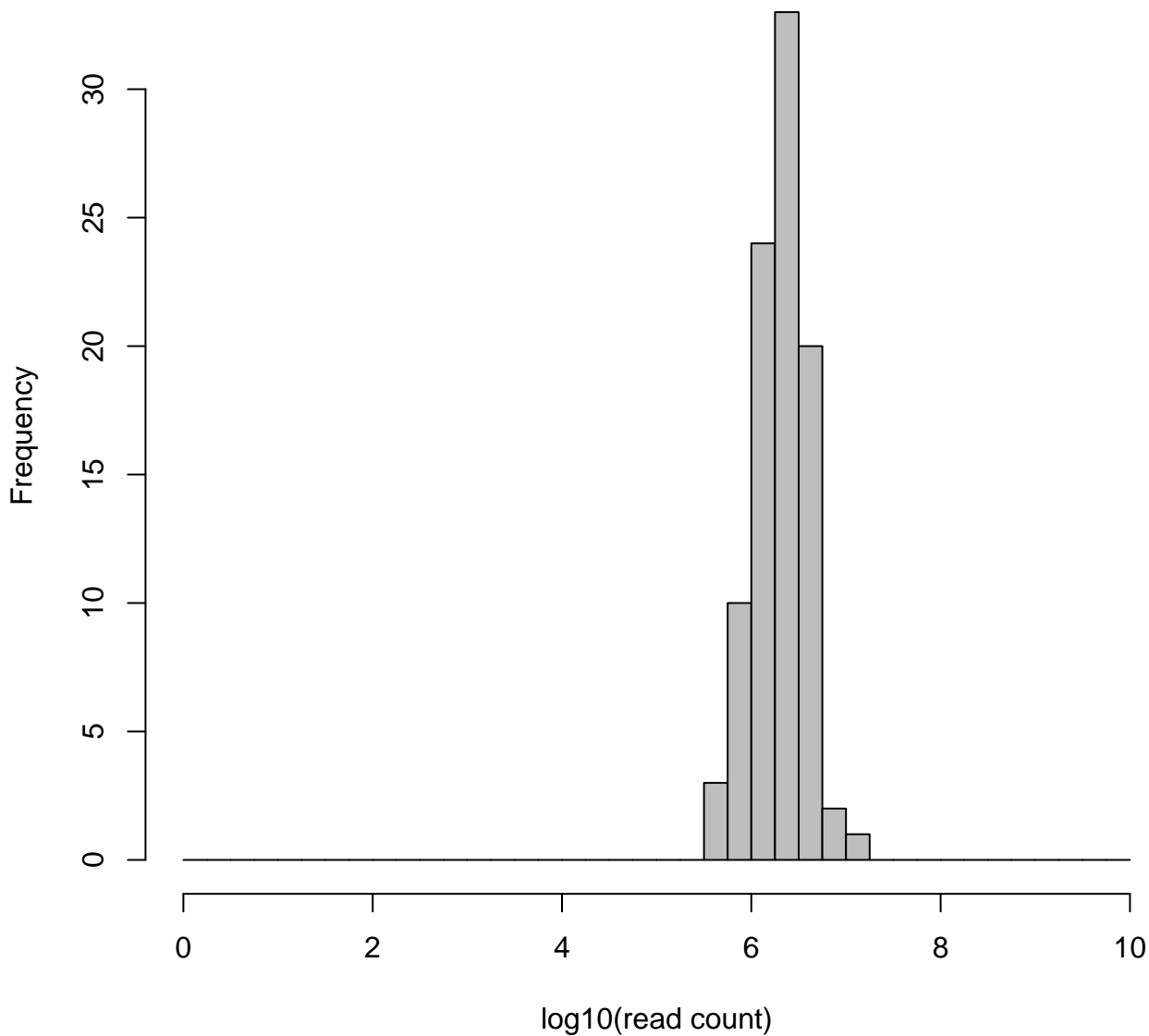
# Read count summary (all) : unique sequence



