

## **Supporting Information**

### **Chromosomal Instability in Enterohaemorrhagic *Escherichia coli* O157:H7: Impact on Adherence, Tellurite Resistance and Colony Phenotype**

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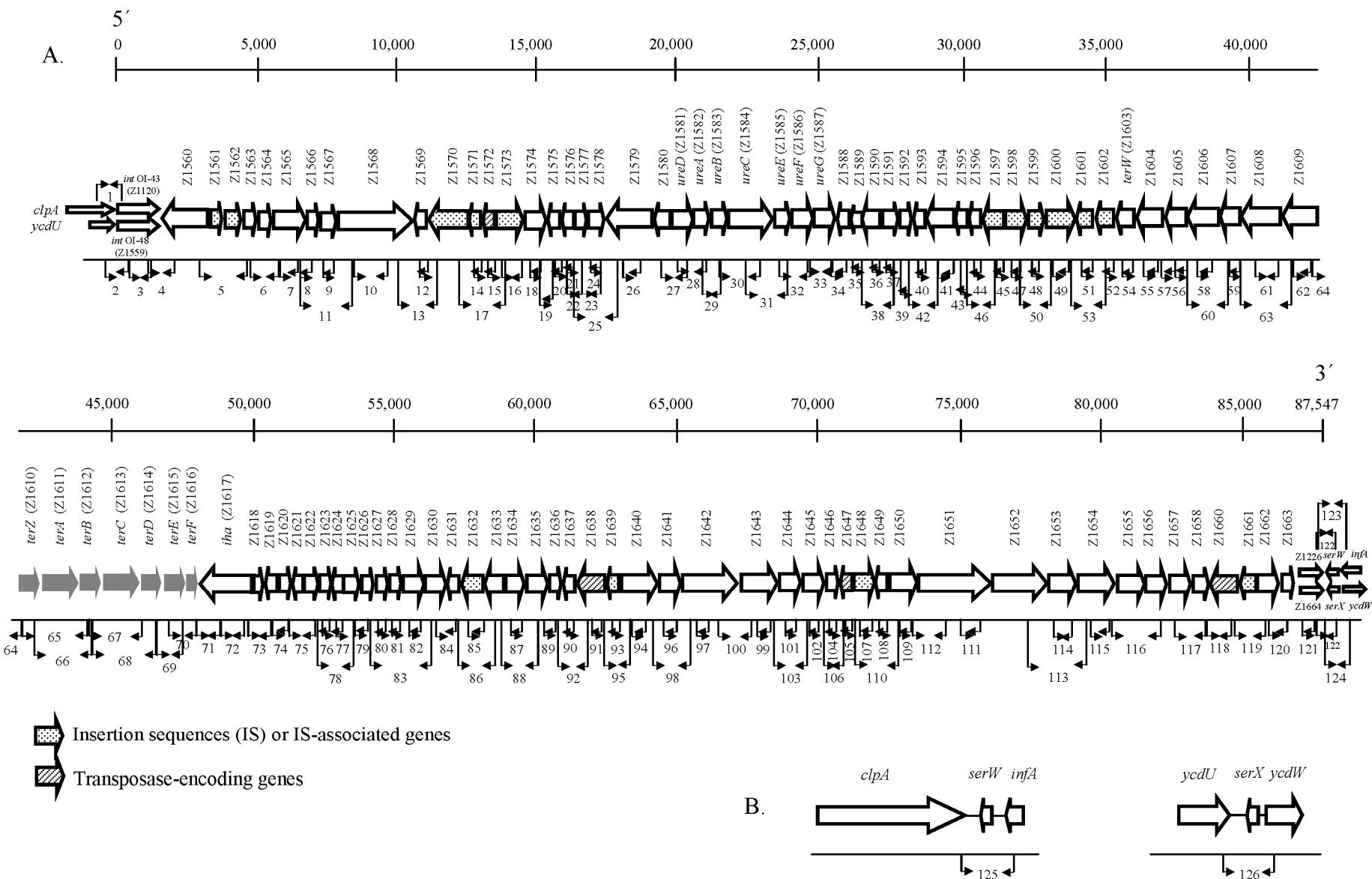
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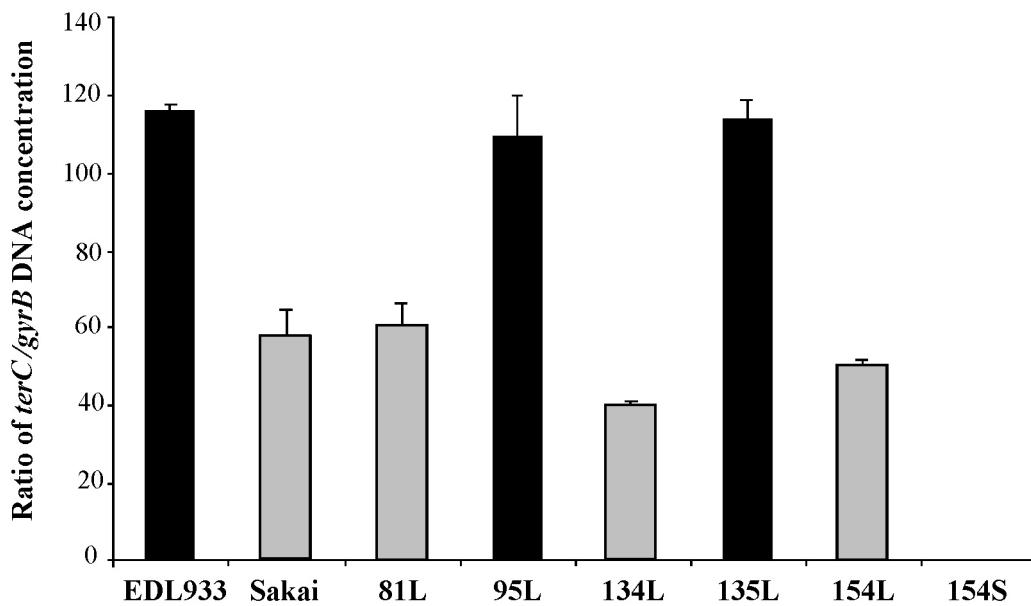
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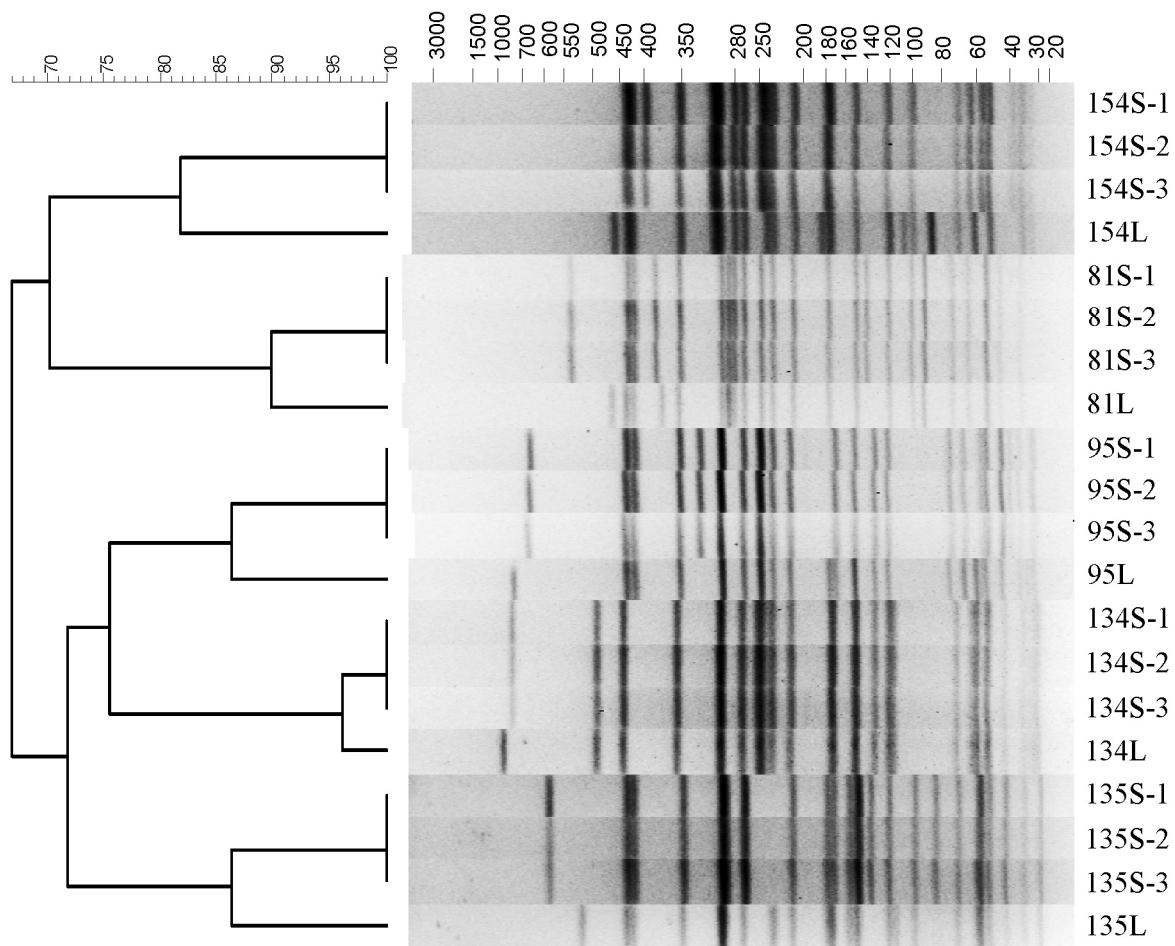
**Fig. S1.** PCR strategy to characterize tellurite resistance ( $\text{Tel}^R$ )-encoding islands and their integration sites in L and S colonies of *E. coli* O157:H7 strains.

