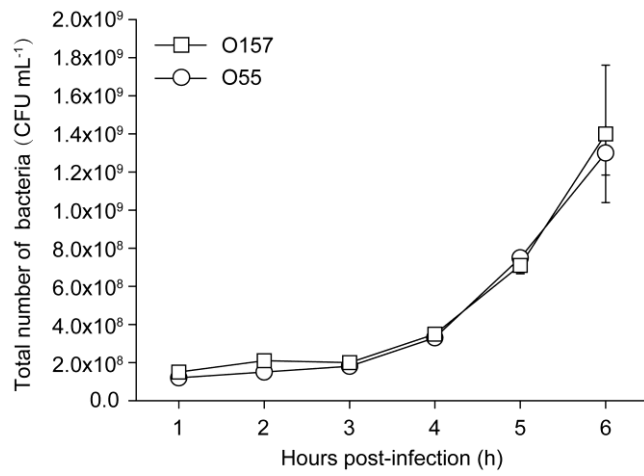
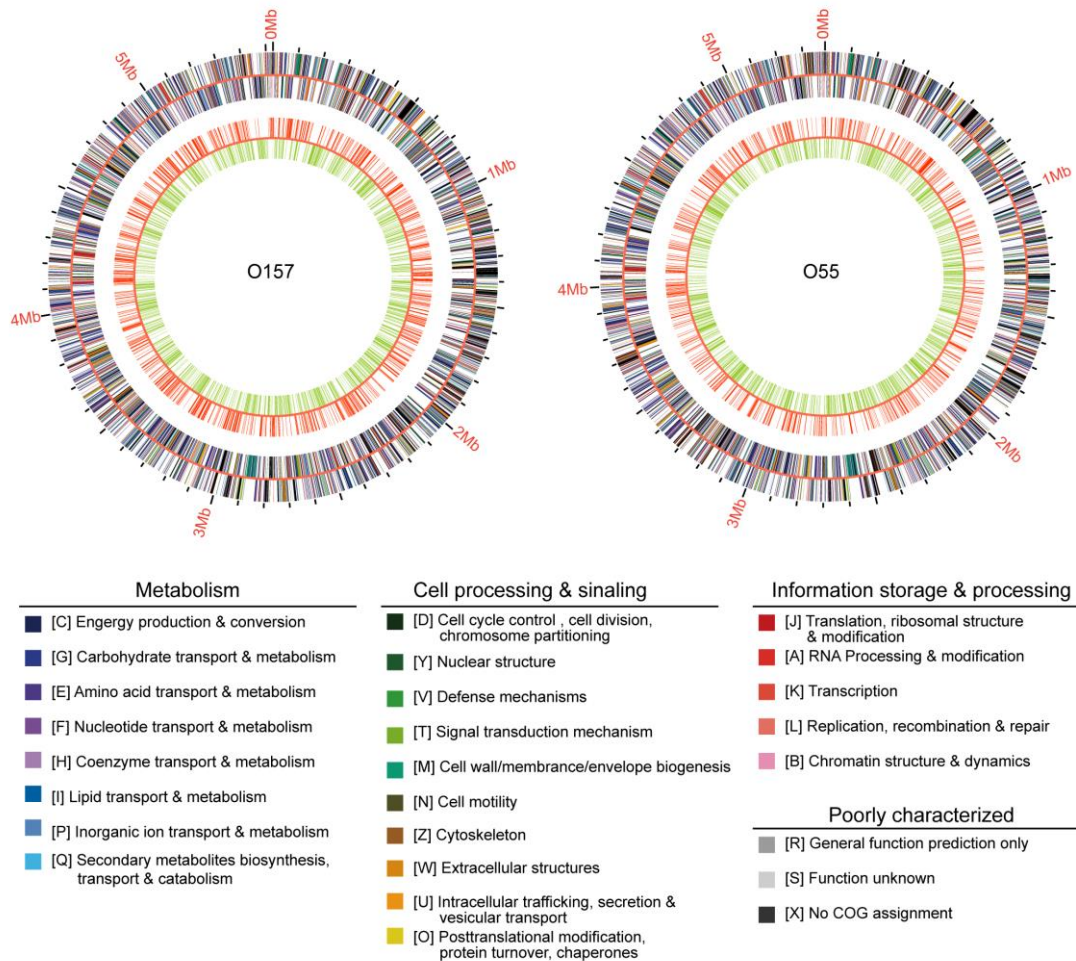


