

Table S1. Bacterial strains and plasmids used in this study

Strain or plasmid	Description	Reference or source
<i>E. coli</i> strains		
JM109	Cloning strain	New England Biolabs
S17-1	Donor strain for diparental conjugation	[1]
<i>R. sphaeroides</i> strains		
2.4.1	wild type	[2]
2.4.1 ΔUdsC	<i>R. sphaeroides</i> 2.4.1 with a scarless deletion of <i>UdsC</i> (3' UTR of RSP_7527)	This study
2.4.1 Δ <i>rpoHII</i>	<i>R. sphaeroides</i> 2.4.1 with a scarless deletion of <i>rpoHII</i>	[3]
2.4.1 OE UdsC	<i>R. sphaeroides</i> 2.4.1 with the plasmid PCV2_udsC for an inducible overexpression of sRNA UdsC	
Plasmids		
pJET1.2/blunt cloning vector	Ap ^r , 2.97 kb	Fermentas
pBBR1	Km ^r , broad-host-range cloning vector	[4]
pCV2	Gen ^r , inducible overexpression plasmid	This study
pCV2_udsC	Gen ^r , inducible overexpression of sRNA UdsC	This study
pPHU231:mVenus	Gen ^r , EVC	[5]
pP-Prp <i>HIII</i> :mVenus	Sp ^r , transcriptional fusion of <i>rpoHII</i> promoter sequence to mVenus	This study
pP- <i>PtorF</i> :mVenus	Sp ^r , transcriptional fusion of <i>torF</i> promoter sequence to mVenus	This study

Ap^r: Ampicillin, Km^r: Kanamycin, Gen^r: Gentamycin, Sp^r: Spectinomycin

Table S2. Oligodeoxynucleotide sequences for cloning, northern blot and *in vitro* transcription

Oligodeoxynucleotide	Sequence 5'-3'	Reference or source
Cloning		
7527_sRNA_SacI_for	CGAGAGCTCATAGTCGGCTGAGGCAGTCA	This study
7527_sRNA_mRNA_KpnI_rev	CGAGGTACCAAGAAAAAGGGCTCCGACGC	This study
7527_sRNA_up_EcoRI_for	CGAGAATTCGTTGCCGCAGGTCAGATGC	This study
7527_sRNA_up_XbaI_rev	CGATCTAGACCTCGTGCGCTCATGC	This study
7527_sRNA_dn_XbaI_for	CGATCTAGAGGGCTCCGCCGC	This study
7527_sRNA_dn_HindIII_rev	CGAAAGCTTCCGGTGCCGTTCTTGACC	This study

Bseq_torF_long_HindI II_for	ACTAAAGCTTCCTTATCGACAGGCGCGC	This study
Bseq_torF_nat_Xba_re v	ACTATCTAGAGATGATCTGGATGGCGGCC A	This study
rpoH2_Pro_HindIII_fo r	ACTAAAGCTTGCCCACCATCACGGTTGC	This study
rpoH2_XbaI_rev	ACTATCTAGAGGTATATCCGTCCAGTGCCA T	This study
Northern Blot		
UdsC	CTGCGACAATGACTGCCTCAGCCGA	[6]
5S rRNA	CTTGAGACGCAGTACCATTG	[7]
EMSA		
T7_RpoHII_for	TAATACGACTCACTATAGGGAGACCGGAC ATGTGTTTTTCCG	This study
RpoHII_rev	AGTGCCATCAGGACCCCTG	This study
T7_UdsC_for	TAATACGACTCACTATAGGGAGAGATAGTC GGCTGAGGCAGTC	This study
UdsC_rev	CAAAGAAAAAGGGCTCC	This study

Table S3: Log₂fold changes (calculated by DEseq2 analysis) in read counts determined by RNAseq within a UdsC overexpression strain (OE UdsC) after 15 min of IPTG treatment in comparison to the UdsC overexpression without (0 min) IPTG treatment and the UdsC knockout strain (Δ UdsC) in comparison to the wild type (WT). **The Table shows the top 50 downregulated genes for the UdsC overexpression strain with IPTG (15 min) versus without IPTG (0 min).**

