Dataset S1. List of differentially expressed genes in the *hutC* deletion mutant background when compared with wild-type *P. fluorescens* SBW25. The differentially expressed genes were determined based on transcripts comparison normalized using the Median of Gene Expression Ratios methods, following the recommendations of Geneious 9.0.5.

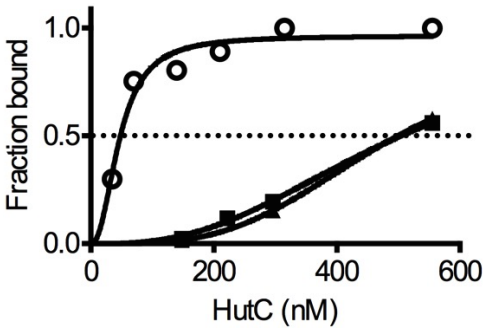

Figure S1. Determination of equilibrium dissociation constant (Kd) for $HutC_{His6}$ binding with P_{hutU} probe DNAs.

The plots were made on EMSA data presented in Figure 1 for the wild-type probe PhutU-325 (open circles), and the EMSA data in Figure 3 for the two mutant probes PhutU-M1 (solid triangles) and PhutU-M2 (solid squares) carrying mutations of the Phut-I and Phut-II repeats respectively.

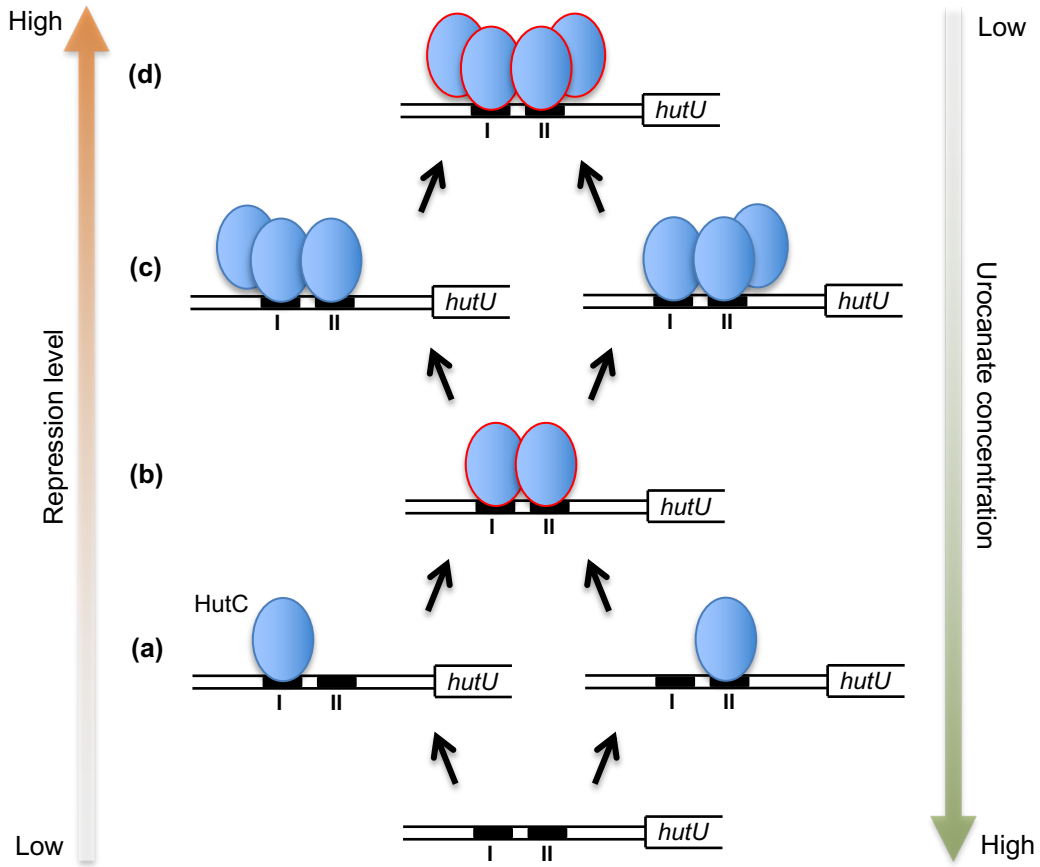

Figure S2. The proposed model of HutC action on the basis of data presented in this work.

When urocanate is present at high concentrations, HutC is dissociated from the P_{hutU} promoter region, and *hut* expression is de-repressed. On the decrease of urocanate, apo-HutC monomer binds to either Phut-I site or Phut-II site (a). However, efficient repression is achieved only when HutC forms a dimer and simultaneously binds to the two half-sites (b). As further decrease of urocanate, HutC forms a trimer (c), and eventually a tetramer, which tightly binds to the Phut site, resulting in stronger repression of the *hut* promoter (d). This dynamic process is reversed on the increase of urocanate.

