

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

Supplementary materials

Mehmet U. Caglar, John R. Houser, Craig S. Barnhart,
Daniel R. Boutz, Sean M. Carroll, Aurko Dasgupta, Walter F. Lenoir,
Bartram L. Smith, Viswanadham Sridhara, Dariya K. Sydykova,
Drew Vander Wood, Christopher J. Marx,
Edward M. Marcotte*, Jeffrey E. Barrick*, Claus O. Wilke*

October 2, 2016

List of Figures

S1	Significantly differentially expressed molecular functions	3
S2	Significantly differentially expressed KEGG pathways for mRNA samples in exponential phase tested for glycerol against glucose	4
S3	Significantly differentially expressed KEGG pathways for mRNA samples in exponential phase tested for gluconate against glucose	5
S4	Significantly differentially expressed KEGG pathways for mRNA samples in exponential phase tested for lactate against glucose	6
S5	Significantly differentially expressed KEGG pathways for protein samples in exponential phase tested for gluconate against glucose	7
S6	Significantly differentially expressed KEGG pathways for protein samples in exponential phase tested for lactate against glucose	8
S7	Significantly differentially expressed KEGG pathways for protein samples in stationary phase tested for glycerol against glucose	9
S8	Significantly differentially expressed KEGG pathways for protein samples in stationary phase tested for gluconate against glucose	10
S9	Significantly differentially expressed KEGG pathways for protein samples in stationary phase tested for lactate against glucose	11
S10	Significantly differentially expressed KEGG pathways for mRNA samples in exponential phase tested for low Mg^{2+} levels against base Mg^{2+}	12
S11	Significantly differentially expressed KEGG pathways for mRNA samples in exponential phase tested for high Mg^{2+} against base Mg^{2+}	13
S12	Significantly differentially expressed KEGG pathways for protein samples in exponential phase tested for high Mg^{2+} against base Mg^{2+}	14
S13	Significantly differentially expressed KEGG pathways for mRNA samples in stationary phase tested for high Mg^{2+} against base Mg^{2+}	15
S14	Significantly differentially expressed KEGG pathways for mRNA samples in exponential phase tested for high Na^+ against base Na^+	16
S15	Significantly differentially expressed KEGG pathways for protein samples in exponential phase tested for high Na^+ against base Na^+	17
S16	Significantly differentially expressed KEGG pathways for mRNA samples in stationary phase tested for high Na^+ against base Na^+	18
S17	Significantly differentially expressed KEGG pathways for protein samples in stationary phase tested for high Na^+ against base Na^+	19
S18	Significantly differentially expressed GO annotations associated with molecular functions for mRNA samples in exponential phase tested for glycerol against glucose	20
S19	Significantly differentially expressed GO annotations associated with molecular functions for mRNA samples in exponential phase tested for lactate against glucose	21
S20	Significantly differentially expressed GO annotations associated with molecular functions for mRNA samples in exponential phase tested for low Mg^{2+} against base Mg^{2+}	22
S21	Significantly differentially expressed GO annotations associated with molecular functions for protein samples in exponential phase tested for high Na^+ against base Na^+	23
S22	Significantly differentially expressed GO annotations associated with molecular functions for protein samples in stationary phase tested for high Na^+ against base Na^+	24
S23	Flux ratios versus ion concentrations	25

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 ▲▲		

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. (A) Exponential phase. (B) Stationary phase.

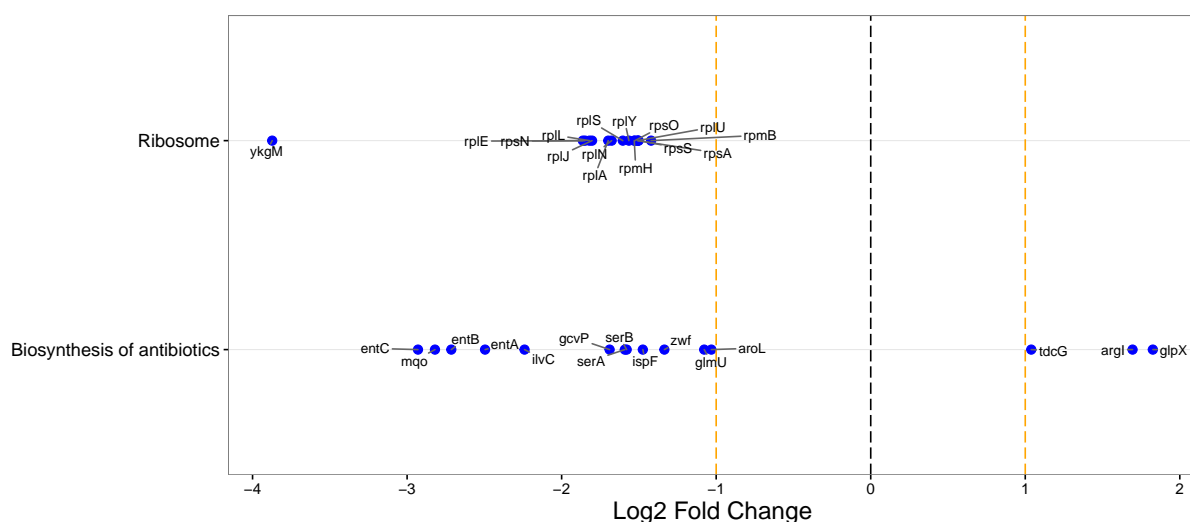


Figure S2: **Significantly differentially expressed KEGG pathways and associated genes with glycerol as carbon source, as determined by mRNA abundances in exponential phase.** The top differentially expressed KEGG pathways are shown along the *y* axis, and the relative fold change of the corresponding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

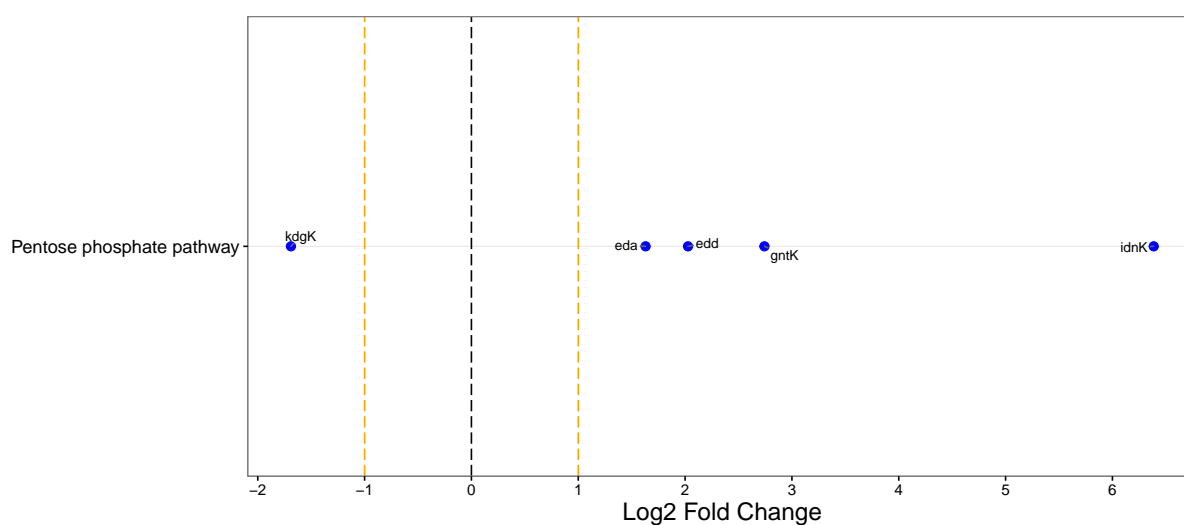


Figure S3: **Significantly differentially expressed KEGG pathways and associated genes with gluconate as carbon source, as determined by mRNA abundances in exponential phase.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding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

