

Supporting information to

Assessing glycolytic flux alterations resulting from genetic perturbations in *E. coli* using a biosensor

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Table S1 DNA oligo sequences for cloning

Abbreviations: -p: promoter region; BSsc: scrambled Cra-binding site

Primer name	Sequence 5'-3'	Description
Promoter regions		
PC028	AACCATUAATACCGCCATTTGG	<i>pfkA</i> -p forw
PC029	AGTTCTTCTCCUTTGTCTCATGACTACCTCTGAACTTTG	<i>pfkA</i> -p rev
PC033	AACCATUCAACGCTGGGATC	<i>ppsA</i> -p forw
PC048	AGTTCTTCTCCUTTGTCTCATCGAACAATCCTTTTGTG	<i>ppsA</i> -p rev
PC035	AACCATUGACGTAAATTCCTG	<i>ppc</i> -p forw
PC049	AGTTCTTCTCCUTTGTCTCATATTACCCAGACACC	<i>ppc</i> -p rev
PC063	ATTACTGGGUCGACGTTTTTTTCATCCGGT	<i>ppsA</i> -p BSsc forw
PC064	ACCCAGTAAUAGTCATATATTTTTTTACTTTTTAAGAC	<i>ppsA</i> -p BSsc rev
Genes		
PC019	AGGAGAAGAACUTTTCACTGGAG	<i>gfp</i> forw
PC021	ATTTGUAGAGCTCATCCATGCC	<i>gfp</i> rev
PC069	ACGACCUGCAGGGAGCAG	<i>mCherry</i> w term rev
PC070	ATGGTTUCCAAGGGCGAG	<i>mCherry</i> forw
Backbone assembly		
PC004	AATGGTUTCTTAGACGTC	p15A rev 1
PC031	ACAAAUGATAGAGGCATCA	p15A forw 1
PC055	ACTCTUCCTTTTTCAATATT	p15A forw 2
PC073	AACTGUACAACCTATATCGTATGGG	p15A forw 2
PC057	AAGAGUATGCCTCGGGCA	Sm/Sp resist. forw
PC060	ACAGTUATTTGCCGACTAC	Sm/Sp resist. rev
PC065	AAACCAUCGAACAATCCTTTTGTG	p15A forw 3
PC071	AGGTCGUGTCCTACTCAGGAG	p15A rev 3
PC072	AATGGTUGCGCTAGCGGAG	p15A forw 4

Table SII **Plasmid list**

Abbreviations: -*p*: promoter region; BSc: scrambled Cra-binding site

Name	Description	Source
pZA11MCS	p15A ori; ampicillin res. (amp), P _{LtetO-1} promoter, MCS	(Lutz, 1997)
pZA14MCS	p15A ori; spectinomycin res. (spec), P _{LtetO-1} promoter, MCS	this study
pGFPppsA	pZA4 + <i>ppsA-p_gfp</i>	this study
pGFPppc	pZA4 + <i>ppc-p_gfp</i>	this study
pGFPpykF	pZA4 + <i>pykF-p_gfp</i>	this study
pFlux	pZA4 + <i>ppsA-p_gfp</i> + <i>ppsA-BSc_mCherry</i>	this study
pMevT	Mevalonate production pathway	(Martin <i>et al</i> , 2003)

Table SIII **List of Bacterial strains**

Name	Description/Genotype	Source
Top10	F ⁻ mcrA Δ(mrr-hsdRMS-mcrBC) φ80lacZΔM15 ΔlacX74 nupG recA1 araD139 Δ(ara-leu)7697 galE15 galk16 rpsL(Str ^R) endA1 λ ⁻	Invitrogen
DH5α	F ⁻ <i>endA1 glnV44 thi-1 recA1 relA1 gyrA96 deoR nupG purB20</i> φ80dlacZΔM15 Δ(<i>lacZYA-argF</i>)U169, <i>hsdR17(r_K⁻ m_K⁺)</i> , λ ⁻	Invitrogen
BW25113	<i>lacI⁺rrnB_{T14} ΔlacZ_{WJ16} hsdR514 ΔaraBAD_{AH33} ΔrhaBAD_{LD78} rph-1 Δ(araB-D)567 Δ(rhaD-B)568 ΔlacZ4787(::rrnB-3) hsdR514 rph-1</i>	Baba <i>et al.</i> 2006
Δ <i>cra</i>	BW25113 JW0078-1, Δ <i>cra</i> (Δ <i>fruR</i>)	Baba <i>et al.</i> 2006
BL21(DE3)	F ⁻ <i>ompT gal dcm lon hsdS_B(r_B⁻m_B⁻)</i> λ(DE3 [<i>lacI lacUV5-T7p07 ind1 sam7 nin5</i>]) [<i>malB⁺</i>] _{K-12} (λ ^S)	Agilent
MG1655	K-12 F ⁻ λ ⁻ <i>ilvG⁻ rfb-50 rph-1</i>	ATCC
W3110	F ⁻ λ ⁻ <i>rph-1 INV(rrnD, rrnE)</i>	Monk <i>et al.</i> 2016
Crooks	ATCC 8739	Monk <i>et al.</i> 2016

Table SIV DNA sequences of the promoter regions. The Cra binding site is highlighted in green, the -35 region in dark gray, the -10 region in light gray and the transcription start site in blue.

ppsA promoter region
CAACGCTGGGATCAGTCTTAAAAAGTAAAAAATATATTTGCTTGAACGATTCACTGTTTTTTCATCCGGTTAAATATGCAAAGATAAATGCGCAGAAATGTGTTCTCAAACCGTTCATTTATCACAAAAGGATTGTTTCG
ppc promoter region
GACGTAAATTCCTGCTATTTATTCGTTTGCTGAAGCGATTTCGCAGCATTGACGTCACCGCTTTTACGTGGCTTTATAAAAAGACGACGAAAAGCAAAGCCCGAGCATA TTCGCGCAATGCGACGTGAAGGATACAGGGCTATCAAACGATAAGATGGGGTGTCTGGGGTAAT
pykF promoter region
CGTAACCTTTCCCTGGAACGTTAAATCTTTGATAACAATTTATTGTCTAACCAAGTTGTATATTTTTGAAACGCTGTTTTGTTTTCTTTTGGATTAATTCAGCGTATA ATGCGCGCCAATTGACTCTTGAATGGTTTCAGCACTTTGGACTGTAGAACTCAACGACTCAAAAACAGGCACTCACGTTGGGCTGAGACACAAGCACACATTCTCTGCACGCTTTTCGATGTCACCTATCCTTAGAGCGAGGCACCACCACCTTCGTAATACCGGATTGCGTTTCCGGCAGTGCGCCAGAAAGCAAGTTTCTCCCATCCTTCTCACTTAAAGACTAAGACTGTC

Table SIII DNA sequence of the pps and pps_scr promoter. TS= transcription start site

pps ATTTGCTTGAACGATTCACTGTTTTTTTCATCCGGTTAAATATGCAAAGATAAATGCGCAGAAATGTGTTTCTCAAACCGTTCATTTATCACAAAAGGATTGTTTCGATG - gfp
 pps_scr ATGACTATTACTGGGTCGACGTTTTTTTCATCCGGTTAAATATGCAAAGATAAATGCGCAGAAATGTGTTTCTCAAACCGTTCATTTATCACAAAAGGATTGTTTCGATG - rfp

Cra binding site / scrambled
-35
-10
TS

Table SVI: blastn parameters considered in this study

Parameter	Value	Comment
word_size	4	To match small sequences
evaluate	1000	To match small sequences
num_threads	28	To fully utilize the machine
max_target_seqs	Exp_read_size	Number of reads in Experiment: to get as much as possible of the reads

Table SVII: List of 504 identified genes with a count threshold ≥ 10 in the original library. The genes are ordered by gene name.

Gene name	Locus tag	Function	1 % low flux	5 % low flux	1 % high flux	5 % high flux
abgT	P46133	Putative transport; Not classified	0	1.66	3.35	3.74
aceA	P0A9G6	Enzyme; Central intermediary metabolism: Glyoxylate bypass	0.98	1.31	0	0
aceB	P08997	Enzyme; Central intermediary metabolism: Glyoxylate bypass	1.36	0.35	0	0
aceK	P11071	Enzyme; Central intermediary metabolism: Glyoxylate bypass	3.95	2.43	0	0
adhE	b1241	Enzyme; Energy metabolism, carbon: Fermentation	0.42	-0.75	-0.66	0.44
adhP	P39451	Enzyme; Energy metabolism, carbon: Anaerobic respiration	3.87	3.73	0	0
aer	P50466	Regulator; Degradation of small molecules: Carbon compounds	0.18	-0.96	-0.23	-0.96
alsC	P32720	Putative transport; Not classified	0	-1.95	0	0
alsK	P32718	Putative regulator; Not classified	2.94	3.48	0	0.15
ampD	P13016	Regulator; Not classified	0	-1.65	0	0
ansB	P00805	Enzyme; Degradation of small molecules: Amino acids	0.17	-1.18	-0.31	-0.1
apt	P69503	Enzyme; Salvage of nucleosides and nucleotides	0.51	1.96	1.71	0.53
araE	P0AE24	Transport; Transport of small molecules: Carbohydrates, organic acids, alcohols	-0.57	-0.16	1.27	0.86
aroG	P0AB91	Enzyme; Amino acid biosynthesis: Phenylalanine	0	-0.14	0.03	0.92
arpA	P23325	Null	1.82	1.67	1.94	0.11
arsB	P0AB93	Transport; Drug/analog sensitivity	0.42	-0.23	-0.01	-0.55
arsC	P0AB96	Enzyme; Drug/analog sensitivity	-0.06	-0.91	-0.55	-0.78
artQ	P0AE34	Transport; Transport of small molecules: Amino acids, amines	-0.51	0	0	0
asd	P0A9Q9	Enzyme; Amino acid biosynthesis: Lysine	1.13	0.95	-0.25	0
asnA	P00963	Enzyme; Amino acid biosynthesis: Asparagine	0.02	-0.65	-0.47	-1.01
asr	P36560	Phenotype; Not classified	0.77	2.22	0	0
atpA	P0ABB0	Enzyme; ATP-proton motive force interconversion	-0.02	-0.64	0.06	0.01
atpB	P0AB98	Enzyme; ATP-proton motive force interconversion	0.54	0.16	0.56	-0.46
atpG	P0ABA6	Enzyme; ATP-proton motive force interconversion	0.5	0.23	0.43	-1.02
bcr	P28246	Transport; Drug/analog sensitivity	0.34	0.31	0.37	0.89
bcsC	P37650	Putative enzyme; Not classified	0.03	0.46	0.24	-1.5
bcsG	P37659	Null	0.39	-0.16	-0.75	-1.26
bdm	P76127	Null	-0.05	-0.24	0	-1.31
betB	P17445	Enzyme; Osmotic adaptation	0.33	-0.12	0	-1.58
cadA	P0A9H3	Enzyme; Degradation of small molecules: Amino acids	0	-2.13	0	0
caiE	P39206	Putative enzyme; Central intermediary metabolism: Pool, multipurpose conversions	0	0.45	0	0

