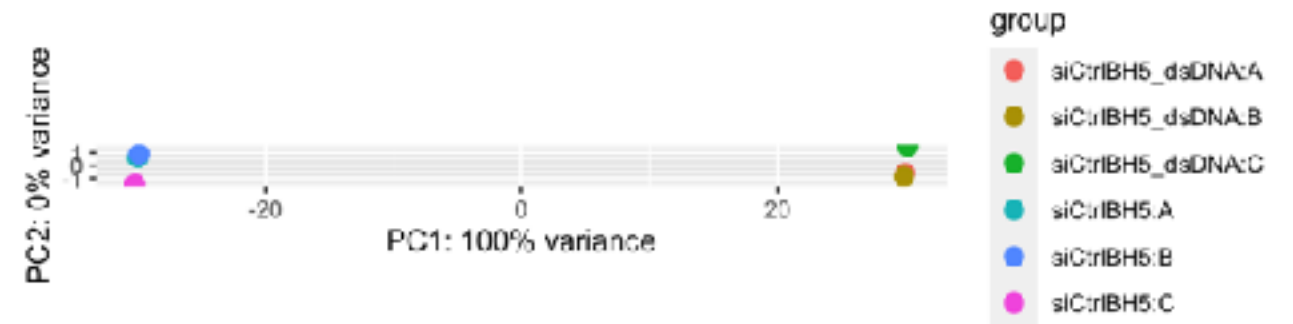
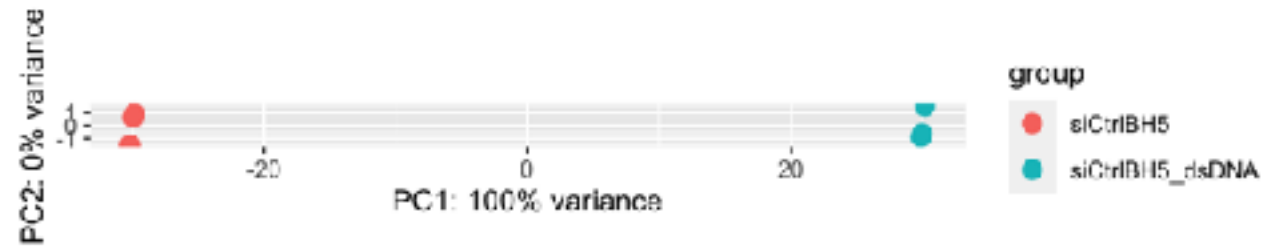
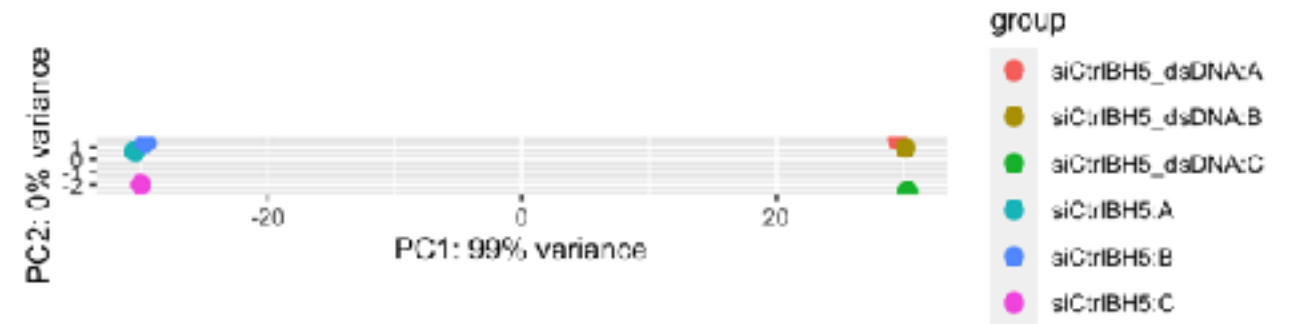
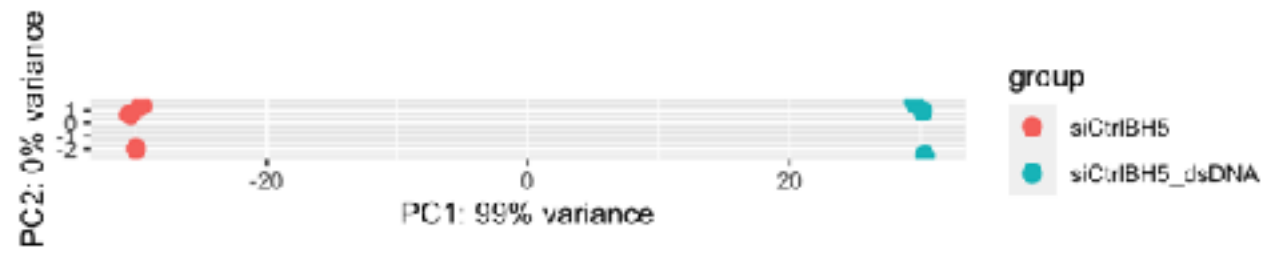
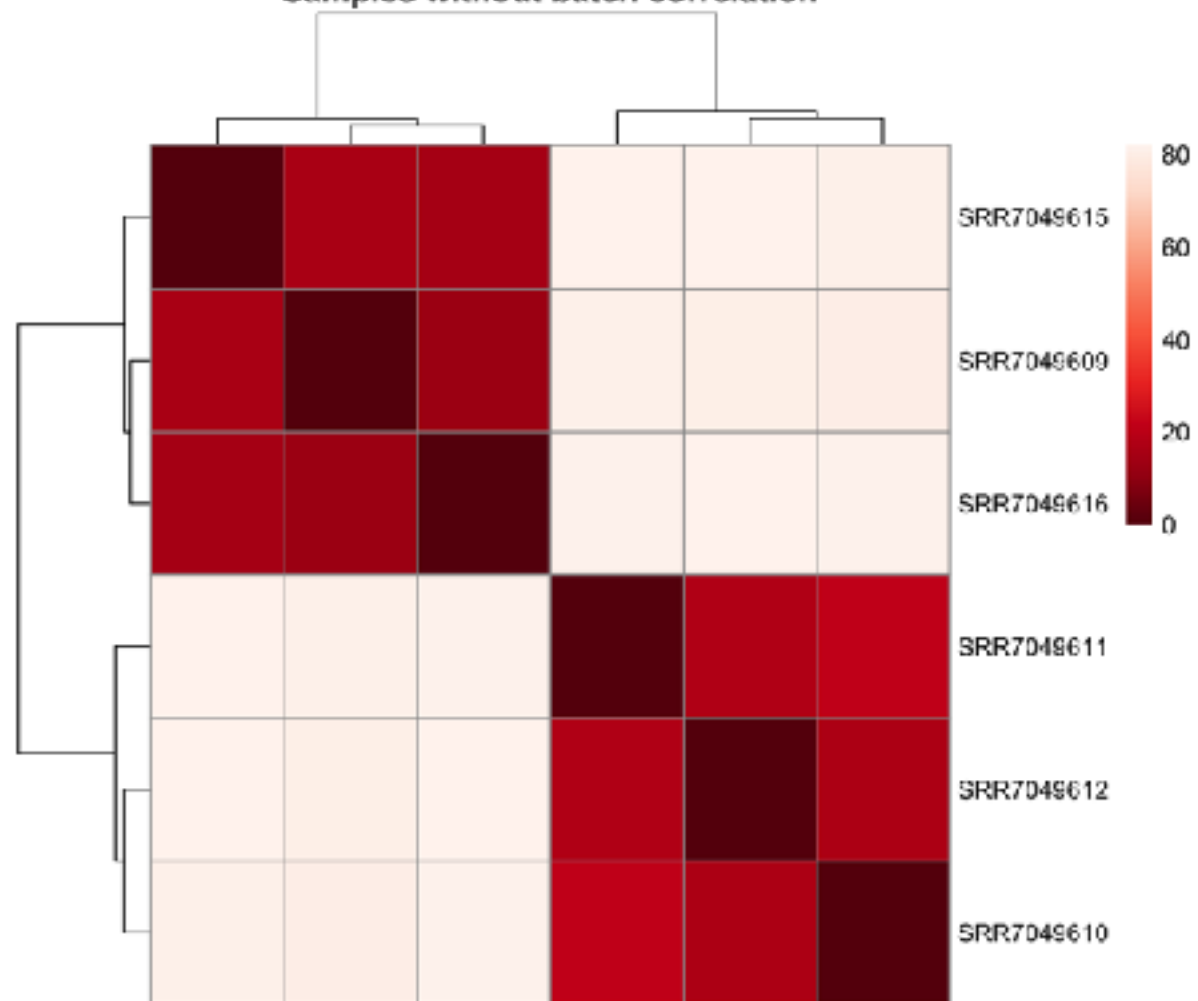


