

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

## Supplementary materials

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## Supplementary Figures

A	mRNA	Protein	
	1.structural constituent of ribosome ▼▼▼ 2.structural molecule activity ▼▼▼		lowMg
			highMg
		1.structural constituent of ribosome ▼▼▼ 2.structural molecule activity ▼▼▼	highNa
	1.structural constituent of ribosome ▼▼▼ 2.structural molecule activity ▼▼▼		glycerol
			gluconate
B			lactate
		1.structural constituent of ribosome ▼▼▼ 2.structural molecule activity ▼▼▼	highNa
			glycerol
			gluconate
			lactate

Figure S1: **Significantly differentially expressed molecular functions, as determined by GO annotations.** For each condition, we show the top-5 differentially expressed molecular functions according to either mRNA or protein abundances. The arrows near pathway names indicate the ratio of significantly up and down regulated genes. if 95%, 80%, 60% or more of the significantly changed genes are up/down regulated then the pathway is labeled with 3, 2, 1 up/down arrows respectively.(A) Exponential phase. (B) Stationary phase.

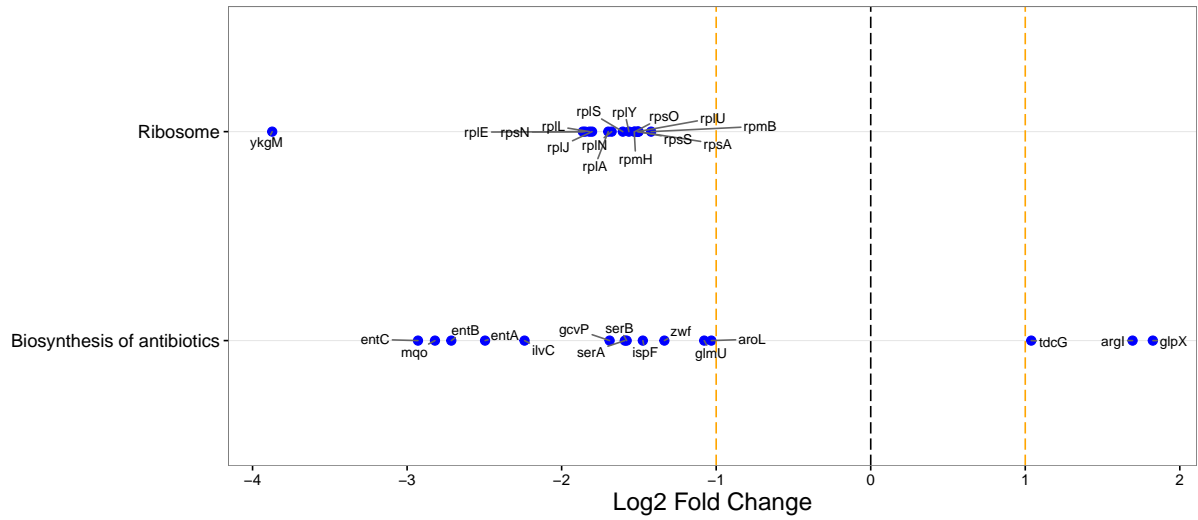


Figure S2: **Significantly differentially expressed KEGG pathways and associated genes with glycerol as carbon source, as determined by mRNA abundances in exponential phase.** The top differentially expressed KEGG pathways are shown along the *y* axis, and the relative fold change of the corresponding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

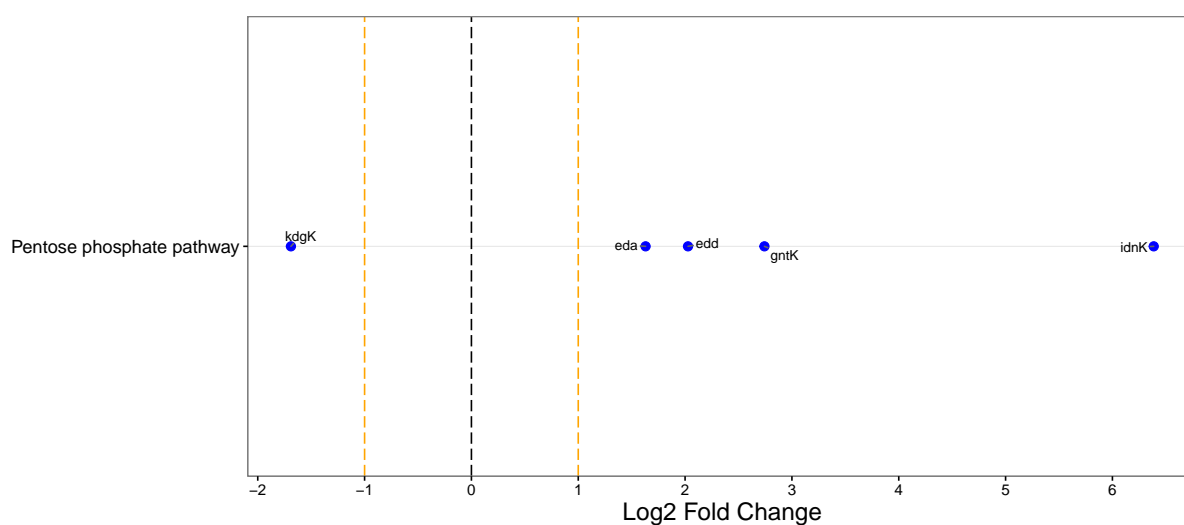


Figure S3: **Significantly differentially expressed KEGG pathways and associated genes with gluconate as carbon source, as determined by mRNA abundances in exponential phase.** The top differentially expressed KEGG pathways are shown along the  $y$  axis, and the relative fold change of the corresponding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

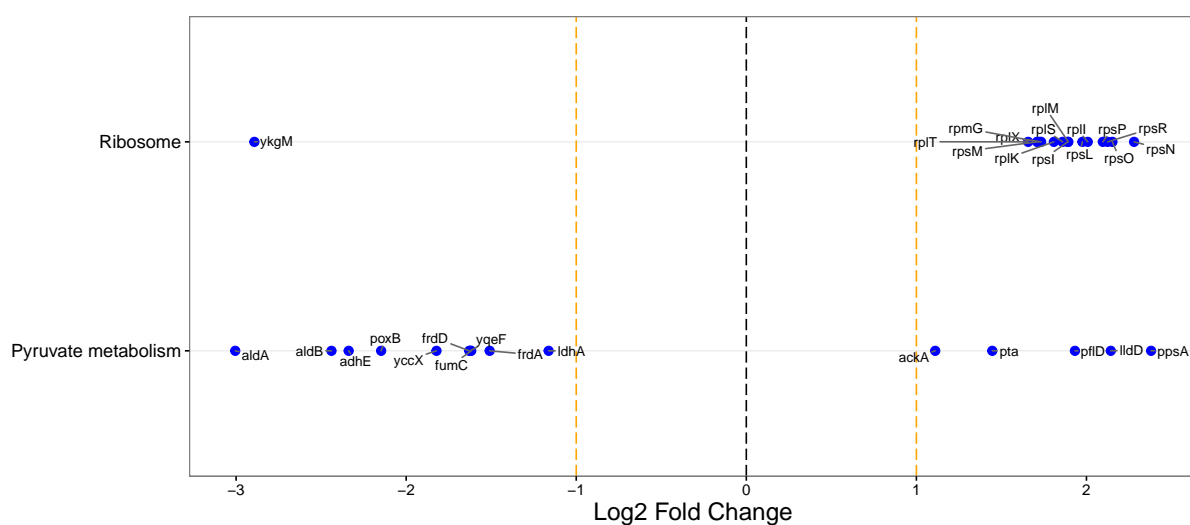


Figure S4: **Significantly differentially expressed KEGG pathways and associated genes with lactate as carbon source, as determined by mRNA abundances in exponential phase.** The top differentially expressed KEGG pathways are shown along the  $y$  axis, and the relative fold change of the corresponding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