Locus	Gene	Function	Log ₂ FC 15 min IPTG vs. 0 min IPTG	Log ₂ FC Δ UdsC vs. WT
RSP_0262	<i>bchX</i>	Chlorophyllide reductase, BchX subunit	-2.77	0,63
RSP_3706	<i>RSP_3706</i>	Hypothetical protein	-2.78	0,43
RSP_0286	<i>bchB</i>	light-independent protochlorophyllide reductase	-2.78	0,73
RSP_0104	<i>nuoF1</i>	Respiratory-chain NADH dehydrogenase,	-2.79	0,54
RSP_0102	<i>nuoCD</i>	NADH dehydrogenase (ubiquinone),	-2.79	0,72
RSP_1816	<i>RSP_1816</i>	Mg chelatase-related protein	-2.80	0,76
RSP_7559	<i>RSP_7559</i>	NA	-2.83	-0,86
RSP_2395	<i>RSP_2395</i>	cytochrome c peroxidase	-2.84	1,32
RSP_3269	<i>gapB</i>	glyceraldehyde-3-phosphate dehydrogenase	-2.85	-0,03
RSP_1284	<i>prkA</i>	Phosphoribulokinase	-2.89	-0,5
RSP_4203	<i>RSP_4203</i>	Putativ glutaredoxin family protein	-2.92	-0,59
RSP_2337	<i>RSP_2337</i>	Hypothetical protein	-2.92	-0,34
RSP_2087	<i>RSP_2087</i>	Hypothetical protein	-2.93	-0,83
RSP_0260	<i>bchZ</i>	putative chlorophyllide reductase, BchZ subunit	-2.94	0,47
RSP_0317	<i>hemN</i>	coproporphyrinogen III oxidase	-2.96	0,26
RSP_2888	<i>RSP_2888</i>	Transcriptional regulator	-2.96	0,36
RSP_7252	<i>RSP_7252</i>	Hypothetical protein	-2.96	0,25
RSP_1256	<i>RSP_1256</i>	enoyl-(acyl carrier protein) reductase	-3.02	-0,82
RSP_0278	<i>RSP_0278</i>	putative light-harvesting complex assembly protein	-3.03	0,74
RSP_0315	<i>pucC</i>	Light-harvesting 1 (B870) complex assembly	-3,12	0,74
RSP_1819	<i>feoA1</i>	Ferrous iron transport protein A	-3,12	-0,68
RSP_0285	<i>bchN</i>	Light-independent protochlorophyllide reductase	-3,13	1,09

RSP_3266	<i>fbpB</i>	Fructose-1,6-bisphosphatase	-3,14	-1,16
RSP_0284	<i>bchF</i>	2-vinyl bacteriochlorophyllide hydratase	-3,15	0,03
RSP_0261	<i>bchY</i>	Chlorophyllide reductase, BchY subunit	-3,17	1,07
RSP_0264	<i>crtF</i>	Hydroxyneurosporene methyltransferase	-3,19	1,03
RSP_1255	<i>RSP_1255</i>	Phosphate acetyltransferase	-3,19	-0,49
RSP_0279	<i>bchG</i>	Bacteriochlorophyll a synthase	-3,20	0,66
RSP_0820	<i>RSP_0820</i>	Putative cytochrome B561	-3,21	0,51
RSP_0259	<i>pufQ</i>	Protein pufQ	-3,24	0,29
NA	3'UTR	NA	-3,27	0,4
RSP_2758	<i>RSP_2758</i>	Hypothetical protein	-3,37	0,46
RSP_2338	<i>RSP_2338</i>	Hypothetical protein	-3,39	-0,18
RSP_0465	<i>RSP_0465</i>	Putative protease	-3,43	0,12
RSP_3044	<i>dorS</i>	DMSO/TMAO-sensor hybrid histidine kinase	-3,45	0,43
RSP_1818	<i>feoB</i>	Fe ²⁺ transport system protein B	-3,46	0,43
RSP_0281	<i>bchE</i>	Mg-protoporphyrin IX monomethylester cyclase	-3,47	0,07
RSP_1817	<i>RSP_1817</i>	Hypothetical protein	-3,48	0,85
RSP_0101	<i>nuoB1</i>	NADH dehydrogenase (ubiquinone)	-3,57	0,04
RSP_2331	<i>ppaZ</i>	PpaZ, a novel pseudoazurin precursor	-3,57	-0,25
RSP_2573	<i>RSP_2573</i>	Hypothetical protein	-3,59	0,67
RSP_0464	<i>RSP_0464</i>	Putative protease	-3,62	0,23
RSP_1283	<i>cfxA</i>	Fructose-bisphosphate aldolase I	-3,65	0,16
RSP_0265	<i>crtE</i>	Geranylgeranyl pyrophosphate synthetase	-3,68	1,17
RSP_1254	<i>RSP_1254</i>	Putative acetate kinase (acetokinase)	-3,71	-0,55
RSP_7547	<i>RSP_7547</i>	Hypothetical protein	-3,82	-0,02
RSP_3788	<i>RSP_3788</i>	Hypothetical protein	-3,83	-0,32
RSP_1285	<i>cbbF1</i>	Fructose-1,6-bisphosphatase I	-4,08	-0,51
RSP_2066	<i>RSP_2066</i>	Hypothetical protein	-4,09	1,4
RSP_3434	<i>RSP_3434</i>	Hypothetical protein	-4,28	0,45
RSP_0468	<i>RSP_0468</i>	Putative 3-octaprenyl-4-hydroxybenzoate lyase	-4,47	0,37

Table S4: Log₂fold changes (calculated by DEseq2 analysis) in read counts determined by RNAseq within a UdsC overexpression strain (OE UdsC) after 15 min of IPTG treatment in comparison to the UdsC overexpression without (0 min) IPTG treatment and the UdsC knockout strain (Δ UdsC) in comparison to the wild type (WT). The Table shows the 22 and 51 genes from Figure 2D, which are colored in red.

