

# Supplemental Information

**Table S1.** Bacterial strains, phages and plasmids.

Strains	Description	Reference or origin
<i>E. coli</i> SCS1	<i>recA1 endA1 gyrA96 thi-1 hsdR17(rK-mK+) supE44 relA1</i>	Stratagene
<i>E. coli</i> UT5600	F- <i>ara-14 leuB6 secA6 lacY1 proC14 tsx-67 Δ(ompT-fepC)266 entA403 trpE38 rfbD1 rpsL109 xyl-5 mtl-1 thi-1</i>	NEB
<i>E. coli</i> Genehogs	F- <i>mcrA Δ(mrr-hsdRMS-mcrBC) φ80 lacZ ΔM15 ΔlacX74 recA1 araD139 Δ(ara-leu)7697 galU galK rpsL (Smr) endA1 nupG fhuA::IS2</i> (confers phage T1 resistance)	Invitrogen
<i>E. coli</i> C-1a	derived from C-1; fertility type F-, prototrophic	[1]
<i>E. coli</i> C-1a (N15)	derived from C-1; fertility type F-, prototrophic; contains the N15 prophage	G. Deho
<i>Y. enterocolitica</i> 83/88/2	serogroup O:5,27; biogroup 2 strain; isolated from man; cured from <i>Yersinia</i> virulence plasmid (pYV)	[2–4]
<i>Y. enterocolitica</i> 29854	serogroup O:5; biogroup 1A strain; isolated from food; contains the PY54 prophage	[2–4]
<i>K. oxytoca</i> CCUG 15788	wild type strain, isolated from a mineral oil emulsion tank in Göteborg, Sweden; contains the φKO2 prophage	[5]
Phages	Description	Reference or Origin
PY54	46.3 kb; isolated from <i>Y. enterocolitica</i> strain 29854	[2–4]
PY54-35Tc	PY54 mutant; Tcr inserted into ORF35	This work
N15	46.3 kb; isolated from sewage	[6–8]
N15-D04	N15 mutant; Cmr inserted into ORF36	[9]
φKO2	51.6 kb, isolated from <i>K. oxytoca</i> strain CCUG 15788	[5]
Plasmids	Description	Reference or Origin
pBR329	4.2 kb cloning vector, pMB1 replicon; Apr, Cmr, Tcr	[10]
pMS470Δ8cat	6.9 kb cloning vector, pMB1 replicon, <i>Ptac/ lacI</i> ; T7 gene Shine-Dalgarno sequence; Apr, Cmr	[11]
pIV2	3.6 kb <i>Yersinia</i> cloning vector; Kmr	[12]
pLitmus38	2.8 kb cloning vector; Apr	NEB
pKKlux	7.7 kb promoter probe vector; pMB1 replicon; promoterless <i>luxAB</i> genes from <i>Vibrio harveyi</i> ; T1T2 of <i>rrnB</i> ; Apr	[13]
pKKL700lux	9.3 kb; derived from pKKlux, contains the <i>Solanum tuberosum</i> ST-LS promoter; Apr	[13]

