Supplementary Information

Proteomics Reveals Selective Remodeling of the Growth-Phase Response by Subinhibitory Carbenicillin in *Salmonella*

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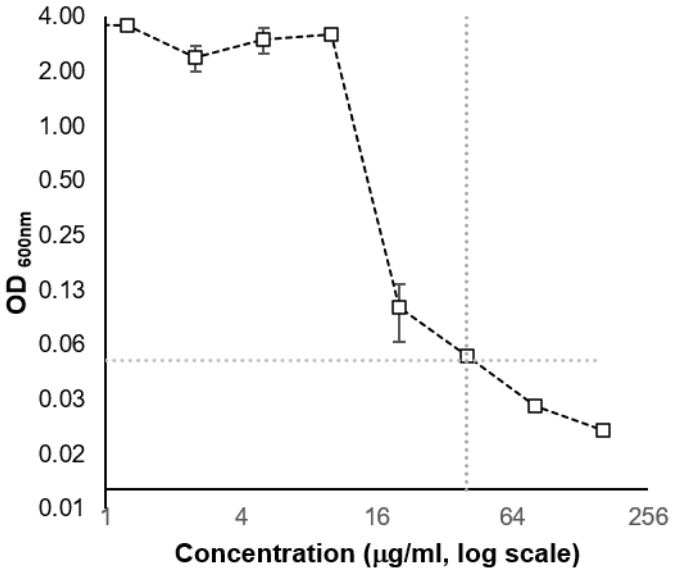
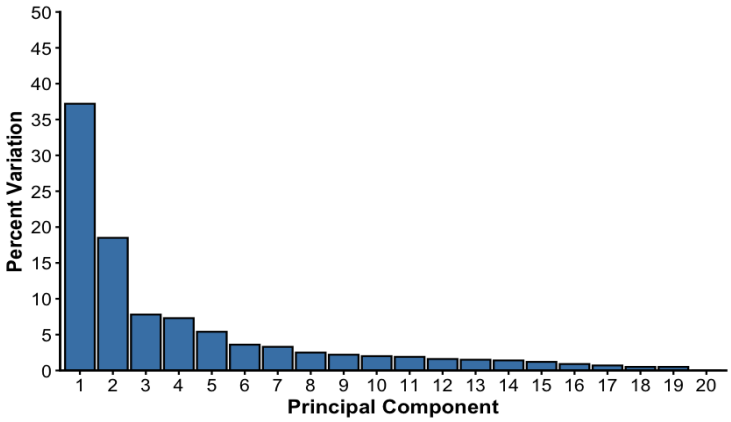
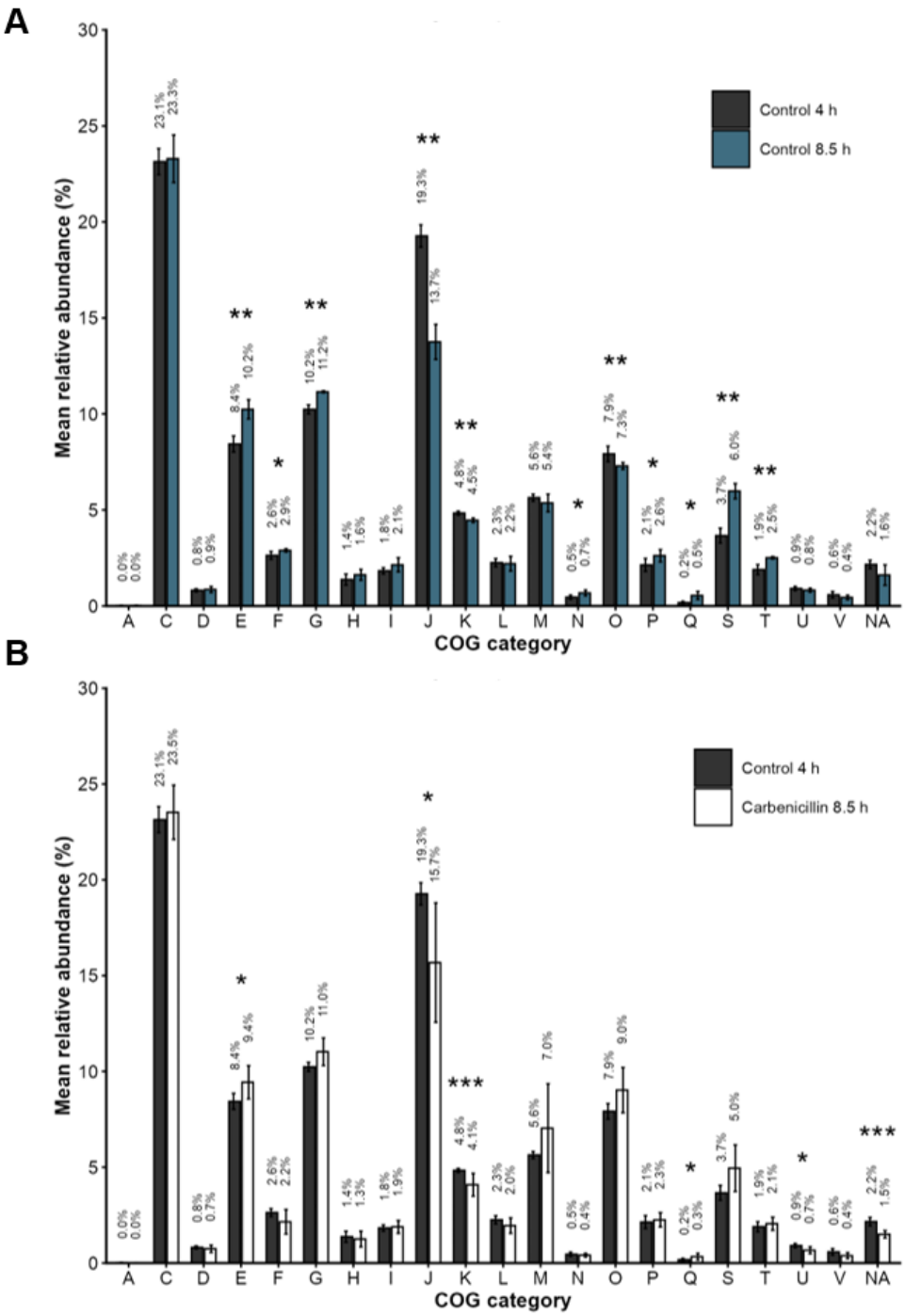
Supplementary Figures



