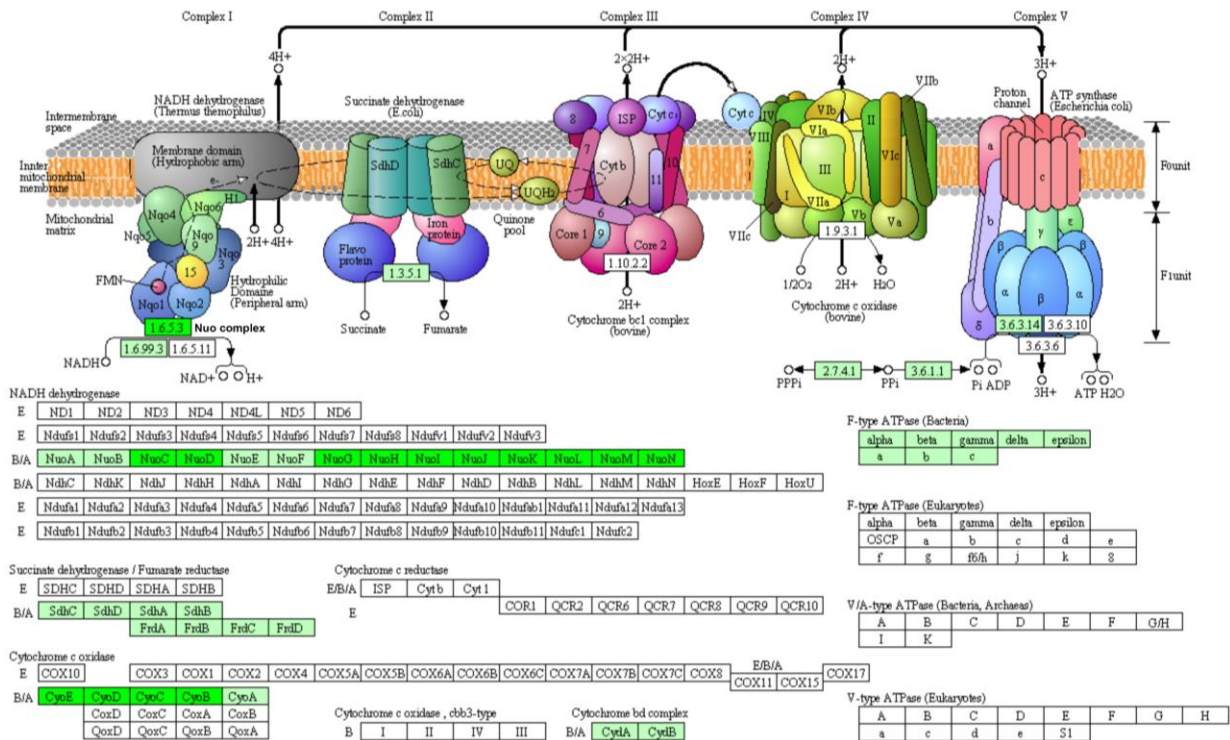Supplementary figure 1 - PCA analysis of transcriptomics data of the coexisting ecotypes data set as obtained from Le Gac et al. (Le Gac, et al. 2012). Genes are treated as variables, strains as observations. Dots of identical shape and color represent replicate cultures. Circular/red dots represent ancestral strains, square/green dots represent L ecotypes and diamond shaped/blue dots S ecotypes. It is expected that dots of equal shape and color will group together because ideally they should exhibit identical expression levels for each gene. **A)** PCA plot of the observations on the first two PC's. Except for two outliers (one ancestral and one S ecotype) observations group together according to their label. **B)** PCA plot of the observations on the first two PCs after removing the outliers from the data set. As can be seen, the observations group together far better according to their label when removing the outliers. To reduce noise on the part of the transcriptomics data, the two microarrays corresponding to the outlier observations were discarded.
