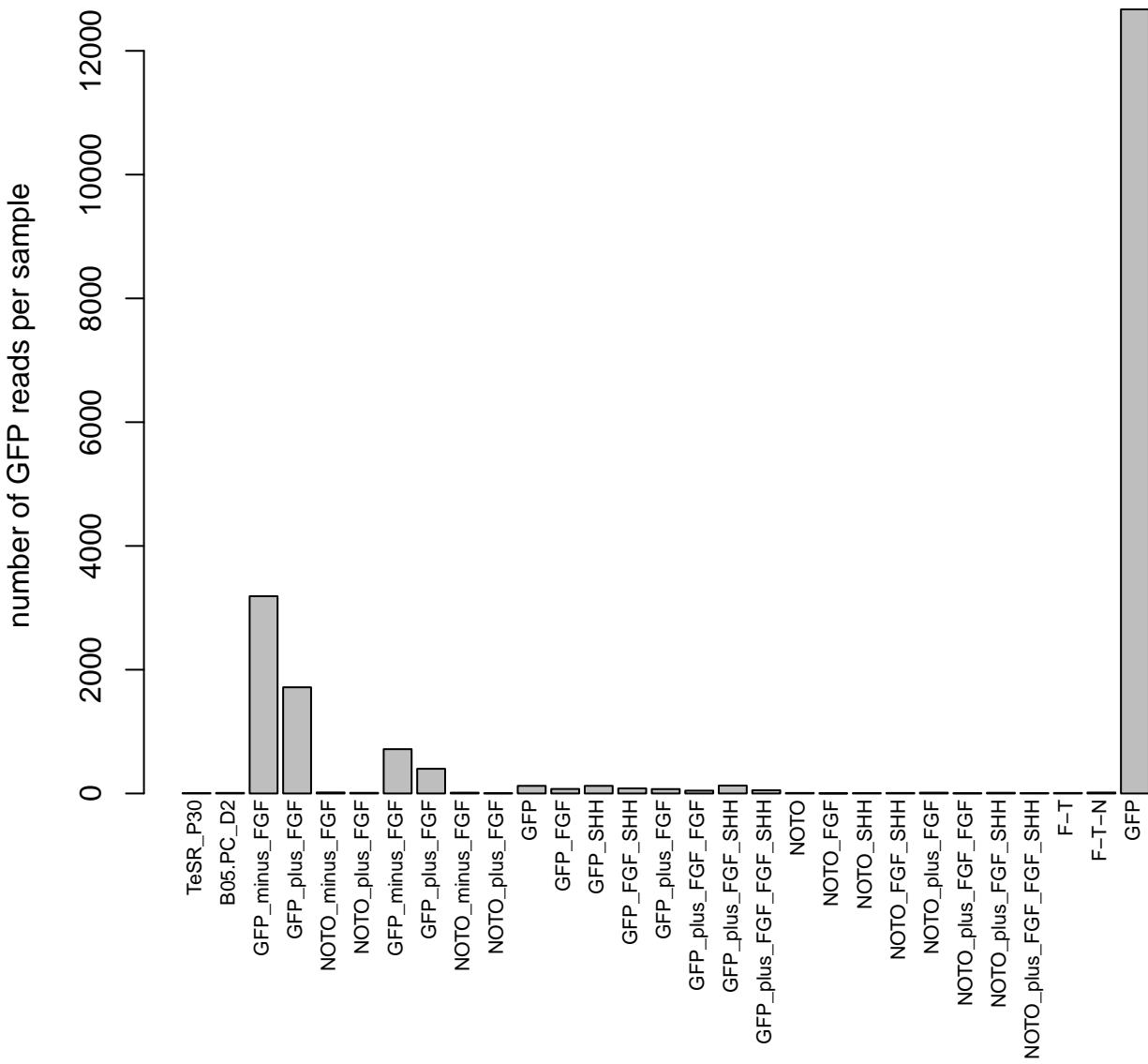
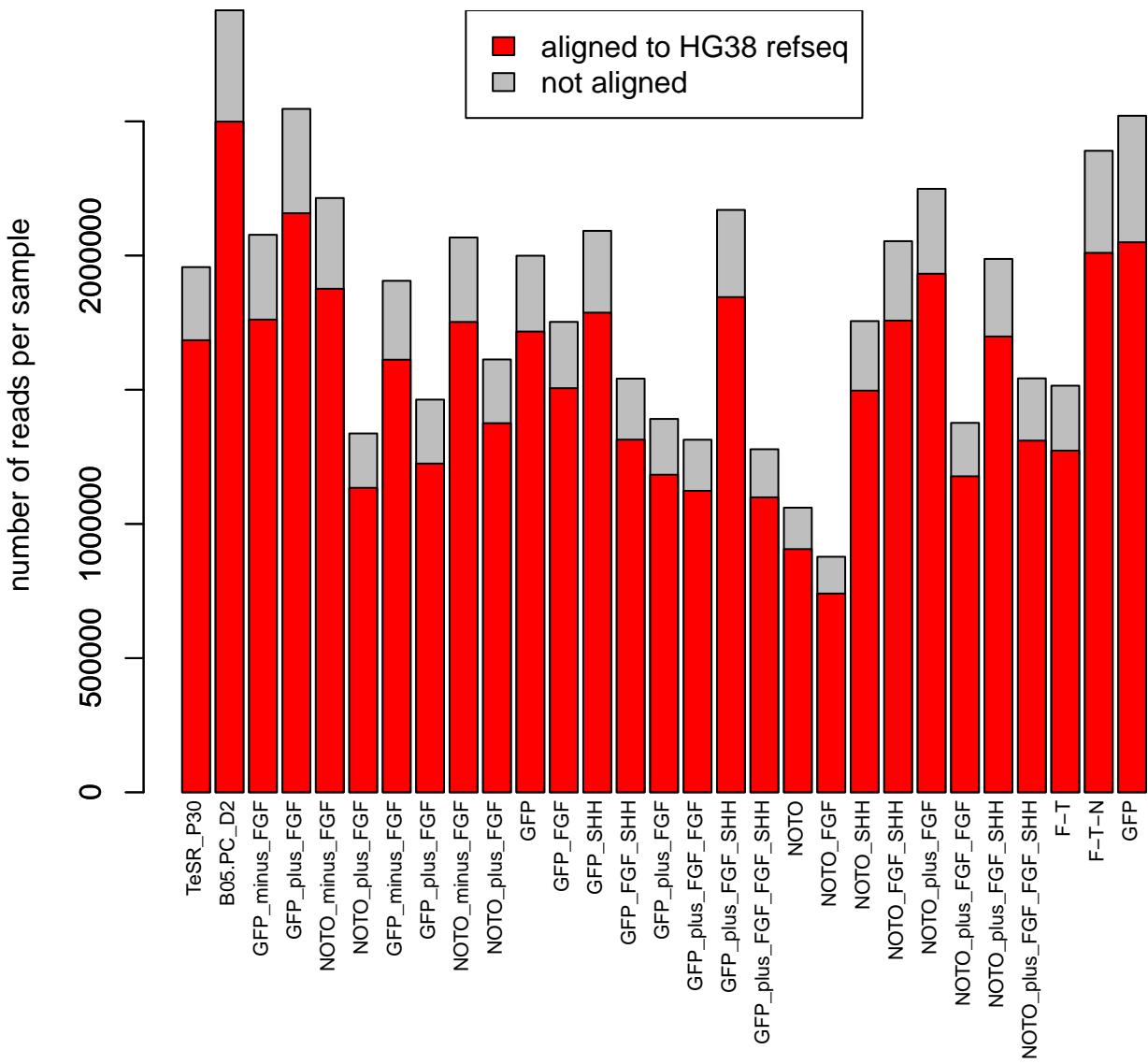


