

Supplementary Information

A: Determination of conversion factors from OD 600 nm to cell dry weight concentration

In preliminary experiments, optical density of appropriately diluted fermentation broth from the primary reactor was measured in triplicates at 600 nm on a spectrophotometer (Amersham Biosciences/GE Healthcare, Amersham, United Kingdom). In parallel, quadruplicate determination of biomass concentration was conducted. 5 ml of broth were centrifuged in weighted glass tubes at 2500 g and 4 °C for 7.5 min. Supernatant was immediately decanted and the pellet washed by resuspending in 5 ml of freshly prepared 150 mM NH_4HCO_3 . The suspension was centrifuged again and the washing repeated once. After a final centrifugation the pellet was dried at 105 °C for at least two days and the new weight of the glass tubes measured. The ratio CDW [g/l] / OD 600 nm was calculated and averaged over all samples to yield conversion factors for each strain. Conversion factors were 0.324 for *E. coli* MG1655 and 0.321 for *E. coli* SR and used in all subsequent experiments to convert OD 600 nm measurements to cell dry weight concentration [g/l].

Table S1: OD 600 nm and CDW [g/l] data from preliminary experiments.

<i>E. coli</i> MG1655			<i>E. coli</i> SR		
OD 600 nm	CDW [g/l]	Ratio CDW / OD	OD 600 nm	CDW [g/l]	Ratio CDW / OD
Experiment 1			Experiment 1		
8.600	2.545	0.296	8.600	2.975	0.346
8.463	2.875	0.340	8.567	2.925	0.341
8.200	2.550	0.311	8.217	2.815	0.343
8.250	2.555	0.310	8.250	2.865	0.347
Experiment 2			Experiment 2		
8.800	2.720	0.309	9.300	2.665	0.287
8.567	3.140	0.367	9.467	2.790	0.295
8.317	2.925	0.352	9.000	2.715	0.302
8.600	2.685	0.312	9.133	2.790	0.305
Conversion Factor			0.321		
0.324					

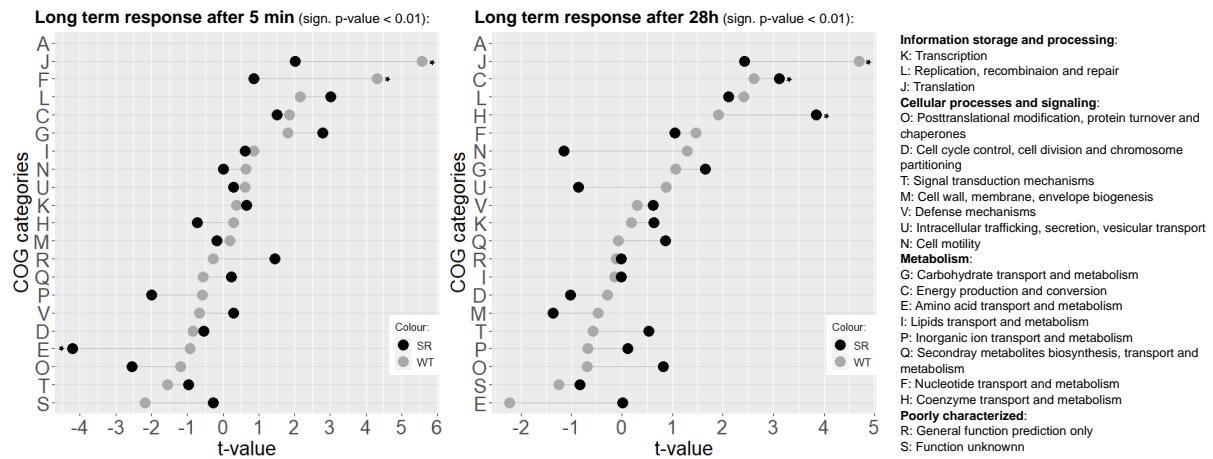


Fig. A3: Left: COG categories long term response 5min STR vs STR 0h WT vs SR; Right: COG categories long term response 28h STR vs STR 0h WT vs SR. Sign. categories are indicated with an asterisk.

