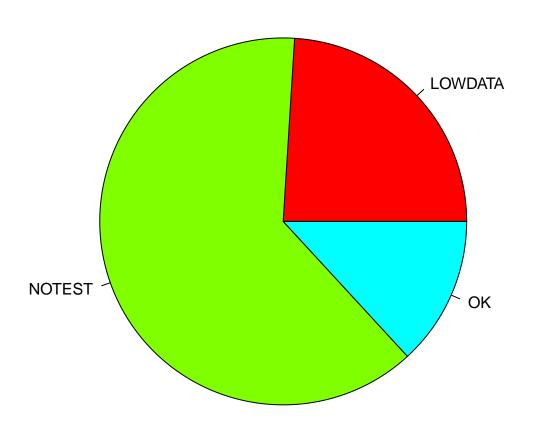
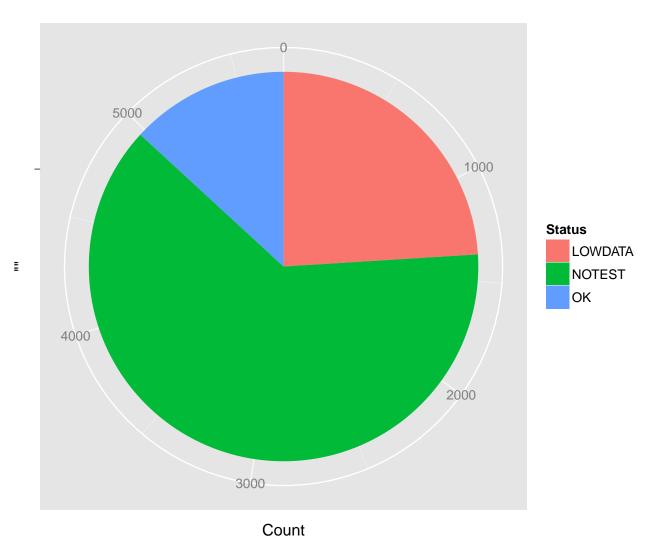