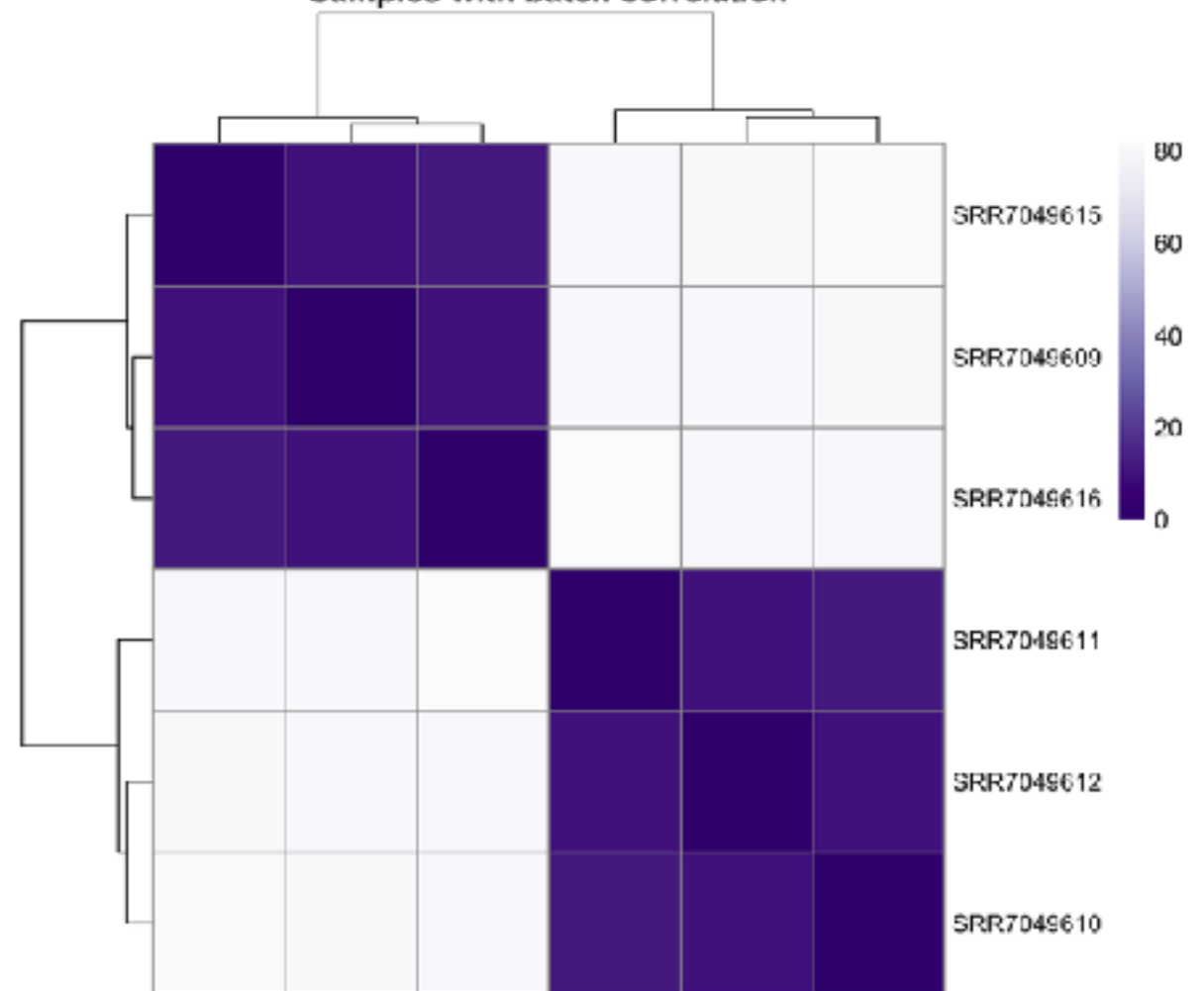
# featureCounts



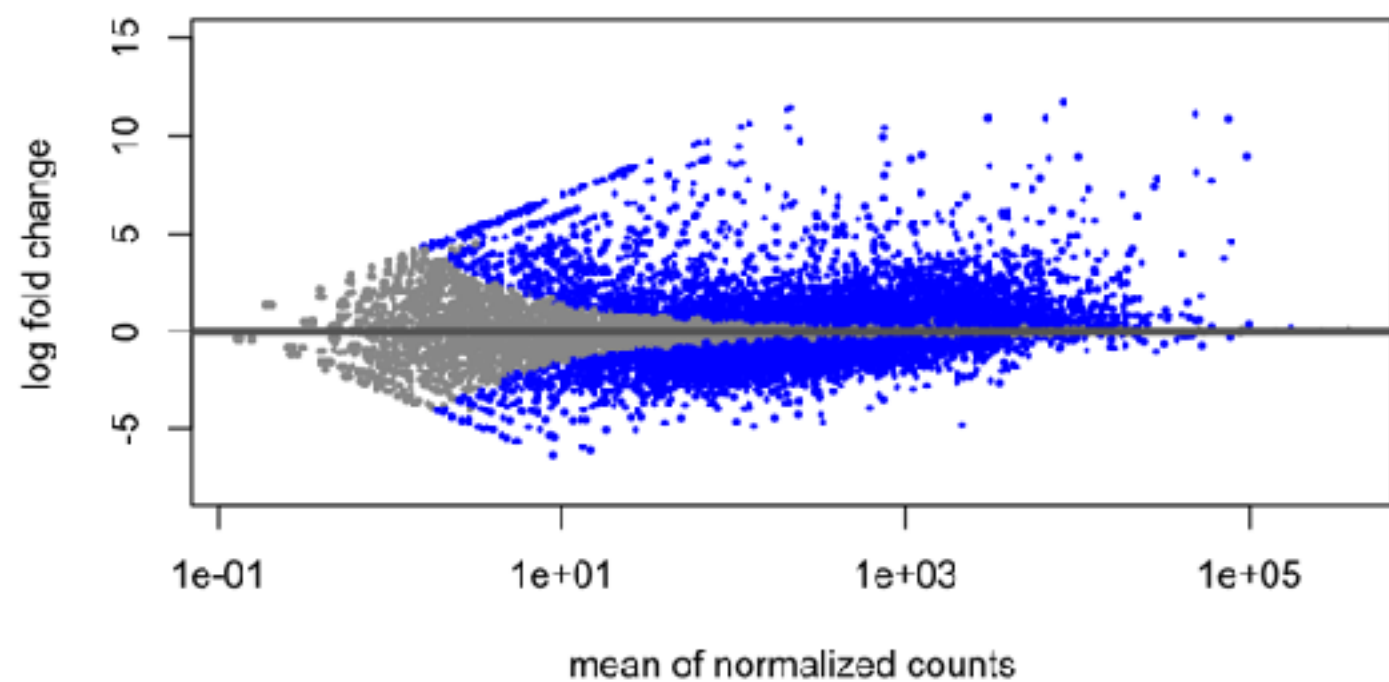
Samples without batch correlation



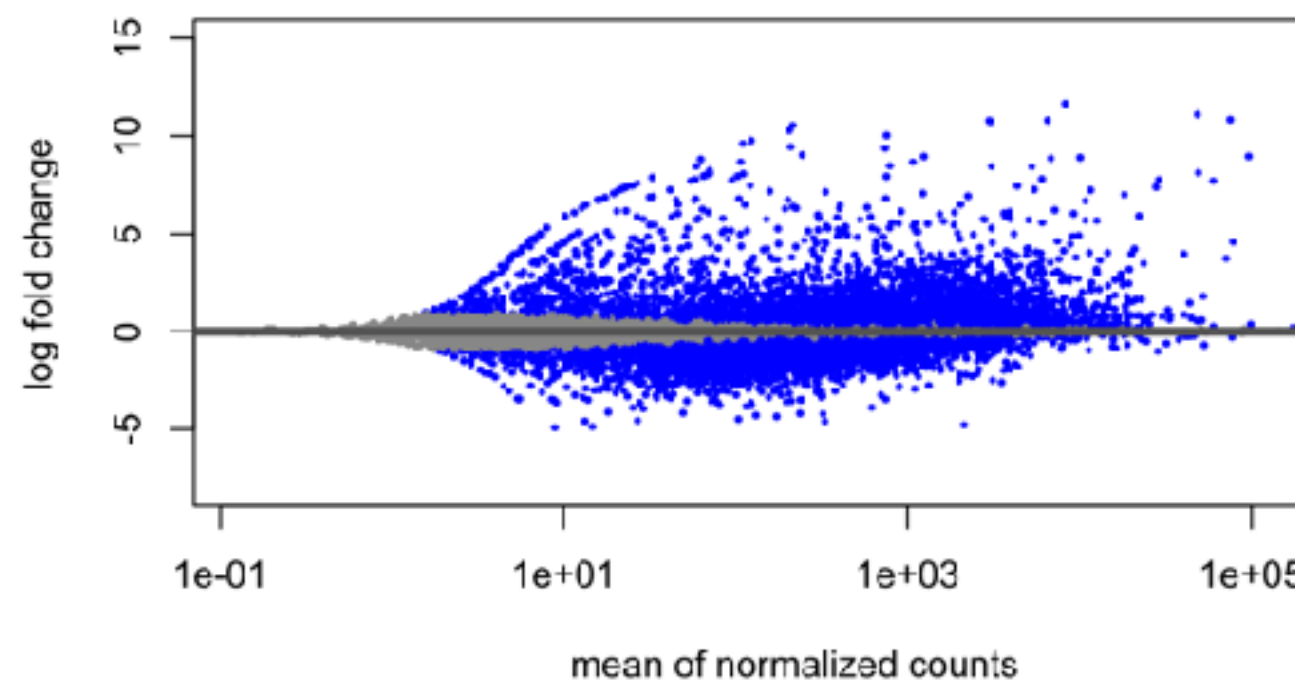
Samples with batch correlation



**Heteroskedasticity assessment**



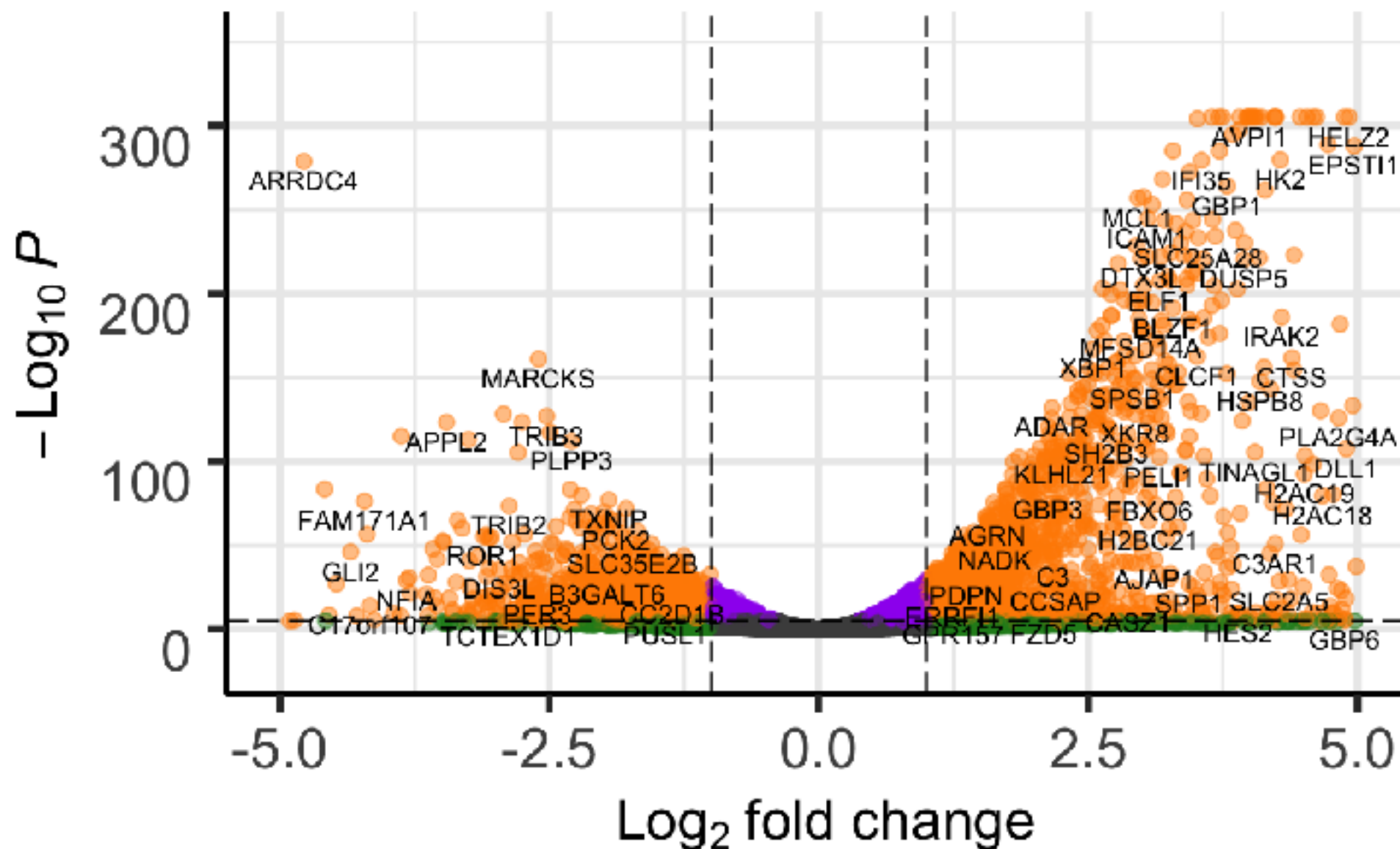