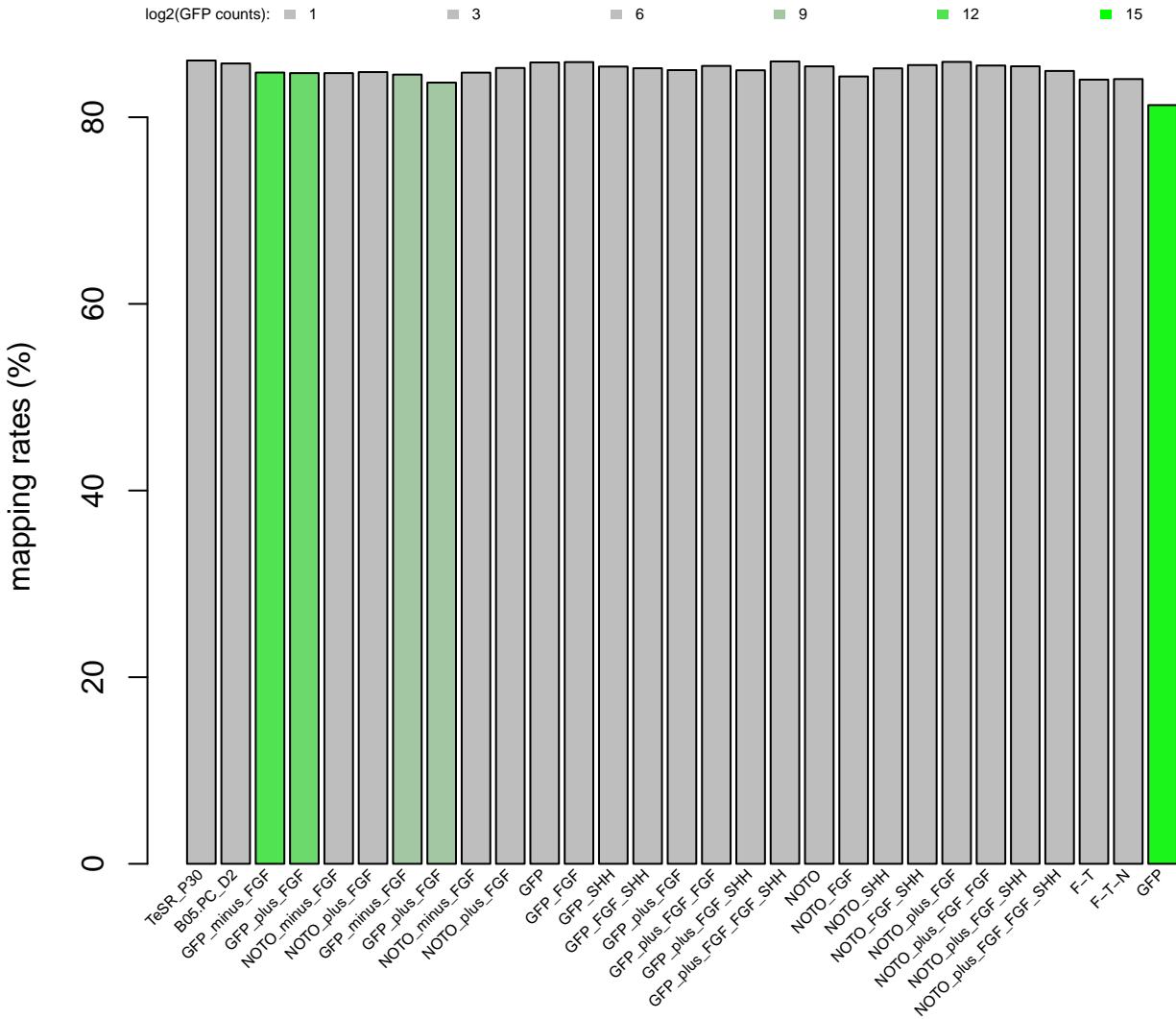
## number of reads aligned to EGFP sequence sample



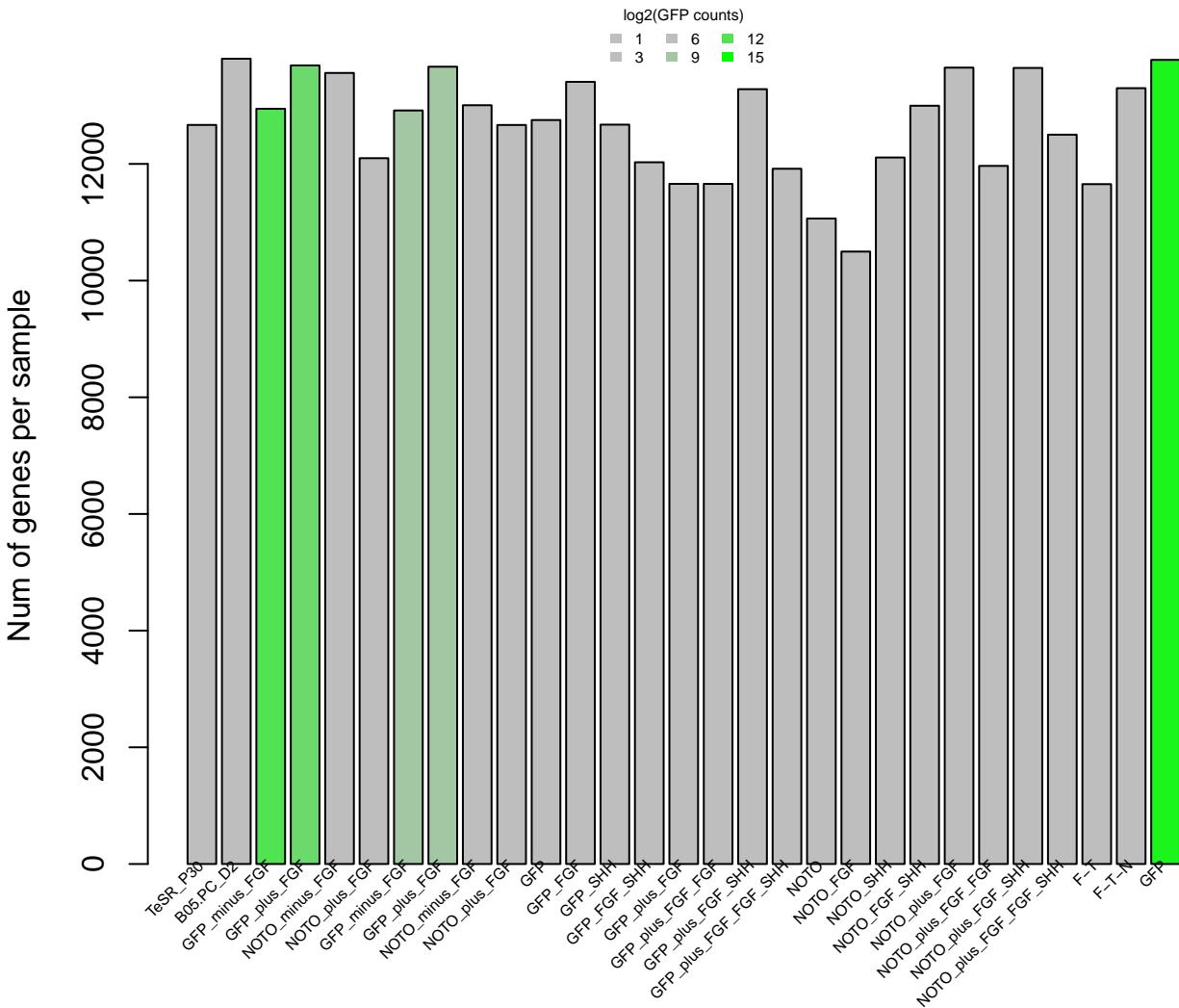
number of raw reads per sample,  
before or after alignmented to human refseq



