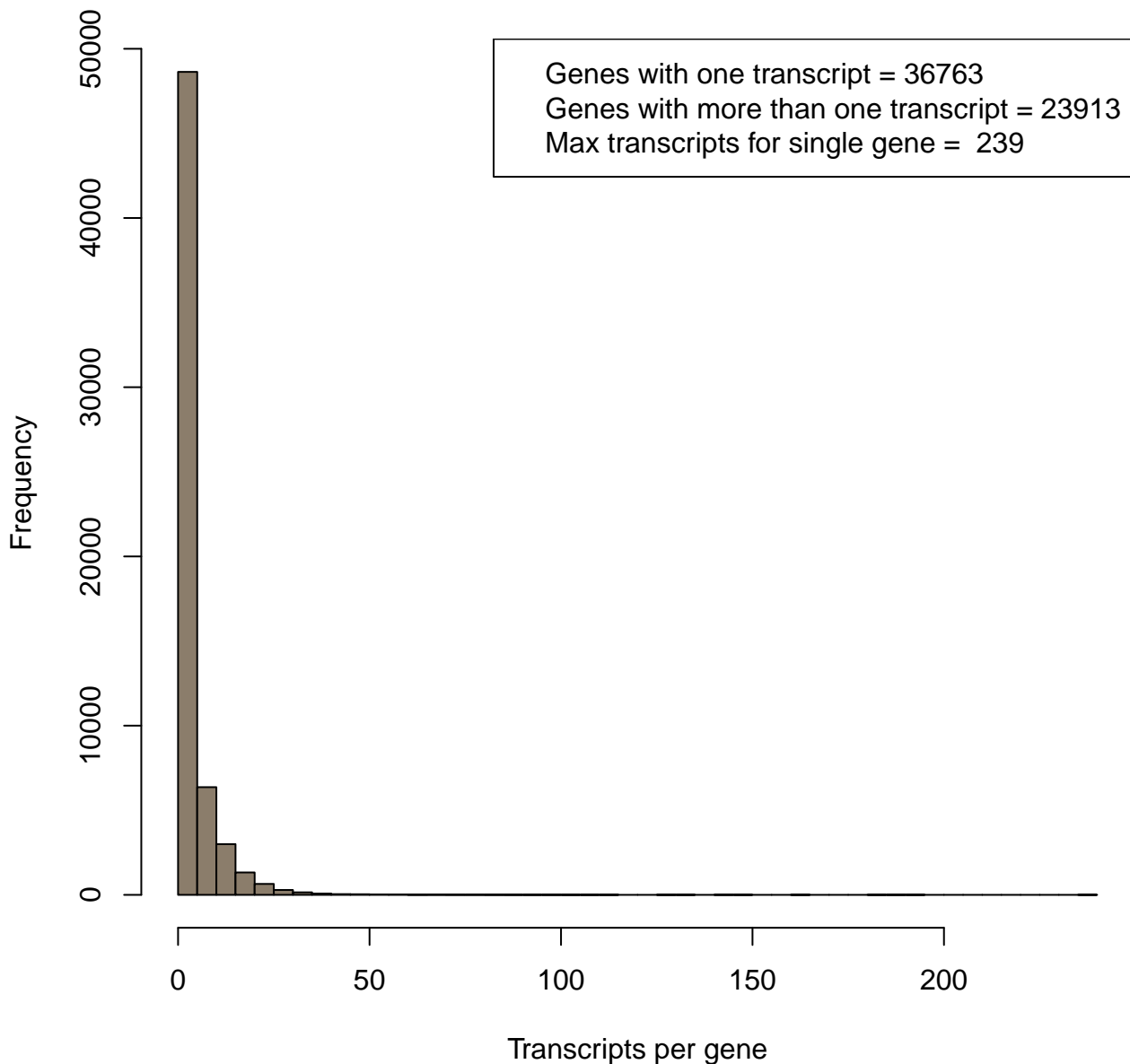
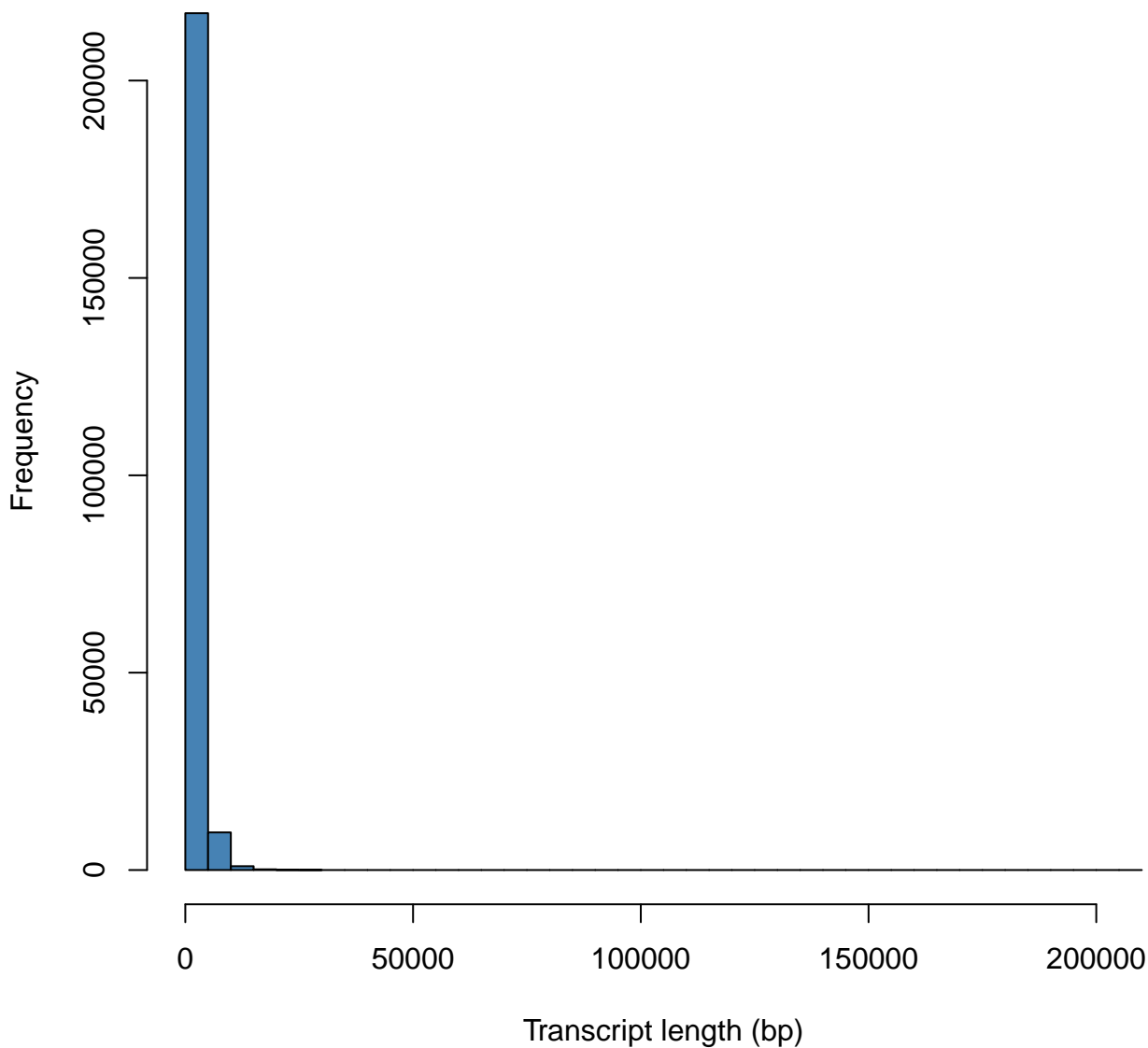


