SUPPLEMENTARY INFORMATION

Transcriptional regulation by BglJ-RcsB, a pleiotropic heteromeric transcriptional activator in *Escherichia coli*

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The supplementary information includes Tables S1 (*E. coli* K12 strains), S2 (Plasmids), S3 (Oligonucleotides), and supplementary references (52,53).

Table S1 ***E. coli* K12 *s*trains**

Strain	relevant genotype [a]	Reference / Construction [a]
BW30270	= MG1655 *rph*$^+$ Laboratory collection No S3839	Datsenko and Wanner, deposited at the Coli Genetic Stock Center #7925
S1734	*bglJ*$_C$ (constitutive *bglJ* expression, allele *yjjQ/bglJ*-Y6::mTn10-cmR)	(31)
BRE2055	BRE2047 Δ*crp96 zhd-732*::Tn10	(52)
S541	Δ*bgl* Δ*lacZ ara thi*	(26)
S3010	S541 Δ*hns*::kanR$_{KD4}$	(4)
S3910	S541 *bglJ*$_c$ (cmR)	S541 x T4*GT7* (S1734)
S3974	BW30270 *ilvG*$^+$ (not motile)	(4)
S4197	S3974 Δ*lacZ*	(4)
T314	S4197 Δ*leuO*$_{FRT}$ Δ(*yjjP-yjjQ-bglJ*)$_{FRT}$	(20)
T1032	S4197 Δ*leuO*$_{FRT}$ *bglJ*$_c$ (cmR)	(20)
T15	S4197 *ΔrcsB*::kanR$_{KD4}$	(4)
T23	S4197 Δ(*yjjP-yjjQ-bglJ*)$_{FRT}$	(20)
T75	S3974 Δ(*yjjP-yjjQ-bglJ*)$_{FRT}$	(20)
T1030	S4197 *bglJ*$_c$ (cmR, Bgl$^+$)	S4197 x T4*GT7* (S1734)
T1048	S3974 Δ(*yjjP-yjjQ-bglJ*)$_{FRT}$ Δ*hns*$_{FRT}$ *stpA*::Tet^R	(20)
T1166	S3974 *bglJ*$_C$ (cmR, Bgl$^+$)	x T4*GT7* (S1734)
Strains with insertions of promoter *lacZ* fusions at *attB* (derivatives of T314)		
T1188	attB::[*PchiA lacZ* spec^R]	T314/pLDR8 x pKESL9
T1478	attB::[*PchiA lacZ* spec^R] *bglJ*$_c$ (cmR)	T1188 x T4GT7 (S1734)
T1772	attB::[*PchiA lacZ* spec^R] *bglJ*$_c$ (cmR) *ΔrcsB*::kanR$_{KD4}$	T1478 x T4GT7 (T15)
T1191	attB::[*PmolR lacZ* spec^R]	T314/pLDR8 x pKESL3
T1441	attB::[*PmolR lacZ* spec^R] *bglJ*$_c$ (cmR)	T1191 x T4GT7 (S1734)
T1773	attB::[*PmolR lacZ* spec^R] *bglJ*$_c$ (cmR) *ΔrcsB*::kanR$_{KD4}$	T1441 x T4GT7 (T15)
T1226	attB::[*PmolR*$_{mut}$ *lacZ* spec^R]	T314/pLDR8 x pKESL13
T1444	attB::[*PmolR*$_{mut}$ *lacZ* spec^R] *bglJ*$_c$ (cmR)	T1226 x T4GT7 (S1734)
T1181	attB::[*PsfsB lacZ* spec^R]	T314/pLDR8 x pKESL5
T1436	attB::[*PsfsB lacZ* spec^R] *bglJ*$_c$ (cmR)	T1181 x T4GT7 (S1734)
T1774	attB::[*PsfsB lacZ* spec^R] *bglJ*$_c$ (cmR) *ΔrcsB*::kanR$_{KD4}$	T1436 x T4GT7 (T15)
T1228	attB::[*PsfsB*$_{mut}$ *lacZ* spec^R]	T314/pLDR8 x pKESL15
T1446	attB::[*PsfsB*$_{mut}$ *lacZ* spec^R] *bglJ*$_c$ (cmR)	T1228 x T4GT7 (S1734)
T1186	attB::[*PyecT lacZ* spec^R]	T314/pLDR8 x pKESL8
T1476	attB::[*PyecT lacZ* spec^R] *bglJ*$_c$ (cmR)	T1186 x T4GT7 (S1734)
T1775	attB::[*PyecT lacZ* spec^R] *bglJ*$_c$ (cmR) *ΔrcsB*::kanR$_{KD4}$	T1476 x T4GT7 (T15)
T1189	attB::[*PygiZ lacZ* spec^R]	T314/pLDR8 x pKESL10
T1438	attB::[*PygiZ lacZ* spec^R] *bglJ*$_c$ (cmR)	T1189 x T4GT7 (S1734)
T1776	attB::[*PygiZ lacZ* spec^R] *bglJ*$_c$ (cmR) *ΔrcsB*::kanR$_{KD4}$	T1438 x T4GT7 (T15)
T1236	attB::[*PygiZ*$_{mut}$ *lacZ* spec^R]	T314/pLDR8 x pKESL20
T1450	attB::[*PygiZ*$_{mut}$ *lacZ* spec^R] *bglJ*$_c$ (cmR)	T1236 x T4GT7 (S1734)

