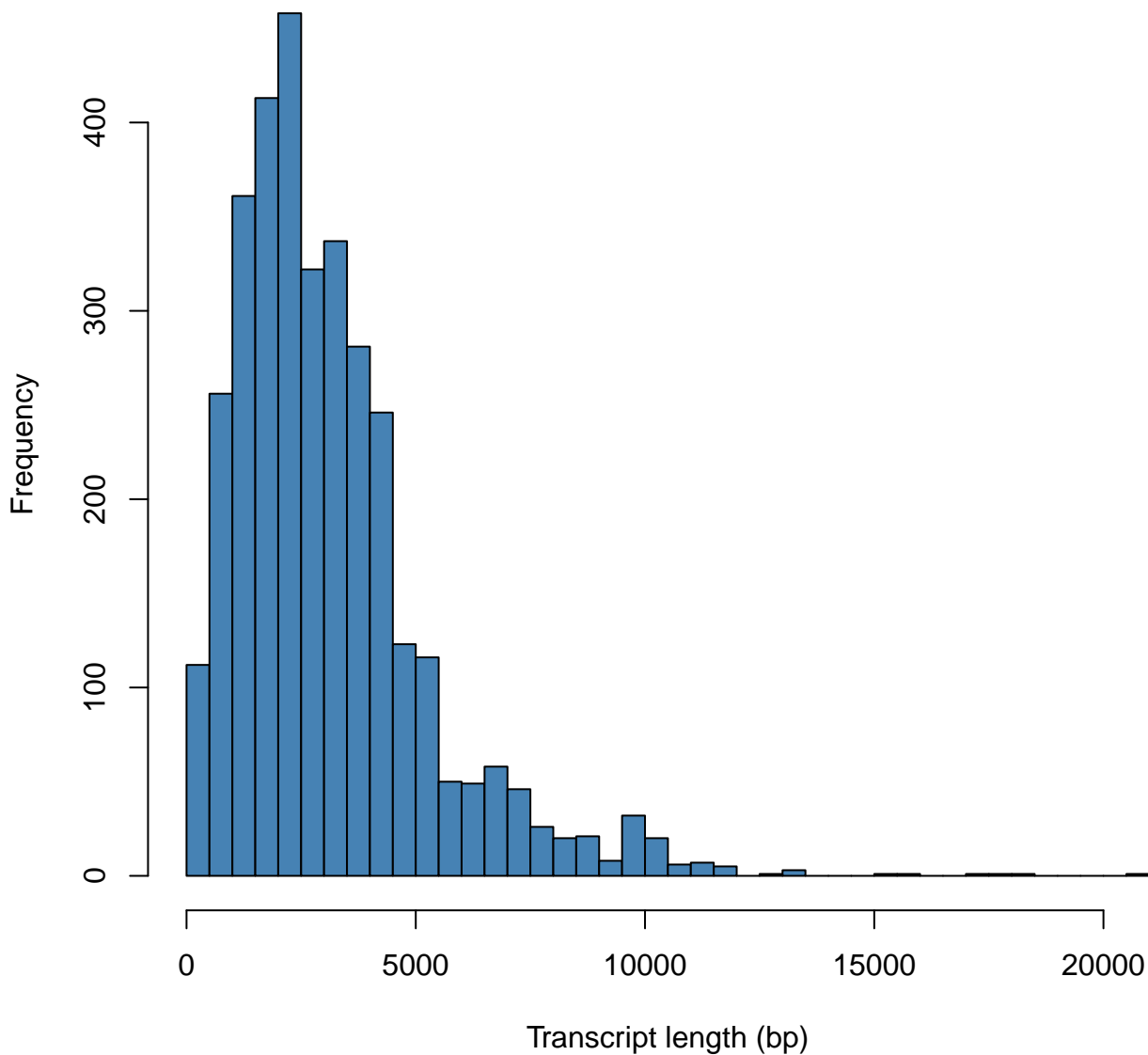