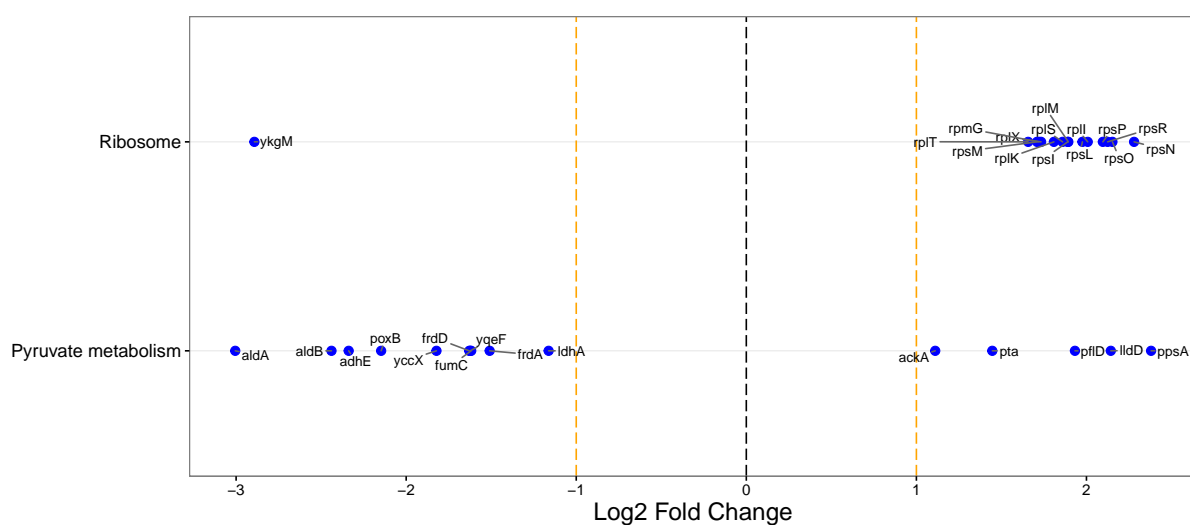


Figure S4: **Significantly differentially expressed KEGG pathways and associated genes with lactate as carbon source, as determined by mRNA abundances in exponential phase.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding genes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

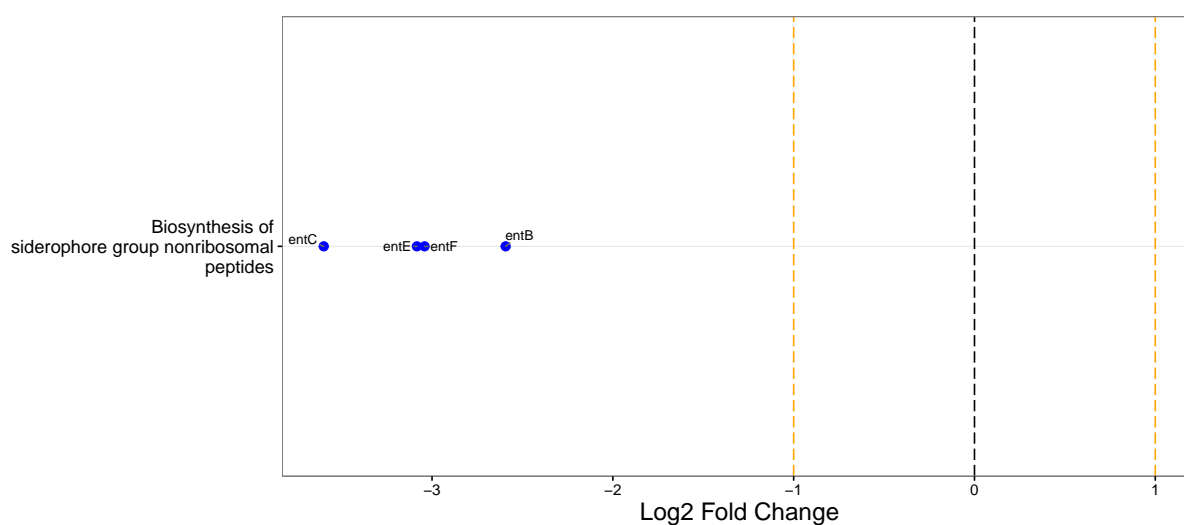


Figure S5: **Significantly differentially expressed KEGG pathways and associated genes with gluconate as carbon source, as determined by protein abundances in exponential phase.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding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

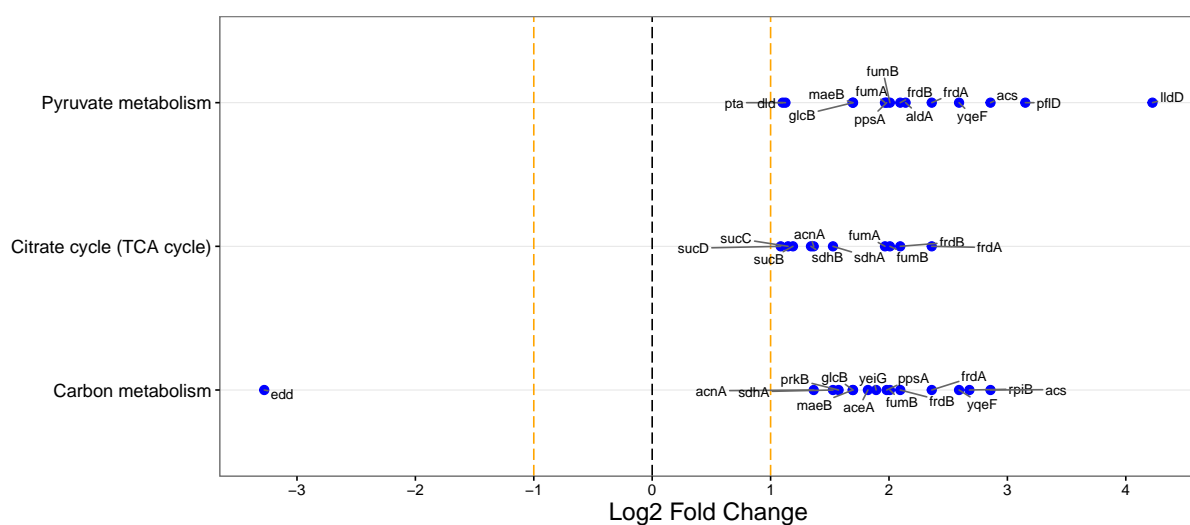


Figure S6: **Significantly differentially expressed KEGG pathways and associated genes with lactate as carbon source, as determined by protein abundances in exponential phase.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding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

