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

Supplementary material

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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
1. structural constituent of ribosome 2. structural molecule activity		lactate

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 generated by GO annotations.** For each condition, we show the top-5 differentially expressed MF as determined by 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 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 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 S4: **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.
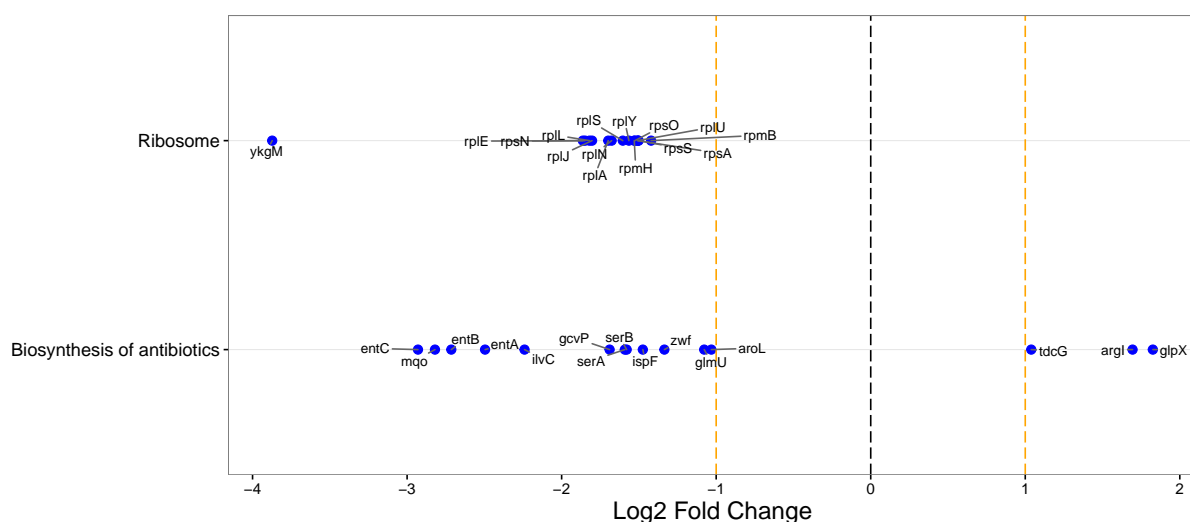
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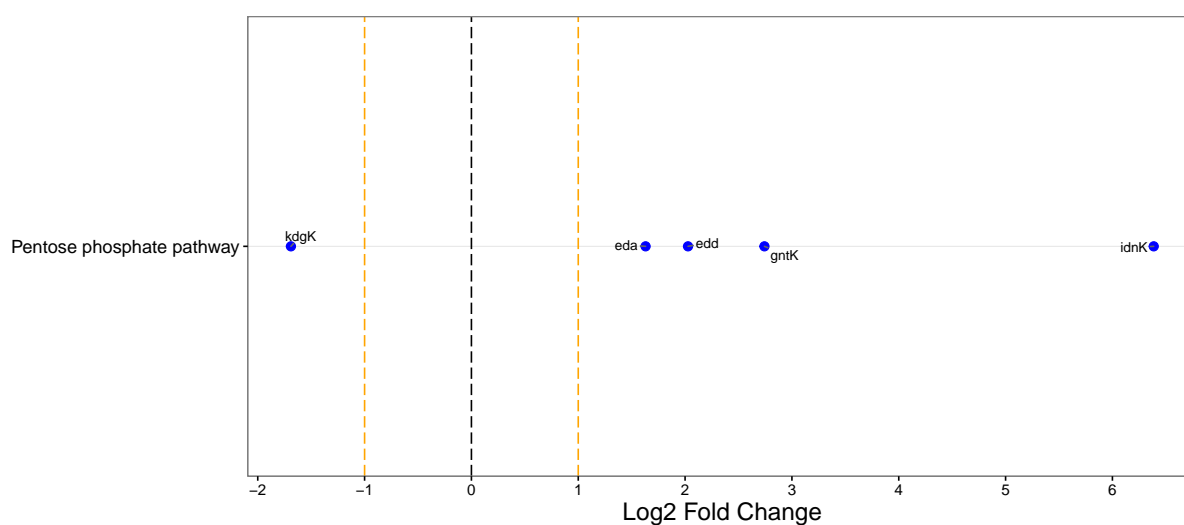
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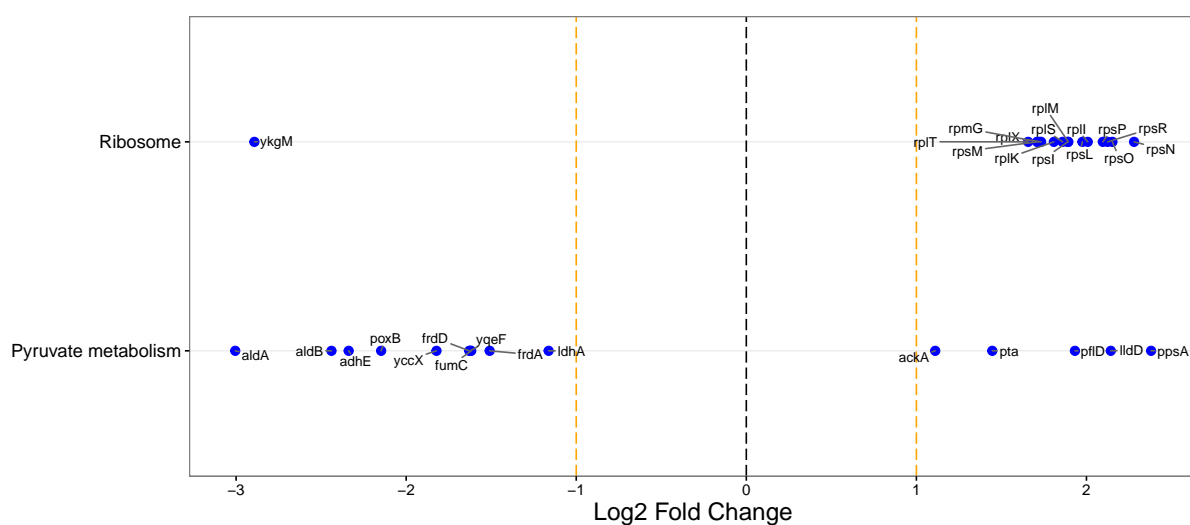
Figure S7: **Significantly differentially expressed KEGG pathways and associated genes with glycerol as carbon source in stationary phase, as determined by protein abundances.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding 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.