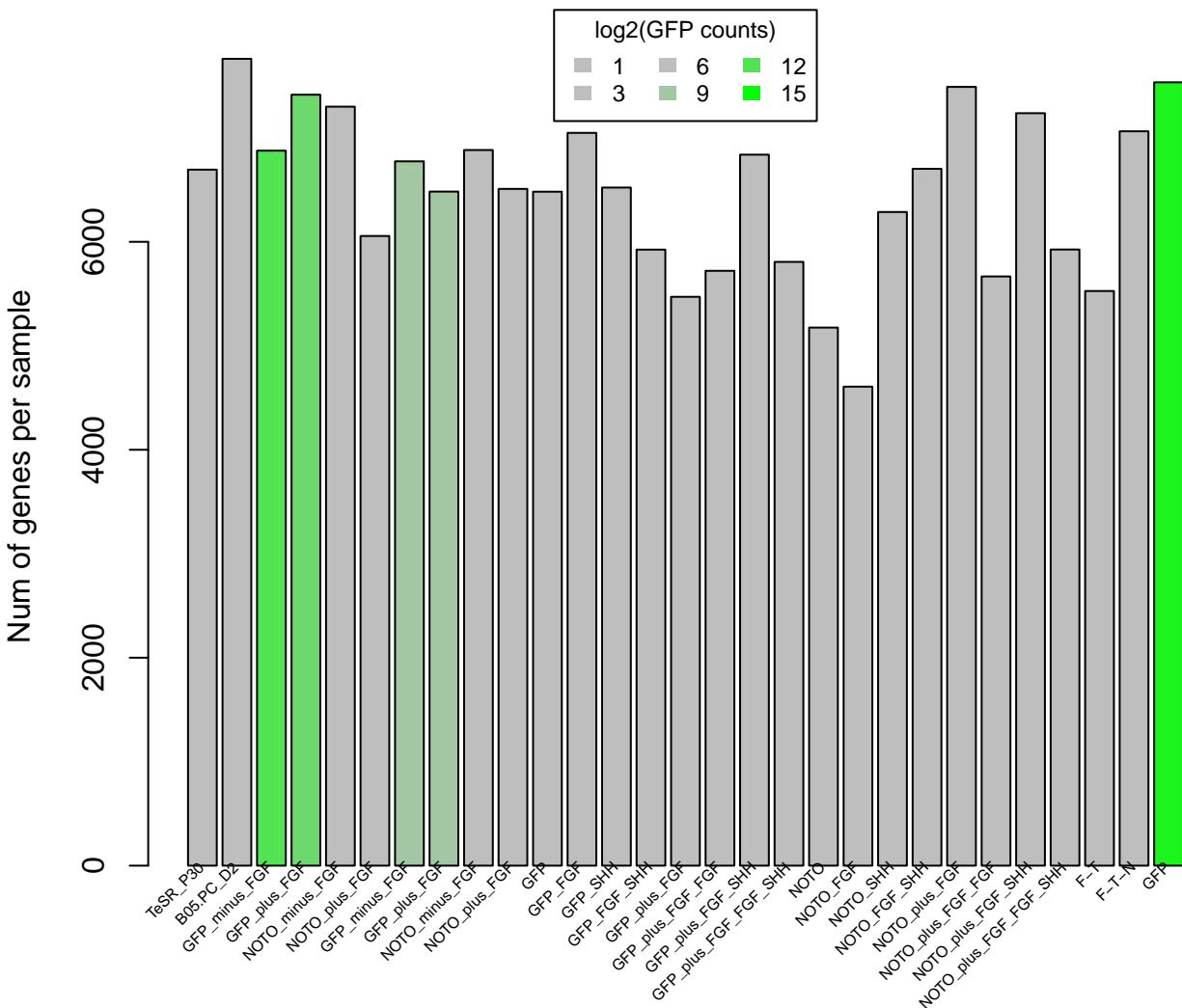
## overall mapping rate

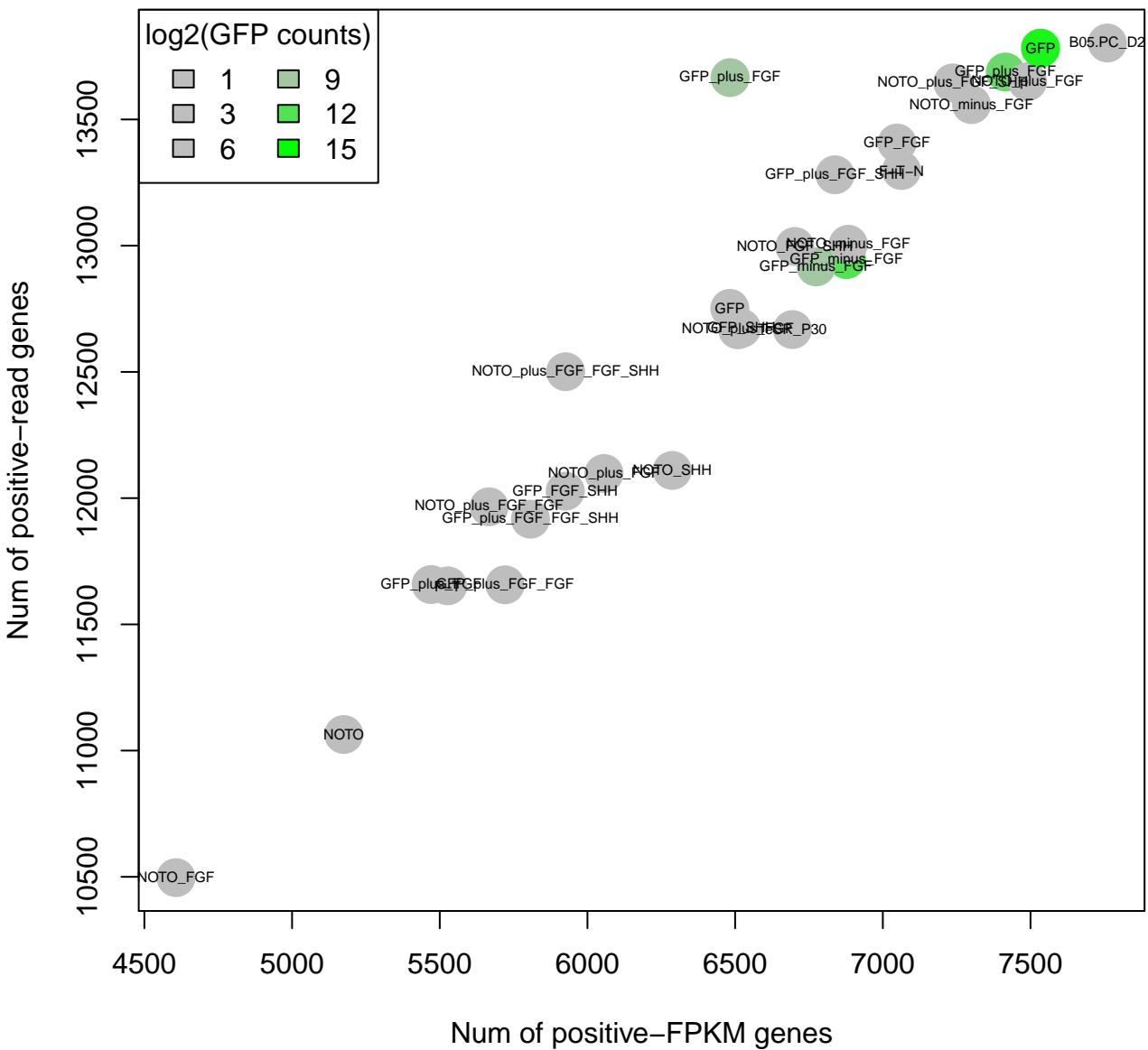


## Numbers of genes detected with at least one read