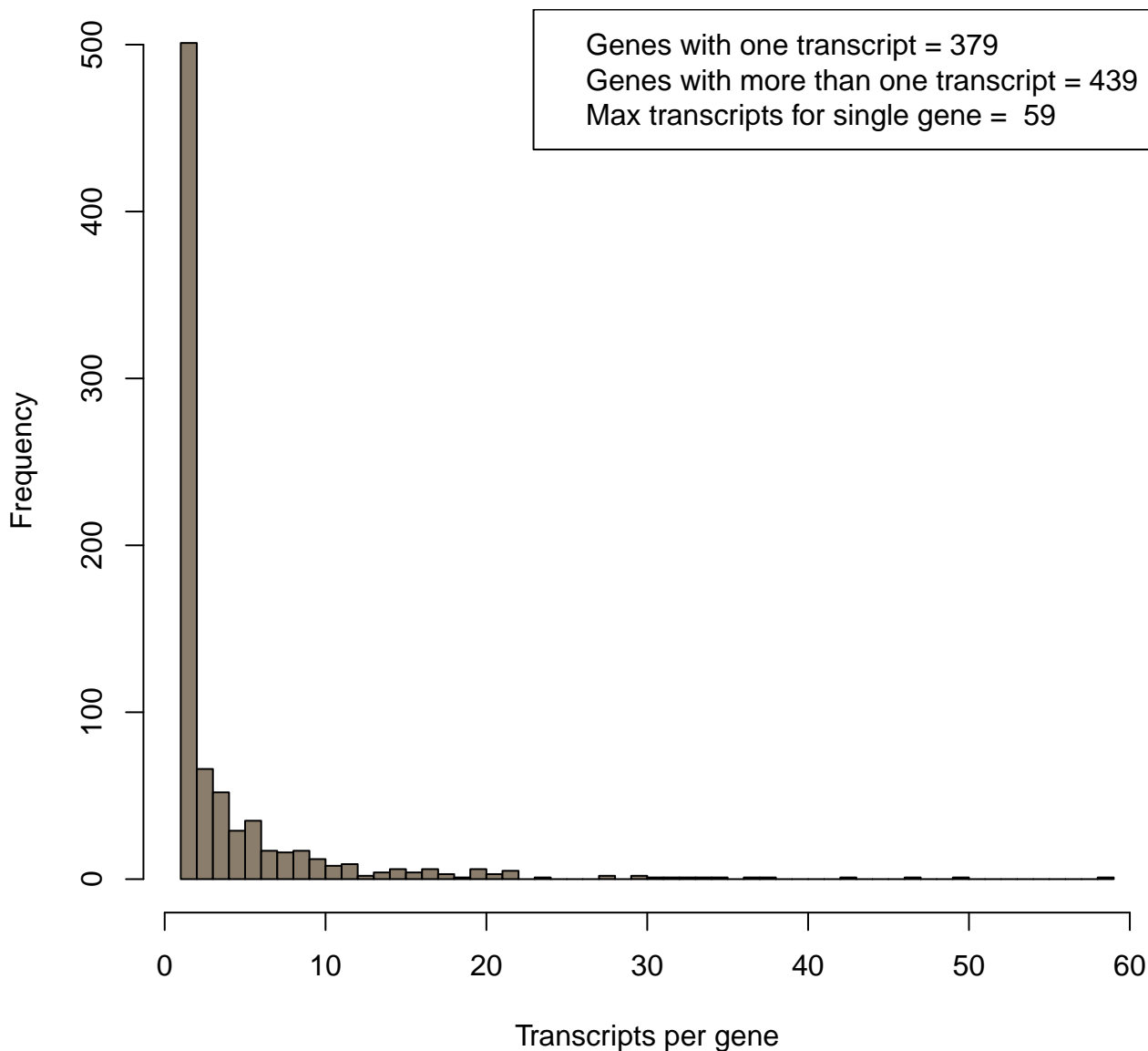


