

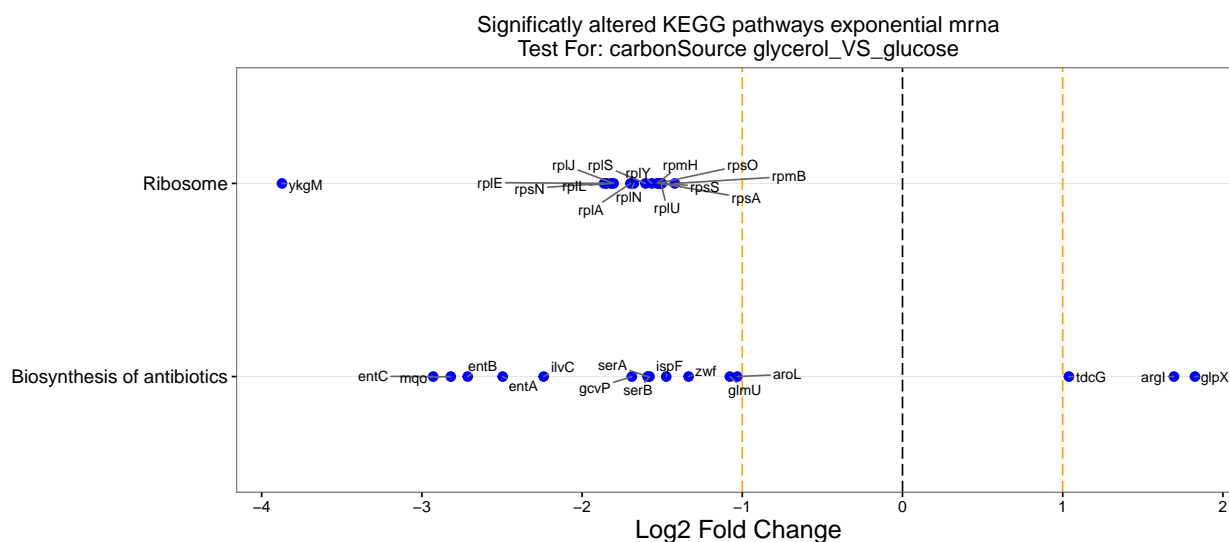
# Supplementary figures for significantly altered pathways

