Table S1, related to Star Methods (Strain and culture conditions) Bacterial Strains. Details of construction of strains can be found in full methods for strains constructed in this work, or in the respective cited reference.

Strain	Genotype
86-24	Stx2A+ EHEC strain serotype O157:H7
EDL933	Stx2A+-Stx1 EHEC strain serotype O157:H7
Sakai	Stx2A+-Stx1 EHEC strain serotype O157:H7
JHD01	86-24 phage *N* antiterminator isogenic mutant
JHD02	86-24 phage *Q* antiterminator isogenic mutant
JHD03	86-24 phage *SR* holins isogenic double mutant
JHD04	86-24 phage *cro* regulatory protein isogenic mutant
JHD05	86-24 *espA* translocon isogenic mutant
JHD06	86-24 Δ*N*- complemented pJHD13
JHD07	86-24 Δ*Q*- complemented pJHD14
JHD08	86-24 ΔΔ*SR*- complemented pJHD15
JHD09	86-24 Δ*cro*-complemented pJHD16
JHD10	86-24*cro*-pet21a in BL21
JHD11	Sakai*cro*-pet21a in BL21
JHD12	EDL933*cro*-pet21a in BL21
JHD13	86-24 Δ*cro* complemented pJHD020
JHD14	86-24 Δ*cro* complemented pJHD021
JHD15	EDL933 phage *cro*-stx2 isogenic mutant
JHD16	EDL933 phage *cro*-stx1 isogenic mutant
JHD17	EDL933 phage *cro*-cryptic isogenic mutant
JHD18	EDL933 phage-*cro*-stx2-stx1 double mutant
JHD19	EDL933 phage-*cro*-stx2-cryptic double mutant
JHD20	EDL933 phage-*cro*-stx2-sxt1-cryptic triple mutant
JHD21	Sakai phage *cro*-stx2 isogenic mutant
JHD22	Sakai phage *cro*-stx1 isogenic mutant
JHD23	Sakai phage *cro*-cryptic isogenic mutant
JHD24	Sakai phage-*cro*-stx2-stx1 double mutant
JHD25	Sakai phage-*cro*-stx2-cryptic double mutant

JHD26	Sakai phage-*cro*-stx2-sxt1-cryptic triple mutant
BL21	F- ompT hsdSB(rB-, mB-) gal dcm (DE3)
TOPO10	Host *E. coli* strain for protein expression
E. coli W3350	*galK2(Oc) galT22 IN(rrnD-rrnE)1*
Citrobacter rodentium DBS100	WT murine pathogen
Citrobacter rodentium C.r-j11	*C. rodentium* with EHEC *ler* promoter region
Citrobacter rodentium-C.r-j11-pcro	*C.rodentium C.r-j11 complemented* pJHD016

Table S2, related to Star Methods. Oligonucleotides used in this study.

	Primers used for mutagenesis and cloning
N-86-24red-F	CACCACCAAAGTTCATCAGGAGGTCTATATGACACGCAGAACTCAGTT CAGTGTAGGCTGGAGCTGCTTC
N-86-24red-R	TCACCTCAAATAAGTGGTTTGCTGCCTAATTTCATTTTCTGGCGACCAA CCCATATGAATATCCTCCTT
Ncomp-F	GTTTCTGCGGCCGCATCAGGAGGTCTATATGACA clone *N* antiterminator in PWSK129
Ncomp-R	GTTTCTGGATCCTCATTTTCTGGCGACCAAC clone *N* antiterminator in PWSK129
Q-86-24red-F	AAGGGAAAAGACACGCTATCGTCAACGGTGTTCTTATGGTTCACCGCG GATGTGTAGGCTGGAGCTGCTTC
Q-86-24red-R	TCGACTGCGTGGCAATGTAACCACTCTTATCATGATATGCAGATTTTTA CGCCATATGAATATCCTCCTT
Qcomp-F	GTTTCTGCGGCCGCGACACGCTATCGTCAACG clone *Q* antiterminator in PWSK129
Qcomp-R	GTTTCTGGATCCCATGATATGCAGATTTTTACGATC clone *Q* antiterminator in PWSK129
SR-86-24red-F	ACGGGGAGTCAGGGCCATCAGTAAACAGCTGCTGGCCTTTTTCATGTT GTGTGTAGGCTGGAGCTGCTTC
SR-86-24red-R	TTATCTGTCGATTCCCCAGCACGCCAGCGCGCTCTCCTGGTCACGACG GGATCCATATGAATATCCTCCTT
SR-lysis-comp-F	GTTTCTGCGGCCGCGCCATCAGTAAACAGCTGCT clone *SR* lysis in PWSK129
SR-lysis-comp-R	GTTTCTGGATCCTTATCTGTCGATTCCCCAGC clone *SR* lysis in PWSK129
Cro-86-24red-F	TGCGGATGATTTATCAAAATGGTAAAGTTGTTCTGTGTGATAAACGGAG GCAGTGTAGGCTGGAGCTGCTTC
Cro-86-24red-R	TCCATTGTGAAAATAGCGGTGTTACTTATGCAGCCGATGCTCTACGCG ATACCATATGAATATCCTCCTT
Cro-comp-F	GTTTCTGCGGCCGCCTGTGTGATAAACGGAGGCA clone regulatory *cro* in PWSK129
Cro-comp-R	GTTTCTGGATCCTCCATTGTGAAAATAGCGGTG clone regulatory *cro* in PWSK129
Cro-pet21a-F	GTTTCTGGATCCATGAGTAATGAACTACTACGC clone 86-24-*cro* in PET21a
Cro-pet21a-F	GTTTCTGCGGCCGCTGCAGCCGATGCTCTACG clone 86-24-*cro* in PET21a
CroSak-pet21F	GTTTCTGGATCCATGAGCAACCTACGAAAATATC clone Sakai-*cro* in PET21a
CroSak-pet21R	GTTTCTGCGGCCGCAGCGGCTTTGTGCTCCG clone Sakai-*cro* in PET21a
CroEdl-pet21F	GTTTCTGGATCCATGCAAAATCTTGATGAGCCG clone EDL933-*cro* in PET21a
CroEdl-pet21R	GTTTCTGCGGCCGCTGCAGCCAGAAGGTTCTTTT clone EDL933-*cro* in PET21a
CroSak-comF	GTTTCTGCGGCCGCGTGGTTACTATGGAGGGCAT clone VT-Stx2-*cro* in pWSK129
CroSak-comR	GTTTCTGGATCCATTAAGCGGCTTTGTGCTCC clone VT-Stx2-*cro* in pWSK129
CroEdl-comF	GTTTCTGCGGCCGCGTACTGAAAGTACGAAAAAGGATA clone BP933W-*cro* in pWSK129
CroEdl-comR	GTTTCTGGATCCATAGCGGTGTTACTTATGCAG clone BP933W-*cro* in

