

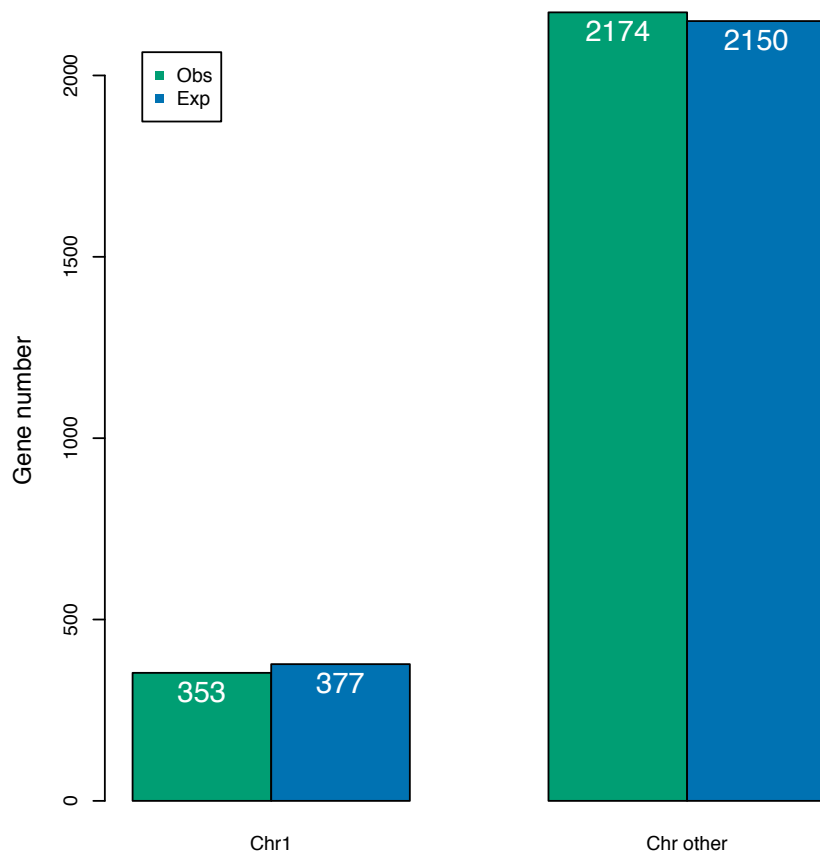
Filtering criteria:  
dgl <- dgl[aveLogCPM(dgl) > 0,] +  
dgl <- dgl[rowSums(cpm(dgl)>=1) >= 3,]