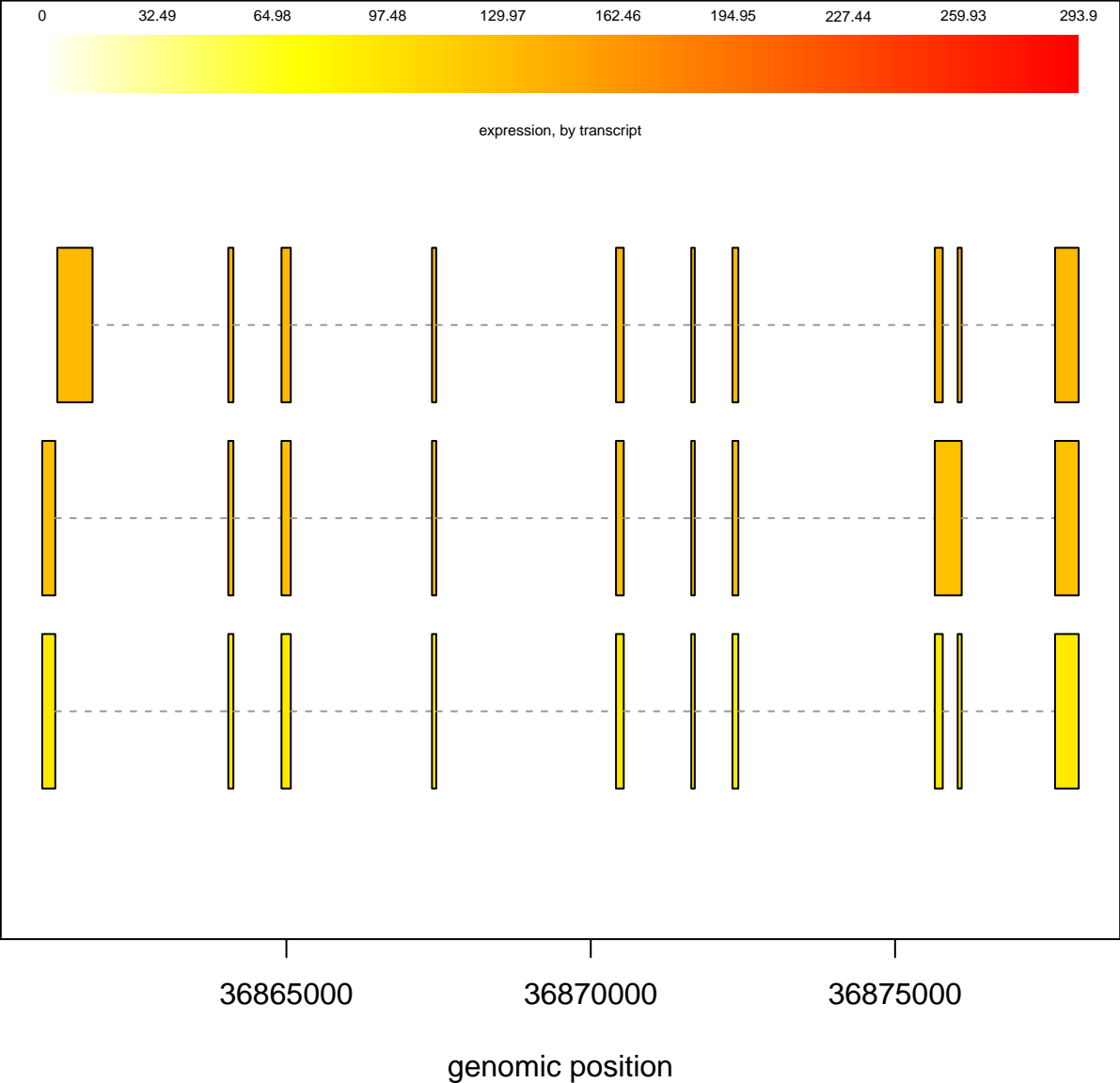
**Distribution of transcript lengths**



## Distribution of transcript count per gene

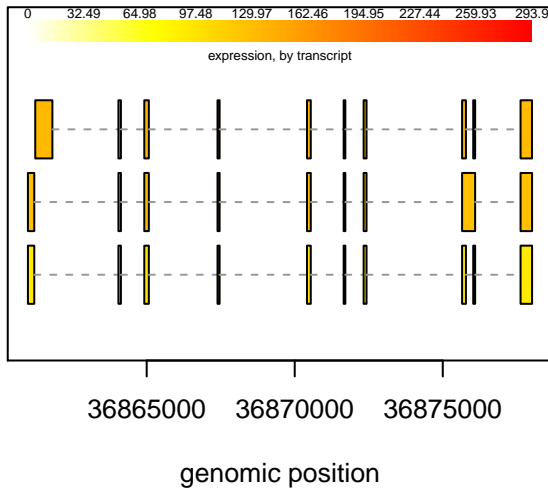


