

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	mRNA	Protein	
			lowMg
			highMg
		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 next to pathway names indicate the proportion of up- and down-regulated genes among the significantly differentially expressed genes in this pathway. One up arrow indicates that 60% or more of the genes are up-regulated, two arrows correspond to 80% or more genes, and three arrows correspond to 95% or more genes being up-regulated. Similarly, down arrows indicate the proportion of down-regulated genes. (A) Exponential phase. (B) Stationary phase.

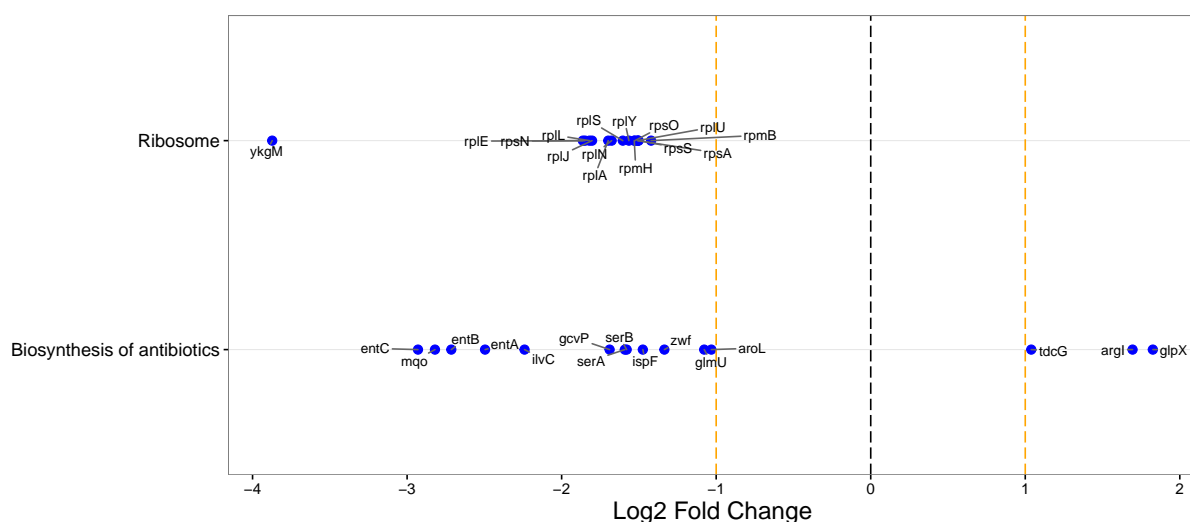


Figure S2: **Significantly differentially expressed KEGG pathways and associated genes with glycerol as carbon source, as determined by mRNA abundances in exponential phase.** The top differentially expressed KEGG pathways are shown along the *y* axis, and the relative fold change of the corresponding 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.

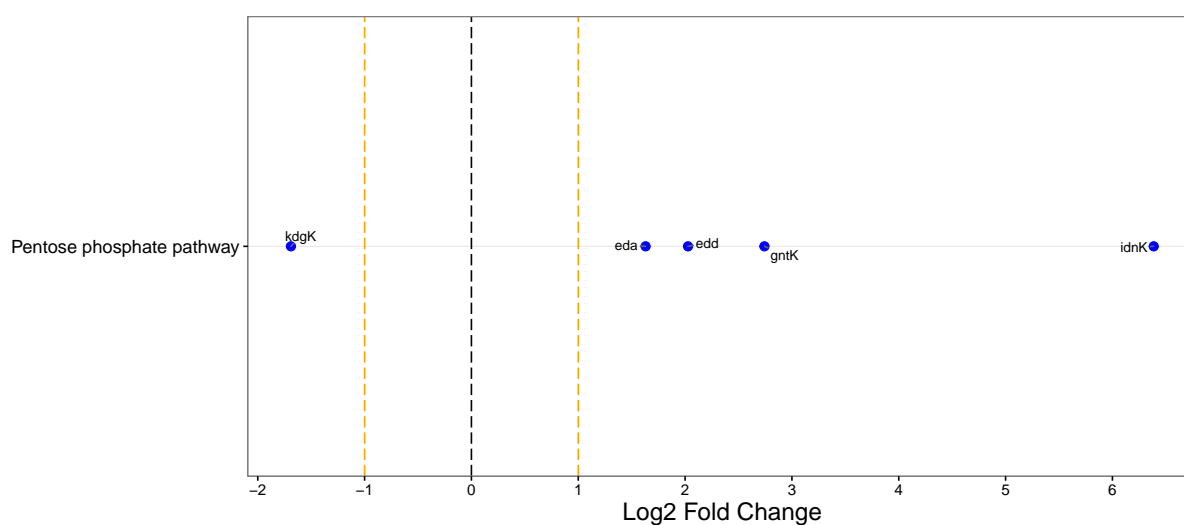


Figure S3: **Significantly differentially expressed KEGG pathways and associated genes with gluconate as carbon source, as determined by mRNA abundances in exponential phase.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding 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.

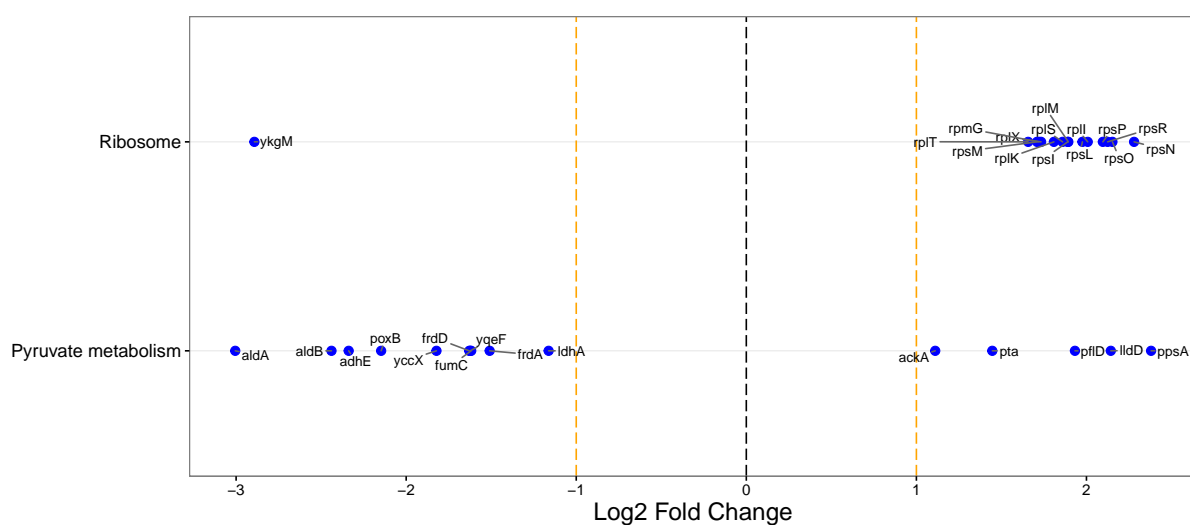


Figure S4: **Significantly differentially expressed KEGG pathways and associated genes with lactate as carbon source, as determined by mRNA abundances in exponential phase.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding genes 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.