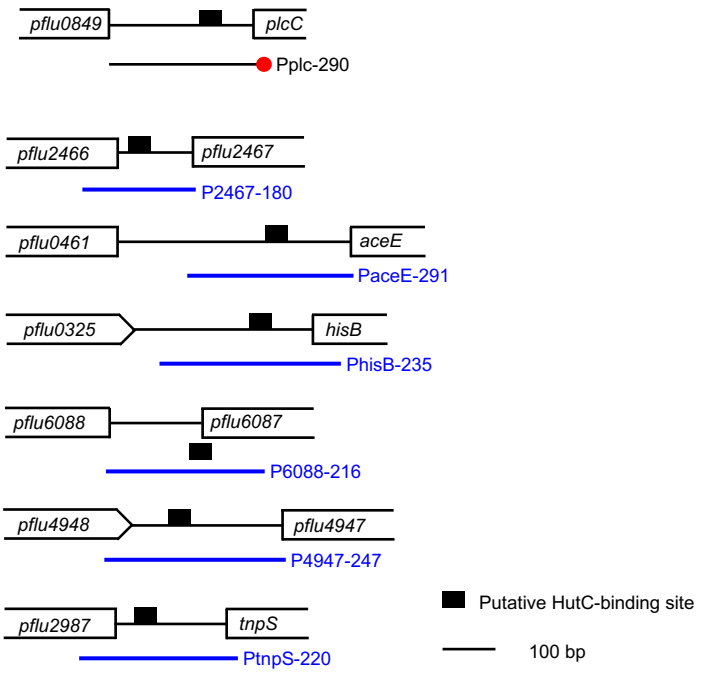

Figure S3. Probe DNAs used for EMSAs analysis of the predicted HutC binding sites. The Pplc-290 probe was labelled by biotin at 3'-end, whereas other probes were DIG-labelled at both ends.

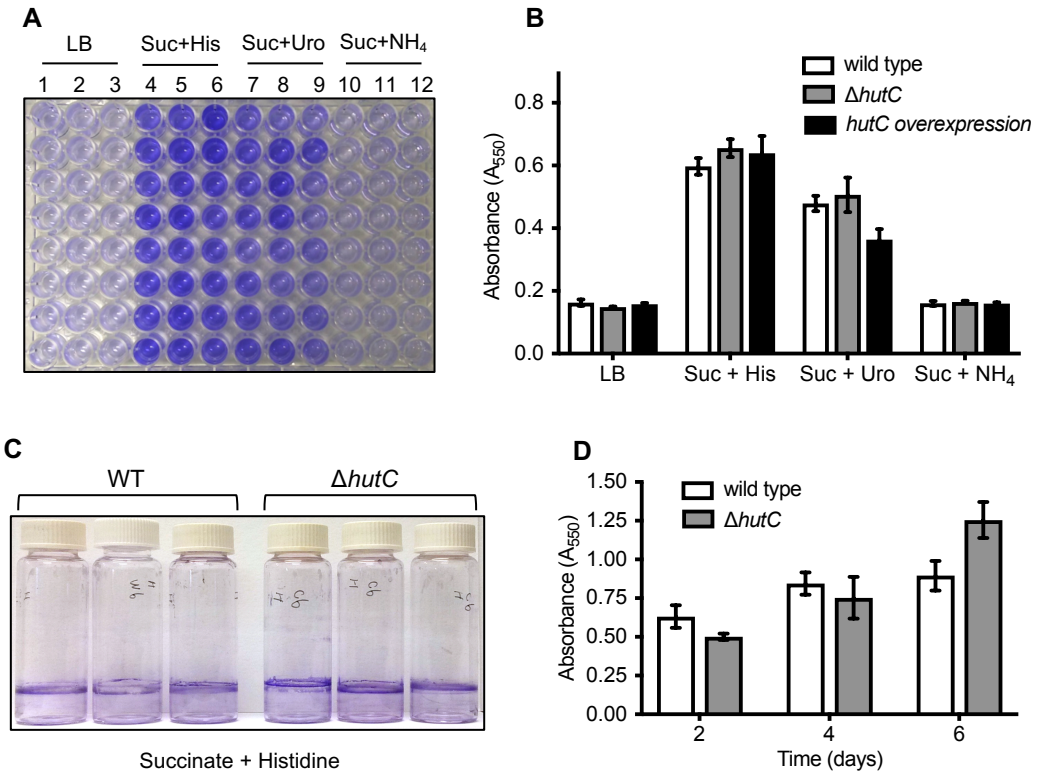

Figure S4. Assays for biofilm formation by wild-type SBW25 and its Δ*hutC* mutant.

(A) Bacteria were grown in a 96-well microtiter plate at 28°C for 3 days with eight replicates for each strain and each medium. Wild type: column 1, 4, 7 and 10; mutant Δ*hutC,* column 2, 5, 8 and 11; mutant over-expressing *hutC*, column, 3, 6, 9 and 12. Biofilm was stained by crystal violet and solubilized for measuring absorbance at A_{550} nm. **(B)** Absorbance data are means and standard errors of eight repeats. **(C)** Biofilm formed when bacteria were grown in glass tubes under shaken conditions for 6 days at 28°C. **(D)** Data of absorbance (A_{550}) for biofilms formed by bacteria grown in minimal salt medium supplemented with succinate (20 mM) and histidine (10 mM) for 2, 4 and 6 days. Data are means and standard errors of three repeats.