	pWSK129
EspA-86-24red-F	TTATTTACCAAGGGATATTGCTGAAATAGTTCTATATTGTAGAGATTGC GTGTAGGCTGGAGCTGCTTC
EspA-86-24red-R	ATGGATACATCAAATGCAACATCCGTTGTTAATGTGAGTGCGAGTTCTT CCCATATGAATATCCTCCTT
Cro-stx2edl-F	GTACTGAAAGTACGAAAAAGGATATTCCTATGCAAAATCTTGATGAGCC GTGTAGGCTGGAGCTGCTTC
Cro-stx2edl-R	CCATTGTGAAAATAGCGGTGTTACTTATGCAGCCAGAAGGTTCTTTTTG CCCATATGAATATCCTCCTT
Cro-stx1edl-F	TTAGAGGTGAAAGGCCATGATGAAAGAGCGGGTACTGCTTAGGCGGC TTGTGTAGGCTGGAGCTGCTTC
Cro-stx1edl-R	GGGCAATTTTGTTCATTGCGGTCTCCTTAGCATTAATCACACACCCATT ACCATATGAATATCCTCCTT
Cro-crypticedl-F	GGTTGCATGTACTAAGGAGGTTGTATGGAACAACGCATAACCCTGAAA GGTGTAGGCTGGAGCTGCTTC
Cro-crypticedl-R	TAAGAGCGGGGTTATTTATGCTGTTGTTTTTTTGTTACTCGGGAAGGGC TCCATATGAATATCCTCCTT
Cro-stx2Sak-F	TTCGTGGTTACTATGGAGGGCATATGAGCAACCTACGAAAATATCGAG AGGTGTAGGCTGGAGCTGCTTC
Cro-stx2Sak-R	CGCTTATTAAGCGGCTTTGTGCTCCGGCGGGAACACGTCATCAAGACT TACCATATGAATATCCTCCTT
Cro-stx1Sak-F	CCCAATGGATTTGCCGCTGATGTTTGCTCACCCGGTTAGAGGTGAAAG GCGTGTAGGCTGGAGCTGCTTC
Cro-stx1Sak-R	GAGACCGCAATGAACAAAATTGCCCAGCAGCGAAAAAAAATCGGAGTT TCGCCATATGAATATCCTCCTT
Cro-crypticSak-F	GGTGATAATGGTTGCATGTACTAAGGAGGTTGTATGGAACAACGCATA ACGTGTAGGCTGGAGCTGCTTC
Cro-crypticSak-R	TGTAAGAGCGGGGTTATTTATGCTGTTGTTTTTTTGTTACTCGGGAAGG GCCATATGAATATCCTCCTT
CrostxledlF	TTAGAGGTGAAAGGCCATGA
CrostxledlR	TAATGGGTGTGTGATTAATGCT
CrocrypedlF	GTTGCATGTACTAAGGAGGT
CrocrypedlR	TAAGAGCGGGGTTATTTATGC
Crostx1SakF	CCCAATGGATTTGCCGCT
Crostx1SakR	GAGACCGCAATGAACAAAATTG
CrocrypSakF	GGTGATAATGGTTGCATGTACT
CrocrypSakR	TGTAAGAGCGGGGTTATTTATG
CRlerF	GAGCTCGGTACCCGGGGATCTTAAATGTTATTCAGAGATGTTAC
CRlerR	GATTAATTGTTGGTCCTTCCT
EHlerPF	CCTCATGCTTTAATATTTTAAGCTA
EHlerPRev	GTATAGGAACTTCGAAGCAGCTCCAGCCTACACAGTATCATATAGCAT CATATAGTGT
CMf	TGTGTAGGCTGGAGCTGCTTC
CMr	ATCGGGTACGCGATCTGTTGCCCTGGAAAGTTGATCTGAGCTCTCAGT AACCATATGAATATCCTCCTTAGT
Tris66F	TTACTGAGAGCTCAGATCAAC
Tris66R	CGACCTGCAGGCATGCAAGCATGGACACCTCACTTGCTC
FlaRzF	TGCAAAAACAACTGGAAGGAACCCAGAAGTATATTAATGAGCAGTGCA GAGACTACAAAGACCATGACGG
FlagRzR	CGCTGGAAGCGCGGGTGTATTGCTCACAATAATTGCATGAGTTGCCCA TCCATATGAATATCCTCCTTAG
RzBorF	ATGAACCGTGTTCTGTGTGTG
RzBorR	GCTGGCCCTGCTTATTACAG