ccmC	P0ABM1	Transport; Protein, peptide secretion	-0.81	0	0	0
ccmD	P0ABM5	Transport; Protein, peptide secretion	-3.77	-1.75	0.45	0.25
cfa	P0A9H7	Enzyme; Fatty acid and phosphatidic acid biosynthesis	0.94	0.71	0	0
chbG	P37794	Enzyme; Degradation of small molecules: N,N'-diacetylchitobiose	2.62	2.31	0	0
cheR	P07364	Enzyme; Chemotaxis and mobility	2.92	0.14	0	0
cheW	P0A964	Regulator; Chemotaxis and mobility	2.02	1.15	0	0
chiA	P13656	Putative enzyme; Not classified	-0.56	0.11	0	0.09
citA	P77510	Regulator; Degradation of small molecules: Carbon compounds	1.32	0.28	0.44	1.25
citB	P0AEF4	Regulator; Degradation of small molecules: Carbon compounds	0	-0.97	0	-1.39
citC	P77390	Enzyme; Central intermediary metabolism: Pool, multipurpose conversions	-0.15	-0.44	-0.1	-0.38
clcA	P37019	Transport; Not classified	-0.05	0.06	0	0
clpS	P0A8Q6	Null	0	-1.42	0	0
cobS	P36561	Enzyme; Biosynthesis of cofactors, carriers: Cobalamin	-4.01	-3.6	-1.78	-0.61
cpdA	P0AEW4	Regulator; Degradation of small molecules: Carbon compounds	-0.23	0.61	2.53	0
cpsB	P24174	Enzyme; Central intermediary metabolism: Sugar-nucleotide biosynthesis, conversions	-0.12	-0.43	0.18	0.61
cpsG	P24175	Enzyme; Central intermediary metabolism: Pool, multipurpose conversions	-1.3	-0.73	-0.45	0
cpxA	P0AE82	Putative regulator; Global regulatory functions	0.31	1.19	1.68	0.19
creC	P08401	Enzyme; Global regulatory functions	0	-2.23	0	0
csiE	P54901	Null	0.14	0.43	-0.37	-1.25
csiR	P37338	Regulator; Not classified	-1.86	-0.94	-1.46	0
cynR	P27111	Regulator; Central intermediary metabolism: Pool, multipurpose conversions	0.7	1.24	0	0
dadA	P0A6J5	Enzyme; Degradation of small molecules: Amino acids	-0.31	-0.31	-0.1	0.16
dapB	P04036	Enzyme; Amino acid biosynthesis: Lysine	0.03	0.07	0	0
dcp	P24171	Enzyme; Degradation of proteins, peptides, glyco	2.26	1.68	0	0
dcuC	P0ABP3	Transport; Transport of small molecules: Carbohydrates, organic acids, alcohols	2.94	3.48	0	0.15
ddlB	P07862	Enzyme; Murein sacculus, peptidoglycan	0	-0.93	0	-1.59
ddpX	P77790	Null	-0.43	1.42	0.4	0
deoC	P0A6L0	Enzyme; Salvage of nucleosides and nucleotides	1.1	1.2	0.16	-0.7
dsbA	P0AEG4	Enzyme; Proteins - translation and modification	0	-0.45	-0.29	0
dusB	P0ABT5	Enzyme; tRNA modification	2.74	2.12	0	-1.6
eamA	P31125	Null	-0.21	0.46	0	0
ecnA	P0ADB4	Null	0.05	0.39	0.09	0.41
elbA	P75987	Null	-0.2	0	0	0
envY	P10805	Structural component; Outer membrane constituents	1.95	1.73	0	-1.46
etp	P0ACZ2	Enzyme; Not classified	0.27	-0.44	0.24	0.8

eutG	P76553	Putative enzyme; Degradation of small molecules: Amines	-1.14	0.26	-0.42	-0.97
eutQ	P76555	Putative enzyme; Not classified	-0.23	-1.21	-0.45	-0.61
eutT	P65643	Null	-0.31	-0.78	-0.09	-0.07
fabF	P0AAI5	Enzyme; Fatty acid and phosphatidic acid biosynthesis	-0.31	0	0	0
fadB	P21177	Enzyme; Degradation of small molecules: Fatty acids	0.53	-0.7	0	0.32
fdnG	P24183	Enzyme; Energy metabolism, carbon: Anaerobic respiration	-0.37	0.91	0	0
fepE	P26266	Transport; Transport of small molecules: Cations	0	0.63	0	0
fhiA	Q47153	Null	0	0.09	0	0
fimC	P31697	Factor; Surface structures	-1.57	-0.58	-1.62	-0.18
fimG	P08190	Structural component; Surface structures	0	-1.77	0	0
fkpA	P45523	Enzyme; Proteins - translation and modification	-0.45	-0.05	-0.69	-2.02
flgD	P75936	Putative structure; Surface structures	-1.72	0.26	0.14	-0.85
flgG	P0ABX5	Structural component; Surface structures	1.66	1.69	0.37	-0.31
flgI	P0A6S3	Putative structural component; Surface structures	0.76	0.24	-2.71	-0.56
flgK	P33235	Structural component; Surface structures	2.2	2.59	0	0
fliB	P76299	Structural component; Not classified	3.07	2.18	0	0
fliD	P24216	Putative structure; Surface structures	-0.36	-0.53	-0.82	-0.45
fliG	P0ABZ1	Structural component; Surface structures	0.47	0.06	0	-1.21
fliH	P31068	Transport; Surface structures	0.07	-0.01	0.12	0.09
fliM	P06974	Structural component; Surface structures	3.22	2.01	0	0
fliO	P22586	Putative structure; Surface structures	2.98	2.38	-0.48	0.01
fliP	P0AC05	Putative structure; Surface structures	1.75	1.17	0	0
fliQ	P0AC07	Putative structure; Surface structures	-0.75	-0.05	0.39	-0.46
fliS	P26608	Regulator; Surface structures	1.01	0.14	0	0
fliZ	P52627	Structural component; Unknown	-0.03	-0.83	-0.81	-0.61
frdA	P00363	Enzyme; Energy metabolism, carbon: Anaerobic respiration	0.8	0	0	0
frmB	P51025	Enzyme; Formaldehyde degradation	-0.34	0.76	0	0.54
frvR	P32152	Putative regulator; Not classified	0.09	-0.23	-0.05	0.05
fsaA	P78055	Null	2.88	2.45	0.58	0
galM	P0A9C3	Enzyme; Central intermediary metabolism: Pool, multipurpose conversions	-0.42	-0.32	-0.11	-0.22
galR	P03024	Regulator; Degradation of small molecules: Carbon compounds	-0.74	1.6	-2.14	-0.73
galS	P25748	Regulator; Degradation of small molecules: Carbon compounds	0.28	2	-2.82	-0.86
gapC	P33898	Null	0	-2.52	0	0
gatA	P69828	Enzyme; Transport of small molecules: Carbohydrates, organic acids, alcohols	2.94	3.48	0	0.15
gatC	P69831	Transport; Transport of small molecules: Carbohydrates, organic acids, alcohols	3.66	3.28	0	0
gatZ	P0C8J8	Putative enzyme; Not classified	0.6	0.57	0	0

glnG	POAFB8	Regulator; Amino acid biosynthesis: Glutamine	-0.74	0.22	0	0
glpD	P13035	Enzyme; Energy metabolism, carbon: Aerobic respiration	1.24	0.13	-0.36	-0.76
gltX	P04805	Enzyme; Aminoacyl tRNA synthetases, tRNA modification	0.04	-0.64	-0.54	-1.47
gpp	P25552	Enzyme; Global regulatory functions	-0.52	-0.34	-0.09	-1.5
gspH	P41443	Putative transport; Not classified	-0.29	-0.76	-0.35	-0.37
gspJ	P45761	Putative transport; Not classified	0.3	-0.34	0.3	-0.89
gst	POA9D2	Enzyme; Biosynthesis of cofactors, carriers: Thioredoxin, glutaredoxin, glutathione	0.99	-0.65	3.55	0.82
gyrB	POAES6	Enzyme; DNA - replication, repair, restriction/modification	-0.22	-0.53	-0.3	-0.38
hcr	P75824	Putative enzyme; Not classified	0.22	-0.74	-0.08	-1.07
hdeB	POAET2	Null	0	1.43	0	-0.05
hdeD	POAET5	Null	0.21	0.01	-0.66	0
hemE	P29680	Enzyme; Biosynthesis of cofactors, carriers: Heme, porphyrin	0.85	0.04	0.52	-0.3
hemN	P32131	Enzyme; Biosynthesis of cofactors, carriers: Heme, porphyrin	0.17	0.74	0	0
hipA	P23874	Enzyme; Protein modification	1.72	1.45	-2.48	0
hisH	P60595	Enzyme; Amino acid biosynthesis: Histidine	-0.84	-0.72	-0.15	-1.23
holC	P28905	Enzyme; DNA - replication, repair, restriction/modification	-1.96	0.27	-0.1	-0.97
hslV	POA7B8	Enzyme; Degradation of proteins, peptides, glyco	-1.69	-2.59	0	0
htrE	P33129	Putative membrane; Surface structures	0	-4.2	-0.54	-0.01
hyaB	POACD8	Enzyme; Energy metabolism, carbon: Aerobic respiration	-0.3	-0.51	0	0
hybE	POAAN1	Phenotype; Energy metabolism, carbon: Anaerobic respiration	0	-0.86	0	0
hybF	POA703	Regulator; Energy metabolism, carbon: Anaerobic respiration	0	-1.78	0	0
hycF	P16432	Putative enzyme; Energy metabolism, carbon: Fermentation	0	0.95	0	0
hych	POAEV7	Factor; Energy metabolism, carbon: Fermentation	1.02	-1.16	0	-0.63
hyfD	P77416	Enzyme; Energy metabolism, carbon: Anaerobic respiration	-1.87	-0.57	0	-1.18
hyfJ	P77453	Putative factor; Not classified	1.46	0.79	0	0
hyfR	P71229	Putative regulator; Not classified	1.11	-0.4	1.08	0.21
ilvB	P08142	Enzyme; Amino acid biosynthesis: Isoleucine, Valine	2.23	1.13	0.97	0
ilvN	POADF8	Enzyme; Amino acid biosynthesis: Isoleucine, Valine	0.54	-0.14	0	-0.32
imp	P31554	Phenotype; Adaptations, atypical conditions	-1.09	0.6	0	-0.78
intF	P71298	Phage or Prophage Related	1.27	1.67	-0.7	0
kbaZ	POC8K0	Putative enzyme; Not classified	0.59	-0.16	-0.1	0.11
kdpD	P21865	Enzyme; Global regulatory functions	0.55	0.96	0.25	-0.23
kdsC	POABZ4	Null	0.08	0	-0.16	0.59