transcripts from gene NCF4: hcc1395\_normal\_rep1, FPKM

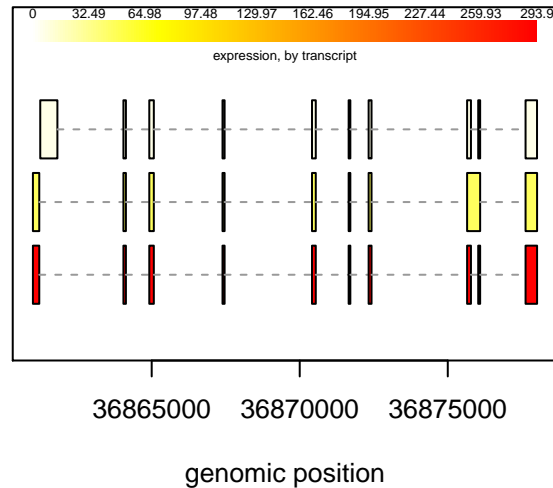


# NCF4

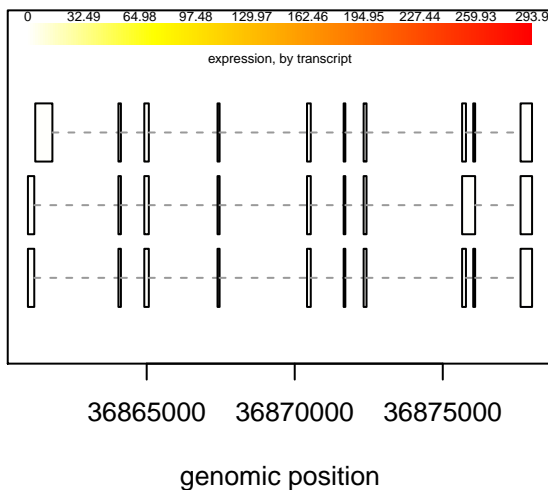