LamCroF	ATGTACTAAGGAGGTTGTATG
LamCroR	TGCATACACCATAGGTGTG
Stx2AF	ATGAAGTGTATATTATTTAAATGGG
Stx2AR	TTTACCCGTTGTATATAAAAACTG
	Oligonucleotides used for Real Time PCR
Ler-F	CGACCAGGTCTGCCCTTCT
Ler-R	GCGCGGAACTCATCGAAA
Tir-F	CCATGGAGAGCAGACGTAGCT
Tir-R	CGGTGATCCTGGATTTAACCTT
sepL-F	GCCTGGGATTCGCAAAGGT
sepL-R	CTCTTGCATATCATTGAGCAGCTT
espA-F	TCAGAATCGCAGCCTGAAAA
espA-R	CGAAGGATGAGGTGGTTAAGCT
rpoA-F	GCGCTCATCTTCTTCCGAAT
rpoA-R	CGCGGTCGTGGTTATGTG
cro-86-24F	GTGAGGAATGGAAGCGACTC
cro-86-24R	TGGTCAAGATAGCCAACTGAAG
cI-86-24F	CGTGAGTTGAGAAGGGCTAAC
cI-86-24R	ATCGCGGGTAACACTAATGC
dinIF	GTACTGATACGTGGCCTTCA
dinIR	GAACTTTCCCGCCGTATTCA
fliC-F	GTCATCCTTCGCGCTGTTAA
fliC-R	TCTGCGCTGTCGAGTTCTAT
NantiF	GTAGGGCGGTGTAATACTTC
NantiR	ATTAGCTAACGGCGTACTGG
phnB-F	CTGTCCTGCGCTGATTTTG
phnB-R	GGCGCTGAACTGCTCTATAA
proPF	ACCGCTTGGCGGACTCTT
proPR	TCTTCTGGCGACCATATTTATC
rncF	GCTCAGAATAGAGTCGCCTA
rncR	CAGCAGGCATTAACTCATCG
trpDF	GCGCGGTAAGCTGCCTAT
trpDR	GTAAGCTTCGACAATCGCCT
wcaMF	GTGATATTCGCCACGACAAAG
wcaMR	GGAAGCACTTACGATAATAATTAC
Cr-rpoA-F	ACGTCAGCCGGAAGTGAAAGAAGA
Cr-rpoA-R	AGCGGACAGTCAATTCCAGATCGT
Cr-espA-F	ACGAGGTAACAACCATGCGAGTGT
Cr-espA-R	CTGCCTGGCATTGCTTTCCAGAAT
	Oligonucleotides used for EMSAS
Ler-173 F	CGGGATCCCGATGATTTTCTTCTATATCATTG
Ler-42 R	CGGAATTCCGCGACCTTATCAGGAAGGACC
KanF	CCGGAATTGCCAGCTGGGGCG
KanR	TCTTGTTCAATCATGCGAAACGATCC
OrprmFv	CGCCAGATTCGATTTGCGAAT
OrprmRv	ACTAGAAGCCTCTTTTCGCC

Table S3, related to Star Methods. Plasmids.

	Genotype
pet21a	N-terminal His-Tag vector
pWSK129	pLG339*ori*, *kan, lacZ*α
pkd4	λ red template plasmid
pkd46	λ red recombinase expression plasmid
pcp20	TS replication and thermal induction of FLP synthesis
pJHD013	86-24 phage *N* antiterminator in pwsk129
pJHD014	86-24 phage *Q*- antiterminator in pwsk129
pJHD015	86-24 phage *SR*- holins in pwsk129
pJHD016	86-24 phage *cro*-transcription factor in pWSK129
pJHD017	86-24 phage *cro*-transcription factor in pet21a
pJHD018	EDL933-933w- *cro*-transcription factor in pet21a
pJHD019	Sakai-Vt-Stx2- *cro*-transcription factor in pet21a
pJHD020	EDL933-933w- *cro*-transcription factor in pWSK129
pJHD021	Sakai-Vt-Stx2- *cro*-transcription factor in pWSK129
pRS551	lacZ reporter gene fusion vector