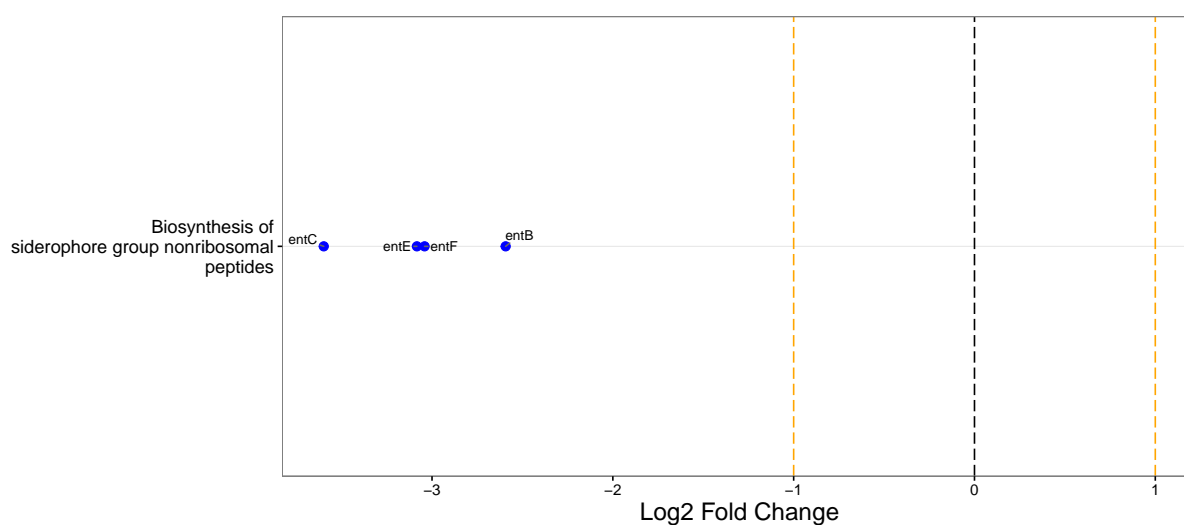
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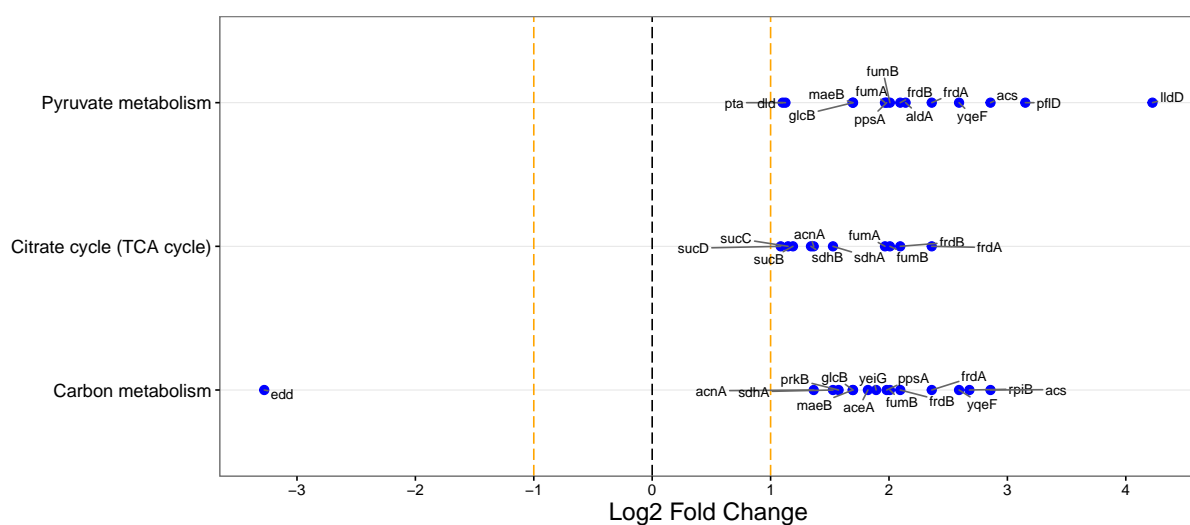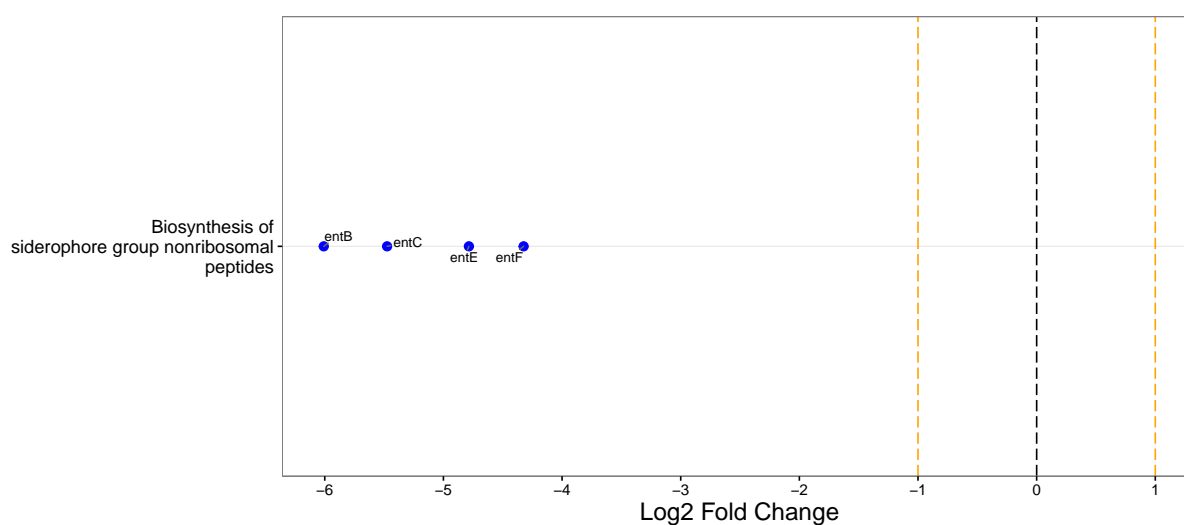
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Figure S10: **Significantly differentially expressed KEGG pathways and associated genes with low Mg^{+2} levels in exponential phase, as determined by mRNA abundances.** The top differentially expressed KEGG pathways are shown along the y axis, and 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.