## hcc1395\_normal\_rep1



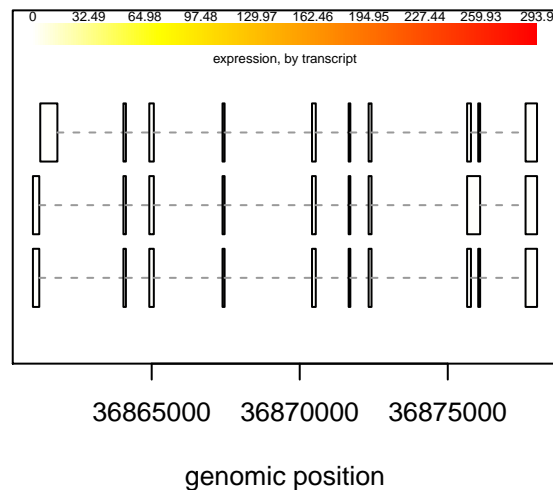
## hcc1395\_normal\_rep2



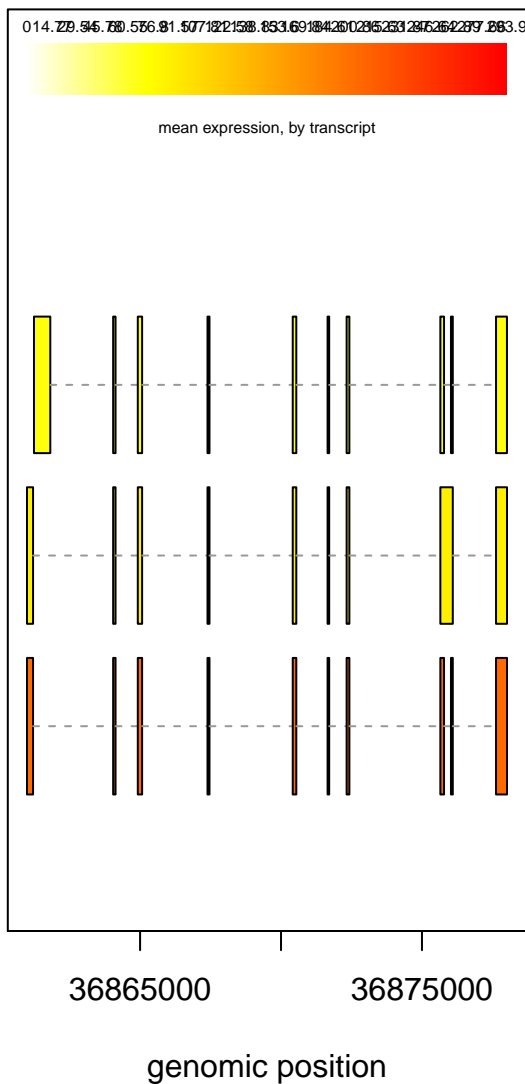
## hcc1395\_tumor\_rep1