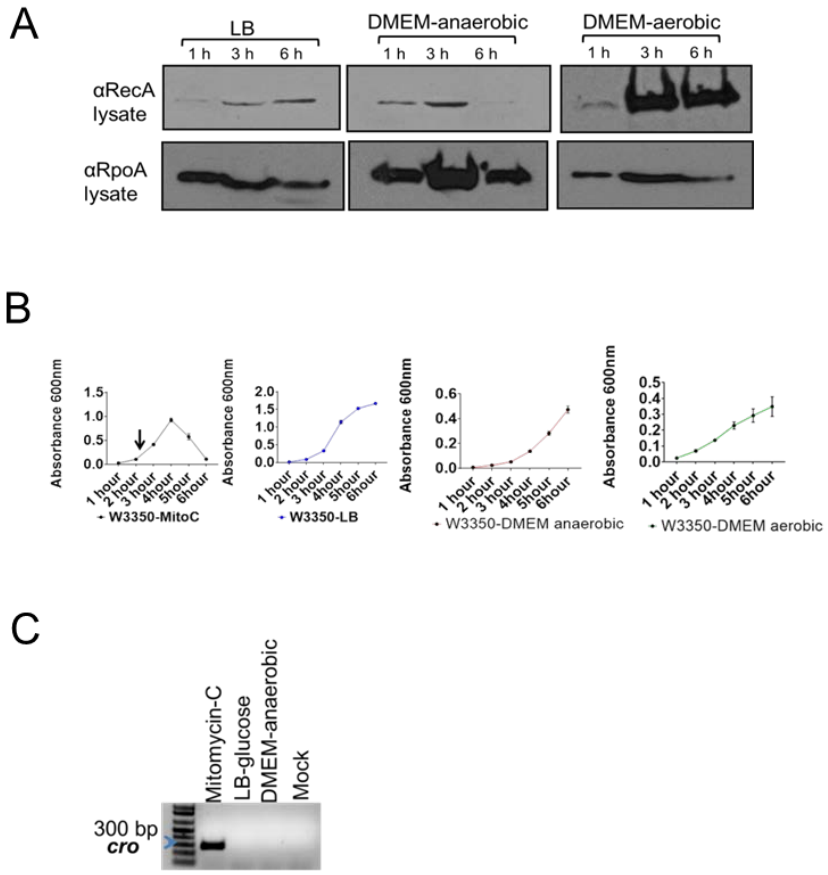


Figure S1. Related to Figure 1. Bacteriophage activity in *E. coli* W3350.

(A) Protein levels of the DNA repair protein, RecA, from whole-cell lysate of *E. coli* W3350 in LB aerobic, DMEM anaerobic and DMEM aerobic conditions. RpoA levels serves as a loading control (B) Growth curves of *E. coli* W3350 using LB-mitomycin C, LB-glucose, DMEM anaerobic and DMEM aerobic. The experiments were conducted with 9 biological replicates. Data are represented as mean ± SEM. (C) Bacteriophage particles isolated from *E. coli* W3350 using PEG8000 under LB mitomycin C, LB-glucose, DMEM anaerobic and DMEM aerobic conditions, and PCR reaction was performed targeting the *cro* gene as readout.