**Restored heteroskedasticity**



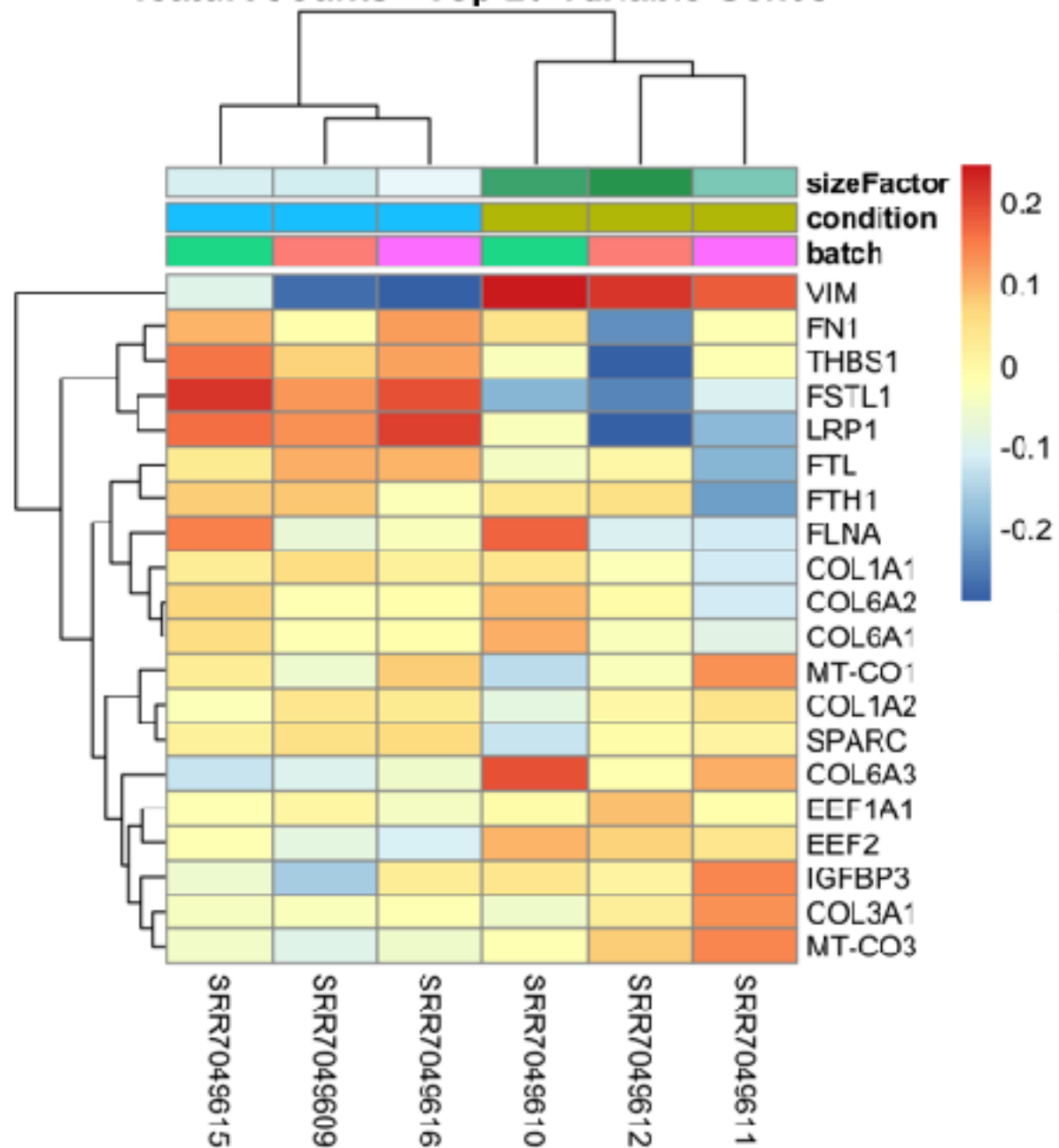
# featureCounts DESeq2 results

Differential Expression Analysis

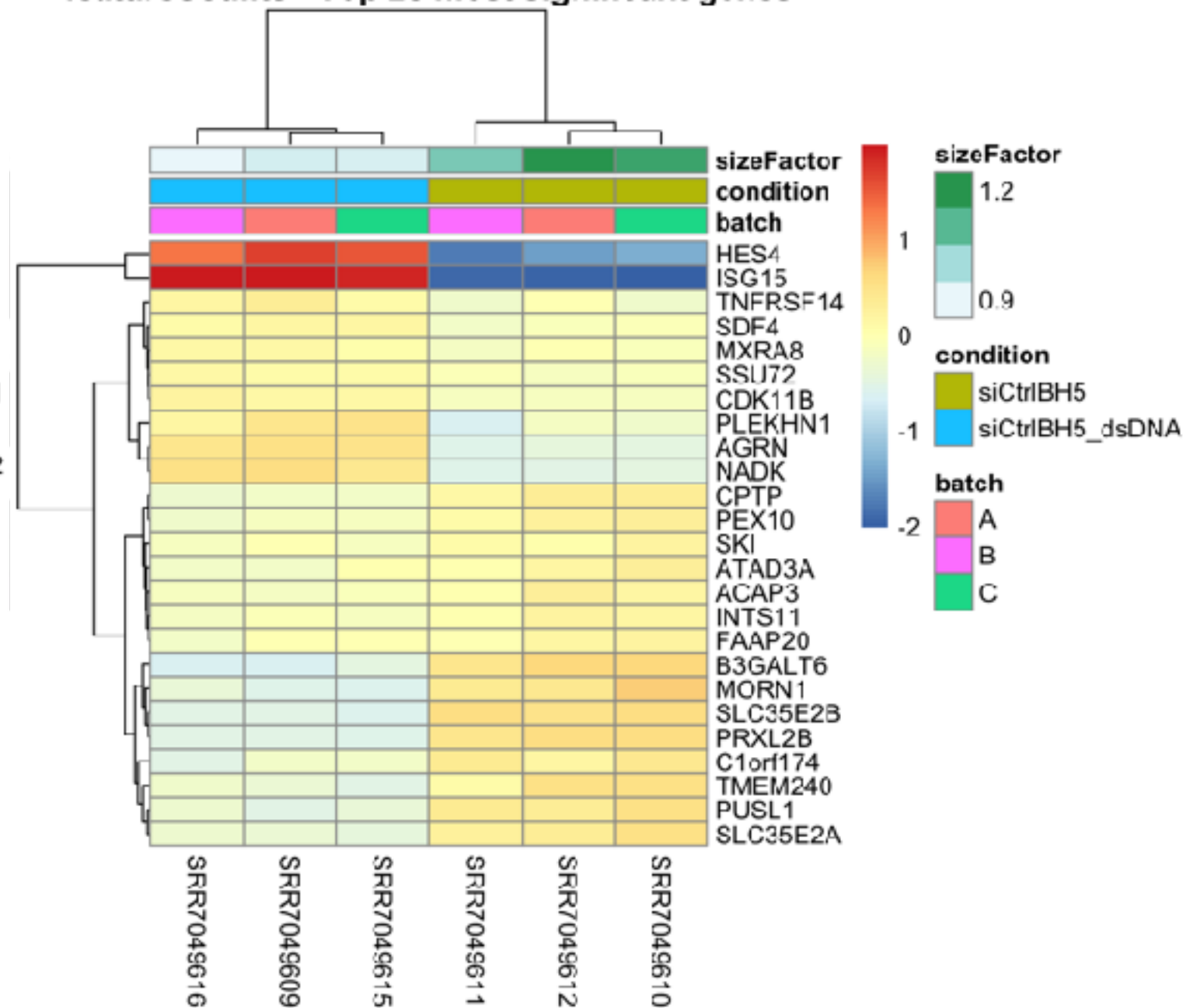
● NS ●  $\text{Log}_2$  FC ● p-value ● p – value and  $\text{log}_2$  FC