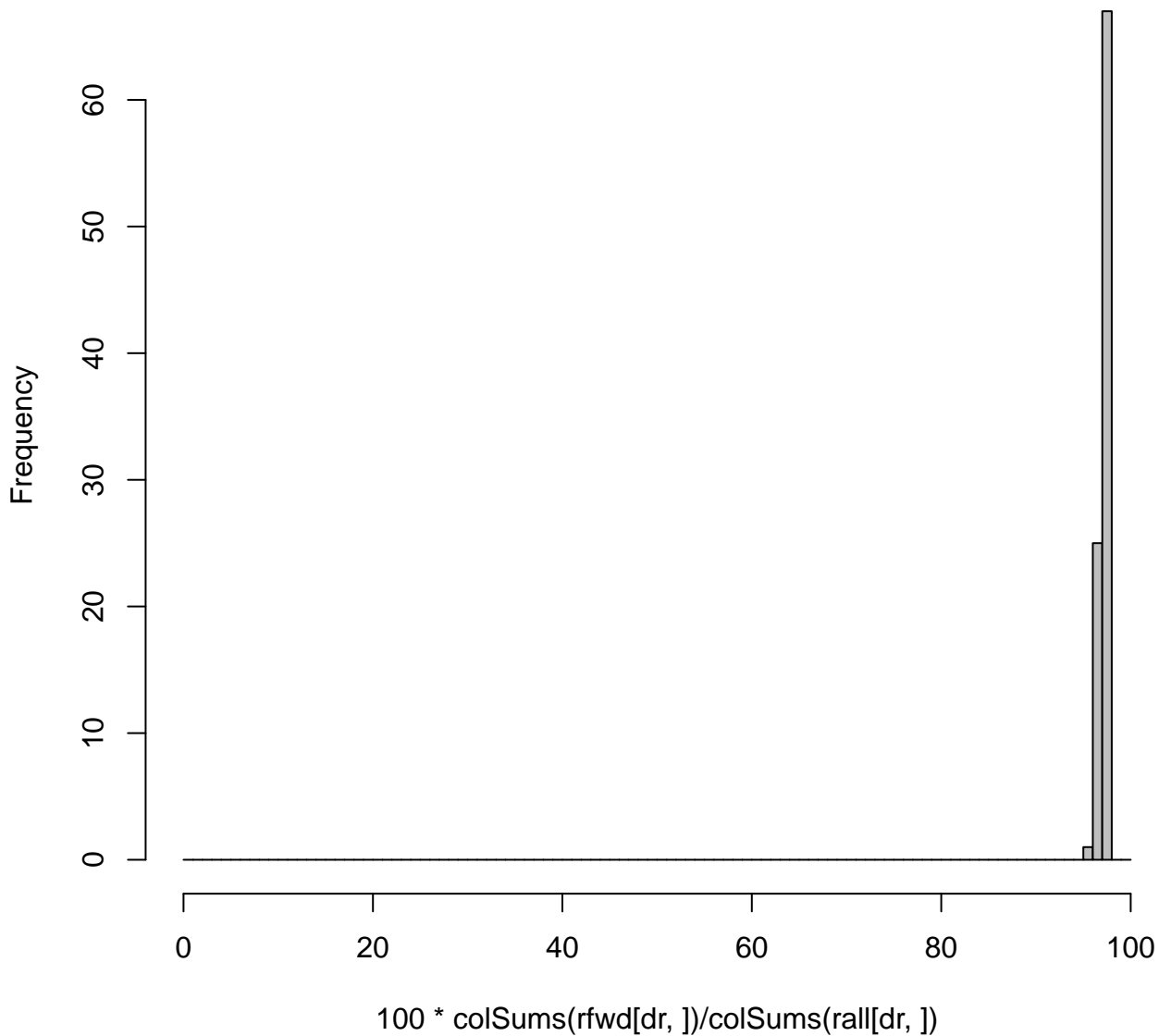
# Read count summary (all) : mapped read