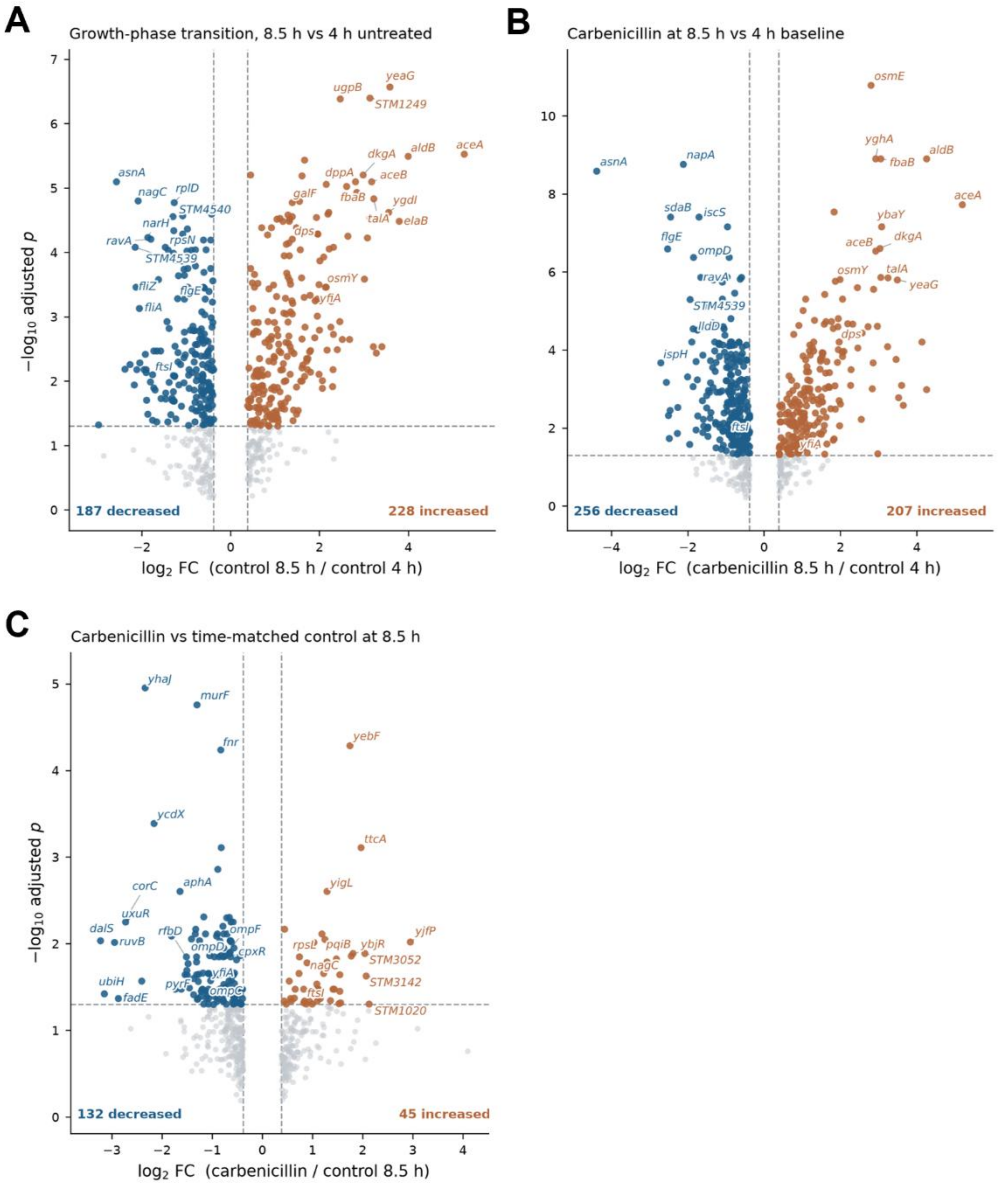
Supplementary Figure S1. Minimum inhibitory concentration of carbenicillin for *S.* Typhimurium. Cultures were grown in LB0 (initial OD_{600} = 0.05) with increasing carbenicillin concentrations (0 – 80 µg/mL) for 24 h at 37°C and 250 rpm. Growth was assessed by OD_{600}, identifying an MIC of 40 µg/mL. Data are presented as mean ± SD from three independent biological replicates.



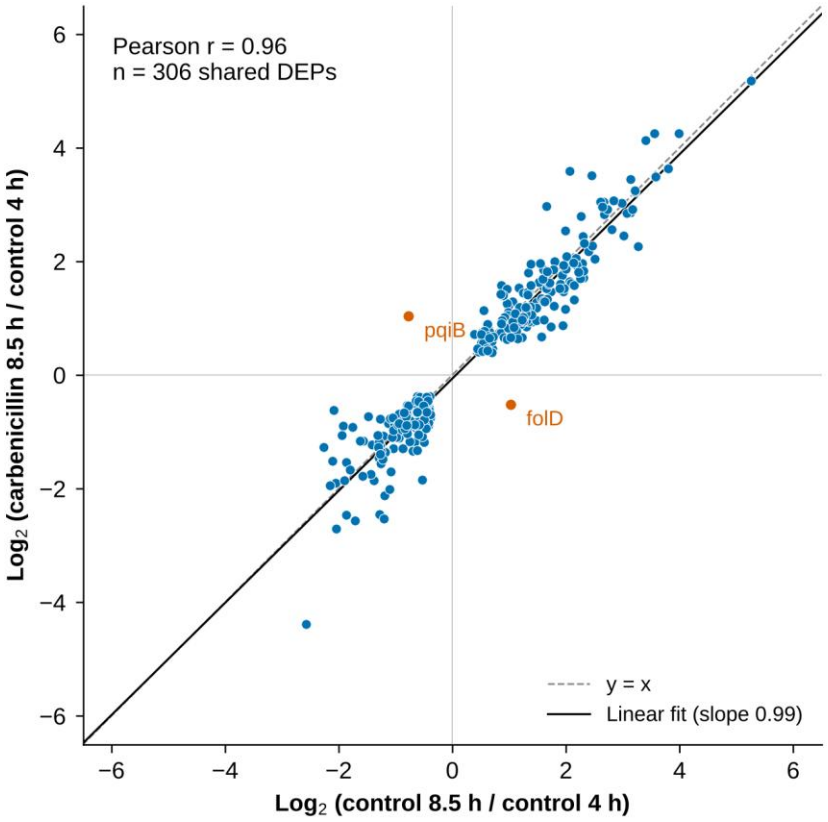
Supplementary Figure S2. Variance explained by principal components of the *S.* Typhimurium proteome. Scree plot showing the percentage of variance explained by each component of the $\log_2$-transformed, imputed, normalized, mean-centred, and unit-variance-scaled protein-abundance matrix. The analysis included untreated cultures at 4 h (n = 7) and 8.5 h (n = 5), and carbenicillin-exposed cultures at 8.5 h (n = 8; 10 µg/mL for 4.5 h). PC1 and PC2 explained 37.2% and 18.5% of the variance, respectively (55.7% combined). The corresponding PCA plot is shown in Figure 2B.