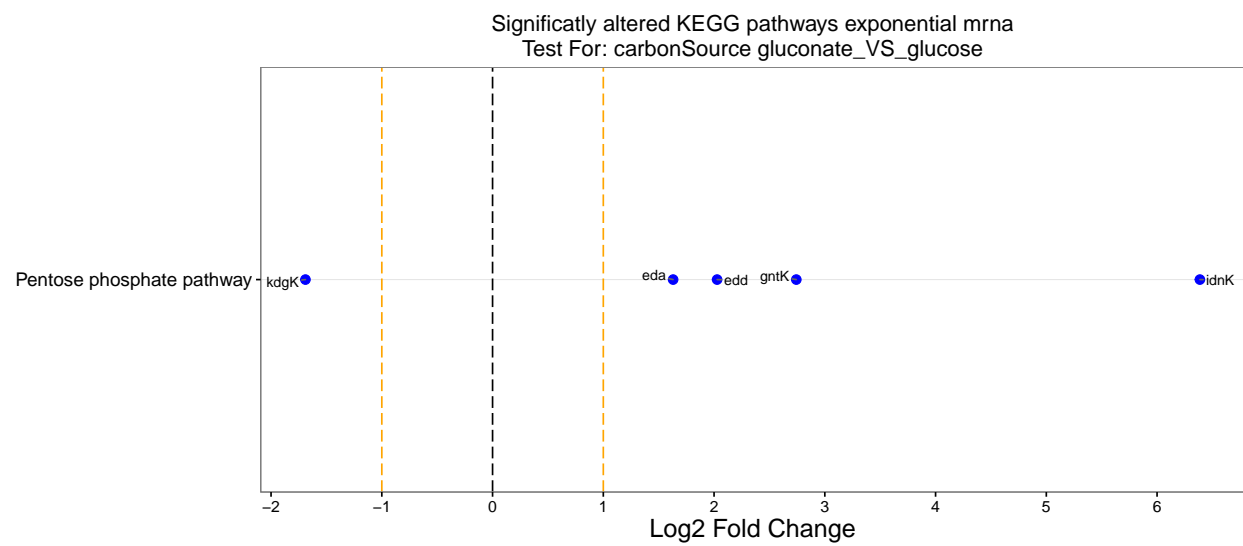
Mehmet Umut Caglar

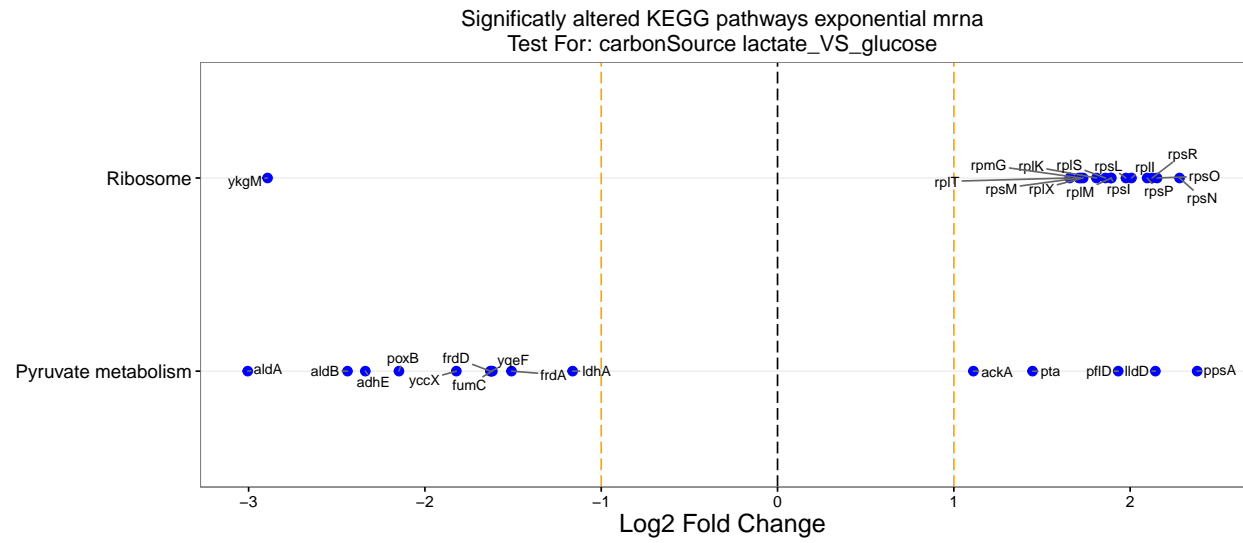
09 August, 2016

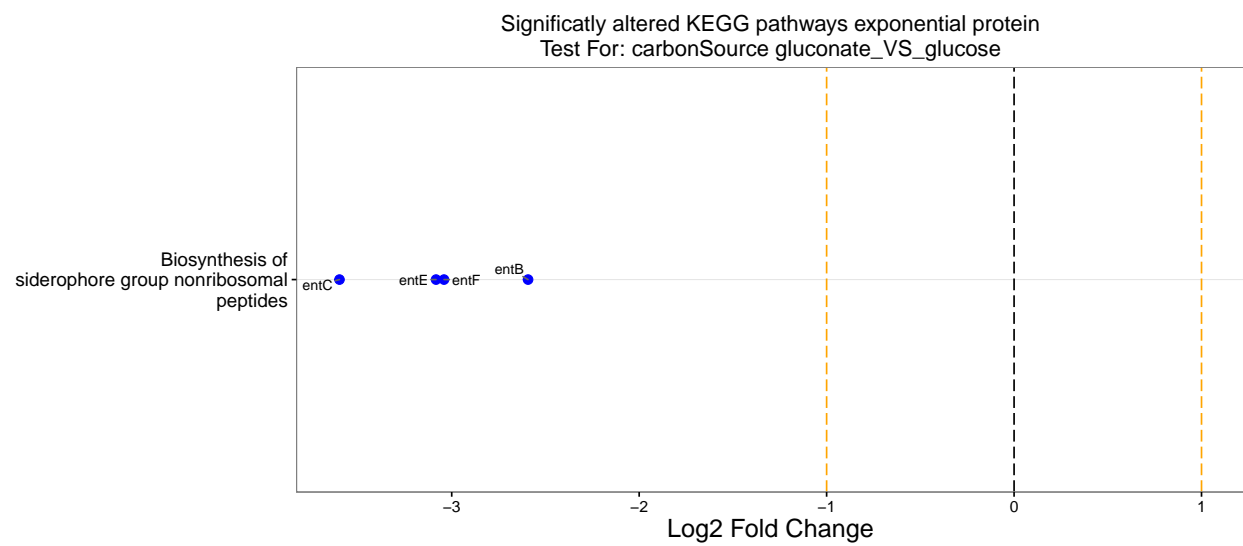
Significantly altered pathways and significantly altered genes within the pathways with respect to different external conditions are shown. Gene alterations are ordered with respect to change in expression levels and filtered by log change and adjusted P values. Only (1) The genes that change more than 2 fold and with an adjusted p value less than 0.05 are shown. (2) The pathways that change with an adjusted p value less than 0.05 are shown (3) If the number of genes that satisfy the property “1” is more than 15 only 15 of them are shown. (4) If the number of pathways that satisfy property “2” is more than 10 only 10 of them are shown