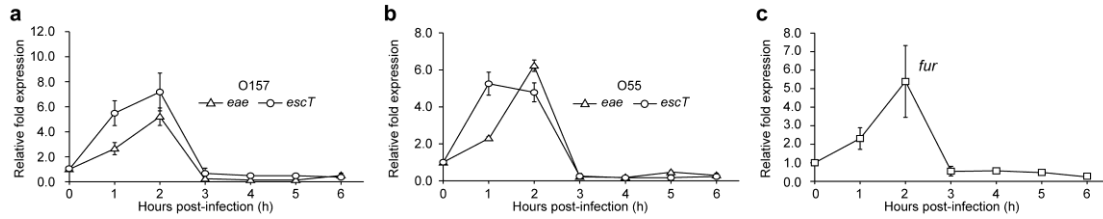
## Supplementary figures



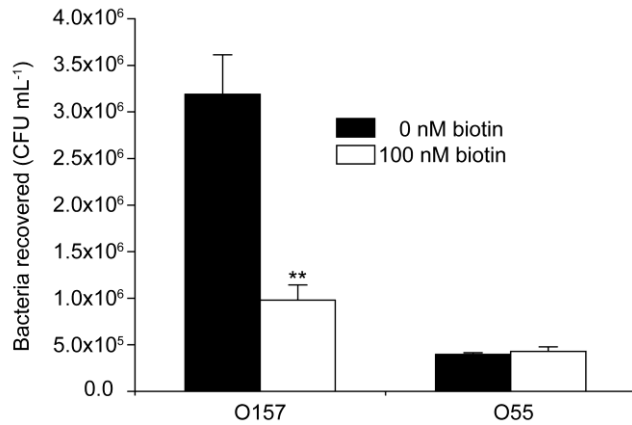
**Supplementary Figure 1.** The total numbers of attached and non-attached bacteria after 1 h to 6 h incubation of O157 or O55 with HeLa epithelial cells. Data are presented as means  $\pm$  s.d.; n=3.



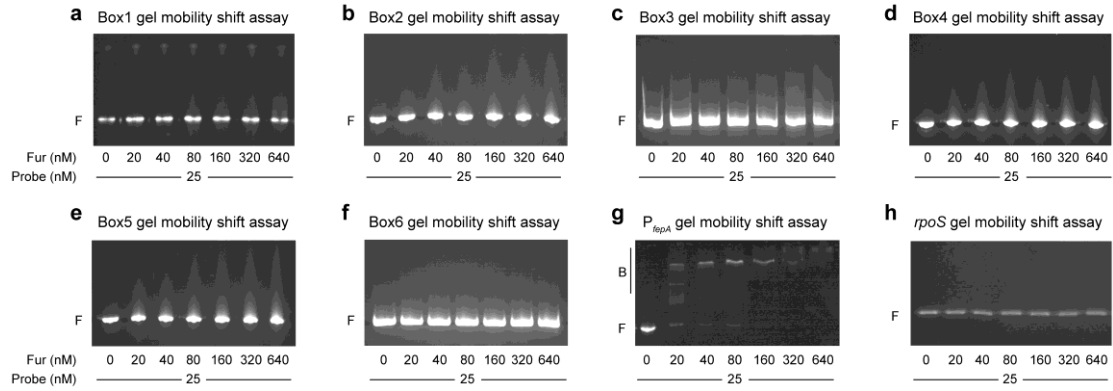
**Supplementary Figure 2.** Distribution of differentially expressed genes in the O157 and O55 genomes. From the outside in, circle 1 demonstrates the size in base pairs. Circles 2 and 3 indicate the CDSs in the clockwise and anti-clockwise directions, analyzed using the COG database (colors were assigned according the COG functional classes, see key). Circle 4 shows the position of the genes that are up-regulated 3 h after attachment of O157 or O55 to HeLa cells (colored orange). Circle 5 shows the position of genes that are down-regulated 3 h after attachment of O157 or O55 to HeLa cells (colored green).