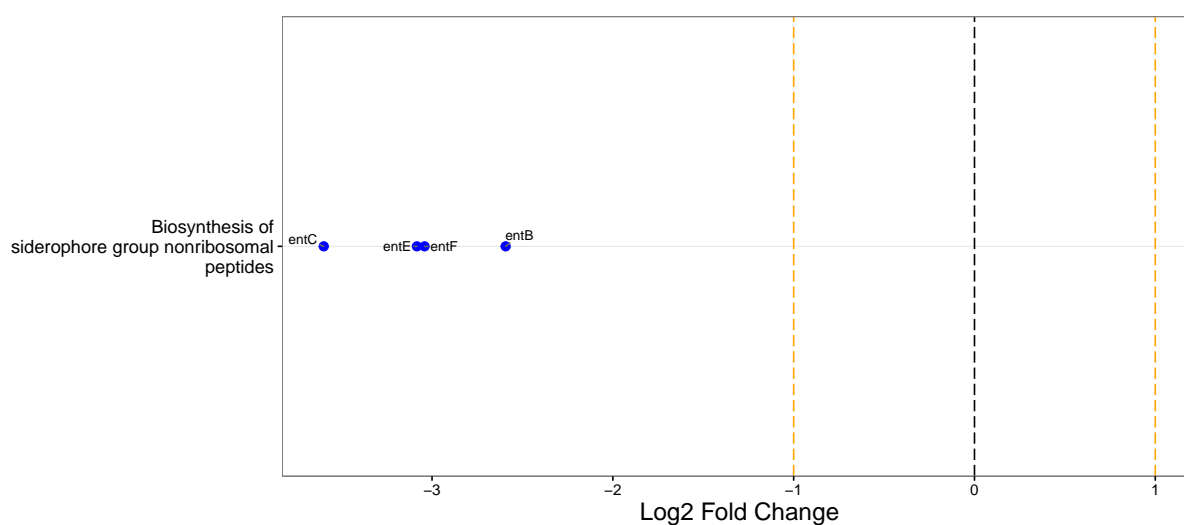


Figure S5: **Significantly differentially expressed KEGG pathways and associated genes with gluconate as carbon source, as determined by protein abundances in exponential phase.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding 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.

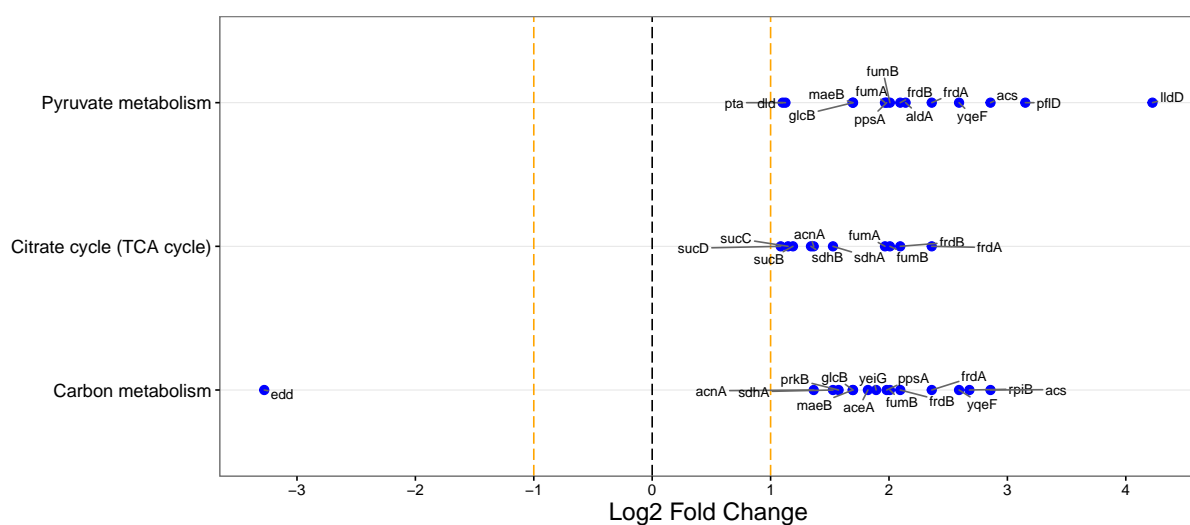


Figure S6: **Significantly differentially expressed KEGG pathways and associated genes with lactate as carbon source, as determined by protein abundances in exponential phase.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding 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.

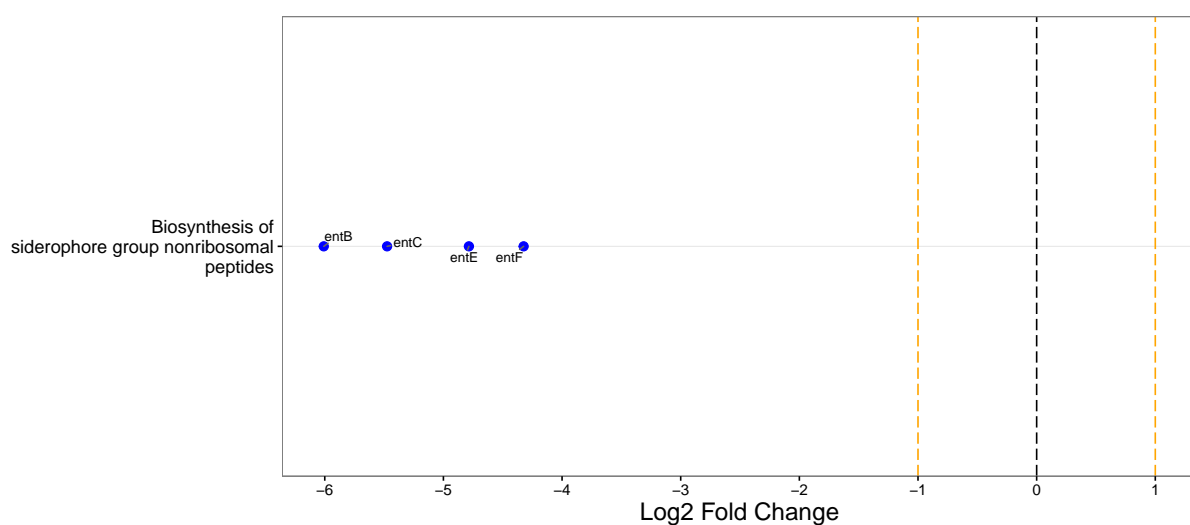


Figure S7: **Significantly differentially expressed KEGG pathways and associated genes with glycerol as carbon source, as determined by protein abundances in stationary phase.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding 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.