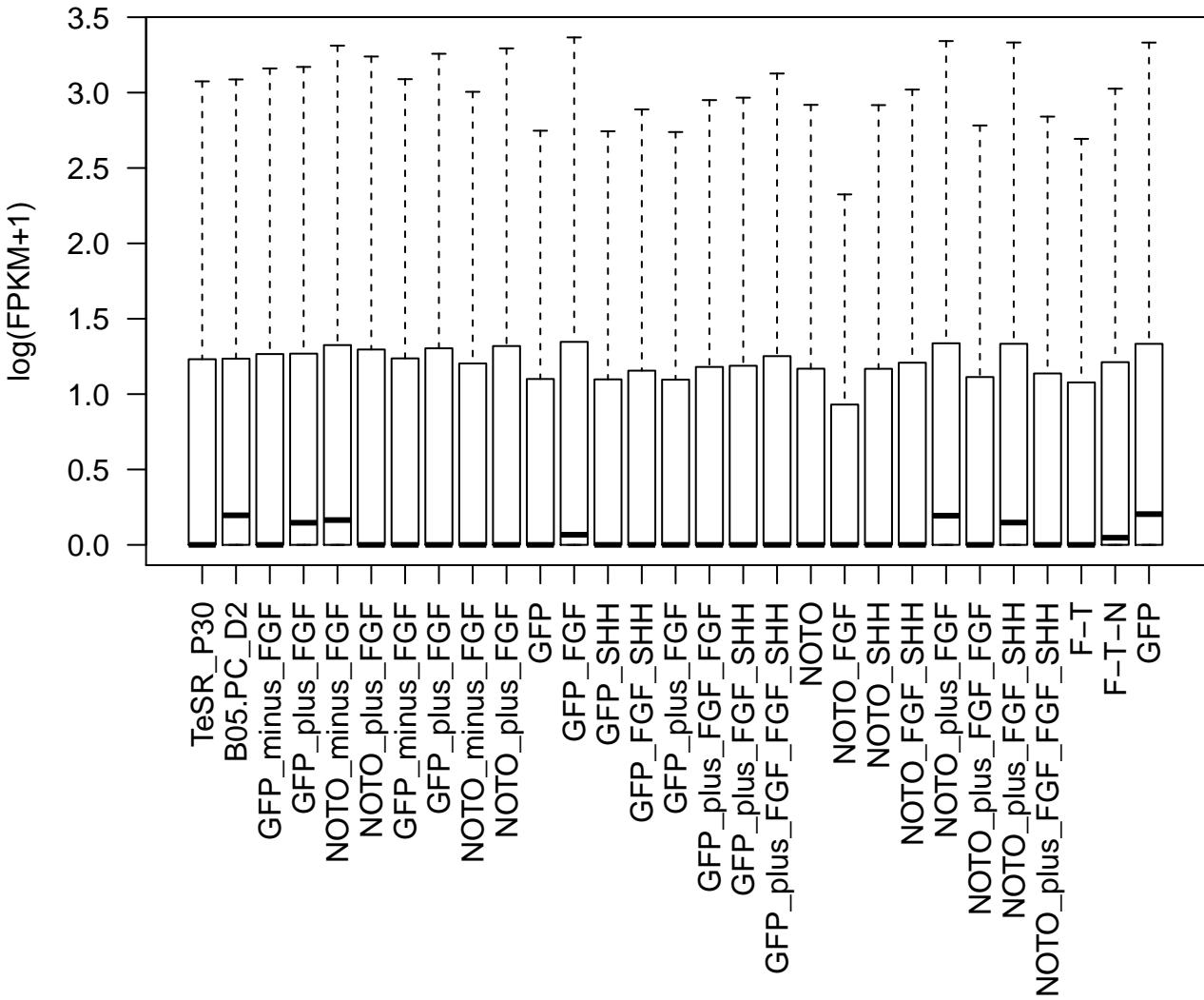


## Numbers of genes detected with non-zero FPKM

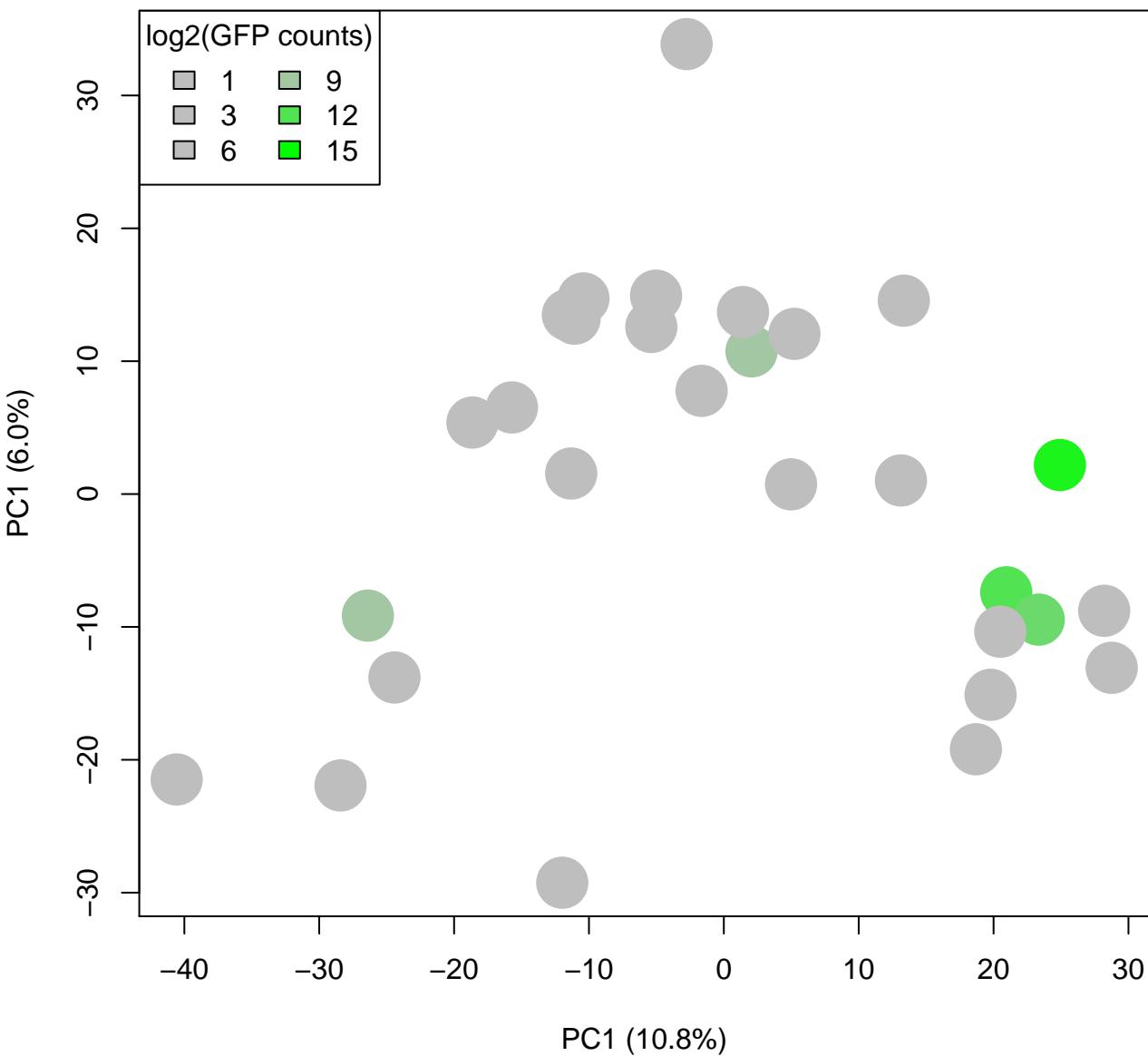




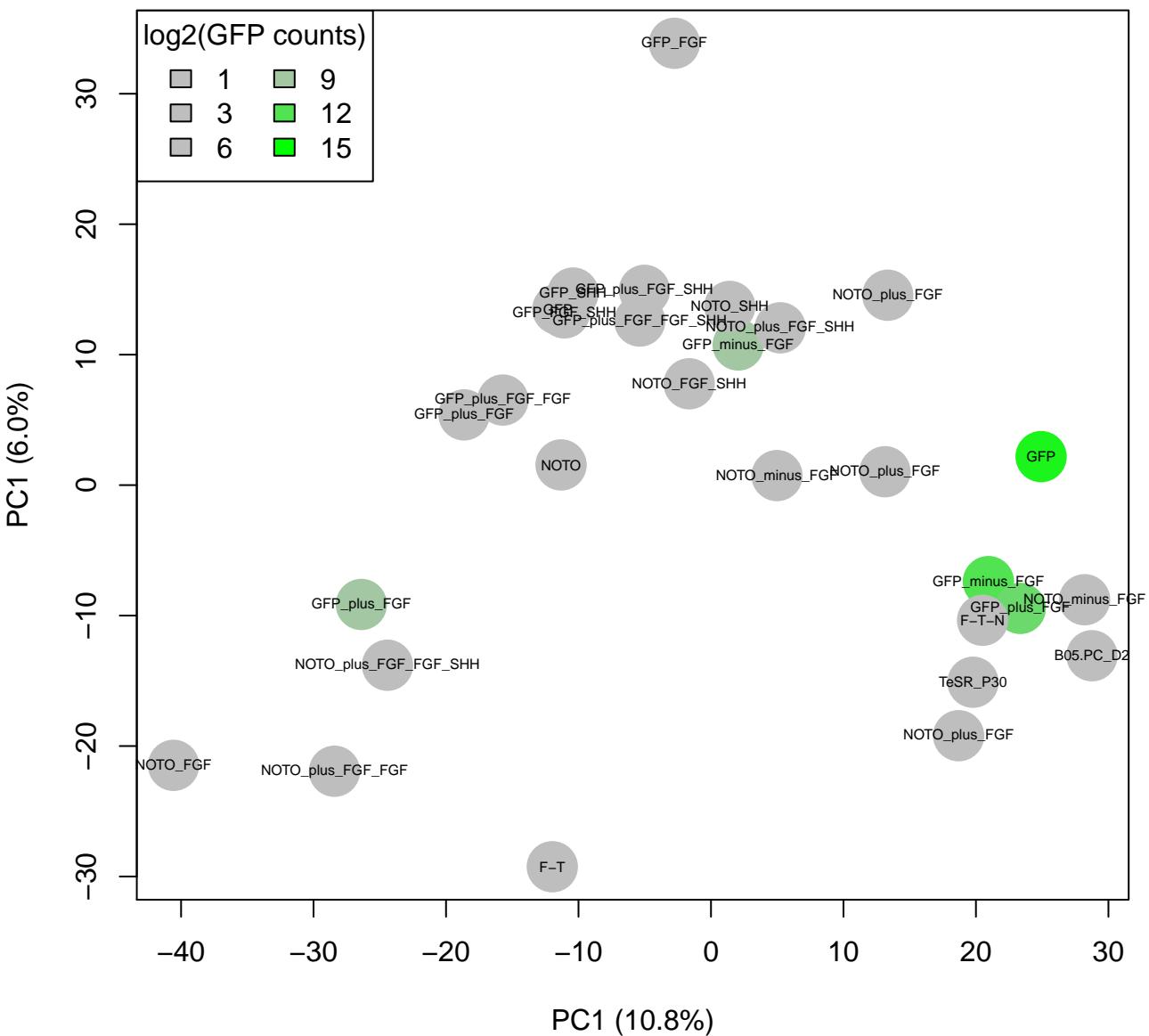