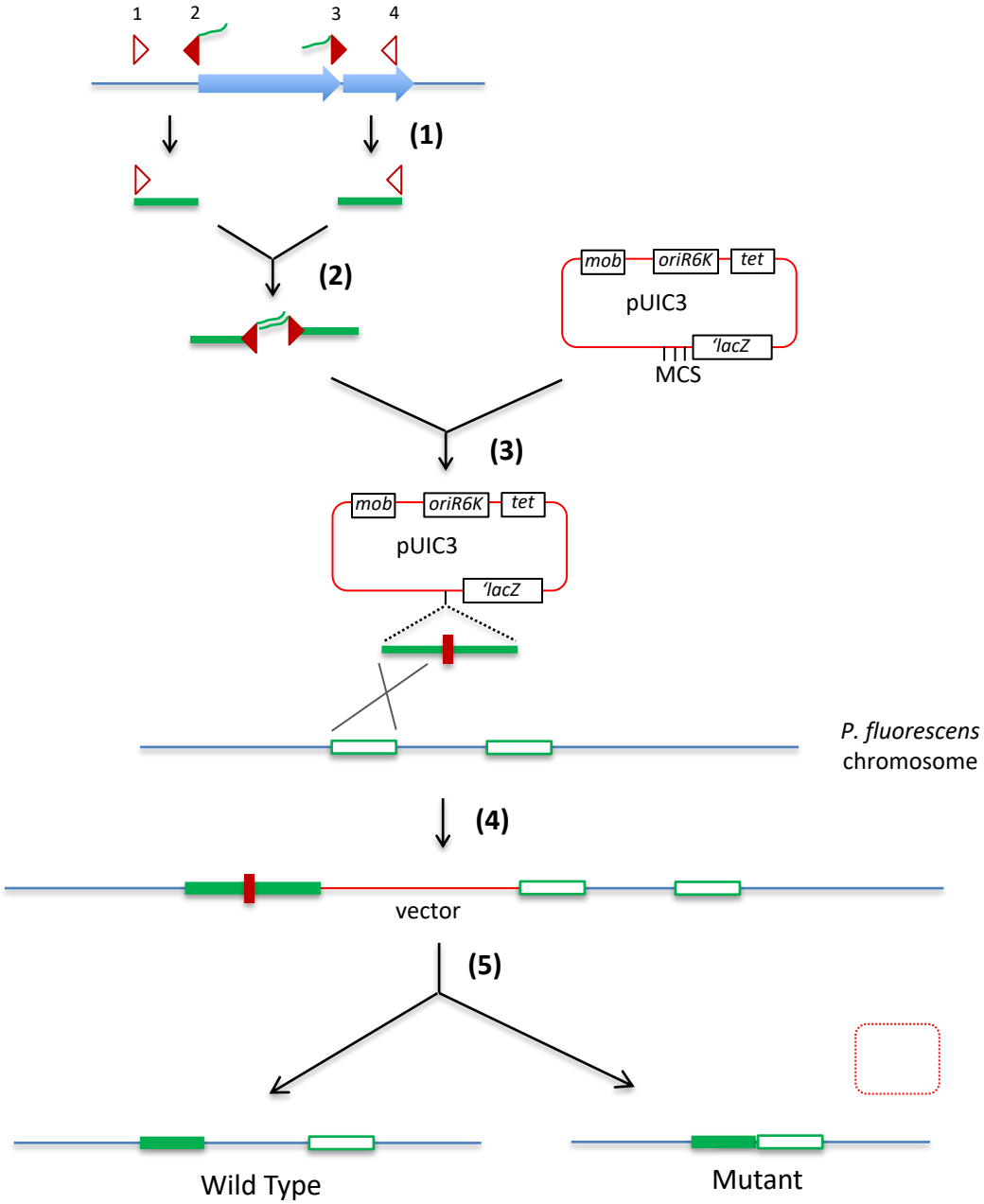

Figure S5. Gene deletion in *Pseudomonas* by SOE-PCR and a two-step allelic-exchange strategy.

(1) Two pairs of primers were designed to amplify the flanking DNA regions, and gene deletion or substitution mutation can be introduced into the overlapping sequence of the two outward facing primers. **(2)** The PCR products were then joined together in a second PCR using the two inward facing primers. **(3)** The resultant PCR product was then cloned into the plasmid vector pCR8/GW/TOPO using the TA Cloning Kit from Invitrogen Ltd. After sequence identity was confirmed by DNA sequencing, the insert DNA is then sub-cloned into the suicide-integration vector pUIC3 (Mob^+). **(4)** The recombinant plasmid was then mobilized into *Pseudomonas* by a standard procedure of tri-parental conjugation on agar plate with the help of pRK2013 (Tra^+). Integration by single homologous recombination was selected on LB agar supplemented with nitrofurantoin (100 µg/ml, to counter-select *E. coli*) and tetracycline (15 µg/ml). (5) To select for excision of the plasmid vector, purified single crossover mutants were subjected to cycloserine enrichment as previously described (Zhang and Rainey, 2007). The double crossover mutants were tet-sensitive and produced white colonies on LB agar containing X-gal (60 µg/ml). The desired mutants can be distinguished from wild-type revertants by PCR and DNA sequencing.

Table S1. Stoichiometric analysis of the $HutC_{His6}$-P_{hutU} complexes performed using the Hilmar Bading's method on the basis of EMSA gel image shown in Figure 1.

