

# The *E. coli* molecular phenotype under different growth conditions

## Supplementary material

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## Supplementary Figures associated with differentially expressed KEGG pathways

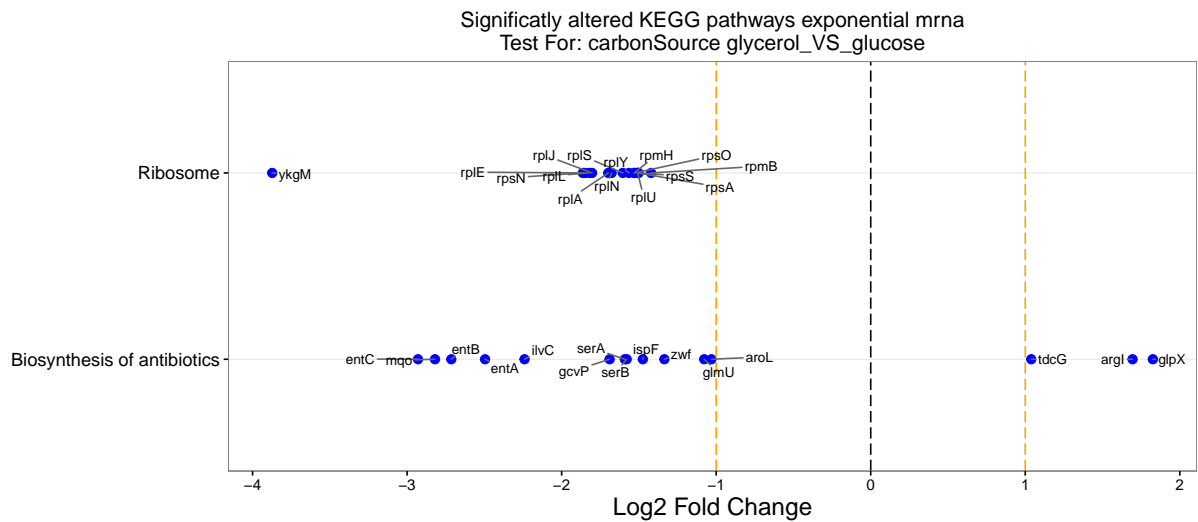


Figure S1: **Significantly differentially expressed KEGG pathways and associated genes with glycerol as carbon source in exponential phase, as determined by mRNA abundances.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding genes is shown along the x axis. In figure we show up to 10 most significantly changed pathways and for each pathway we show up to 15 of the most significantly changing genes.

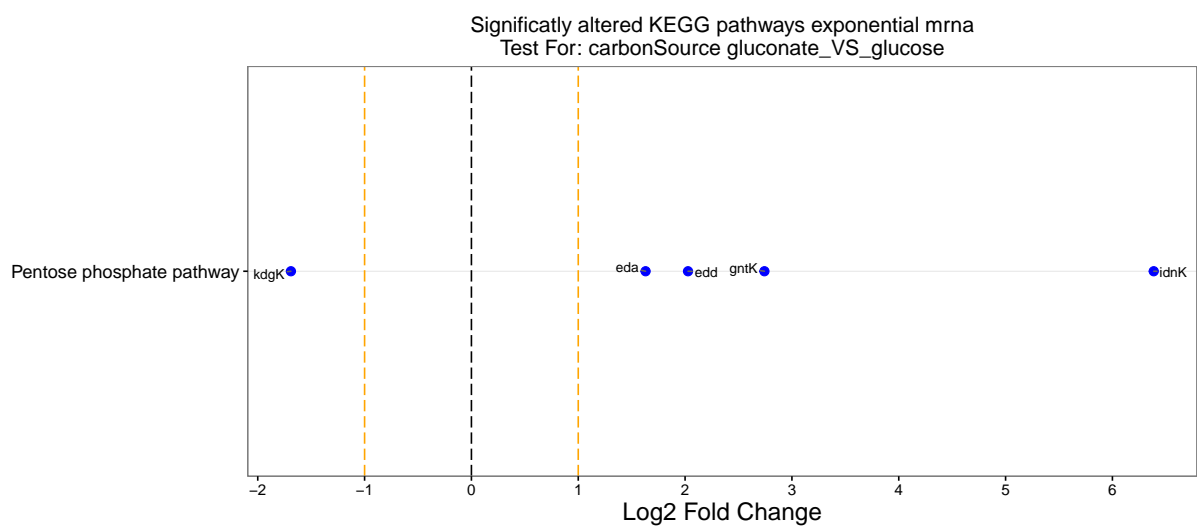


Figure S2: **Significantly differentially expressed KEGG pathways and associated genes with gluconate as carbon source in exponential phase, as determined by mRNA abundances.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding genes is shown along the x axis. In figure we show up to 10 most significantly changed pathways and for each pathway we show up to 15 of the most significantly changing genes.