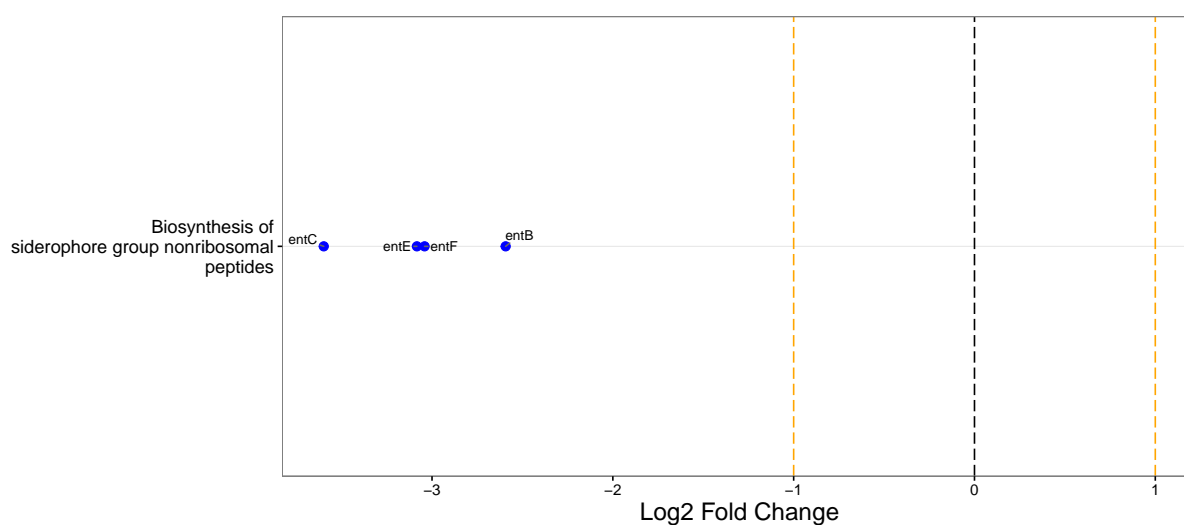


Figure S5: **Significantly differentially expressed KEGG pathways and associated genes with gluconate as carbon source, as determined by protein abundances in exponential phase.** The top differentially expressed KEGG pathways are shown along the  $y$  axis, and the relative fold change of the corresponding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



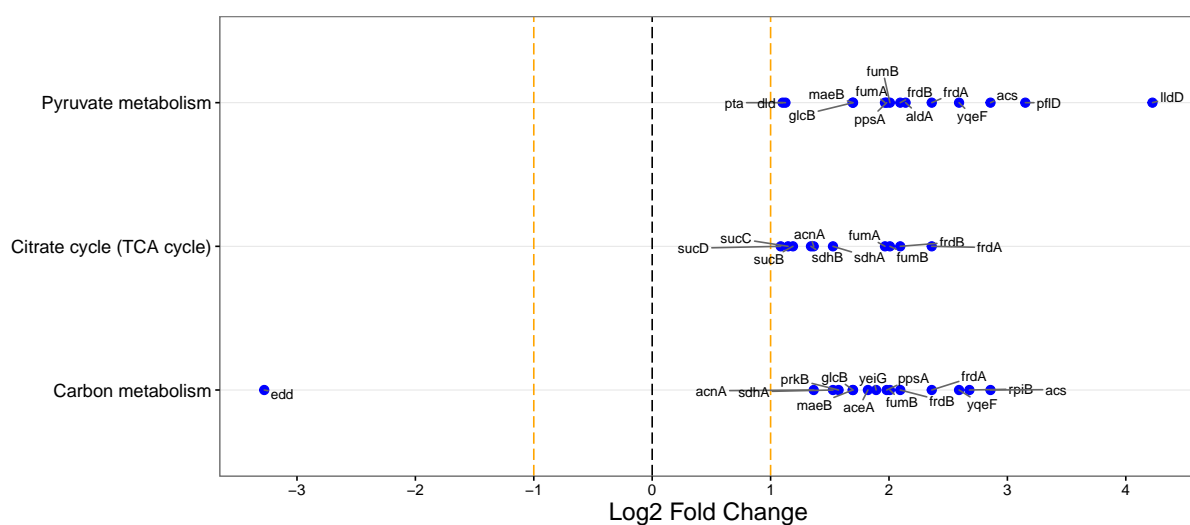


Figure S6: **Significantly differentially expressed KEGG pathways and associated genes with lactate as carbon source, as determined by protein abundances in exponential phase.** The top differentially expressed KEGG pathways are shown along the  $y$  axis, and the relative fold change of the corresponding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

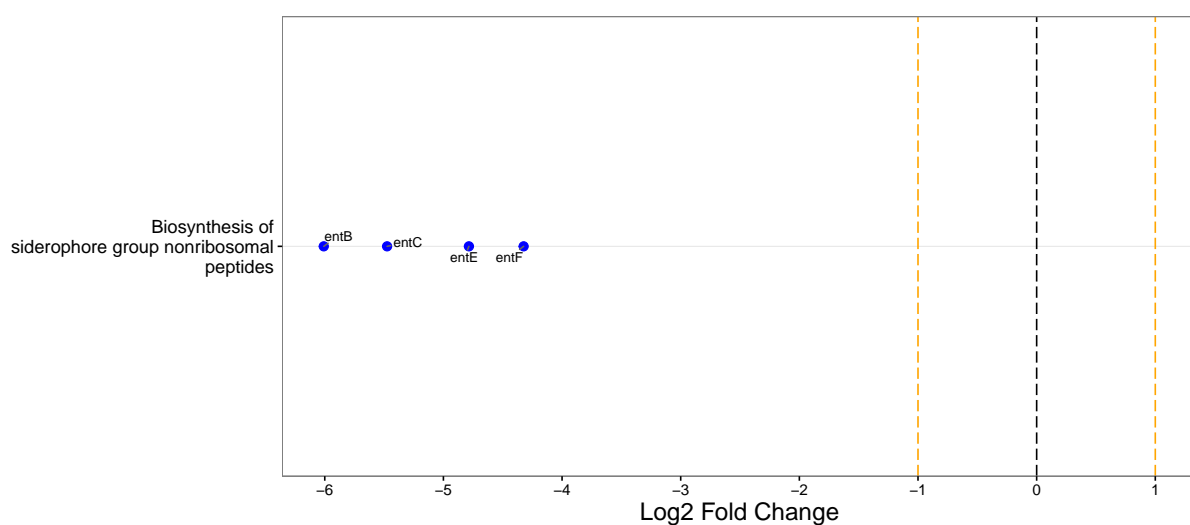


Figure S7: **Significantly differentially expressed KEGG pathways and associated genes with glycerol as carbon source, as determined by protein abundances in stationary phase.** The top differentially expressed KEGG pathways are shown along the  $y$  axis, and the relative fold change of the corresponding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