Table S1	***E. coli* K12 *s*trains**	
Strain	**relevant genotype** [a]	**Reference / Construction** [a]
T1184	attB::[*PyidL lacZ* spec^R]	T314/pLDR8 x pKESL7
T1474	attB::[*PyidL lacZ* spec^R] *bglJ$_c$* (cmR)	T1184 x T4GT7 (S1734)
T1777	attB::[*PyidL lacZ* spec^R] *bglJ$_c$* (cmR) *ΔrcsB*::kanR$_{KD4}$	T1474 x T4GT7 (T15)
T1579	attB::[*PyidL$_{mut}$ lacZ* spec^R]	T314/pLDR8 x pKESL92
T1581	attB::[*PyidL$_{mut}$ lacZ* spec^R] *bglJ$_c$* (cmR)	T314/pLDR8 x pKESL92
T1177	attB::[*PykiA lacZ* spec^R]	T314/pLDR8 x pKESL1
T1472	attB::[*PykiA lacZ* spec^R] *bglJ$_c$* (cmR)	T1177 x T4GT7 (S1734)
T1778	attB::[*PykiA lacZ* spec^R] *bglJ$_c$* (cmR) *ΔrcsB*::kanR$_{KD4}$	T1472 x T4GT7 (T15)
T1552	attB::[*PykiA$_{mut}$ lacZ* spec^R]	T314/pLDR8 x pKESL41
T1557	attB::[*PykiA$_{mut}$ lacZ* spec^R] *bglJ$_c$* (cmR)	T314/pLDR8 x pKESL41
T1179	attB::[*PynbA lacZ* spec^R]	T314/pLDR8 x pKESL2
T1326	attB::[*PynbA lacZ* spec^R] *bglJ$_c$* (cmR)	T1179 x T4GT7 (S1734)
T1779	attB::[*PynbA lacZ* spec^R] *bglJ$_c$* (cmR) *ΔrcsB*::kanR$_{KD4}$	T1326 x T4GT7 (T15)
T1224	attB::[*PynbA$_{mut}$ lacZ* spec^R]	T314/pLDR8 x pKESL12
T1442	attB::[*PynbA$_{mut}$ lacZ* spec^R] *bglJ$_c$* (cmR)	T1224x T4GT7 (S1734)
T1183	attB::[*PynjI lacZ* spec^R]	T314/pLDR8 x pKESL6
T1327	attB::[*PynjI lacZ* spec^R] *bglJ$_c$* (cmR)	T1183 x T4GT7 (S1734)
T1780	attB::[*PynjI lacZ* spec^R] *bglJ$_c$* (cmR) *ΔrcsB*::kanR$_{KD4}$	T1327 x T4GT7 (T15)
T1230	attB::[*PynjI$_{mut}$ lacZ* spec^R]	T314/pLDR8 x pKESL16
