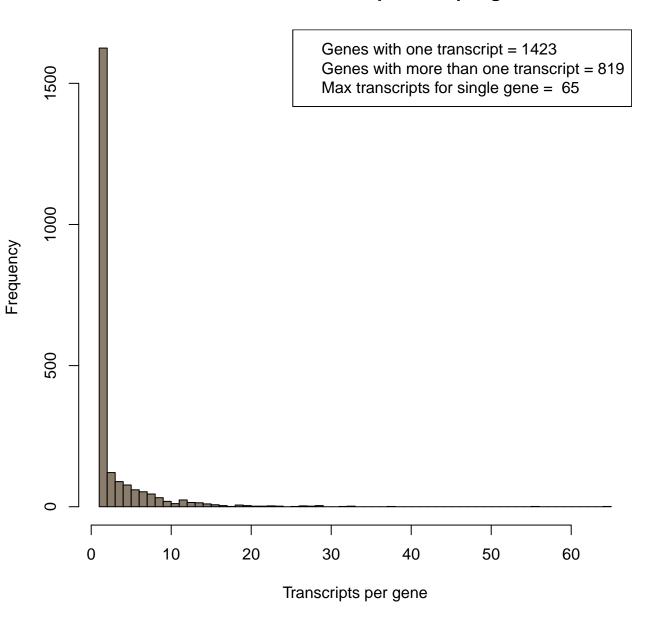
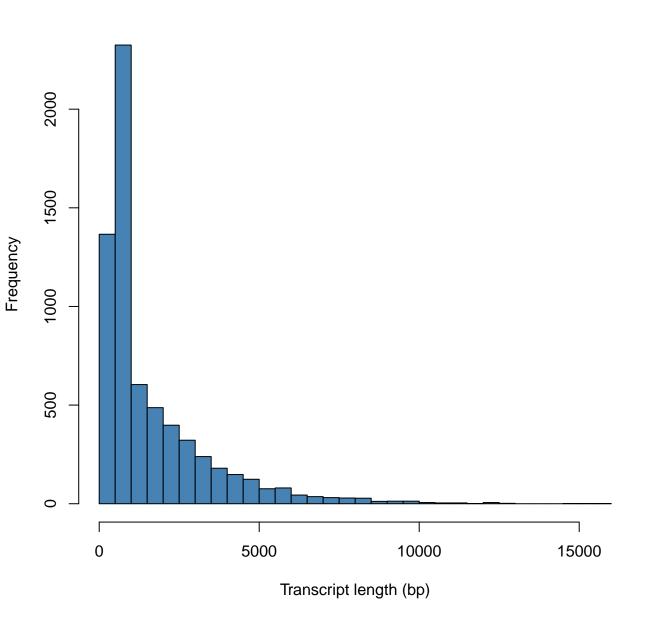
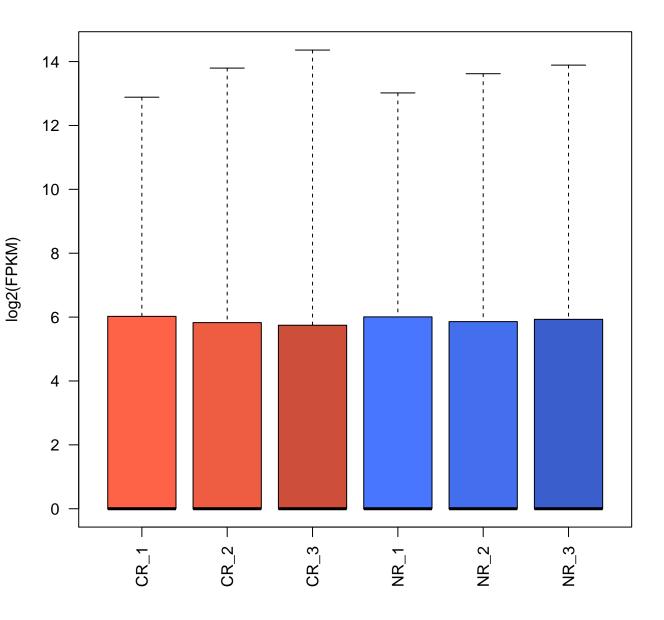
## Distribution of transcript count per gene



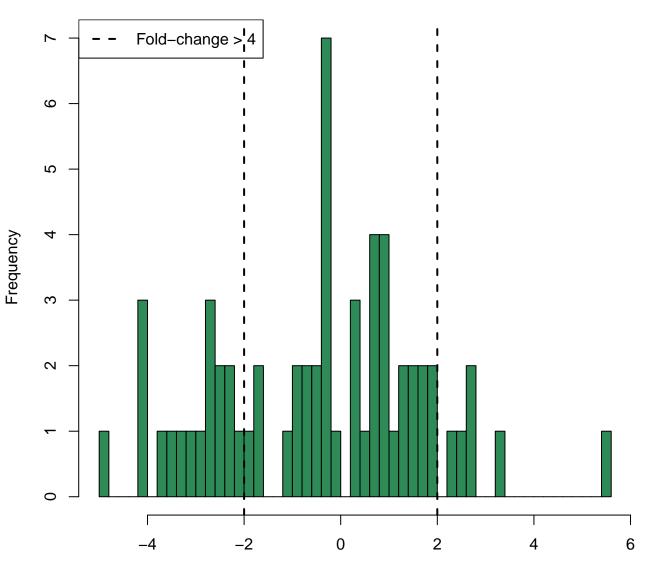
# **Distribution of transcript lengths**



## Distribution of FPKMs for all 6 libraries



# Distribution of differential expression values



log2(Fold change) carcinoma vs normal

### carcinoma vs normal FPKMs