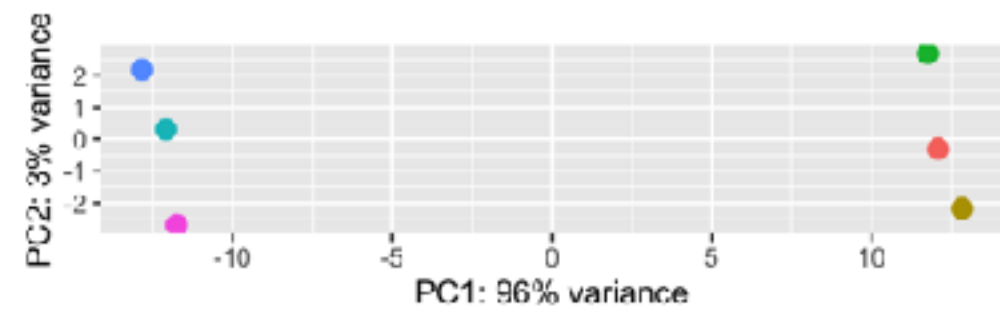
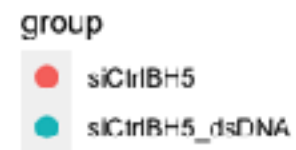
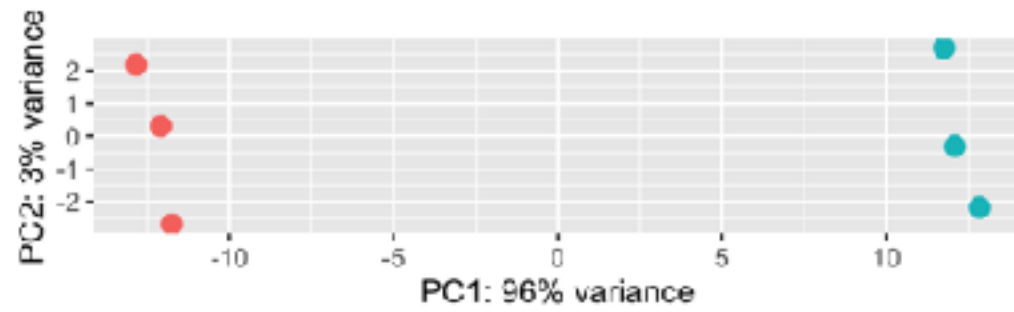
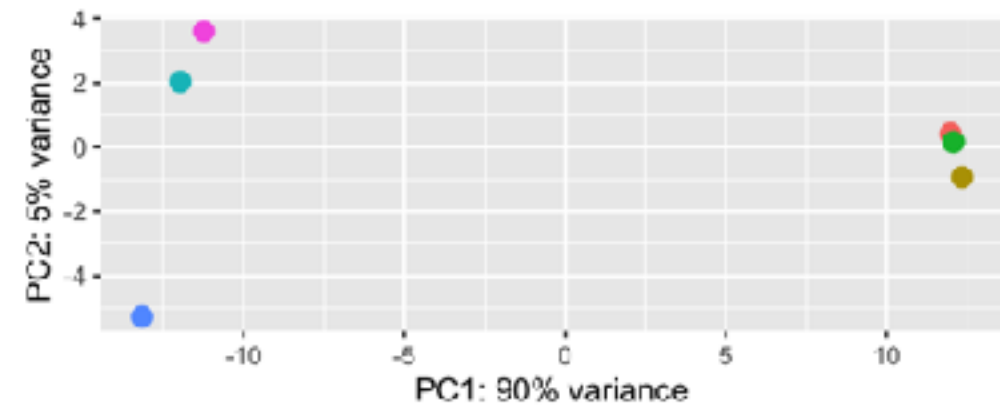
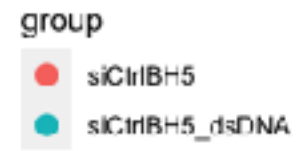
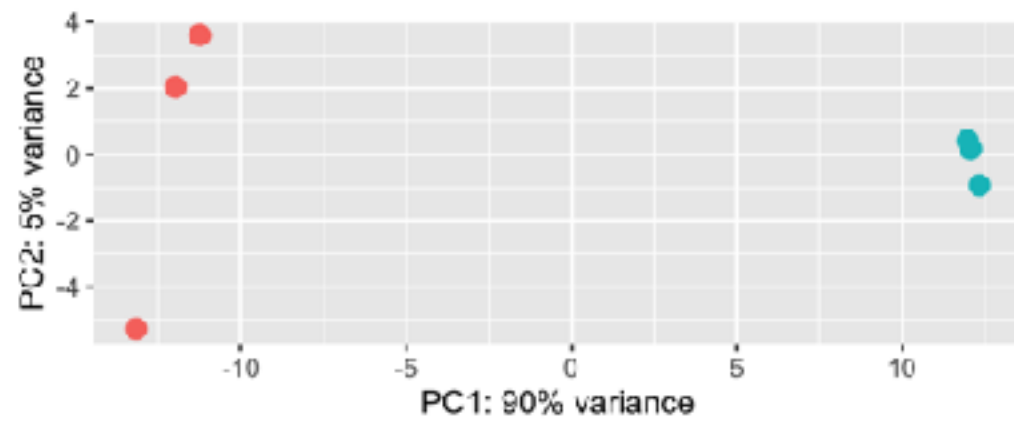
featureCounts - Top 20 Variable Genes



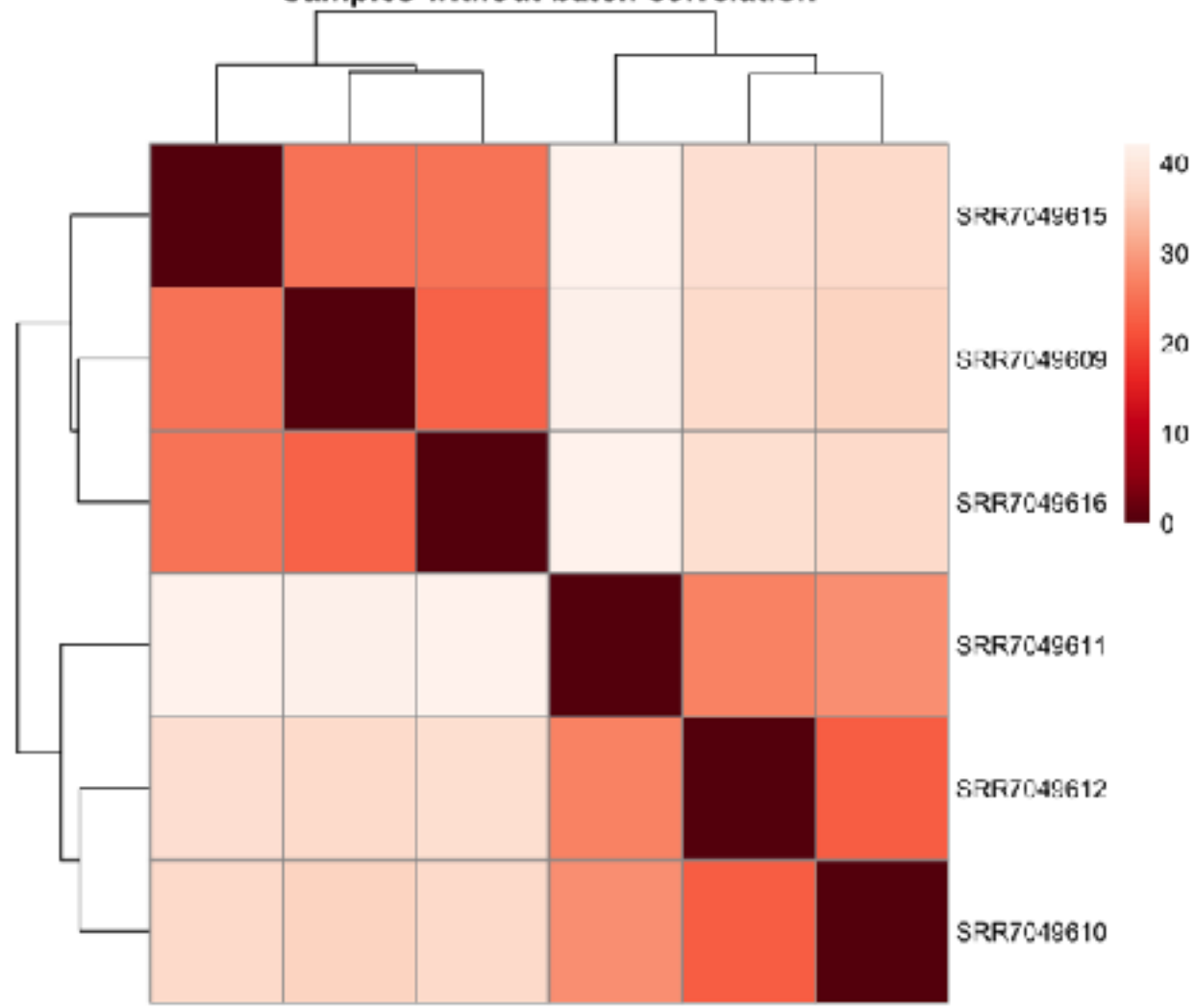
featureCounts - Top 25 most significant genes