Locus	Gene	Function	Log ₂ FC 15 min IPTG vs. 0 min IPTG	Log ₂ FC Δ UdsC vs. WT
RSP_0265	<i>crtE</i>	Geranylgeranyl pyrophosphate synthetase	-3,68	1,17
RSP_0264	<i>crtF</i>	Hydroxyneurosporene methyltransferase	-3,19	1,03
RSP_0261	<i>bchY</i>	Chlorophyllide reductase, BchY subunit	-3,17	1,07
RSP_0285	<i>bchN</i>	light-independent protochlorophyllide reductase	-3,13	1,09
RSP_0315	<i>pucC</i>	Light-harvesting 1 (B870) complex assembly	-3,12	1,11
RSP_2395	<i>RSP_2395</i>	BCCP, cytochrome c peroxidase	-2,84	1,32
RSP_6125	<i>RSP_6125</i>	hypothetical protein	-2,74	1,44
RSP_6138	<i>RSP_6138</i>	hypothetical protein	-2,68	1,67
RSP_1406	<i>RSP_1406</i>	hypothetical protein	-2,49	1,21
RSP_3070	<i>RSP_3070</i>	hypothetical protein	-1,89	1,05
RSP_1480	<i>oppB</i>	ABC oligopeptide transporter	-1,87	1,74
RSP_0254	<i>dxsA</i>	1-deoxy-D-xylulose-5-phosphate synthase	-1,74	1,09
RSP_1574	<i>RSP_1574</i>	Cytochrome b562	-1,72	1,17

RSP_2085	RSP_2085	hypothetical protein	-1,65	1,12
RSP_6137	RSP_6137	transcriptional regulator, TetR family	-1,59	1,27
RSP_0293	RSP_0293	hypothetical protein	-1,25	1,19
RSP_0294	RSP_0294	hypothetical protein	-1,23	1,17
RSP_2864	<i>cbbE</i>	Pentose-5-phosphate-3-epimerase	-1,21	1,17
RSP_1278	<i>cbbZ</i>	phosphoglycolate phosphatase	-1,15	1,11
RSP_0095	<i>smoS</i>	sorbitol dehydrogenase	-1,05	1,44
RSP_0576	RSP_0576	Na ⁺ /solute-symporter	-1,04	1,11
RSP_0660	RSP_0660	hypothetical protein	-1,04	1,07
RSP_1718	<i>rplW</i>	50S ribosomal protein L23	1,09	-1,20
RSP_1733	<i>rpmD</i>	Ribosomal protein L30	1,13	-1,39
RSP_0047	<i>cheB2</i>	chemotaxis methyltransferase, CheB2	1,15	-2,25
RSP_0037	<i>flgM</i>	Putative FlgM, negative regulator of flagellin	1,29	-3,16
NA	<i>sRNA_00061</i>	NA	1,41	-2,73
RSP_1049	<i>pheAa</i>	chorismate mutase	1,59	-1,26
RSP_3388	RSP_3388	putative Isocitrate/isopropylmalate dehydrogenase	1,60	-1,86
RSP_0042	<i>cheA3</i>	Chemotaxis histidine protein kinase, CheA3	1,67	-1,93
RSP_0044	<i>tlpT</i>	putative cytoplasmic chemoreceptor, TlpT	1,85	-2,87
RSP_0043	<i>cheY6</i>	chemotaxis response regulator, CheY6	1,99	-2,16
RSP_3386	RSP_3386	TRAP-T family transporter	2,12	-1,01
RSP_3389	RSP_3389	Isocitrate/isopropylmalate dehydrogenase	2,13	-2,40
RSP_0045	<i>slp</i>	chromosome partitioning protein	2,26	-2,31
RSP_6169	RSP_6169	hypothetical protein	2,48	-1,69
RSP_0046	<i>cheW4</i>	Chemotaxis protein, CheW4	2,61	-2,65
RSP_3387	RSP_3387	TRAP-T family transporter	2,74	-1,81
RSP_0084	RSP_0084	hypothetical protein	2,86	-1,67
RSP_0032	<i>fliA</i>	sigma factor FliA (Sigma-28 group, flagellar)	2,88	-1,82
NA	<i>UdsC</i>	NA	2,91	-3,46
RSP_0079	<i>flgF</i>	flagellar proximal rod protein FlgF	2,95	-2,29
RSP_0051	<i>torF</i>	Torf protein	3,02	-1,25
RSP_0073	<i>flgL</i>	flagellar hook-associated protein 3 FlgL	3,08	-2,19
RSP_0059	<i>fliL</i>	flagellar biosynthesis protein, FliL	3,15	-2,40
RSP_0076	<i>flgI</i>	flagellar P-ring protein	3,15	-2,57
RSP_0054	<i>fliG</i>	Probable flagellar motor switch protein FliG	3,25	-1,39
RSP_0065	<i>fliR</i>	Flagellar protein FliR	3,29	-1,65
RSP_6086	RSP_6086	hypothetical protein	3,33	-2,04
RSP_6092	RSP_6092	hypothetical protein	3,34	-2,29
RSP_0081	<i>flgD</i>	Flagellar scaffolding protein FlgD	3,35	-2,82
RSP_0064	<i>fliQ</i>	Flagellar protein FliQ	3,38	-2,71
RSP_0074	<i>flgK1</i>	FlgK flagellar hook-associated protein 1	3,40	-2,44
RSP_0033	RSP_0033	hypothetical protein	3,40	-2,59
RSP_0080	<i>flgE</i>	flagellar hook protein FlgE	3,41	-2,98
RSP_0077	<i>flgH</i>	Flagellar L-ring protein	3,48	-2,08
RSP_0072	RSP_0072	possible invasion protein	3,50	-2,42
RSP_0078	<i>flgG</i>	Flagellar distal rod protein	3,51	-2,74
RSP_0231	<i>motB</i>	flagellar MotB protein	3,51	-2,70
RSP_6093	<i>flgJ</i>	FlgJ	3,53	-1,83
RSP_0060	<i>fliM</i>	Flagellar switch protein FliM	3,54	-2,20
RSP_0066	<i>flhB</i>	Flagellar protein FlhB	3,60	-2,32
RSP_0062	<i>fliO</i>	Flagellar protein FliO	3,74	-2,64
RSP_0058	<i>fliK</i>	FliK, flagellar hook-length control protein	3,77	-2,01

