

Figure S1. Detection of non-syntenic IGRs. Genomic locations of orthologous genes (black dots) in *Salmonella enterica* and *Escherichia coli* are plotted on the x and y axes, respectively. Those IGRs neighboring non-syntenic genes (*i.e.*, dots not aligned on the diagonal) were examined to identify non-syntenic IGRs.

Figure S2. 3' RACE analysis of *E. coli* sRNAs. (A) PCR bands observed for EcsR1 and EcsR2 from a modified 3' RACE protocol. The amplicons were sequenced and the predicted 3' ends for EcsR1 and EcsR2 are shown in (B) and (C), respectively.

Figure S3. Evolution of a new sRNA promoter in *Salmonella*. Sequences immediately upstream of STM14_1869 and its orthologs in *E. coli* MG1655, *Enterobacter aerogenes* KCTC 2190, *Klebsiella pneumoniae* HS11286, and *Serratia marcescens* FG194 are aligned. Numbers of RNA-seq reads mapping to this region are shown (black, *Salmonella*; blue, *E. coli*). The new *Salmonella* σ^{70} promoter and sRNA transcription start site are boxed. Phylogenetic tree is based on Petty et al. 2010.

Figure S4. Fragmentary EcsR1 is not transcribed in *Salmonella*. Transcript levels of forward (red) and reverse (blue) strands of the *nifJ-uspF* IGR in *Salmonella* is shown. Transcription start site (TSS) of *uspF* is apparent, but neither the small 5' portion of EcsR1 nor the *micC* gene are expressed.

Figure S5. EcsR1 abundance in *E. coli* strains. (A) Histogram showing the fold difference in expression of EcsR1 in an Hfq-deleted strain compared to wild-type strain (normalized to 1). Asterisks indicate $p < 0.01$. (B) Ct values of EcsR1 qPCR with wild-type *E. coli* carrying pBAD with cloned EcsR1, and with wild-type *E. coli*

with empty pBAD, when grown in LB to $OD_{600} \approx 0.5$ and induced with 0.2% arabinose for 15 minutes. Asterisks indicate $p < 0.01$.

Figure S6. Nucleotide substitutions in the corresponding FNR- and CRP-binding sites of *E. coli* and *Salmonella*. Sequences homologous to the putative FNR- and CRP-binding regions (yellow and blue, respectively; overlapping region in green) upstream of EcsR1 contain multiple nucleotide substitutions (marked by asterisks).

Table S1. Genes neighboring unique IGRs in *E. coli* and *Salmonella*

<i>E. coli</i>			<i>Salmonella</i>		
Gene	Left end ^a	Right end ^a	Gene	Left end ^a	Right end ^a
<i>ykgJ</i>	303077	303406	STM14_2096	1839558	1839962
<i>ykgM</i>	311738	312001	<i>rpmE2</i>	527046	527306
<i>ykgD</i>	319451	320305	STM14_0657	619952	620806
<i>emrE</i>	567538	567870	STM14_1998	1756592	1756930
<i>ybcL</i>	570116	570667	STM14_1226	1130516	1131064
<i>rzpD</i>	577330	577791	STM14_2458	2116355	2116840
<i>nobD</i>	580057	580602	STM14_3192	2809024	2809569
<i>ompT</i>	583903	584856	<i>pgtE</i>	2557607	2558545
<i>cusC</i>	594823	596196	STM14_0408	393112	394569
<i>hyaA</i>	1031362	1032480	STM14_2161	1895517	1896635
<i>appB</i>	1038519	1039655	STM14_2168	1902638	1903774
<i>torD</i>	1061022	1061621	<i>torD</i>	4033878	4034510
<i>ymfR</i>	1204772	1204954	STM14_2451	2112246	2112428
<i>pinE</i>	1208908	1209462	<i>hin</i>	2935077	2935649
<i>umuC</i>	1230409	1231677	<i>umuC</i>	2091297	2092565
<i>intR</i>	1410024	1411259	STM14_1140	1056587	1057879
<i>ydaV</i>	1420007	1420753	STM14_1152	1065589	1066338
<i>ompN</i>	1433784	1434917	<i>ompN</i>	1559653	1560786
<i>rzpQ</i>	1637054	1637551	STM14_2272	1976912	1977445
<i>rrrQ</i>	1637548	1638081	STM14_1451	1303335	1303874
<i>relE</i>	1643370	1643657	STM14_5341	4704513	4704797
<i>ydhR</i>	1744724	1745029	STM14_4166	3625984	3626295
<i>ydhU</i>	1747587	1748372	<i>phsC</i>	2188873	2189637
<i>fliC</i>	2000134	2001630	<i>fljB</i>	2933465	2934985
<i>yedV</i>	2034818	2036176	<i>copS</i>	1140624	1141988
<i>hiuH</i>	2036980	2037393	STM14_1243	1142797	1143207
<i>yedY</i>	2037502	2038506	STM14_4072	3561997	3563001
<i>zinT</i>	2039399	2040049	STM14_1523	1355815	1356462
<i>yeeN</i>	2054882	2055598	<i>yeeN</i>	4765498	4766214
<i>glf</i>	2105250	2106353	STM14_0838	784514	785665
<i>gatD</i>	2169857	2170897	STM14_3943	3443499	3444542
<i>rcnR</i>	2183546	2183818	<i>yohL</i>	3203592	3203864
<i>ccmH</i>	2289380	2290432	<i>ccmH_2</i>	4026013	4027056
<i>yfdN</i>	2470409	2470903	STM14_2468	2122501	2123025
<i>dsdC</i>	2474716	2475651	<i>dsdC</i>	4015641	4016564
<i>dsdA</i>	2477224	2478552	<i>dsdA</i>	4018145	4019467
<i>murQ</i>	2543795	2544691	<i>murQ</i>	2768132	2769025
<i>yqeI</i>	2986524	2987333	<i>marT</i>	3971890	3972678

