Supplementary data

Type I CRISPR-Cas provides robust immunity but incomplete attenuation of phage-induced cellular stress

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Supplementary figures

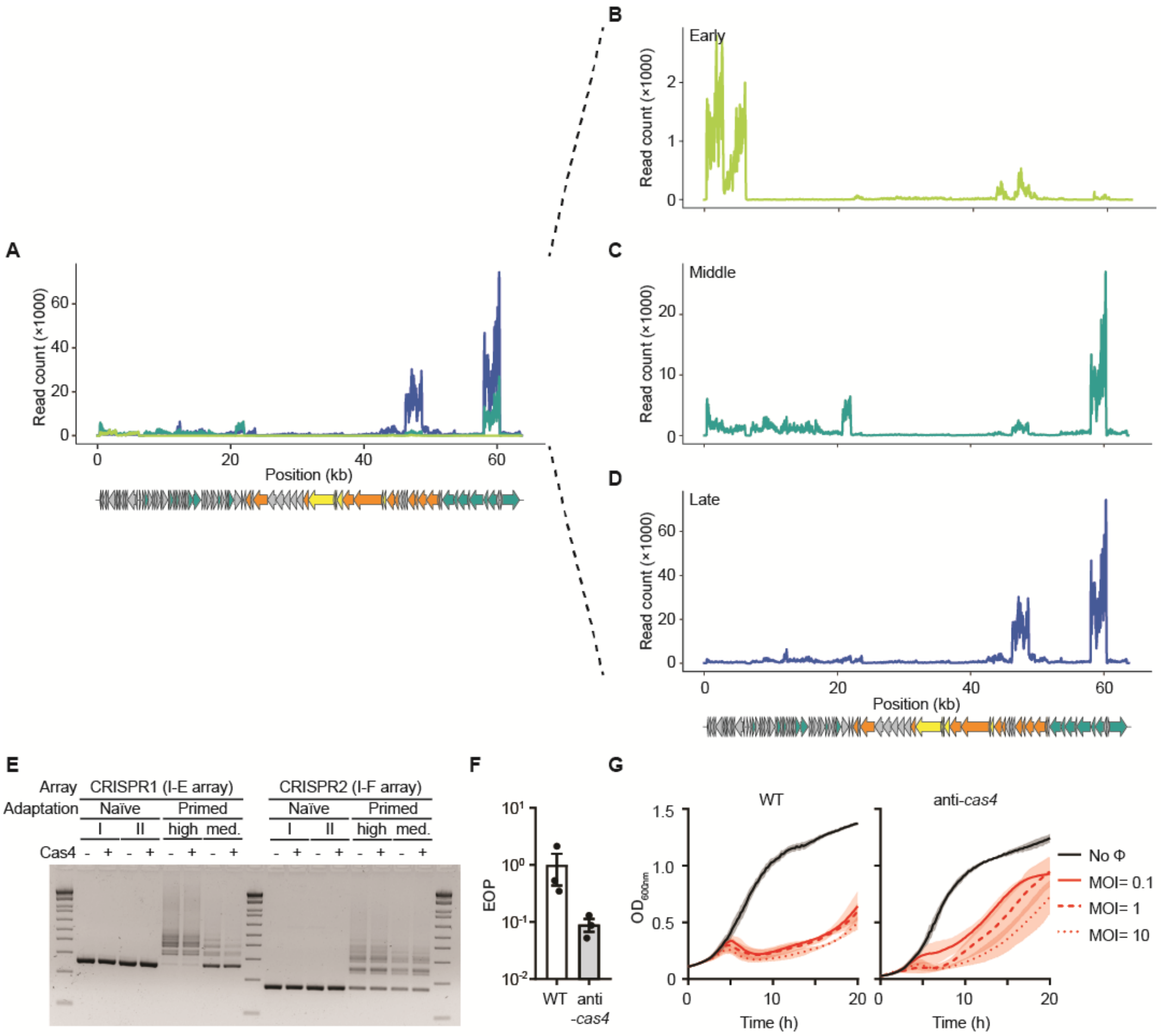

Figure S1. Phage genes are highly expressed during late infection. A. RNA read density plot across the JS26 genome at **B.** early (5 mpi), **C.** mid (20 mpi) and **D.** late (40 mpi) infection. For ease of visualisation, reads from either strand are shown in a single plot (note: no reads mapped to non-coding regions). One representative replicate per time point is shown. **E.** Type I-E and I-F array expansion during naïve (I, pPF953 and II, pPF719) and primed CRISPR adaptation (type I-E array expansion: high, pPF1233; medium, pPF1048 and type I-F array expansion: high, pPF1242; medium: pPF1243) during *cas4* overexpression (pPF2291, empty vector: pPF783) after 3 days of passaging. **F.** Plaquing efficiency and **G.** infection in liquid culture of *Serratia* with (anti-*cas4*, pPF2786) or without (WT, pPF1755, empty vector) CRISPR-dCas9 silencing vector. In E, F and G experiments were performed in three biological triplicates.

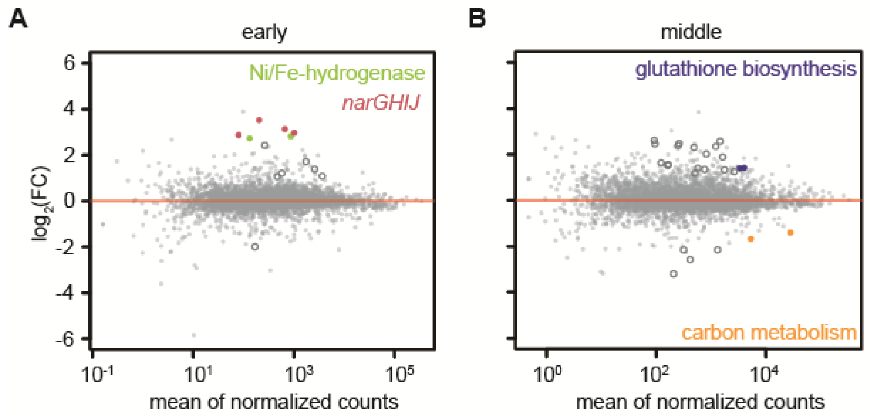

Figure S2. The host has a small early and mid response to phage infection. Expression landscape in *Serratia* during **A.** early (5 mpi) and **B.** mid (20 mpi) infection. Genes significantly differentially expressed ($\log_2(FC)>1.5$ and padj<0.05) are represented as coloured dots or empty circles.

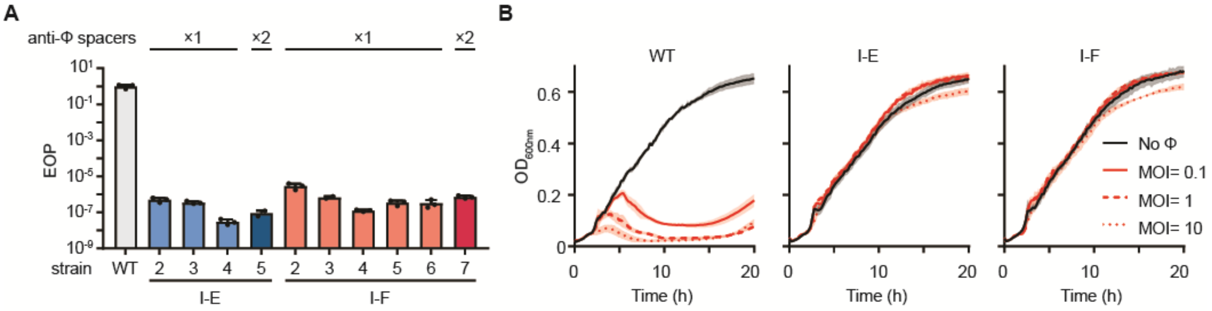

Figure S3. Type I CRISPR-Cas systems provide robust immunity against JS26.A. EOP assay on strains carrying anti-JS26 spacers in the CRISPR native arrays CRISPR1 (I-E) and CRISPR2 (I-F). Anti-JS26 I-E strains: 2 (PCF552), 3 (PCF554), 4 (PCF556), 5 (PCF558, ×2 anti-JS26 spacers) and anti-JS26 I-F strains: 2 (PCF562), 3 (PCF568), 4 (PCF574), 5 (PCF577), 6 (PCF579), 7 (PCF580, ×2 anti-JS26 spacers). **B.** Plate reader assay for *Serratia* WT and strains with anti-JS26 spacers in the I-E (PCF524) and I-F (PCF525) array uninfected (moi=0) or infected with JS26 (moi=0.1, 1 and 10). Data are represented as mean of biological triplicates ± SD (n=3).

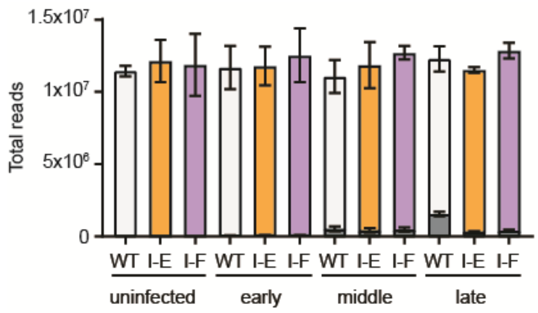

Figure S4. CRISPR immunity results in a reduced number of reads mapping to JS26 during late infection. Total number of reads mapping to *Serratia* WT (pale grey) and strains carrying anti-phage spacers in the I-E (orange, PCF524), and I-F (purple, PCF525) CRISPR arrays during early (5 mpi), mid (20 mpi) and late (40 mpi) infection. Total number of reads mapping to JS26 are represented as dark grey bars.