A. Physical map of O island (OI) 48 and its flanks in *E. coli* O157:H7 strain EDL933 and positions of primers used to map  $\text{Tel}^R$ -encoding islands. Large arrows indicate ORFs of OI 48 (designations above arrows). Striped arrows denote putative transposases. Dotted arrows indicate insertion sequences (IS) and IS-associated genes. *ter* genes are grey. The duplicated arrows at the 5' and 3'ends of the island indicate respective ORFs at these positions in OI 48 (Z1559 [putative P4-family integrase of OI 48] and Z1664, respectively; lower arrows) and in OI 43 (Z1120 [putative P4-family integrase of OI 43] and Z1226, respectively; upper arrows). Moreover, genes upstream of the first ORF of OI 48 (*ycdU*) and OI 43 (*clpA*) and downstream of the last ORF of OI 48 (*serX*, *ycdW*) and OI 43 (*serW*, *infA*) are indicated by double arrows. The scale (in bp) is above the graph. Small arrows indicate positions of PCR primers; the numbers below the small arrows indicate PCR numbers in Table S1, which describes PCR conditions.

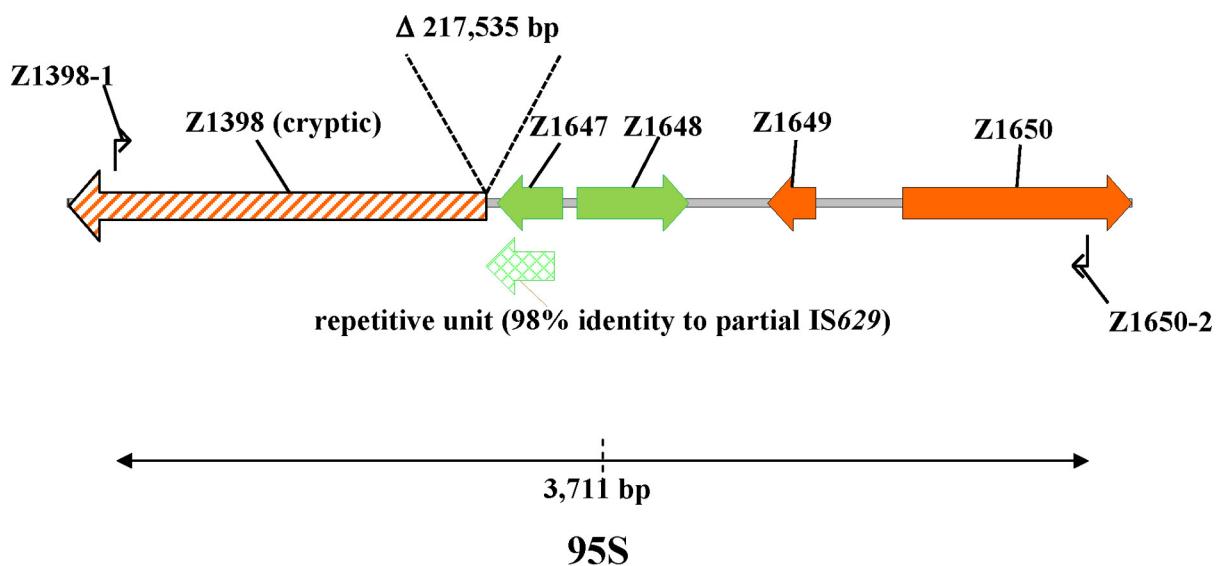
B. Strategy to investigate occupancy of *serW* and *serX*, the respective integration sites for OI 43 and OI 48 in EDL933.