<i>ygeX</i>	3005532	3006728	STM14_1136	1052217	1053431
<i>gpr</i>	3145919	3146959	STM14_2960	2573772	2574770
<i>exuT</i>	3243126	3244544	STM14_3791	3312670	3313974
<i>ybjA</i>	3665814	3667211	STM14_4612	4032288	4033688
<i>yjdL</i>	4352977	4354434	<i>yjdL</i>	2753703	2755163
<i>cadC</i>	4358419	4359957	<i>cadC</i>	2748184	2749728
<i>yjgH</i>	4470837	4471232	STM14_1869	1635982	1636371
<i>yjgI</i>	4471363	4472076	STM14_2022	1777978	1778691
<i>sgcR</i>	4524129	4524911	STM14_1957	1716544	1717335
<i>lsrK</i>	1596641	1598233	<i>ydeV</i>	4294190	4295782
<i>yedK</i>	2007845	2008513	STM14_1484	1334473	1335144
<i>yiaY</i>	3754699	3755850	STM14_4863	4267391	4268644
<i>ykgB</i>	316950	317543	STM14_0661	622753	623313
<i>ykgC</i>	317900	319225	STM14_0658	621022	622347
<i>yaiL</i>	375996	376535	STM14_5039	4428432	4428971
<i>ybgQ</i>	748945	751392	<i>stdB</i>	3208362	3210851
<i>torS</i>	1052657	1055401	<i>torS</i>	4040144	4042879
<i>feaB</i>	1445543	1447042	STM14_3782	3307225	3308709
<i>yodB</i>	2040392	2040922	STM14_1512	1347423	1347953
<i>ccmA</i>	2295043	2295666	<i>ccmA_2</i>	4031665	4032282
<i>yjgJ</i>	4472147	4472740	STM14_2021	1777310	1777900
<i>yjhH</i>	4522128	4523033	STM14_4252	3710729	3711634
<i>sgcX</i>	4528553	4529674	STM14_1951	1711775	1712893
<i>ykgO</i>	311598	311738	<i>rpmJ_1</i>	527312	527452
<i>ymfL</i>	1202491	1203048	STM14_2472	2125175	2125729
<i>yeeJ</i>	2042962	2050038	<i>sinH</i>	2700161	2702353
<i>frmR</i>	378830	379105	STM14_1969	1728800	1729075
<i>ydfU</i>	1641279	1642328	STM14_2767	2391120	2392109
<i>yoaC</i>	1892157	1892456	STM14_0383	371424	371747
<i>yjjN</i>	4594013	4595035	STM14_3725	3262486	3263502

^aLeft and right ends of genes according to *E. coli* MG1655 (NC_000913.2) or *Salmonella* Typhimurium (NC_016856.1).

Table S2. *E. coli* strains used in this study.

Accession No.	Description
NC_017626.1	<i>Escherichia coli</i> 042
NC_008253.1	<i>Escherichia coli</i> 536
NC_011748.1	<i>Escherichia coli</i> 55989
NC_017631.1	<i>Escherichia coli</i> ABU 83972
NC_008563.1	<i>Escherichia coli</i> APEC O1
NC_020163.1	<i>Escherichia coli</i> APEC O78
NC_010468.1	<i>Escherichia coli</i> ATCC 8739
NC_012967.1	<i>Escherichia coli</i> B str. REL606
NC_012947.1	<i>Escherichia coli</i> BL21-Gold(DE3)pLysS AG'
NC_012892.2	<i>Escherichia coli</i> BL21(DE3)
NC_012971.2	<i>Escherichia coli</i> BL21(DE3)
NC_012759.1	<i>Escherichia coli</i> BW2952
NC_004431.1	<i>Escherichia coli</i> CFT073
NC_017625.1	<i>Escherichia coli</i> DH1
NC_017638.1	<i>Escherichia coli</i> DH1
NC_009801.1	<i>Escherichia coli</i> E24377A
NC_011745.1	<i>Escherichia coli</i> ED1a
NC_017633.1	<i>Escherichia coli</i> ETEC H10407
NC_009800.1	<i>Escherichia coli</i> HS
NC_011741.1	<i>Escherichia coli</i> IAI1
NC_011750.1	<i>Escherichia coli</i> IAI39
NC_017628.1	<i>Escherichia coli</i> IHE3034
NC_022648.1	<i>Escherichia coli</i> JJ1886
NC_016902.1	<i>Escherichia coli</i> KO11FL
NC_017660.1	<i>Escherichia coli</i> KO11FL
NC_011993.1	<i>Escherichia coli</i> LF82
NC_022364.1	<i>Escherichia coli</i> LY180
NC_017644.1	<i>Escherichia coli</i> NA114
NC_013353.1	<i>Escherichia coli</i> O103:H2 str. 12009
NC_018650.1	<i>Escherichia coli</i> O104:H4 str. 2009EL-2050
NC_018661.1	<i>Escherichia coli</i> O104:H4 str. 2009EL-2071
NC_018658.1	<i>Escherichia coli</i> O104:H4 str. 2011C-3493
NC_013364.1	<i>Escherichia coli</i> O111:H- str. 11128
NC_011601.1	<i>Escherichia coli</i> O127:H6 str. E2348/69
NC_011353.1	<i>Escherichia coli</i> O157:H7 str. EC4115