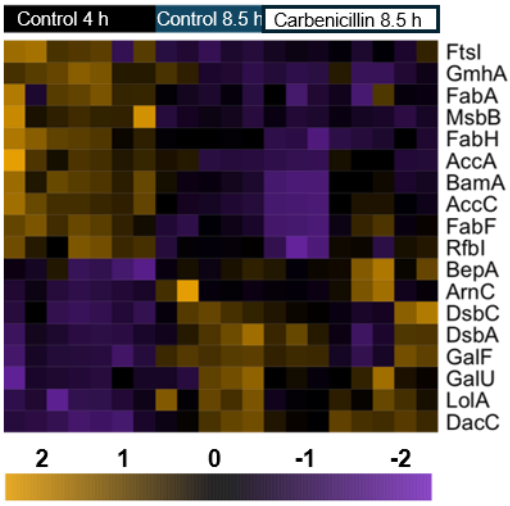
Supplementary Figure S3. Functional classification of the *S.* Typhimurium proteome according to Clusters of Orthologous Groups. Relative COG abundances were calculated as percentages of the total COG-assigned protein abundance. (A) Comparison of untreated cultures at 4 h (n = 7) and 8.5 h (n = 5). (B) Comparison of untreated cultures at 4 h and carbenicillin-exposed cultures at 8.5 h (n = 8, 10 µg/mL for 4.5 h). Bars represent mean ± SD across biological replicates. Statistical significance was assessed using the Mann–Whitney U test with Benjamini–Hochberg correction for multiple testing; adjusted $p < 0.05$ (*), $p < 0.01$ (**),$p < 0.001$ (***).



Supplementary Figure S4. Volcano plots show three pairwise comparisons: (A) untreated cultures at 8.5 h versus untreated cultures at 4 h; **(B**) carbenicillin-exposed cultures at 8.5 h versus the untreated 4 h baseline; and **(C)** carbenicillin-exposed cultures at 8.5 h versus time-matched untreated controls. Dashed lines mark the thresholds ($|\log_2 \text{fold change}| \geq 0.3785$ and Benjamini–Hochberg-adjusted $p < 0.05$). Orange and blue indicate increased and decreased abundance, respectively; gray indicates proteins that did not meet both criteria.



Supplementary Figure S5. Concordance of shared DEPs between untreated and carbenicillin-treated cultures. Log_2 fold changes of the 306 shared DEPs at 8.5 h relative to the common 4 h baseline were strongly correlated (Pearson r = 0.96; linear fit slope = 0.99). The dashed line indicates y = x and the solid line the linear fit. PqiB and FolD (orange) were the only shared DEPs with opposite directions of change between conditions.



Supplementary Figure S6. Relative abundance patterns of envelope-associated proteins across growth-phase and carbenicillin-exposure conditions. Protein abundances in heatmap are shown for logarithmic-phase control cultures (4 h), untreated cultures at 8.5 h, and carbenicillin-exposed cultures at 8.5 h. Columns represent individual biological replicates and rows represent individual proteins. Protein abundances were standardized as row-wise Z-scores across samples, with yellow indicating higher and purple indicating lower relative abundance for each protein.

Supplementary Tables

Supplementary Table S3. Proteins discussed in Section 2.3 with their fold changes in untreated (4 h → 8.5 h) and carbenicillin-exposed (4 h → 8.5 h carbenicillin) cultures relative to the 4 h baseline.

Protein	UniProt ID	Description (gene name)	4 h → 8.5 h	4 h → 8.5 h carbenicillin
Translation and transcription				
RplA	P0A2A3	Large ribosomal subunit protein uL1 (*rplA*)	0.70	0.77[1]
RplB	P60428	Large ribosomal subunit protein uL2 (*rplB*)	0.49	0.51
RplC	P60446	Large ribosomal subunit protein uL3 (*rplC*)	0.51	0.47
RplD	P60726	Large ribosomal subunit protein uL4 (*rplD*)	0.41	0.59
RplE	P62405	Large ribosomal subunit protein uL5 (*rplE*)	0.75	0.65
RplF	P66313	Large ribosomal subunit protein uL6 (*rplF*)	0.51	0.53
RplI	Q8ZK80	Large ribosomal subunit protein bL9 (*rplI*)	0.67	0.62
RplK	P0A7K0	Large ribosomal subunit protein uL11 (*rplK)*	0.64	0.63
RplM	P0AA13	Large ribosomal subunit protein uL13 (*rplM*)	0.49	0.56
RplN	Q7CPL5	Large ribosomal subunit protein uL14 (*rplN*)	0.52	0.47
RplO	P66073	Large ribosomal subunit protein uL15 (*rplO*)	0.58	0.69
RplP	Q7CPL4	Large ribosomal subunit protein uL16 (*rplP*)	0.58	0.55
RplQ	Q7CPL7	Large ribosomal subunit protein bL17 (*rplQ*)	0.48	0.47
RplS	P0A2A1	Large ribosomal subunit protein bL19 (*rplS*)	0.49	0.49
RplT	P0A7L6	Large ribosomal subunit protein bL20 (*rplT*)	0.58	0.69
RplU	Q7CPP7	Large ribosomal subunit protein bL21 (*rplU*)	0.73	0.77
RplV	P61179	Large ribosomal subunit protein uL22 (*rplV*)	0.46	0.56
RplX	P60626	Large ribosomal subunit protein uL24 (*rplX*)	0.53	0.56
RplY	Q7CQ71	Large ribosomal subunit protein bL25 (*rplY*)	0.42	0.39
RpmB	P0A2A5	Large ribosomal subunit protein bL28 (*rpmB*)	0.66	0.85[1]
RpmC	P66170	Large ribosomal subunit protein uL29 (*rpmC*)	0.41	0.44
RpmD	P0A2A7	Large ribosomal subunit protein uL30 (*rpmD*)	0.67	0.76[1]
RpmF	P0A7N6	Large ribosomal subunit protein bL32 (*rpmF*)	0.40	0.48
RpsA	Q7CQT9	30S ribosomal protein S1 (*rpsA*)	0.61	0.55
RpsB	P66541	Small ribosomal subunit protein uS2 (*rpsB*)	0.71	0.74
RpsD	O54297	Small ribosomal subunit protein uS4 (*rpsD*)	0.63	0.79[1]
RpsE	P0A7W4	Small ribosomal subunit protein uS5 (*rpsE*)	0.70	0.69
RpsG	P0A2B3	Small ribosomal subunit protein uS7 (*rpsG*)	0.63	0.66
RpsI	P66643	Small ribosomal subunit protein uS9 (*rpsI*)	0.70	0.68
RpsJ	P67904	Small ribosomal subunit protein uS10 (*rpsJ*)	0.59	0.61
RpsK	O54296	Small ribosomal subunit protein uS11 (*rpsK*)	0.66	0.59
RpsL	P0A7S6	Small ribosomal subunit protein uS12 (*rpsL*)	0.66	1.10[1]
RpsN	P66409	Small ribosomal subunit protein uS14 (*rpsN*)	0.36	0.60
RpsO	P66431	Small ribosomal subunit protein uS15 (*rpsO*)	1.98	1.77
RpsR	Q8ZK81	Small ribosomal subunit protein bS18 (*rpsR*)	0.63	0.53
RpsS	P66491	Small ribosomal subunit protein uS19 (*rpsS*)	0.67	0.77
RpsU	P68684	Small ribosomal subunit protein bS21 (*rpsU*)	0.47	0.59
Tig	P66932	Trigger factor (*tig*)	0.54	0.51
BipA	H9L427	Large ribosomal subunit assembly factor BipA (*bipA*)	0.56	0.63