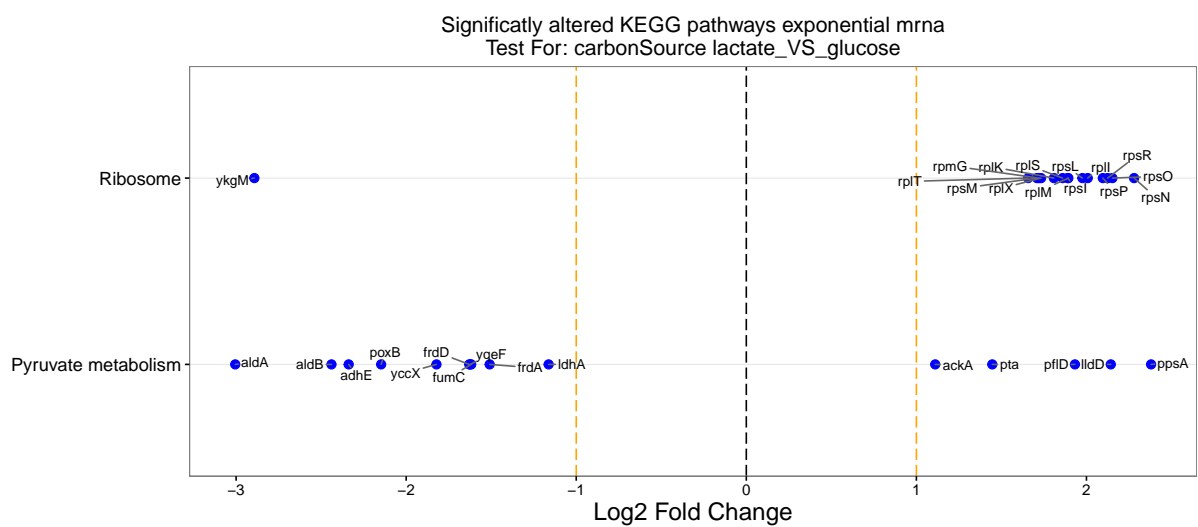


Figure S3: **Significantly differentially expressed KEGG pathways and associated genes with lactate as carbon source in exponential phase, as determined by mRNA abundances.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding genes is shown along the x axis. In figure we show up to 10 most significantly changed pathways and for each pathway we show up to 15 of the most significantly changing genes.

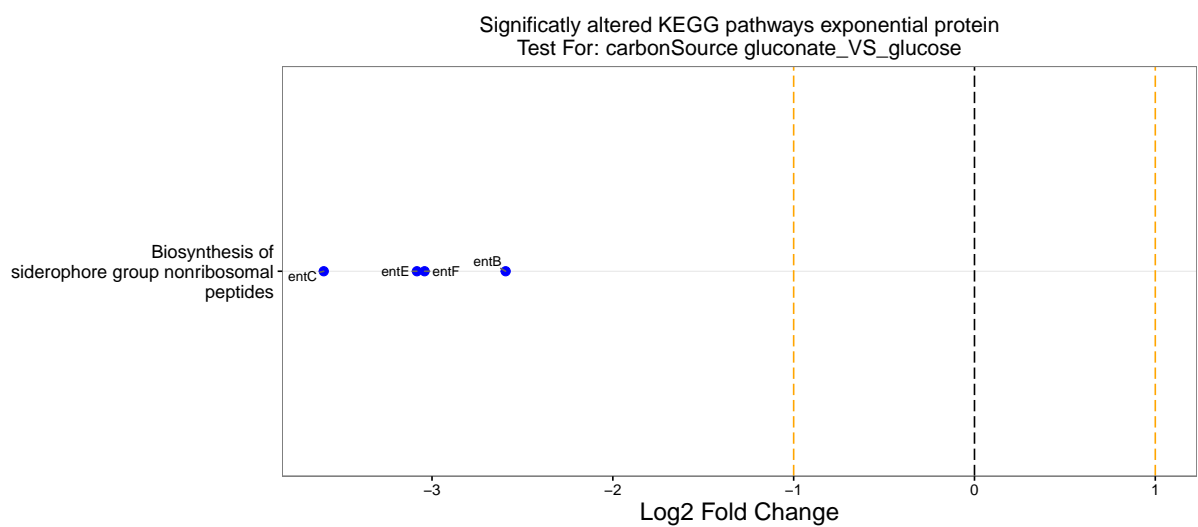


Figure S4: **Significantly differentially expressed KEGG pathways and associated genes with gluconate as carbon source in exponential phase, as determined by protein abundances.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding genes is shown along the x axis. In figure we show up to 10 most significantly changed pathways and for each pathway we show up to 15 of the most significantly changing genes.

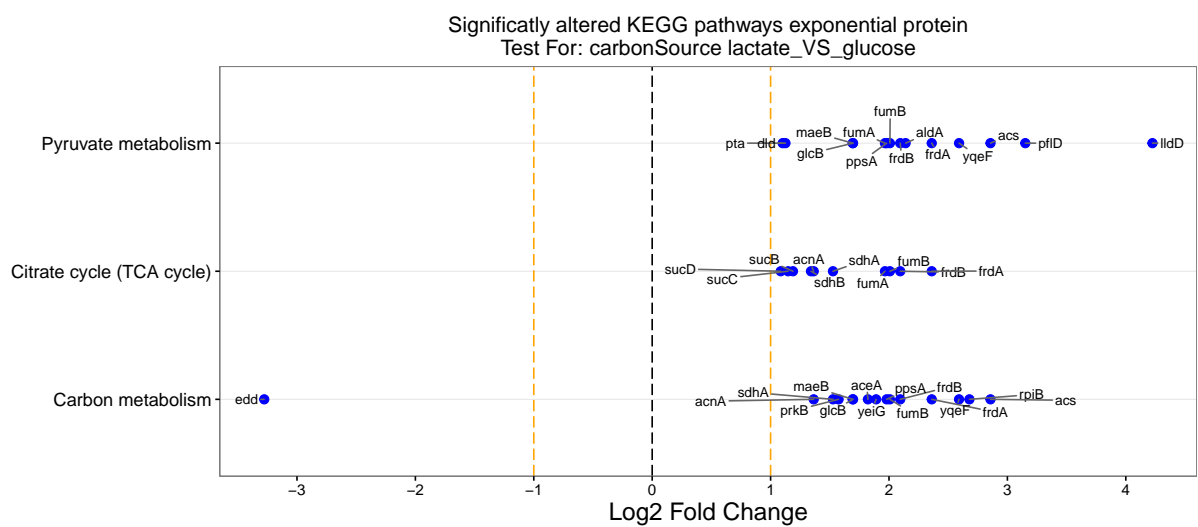


Figure S5: **Significantly differentially expressed KEGG pathways and associated genes with lactate as carbon source in exponential phase, as determined by protein abundances.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding genes is shown along the x axis. In figure we show up to 10 most significantly changed pathways and for each pathway we show up to 15 of the most significantly changing genes.