NC_002655.2	<i>Escherichia coli</i> O157:H7 str. EDL933
NC_002695.1	<i>Escherichia coli</i> O157:H7 str. Sakai
NC_013008.1	<i>Escherichia coli</i> O157:H7 str. TW14359
NZ_CM000662.1	<i>Escherichia coli</i> O157:H7 str. TW14588
NC_013361.1	<i>Escherichia coli</i> O26:H11 str. 11368
NC_013941.1	<i>Escherichia coli</i> O55:H7 str. CB9615
NC_017656.1	<i>Escherichia coli</i> O55:H7 str. RM12579
NC_017646.1	<i>Escherichia coli</i> O7:K1 str. CE10
NC_017634.1	<i>Escherichia coli</i> O83:H1 str. NRG 857C
NC_017663.1	<i>Escherichia coli</i> P12b
NC_011742.1	<i>Escherichia coli</i> S88
NC_011415.1	<i>Escherichia coli</i> SE11
NC_013654.1	<i>Escherichia coli</i> SE15
NC_010498.1	<i>Escherichia coli</i> SMS-3-5
NC_017652.1	<i>Escherichia coli</i> str. 'clone D i14'
NC_017651.1	<i>Escherichia coli</i> str. 'clone D i2'
NC_010473.1	<i>Escherichia coli</i> str. K-12 substr. DH10B
NC_020518.1	<i>Escherichia coli</i> str. K-12 substr. MDS42 DNA
NC_000913.2	<i>Escherichia coli</i> str. K-12 substr. MG1655
NZ_AKBV01000001.1	<i>Escherichia coli</i> str. K-12 substr. MG1655 strain K-12
NZ_AKVX01000001.1	<i>Escherichia coli</i> str. K-12 substr. MG1655 strain K-12
NZ_CM000960.1	<i>Escherichia coli</i> str. K-12 substr. MG1655star strain
NC_007779.1	<i>Escherichia coli</i> str. K-12 substr. W3110
NC_017632.1	<i>Escherichia coli</i> UM146
NC_011751.1	<i>Escherichia coli</i> UMN026
NZ_AGTD01000001.1	<i>Escherichia coli</i> UMN18
NC_017641.1	<i>Escherichia coli</i> UMNK88
NC_007946.1	<i>Escherichia coli</i> UTI89
NC_017635.1	<i>Escherichia coli</i> W
NC_017664.1	<i>Escherichia coli</i> W
NC_017906.1	<i>Escherichia coli</i> Xuzhou21

Table S3. *Salmonella* strains used in this study.

Accession No.	Description
NC_021814.1	<i>Salmonella enterica</i> subsp. <i>enterica</i> Typhimurium var. 5
NC_016863.1	<i>Salmonella enterica</i> subsp. <i>enterica</i> Typhimurium str. UK-1
NC_021151.1	<i>Salmonella enterica</i> subsp. <i>enterica</i> Typhimurium str. U288
NC_016860.1	<i>Salmonella enterica</i> subsp. <i>enterica</i> Typhimurium str. T000240
NC_016857.1	<i>Salmonella enterica</i> subsp. <i>enterica</i> Typhimurium str. ST4/74
NC_016810.1	<i>Salmonella enterica</i> subsp. <i>enterica</i> Typhimurium str. SL1344
NC_022544.1	<i>Salmonella enterica</i> subsp. <i>enterica</i> Typhimurium str. DT2
NC_022569.1	<i>Salmonella enterica</i> subsp. <i>enterica</i> Typhimurium str. DT104
NC_016854.1	<i>Salmonella enterica</i> subsp. <i>enterica</i> Typhimurium str. D23580
NC_017046.1	<i>Salmonella enterica</i> subsp. <i>enterica</i> Typhimurium str. 798
NC_016856.1	<i>Salmonella enterica</i> subsp. <i>enterica</i> Typhimurium str. 14028S
NC_021820.1	<i>Salmonella enterica</i> subsp. <i>enterica</i> Typhimurium str. 08-1736
NC_021176.1	<i>Salmonella enterica</i> subsp. <i>enterica</i> Typhi str. Ty21a
NC_004631.1	<i>Salmonella enterica</i> subsp. <i>enterica</i> Typhi str. Ty2
NC_016832.1	<i>Salmonella enterica</i> subsp. <i>enterica</i> Typhi str. P-stx-12
NC_003198.1	<i>Salmonella enterica</i> subsp. <i>enterica</i> Typhi str. CT18
NC_022525.1	<i>Salmonella enterica</i> subsp. <i>enterica</i> Thompson str. RM6836
NC_011094.1	<i>Salmonella enterica</i> subsp. <i>enterica</i> Schwarzengrund str. CVM19633
NC_021984.1	<i>Salmonella enterica</i> subsp. <i>enterica</i> Pullorum str. S06004
NC_012125.1	<i>Salmonella enterica</i> subsp. <i>enterica</i> Paratyphi C strain RKS4594
NC_010102.1	<i>Salmonella enterica</i> subsp. <i>enterica</i> Paratyphi B str. SPB7
NC_006511.1	<i>Salmonella enterica</i> subsp. <i>enterica</i> Paratyphi A str. ATCC 9150
NC_011147.1	<i>Salmonella enterica</i> subsp. <i>enterica</i> Paratyphi A str. AKU_12601
NC_021902.1	<i>Salmonella enterica</i> subsp. <i>enterica</i> Newport str. USMARC-S3124.1
NC_011080.1	<i>Salmonella enterica</i> subsp. <i>enterica</i> Newport str. SL254
NC_020307.1	<i>Salmonella enterica</i> subsp. <i>enterica</i> Javiana str. CFSAN001992
NC_011083.1	<i>Salmonella enterica</i> subsp. <i>enterica</i> Heidelberg str. SL476
NC_021812.2	<i>Salmonella enterica</i> subsp. <i>enterica</i> Heidelberg str. CFSAN002069
NC_017623.1	<i>Salmonella enterica</i> subsp. <i>enterica</i> Heidelberg str. B182
NC_021810.1	<i>Salmonella enterica</i> subsp. <i>enterica</i> Heidelberg str. 41578
NC_016831.1	<i>Salmonella enterica</i> subsp. <i>enterica</i> Gallinarum/pullorum
NC_022221.1	<i>Salmonella enterica</i> subsp. <i>enterica</i> Gallinarum/pullorum
NC_011274.1	<i>Salmonella enterica</i> subsp. <i>enterica</i> Gallinarum str. 287/91
NC_011294.1	<i>Salmonella enterica</i> subsp. <i>enterica</i> Enteritidis str. P125109
NC_011205.1	<i>Salmonella enterica</i> subsp. <i>enterica</i> Dublin str. CT_02021853