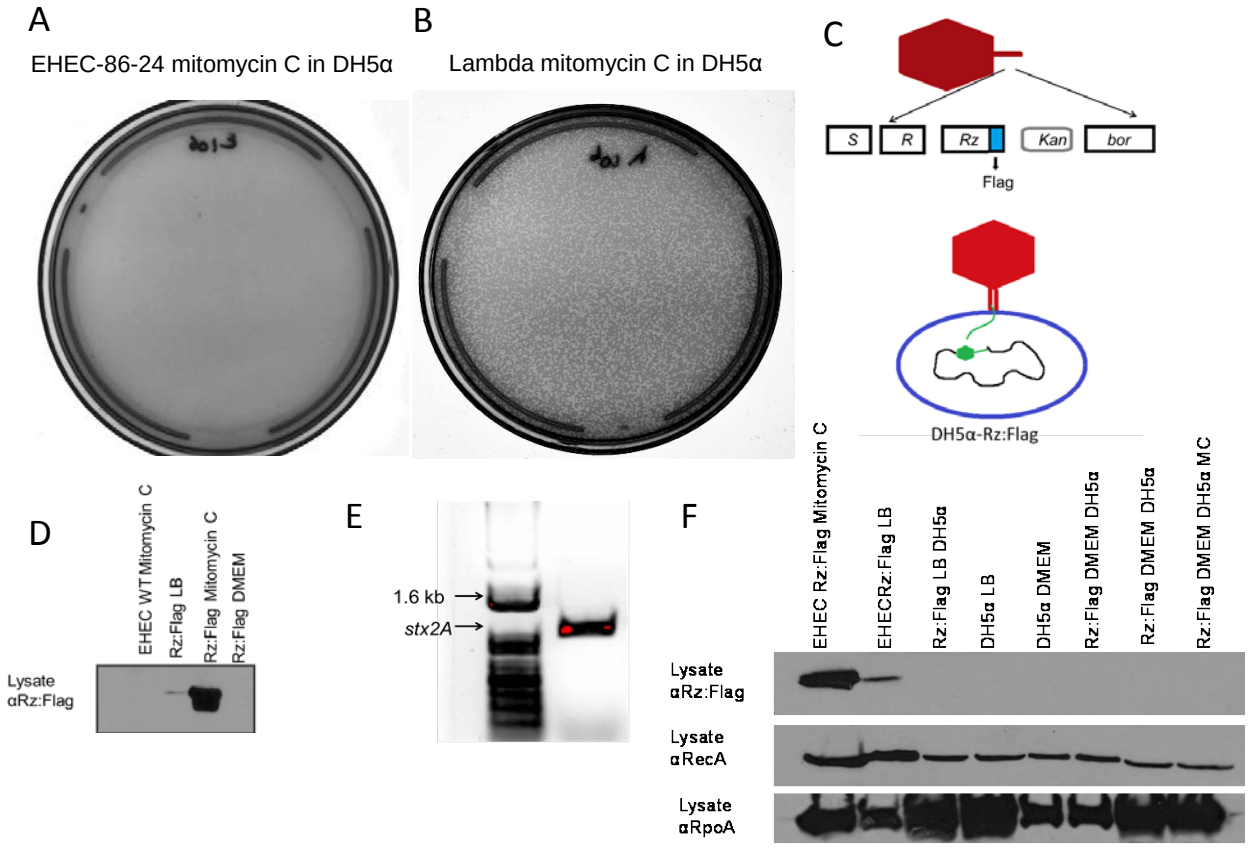


Figure S2. Related to Figure 1. Differences between EHEC 8624 and *E. coli* W3350 bacteriophages.

EHEC and *E. coli* W3350 were grown in LB medium and treated with Mitomycin C (10 µg/ml), centrifuged, filter sterilized and serially diluted in SM buffer and an aliquot (100 µl) was mixed with host strain *E. coli* (DH5α), incubated and poured onto LB plates to be incubated overnight. Plaques were visualized with a digital camera.

(A) EHEC Stx2 bacteriophage did not form plaques on *E. coli* DH5α.

(B) Lambda phage from strain W3350 was able to produce thousands of plaques on *E.*

coli DH5α. (C) Cartoon depicting the strategy to Flag-tag *Rz* gene from the 8624 bacteriophage, which is a non-essential gene for bacteriophage. *Rz* is a gene located downstream of the lysis genes *SR*, and between *Rz* flag and *bor* a kanamycin resistant gene was introduced as a selection marker. (D) Western Blot experiment of EHEC 8624 *Rz*-flag strain where the bacterium was grown on different conditions, Mitomycin C, LB, and DMEM anaerobic for 6 hours to obtain whole cell lysate to be probed against anti-Flag antibody (Sigma) . WT EHEC was added to test the specificity of the Flag antibody. The Flag tag was highly expressed by the *Rz*-Flag 8624 strain in Mitomycin C. In the absence of mitomycin C it was expressed at lower levels in LB and not in DMEM. (E) PCR of DH5α clone transduced with 8624 *Rz*:Flag bacteriophage depicting the presence of *stx2A* gene in the chromosome. (F) Western blot of DH5α transduced with *Rz*:Flag bacteriophage under different growth conditions. The first to lines are EHEC 8624 *Rz*:flag under mitomycin C and LB conditions used as positive controls. (D) Western Blot experiment of EHEC 8624 Rz-flag strain where the bacterium was grown on different conditions, Mitomycin C, LB, and DMEM anaerobic for 6 hours to obtain whole cell lysate to be probed against anti-Flag antibody (Sigma) . WT EHEC was added to test the specificity of the Flag antibody. The Flag tag was highly expressed by the Rz-Flag 8624 strain in Mitomycin C. In the absence of mitomycin C it was expressed at lower levels in LB and not in DMEM. (E) PCR of DH5α clone transduced with 8624 Rz:Flag bacteriophage depicting the presence of *stx2A* gene in the chromosome.

(F) Western blot of DH5α transduced with Rz:Flag bacteriophage under different growth conditions. The first to lines are EHEC 8624 Rz:flag under mitomycin C and LB conditions used as positive controls.