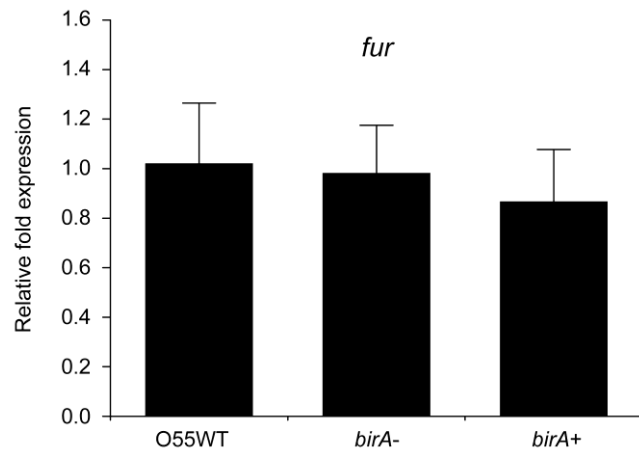
**Supplementary Figure 3.** (a) qRT-PCR quantification of the changes in expression of *eae* and *escT* in O157 incubated with HeLa cells from 1 to 6 h. (b) qRT-PCR quantification of the changes in the expression of *eae* and *escT* in O55 incubated with HeLa cells from 1 to 6 h. (c) qRT-PCR quantification of the changes in the expression of *fur* in O157 incubated with HeLa cells from 1 to 6 h. The expression of *eae*, *escT*, and *fur* in DMEM-grown O157 or O55 is represented as 1 (0 h), and all other values of expression from 1 h to 6 h are expressed relative to this value. Data are presented as means  $\pm$  s.d.; n=3.



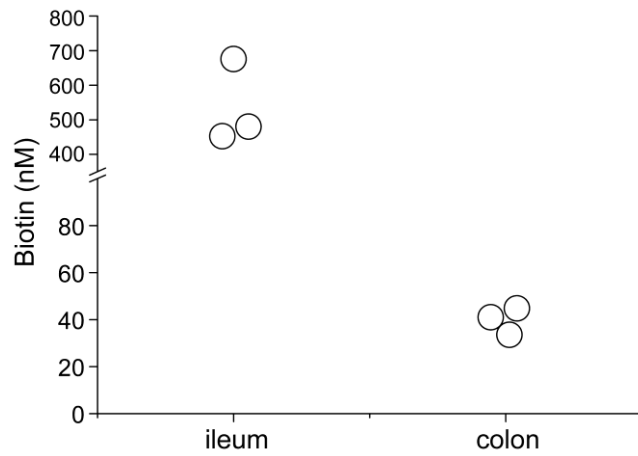
**Supplementary Figure 4.** Adherence of O157 and O55 to Caco-2 cells in the presence of 0 or 100 nM biotin. Caco-2 cells were grown to confluence in 6-well plates. Cell cultures were infected with exponential-phase O157 or O55 ( $10^8$  bacteria/well) for 3 h at 37 °C in a 5% CO<sub>2</sub> atmosphere. The attachment efficiency was represented by the colony-forming units (CFU) per milliliter. Data are presented as means  $\pm$  s.d.; n=3. \*\*  $P \leq 0.01$ . All  $P$  values were calculated using Student's  $t$ -test.



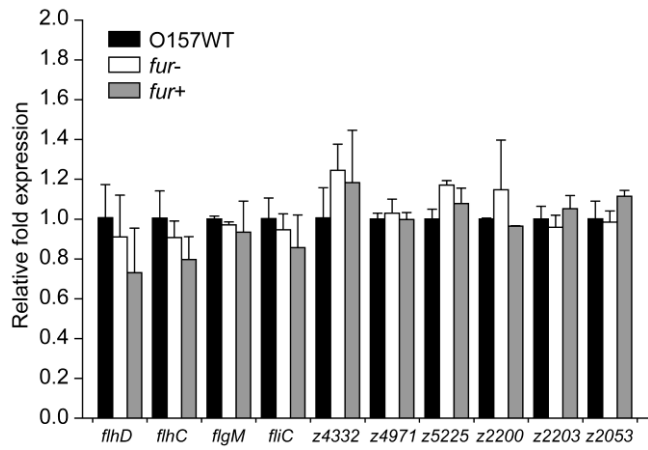
**Supplementary Figure 5. The interaction of Fur with the predicted Fur boxes located within the LEE region. (a-f)** Gel mobility shift analysis of Fur with the predicted Fur boxes (Box1 to Box6 in Supplementary Table 6) located within the O157 LEE region. **(g)** Gel mobility shift analysis of Fur with the *fepA* promoter region (positive control). The positions of the bound (denoted with “B”) and free (denoted with “F”) probe are shown on the left. **(h)** Gel mobility shift analysis of Fur with *rpoS* (negative control). For each assay, the concentrations of the probe and purified Fur are indicated at the bottom of each lane. Full gels are shown in Supplementary Figure 10.