NC_021818.1	<i>Salmonella enterica</i> subsp. <i>enterica</i> Cubana str. CFSAN002050
NC_006905.1	<i>Salmonella enterica</i> subsp. <i>enterica</i> Choleraesuis str. SC-B67
NC_021844.1	<i>Salmonella enterica</i> subsp. <i>enterica</i> Bareilly str. CFSAN000189
NC_011149.1	<i>Salmonella enterica</i> subsp. <i>enterica</i> Agona str. SL483
NC_022991.1	<i>Salmonella enterica</i> subsp. <i>enterica</i> Agona str. 24249
NC_010067.1	<i>Salmonella enterica</i> subsp. <i>arizonae</i> 62:z4
NC_015761.1	<i>Salmonella bongori</i> NCTC 12419
NC_021870.1	<i>Salmonella bongori</i> N268-08

Table S4. *E. coli* genes affected by EcsR1.

Gene ID	Fold Change (Log2) ^a	P value
<i>yjdK</i>	-4.44	6.6E-09
<i>narK</i>	-4.25	2.1E-02
<i>nirB</i>	-4.13	2.8E-02
<i>ansB</i>	-3.79	7.0E-07
<i>garP</i>	-3.78	1.7E-05
<i>ynfK</i>	-3.51	7.0E-07
<i>tdcA</i>	-3.51	7.0E-07
<i>bssR</i>	-3.22	2.5E-04
<i>yhbU</i>	-3.19	2.0E-05
<i>ychH</i>	-3.13	9.2E-06
<i>focA</i>	-3.12	9.8E-06
<i>dmsA</i>	-3.05	4.0E-02
<i>gntK</i>	-2.99	2.0E-05
<i>ydjX</i>	-2.97	3.1E-04
<i>yehD</i>	-2.94	3.4E-04
<i>chiP</i>	-2.85	1.2E-02
<i>yahN</i>	-2.80	1.2E-03
<i>narG</i>	-2.76	2.1E-02
<i>abrB</i>	-2.64	7.8E-04
<i>yjjM</i>	-2.61	5.9E-04
<i>ysaA</i>	-2.61	7.8E-04
<i>uspC</i>	-2.46	1.6E-03
<i>araF</i>	-2.40	1.2E-03
<i>garD</i>	-2.32	7.3E-03
<i>raiA</i>	-2.28	2.8E-03
<i>galS</i>	-2.26	4.1E-03
<i>wrbA</i>	-2.18	1.8E-02
<i>mocA</i>	-2.11	2.9E-02
<i>melR</i>	-2.11	1.9E-02
<i>yecH</i>	-2.10	2.8E-02
<i>yggA</i>	-2.01	3.1E-02
<i>ilvC</i>	-1.88	4.5E-02
<i>yfeC</i>	-1.87	4.4E-02
<i>yjcD</i>	1.89	3.7E-02
<i>purL</i>	1.97	2.4E-02

<i>purE</i>	2.08	3.7E-02
<i>ybjX</i>	2.14	1.7E-02
<i>dhaM</i>	2.15	7.3E-03
<i>nrdE</i>	2.18	1.6E-02
<i>yrfG</i>	2.20	3.1E-02
<i>yjjZ</i>	2.22	4.5E-02
<i>fepC</i>	2.36	3.0E-02
<i>uhpT</i>	3.52	7.0E-07

^aA negative value indicates lower gene expression in the sRNA-overexpression strain compared to control strain.

Table S5. Genes inhibited by *uspF-ompN* sRNA in *E. coli*.

Gene	GO Number and Functional Assignment ^a		FNR ^b	CRP ^b
<i>abrB</i>	GO:0031090	Organelle membrane	-	-
<i>araF</i>	GO:0016052	Carbohydrate catabolic process	-	Y
<i>dmsA</i>	GO:0031090	Organelle membrane	Y	-
<i>focA</i>	GO:0031090	Organelle membrane	Y	Y
	GO:0016052	Carbohydrate catabolic process		
<i>galS</i>	GO:0016052	Carbohydrate catabolic process	-	Y
<i>garD</i>	GO:0016052	Carbohydrate catabolic process	-	-
<i>garP</i>	GO:0031090	Organelle membrane	Y	-
	GO:0016052	Carbohydrate catabolic process		
<i>melR</i>	GO:0016052	Carbohydrate catabolic process	-	Y
<i>narG</i>	GO:0031090	Organelle membrane	Y	-
	GO:0042126	Nitrate metabolic process		
<i>narK</i>	GO:0031090	Organelle membrane	Y	-
	GO:0042126	Nitrate metabolic process		
<i>nirB</i>	GO:0042126	Nitrate metabolic process	Y	Y

^aGene ontology (GO) analysis using DAVID (Huang et al. 2009). Only overrepresented GO terms ($p < 0.05$) are shown.

^bBased on (Constantinidou et al. 2006; Keseler et al. 2013). Y indicates that FNR or CRP is known to regulate gene expression.

Table S6. *Salmonella* genes affected by EcsR1.