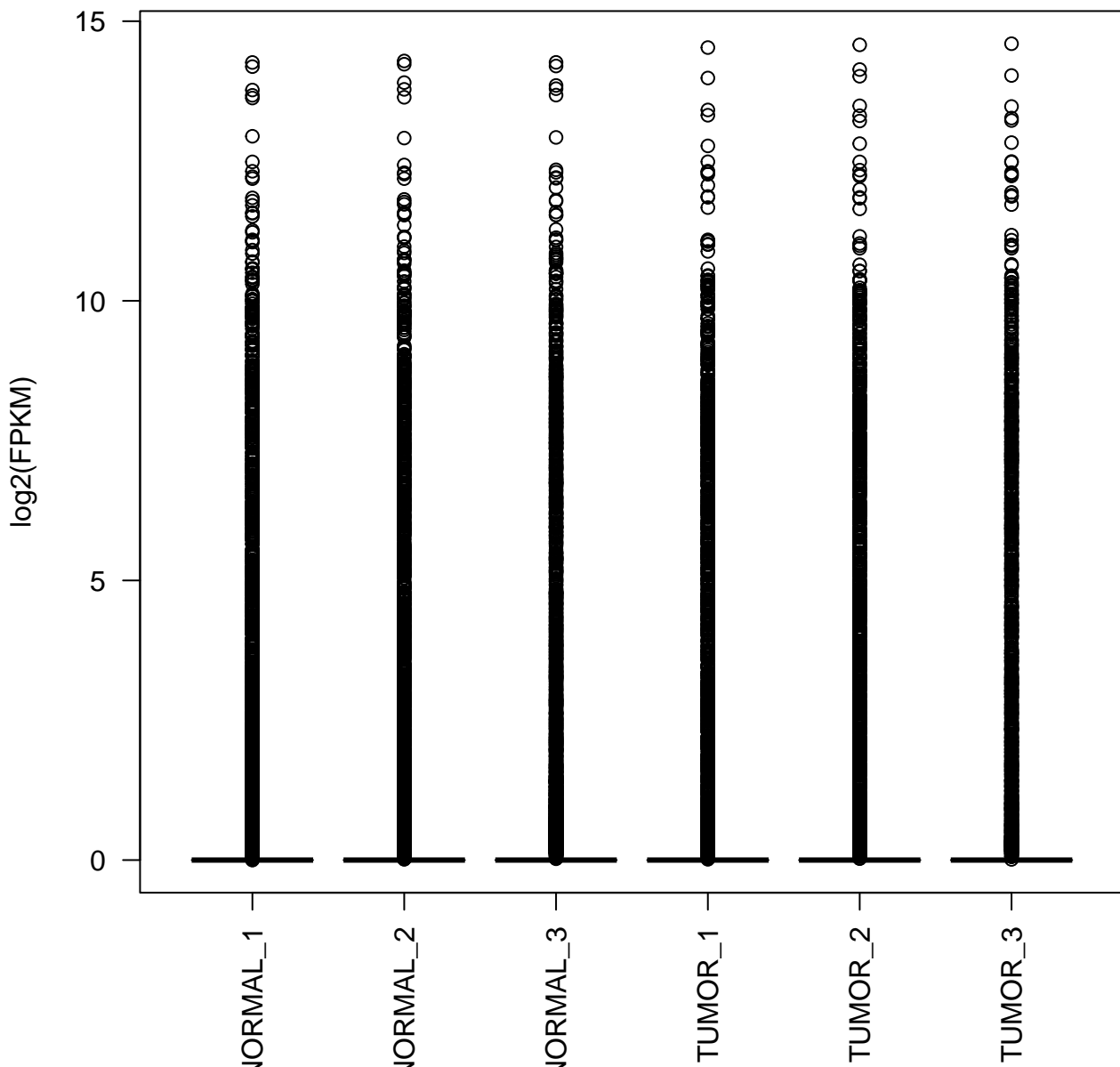
## Distribution of transcript count per gene