lgt	P60955	Enzyme; Macromolecule synthesis, modification: Phospholipids	0.89	0.51	1.05	1.4
lit	P11072	Membrane; Phage or Prophage Related	-2.72	0.59	0	0
livM	P22729	Transport; Transport of small molecules: Amino acids, amines	0.4	0	0.08	-1.26
lsrD	P0AFS1	Transport; Transport of small molecules: Carbohydrates, organic acids, alcohols	1.13	-1.17	0	0
lysC	P08660	Enzyme; Amino acid biosynthesis: Lysine	-0.14	-0.73	-0.18	-0.16
mdfA	P0AEY8	Transport; Transport of small molecules: Other	2.48	1.86	-2.39	-3.38
mdlA	P77265	Null	-1.48	0	0	0
mdlB	P0AAG5	Null	1.82	0.75	0.65	0.55
mdtA	P76397	Putative membrane; Not classified	0.06	-0.51	0.34	-1.6
menD	P17109	Enzyme; Biosynthesis of cofactors, carriers: Menaquinone, ubiquinone	-0.02	-0.43	0.08	0.02
menE	P37353	Enzyme; Biosynthesis of cofactors, carriers: Menaquinone, ubiquinone	1.15	1.72	0	0
metJ	P0A8U6	Regulator; Amino acid biosynthesis: Methionine	0.45	-0.23	0.19	0.18
metL	P00562	Enzyme; Amino acid biosynthesis: Methionine	-0.96	-0.08	0	-0.31
mgsA	P0A731	Enzyme; Central intermediary metabolism: Pool, multipurpose conversions	-0.2	-0.42	0	0
mhpD	P77608	Enzyme; Degradation of small molecules: Carbon compounds	1.56	0.14	0.69	0
mhpR	P77569	Regulator; Not classified	-0.44	1.51	0	0
mhpT	P77589	Putative transport; Not classified	2.76	2.54	-2.45	-2.38
mngA	P54745	Enzyme; Proteins - translation and modification	0	0.22	0	0
molR	P33345	Null	0	-0.52	0	0
mraW	P60390	Enzyme; rRNA modification	-1.45	-0.86	0	0
mrcA	P02918	Enzyme; Murein sacculus, peptidoglycan	-0.54	-0.13	-0.33	-1.46
mrcB	P02919	Enzyme; Murein sacculus, peptidoglycan	0.58	-0.33	0.2	-0.35
mrp	P0AF08	Putative enzyme; Not classified	0.3	-0.94	-0.2	0.2
msrA	P0A744	Enzyme; Proteins - translation and modification	-0.13	-1.14	0	0
murD	P14900	Enzyme; Murein sacculus, peptidoglycan	-0.11	-1.29	-0.59	-1.39
mutT	P08337	Enzyme; 2'-Deoxyribonucleotide metabolism	-1.17	-0.54	0	-0.32
nagA	P0AF18	Enzyme; Central intermediary metabolism: Amino sugars	0	-3.25	0	0
nagC	P0AF20	Regulator; Central intermediary metabolism: Amino sugars	-3.09	-2.02	-0.41	-0.11
nagZ	P75949	Null	1.34	-0.71	0.65	0
nanK	P45425	Putative regulator; Not classified	3.85	2.98	0	0
napD	P0A9I5	Null	0	-2.19	0	0
nfo	P0A6C1	Enzyme; Degradation of DNA	2.18	-1.09	0	0
nikC	P0AFA9	Transport; Transport of small molecules: Cations	-0.22	-0.8	-0.65	-1.44
nlpB	P0A903	Membrane; Macromolecule synthesis, modification: Lipoprotein	0.14	-0.2	-0.08	-0.5
nohA	P31061	Phage or Prophage Related	1.72	1.08	0	0

nrdD	P28903	Enzyme; 2'-Deoxyribonucleotide metabolism	0	0.12	0	0
ogt	P0AFH0	Enzyme; DNA - replication, repair, restriction/modification	0.95	0.14	0	0
ompC	P06996	Membrane; Outer membrane constituents	-1.11	-0.72	1.02	1.26
oppD	P76027	Transport; Not classified	1.5	0.85	0	0
pcm	P0A7A5	Enzyme; Proteins - translation and modification	2.95	2.69	0	0
pepQ	P21165	Enzyme; Degradation of proteins, peptides, glyco	-0.05	-1.29	0.35	-1.17
pflD	P32674	Enzyme; Energy metabolism, carbon: Anaerobic respiration	-0.02	-0.62	-0.4	-0.73
pfs	P0AF12	Null	-0.26	-0.52	0.12	-0.4
phnA	P0AFJ1	Null	-0.4	0	0	0
phnC	P16677	Transport; Central intermediary metabolism: Phosphorus compounds	2.9	2.59	0	-1.23
phnG	P16685	Enzyme; Central intermediary metabolism: Phosphorus compounds	1.13	-1.09	-0.05	-0.16
phnH	P16686	Enzyme; Central intermediary metabolism: Phosphorus compounds	0.41	-0.37	0	0
phoA	P00634	Enzyme; Central intermediary metabolism: Phosphorus compounds	0.63	-1.51	0	0
phoH	P0A9K1	Regulator; Central intermediary metabolism: Phosphorus compounds	0.34	0.03	-0.2	0.08
phoU	P0A9K7	Regulator; Global regulatory functions	-0.06	-0.48	-1.24	-2.33
pncA	P21369	Null	-0.74	1	0.73	0.32
pntA	P07001	Enzyme; Central intermediary metabolism: Pool, multipurpose conversions	0.53	0.44	0	-0.66
potB	P0AFK4	Transport; Transport of small molecules: Amino acids, amines	-0.21	-1.7	-0.31	-0.28
pphA	P55798	Regulator; Not classified	0.67	0.66	0	-0.94
ppk	P0A7B1	Enzyme; Central intermediary metabolism: Phosphorus compounds	3.23	3.04	0.44	0
psd	P0A8K1	Enzyme; Macromolecule synthesis, modification: Phospholipids	-1	-0.59	1.3	0
purH	P15639	Enzyme; Purine ribonucleotide biosynthesis	0.43	0.03	-0.12	-1.15
purR	P0ACP7	Regulator; Purine ribonucleotide biosynthesis	0.83	0.81	-0.65	-0.61
pyrB	P0A786	Enzyme; Pyrimidine ribonucleotide biosynthesis	-0.2	0	0	0
paaC	P76079	Enzyme; Phenylacetic acid degradation	0.1	-0.4	-0.65	-1.42
paaF	P76082	Enzyme; Phenylacetic acid degradation	0.15	-0.08	0.15	-0.22
paal	P76084	Enzyme; Phenylacetic acid degradation	2.82	2.13	0.06	-1.09
qor	P28304	Enzyme; Energy metabolism, carbon: Electron transport	0.12	-0.23	-0.4	-0.27
racR	P76062	Phage or Prophage Related	0.1	0.35	0	0
radA	P24554	Putative enzyme; Degradation of proteins, peptides, glycopeptides	-0.64	-0.8	0	0
rarA	P0AAZ4	Putative enzyme; Not classified	1.07	1.99	0	0.43
rbbA	P37624	Putative transport; Not classified	-0.21	-0.55	0.34	-0.23
rbsC	P0AGI1	Transport; Transport of small molecules:	-0.17	-0.58	-0.32	-0.69

		Carbohydrates, organic acids, alcohols				
rcsF	P69411	Regulator; Surface polysaccharides & antigens	0	-1.08	0	0
rep	P09980	Enzyme; DNA - replication, repair, restriction/modification	0.43	-0.28	0	-0.75
rffG	P27830	Enzyme; Central intermediary metabolism: Sugar-nucleotide biosynthesis, conversions	0	0.46	0.09	0
rimJ	POA948	Enzyme; Ribosomes - maturation and modification	3.51	2.73	0	0
rne	P21513	Enzyme; Degradation of RNA	-0.01	-0.39	-0.17	-1.14
rob	POACIO	Factor; DNA - replication, repair, restriction/modification	-0.64	0.4	0	0.45
rpe	POAG07	Enzyme; Central intermediary metabolism: Non-oxidative branch, pentose pathway	0.01	0.15	-0.39	0
rph	P0CG19	Enzyme; Degradation of RNA	0.02	-0.54	-1.76	0
rpiA	POA7Z0	Enzyme; Central intermediary metabolism: Non-oxidative branch, pentose pathway	-2.24	-1.97	1.22	2.2
rplW	POADZ0	Structural component; Ribosomal proteins - synthesis, modification	-0.6	-0.66	-0.21	-0.33
rpmD	POAG51	Structural component; Ribosomal proteins - synthesis, modification	-0.05	1.78	0	0.57
rpmF	POA7N4	Structural component; Ribosomal proteins - synthesis, modification	0.31	-0.87	-0.43	-1.49
rseC	P46187	Regulator; Global regulatory functions	0.2	0	0	0
rssA	POAFR0	Null	2.78	2.52	0	0
rsuA	POAA43	Enzyme; rRNA modification	0.86	0	0.07	0
rsxC	P77611	Putative membrane; Not classified	0	0.07	0	0.55
sbcD	POAG76	Enzyme; Degradation of DNA	0	0	0	-0.25
secG	POAG99	Transport; Protein, peptide secretion	0	-2.71	0	0
selD	P16456	Enzyme; Aminoacyl tRNA synthetases, tRNA modification	0.25	0.52	0	0
sfmC	P77249	Putative factor; Surface structures	0.41	0.62	0	-0.84
sgbU	P37679	Putative enzyme; Central intermediary metabolism: Pool, multipurpose conversions	0.57	-0.15	-0.08	-0.13
sgcB	P58035	Null	-1.08	0	0	0
sgcQ	P39364	Putative enzyme; Not classified	0	-0.47	0.36	1.16
sgrR	P33595	Transport; Not classified	0	-1.42	0	0
slyA	POA8W2	Regulator; Adaptations, atypical conditions	0.59	-0.03	-1.08	0.38
slyX	POA8R4	Null	0.51	-0.06	0.08	0.32
soxS	POA9E2	Regulator; Global regulatory functions	0	0.54	0	0
speB	P60651	Enzyme; Central intermediary metabolism: Polyamine biosynthesis	0	-1	-1.14	0
ssnA	Q46812	Putative structure; Not classified	2.54	2.44	2.47	3
ssuD	P80645	Null	1.94	0.95	-0.42	0
stfQ	P77515	Phage or Prophage Related	3.07	2.67	-0.17	0
stfR	P76072	Phage or Prophage Related	3.07	2.67	-0.17	0
sucC	POA836	Enzyme; Energy metabolism, carbon: TCA cycle	0.47	0.09	0.59	0.41