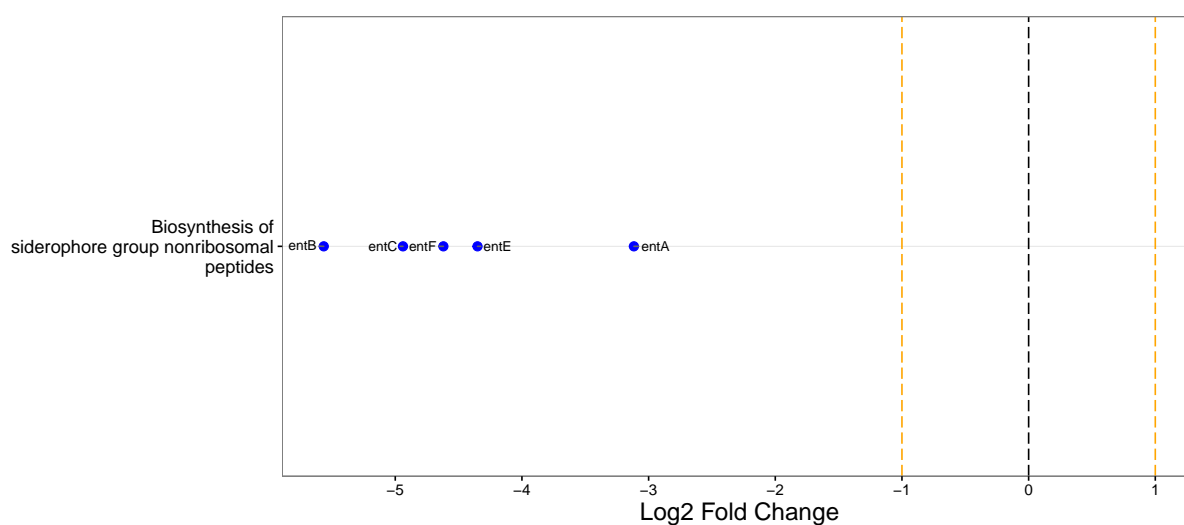Figure S11: **Significantly differentially expressed KEGG pathways and associated genes with high Mg^{+2} levels in exponential phase, as determined by mRNA abundances.** The top differentially expressed KEGG pathways are shown along the y axis, and the relative fold change of the corresponding genes 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.