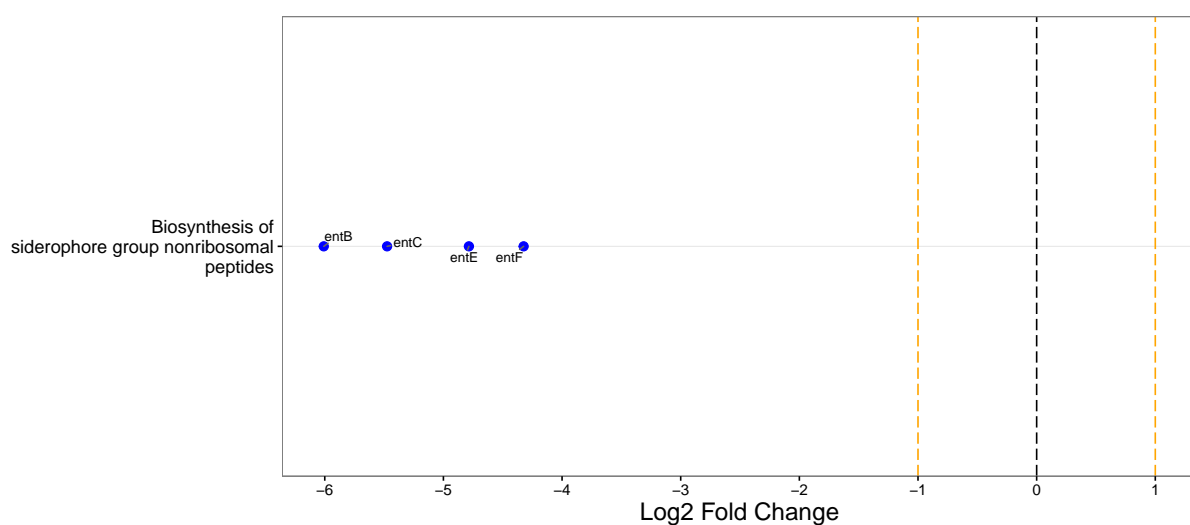


Figure S7: **Significantly differentially expressed KEGG pathways and associated genes with glycerol as carbon source, as determined by protein abundances in stationary phase.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding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

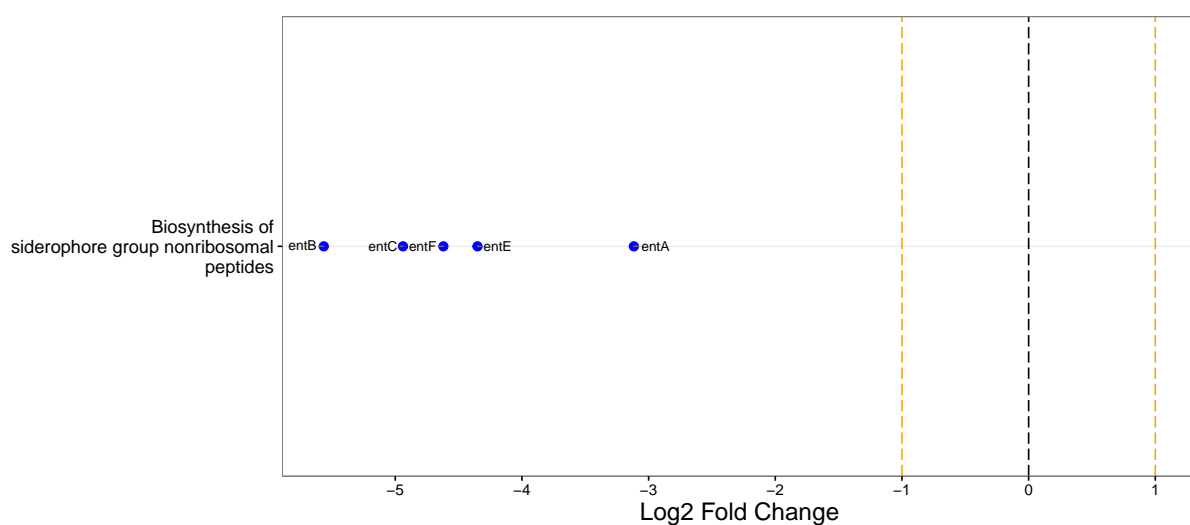


Figure S8: **Significantly differentially expressed KEGG pathways and associated genes with gluconate as carbon source, as determined by protein abundances in stationary phase.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding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

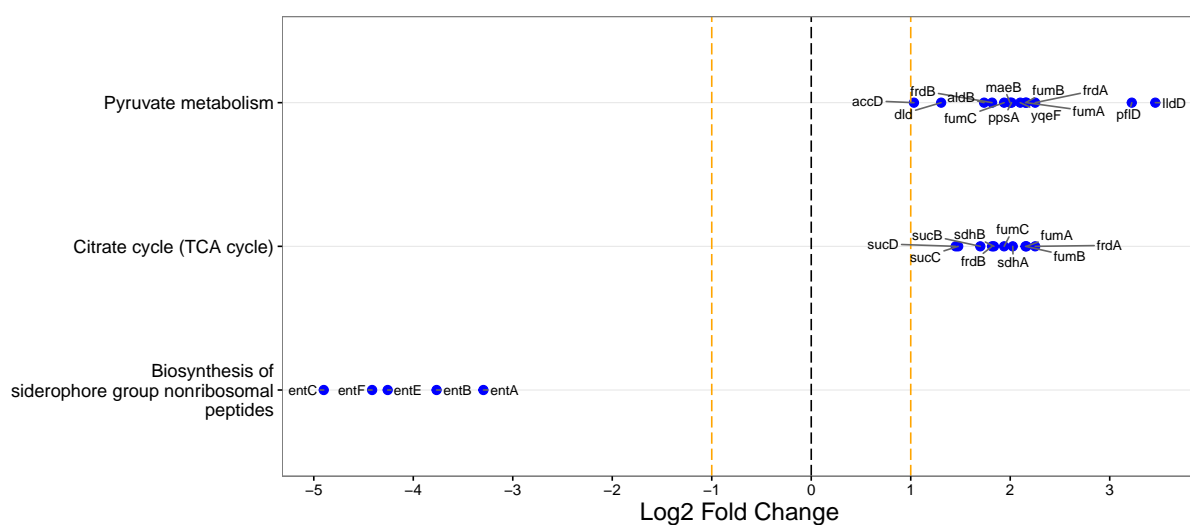


Figure S9: **Significantly differentially expressed KEGG pathways and associated genes with lactate as carbon source, as determined by protein abundances in stationary phase.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding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