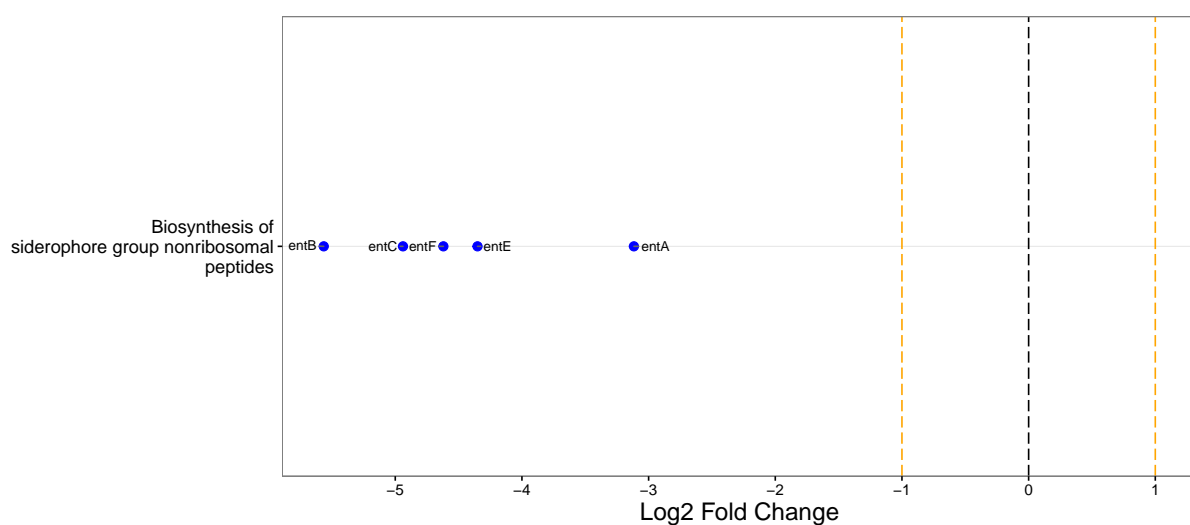


Figure S8: **Significantly differentially expressed KEGG pathways and associated genes with gluconate as carbon source, as determined by protein abundances in stationary phase.** The top differentially expressed KEGG pathways are shown along the  $y$  axis, and the relative fold change of the corresponding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

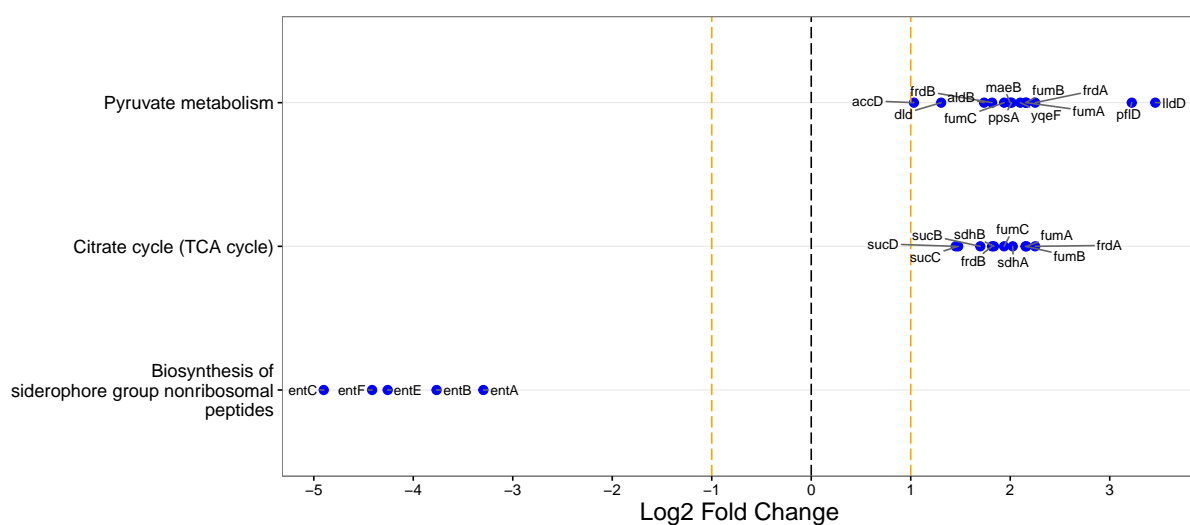


Figure S9: **Significantly differentially expressed KEGG pathways and associated genes with lactate as carbon source, as determined by protein abundances in stationary phase.** The top differentially expressed KEGG pathways are shown along the  $y$  axis, and the relative fold change of the corresponding genes is shown along the  $x$  axis. We show up to 10 of the most significantly changed pathways and for each pathway, we show up to 15 of the most significantly changing genes.

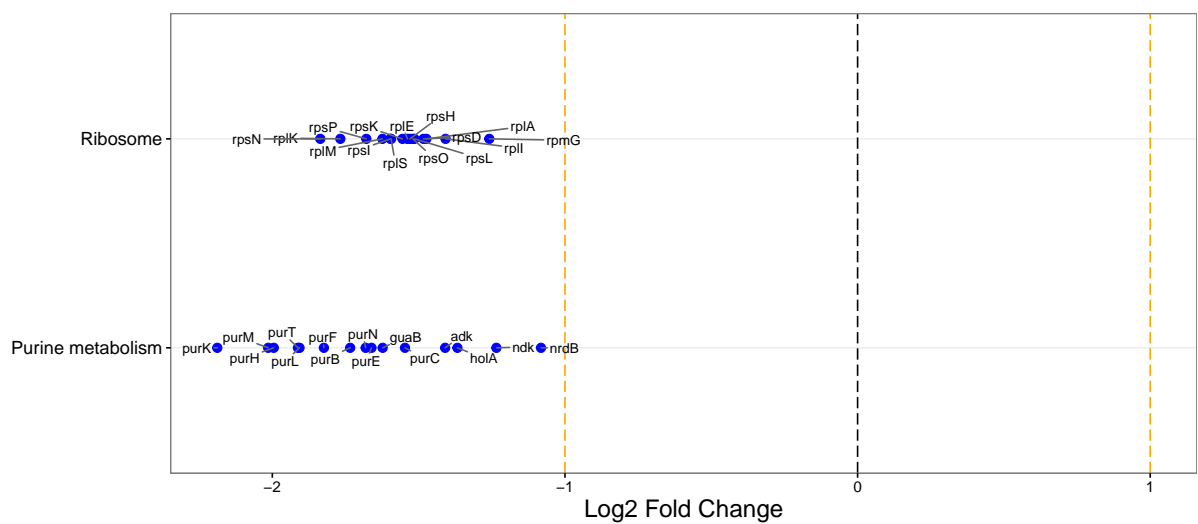


Figure S10: **Significantly differentially expressed KEGG pathways and associated genes with low  $Mg^{2+}$  levels, as determined by mRNA abundances in exponential phase.** The top differentially expressed KEGG pathways are shown along the  $y$  axis, and the relative fold change of the corresponding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

