SUPPLEMENTAL MATERIAL

Supplemental Tables S1 and S2 published separately

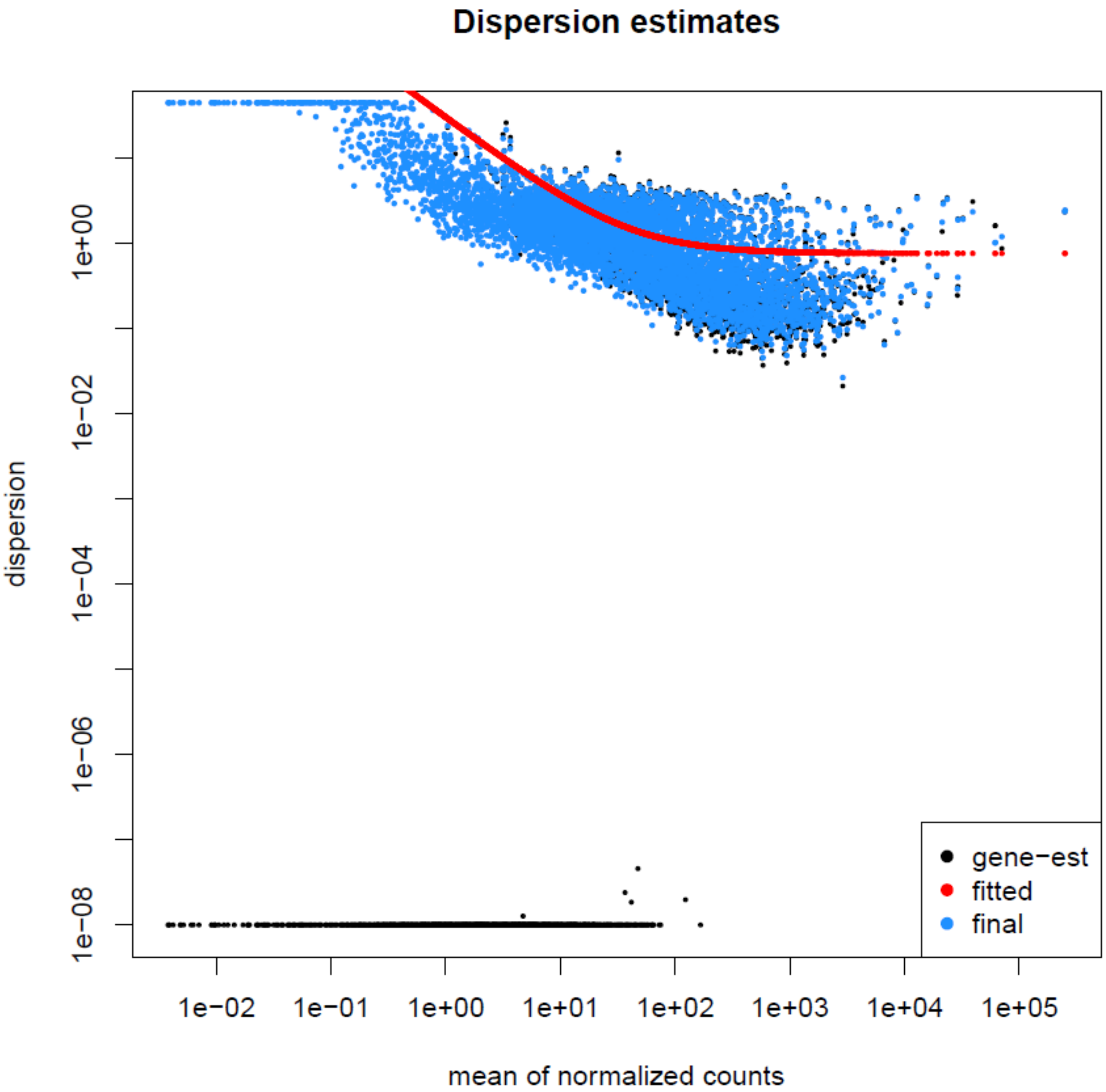

FIG. S1 Dispersion plot by the mean of normalized counts for each gene generated by DESeq2 fits the assumption of the tool. Black dots- estimate of dispersion of each gene expression within the data set. Blue dots- actual gene expression dispersion. Red line-the assumption of DESeq2 is that the collapsed points will center around the fitted line in terms of dispersion and mean.