tam	P76145	Enzyme; Detoxification	1	-1.27	0	0
tar	P07017	Regulator; Chemotaxis and mobility	-1.38	-0.8	-1	0
tdcD	P11868	Putative enzyme; Not classified	-0.25	-2.17	0	0
tehB	P25397	Enzyme; Drug/analog sensitivity	-0.5	0.17	0	0
tesA	P0ADA1	Enzyme; Fatty acid and phosphatidic acid biosynthesis	1.19	0.73	0.89	1.27
tesB	P0AGG2	Enzyme; Fatty acid and phosphatidic acid biosynthesis	0	-0.01	0	0
tfaD	P77699	Phage or Prophage Related	-0.81	-0.06	-0.01	1.04
tfaE	P09153	Phage or Prophage Related	-0.34	0.33	0.19	0.59
tfaS	P77326	Phage or Prophage Related	-0.29	0.33	0.24	0.67
this	O32583	Factor; Biosynthesis of cofactors, carriers: Thiamine	-1.19	-0.98	0	0
tktA	P27302	Enzyme; Central intermediary metabolism: Non-oxidative branch, pentose pathway	-0.64	-0.27	0.35	1.17
tktB	P33570	Enzyme; Central intermediary metabolism: Non-oxidative branch, pentose pathway	-1.98	-1.06	-0.43	-1.17
tldD	P0AGG8	Phenotype; Not classified	0.91	0.4	0.79	0.43
tmk	P0A720	Enzyme; 2'-Deoxyribonucleotide metabolism	-0.51	-1.6	-0.43	-1.2
torS	P39453	Enzyme; Energy metabolism, carbon: Anaerobic respiration	0.36	-0.27	0	0
tpr	P02338	Factor; Basic proteins - synthesis, modification	-0.64	0.85	0	0.51
trg	P05704	Regulator; Chemotaxis and mobility	-0.12	2	0	0
trkH	P0AFZ7	Transport; Transport of small molecules: Cations	-0.51	0.47	0	0
trxC	P0AGG4	Putative enzyme; Not classified	-0.75	0.45	0	0
uhpA	P0AGA6	Regulator; Transport of small molecules: Carbohydrates, organic acids, alcohols	-0.46	-0.16	-0.58	-0.44
ulaE	P39305	Putative enzyme; Central intermediary metabolism: Pool, multipurpose conversions	3.12	1.97	0.36	0.22
ulaF	P39306	Putative enzyme; Not classified	2.19	1.16	0	0
uup	P43672	Factor; DNA - replication, repair, restriction/modification	0	0	-0.26	0.29
uxaA	P42604	Enzyme; Degradation of small molecules: Carbon compounds	-0.64	0.72	0	0.97
uxuB	P39160	Enzyme; Degradation of small molecules: Carbon compounds	2.59	2.71	0	0
wbbI	P37749	Enzyme; Lipopolysaccharide biosynthesis	0	-1.27	0	0
wcaA	P77414	Putative regulator; Not classified	0.17	-0.89	0	0
wcaC	P71237	Putative enzyme; Not classified	-0.55	-1.26	-0.62	-0.21
wcaI	P32057	Putative enzyme; Not classified	-0.05	-0.06	0	0
wrbA	P0A8G6	Enzyme; Not classified	-0.47	-0.79	-0.72	-0.07
wzc	P76387	Enzyme; Not classified	-0.37	-0.07	0	0
wzzE	P0AG00	Putative transport; Not classified	-1.6	-0.91	-0.76	0
xerC	P0A8P6	Enzyme; Cell division	0	0.13	-1.07	-0.67
yadD	P31665	Null	-1.19	-0.78	0	0
yafL	Q47151	Putative membrane; Not classified	2.43	1.46	0	0
yafM	Q47152	Null	-0.07	0.43	0	0

yafN	Q47156	Null	1.81	1.53	0	0
yafT	P77339	Putative enzyme; Not classified	3.17	2.21	0	0
yafW	Q47684	Phage or Prophage Related	0.82	0.13	0	0
yagl	P77300	Phage or Prophage Related	-0.16	-0.68	-0.16	-0.16
yagM	P71296	Phage or Prophage Related	2.75	2.09	0	0
yagP	P75684	Putative regulator; Not classified	2.57	3.18	0	0
yagU	P0AAA1	Null	1.1	-1.18	0	0
yagZ	P0AAA3	Structural component; Surface structures	-0.22	1.15	0	0
yahF	P77187	Putative enzyme; Not classified	1.22	0.36	-0.26	0
yahG	P77221	Null	1.23	0.96	0	0
yahH	/	#N/A	1.21	0.83	0.64	-0.28
yahI	P77624	Putative enzyme; Not classified	1.12	2.16	1.73	0
yahO	P75694	Null	0.71	2.39	0	0
yaiF	P75697	Null	1.84	-0.84	0	0
yaiV	P0AAP5	Null	0	-0.3	0	0
ybaA	P0AAQ6	Null	0.93	1.44	-1.4	-1.65
ybaB	P0A8B5	Factor; DNA - replication, repair, restriction/modification	0.66	0.63	1.01	-0.07
ybaL	P39830	Putative transport; Not classified	3.71	4	0	0
ybaV	P0AAR8	Null	-1.57	0	0	0
ybaY	P77717	Phenotype; Not classified	0.24	-0.12	0.01	-0.52
ybbA	P0A9T8	Putative transport; Not classified	0	-0.99	0	0
ybbN	P77395	Putative enzyme; Not classified	0	-0.1	0	0
ybcD	P77528	Phage or Prophage Related	1.86	0.57	0	0
ybcV	P77598	Phage or Prophage Related	-0.33	0.99	0.69	1
ybdM	P77174	Null	0.73	0.45	-1.76	-2.66
ybdN	P77216	Null	-0.76	0	0	0
ybdZ	P18393	Enzyme; Biosynthesis of cofactors, carriers: Enterochelin	0.15	0	0	0
ybeA	P0A8I8	Enzyme; rRNA modification	0	-0.04	0	0
ybeL	P0AAT9	Phenotype; Not classified	2.44	0.86	0	0
ybeX	P0AE78	Putative transport; Not classified	-0.09	-0.1	0.54	-1.12
ybgJ	P0AAV4	Putative enzyme; Not classified	0	0.25	0	0
ybgO	P75748	Null	0	-1.53	0	0
ybhP	P0AAW1	Null	2.12	2.05	-0.37	0
ybiJ	P0AAX3	Null	-0.17	0.38	0	0
ybjD	P75828	Null	-0.64	0.86	0	0
ybjH	P0AAY4	Null	0.62	-0.13	-0.75	-1.89
ybjI	P75809	Enzyme; Biosynthesis of cofactors, carriers: Riboflavin	0	0.34	0	0
ycaO	P75838	Null	-0.47	0.41	-1.26	0.28
ycbB	P22525	Enzyme; Murein sacculus, peptidoglycan	0.96	-0.22	0	0
ycbF	P40876	Putative factor; Surface structures	2.28	2.26	0	0.63

ycbV	P75860	Putative structural component; Surface structures	0.43	3.11	0	0
ycbW	P75862	Null	0.17	-0.57	-0.22	-0.09
yccF	P0AB12	Null	0.89	1.18	0	0
yccV	P0AB20	Null	0	-1.01	-0.63	-1.19
yccX	P0AB65	Null	0.88	-0.5	0	0
ycdM	P75898	Enzyme; Pyrimidine nitrogen catabolism	1.34	0.76	0	0
ycdN	P75901	Null	-0.43	0.08	0	0
ycdP	P69432	Enzyme; Surface polysaccharides and antigens	-0.3	0.91	0	-0.57
yceK	P0AB31	Null	0	-0.44	0	0
ycfM	P0AB38	Null	-1.38	-0.59	-0.73	-1.19
ycfZ	P75961	Putative factor; Not classified	2.5	2.39	0	0
ycgH	Null	Phage or Prophage Related	0.7	0.55	-0.23	0.3
ycgY	P76012	Null	-0.17	0	0	0
ycil	P0AB55	Null	-0.04	-0.6	-0.6	-0.65
yciQ	P45848	Null	-0.52	-1.65	0	0
ycjN	P76042	Putative transport; Not classified	-0.57	1.19	0	0
ycjW	P77615	Putative regulator; Not classified	0.73	0.09	0	0
ydaG	P76061	Phage or Prophage Related	0.12	-1.28	0	-1.98
ydaL	P76053	Null	0	-1.48	0.77	0.29
ydaT	P76064	Phage or Prophage Related	0.22	-1.97	-1.53	-0.96
ydaV	P77546	Phage or Prophage Related	0.48	0.28	-0.3	0.68
ydaW	P76066	Phage or Prophage Related	-0.13	-0.36	0.45	0.04
ydbA	P33666	Null	1.78	0.42	0	0
ydcI	P77171	Putative regulator; Not classified	0	-1.37	0	0
ydcQ	P67697	Null	-0.28	-0.56	0.45	0.26
ydcR	P77730	Putative regulator; Not classified	2.89	1.42	0	0
ydcT	P77795	Putative transport; Not classified	0	0	-0.29	0
ydeA	P31122	Transport; Transport of small molecules: sugars	0	-2.08	0	0
ydeN	P77318	Putative enzyme; Not classified	0.57	0.09	0.17	-0.47
ydeO	P76135	Regulator; Not classified	0	-0.7	0	0
ydeU	P32051	Null	2.6	1.99	0	0
ydeV	P77432	Enzyme; Not classified	1.5	1.14	0	0
ydfB	P29009	Phage or Prophage Related	-0.59	-0.78	-0.66	-0.69
ydfK	P76154	Phage or Prophage Related	2.55	1.55	0	0
ydgD	P76176	Null	-1.21	0.35	-0.79	-0.15
ydhS	P77148	Putative enzyme; Not classified	-0.38	-1.07	1.06	0
ydiK	P0AFS7	Null	1.36	0	0	0
ydiV	P76204	Null	0	-2.23	0	0
ydjN	P77529	Putative enzyme; Not classified	0.77	-1.13	0	0
yeaB	P43337	Null	2.84	2.7	-1.44	-0.59
yeaL	P0ACY6	Null	0.72	0.09	0	0
yeaP	P76245	Null	0.75	-0.08	0.61	-0.41