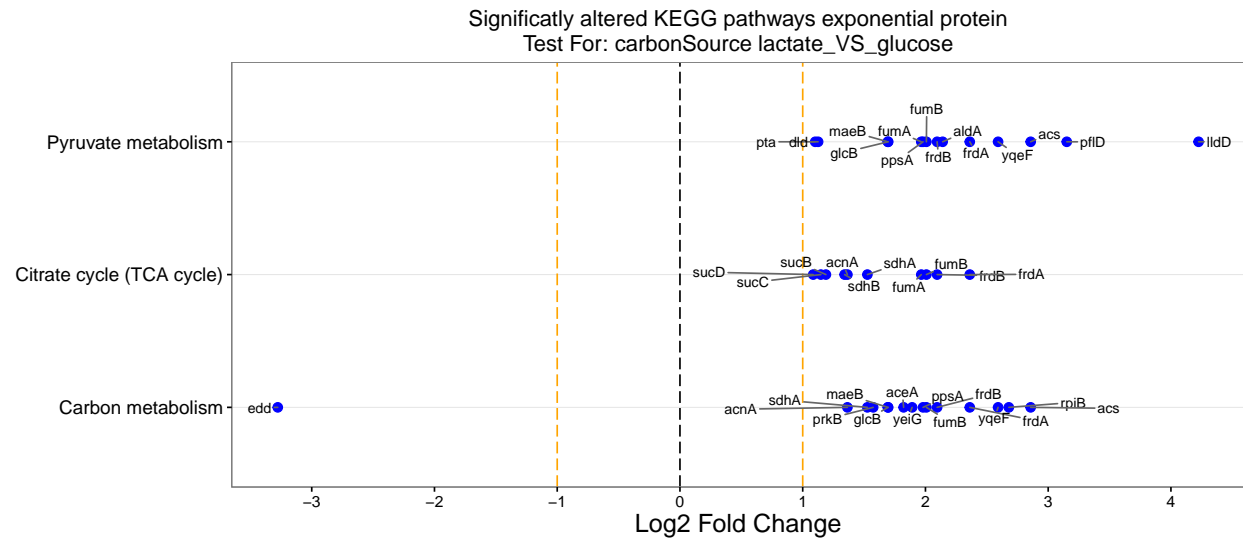
## Figures related with KEGG Pathway

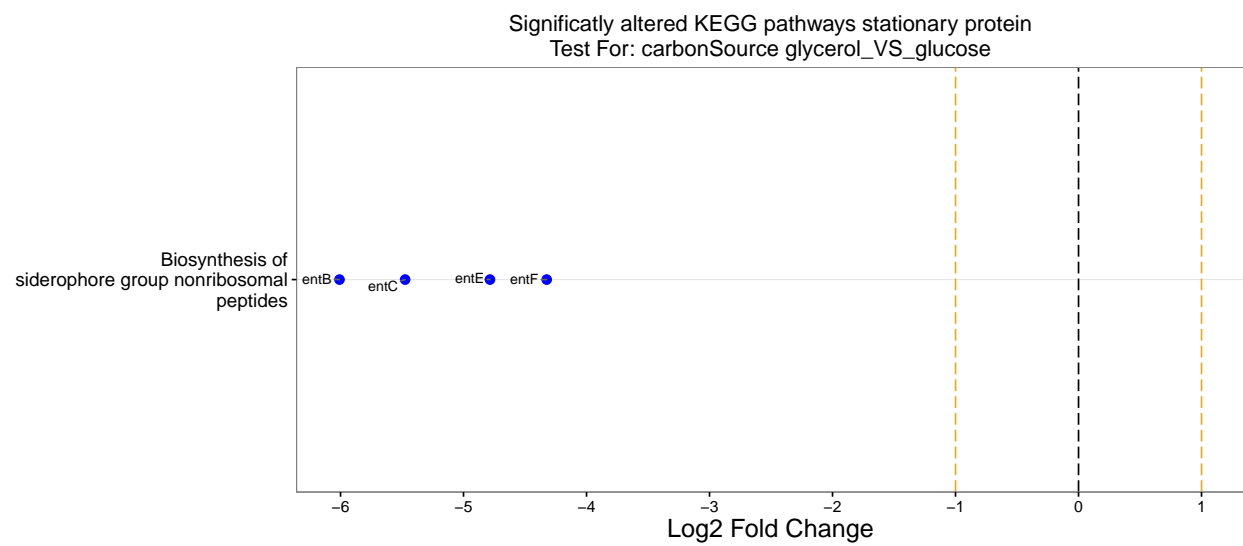


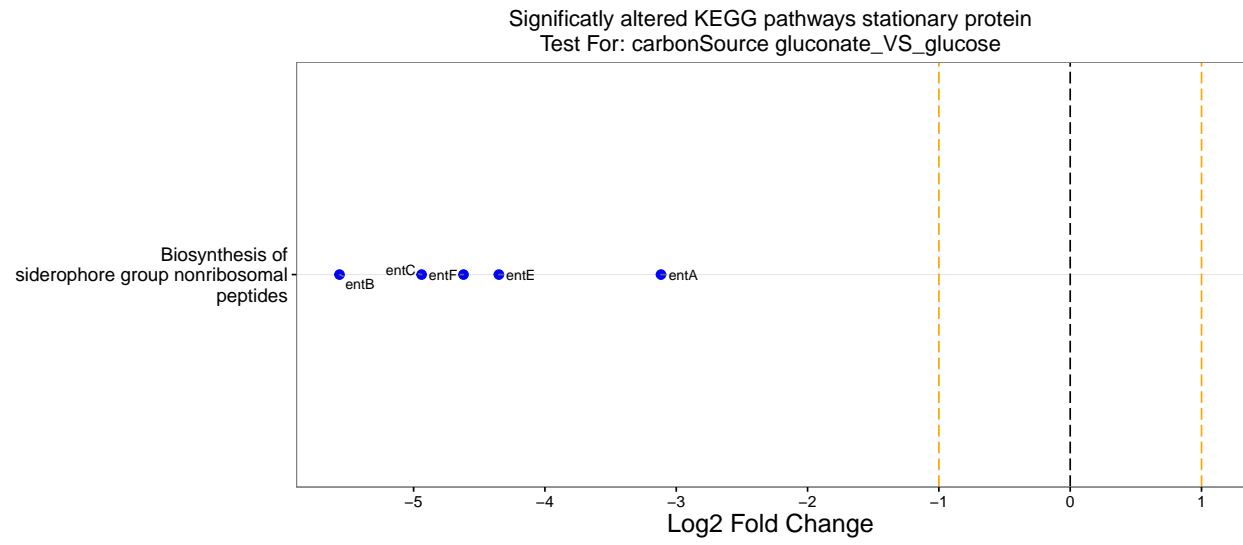


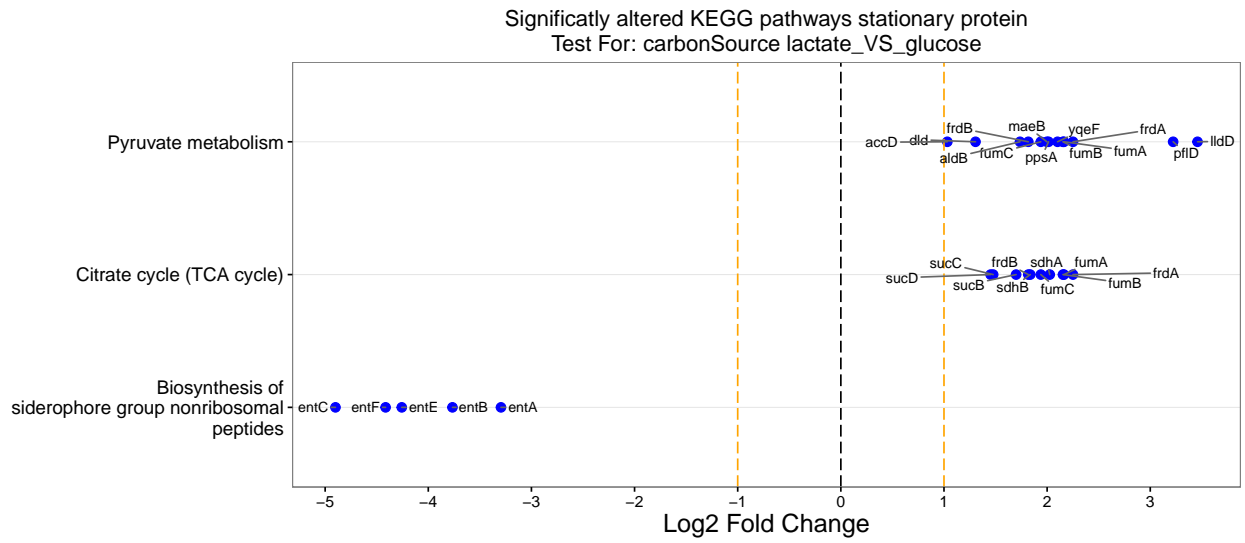




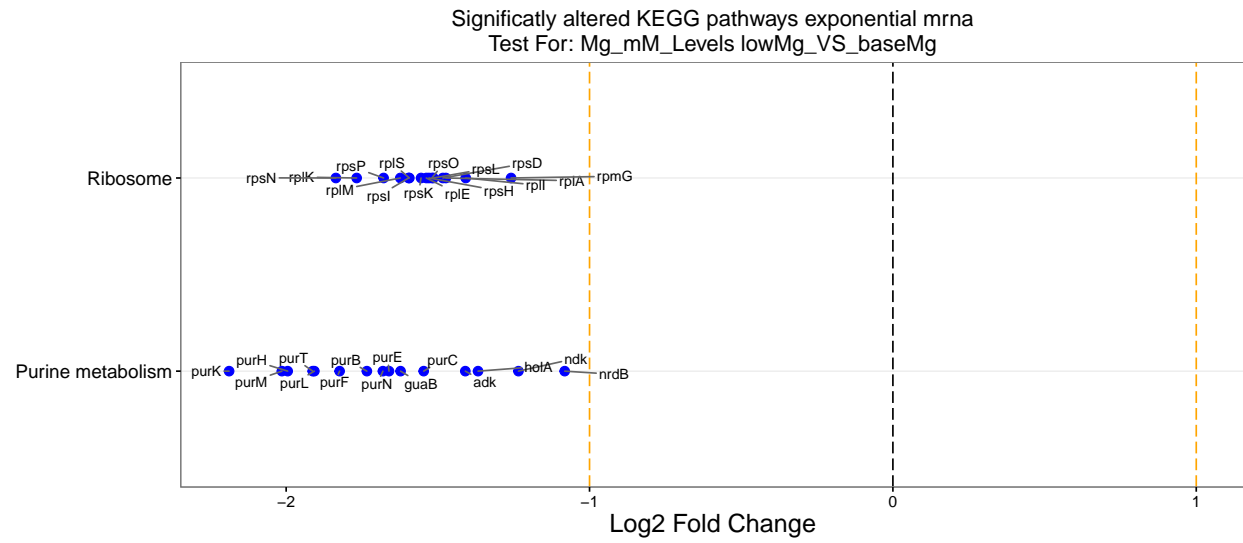