T1448	attB::[*PynjI$_{mut}$ lacZ* spec^R] *bglJ$_c$* (cmR)	T1230 x T4GT7 (S1734)
T1180	attB::[*PyqhG lacZ* spec^R]	T314/pLDR8 x pKESL4
T1473	attB::[*PyqhG lacZ* spec^R] *bglJ$_c$* (cmR)	T1180 x T4GT7 (S1734)
T1781	attB::[*PyqhG lacZ* spec^R] *bglJ$_c$* (cmR) *ΔrcsB*::kanR$_{KD4}$	T1473 x T4GT7 (T15)
T568	attB::[*Pbgl* t1$_{RAT}$ *bglG lacZ* spec^R]	(4)
T1432	T568 *bglJ$_c$* (cmR)	T568 x T4GT7 (S1734)
T1500	T568 Δ*crp96 zhd-732*::Tn10	T568 x T4GT7 (BRE2055)
T1502	T568 Δ*crp96-zhd-732*::Tn10 *bglJ$_c$* (cmR)	T1432 x T4GT7 (BRE2055)
T729	T568 *hns$_{FRT}$*	(4)
T580	attB::[*Pbgl*_BglJ-RcsB$_{mut1}$ t1$_{RAT}$ *bglG lacZ* spec^R]	(4)
T1434	T580 *bglJ$_c$* (cmR)	T580 x T4GT7 (S1734)
T1501	T580 Δ*crp96 zhd-732*::Tn10	T580 x T4GT7 (BRE2055)
T1503	T580 *bglJ$_c$* (cmR) Δ*crp96 zhd*-732::Tn10	T1434 x T4GT7 (BRE2055)
T735	T580 *hns$_{FRT}$*	(4)
T1413	attB::[*Pbgl*_CRP$_{mut}$ t1$_{RAT}$ *bglG lacZ* spec^R]	T314/pLDR8 x pKESL46
T1507	T1413 *bglJ$_c$* (cmR)	T1413 x T4GT7 (S1734)
T1504	T1413 Δ*crp*96 *zhd-732*::Tn10	T1413 x T4GT7 (BRE2055)
T1550	T1413 *bglJ$_c$* (cmR) Δ*crp96 zhd-732*::Tn10	T1507 x T4GT7 (BRE2055)
T1543	T1413 Δ*hns*::kan$_{KD4}$	T1413 x T4GT7 (S3010)
T1465	attB::[*Pbgl*_BglJ-RcsB$_{mut1}$_CRP$_{mut}$ t1$_{RAT}$ *bglG lacZ* spec^R]	T314/pLDR8 x pKESL47
T1493	T1465 *bglJ$_c$* (cmR)	T1465 x T4GT7 (S1734)
T1506	T1465 Δ*crp96 zhd-732*::Tn10	T1465 x T4GT7 (BRE2055)
T1530	T1465 *bglJ$_c$* (cmR) Δ*crp96 zhd-732*::Tn10	T1493 x T4GT7 (BRE2055)
T1545	T1465 Δ*hns*::kan$_{KD4}$	T1465 x T4GT7 (S3010)

