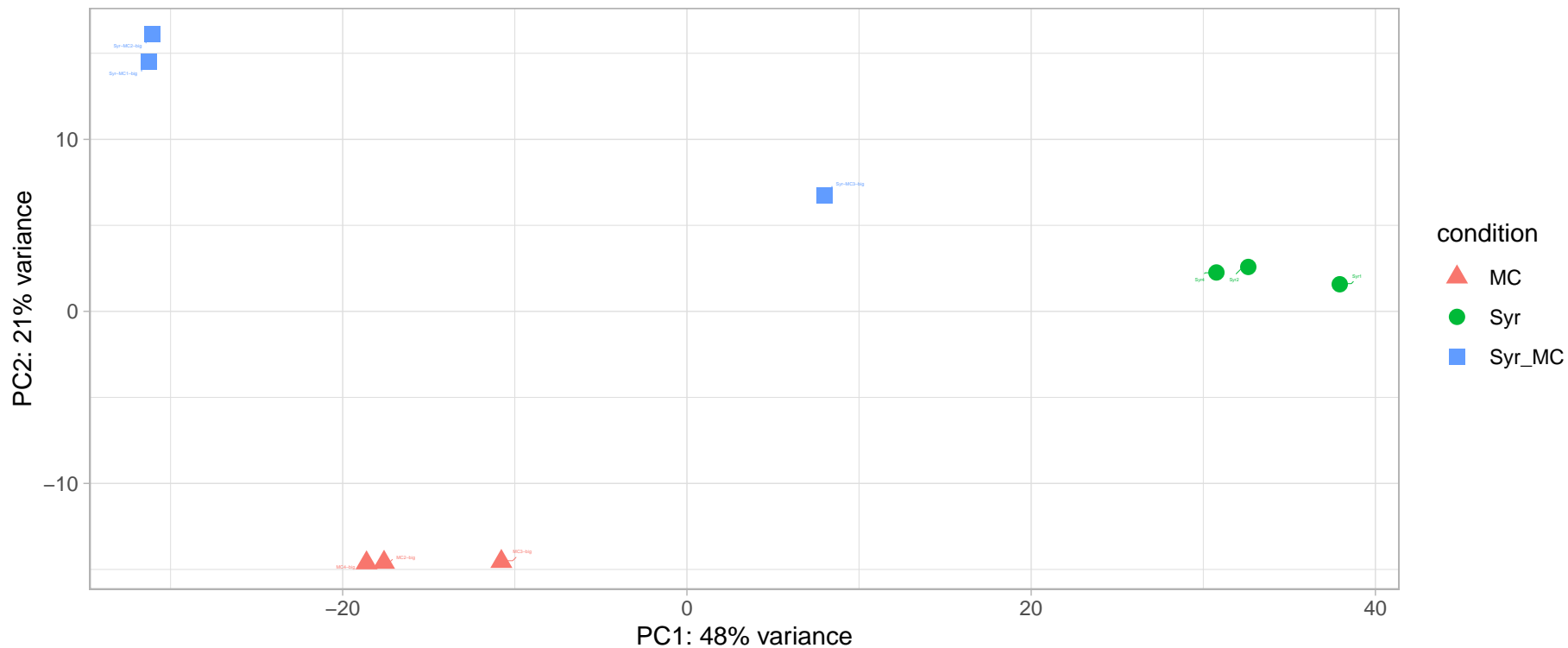


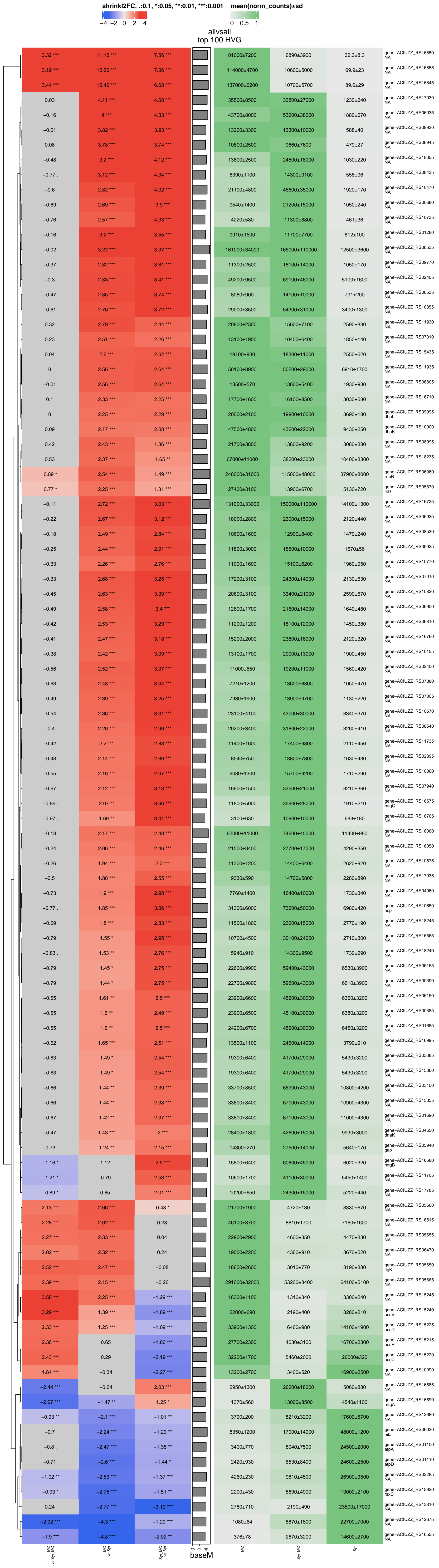
vsd PCA of the