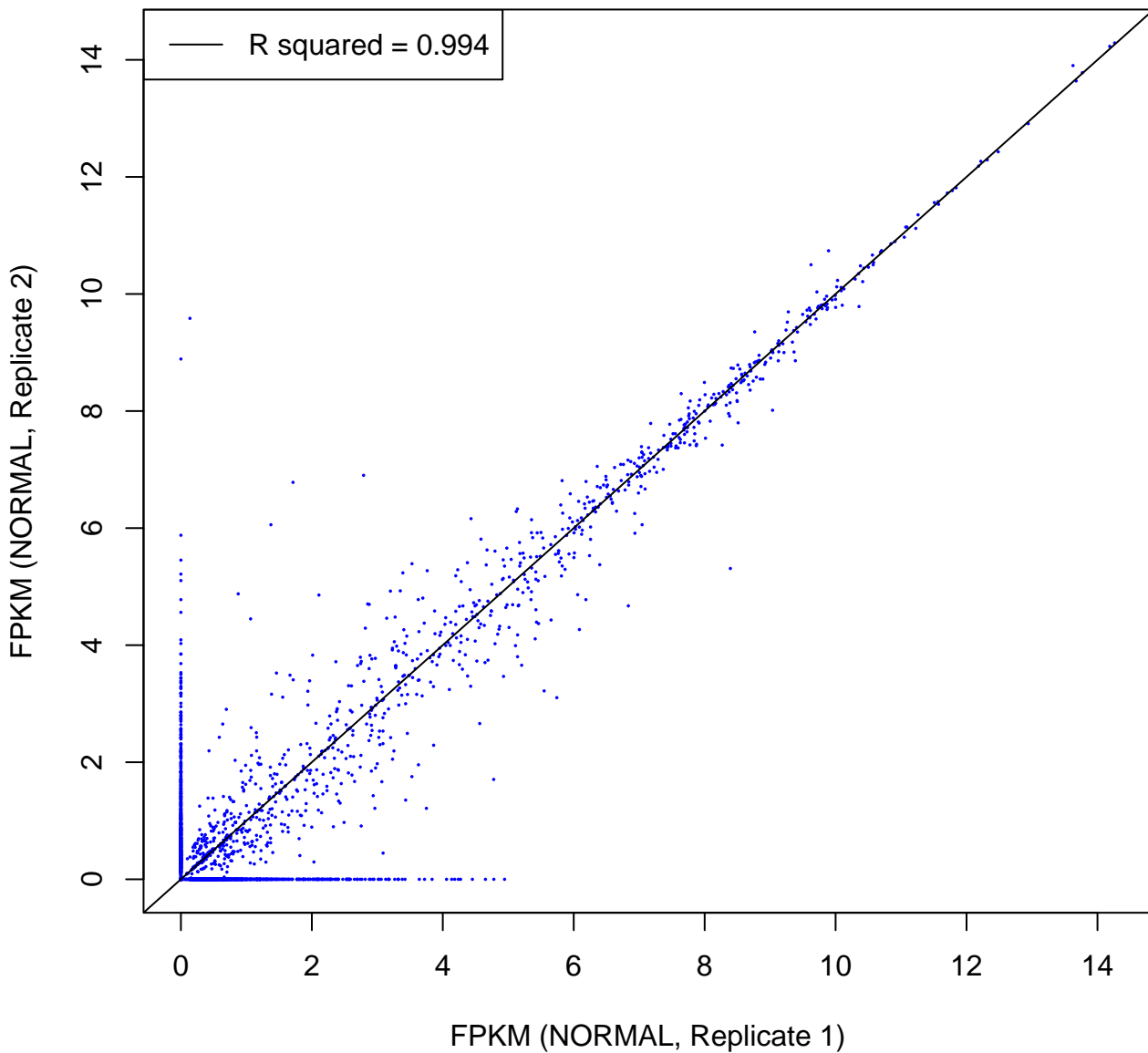
**Distribution of transcript lengths**