Protein	UniProt ID	Description (gene name)	4 h → 8.5 h	4 h → 8.5 h carbenicillin
PrfC	Q56121	Peptide chain release factor 3 (*prfC*)	0.74	0.72
FusA	P0A1H3	Elongation factor G (*fusA*)	0.66	0.73
Tsf	P64052	Elongation factor Ts (*tsf*)	0.57	0.69
Efp	P64036	Elongation factor P (*efp*)	0.71	0.62
EfpL	P64046	Elongation factor protein EfpL (*efpL*)	0.73	0.52
IleS	Q8ZRZ0	Isoleucine-tRNA ligase (*ileS*)	0.72	0.65
LeuS	Q8ZQZ6	Leucine-tRNA ligase (*leuS*)	0.72	0.54
LysS	P28354	Lysine-tRNA ligase (*lysS*)	0.63	0.67
AsnS	P58696	Asparagine-tRNA ligase (*asnS*)	0.73	0.69
ThrS	Q8ZPS9	Threonine-tRNA ligase (*thrS*)	0.68	0.63
Hpf	P26983	Ribosome hibernation promoting factor (*hpf*)	2.09	1.92
YfiA (RaiA)	Q7CQ00	Ribosome associated factor (*yfiA*)	3.86	1.84
RpoA	P0A7Z7	DNA-directed RNA polymerase subunit alpha (*rpoA*)	0.64	0.73
RpoB	P06173	DNA-directed RNA polymerase subunit beta (*rpoB*)	0.73	0.65
NusA	P37430	Transcription termination/antitermination protein NusA (*nusA*)	0.74	0.73
NusB	Q8ZRD3	Transcription antitermination protein NusB (*nusB*)	0.77	0.62
Glycolysis				
PtsG	P37439	PTS system glucose-specific EIICB component (*ptsG*)	0.74	0.66
Glk	Q93IM5	Glucokinase (*glk*)	0.64[1]	0.21
YeaD	Q8ZPV9	Putative glucose-6-phosphate 1-epimerase (*yeaD*)	1.98	1.30[1]
Pgi	Q8ZKI4	Glucose-6-phosphate isomerase (*pgi*)	0.94[1]	0.90[1]
PfkA	P65692	ATP-dependent 6-phosphofructokinase (*pfkA*)	1.65	1.43[1]
PfkB	Q8ZPT5	Phosphofructokinase (*pfkB*)	4.51	4.16
Fbp	Q8ZK67	Fructose-1,6-bisphosphatase class 1 (*fbp*)	0.77[1]	0.81[1]
FbaB	Q7CQ97	Fructose-bisphosphate aldolase class 1 (*fbaB*)	6.11	8.29
TpiA	Q8ZKP7	Triosephosphate isomerase (*tpiA*)	1.36	1.38
GapA	P0A1P0	Glyceraldehyde-3-phosphate dehydrogenase (*gapA*)	0.89[1]	1.17[1]
Pgk	P65702	Phosphoglycerate kinase (*pgk*)	0.97[1]	1.19[1]
GpmA	Q8ZQS2	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase (*gpmA*)	1.44	1.34
Eno	P64076	Enolase (*eno*)	0.91[1]	1.16[1]
PykA	Q8ZNW0	Pyruvate kinase II (*pykA*)	0.75	0.54
Pentose phosphate pathway				
STM2340	Q8ZND5	Transketolase	0.71	0.44
TktA	Q8ZM63	Transketolase (*tktA*)	0.76	0.77
TktB	Q8ZN82	Transketolase (*tktB*)	6.35	8.28
TalA	Q8ZN83	Transaldolase A (*talA*)	9.31	9.47
Rpe	Q8ZLK4	Ribulose-phosphate 3-epimerase (*rpe*)	1.85	2.63
RpiA	P66692	Ribose-5-phosphate isomerase A (*rpiA*)	3.03	2.48
RbsK	Q8ZKV8	Ribokinase (*rbsK*)	2.37	2.72
Pgm	Q8ZQW9	Phosphoglucomutase (*pgm*)	1.70	1.38[1]
DeoB	P63923	Phosphopentomutase (*deoB*)	1.53	1.37
PrsA (Prs)	P0A1V6	Ribose-phosphate pyrophosphokinase (*prs*)	0.77	0.60