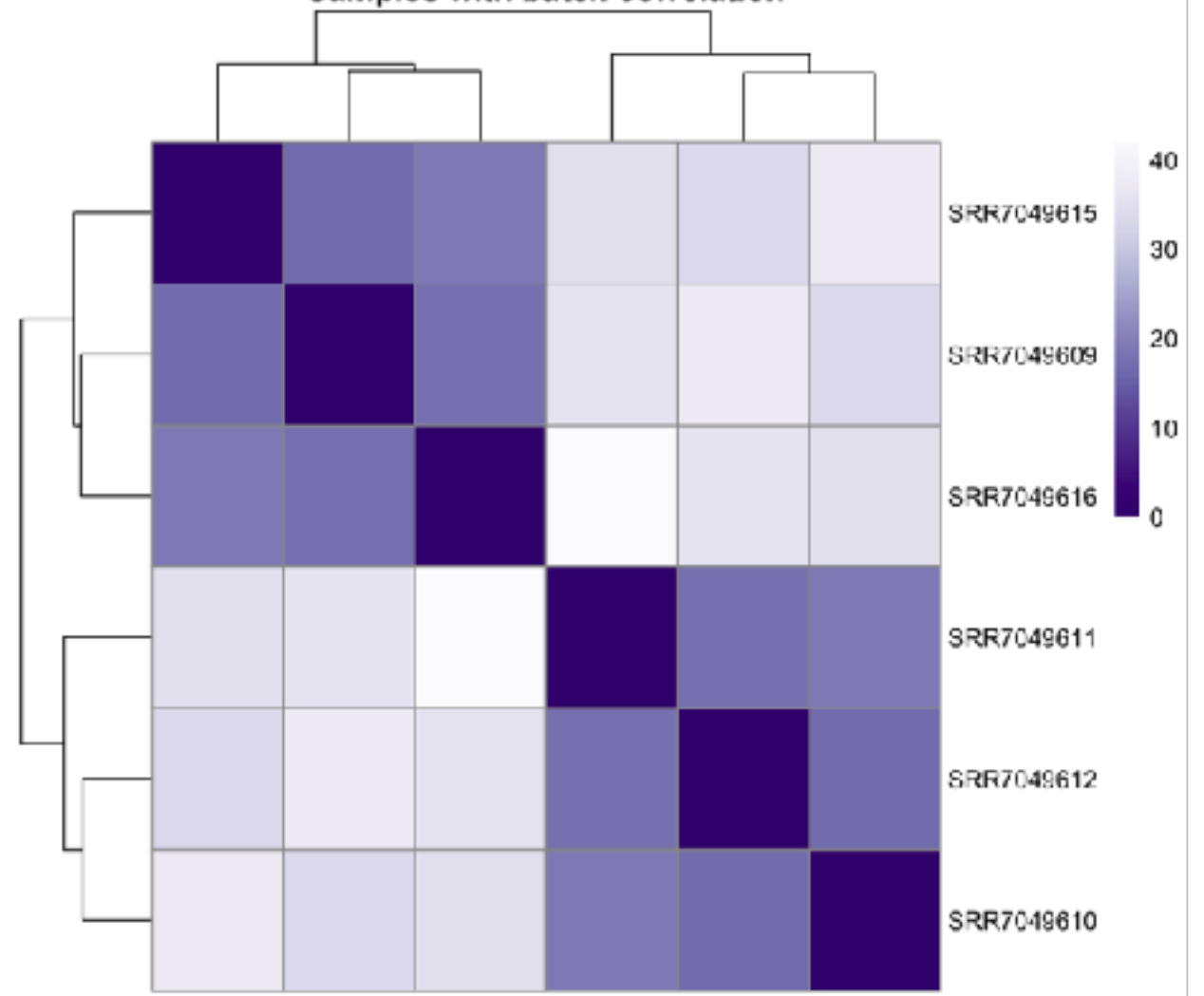
# kallisto



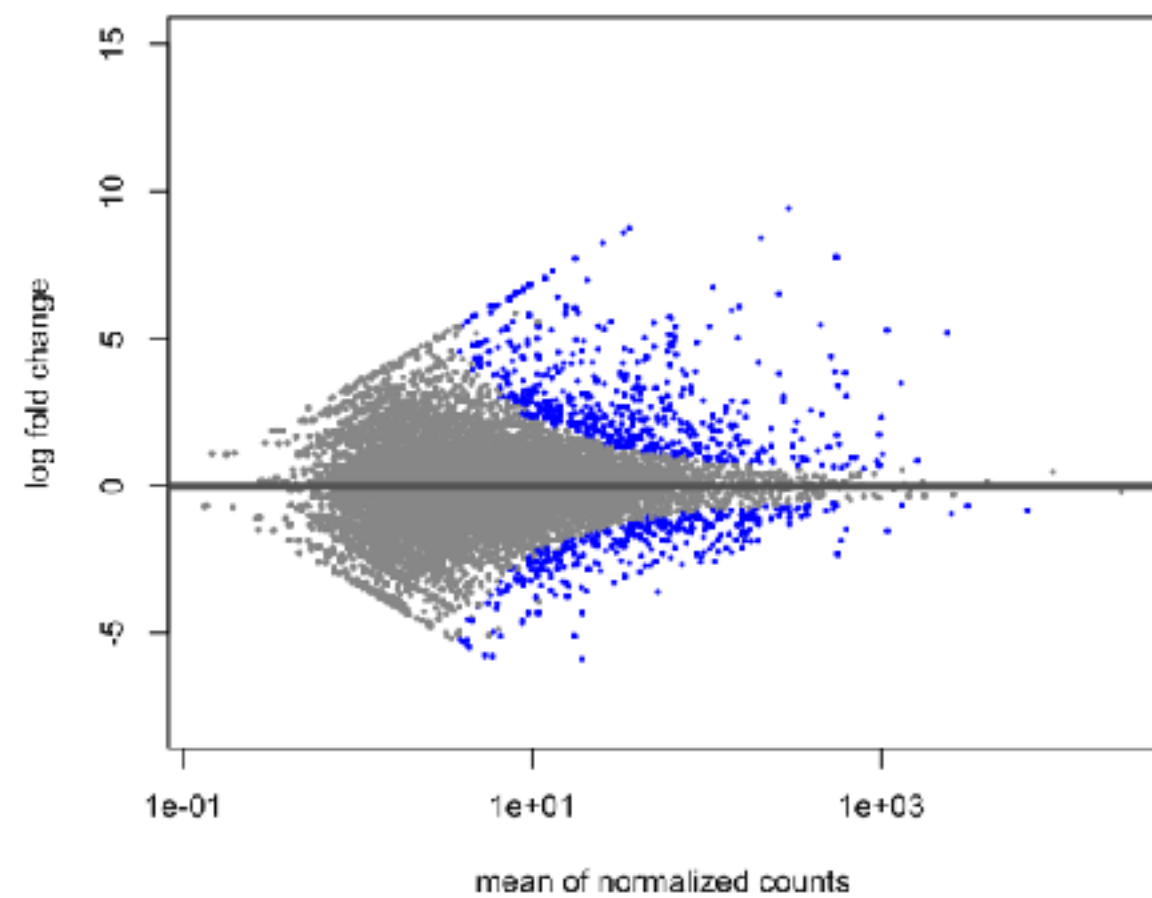
Samples without batch correlation



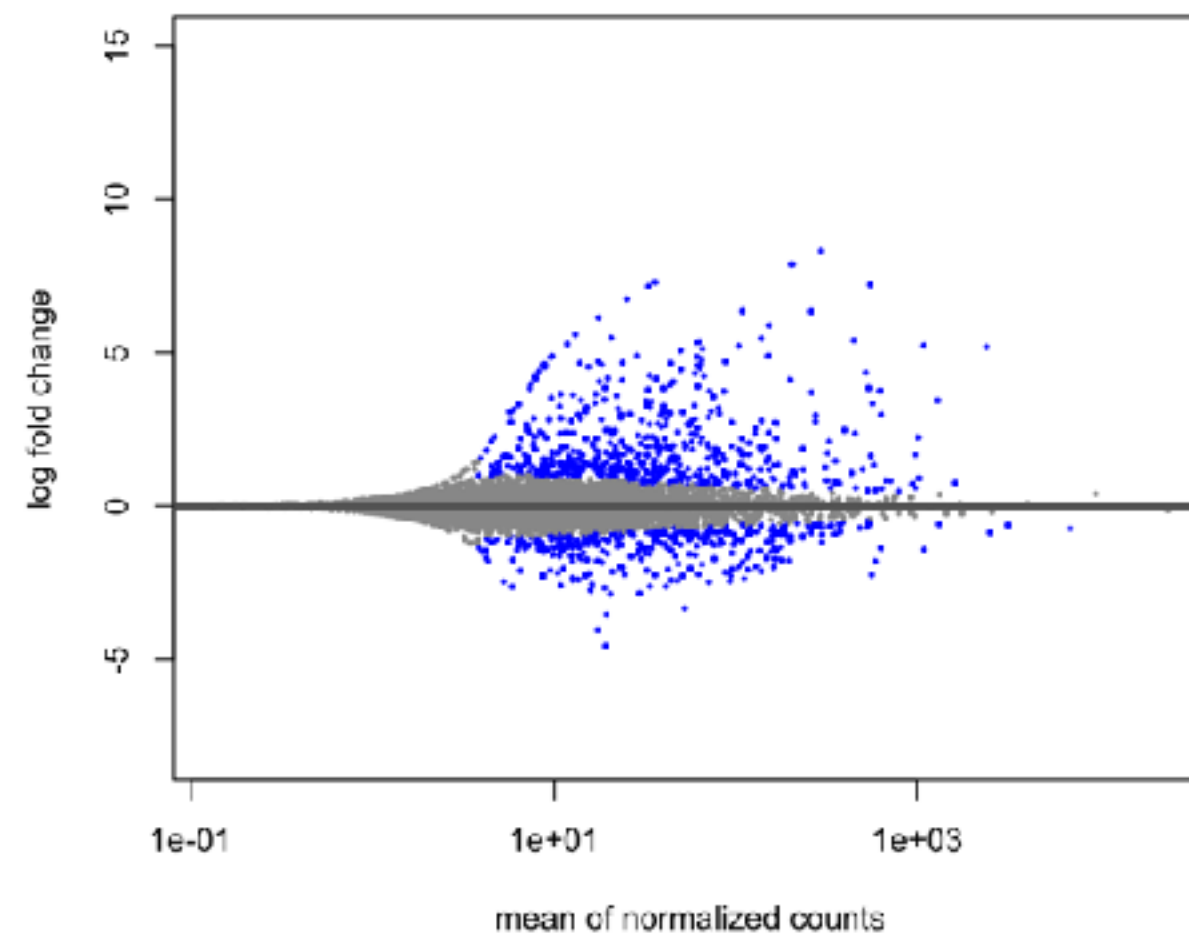
Samples with batch correlation



**Heteroskedasticity assessment**



**Restored heteroskedasticity**

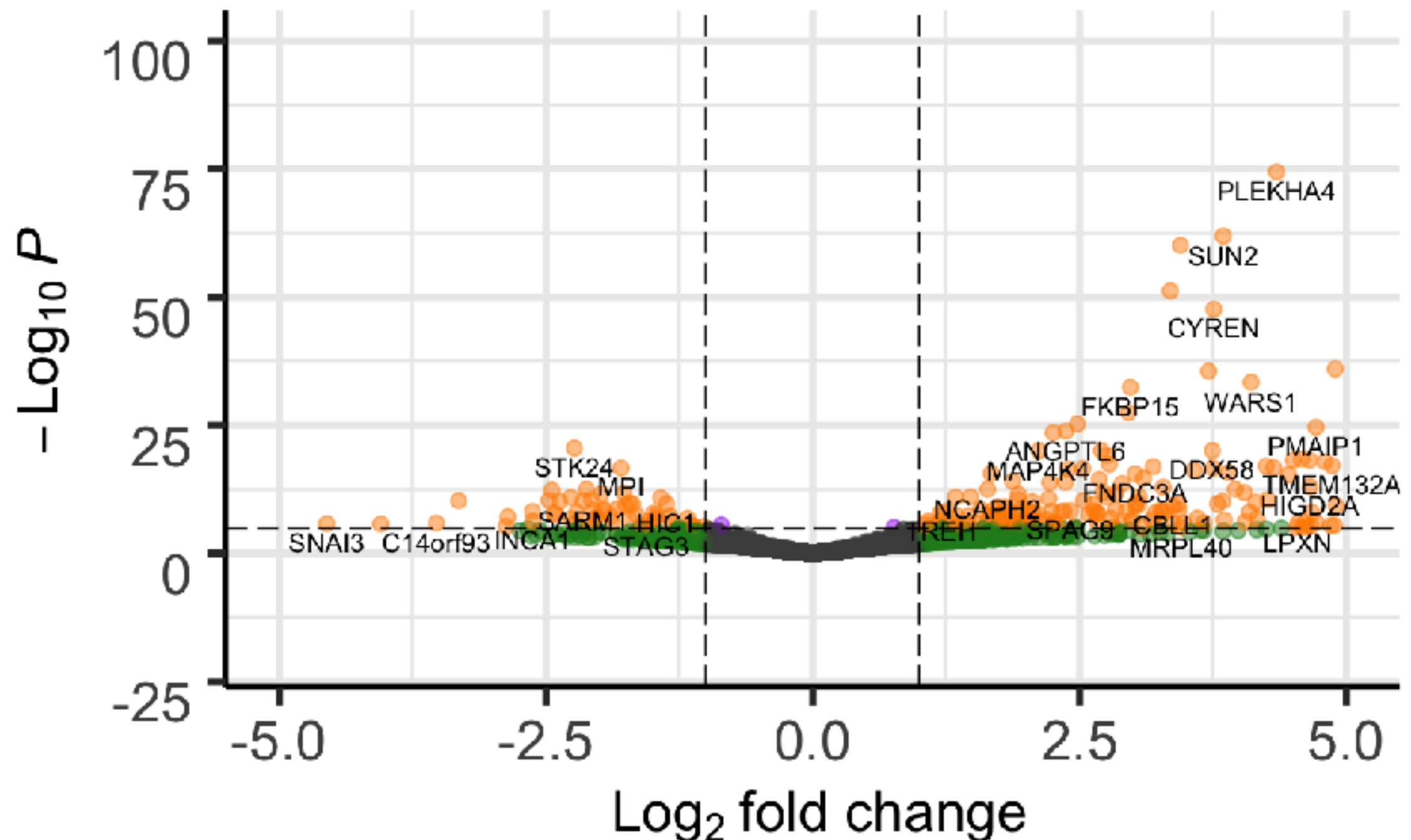