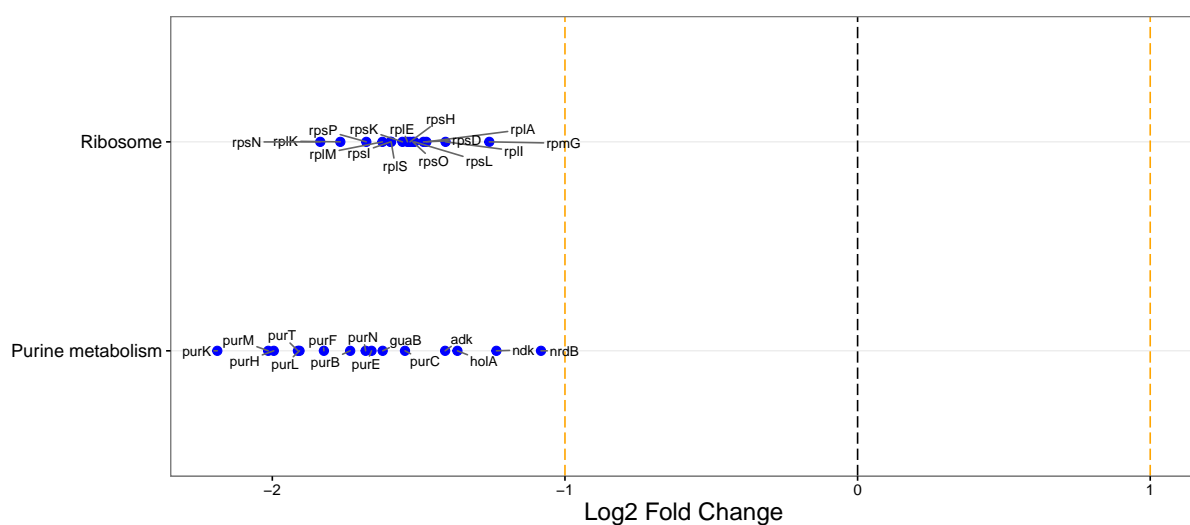


Figure S10: **Significantly differentially expressed KEGG pathways and associated genes with low Mg^{2+} levels, as determined by mRNA abundances in exponential phase.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding genes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

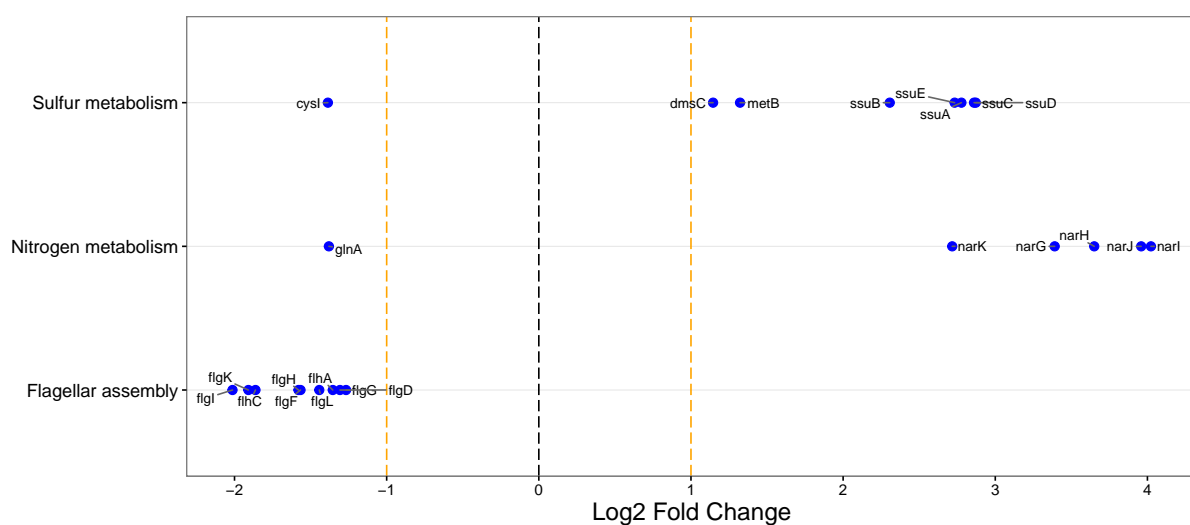


Figure S11: **Significantly differentially expressed KEGG pathways and associated genes with high Mg^{2+} levels, as determined by mRNA abundances in exponential phase.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding genes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

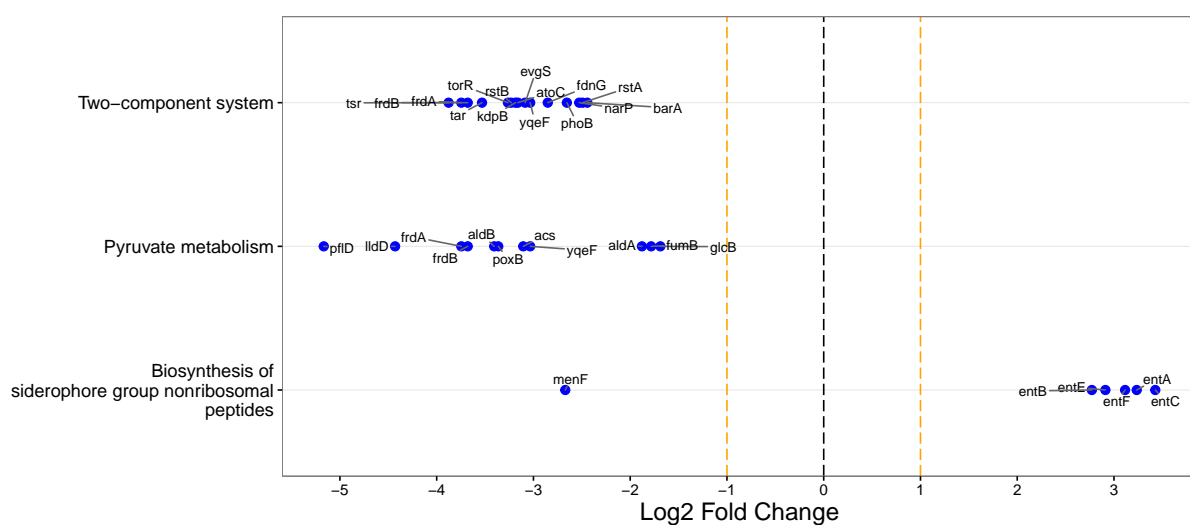


Figure S12: **Significantly differentially expressed KEGG pathways and associated genes with high Mg^{2+} levels, as determined by protein abundances in exponential phase.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding genes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

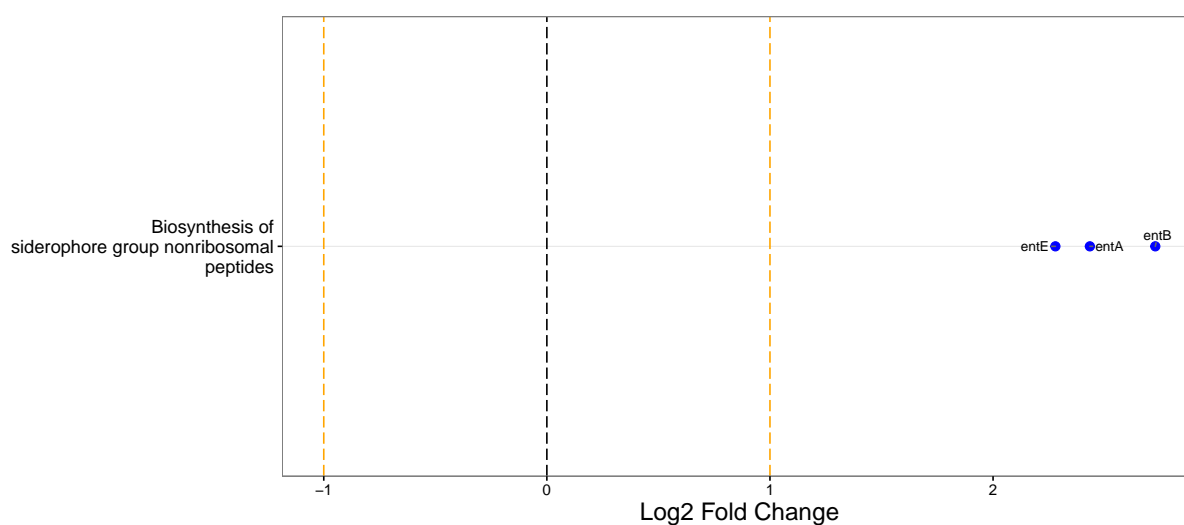


Figure S13: **Significantly differentially expressed KEGG pathways and associated genes with high Mg^{2+} levels, as determined by mRNA abundances in stationary phase.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding genes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