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Pgl	Q8ZQR4	6-phosphogluconolactonase (*pgl*)	9.27	9.36
Glycogen synthesis				
GlgC	P05415	Glucose-1-phosphate adenylyltransferase (*glgC*)	2.28	1.93
GlgA	P05416	Glycogen synthase (*glgA*)	2.26	2.30
GlgB	Q8ZLG5	1,4-alpha-glucan branching enzyme GlgB (*glgB*)	1.36	1.27[1]
Pyruvate, lactate, acetate and ethanol metabolism				
AceE	Q8ZRT2	Pyruvate dehydrogenase E1 component (*aceE*)	0.77[1]	0.71
AceF	Q8ZRT1	Acetyltransferase component of pyruvate dehydrogenase complex (*aceF*)	0.68	0.69
PflB	Q7CQU1	Formate acetyltransferase (*pflB*)	0.69	0.73
LldD	Q8ZL61	L-lactate dehydrogenase (*lldD*)	0.38	0.28
LdhA	Q8ZP91	NAD-dependent fermentative D-lactate dehydrogenase (*ldhA*)	2.16	2.12
Dld	Q8ZNM7	Quinone-dependent D-lactate dehydrogenase (*dld*)	3.88	2.77
Acs	Q8ZKF6	Acetyl-coenzyme A synthetase (*acs*)	2.44	2.28
AldB	Q8ZL72	Aldehyde dehydrogenase B (*aldB*)	15.91	19.03
STM1627	Q8ZPA8	S-(hydroxymethyl)glutathione dehydrogenase	3.44	3.63
AdhP	Q7CQI9	Alcohol dehydrogenase (*adhP*)	4.92	5.44
AdhE	Q8ZP45	Aldehyde-alcohol dehydrogenase (*adhE*)	1.82	1.87
TCA cycle and glyoxylate bypass				
PckA	P41033	Phosphoenolpyruvate carboxykinase (ATP) (*pckA*)	0.91[1]	0.84[1]
GltA	O68883	Citrate synthase (*gltA*)	0.93[1]	1.29[1]
PrpC	Q56063	2-methylcitrate synthase (*prpC*)	n.d.[2]	n.d.[2]
AcnA	Q8ZP52	Aconitate hydratase A (*acnA*)	4.97	4.99
AcnB	Q8ZRS8	Aconitate hydratase B (*acnB*)	1.06[1]	1.01[1]
IcdA	Q8ZPZ0	Isocitrate dehydrogenase [NADP] (*icdA*)	1.06[1]	1.26[1]
SucA	Q8ZQU1	2-oxoglutarate dehydrogenase E1 component (*sucA*)	0.81[1]	0.94[1]
SucB	Q7CQX4	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex (*sucB*)	0.82[1]	1.02[1]
SucC	P66869	Succinate-CoA ligase [ADP-forming] subunit beta (*sucC*)	0.84[1]	1.04[1]
SucD	Q8ZQU0	Succinate-CoA ligase [ADP-forming] subunit alpha (*sucD*)	0.89[1]	1.10[1]
SdhA	Q8ZQU3	Succinate dehydrogenase flavoprotein subunit (*sdhA*)	0.91[1]	0.80[1]
SdhB	Q8ZQU2	Succinate dehydrogenase iron-sulfur subunit (*sdhB*)	0.99[1]	0.91[1]
SdhC	P63725	Succinate dehydrogenase cytochrome b556 subunit (*sdhC*)	0.77[1]	1.32[1]
SdhD	Q7CQX5	Succinate dehydrogenase hydrophobic membrane anchor subunit (*sdhD*)	1.55	2.87[1]
FrdA	Q7CP97	Fumarate reductase flavoprotein subunit (*frdA*)	0.73[1]	0.63
FrdB	Q8ZKB4	Fumarate reductase iron-sulfur subunit (*frdB*)	0.73	0.59
FrdC	P67638	Fumarate reductase subunit C (*frdC*)	1.11[1]	1.09[1]
Mdh	P25077	Malate dehydrogenase (*mdh*)	0.85[1]	1.23[1]
FumA	P40720	Fumarate hydratase class I, aerobic (*fumA*)	0.75	0.63
FumB	Q8ZKE2	Fumarate hydratase class I (*fumB*)	0.43	0.48
FumC	Q8ZPL7	Fumarate hydratase class II (*fumC*)	4.65	3.51
AceA	P51066	Isocitrate lyase (*aceA*)	38.23	36.40
AceB	Q8ZKL4	Malate synthase (*aceB*)	8.99	7.57

Protein	UniProt ID	Description (gene name)	4 h → 8.5 h	4 h → 8.5 h carbenicillin
Nucleotide metabolism				
CarB	P14846	Carbamoyl phosphate synthase large chain (*carB*)	2.35	1.96
PyrB	P0A1Z4	Aspartate carbamoyltransferase catalytic subunit (*pyrB*)	4.96	3.28
PyrC	P06204	Dihydroorotase (*pyrC*)	2.54	1.92
NrdD	Q9L646	Anaerobic ribonucleoside-triphosphate reductase (*nrdD*)	0.27	0.18
PurU	Q8ZP42	Formyltetrahydrofolate deformylase (*purU*)	1.53	0.96[1]
Cell envelope				
FtsI	Q7CR83	Peptidoglycan D,D-transpeptidase FtsI (PBP3) (*ftsI*)	0.30	0.53
BamA	Q8ZRP0	Outer membrane protein assembly factor BamA (*bamA*)	0.66	0.55
AccA	P0A1C3	Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha (*accA*)	0.63	0.57
AccC	Q7CPM0	Biotin carboxylase (*accC*)	0.67	0.66
FabH	O85139	Beta-ketoacyl-[acyl-carrier-protein] synthase III (*fabH*)	0.69	0.47
FabA	P64105	3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase (*fabA*)	0.63	0.63
FabF	Q8ZQ14	3-oxoacyl-[acyl-carrier-protein] synthase 2 (*fabF*)	0.71	0.74
GmhA	P63223	Phosphoheptose isomerase (*gmhA*)	0.72	0.60
MsbB	H9L440	Lipid A biosynthesis acyltransferase (LpxM) (*msbB*)	0.27	0.28
RfbI	P26395	Protein RfbI (*rfbI*)	0.65	0.53
LolA	Q8ZQD4	Outer-membrane lipoprotein carrier protein (*lolA*)	2.61	2.06
BepA	P66950	Beta-barrel assembly-enhancing protease (*bepA*)	1.44	1.68
DsbA	P0A2H9	Thiol:disulfide interchange protein DsbA (*dsbA*)	2.47	1.95
DsbC	P55890	Thiol:disulfide interchange protein DsbC (*dsbC*)	2.28	2.03
DacC	Q8ZQL1	Serine-type D-Ala-D-Ala carboxypeptidase (*dacC*)	3.86	3.83
GalU	Q7CQF2	UTP--glucose-1-phosphate uridylyltransferase (*galU*)	1.37	1.33
GalF	P0A2K7	UTP--glucose-1-phosphate uridylyltransferase (*galF*)	2.62	2.08
ArnC (PmrF)	O52324	Undecaprenyl-phosphate 4-deoxy-4-formamido-L-arabinose transferase (*arnC*)	2.79	2.43
YbjR	Q8ZQF3	N-acetylmuramoyl-L-alanine amidase (*ybjR*)	n.d.[2]	n.d.[2]
NagC	Q8ZQX9	Transcriptional repressor of nag (N-acetylglucosamine) operon (NagC/XylR family) (*nagC*)	0.24	0.65
RffG	Q9L6R3	dTDP-glucose 4,6-dehydratase (*rffG*)	0.28[1]	0.56[1]
FolD	P58688	Bifunctional protein FolD (*folD*)	2.04	0.70
PqiB	Q8ZQ71	Paraquat-inducible protein B (*pqiB*)	0.59	2.05
Stress adaptation and cellular protection				
UspA	Q8ZLD7	Universal stress protein A (*uspA*)	2.60	3.00
UspF	P67091	Universal stress protein F (*uspF*)	2.44	2.13
UspG	P67093	Universal stress protein G (*uspG*)	3.02	3.22
OsmY	Q7CP68	Osmotically-inducible protein Y (*osmY*)	4.38	3.95
OsmE	Q7CQP3	Osmotically-inducible putative lipoprotein OsmE (*osmE*)	4.79	6.92
Dps	Q7CQV9	DNA protection during starvation protein (*dps*)	2.60	3.89
IraP	Q7CR46	Anti-adapter protein IraP (*iraP*)	4.19	3.12
KatG	P17750	Catalase-peroxidase (*katG*)	1.48	1.71
SodC1	P0CW86	Superoxide dismutase [Cu-Zn] 1 (*sodC1*)	3.48	4.00
SodC2	O68901	Superoxide dismutase [Cu-Zn] 2 (*sodC*)	5.47	11.44
TrxA	P0AA28	Thioredoxin 1 (*trxA*)	2.44	2.15