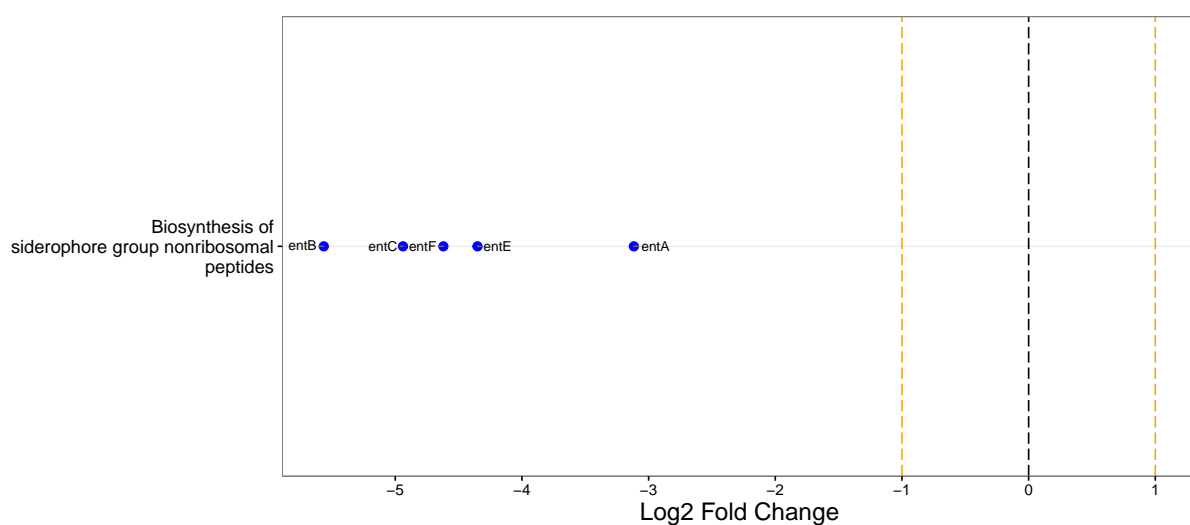


Figure S8: **Significantly differentially expressed KEGG pathways and associated genes with gluconate as carbon source, as determined by protein abundances in stationary phase.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding 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.

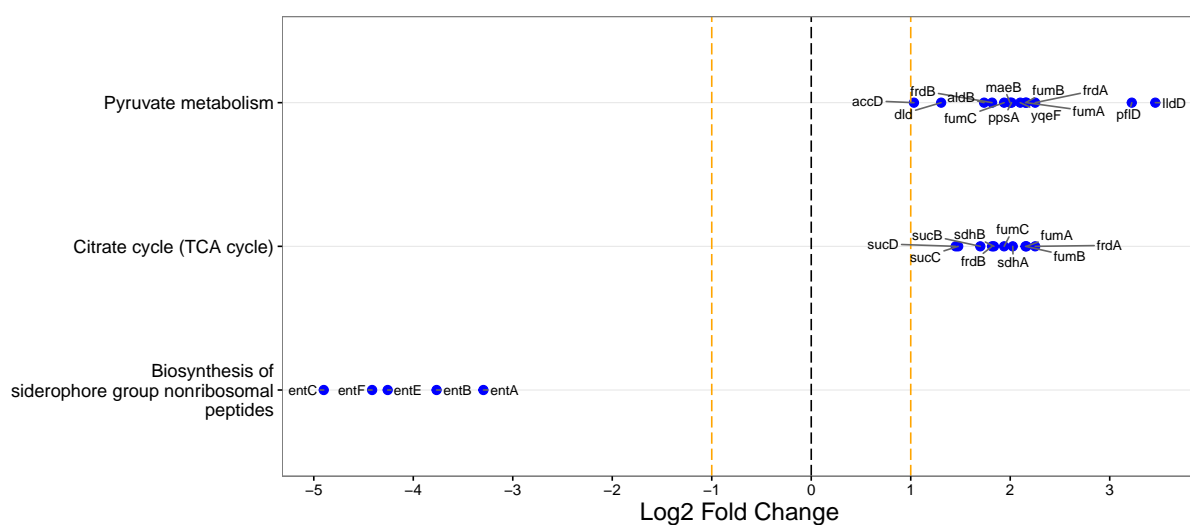


Figure S9: **Significantly differentially expressed KEGG pathways and associated genes with lactate as carbon source, as determined by protein abundances in stationary phase.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding 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.

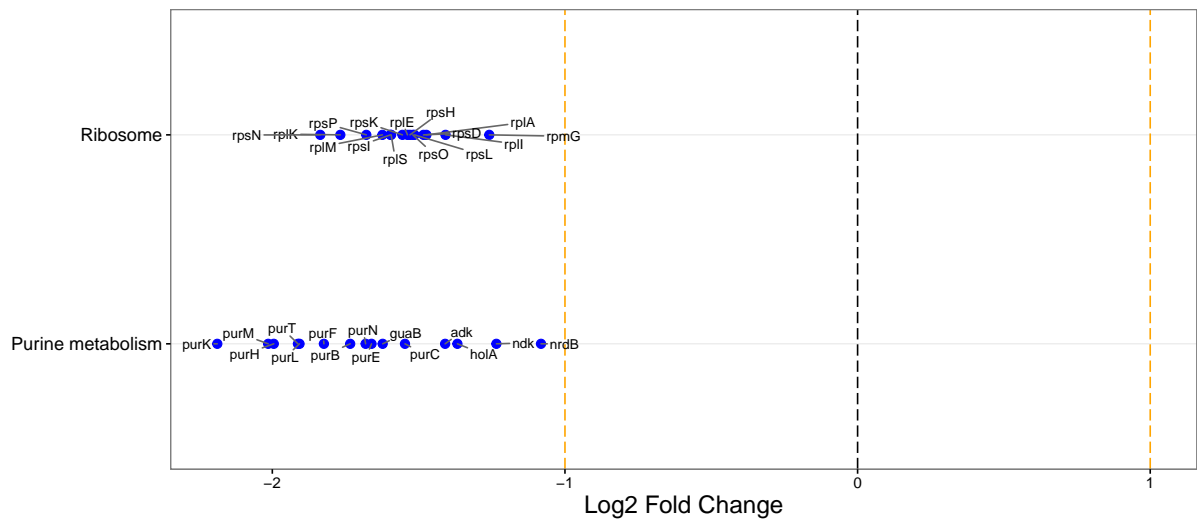


Figure S10: **Significantly differentially expressed KEGG pathways and associated genes with low Mg^{2+} levels, as determined by mRNA abundances in exponential phase.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding genes 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.