## gene expression levels across the samples



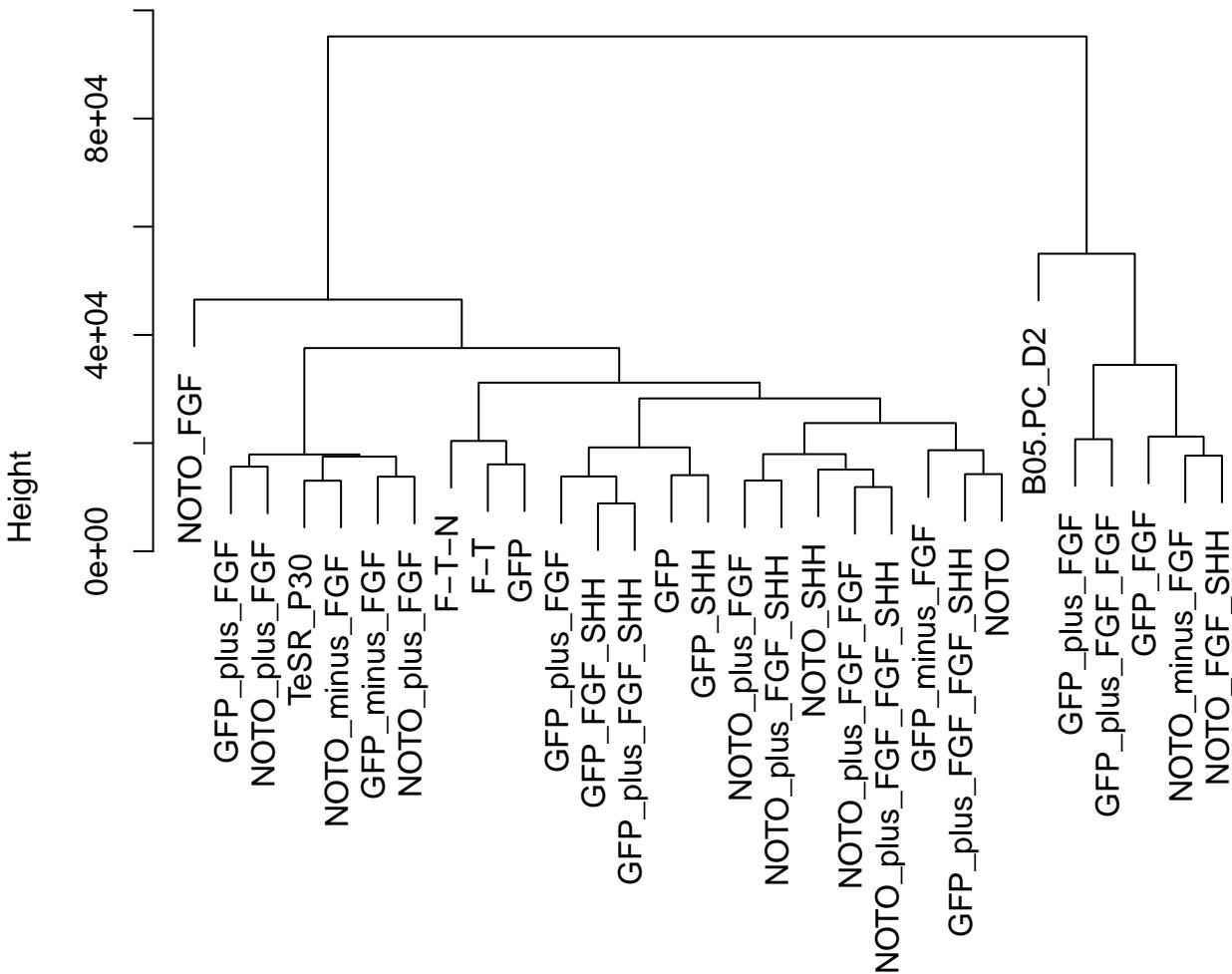
# PCA of 12,224 genes expressed in at least one sample