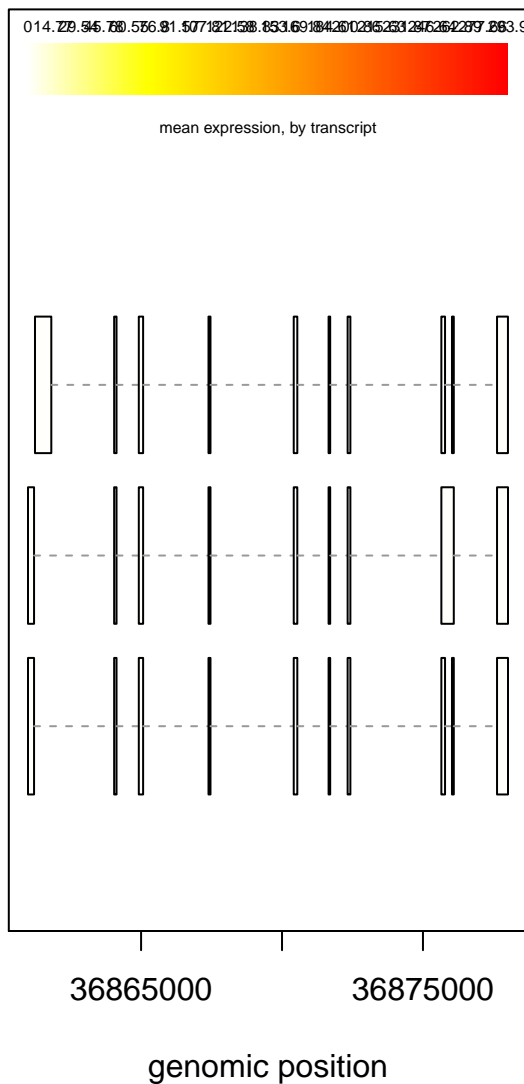
## hcc1395\_tumor\_rep2



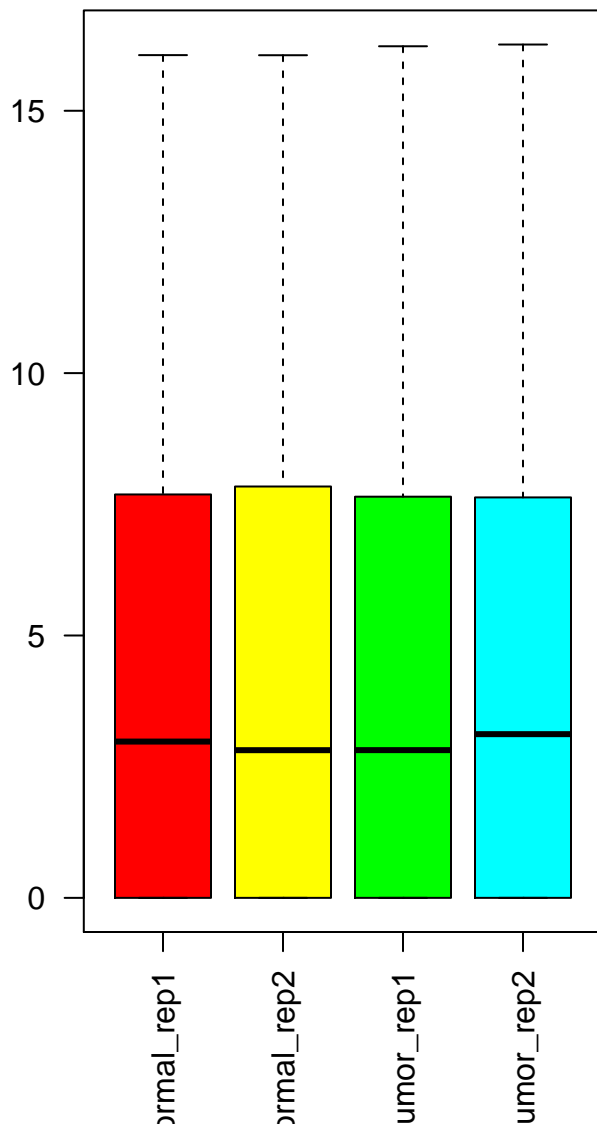
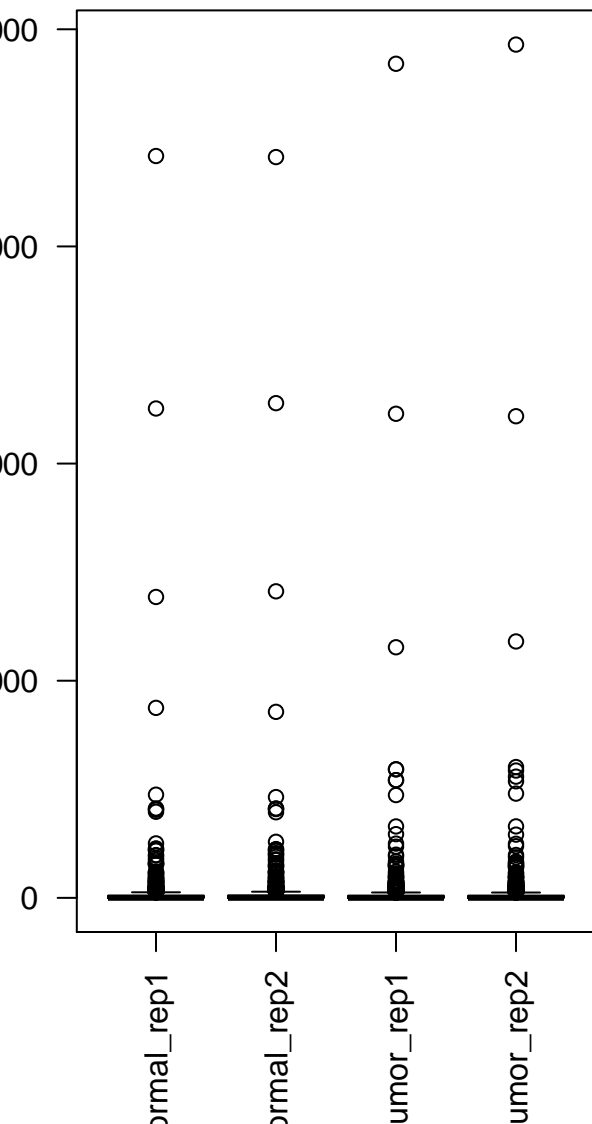
## NCF4: normal