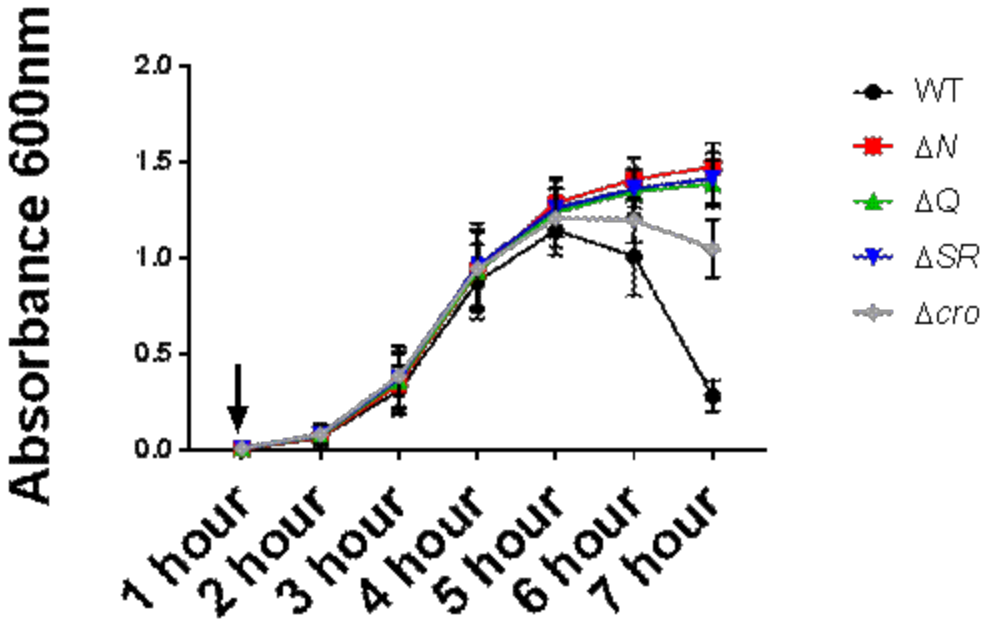


Figure S3.Related to Figures 2 and 3. EHEC 8624 bacteriophage mutants are lysogenic

Growth curves of EHEC 8624 WT (Black line) and isogenic bacteriophage mutations Δ*N* (Red line), Δ*Q* (Green line) Δ*SR* (Blue line) and Δ*cro* (Grey line). The strains were grown in LB medium supplemented with a low concentration of Mitomycin C (200 ng/ml) under aerobic conditions, and induction was done at the beginning of the experiment (0 hour) (n=3, error bars, standard deviation).

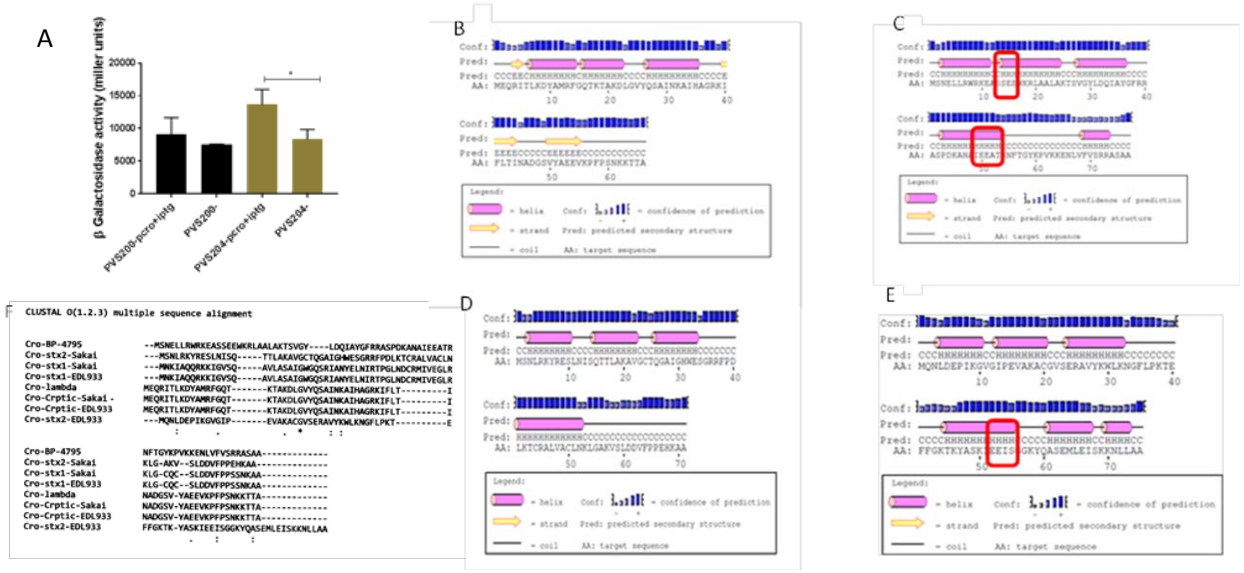


Figure S4. Related to Figure 4. Cro regulation of ler and Different Cro proteins.

(A) Beta galactosidase assay of *ler*-lacZ fusions in *E. coli* K-12 MC4100 in the absence (vector control) or presence of pCro. IPTG is used in all cultures because it induces cro expression. Cultures were grown in DMEM. pVS204 contains the -343 to +86 regulatory region of *ler*. pVS200 does not contain *ler* P2 promoter (Sharp and Sperandio, 2007) . P<0.05 as significant. (B) The presence of acidic patches in the DNA domain of a transcription factor are required for transcriptional activation(Bushman and Ptashne, 1988; Ko et al., 2008). Cro proteins from the different phages were evaluated using the software Protein Sequence Analysis Workbench (PSPIRED)(Buchan et al., 2013). a, Lambda (λ) Cro protein, accession number NP_040629.1 was used for comparison purposes showing the software's accuracy to predict the Cro DNA binding domain at amino acid residual 30 , QSANK showed as pink bars. Noticeably, this domain does not contain acidic patches which is typical for this type of Cro. (C) EHEC 86-24 Cro