# PCA of 12,224 genes expressed in at least one sample



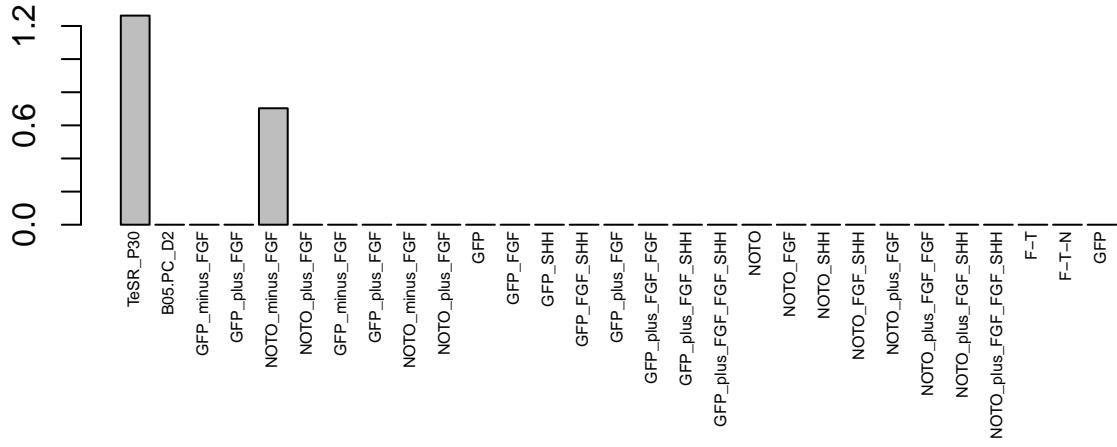
# Cluster Dendrogram



dist(t(fpkmMat.nz + 1))  
hclust (\*, "complete")

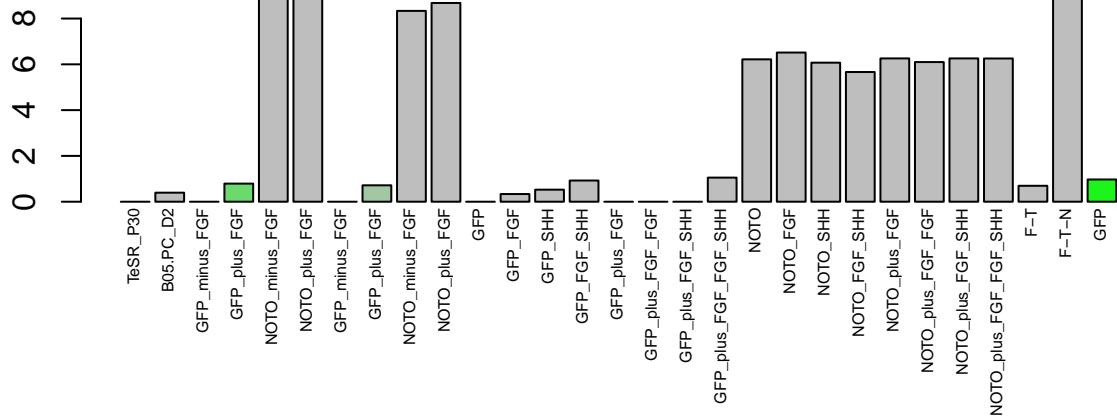
# POU5F1

log(FPKM+1)



# NOTO

log(FPKM+1)



log(FPKM+1)

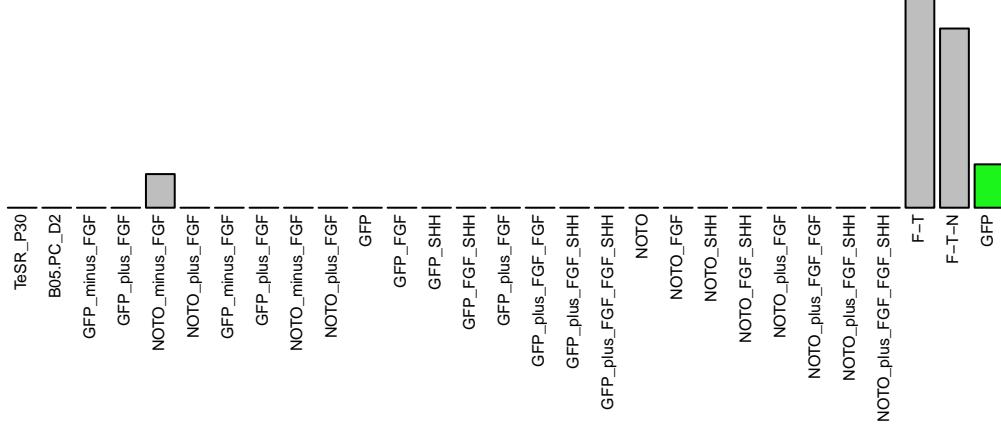
log(FPKM+1)

0.0 1.5 3.0

0.0 1.0

██████████

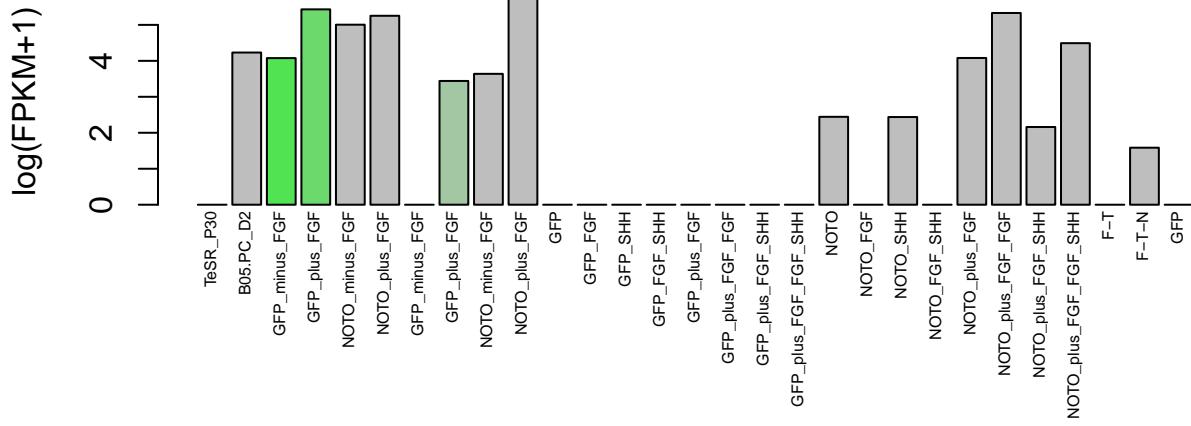
██████████



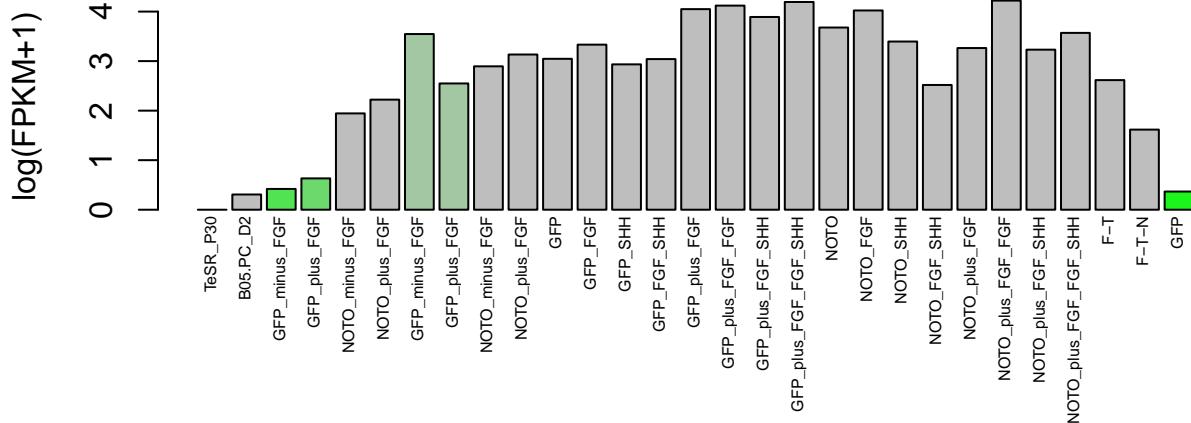
**FOXA2**

**SHH**

# SAMD3



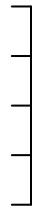
# NOG



log(FPKM+1)

log(FPKM+1)