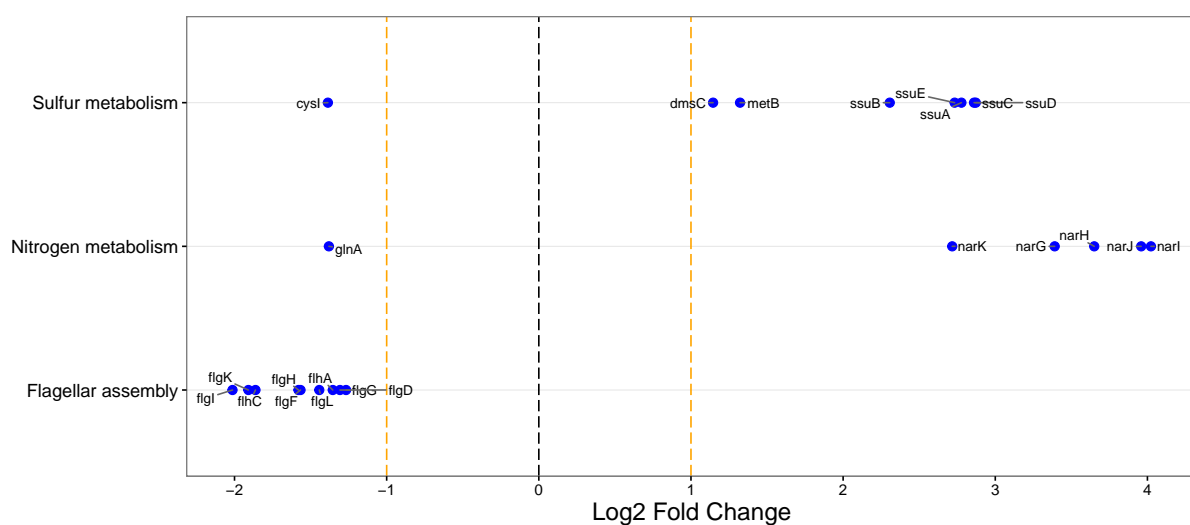


Figure S11: **Significantly differentially expressed KEGG pathways and associated genes with high Mg^{2+} levels, as determined by mRNA abundances in exponential phase.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding genes 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.

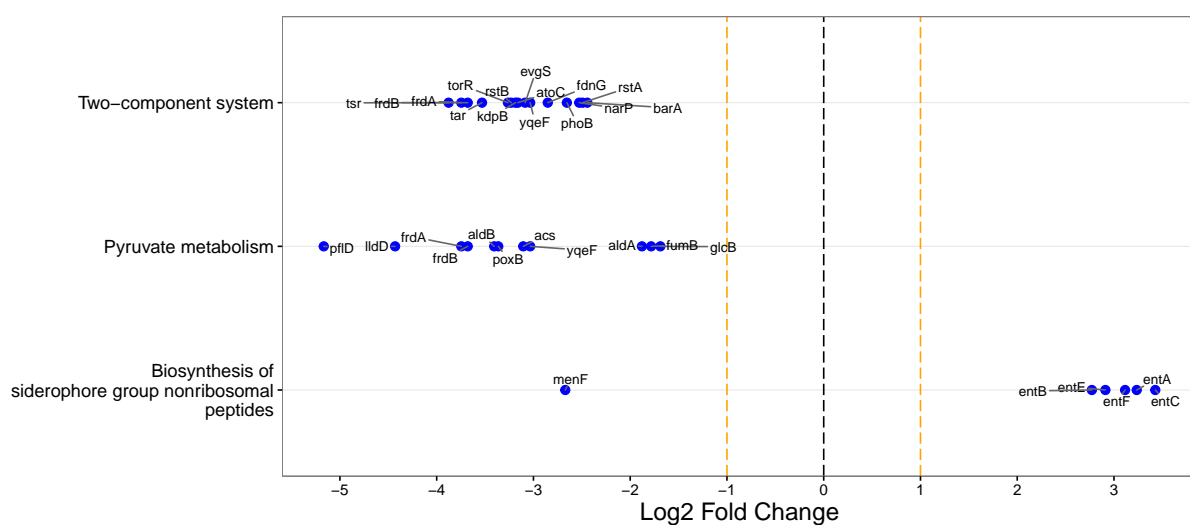


Figure S12: **Significantly differentially expressed KEGG pathways and associated genes with high Mg^{2+} levels, as determined by protein abundances in exponential phase.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding genes 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.

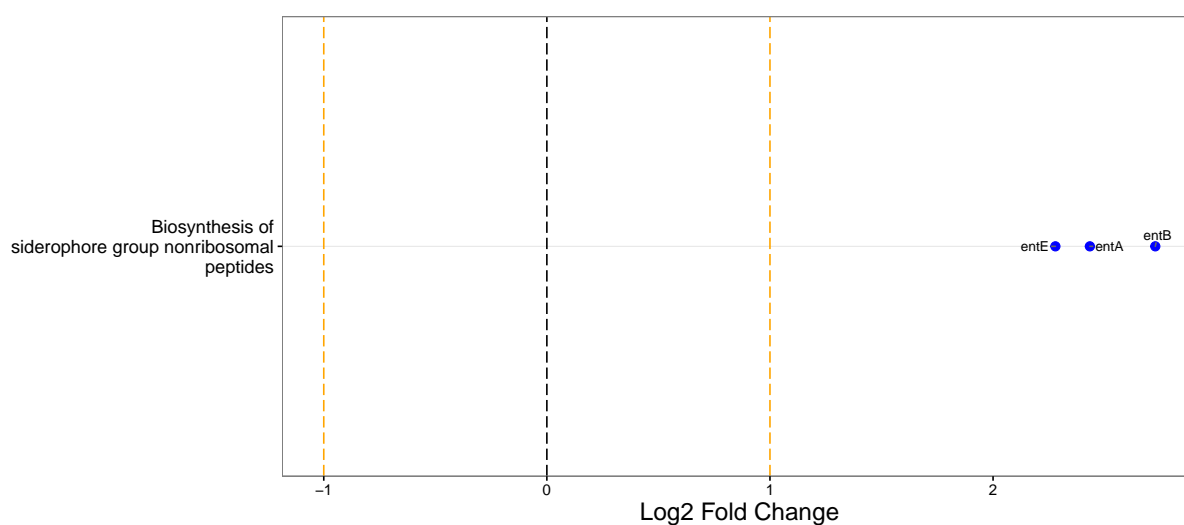


Figure S13: **Significantly differentially expressed KEGG pathways and associated genes with high Mg^{2+} levels, as determined by mRNA abundances in stationary phase.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding genes 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.