accession number YP_001449261.1 contains two domains , at residuals 20 and 50 which have acidic patches SEE and EE-T respectively (red boxes). (D) EHEC Sakai VT-Stx2 Cro accession number WP_000067727, does not have any residual patches in the predicted helix domains. (E) EHEC EDL933 933W Cro accession number NP_286964, contain one domain at residual 50 with acid patch EE-S (red box). (F) Clustal Omega alignments of all the Cro used in the study. Phage BP-4795 Cro is 100 percent identical to EHEC strain 86-24 phage Cro. EHEC strain EDL933 contain three different phages: Shiga toxin 2 (Stx2) phage (ΦBP933W), Shiga toxin 1 (Stx1) phage (ΦCP933V) and Cryptic phage. EHEC strain Sakai contain also three different phages: Shiga toxin 2 (Stx2) phage (ΦVTX2), Shiga toxin 1 (Stx1) phage (ΦECs2989), and Cryptic phage (Φ ECs0275). Lambda phage Cro was added for comparison purposes. Cro accession numbers used in the alignment were : YP_001449261.1, NP_040629.1, WP_000067727, NP_286964.1 , WP_000437875, WP_000437875.1, WP_001033078.1. (E) EHEC EDL933 933W Cro accession number NP_286964, contain one domain at residual 50 with acid patch EE-S (red box). (F) Clustal Omega alignments of all the Cro used in the study. Phage BP-4795 Cro is 100 percent identical to EHEC strain 86-24 phage Cro. EHEC strain EDL933 contain three different phages: Shiga toxin 2 (Stx2) phage (ΦBP933W), Shiga toxin 1 (Stx1) phage (ΦCP933V) and Cryptic phage. EHEC strain Sakai contain also three different phages: Shiga toxin 2 (Stx2) phage (ΦVTX2), Shiga toxin 1 (Stx1) phage (ΦECs2989), and Cryptic phage (Φ ECs0275). Lambda phage Cro was added for comparison purposes. Cro accession numbers used in the alignment were : YP_001449261.1, NP_040629.1,

WP_000067727, NP_286964.1 , WP_000437875, WP_000437875.1,

WP_001033078.1.

A Down regulated genes affected by Δ*cro*

Virulence	Dna-repair	Peptidoglycan-cell-wall	Metabolism	Hypothetical-protein	tRNA-rRNA	Phage-related	Transport	Total
49	52	30	181	87	81	42	62	584

B Up-regulated genes affected by Δ*cro*

Virulence	Dna-repair	Peptidoglycan-cell-wall	Metabolism	Hypothetical-protein	tRNA-rRNA	Phage-related	Transport	Total
9	40	23	84	64	44	15	28	307

C TypeIII-Secretion system Down regulated genes in Δ*cro*.

Gene name	Fold Change	Biological function
espA	0.061	protein EspA
espD	0.081	protein EspD
Z5111	0.105	Tir chaperone protein (CesT) family
Z3071	0.119	secretion protein EspJ
Z5104	0.122	pathogenicity island 2 effector protein SseE
espF	0.179	secretion protein EspF
espB	0.247	Enterobacterial EspB protein
Z3921	0.249	T3SS effector protein NleG8
Z5102	0.297	EscG/YscG/SsaH family type III secretion system
Z5125	0.329	type III secretion system protein SepD
sepZ	0.338	type III secretion system protein SepZ
Z5121	0.359	Hypothetical protein (type III secretion)
Z5116	0.365	type III secretion system protein SepQ
Z5114	0.408	regulation of protein secretion, Tir chaperone protein (CesT) family (hypothetical protein)
Z1829	0.478	type III secretion protein GogB

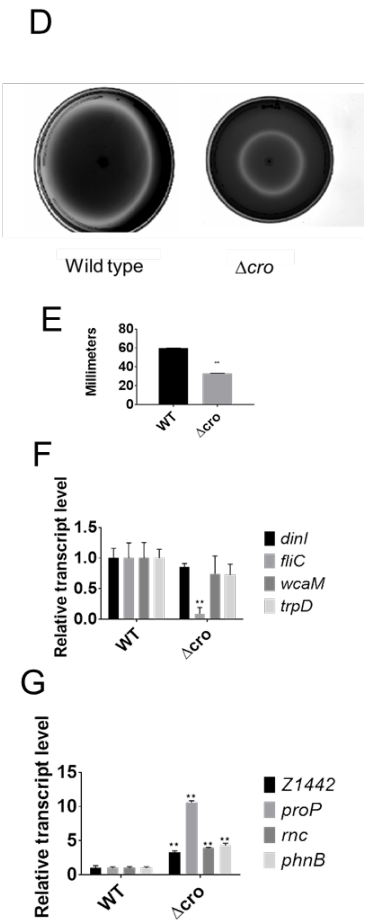


Figure S5. Related to Figures 1-4. Microarray analysis of EHEC 8624 Δ*cro* grown anaerobically in DMEM. (A-B). Transcriptomic profile of a mutation in the bacteriophage transcription factor, *cro,* where approximately 800 genes were affected and grouped in categories. Majority of the affected genes were down regulated in Δ*cro* (approximately 500) and the remaining genes were up regulated in Δ*cro* (300).