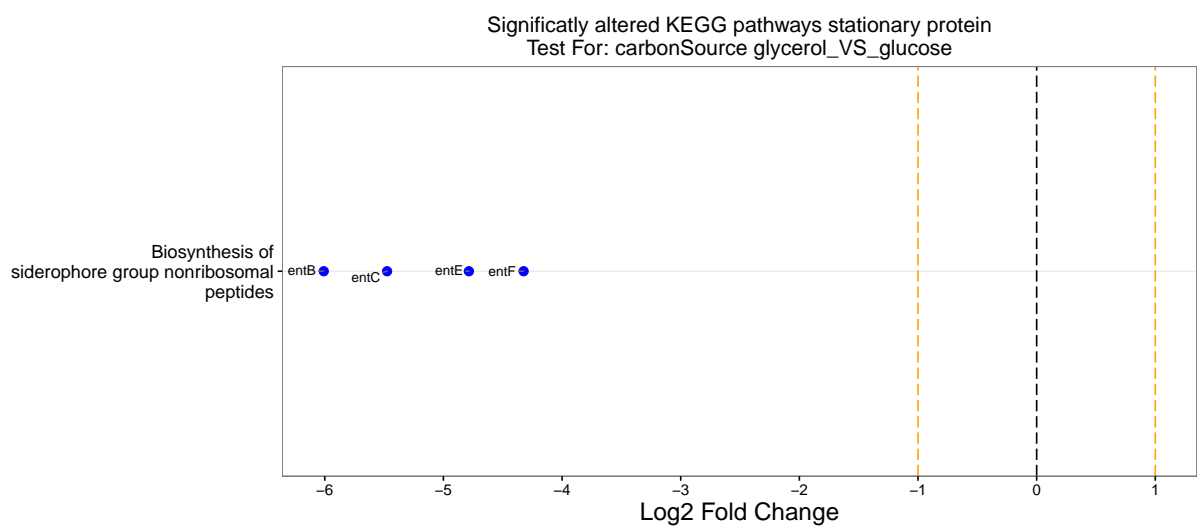


Figure S6: **Significantly differentially expressed KEGG pathways and associated genes with glycerol as carbon source in stationary phase, as determined by protein abundances.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding genes is shown along the x axis. In figure we show up to 10 most significantly changed pathways and for each pathway, we show up to 15 of the most significantly changing genes.

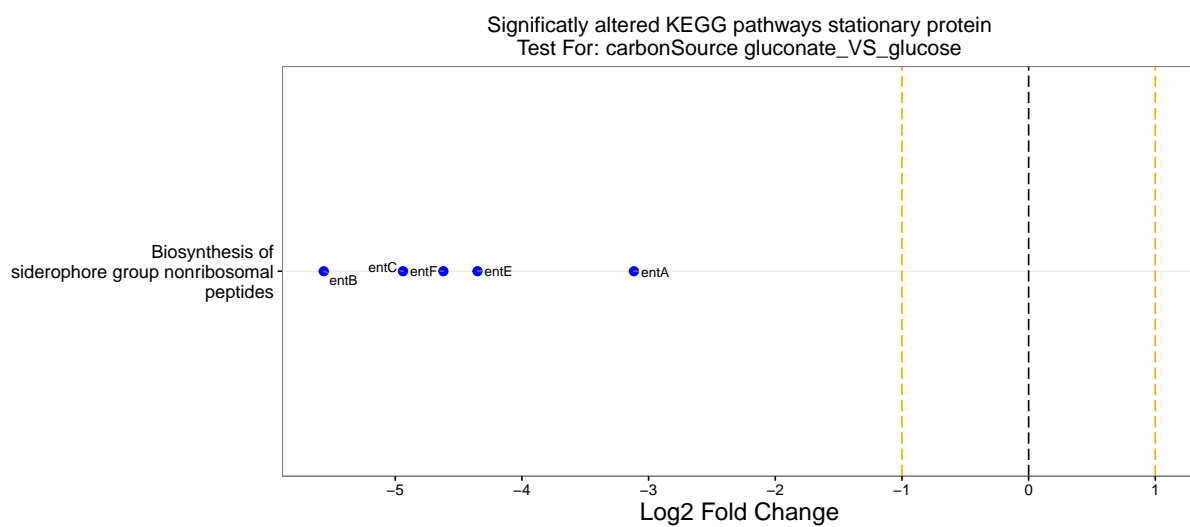


Figure S7: **Significantly differentially expressed KEGG pathways and associated genes with gluconate as carbon source in stationary phase, as determined by protein abundances.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding genes is shown along the x axis. We show up to 10 most significantly changed pathways and for each pathway, we show up to 15 of the most significantly changing genes.

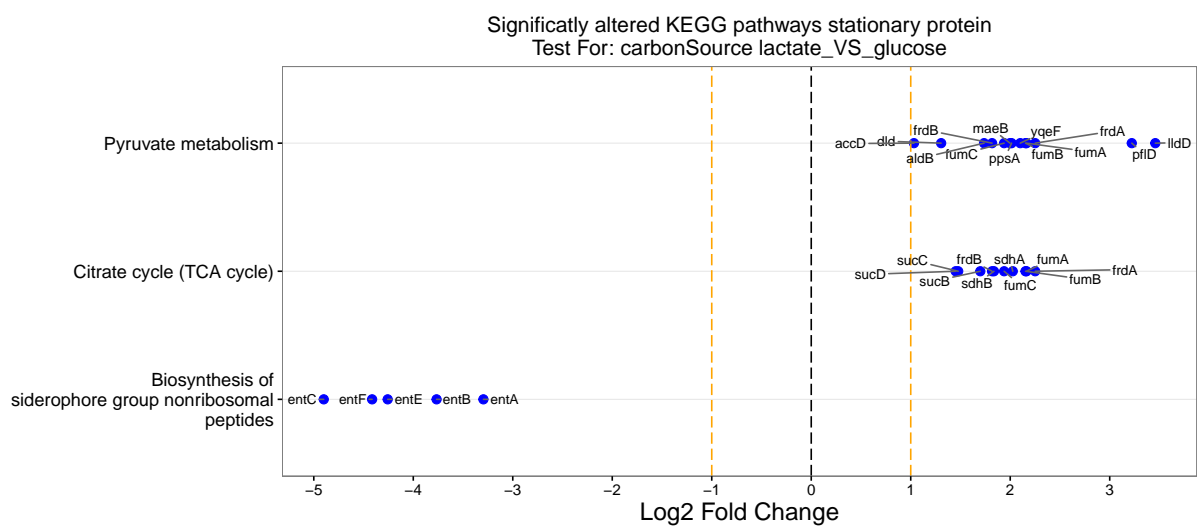


Figure S8: **Significantly differentially expressed KEGG pathways and associated genes with lactate as carbon source in stationary phase, as determined by protein abundances.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding genes is shown along the x axis. We show up to 10 most significantly changed pathways and for each pathway, we show up to 15 of the most significantly changing genes.