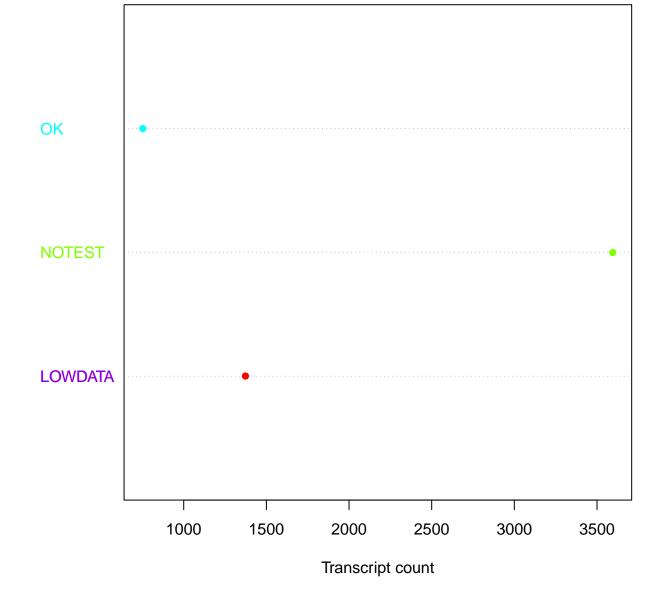
#### Status counts reported by Cuffdiff



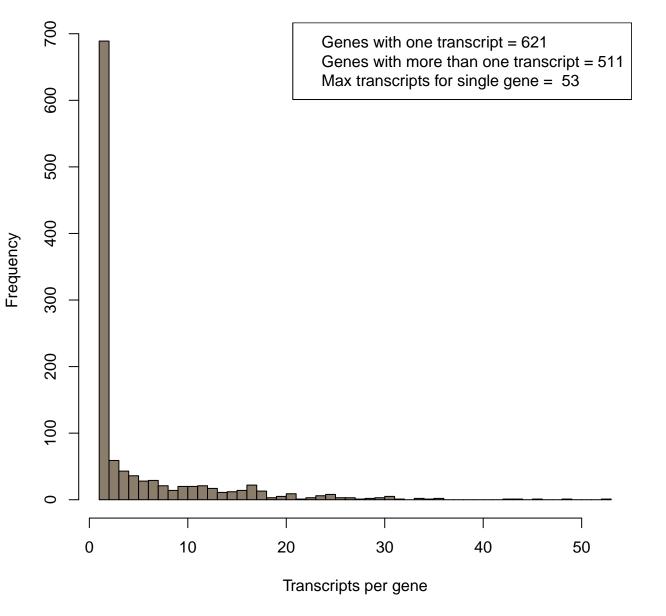


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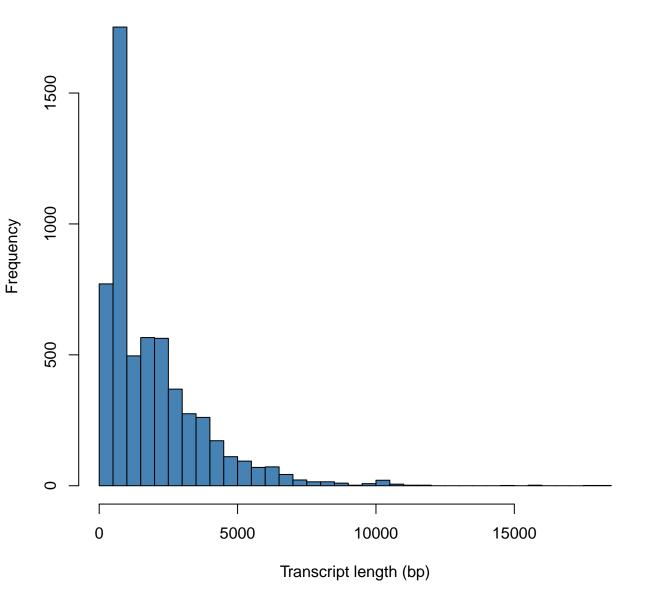
Tutorial\_Part3\_Supplementary\_R\_output.pdf



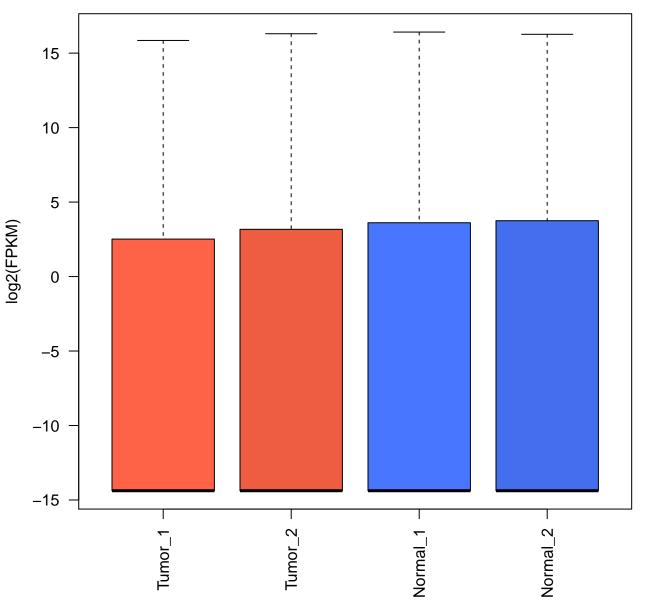
### Distribution of transcript count per gene