**Supplementary Figure 6.** Repetition of Figure 5d (O55). qRT-PCR quantification of the change in the expression of *fur* in the O55 wild-type strain and its *birA*-mutant and complemented strains. Data are presented as means  $\pm$  s.d.; n=3.



**Supplementary Figure 7.** Quantification of the molarity of biotin in the ileal content and colonic content obtained from mice fed a normal diet. The graph represents a typical experiment with 3 mice in each group.



**Supplementary Figure 8.** qRT-PCR quantification of the changes in expression of *flhDC*, flagellum synthetic genes, and genes encoding initial adhesins in the O157 wild-type strain and its *fur*-mutant and complemented strains. Data are presented as means  $\pm$  s.d.; n=3.



Fig. 3h

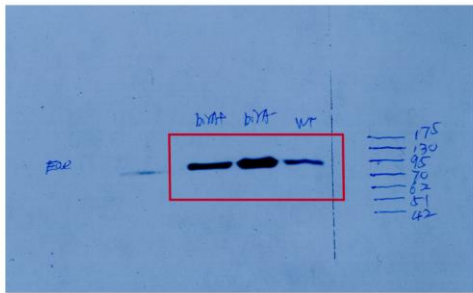


Fig. 3h

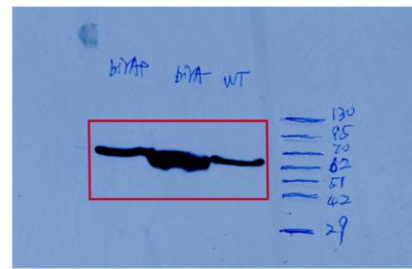
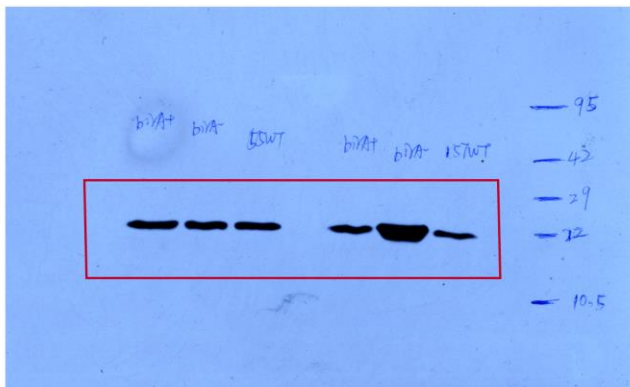


Fig. 5e



**Supplementary Figure 9.** Scans of the western blots. Boxes highlight lanes used in the figures.

Fig. 4a

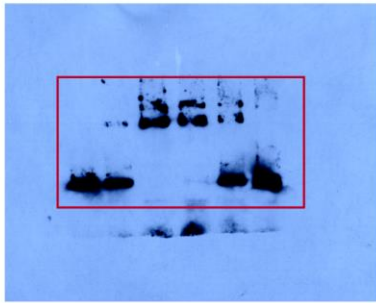


Fig. 4b

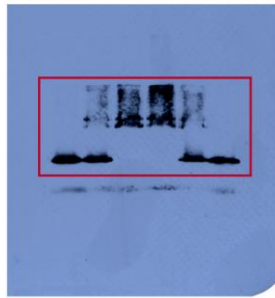


Fig. 4c

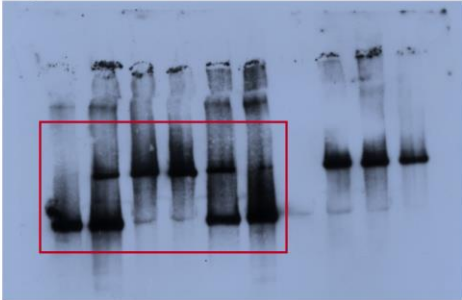
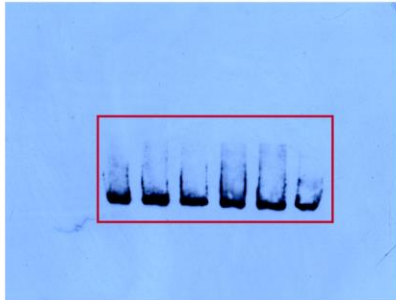
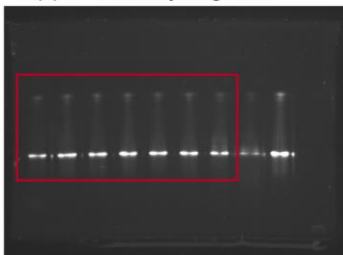