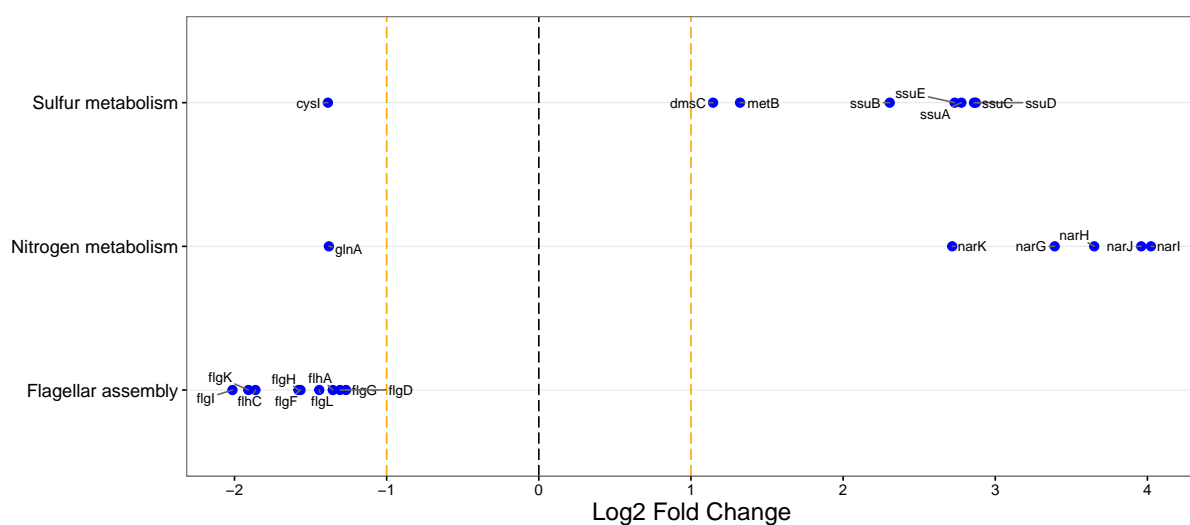


Figure S11: **Significantly differentially expressed KEGG pathways and associated genes with high  $\text{Mg}^{2+}$  levels, as determined by mRNA abundances in exponential phase.** The top differentially expressed KEGG pathways are shown along the  $y$  axis, and the relative fold change of the corresponding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

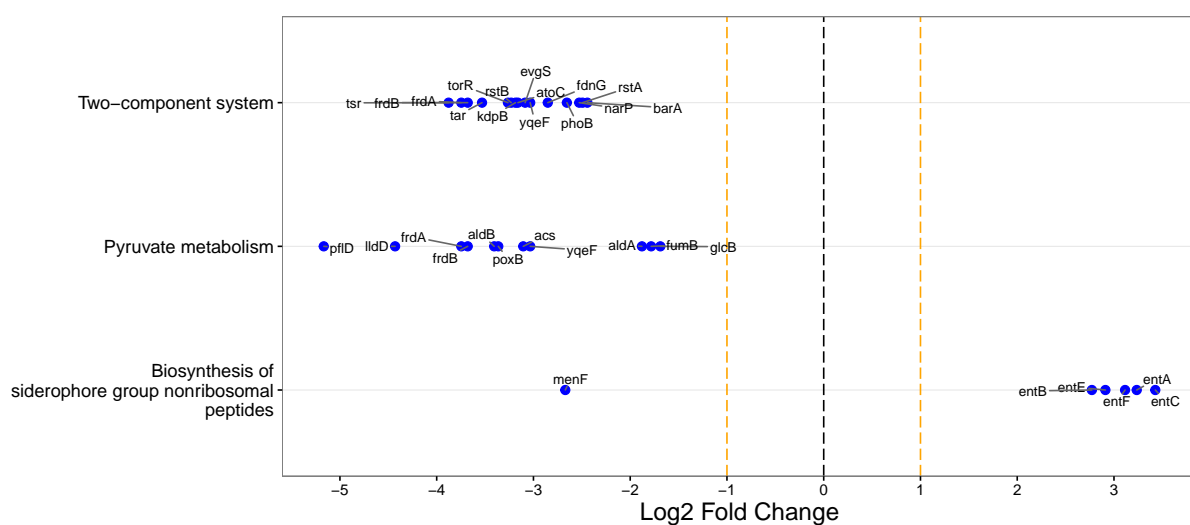


Figure S12: **Significantly differentially expressed KEGG pathways and associated genes with high  $Mg^{2+}$  levels, as determined by protein abundances in exponential phase.** The top differentially expressed KEGG pathways are shown along the  $y$  axis, and the relative fold change of the corresponding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

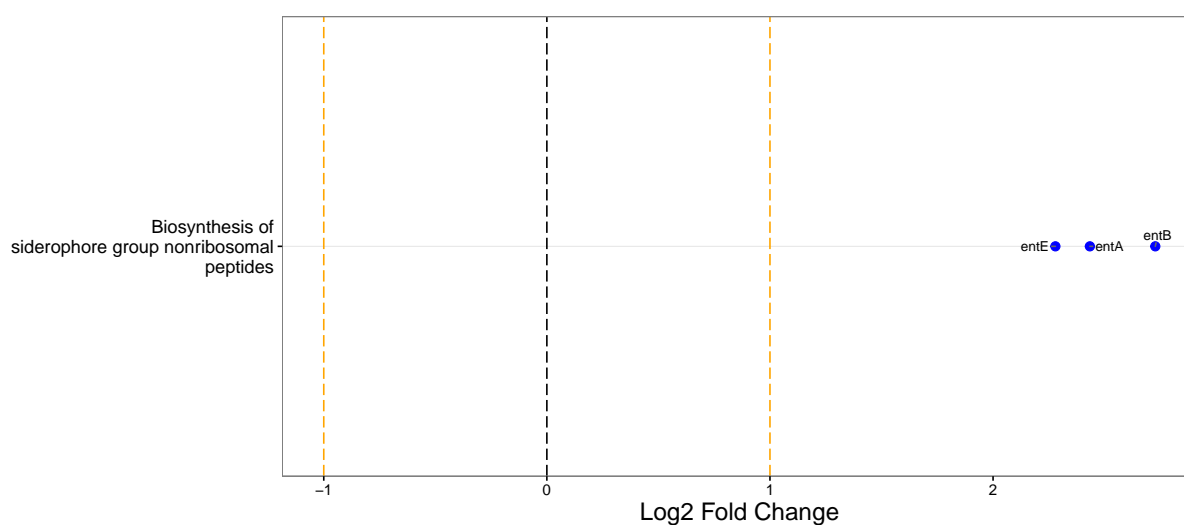


Figure S13: **Significantly differentially expressed KEGG pathways and associated genes with high  $\text{Mg}^{2+}$  levels, as determined by mRNA abundances in stationary phase.** The top differentially expressed KEGG pathways are shown along the  $y$  axis, and the relative fold change of the corresponding genes is shown along the  $x$  axis. We show up to 10 of the most significantly changed pathways and for each pathway, we show up to 15 of the most significantly changing genes.