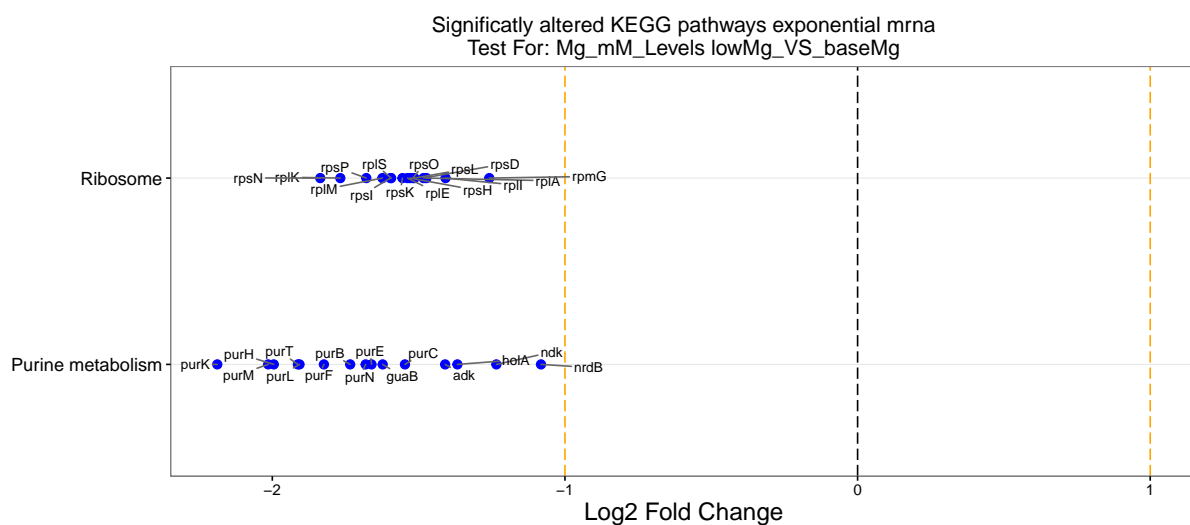


Figure S9: **Significantly differentially expressed KEGG pathways and associated genes with low  $Mg^{+2}$  levels in exponential phase, as determined by mRNA abundances.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding genes is shown along the x axis. We show up to 10 most significantly changed pathways and for each pathway, we show up to 15 of the most significantly changing genes.

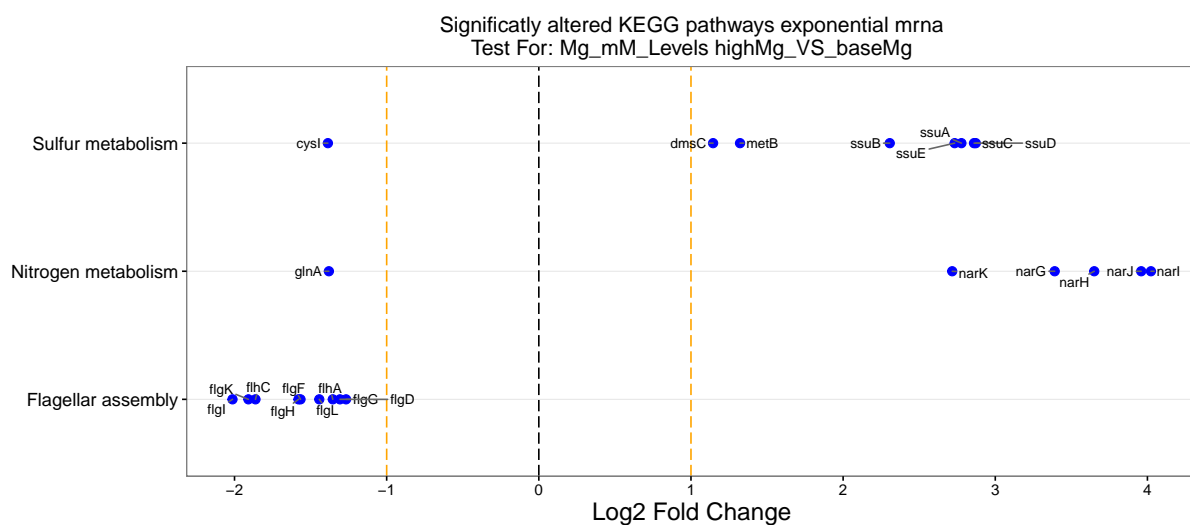


Figure S10: **Significantly differentially expressed KEGG pathways and associated genes with high  $Mg^{+2}$  levels in exponential phase, as determined by mRNA abundances.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding genes is shown along the x axis. We show up to 10 most significantly changed pathways and for each pathway, we show up to 15 of the most significantly changing genes.