Protein	UniProt ID	Description (gene name)	4 h → 8.5 h	4 h → 8.5 h carbenicillin
YibF	Q8ZL68	Glutathione S-transferase (*yibF*)	4.55	3.82
DegP	P26982	Periplasmic serine endoprotease DegP (*degP*)	1.43	1.31[1]
HtpG	P58480	Chaperone protein HtpG (*htpG*)	0.58	0.51
RpoS	P0DM81	RNA polymerase sigma factor RpoS (*rpoS*)	n.d.[2]	n.d.[2]
Nutrient acquisition				
OppA	P06202	Periplasmic oligopeptide-binding protein OppA (*oppA*)	2.92	3.90
DppA	Q8ZLA9	Dipeptide transport protein (*dppA*)	6.98	5.89
GltL	Q7CQY9	Glutamate/aspartate transporter (*gltL*)	4.27	3.06
GsiB	Q8ZQM3	Glutathione-binding protein GsiB (*gsiB*)	2.13	1.99
UgpB	Q7CPK0	sn-glycerol-3-phosphate-binding periplasmic protein UgpB (*ugpB*)	5.51	4.84
ModA	Q8ZQR7	Molybdate-binding protein ModA (*modA*)	3.90	2.87
Environmental sensing and motility				
NarL	Q8ZP34	Nitrate/nitrite response regulator protein NarL (*narL*)	0.57	0.60
RstA	Q8ZPL3	Response regulator in two-component regulatory system with RstB (OmpR family) (*rstA*)	0.21	0.42
FliA	P0A2E8	RNA polymerase sigma factor FliA (*fliA*)	0.24	0.27
FliL	P26417	Flagellar protein FliL (*fliL*)	0.46	0.25
FlgE	P0A1J1	Flagellar hook protein FlgE (*flgE*)	0.44	0.17
FljB	P52616	Phase 2 flagellin (*fljB*)	2.38	1.35[1]
FlgK	P0A1J5	Flagellar hook-associated protein 1 (*flgK*)	2.67	1.56[1]
Respiration				
AtpF	Q7CPE4	ATP synthase subunit b (*atpF*)	0.58	0.63
AtpG	Q8ZKW8	ATP synthase gamma chain (*atpG*)	0.65	0.67
AtpB	Q7CPE3	ATP synthase subunit a (*atpB*)	1.33[1]	0.55
AtpH	Q7CPE5	ATP synthase subunit delta (*atpH*)	0.78[1]	0.52
NuoH	Q60010	NADH-quinone oxidoreductase subunit H (*nuoH*)	0.63	0.44
NuoI	Q7CQ51	NADH-quinone oxidoreductase subunit I (*nuoI*)	1.07[1]	0.71
Ndh	Q8ZQ05	Respiratory NADH dehydrogenase 2 (*ndh*)	0.84[1]	0.29
CybC	P63727	Soluble cytochrome b562 (*cybC*)	2.37[1]	1.54[1]

Fold change: ratio of arithmetic mean normalized protein abundance (later/earlier condition), rounded to two decimals. Ratios of differentially abundant proteins correspond to Supplementary Table S2; other ratios were calculated from the condition means in Supplementary Table S1. [1] Not differentially abundant in this comparison. [2] n.d., not detected in any replicate of one of the two conditions; ratio not calculable.

Supplementary Table S4. Selected proteins discussed in Section 2.4, including differentially abundant proteins and nonsignificant comparators. Fold changes are shown for (i) untreated cultures at 8.5 h relative to untreated cultures at 4 h (4 h → 8.5 h) and (ii) carbenicillin-exposed cultures at 8.5 h relative to time-matched untreated controls (8.5 h → 8.5 h carbenicillin).