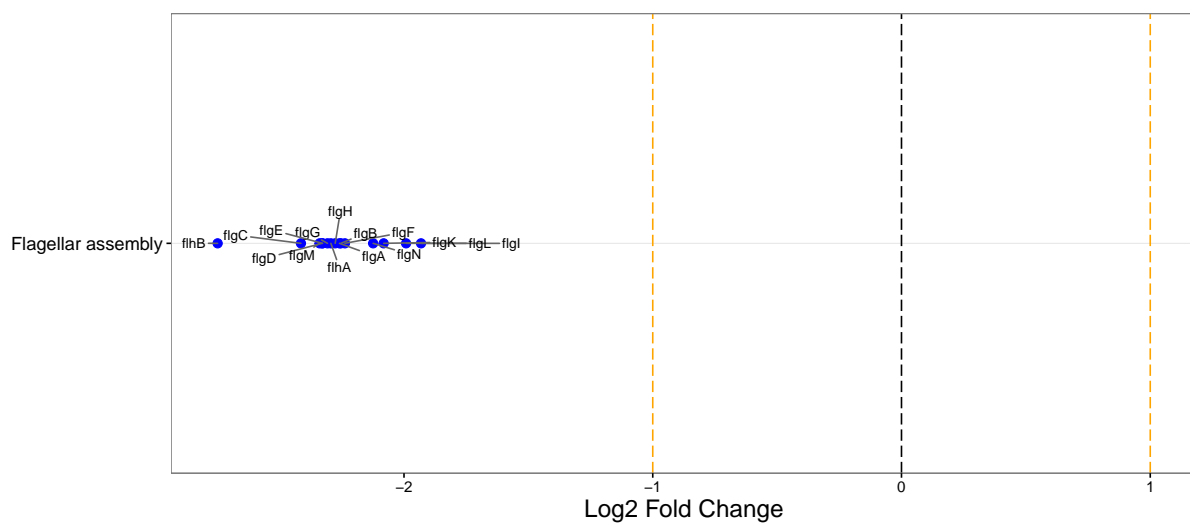


Figure S14: **Significantly differentially expressed KEGG pathways and associated genes with high Na^+ levels, as determined by mRNA abundances in exponential phase.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding genes is 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.

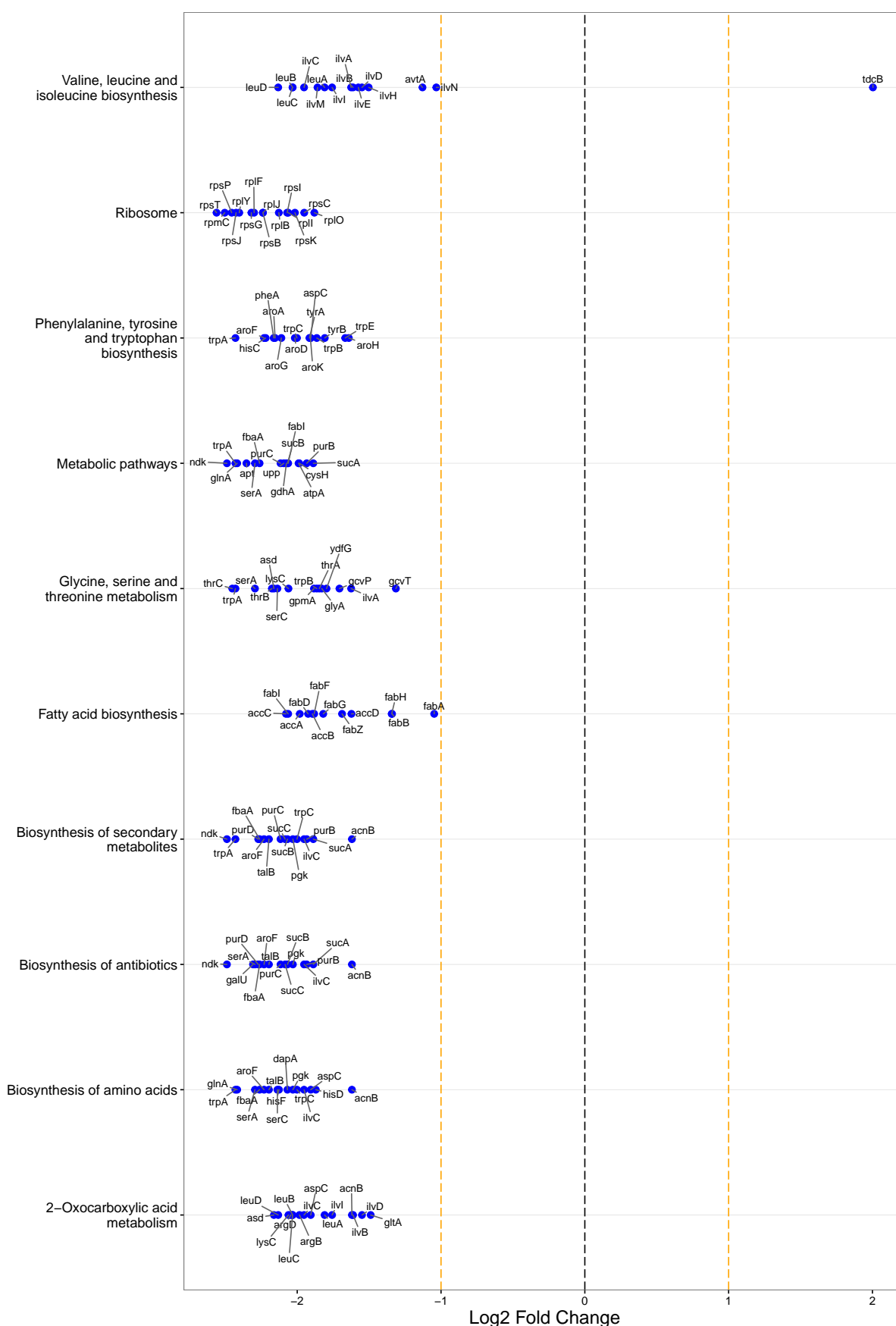


Figure S15: Significantly differentially expressed KEGG pathways and associated genes with high Na^+ levels, as determined by protein abundances in exponential phase. The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding genes is 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.