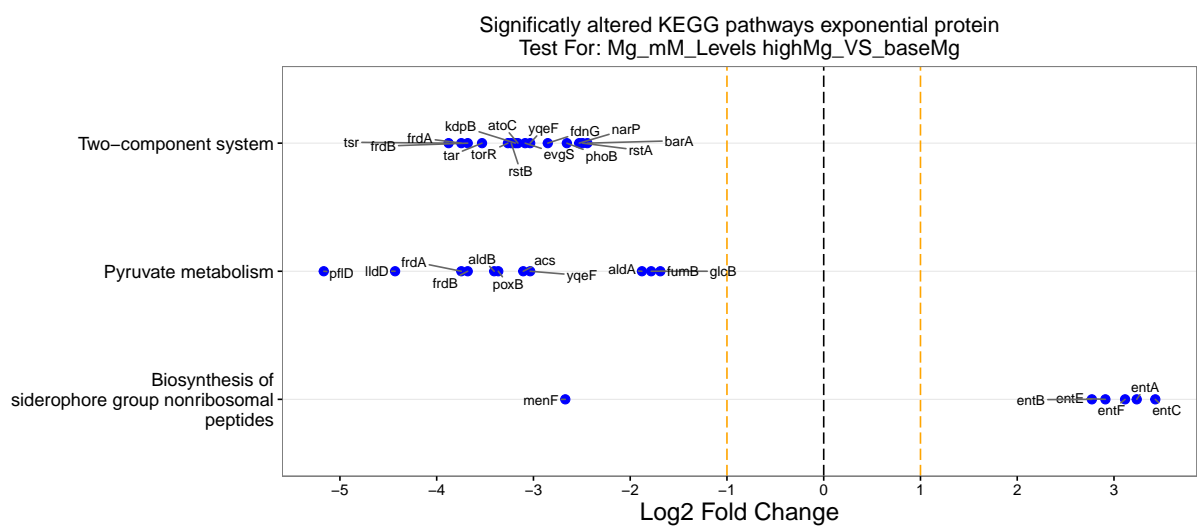


Figure S11: **Significantly differentially expressed KEGG pathways and associated genes with high  $Mg^{+2}$  levels in exponential phase, as determined by protein abundances.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding genes is shown along the x axis. We show up to 10 most significantly changed pathways and for each pathway, we show up to 15 of the most significantly changing genes.

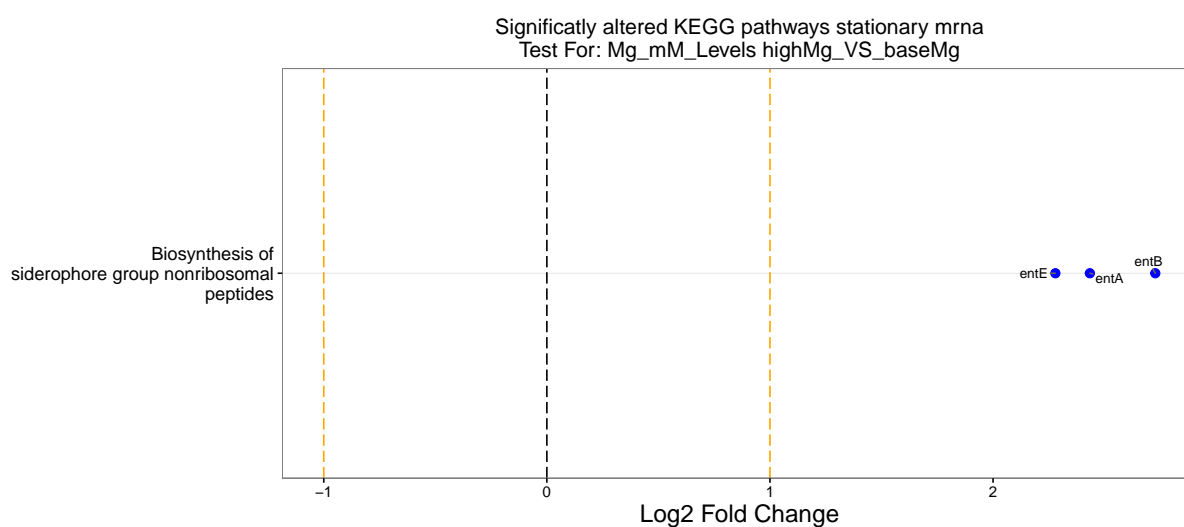


Figure S12: **Significantly differentially expressed KEGG pathways and associated genes with high  $\text{Mg}^{+2}$  levels in stationary phase, as determined by mRNA abundances.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding genes is shown along the x axis. We show up to 10 most significantly changed pathways and for each pathway, we show up to 15 of the most significantly changing genes.

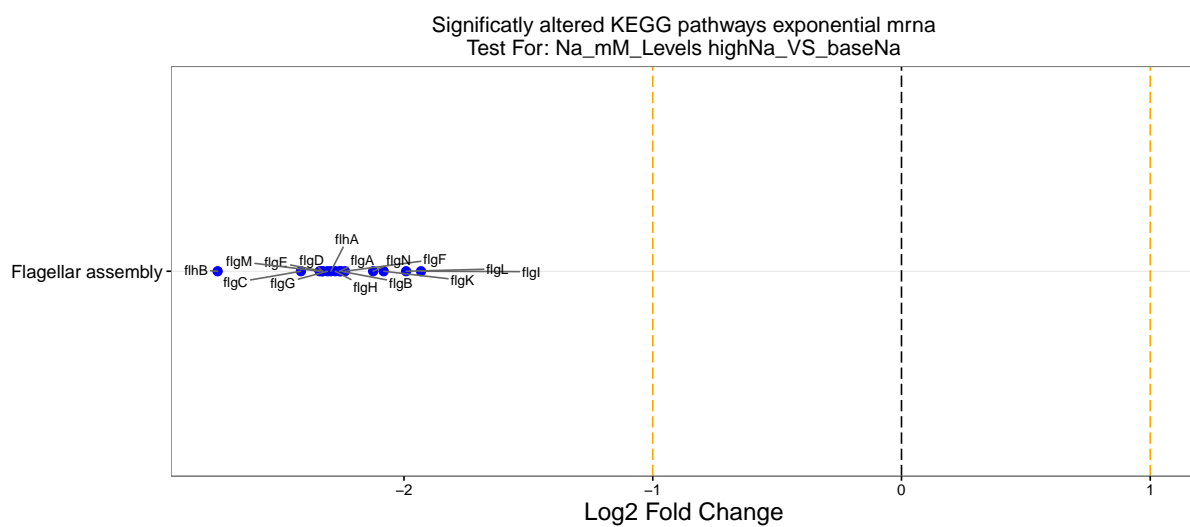


Figure S13: **Significantly differentially expressed KEGG pathways and associated genes with high  $\text{Na}^{+1}$  levels in exponential phase, as determined by mRNA abundances.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding genes is shown along the x axis. We show up to 10 most significantly changed pathways and for each pathway, we show up to 15 of the most significantly changing genes.