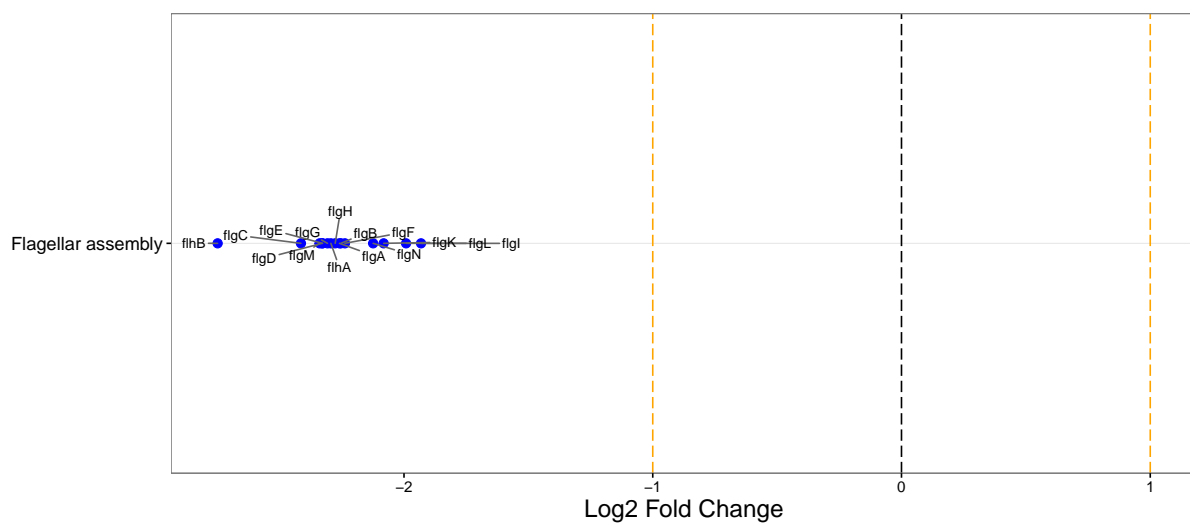


Figure S14: **Significantly differentially expressed KEGG pathways and associated genes with high Na^+ levels, as determined by mRNA abundances in exponential phase.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding genes is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

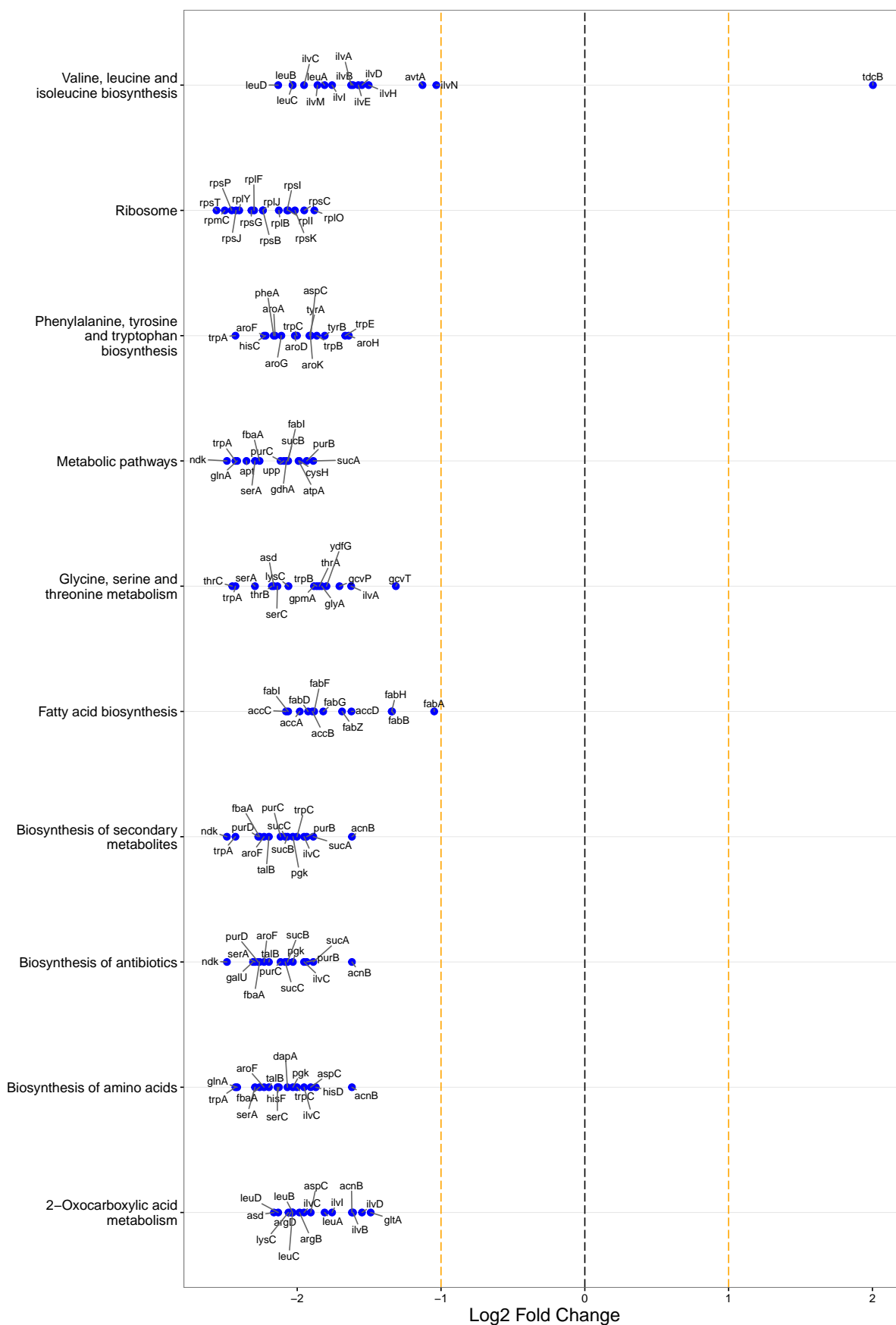


Figure S15: Significantly differentially expressed KEGG pathways and associated genes with high Na^+ levels, as determined by protein abundances in exponential phase. The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding genes is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