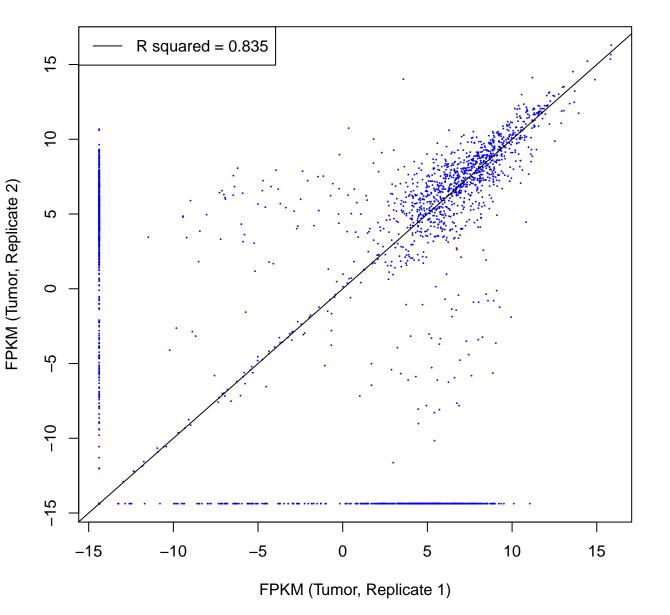
# Distribution of transcript lengths



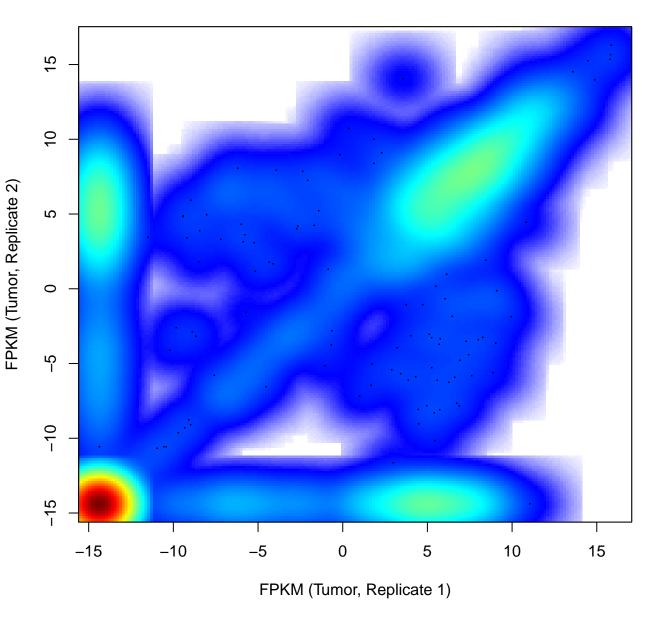
## Distribution of FPKMs for all 4 libraries