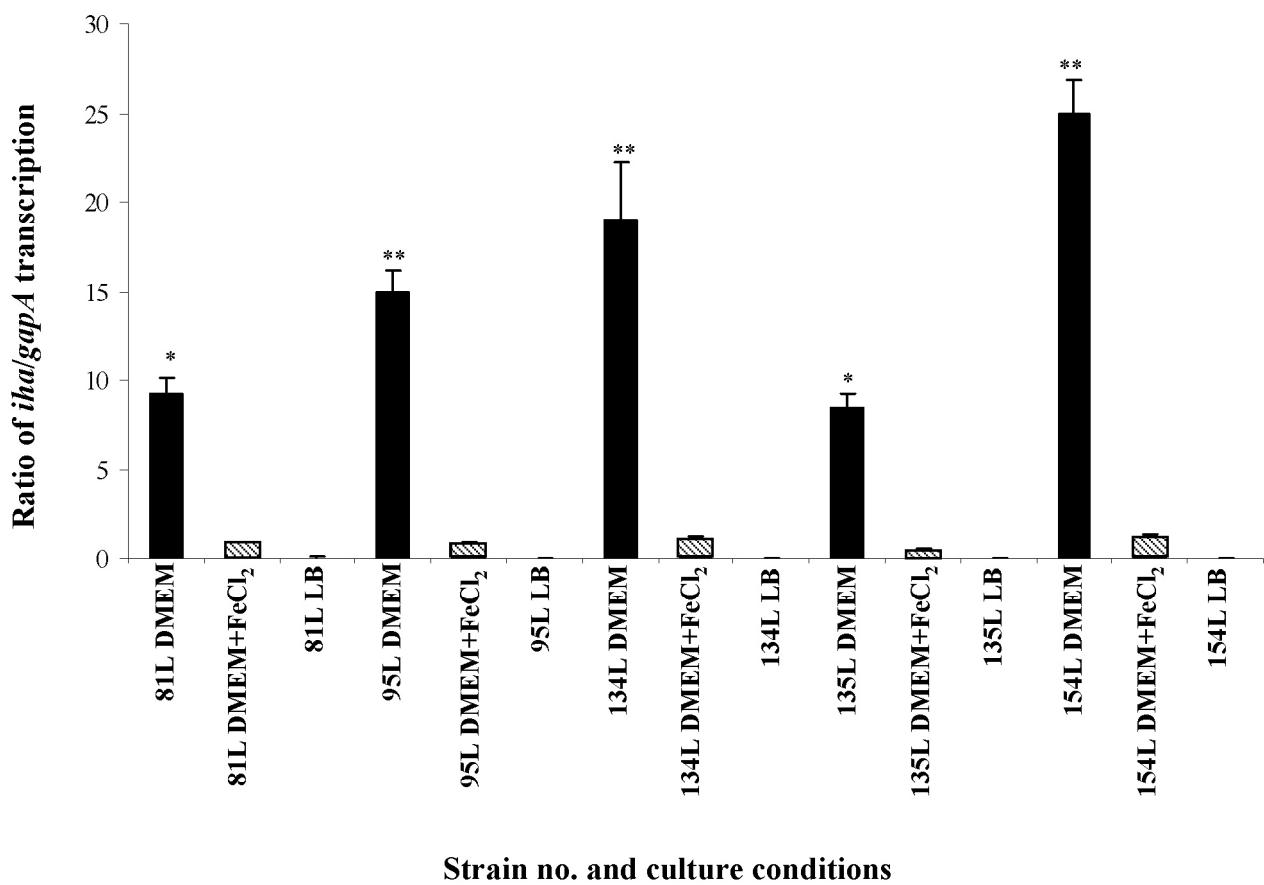
**Fig. S2.** Number of copies of Tel<sup>R</sup>-encoding island in L strains. The *terC* DNA was quantified using light-cycler PCR and normalized to *gyrB* DNA. The *terC/gyrB* DNA ratio for each strain represents a mean  $\pm$  standard deviation from three independent experiments. Strains with two copies or one copy of *terC* are depicted by black or grey bars, respectively. Strains EDL933 (GenBank accession no. AE005174; 2 copies of the *ter* cluster), Sakai RIMD 0509952 (GenBank accession no. NC\_002695; 1 copy of the *ter* cluster), and 154S (lacking the *ter* cluster) were used as controls.



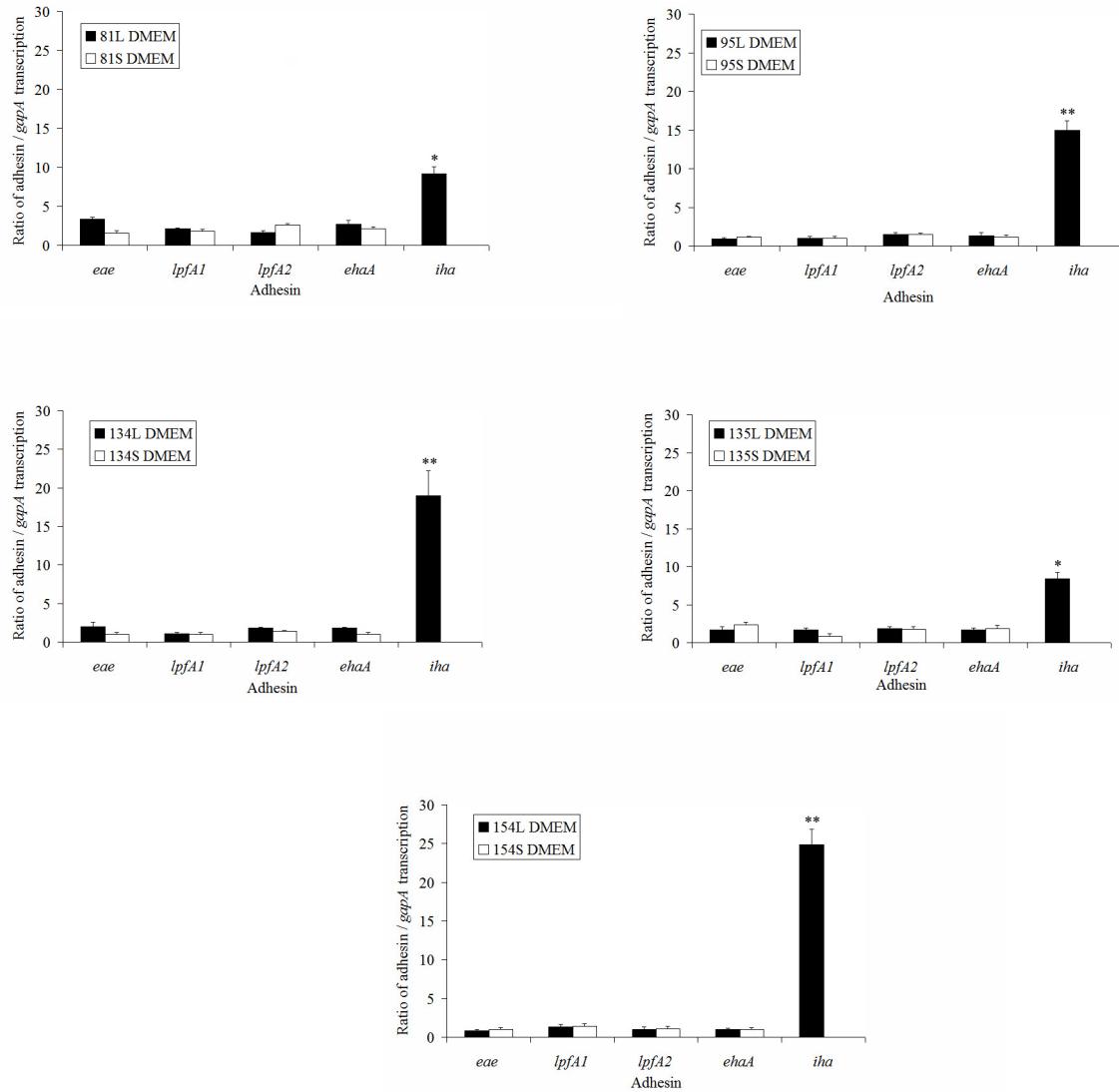
**Fig. S3.** PFGE of *Xba*I-digested genomic DNA from L and S strains. Chromosomal DNA from strains 81L, 95L, 134L, 135L, and 154 L and from three independent S colonies derived from each L strain was digested with *Xba*I and subjected to PFGE as described in Experimental procedures. The cluster analysis was performed using UPGMA (Unweighted Pair Group Method with Arithmetic Mean) in BioNumerics software 5.1. Strain numbers are shown to the right from the gel (three independent S colonies derived from each L strain are designated by strain number and the end numbers 1 to 3). Molecular weight scale (based on *Xba*I-digested DNA of *Salmonella enterica* serovar Braenderup strain H9812) is given above the gel.