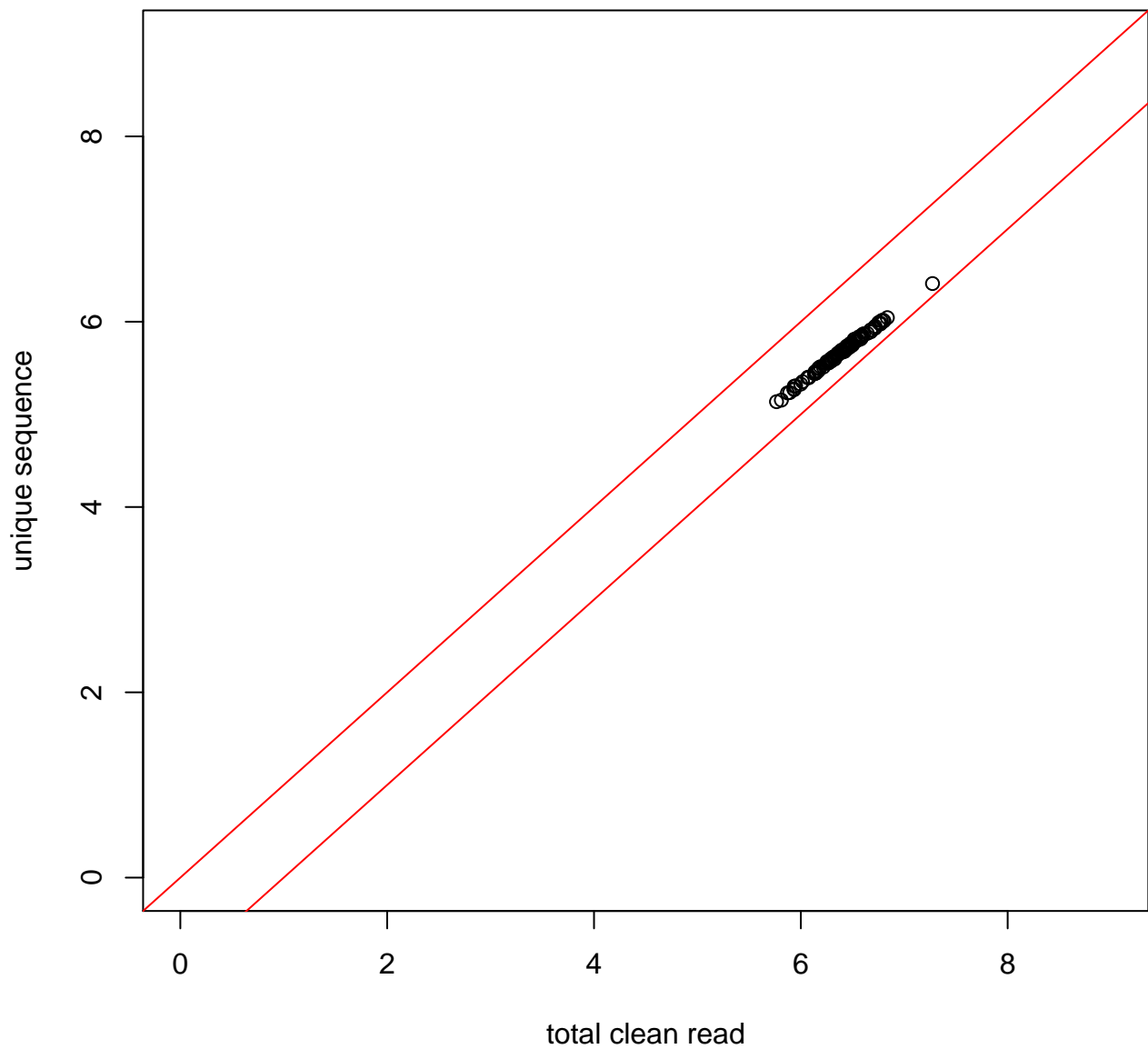


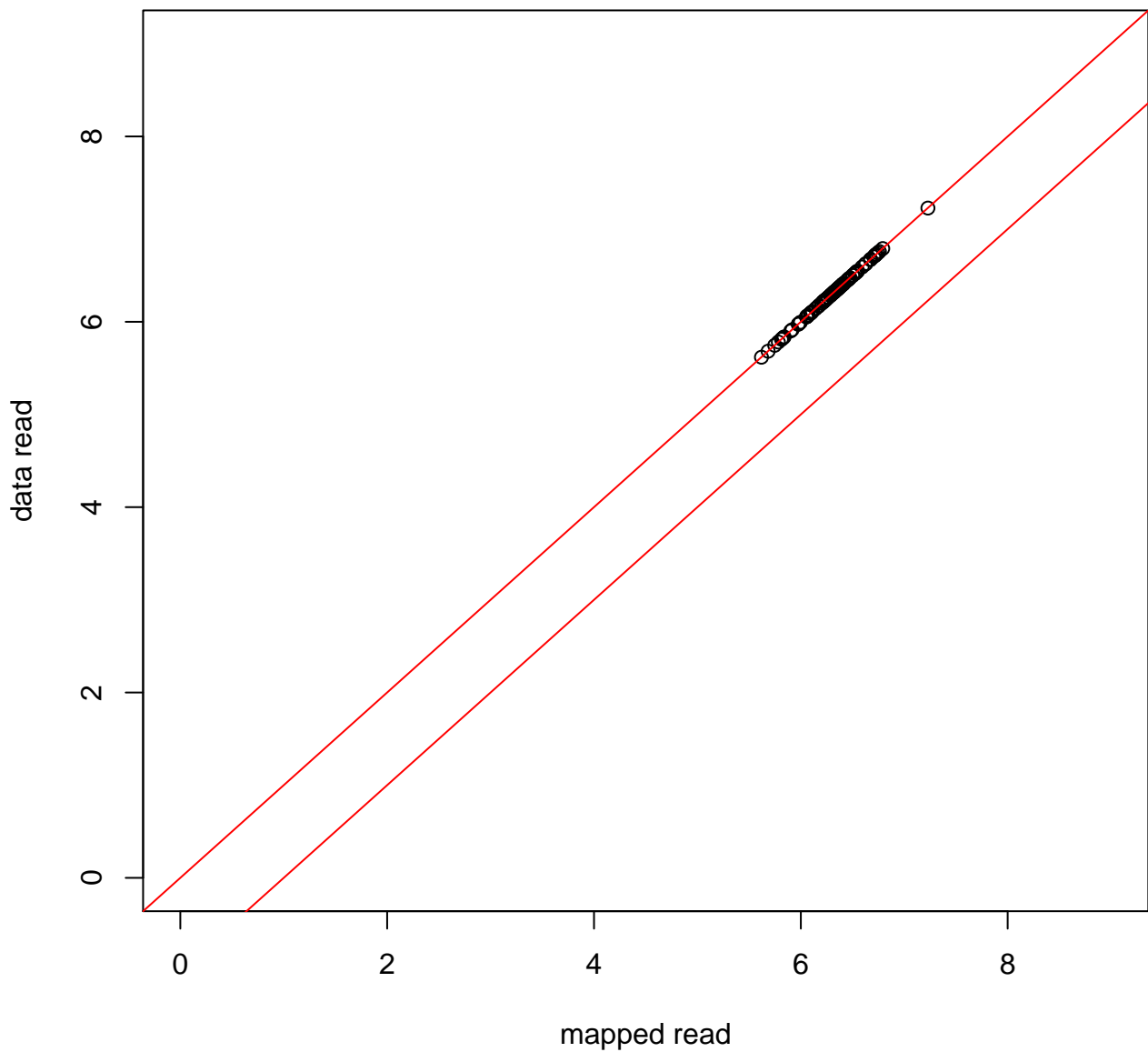
# Read count summary (all) : data read



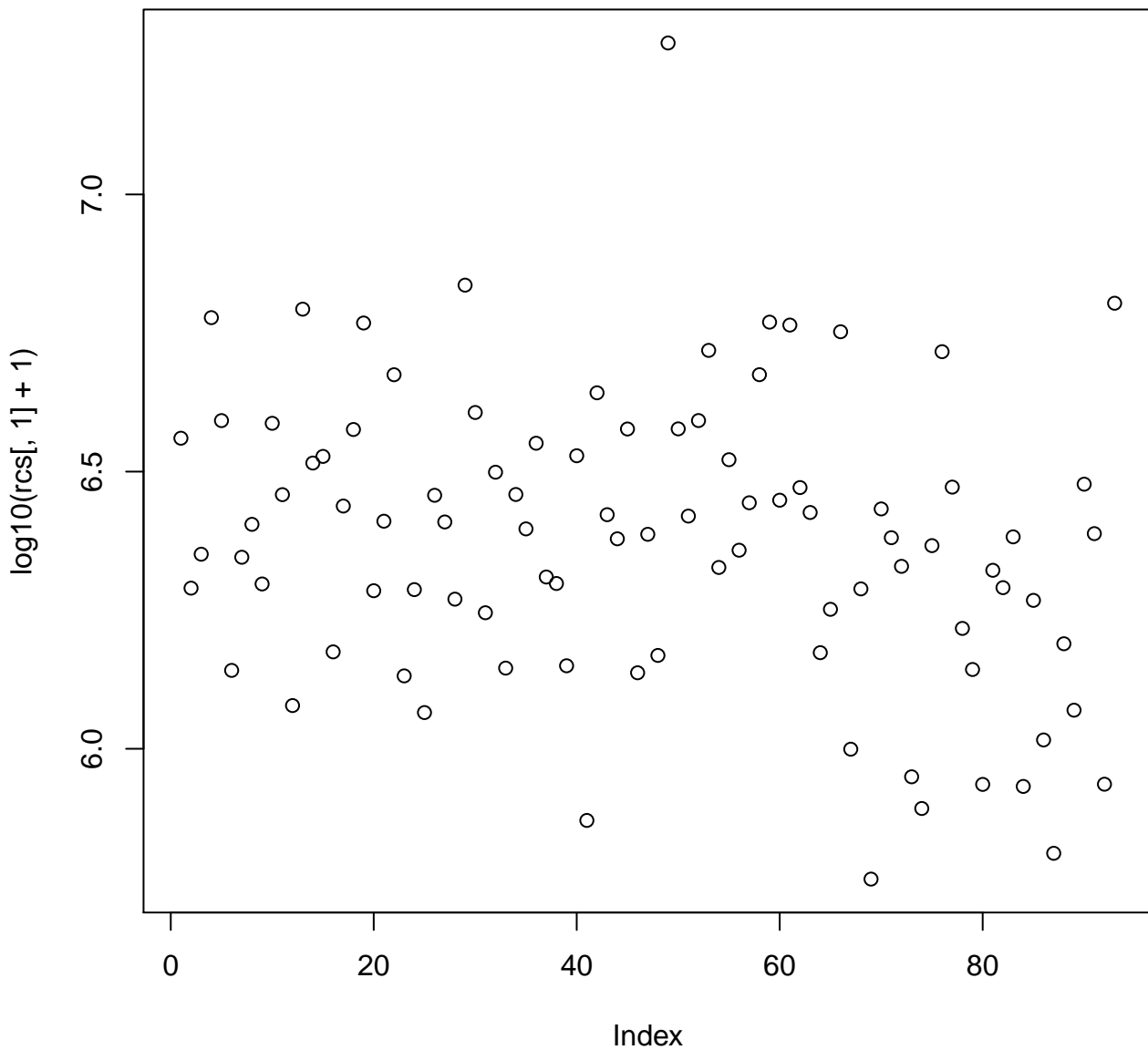
# Read count summary (all) : strand specificity