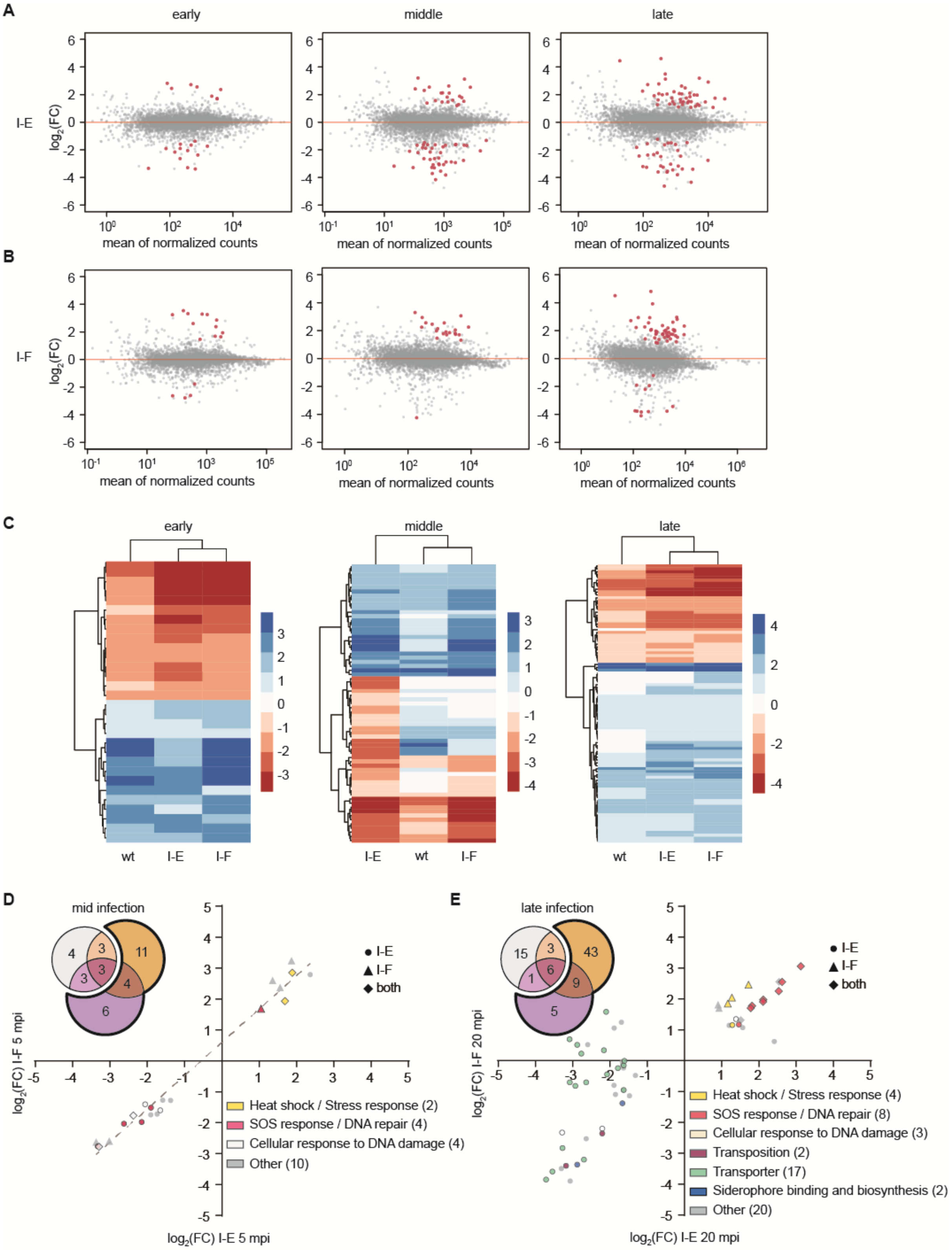

Figure S5. Type I-E and I-F targeting results in different transcriptomic landscapes. Expression landscape in **A.** type I-E and **B.** type I-F targeting strains during early, mid and late infection. Genes significantly differentially expressed ($\log_2(FC)>1.5$ and $padj<0.05$) are represented as red dots. **C.** Heat map of significantly differentially expressed genes in *Serratia* WT and type I-E and I-F targeting strains throughout infection. Comparison of expression landscape in the type I-E and type I-F targeting strains during **D.** early and **E.** mid infection. Number of genes significantly differentially expressed only in the I-E (●, orange in Venn diagram), the I-F (▲, purple in Venn diagram) or in both strains (◆, brown in Venn diagram) were classified into gene ontology.

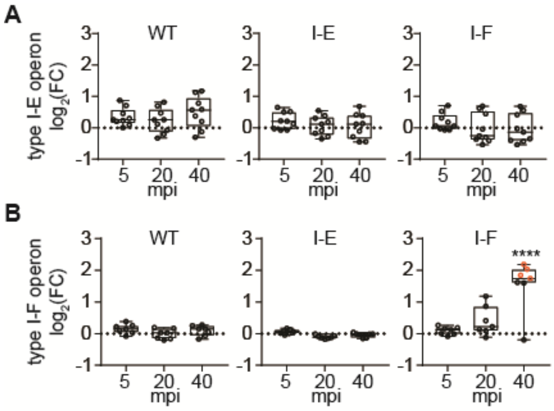

Figure S6. The type I-F CRISPR-Cas operon is upregulated upon type I-F targeting. Expression profile of genes encoded in the **A.** type I-E and **B.** type I-F CRISPR-Cas operon in *Serratia* WT and type I-E and type I-F targeting strains throughout infection. Genes significantly upregulated are represented as red dots. Statistical significance was calculated using a two-way ANOVA and a Tukey's test for multiple comparison. **** indicates a padj<0.0001.

Supplementary tables

Table S1. Primer list

Name	**Sequence**	Description/ Binding site
General cloning		
PF2296	TTTTACTAGTGATCGCCATCGCAATCTGAC	JS26 Tape measure gene with SpeI site fwd
PF2297	TTTTGGTACCAGTCCGGGCGTACCAATCAG	JS26 Tape measure gene with KpnI site rev
PF1403	AGCTCCTGAAAATCTCGATAAC	Screening primer pPF1257/58 fwd
PF1732	ATAAGATCTTGTTATCCGCTCACAAAGC	Screening primer pPF1257/58 rev
PF4692	GTTTTTTTGGGCTAGCGAATTCAAAGAGGAGAAATTAACTATGTCCCGCGGGGTGAC	*cas4* (*gp81*) + RBS, overlap with pPF783 (EcoRI) for pPF2291 fwd
PF4693	GTCATCCACTGCAGCATGCTTAATCTTCTTCGCCTTCTTCTTC	*cas4* (*gp81*), overlap with pPF783 (SphI) for construction of pPF2291 rev
PF2346	CTGCAAAAATGCAGTAATATCAAGAAGTTTTACATTGATTGGCTCCAATTCTTGGAG	Protospacer targeted by spacer 1 in CRISPR2 for pPF1242/43 fwd
PF2348	TTTTCCATGGTCTATTCCTGCAAAAATGCAGTAATATCAAG	Protospacer targeted by spacer 1 in CRISPR2 for pPF1242 (GAA_PAM) rev
PF2349	TTTTCCATGGTCTATGCCTGCAAAAATGCAGTAATATCAAG	Protospacer targeted by spacer1 in CRISPR2 for pPF1243 (GCA_PAM) rev
CRISPR expansion PCRs		
PF1989	TAAGTTAGTGTTCTTTAACAAGCAGGA	CRISPR1 expansion screening fwd
PF1887	GTTAAGTCAGCAGGCGTTTAGTCG	CRISPR1 expansion screening rev
PF633	GTGGATCTGGATGGACTGC	CRISPR1 expansion screening fwd
PF2177	TTACTGAATTCAGGCGTTTCGTCGTTTTGTG	CRISPR1 expansion screening rev
PF1990	CACGAAAATGATAATTGATGCTGAT	CRISPR2 expansion screening fwd
PF1888	CATCTGATGCTGACGACACTG	CRISPR2 expansion screening rev
Transposon mutagenesis / Arbitrary PCR		
PF106	GACCACACGTCGACTAGTGCNNNNNNNNNNAGAG	Random primed PCR primer 1
PF107	GACCACACGTCGACTAGTGCNNNNNNNNNNACGCC	Random primed PCR primer 2
PF108	GACCACACGTCGACTAGTGCNNNNNNNNNNGATAC	Random primed PCR primer 3
PF109	GACCACACGTCGACTAGTGC	Random primed PCR adapter primer
PF226	CATAAGGGACTCCTCATTAAG	Nested primer
PF1212	CGGGAATTCTCATGTTTGAC	Nested primer
RNA extraction DNA contamination screening		
PF796	ATAGAATTCAGGAGGAATATAATGGGTACTTCTGAGTTACTTAAGC	*flhDC* forward
PF797	GATCCCGGGTCAGACTGCGTGTTTTACTTG	*flhDC* reverse

Table S2. Plasmid list

Name	Features	Description	Construction	Reference
Priming vectors				
pPF1125	RP4/oriT, pBR322_origin, CmR, mCherry, lacI/T5	Phage priming vector with I-E PPS (spacer 1 CGT PAM)		(1)
pPF1126	RP4/oriT, pBR322_origin, CmR, mCherry, lacI/T5	Phage priming vector with I-F PPS (spacer 2 GT PAM)		(1)
pPF1257	RP4/oriT, pBR322_origin, CmR, mCherry, lacI/T5	Phage priming vector with I-E PPS (spacer 1 CGT PAM) with tail tape measure gene insert (*gp61*)	PF2296/PF2297 into pPF1125 (SpeI, KpnI)	This study
pPF1258	RP4/oriT, pBR322_origin, CmR, mCherry, lacI/T5	Phage priming vector with I-F PPS (spacer 2 GT PAM) with tail tape measure gene insert (*gp61*)	PF2296/PF2297 into pPF1126 (SpeI, KpnI)	This study
***cas4* heterologous expression**				
pPF783	OriT, p15A, GmR, AraC	Expression vector		Jackson, unpublished
pPF2291	OriT, p15A, GmR, AraC	*cas4* (*gp81*) expression vector	PF4692/PF4693 (JS26) into pPF783 (EcoRI, SphI)	This study
Adaptation assay				
pPF719	RP4/oriT, pBR322_origin, TcR, mCherry, lacI/T5	Naïve control priming plasmid (no protospacer)		(2)
pPF953	RP4/oriT, pBR322_origin, TcR, mCherry, lacI/T5	Naïve control priming plasmid (no protospacer)		(1)
pPF1233	RP4/oriT, pBR322_origin, TcR, mCherry, lacI/T5	Type I-E priming plasmid containing protospacer from CRISPR1 spacer 1 (CGT_PAM)		(3)
pPF1048	RP4/oriT, pBR322_origin, TcR, mCherry, lacI/T5	Type I-E priming plasmid containing protospacer from CRISPR1 spacer 1 (TCA_PAM)		(2)
pPF1242	RP4/oriT, pBR322_origin, TcR, mCherry, lacI/T5	Type I-F priming plasmid containing protospacer from CRISPR2 spacer 1 (GAA_PAM)	PF2346/PF2348 into pPF953 (NcoI/XhoI)	Jackson, unpublished
pPF1243	RP4/oriT, pBR322_origin, TcR, mCherry, lacI/T5	Type I-F priming plasmid containing protospacer from CRISPR2 spacer 1 (GCA_PAM)	PF2346/PF2348 into pPF953 (NcoI/XhoI)	Jackson, unpublished
CRISPRi				
pPF1755	oriT, RK2, KmR, AraC, dCas9	dCas9 HF expression vector		Jackson and Yin, unpublished
pPF2786	oriT, RK2, KmR, AraC, dCas9	dCas9 HF expression vector with gRNA targeting *cas4* (*gp81* in JS26)	pPF1755 (BsaI) + PF5506/PF5507	Malone and Harding, unpublished