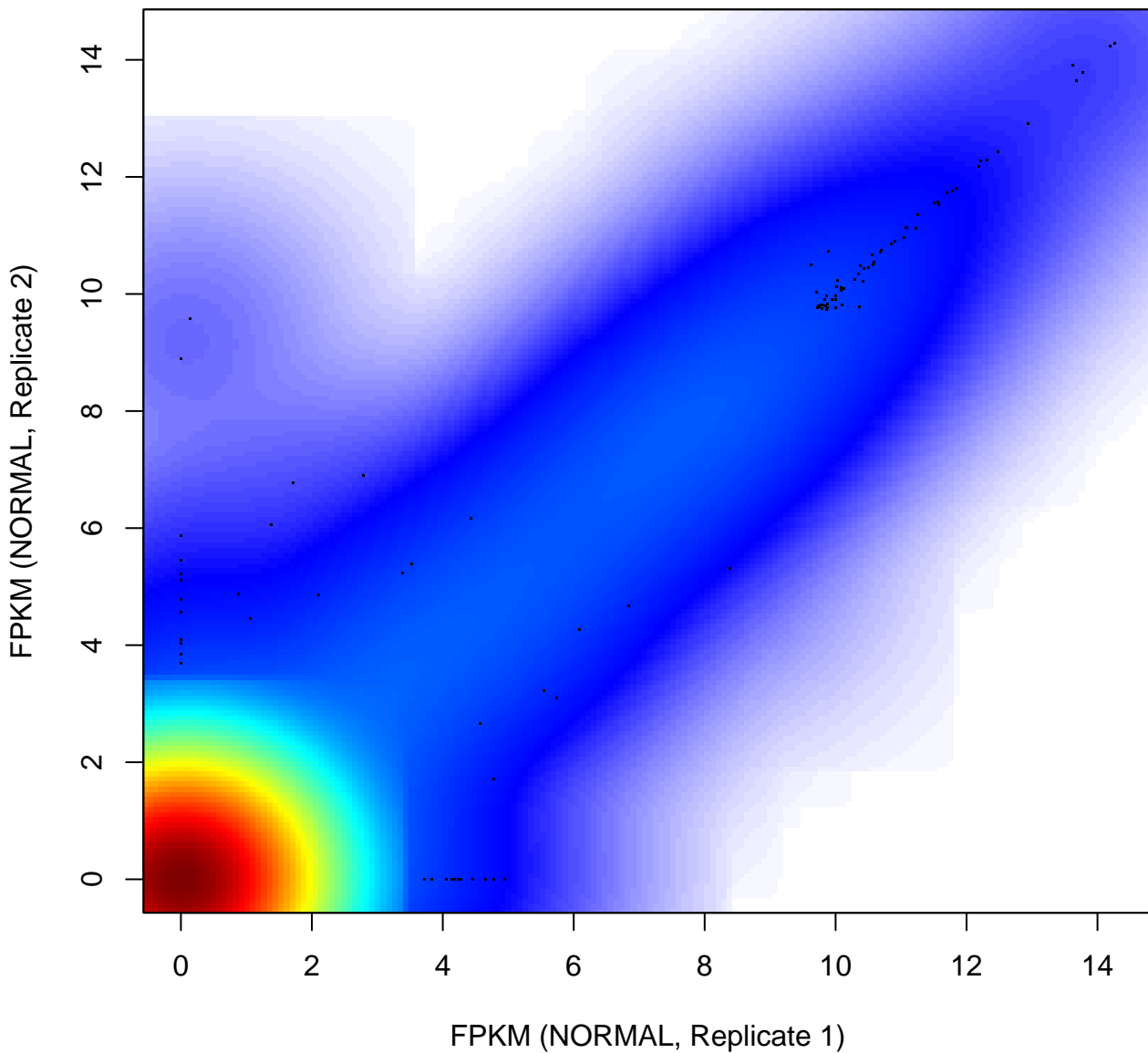
**Distribution of FPKMs for all 6 libraries**



