Transcriptomic Monitoring of *Escherichia coli* Growth

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Background and Motivation

Analysis of the transcriptome is a powerful tool for understanding genetic regulatory processes. Prerequisite to any transcriptomic analysis is biological sampling and statistical data analysis. Exemplified by transcriptomic monitoring of bacterial growth we established a data processing pipeline for the analysis of RNASeq data. The goal was to find strongly regulated genes during exponential growth of *Escherichia coli*.

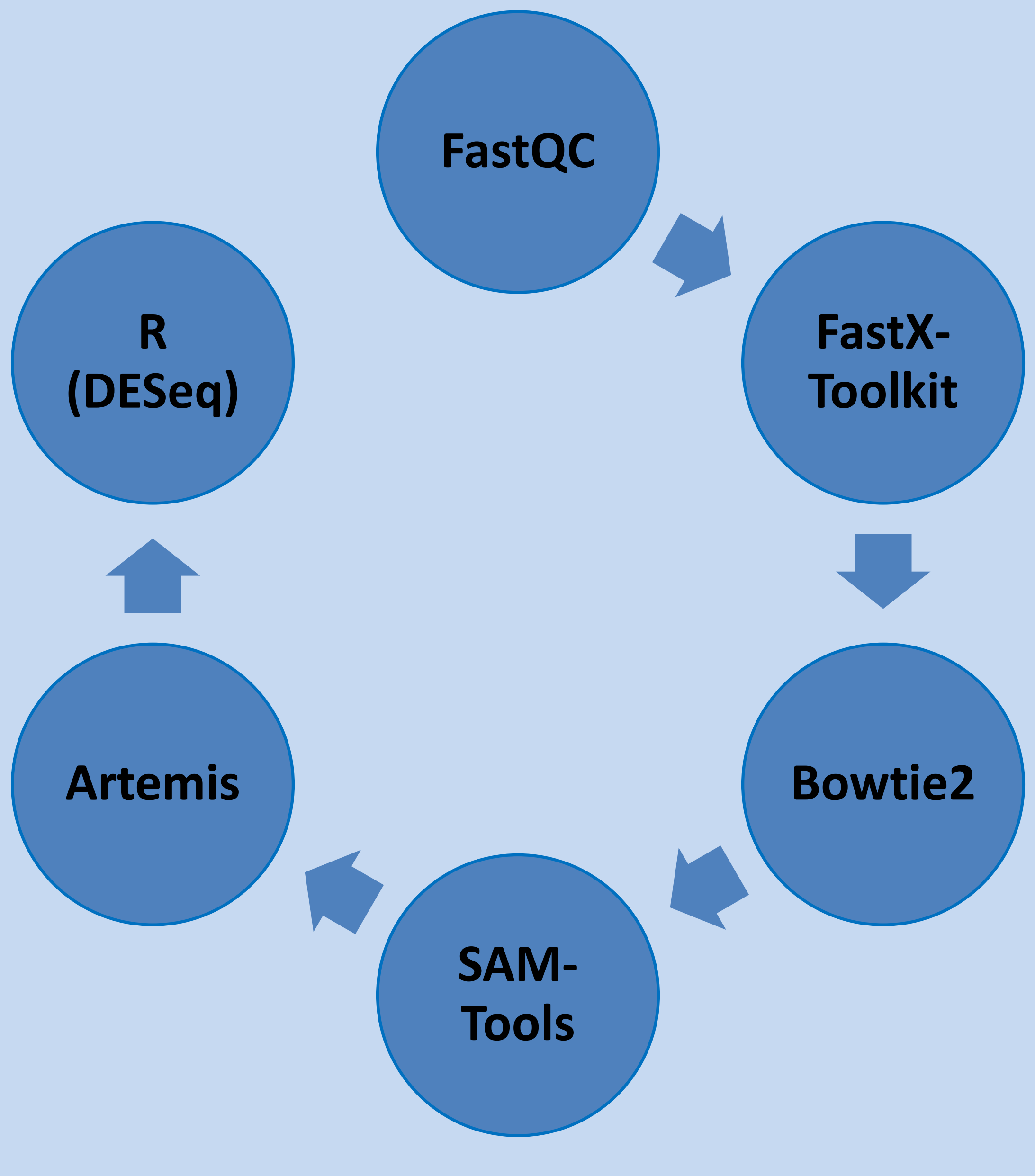
Material and Methods

Escherichia coli **strain K12 (DSM-No 498) was grown as batch culture with DSM medium 1 at 37°C in Erlenmeyer flasks. Cultures were shaken at 150 rpm. Three biologically replicates were incubated from one inoculum (OD_{600} of 1.4; 1:10) and sampled at four different time-points (45 min, 3 h, 5 h, 7 h) covering major growth states at average OD_{600} of 0.14, 0.80, 1.69, and 1.78, respectively. mRNA extraction, sequencing and annotation was performed following standard protocols and software (see Figure 1).**