Gene ID	Fold Change (Log2) ^a	P value
STM14_1513	-3.86	5.5E-19
STM14_1514	-3.74	4.5E-16
<i>speF</i>	-3.69	6.0E-03
<i>potE</i>	-3.69	3.8E-05
STM14_0819	-3.49	3.0E-09
<i>yfiD</i>	-2.84	1.0E-07
<i>mgtC</i>	-2.46	6.3E-05
STM14_0421	-2.38	1.3E-03
STM14_5479	-2.37	3.0E-02
<i>yciG</i>	-2.32	3.9E-03
<i>yiaG</i>	-2.30	2.0E-07
<i>osmB</i>	-2.24	2.3E-03
<i>rcsA</i>	-2.21	4.9E-02
<i>ymdF</i>	-2.16	1.3E-06
<i>yiaD</i>	-2.11	7.3E-06
STM14_1526	-2.01	1.4E-03
<i>hisC</i>	-2.01	2.9E-04
STM14_1550	-2.01	2.9E-02
<i>aceE</i>	-1.98	1.5E-02
<i>ybiJ</i>	-1.92	4.7E-03
<i>ecnB</i>	-1.88	2.9E-04
<i>mgtB</i>	-1.85	4.2E-02
<i>hisH</i>	-1.79	6.0E-03
STM14_2239	-1.79	3.2E-04
STM14_3661	-1.72	1.2E-02
<i>rpsV</i>	-1.71	2.6E-04
STM14_1529	-1.71	3.2E-03
<i>marR</i>	-1.70	1.9E-02
<i>pliC</i>	-1.68	1.1E-02
<i>pta</i>	-1.61	1.4E-03
<i>nrdD</i>	-1.60	1.0E-02
<i>aceF</i>	-1.60	1.3E-03
<i>marB</i>	-1.57	4.7E-02
<i>ycdF</i>	-1.54	1.6E-02
STM14_5430	-1.50	8.0E-03
<i>ycfS</i>	-1.49	1.0E-02
<i>spy</i>	-1.49	4.2E-03

STM14_2188	-1.47	2.9E-02
<i>yhbO</i>	-1.46	3.9E-02
<i>marA</i>	-1.46	2.9E-02
<i>chaA</i>	-1.43	7.8E-03
STM14_949	-1.41	3.1E-02
<i>yhdV</i>	-1.40	8.8E-03
<i>ybhF</i>	-1.39	2.9E-02
STM14_2282	-1.36	2.2E-02
STM14_1521	-1.36	2.2E-02
<i>ygiM</i>	-1.34	2.5E-02
<i>htrA</i>	-1.33	1.4E-02
<i>hisD</i>	-1.32	4.9E-02
STM14_1528	-1.32	8.9E-03
<i>gcd</i>	-1.31	2.7E-02
<i>ecnR</i>	-1.29	2.4E-02
<i>katE</i>	-1.29	3.4E-02
<i>elaB</i>	-1.28	3.3E-02
STM14_2074	-1.26	2.0E-02
<i>chaB</i>	-1.20	5.1E-02
<i>phoB</i>	1.18	4.2E-02
<i>flhD</i>	1.21	3.3E-02
<i>csrB</i>	1.32	2.5E-02
<i>oafA</i>	1.34	2.5E-02
<i>sinR</i>	1.37	2.3E-02
<i>fdnG</i>	1.41	1.0E-02
<i>aer</i>	1.51	3.3E-02
<i>pstS</i>	1.51	3.6E-03
<i>trg</i>	1.55	2.5E-02
STM14_3479	1.59	1.1E-03
STM14_3799	1.60	2.3E-03
<i>fimD</i>	1.64	1.2E-02
<i>modA</i>	1.65	7.6E-03
<i>yneB</i>	1.66	2.6E-02
STM14_1163	1.66	6.0E-03
<i>fdnH</i>	1.74	4.6E-03
<i>ssaJ</i>	1.75	1.6E-02
<i>tsx</i>	1.79	5.7E-04
<i>sopA</i>	1.82	9.1E-05
<i>ompF</i>	1.91	2.0E-04
<i>avrA</i>	1.93	2.9E-02
<i>araC</i>	2.06	8.1E-03
<i>hilD</i>	2.12	1.5E-06
<i>prgK</i>	2.13	3.1E-02

STM14_2342	2.13	5.0E-05
STM14_5184	2.21	1.4E-03
<i>invC</i>	2.23	4.5E-02
<i>fimC</i>	2.24	5.7E-04
<i>fimZ</i>	2.25	3.6E-05
<i>hilA</i>	2.27	4.9E-05
<i>invE</i>	2.30	4.2E-02
<i>invG</i>	2.30	4.5E-02
<i>sicP</i>	2.35	1.0E-07
<i>spaQ</i>	2.40	6.2E-03
<i>sipD</i>	2.41	6.3E-03
<i>nmpC</i>	2.44	7.5E-08
<i>iagB</i>	2.44	1.3E-07
<i>prgH</i>	2.50	1.6E-02
STM14_0643	2.50	1.5E-02
<i>spaP</i>	2.55	2.9E-02
<i>sipC</i>	2.59	2.2E-02
<i>sopD</i>	2.63	2.9E-02
STM14_2387	2.63	2.0E-04
<i>sptP</i>	2.69	3.2E-03
<i>invA</i>	2.72	2.5E-03
STM14_1486	2.73	9.1E-05
<i>pipC</i>	2.77	4.1E-05
<i>sprB</i>	2.78	2.2E-03
<i>sipB</i>	2.89	1.3E-02
<i>sopE2</i>	2.90	3.4E-02
<i>iacP</i>	3.06	2.2E-03
STM14_5186	3.06	1.1E-08
<i>spaR</i>	3.10	3.5E-04
<i>rrfF</i>	3.10	1.0E-07
<i>hilC</i>	3.16	1.1E-08
<i>fimA</i>	3.16	1.5E-10
STM14_1487	3.17	1.2E-02
<i>sicA</i>	3.18	4.7E-02
STM14_5121	3.19	2.9E-02
STM14_5188	3.19	2.1E-14
STM14_1235	3.23	8.5E-09
STM14_1612	3.26	2.9E-04
STM14_5122	3.34	2.5E-02
<i>invI</i>	3.36	2.6E-02
STM14_5187	3.49	4.2E-05
<i>invB</i>	3.63	1.4E-02
STM14_3464	4.03	4.1E-02

STM14_4689	4.11	1.4E-04
STM14_5118	4.26	1.0E-05
STM14_5119	4.34	2.5E-05
STM14_5120	4.46	2.2E-04
STM14_5117	4.57	8.5E-09

^aA negative value indicates lower gene expression in the sRNA-overexpression strain compared to control strain.