(C) Summary of genes affected (down regulated) in the T3SS comprising genes related to the needle apparatus such as *espA,* and secreted encoded effectors like *espF*.

(D) Motility plates were conducted using a low concentration of agar (0.25%) in DMEM anaerobically at 37^0C overnight. Wild type EHEC 86-24 and isogenic Δ*cro* were grown

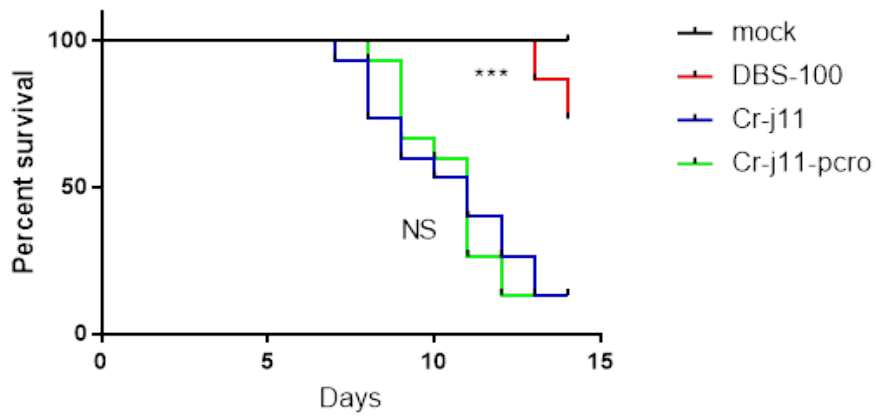
in LB medium overnight, plates were stabbed in the middle with the respective strain and incubated anaerobically overnight.

(E) Motility experiments were conducted in triplicates at three independent times having a total of 9 replicates, the diameter was measured and a Student's *t-test* was conducted showing statistical significance at $p<0.01$ (**). qRT-PCR of selected genes from the microarray experiments. RNA was extracted from EHEC 86-24 strains grown anaerobically in DMEM to an OD_{600} of 0.6 (n=6 replicates per strain; asterisks, *p<0.01*; Student's *t*-test.

(F) Up-regulated genes and

(G) Down regulated genes affected by Δ*cro* compared to wild type (WT) EHEC.

A



B

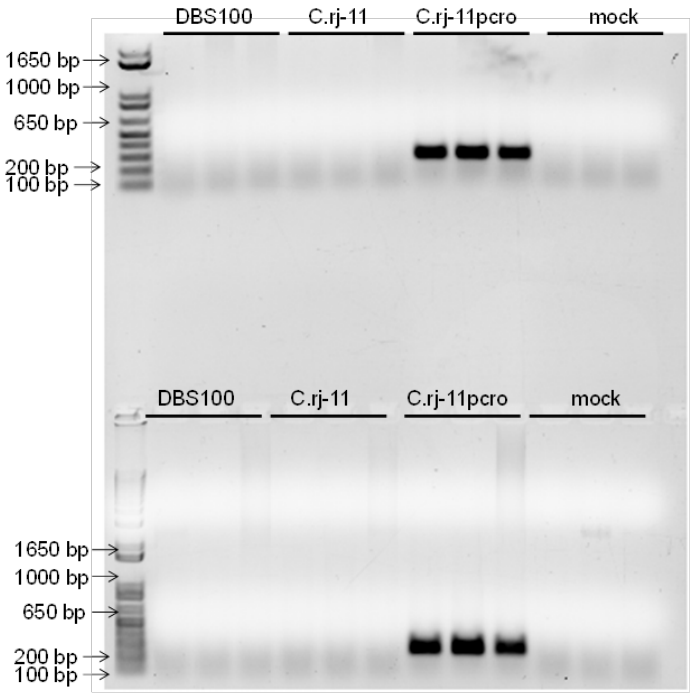


Figure S6. Related to Figures 5 and 6. The disease prognosis in mice can be influenced utilizing the EHEC 8624 bacteriophage Cro expressed in Trans

(A) Survival curves of mouse after infection with mock (PBS) and different *C. rodentium*

strains. The curves show a drastically difference between *Cr*-j11, *Cr*-j11-pcro and *C. rodentium* DBS100. There was a highly statistical significance comparing DBS100 either *Cr*-j11 or *Cr*-j11-pcro (***$p<0.01$). Nonetheless, there was not statistical significance within *Cr*-j11 and *Cr*-j11-pcro (n=15, analysis was done using Mantel-cox, and Grehan-Breslow-Wilcoxon tests in GraphPad prism). (B) 8624 *cro* phage gene isolated from mouse distal colon. The RNA from distal colon was extracted and cDNA converted . PCR reaction was conducted using primers to target the cro gene complemented in trans into pwsk129 plasmid. Each lane denotes a single mouse from different groups.