RSP_0233	<i>motA</i>	Flagellar motor protein MotA	3,77	-1,40
RSP_0082	<i>flgC</i>	flagellar basal-body rod protein FlgC	3,83	-2,77
RSP_0035	<i>RSP_0035</i>	hypothetical protein	3,87	-2,56
RSP_0067	<i>RSP_0067</i>	hypothetical protein	3,89	-2,80
RSP_0061	<i>fliN</i>	Flagellar motor switch FliN protein	3,97	-2,08
RSP_0063	<i>fliP</i>	Flagellar transport protein FliP	4,00	-2,08
RSP_0036	<i>flgA</i>	flagellar basal-body P-ring formation protein FlgA	4,02	-2,49
RSP_0034	<i>flhA</i>	flagellar biosynthesis protein, FlhA	4,05	-2,48
RSP_0083	<i>flgB</i>	Flagellar proximal rod protein FlgB	4,65	-2,19

Table S5: Log₂fold changes (calculated by DEseq2 analysis) in read counts determined by RNAseq within a UdsC overexpression strain (OE UdsC) after 15 min of IPTG treatment in comparison to the UdsC overexpression without (0 min) IPTG treatment and the UdsC knockout (ΔUdsC) in comparison to the wild type (WT). The Table shows 27 genes of the motility gene cluster that are not or slightly regulated.