Table S7. *Salmonella* processes affected by EcsR1.

GO Number ^a	GO Description	Genes	Regulation	P value
GO:0009405	Pathogenesis	<i>sicA, invE, invG, hilA, invB, sipB, invA, sipC, sipD, invC, spaP, spaQ, spaR, prgH, sptP, invI, prgK, sopE2, sicP, pipC, sopD, iagB</i>	Up	2.20E-25
GO:0008104	Protein localization	<i>sopD, invE, invG, invB, invA, invC, spaP, spaQ, spaR, ssaJ, prgK</i>	Up	1.30E-05
GO:0015031	Protein transport	<i>sopD, invE, invG, invB, invA, invC, spaP, spaQ, spaR, ssaJ, prgK</i>	Up	1.60E-05
GO:0045184	Establishment of protein localization	<i>sopD, invE, invG, invB, invA, invC, spaP, spaQ, spaR, ssaJ, prgK</i>	Up	1.60E-05
GO:0032940	Secretion by cell	<i>invE, invG, invB, invA, invC, spaP, spaQ, ssaJ,</i>	Up	9.00E-05

prgK

GO:0046903	Secretion	<i>invE, invG, invB, invA, invC, spaP, spaQ, ssaJ, prgK</i>	Up	9.00E-05
GO:0009306	Protein secretion	<i>invE, invG, invB, invA, invC, spaP, spaQ, ssaJ, prgK</i>	Up	9.00E-05
GO:0005576	Extracellular region	<i>sipB, sipC, sipD, sptP, sopE2</i>	Up	7.10E-03
GO:0009279	Cell outer membrane	<i>fimD, invG, nmpC, ssaJ, ompF, tsx, prgk</i>	Up	5.40E-02

^aGene ontology (GO) analysis using DAVID (Huang et al. 2009).