Table S3. Strain list

Species	Strain	Description	Notes	Construction	Reference
E. coli	DH5α	Cloning strain			Gibco/BRL
E. coli	ST18	Auxotrophic donor for biparental conjugation	Requires ALA		(4)
Serratia sp. ATCC 39006	LacA	*lac* EMS mutant, denoted WT			(5)
Receptor mutants					
Serratia sp. ATCC 39006	PCF619	*flgI*::mini-Tn5, flagella mutant	KmR	transposon mutagenesis	This study
Serratia sp. ATCC 39006	PCF620	*flhD*::mini-Tn5, flagella mutant	KmR	transposon mutagenesis	This study
Serratia sp. ATCC 39006	PCF621	*fliR*::mini-Tn5, flagella mutant	KmR	transposon mutagenesis	This study
Serratia sp. ATCC 39006	PCF623	*flhC*::mini-Tn5, flagella mutant	KmR	transposon mutagenesis	This study
Serratia sp. ATCC 39006	PCF879	Δ*flhDC*, flagella master transcriptional regulator knock-out	CmR		(6)
Strains with spacers in native CRISPR arrays					
Serratia sp. ATCC 39006	PCF524	anti-JS26 spacer in type I-E system		plasmid loss with pPF1257	This study
Serratia sp. ATCC 39006	PCF552	anti-JS26 spacer in type I-E system		plasmid loss with pPF1257	This study
Serratia sp. ATCC 39006	PCF554	anti-JS26 spacer in type I-E system		plasmid loss with pPF1257	This study
Serratia sp. ATCC 39006	PCF556	anti-JS26 spacer in type I-E system		plasmid loss with pPF1257	This study
Serratia sp. ATCC 39006	PCF558	anti-JS26 spacer in type I-E system		plasmid loss with pPF1257	This study
Serratia sp. ATCC 39006	PCF525	anti-JS26 spacer in type I-F system		plasmid loss with pPF1258	This study
Serratia sp. ATCC 39006	PCF562	anti-JS26 spacer in type I-F system		plasmid loss with pPF1258	This study
Serratia sp. ATCC 39006	PCF568	anti-JS26 spacer in type I-F system		plasmid loss with pPF1258	This study
Serratia sp. ATCC 39006	PCF574	anti-JS26 spacer in type I-F system		plasmid loss with pPF1258	This study
Serratia sp. ATCC 39006	PCF577	anti-JS26 spacer in type I-F system		plasmid loss with pPF1258	This study
Serratia sp. ATCC 39006	PCF579	anti-JS26 spacer in type I-F system		plasmid loss with pPF1258	This study
Serratia sp. ATCC 39006	PCF580	anti-JS26 spacer in type I-F system		plasmid loss with pPF1258	This study

Table S4. Spacers in native CRISPR arrays

Strain name	a.k.a.	No. of new spacers	Sequence	Protospacer
PCF524	I-E_1	1	AAACTCGGCGGTACCGAGGGCGCGGCCTTCCA	Phage tape measure gene
PCF554	I-E_3	4	TAGGCCCACCCGCGAGCGGGTGTTCCTTCTTC	oriT
			GCCACGCCCACCGAGTCAGCGGCACCCTTGAT	Phage tape measure gene
			CGTGGCGCTTTCTCATAGCTCACGCTGTAGGT	pBR322_origin
			GGTGAACACTATCCCATATCACCAGCTCACCG	Cm resistance
PCF556	I-E_4	3	GCCGCTTTGTTGGCCTCCGCAAACTGGCGAAT	Phage tape measure gene
			CGTGGCGCTTTCTCATAGCTCACGCTGTAGGT	pBR322_origin
			GGTGAACACTATCCCATATCACCAGCTCACCG	Cm resistance
PCF558	I-E_5	5	GCGCGTGCTGCCGAGGACGGCGGGAAGGCTGA	Phage tape measure gene
			AGTGGAAGCGGCGATGGCGGAGCTGAATTACA	*lacI*
			ATTGCAGCGATCGAGCAGCAACTGCAGGCGGC	Phage tape measure gene
			CGTGGCGCTTTCTCATAGCTCACGCTGTAGGT	pBR322_origin
			GGTGAACACTATCCCATATCACCAGCTCACCG	Cm resistance
PCF525	I-F_1	1	TGATACTCGTCGAGGTTAGCCATCAGGGTGTT	Phage tape measure gene
PCF562	I-F_2	1	ACGATCGAGTCGAAGGCCACGCCCACCGAGTC	Phage tape measure gene
PCF568	I-F_3	2	TTGATGCCCATCTGCAGGTAGTCGTTGAGTTC	Phage tape measure gene
			ACTTCAAGAACTCTGTAGCACCGCCTACATAC	pBR322_origin
PCF574	I-F_4	2	GAACATATMGGACCATTMGGCAGTCCCGTTCT	Phage tape measure gene
			AGTTWTGATTTAAACGTGGCCAATATGGACAA	Cm resistance
PCF577	I-F_5	1	GGTAATGGCACCCATGTCGCCCTGCAGCGCTT	Phage tape measure gene
PCF579	I-F_6	2	CAGGACTCCTCCCTGCAGGACGGCGAGTTCAT	mCherry
			ATTTTATCGCCCCGGGTTGTCAGCCGGTCACG	Phage tape measure gene
PCF580	I-F_7	3	AATGTGCTGTTAAGCAGCAGCGCCTGGTCCCTC	Phage tape measure gene
			TGGGCCAACTTTTGGCGAAAATGAGACGTTGA	plasmid backbone
			CTTGATGCCCATCTGCAGGTAGTCGTTGAGTT	Phage tape measure gene

Table S5. JS26 genome annotation

ORF	Protein function	Start (bp)	Stop (bp)	Length (bp)	Proteomic hit[(1)]	Strand
gp01	Hypothetical protein CDS	752	895	144		-
gp02	Hypothetical protein CDS	892	1218	327		-
gp03	Hypothetical protein CDS	1205	1690	486		-
gp04	Hypothetical protein CDS	1693	1989	297		-
gp05	Hypothetical protein CDS	1989	2972	984		-
gp06	Hypothetical protein CDS	3080	3292	213		-
gp07	Hypothetical protein CDS	3279	3593	315		-
gp08	Hypothetical protein CDS	3586	3756	171		-
gp09	DnaA C-terminal domain containing protein CDS	3758	4243	486		-
gp10	Hypothetical protein CDS	4268	4543	276		-
gp11	Hypothetical protein CDS	4540	4860	321		-
gp12	Hypothetical protein CDS	4895	6073	1179		-
gp13	Hypothetical protein CDS	6099	6314	216		-
gp14	Hypothetical protein CDS	6676	6918	243		+
gp15	Hypothetical protein CDS	7132	7422	291		+
gp16	NAD-dependent DNA ligase CDS	7497	8003	507		+
gp17	Hypothetical protein CDS	7993	8622	630		+
gp18	Hypothetical protein CDS	8612	8881	270		+
gp19	Phage protein CDS	8932	9294	363		+
gp20	Hypothetical protein CDS	9297	9860	564		+
gp21	Hypothetical protein CDS	9853	10119	267		+
gp22	Phage protein CDS	10112	10900	789		+
gp23	Hypothetical protein CDS	10985	11248	264		+
gp24	Putative ssDNA binding protein CDS	11248	11775	528		+
gp25	Hypothetical protein CDS	11753	12046	294		+
gp26	Hypothetical protein CDS	12043	12231	189		+
gp27	Nucleoside Triphosphate Pyrophosphohydrolase CDS	12218	12589	372		+
gp28	Hypothetical protein CDS	12636	13031	396		+
gp29	Hypothetical protein CDS	13031	13384	354		+
gp30	Hypothetical protein CDS	13381	13614	234		+
gp31	Hypothetical protein CDS	13611	14000	390		+
gp32	Putative methylase CDS	13990	14718	729		+
gp33	DNA recombination-dependent growth factor C CDS	14720	15844	1125		+
gp34	Hypothetical protein CDS	16013	16396	384		+
gp35	Hypothetical protein CDS	16393	16671	279		+
gp36	Hypothetical protein CDS	16768	17406	639		+
gp37	Hypothetical protein CDS	17406	17717	312		+
gp38	Hypothetical protein CDS	17710	18429	720		+
gp39	Putative Nucleoside 2-deoxyribosyltransferase CDS	18429	18836	408		+
gp40	Hypothetical protein CDS	18907	19320	414		+
gp41	Hypothetical protein CDS	19492	19800	309		+

ORF	Protein function	Start (bp)	Stop (bp)	Length (bp)	Proteomic hit	Strand
gp42	Hypothetical protein CDS	19800	20045	246		+
gp43	N-6-adenine-methyltransferase CDS	20042	20749	708		+
gp44	Phage protein CDS	20884	21921	1038		+
gp45	Hypothetical protein CDS	21936	22124	189		+
gp46	Phage protein CDS	22284	22553	270		-
gp47	Phage capsid and scaffold CDS	22550	23314	765	x	-
gp48	Hypothetical protein CDS	23326	23655	330		-
gp49	Putative capsid protein CDS	23663	25786	2124	x	-
gp50	Hypothetical protein CDS	25796	27043	1248	x	-
gp51	Hypothetical protein CDS	27054	28199	1146	x	-
gp52	Phage protein CDS	28212	29228	1017	x	-
gp53	Phage protein CDS	29241	30191	951	x	-
gp54	Phage protein CDS	30194	31156	963	x	-
gp55	Tail fiber protein CDS	31156	31890	735	x	-
gp56	Putative tail assembly protein CDS	31902	35720	3819	x	-
gp57	Putative tail assembly protein CDS	35707	35928	222		-
gp58	Putative tail assembly protein CDS	35928	36170	243		-
gp59	Putative tail assembly protein CDS	36181	37002	822	x	-
gp60	Putative distal tail protein	37013	38698	1686	x	-
gp61	Putative tail length tape measure protein CDS	38709	42851	4143	x	-
gp62	Putative tail assembly protein CDS	42844	43089	246		-
gp63	Putative tail assembly protein CDS	43086	43547	462		-
gp64	Putative tail protein CDS	43677	44816	1140	x	-
gp65	Putative minor tail protein CDS	44829	45371	543	x	-
gp66	Phage protein CDS	45368	45985	618	x	-
gp67	Phage protein CDS	45987	46361	375	x	-
gp68	hypothetical protein CDS	46364	46735	372		-
gp69	Phage major capsid protein CDS	46799	47863	1065	x	-
gp70	Capsid decoration protein CDS	47874	48275	402	x	-
gp71	Head-tail preconnector protein GP5 CDS	48286	49575	1290	x	-
gp72	Phage portal protein CDS	49581	51284	1704	x	-
gp73	Head-tail joining protein CDS	51284	51538	255	x	-
gp74	Hypothetical protein CDS	51549	51857	309		-
gp75	Terminase large subunit CDS	51972	53630	1659		-
gp76	Terminase small subunit CDS	53614	54240	627		-
gp77	DNA helicase, phage-associated CDS	54240	55727	1488		-
gp78	VRR-NUC domain protein CDS	55714	56001	288		-
gp79	DNA polymerase B region CDS	55998	58064	2067		-
gp80	Putative ligase CDS	58157	58741	585		-
gp81	Putative Cas4 CDS	58762	60057	1296		-
gp82	Hypothetical protein CDS	60057	60458	402		-
gp83	Hypothetical protein CDS	60682	60942	261		+
gp84	DNA primase/helicase, phage-associated CDS	60952	63522	2571		+

(1) Details provided in Table S6.