Locus	Gene	Function	Log ₂ FC 15 min IPTG vs. 0 min IPTG	Log ₂ FC ΔUdsC vs. WT
RSP_1303	<i>flgE1</i>	putative flagellar hook protein	-0,13	-0,34
RSP_1304	<i>RSP_1304</i>	flagellar hook-associated protein	-1,33	-0,31
RSP_1305	<i>RSP_1305</i>	putative flagellar hook-associated protein	-0,28	-1,04
RSP_1307	<i>flgI1</i>	flagellar P-ring protein precursor	-0,35	-0,94
RSP_1306	<i>RSP_1306</i>	PAS sensor Signal Transduction Histidine Kinase	0,76	0,03
RSP_1308	<i>RSP_1308</i>	hypothetical protein	-0,71	0,18
RSP_1309	<i>fliP1</i>	Type III secretion system inner membrane P protein	0,03	-0,91
RSP_1310	<i>RSP_1310</i>	hypothetical protein	0,59	1,07
RSP_1311	<i>fliH1</i>	putative flagellar biosynthesis/type III secretory pathway protein	-0,97	1,80
RSP_1312	<i>fliF</i>	putative flagellar M-ring protein	0,24	-0,39
RSP_1313	<i>RSP_1313</i>	possible flagellar synthesis protein	-0,67	-0,44
RSP_1314	<i>RSP_1314</i>	hypothetical protein	-0,85	-0,08
RSP_1315	<i>RSP_1315</i>	hypothetical protein	-1,31	0,60
RSP_1316	<i>motA1</i>	flagellar motor protein	0,69	-0,25
RSP_1318	<i>RSP_1318</i>	hypothetical protein	0,04	-0,18
RSP_1319	<i>RSP_1319</i>	possible invasion protein	0,06	-0,19
RSP_1320	<i>flhA1</i>	Flagellar biosynthesis pathway, component FlhA	-0,02	-0,80
RSP_1321	<i>fliR1</i>	Flagellar biosynthesis pathway, component FliR	-0,35	-1,46
RSP_1322	<i>fliB</i>	flagellar biosynthesis pathway, component FliB	-0,17	-0,21
RSP_6155	<i>RSP_6155</i>	hypothetical protein	0,36	0,53
RSP_1323	<i>RSP_1323</i>	hypothetical protein	0,23	0,84
RSP_1324	<i>flgH1</i>	flagellar L-ring protein precursor	0,32	0,48
RSP_1325	<i>RSP_1325</i>	putative flagellar basal-body P-ring formation protein FlgA	-0,40	0,30
RSP_1326	<i>RSP_1326</i>	putative flagellar basal body rod protein	-0,41	0,22
RSP_1327	<i>RSP_1327</i>	putative flagellar basal body rod protein	0,07	0,04
RSP_1328	<i>RSP_1328</i>	flagellar biosynthetic protein FliQ	0,16	0,25
RSP_1329	<i>fliE1</i>	putative flagellar hook-basal body complex protein	-0,81	-1,31