Figure S1

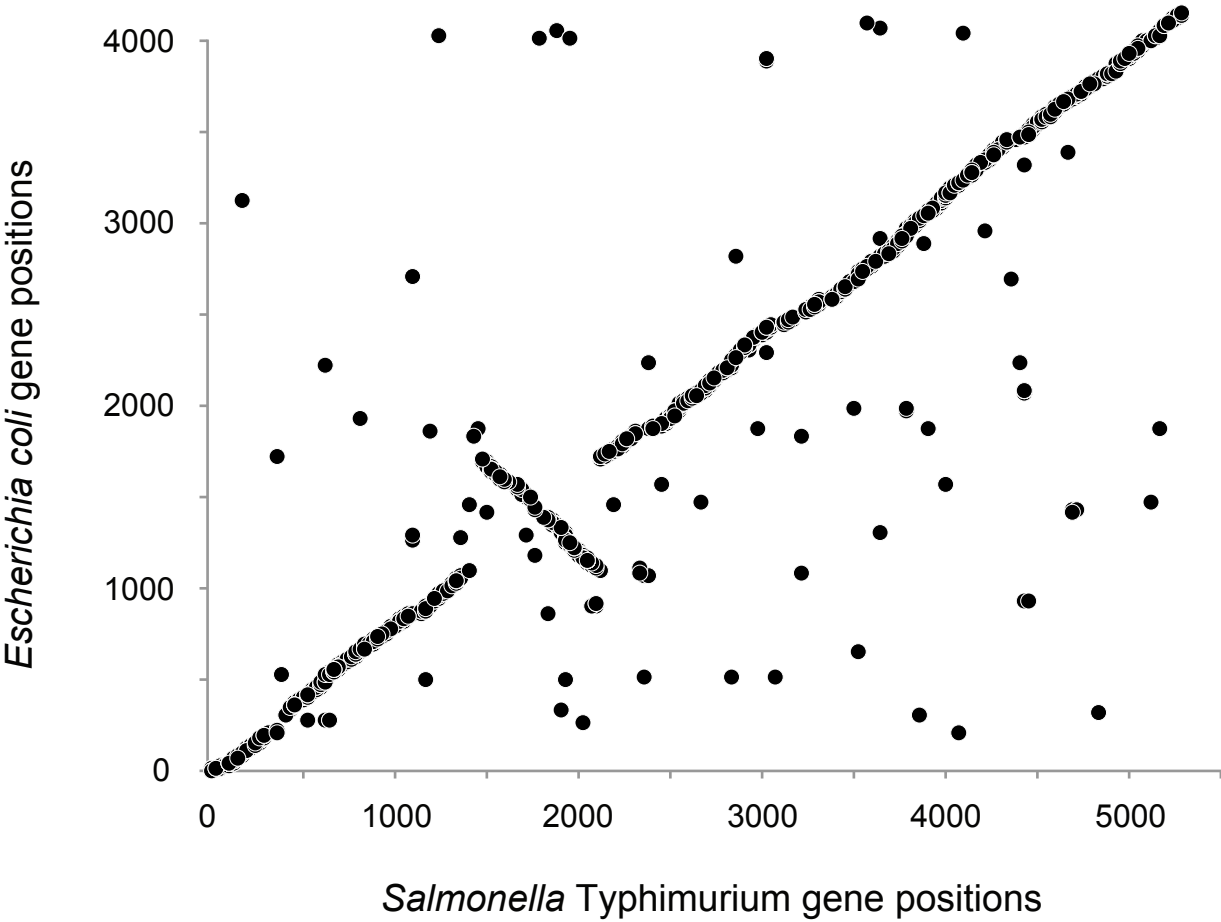


Figure S2

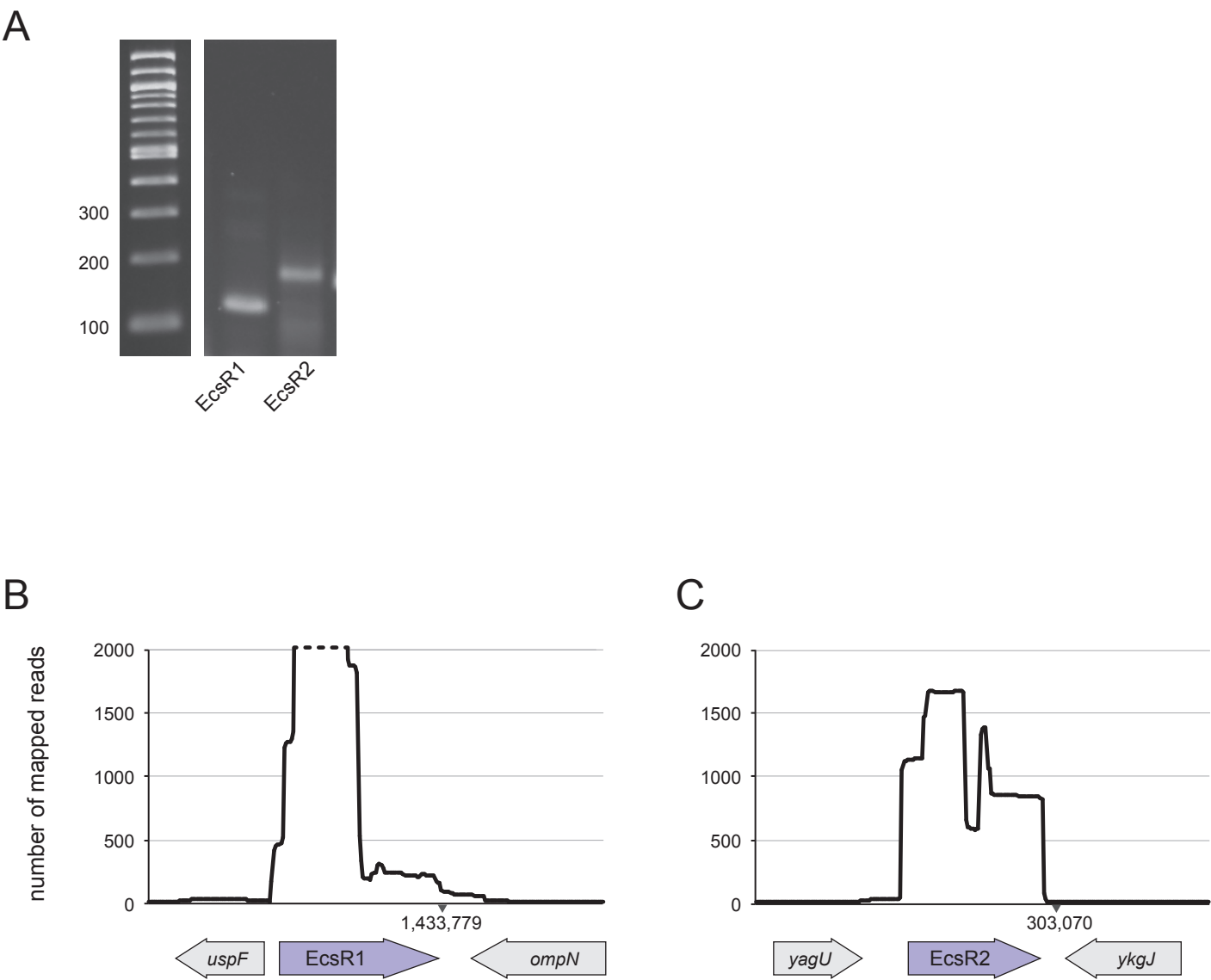


Figure S3

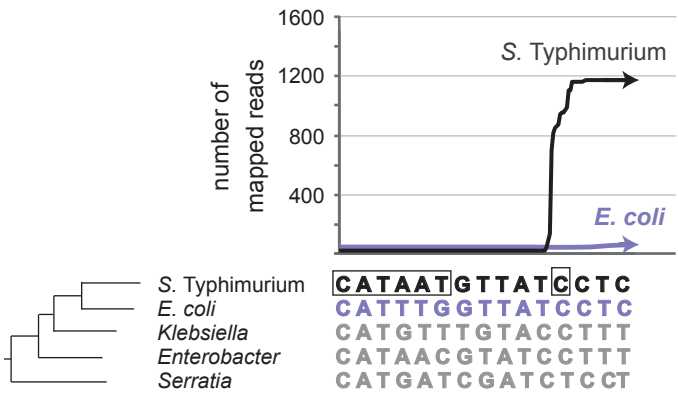


Figure S4

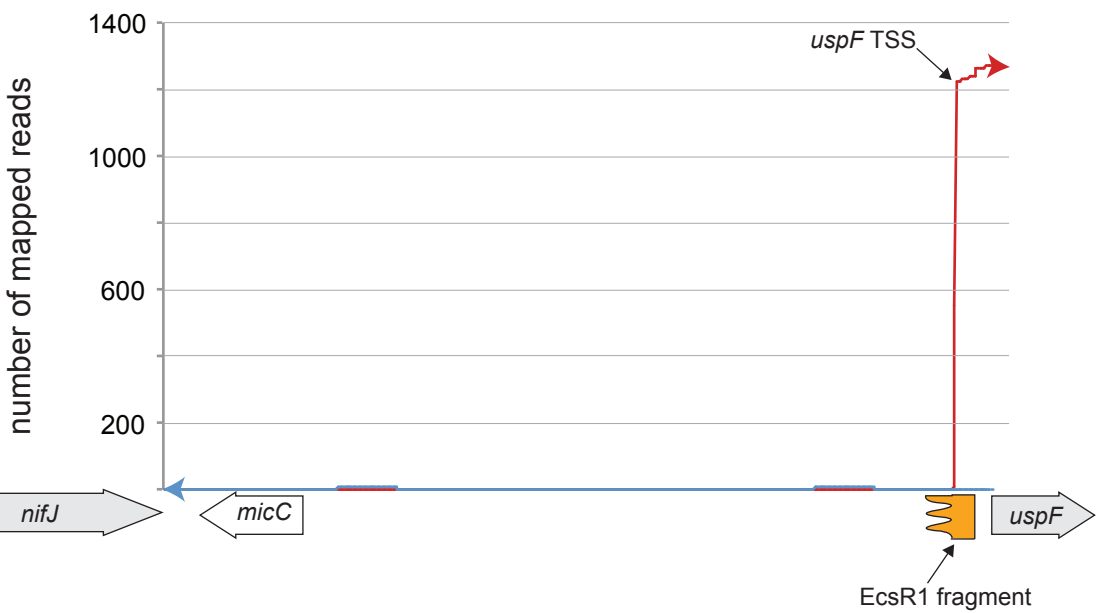
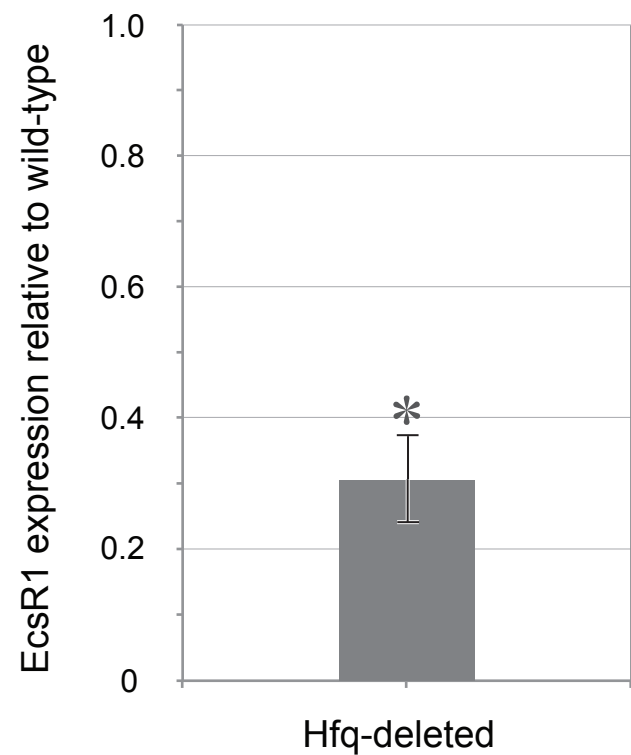