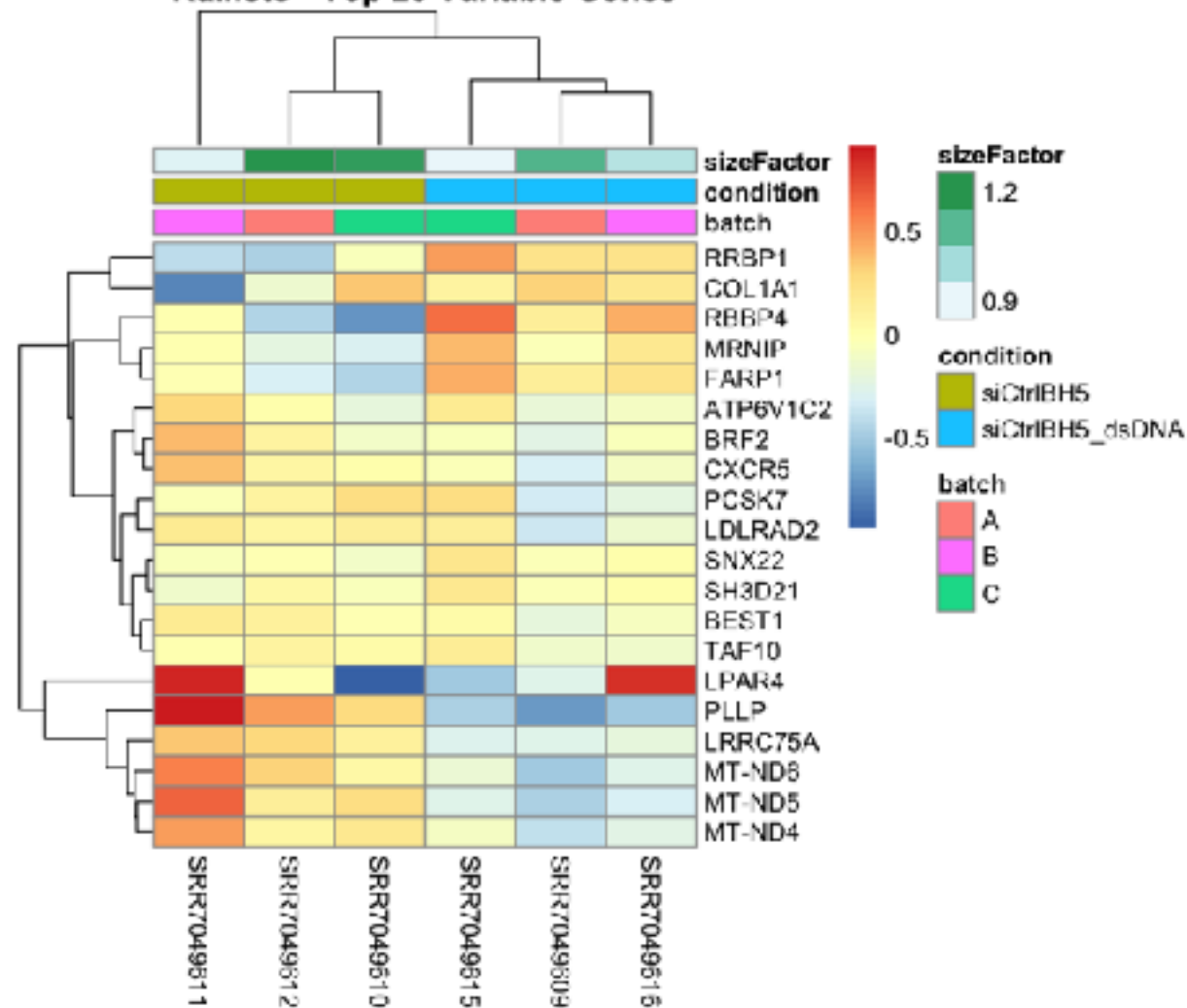
# Kallisto DESeq2 results

Differential Expression Analysis

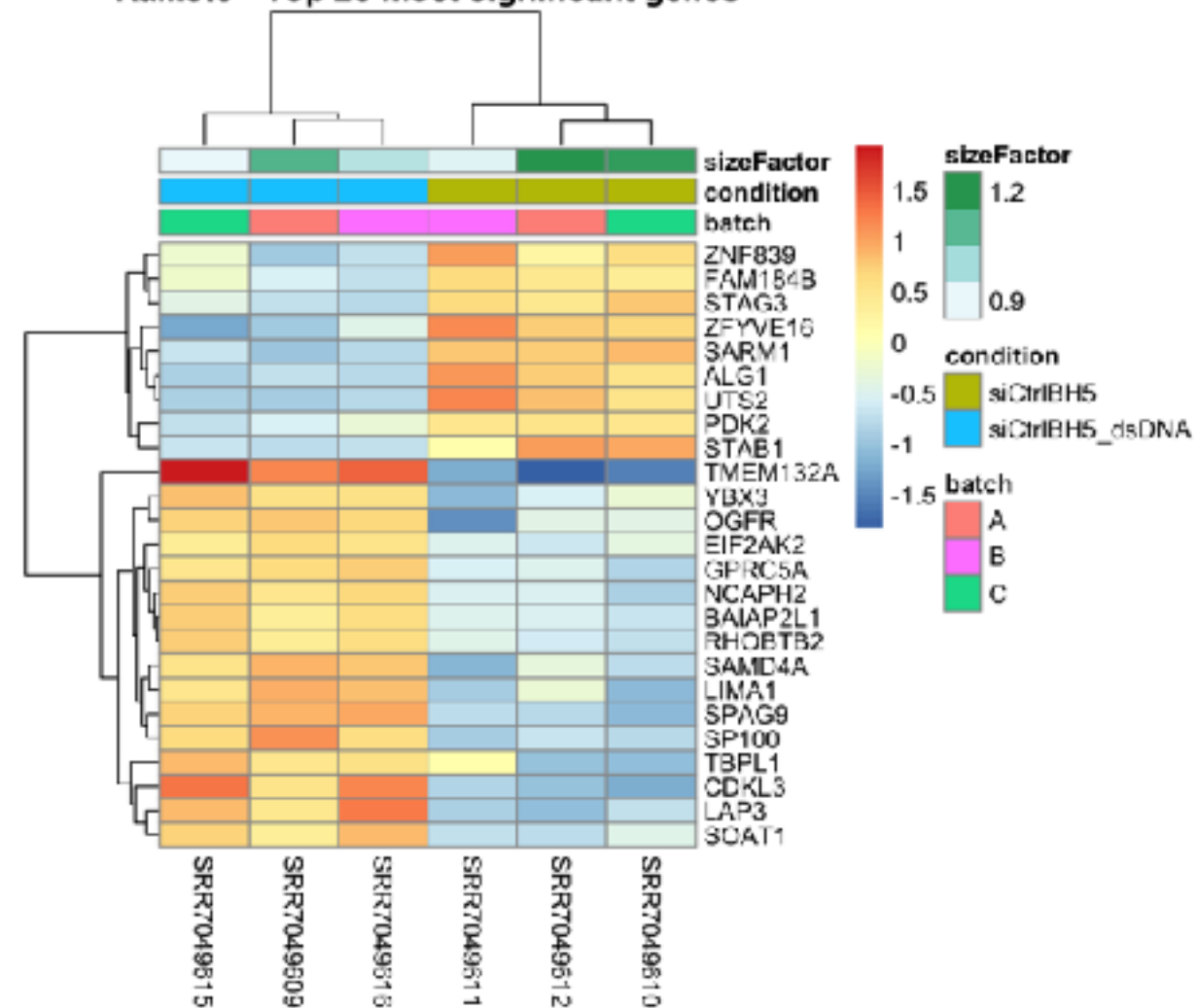
● NS ●  $\text{Log}_2$  FC ● p-value ● p – value and  $\text{log}_2$  FC



Kallisto - Top 20 Variable Genes