	Migration Distance (cm)	HutC Molecular Weight (KDa)	Number of HutC
Complex d	4.75	119.74	4.19
Complex c	5.25	91.67	3.21
Complex b	5.80	66.38	2.32
Complex a	6.50	40.38	1.41
Free DNA	8.00	--	--

Table S2. Predicted HutC-binding sites in *P. fluorescens* SBW25

p-value	Matched Sequence[a]	Motif Location			Putative or established function of candidate genes[b]
		Start	End	Distance to candidate genes	
8.49E-09	TATA**TGTA**TA**TACA**AA	396038	396053	27 bp	PFLU0358: HutF
9.13E-09	TGCT**TGTA**TG**TACA**AG	397745	397760	71 bp	PFLU0361: HutU
1.21E-06	TCCA**TGTA**TA**AACA**AG	2682811	2682826	81bp to PFLU2467	PFLU2466: hypothetical protein. PFLU2467: AraC family transcriptional regulator.
2.49E-06	TATT**TGTA**TA**CAAA**AG	4800553	4800568	108 bp	PFLU4355: Xanthine/uracil permeases family protein.
3.69E-06	TATT**TGTA**TG**CACA**GA	6665739	6665754	120bp to PFLU6088	PFLU6087: N-acetylmuramoyl-L-alanine amidase in peptidoglycan catabolism. PFLU6088: GTP cyclohydrolase
4.59E-06	GATA**TGTT**TG**TACA**AG	3934565	3934580		
6.34E-06	TGTA**TGTA**TA**TACA**GC	957430	957445	40bp to PFLU0848	PFLU0848: Plc, phosphatidylcholine-hydrolyzing phospholipase C. PFLU0849: 5-dehydro-4-deoxyglucarate dehydratase, involved in D-glucarate degradation.
6.47E-06	TGTT**TGAA**TA**TTCA**AA	5361498	5361513	130 bp	PFLU4885: hypothetical protein. A LTXXQ domain-containing protein, which shows similarity to a pilus assembly protein.
7.22E-06	TGTA**TGCA**AA**TACA**AA	2875177	2875192	Overlap PFLU2604 start codon	PFLU2604: hypothetical protein, which shows similarity to the GCN5 family acetyltransferase.
8.74E-06	TGCT**TGTT**TA**TATA**AG	3019426	3019441	123bp	PFLU2736: hypothetical protein.
8.93E-06	TGTT**TGCA**TG**TTCA**AA	1819996	1820011	386 bp	PFLU1658: Fnl2, NAD dependent epimerase/dehydratase.
9.06E-06	TGTT**CGTT**TG**TACA**AG	5428854	5428869	155 bp	PFLU4947: hypothetical protein. Its identified ortholog is pilus assembly protein PilZ.
9.13E-06	TGCA**TGTA**TG**TGCA**TG	5770150	5770165	PFLU5255 coding region, 34bp from its start codon	PFLU5255: Hypothetical protein. Its ortholog is ribosome maturation protein RimP, which is important for maturation of the 30S ribosomal subunit.
1.14E-05	TATG**TGGA**TA**TAAA**AA	3125190	3125205		
1.15E-05	TATA**TCAA**TT**TACA**AG	1851392	1851407		

1.23E-05	CATA**TATA**TA**TAAA**AA	192404	192419	447 bp	PFLU0172: hypothetical protein.
1.56E-05	TATT**TATT**TA**TATA**AA	817631	817646	95bp to PFLU0709	PFLU0709: RspL, alternate sigma factor. PFLU0710: No information.
1.57E-05	TATT**TGTA**TG**TAGG**AC	4575786	4575801		
1.79E-05	GATT**TTTA**TA**TAGA**AG	4674453	4674468		
2.36E-05	TTTA**TGTT**TA**TAAA**AA	5295164	5295179	210 bp	PFLU4815: putative glutathione S-transferase like protein.
2.36E-05	TTTT**TGCA**TG**TACA**AC	3711537	3711552	230 bp to PFLU3353, overlap PFLU3354 start codon	PFLU3353: putative amidase, its ortholog is acyl-homoserine lactone acylase subunit beta, which is involved in quorum sensing. PFLU3354: hypothetical protein.
2.36E-05	TACC**TATA**TA**TACC**AG	5252378	5252393		
2.62E-05	TACT**CGTA**TT**TAGA**AG	3126232	3126247		
2.97E-05	TACT**CGTA**TA**TACA**TT	520016	520031	150bp to PFLU0460	PFLU0460: AceE, pyruvate dehydrogenase subunit E1. PFLU0461: bifunctional glutamine-synthetase adenylyltransferase/deadenyltransferase.
3.04E-05	TATT**TCGA**TA**CACA**AA	4779233	4779248	199 bp	PFLU4327: putative sulfatase.
3.17E-05	TATT**TGAC**TA**TAAA**AA	3433087	3433102	PFLU3141 coding region, 7bp from its start codon	PFLU3141: LipB, lipase.
3.19E-05	CAGT**TGTA**TG**CACA**TG	360518	360533	106 bp	PFLU0327: HisB, imidazoleglycerol-phosphate dehydratase.
3.29E-05	TATT**TATA**TG**AATA**AA	4501472	4501487	318 bp	PFLU4069: hypothetical protein.
3.37E-05	GATT**TGTA**TA**AATA**AG	2182043	2182058	247 bp	PFLU2013: CycA, D-serine/D-alanine/glycine transporter.
3.43E-05	TATA**TCGA**TA**TTCA**AG	4573285	4573300		
3.43E-05	TATT**CGTA**CA**TAGA**AG	6418864	6418879	106 bp	PFLU5862: ArgA, N-acetylglutamate synthase involved in arginine biosynthesis pathway.
3.54E-05	TATT**TTTT**TG**TAAA**AG	2045361	2045376	21 bp	PFLU1874: putative transporter-like acyltransferase protein. Its ortholog is glycerol acyltransferase.
3.54E-05	TATC**TGTC**TG**TACG**AA	4678701	4678716		
3.54E-05	TATG**TGTA**TG**AGCA**AG	1584681	1584696		
3.63E-05	TAAT**TGGT**TG**TACA**AG	3192681	3192696		
3.67E-05	TAAT**TGTG**AG**TACA**AG	6160944	6160959	275 bp	PFLU5623: GlcB, malate synthase G.
3.68E-05	TTTT**TGTA**GG**TAAA**AG	3761310	3761325		
3.79E-05	TATA**TGTC**GA**TCCA**AA	1060899	1060914		
3.79E-05	TATA**TGTG**AA**TACA**GA	3527700	3527715	91bp to PFLU3219	PFLU3218: putative TonB-dependent outer membrane receptor. PFLU3219: SyrP-like protein. SyrP is a regulatory protein involved in syringomycin production and virulence in *P. syringae*.
3.93E-05	GATA**TGCA**TA**TTCA**AA	4101662	4101677	Overlap PFLU3705 start codon	PFLU3705: hypothetical protein.
4.04E-05	TATA**TGAA**CA**TTCA**AA	4570067	4570082	PFLU4126B coding region, 27bp from its start	PFLU4126B: hypothetical protein.