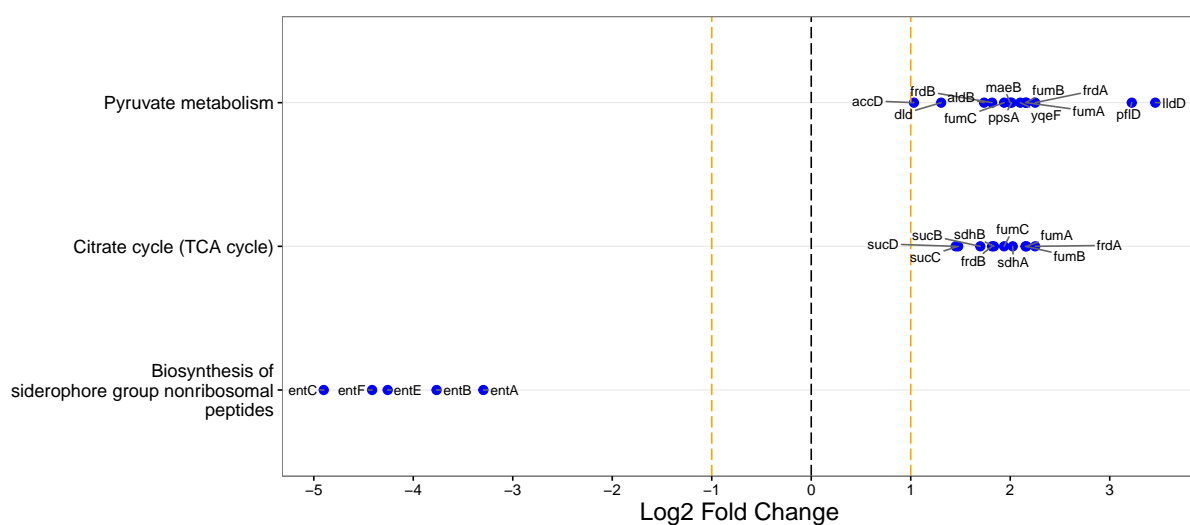
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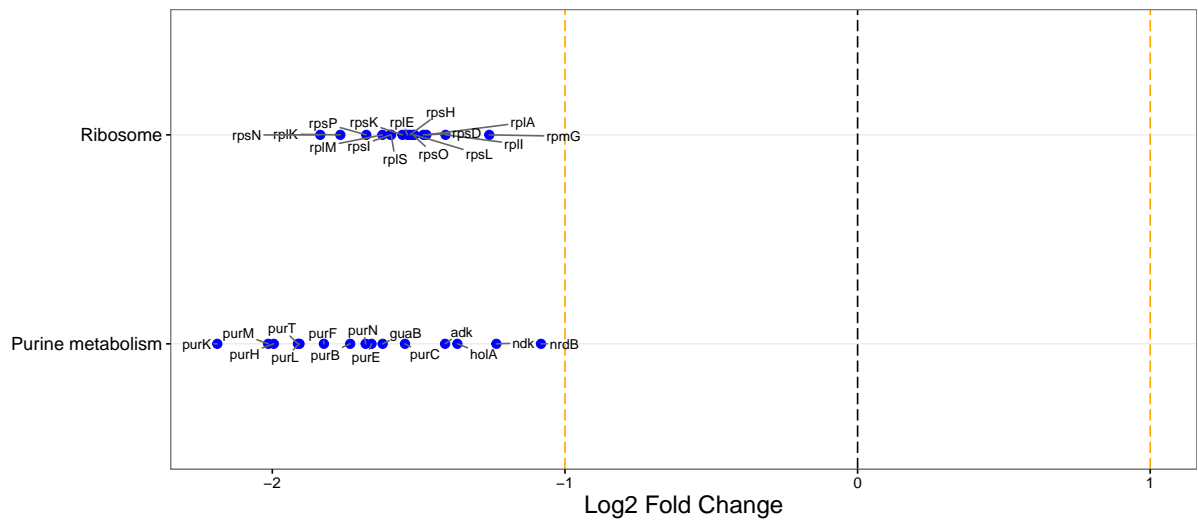
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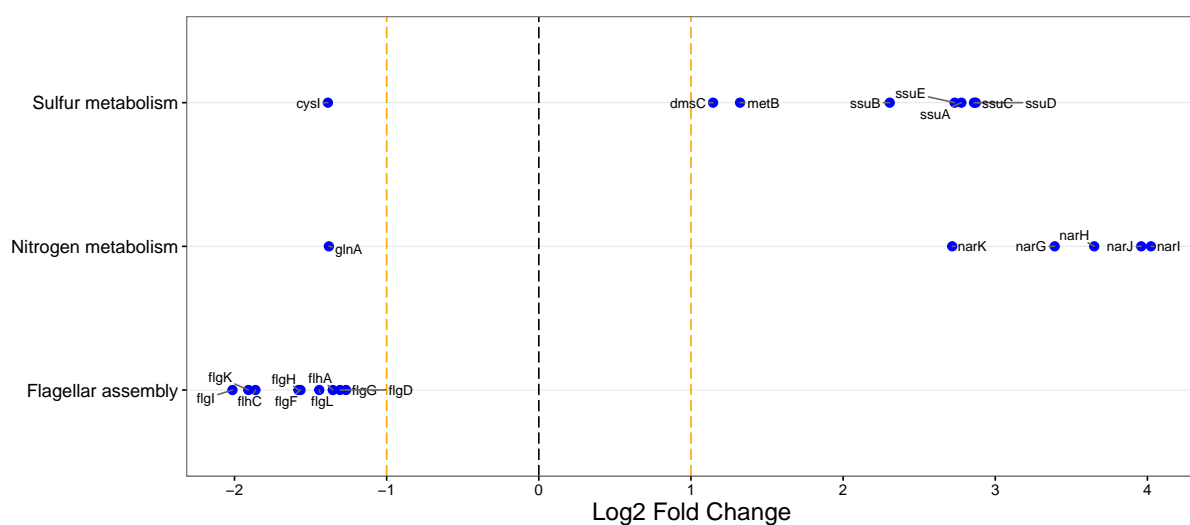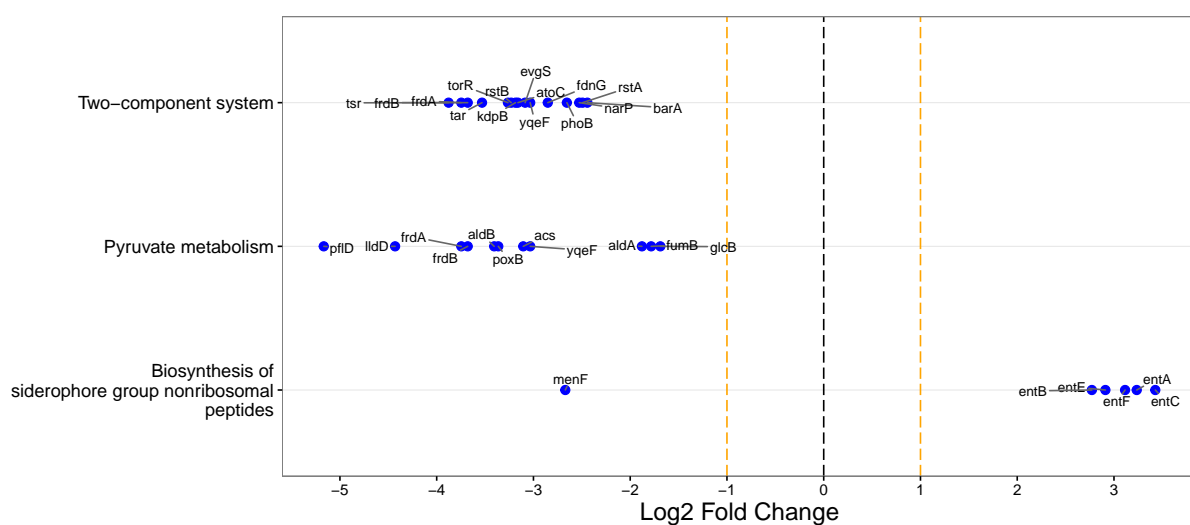
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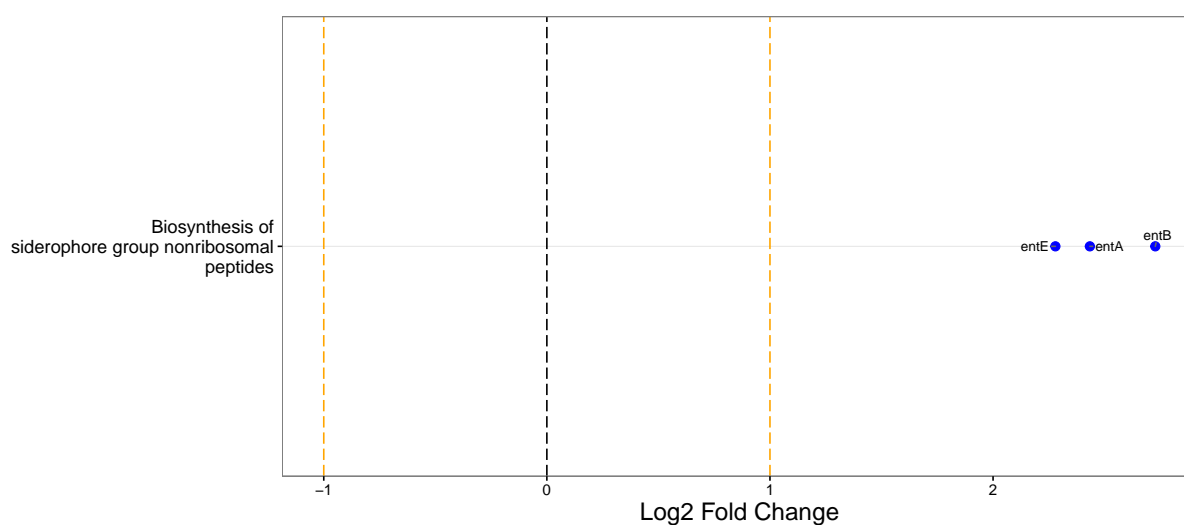