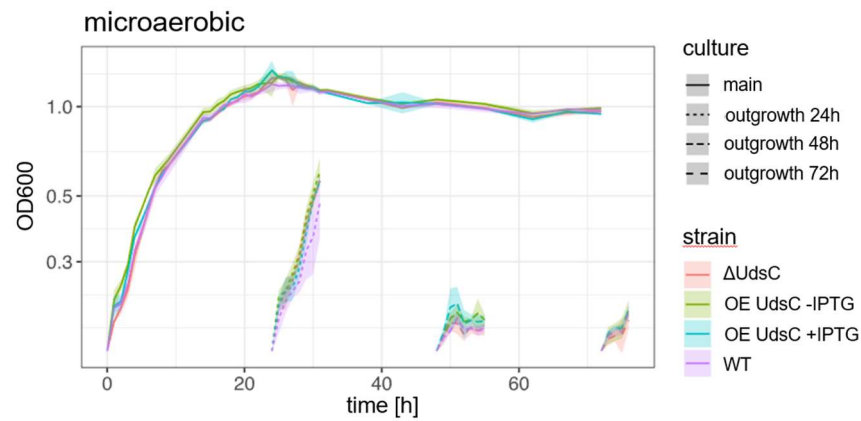
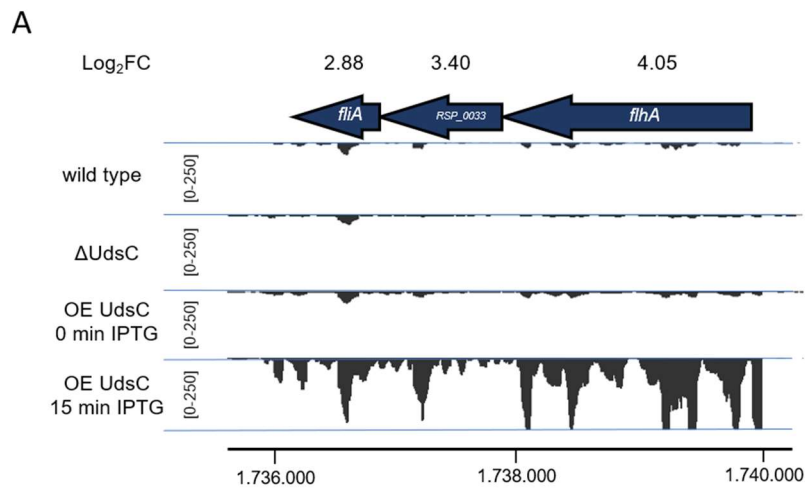
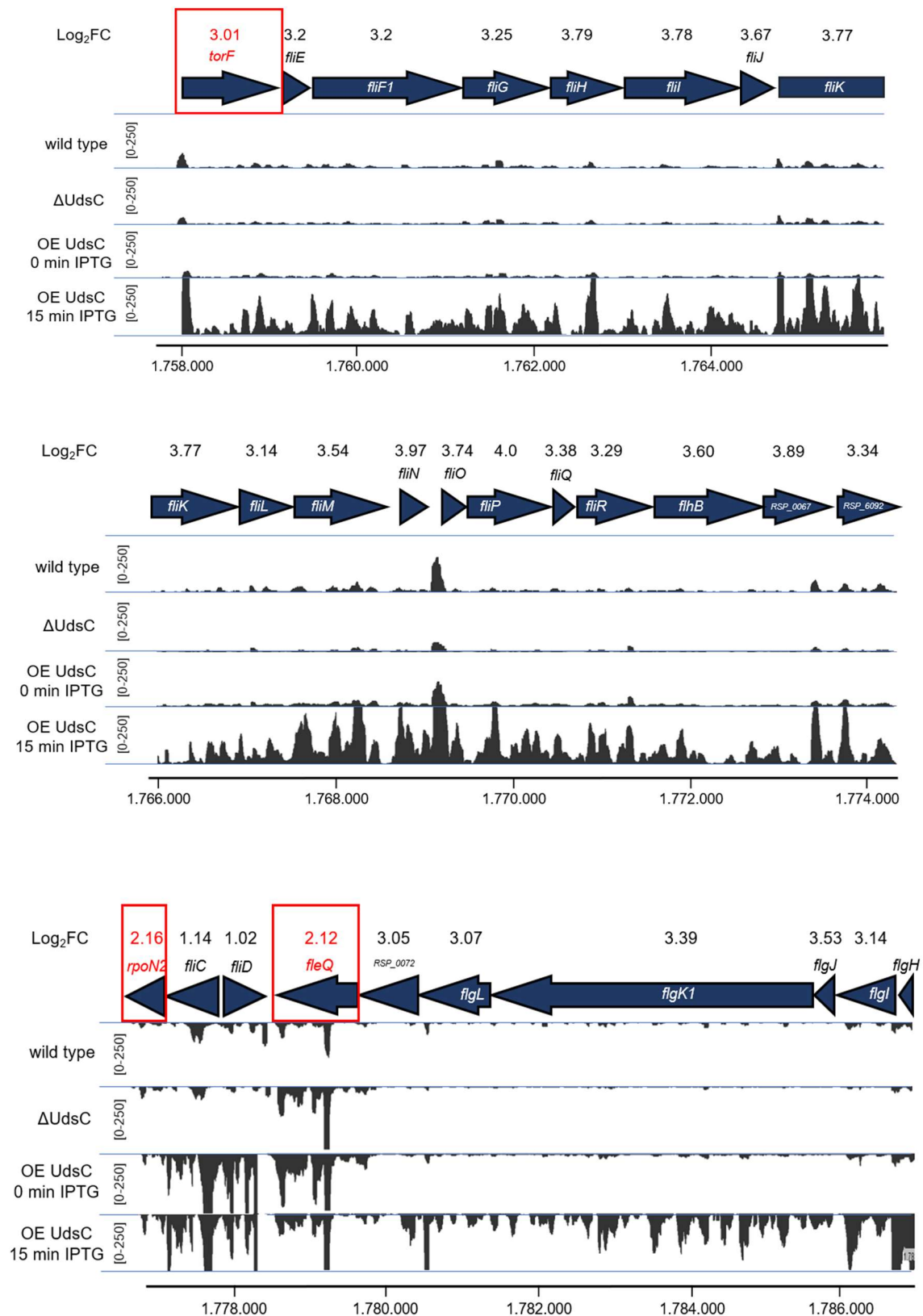