male bias

female bias

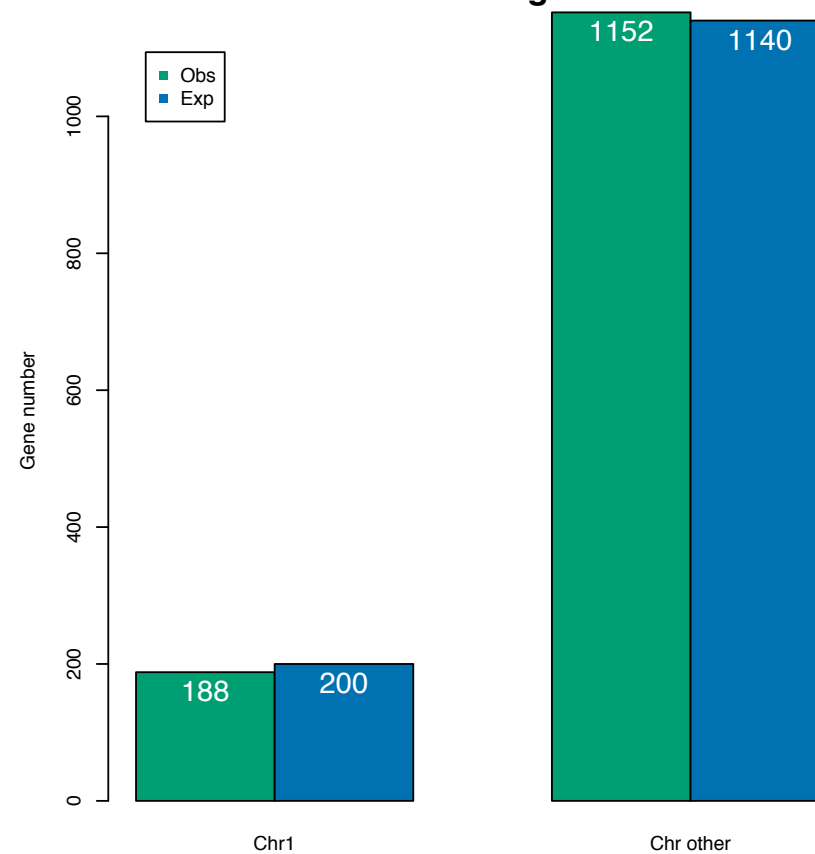
### Sex chromosome vs autosomes

DE XYtestis vs XXovary  
FDR=0.05 logFC=1



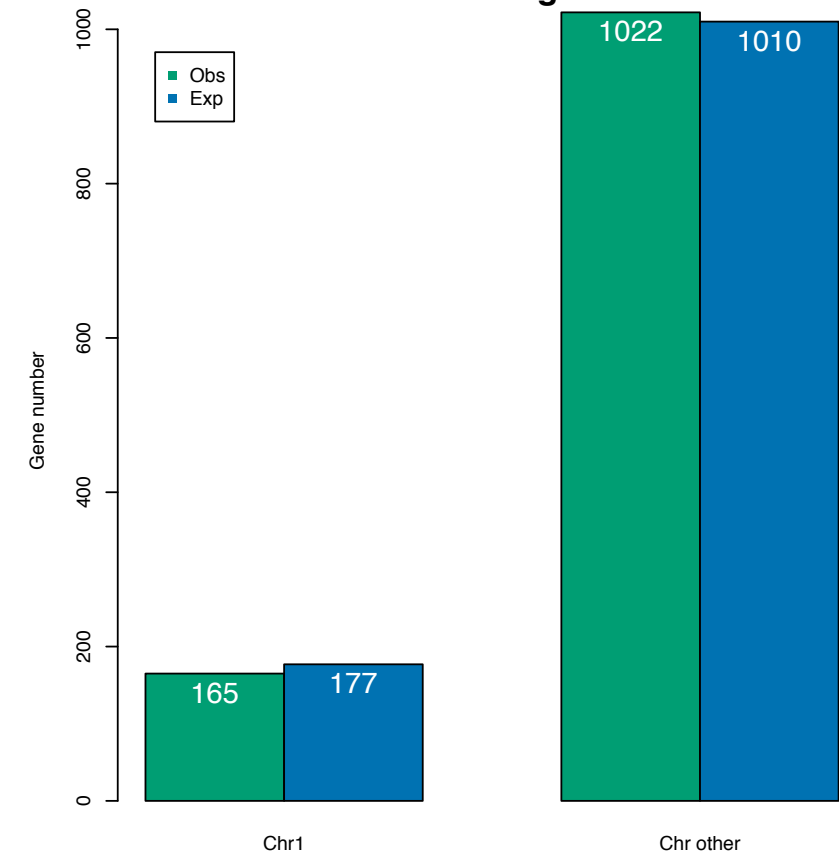
chisq = 0.17

Up XYtestis  
FDR=0.05 logFC=1



chisq = 0.35