Fig. 4d



Supplementary Fig. 5a



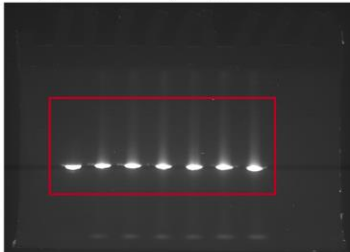
Supplementary Fig. 5b



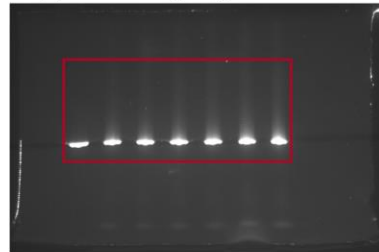
Supplementary Fig. 5c



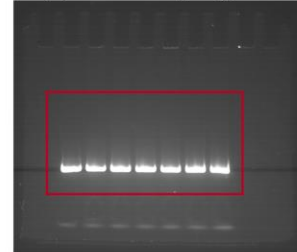
Supplementary Fig. 5d



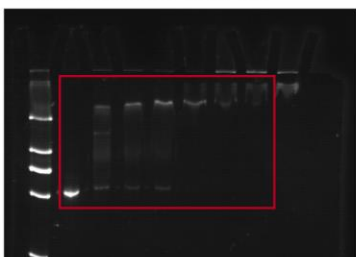
Supplementary Fig. 5e



Supplementary Fig. 5f



Supplementary Fig. 5g



Supplementary Fig. 5h



**Supplementary Figure 10.** Full blots and gels of the EMSAs. Boxes highlight lanes used in the figures.

## Supplementary Tables

**Supplementary Table 1. Statistics for the RNA-seq data sets**

	DMEM-grown O157	HeLa-attached O157	DMEM-grown O55	HeLa-attached O55
Total number of reads	12,604,656	12,353,582	26,056,440	11,822,200
Average read length (bp)	74.20	78.34	74.56	76.13
Low-quality reads	1,186,530	1,126,642	2,530,852	1,222,395
Multi-mapped reads	336,973	773,344	136,363	68,528
Reads mapped to bacterial genome	9,916,754	4,917,044	20,979,282	1,347,940
Mapping success rate (%)	92.05	46.71	94.34	13.70
Reads mapped to host genome	/	5,084,499	/	7,979,625
Contamination rate with host RNA (%)	/	48.30	/	81.10
Gene coverage (%)	94.66	87.92	96.17	79.52

**Supplementary Table 2. Statistics for the ChIP-seq data sets**

	Mock-ChIP sample	BirA-ChIP sample
Total number of reads	6,011,222	6,591,200
Average read length (bp)	85.85	86.02
Low-quality reads	723,554	923,893
Multi-mapped reads	255,873	277,694
Reads mapped to bacterial genome	4,669,886	5,091,616
Mapping success rate	92.30%	93.27%
Coverage (fold)	72.52	79.22

**Supplementary Table 3. The interaction of Fur with predicted Fur boxes located in the LEE region and the promoter regions of known LEE regulators in O157, as determined by ChIP-qPCR**

Site_name	Putative Fur box	Start	End	Fold*	Reference
Box1 <sup>†</sup>	AATAATAAATATGTTTAT	4662881	4662898	0.93 ± 0.10	This study
Box2	AATAAAAAATAATTATATT	4670769	4670786	0.94 ± 0.41	This study
Box3	CATTATTATTTTCTATTAC	4673538	4673556	0.80 ± 0.19	This study
Box4	CATAAAGATAATAATCAT	4680198	4680215	0.75 ± 0.13	This study
Box5	TATTATAATTTTATTAT	4687072	4687088	0.94 ± 0.13	This study
Box6	CATATTCATAATAAATAAT	4689132	4689150	1.17 ± 0.18	This study
P <sub>fepA</sub>	TATTATGATAACTATTTGCA	694097	694117	6.68 ± 1.63	<sup>1</sup>
<i>rpoS</i>	none			1.05 ± 0.17	This study
P <sub>hns</sub>	none			0.96 ± 0.25	This study
P <sub>fis</sub>	none			1.03 ± 0.19	This study
P <sub>ihfA</sub>	none			0.84 ± 0.20	This study
P <sub>ihfB</sub>	none			0.81 ± 0.18	This study
P <sub>grlR</sub>	none			1.23 ± 0.22	This study
P <sub>grvA</sub>	none			1.13 ± 0.42	This study
P <sub>qseA</sub>	none			1.10 ± 0.57	This study
P <sub>hha</sub>	none			1.20 ± 0.31	This study
P <sub>gadE</sub>	none			0.70± 0.16	This study
P <sub>hfq</sub>	none			0.71± 0.13	This study
P <sub>etrA</sub>	none			0.63± 0.22	This study
P <sub>eivF</sub>	none			0.79± 0.14	This study
P <sub>rpoS</sub>	none			0.99± 0.23	This study
P <sub>rpoN</sub>	none			0.86± 0.16	This study