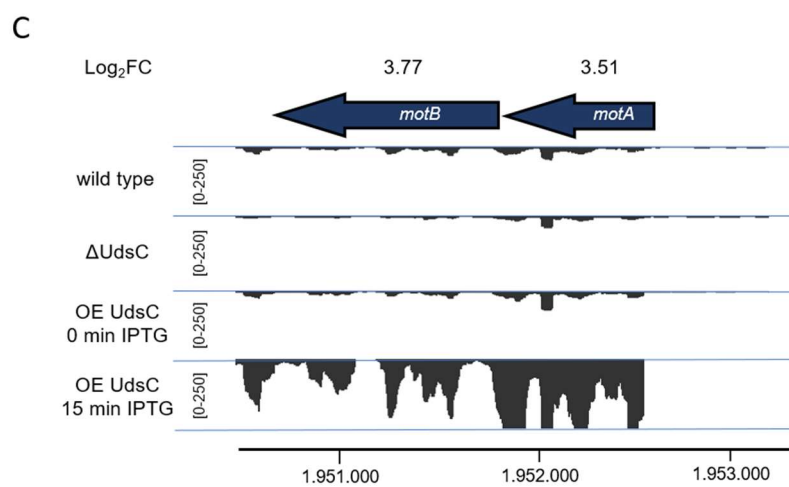
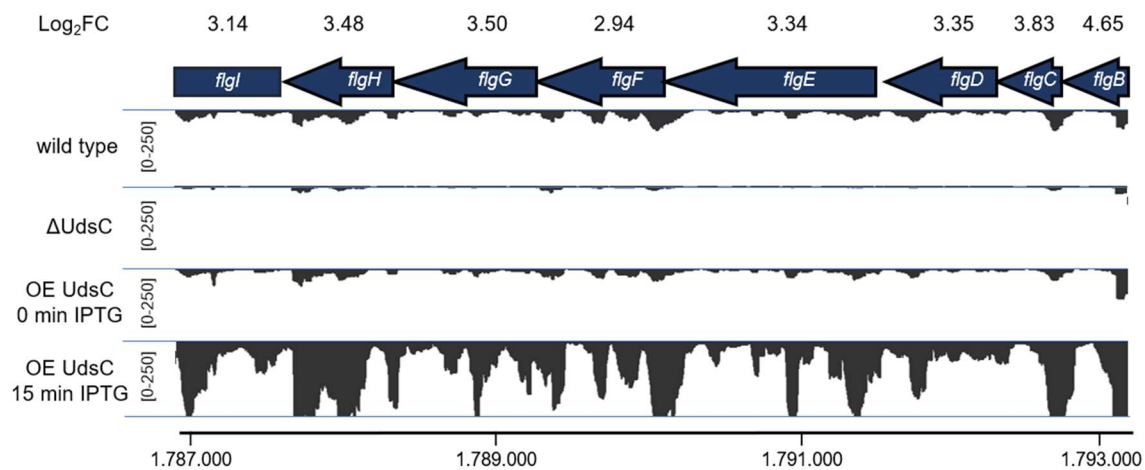