yeaW	P0ABR7	Null	-0.08	0.33	0	0
yeaX	P76254	Putative enzyme; Not classified	0.1	1.03	0	0.93
yebU	P76273	Enzyme; rRNA modification	0	-1.74	0	0
yebV	P64503	Null	0	0.21	0	0
yecE	P37348	Null	0.56	-0.31	0.94	-0.2
yecS	P0AFT2	Putative transport; Not classified	-1.22	0	0	0
yedQ	P76330	Null	-0.9	0.19	-1.34	-1.38
yedY	P76342	Putative enzyme; Not classified	-0.07	-0.98	0	-0.29
yedZ	P76343	Null	3.62	3.43	0	0
yeeA	P33011	Null	0.9	1.71	0	0
yeeO	P76352	Null	0.47	-0.47	0	-1.5
yeeY	P76369	Putative regulator; Not classified	-0.54	-1.99	0	0
yegl	P76393	Putative enzyme; Not classified	0	-0.15	0.15	-1.65
yegL	P76396	Null	-0.18	-0.18	0.31	-0.84
yegP	P76402	Null	0.03	-0.19	-0.18	-0.58
yegX	P76421	Null	-0.15	0	0	0
yehL	P33348	Null	0	-1.89	0	0
yehS	P33355	Null	-0.51	0	0	0
yeiB	P25747	Null	2.41	3.2	0	0
yeiJ	P33021	Putative transport; Not classified	0.31	1.55	0	0
yeiW	P0AFT8	Null	1.07	1.42	0.75	-1.26
yfaO	P52006	Null	3.1	2.76	0	0
yfbG	P77398	Putative enzyme; Not classified	0.29	1.14	2.31	2.14
yfbL	P76482	Putative enzyme; Not classified	-1.96	-0.32	0	0
yfbT	P77625	Putative enzyme; Not classified	-2.52	-2.33	0	0
yfcl	P77768	Null	-1.08	1.85	0	0
yfcU	P77196	Putative membrane; Not classified	0	-2.23	0	0
yfdC	P37327	Putative transport; Not classified	1.29	-0.29	0	-0.45
yfdN	P76510	Phage or Prophage Related	0.83	0.82	0.17	-1.54
yfeO	P67729	Null	1.18	-0.59	0	0
yfeX	P76536	Enzyme; Transport of small molecules: Cations	0	-2.7	0	0
yfgF	P77172	Enzyme; Not classified	1.02	-0.12	0	-0.63
yfgG	P64545	Null	0	0.74	0.3	0.22
yfgH	P65290	Putative membrane; Not classified	0.3	-0.3	0	0
yfgJ	P76575	Null	0	-1.51	0	0
yfhB	P0AD42	Enzyme; Macromolecule synthesis, modification: Phospholipids	2.3	1.06	1.17	0.62
yfhD	P0AGC5	Enzyme; Transporter; Not classified	2.57	1.34	0	-0.98
yfhK	P52101	Putative regulator; Not classified	1.74	0.86	0	0
yfhR	P77538	Putative enzyme; Not classified	0.15	0.42	0	0
yfiL	P11289	Null	0.95	0.58	0	0
yfjM	P52128	Phage or Prophage Related	-1.92	-1.63	0	-0.1
yfjZ	P52141	Phage or Prophage Related	-3.88	-3.16	0.96	1.19
ygaX	P76628	Putative transport; Not classified	0.47	-0.19	0	0

ygbA	P25728	Null	-1.47	-1.24	0	0
ygbJ	Q46888	Putative enzyme; Not classified	0	0.05	0	0
ygcS	Q46909	Putative transport; Not classified	0	0.08	0	0
ygcU	Q46911	Null	2.37	1.18	0	0
ygdH	P0ADR8	Null	0.01	-0.85	-0.15	0.12
ygfM	P64557	Null	-0.05	-1.75	0	0
yggF	P21437	Null	1.51	2.13	0	0
ygiC	P0ADT5	Putative enzyme; Not classified	0	-1.65	0	0
ygiE	P0A8H3	Null	-1.17	0.31	-1.34	-0.11
ygiL	P39834	Putative structural component; Surface structures	0	-0.03	0	0
ygiS	Q46863	Putative transport; Not classified	0	1.78	0	0
ygiJ	P42590	Orf; Not classified	0.64	0.21	1.07	1.07
ygiK	P42592	Enzyme; Not classified	0	0.03	0	0
yhal	P64592	Putative carrier; Not classified	0.91	0.08	0	0
yhbG	P0A9V1	Putative transport; Not classified	-2.22	-0.97	-1.12	0
yhbH	P0AFX0	Putative regulator; Global regulatory functions	0	-2.03	0	0
yhcB	P0ADW3	Null	-1.14	-0.49	-0.48	-0.28
yhcE	P45421	Null	1.03	0.29	0.34	0
yhcE	P45421	Null	2.94	3.48	0	0.15
yhcG	P45423	Null	-0.76	0	0	0
yhcM	P64612	Enzyme; Not classified	0	-1.26	0	0
yhcO	P64616	Null	0.29	0.74	0	0
yhdH	P26646	Putative enzyme; Not classified	0	0.12	0	0
yhdX	P45767	Putative transport; Not classified	-0.88	0	0	0
yhgE	P45804	Putative transport; Not classified	0	-0.59	0	0
yhhW	P46852	Null	-0.3	-0.87	-1.16	-0.41
yhiN	P37631	Putative enzyme; Not classified	1.2	0.7	1.04	0.72
yhiQ	P68567	Enzyme; rRNA modification	-0.14	-0.37	-0.22	-1
yiaN	P37675	Transport; Transport of small molecules: Carbohydrates, organic acids, alcohols	0	0.28	0.35	0
yiaT	P37681	Putative membrane; Not classified	-2.96	-0.99	0	-1.63
yidG	P0ADL6	Null	-2.19	-0.69	0.15	-1.03
yidZ	P31463	Putative regulator; Not classified	-0.93	0.36	1.39	0.31
yifK	P27837	Putative transport; Not classified	-0.43	-1.11	-0.36	0.08
yihS	P32140	Enzyme; Not classified	-0.49	-0.51	0.11	-0.8
yihX	P0A8Y3	Enzyme; Not classified	0.92	-0.1	-0.3	0
yiiT	P0AAB8	Putative regulator; Not classified	-1.21	0.04	-0.27	-1.02
yijF	P32668	Null	0.44	0.37	0.44	0.31
yjaB	P09163	Null	0	0.77	0	0
yjaG	P32680	Null	-0.68	-0.89	-0.42	-0.6
yjaH	P32681	Null	-0.22	-0.63	-0.33	-0.62
yjcQ	P32715	Orf; Not classified	0	-0.51	0	0
yjeK	P39280	Enzyme; Protein modification	0.66	0.44	0.4	-0.7
yjfK	P39293	Null	0.19	-0.53	0	0

yjgK	P0AF96	Putative enzyme; Not classified	-0.12	-0.18	0.13	0.11
yjgM	P39337	Null	0	0.62	0	0
yjgZ	P39351	Null	0.34	0.4	-1.91	0.87
yjhF	P39357	Putative transport; Not classified	0	-0.77	-0.12	0.6
yjiM	P39384	Null	2.26	1.08	2.03	0
yjiN	P39385	Null	0.3	0.09	0.19	0.33
yjiR	P39389	Putative regulator; Not classified	-0.35	0.14	0	-1.69
yjiW	P39394	Null	0	-2.6	0	0
yjjG	P0A8Y1	Enzyme; Degradation of small molecules: Nucleotides	3.36	1.94	3.03	0.9
yjjP	P0ADD5	Putative structure; Not classified	0	-0.58	0	0
yjjU	P39407	Null	-0.49	-0.36	0	0
yjjY	P0ADD9	Null	3.18	2.19	0	0
ykfB	P77162	Phage or Prophage Related	0	-2.02	0	0
ykfC	Q47688	Phage or Prophage Related	2.81	2.42	0	0
ykfF	P75677	Phage or Prophage Related	1.9	1.8	0	0
ykfl	P77692	Phage or Prophage Related	-0.53	1.24	0	0
ykgB	P75687	Null	2.95	2.91	0	0
ykgE	P77252	Putative carrier; Energy metabolism, carbon: Electron transport	1.32	1.15	0	0
ykgF	P77536	Putative carrier; Energy metabolism, carbon: Electron transport	0.19	0	0	0
yliE	P75800	Null	0.04	-0.72	0	0
ymcD	P75885	Null	-2.36	0.49	-0.88	0
ymdB	P0A8D6	Null	-0.74	-1.28	0	0
ymdF	P56614	Null	0	-0.91	0	-0.59
ymfL	P75976	Phage or Prophage Related	0.17	-0.37	0.02	0.59
ymfM	P75977	Phage or Prophage Related	1.41	-0.13	-0.41	-0.42
ymfO	P75980	Phage or Prophage Related	1.3	0.95	-1.6	0
ymfP	P75981	Phage or Prophage Related	0	1.94	0	0
ymfR	P75979	Phage or Prophage Related	-0.71	-0.22	0	0
ymgF	P58034	Null	0	-0.09	0	0
ynaE	P76073	Phage or Prophage Related	2.55	1.55	0	0
ynal	P0AEB5	Null	1.23	0.36	0	0
yncB	P76113	Enzyme; Not classified	0	-1.22	-2.02	-0.68
yncC	P76114	Putative regulator; Not classified	-0.05	-0.97	0	0
yncE	P76116	Putative factor; Not classified	0.28	-0.43	0.29	0.85
yncH	P76118	Null	-1.46	-1.75	0	0
yncK	Null	Phage or Prophage Related	2.8	2.39	0	0
yneE	P76146	Null	0.82	0.82	-0.43	0.22
yneF	P76147	Null	0.27	-1.53	0	0
ynel	P76149	Putative enzyme; Not classified	0.05	-0.39	0	0
yneK	P76150	Null	-0.53	0.17	0	0
ynfD	P76172	Null	-0.37	-0.78	-0.38	-1.39
ynfH	P76173	Putative enzyme; Degradation of small molecules:	-2.12		1.35	2.35