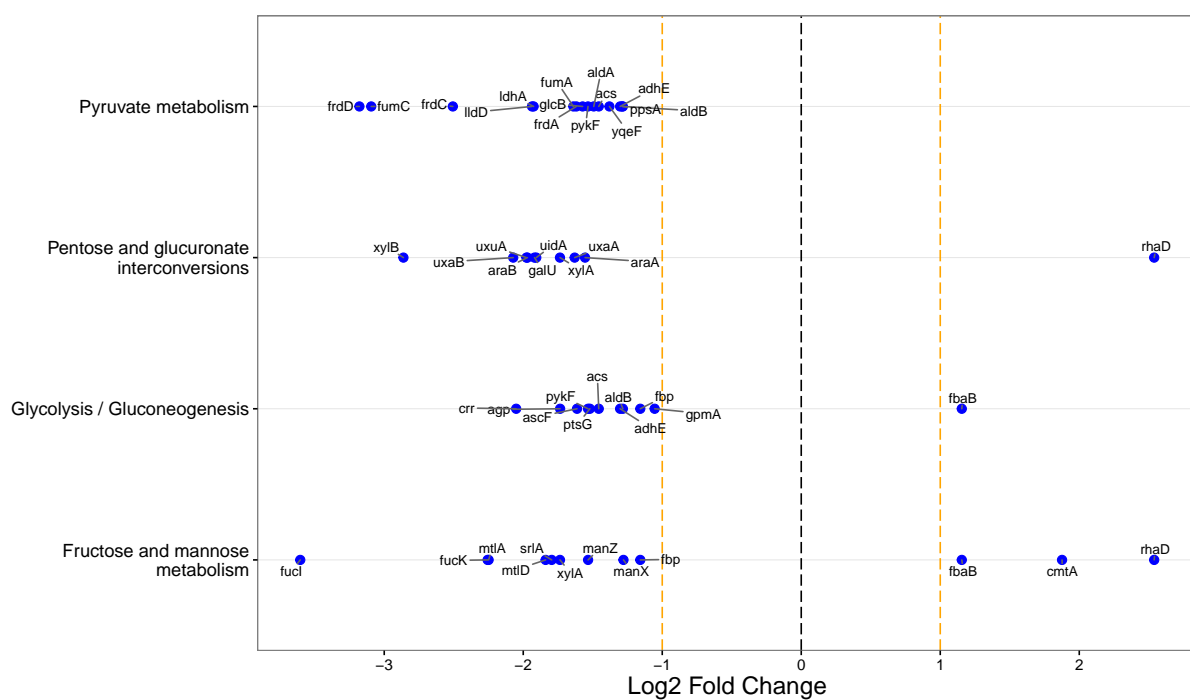


Figure S16: **Significantly differentially expressed KEGG pathways and associated genes with high Na^+ levels, as determined by mRNA abundances in stationary phase.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding genes is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

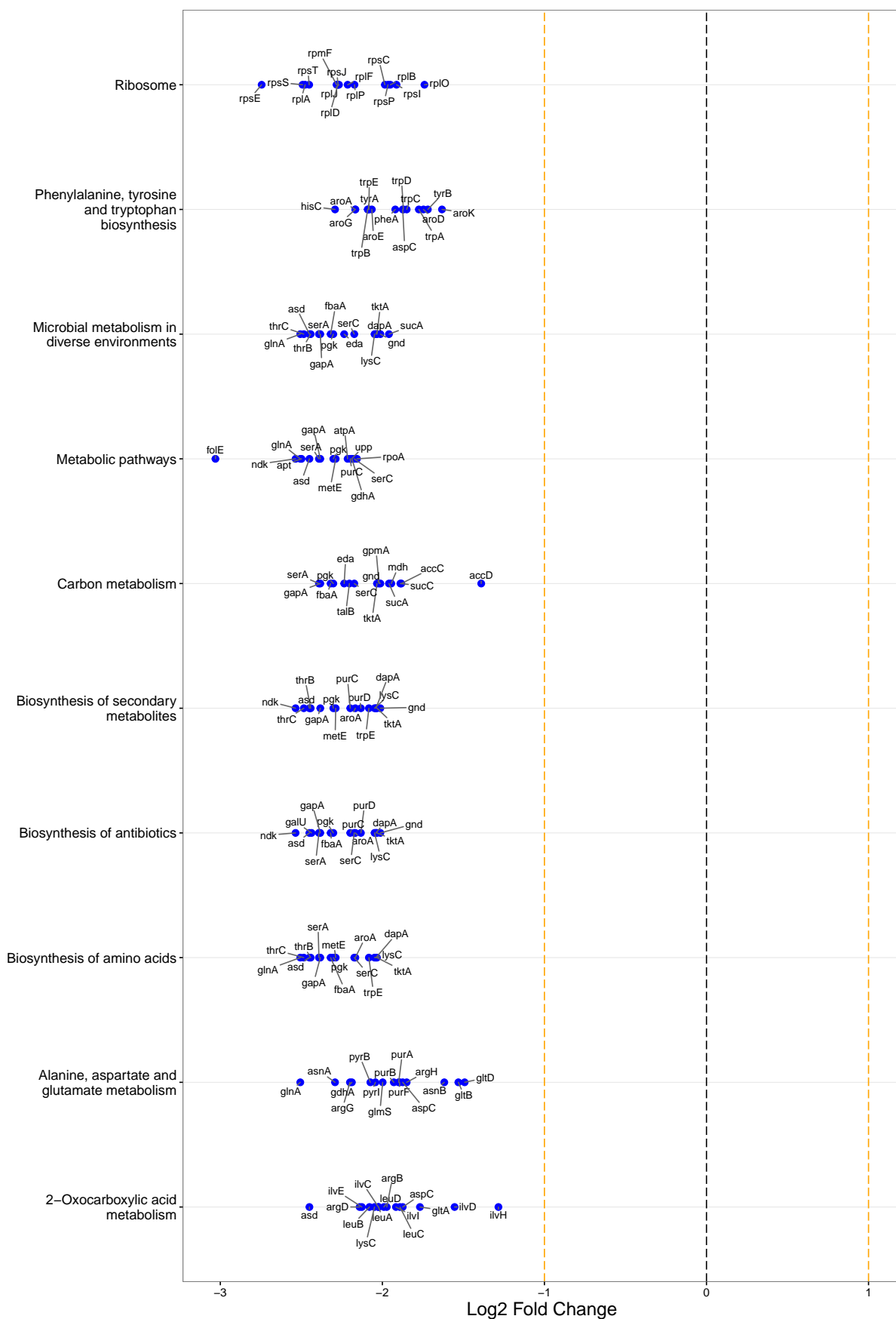


Figure S17: **Significantly differentially expressed KEGG pathways and associated genes with high Na^+ levels, as determined by protein abundances in stationary phase.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding genes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