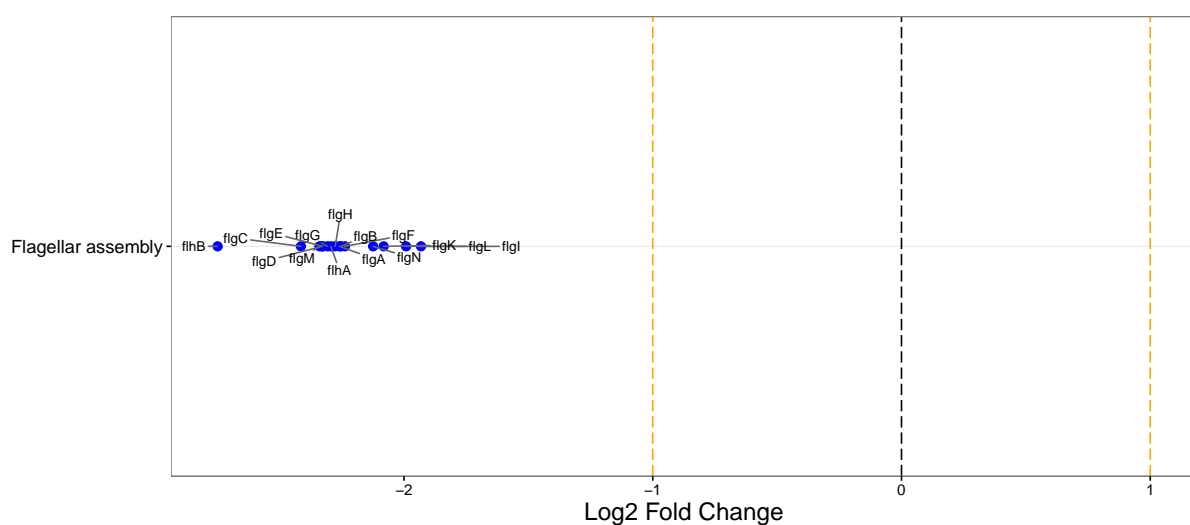


Figure S14: **Significantly differentially expressed KEGG pathways and associated genes with high  $\text{Na}^+$  levels, as determined by mRNA abundances in exponential phase.** The top differentially expressed KEGG pathways are shown along the  $y$  axis, and the relative fold change of the corresponding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

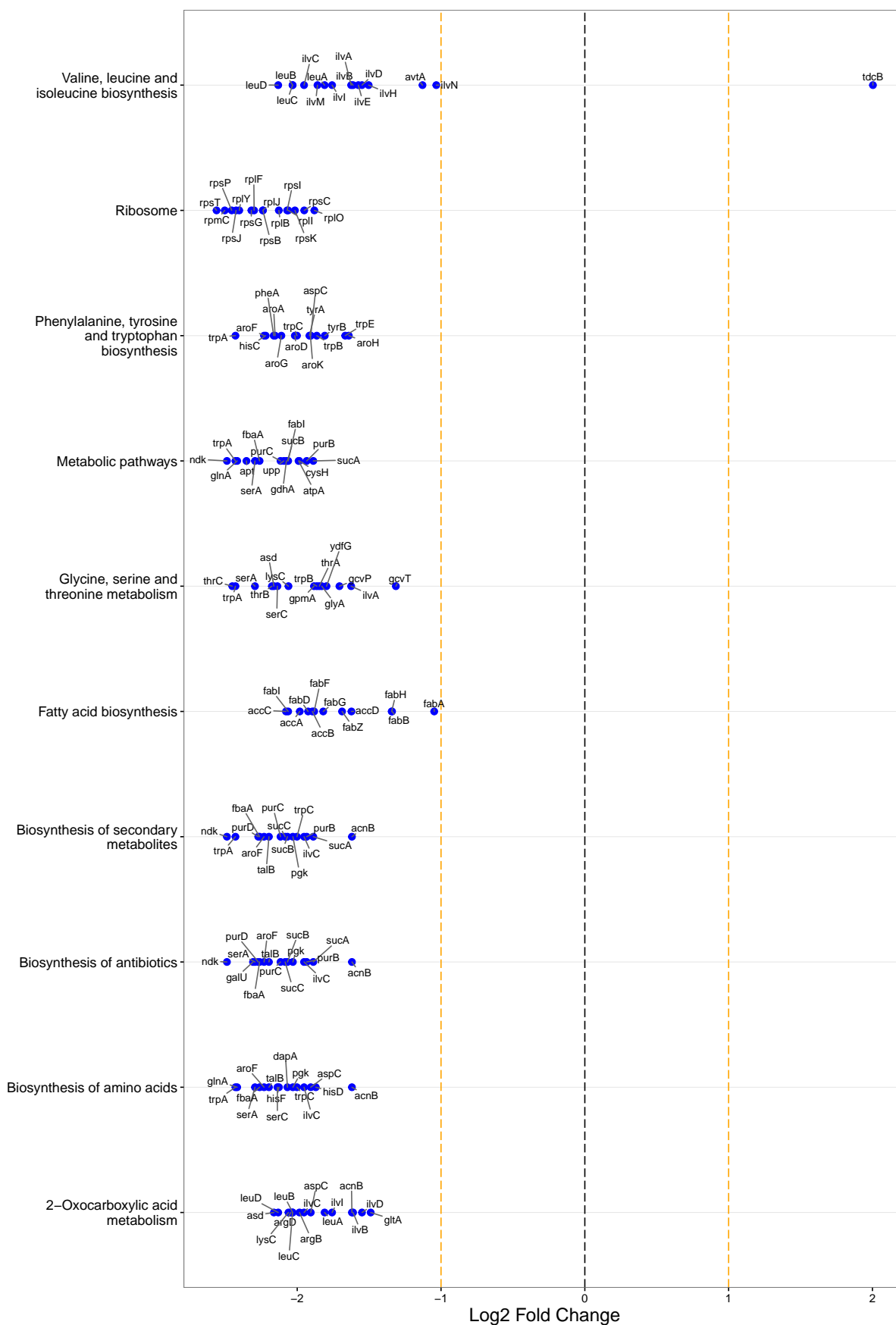


Figure S15: **Significantly differentially expressed KEGG pathways and associated genes with high  $\text{Na}^+$  levels, as determined by protein abundances in exponential phase.** The top differentially expressed KEGG pathways are shown along the  $y$  axis, and the relative fold change of the corresponding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