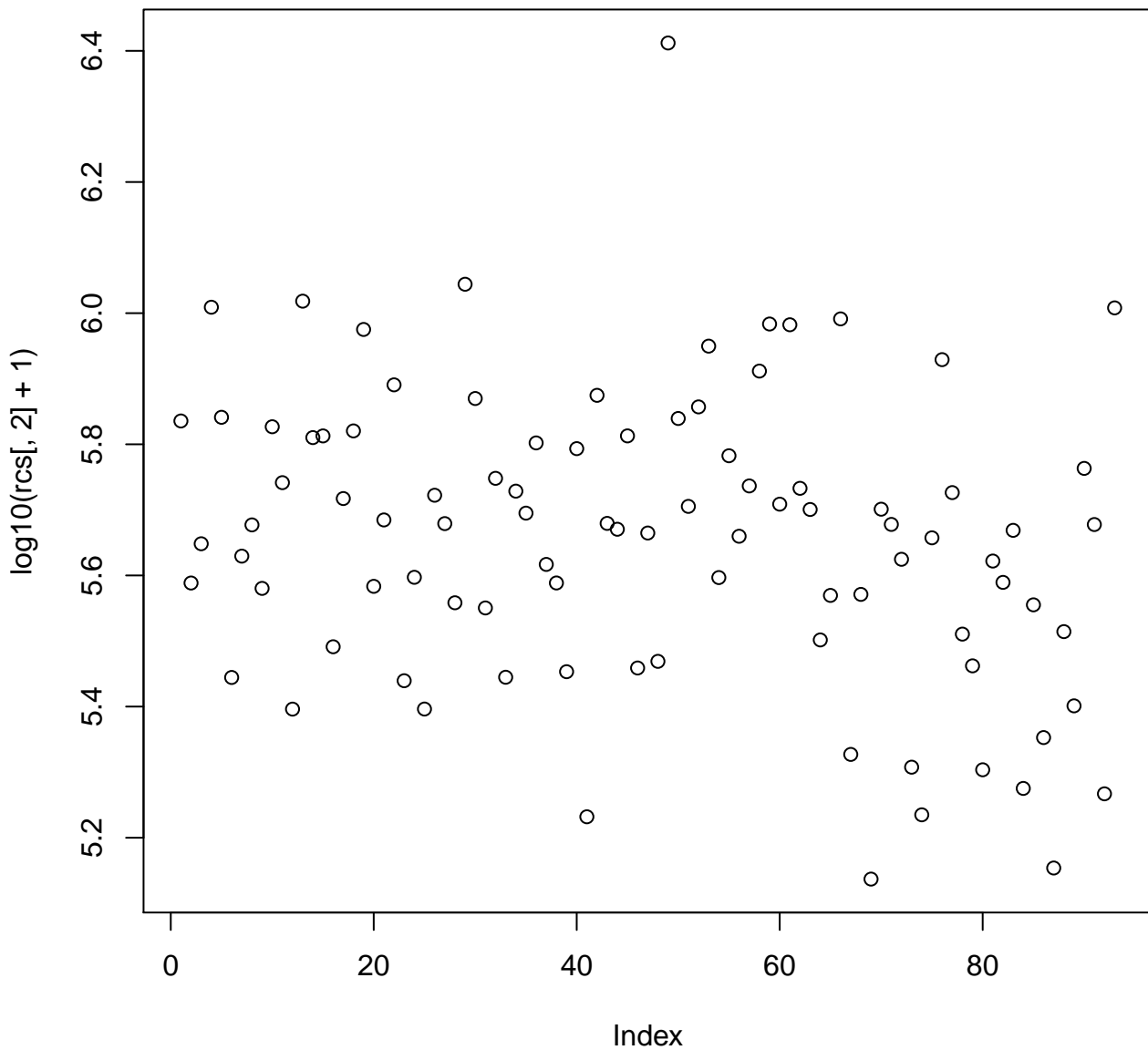




# total clean read

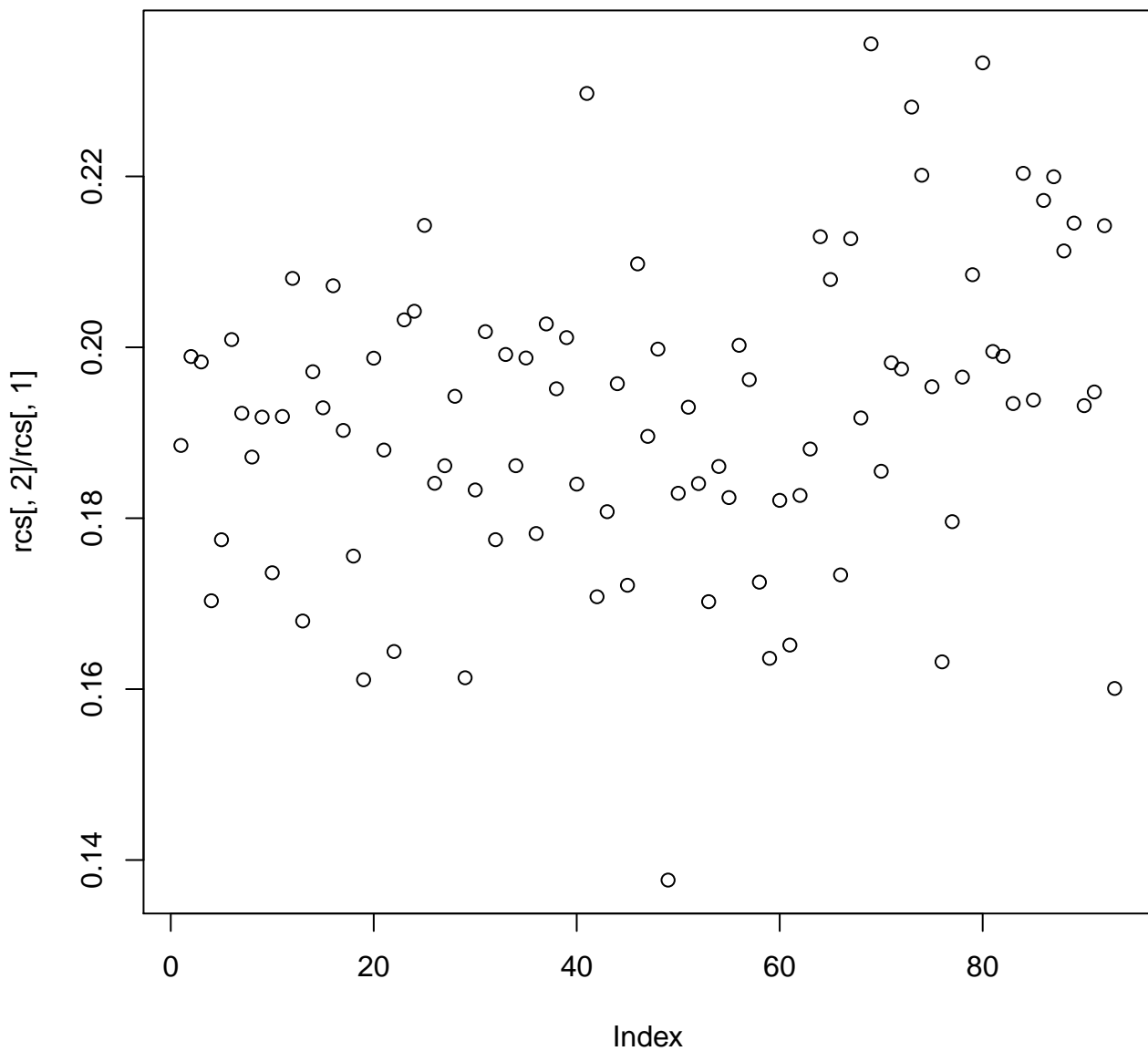