**Fig. S4.** Deletion of OI 48 and the upstream core genome region in strain 95S. The size and genetic organisation of the connecting fragment amplified with primers Z1398-1 and Z1650-2 (small arrows) that spans the internal deletion of OI 48 plus deleted parts of the core chromosome. Position and size of the deleted DNA region (217,535 bp) is indicated above the graph by dotted lines. ORFs with similarity to mobile genetic elements (putative transposases and insertion sequences) are highlighted in green.



**Fig. S5.** *iha* transcription in L strains is upregulated in iron-limited conditions. The *iha*-positive L strains were cultured in DMEM (iron content  $< 0.05 \mu\text{g ml}^{-1}$ ), DMEM with  $10 \mu\text{M FeCl}_2$  (iron content  $0.50 \mu\text{g ml}^{-1}$ ) or LB broth (iron content  $0.59 \mu\text{g ml}^{-1}$ ) and *iha* transcription was determined using quantitative real-time reverse transcription PCR and normalized to *gapA* transcription. The ratio of *iha/gapA* transcription was  $8.4-24.9$ ,  $\leq 1.0$ , and  $\leq 0.04$ , respectively. Data are presented as means  $\pm$  standard deviations from three experiments performed with three independently isolated RNA preparations. Differences between relative transcription of *iha* in DMEM and in each of the other two media are indicated \* ( $p < 0.05$ ) and \*\* ( $p < 0.001$ ) (unpaired Student's *t* test).



**Fig. S6.** Transcription analysis of *iha* and non-*iha* adhesin genes (*eae*, *lpfA1*, *lpfA2*, *ehaA*) in L and S strains grown under iron-limited conditions. The strains were cultured in DMEM (iron content  $< 0.05 \mu\text{g ml}^{-1}$ ) and transcription of each gene was determined using quantitative real-time reverse transcription PCR and normalized to *gapA* transcription. Data are presented as means  $\pm$  standard deviations from three experiments performed with three independently isolated RNA preparations. Differences between relative transcription of *iha* and each of the non-*iha* adhesin genes are indicated \* ( $p < 0.05$ ) and \*\* ( $p < 0.001$ ) (unpaired Student's *t* test).

Table S1. PCR primers and conditions used for mapping and analysis of deletions of Tel<sup>R</sup>-encoding islands.

PCR No.	Primer <sup>a</sup>	Sequence (5' - 3')	Target	PCR conditions <sup>b</sup>			PCR product (bp)	Position of the primer <sup>c</sup>
				Denaturing	Annealing	Extension		
1	clpA-f int-4	CTGTTGGTCGCTGGTGGAC CCATTCCCCCGCCCCTTAC	<i>clpA</i> -integrase OI 43 (left junction of OI 43 and the core genome)	94°C, 30 s	56°C, 60 s	72°C, 60 s	756	2161-2181 <sup>d</sup> 280-260
2	serX-F OI 48 CI-R	TGTCGATTCCCTCTGGCATAA AAGTTGCTCTCGCATTATCC	<i>ycdU</i> -integrase OI 48 (left junction of OI 48 and the core genome)	95°C, 45 s	58°C, 45 s	72°C, 90 s	678	913-932 <sup>e</sup> 397-378
3	int-1 int-2	AATCTGAGAAAGTCGCTATCC CACTGACGGCTTCTTTTAC	integrase OI 43/OI 48	94°C, 30 s	54°C, 60 s	72°C, 60 s	708	435-455 1142-1122
4	Z1559-1 Z1560-2	GAATGAAAGCCAGGATAC ATAAGCCTGTTGATGGA	Z1559-Z1560	94°C, 30 s	50°C, 60 s	72°C, 60 s	767	972-989 1738-1721
5	Z1560-1 Z1563-2	TAGCCAGAACACCAAAAC AGTCAGGCATCCGTAAG	Z1560-Z1563	94°C, 30 s	51°C, 60 s	72°C, 90 s	1,228	3310-3327 4537-4520
6	Z1563-1 Z1565-4	CAGCAGTCAAAGGTGTTA CGGATAAGGATTTCTGG	Z1563-Z1565	94°C, 30 s	49°C, 60 s	72°C, 60 s	743	4708-4725 5450-5433
7	Z1565-1 Z1565-2	AACGCATCTGAATAAAC AGACAACCGCACATACTC	Z1565	94°C, 30 s	51°C, 60 s	72°C, 60 s	688	5849-5866 6536-6518
8	Z1565-3 Z1566-2	TGTCGCACCTAACTTGA ATTTTTCATACCTATAA	Z1565-1566	94°C, 30 s	48°C, 60 s	72°C, 60 s	381	6779-6796 7159-7142