		Carbon compounds				
ynfN	P76157	Phage or Prophage Related	2.98	2.21	0.12	0.69
ynhG	P76193	Enzyme; Murein sacculus, peptidoglycan	-0.18	-0.64	-0.57	-1.38
ynjB	P76223	Null	0	-0.49	0	0
ynjH	P76227	Null	-0.85	-0.57	0	0
ynjI	P76228	Null	2.47	2.3	0	0
yoaB	POAEB7	Putative enzyme; Not classified	2.21	1.87	0	0
yoeA	P76356	Phage or Prophage Related	1.84	-0.84	0	0
yoeB	P69348	Null	-0.15	-1.06	0	0
yohD	P33366	Null	1.34	2.39	0	0
ypfG	P76559	Null	-1.26	-2.51	0	0
ypfN	Q2EET2	Null	0.59	0.04	0.22	0
yqfA	P67153	Putative enzyme; Not classified	0	-1.72	0	0
yqgB	P64567	Null	0.34	-0.17	-1.48	-1.07
yqgC	P64570	Null	0.92	1.33	0	0
yqhD	Q46856	Enzyme; Degradation of small molecules: Carbon compounds	0	-0.25	-0.2	-1.08
yqhG	Q46858	Null	-0.02	-0.77	-0.54	-0.36
yqjK	Q47710	Null	0	-2.97	0	0
yrbC	P0ADV7	Transport; Transport of small molecules: phospholipids	3.04	2.09	0	0
yrfF	P45800	Putative factor; Not classified	1.19	-1.18	0	0
ytjC	P0A7A2	Enzyme; Not classified	0	-1.71	0	0
yaaA	P0A8I3	Null	-0.28	0.15	0.44	-1.54
zraR	P14375	Regulator; Energy metabolism, carbon: Fermentation	0.24	0.51	0.14	-1.66

Table SVIII: List of genes with a high flux phenotype, ordered by 1 % high flux value

Gene name	Locus tag	Function	1 % low flux	5 % low flux	5 % high flux	1 % high flux
ynfH	P76173	Putative enzyme; Degradation of small molecules: Carbon compounds	-2.12		2.35	1.35
rpiA	P0A7Z0	Enzyme; Central intermediary metabolism: Non-oxidative branch, pentose pathway	-2.24	-1.97	2.2	1.22
ompC	P06996	Membrane; Outer membrane constituents	-1.11	-0.72	1.26	1.02

Table SIX: List of genes with a low flux phenotype, ordered by 1% low flux value

Gene name	Locus tag	Function	1 % low flux	5 % low flux	5 % high flux	1 % high flux
aceK	P11071	Enzyme; Central intermediary metabolism: Glyoxylate bypass	3.95	2.43	0	0
adhP	P39451	Enzyme; Energy metabolism, carbon: Anaerobic respiration	3.87	3.73	0	0
nanK	P45425	Putative regulator; Not classified	3.85	2.98	0	0
ybaL	P39830	Putative transport; Not classified	3.71	4.00	0	0
gatC	P69831	Transport; Transport of small molecules: Carbohydrates, organic acids, alcohols	3.66	3.28	0	0
yedZ	P76343	Null	3.62	3.43	0	0
rimJ	P0A948	Enzyme; Ribosomes - maturation and modification	3.51	2.73	0	0
ppk	P0A7B1	Enzyme; Central intermediary metabolism: Phosphorus compounds	3.23	3.04	0	0.44
fliM	P06974	Structural component; Surface structures	3.22	2.01	0	0
yjjY	P0ADD9	Null	3.18	2.19	0	0
yafT	P77339	Putative enzyme; Not classified	3.17	2.21	0	0
ulaE	P39305	Putative enzyme; Central intermediary metabolism: Pool, multipurpose conversions	3.12	1.97	0.22	0.36
yfaO	P52006	Null	3.10	2.76	0	0
stfQ	P77515	Phage or Prophage Related	3.07	2.67	0	-0.17
stfR	P76072	Phage or Prophage Related	3.07	2.67	0	-0.17
flhB	P76299	Structural component; Not classified	3.07	2.18	0	0
yrbC	P0ADV7	Transport; Transport of small molecules: phospholipids	3.04	2.09	0	0
fliO	P22586	Putative structure; Surface structures	2.98	2.38	0.01	-0.48
ykgB	P75687	Null	2.95	2.91	0	0
pcm	P0A7A5	Enzyme; Proteins - translation and modification	2.95	2.69	0	0
gatA	P69828	Enzyme; Transport of small molecules: Carbohydrates, organic acids, alcohols	2.94	3.48	0.15	0
dcuC	P0ABP3	Transport; Transport of small molecules: Carbohydrates, organic acids, alcohols	2.94	3.48	0.15	0
yhcE	P45421	Null	2.94	3.48	0.15	0
alsK	P32718	Putative regulator; Not classified	2.94	3.48	0.15	0
phnC	P16677	Transport; Central intermediary metabolism: Phosphorus compounds	2.90	2.59	-1.23	0
ydcR	P77730	Putative regulator; Not classified	2.89	1.42	0	0
fsaA	P78055	Null	2.88	2.45	0	0.58
yeaB	P43337	Null	2.84	2.70	-0.59	-1.44
paal	P76084	Enzyme; Phenylacetic acid degradation	2.82	2.13	-1.09	0.06
ykfC	Q47688	Phage or Prophage Related	2.81	2.42	0	0
ynck	Null	Phage or Prophage Related	2.80	2.39	0	0

rssA	P0AFR0	Null	2.78	2.52	0	0
mhpT	P77589	Putative transport; Not classified	2.76	2.54	-2.38	-2.45
yagM	P71296	Phage or Prophage Related	2.75	2.09	0	0
dusB	P0ABT5	Enzyme; tRNA modification	2.74	2.12	-1.60	0
chbG	P37794	Enzyme; Degradation of small molecules: N,N'-diacetylchitobiose	2.62	2.31	0	0
ydeU	P32051	Null	2.60	1.99	0	0
uxuB	P39160	Enzyme; Degradation of small molecules: Carbon compounds	2.59	2.71	0	0
yagP	P75684	Putative regulator; Not classified	2.57	3.18	0	0
yfhD	P0AGC5	Enzyme; Transporter; Not classified	2.57	1.34	-0.98	0
ydfK	P76154	Phage or Prophage Related	2.55	1.55	0	0
ynaE	P76073	Phage or Prophage Related	2.55	1.55	0	0
ycfZ	P75961	Putative factor; Not classified	2.50	2.39	0	0
cmr	P0AEY8	Transport; Transport of small molecules: Other	2.48	1.86	-3.38	-2.39
ynjI	P76228	Null	2.47	2.30	0	0
ybeL	P0AAT9	Phenotype; Not classified	2.44	0.86	0	0
yafL	Q47151	Putative membrane; Not classified	2.43	1.46	0	0
yeiB	P25747	Null	2.41	3.20	0	0
ygcU	Q46911	Null	2.37	1.18	0	0
dcp	P24171	Enzyme; Degradation of proteins, peptides, glyco	2.26	1.68	0	0
yoaB	P0AEB7	Putative enzyme; Not classified	2.21	1.87	0	0
flgK	P33235	Structural component; Surface structures	2.20	2.59	0	0
ulaF	P39306	Putative enzyme; Not classified	2.19	1.16	0	0
ybhP	P0AAW1	Null	2.12	2.05	0	-0.37
cheW	P0A964	Regulator; Chemotaxis and mobility	2.02	1.15	0	0
envY	P10805	Structural component; Outer membrane constituents	1.95	1.73	-1.46	0
ssuD	P80645	Null	1.94	0.95	0	-0.42
ykfF	P75677	Phage or Prophage Related	1.90	1.80	0	0
ybcD	P77528	Phage or Prophage Related	1.86	0.57	0	0
yafN	Q47156	Null	1.81	1.53	0	0
fliP	P0AC05	Putative structure; Surface structures	1.75	1.17	0	0
yfhK	P52101	Putative regulator; Not classified	1.74	0.86	0	0
hipA	P23874	Enzyme; Protein modification	1.72	1.45	0	-2.48
nohA	P31061	Phage or Prophage Related	1.72	1.08	0	0
flgG	P0ABX5	Structural component; Surface structures	1.66	1.69	-0.31	0.37
yggF	P21437	Null	1.51	2.13	0	0
oppD	P76027	Transport; Not classified	1.50	0.85	0	0
ydeV	P77432	Enzyme; Not classified	1.50	1.14	0	0
hyfJ	P77453	Putative factor; Not classified	1.46	0.79	0	0
aceB	P08997	Enzyme; Central intermediary metabolism: Glyoxylate bypass	1.36	0.35	0	0

yohD	P33366	Null	1.34	2.39	0	0
ycdM	P75898	Enzyme; Pyrimidine nitrogen catabolism Putative carrier; Energy metabolism, carbon: Electron transport	1.34	0.76	0	0
ykgE	P77252	Phage or Prophage Related	1.32	1.15	0	0
ymfO	P75980	Null	1.30	0.95	0	-1.60
yahG	P77221	Enzyme; Biosynthesis of cofactors, carriers: Menaquinone, ubiquinone	1.23	0.96	0	0
menE	P37353	Enzyme; Amino acid biosynthesis: Lysine	1.15	1.72	0	0
asd	P0A9Q9	Enzyme; Salvage of nucleosides and nucleotides	1.13	0.95	0	-0.25
deoC	P0A6L0	Enzyme; Central intermediary metabolism: Glyoxylate bypass	1.10	1.20	-0.70	0.16
aceA	P0A9G6	Null	0.98	1.31	0	0
yfiL	P11289	Enzyme; Fatty acid and phosphatidic acid biosynthesis	0.95	0.58	0	0
cfa	P0A9H7	Null	0.94	0.71	0	0
ybaA	P0AAQ6	Null	0.93	1.44	-1.65	-1.40
yqgC	P64570	Null	0.92	1.33	0	0
yeeA	P33011	Null	0.90	1.71	0	0
yccF	P0AB12	Regulator; Purine ribonucleotide biosynthesis	0.89	1.18	0	0
purR	P0ACP7	Phage or Prophage Related	0.83	0.81	-0.61	-0.65
yfdN	P76510	Null	0.83	0.82	-1.54	0.17
yneE	P76146	Phenotype; Not classified	0.82	0.82	0.22	-0.43
asr	P36560	Null	0.77	2.22	0	0
yahO	P75694	Phage or Prophage Related	0.71	2.39	0	0
ycgH	Null	Regulator; Central intermediary metabolism: Pool, multipurpose conversions	0.70	0.55	0.30	-0.23
cynR	P27111	Regulator; Not classified	0.70	1.24	0	0
pphA	P55798	Putative enzyme; Not classified	0.67	0.66	-0.94	0
gatZ	POC8J8	Enzyme; Global regulatory functions	0.60	0.57	0	0
kdpD	P21865	Regulator; Degradation of small molecules: Carbon compounds	0.55	0.96	-0.23	0.25
galS	P25748	Regulator; Degradation of small molecules: Carbon compounds	0.28	2.00	-0.86	-2.82
*galR	P03024	Regulator; Degradation of small molecules: Carbon compounds	-0.74	1.60	-0.73	-2.14