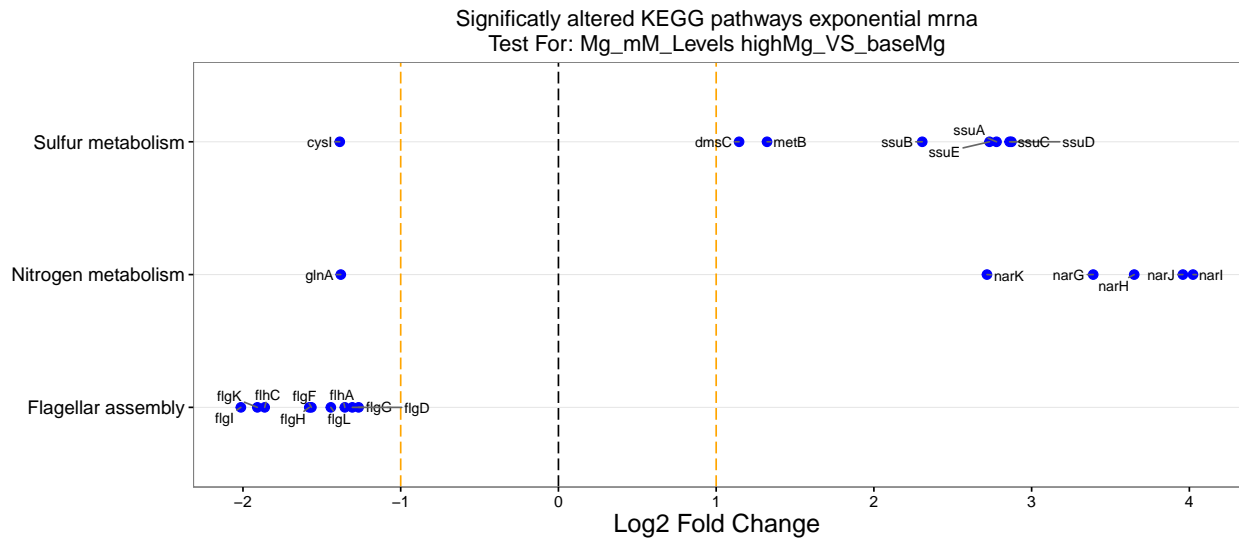


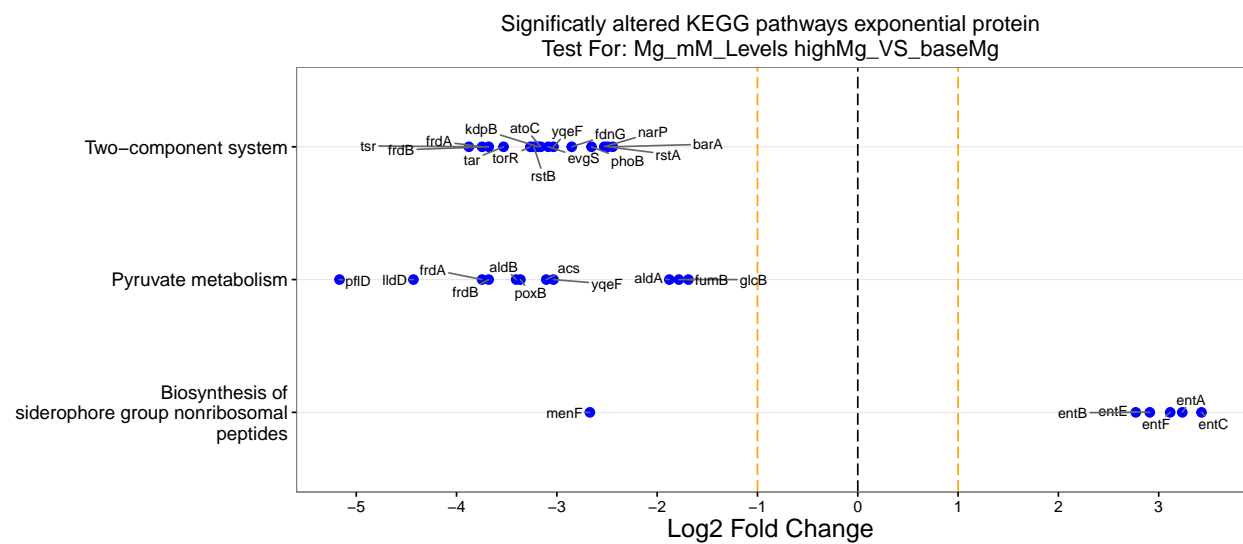


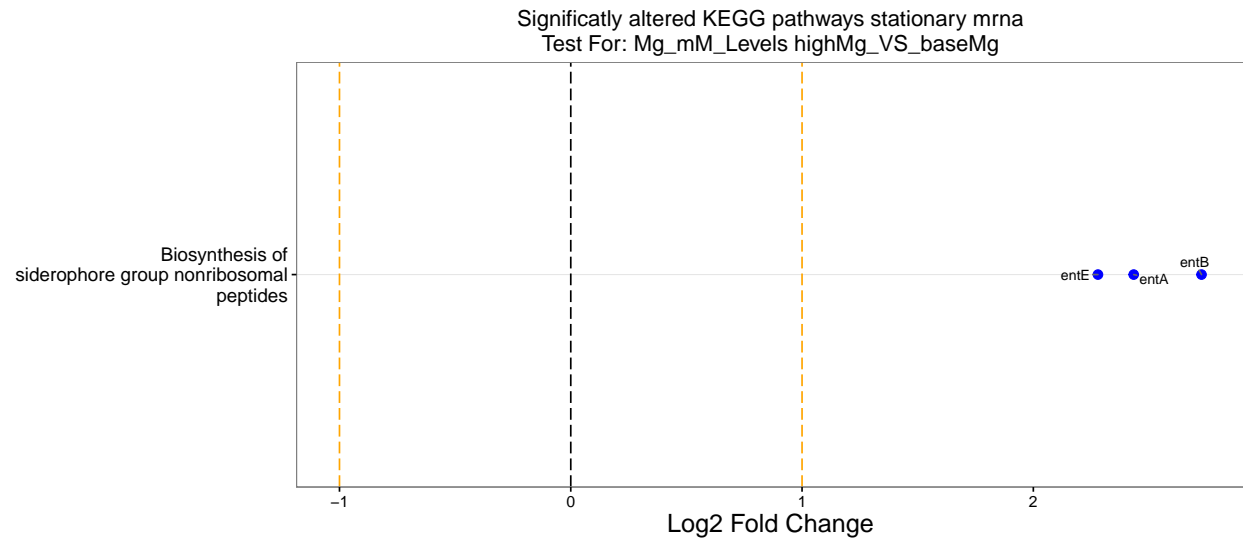


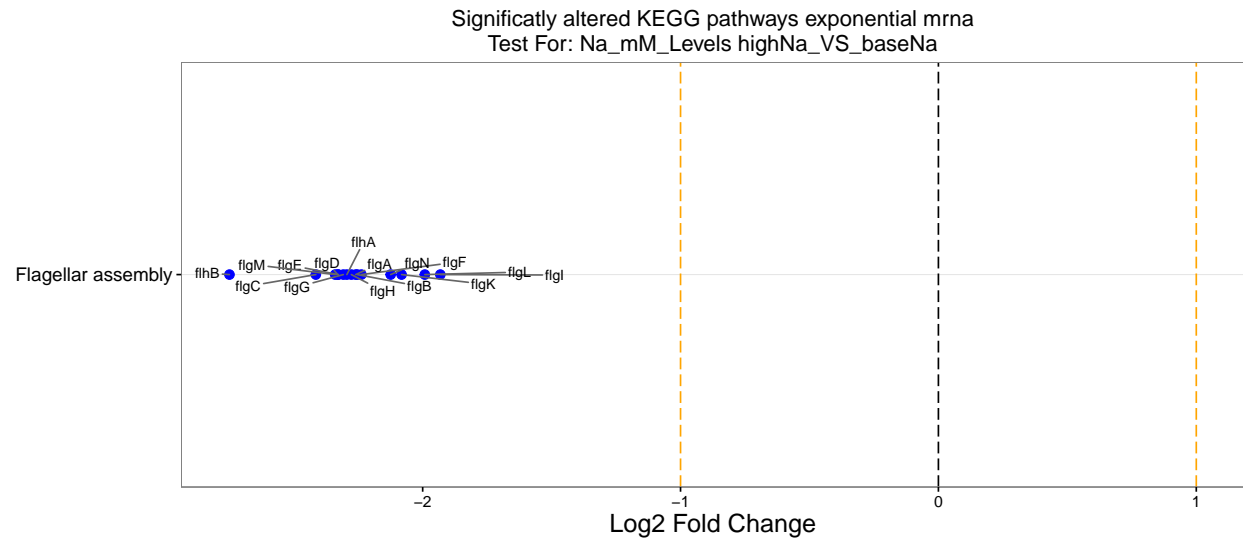


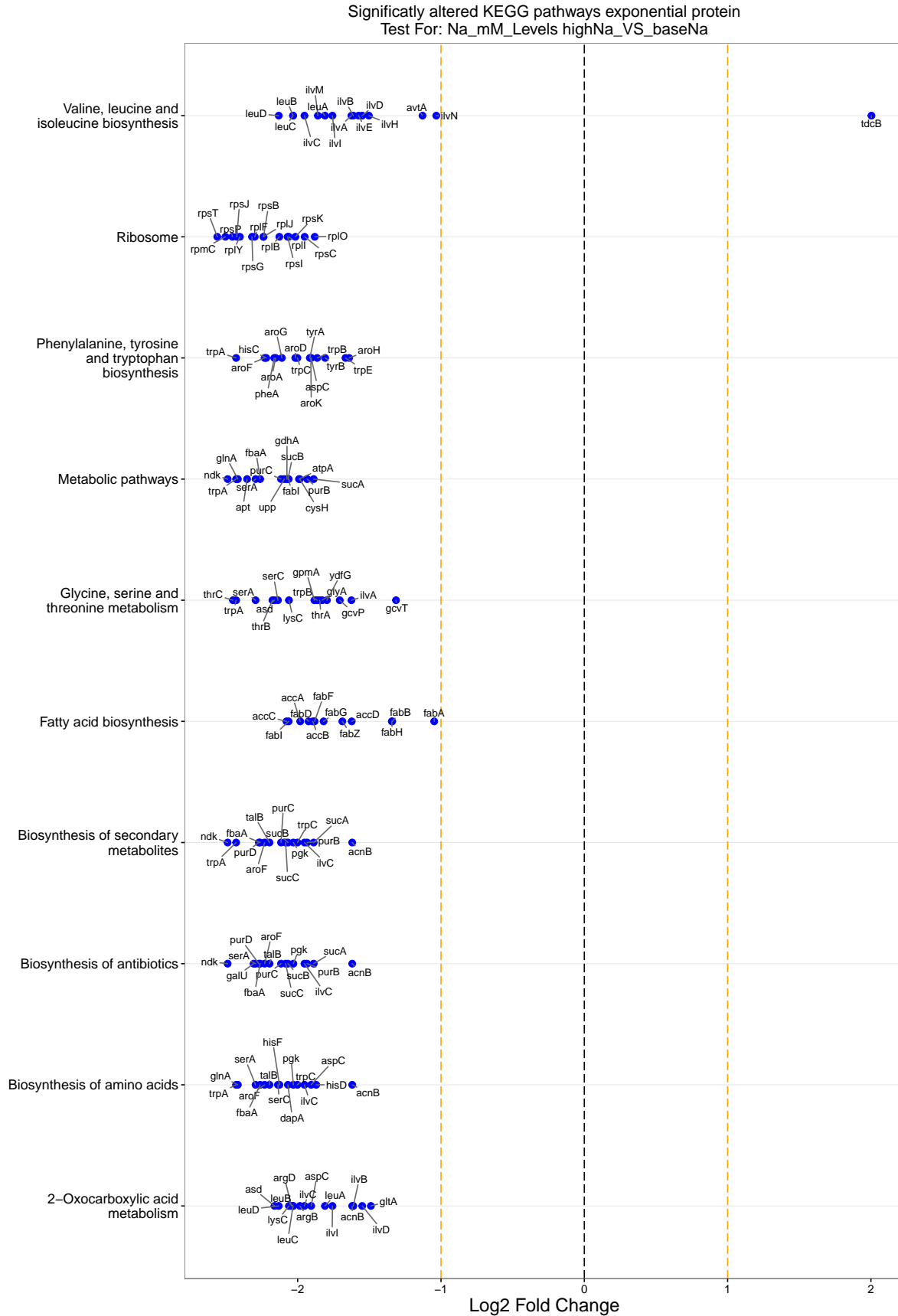


