ESI1. The hierarchical clustering dendogram of the transcriptome in response to an impulse like addition of glucose (above) and ammonium (below).

ESI2. The computer visualized output of Pathway Viewer mapping gene expression and metabolite concentration levels onto KEGG pathways for glycolysis. The normalized expression and metabolite concentration levels, which were analysed with respect to the first steady state (P1), were provided numerically and these numerical values were also colour coded. Each individual pathway diagram represents a particular snapshot for the zero-normalized difference in expression levels and metabolite concentrations. Red indicates high concentrations for metabolites/up-regulation for genes whereas yellow indicates low concentrations for metabolites/down-regulation for genes. Dark blue indicates no change. Therefore different colours along phases would indicate up- or down-regulation of a gene during different phases following the perturbation. Metabolite levels were similarly colour coded in the figures and the colours indicated normalized high- or low-concentration. If no information was available, that particular gene or metabolite was shown in black. The As indicate the response to glucose impulse whereas Bs represent the response to ammonium impulse. If there is more than one gene encoding the enzymes catalysing a particular reaction, this was shown by two different bars connecting the reactant and the product. Accordingly, the colour of the bar and the gene that it represents were the same.

ESI3. The computer visualized output of Pathway Viewer mapping gene expression and metabolite concentration levels onto KEGG pathways for The TCA Cycle. See ESI2 legend for details.

ESI4. The computer visualized output of Pathway Viewer mapping gene expression and metabolite concentration levels onto KEGG pathways for gluconeogenesis. See ESI2 legend for details.

ESI5. The computer visualized output of Pathway Viewer mapping gene expression and metabolite concentration levels onto KEGG pathways for the *de novo* synthesis of purine nucleotides and their salvage pathways. See ESI2 legend for details.

ESI6. The computer visualized output of Pathway Viewer mapping gene expression and metabolite concentration levels onto KEGG pathways for the *de novo* synthesis of pyrimidine nucleotides. See ESI2 legend for details.

ESI7. The computer visualized output of Pathway Viewer mapping gene expression and metabolite concentration levels onto KEGG pathways for the salvage pathways of pyrimidine nucleotides. See ESI2 legend for details.

ESI8. The computer visualized output of Pathway Viewer mapping gene expression and metabolite concentration levels onto KEGG pathways for the folate metabolism. See ESI2 legend for details.

ESI9. The computer visualized output of Pathway Viewer mapping gene expression and metabolite concentration levels onto KEGG pathways for the serine-glycine-threonine metabolism (above), sulphur assimilation (middle), methionine salvage metabolism (below). See ESI2 legend for details.

ESI10. The computer visualized output of Pathway Viewer mapping gene expression and metabolite concentration levels onto KEGG pathways for the aspartate (above) and glutamate (below) metabolisms. See ESI2 legend for details.

ESI11. The raw and processed endo-metabolome data in response to an impulse-like addition of glucose (c) or ammonium (n) into its respective limited culture. The peak identification for the detected metabolites along with the likely success of the identification (out of 1000) is stated in the interest metabolites tabs. The peak areas for all identified peaks and the internal standard are provided in peak area tabs. The peak ratios with respect to the internal standard are provided in peak ratio tabs. The sample normalization within phase, across time and experimental conditions is provided in the normalization tabs. The difference in the normalized mean values for each phase and phase 1 (P1) are provided in the normalized phase differences tabs.