Table S1. *Cont.*

Plasmids	Description	Reference or Origin
pJH136-1	contains the 18 bp palindromic OR3 operator sequence pBR329 Δ[BamHI-HindIII] Ω[PCR, 18 bp, BamHI-HindIII], PY54 32,535–32,552	Figure 5, this work
pJH136-2	contains the 16 bp OR3 operator sequence pBR329 Δ[BamHI-HindIII] Ω[PCR, 16 bp, BamHI-HindIII], PY54 32,536–32,551	Figure 5, this work
pJH136-3	contains 14 bp of the central OR3 operator pBR329 Δ[BamHI-HindIII] Ω[PCR, 14 bp, BamHI-HindIII], PY54 32,537–32,550	Figure 5, this work
pJH136-4	contains the right-arm of the OR3 palindrome pBR329 Δ[BamHI-HindIII] Ω[PCR, 10 bp, BamHI-HindIII], PY54 32,543–32,552	Figure 5, this work
pJH136-5	contains the left-arm of the OR3 palindrome pBR329 Δ[BamHI-HindIII] Ω[PCR, 10 bp, BamHI-HindIII], PY54 32,535–32,544	Figure 5, this work
pJH136-6	contains the 18 bp palindromic OR3 operator with a central A/T nucleotide change pBR329 D[BamHI-HindIII] W[PCR, 18 bp, BamHI-HindIII], PY54 32,535–32,552	Figure 5, this work
pJH136-7	contains the 18 bp palindromic OR3 operator with a central G/C nucleotide change pBR329 D[BamHI-HindIII] W[PCR, 18 bp, BamHI-HindIII], PY54 32,535–32,552	Figure 5, this work
pJH136-8	contains the 18 bp palindromic OR3 operator with a partial adaption to the N15 OR3 operator pBR329 D[BamHI-HindIII] W[PCR, 18 bp, BamHI-HindIII], PY54 32,535–32,552	Figure 5, this work
pJH136-9	contains the 18 bp palindromic OR3 operator with a partial adaption to the N15 OR3 operator pBR329 D[BamHI-HindIII] W[PCR, 18 bp, BamHI-HindIII], PY54 32,535–32,552	Figure 5, this work
pJH136-10	contains the 18 bp palindromic OR3 operator of N15 pBR329 D[BamHI-HindIII] W[PCR, 18 bp, BamHI-HindIII], PY54 32,535–32,552	Figure 5, this work
pJH142-2	PY54 <i>cro</i> gene expression plasmid	This work
pJH192	pMS470D8 <i>cat</i> D[NdeI-HindIII] W[PCR, <i>cro</i> gene, NdeI-HindIII], PY54 32,629–32,831	This work
pJH281	contains the <i>cro</i> gene and the intergenic repressor region pIV2 D[HindIII-XbaI] W[PCR, 308 bp, HindIII-XbaI], PY54 32,525–32,832	Figure 6, this work
pJH282	contains 138 bp of the upstream region of the <i>cI</i> gene pKKluxBamHI D[SmaI-XbaI] W[PCR, 138 bp, SmaI-XbaI], PY54 32,525–32,662	Figure 6, this work
	contains 104 bp of the upstream region of the <i>cI</i> gene pKKluxBamHI D[SmaI-XbaI] W[PCR, 104 bp, SmaI-XbaI], PY54 32,525–32,628	Figure 6, this work