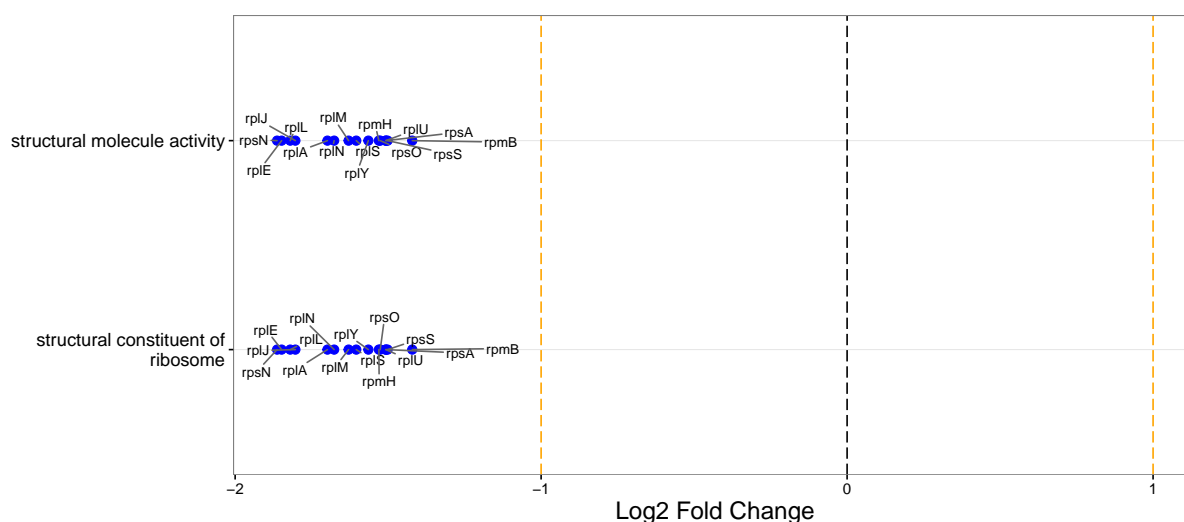


Figure S18: **Significantly differentially expressed GO annotations related with molecular functions and associated genes with glycerol as carbon source, as determined by mRNA abundances in exponential phase.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative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

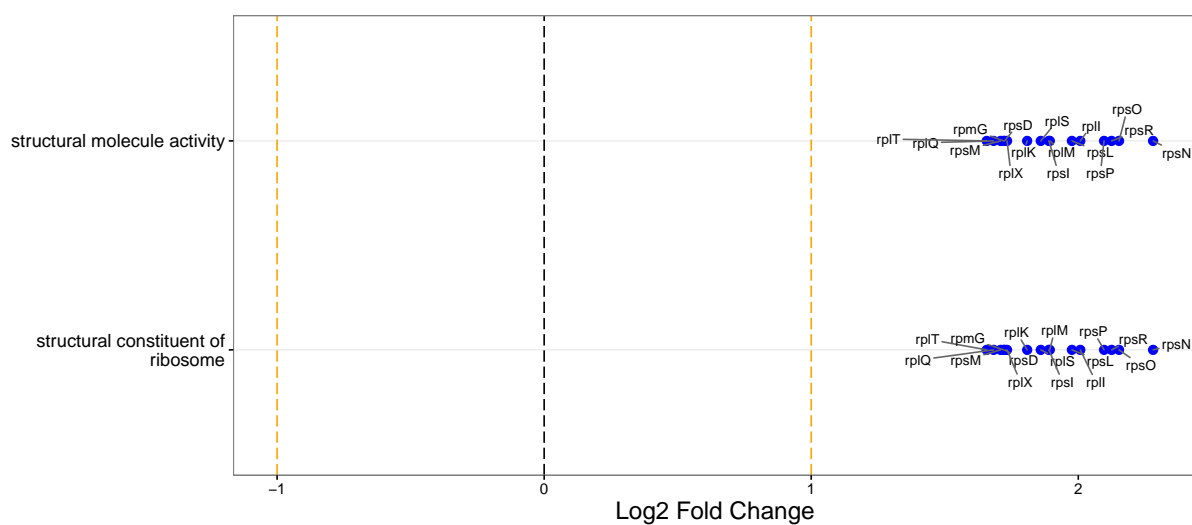


Figure S19: **Significantly differentially expressed GO annotations related with molecular functions and associated genes with lactate as carbon source, as determined by mRNA abundances in exponential phase.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative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

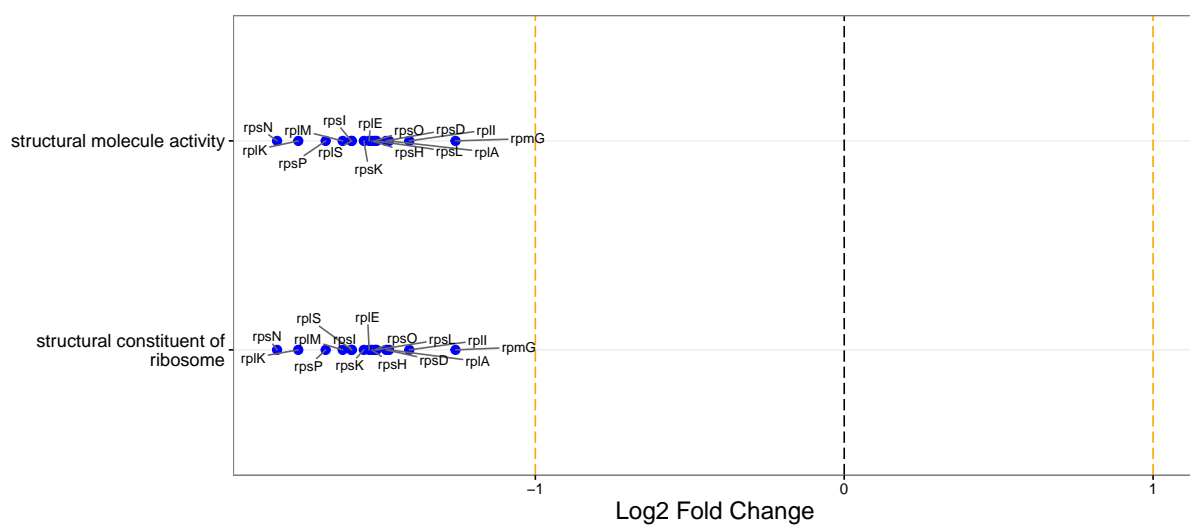


Figure S20: **Significantly differentially expressed GO annotations related with molecular functions and associated genes with low Mg^{2+} levels, as determined by mRNA abundances in exponential phase.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold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

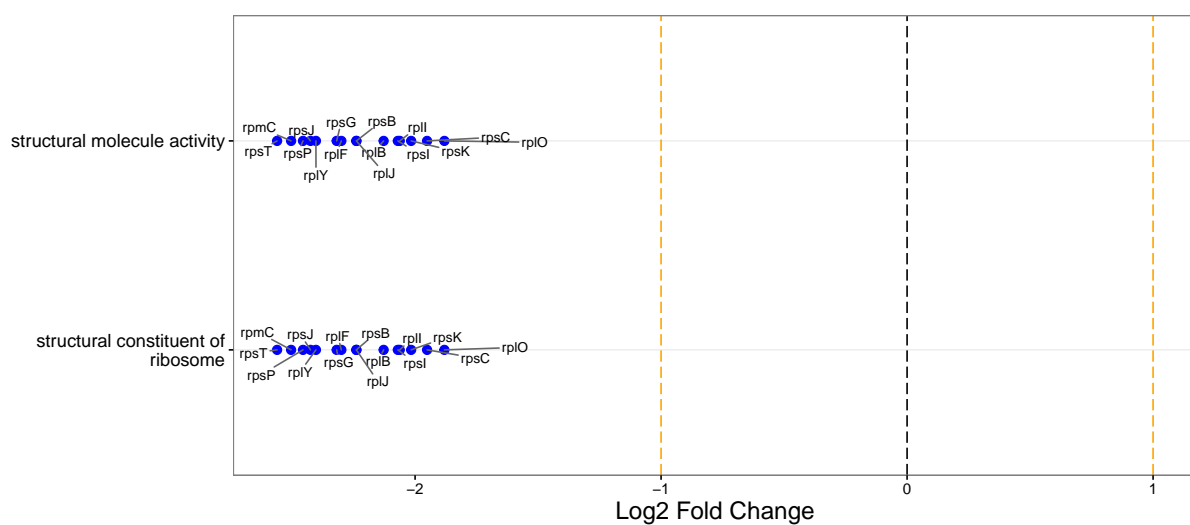


Figure S21: **Significantly differentially expressed GO annotations related with molecular functions and associated genes with high Na^+ levels, as determined by protein abundances in exponential phase.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold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