* Not enriched in 1% low-flux pool

Table SX Growth rate and OD600 after 16 hours of growth in M9 minimal medium containing 5 g/l galactose. The genes were chosen based on their enrichment in the 1% low flux or 1% high flux pools, respectively. Intracellular FBP concentrations of the identified mutants.

Deletion / strain name	max growth rate (h ⁻¹)	OD ₆₀₀ *)	Intracellular FBP concentration (from Fuhrer et al. 2017)
Wild type	0.223 ± 0.06	0.14 ± 0.044	0.2737
Low flux pool			
<i>ΔybaL</i>	0.245 ± 0.001	0.10 ± 0.001	0.2271
<i>Δppk</i>	0.231 ± 0.009	0.13 ± 0.01	-1.1933
<i>ΔyjjY</i>	0.269 ± 0.017	0.09 ± 0.001	-0.4365
<i>ΔaceK</i>	0.215 ± 0.009	0.13 ± 0.01	0.4666
<i>ΔfliM</i>	0.203 ± 0.021	0.10 ± 0.003	-0.1543
<i>ΔyedZ</i>	0.214 ± 0.009	0.11 ± 0.004	0.3831
<i>ΔgatC</i>	0.216 ± 0.000	0.17 ± 0.06	-0.1027
<i>ΔnanK</i>	0.213 ± 0.000	0.19 ± 0.21	0.1724
<i>ΔadhP</i>	0.221 ± 0.007	0.16 ± 0.02	-0.1064
<i>ΔrimJ</i>	0.225 ± 0.002	0.11 ± 0.01	-0.7655
High flux pool			
<i>ΔompC</i>	0.356 ± 0.006	0.51 ± 0.07	2.4256
<i>ΔrpiA</i>	0.308 ± 0.005	0.85 ± 0.44	0.2739
<i>ΔynfH^c</i>	0.212 ± 0.007	0.13 ± 0.02	0.7675

*) at 16 h

LOCUS pCL002_A4_G_mC_ppsp_Scr 3934 bp DNA circular UNA 04-Mar-2014

DEFINITION

FEATURES '-----'ion/Qualifiers
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pFlux
3934 bp

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promoter 149..290

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ORIGIN

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181 ATATATTTGC TTGAACGATT CACCGTTTTT TTCATCCGGT TAAATATGCA AAGATAAATG
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301 GAGAAGAACT TTCTACTGGA GTTGTCCCAA TTCTTGTTGA ATTAGATGGT GATGTTAATG
361 GGCACAAATT TTCTGTCAGT GGAGAGGGTG AAGGTGATGC TACATACGGA AACTCACCC
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1741 AGAACCGTAC ATAAATTGCG GGCTCAGGAT GTCCACGCA AAAGGCAGCG GGCCGCCTTT
1801 AGTCACTTTC AGTTTGGCGG TCTGGGTGCC TTCATACGGA CGGCCCTCGC CTTCGCCTTC
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2641 CCGCTGCGCC TTATCCGGTA ACTATCGTCT TGAGTCCAAC CCGGAAAGAC ATGCAAAGC
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3181 CCATTGCCCA GTCGGCAGCG ACATCCTTCG GCGCGATTTT GCCGGTTACT GCGCTGTACC
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3301 TCCATAGCGT TAAGGTTTCA TTTAGCGCCT CAAATAGATC CTGTTTCAGGA ACCGGATCAA
3361 AGAGTTCCTC CGCCGCTGGA CCTACCAAGG CAACGCTATG TTCTCTTGCT TTTGTCAGCA
3421 AGATAGCCAG ATCAATGTTCG ATCGTGGCTG GCTCGAAGAT ACCTGCAAGA ATGTCATTGC
3481 GCTGCCATTC TCCAAATTGC AGTTCGCGCT TAGCTGGATA ACGCCACGGA ATGATGTCGT
3541 CGTGCAACAAC AATGGTGACT TCTACAGCGC GGAGAATCTC GCTCTCTCCA GGGGAAGCCG
3601 AAGTTTCAA AAGGTCGTTG ATCAAAGCTC GCCGCGTTGT TTCATCAAGC CTTACGGTCA
3661 CCGTAACCAG CAAATCAATA TCACTGTGTG GCTTCAGGCC GCCATCCACT GCGGAGCCGT
3721 ACAAATGTAC GGCCAGCAAC GTCGGTTCGA GATGGCGCTC GATGACGCCA ACTACCTCTG
3781 ATAGTTGAGT CGATACTTCG GCGATCACCG CTTCCCTCAT GATGTTTAAAC TTTGTTTTAG
3841 GGCGACTGCC CTGCTGCGTA ACATCGTTGC TGCTCCATAA CATCAAACAT CGACCCACGG
3901 CGTAACGCGC TTGCTGCTTG GATGCCCGAG GCAT

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Figure S1 Sequence of pFlux.

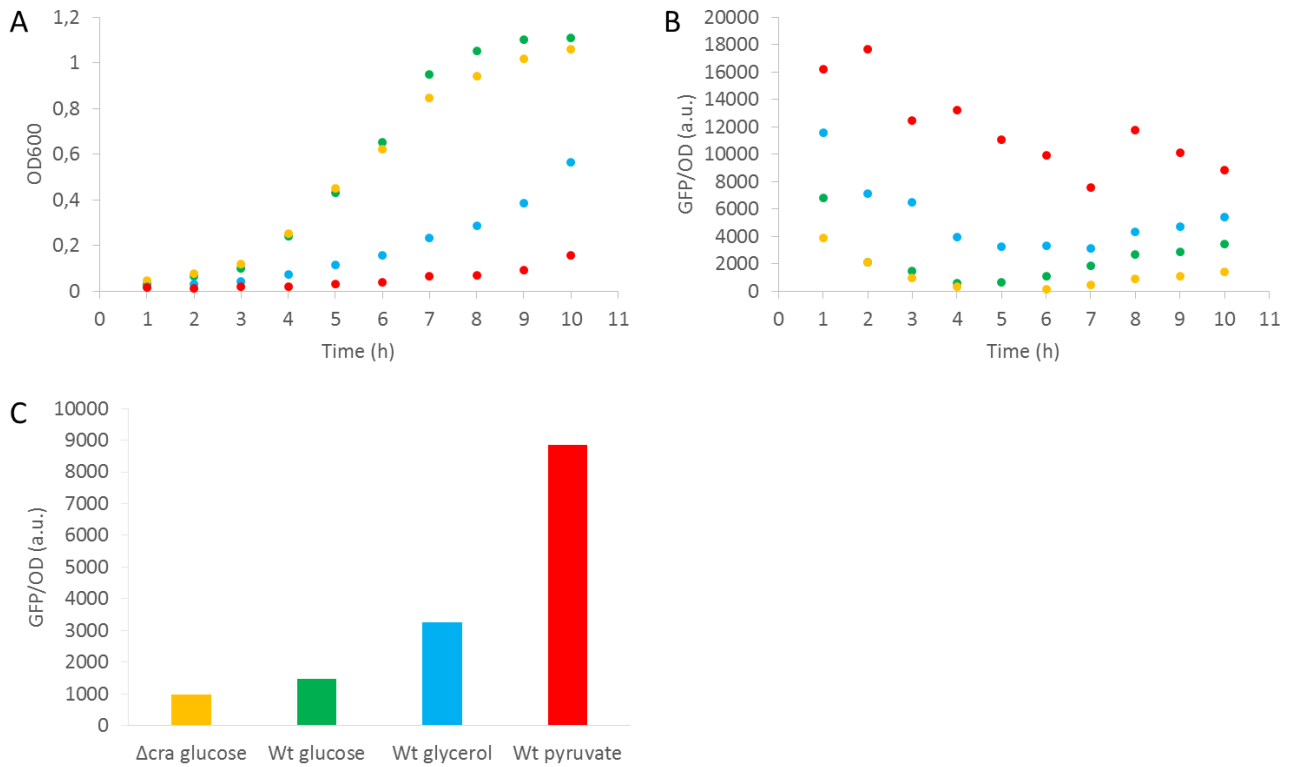


Fig. SII Analysis of growth and fluorescence over time in a plate reader. To identify which time point is suitable for screening by FACS at a single time point, we analysed the growth behavior and the GFP per OD in the wild type harboring pFlux growing in three different carbon sources (glucose: green, glycerol: blue and pyruvate: red), and for the *Δcra* mutant harboring pFlux in glucose (orange). **A** Growth profile of the different strains. **B** Specific fluorescence given in GFP per OD (a.u.). **C** Specific fluorescence measured at OD₆₀₀ = 0.13 ± 0.02

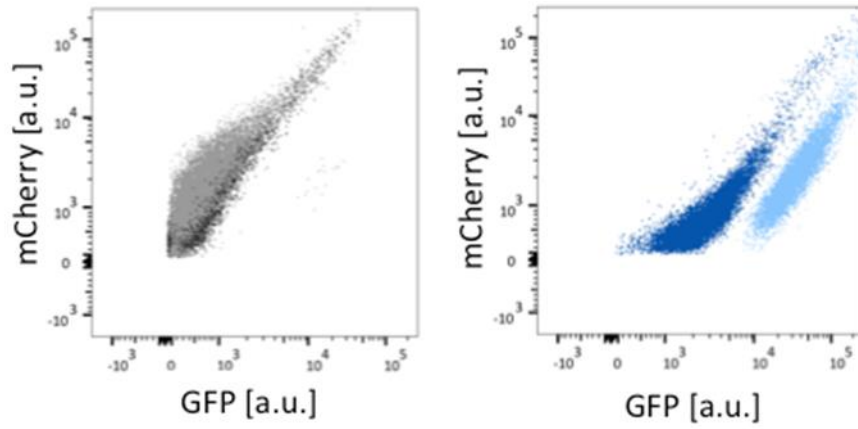


Fig. SIII Flow cytometry dot plots of the GFP versus RFP expression of Δcra (grey) and wild type strains (blue). The cells contain pFlux and were grown in the presence of glucose (dark) and pyruvate (light).