Table S6. Proteomic hits

ORF	Description	# Unique Peptides[1]	# PSMs[2]	Coverage (%)[3]	Sum PEP Score[4]	Score Mascot[5]
gp47	Phage capsid and scaffold CDS	3	10	15.0	17.0	150.3
gp49	Putative capsid protein CDS	68	1241	87.9	951.0	21469.9
gp50	Hypothetical protein CDS	34	1182	74.0	556.2	21306.4
gp51	Hypothetical protein CDS	23	1214	65.9	431.4	20354.0
gp52	Phage protein CDS	63	2108	86.1	694.9	41213.1
gp53	Phage protein CDS	35	1677	76.9	538.7	36132.3
gp54	Phage protein CDS	49	1654	93.4	625.6	30050.2
gp55	Tail fibre protein CDS	16	483	81.1	329.0	7820.9
gp56	Putative tail assembly protein CDS	152	2748	82.4	1967.1	43757.5
gp59	Putative tail assembly protein CDS	28	743	75.5	316.2	11922.2
gp60	Putative distal tail protein	49	1508	64.2	630.7	25676.0
gp61	Putative tape measure protein CDS	223	5751	84.2	3275.0	109573.6
gp64	Putative tail protein CDS	169	14174	84.4	2195.9	254994.2
gp65	Putative minor tail protein CDS	18	682	92.9	361.0	10805.6
gp66	Phage protein CDS	13	291	68.8	248.7	5448.1
gp67	Phage protein CDS	12	234	83.9	152.3	4642.6
gp69	Phage major capsid protein CDS	276	27045	97.2	4065.4	419874.7
gp70	Capsid decoration protein CDS	101	3541	100.0	1375.0	59501.7
gp71	Head-tail preconnector protein CDS	27	373	54.3	297.5	6800.3
gp72	Phage portal protein CDS	124	4507	84.0	1751.1	79681.0
gp73	Head-tail joining protein CDS	10	260	98.8	110.3	5326.1

[1] Unique peptides identified per protein. [2] The number of acquired peptide spectra per protein (PSMs - peptide spectral matches), resulting in the identified [3] sequence coverage (coverage (%)). [4] Protein score calculated as the negative logarithms of the Posterior Error Probability values of PSMs. [5] Score calculated by search engine Mascot.

Table S7. Genes differentially expressed in *Serratia* during phage infection

ORF (CWC46_)	Function	GO molecular function	log2(FC)	lfcSE	padj
Early infection					
RS02465	ribose ABC transporter permease	transport activity	1.39	0.20	1.67E-02
RS05850	NhaA, Na+/H+ antiporter	sodium ion transport / pH regulation	1.21	0.13	1.86E-03
RS10625	Ni/Fe-hydrogenase cytochrome b subunit	unknown	2.73	0.51	1.47E-02
RS10630	cytochrome-c3 hydrogenase	redox activity	2.82	0.53	1.47E-02
RS12605	NarG, nitrate reductase subunit alpha	nitrate reductase activity / electron carrier	2.97	0.64	4.90E-02
RS12610	NarH, nitrate reductase subunit beta	nitrate reductase activity / electron carrier	3.13	0.60	1.47E-02
RS12615	NarJ, nitrate reductase molybdenum cofactor assembly chaperone	nitrate reductase activity / electron carrier	3.52	0.60	1.51E-03
RS12620	NarI, respiratory nitrate reductase subunit gamma	nitrate reductase activity / electron carrier	2.88	0.46	1.51E-03
RS16055	LysR family transcriptional regulator	transcription regulation	1.72	0.27	1.54E-02
RS16060	S-(hydroxymethyl)glutathione dehydrogenase/class III alcohol dehydrogenase	redox activity	1.08	0.13	4.90E-02
RS18585	GalS, HTH-type transcriptional regulator	transcription regulation	-1.99	0.34	1.52E-02
RS19145	PhoB, phosphate regulon transcriptional regulatory protein	transcription regulation / phosphorelay signal transduction	1.06	0.12	3.04E-02
RS21500	hypothetical protein	unknown	2.43	0.45	1.77E-02
Mid infection					
RS00220	LysR family transcriptional regulator	transcription regulation	2.48	0.44	7.18E-03
RS00965	FadB, fatty acid oxidation complex subunit alpha	fatty acid metabolism	2.57	0.40	3.43E-04
RS00970	FadA, acetyl-CoA C-acyltransferase	fatty acid metabolism	2.30	0.39	4.03E-03
RS03770	PutA, trifunctional transcriptional regulator/proline dehydrogenase/L-glutamate gamma-semialdehyde dehydrogenase	transcription regulation / amino acid biosynthesis	2.34	0.28	2.94E-07
RS05275	iron permease FTR1	iron transport	-2.16	0.40	1.92E-02
RS05850	NhaA, Na+/H+ antiporter	sodium ion transport	2.02	0.22	8.06E-08
RS05855	NhaR, transcriptional activator	transcription regulation / sodium ion transport	1.35	0.15	2.24E-04
RS06280	PdhR, pyruvate dehydrogenase complex transcriptional repressor	transcription regulation / pyruvate dehydrogenase	-1.68	0.29	2.93E-02
RS06285	AceE, pyruvate dehydrogenase (acetyl-transferring), homodimeric type	pyruvate dehydrogenase	-1.40	0.20	1.46E-02
RS07090	DUF2502 domain-containing protein	unknown	1.56	0.27	4.87E-02

ORF (CWC46_)	Function	GO molecular function	log2(FC)	lfcSE	padj
RS07105	DUF1107 domain-containing protein	unknown	1.88	0.17	1.43E-10
RS07620	FadE, acyl-CoA dehydrogenase	fatty acid metabolism	1.40	0.21	1.84E-02
RS10685	DUF2002 domain-containing protein	unknown	2.61	0.30	5.37E-08
RS10950	hypothetical protein	unknown	2.46	0.36	1.94E-04
RS11860	glycine zipper 2TM domain-containing protein	outer membrane	2.39	0.46	2.21E-02
RS12150	esterase	carbohydrate metabolism	-2.16	0.39	1.46E-02
RS15300	CutC, copper homeostasis protein	copper ion homeostasis	1.17	0.15	1.71E-02
RS16060	FrmA, S-(hydroxymethyl)glutathione dehydrogenase/class III alcohol dehydrogenase	glutathione biosynthesis	1.41	0.20	1.46E-02
RS16065	FghA, S-formylglutathione hydrolase	glutathione biosynthesis	1.40	0.22	3.98E-02
RS16520	LamB/YcsF family protein	carbohydrate metabolism	1.63	0.24	4.03E-03
RS18615	ABC transporter substrate-binding protein	transport	-3.20	0.57	2.12E-03
RS18620	TonB-dependent siderophore receptor	siderophore transport	-2.58	0.51	1.92E-02
RS18680	MenD, 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylic-acid synthase	menaquinone biosynthesis	1.33	0.18	1.46E-02
RS18685	MenF, isochorismate synthase	menaquinone biosynthesis	1.24	0.14	6.43E-04
RS21855	ABC transporter substrate-binding protein	polyamine transport	1.52	0.24	2.59E-02
Late infection					
RS00005	AspA, aspartate ammonia-lyase	TCA cycle	-1.25	0.18	1.09E-02
RS00015	anaerobic C4-dicarboxylate transporter	C4-dicarboxylate transport	-1.49	0.19	2.98E-04
RS01325	XylR, xylose operon transcription regulator	transcription regulation	1.25	0.19	3.09E-02
RS01395	HAMP domain-containing protein	chemotaxis	-1.40	0.23	1.94E-02
RS01725	ABC transporter ATP-binding protein	peptide transport	1.47	0.26	2.82E-02
RS01730	L-Ala-D/L-Glu epimerase	amino acid catabolism	1.63	0.24	9.06E-04
RS01970	carbon starvation protein A	cellular response to starvation	-4.49	0.27	1.56E-45
RS01975	phosphoenolpyruvate carboxylase	TCA cycle	1.22	0.10	2.46E-08
RS02115	LigB, NAD-dependent DNA ligase	DNA replication	1.60	0.29	2.32E-02
RS02180	nitrogen regulation protein NR(II)	transcription regulation / phosphorelay signal transduction	-0.98	0.12	4.57E-02
RS03125	malate permease	organic anion transport	-3.43	0.78	1.47E-02