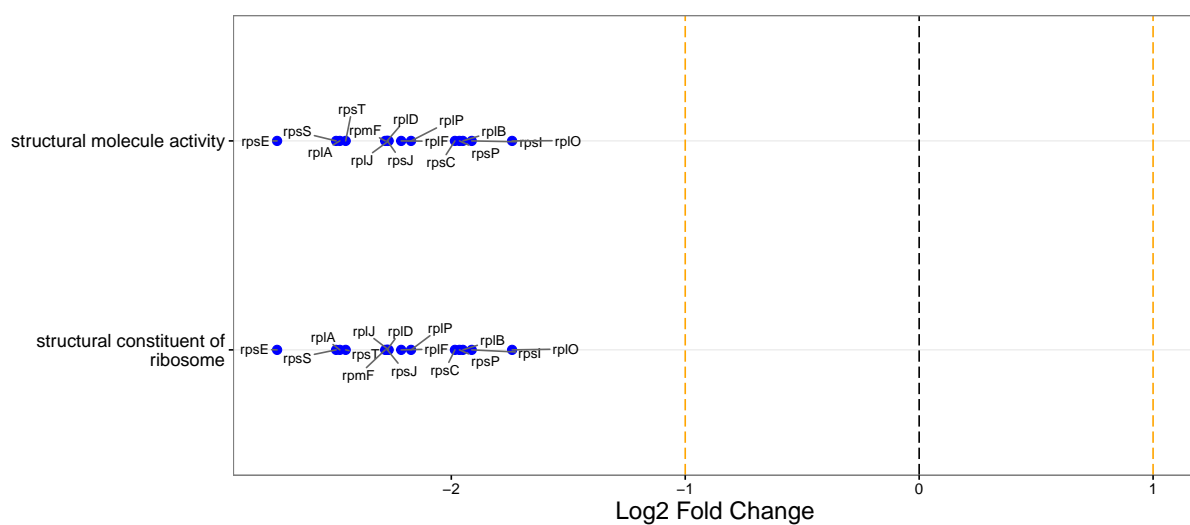


Figure S22: **Significantly differentially expressed GO annotations related with molecular functions and associated genes with high Na^+ levels, as determined by protein abundances in stationary phase.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold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

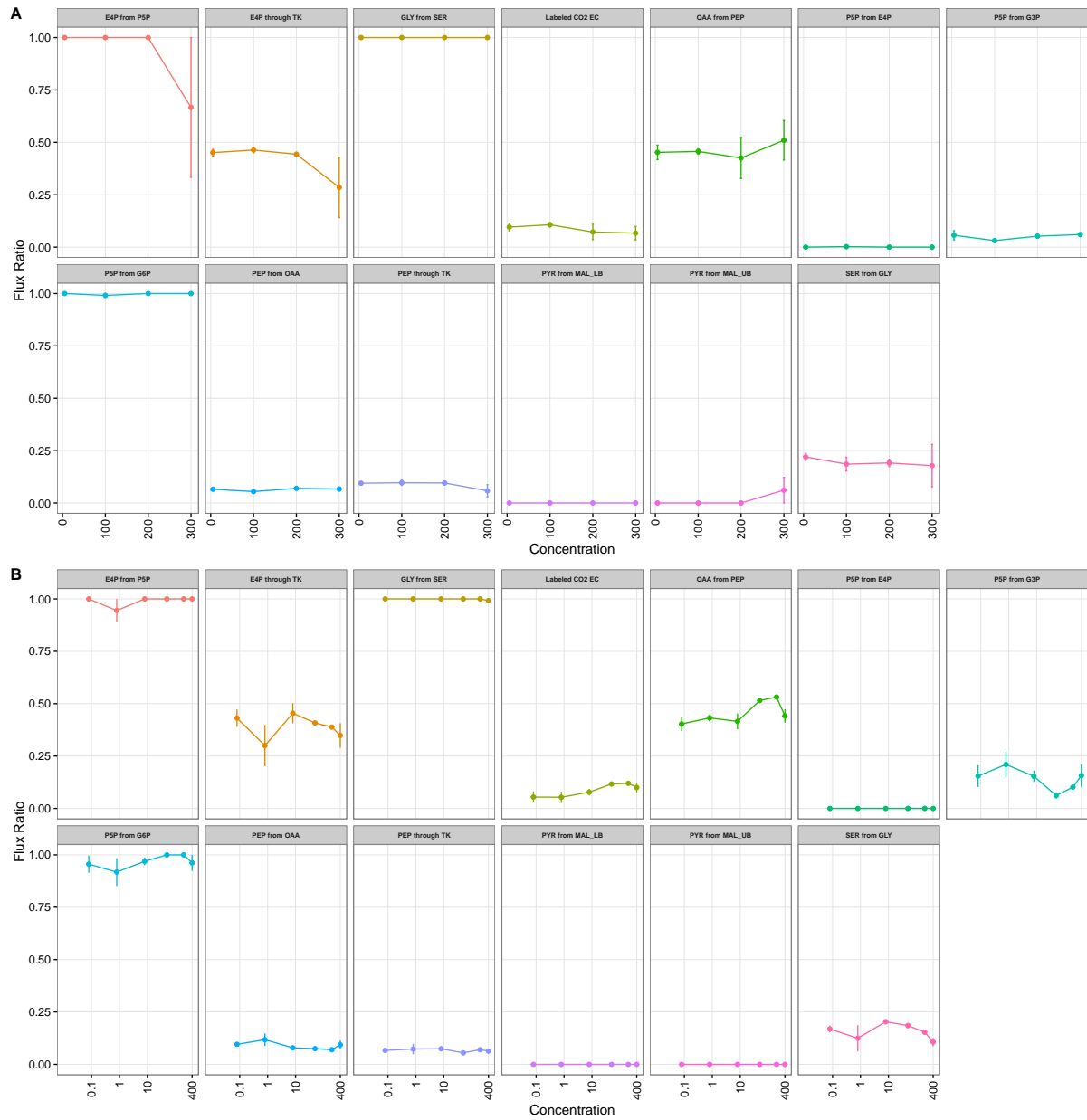


Figure S23: **Flux ratios versus ion concentrations.** 13 different flux were measured with respect to four different Na^+ and five different Mg^{2+} concentrations. (A) Concentrations with respect to changing Na^+ concentrations. (B) Concentrations with respect to changing Mg^{2+} concentrations. There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