PCR No.	Primer <sup>a</sup>	Sequence (5' - 3')	Target	PCR conditions <sup>b</sup>			PCR product (bp)	Position of the primer <sup>c</sup>
				Denaturing	Annealing	Extension		
119	Z1660-1	ATGATGTCGCTGTTGCTG	Z1660-Z1662	94°C, 30 s	55°C, 60 s	72°C, 60 s	779	85124-85141
	Z1662-2	TAGCCGTTATCGCAGACC						85902-85885
120	Z1662-1	GCTACTCCCTCGTGTG	Z1662-Z1663	94°C, 30 s	54°C, 60 s	72°C, 60 s	512	85899-85916
	Z1663-2	CGATACAGGGCAACAGTG						86410-86393
121	Z1664-1	CTGGCTGAAATCTCGGTGCTG	Z1226, Z1664 <sup>f</sup>	94°C, 30 s	57°C, 60 s	72°C, 60 s	327	86689-86709
	Z1664-2	GATCACCCCTCGCTCAAACAC						87015-86995
122	LG-1	AAATCAGCGAAGCGAACAA	Z1226/Z1664 - <i>serW/serX</i>	94°C, 30 s	54°C, 60 s	72°C, 60 s	694	86936-86953
	SerWX-2	TGTCCGAGTGGCTGAAGG						25-8 <sup>g</sup>
123	LG43	GTAAACCAATCCCCGACAACC	Z1226- <i>infA</i> (right junction of OI 43 and the core genome)	94°C, 30 s	55°C, 60 s	72°C, 60 s	781	87188-87208
	InfA-r	CCTGACGGCGACAAAGTGAC						79-59 <sup>h</sup>
124	OI 48 CI-F	TTTGCCAGTATGCTCAAAGA	Z1664 downstr- <i>ycdW</i> (right junction of OI 48 and the core genome)	95°C, 45 s	58°C, 45 s	72°C, 90 s	505	87420-87401
	serX-R	GGTATCGAACGTTGGGTGAT						75-56 <sup>i</sup>
125	SerW-3	CGCTGGATAAAAGAGAAAAATG	<i>serW</i> intact	94°C, 30 s	54°C, 60 s	72°C, 90 s	859	2201-2221 <sup>d</sup>
	SerW-4	GCAAAAACATACATCCGCATCC						98-78 <sup>h</sup>
126	serX-F	TGTCGATTCCCTCTGGCATAA	<i>serX</i> intact	95°C, 45 s	60°C, 45 s	72°C, 90 s	624	913-932 <sup>e</sup>
	serX-R	GGTATCGAACGTTGGGTGAT						75-56 <sup>i</sup>

PCR No.	Primer <sup>a</sup>	Sequence (5' - 3')	Target	PCR conditions <sup>b</sup>			PCR product (bp)	Position of the primer <sup>c</sup>
				Denaturing	Annealing	Extension		
127	Z1565F Z1638R	TGAAAGTCTGGCGATGAGTG GTACTACCGTCAGCCGGAAA	internal deletion of OI 48 in strain 134S	95°C, 45 s	60°C, 30 s	68°C, 240 s	2,017	6257-6276 62046-62027
128	Z1567F Z1648R	ATGCTGGCGGGATATTACTG GGATTTCAGCGTCATGTT	internal deletion of OI 48 in strains 81S/154S	95°C, 45 s	60°C, 30 s	68°C, 240 s	4,825/ 2,379	7831-7850 71571-71552
129	134S-F2 134S-R2	CAGAGTTGTACCGGTTATTGAGG CCATTTCGTAATTGGGATTAGC	walking primer for sequencing of PCR product 127	- -	59°C 59°C	- -	- -	n.a. <sup>j</sup> n.a.
130	81S-F2 81S-F3 81S-F4 81S-R2 81S-R3 81S-R4 154S-R2	ACGTTAGTGTGCCAGTTCC ATGATGTCGCTGTTGCTGAC GCCCTAATTATCCTCCCGAAT ACCGGCCAGTCTGCTATG TGCGGTCATCACGAACATAC ATACGGCGGGAGACTTTTC GTTCCATTGCCCAAAGATT	walking primer for sequencing of PCR products 128	- - - - - - -	59°C 59°C 59°C 59°C 59°C 59°C 59°C	- - - - - - -	- - - - - - -	n.a. n.a. n.a. n.a. n.a. n.a. n.a.
131	RecAF RecAR	CCGGTAAAACCACGCTGAC CCTGACCGATCTCTCACCT	RecA	95°C, 30 s	54°C, 45 s	72°C, 60 s	693	212-230 <sup>k</sup> 904-885 <sup>k</sup>
132	TerE1 TerE2	TAAAAGGCGCAACGTATCTCTGA CCGTCCCCGTTGTCGTTGTAA	TerE	95°C, 30 s	58°C, 45 s	72°C, 60 s	399	46020-46043 46418-46396

PCR No.	Primer <sup>a</sup>	Sequence (5' - 3')	Target	PCR conditions <sup>b</sup>			PCR product (bp)	Position of the primer <sup>c</sup>
				Denaturing	Annealing	Extension		
133	Z1567F	ATGCTGGCGGGATATTACTG	5' junction of internal deletion in strain 81L  walking primer for sequencing	94°C, 30 s	53°C, 30 s	68°C, 5 m	3,464	7831-7850
	Z1568-4	ATCGCAGAAAATGAAACC		-	-	-		9981-9964
	81S-F2	ACGTTAGTGTGCCAGTTCC		-	59°C	-	-	n.a.
	81S-F3	ATGATGTCGCTGTTGCTGAC		-	59°C	-	-	n.a.
	Z1568-R1	ACCTGAGGTAATTGCGCTTT		-	59°C	-	-	9360-9341
	Z1568-R2	CCAGCGCAGCAGGTACAC		-	59°C	-	-	8846-8829
134	Z1637F	CGCTGATTGACTTTCGGTAAT	3' junction of internal deletion in strain 81L  walking primer for sequencing <sup>l</sup>	94°C, 30 s	61°C, 30 s	68°C, 10 m	~6,200	60841-60861
	Z1648R	GGATTTCAGCGTCATGTT		-	-	-		71571-71552
	Z1637/38F	ATTCTGGTACCGGTTGATGC		-	59°C	-	-	61342-61361
	81S-R2	ACCGGCCAGTCTGCTATG		-	59°C	-	-	n.a.
	81S-R3	TGCGGTCACTACGAACATAC		-	59°C	-	-	n.a.
	81S-R4	ATACGGCGGGAGACTTTTC		-	59°C	-	-	n.a.
	81S-R5	CGGAACGTTACCTCACAGC		-	59°C	-	-	n.a.