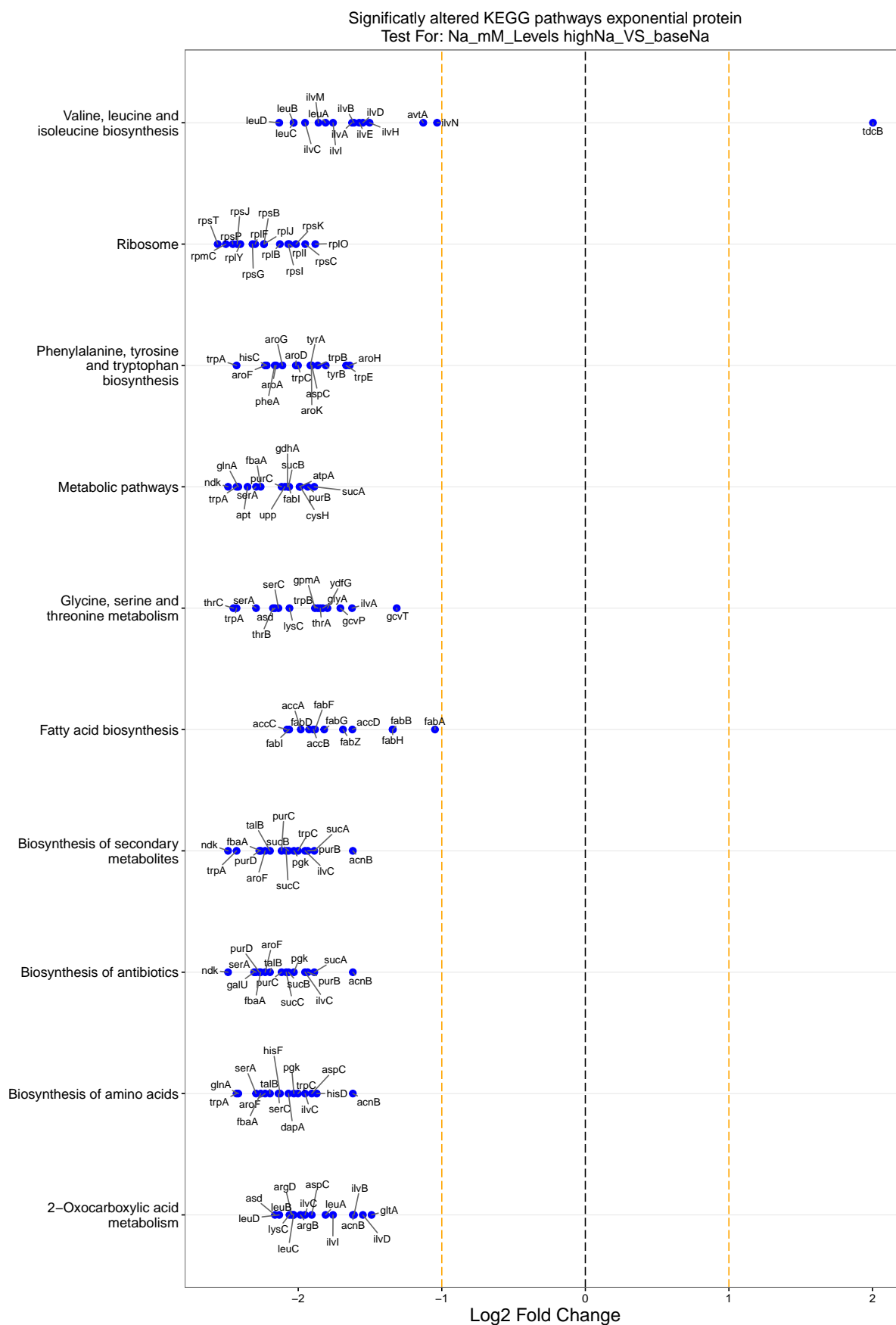


Figure S14: Significantly differentially expressed KEGG pathways and associated genes with high  $\text{Na}^{+1}$  levels in exponential phase, as determined by protein abundances. The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding genes is shown along the x axis. We show up to 10 most significantly changed pathways and for each pathway, we show up to 15 of the most significantly changing genes.

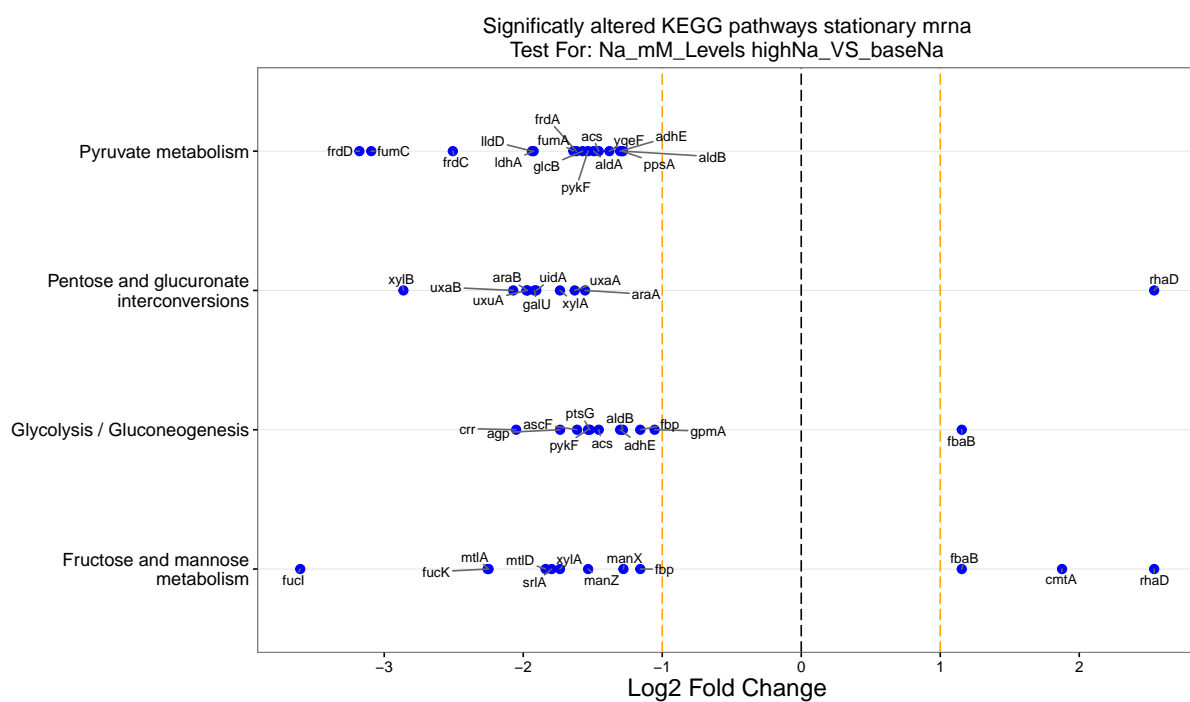


Figure S15: **Significantly differentially expressed KEGG pathways and associated genes with high  $\text{Na}^{+1}$  levels in stationary phase, as determined by mRNA abundances.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding genes is shown along the x axis. We show up to 10 most significantly changed pathways and for each pathway, we show up to 15 of the most significantly changing genes.