[a] Strain construction was performed as described previously (15,26). Bacteriophage T4*GT7* (28) was used for transduction with the donor strains given in brackets. Transductants of the *bglJ$_c$* (cmR) allele were selected on LB chloramphenicol plates and analyzed by PCR. Co-transduction of Δ*crp96* with *zhd-732*::Tn10 was screened on MacConkey Maltose plates, and Maltose negative colonies were taken. Integration of reporter constructs into the phage λ *attB* site was performed using origin-less re-ligated BamHI fragments of the plasmids, which carry a promoter *lacZ* fusion, the *attP*-site for integration, and the *aadA* gene for selection on LB spectinomycin plates. These orgin-less circular DNA molecules were used to transform strain T314 carrying the *int* expressing helper-plasmid pLDR8 (25,26).

Table S2	**Plasmids**	
Plasmid	**Features** [a, b]	**Reference / Construction** [c, d, e]
pDCRP	*crp* in pBR-ori ampR	(35)
pDCRP-H159L	*crp*-H159L (CAC->CTG) in pBR-ori ampR	(35)
pDCRP-H19L (=pKES324)	*crp*-H19L (CAC->CTC) in pBR-ori ampR	this work [c]
pDCRP-K101E (=pKES328)	*crp*-K101E (AAA->GAA) in pBR-ori ampR	this work [c]
pDctrl (=pKES325)	vector control for pDCRP (= pBR-ori ampR), sequence at BamHI, SalI fusion is GAATTCCCGGGGATCcgaccgatgcccttga	pDCRP BamHI, SalI, re-ligated
pFMAC20	*E-Pbgl t1 bglG lacZ* p15A-ori kanR attP specR	(53)
pFMAC19	pFMAC20 with CAATTG insertion at -61,5 relative to *P2bgl*	(53)
pKES209	pFMAC20 with CAATTG insertion at -69,5 relative to *P2bgl*	this work [d]
pKES203	pFMAC20 with CAATTG insertion at -80,5 relative to *P2bgl*	this work [d]
pKES205	pFMAC20 with CAATTG insertion at -84,5 relative to *P2bgl*	this work [d]
pKES207	pFMAC20 with CAATTG insertion at -88,5 relative to *P2bgl*	this work [d]
pLDR8	cI_{857} P_R λ-*int* in pSC101 rep^{ts} kanR	(25)
pKES268	*PlacUV5* MCS *lacZ* p15A-ori kanR attP specR	this work [e]
pKESL9	*PchiA* (pos:3468190-3467882) *lacZ*	cloned PCR fragment T672, T673
pKESL3	*PmolR*(*yehH*) (pos:2194338-2194505) *lacZ*	cloned PCR fragment T658, T659
pKESL13	$PmolR_{mut}$ (TTCTTT**aga**AAAT**ag**CTAAAG) *lacZ*	T699 for mutagenesis
pKES329	*PmolR* 5bp insertion *lacZ*	this work [f]
pKES330	*PmolR* 10bp insertion *lacZ*	this work [f]
pKESL5	*PsfsB* (pos:3332698-3352942) *lacZ*	cloned PCR fragment T662, T663
pKESL15	$PsfsB_{mut}$ (ATCTTT**ga**ATAT**ag**TGAATA) *lacZ*	T701 for mutagenesis
pKESL8	*PyecT* (pos:1959790-1960001) *lacZ*	cloned PCR fragment T676, T677
pKESL4	*PyqhG* (pos:3155455-3155686) *lacZ*	cloned PCR fragment T660, T661
pKESL10	*PygiZ* (pos:3170219-3170566) *lacZ*	cloned PCR fragment T674, T675
pKESL20	$PygiZ_{mut}$ (GGATAA**ga**ATTT**ag**TGAAAA) *lacZ*	T705 for mutagenesis
pKESL7	*PyidL* (pos:3858054-3878320) *lacZ*	cloned PCR fragment T668, T669
pKESL92	$PyidL_{mut}$ (GCAGTCAGAT**ag**TTAAAATA) *lacZ*	T816 for mutagenesis
pKES331	*PyidL* 5bp insertion *lacZ*	this work [f]
pKES332	*PyidL* 10bp insertion *lacZ*	this work [f]
pKESL1	*PykiA* (pos:0407683-0407892) *lacZ*	cloned PCR fragment T654, T655
pKESL41	$PykiA_{mut}$ (GGAGGGCATTTT**ag**TGAAAT) *lacZ*	T765 and T812 for mutagenesis
pKESL2	*PynbA* (pos:1475436-1475662) *lacZ*	cloned PCR fragment T656, T657
pKESL12	$PynbA_{mut1}$ (ACCTTG**ga**ATAT**ag**TGAATT) *lacZ*	T698 for mutagenesis
pKESL6	*PynjI* (pos:1843066-1842886) *lacZ*	cloned PCR fragment T664, T665
pKESL16	$PynjI_{mut1}$ (TTCGAG**ga**ATAT**ag**TGAAAT) *lacZ*	T702 for mutagenesis
pKENV61	*Pbgl* $t1_{RAT}$ *bglG lacZ*	(50)
pKES222	*Pbgl*_BglJ-$RcsB_{mut1}$ (AACTTTATAAATagCTAAAAT) $t1_{RAT}$ *bglG lacZ*	(4)
pKESL46	*Pbgl*_CRP_{mut} (AACacCGACGATCCTCATTTT) $t1_{RAT}$ *bglG lacZ*	primer T770 for mutagenesis amplified from template pKENV61
pKESL47	*Pbgl*_BglJ-$RcsB_{mut1}$_CRP_{mut} $t1_{RAT}$ *bglG lacZ*	primer T770 for mutagenesis amplified from template pKES222