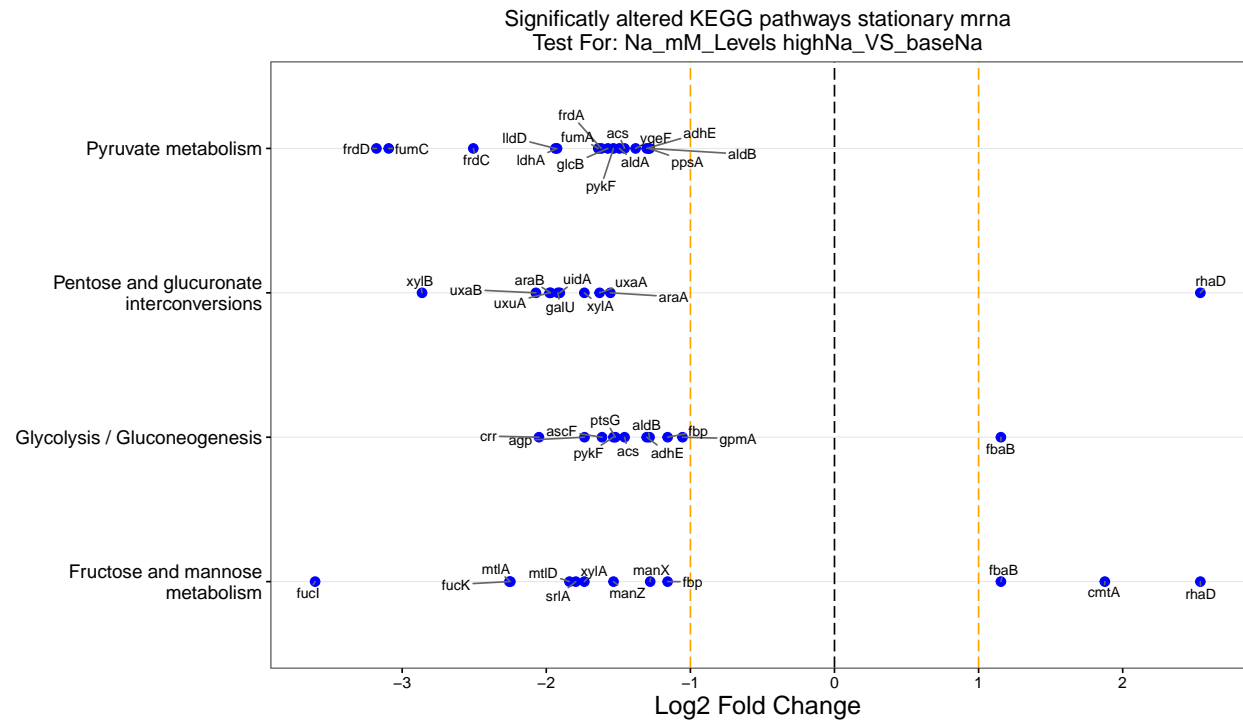




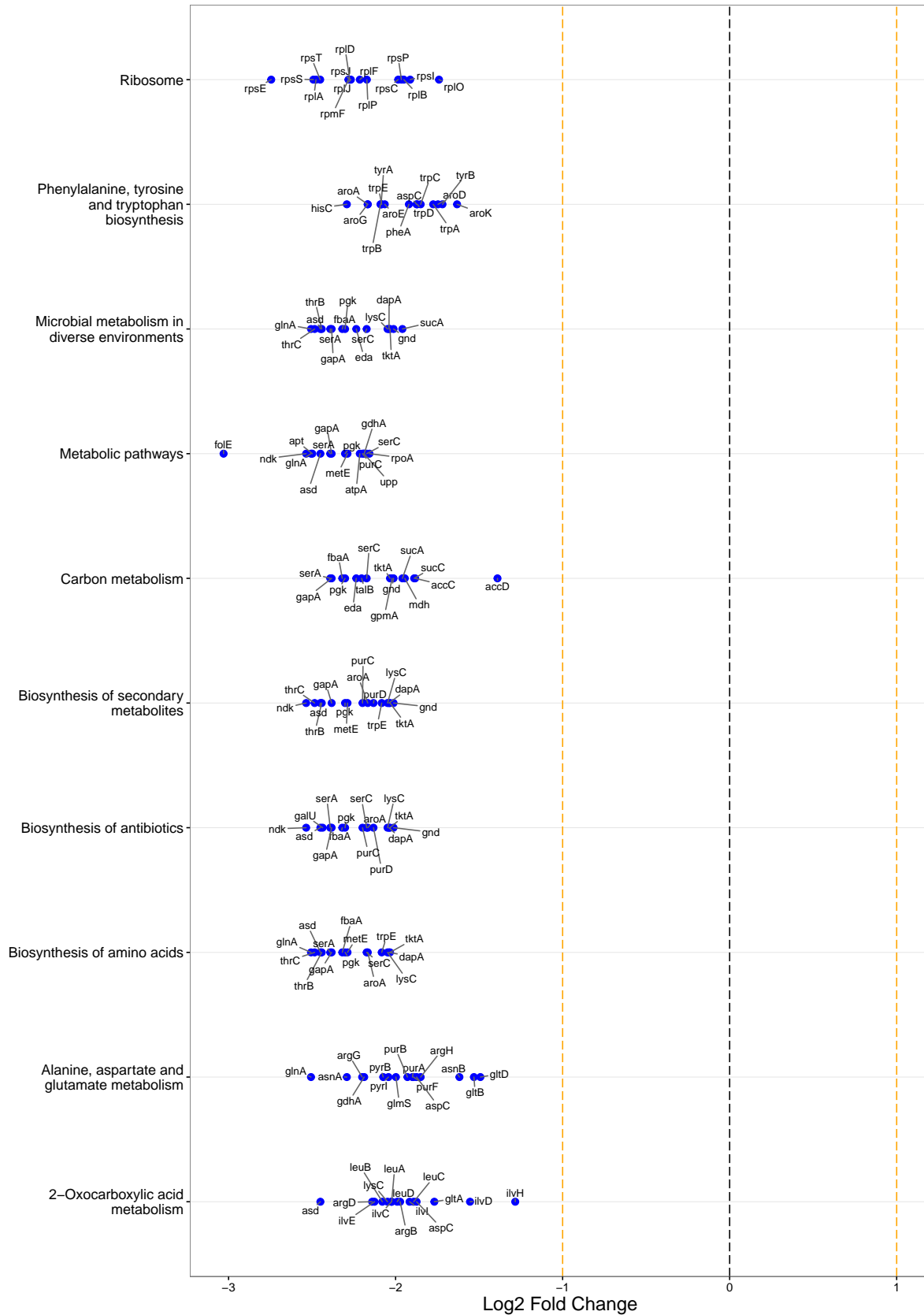






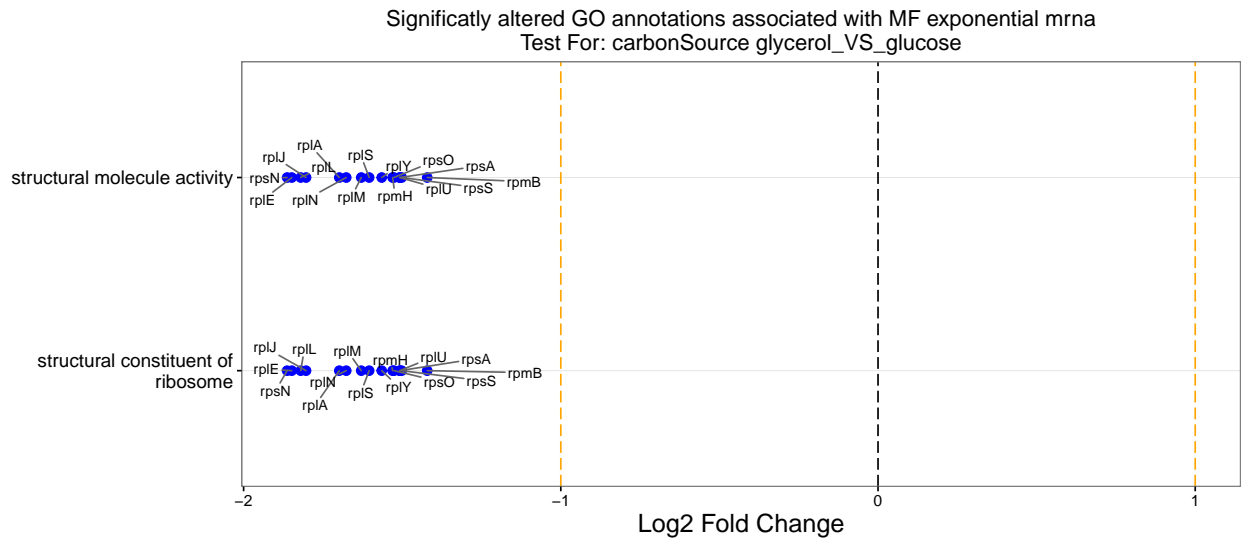


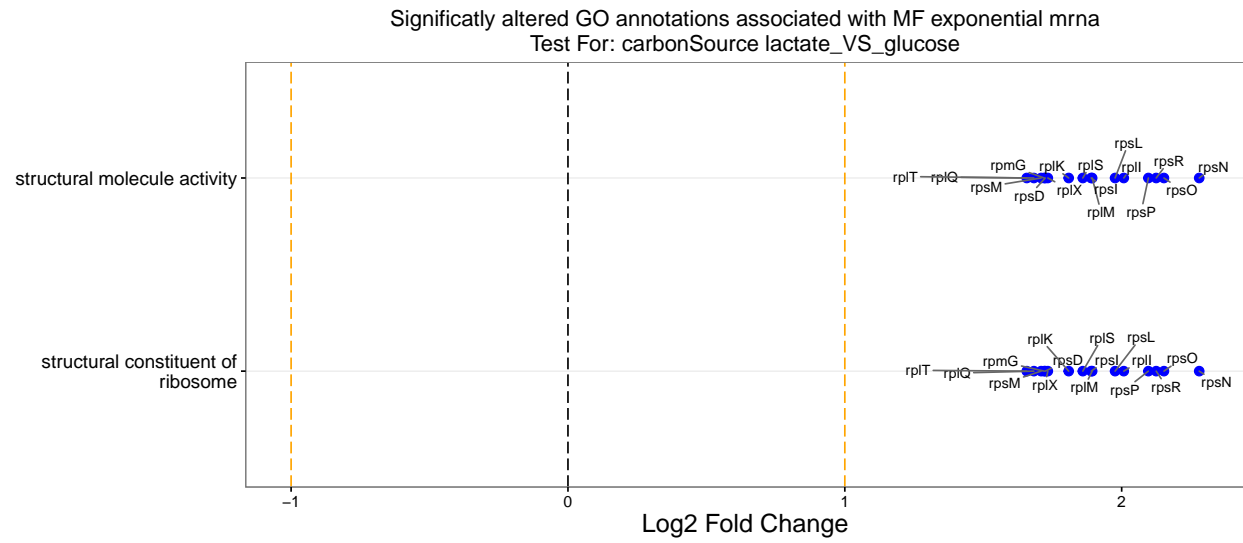
Significantly altered KEGG pathways stationary protein  