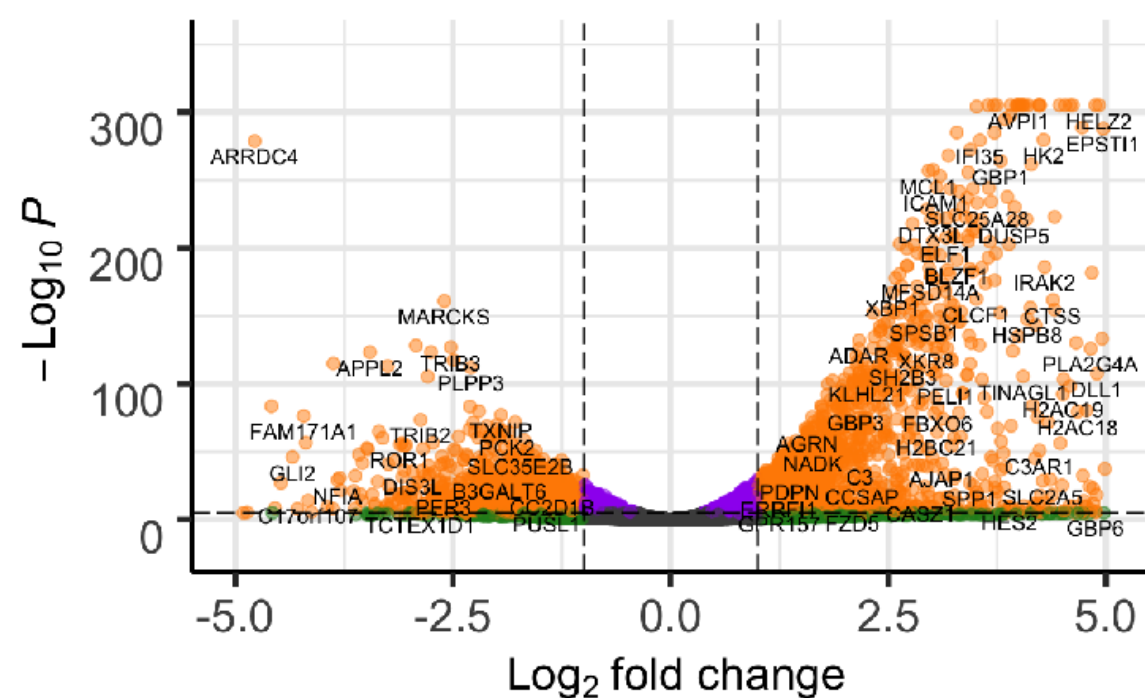
Kallisto - Top 25 most significant genes



## featureCounts DESeq2 results

Differential Expression Analysis

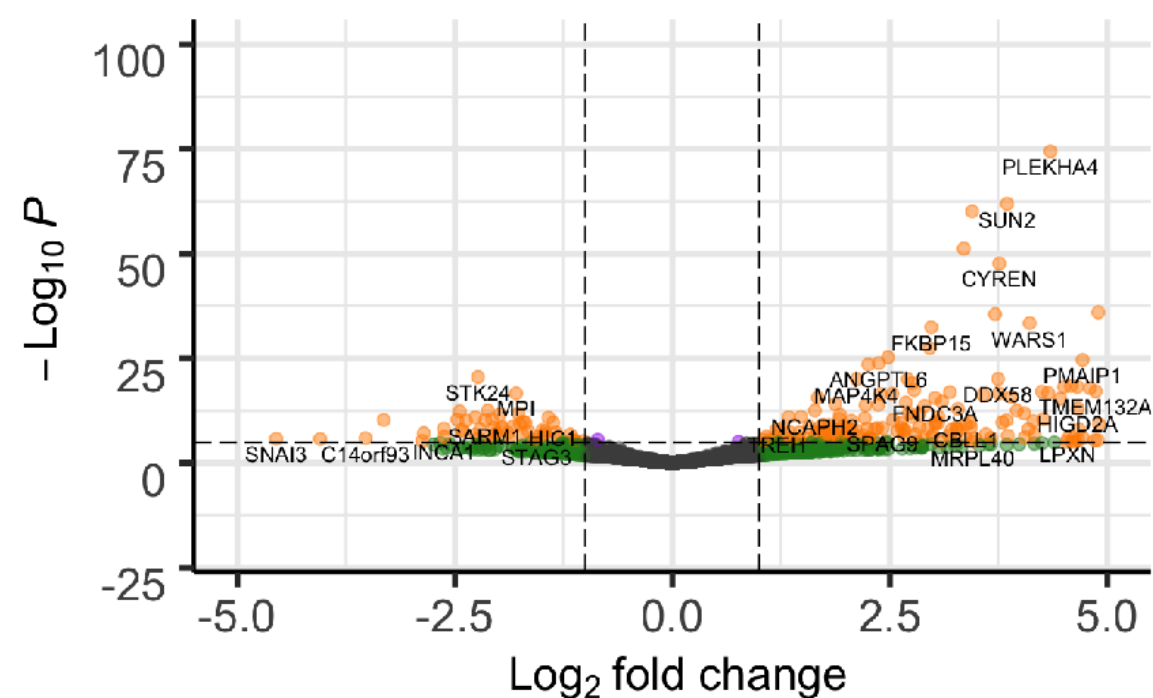
● NS ● Log<sub>2</sub> FC ● p-value ● p-value and log<sub>2</sub> FC



