



Additional data file 5

Integration of transcriptome and metabolome data during the comparison of ancestral and evolved strains in excess-nutrient adaptive evolution (MG/MGAdp and DH/DHAdp). Metabolic overview for *E. coli* illustrating the results of high-throughput transcriptome and metabolome experiments in a global metabolic pathway context generated by Pathway Tools. Gene expression levels are mapped to reaction steps involved in a metabolism, and the range of data values levels in a given experimental dataset is mapped to a spectrum of colours according to the \log_2 ratio scale on the lower right inset. Similarly, for metabolomics data, compound nodes are coloured according to the data value for the corresponding compound. The inner inset shows the ratio-intensity plot of the gene expression data displaying the $\log_2(Ri/Gi)$ ratio for each element on the array as a function of the $\log_{10}(Ri*Gi)$ product intensities. (1- Biosynthesis - Aminoacyl-tRNAs, 2- Biosynthesis - Cofactors, prosthetic group and electron carriers, 3- Biosynthesis - Amino acids, 4- Biosynthesis - Fattyacids and lipids, 5- Biosynthesis - Cell structure, 6- Biosynthesis - Amines and polyamines, 7- Biosynthesis - Secondary metabolites, 8- Biosynthesis - Sugars and polysaccharides, 9- Biosynthesis - Nucleosides and nucleotides, 9a- Biosynthesis -Signal transduction pathways, 10- Respiration, 11- Pentose phosphate pathway, 12- Glycolysis, 13- Fermentation, 14- Superpathway of glycolysis and Entner-Doudoroff, 15- Degradation - Sugars and polysaccharides, 16- Degradation - Sugar derivatives, 17- Degradation - Fattyacids and lipids, 18- Degradation - Alcohols, 19- Degradation - Amino acids, 20- Degradation - Inorganic nutrients, 21- Degradation - Amines and polyamines, 22- Degradation - Nucleosides and nucleotides, 23- Degradation - Aromatic compounds, 24- Degradation - Carboxylates.)