0.0 1.0 2.0



T6SR\_P30 |  
B05,PC\_D2 |  
GFP\_minus\_FGF |  
GFP\_plus\_FGF |  
NOTO\_minus\_FGF |  
NOTO\_plus\_FGF |  
GFP\_minus\_FGF |  
GFP\_plus\_FGF |  
NOTO\_minus\_FGF |  
NOTO\_plus\_FGF |  
GFP |  
GFP\_FGF |  
GFP\_SHH |  
GFP\_FGF\_SHH |  
GFP\_plus\_FGF |  
GFP\_plus\_FGF\_FGF |  
GFP\_plus\_FGF\_SHH |  
GFP\_plus\_FGF\_FGF\_SHH |  
NOTO |  
NOTO\_FGF |  
NOTO\_SHH |  
NOTO\_FGF\_SHH |  
NOTO\_plus\_FGF |  
NOTO\_plus\_FGF\_FGF |  
NOTO\_plus\_FGF\_SHH |  
NOTO\_plus\_FGF\_FGF\_SHH |  
F-T |  
F-T-N |  
GFP |

T6SR\_P30 |  
B05,PC\_D2 |  
GFP\_minus\_FGF |  
GFP\_plus\_FGF |  
NOTO\_minus\_FGF |  
NOTO\_plus\_FGF |  
GFP\_minus\_FGF |  
GFP\_plus\_FGF |  
NOTO\_minus\_FGF |  
NOTO\_plus\_FGF |  
GFP |  
GFP\_FGF |  
GFP\_SHH |  
GFP\_FGF\_SHH |  
GFP\_plus\_FGF |  
GFP\_plus\_FGF\_FGF |  
GFP\_plus\_FGF\_SHH |  
GFP\_plus\_FGF\_FGF\_SHH |  
NOTO |  
NOTO\_FGF |  
NOTO\_SHH |  
NOTO\_FGF\_SHH |  
NOTO\_plus\_FGF |  
NOTO\_plus\_FGF\_FGF |  
NOTO\_plus\_FGF\_SHH |  
NOTO\_plus\_FGF\_FGF\_SHH |  
F-T |  
F-T-N |  
GFP |

## CHRD2

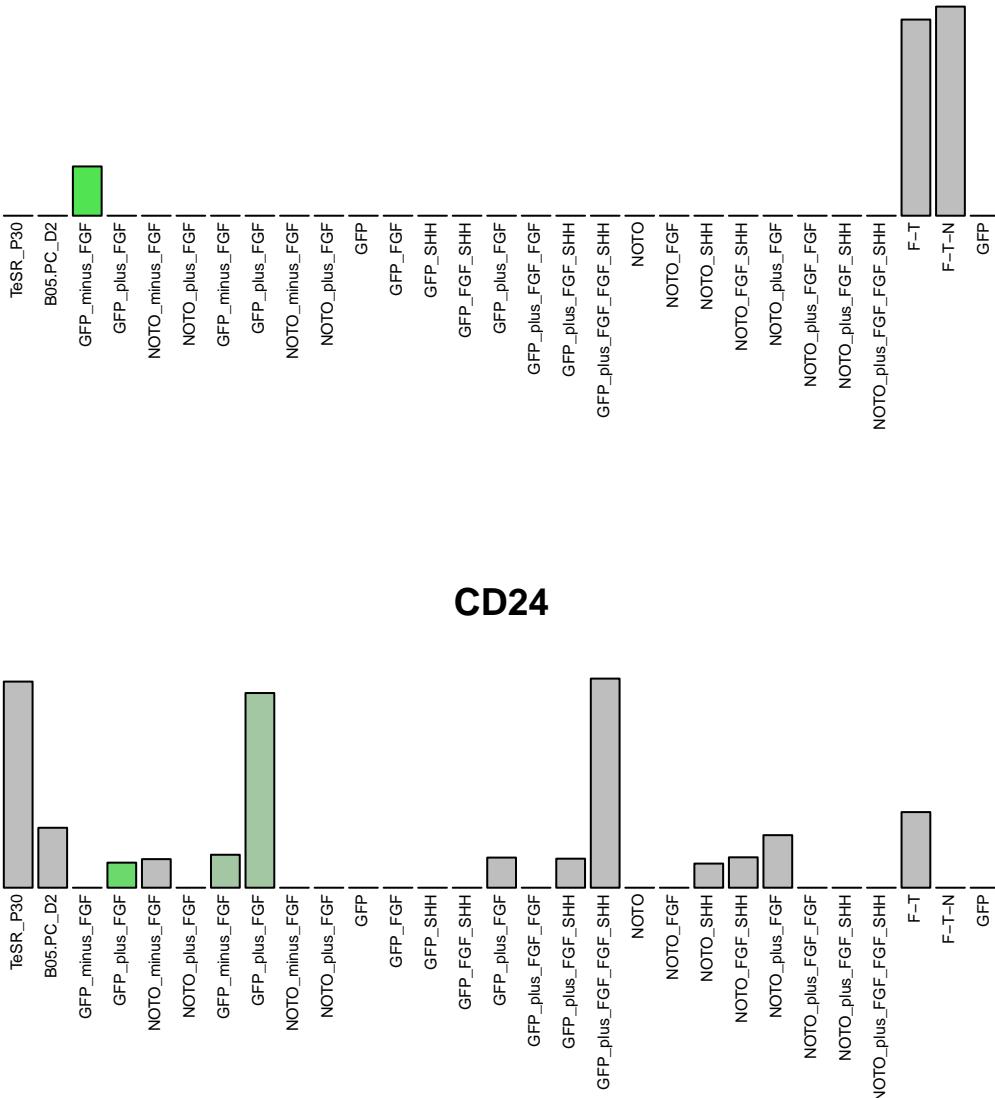
## CHRD

log(FPKM+1)