PCR No.	Primer <sup>a</sup>	Sequence (5' - 3')	Target	PCR conditions <sup>b</sup>			PCR product (bp)	Position of the primer <sup>c</sup>
				Denaturing	Annealing	Extension		
135	Z1565F	TGAAAGTCTGGCGATGAGTG	5' junction of internal deletion in strain 134L  walking primer for sequencing	95°C, 30 s	45°C, 30 s	68°C, 5 m	3197	6257-6276
	Z1567-2	TACGCCTCAGAATAATAC		-	59°C	-	-	8140-8123
	134S-F2	CAGAGTTGTACCGGTTATTGAGG		-	59°C	-	-	n.a.
	134L-F1	GTGCTGCTGGTTACCTCGTT		-	59°C	-	-	n.a.
	ECs5244-2	CCAGCCTTCCCAGCAATCGTC		-	59°C	-	-	n.a.
	134L-R1	CTGGAAAGTCAGGGCGAATA		-	59°C	-	-	n.a.
	ECs5244-1	TCAGCAACAGCGACATCATCC		-	59°C	-	-	n.a.
	134S-R2	CCATTTCGTAATTGGGATTAGC		-	59°C	-	-	n.a.
136	Z1636-1	GTTTTCTGGGCTTGTCTC	3' junction of internal deletion in strain 134L  walking primer for sequencing	95°C, 30 s	53°C, 30 s	68°C, 5 m	1,446	60601-60618
	Z1638R	GGATTTCAGCGTCATGTT		-	52°C	-	-	31082-31063
	Z1638-2	GGCAGAACAGAAAAAGC		-	52°C	-	-	61529-61512

PCR No.	Primer <sup>a</sup>	Sequence (5' - 3')	Target	PCR conditions <sup>b</sup>			PCR product (bp)	Position of the primer <sup>c</sup>
				Denaturing	Annealing	Extension		
137	Z1567F	ATGCTGGCGGGATATTACTG	5' junction of internal deletion in strain 154L  walking primer for sequencing	94°C, 30 s	61°C, 30 s	68°C, 10 m	3,213	7831-7850
	Z1574R	CGACTGCTGCACCTTCATAA		-	59°C	-	-	15403-15384
	ECs5244-2	CCAGCCTTCCCAGCAATCGTC		-	59°C	-	-	n.a.
	81S-F3	ATGATGTCGCTGTTGCTGAC		-	59°C	-	-	n.a.
	Z1573R	ACAGGGCTTACCTGTCAGC		-	59°C	-	-	14772-14753
	Z1573-2	CCGCTCATCACTTTGTTT		-	50°C	-	-	14384-14367
	ECs5243-1	GCGATT CGTATGGTTCTGGA		-	59°C	-	-	n.a.
	ECs5244-1	TCAGCAACAGCGACATCATCC		-	59°C	-	-	n.a.

PCR No.	Primer <sup>a</sup>	Sequence (5' - 3')	Target	PCR conditions <sup>b</sup>			PCR product (bp)	Position of the primer <sup>c</sup>
				Denaturing	Annealing	Extension		
138	Z1640F	CTGCTGGATTACGGGACAT	3' junction of internal deletion in strain 154L	94°C, 30 s	60°C, 30 s	68°C, 10 m	6,424	63370-63389
	Z1648R	GGATTTCAGCGTCATGTT		-	-	-	-	71571-71552
	Z1640-3	GTTTGTGGCTGGTGTCTG		walking primer for	-	54°C	-	63786-63803
	Z1641-1	GAAATGACGACAGAGAGG		sequencing	-	50°C	-	64220-64237
	Z1642-3	GAAAAGATGGACAAACAG		-	49°C	-	-	64863-64880
	Z1642F	GAGAAGGCTGGCGCTATTAA		-	59°C	-	-	65291-65310
	Z1642F2	TCAGGAACATGGTGCCAGTA		-	59°C	-	-	65800-65819
	ECs5244-2	CCAGCCTTCCCAGCAATCGTC		-	59°C	-	-	n.a.
	81S-F3	ATGATGTCGCTGTTGCTGAC		-	59°C	-	-	n.a.
	ECs5243-1	GCGATTCTGATGGTTCTGGA		-	59°C	-	-	n.a.
	ECs5244-1	TCAGAACAGCGACATCATCC		-	59°C	-	-	n.a.
	Z1647R	AAACCGTGCAGAAGTGGAAC		-	59°C	-	-	71046-71027
	Z1642/43R	CACACCTGGAAAATCCATGC		-	59°C	-	-	67171-67152
	Z1642R	AATGGAGTCTTCCGACCTT		-	59°C	-	-	66661-66642

a. Primers were derived from the sequence of O island (OI) 48 of *E. coli* O157:H7 strain EDL933 (GenBank accession number AE005174; genomic position 1454242 to 1541789), which is identical in its nucleotide sequence to OI 43 of EDL933, and from the genes flanking OI 48 (*ycdU*, *serX*, *ycdW*) and OI 43 (*clpA*, *serW*, *infA*) in the genome of strain EDL933.

b. All PCRs included 30 cycles as indicated, preceded by denaturation (94°C, 5 min) and followed by a final extension (72°C, 5 min).

- c. Positions of PCR primers within the sequence of OI 48 of *E. coli* O157:H7 strain EDL933 are indicated unless specified otherwise; position of the first nucleotide of OI 48 (1454242) is considered as position 1.
- d. Position of the primer within *clpA* (Z1119), which is located directly upstream of the integrase gene of OI 43 in strain EDL933 (Fig. S1A).
- e. Position of the primer within *ycdU* (Z1558), which is located directly upstream of the integrase gene of OI 48 in strain EDL933 (Fig. S1A).
- f. Last genes of OI 43 and OI 48, respectively.
- g. Positions of the primer within *serW* and *serX* genes (which are 100% identical).
- h. Position of the primer within *infA* (Z1228), which is located downstream of OI 43 (Fig. S1A).
- i. Position of the primer within *ycdW* (Z1666) which is located downstream of OI 48 (Fig. S1A).
- j. n.a., not applicable
- k. Position of the primer within *recA*(Z4002).
- l. Full sequencing of the PCR product was not possible due to the presence of an additional IS629 besides Z1638/Z1339 in the PCR fragment. However, the existence of two IS elements has been verified by restriction digestion with *HindIII*, a single cutting enzyme in IS629, which resulted in three restriction fragments of the expected size (data not shown). According to sequencing data additional *HindIII* restriction sites in flanking regions were excluded.

Table S2. PCR primers for analysis of the core genome deletions in strain 95S.

