

Additional data file 10

Integration of transcriptome and metabolome data during the comparison of ancestral and evolved strains in prolonged stationary phase evolution (MG/MGStat and DH/DHStat). 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 log₂ 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 log₂(Ri/Gi) ratio for each element on the array as a function of the log₁₀(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.)