ORF (CWC46_)	Function	GO molecular function	log2(FC)	lfcSE	padj
RS03335	GntP family transporter	gluconate transport	-1.41	0.24	2.82E-02
RS03345	aldolase	unknown	-1.45	0.20	1.38E-03
RS03355	NAD(P)-dependent oxidoreductase	redox activity	-1.41	0.25	3.64E-02
RS03495	agmatine deiminase	putrescine biosynthesis	1.95	0.28	1.10E-04
RS03720	ilv operon leader peptide	branched-chain amino acid biosynthesis	1.78	0.35	2.82E-02
RS03725	acetolactate synthase 2 catalytic subunit	branched-chain amino acid biosynthesis	2.26	0.25	5.40E-09
RS03730	acetolactate synthase 2 small subunit	branched-chain amino acid biosynthesis	1.44	0.22	5.15E-03
RS03770	PutA, trifunctional transcriptional regulator/proline dehydrogenase/L-glutamate gamma-semialdehyde dehydrogenase	transcription regulation / amino acid biosynthesis	2.89	0.22	5.53E-23
RS05535	YjeF, bifunctional ADP-dependent NAD(P)H-hydrate dehydratase/NAD(P)H-hydrate epimerase	nucleotide metabolism	1.79	0.35	2.63E-02
RS05725	oxidative stress defence protein	oxidative stress	1.17	0.12	2.65E-04
RS05795	bifunctional aspartate kinase/homoserine dehydrogenase I	L-lysine, L-methionine, L-threonine biosynthesis / amino acid biosynthesis	1.22	0.19	3.17E-02
RS05840	DnaK, molecular chaperone	heat shock response/ protein folding	1.88	0.29	9.06E-04
RS05845	DnaJ, molecular chaperone	heat shock response/ protein folding	1.77	0.29	2.86E-03
RS05850	NhaA, Na+/H+ antiporter	sodium ion transport	1.95	0.17	1.60E-12
RS05855	NhaR, transcriptional activator	transcription regulation / sodium ion transport	1.07	0.14	2.32E-02
RS06280	PdhR, pyruvate dehydrogenase complex transcriptional repressor	transcription regulation / pyruvate dehydrogenase	-1.39	0.19	1.61E-03
RS06285	AceE, pyruvate dehydrogenase (acetyl-transferring), homodimeric type	pyruvate dehydrogenase	-1.43	0.12	9.85E-10
RS06290	pyruvate dehydrogenase complex dihydrolipoyllysine-residue acetyltransferase	pyruvate dehydrogenase	-1.23	0.17	6.06E-03
RS07090	DUF2502 domain-containing protein	unknown	2.39	0.18	5.78E-21
RS07105	DUF1107 domain-containing protein	unknown	1.94	0.21	3.50E-08
RS07300	CysJ, NADPH-dependent assimilatory sulfite reductase flavoprotein subunit	cysteine biosynthesis / amino acid biosynthesis	1.91	0.41	4.57E-02
RS09040	inositol-1-monophosphatase	inositol phosphate dephosphorylation	-1.27	0.18	8.35E-03
RS09050	IscR, Fe-S cluster assembly transcriptional regulator	regulation of transcription	1.66	0.22	1.40E-04
RS09545	transmembrane protein	membrane	1.24	0.12	2.13E-05
RS09860	ManC, mannose-1-phosphate guanylyltransferase/mannose-6-phosphate isomerase	LPS biosynthesis	1.17	0.17	2.48E-02
RS10405	acetate kinase	organic acid metabolism	-1.11	0.13	2.16E-03
RS10615	HydA, hydrogenase (NiFe) small subunit	redox activity	-1.95	0.33	2.69E-03

ORF (CWC46_)	Function	GO molecular function	log2(FC)	lfcSE	padj
RS10685	DUF2002 domain-containing protein	unknown	4.10	0.24	1.57E-46
RS10690	hypothetical protein	unknown	3.65	0.74	2.86E-03
RS10950	hypothetical protein	unknown	2.10	0.29	2.94E-05
RS10955	sugar ABC transporter permease	sugar transport	2.22	0.32	8.23E-05
RS11350	FlhC, flagellar transcriptional regulator	transcriptional regulation of flagellum assembly	-1.45	0.19	5.57E-04
RS11375	HAMP domain-containing protein	chemotaxis	-1.11	0.15	2.25E-02
RS11380	CheR, protein-glutamate O-methyltransferase	chemotaxis	-0.95	0.11	3.32E-02
RS11400	FlhB, flagellar type III secretion system protein	flagellum assembly	-1.09	0.12	3.36E-03
RS11430	FlgB, flagellar basal body rod protein	flagellum assembly	-1.19	0.18	4.15E-02
RS11540	FliG, flagellar motor switch protein	flagellum assembly	-1.20	0.19	3.68E-02
RS11545	FliF, flagellar basal body M-ring protein FliF	flagellum assembly	-1.11	0.16	4.36E-02
RS11550	FliE, flagellar hook-basal body complex protein FliE	flagellum assembly	-1.27	0.16	1.17E-03
RS11580	hypothetical protein	unknown	-1.12	0.13	3.82E-03
RS11585	DegT/DnrJ/EryC1/StrS family aminotransferase	transaminase activity	-1.13	0.16	3.10E-02
RS11860	glycine zipper 2TM domain-containing protein	outer membrane	3.89	0.32	2.72E-22
RS12135	PTS beta-glucoside transporter subunit IIABC	transport	-2.46	0.38	1.16E-04
RS12140	6-phospho-beta-glucosidase	carbohydrate metabolism	-2.77	0.35	1.68E-07
RS12145	carbohydrate porin	transport	-3.19	0.49	1.91E-05
RS12150	esterase	carbohydrate metabolism	-3.34	0.36	2.25E-11
RS12155	hypothetical protein	unknown	-3.00	0.47	5.99E-05
RS12185	non-ribosomal peptide synthetase	catalytic activity	-1.47	0.25	1.94E-02
RS12280	DUF2091 domain-containing protein	unknown	1.54	0.24	5.24E-03
RS12340	osmotically-inducible lipoprotein OsmB	oxidative stress	1.72	0.28	3.91E-03
RS12875	ShlB/FhaC/HecB family hemolysin secretion/activation protein	protein transport	-1.29	0.20	1.94E-02
RS13350	NAD(P)(+) transhydrogenase (Re/Si-specific) subunit alpha	redox activity	2.02	0.31	5.57E-04
RS13355	NAD(P)(+) transhydrogenase (Re/Si-specific) subunit beta	redox activity	2.35	0.39	6.84E-04
RS13465	SfrC, virulence effector protein	virulence factor	-1.13	0.15	1.50E-02

ORF (CWC46_)	Function	GO molecular function	log2(FC)	lfcSE	padj
RS13470	SrfB, virulence protein	virulence factor	-1.15	0.17	3.55E-02
RS13475	hypothetical protein	virulence factor	-1.13	0.14	8.20E-03
RS13630	MFS transporter	transport	2.36	0.43	2.86E-03
RS13785	DtpA, dipeptide/tripeptide permease	peptide transport	-1.81	0.35	2.63E-02
RS14540	23S rRNA (guanine(745)-N(1))-methyltransferase	rRNA methylation / rRNA processing	-1.15	0.16	1.77E-02
RS14885	FkbM family methyltransferase	unknown	-1.10	0.15	3.52E-02
RS15300	CutC, copper homeostasis protein	copper ion homeostasis	1.27	0.16	2.29E-03
RS15650	FAA hydrolase family protein	catalytic activity	-1.38	0.18	1.38E-03
RS15655	hypothetical protein	organic anion transport	-2.19	0.28	3.63E-06
RS15675	hypothetical protein	catalytic activity	1.56	0.30	4.31E-02
RS15785	DmsD, Tat proofreading chaperone	protein folding	1.53	0.20	3.75E-04
RS15945	DUF2593 domain-containing protein	unknown	1.88	0.37	2.32E-02
RS16005	serine hydrolase	proteolysis	1.28	0.16	9.18E-04
RS16160	DUF2807 domain-containing protein	unknown	1.50	0.26	2.32E-02
RS16165	cytochrome P450	redox activity	1.63	0.25	2.29E-03
RS16175	hypothetical protein	unknown	1.40	0.24	3.32E-02
RS16270	hypothetical protein	unknown	1.46	0.16	1.49E-05
RS16275	ABC transporter ATP-binding protein	transport	1.39	0.24	3.90E-02
RS16280	hypothetical protein	unknown	1.48	0.26	2.82E-02
RS16385	hypothetical protein	unknown	-1.99	0.35	3.39E-03
RS16390	hypothetical protein	unknown	-2.19	0.48	3.78E-02
RS16540	hypothetical protein	unknown	1.31	0.14	1.91E-05
RS17240	anaerobic C4-dicarboxylate transporter	C4-dicarboxylate transport	-1.41	0.22	1.09E-02
RS17330	alanyl-tRNA editing protein	tRNA aminoacylation	-1.75	0.27	1.09E-03
RS18075	cytochrome bd-I ubiquinol oxidase subunit I	aerobic electron transport chain	-1.59	0.26	7.35E-03
RS18615	ABC transporter substrate-binding protein	transport	-2.49	0.51	1.09E-02
RS18620	TonB-dependent siderophore receptor	siderophore transport	-2.18	0.42	8.42E-03

ORF (CWC46_)	Function	GO molecular function	**log2(FC)**	lfcSE	padj
RS18660	MenE, o-succinylbenzoate--CoA ligase	menaquinone biosynthesis	1.71	0.24	5.24E-04
RS18665	MenC, o-succinylbenzoate synthase	menaquinone biosynthesis	1.63	0.27	6.06E-03
RS18670	MenB, 1, 4-dihydroxy-2-naphthoyl-CoA synthase	menaquinone biosynthesis	1.73	0.27	1.70E-03
RS18675	MenH, 2-succinyl-6-hydroxy-2%2C4-cyclohexadiene-1-carboxylate synthase	menaquinone biosynthesis	1.88	0.26	1.25E-04
RS18680	MenD, 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylic-acid synthase	menaquinone biosynthesis	1.66	0.15	2.47E-10
RS18685	MenF, isochorismate synthase	menaquinone biosynthesis	1.61	0.10	2.72E-22
RS18725	NrdA, ribonucleoside-diphosphate reductase subunit alpha	DNA replication	1.26	0.17	3.84E-03
RS20365	IS1 family transposase	transposition	-2.43	0.48	8.42E-03
RS20700	PigA, butyryl-CoA dehydrogenase	antibiotic biosynthesis	1.82	0.37	3.97E-02
RS21305	IolD, 3D-(3%2C5/4)-trihydroxycyclohexane-1%2C2-dione acylhydrolase (decyclizing)	inositol catabolism	1.31	0.22	4.15E-02
RS21820	acetolactate synthase AlsS	valine biosynthesis / amino acid biosynthesis	1.17	0.18	4.77E-02
RS21855	hypothetical protein	unknown	1.64	0.23	5.00E-04
RS22235	hypothetical protein	unknown	1.79	0.20	6.19E-07
RS22565	OsmY, molecular chaperone	protein folding	1.57	0.14	1.96E-10
RS22725	MFS transporter	transport	-1.43	0.21	2.96E-03
RS22750	LysR family transcriptional regulator	transcriptional regulation	-1.36	0.13	2.85E-07