Down XXovary  
FDR=0.05 logFC=1



chisq = 0.32

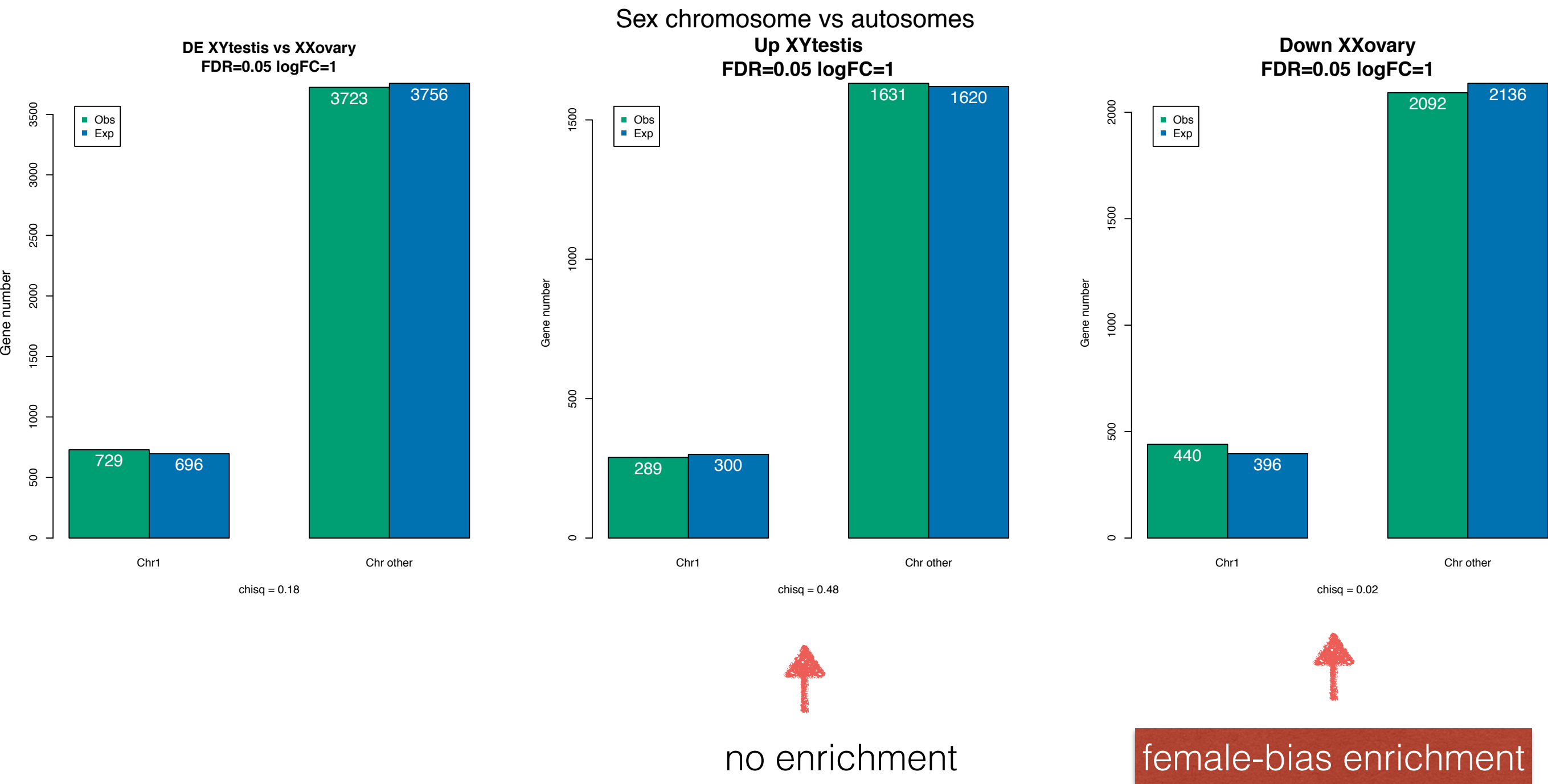


no enrichment



no enrichment

Filtering criteria:  
`dgl <- dgl[aveLogCPM(dgl) > 0,]`



Filtering criteria:  
dgl <- dgl[rowSums(cpm(dgl)) >= 2,]