Test For: Na\_mM\_Levels highNa\_VS\_baseNa

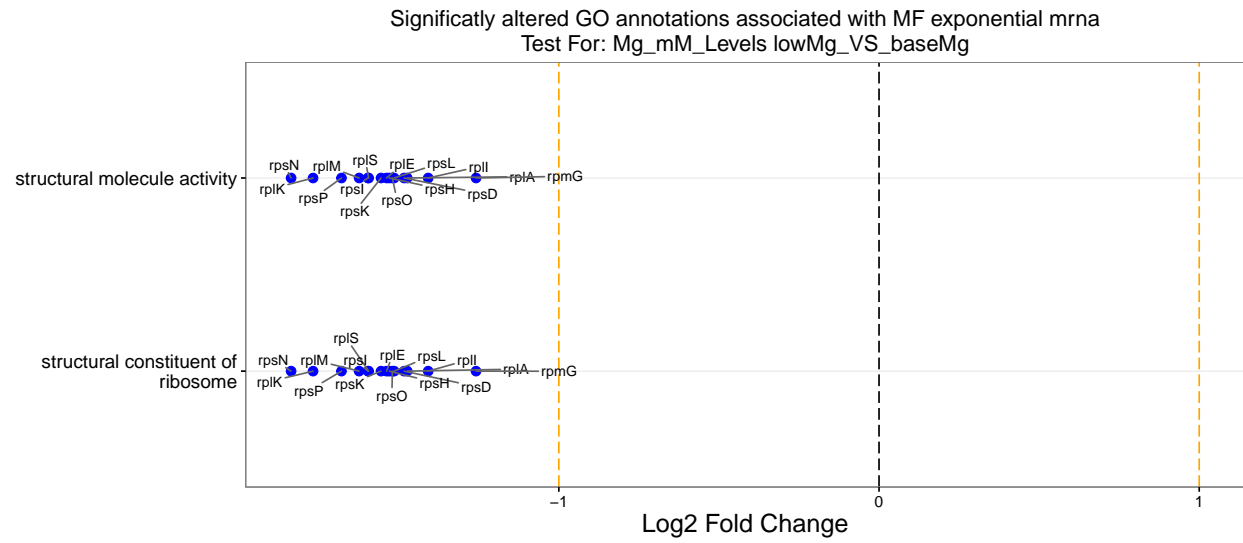




Figures related with GO Annotations associated with Molecular Function







Volcano plot showing Log2 Fold Change (X-axis) versus Log2 Fold Change (Y-axis). The X-axis ranges from -3 to 1, with a vertical dashed line at -1 and a solid vertical line at 0. The Y-axis labels are "structural molecule activity" and "structural constituent of ribosome".

Key data points (Gene Name, Log2 Fold Change):

Gene Name	Log2 Fold Change
rpsT	-2.8
rpsJ	-2.7
rpsG	-2.6
rplB	-2.5
rplI	-2.4
rpsK	-2.3
rpsC	-2.2
rplO	-2.1
rpmC	-2.8
rpsP	-2.7
rplY	-2.6
rplF	-2.5
rplJ	-2.4
rpsB	-2.3
rplB	-2.2
rplI	-2.1
rpsK	-2.0
rpsC	-1.9
rplO	-1.8