				codon	
4.14E-05	TATA**GGTA**TG**TTAA**AA	1818852	1818867		
4.18E-05	TATA**TTTA**CG**TGCA**AA	2720248	2720263		
4.37E-05	TATT**TGGA**TG**TAAC**AA	3164038	3164053	2 bp	PFLU2900: hypothetical protein.
4.45E-05	CACT**TTTA**TG**TAAA**AA	3431252	3431267	79bp from PFLU3140	PFLU3139: hypothetical protein. PFLU3140: putative lipoprotein.
4.45E-05	CCAC**TGTC**CG**AACA**AC	377028	377043	300 bp	PFLU0344: NtrB, nitrogen-specific signal transduction histidine kinase.
4.45E-05	TATA**TGGA**TG**CAAA**AA	3468310	3468325	71bp to PFLU3176	PFLU3176: aspartate aminotransferase, which catalyzes the interconversion of aspartate and α-ketoglutarate to oxaloacetate and glutamate. PFLU3177: hypothetical protein. Its ortholog is NAD-dependent dehydratase.
4.45E-05	TATA**TTTA**TG**ACCA**AA	4101101	4101116		
4.56E-05	TATA**TCTT**TG**TCCA**AA	5824380	5824395	PFLU5305 coding region, 74bp from its start codon	PFLU5305: putative plasmid partitioning protein.
4.56E-05	TACA**TATT**TG**TAGA**AA	6297047	6297062		
4.61E-05	TATT**TCCA**TG**TACA**CA	6639456	6639471	80bp to PFLU6064	PFLU6064: GntR family transcriptional regulator. PFLU6065: putative regulatory protein.
4.71E-05	TACT**TCTA**GA**TGCA**AG	960179	960194	Overlap PFLU0851 start codon	PFLU0851: putative sugar ABC transporter membrane protein. Its ortholog is glucarate transporter.
4.81E-05	TACT**AGTA**TA**TAGA**GG	1612714	1612729	81bp to PFLU1465	PFLU1465: NadB, L-aspartate oxidase, which participates in alanine and aspartate metabolism. PFLU1467: AlgU, a sigma factor, which regulates genes involved in alginate biosynthesis.
4.95E-05	TATT**TGTA**CA**CACG**AG	2357140	2357155	287 bp	PFLU2175: hypothetical protein.
5.15E-05	TATT**GGTC**AA**TACA**AG	3188737	3188752		
5.28E-05	TATA**GGTA**CA**AACA**AG	4575654	4575669		
5.47E-05	TATT**TCTG**TG**TACA**CG	202548	202563		
5.74E-05	TATA**TGTA**CG**TATA**CG	2930280	2930295	Overlap PFLU2657 start codon, 230bp upstream of PFLU2658	PFLU2657: putative sulfite reductase. PFLU2658: hypothetical protein.
5.89E-05	TTCA**TGTC**TA**AACA**AA	2052141	2052156	305 bp	PFLU1879: hypothetical protein.
5.89E-05	TCTA**TGCA**TG**TCCA**AA	2691737	2691752	370 bp	PFLU2477: hypothetical protein.
5.99E-05	CACA**TGTA**CA**TACA**GA	2409875	2409890	260 bp	PFLU2222: putative ABC transporter membrane protein.
5.99E-05	TACA**TGTA**GA**TACT**CA	3192340	3192355	414 bp	PFLU2927: hypothetical protein.
5.99E-05	TACT**TGGA**GA**TACA**CA	5654723	5654738	228bp to PFLU5155, 0bp to PFLU5156	PFLU5155: putative MerR family transcriptional regulator. PFLU5156: hypothetical protein with very high similarity to antibiotic biosynthesis monooxygenase.
5.99E-05	AATA**CGTA**TG**TTCA**AA	2065013	2065028	Overlap PFLU1890 start codon	PFLU1890: hypothetical protein.