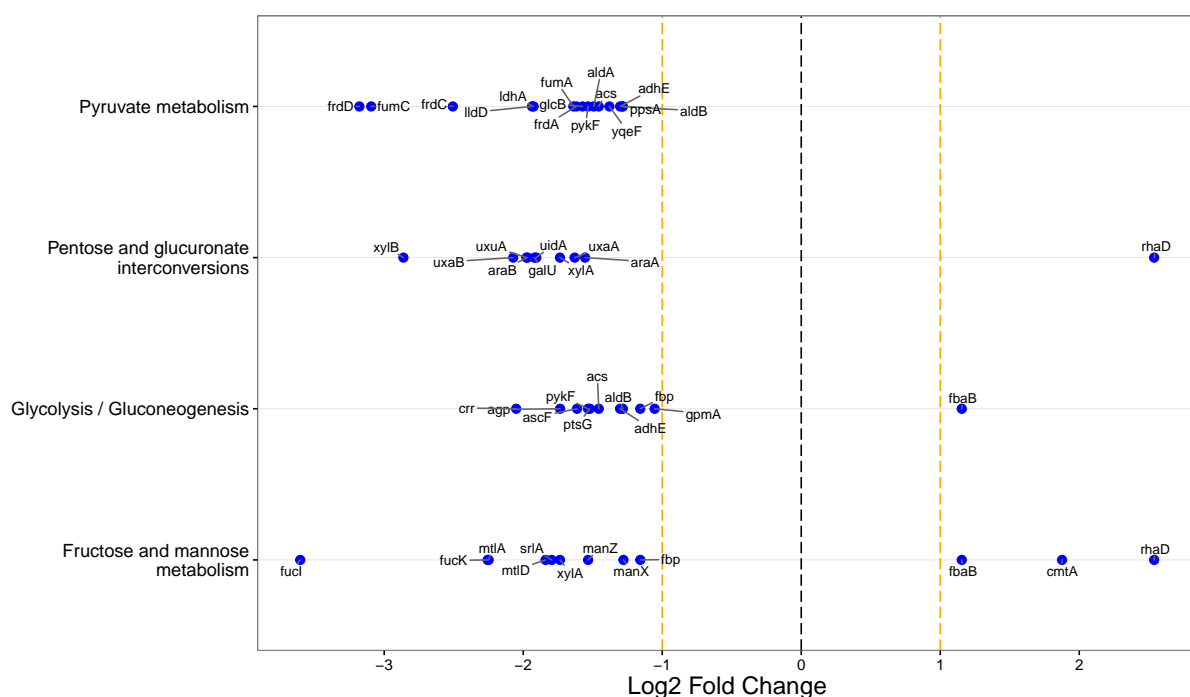


Figure S16: **Significantly differentially expressed KEGG pathways and associated genes with high Na^+ levels, as determined by mRNA abundances in stationary phase.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding genes is 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.

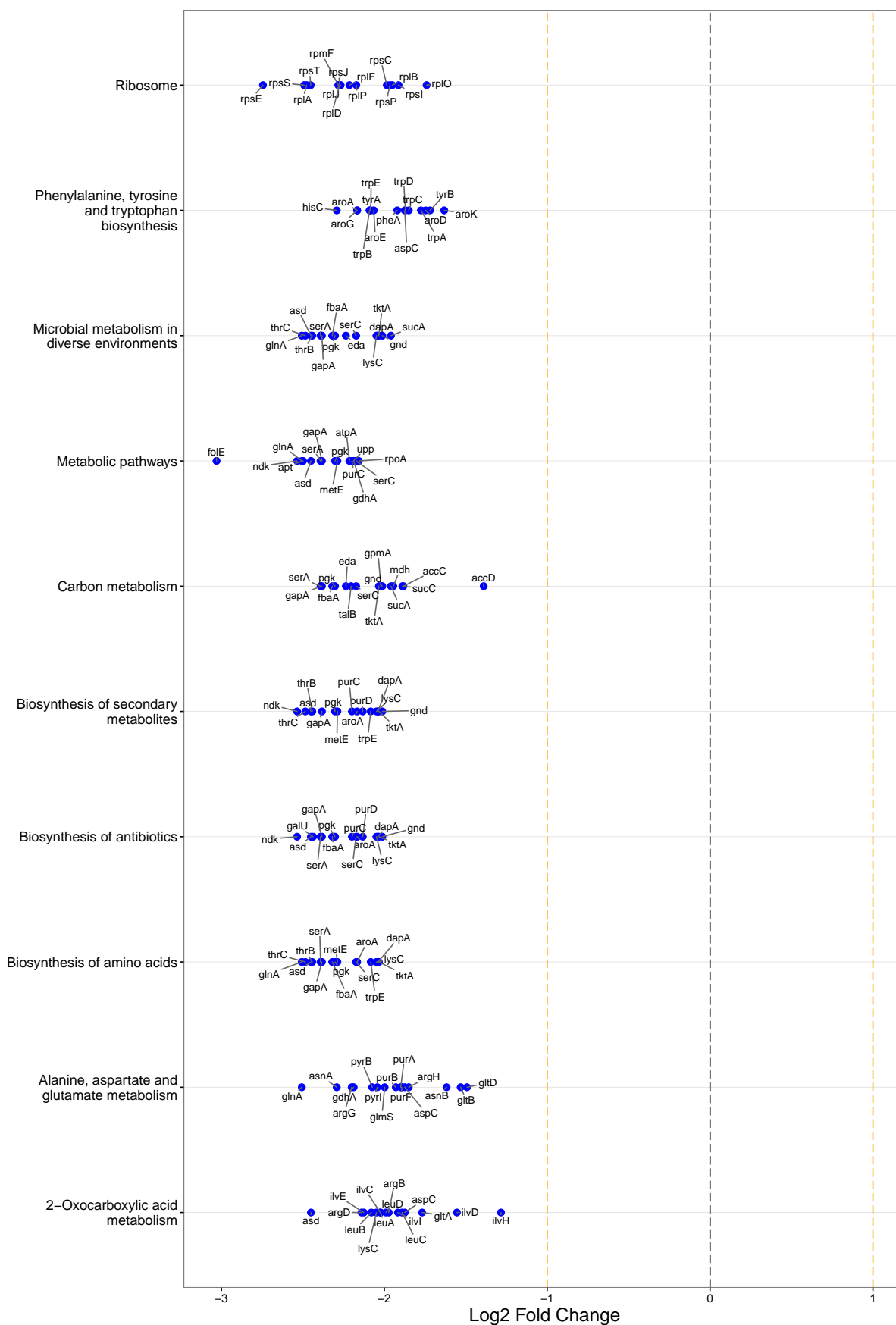


Figure S17: **Significantly differentially expressed KEGG pathways and associated genes with high Na^+ levels, as determined by protein abundances in stationary phase.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding genes 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.

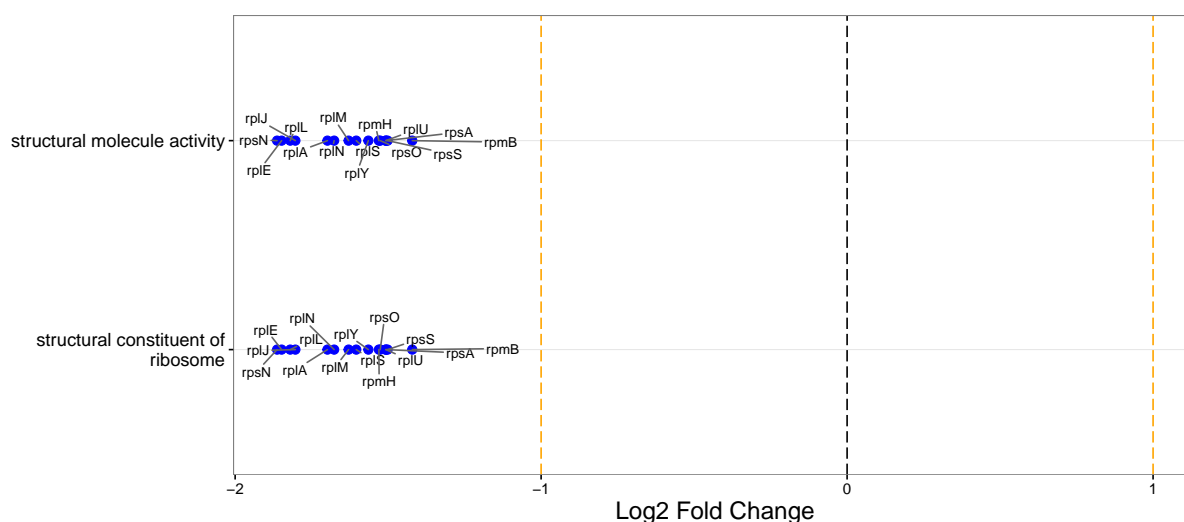


Figure S18: **Significantly differentially expressed GO annotations related with molecular functions and associated genes with glycerol as carbon source, as determined by mRNA abundances in exponential phase.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative 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.