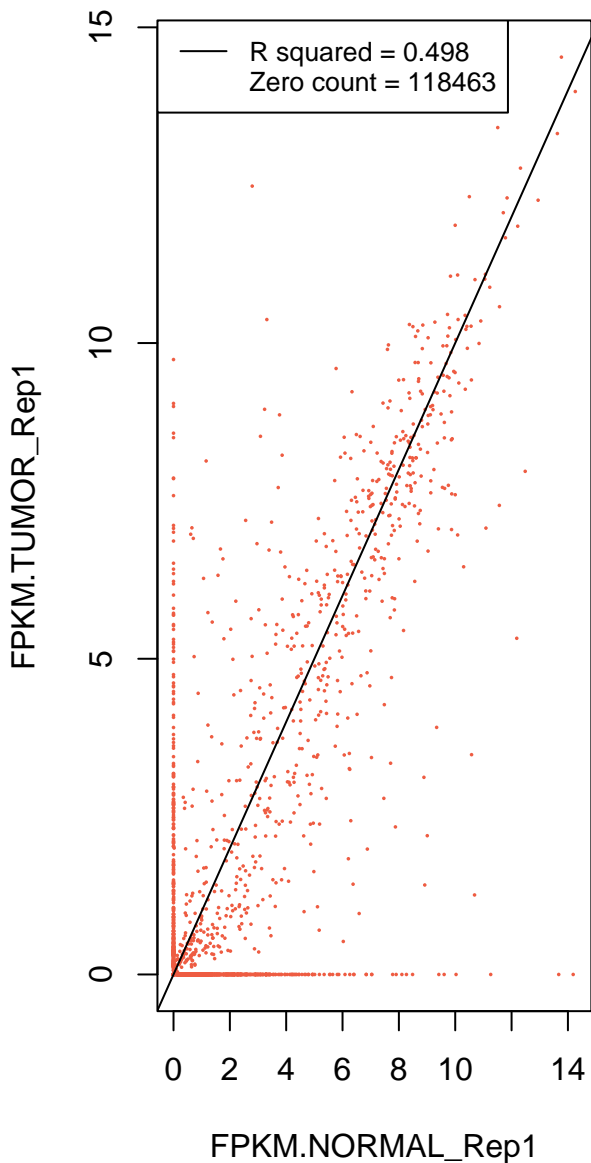
# Comparison of expression values for a pair of replicates



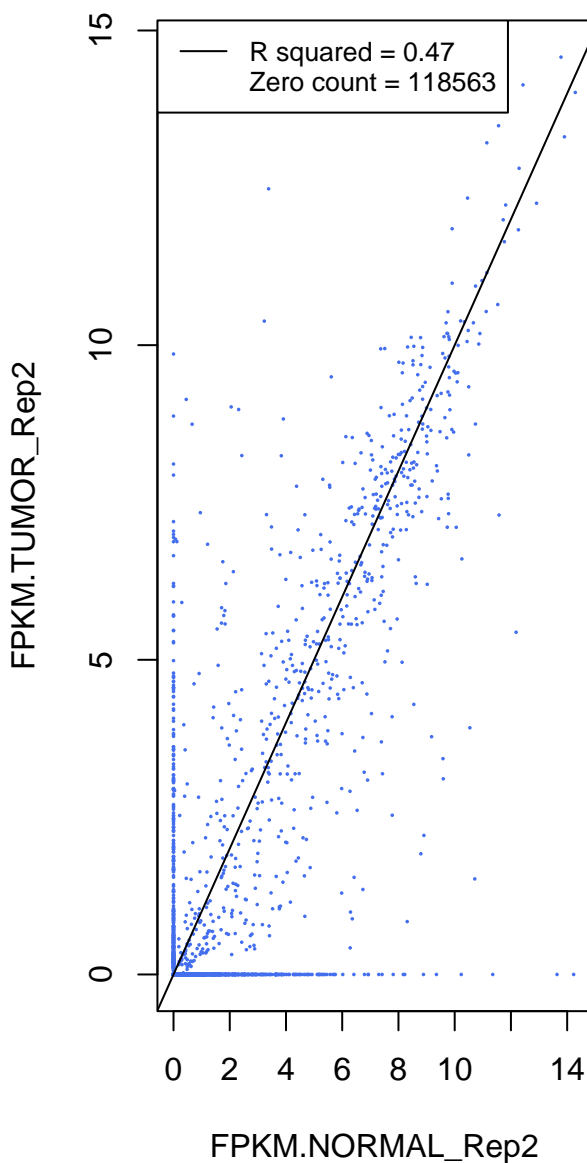
# Comparison of expression values for a pair of replicates