6.05E-05	TATT**TGGA**TG**AACC**AA	2069374	2069389		
6.05E-05	TATT**GGTA**TG**TGCA**TA	3168701	3168716		
6.17E-05	TACA**TGGA**AA**TCCA**AG	2730579	2730594	433 bp	PFLU2516: hypothetical protein, a TetR family transcriptional regulator.
6.17E-05	TATT**TGTT**TG**ATCA**AG	1968004	1968019	55bp to PFLU1804	PFLU1803: Gcl, glyoxylate carboligase, which participates in glycolate degradation. PFLU1804: hypothetical protein. Its ortholog is GlcG protein with unknown function.
6.21E-05	TATT**CGTA**AG**TACA**CG	2958127	2958142	31 bp	PFLU2681: PepN, aminopeptidase.
6.24E-05	AATT**TGTA**GG**TTCA**AG	4649122	4649137	63 bp	PFLUt63: tRNA-Glu.
6.25E-05	TACT**CGTA**TG**AAGA**AG	5761130	5761145	Overlap PFLU5248 start codon	PFLU5248: osmotically inducible protein Y.
6.32E-05	TGTT**TTTA**TA**TACA**GT	54429	54444	16 bp	PFLU0054: hypothetical protein with very high similarity to DNA repair photolyase.
6.32E-05	TGAT**CGTA**TC**TACA**AG	4367523	4367538		
6.37E-05	TGCG**TTTA**TC**TACA**AG	5381873	5381888		
6.37E-05	TTCA**TGTA**TG**TACT**GG	5604071	5604086	447 bp	PFLU5103: hypothetical protein.
6.43E-05	TGCA**TGGA**TT**TACA**AT	829311	829326	248 bp	PFLU0727: RspB, putative type III secretion protein.
6.43E-05	TGTA**TGTA**TT**AATA**AA	2164052	2164067	22bp to PFLU1992	PFLU1992: hypothetical protein, showing high similarity to amidase. PFLU1993: GntR family transcriptional regulator.
6.49E-05	CACA**TGGA**TG**TACA**CA	4109407	4109422		
6.52E-05	TGTT**TTTT**TC**TACA**AG	5256428	5256443		
6.62E-05	TACT**CGTC**TG**TACG**AG	5539401	5539416	65bp to PFLU5040	PFLU5040: PTS system sucrose-specific transporter subunit IIBC. PFLU5041: trehalose operon transcriptional repressor.
6.68E-05	TGTT**TGTA**TA**GACA**GT	1303654	1303669	93bp to PFLU1167	PFLU1166: hypothetical protein. PFLU1167: putative regulatory protein, its ortholog is transcriptional repressor PrtR which regulates pyocin-producing genes.
6.78E-05	TGTA**TGCA**TA**TACA**GT	1304632	1304647	441 bp	PFLU1169: hypothetical protein.
6.79E-05	TGAA**TGTG**TA**AACA**AA	3336181	3336196		
6.86E-05	TGTA**CGTA**TT**TACC**AA	3708943	3708958	134 bp	PFLUt50: tRNA-Cys.
6.86E-05	TGTC**TGTA**TG**CAAA**AA	3777730	3777745		
6.95E-05	TGTC**GGTA**TA**AACA**AG	4334862	4334877	147 bp	PFLU3927: DNA-binding ATP-dependent protease La; heat shock K-protein.
6.99E-05	GGCA**TATA**TC**TACA**AG	3832062	3832077		
7.03E-05	AGCA**TGGA**TA**TACA**AC	6590392	6590407	447 bp	PFLU6027: hypothetical protein.
7.04E-05	TGTT**TATA**AA**TGCA**AA	5351550	5351565	292bp to PFLU4872	PFLU4870: aromatic amino acid transport protein. PFLU4872: hypothetical protein with high similarity to leucyl aminopeptidase (aminopeptidase T).
7.04E-05	TGTA**TGTT**TG**TACA**GC	1918052	1918067	25 bp	PFLU1750: hypothetical protein, a highly conserved transcriptional regulator in *Pseudomonas*.
7.13E-05	TGTA**TGGA**TG**TACA**GC	2337963	2337978	69 bp	PFLU2157: TopB, DNA topoisomerase III.