Primer	Sequence (5'- 3')	Target	Annealing temperature	PCR product (bp)
ycdU-1 ycdU-2	GTGGGATTCTGGCCCTGGTGC GCGTACCGCCTGGAGAAGCG	Z1558 ( <i>ycdU</i> )	59°C	538
Z1549-1 Z1549-2	GCACTGAGCCCATCTATC ATTCCGGCACATAGTCCAG	Z1549	55°C	554
Z1539-1 Z1539-2	AGCCATCACTATCACAAAGCAA CCTTCAGGGATTAAGTGCAAA	Z1539	58°C	494
Z1528-1 Z1528-2	TGATTGCTAACGGAGCATTG GCAGCGCGATAAAAATAC	Z1528	59°C	712
Z1522-1 Z1522-2	GCATTTCAACCTCATCC TCCACCTTCCCTATTCC	Z1522	54°C	674
Z1513-1 Z1513-2	CCAGGCGAATCATAAGAC TCGCTGAACCGCATTATC	Z1513	55°C	607
Z1505-1 Z1505-2	AATCAGCCGAACACAAC CTGGATGGCGGTAATGAC	Z1505	55°C	574
Z1495-1 Z1495-2	GGCAACTGTTACGCACTC CGAATGCCTCACGAATAAC	Z1495	55°C	1224
Z1486-1 Z1486-2	CCGAATGATGATGAAACC ACATCCTGCTTACCATCC	Z1486	54°C	791
Z1477-1 Z1477-2	CGTGAAGCCTGGTTGTC GCCCTGAATAACCTCTG	Z1477	55°C	784
LP43 LP44	ATCCTATTCCCGGGAGTTACG GCGTCATCGTATACACAGGAGC	Z1464	57°C	584
wrbA1 wrbA2	ATGGCTAAAGTTCTGGTG CTCCTGTTGAAGATTAGC	Z1423	53°C	600
Z1409-1 Z1409-2	TGCGTAACCAATCACCGTAA CTGAATTAAATCGGCGCTCTC	Z1409	59°C	605
Z1408-1 Z1408-2	GGCTCCCTTGTGGAGCCTTTT CGCCAGTAAGGTGTTGGTTCCCG	Z1408	57°C	155

Primer	Sequence (5'- 3')	Target	Annealing temperature	PCR product (bp)
Z1406-1 Z1406-2	TCCTGATGATGGCAGCAAAGACG GGGCCACGTTGACCCTGCTC	Z1406	57°C	120
Z1405-1 Z1405-2	CGCTGTTGGCCTCGCAGGC ACCTTGATCGAAAAGCGGCA	Z1405	58°C	162
Z1404-1 Z1404-2	GCGCGTAGTGGACGTGGTGG GACGCCAGCTGCGTTGCTG	Z1404	59°C	259
Z1403-1 Z1403-2	ACACAGCACATCGCGACCCG TCAGCAGATCCAGGCAGTGG	Z1403	59°C	364
Z1402-1 Z1402-2	CACAGGGCAACAGGGCGAC TTCCGTTGGCCCCGTGGAGA	Z1402	60°C	504
Z1401-1 Z1401-2	TTGCGCAGGCTGGCTACGTC TGGCGCTGTTCCCATGGCTG	Z1401	59°C	946
Z1400-1 Z1400-2	AGCGTTACCCAGCGCTTCCG CGCAGGCTAACCCGGAGCTG	Z1400	59°C	647
Z1399-1 Z1399-2	GACCTCGGGAGCGATTGCGG CATTGGCGAGCGCTTGCTGC	Z1399	59°C	241
Z1398-1 Z1398-2	GCAGGGCTGGTGCCGACAGAG GAAGTGCAGCGAGCTGGAA	Z1398	60°C	1174
Z1397-1 Z1397-2	TCGTCATGGTGTGCGTGCCC ATCCTTCCCCACCCGGCTC	Z1397	59°C	666
Z1396-1 Z1396-2	TAGCGTTGGTGCGCACTGGG CAGCGTGATGCCTGCCGTGA	Z1396	59°C	775
Z1395-1 Z1395-2	CCTGCTGGTGACGTGGCTGG ACGGCAAACCTCCAGAGCGCC	Z1395	59°C	917
Z1394-1 Z1394-2	ACAGCCCGCAGGTGATTG TCAATGGGCGGCGGTAAAC	Z1349	58°C	352
Z1376-1 Z1376-2	TCCACGGGGCTGAAAATC GGAGAGCGTTTCGTCAC	Z1376	56°C	375
Z1349-1 Z1349-2	GTGAGGGCGTTATTTG GCATTCAGTCCCAGTGTGTC	Z1349	56°C	844

Primer	Sequence (5'- 3')	Target	Annealing temperature	PCR product (bp)
Z1329-1 Z1329-3	GCAGTTCCGGTAATCCTGTG AATCCAGGAAATTGCAGCAC	Z1329	60°C	331
Z1309-1 Z1309-2	ACCGATCATTGTTGGCAGT GAAACTCCTGTTCGGCGTA	Z1309	60°C	543
Z1297-1 Z1297-2	GGCTGACGGTGGTGAAAATAC GTTTGCTGATTTCGCCACAC	Z1297	56°C	405
Z1280-1 Z1280-2	AAATCCTGACGCTGCCTCTG CAGGTCGGTAAGCATTCCAC	Z1280	58°C	602
Z1270-1 Z1270-2	ATCCCTCGTCCGTCTTGTGCG TGGCTGATTCTCTCGGTTTC	Z1270	57°C	438
Z1256-1 Z1256-2	TGGCACTAGCGGCATTACATC CCGAGGAGGCGTCAAGGAAAA	Z1256	57°C	327
Z1243-1 Z1243-2	CAGGGCGAGCAATGTAAGGTG ATGATGCTGCCGTTTGCTTG	Z1243	55°C	225
Z1232-1 Z1232-2	TTTGATGTAGCCGTTTCCAG CCGTGGAGTTCTGCTTGTGC	Z1232	56°C	406
clpA-1 clpA-2	GAATCAGCTTGCAGCGTGG TTCGTCCAGCAGCAGCACCG	Z1119 ( <i>clpA</i> )	59°C	1168
Z1118-1 Z1118-2	TTCGCGACGCGCTAAACCG TGGTTCTGCAACCTCGGCGG	Z1118	59°C	198
Z1117-1 Z1117-2	TGCCTTTGGCCCTGGTGG CATCTGCCCTGAAGGCAGCG	Z1117	59°C	125
Z1116-1 Z1116-2	TGCTCGCGCCCAGGAGTTG ACCTGCGCACGACCCTTCAG	Z1116	59°C	838
Z1115-1 Z1115-2	TGCTGGCGACCGGAAAGCTG CCGGATCGCCTAACGCCGAC	Z1115	59°C	804
Z1112-1 Z1112-2	CGCCGACGGTATTCAAGCCCC ATGCCCTTACCTTGCAGCG	Z1112	59°C	649
Z1110-1 Z1110-2	CTGGCGTCTGGGGCCAAGTG CAGCCACAGCACGCGTGAGA	Z1110	59°C	595