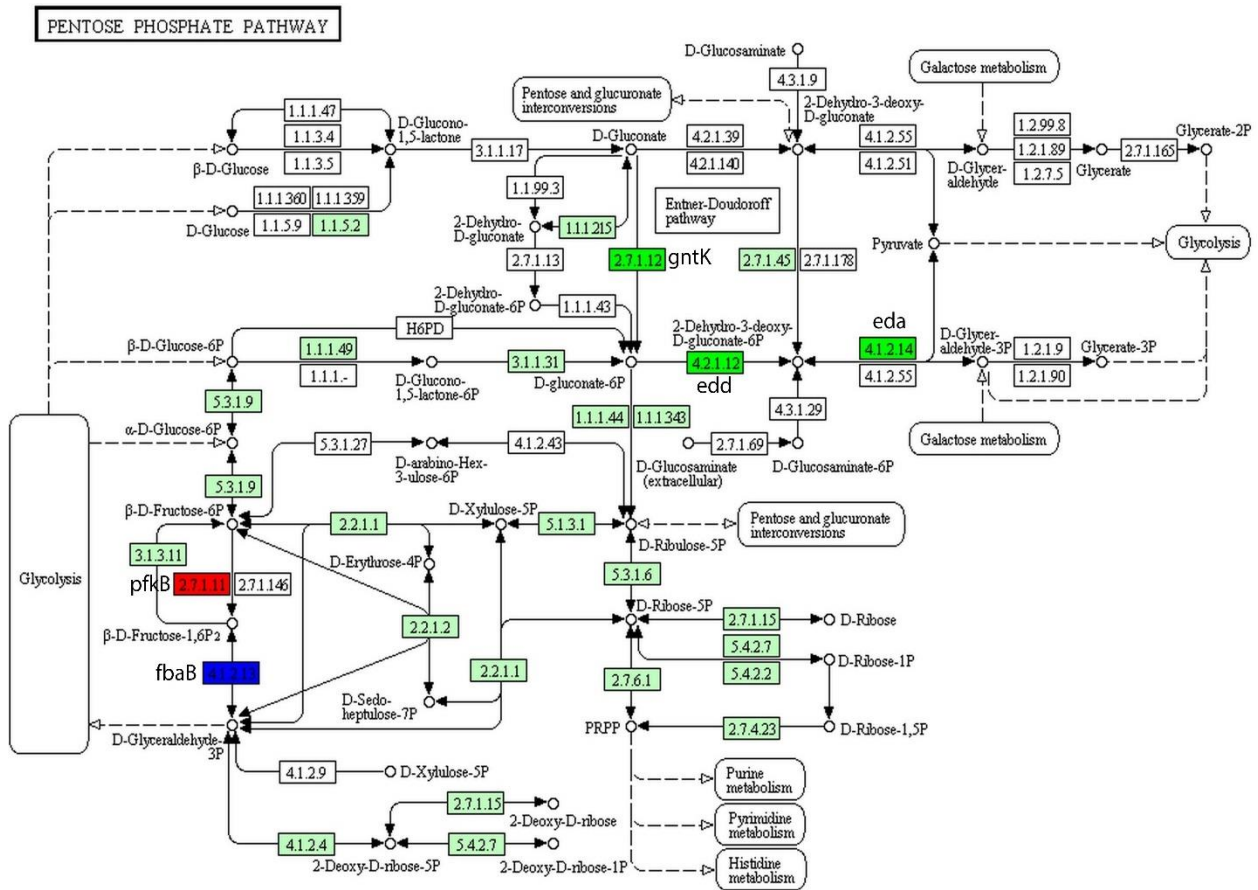
Supplementary figure 2 – Mapping of the inferred subnetwork from all four lines of the Amikacin resistance data set to the oxidative phosphorylation from KEGG pathways. Light green boxes correspond to genes/gene products present in *E.coli MDS 42*.Green boxes correspond to genes/gene products present in the inferred subnetwork which are down regulated as compared to the ancestral strain. It can be seen that NADH dehydrogenase and cytochrome oxidase complexes are down regulated in the AMK resistant strains.