7.16E-05	TGTA**TGTA**TG**AACA**GT	3123864	3123879	20 bp	PFLU2842: hypothetical protein. Its ortholog is ATP-dependent hsl protease ATP-binding subunit hslU.
7.18E-05	TGTA**ATTG**TA**TACA**AG	1967841	1967856	22bp to PFLU1803	PFLU1803: Gcl, glyoxylate carboligase, which participates in glycolate degradation. PFLU1804: hypothetical protein. Its ortholog is GlcG protein with unknown function.
7.24E-05	TGCG**TGAA**TA**TCCA**AA	5683522	5683537	33 bp	PFLU5187: putative amino acid transporter membrane protein.
7.24E-05	CGAA**TGTT**TG**TACA**AA	127586	127601		
7.27E-05	TGGT**TGTC**TG**TTCA**AA	2366894	2366909		
7.27E-05	GGAT**TGCA**TG**TACA**AG	4094071	4094086	Overlap PFLU3698 start codon, 374bp upstream of PFLU3699	PFLU3698: putative TonB-dependent outer membrane receptor protein. PFLU3699: putative GGDEF domain signaling protein.
7.29E-05	TGCT**TGTA**AA**GATA**AA	445895	445910	99bp to PFLU0402	PFLU0402: PriA, primosome assembly protein. PFLU0403: RpmE, 50S ribosomal protein L31.
7.39E-05	TGCA**TTTA**TA**TCCA**CA	2201527	2201542		
7.44E-05	TGCT**TATC**GA**TACA**AA	2574931	2574946	122 bp	PFLU2365: putative TonB-dependent siderophore receptor.
7.52E-05	GGTA**GGGA**TA**TACA**AA	3018076	3018091	5 bp	PFLU2734: hypothetical protein.
7.61E-05	GGTA**TGTA**TA**TACG**TA	3255865	3255880	32bp from PFLU2987	PFLU2987: putative phage cointegrase resolution protein. PFLU2988: TnpS, cointegrase.
7.87E-05	CGTA**GGTA**TA**TACA**CA	5503929	5503944	116 bp	PFLU5008: XerD, site-specific tyrosine recombinase.
7.87E-05	TGCA**TGAA**TA**GATA**AA	5540677	5540692	21 bp	PFLU5042: putative regulatory protein.
7.92E-05	TGCA**GGTC**TG**TACA**AC	2315111	2315126		
7.98E-05	TGCT**GGTC**TG**TACA**AT	4750305	4750320	24 bp	PFLU4307: TenA family transcriptional regulator.
7.98E-05	TGTT**TGTC**TG**AAAA**AA	2489624	2489639	351 bp	PFLU2290: putative acetyl-CoA synthetase.
8.08E-05	TGTT**TGTC**TG**AAAA**AA	2490009	2490024		
8.14E-05	TGCA**TCTA**TG**TAAA**TA	3330114	3330129		
8.25E-05	TGTT**TGTC**TG**TGAA**AA	3391717	3391732		
8.32E-05	TGCA**TCAA**TG**TAAA**AA	792973	792988		
8.35E-05	TGCA**TGTA**TA**CCGA**AG	2443235	2443250		
8.38E-05	AGCT**TTTA**TA**TTCA**AG	3752558	3752573		
8.49E-05	GGCT**TCTA**TA**AACA**AG	4361503	4361518		
8.57E-05	TGCA**TGTA**TA**TAAT**GG	5544003	5544018	34 bp	PFLU5044: inosine 5'-monophosphate dehydrogenase.
8.57E-05	CGTA**TCTA**TG**CACA**AG	1513619	1513634		
8.67E-05	TGTT**TCGG**TG**TACA**AG	4620202	4620217		
8.67E-05	TGCG**TGTG**TG**TACA**CG	2550391	2550406		
8.87E-05	TGCT**TGTA**GA**AACC**AA	5013760	5013775		
8.99E-05	TGCT**TGCA**TA**GCCA**AA	1627083	1627098		
8.99E-05	TGCA**TGTT**TA**TCCA**CA	5014262	5014277		
9.14E-05	TGCT**TCTG**TG**TACA**TA	1360685	1360700		

9.23E-05	CGCA**TGTT**TG**TAGA**AA	2011553	2011568		
9.23E-05	TGCA**TTTA**TG**TCCC**AA	6232815	6232830	Overlap PFLU5686 start codon	PFLU5686: BetA, choline dehydrogenase
9.23E-05	CGCA**AATA**TG**TACA**AA	935972	935987	157 bp	PFLU0826: DppA3, dipeptide ABC transporter substrate-binding protein.
9.26E-05	TGTT**TGTC**TG**TACG**TA	3251963	3251978	80 bp	PFLU2983: putative lipoprotein.
9.28E-05	TGCT**TGTA**AG**TTTA**AA	6251444	6251459	90 bp	PFLU5700: hypothetical protein.
9.32E-05	TGCA**GGTA**GA**GACA**AG	3028964	3028979	PFLU2745 coding region, 24bp from its start codon	PFLU2745: putative ABC transporter mannitol-binding protein.
9.39E-05	TGCT**TTTT**TG**TTCA**AG	75295	75310	100 bp	PFLU0074: ZnuC, high-affinity zinc ABC transporter ATP-binding protein.
9.39E-05	TGTT**TGCA**GG**TACA**CG	709299	709314	401 bp	PFLU0626: SpeA, arginine decarboxylase.
9.46E-05	TGTT**TGTG**TG**AACA**GG	2914511	2914526	286 bp	PFLU2640: putative substrate-binding transport protein.
9.46E-05	TGCT**TGTA**AG**AAAA**AG	6506555	6506570		
9.46E-05	TGCA**TATA**TG**ACCA**AG	6578846	6578861	77bp to PFLU6018	PFLU6017: Homologue of a type VI secretion protein. PFLU6018: Homologue of the type VI secretion protein ImpA.
9.48E-05	TGCT**GGGA**TG**TACA**CA	52910	52925	149 bp	PFLU0053: AdhB, alcohol dehydrogenase cytochrome C subunit.
9.57E-05	TGCT**TGTC**TG**CACG**AA	875808	875823	7bp to PFLU0773	PFLU0772: a type IV pilus-like protein. PFLU0773: hypothetical protein. Its ortholog is pilus assembly protein PilV.
9.57E-05	GGCA**AGTA**GG**TACA**AA	1909814	1909829	73 bp	PFLU1740: putative two-component system response regulator, LuxR family transcriptional regulator.
9.57E-05	TGCA**GGTA**CG**TGCA**AA	3122089	3122104	240 bp	PFLU2839: hypothetical protein.
9.57E-05	TGCA**TGGA**TG**AACG**AG	486244	486259	62bp to PFLU0439	PFLU0438: homologue of 3-oxoacyl-ACP synthase in fatty acid biosynthesis. PFLU0439: putative chromosome partitioning ParA-like protein.
9.64E-05	CGCA**TGGA**TG**TGCA**AG	1174625	1174640	398 bp	PFLU1062: RecO, DNA repair protein.
9.72E-05	TGCT**TGTA**CG**TCCA**GG	3067587	3067602	257 bp	PFLU2774: 3-phosphoshikimate 1-carboxyvinyltransferase involved in aromatic amino acid biosynthesis.
9.75E-05	TGCA**TGCC**AG**TACA**AG	3799694	3799709	197 bp	PFLU3431: hypothetical protein.
9.82E-05	GGCT**TGAA**TG**TGCA**AG	4276360	4276375		
9.93E-05	GGCA**TGGA**TG**TACA**TG	6436208	6436223	235 bp	PFLU5879: 2-octaprenyl-6-methoxyphenyl hydroxylase, which is involved in ubiquinone biosynthesis and oxidation-reduction process.