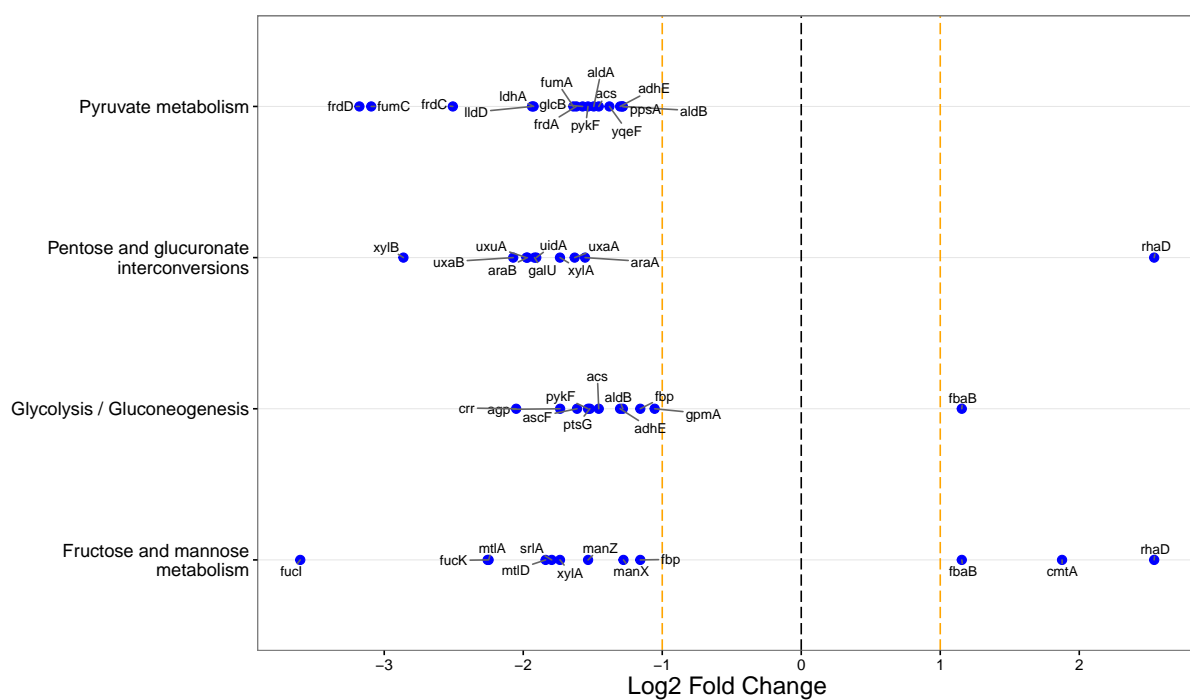


Figure S16: **Significantly differentially expressed KEGG pathways and associated genes with high  $\text{Na}^+$  levels, as determined by mRNA abundances in stationary phase.** The top differentially expressed KEGG pathways are shown along the  $y$  axis, and the relative fold change of the corresponding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

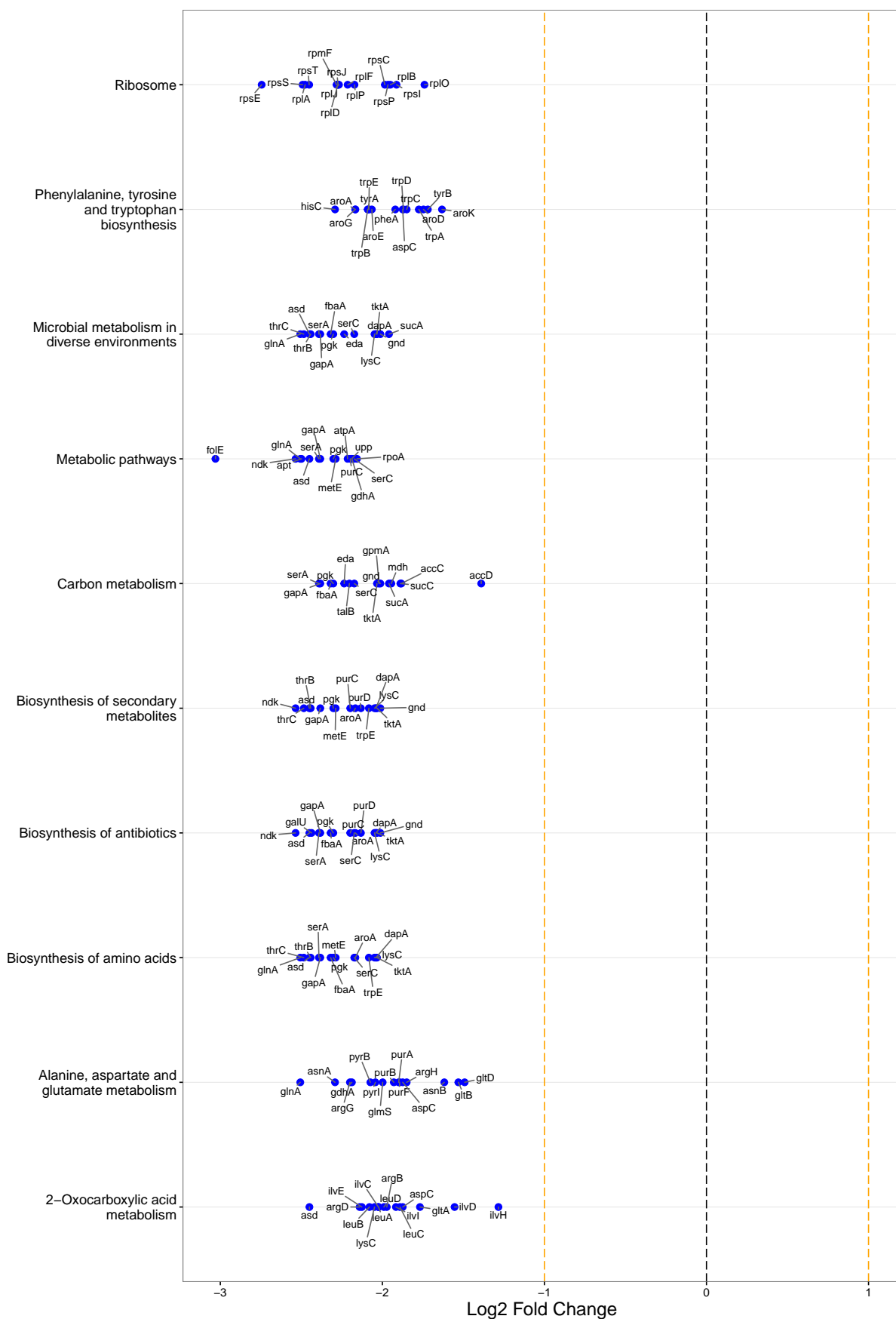


Figure S17: **Significantly differentially expressed KEGG pathways and associated genes with high  $\text{Na}^+$  levels, as determined by protein abundances in stationary phase.** The top differentially expressed KEGG pathways are shown along the  $y$  axis, and the relative fold change of the corresponding genes is shown along the  $x$  axis. We show up to 10 of the most significantly changed pathways and for each pathway, we show up to 15 of the most significantly changing genes.

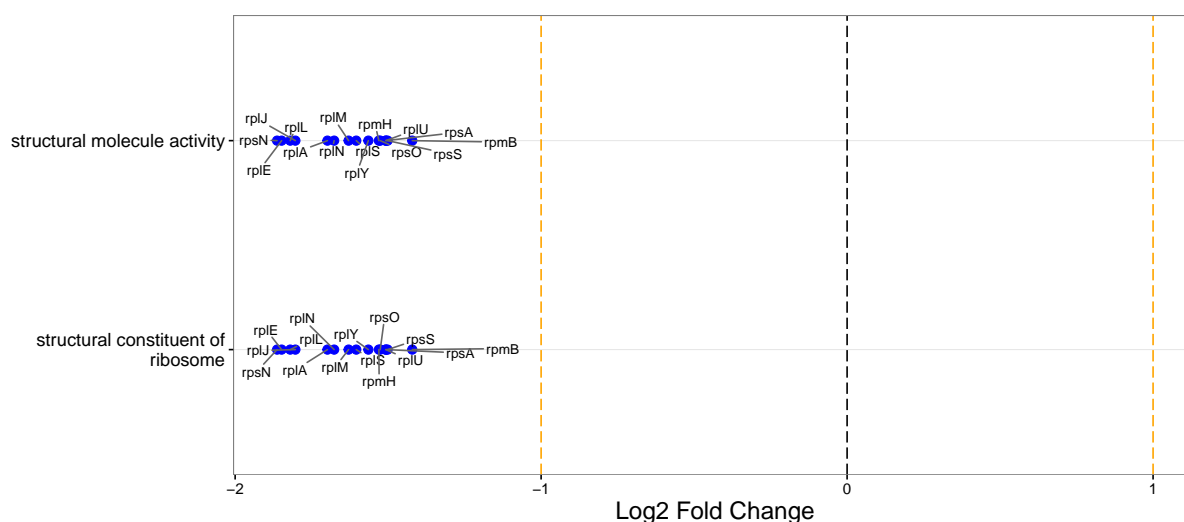


Figure S18: **Significantly differentially expressed GO annotations related with molecular functions and associated genes with glycerol as carbon source, as determined by mRNA abundances in exponential phase.** The top differentially expressed KEGG pathways are shown along the  $y$  axis, and the relative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