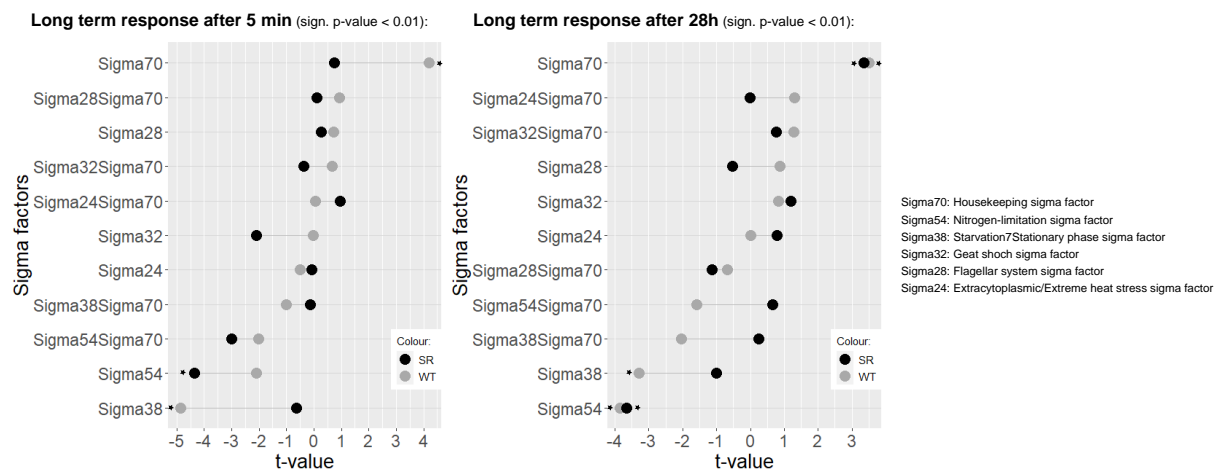


Fig. A4: Left: Sigma factors long term response 5min STR vs STR 0h WT vs SR. Right: Sigma factors long term response 28h STR vs STR 0h WT vs SR. Sign. categories are indicated with an asterisk. Sigma70: Housekeeping; Sigma54: Nitrogen-limitation; Sigma38: Starvation/Stationary phase; Sigma 32: Heat shock; Sigma28: Flagellar system; Sigma24: Extracytoplasmic/Extreme heat stress

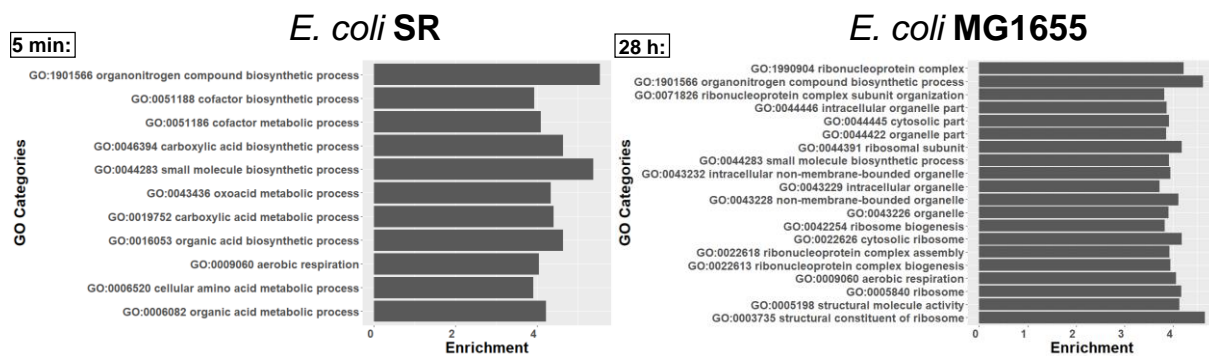


Fig. A5: Left: GO categories long term response 28h STR vs STR0 SR. Top 20 significantly upregulated. No sign. down regulated categories. Right: GO categories long term response 28h STR vs STR0 WT. Top 20 significantly upregulated. No sign. down regulated categories.