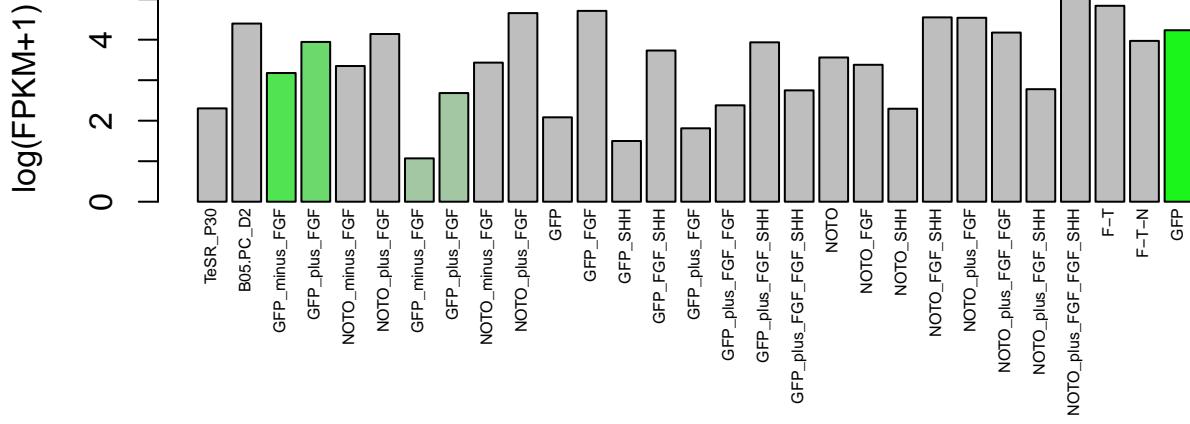
log(FPKM+1)

T

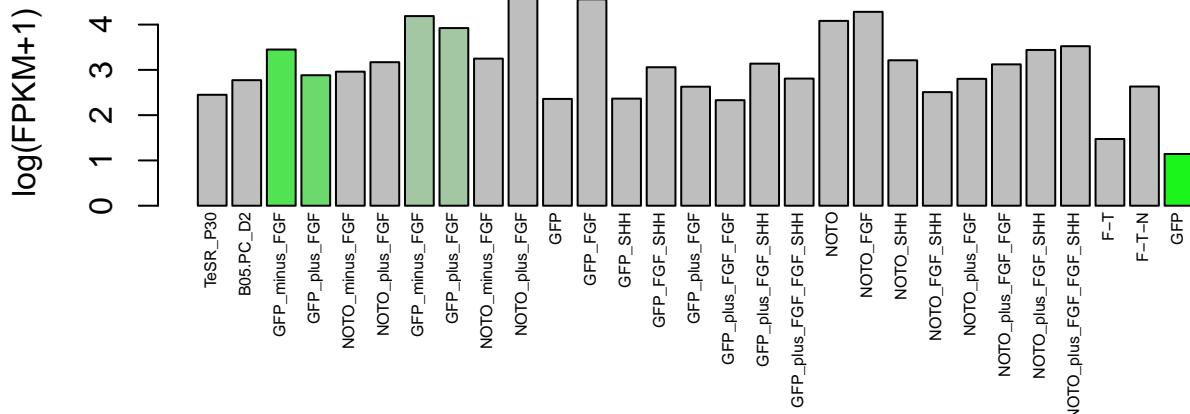
## CD24



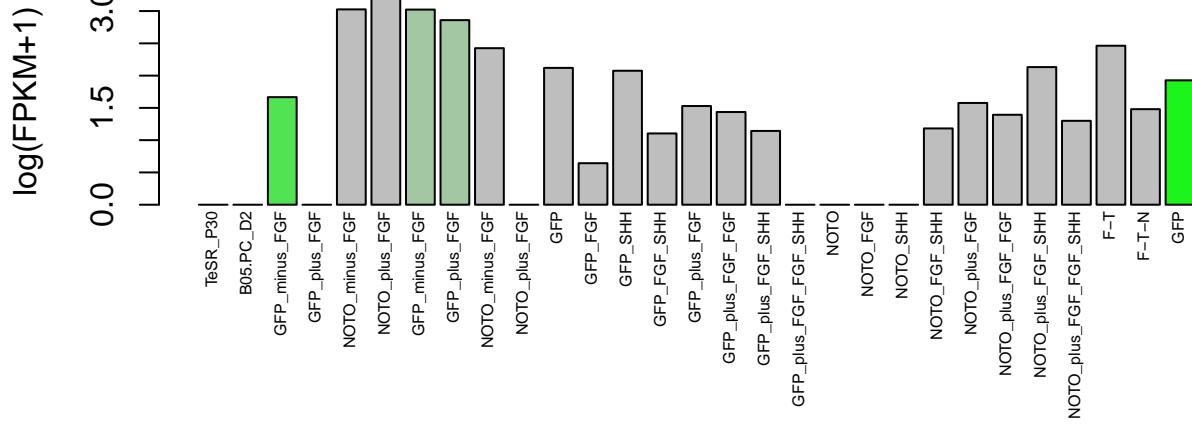
## KRT8



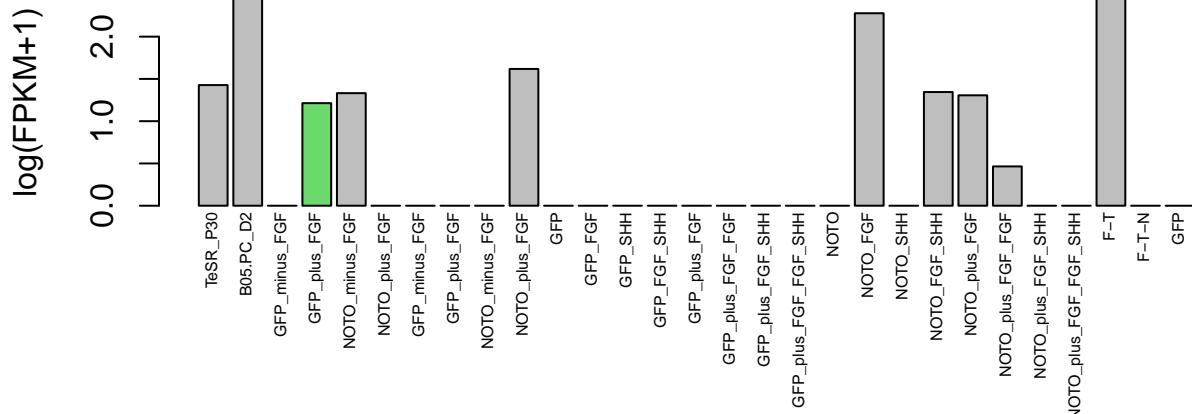
## KRT18



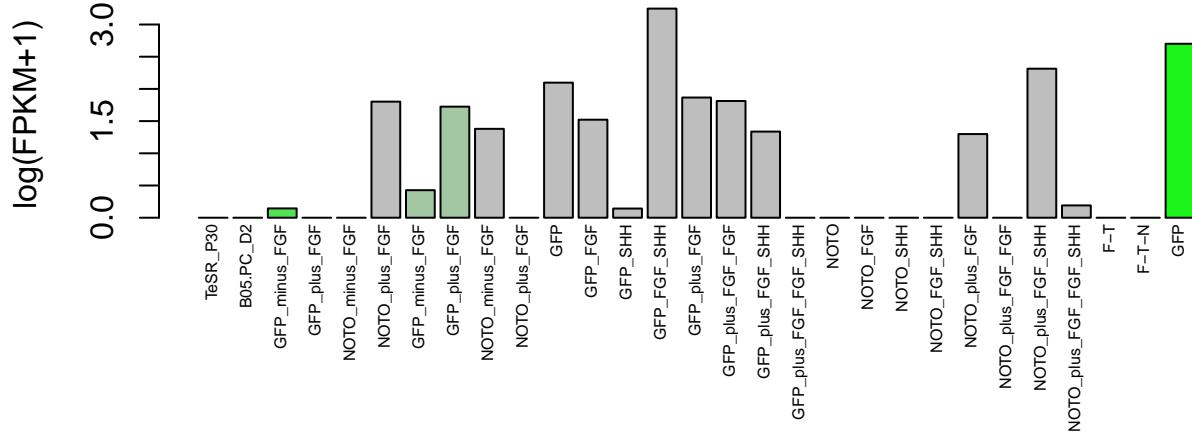
# KRT19



# CAV1



# HAPLN1



Analysed by Peikai on: Sat May 09 23:32:55 2020