top 1000 HVGs



% sdev

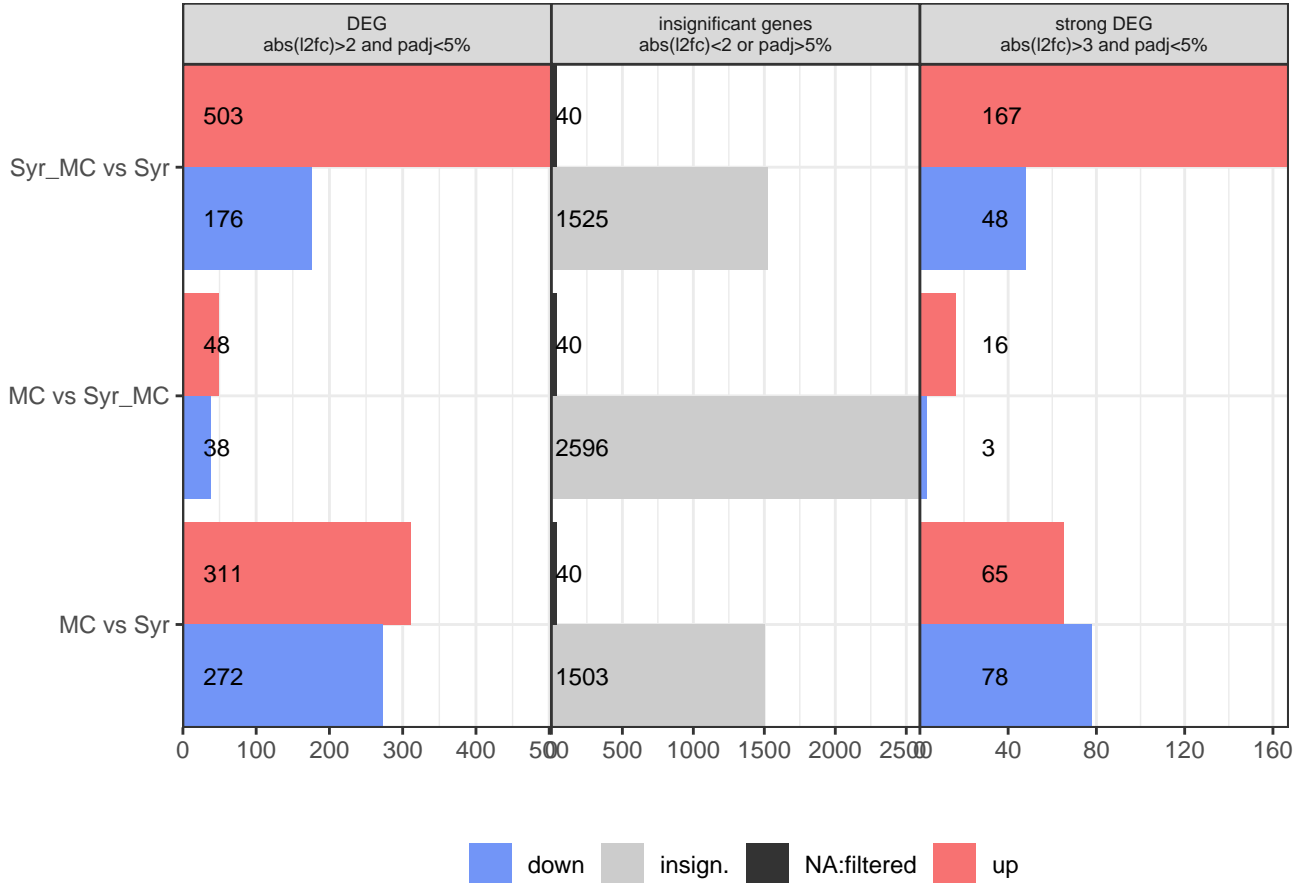
50  
40  
30  
20  
10  
0