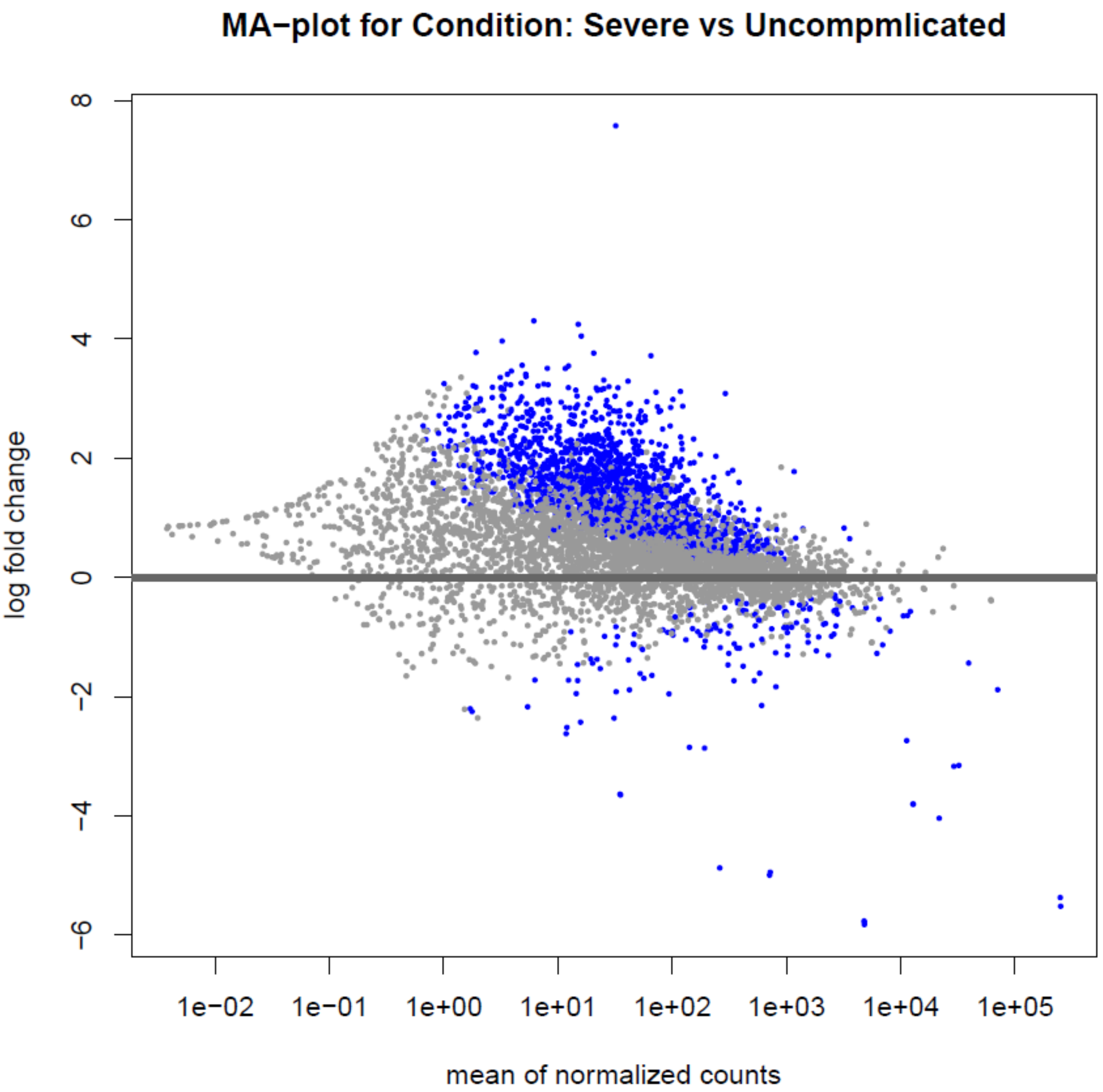

FIG. S2 MA plot. Plots the base 2 log fold change (M=$\log_2(FC_{upregulated}/FC_{downregulated})$ versus the mean of the feature counts, normalized for sample size (A= ½ $\log_2(n_{upregulated})(n_{downregulated})$. Blue points indicate genes which are significantly differentially expressed, at the $p \leq 0.1$ (DESeq2) level.