Protein	UniProt ID	Description (gene name)	4 h → 8.5 h	8.5 h → 8.5 h carbenicillin
Translation				
RpsL	P0A7S6	Small ribosomal subunit protein uS12 (*rpsL*)	0.66	1.67
YfiA	Q7CQ00	Ribosome associated factor (RaiA) (*yfiA*)	3.86	0.48
Carbon metabolism and transport				
FbaB	Q7CQ97	Fructose-bisphosphate aldolase class 1 (*fbaB*)	6.11	1.36
ModA	Q8ZQR7	Molybdate-binding protein ModA (*modA*)	3.90	0.74
Motility and signal transduction				
FljB	P52616	Phase 2 flagellin (*fljB*)	2.38	0.57
FlgK	P0A1J5	Flagellar hook-associated protein 1 (*flgK*)	2.67	0.58
FlgE	P0A1J1	Flagellar hook protein FlgE (*flgE*)	0.44	0.40
FliL	P26417	Flagellar protein FliL (*fliL*)	0.46	0.54
Tcp	Q02755	Methyl-accepting chemotaxis citrate transducer (*tcp*)	1.28[1]	0.68
FlgB	P16437	Flagellar basal body rod protein FlgB (*flgB*)	0.08[1]	2.57
CpxR	Q8ZKR6	Transcriptional regulatory protein CpxR (*cpxR*)	1.91	0.58
Fnr	P0A2T8	Fumarate and nitrate reduction regulatory protein (*fnr*)	1.65	0.56
NarP	Q8ZNI1	Response regulator in two-component regulatory system with NarQ (*narP*)	1.00[1]	0.63
PhoB	Q7CR43	Phosphate regulon transcriptional regulatory protein PhoB (*phoB*)	0.84[1]	0.59
RpoD	P0A2E3	RNA polymerase sigma factor RpoD (*rpoD*)	1.21[1]	0.66
Stress protection and protein quality control				
KatG	P17750	Catalase-peroxidase (*katG*)	1.48	1.16[1]
TrxA	P0AA28	Thioredoxin 1 (*trxA*)	2.44	0.88[1]
OsmY	Q7CP68	Osmotically-inducible protein Y (*osmY*)	4.38	0.90[1]
OsmE	Q7CQP3	Osmotically-inducible putative lipoprotein OsmE (*osmE*)	4.79	1.44
DegP	P26982	Periplasmic serine endoprotease DegP (*degP*)	1.43	0.92[1]
HtpG	P58480	Chaperone protein HtpG (*htpG*)	0.58	0.89[1]
STM1251	Q8ZPY6	Molecular chaperone (Small heat shock protein)	4.18	2.88
Nucleotide metabolism				
CarA	P14845	Carbamoyl phosphate synthase small chain (*carA*)	2.48	0.56
CarB	P14846	Carbamoyl phosphate synthase large chain (*carB*)	2.35	0.84[1]
PyrB	P0A1Z4	Aspartate carbamoyltransferase catalytic subunit (*pyrB*)	4.96	0.66[1]
PyrC	P06204	Dihydroorotase (*pyrC*)	2.54	0.76[1]
PyrI	P08421	Aspartate carbamoyltransferase regulatory chain (*pyrI*)	n.d.[2]	0.41
PyrF	P07691	Orotidine 5'-phosphate decarboxylase (*pyrF*)	n.d.[2]	0.39
PyrG	P65921	CTP synthase (*pyrG*)	0.83[1]	0.61
PyrH	P65933	Uridylate kinase (*pyrH*)	0.62[1]	0.69
PurC	P65889	Phosphoribosylaminoimidazole-succinocarboxamide synthase (*purC*)	1.53	0.65
PurU	Q8ZP42	Formyltetrahydrofolate deformylase (*purU*)	1.53	0.63
Hpt	O33799	Hypoxanthine phosphoribosyltransferase (*hpt*)	n.d.[2]	0.54

Protein	UniProt ID	Description (gene name)	4 h → 8.5 h	8.5 h → 8.5 h carbenicillin
NrdD	Q9L646	Anaerobic ribonucleoside-triphosphate reductase (*nrdD*)	0.27	0.66
UshA	P06196	Silent protein UshA(0) (*ushA*)	0.74[1]	0.44
PurA	P65882	Adenylosuccinate synthetase (*purA*)	1.04[1]	1.02[1]
PurB	Q8ZPZ6	Adenylosuccinate lyase (*purB*)	0.96[1]	1.08[1]
PurH	P26978	Bifunctional purine biosynthesis protein PurH (*purH*)	1.18[1]	0.86[1]
PurL	P74881	Phosphoribosylformylglycinamidine synthase (*purL*)	1.28[1]	0.89[1]
GuaA	Q8ZN60	GMP synthase [glutamine-hydrolyzing] (*guaA*)	0.97[1]	0.82[1]
GuaB	Q8ZN59	Inosine-5'-monophosphate dehydrogenase (*guaB*)	1.08[1]	0.64[1]
PrsA (Prs)	P0A1V6	Ribose-phosphate pyrophosphokinase (*prs*)	0.77	0.78[1]
GlnA	P0A1P6	Glutamine synthetase (*glnA*)	0.44	0.89[1]
Ppx	P0A269	Exopolyphosphatase (*ppx*)	0.31	0.55
Ndk	P65534	Nucleoside diphosphate kinase (*ndk*)	0.90[1]	0.93[1]
Udp	P0A1F6	Uridine phosphorylase (*udp*)	0.79[1]	1.31[1]
Cofactor metabolism				
RibD	Q8ZRD4	Riboflavin biosynthesis protein RibD (*ribD*)	1.03[1]	0.66
UbiH	Q8ZM73	2-octaprenyl-6-methoxyphenol hydroxylase (*ubiH*)	n.d.[2]	0.11
HemB	Q7CR48	Delta-aminolevulinic acid dehydratase (*hemB*)	0.84[1]	0.51
FolD	P58688	Bifunctional protein FolD (*folD*)	2.04	0.34
MetK	P66764	S-adenosylmethionine synthase (*metK*)	0.62	0.64
PdxH	Q8ZPM9	Pyridoxine/pyridoxamine 5'-phosphate oxidase (*pdxH*)	1.24[1]	0.65
CbiC	Q05601	Cobalt-precorrin-8 methylmutase (*cbiC*)	1.28[1]	0.68
CbiH	Q05590	Probable cobalt-factor III C(17)-methyltransferase (*cbiH*)	1.21[1]	0.57
CbiL	Q05593	Cobalt-precorrin-2 C(20)-methyltransferase (*cbiL*)	1.18[1]	0.68
EutB	P19264	Ethanolamine ammonia-lyase large subunit (*eutB*)	n.d.[2]	0.47
PduA	P0A1C7	Bacterial microcompartment shell protein PduA (*pduA*)	0.69[1]	0.48
Respiration and energy conservation				
AtpB	Q7CPE3	ATP synthase subunit a (*atpB*)	1.33[1]	0.41
AtpH	Q7CPE5	ATP synthase subunit delta (*atpH*)	0.78[1]	0.67
NuoH	Q60010	NADH-quinone oxidoreductase subunit H (*nuoH*)	0.63	0.70
NuoI	Q7CQ51	NADH-quinone oxidoreductase subunit I (*nuoI*)	1.07[1]	0.67
CybC	P63727	Soluble cytochrome b562 (*cybC*)	2.37[1]	0.65
AtpF	Q7CPE4	ATP synthase subunit b (*atpF*)	0.58	1.10[1]
AtpG	Q8ZKW8	ATP synthase gamma chain (*atpG*)	0.65	1.03[1]
Chromosome organization, cell division and peptidoglycan synthesis				
DnaN	P26464	Beta sliding clamp (*dnaN*)	2.31	0.36
MukF	Q8ZQB7	Chromosome partition protein MukF (*mukF*)	1.74	0.40
MatP	Q8ZQ68	Macrodomain Ter protein (*matP*)	0.63[1]	0.48
MaoP	Q7CPD8	Macrodomain Ori protein (*maoP*)	4.43	0.56
RuvB	P66755	Holliday junction branch migration complex subunit RuvB (*ruvB*)	2.78[1]	0.13
MinE	P65363	Cell division topological specificity factor (*minE*)	1.04[1]	0.70
ZapD	P67693	Cell division protein ZapD (*zapD*)	1.04[1]	0.53
RecA	P65977	Protein RecA (*recA*)	1.13[1]	0.76[1]
LexA	P0A273	LexA repressor (*lexA*)	1.87[1]	1.04[1]