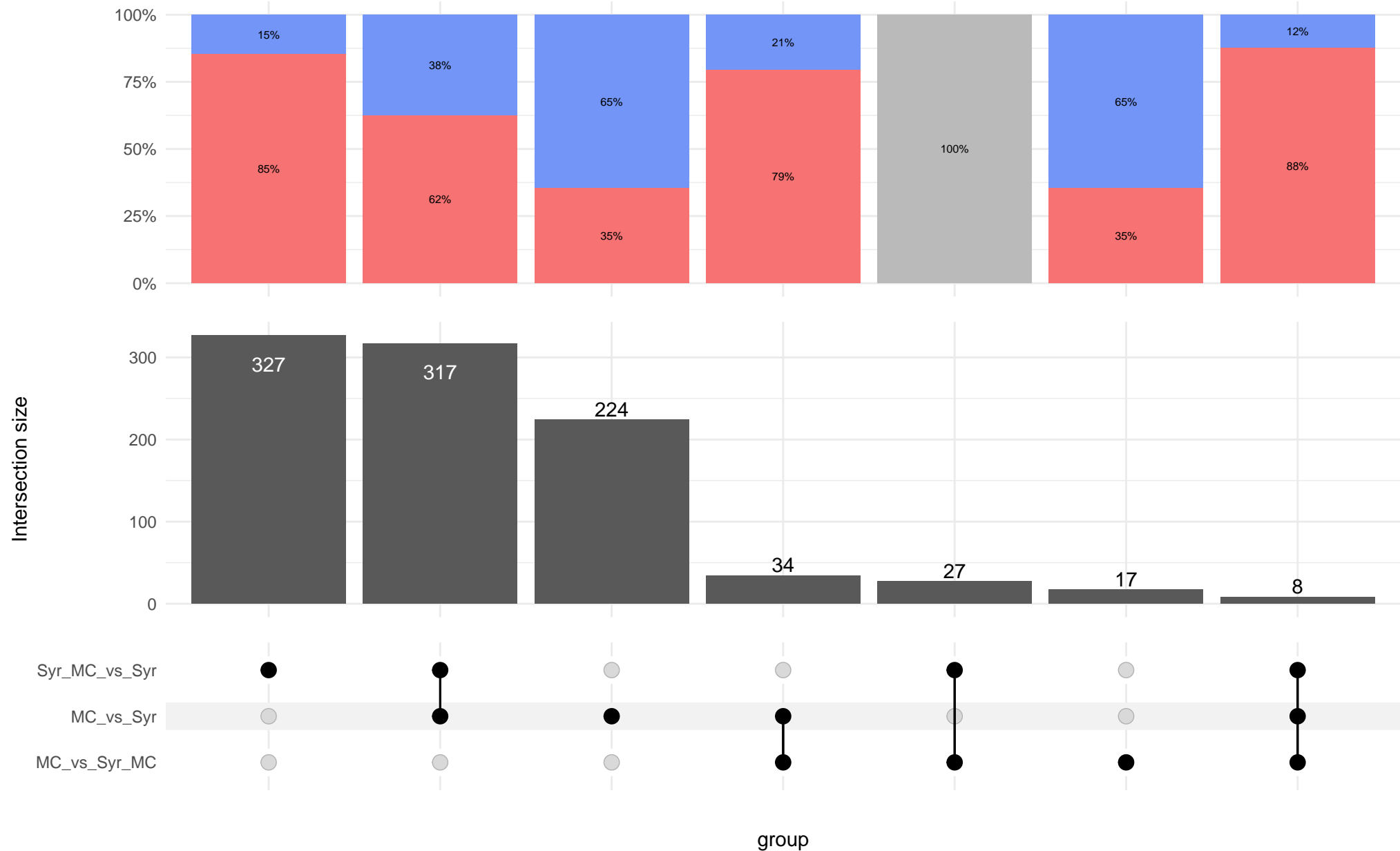
# Overview, l2fcshrunk

## number of up/down regulated DEGs



