

## Description of Additional Supplementary Files

File Name: Supplementary Data 1

Description: Fold change and intracellular concentrations ( $\mu\text{M}$ ) of measured metabolites in *E. coli* BW25113 in the switch from growth to starvation and back to growth. Fold change is calculated to the first time point  $t_0$ . Compound information contains KEGG, metabolite name, BIGG identifier and the corresponding subsystem.

File Name: Supplementary Data 2

Description: Expression of genes shown as TPM (Transcripts Per kilobase Million) of *E. coli* BW25113 in the switch from growth to starvation and back to growth.

File Name: Supplementary Data 3

Description: Process time in h, optical density at 600 nm (OD600), growth rate ( $\mu$ ), reactor volume  $V_r$  in Liter and the corresponding metabolite and transcript samples during the shift of starvation and growth. Samples for metabolomics were collected at 35 time points; samples for transcriptomics were collected at 29 time points.

File Name: Supplementary Data 4

Description: Process data including process time (h), agitation (RPM), dissolved oxygen DO (%), gas flow inlet ( $\text{sL}\cdot\text{min}^{-1}$ ), pH, temperature ( $^{\circ}\text{C}$ ), gas flow outlet ( $\text{sL}\cdot\text{h}^{-1}$ ), oxygen concentration  $\text{O}_2$  (%), carbon dioxide concentration  $\text{CO}_2$  (%), oxygen uptake rate OUR ( $\text{mmol}\cdot\text{h}^{-1}$ ), carbon production rate CPR ( $\text{mmol}\cdot\text{h}^{-1}$ ), specific oxygen uptake rate  $q_{\text{O}_2}$  ( $\text{mmol}\cdot\text{h}^{-1}\cdot\text{g}^{-1}$ ) and specific carbon production rate  $q_{\text{CO}_2}$  ( $\text{mmol}\cdot\text{h}^{-1}\cdot\text{g}^{-1}$ ) during the shift of starvation and growth.

File Name: Supplementary Data 5

Description: Transcription factor activity ( $\log_{10}$ ) calculated by Network Component Analysis and the 95% confidence interval of 100 calculations with randomised starting points.

File Name: Supplementary Data 6

Description: Correlation coefficients of 123 metabolites and 125 transcription factor activities using Hill-type parameters

File Name: Supplementary Data 7

Description: 513 correlation coefficients of metabolite- transcription factor pairs that fulfill the distance filter.

File Name: Supplementary Data 8

Description: Connectivity matrix of the transcriptional regulatory network between all transcriptional regulators and genes in *E. coli*. Adapted from RegulonDB and EcoCyc. 1 indicates activation; -1 indicates inhibition by the transcriptional regulator.

File Name: Supplementary Data 9

Description: Gene expression input ( $\log_{10}$ ) for Network Component Analysis.

File Name: Supplementary Data 10

Description: Reporting standards for metabolite measurement