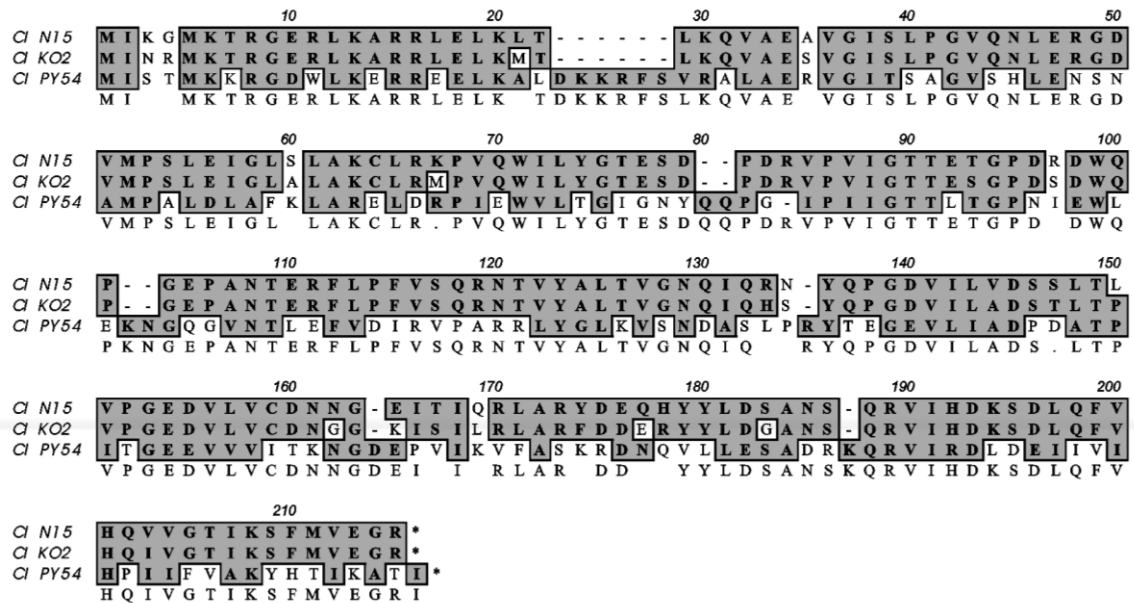
Table S1. *Cont.*

Plasmids	Description	Reference or Origin
pJH283	contains 80 bp of the upstream region of the <i>cI</i> gene pKKluxBamHI D[SmaI-XbaI] W[PCR, 80 bp, SmaI-XbaI], PY54 32,525–32,604	Figure 6, this work
pJH284	contains 59 bp of the upstream region of the <i>cI</i> gene pKKluxBamHI D[SmaI-XbaI] W[PCR, 59 bp, SmaI-XbaI], PY54 32,525–32,583	Figure 6, this work
pJH287	contains 64 bp of the upstream region of the <i>cro</i> gene including a single nucleotide polymorphism at 1st position of the P1 TATA (-10) box pKKluxBamHI D[SmaI-XbaI] W[PCR, 64 bp, SmaI-XbaI], PY54 32,565–32,628	Figure 6, this work
pJH288	contains 64 bp of the upstream region of the <i>cro</i> gene including a single nucleotide polymorphism at 3rd position of the P1 TATA (-10) box pKKluxBamHI D[SmaI-XbaI] W[PCR, 45 bp, SmaI-XbaI], PY54 32,584–32,628	Figure 6, this wor
pJH289	contains 36 bp of the upstream region of the <i>cro</i> gene pKKluxBamHI D[SmaI-XbaI] W[PCR, 36 bp, SmaI-XbaI], PY54 32,593–32,628	Figure 6, this work
pJH290	contains 21 bp of the upstream region of the <i>cro</i> gene pKKluxBamHI D[SmaI-XbaI] W[PCR, 21 bp, SmaI-XbaI], PY54 32,608–32,628	Figure 6, this work
pJH291	pKKluxBamHI D[SmaI-XbaI] W[PCR, 60 bp, SmaI-XbaI], PY54 32,525–32,584	Figure 6, this work
pJH292	pKKluxBamHI D[SmaI-XbaI] W[PCR, 75 bp, SmaI-XbaI], PY54 32,525–32,599	Figure 6, this work
pJH293	pKKluxBamHI D[SmaI-XbaI] W[SmaI-XbaI, PY54 32,524–32,778]	Figure 7, this work
pJH294	pKKluxBamHI D[SmaI-XbaI] W[SmaI-XbaI, PY54 32,524–32,803]	Figure 7, this work
pJH295	pKKluxBamHI D[SmaI-XbaI] W[SmaI-XbaI, PY54 32,524–32,828]	Figure 7, this work
pJH296	pKKluxBamHI D[SmaI-XbaI] W[SmaI-XbaI, PY54 32,524–32,831]	Figure 7, this work
pJH297	contains an OR3 mutation pKKluxBamHI D[SmaI-XbaI] W[SmaI-XbaI, PY54 32,524–32,831]	Figure 7, this work

**Table S2.** Purification of the PY54 Cro repressor.

Fraction	Purification Step	Protein [mg] <sup>a</sup>	Recovery [%]	Purity [%]
I	Crude extract <sup>b</sup>	229.2	100	9
II	Heparin-Sepharose <sup>TM</sup>	55.5	24.2	55
III	DEAE-Sepharce <sup>TM</sup>	50.5	22.0	73
IV	CM-Sepharose <sup>TM</sup> fast flow	34.6	15.1	94

<sup>a</sup> From laser densitometrical measurement on gels; <sup>b</sup> From 29.55 g of cell paste.



**Figure S1.** Sequence analysis of PY54 CI. Alignment of the amino acid sequences of the CI/CB prophage repressors of PY54, φKO2 and N15. Similar and identical residues at corresponding positions are shown in light grey and dark grey, respectively.

## References

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