# unique sequence

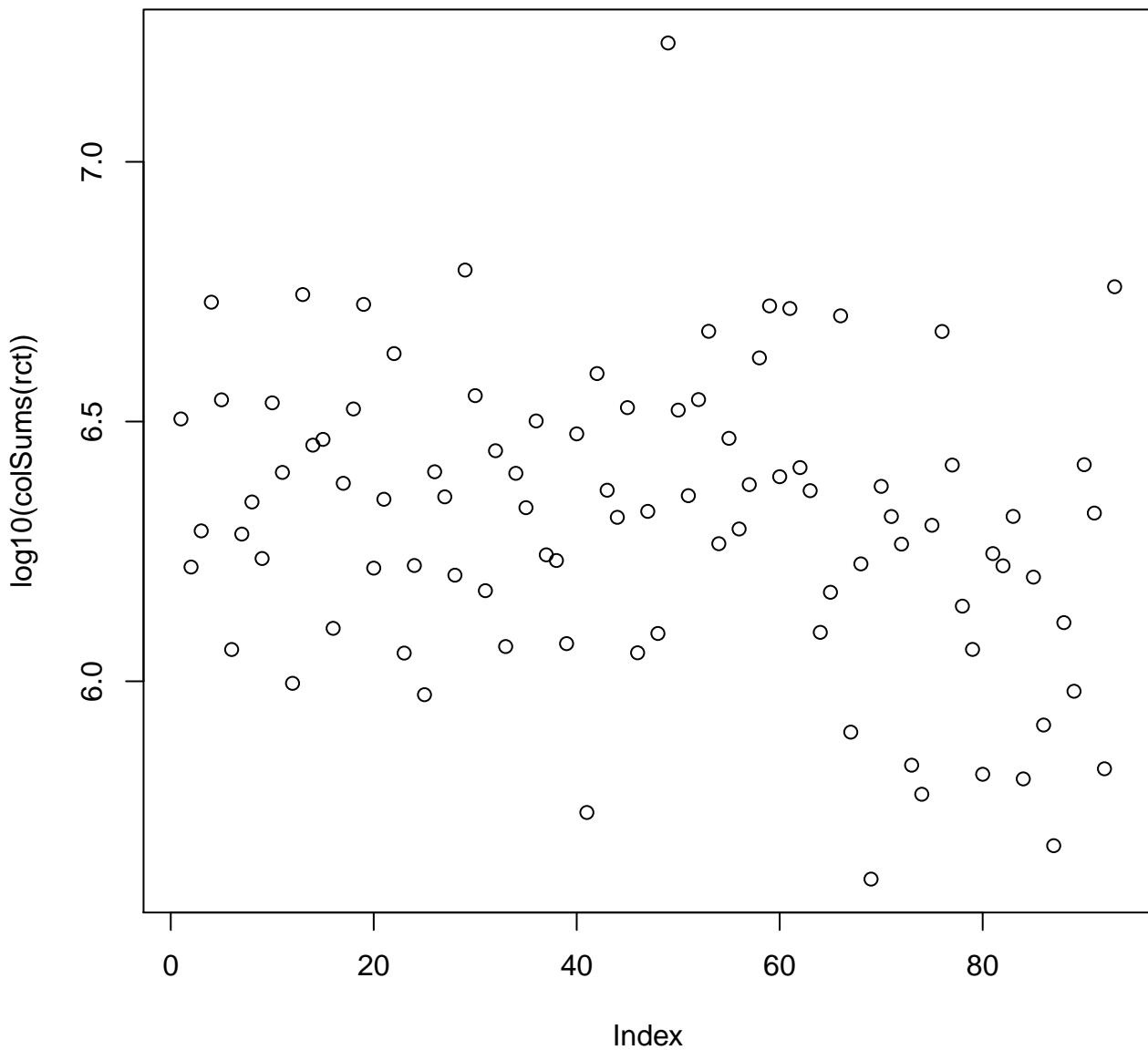




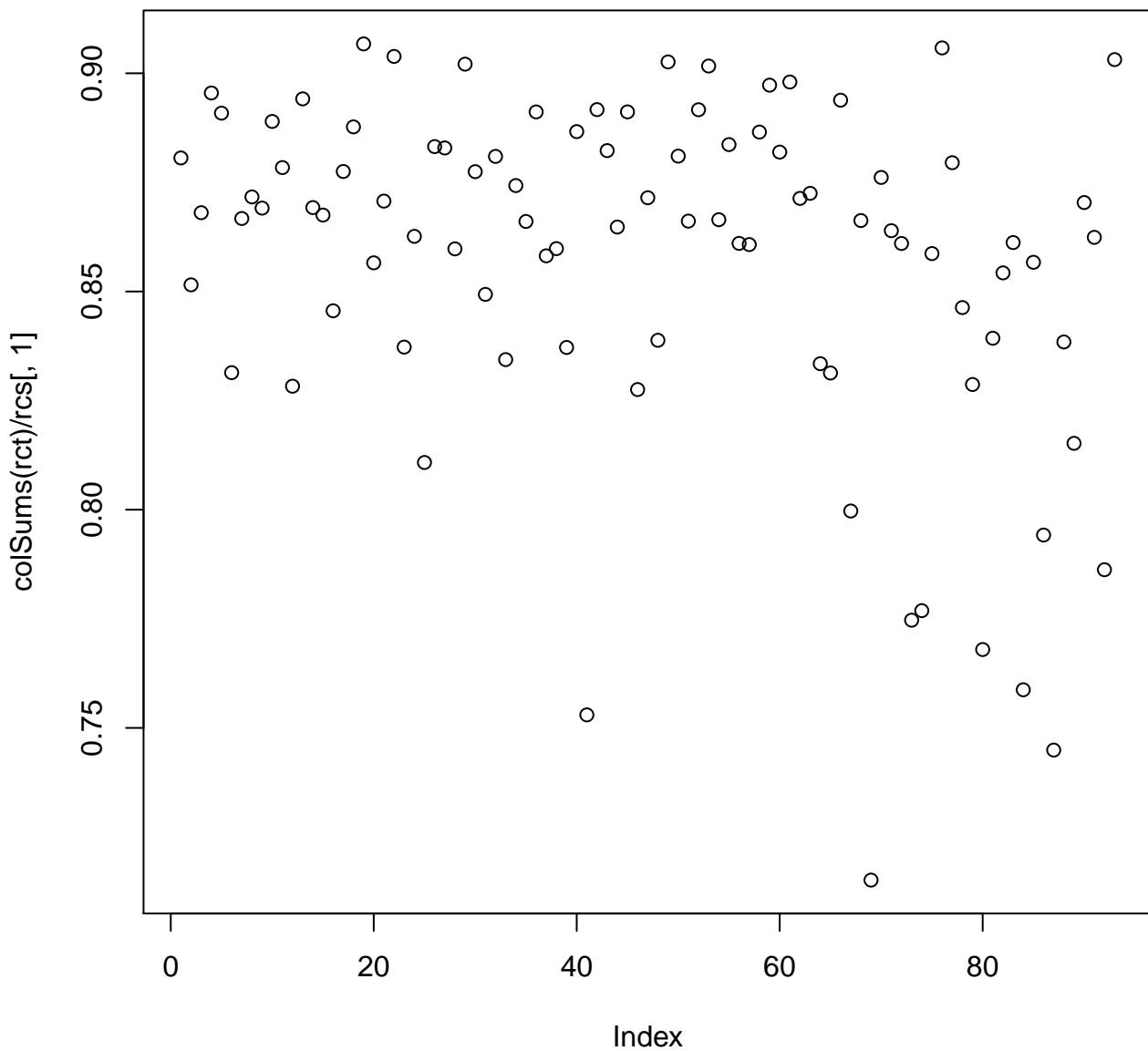