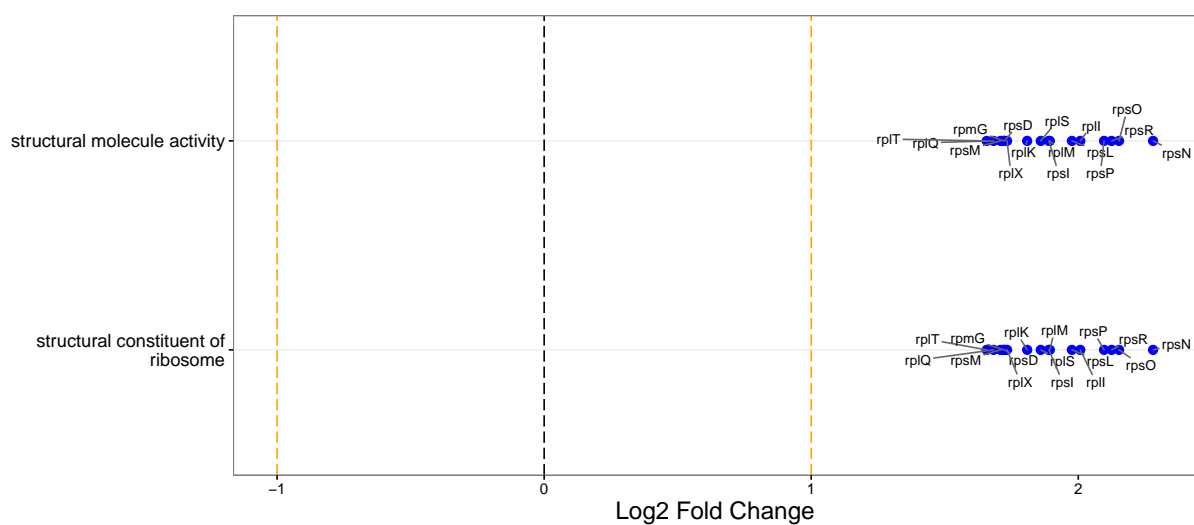


Figure S19: **Significantly differentially expressed GO annotations related with molecular functions and associated genes with lactate as carbon source, as determined by mRNA abundances in exponential phase.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative 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.

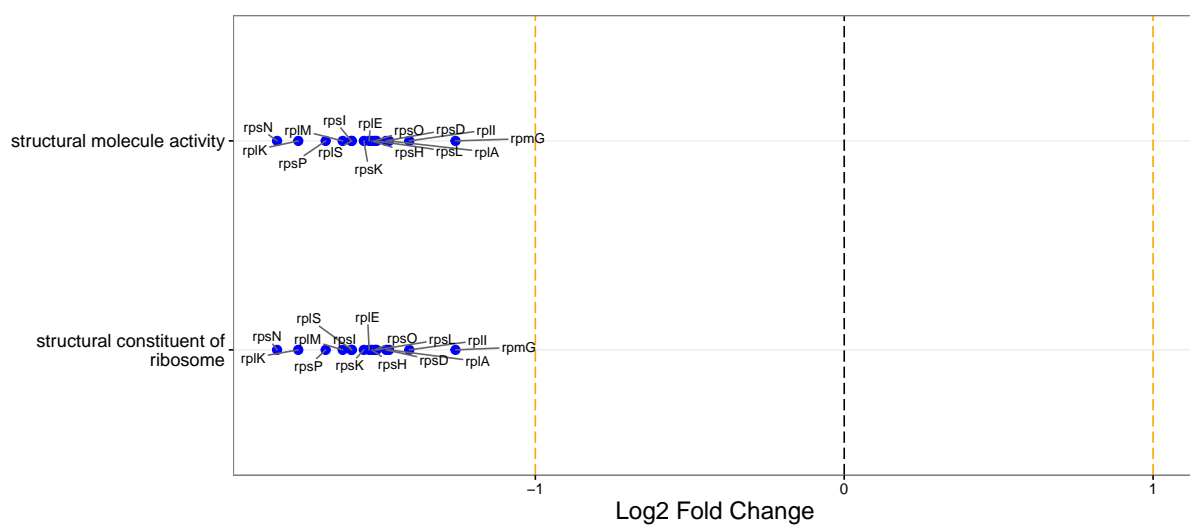


Figure S20: **Significantly differentially expressed GO annotations related with molecular functions and associated genes with low Mg^{2+} levels, as determined by mRNA abundances in exponential phase.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold 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.

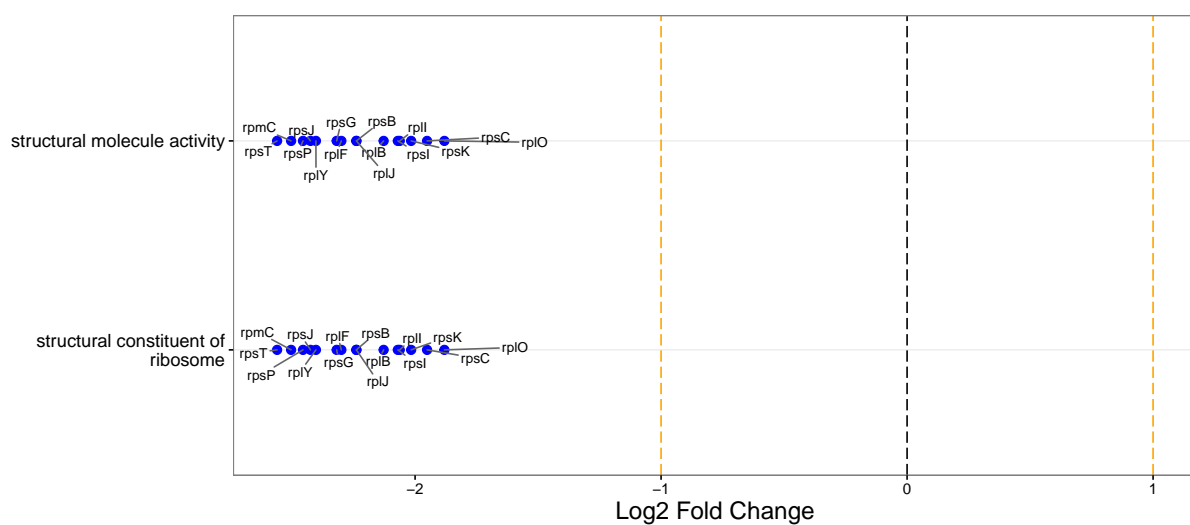


Figure S21: **Significantly differentially expressed GO annotations related with molecular functions and associated genes with high Na^+ levels, as determined by protein abundances in exponential phase.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold 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.