[a] Conserved palindromic half sites (Phut-I and Phut-II) are highlighted in bold font.

[b] Genes shown here contain the related HutC-binding site in their regulatory region spanning from -500 bp to +100 bp relative to the first nucleotide of the start codon. Candidates in red font have been subjected to experimental verification by EMSA with purified $HutC_{His6}$.

Table S3. Oligonucleotides used in this work

Primer	**Sequence (5′ - 3′)[a]**	**Application**
HutC-ProF	aaatttaccatgggccatcatcatcatcatCCGACTCC GCCCGCCAAGTCTC	Expression of HutC protein from SBW25
HutC-ProR	aaatttgaagcttGCGCCAGACGCTTATTGCACTC AT	
PhutU_D	aaatttactagtATTTGTTACCGAATGCCCCAGC	Amplifying PhutU-325 probe DNA
Bio-UR[b]	GCTTGTTACCGTGGGCGGCACGGAT	
PhutU_B	aaatttactagtGTCGGTACATCTATGACTGAAAC	Mutagenizing Phut-I site in P_{hutU} promoter
PhutU-mut1	cttgtacaccggAGCATATGCAATCGAG	
PhutU-mut2	catatgctccggTGTACAAGTAAAGATGTG	
hutU-T7R2	TGTTCATCAGCATGCGCAGC	
PhutU-mut3	atctttacggccACATACAAGCATATGCAA	Mutagenizing Phut-II site in P_{hutU} promoter with primers PhutU_B and hutU-T7R2
PhutU-mut4	ttgtatgtggccGTAAAGATGTGTGCGTAA	
hutU-M1	ttacggccacaccggAGCATATGCAATCGAGCGG CCA	Mutagenizing Phut-I and Phut-II site in P_{hutU} promoter with primers PhutU_B and hutU-T7R2
hutU-M2	atgctccggtgtggccGTAAAGATGTGTGCGTAAG AG	
PhutU_Rev	aaatttctgcagAGCTTGTTACCGTGGGCGGC	P_{hutU} transcriptional fusion to lacZ with primer PhutU_D
ntrB-SpeI	gactaGTATTACCGGCAACACCCCGGTCGA	Amplifying PntrBC-154 probe DNA
Bio-ntrR3[b]	ATGAAGGTTGTTCAGGAAGTGG	
ntrB-HindIII	gaagcttGCTGATGGTCATTGGGACCTCTT	Mutagenizing Phut site in P_{ntrBC} promoter
PntrBM2-1	TCATGGGATGGCACACCTTAC	
PntrBM2-2	tgccaccacttaggtcACACTGATCCATCCCCCACT	
PntrBM2-3	agtgtgacctaagtgGTGGCATGCCCGGACGGCC CGCGT	
P2467-F	GAAGGACTTGGGTTCACCGT	Amplifying P2467 probe DNA
P2467-R	CATGGGCATGCACATCGATC	
PaceE-F	CATAGTTGTTGGCAGGGAAC	Amplifying PglnE probe DNA
PaceE-R	TCTTGCATGGCTTGCTCCAG	
PhisB-F	AGCCACCTCGTTCTTTCAGT	Amplifying PhisB probe DNA
PhisB-R	TTACGTTCGGCCATCACCAG	
P6088-F	TTGCGTATCTGTGTGGCGTG	Amplifying PamiA probe DNA
P6088-R	CATGAGCAGGTCCATCGTTG	
P4947-F	GCGTCCAGCTTCGTTATGATG	Amplifying PpilZ probe DNA
P4947-R	CATGGTGAGATCGCCATCCA	
P2987-F	CATGGGAGGCCTTTGTGTAC	Amplifying PtnpS probe DNA
P2987-R	AGGCGTGCCGTTTGAACTAC	
Bio-plc[b]	CTGCGAGTTCAAGACCTGACAT	Amplifying PplcC probe DNA
plc-R	ggactagtGGACTTCAGTTCTTGTGGATTC	
ntrB-SpeI	gactaGTATTACCGGCAACACCCCGGTCGA	Transcriptional *lacZ* fusion to P_{ntrBC}
ntrB-HindIII	gaagcttGCTGATGGTCATTGGGACCTCTT	
plc-F	ggaagcttCTGCGAGTTCAAGACCTGACAT	P_{plcC} transcriptional fusion to *lacZ* with primer plc-R
hutC7	gaagatCTGCAAGGATTCCCTGTGCC	*hutC* overexpression with primer HutC-ProR
hutF1	gaagatCTGATCTGACGCGACAGTTC	*hutC* deletion

hutC-del2	aagctatgacGCACAGGGAATCCTTGCAG	
hutC-del3	attccctgtgCGTCATAGCTTGGAAGGAC	
hutD1	gaagatctTGGGTCAGTTCGATCAGGC	

[a] Artificial sequences integrated into the primers are shown in lowercase with restriction sites underlined.
[b] Primers are labeled by biotin at the 5′ end.