Figure S16: **Significantly differentially expressed KEGG pathways and associated genes with high  $\text{Na}^{+1}$  levels in stationary phase, as determined by protein abundances.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding genes is shown along the x axis. We show up to 10 most significantly changed pathways and for each pathway, we show up to 15 of the most significantly changing genes.

### Supplementary Figures related with GO Annotations associated with Molecular Function

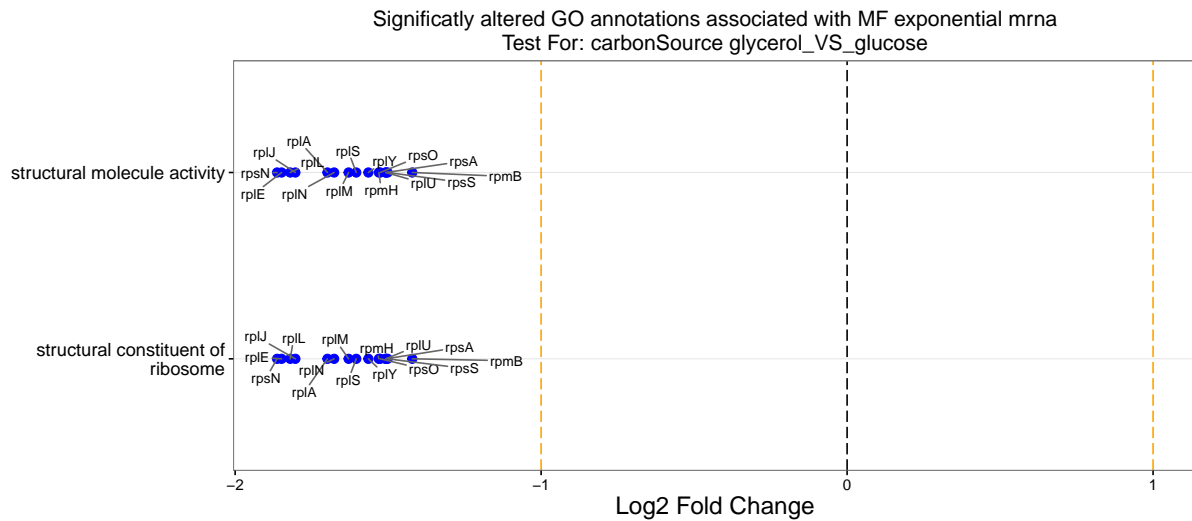


Figure S17: **Significantly differentially expressed GO annotations related with molecular functions and associated genes with glycerol as carbon source in exponential phase, as determined by mRNA abundances.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding genes is shown along the x axis. We show up to 10 most significantly changed pathways and for each pathway, we show up to 15 of the most significantly changing genes.

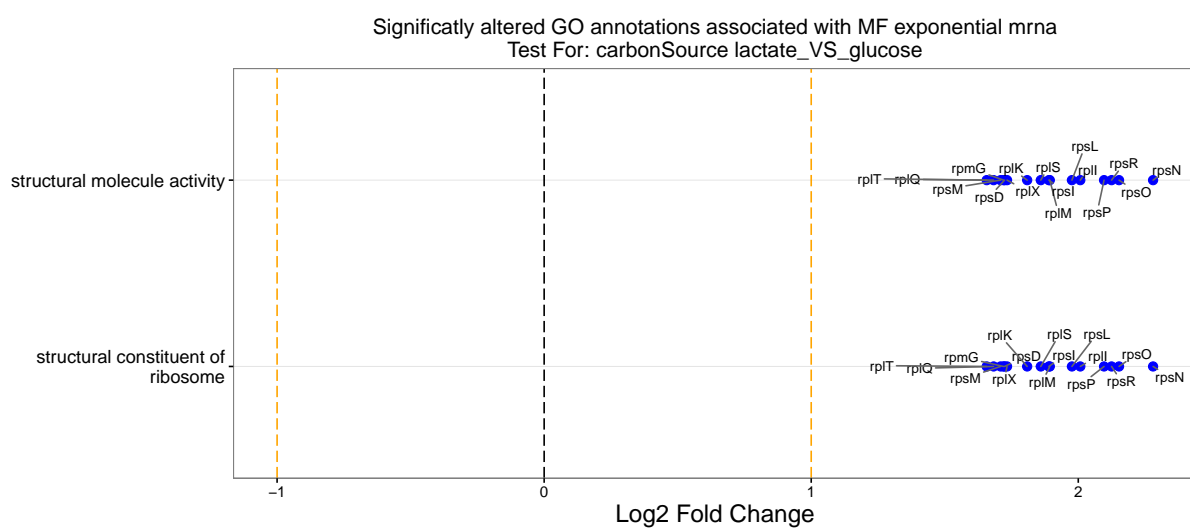


Figure S18: **Significantly differentially expressed GO annotations related with molecular functions and associated genes with lactate as carbon source in exponential phase, as determined by mRNA abundances.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding genes is shown along the x axis. We show up to 10 most significantly changed pathways and for each pathway, we show up to 15 of the most significantly changing genes.

