Deliverable 2

We used DESeq2 package in r to normalize the count files obtained to generate the list of differentially expressed genes

The statistical methods used for obtaining the differentially expressed genes include:

- P adjusted value (transformation of P value after accounting for multiple testing) – DESeq2 adjust p value from wald test using benjamini and hochberg method (BH-adjusted p values) which is presented in the column of padj in the results object. **This helped us control any false discovery rate.**
- Log2 fold change

Statistical Method	Cut-off selected
Log2 fold change	{Lesser than -2 for downregulated genes, Greater than 2 for upregulated genes}
Padjusted	Lesser than 0.05