Figure S5

A



B

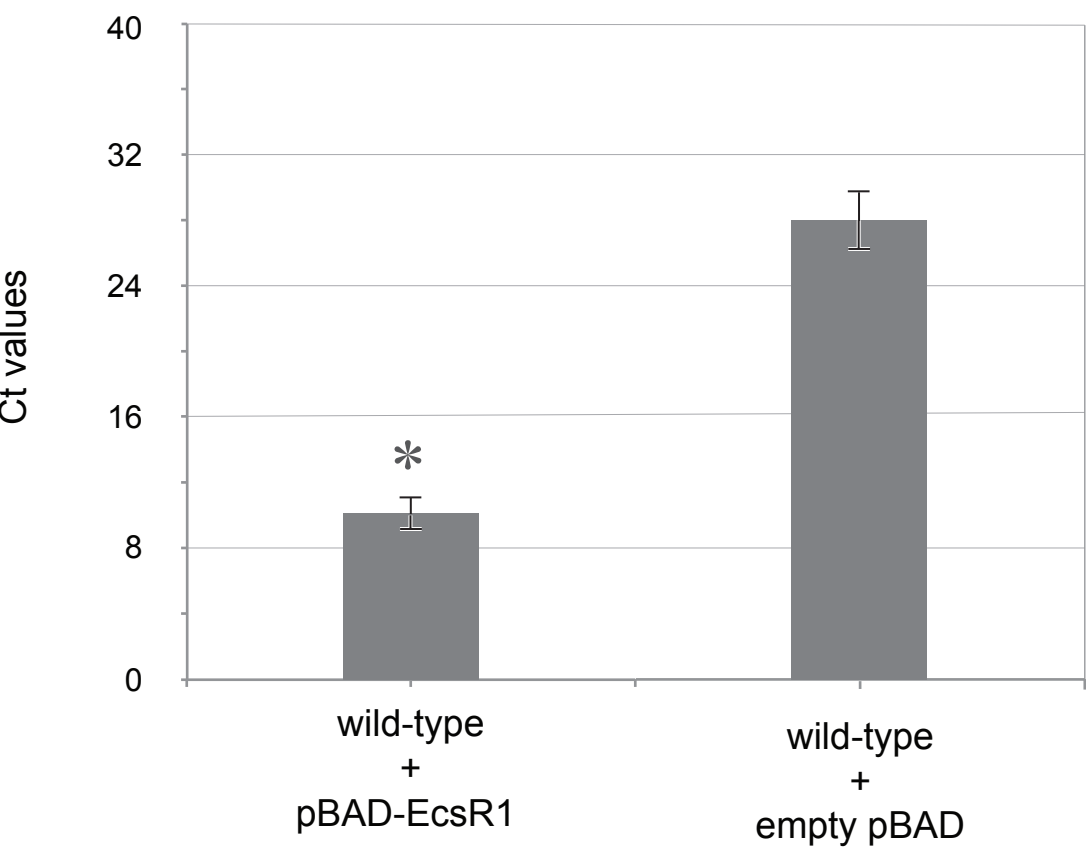


Figure S6

	FNR-binding site	CRP-binding site
<i>E. coli</i>	TTGCCTCTCCT	CAACGTGGCTAATCACGCGTG
<i>S. Typhimurium</i>	TTGCTTCAGCTT	CAACATGCGAAATCACGCGTG
	* ** *	* **