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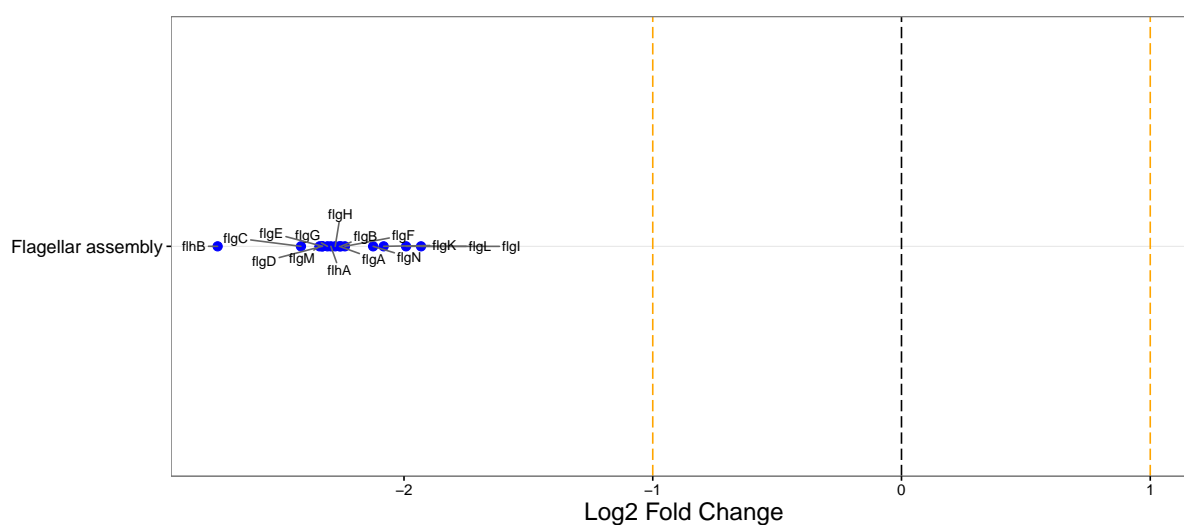
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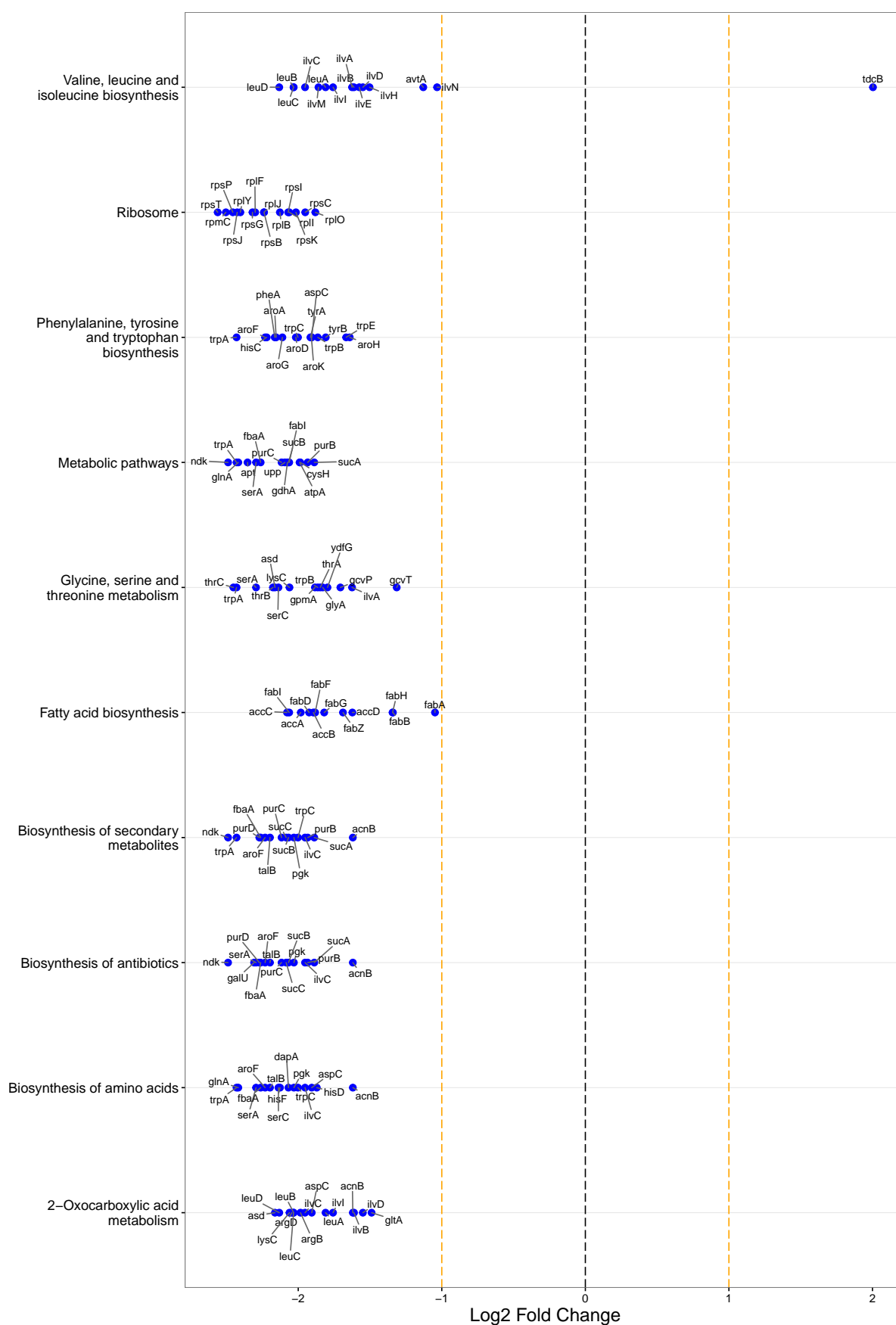
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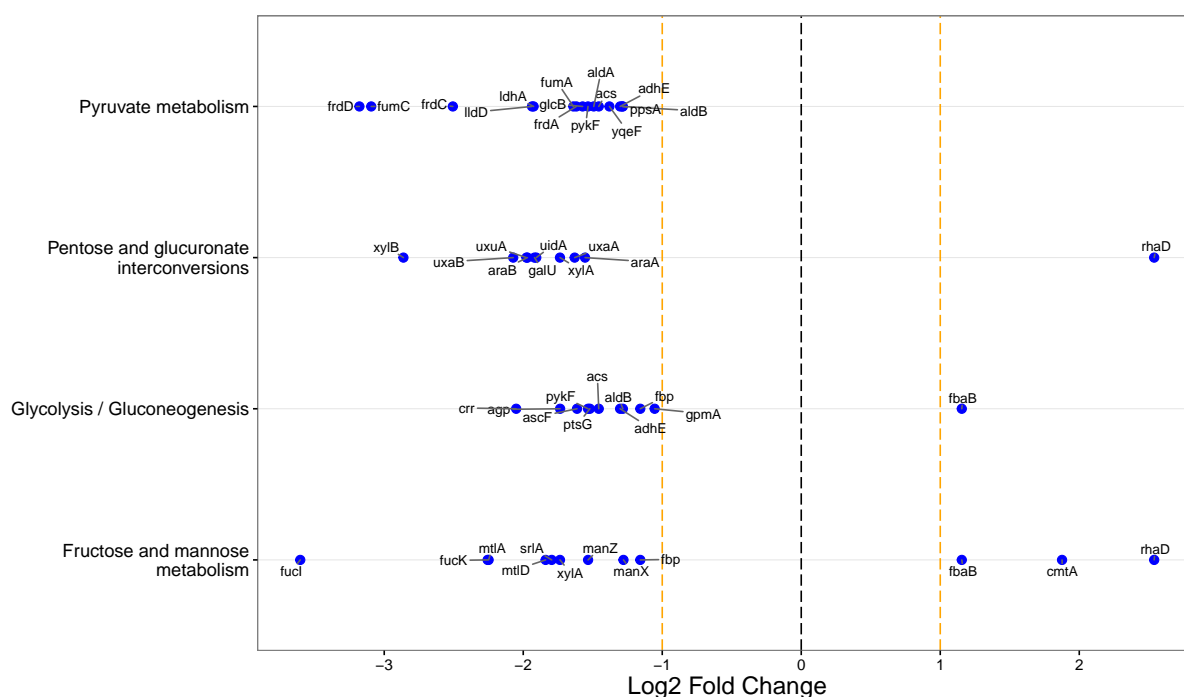
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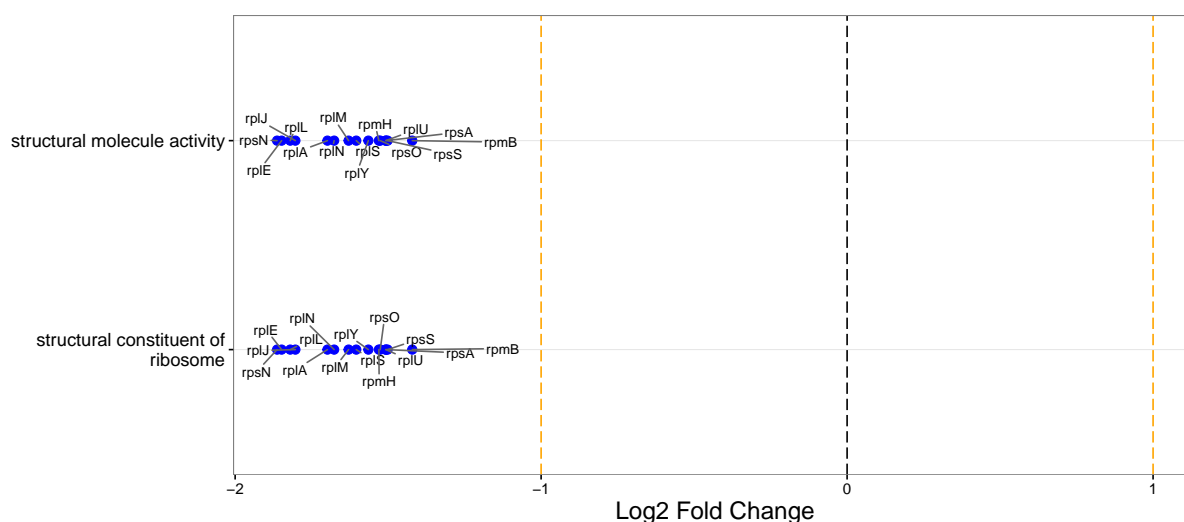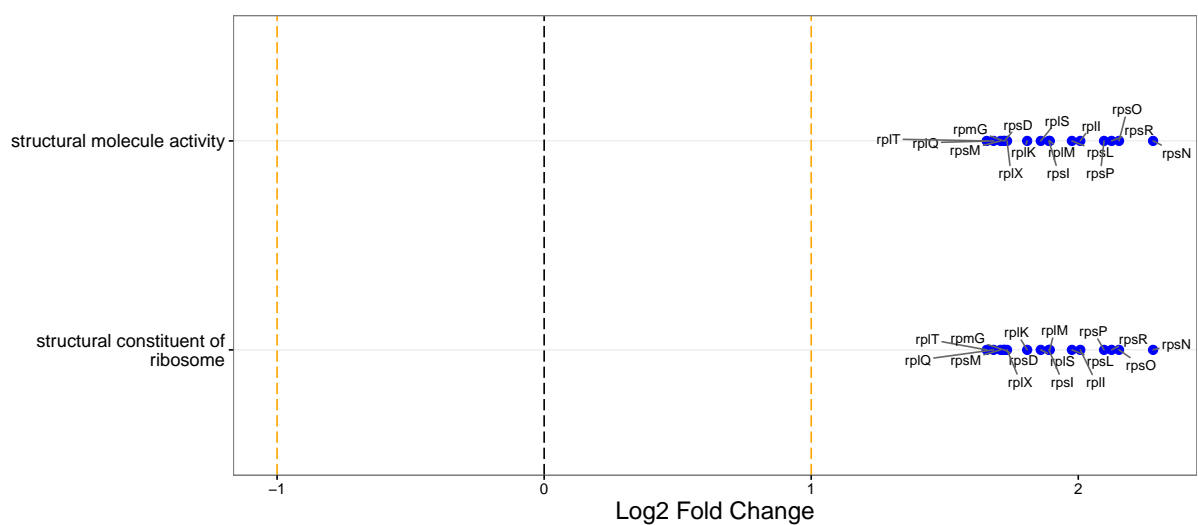
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Figure S20: **Significantly differentially expressed GO annotations related with molecular functions and associated genes with low Mg^{+2} levels in exponential phase, as determined by mRNA abundances.** The top differentially expressed KEGG pathways 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.