## NCF4: tumor

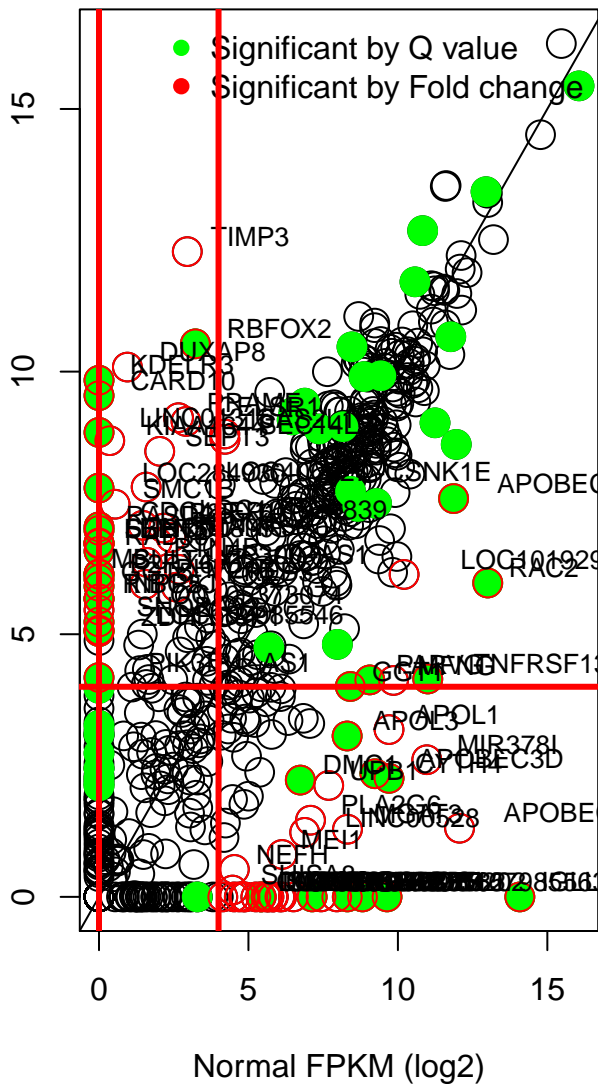


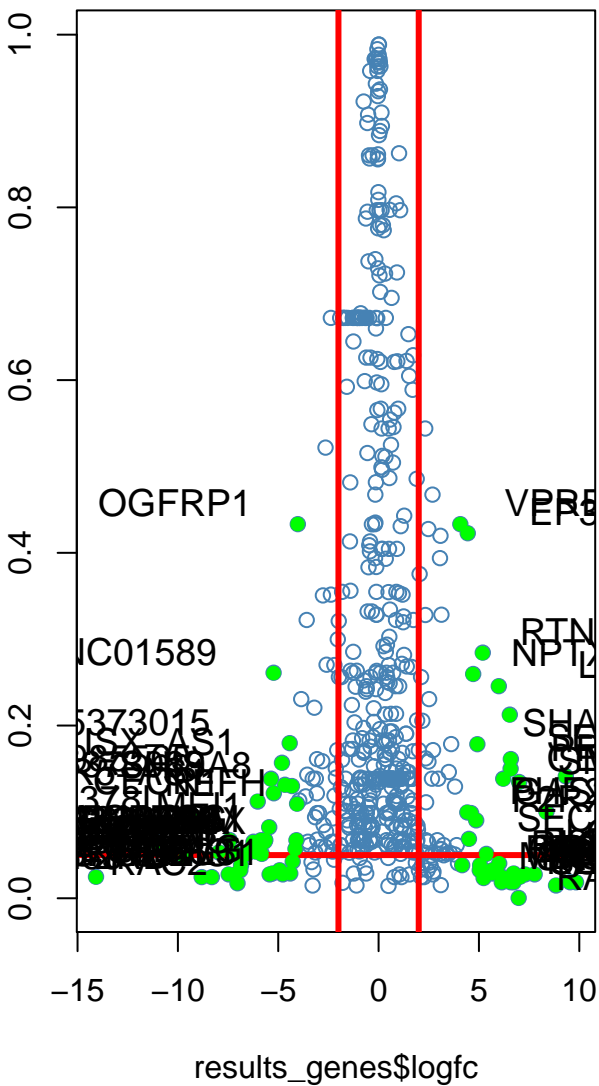
**Distribution of FPKMs for all 6 samples****formed distribution of FPKMs for all 6**