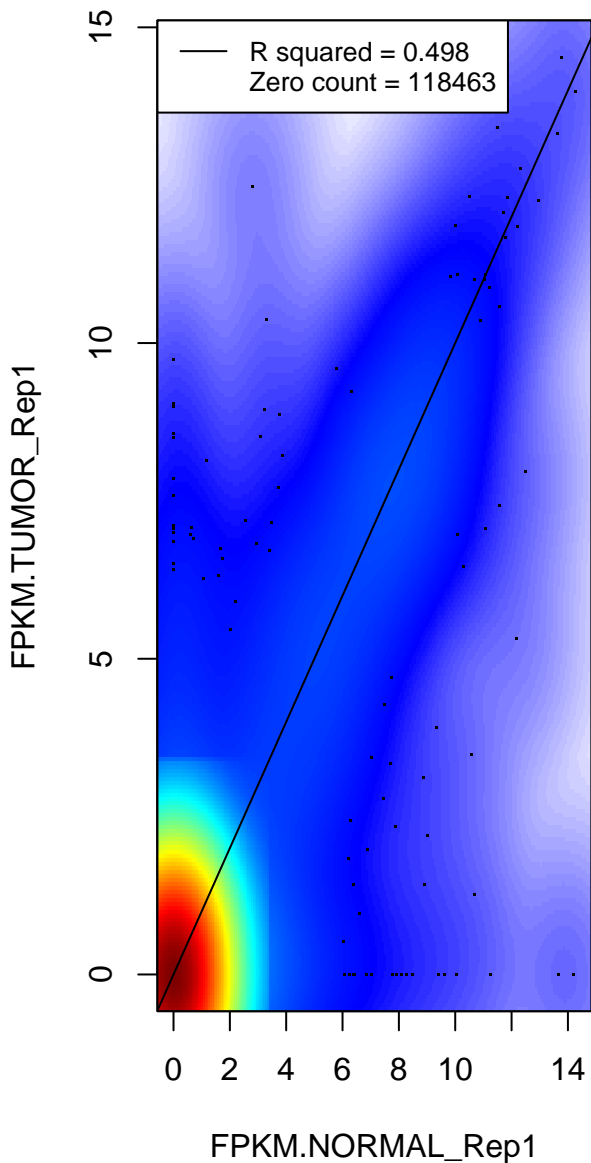
**NORMAL\_1 vs TUMOR\_1**



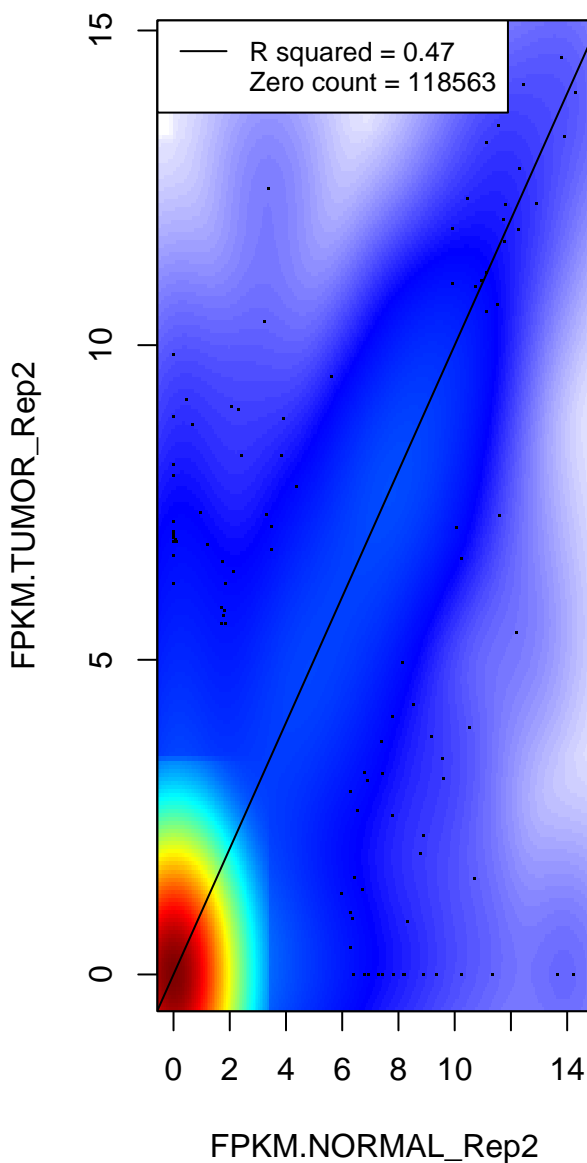
**NORMAL\_2 vs TUMOR\_2**



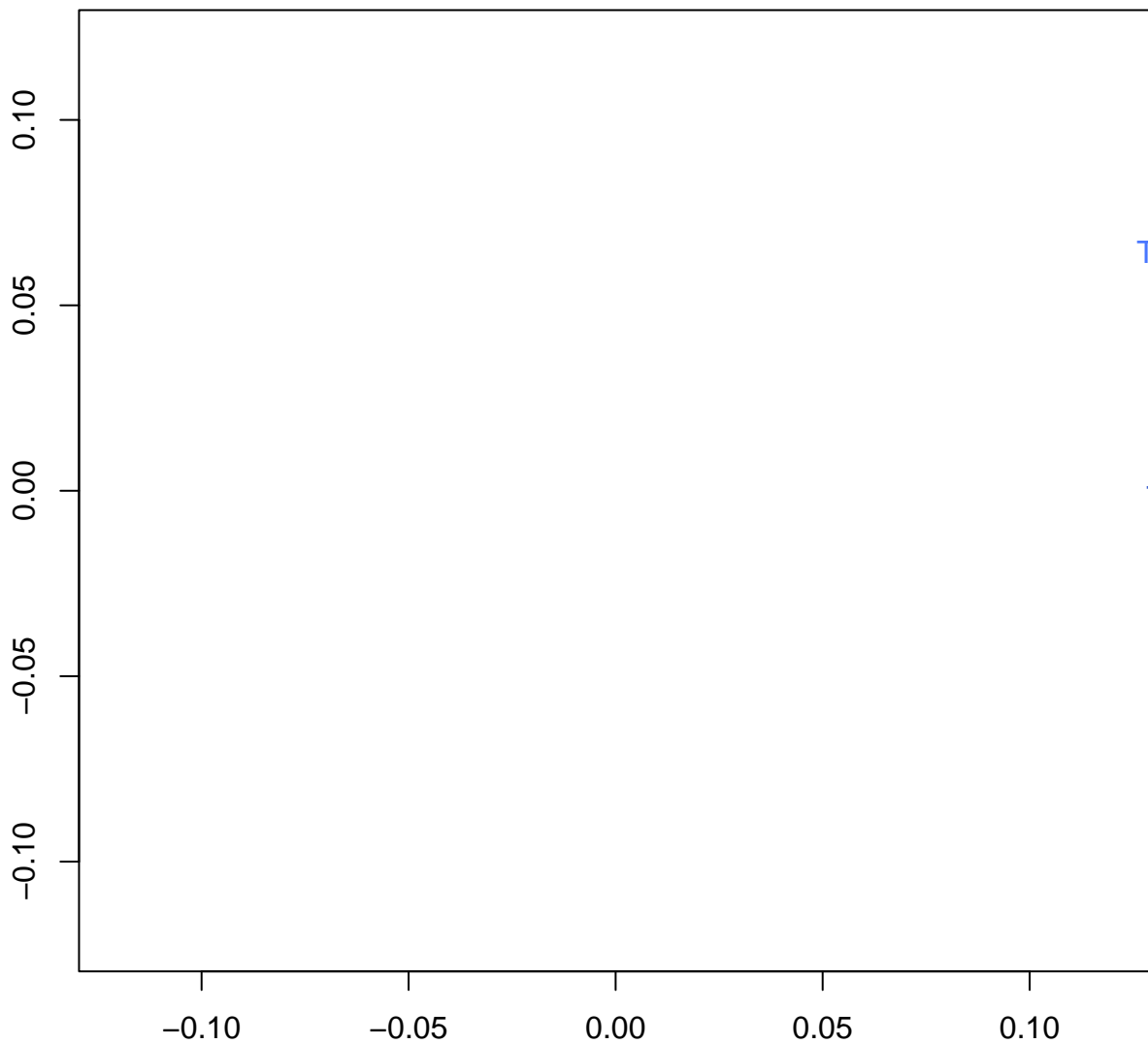