[a] Unless otherwise stated the vector backbone of the plasmids carry a p15A derived origin of replication, the *neo* gene conferring kanamycin resistance (kanR), the *aadA* gene conferring spectinomycin resistance (specR), and the phage λ attP site, as described (26).

[b] Positions in brackets refer to the reference genome sequence NC_000913 of *E. coli* K12 strain MG1655. Sequences in bracket refer to presumptive BglJ-RcsB binding sites with site-specific mutations shown in lower case bold letters.

[c] Plasmids expressing *crp* mutants were constructed by cloning overlapping PCR fragments into the SalI, BamHI digested pDcrp plasmid DNA. The PCR fragments were generated using oligonucleotides T870 and T871 for mutagenesis of residue 19, oligonucleotides T940 and T941 for mutagenesis of residue 101, oligonucleotides T24 and S527 for amplification, and pDCRP as template.

[d] Plasmids carrying 6bp CAATTG insertions within the *bgl* regulatory region were generated by MunI digestion of plasmids carrying insertions of *lacO* (53). *E-Pbgl* carries a 1 bp exchange from A to G at position -79/-99 relative to the transcription start sites of *P2bgl* and *Pbgl* generating an EcoRI-site (53).

[e] Plasmid pKES268 was used as cloning vector, pKES268 carries a *lacUV5* promoter fragment flanked by a SalI restriction site (upstream) and a multiple cloning site (MCS) including a XbaI site (downstream). The SalI and XbaI sites were used for cloning of promoter fragments amplified by PCR using cells of strain BW30270 as template.

[f] The derivatives of *PmolR* and *PyidL lacZ* fusions with 5bp and 10 bp duplications in between the BglJ-RcsB binding site and the promoter were constructed by overlapping PCR using oligonucleotides T932 and T933 (*PmolR* +5bp), T934 and T935 (*PmolR* +10bp), T936 and T937 (*PyidL* +5bp), and T938 and T939 (*PyidL* +10bp).