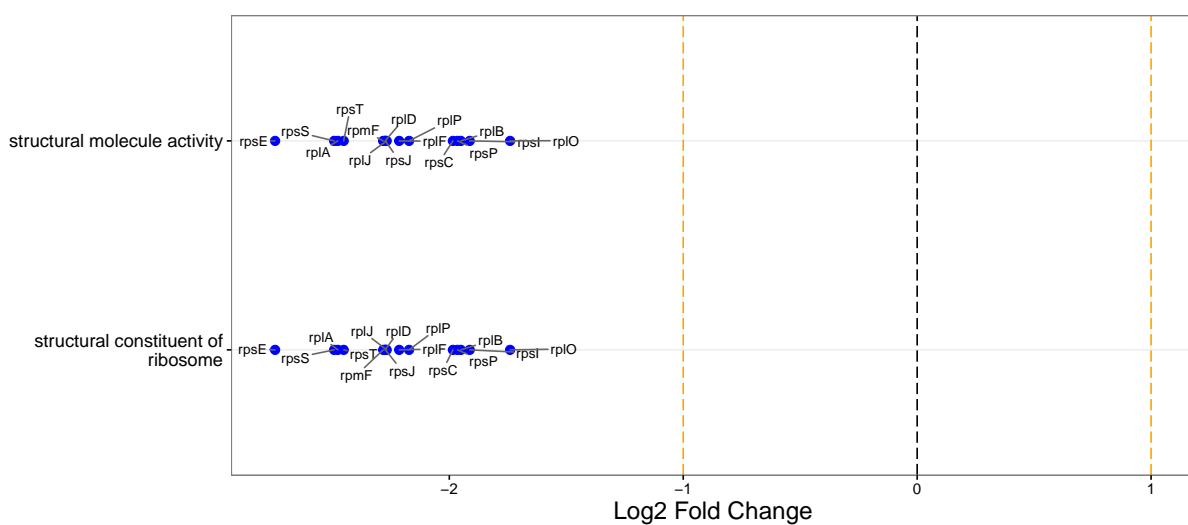


Figure S22: **Significantly differentially expressed GO annotations related with molecular functions and associated genes with high Na^+ levels, as determined by protein abundances in stationary phase.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold 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.

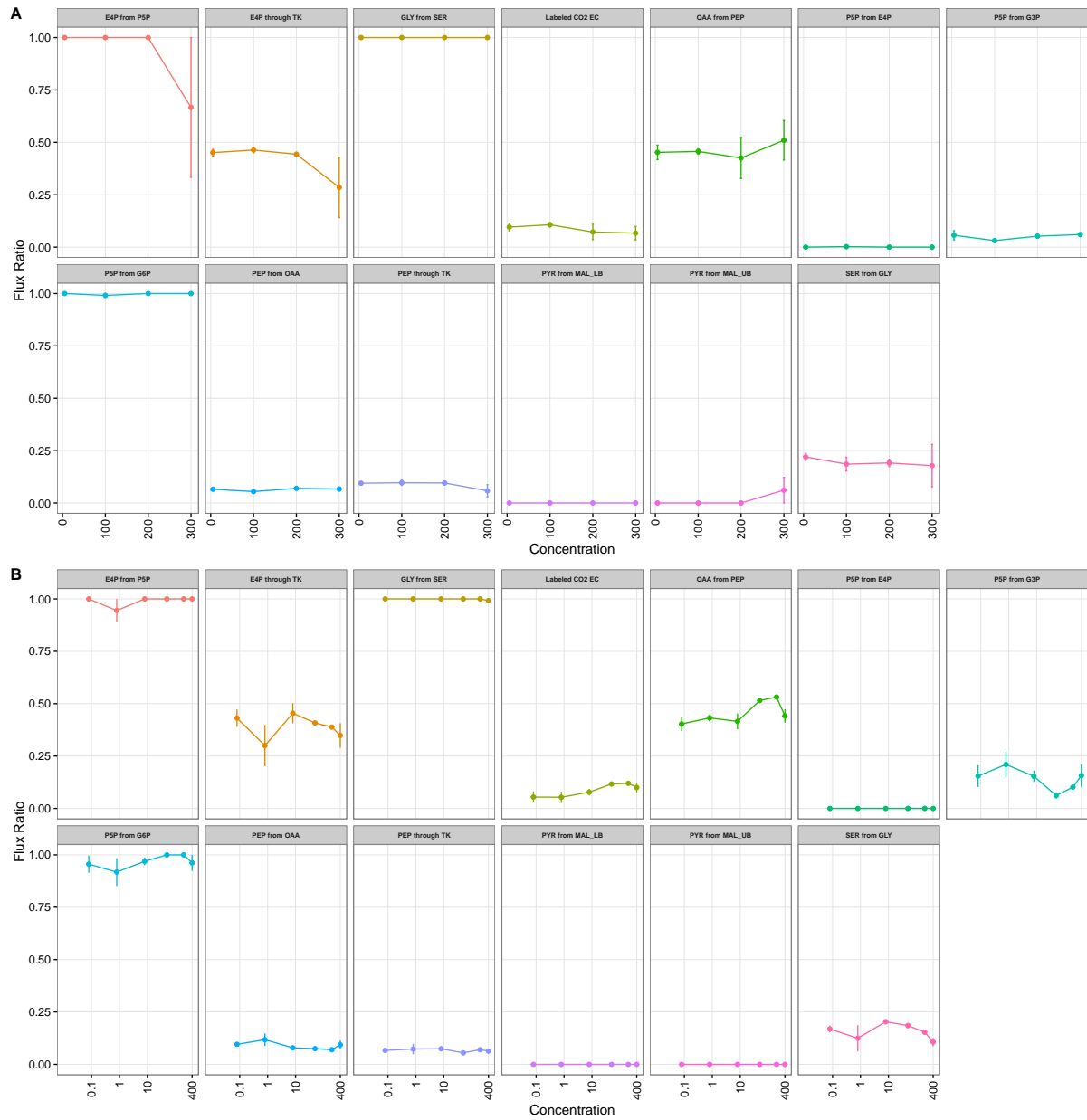


Figure S23: **Flux ratios versus ion concentrations.** 13 different flux were measured with respect to four different Na⁺ and five different Mg²⁺ concentrations. (A) Concentrations with respect to changing Na⁺ concentrations. (B) Concentrations with respect to changing Mg²⁺ concentrations. There was no significant trend of increase or decrease in flux ratios with respect to either Na⁺ or Mg²⁺ concentrations (Supplementary Table 5).