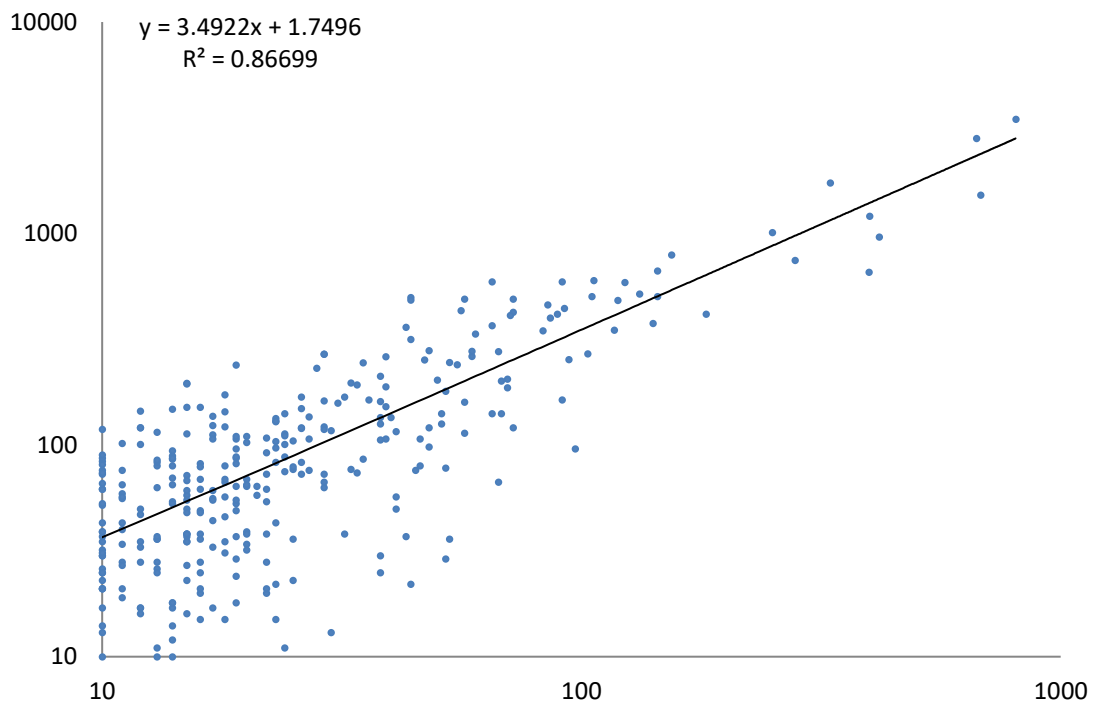


Figure SIV Log scale dot plot of the individual gene coverage for the duplicates of the 1 % low flux pool. Each dot represents one gene. The plot shows the raw numbers before normalization. A linear regression line is presented with a R^2 of 0.86699.

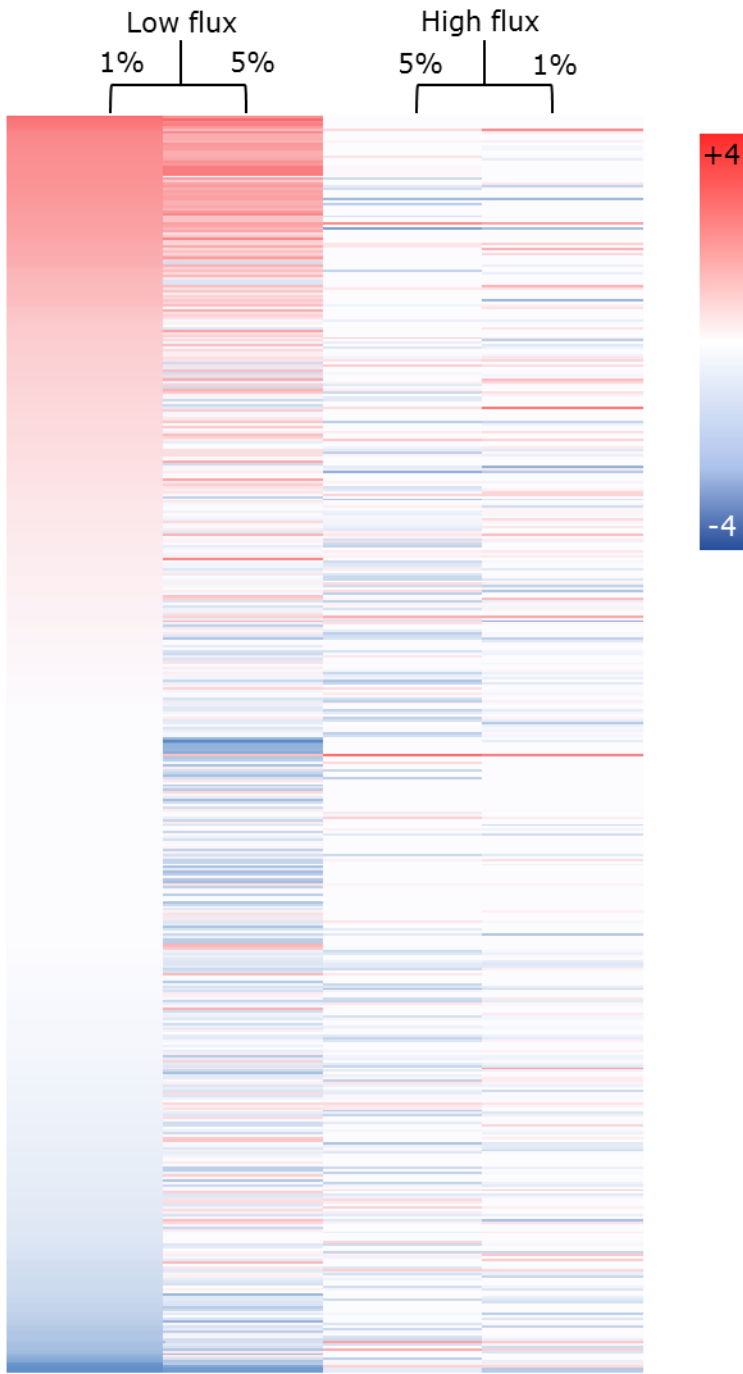


Fig. SV Heat map of the 504 genes identified in the low flux pools and high flux pools compared to the total knockout library. Enrichment is shown in red and depletion in blue. The genes are sorted according to their abundance in the 1% low flux pool.

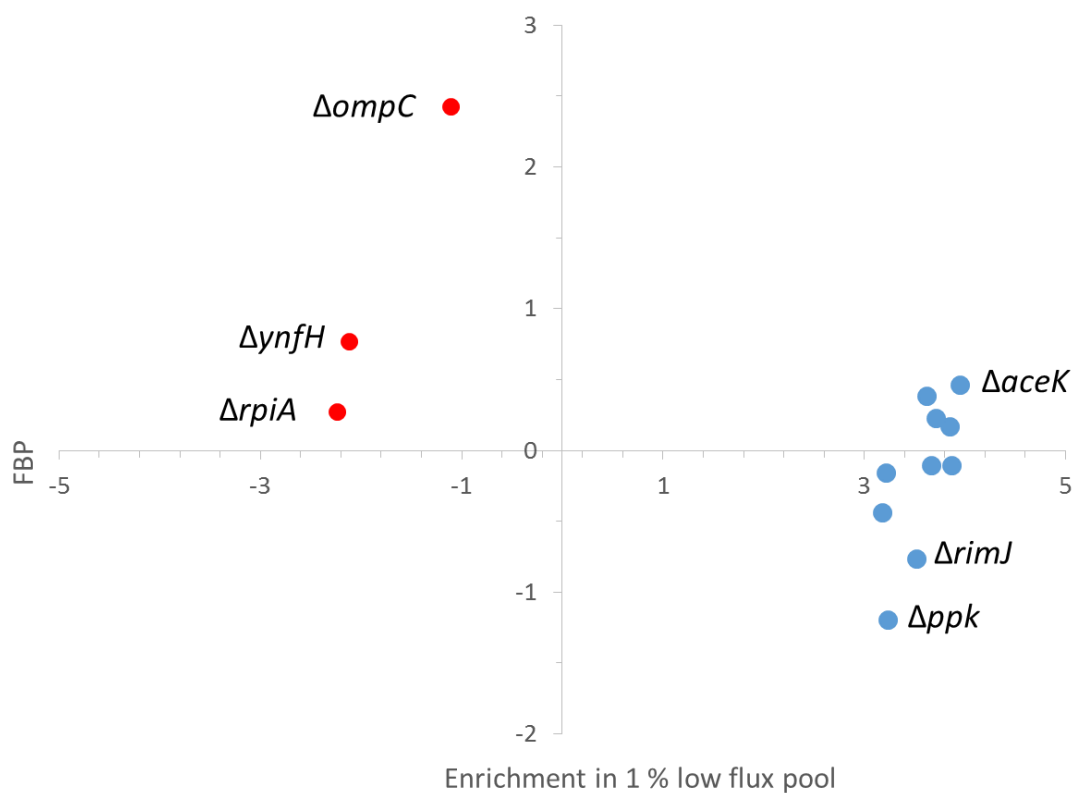


Fig. SVI: Comparison of the enrichment factor in the 1% low flux pool to the measured intracellular FBP concentration (a.u.) during growth on glucose (adopted from Fuhrer et al, 2017) The 10 highest enriched strains in the 1% low flux pools (blue) are shown together with the three identified mutants enriched in the high flux pools (red).