Table S3 Oligonucleotides

No	Sequence [a]	Purpose
S527	AAGAATTCGCCGGCTTCCATTCAGGT	*crp* cloning, maps in vector backbone
T24	GAAAAGTGCCACCTGACGTCTAA	*crp* cloning, maps in vector backbone
T265	GCGCGAATTCCTGTAGAACGA	5'RACE EcoRI
T268	AUAUGCGCGAAUUCCUGUAGAACGAACACUAGAAGAAA	5'RACE RNA adapter
T654	gtcagtcgacTAATTCCTCGCCTTCCCCTTG	PykiA cloning
T655	gtcatctagaTGCACGCCACCATTCATCAT	PykiA cloning
T656	gtcagtcgacCGGGAACAAGCGATGAGAAAA	PynbA cloning
T657	gtcatctagaTATCTGGTAGAGCGTCATTATCAATCCT	PynbA cloning
T658	gtcagtcgacGGTCATCAGGTGAAATAATCCCCC	PmolR cloning
T659	gtcatctagaAGTGTCTCATTCTGCATCCCTGTAATT	PmolR cloning
T660	gtcagtcgacGACCAGTTCGGCGGCTAACAT	PyqhG cloning
T661	gtcatctagaAAGTATTATTTTCATCTGTTTTTCACCTCTCC	PyqhG cloning
T662	gtcagtcgacCGTTAATCCCCTCCCCTCATC	PsfsB cloning
T663	gtcatctagaATTACTTTCCATTTTTCCTCACTCCTTA	PsfsB cloning
T664	gtcagtcgacAAAGTCCGCCAGCAGATGAAGTC	PynjI cloning
T665	gtcatctagaCTTTTTTCATCACATTCCCTGTTATTACATACT	PynjI cloning
T666	gtcagtcgacCGGGTGGGGGATAATTCA	PyiaBA cloning
T667	gtcatctagaCTTTGAGGTTTTCATAACGATCTCCATAT	PyiaBA cloning
T668	gtcagtcgacGTATCTGTTTTGCGGACCTTCCAC	PyidL cloning
T669	gtcatctagaCAATTTTCCATTCATTTTAATATCCCTCC	PyidL cloning
T670	gtcagtcgacGACTTTCGCCTTTATTTGGGTGG	PyigGF cloning
T671	gtcatctagaTCTGGAAATCTTACCGTTAGATGTTGG	PyigGF cloning
T672	gtcagtcgacGTTGTTGCTAAAGTTCTGGGCTAATT	PchiA cloning
T673	gtcatctagaCCCTTGTGACGTAAAAACTGCAAA	PchiA cloning
T674	gtcagtcgacCAGGATGTTGCTCATTTTTTAACCTC	PygiZ cloning
T675	gtcatctagaTTTCTGCTTTAACATATATCAGTACGCTCAT	PygiZ cloning
T676	gtcagtcgacCTGGGTATTGAGACTGTAGAGCGTATGTAA	PyecT cloning
T677	gtcatctagaAAACACTGCGGTATTCCTTAAATTCA	PyecT cloning
T698	5'phos TGAGTCCCCAATACCTTG**ga**ATAT**ag**TGAATTTTTAATGAAACGG	PynbA mutagenesis
T699	5'phos GACAGCGCCTTTTCTTT**aga**AAAT**ag**CTAAAGTTGTTTTCTTGC	PmolR mutagenesis
T701	5'phos AATAGGGATGTGCATCTTT**ga**ATAT**ag**TGAATATTCACACTCTTTACAG	PsfsB mutagenesis
T702	5'phos TCTTTCGTGCTATTCGAG**ga**ATAT**ag**TGAAATATCCAGCGGA	PynjI mutagenesis
T705	5'phos TCACCGATGCAGGATAA**ga**ATTT**ag**TGAAAATGACAATACTGATAG	PygiZ mutagenesis
T707	gtcatctagaCGCCAACATCAACAGCAATC	*ynbA* 5-'RACE
T708	gtcatctagaCCGAACAATAAGCCCCATCATAAT	*ynjI* 5'-RACE
T709	gtcatctagaATTGTATTCTTGTCGCAGGCATGA	*yecT* 5'-RACE
T710	gtcatctagaCTTCTTCACCTTCTCCGCAATCAG	*molR* 5'-RACE
T711	gtcatctagaCTGCGTGGTCTTTTCTTTATCATCTTT	*yqhG* 5'-RACE
T712	gtcatctagaAAGCCACCAACCACAAACCAG	*ygiZ* 5'-RACE
T713	gtcatctagaGGCTTTCGCAATAATCATCTCTCC	*sfsB* 5'-RACE