**NORMAL\_1 vs TUMOR\_1**



**NORMAL\_2 vs TUMOR\_2**

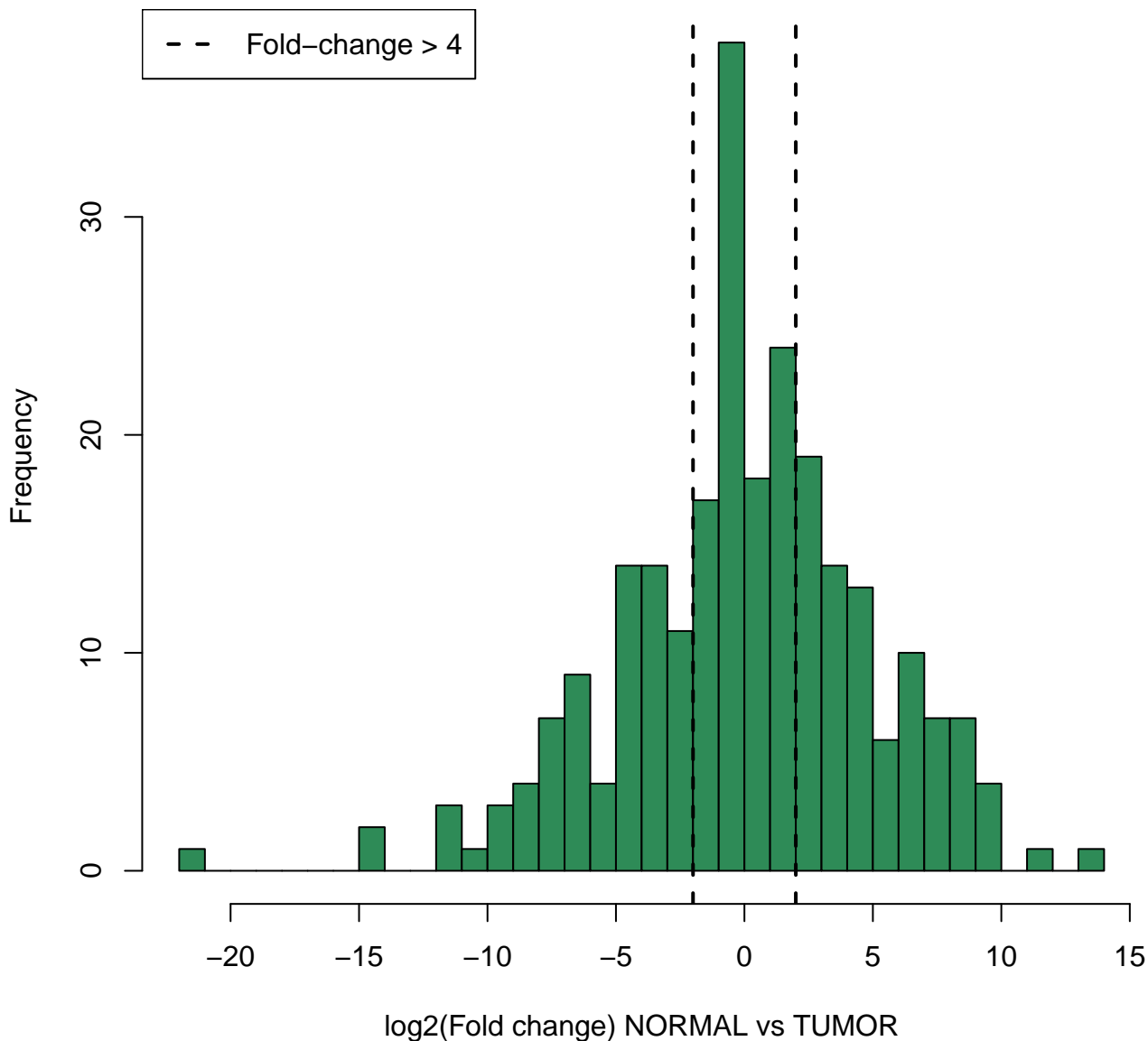


**MDS distance plot (all non-zero genes)**

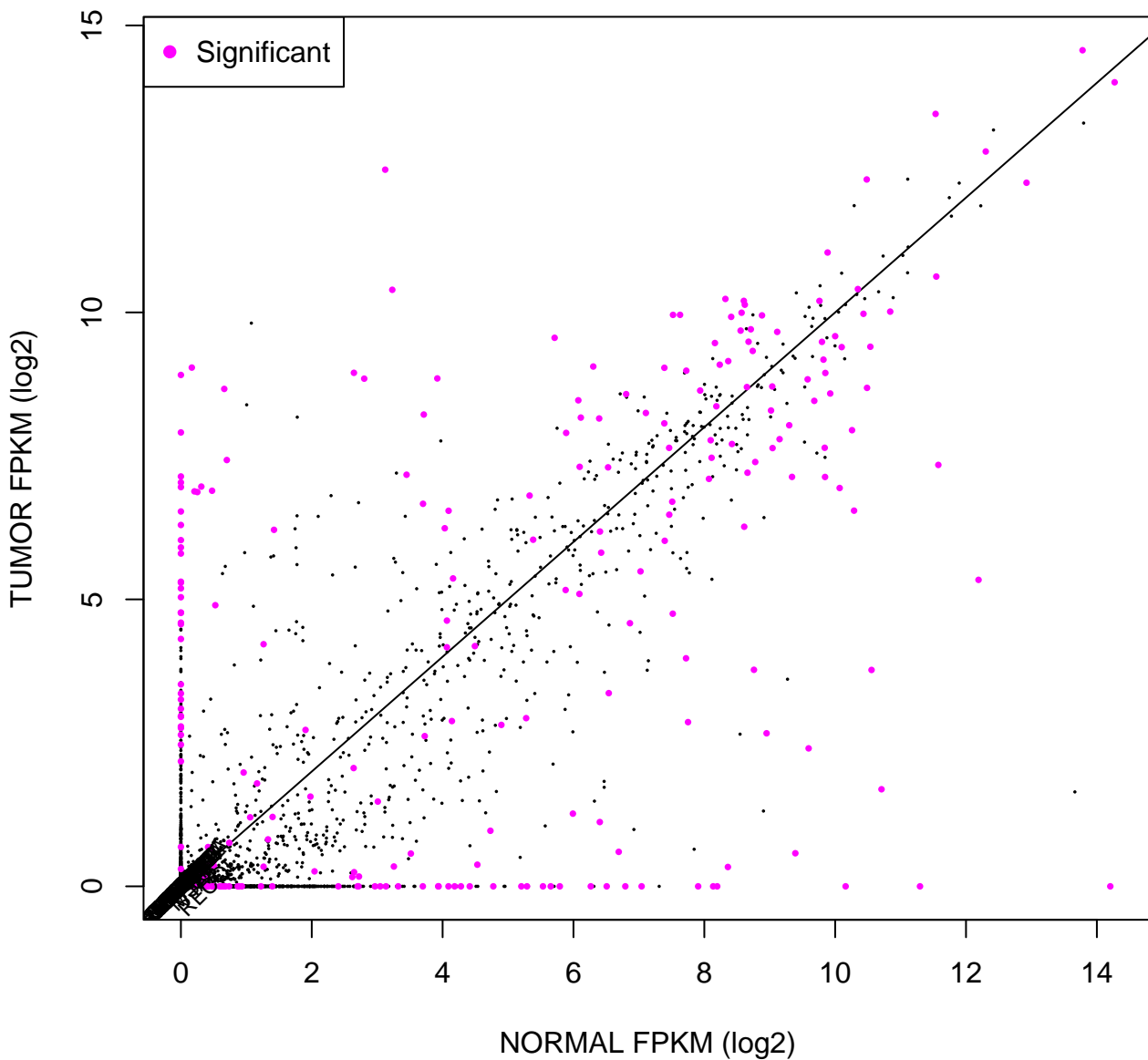




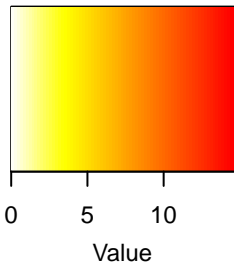
# Distribution of differential expression values



# NORMAL vs TUMOR FPKMs



Color Key



sig DE Transcripts