Table S8. Genes differentially expressed in *Serratia* I-E anti-JS26 strain

DE in strains	locus_tag	product	GO molecular function	$\log_2$(FC)	lfcSE	padj
Early infection						
wt, I-E, I-F	RS02465	ribose ABC transporter permease	sugar transport	1.71	0.26	9.54E-03
wt, I-E, I-F	RS10625	Ni/Fe-hydrogenase cytochrome b subunit	anaerobic respiration	2.82	0.54	1.32E-02
wt, I-E, I-F	RS12610	NarH, nitrate reductase subunit beta	nitrate reductase activity	2.72	0.44	8.89E-04
wt, I-E	RS12605	NarG, nitrate reductase subunit alpha	nitrate reductase activity	2.56	0.40	8.89E-04
wt, I-E	RS18585	GalS, HTH-type transcriptional regulator	transcriptional regulation	-3.38	0.44	4.99E-07
wt, I-E	RS21500	hypothetical protein	unknown	2.45	0.41	3.83E-03
I-E, I-F	RS00965	FadB, fatty acid oxidation complex subunit alpha	fatty acid metabolism	-2.37	0.41	8.27E-03
I-E, I-F	RS02455	ribokinase	D-ribose metabolism	1.69	0.28	2.34E-02
I-E, I-F	RS02475	RbsD, D-ribose pyranase	monosaccharide metabolism	1.89	0.33	2.66E-02
I-E, I-F	RS10190	FadL, long-chain fatty acid transporter	fatty acid transport	-3.29	0.41	1.11E-07
I-E	RS00220	LysR family transcriptional regulator	transcriptional regulation	-2.64	0.50	1.37E-02
I-E	RS00970	FadA, acetyl-CoA C-acyltransferase	fatty acid metabolism	-2.06	0.38	2.66E-02
I-E	RS01640	PtsN, PTS IIA-like nitrogen-regulatory protein	regulation of ion transmembrane transport	-1.74	0.31	4.37E-02
I-E	RS02470	RbsA, ribose ABC transporter ATP-binding protein	sugar transport	2.37	0.33	1.15E-04
I-E	RS05265	FCD domain-containing protein	transcriptional regulation	-3.34	0.65	9.99E-03
I-E	RS07620	FadE, acyl-CoA dehydrogenase	fatty acid metabolism	-1.65	0.28	3.17E-02
I-E	RS10010	GspB, type II secretion system assembly factor	protein secretion	-1.91	0.32	1.32E-02
I-E	RS13615	LysR family transcriptional regulator	transcriptional regulation	-1.90	0.36	4.37E-02
I-E	RS17740	amino acid adenylation domain protein	nucleotidyltransferase activity	-1.59	0.24	1.32E-02
I-E	RS19320	methyl-accepting chemotaxis protein	chemotaxis	-1.37	0.20	1.67E-02
I-E	RS22460	sigma-54-dependent Fis family transcriptional regulator	transcriptional regulation	-2.16	0.43	4.37E-02
Mid-infection						
wt, I-E, I-F	RS05850	NhaA, Na+/H+ antiporter	sodium transport	2.13	0.30	8.18E-05
wt, I-E, I-F	RS05855	NhaR, transcriptional activator	sodium transport	1.47	0.20	1.62E-03
wt, I-E, I-F	RS07090	DUF2502 domain-containing protein	unknown	2.30	0.31	1.49E-05

DE in strains	locus_tag	product	GO molecular function	$\log_2$(FC)	lfcSE	padj
wt, I-E, I-F	RS10685	DUF2002 domain-containing protein	unknown	3.20	0.44	1.31E-06
wt, I-E, I-F	RS18615	ABC transporter substrate-binding protein	transporter	-4.16	0.69	7.14E-05
wt, I-E, I-F	RS18685	MenF, isochorismate synthase	menaquinone biosynthesis	1.88	0.20	6.62E-08
wt, I-E	RS05275	iron permease FTR1	iron transport	-3.02	0.49	1.88E-04
wt, I-E	RS07105	DUF1107 domain-containing protein	unknown	1.59	0.21	3.61E-04
wt, I-E	RS18620	TonB-dependent siderophore receptor	siderophore transport	-3.82	0.64	9.40E-05
I-E, I-F	RS07645	DNA polymerase IV	DNA repair / SOS response	2.12	0.30	9.40E-05
I-E, I-F	RS08295	RecA, recombinase	DNA repair / SOS response	2.53	0.39	1.79E-04
I-E, I-F	RS08300	RecX, recombination regulator	DNA repair / SOS response	2.11	0.31	1.91E-04
I-E, I-F	RS08850	RseA, anti-sigma-E factor	anti-sigma binding	1.51	0.17	2.08E-05
I-E, I-F	RS09495	SulA, cell division inhibitor	cellular response to DNA damage stimulus / SOS response	2.62	0.25	1.12E-12
I-E, I-F	RS14825	hypothetical protein	unknown	2.54	0.36	1.49E-05
I-E, I-F	RS21055	RecN, DNA repair protein	DNA repair/ SOS response	3.12	0.30	2.78E-13
I-E, I-F	RS21370	DinI family protein	DNA repair/ SOS response	1.82	0.33	1.33E-02
I-E, I-F	RS22350	LexA, repressor	DNA repair / SOS response	1.78	0.19	1.46E-07
I-E	RS01460	tripartite tricarboxylate transporter substrate binding protein	transport	-2.16	0.37	2.92E-03
I-E	RS01920	polysaccharide deacetylase	carbohydrate metabolism	-1.67	0.25	2.43E-03
I-E	RS01925	MFS transporter	transport	-1.78	0.28	2.90E-03
I-E	RS01930	NAD(P)-dependent oxidoreductase	redox activity	-1.64	0.29	2.52E-02
I-E	RS03205	dicarboxylate/amino acid:cation symporter	transporter	-2.08	0.42	3.29E-02
I-E	RS05985	DNA polymerase II	DNA repair / SOS response	1.46	0.21	3.89E-03
I-E	RS06370	sugar ABC transporter substrate-binding protein	sugar transport	-2.93	0.51	7.16E-04
I-E	RS06375	sugar ABC transporter permease	sugar transport	-3.08	0.59	3.23E-03
I-E	RS06380	carbohydrate ABC transporter permease	sugar transport	-2.64	0.58	2.85E-02
I-E	RS06810	aldolase	catalytic activity	-3.30	0.74	1.90E-02
I-E	RS06815	ATP-grasp domain-containing protein	TCA cycle	-3.07	0.59	2.92E-03
I-E	RS06820	LucA, siderophore biosynthesis protein	siderophore biosynthesis	-2.88	0.54	2.90E-03

DE in strains	locus_tag	product	GO molecular function	$\log_2$(FC)	lfcSE	padj
I-E	RS06825	MFS transporter	transport	-2.70	0.62	4.99E-02
I-E	RS06850	IS200/IS605 family transposase	DNA recombination/ transposition	-2.21	0.48	4.64E-02
I-E	RS08845	RpoE, RNA polymerase sigma factor	transcriptional regulation / envelope stress response	1.28	0.17	2.90E-03
I-E	RS08855	RseB, sigma-E factor regulatory protein	anti-sigma binding / regulation of polysaccharide biosynthetic process / envelope stress response	1.20	0.16	9.81E-03
I-E	RS10855	ABC transporter ATP-binding protein	transport	-3.54	0.61	2.21E-04
I-E	RS10860	ABC transporter permease	transport	-3.28	0.56	3.23E-04
I-E	RS10865	ABC transporter permease	transport	-3.72	0.56	1.04E-05
I-E	RS10870	EntS, enterobactin transporter	cellular response to DNA damage stimulus / response to antibiotic	-3.29	0.59	7.39E-04
I-E	RS12165	SbnA, 2,3-diaminopropionate biosynthesis protein	siderophore biosynthesis	-1.67	0.30	2.80E-02
I-E	RS13735	arabinose ABC transporter substrate-binding protein	transport	-1.88	0.33	7.61E-03
I-E	RS13920	OppF, oligopeptide ABC transporter ATP-binding protein	protein transport	-1.63	0.17	1.60E-07
I-E	RS13925	OppD, oligopeptide ABC transporter ATP-binding protein OppD	protein transport	-1.61	0.21	2.54E-04
I-E	RS14775	ferrous iron transport protein A	iron transport / cellular response to DNA damage stimulus	-2.21	0.41	8.36E-03
I-E	RS16865	alcohol dehydrogenase	redox activity	-1.66	0.32	4.99E-02
I-E	RS17020	hypothetical protein	unknown	-2.64	0.53	9.81E-03
I-E	RS17315	cysteine synthase family protein	amino acid biosynthesis	-1.48	0.22	3.89E-03
I-E	RS17750	chlorinating enzyme	unknown	-1.89	0.25	4.76E-05
I-E	RS17755	hypothetical protein	unknown	-1.64	0.29	2.29E-02
I-E	RS17760	EamA/RhaT family transporter	transport	-1.63	0.27	9.81E-03
I-E	RS17765	thioesterase	hydrolase activity	-1.85	0.27	3.61E-04
I-E	RS18320	glutamate/aspartate ABC transporter substrate-binding protein	amino acid transport	-1.69	0.30	1.77E-02
I-E	RS18585	GalS, HTH-type transcriptional regulator	transcriptional regulation	-2.60	0.51	8.36E-03
I-E	RS18590	MglB, galactose/glucose ABC transporter substrate-binding protein	sugar transport	-2.77	0.39	1.42E-05
I-E	RS18595	MglA, galactose/methyl galactoside ABC transporter ATP-binding protein	sugar transport	-2.88	0.58	7.85E-03
I-E	RS18600	MglC, galactose/methyl galactoside ABC transporter permease	sugar transport	-3.08	0.62	5.42E-03
I-E	RS19145	PhoB, phosphate regulon transcriptional regulatory protein	transcription regulation	1.57	0.25	9.81E-03
I-E	RS20365	IS1 family transposase	transposition	-3.18	0.59	1.60E-03