--- Fold change  $>2$  and  $<-2$

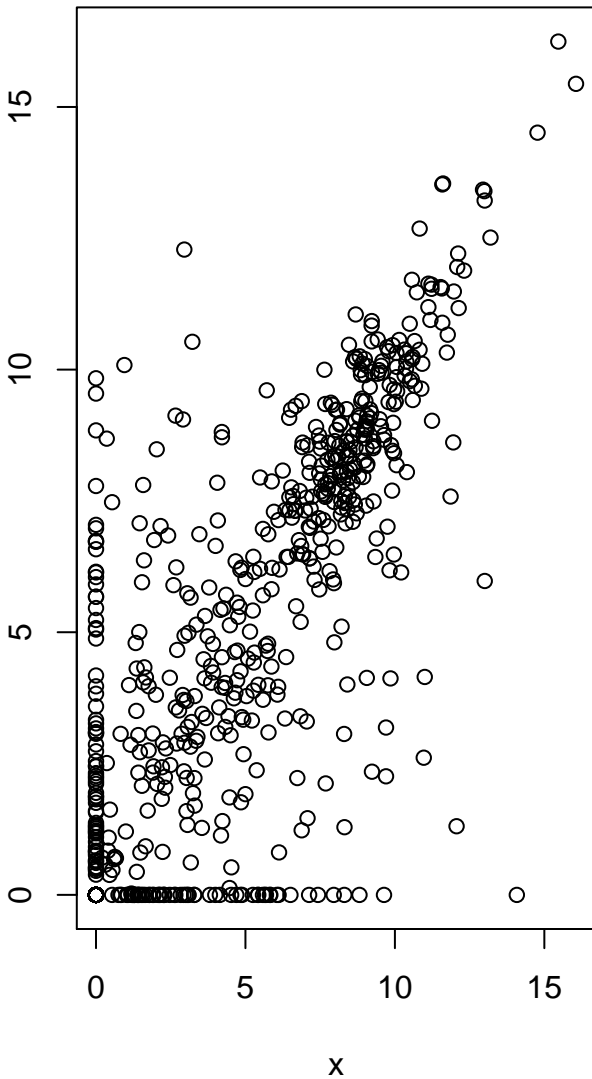
log<sub>2</sub>(Fold change) Tumor vs Normal



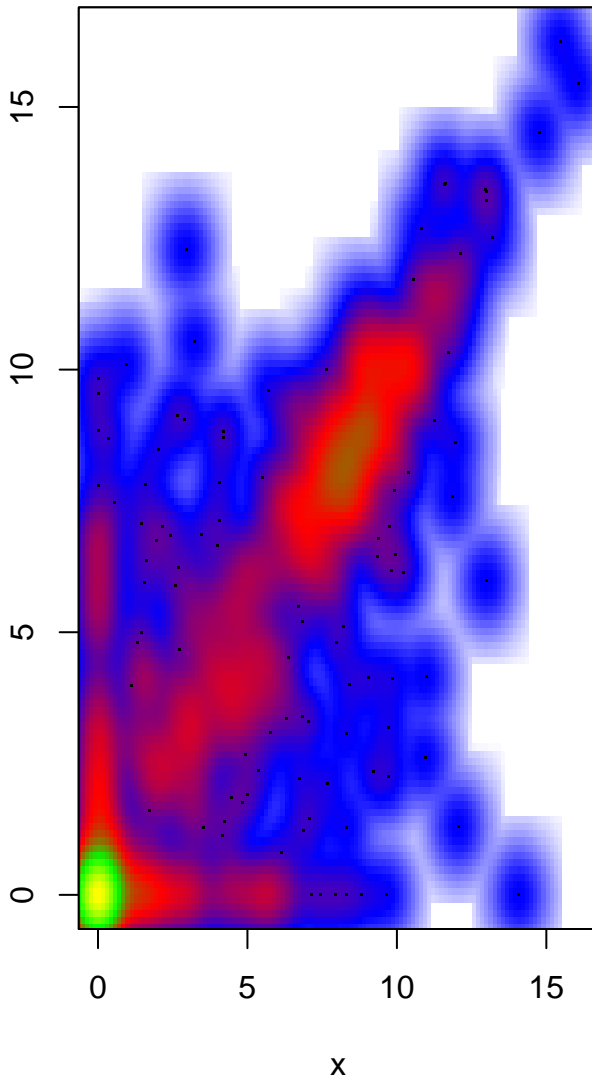




**Scatter plot of DEGs**



**Density plot of DEGs**



## Significant genes