Table S3 Oligonucleotides

No	Sequence [a]	Purpose
T714	gtcatctagaAATAGCCAGCGACCGATCCTG	*ykiA* 5'-RACE
T715	gtcatctagaTGTAGAAGAAACCCACCAGGCATT	*chiA* 5'-RACE
T716	gtcatctagaTGAGTTGGCGATAAGCGGTTT	*yidL* 5'-RACE
T765	5'phos AACGGGAGGGCATTTT**ag**TGAAATATCCTTTCTTTAGCCCATAA	*ykiA* mutagenesis
T770	5'phos CTATTGATAAAAATATGACCATGCTCG**gt**GTTATTAACTTTGTGTAATTTTAG	*bgl* CRP mutagenesis
T812	5'phos TTATGGGCTAAAGAAAGGATATTTCA**ct**AAAATGCCCTCCCGTT	*ykiA* mutagenesis
T816	5'phos TCGGGTCAGGCAGTCAGAT**ag**TTAAAATACAAACGTCGTATCC	*yidL* mutagenesis
T820	GTTGTCGCTGTAATGTTTGTGTTCG	*ynjI*, qRT-PCR
T821	CCGAACAATAAGCCCCATCATAA	*ynjI*, qRT-PCR
T822	CATTATCTCTTGCCAGGCTTACGC	*yecT*, qRT-PCR
T823	GAGATTGTATTCTTGTCGCAGGCA	*yecT*, qRT-PCR
T828	TGGCATCGCTCAGGACATTCATC	*chiA*, qRT-PCR
T829	CAGGATAAATGGAAGTCAGAAGGCAAAG	*chiA*, qRT-PCR
T832	CGGTAACGGGCTCTCTCAAGGTAG	*molR*, qRT-PCR
T833	CCAGCCACGGTAAAACAGCATC	*molR*, qRT-PCR
T838	CATACCTACGCCGACGAGCATTAC	*yidL*, qRT-PCR
T839	GCAGTGTTATTTGTTCGCCATTCTTTA	*yidL*, qRT-PCR
T870	GGTACTTATGAATG**a**GGCAATGAGACAAGAACCATT	*crp*-H19L
T871	CTTGTCTCATTGCC**t**CATTCATAAGTACCCATCCAAGA	*crp*-H19L
T932	AAAGTTGTTttcttTTCTTGCGATTTTGTCTCTCTCTA	*PmolR*+5bp cloning
T933	AATCGCaagaaAAGAAAACAACTTTAGGAATTTATAAAGAAAAGGC	*PmolR*+5bp cloning
T934	AAGTTGTTttcttgcgatTTCTTGCGATTTTGTCTCTCTCTA	*PmolR*+10bp cloning
T935	CAAGAAatcgcaagaaAACAACTTTAGGAATTTATAAAGAAAAGGC	*PmolR*+10bp cloning
T936	CTTAAAATAcaaacCAAACGTCGTATCCCTGAACGGATT	*PyidL*+5bp cloning
T937	GGATACGACgtttgGTTTGTATTTTAAGAATCTGACTGCCT	*PyidL*+5bp cloning
T938	ACAAACgtcgacaaacGTCGTATCCCTGAACGGATT	*PyidL*+10bp cloning
T939	CGACgtttgtcgacGTTTGTATTTTAAGAATCTGACTGCCTG	*PyidL*+10bp cloning
T940	ATTTCGTACAAA**g**AATTTCGCCAATTGATTCAG	*crp*-K101E
T941	TTGGCGAAATT**c**TTTGTACGAAATTTCAGCCAC	*crp*-K101E

[a] Bases of the oligonucleotide which match the template are in capital letters, while other bases are in lower case letters. Mutations are indicated with lower case letters in bold. Restrictions sites are underlined. 5 and 10 bp sequence duplications (oligonucleotides T932-T939) are shown in lowercase and underlined letters.

SUPPLEMENTARY REFERENCES

52. Bremer, E., Gerlach, P. and Middendorf, A. (1988) Double negative and positive control of *tsx* expression in *Escherichia coli*. *J. Bacteriol.*, **170**, 108-116.
53. Caramel, A. and Schnetz, K. (1998) Lac and Lambda repressor relieve silencing of the *Escherichia coli bgl* promoter. Activation by alteration of a repressing nucleoprotein complex. *J. Mol. Biol.*, **284**, 875-883.