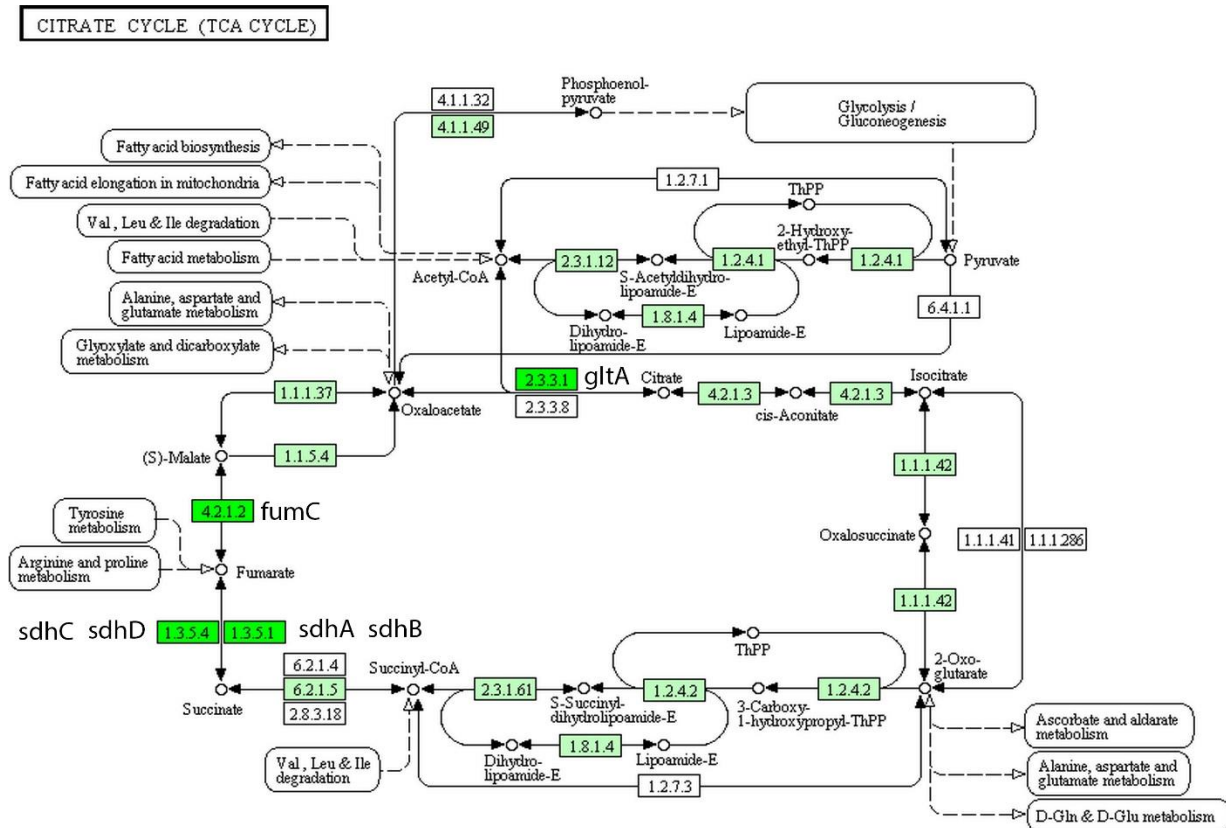
Supplementary figure 3 - Mapping of the inferred subnetwork from the coexisting ecotypes data set to the TCA cycle from KEGG pathways. Light green boxes correspond to genes/gene products present in *E.coli B REL606*. Green boxes correspond to genes/gene products present in the inferred subnetwork and up-regulated in the S ecotype as compared to the L ecotype. It can be seen that multiple components of the TCA cycle are up-regulated in the S ecotype as compared to the L ecotype.

Supplementary figure 4 – Mapping of the inferred subnetwork from the coexisting ecotypes data set to the pentose phosphate pathway from KEGG pathways. Light green boxes correspond to genes/gene products present in *E.coli B REL606*. Green boxes correspond to genes/gene products present in the inferred subnetwork and up-regulated in the S ecotype as compared to the L ecotype. Red boxes correspond to genes/gene products present in the inferred subnetwork and overexpressed in the L ecotype as compared the S ecotype. Blue boxes correspond to genes/gene products present in the inferred subnetwork and mutated in the L ecotype. It can be seen that multiple components of the Entner-Doudoroff pathway are up-regulated in the S ecotype as compared to the L ecotype implying S-specific uptake of gluconate.