Primer	Sequence (5'- 3')	Target	Annealing temperature	PCR product (bp)
Z1109-1 Z1109-2	CAGCCGCCCTGGAAGATGGC ATTGCCAGGTTGTCGGCGG	Z1109	59°C	344
Z1108-1 Z1108-2	CGCGCTCCGATTACCGGAC CGCTTCGCCAACAAAGCTGCG	Z1108	59°C	617
Z1107-1 Z1107-2	AGCATTTCGCCGTGGGTGTAG GCAGGGGATGTGTGGTAAAAC	Z1107	57°C	762
Z1097-1 Z1097-2	CGCGGAAAATATTCCAACAG TCATCAGCAAATCCAAGCAC	Z1097	59°C	573
Z1087-1 Z1087-2	TGGTTTGCTGGTGGGTATTGG CGGCATCTTGGTAACCTTGG	Z1087	55°C	500
Z1074-1 Z1074-2	TCGGCATCTCAATCTGGCTAC CATTGGCGTTTAGTCGTATC	Z1074	56°C	908
Z1063-1 Z1063-2	ATTCCGAAGTTGGCGATGATG GCCGTAGTTTGCCTTTTG	Z1063	56°C	443
Z1054-1 Z1054-2	TTTGCTTCcccATTCCttAC CTCTTTGccCTTACCTTC	Z1054	56°C	480
Z1045-1 Z1045-2	TTACCCACCGAGCCAATGACC TCCACTCAGCCTAACCTCAGC	Z1045	58°C	998
Z1035-1 Z1035-2	TAGCAGGAACCACAGACCAAG TGGCGTCTATTCAAGGTGGAG	Z1035	57°C	347
Z1026-1 Z1026-2	ACCCATAATGCCGTATCAG GGATACTACCCGCACGATGAC	Z1026	58°C	826
Z1017-1 Z1017-2	CCACGGTAATAATCGCAAGG TGATTCGCACCACCTCTCC	Z1017	58°C	436

All primers were designed in this study except for LP43 and LP44 (Friedrich *et al.*, 2002) and wrbA1 and wrbA2 (Bielaszewska *et al.*, 2006b).

Table S3. Quantitative real time RT-PCR assays to determine transcription of *iha* and non-*iha* adhesins in L and S strains.

Primer	Sequence (5' - 3')	Target	Annealing temperature	PCR product (bp)	Reference
GapA_for GapA_rev	GTTGTCGCTGAAGCAACTGG AGCGTTGGAAACGATGTCCT	<i>gapA</i>	53°C - 60°C	171	Blumer <i>et al.</i> , 2005
K14924 K14925	TTACCAGCGATACCAAGAGC CAACATGACCGATGACAAGG	<i>eae</i>	59°C	126	Chen <i>et al.</i> , 2007
CMD306 CMD307	GGCTGAATCTGCAGGAAAGCAACA TGCAGGCTGACAGAACATCCACA	<i>iha</i>	60°C	95	Léveillé <i>et al.</i> , 2006
ehaA-F ehaA-R1	AGCGTTAGGGGCACAGGAAG CCTCGCTGCCACTGACAATA	<i>ehaA</i>	54°C	161	This study <sup>a</sup>
LPFA1-CF LPFA1-CR1	GGTTGGTGACAAATCCCCG CGTCTGGCCTTACTCAGA	<i>lpfA1</i> (O157/OI-141)	53°C	244	Torres <i>et al.</i> , 2009
LPFA2-F1 LPFA2-CR	GCAGGTCACCTACAGGGGGC GCTAATACCAGCGGCAGCATCGT	<i>lpfA2</i> (O157/OI-154)	57°C	306	This study <sup>b</sup> Torres <i>et al.</i> , 2009

- a. The primers were derived from a 851-bp fragment of *ehaA* passenger domain sequenced in our laboratory, which was 100% identical in all L and S strains and also to the respective sequences in EHEC O157:H7 strains EDL933 and Sakai (data not shown).
- b. The primer was derived from the sequence of *lpfA2* of strain EDL933 (GenBank accession no. AE005174).

Table S4. Plasmids and *E. coli* constructs used in this study.

Plasmid or construct	Description	Source or reference
<b>Plasmids</b>		
pWKS30	<i>ori pSC101, bla</i>	Wang and Kushner, 1991
pWKS30 <i>iha</i>	pWKS30 with a 2,916-bp fragment containing <i>iha</i> from EHEC O157:H7 Sakai (RIMD 0509952)	This study
pKD3	<i>bla FRT cat oriRγ</i>	Datsenko and Wanner, 2000
pKD46	<i>bla araC-ParaB-γ-β-exo oriR101 repA101 (ts)</i>	Datsenko and Wanner, 2000
pKD4	<i>kan FRT cat oriRγ</i>	Datsenko and Wanner, 2000
pKD4 <i>iha</i>	pKD4 with a 2,916-bp fragment ( <i>BstBI/HindIII</i> ) containing <i>iha</i> from EHEC O157:H7 Sakai (RIMD 0509952)	This study
pCP20	<i>bla cat flp (ts)</i>	Cherepanov and Wackernagel, 1995
pGEM-T easy	<i>bla lacZα</i>	Promega
pTerE	pGEM-T Easy containing a 399-bp internal <i>terE</i> fragment	This study
<b>Constructs</b>		
154LΔ <i>iha</i>	154LΔ <i>iha</i>	This study
154LΔ <i>iha</i> /pWKS30 <i>iha</i>	154LΔ <i>iha</i> containing pWKS30 <i>iha</i> , Ap <sup>R</sup>	This study
154LΔ <i>iha</i> /pWKS30	154LΔ <i>iha</i> containing pWKS30, Ap <sup>R</sup>	This study
154S <i>glmS::iha</i>	154S chromosomally complemented (downstream of <i>glmS</i> ) with <i>iha</i> from EHEC O157:H7 Sakai (RIMD 0509952), Km <sup>R</sup>	This study
SakaiΔ <i>iha</i>	EHEC O157:H7 Sakai (RIMD 0509952)Δ <i>iha</i>	This study
SakaiΔ <i>iha</i> <i>glmS::iha</i>	EHEC O157:H7 SakaiΔ <i>iha</i> chromosomally complemented (downstream of <i>glmS</i> ) with <i>iha</i> from EHEC O157:H7 Sakai (RIMD 0509952), Km <sup>R</sup>	This study

Table S5. Primers used for construction of *iha* deletion and complementation mutants.

Primer <sup>a</sup>	Sequence (5' - 3')
del_iha_for	GTATTTGTATTGTCTGCCGGTTAACATGATCGGAGATTAGTAATATGGTAGGCTGGAGCTGCTT
del_iha_rev	TGCAGTGGCAACGTATTCTACCGTCAGTGATAGCGTTTGTATTATCACATATGAATATCCTCCTAGTTCTA
iha_for2	GGTTTCGAACAATGTGGGCTGACATGA
iha_rev	CGGTAGCTGCAAAACTTAACG
iha-pKD4_for	CCTTTTGCGTGGCCAGTGCCAAGCTGCATGCAGATTGCAGCATTACACAACAATGTGGGCTGACATGA
iha-pKD4_rev	AAAGTATAGGAACCTCGAACGCAGCTCCAGCCTACACAATCGCTCAAGACCGGTAGCTGCAAAACTTAACG
iha-int_for	AACTCCATTAATTGATATTATTCCCTGTGTATCCATTATTAAACAAATGTGGGCTGACATGA
iha-int_rev	ACTTACCAGCATTAATAATCTAACCTCATTCCATATAATTACCTCAGCTACGGCTGACATGGGAATTAG

a. All primers were designed in this study.