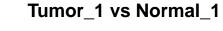


#### Comparison of expression values for a pair of replicates

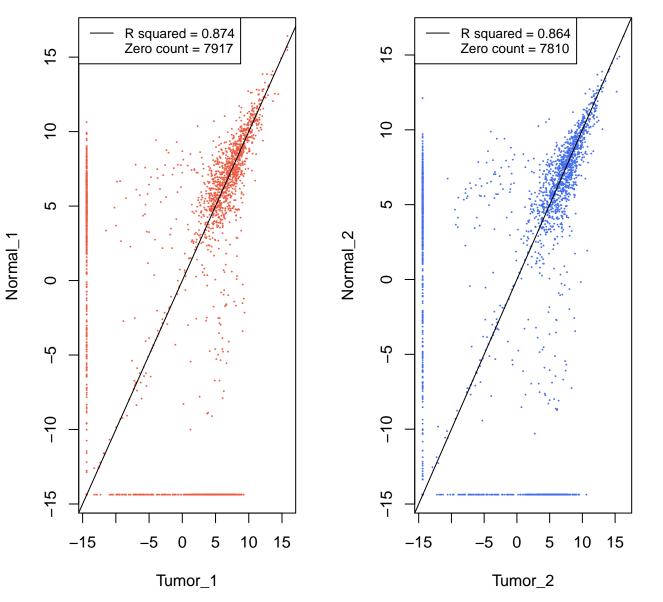


#### Comparison of expression values for a pair of replicates





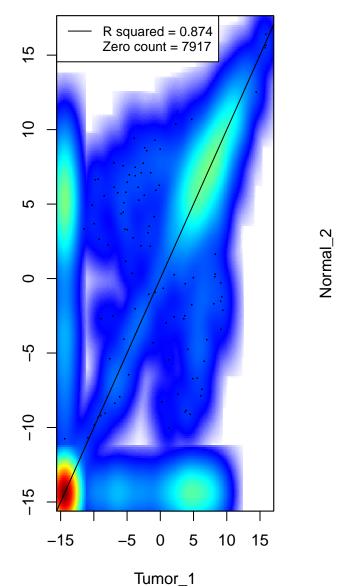
### Tumor\_2 vs Normal\_2

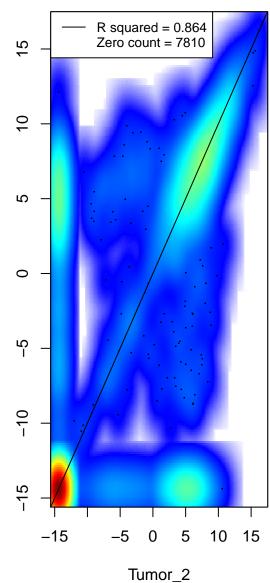


Normal\_1

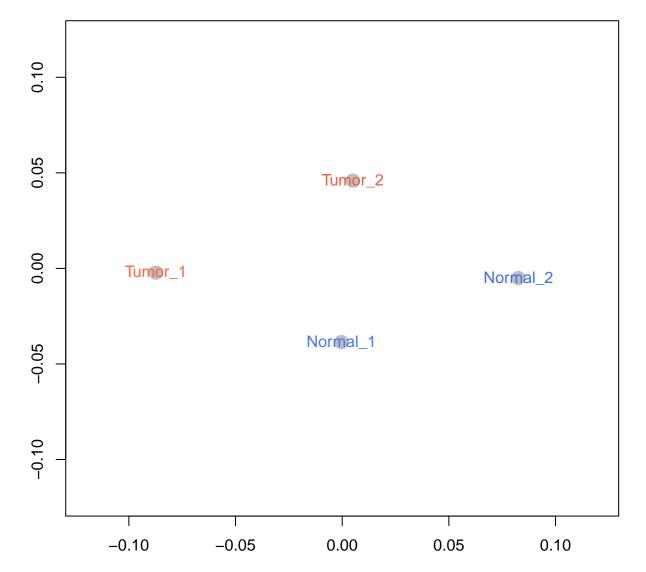
### Tumor\_1 vs Normal\_1

### Tumor\_2 vs Normal\_2

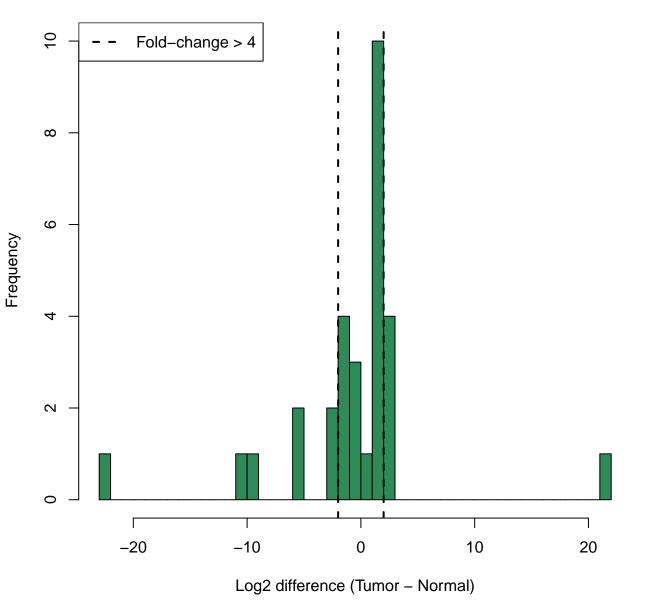




### MDS distance plot (all non-zero genes)



#### Distribution of differential expression values



#### **Tumor vs Normal FPKMs**