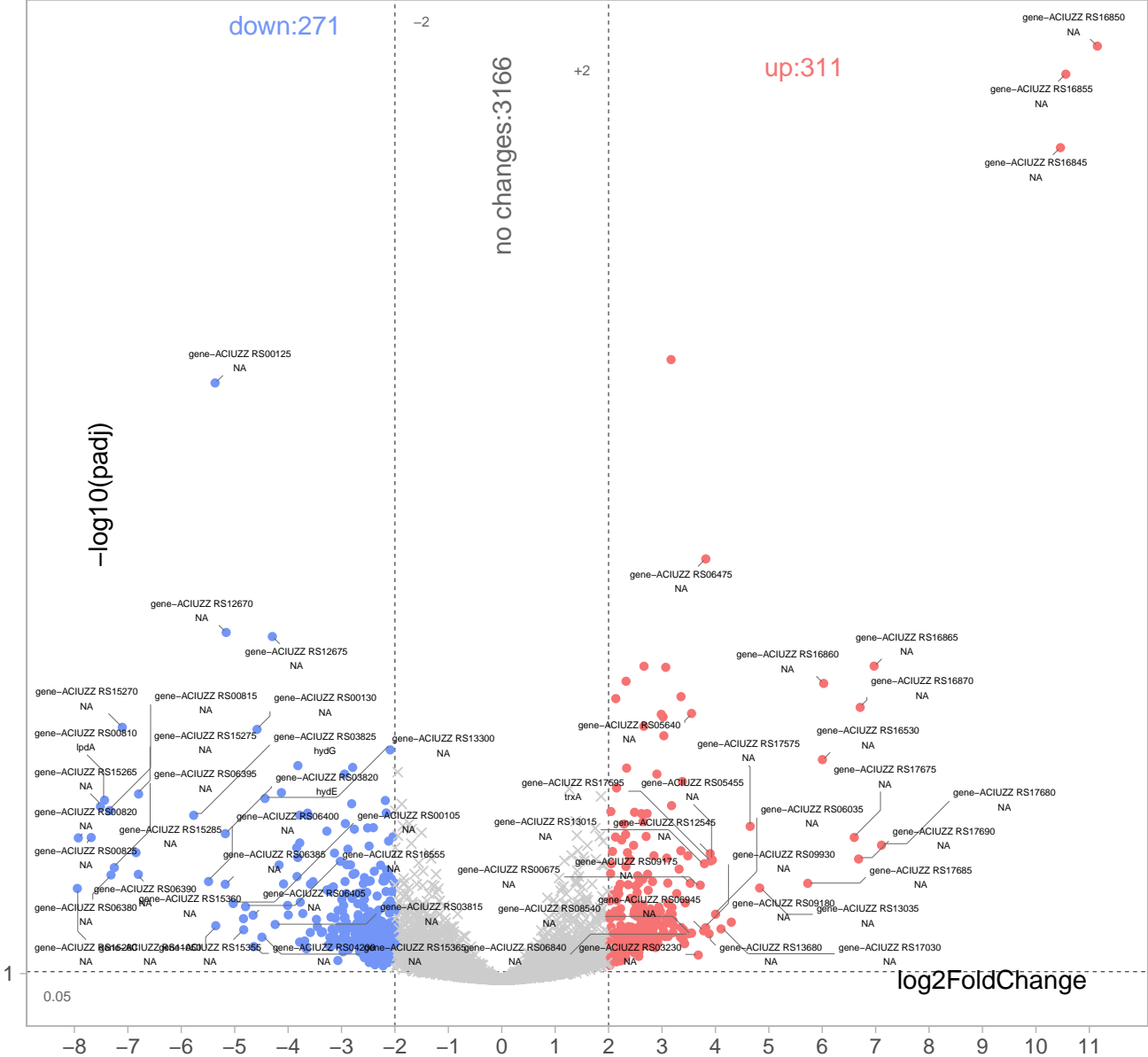
# UpSetR overlap of DEGs (abs(lfc)>2 & padj<5%), l2fcshrunk