**unique sequence / total clean read**



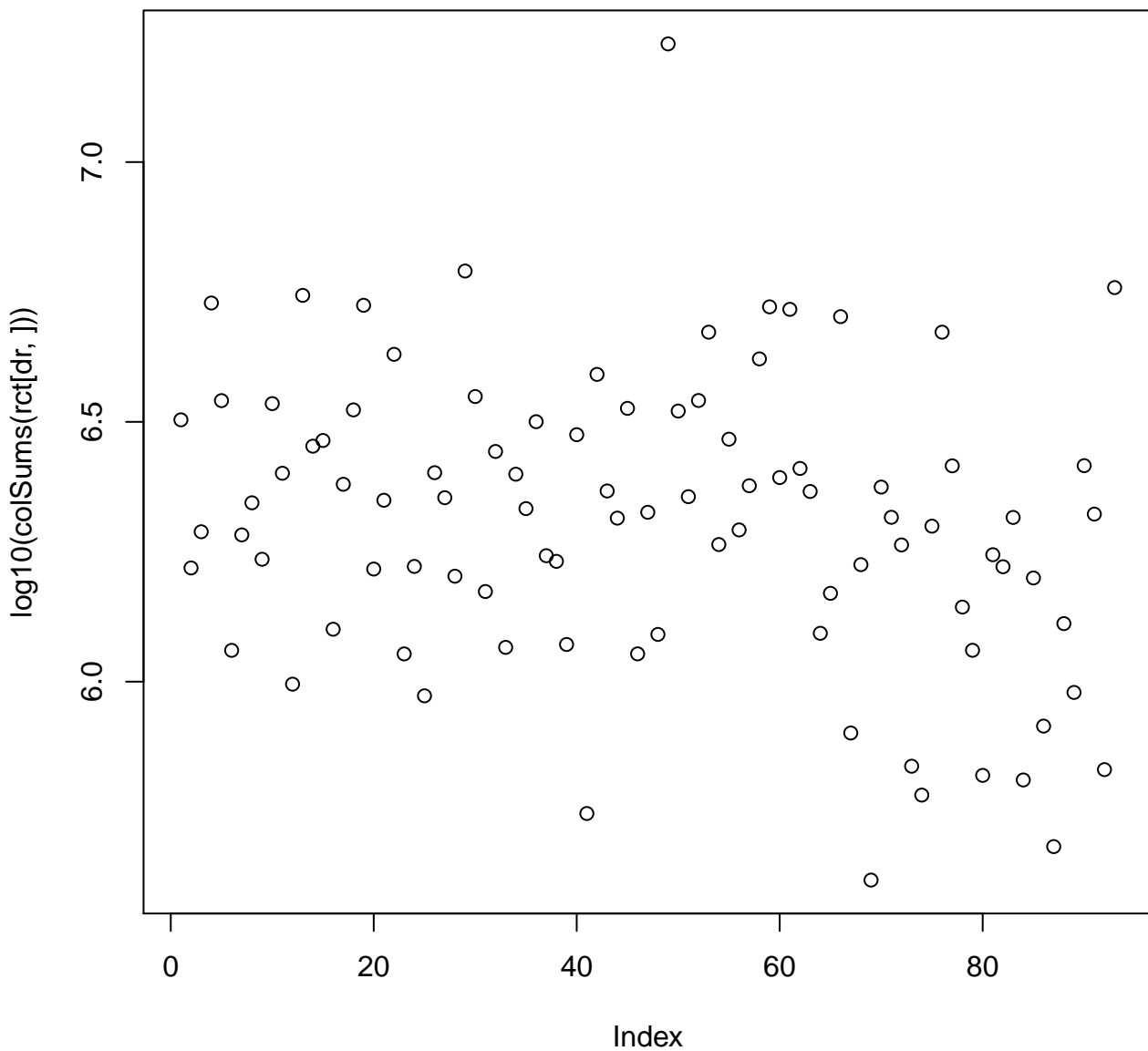
# mapped read



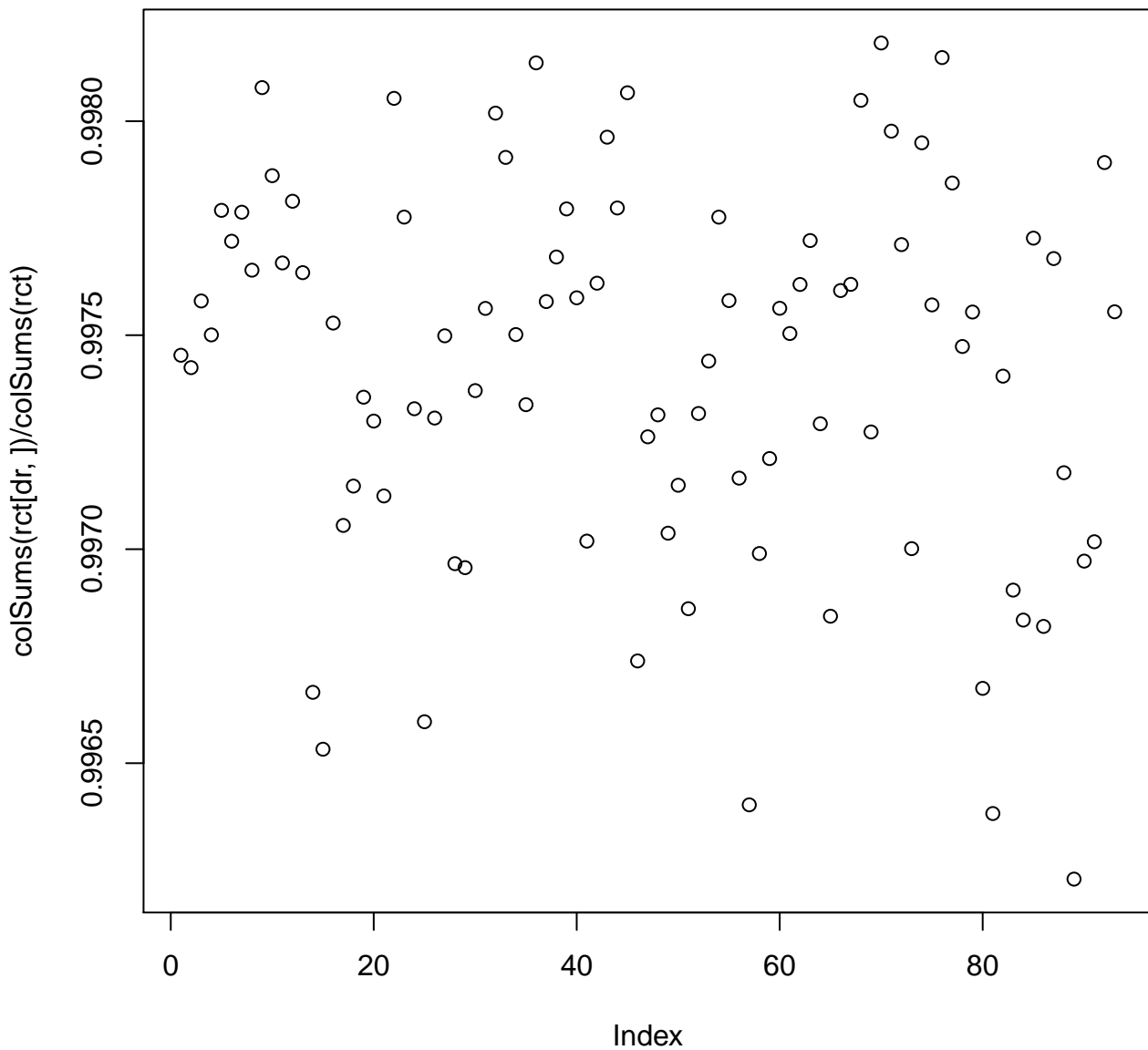
mapped read / total clean read



# data read



**data read / mapped read**



# strand specificity