Results and Discussion

The OD_{600} of all three biological replicates ranged between 1.76 and 1.81 after 7 h of growth. The clustered expression pattern of time-course changes are shown in Figure 2. Interpretation of the results will be presented. For a first insight into gene regulatory processes with focussed our analysis on expressed enzymes, i.e. proteins with allocated EC numbers. 204/257 individual enzymes were found to be significantly up/down-regulated between time-point 45 min and 5 h (see Figure 3). These could be allocated to 97 pathway categories (see Table 1).

Figure 1



FastQC

FastX-Toolkit

Bowtie2

SAM-Tools

Artemis

R (DESeq)

Figure 2

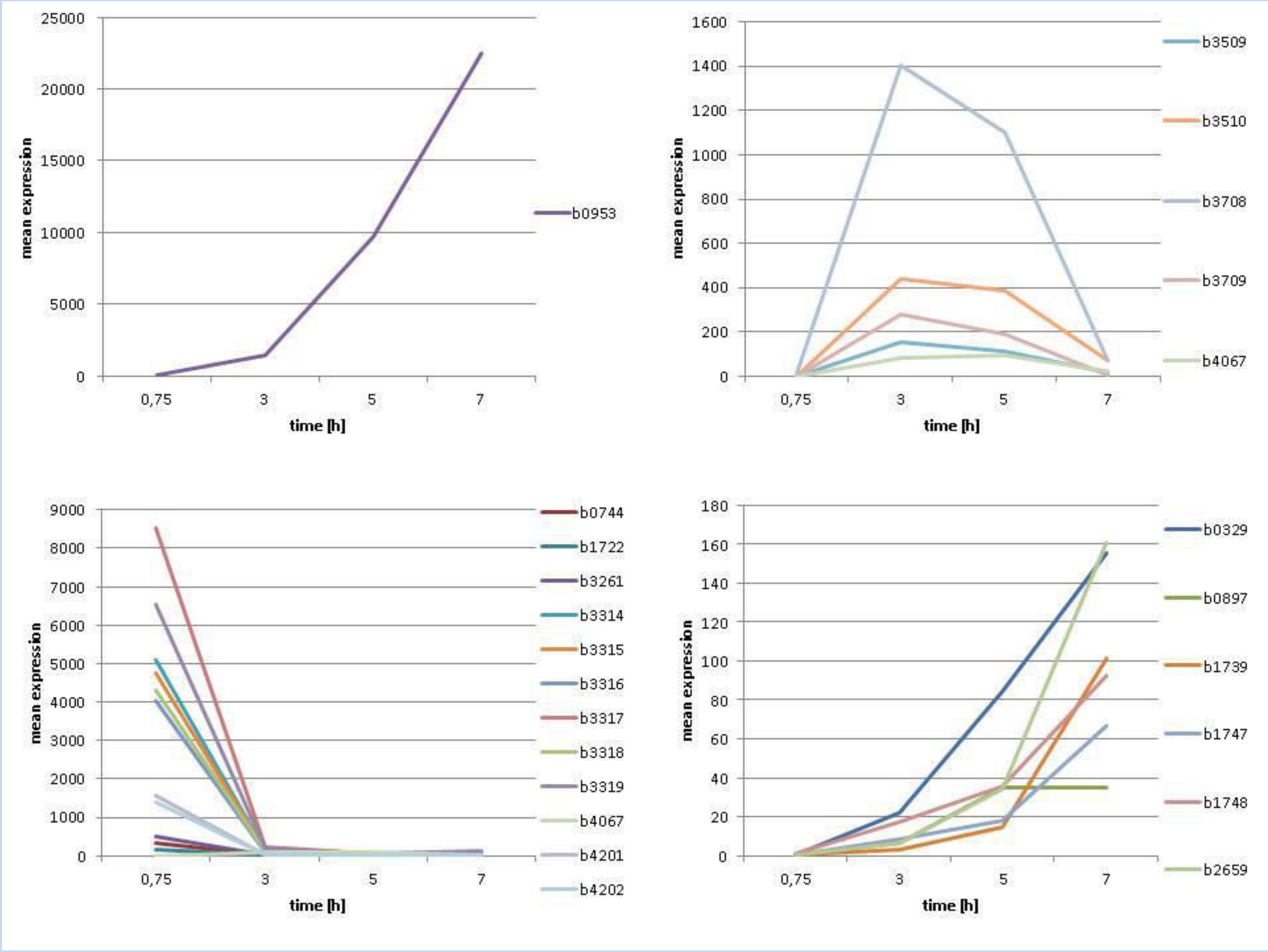
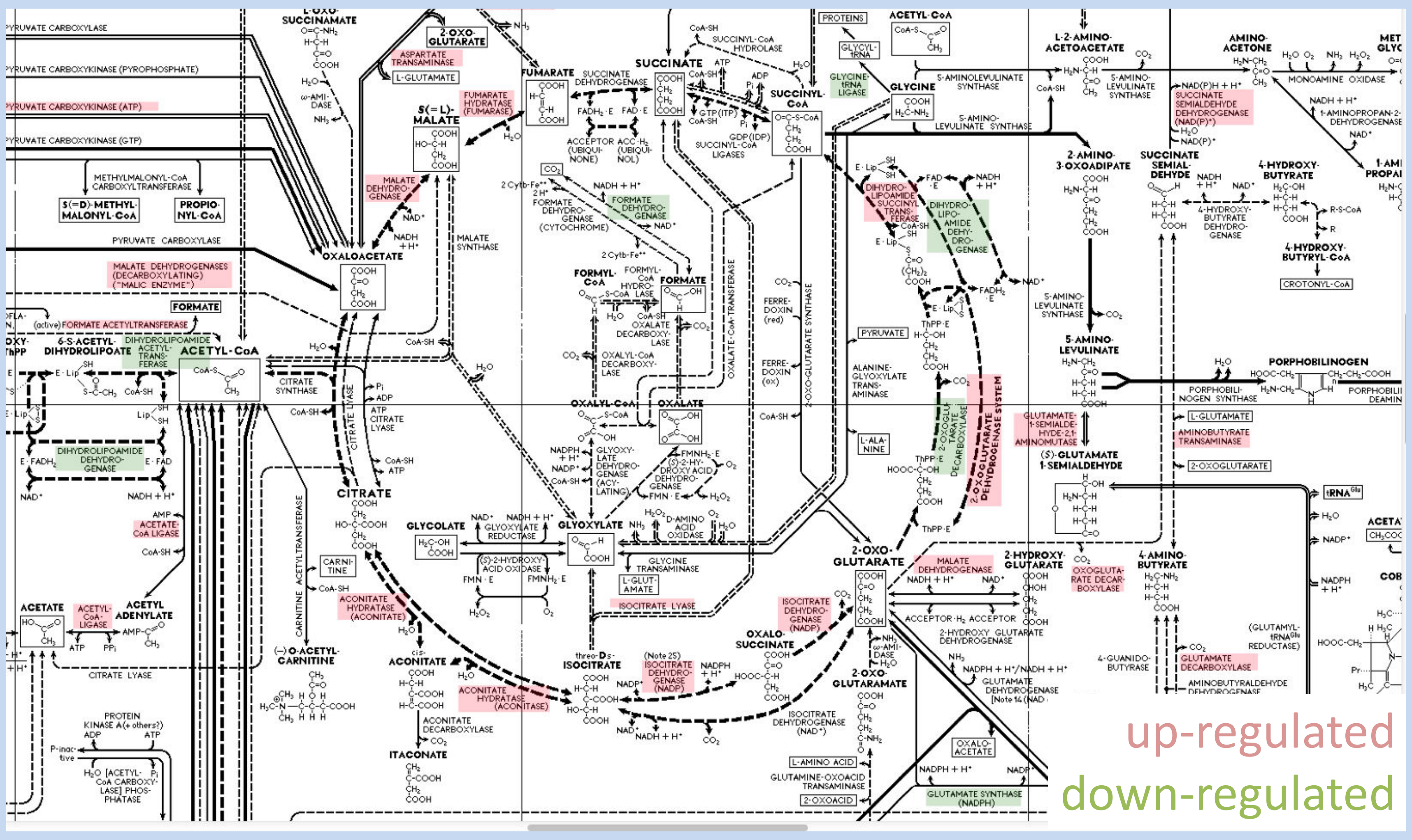


Table 1

Gene ID	Gene Name	Annotation
b3509	*hdeB*	acid resistent protein
b3510	*hdeA*	acid resistent protein
b3708	*tnaA*	tryptophanase/L-cystein desulfhydrase
b3709	*tnaB*	tryptophane transporter
b4067	*actP*	acetat transporter

Figure 3



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