Protein	UniProt ID	Description (gene name)	4 h → 8.5 h	8.5 h → 8.5 h carbenicillin
GlmS	Q8ZKX1	Glutamine-fructose-6-phosphate aminotransferase [isomerizing] (*glmS*)	1.00[1]	0.64
MurF	Q8ZRU6	UDP-N-acetylmuramoyl-tripeptide-D-alanyl-D-alanine ligase (*murF*)	n.d.[2]	0.40
FtsI	Q7CR83	Peptidoglycan D,D-transpeptidase FtsI (PBP3) (*ftsI*)	0.30	1.79
YbjR	Q8ZQF3	N-acetylmuramoyl-L-alanine amidase (*ybjR*)	n.d.[2]	3.41
NagC	Q8ZQX9	Transcriptional repressor of nag (N-acetylglucosamine) operon (NagC/XylR family) (*nagC*)	0.24	2.77
MrcB	Q8ZRQ3	Penicillin-binding protein 1B (PBP1b) (*mrcB*)	1.26[1]	0.92[1]
MurA	P65454	UDP-N-acetylglucosamine 1-carboxyvinyltransferase (*murA*)	0.95[1]	0.88[1]
MurD	Q8ZRU4	UDP-N-acetylmuramoylalanine-D-glutamate ligase (*murD*)	0.89[1]	1.34[1]
MurE	Q8ZRU7	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2,6-diaminopimelate ligase (*murE*)	0.61[1]	1.61[1]
MurG	Q8ZRU3	UDP-N-acetylglucosamine-N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase (*murG*)	1.60[1]	0.89[1]
FtsZ	Q8ZRU0	Cell division protein FtsZ (*ftsZ*)	0.91[1]	1.16[1]
FtsA	Q7CR80	Cell division protein FtsA (*ftsA*)	0.96[1]	1.47[1]
LPS, envelope and outer membrane				
FabH	O85139	Beta-ketoacyl-[acyl-carrier-protein] synthase III (*fabH*)	0.69	0.68
LpxA	P32200	Acyl-[acyl-carrier-protein]-UDP-N-acetylglucosamine O-acyltransferase (*lpxA*)	0.83[1]	0.68
WaaB	Q06994	Lipopolysaccharide 1,6-galactosyltransferase (*waaB*)	3.25[1]	0.42
MsbA	P63359	ATP-dependent lipid A-core flippase (*msbA*)	1.81[1]	0.44
YedD	Q06399	Uncharacterized lipoprotein YedD (*yedD*)	0.87[1]	0.76
RfbD	P26392	dTDP-4-dehydrorhamnose reductase (*rfbD*)	1.90	0.35
RfbJ	P0A1P4	CDP-abequose synthase (*rfbJ*)	1.49	0.54
RfbF	P26396	Glucose-1-phosphate cytidylyltransferase (*rfbF*)	0.82[1]	0.61
WecB	Q9L6R5	UDP-N-acetylglucosamine 2-epimerase (*wecB*)	n.d.[2]	0.43
RffG	Q9L6R3	dTDP-glucose 4,6-dehydratase (*rffG*)	0.28[1]	1.98
GalU	Q7CQF2	UTP--glucose-1-phosphate uridylyltransferase (*galU*)	1.37	0.97[1]
GalE	P22715	UDP-glucose 4-epimerase (*galE*)	0.65	1.61[1]
GlmU	Q8ZKX0	Bifunctional protein GlmU (*glmU*)	1.13[1]	0.93[1]
KdsB	Q8ZQC0	3-deoxy-manno-octulosonate cytidylyltransferase (*kdsB*)	0.86[1]	0.84[1]
MdoB	Q8ZJX6	Phosphoglycerol transferase I (*mdoB*)	0.55	0.74
MdoH	Q8ZQ26	Glucans biosynthesis glucosyltransferase H (*mdoH*)	0.48	1.66
PqiB	Q8ZQ71	Paraquat-inducible protein B (*pqiB*)	0.59	3.50
FadD	P63521	Long-chain-fatty-acid-CoA ligase (*fadD*)	n.d.[2]	2.64
YafH (FadE)	Q8ZRJ7	Acyl-coenzyme A dehydrogenase (*fadE*)	n.d.[2]	0.14
FadI	Q8ZNA6	3-ketoacyl-CoA thiolase YfcY (*fadI*)	n.d.[2]	1.85
SecY	Q8ZLM0	Protein translocase subunit SecY (*secY*)	0.71[1]	0.73
TatA	P0A2H3	Sec-independent protein translocase protein TatA (*tatA*)	n.d.[2]	0.59

Protein	UniProt ID	Description (gene name)	4 h → 8.5 h	8.5 h → 8.5 h carbenicillin
Lgt	P60959	Phosphatidylglycerol-prolipoprotein diacylglyceryl transferase (*lgt*)	1.71[1]	0.46
OmpD	P37592	Outer membrane porin protein OmpD (*ompD*)	0.69	0.40
OmpC	P0A263	Outer membrane porin C (*ompC*)	0.82[1]	0.46
OmpF	P37432	Outer membrane porin F (*ompF*)	1.22[1]	0.60
YejA	Q8ZNK0	ABC transporter periplasmic binding protein (*yejA*)	n.d.[2]	0.19

Fold change: ratio of arithmetic mean normalized protein abundance (8.5 h untreated/4 h untreated or 8.5 h carbenicillin-exposed/8.5 h untreated, respectively), rounded to two decimals. Ratios of differentially abundant proteins correspond to Supplementary Table S2; other ratios were calculated from the condition means in Supplementary Table S1. [1] Not differentially abundant in this comparison. [2] n.d., not detected in any replicate of one of the two conditions; ratio not calculable.