contrary down up



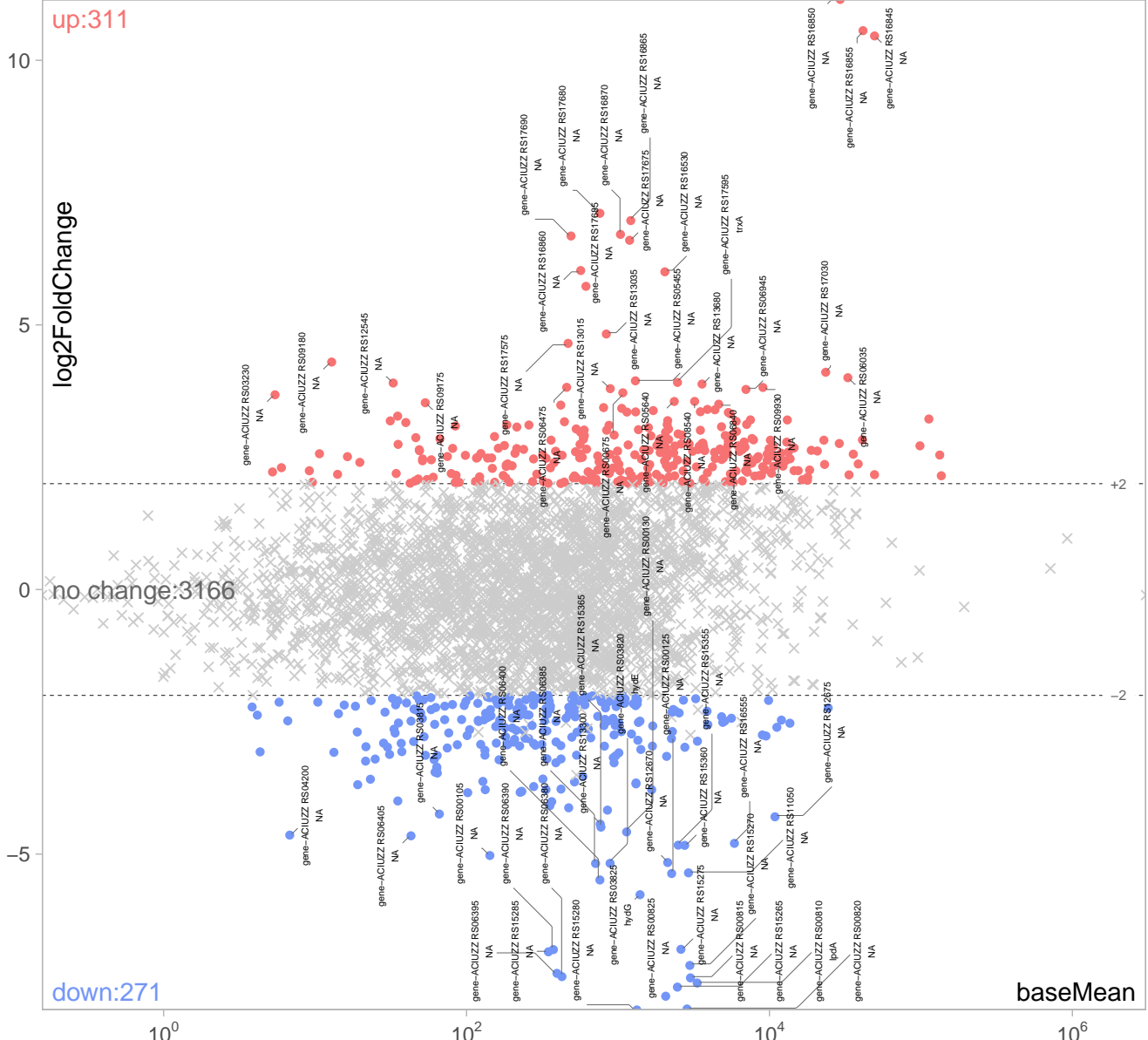
[illegible][illegible]

Volcano: MC compared to Syr



red/blue = DEG, higher = smaller padj

MAplot: MC compared to Syr



red/blue = DEG, more to the right = higher overall expression, x = insig.



Volcano plot showing log<sub>2</sub>FoldChange (x-axis) versus log<sub>10</sub>(padj) (y-axis). The plot is divided into three regions: down-regulated (blue, left), no changes (grey, center), and up-regulated (red, right). The y-axis is log<sub>10</sub>(padj) and the x-axis is log<sub>2</sub>FoldChange. A horizontal dashed line at y=1 indicates a significance threshold. A vertical dashed line at x=-2 separates down-regulated from no changes. A vertical dashed line at x=2 separates no changes from up-regulated. The plot shows a large number of genes, with many labeled with gene names and accession numbers. The up-regulated region shows a dense cluster of red points, while the down-regulated region shows a cluster of blue points. The no changes region is a large grey cloud of points.

red/blue = DEG, higher = smaller padj

[illegible]

red/blue = DEG, more to the right = higher overall expression, x = insig.



# Dispersion Estimation of DESeq2

blue circles are removed due to abnormal high dispersion

blue points are dispersion corrected to fit the red target