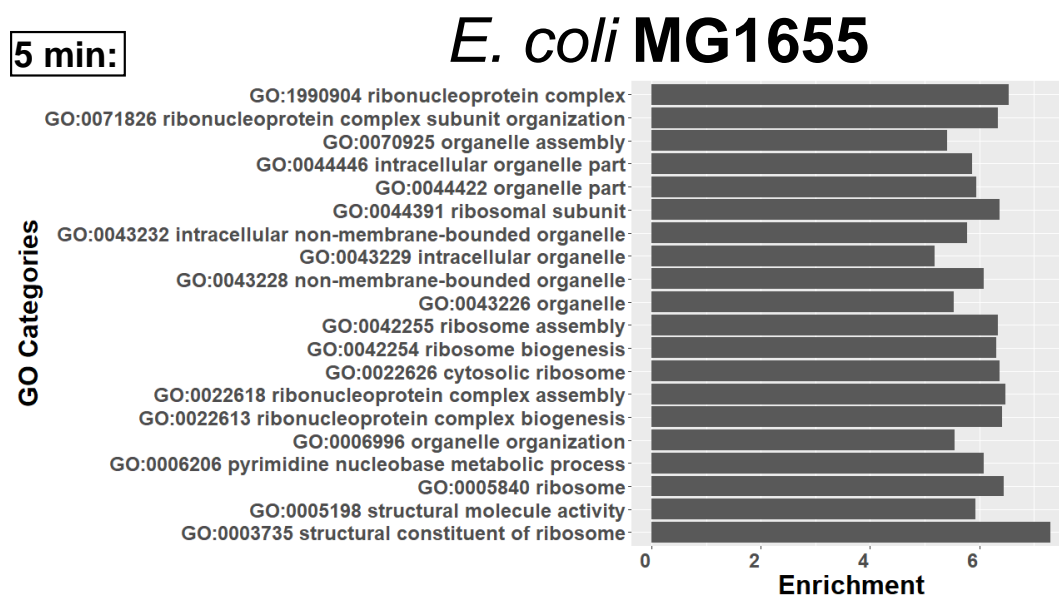


Fig. A6: GO categories long term response 5min STR vs STR0 WT. Top 20 significantly upregulated. No sign. down regulated categories.

C: NtrC-mediated operons

Table S2: NtrC-mediated operons (Brown *et al.*, 2014); *E. coli* MG1655

Operons	Log ₂ FC ^a		Function/Pathway
	5min short	28h long	
<u><i>glnK-amtB</i></u>	3.81	4.09	GlnK - Nitrogen regulatory protein, AmtB – ammonia transport
<u><i>gltIJKL</i></u>	1.14	0.94	Glutamate / aspartate ABC transport
<i>dicC</i>			DNA-binding transcriptional repressor
<u><i>glnHPQ</i></u>	3.41	3.37	Glutamine ABC transport
<u><i>yeaGH</i></u>	2.98	2.69	YeaG is a serine protein kinase
<u><i>ycdMLKJIHG</i></u>	4.01	4.05	Pyrimidine degradation
<i>flgMN</i>	0.29	0.84	Regulation of flagellar synthesis and flagellar biosynthesis protein
<u><i>ddpXABCDF</i></u>	4.25	4.49	D-ala-D-ala dipeptide transport and dipeptidase
<u><i>astCADBE</i></u>	4.84	4.81	Arginine catabolic pathway
<i>fliC</i>	0.46	0.41	Flagellar biosynthesis component
<u><i>Nac-cbl</i></u>	4.14	3.94	Nitrogen limitation response-adpater for sigma 70 dependent genes
<u><i>hisJQMP</i></u>	1.24	1.64	Histidine ABC transporter
<u><i>argT</i></u>	3.32	3.44	Lysine/arginine/ornithine ABC transporter
<u><i>relA</i></u>	1.29	1.60	GDP pyrophosphokinase involved in stringent response
<i>ssrS</i>	-	-	6S RNA involved stationary phase regulation of transcription
<u><i>yqiG</i></u>	3.03	2.79	Putrescine degradative pathway
<u><i>yhdWXYZ</i></u>	2.75	2.36	Polar amino acid transport
<u><i>glnALG</i></u>	2.57	1.99	Glutamine biosynthesis pathway (ammonia assimilation) and nitrogen regulation
<i>soxR</i>	0.30	0.27	SoxR transcriptional regulator
<i>yjcZ-proP</i>	-0.39	-0.26	Hypothetical protein (YjcZ) + symporter (proP)
<i>potFGHI</i>	0.92	0.82	Putrescine transport

^a Underlining indicates significant differential expression. Logarithmic ratios are always given for the first gene in the transcription unit.