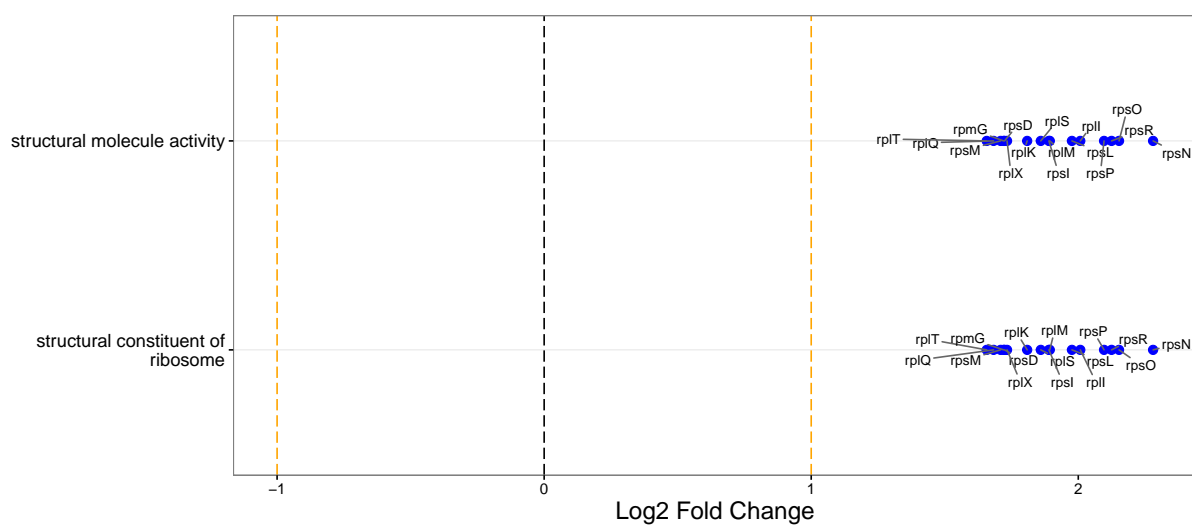


Figure S19: **Significantly differentially expressed GO annotations related with molecular functions and associated genes with lactate as carbon source, as determined by mRNA abundances in exponential phase.** The top differentially expressed KEGG pathways are shown along the  $y$  axis, and the relative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

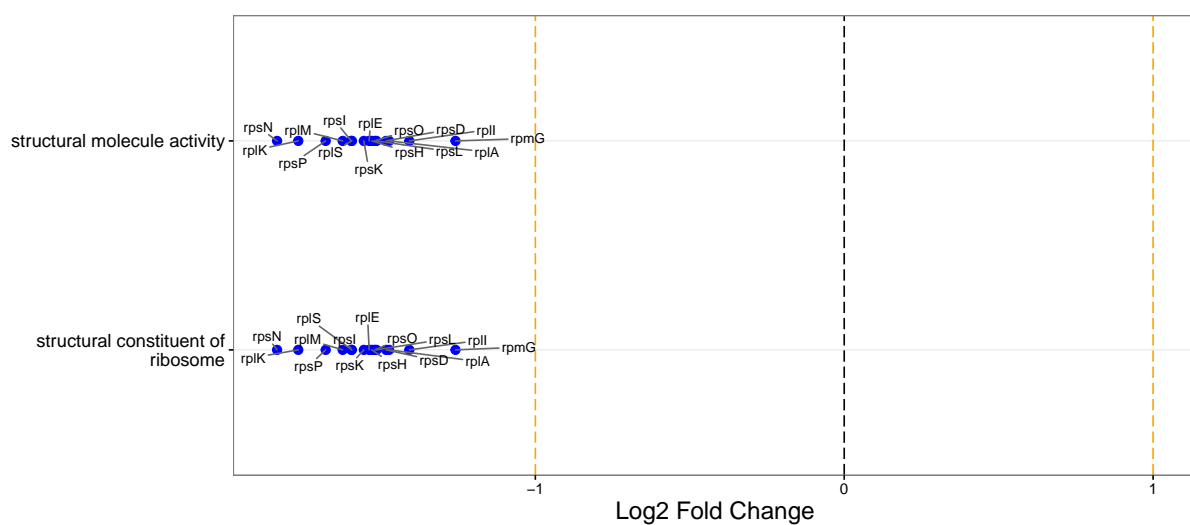


Figure S20: **Significantly differentially expressed GO annotations related with molecular functions and associated genes with low  $Mg^{2+}$  levels, as determined by mRNA abundances in exponential phase.** The top differentially expressed KEGG pathways are shown along the  $y$  axis, and the relative fold change of the corresponding genes is shown along the  $x$  axis. We show up to 10 of the most significantly changed pathways and for each pathway, we show up to 15 of the most significantly changing genes.

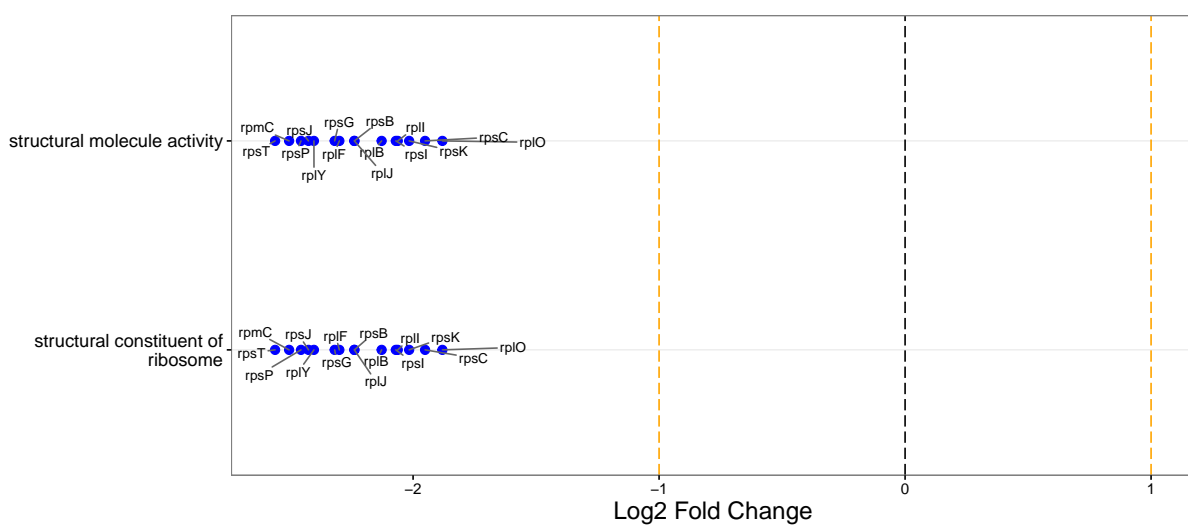


Figure S21: **Significantly differentially expressed GO annotations related with molecular functions and associated genes with high  $\text{Na}^+$  levels, as determined by protein abundances in exponential phase.** The top differentially expressed KEGG pathways are shown along the  $y$  axis, and the relative fold change of the corresponding genes is shown along the  $x$  axis. We show up to 10 of the most significantly changed pathways and for each pathway, we show up to 15 of the most significantly changing genes.