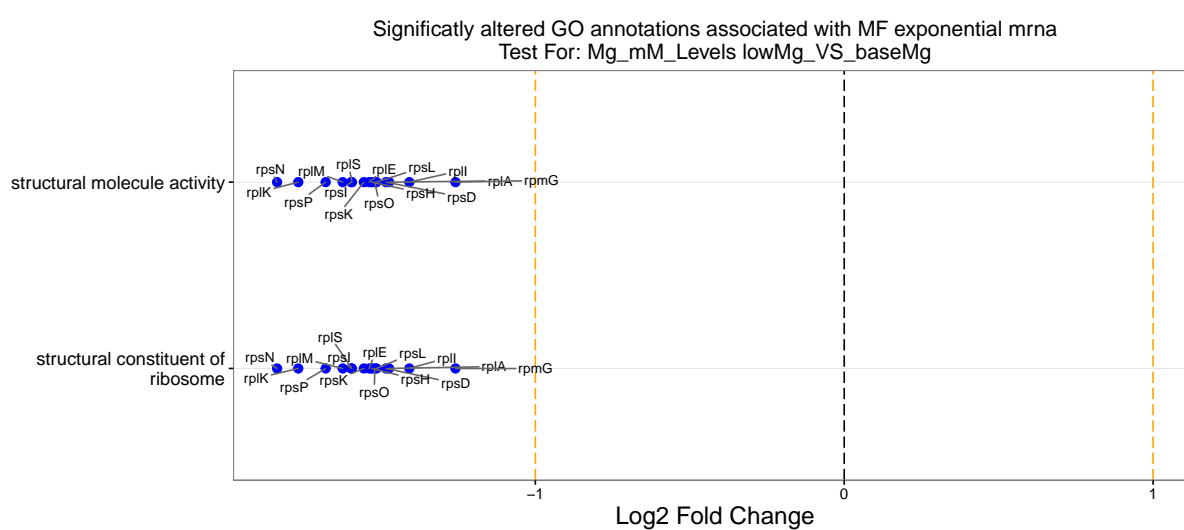


Figure S19: **Significantly differentially expressed GO annotations related with molecular functions and associated genes with low  $Mg^{+2}$  levels in exponential phase, as determined by mRNA abundances.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding genes is shown along the x axis. We show up to 10 most significantly changed pathways and for each pathway, we show up to 15 of the most significantly changing genes.

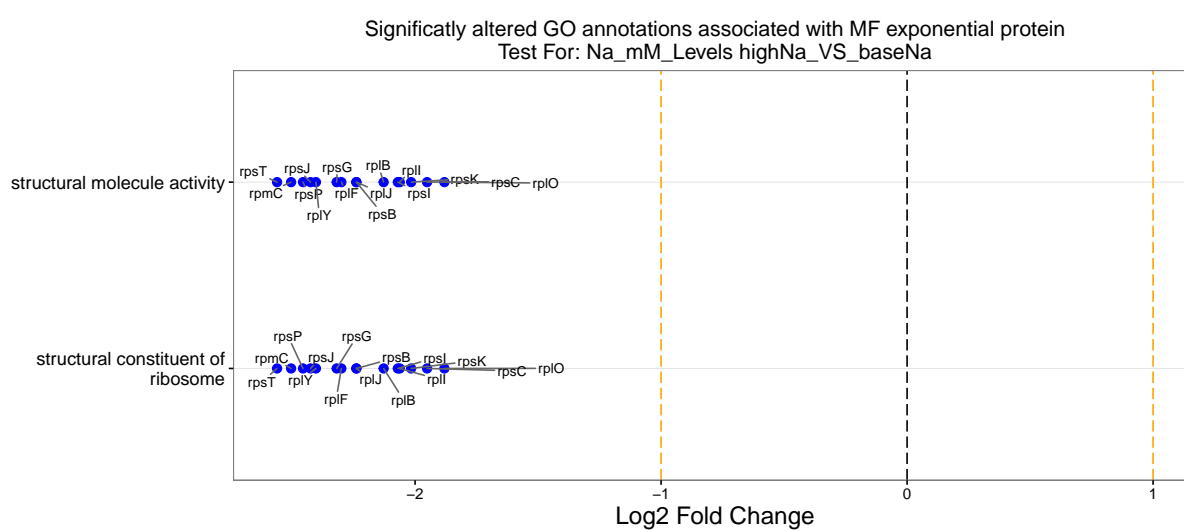


Figure S20: **Significantly differentially expressed GO annotations related with molecular functions and associated genes with high  $\text{Na}^{+1}$  levels in exponential phase, as determined by protein abundances.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding genes is shown along the x axis. We show up to 10 most significantly changed pathways and for each pathway, we show up to 15 of the most significantly changing genes.







Figure S22: This frog was uploaded via the project menu.

Item	Quantity
Widgets	42
Gadgets	13

Table 1: An example table.

## 1 Introduction

Your introduction goes here! Some examples of commonly used commands and features are listed below, to help you get started. If you have a question, please use the help menu (“?”) on the top bar to search for help or ask us a question.

## 2 Some examples to get started

### 2.1 How to include Figures

First you have to upload the image file from your computer using the upload link the project menu. Then use the `includegraphics` command to include it in your document. Use the figure environment and the caption command to add a number and a caption to your figure. See the code for Figure S22 in this section for an example.

### 2.2 How to add Comments

Comments can be added to your project by clicking on the comment icon in the toolbar above. To reply to a comment, simply click the reply button in the lower right corner of the comment, and you can close them when you’re done.

Comments can also be added to the margins of the compiled PDF using the `todo` command, as shown in the example on the right. You can also add inline comments:

This is an inline comment.

Here’s a comment in the margin!

### 2.3 How to add Tables

Use the `table` and `tabular` commands for basic tables — see Table 1, for example.

### 2.4 How to write Mathematics

$\text{\LaTeX}$  is great at typesetting mathematics. Let  $X_1, X_2, \dots, X_n$  be a sequence of independent and identically distributed random variables with  $E[X_i] = \mu$  and  $\text{Var}[X_i] = \sigma^2 < \infty$ , and let

$$S_n = \frac{X_1 + X_2 + \dots + X_n}{n} = \frac{1}{n} \sum_i^n X_i$$

denote their mean. Then as  $n$  approaches infinity, the random variables  $\sqrt{n}(S_n - \mu)$  converge in distribution to a normal  $\mathcal{N}(0, \sigma^2)$ .

## 2.5 How to create Sections and Subsections

Use section and subsections to organize your document. Simply use the section and subsection buttons in the toolbar to create them, and we'll handle all the formatting and numbering automatically.

## 2.6 How to add Lists

You can make lists with automatic numbering ...

1. Like this,
2. and like this.

... or bullet points ...

- Like this,
- and like this.

We hope you find Overleaf useful, and please let us know if you have any feedback using the help menu above.