DE in strains	locus_tag	product	GO molecular function	$\log_2$(FC)	lfcSE	padj
I-E	RS21295	sugar ABC transporter substrate-binding protein	sugar transport	-2.10	0.40	1.24E-02
I-E	RS21500	hypothetical protein	unknown	2.41	0.38	3.29E-04
I-E	RS22190	malate dehydrogenase	TCA cycle / anaerobic respiration	-1.32	0.20	1.82E-02
I-E	RS22235	RcnB, Nickel/cobalt homeostasis protein	cellular response to DNA damage	1.39	0.23	3.42E-02
Late infection						
wt, I-E, I-F	RS05850	NhaA, Na+/H+ antiporter	sodium transport	1.75	0.26	1.24E-03
wt, I-E, I-F	RS07090	DUF2502 domain-containing protein	unknown	2.78	0.27	7.97E-14
wt, I-E, I-F	RS07105	DUF1107 domain-containing protein	unknown	2.11	0.18	3.44E-14
wt, I-E, I-F	RS09545	YccA, transmembrane protein	negative regulation of apoptosis	1.47	0.26	4.01E-02
wt, I-E, I-F	RS09860	mannose-1-phosphate guanylyltransferase/mannose-6-phosphate isomerase	polysaccharide biosynthetic process	1.27	0.17	4.38E-03
wt, I-E, I-F	RS10685	DUF2002 domain-containing protein	unknown	4.61	0.38	3.45E-23
wt, I-E, I-F	RS10690	hypothetical protein	unknown	4.45	0.76	1.04E-04
wt, I-E, I-F	RS11860	glycine zipper 2TM domain-containing protein	unknown	3.49	0.65	1.24E-03
wt, I-E, I-F	RS12140	6-phospho-beta-glucosidase	carbohydrate metabolism	-3.40	0.60	6.41E-04
wt, I-E, I-F	RS12150	esterase	carbohydrate metabolism	-3.39	0.59	4.70E-04
wt, I-E, I-F	RS12155	hypothetical protein	unknown	-3.26	0.65	4.39E-03
wt, I-E, I-F	RS12340	OsmB, osmotically-inducible lipoprotein	osmotic stress	2.25	0.39	2.20E-03
wt, I-E, I-F	RS15300	CutC, copper homeostasis protein	copper homeostasis	1.32	0.18	4.75E-03
wt, I-E, I-F	RS15785	DmsD, Tat proofreading chaperone	protein folding	1.92	0.22	6.77E-07
wt, I-E, I-F	RS16005	serine hydrolase	proteolysis	1.65	0.31	3.29E-02
wt, I-E, I-F	RS16385	hypothetical protein	unknown	-2.34	0.39	1.17E-03
wt, I-E, I-F	RS18680	MenD, 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylic-acid synthase	menaquinone biosynthesis	1.75	0.32	1.89E-02
wt, I-E, I-F	RS18685	MenF, isochorismate synthase	menaquinone biosynthesis	1.98	0.13	1.17E-22
wt, I-E, I-F	RS22235	hypothetical protein	unknown	1.99	0.26	1.47E-05
wt, I-E, I-F	RS22565	OsmY, molecular chaperone	protein folding / Response to osmotic stress	1.85	0.29	1.40E-03
wt, I-E	RS05725	oxidative stress defence protein	Oxidative stress response	1.50	0.24	1.27E-02
wt, I-E	RS05840	DnaK, molecular chaperone	protein folding	1.70	0.29	9.73E-03

DE in strains	locus_tag	product	GO molecular function	$\log_2$(FC)	lfcSE	padj
wt, I-E	RS11350	FlhC, flagellar transcriptional regulator	flagella	-1.47	0.24	1.68E-02
wt, I-E	RS12145	carbohydrate porin	carbohydrate transport	-4.62	1.19	4.21E-02
wt, I-E	RS12280	DUF2091 domain-containing protein	unknown	1.61	0.30	3.35E-02
wt, I-E	RS12875	ShlB/FhaC/HecB family hemolysin secretion/activation protein	protein transport	-1.23	0.19	4.01E-02
wt, I-E	RS16390	hypothetical protein	unknown	-2.45	0.40	6.41E-04
wt, I-E	RS16540	hypothetical protein	unknown	1.74	0.29	7.71E-03
wt, I-E	RS17330	alanyl-tRNA editing protein	tRNA modification	-1.49	0.26	3.29E-02
I-E, I-F	RS01685	oligopeptidase A	proteolysis	1.22	0.19	4.69E-02
I-E, I-F	RS03060	IbpA, heat shock protein	Heat shock response	1.49	0.26	3.61E-02
I-E, I-F	RS04105	DNA helicase II	DNA repair	1.31	0.21	3.29E-02
I-E, I-F	RS07645	DinB, DNA polymerase IV	DNA repair / SOS response	2.21	0.24	1.05E-08
I-E, I-F	RS08295	RecA, recombinase	DNA repair / SOS response	2.91	0.34	3.84E-09
I-E, I-F	RS08300	RecX, recombination regulator	DNA repair / SOS response	2.49	0.27	7.58E-10
I-E, I-F	RS09495	SulA, cell division inhibitor	SOS response	2.62	0.20	8.71E-22
I-E, I-F	RS09530	HspQ, heat shock protein	Heat shock response	2.04	0.27	3.27E-05
I-E, I-F	RS10830	isochorismate synthase	siderophore biosynthesis	-3.62	0.75	5.76E-03
I-E, I-F	RS10845	MbtH family protein	siderophore biosynthesis	-3.60	0.71	2.91E-03
I-E, I-F	RS10855	ABC transporter ATP-binding protein	transport	-3.45	0.74	1.07E-02
I-E, I-F	RS13235	stress protein	tellurium resistance / response to stress	1.48	0.26	3.29E-02
I-E, I-F	RS13240	TerD, tellurium resistance	tellurium resistance / response to stress	1.51	0.22	3.59E-03
I-E, I-F	RS14825	hypothetical protein	unknown	3.13	0.36	1.06E-09
I-E, I-F	RS15240	RuvB, Holliday junction branch migration DNA helicase	DNA repair/ SOS response	1.33	0.19	7.50E-03
I-E, I-F	RS16835	6-phospho-beta-glucosidase	carbohydrate metabolism	-1.51	0.21	2.02E-03
I-E, I-F	RS21055	RecN, DNA repair protein	DNA repair/ SOS response	3.19	0.23	2.24E-25
I-E, I-F	RS21370	DinI family protein	DNA repair/ SOS response	2.06	0.30	1.59E-04
I-E, I-F	RS22350	LexA, repressor	SOS response	1.96	0.17	4.37E-14
I-E	RS05025	sucrose-6-phosphate hydrolase	sucrose metabolism	1.29	0.19	1.71E-02
I-E	RS05275	iron permease FTR1	iron transport	-3.04	0.52	4.70E-04

DE in strains	locus_tag	product	GO molecular function	$\log_2$(FC)	lfcSE	padj
I-E	RS05280	EfeM/EfeO family lipoprotein	unknown	-2.46	0.49	1.14E-02
I-E	RS05985	DNA polymerase II	DNA repair	1.47	0.18	1.42E-04
I-E	RS06540	UvrA, excinuclease ABC subunit	DNA repair / SOS response	1.41	0.21	8.94E-03
I-E	RS06820	LucA, siderophore biosynthesis protein	siderophore biosynthesis	-3.17	0.70	1.74E-02
I-E	RS06825	MFS transporter	siderophore biosynthesis	-3.17	0.76	4.01E-02
I-E	RS06855	TonB-dependent siderophore receptor	siderophore receptor	-2.76	0.63	3.82E-02
I-E	RS07775	hypothetical protein	unknown	2.07	0.42	3.29E-02
I-E	RS07980	RNA-directed DNA polymerase	RNA-dependent DNA replication	-2.22	0.44	1.73E-02
I-E	RS08430	ClpB, ATP-dependent chaperone	protein folding / heat shock response	1.07	0.13	1.11E-02
I-E	RS08845	RpoE, RNA polymerase sigma factor	transcription regulation	1.07	0.14	3.66E-02
I-E	RS08850	RseA, anti-sigma-E factor	anti sigma factor	1.16	0.16	2.10E-02
I-E	RS10165	hypothetical protein	unknown	-1.61	0.28	1.71E-02
I-E	RS10825	2,3-dihydroxybenzoate-AMP ligase	siderophore biosynthesis	-3.55	0.77	1.11E-02
I-E	RS10835	TonB-dependent siderophore receptor	siderophore receptor	-4.35	0.76	1.59E-04
I-E	RS10840	enterochelin esterase	siderophore dependant iron intake	-3.81	0.71	1.04E-03
I-E	RS10860	ABC transporter permease	transport	-3.25	0.59	1.19E-03
I-E	RS10870	EntS, enterobactin transporter	cellular response to DNA damage stimulus / response to antibiotic	-3.21	0.62	2.95E-03
I-E	RS10895	6-phospho-beta-glucosidase	carbohydrate metabolic process	-1.63	0.31	4.19E-02
I-E	RS11325	cytochrome b562	electron transfer activity	2.08	0.43	3.29E-02
I-E	RS12165	SbnA, 2,3-diaminopropionate biosynthesis protein	diaminopropionate biosynthesis	-1.56	0.28	3.29E-02
I-E	RS14775	ferrous iron transport protein A	iron transport	-2.38	0.46	8.88E-03
I-E	RS15245	RuvA, Holliday junction branch migration protein	DNA repair/ SOS response	1.11	0.14	1.59E-02
I-E	RS16715	AAA ATPase	unknown	-2.05	0.38	1.05E-02
I-E	RS16720	DUF4435 domain-containing protein	unknown	-2.49	0.43	1.40E-03
I-E	RS16840	PTS lactose/cellobiose transporter subunit IIA	carbohydrate transport	-1.82	0.32	9.63E-03
I-E	RS21500	hypothetical protein	unknown	2.73	0.61	3.29E-02

Table S9. Genes differentially expressed in *Serratia* I-F anti-JS26 strain

DE in strains	locus_tag	product	GO molecular function	$\log_2$(FC)	lfcSE	padj
Early infection						
wt, I-E, I-F	RS02465	ribose ABC transporter permease	sugar transport	1.65	0.25	7.13E-03
wt, I-E, I-F	RS10625	Ni/Fe-hydrogenase cytochrome b subunit	anaerobic respiration	3.53	0.56	8.27E-05
wt, I-E, I-F	RS12610	NarH, nitrate reductase subunit beta	nitrate reduction	3.28	0.66	1.44E-02
wt, I-F	RS05850	NhaA, Na+/H+ antiporter	sodium transport	1.46	0.22	1.56E-02
wt, I-F	RS10630	cytochrome-c3 hydrogenase	redox process	3.25	0.39	1.50E-08
wt, I-F	RS12615	NarJ, nitrate reductase molybdenum cofactor assembly chaperone	anaerobic respiration	3.32	0.67	1.56E-02
I-E, I-F	RS00965	FadB, fatty acid oxidation complex subunit alpha	fatty acid metabolism	-1.77	0.25	6.62E-04
I-E, I-F	RS02455	ribokinase	D-ribose catabolism	1.93	0.14	2.26E-17
I-E, I-F	RS02475	D-ribose pyranase	D-ribose catabolism	2.85	0.56	1.62E-02
I-E, I-F	RS10190	FadL, long-chain fatty acid transporter	fatty acid transport	-2.78	0.26	1.91E-14
I-F	RS02450	RbsR, transcriptional regulator	transcriptional regulation	1.68	0.16	5.22E-09
I-F	RS03200	hypothetical protein	unknown	-2.60	0.37	4.31E-05
I-F	RS04170	GlpC, anaerobic glycerol-3-phosphate dehydrogenase subunit C	anaerobic respiration	2.37	0.35	2.28E-04
I-F	RS10635	HyaD/HybD family hydrogenase maturation endopeptidase	protein processing	2.60	0.38	6.98E-05
I-F	RS10885	PRD domain-containing protein	transcription regulation	-2.63	0.44	1.68E-03
I-F	RS16980	SpeF, ornithine decarboxylase	spermidine biosynthesis	3.24	0.61	5.32E-03
Mid-infection						
wt, I-E, I-F	RS05850	NhaA, Na+/H+ antiporter	sodium transport	2.14	0.28	1.73E-05
wt, I-E, I-F	RS05855	NhaR, transcriptional activator	sodium transport	1.46	0.18	3.43E-04
wt, I-E, I-F	RS07090	DUF2502 domain-containing protein	unknown	2.24	0.32	1.52E-04
wt, I-E, I-F	RS10685	DUF2002 domain-containing protein	unknown	3.29	0.44	1.12E-06
wt, I-E, I-F	RS18615	ABC transporter substrate-binding protein	transport	-4.24	0.96	3.15E-02
wt, I-E, I-F	RS18685	MenF, isochorismate synthase	menaquinone biosynthesis	1.73	0.16	8.27E-10
wt, I-F	RS11860	glycine zipper 2TM domain-containing protein	unknown	2.94	0.56	8.06E-03
I-E, I-F	RS07645	DNA polymerase IV	DNA repair / SOS response	1.97	0.26	3.34E-05