Table S3: NtrC-mediated operons (Brown *et al.*, 2014); *E. coli* SR

Operons	Log ₂ FC ^a		Function/Pathway
	5min short	28h long	
<u><i>glnK-amtB</i></u>	4.05	2.67	GlnK - Nitrogen regulatory protein, AmtB – ammonia transport
<i>gltIJKL</i>	0.25	-0.29	Glutamate / aspartate ABC transport
<i>dicC</i>	-0.09	-0.25	DNA-binding transcriptional repressor
<u><i>glnHPQ</i></u>	2.82	2.45	Glutamine ABC transport
<u><i>yeaGH</i></u>	1.30	0.89	YeaG is a serine protein kinase
<u><i>ycdMLKJIHG</i></u>	3.18	2.83	Pyrimidine degradation
<i>flgMN</i>	0.63	0.73	Regulation of flagellar synthesis and flagellar biosynthesis protein
<u><i>ddpXABCDF</i></u>	4.71	3.12	D-alanine-D-alanine dipeptide transport and dipeptidase
<u><i>astCADBE</i></u>	4.11	3.93	Arginine catabolic pathway
<i>fliC</i>	0.05	0.17	Flagellar biosynthesis component
<u><i>Nac-cbl</i></u>	3.13	1.42	Nitrogen limitation response-adaptor for sigma 70 dependent genes
<i>hisJQMP</i>	0.77	0.59	Histidine ABC transporter
<u><i>argT</i></u>	2.51	2.01	Lysine/arginine/ornithine ABC transporter
<i>relA</i>	1.35	1.79	GDP pyrophosphokinase involved in stringent response
<i>ssrS</i>	-	-	6S RNA involved stationary phase regulation of transcription
<u><i>ygiG</i></u>	2.06	2.16	Putrescine degradative pathway
<i>yhdWXYZ</i>	2.00	1.21	Polar amino acid transport
<i>glnALG</i>	2.64	-0.11	Glutamine biosynthesis pathway (ammonia assimilation) and nitrogen regulation
<i>soxR</i>	0.34	1.12	SoxR transcriptional regulator
<i>yjcZ-proP</i>	-0.77	-0.39	Hypothetical protein (YjcZ) + symporter (proP)
<u><i>potFGHI</i></u>	0.44	-1.91	Putrescine transport

^a Underlining indicates significant differential expression. Logarithmic ratios are always given for the first gene in the transcription unit.

D: Motility Assay of *E. coli* MG1655

A 5 ml overnight preculture of *E. coli* MG1655 in 2xTY medium was incubated at 37 °C and 130 rpm. On the next day, a tube containing motility agar (10 g/l tryptone, 3 g/l yeast extract, 5 g/l NaCl, 0.5 g/l triphenyl-tetrazolium chloride and 0.4 % agar-agar) was inoculated by dipping a thin sterile steel wire into the liquid preculture and stabbing the wire into the motility agar. The culture was incubated without shaking at 37 °C overnight. The spreading of cells as indicated by the expanse of red color from reduction of triphenyl-tetrazolium chloride to triphenylformazan was recorded on the next morning. The formation of a cloudy deep red colored zone indicates strong motility and cell viability.



Fig. A7: Motility Assay of *E. coli* MG1655.

E: Glucose-specific phosphotransferase system components

Table S6: Logarithmic expression ratio and percentage change of mean expression levels from three glucose-specific phosphotransferase system components identified in *E. coli* MG1655.

Gene	Log ₂ FC ^a of <i>E. coli</i> SR vs MG1655 (S/S)		Relative Mean Expression Level <i>E. coli</i> SR to <i>E. coli</i> MG1655	
	5 min	28 h	5 min	28 h
<u><i>ptsG</i></u>	-0.35	0.67	+ 21.58 %	+ 58.98 %
<u><i>ptsH</i></u>	0.57	0.68	+ 48.01 %	+ 60.32 %
<u><i>ptsI</i></u>	0.31	0.23	+ 23.82 %	+ 17.28 %

^a Underlining indicates significant differential expression.