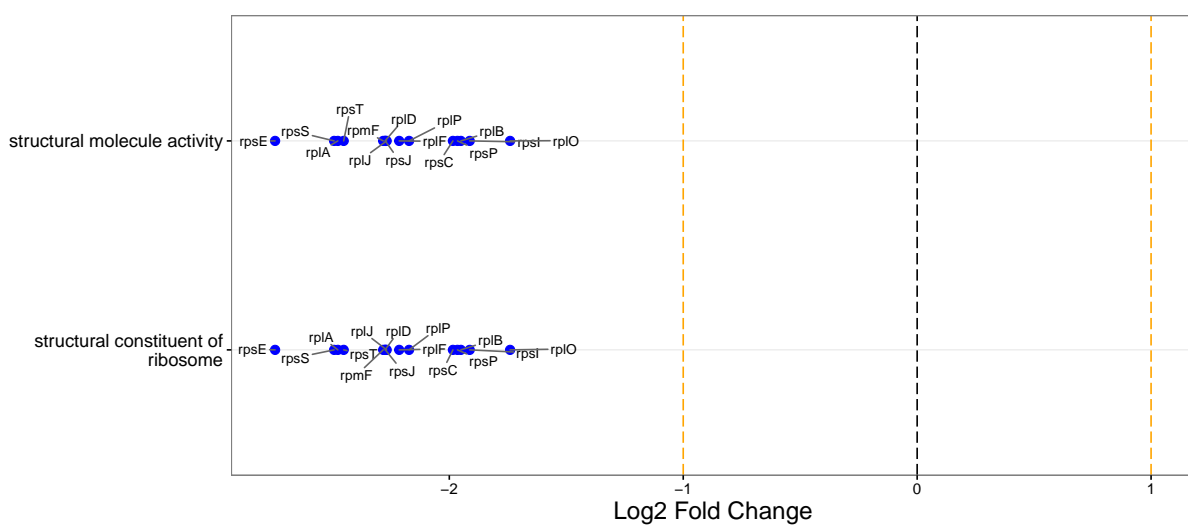


Figure S22: **Significantly differentially expressed GO annotations related with molecular functions and associated genes with high  $\text{Na}^+$  levels, as determined by protein abundances in stationary phase.** The top differentially expressed KEGG pathways are shown along the  $y$  axis, and the relative fold change of the corresponding genes is shown along the  $x$  axis. We show up to 10 of the most significantly changed pathways and for each pathway, we show up to 15 of the most significantly changing genes.

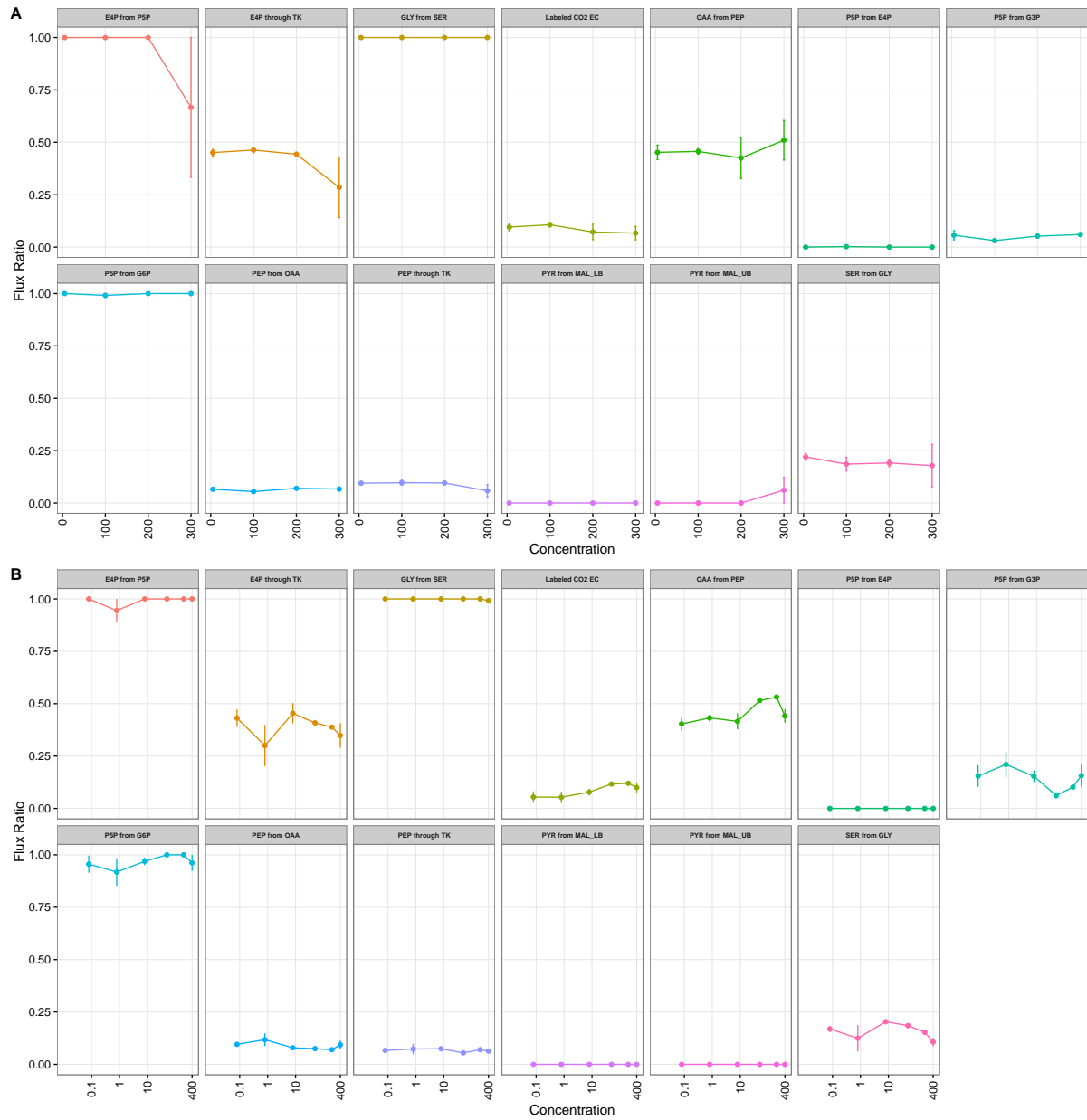


Figure S23: **Flux ratios versus ion concentrations.** 13 different flux were measured with respect to four different Na<sup>+</sup> and five different Mg<sup>2+</sup> concentrations. (A) Concentrations with respect to changing Na<sup>+</sup> concentrations. (B) Concentrations with respect to changing Mg<sup>2+</sup> concentrations. There was no significant trend of increase or decrease in flux ratios with respect to either Na<sup>+</sup> or Mg<sup>2+</sup> concentrations (Supplementary Table 5).