DE in strains	locus_tag	product	GO molecular function	$\log_2$(FC)	lfcSE	padj
I-E, I-F	RS08295	RecA, recombinase	DNA repair / SOS response	2.25	0.38	3.11E-03
I-E, I-F	RS08300	RecX, recombination regulator	DNA repair / SOS response	1.91	0.30	2.68E-03
I-E, I-F	RS08850	RseA, anti-sigma-E factor	anti-sigma binding	1.31	0.19	3.50E-02
I-E, I-F	RS09495	SulA, cell division inhibitor	cellular response to DNA damage stimulus / SOS response	2.55	0.28	1.81E-09
I-E, I-F	RS14825	hypothetical protein	unknown	2.56	0.49	1.31E-02
I-E, I-F	RS21055	RecN, DNA repair protein	DNA repair/ SOS response	3.06	0.26	2.47E-18
I-E, I-F	RS21370	DinI family protein	DNA repair/ SOS response	1.78	0.25	7.05E-04
I-E, I-F	RS22350	LexA, repressor	DNA repair / SOS response	1.70	0.27	8.06E-03
I-F	RS00630	RNA-binding S4 domain protein	response to heat	1.70	0.28	1.31E-02
I-F	RS03060	IbpA, heat shock protein	heat shock response	2.04	0.29	2.23E-04
I-F	RS03065	IbpB, heat shock chaperone	heat shock response	1.85	0.29	3.31E-03
I-F	RS09530	HspQ, heat shock protein	heat shock response	2.45	0.37	1.93E-04
I-F	RS22385	FxsA, cytoplasmic membrane protein	unknown	1.81	0.34	4.96E-02
Late infection						
wt, I-E, I-F	RS05850	NhaA, Na+/H+ antiporter	sodium transport	1.74	0.17	1.22E-09
wt, I-E, I-F	RS07090	DUF2502 domain-containing protein	unknown	2.92	0.38	3.19E-07
wt, I-E, I-F	RS07105	DUF1107 domain-containing protein	unknown	2.60	0.41	2.10E-04
wt, I-E, I-F	RS09545	transmembrane protein	negative regulation of apoptotic process	1.71	0.26	2.50E-03
wt, I-E, I-F	RS09860	Mannose-1-phosphate guanylyltransferase/mannose-6-phosphate isomerase	polysaccharide biosynthetic process	1.40	0.21	1.03E-02
wt, I-E, I-F	RS10685	DUF2002 domain-containing protein	unknown	4.80	0.48	2.61E-15
wt, I-E, I-F	RS10690	hypothetical protein	unknown	4.49	1.02	1.40E-02
wt, I-E, I-F	RS11860	glycine zipper 2TM domain-containing protein	unknown	3.92	0.33	2.61E-21
wt, I-E, I-F	RS12140	6-phospho-beta-glucosidase	carbohydrate metabolism	-3.44	0.79	2.50E-02
wt, I-E, I-F	RS12150	esterase	carbohydrate metabolism	-3.77	0.85	1.78E-02
wt, I-E, I-F	RS12155	hypothetical protein	unknown	-3.77	0.87	2.25E-02
wt, I-E, I-F	RS12340	OsmB, osmotically-inducible lipoprotein	osmotic stress	2.22	0.47	4.18E-02
wt, I-E, I-F	RS15300	CutC, copper homeostasis protein	copper homeostasis	1.48	0.23	1.34E-02

DE in strains	locus_tag	product	GO molecular function	log$_2$(FC)	lfcSE	padj
wt, I-E, I-F	RS15785	DmsD, Tat proofreading chaperone	protein folding	2.26	0.35	3.10E-04
wt, I-E, I-F	RS16005	serine hydrolase	proteolysis	1.97	0.37	1.82E-02
wt, I-E, I-F	RS16385	hypothetical protein	unknown	-2.21	0.42	1.24E-02
wt, I-E, I-F	RS18680	MenD, 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylic-acid synthase	menaquinone biosynthesis	1.61	0.19	9.01E-06
wt, I-E, I-F	RS18685	MenF, isochorismate synthase	menaquinone biosynthesis	1.96	0.12	1.79E-25
wt, I-E, I-F	RS22235	hypothetical protein	unknown	2.03	0.35	6.04E-03
wt, I-E, I-F	RS22565	OsmY, molecular chaperone	protein folding / Response to osmotic stress	2.06	0.38	1.29E-02
wt, I-F	RS03770	PutA, trifunctional transcriptional regulator/proline dehydrogenase/L-glutamate gamma-semialdehyde dehydrogenase	proline biosynthetic process/ transcriptional regulation	2.81	0.62	2.56E-02
wt, I-F	RS05855	NhaR, transcriptional activator	sodium transport	1.14	0.16	3.05E-02
wt, I-F	RS10950	hypothetical protein	unknown	2.93	0.53	1.58E-03
wt, I-F	RS10955	sugar ABC transporter permease	sugar transport	2.71	0.53	8.00E-03
wt, I-F	RS12185	non-ribosomal peptide synthetase	catalytic activity	-1.94	0.31	2.27E-03
wt, I-F	RS18615	ABC transporter substrate-binding protein	transport	-4.10	0.94	1.82E-02
wt, I-F	RS18670	MenB, 1,2C4-dihydroxy-2-naphthoyl-CoA synthase	menaquinone biosynthesis	1.56	0.26	1.40E-02
wt, I-F	RS18675	MenH, 2-succinyl-6-hydroxy-2%2C4-cyclohexadiene-1-carboxylate synthase	menaquinone biosynthesis	1.81	0.28	2.73E-03
I-E, I-F	RS01685	oligopeptidase A	proteolysis	1.53	0.25	1.45E-02
I-E, I-F	RS03060	IbpA, heat shock protein	heat shock response	1.75	0.23	9.21E-05
I-E, I-F	RS04105	UvrD, DNA helicase II	DNA repair	1.20	0.14	1.30E-03
I-E, I-F	RS07645	DinB, DNA polymerase IV	DNA repair / SOS response	1.91	0.17	2.06E-12
I-E, I-F	RS08295	RecA, recombinase	DNA repair / SOS response	2.32	0.23	6.28E-11
I-E, I-F	RS08300	RecX, recombination regulator	DNA repair / SOS response	2.03	0.17	2.26E-14
I-E, I-F	RS09495	SulA, cell division inhibitor	SOS response	2.36	0.18	7.71E-19
I-E, I-F	RS09530	HspQ, heat shock protein	Heat shock response	2.08	0.24	7.63E-08
I-E, I-F	RS10830	isochorismate synthase	siderophore biosynthesis	-3.82	0.83	1.24E-02
I-E, I-F	RS10845	MbtH family protein	siderophore biosynthesis	-3.75	0.92	4.67E-02
I-E, I-F	RS10855	ABC transporter ATP-binding protein	transport	-3.80	0.92	3.88E-02
I-E, I-F	RS13235	stress protein	tellurium resistance / response to stress	1.87	0.31	4.60E-03

DE in strains	locus_tag	product	GO molecular function	$\log_2$(FC)	lfcSE	padj
I-E, I-F	RS13240	Tellurium resistance	tellurium resistance / response to stress	1.73	0.30	1.54E-02
I-E, I-F	RS14825	hypothetical protein	unknown	2.56	0.39	1.09E-04
I-E, I-F	RS15240	RuvB, Holliday junction branch migration DNA helicase	DNA repair/ SOS response	1.12	0.14	1.34E-02
I-E, I-F	RS16835	6-phospho-beta-glucosidase	carbohydrate metabolic process	-1.21	0.15	3.21E-03
I-E, I-F	RS21055	RecN, DNA repair protein	DNA repair/ SOS response	2.95	0.19	5.09E-34
I-E, I-F	RS21370	DinI family protein	DNA repair/ SOS response	1.75	0.17	4.05E-09
I-E, I-F	RS22350	LexA, repressor	SOS response	1.63	0.15	1.59E-09
I-F	RS00620	IgaA, intracellular growth attenuator family protein	signal transduction / stress response	1.25	0.18	2.50E-02
I-F	RS00630	RNA-binding S4 domain protein	cellular response to heat	1.50	0.24	1.40E-02
I-F	RS01030	RmuC, DNA recombination protein	DNA recombination	1.96	0.29	3.22E-04
I-F	RS01690	RsmJ, 16S rRNA (guanine(1516)-N(2))-methyltransferase	rRNA methylation	1.36	0.22	3.80E-02
I-F	RS03065	IbpB, heat shock chaperone	heat shock response	1.65	0.24	1.34E-03
I-F	RS06570	Cas5f, type I-F CRISPR-associated protein	CRISPR type I-F immunity	1.74	0.34	4.88E-02
I-F	RS06575	Cas8f, type I-F CRISPR-associated protein	CRISPR type I-F immunity	1.84	0.31	7.98E-03
I-F	RS06580	Cas3, type I-F CRISPR-associated helicase	CRISPR type I-F immunity	2.03	0.26	6.03E-06
I-F	RS06585	Cas1, type I-F CRISPR-associated endonuclease	CRISPR type I-F immunity	2.19	0.29	1.20E-05
I-F	RS12180	cyclic peptide export ABC transporter	transport	-1.91	0.33	9.01E-03
I-F	RS13245	TerB, tellurite resistance	tellurium resistance	1.72	0.31	2.52E-02
I-F	RS22385	FxsA cytoplasmic membrane protein	unknown	1.41	0.21	9.86E-03

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