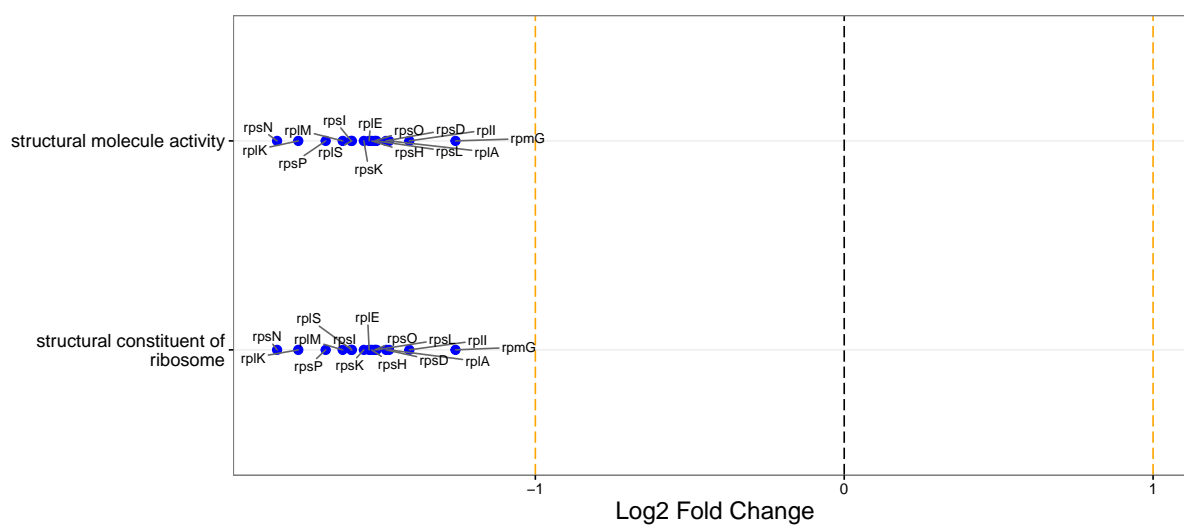
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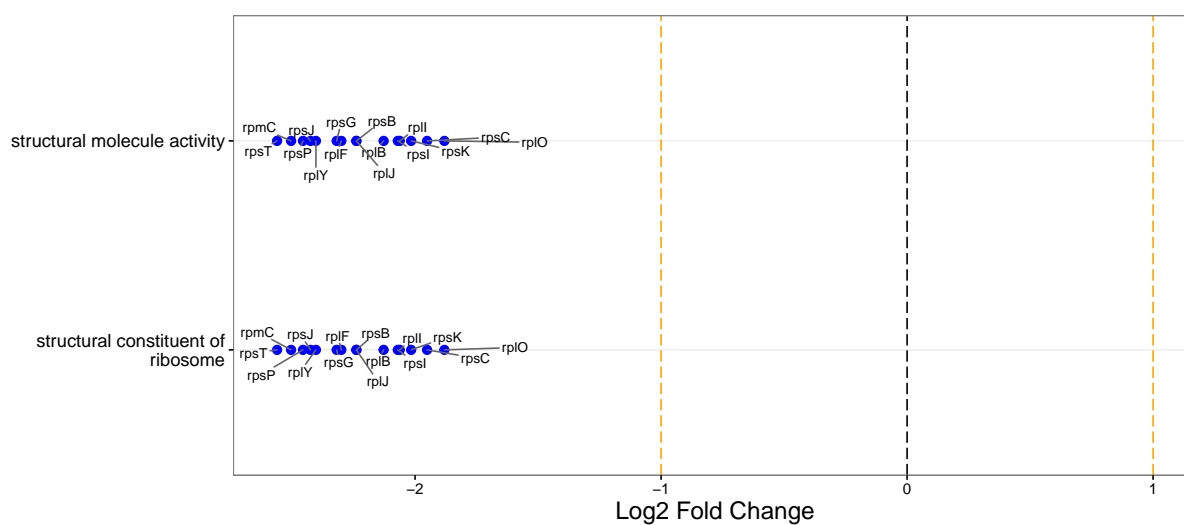
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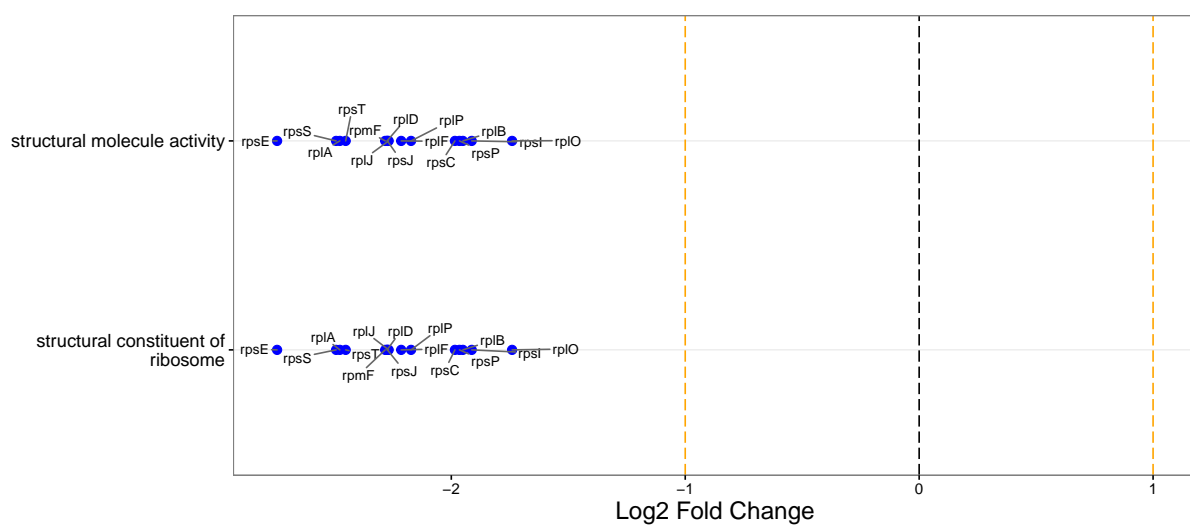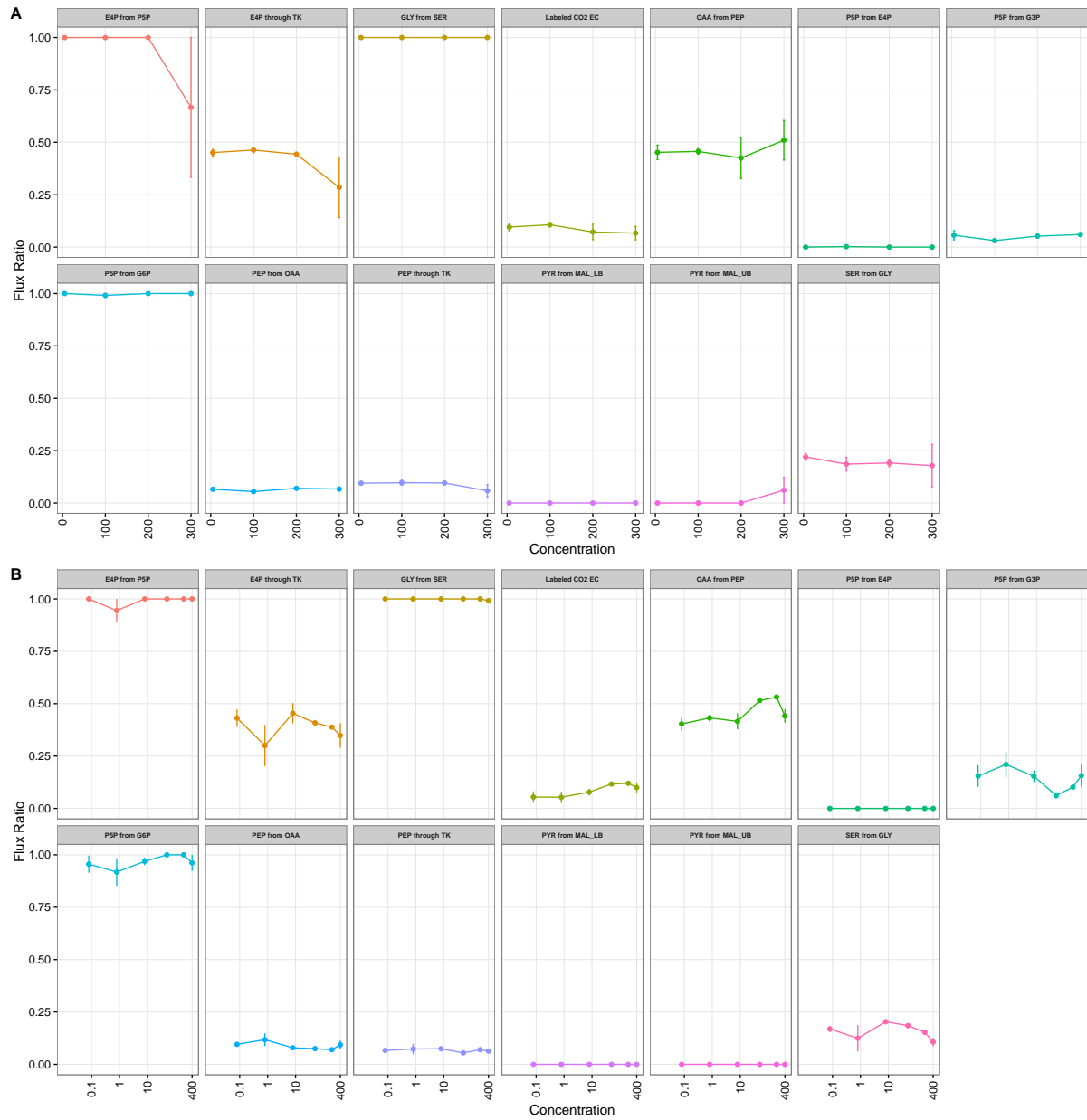
Figure S23: **Flux changes with respect to salt stresses in exponential phase.** 13 different flux were measured with respect to four different Na and five different Mg2+ concentrations. (A) Concentrations with respect to changing Na+ concentrations. (B) Concentrations with respect to changing Mg2+ concentrations. There is no significant trend of increase or decrease in exponential phase flux measurements with respect to either Mg2+ or Na+ concentrations after fdr correction for multiple testing. Correction. The only significant trend was for labelled CO2 EC branch at exponential phase with respect to Mg2+ concentrations before multiple testing (P=.02), but even for this branch, after multiple testing correction corresponding p value increases to .4.