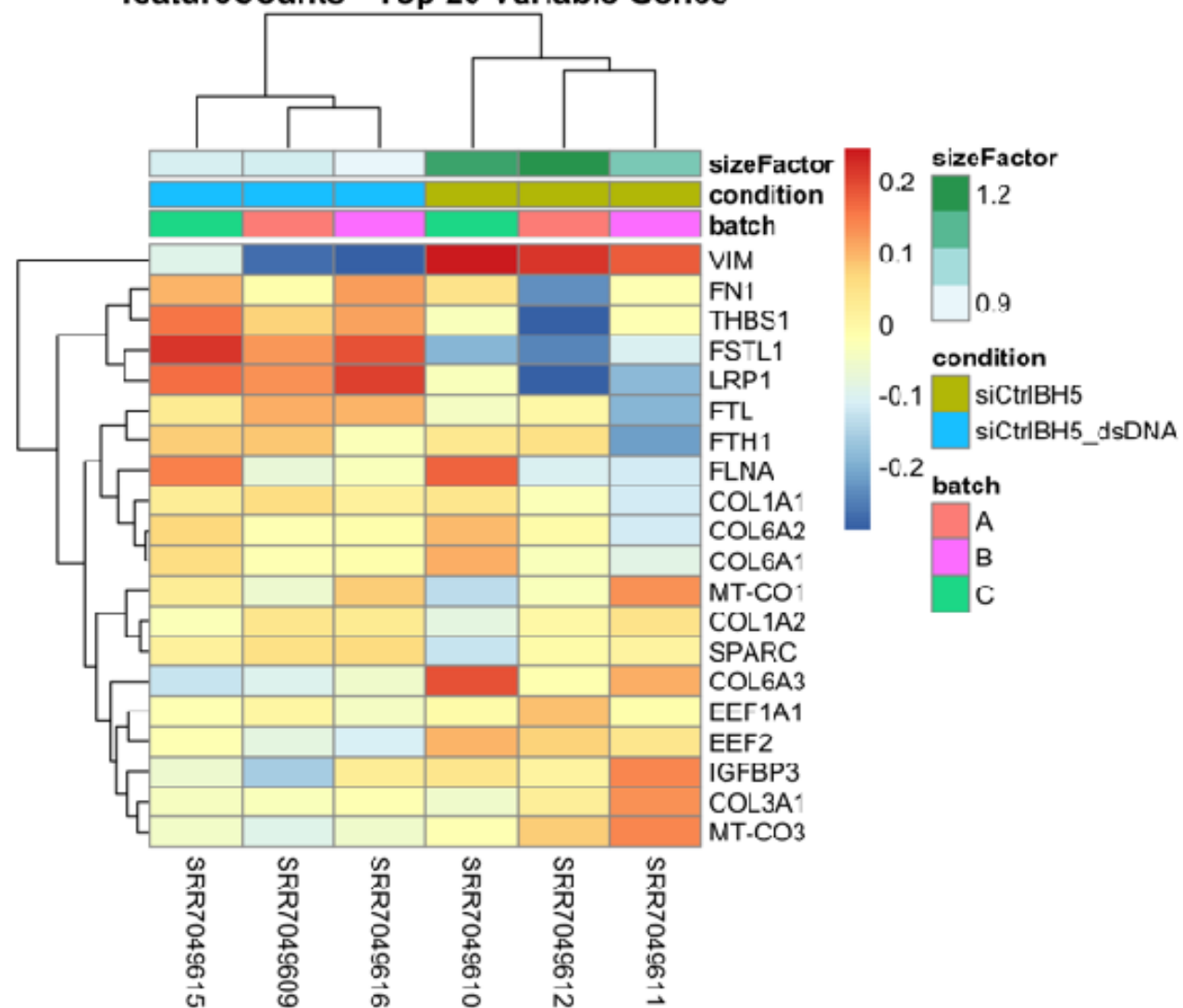
## Kallisto DESeq2 results

Differential Expression Analysis

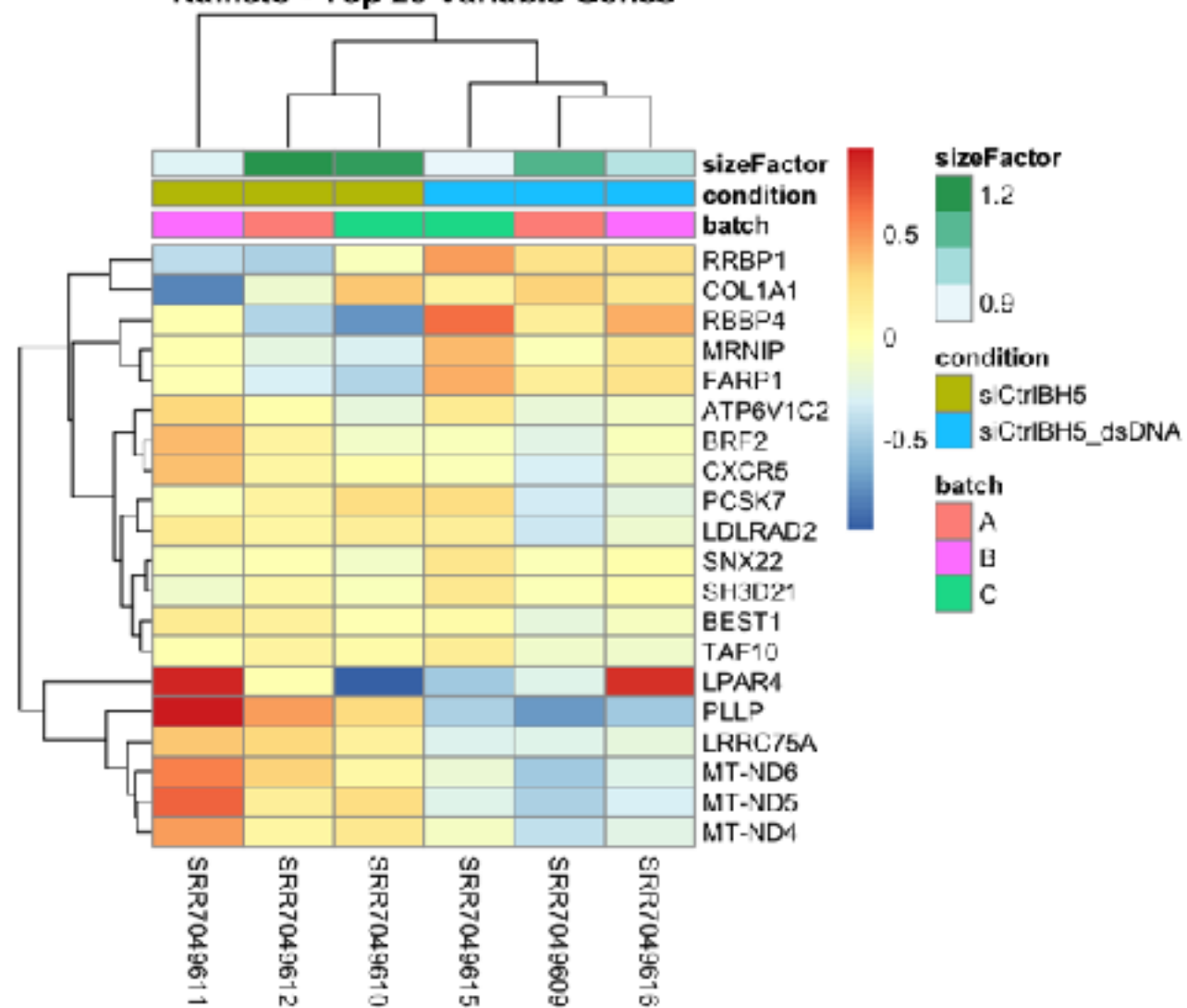
● NS ● Log<sub>2</sub> FC ● p-value ● p-value and log<sub>2</sub> FC



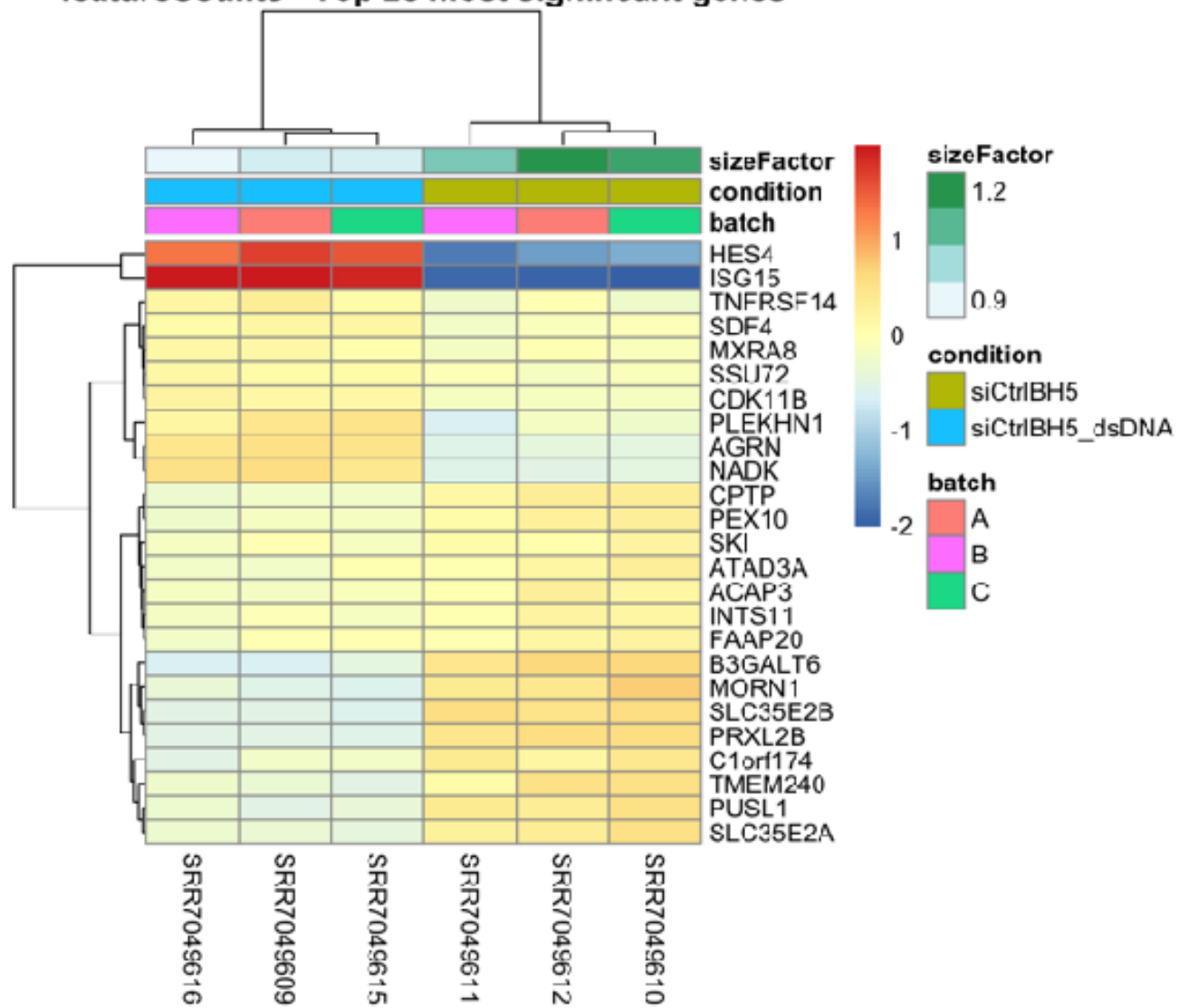
featureCounts - Top 20 Variable Genes



Kallisto - Top 20 Variable Genes



featureCounts - Top 25 most significant genes



Kallisto - Top 25 most significant genes

