

S1 Table

	DESeq2	NOISeq
Prefiltering count data (NOISeq function used for both)	<code>filtered.data</code> <code>method=1</code> <code>cv.cutoff=10</code> <code>cpm=5</code>	<code>filtered.data</code> <code>method=1</code> <code>cv.cutoff=10</code> <code>cpm=5</code>
Calculating differential expression statistics	<code>estimateSizeFactors</code> <code>estimateDispersions</code> <code>nbinomWaldTest</code>	<code>noiseqbio</code> <code>k=0.5</code> <code>norm=rpk</code> <code>lc=1</code> <code>r=50</code> <code>adj=1.5</code> <code>nclust=15</code> <code>aOper=0.9</code> <code>random.seed=12345</code> <code>filter=0</code>
Reporting differentially expressed genes	<code>results</code> <code>independentFiltering=FALSE</code> <code>padj<0.2</code> <code>abs(log2FoldChange)>0.5</code>	<code>degenes</code> <code>q=0.95</code>