Figure S1: Growth curves of WT, UdsC knockout strain (Δ UdsC) and the UdsC overexpression strain (OE UdsC strain (with or without IPTG added) under microaerobic conditions. The cultures were incubated for 72 h. 24, 48 and 72 h after inoculation, part of the cultures was diluted into fresh medium and outgrowth was monitored, while the remaining culture was further incubated for monitoring the OD. The lines represent the mean of biological triplicates and the standard deviations are indicated (shade).

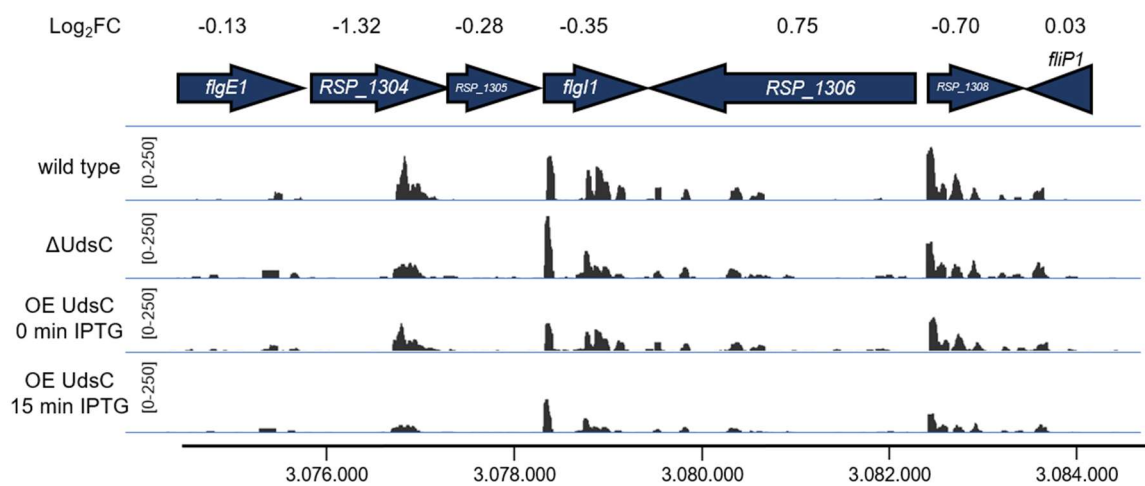


B





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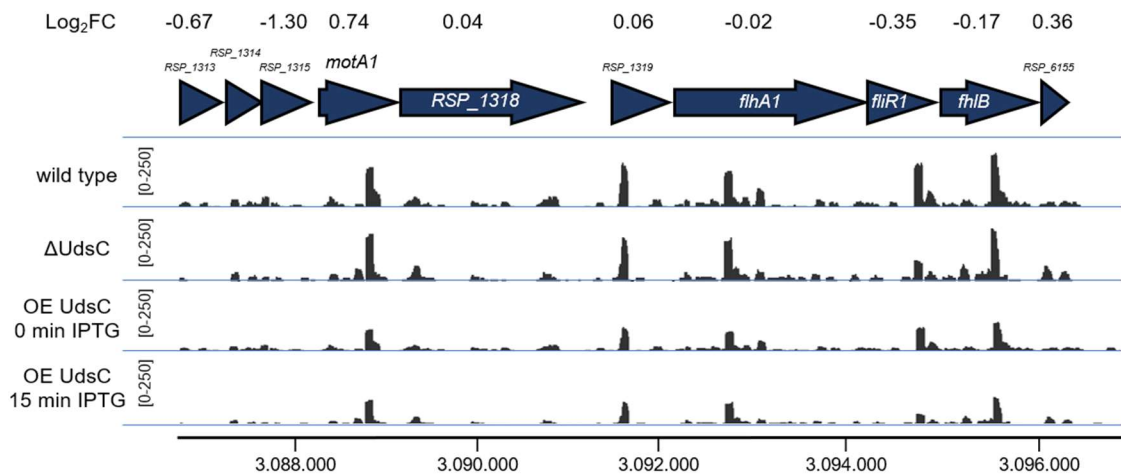


Figure S2: Effect of UdsC on expression of the motility genes from RNAseq visualized by the Integrated Genome Browser. Wild type, UdsC deletion strain (Δ UdsC) and UdsC overexpression (OE UdsC) with and without IPTG (0 min IPTG or 15 min IPTG) were cultivated under microaerobic conditions and total RNA was isolated for RNA sequencing as described in materials and methods. The Log₂fold change (Log₂FC) of UdsC overexpression strain (OE UdsC) with IPTG (15 min) versus without IPTG (0 min) is indicated. Genes for important regulators of the flagella genes are marked in red.

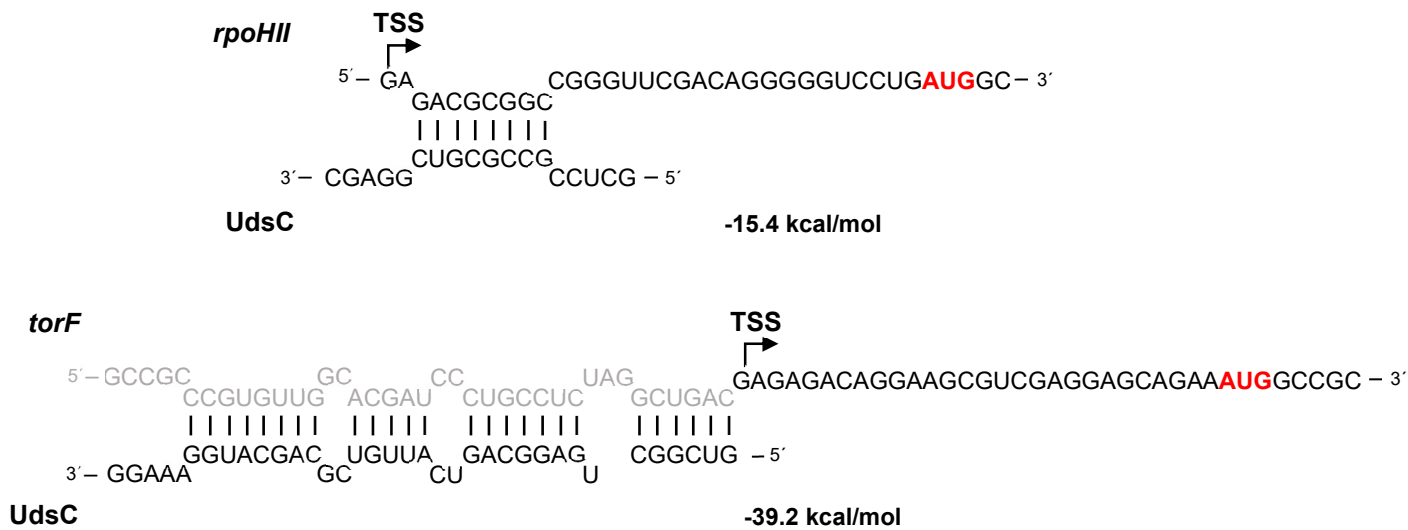


Figure S3: (A) Predicted base pairing between UdsC and *rpoHII* mRNA transcript by IntaRNA webtool [8]. The transcription start site (TSS) is indicated by an arrow and the start codon AUG is shown in red. (B) The predicted binding site for *torF* locates directly upstream of the transcriptional start site (TSS), which would exclude a binding of UdsC to *torF* mRNA.

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