\* , Fold enrichment measured by ChIP-qPCR, and values shown are the means ± SD of three independent experiments. <sup>†</sup>, Using a bioinformatics method allowing no more than two mismatches compared with the standard Fur box (Fur binding sequences, N A T W A T N A T W A T N A T W A T; N= any nucleoside; W=A or T) <sup>2</sup>, six putative Fur boxes (Box1 to Box6) were predicted within the O157 LEE pathogenicity island.

**Supplementary Table 4. Strains and plasmids used in this study**

Strains	Genotype or description	Source or reference
G2734	Wild-type EHEC O157:H7 EDL933	ATCC*
G2583	Wild-type EPEC O55:H7 CB9615	BfR†
H2164	<i>birA</i> deletion mutant in G2734 (pLW1629)	This work
H2257	<i>birA</i> deletion mutant in G2583 (pLW1629)	This work
H2165	<i>fur</i> deletion mutant in G2734	This work
H2258	<i>fur</i> deletion mutant in G2583	This work
H2259	<i>birA</i> and <i>fur</i> double deletion mutant in G2734	This work
H2404	<i>birA</i> and <i>fur</i> double deletion mutant in G2583	This work
H2400	H2164 containing pLW1693	This work
H2401	H2257 containing pLW1693	This work
H2205	H2164 containing pLW1630	This work
H2204	H2257 containing pLW1630	This work
H2402	H2165 containing pLW1694	This work
H2403	H2258 containing pLW1694	This work
H2212	H2165 containing pLW1633	This work
H2211	H2258 containing pLW1633	This work
H2206	DH5 $\alpha$ containing pLW1631	This work
H2207	BL21 containing pLW1631	This work
H2213	DH5 $\alpha$ containing pLW1634	This work
H2214	BL21 containing pLW1634	This work
H2261	H2164 containing pLW1658	This work
H2262	H2257 containing pLW1658	This work
H2264	H2165 containing pLW1659	This work
H2265	H2258 containing pLW1659	This work
H2405	G2734, intimin tagged with His tag	This work
H2406	H2164, intimin tagged with His tag	This work
H2407	H2400, intimin tagged with His tag	This work
H2408	G2734, Tir tagged with His tag	This work
H2409	H2164, Tir tagged with His tag	This work
H2410	H2400, Tir tagged with His tag	This work
H2411	G2734, Fur tagged with 3 $\times$ FLAG tag	This work
H2412	H2164, Fur tagged with 3 $\times$ FLAG tag	This work
H2413	H2400, Fur tagged with 3 $\times$ FLAG tag	This work
H2414	G2583, Fur tagged with 3 $\times$ FLAG tag	This work
H2415	H2257, Fur tagged with 3 $\times$ FLAG tag	This work
H2416	H2401, Fur tagged with 3 $\times$ FLAG tag	This work
G4937	EHEC O157:H7 ( <i>eae+</i> , <i>stx1+</i> , <i>stx2+</i> )	<sup>3</sup>
G4938	EHEC O157:H7 ( <i>eae+</i> , <i>stx2+</i> )	<sup>4</sup>
G1334	EHEC O157:H7 ( <i>eae+</i> , <i>stx1+</i> , <i>stx2+</i> )	BfR

G2534	EHEC O157:H7 ( <i>eae+</i> , <i>stx1+</i> , <i>stx2+</i> )	BfR
G4940	EHEC O157:H- ( <i>eae+</i> , <i>stx2+</i> )	5
G2537	EHEC O157:H- ( <i>eae+</i> , <i>stx1+</i> , <i>stx2+</i> )	BfR
G4947	EHEC O111:H8 ( <i>eae+</i> , <i>stx1+</i> )	Lab collection
G4948	EHEC O111:H8 ( <i>eae+</i> , <i>stx1+</i> , <i>stx2+</i> )	6
G4950	EHEC O111:H- ( <i>eae+</i> , <i>stx1+</i> , <i>stx2+</i> )	Lab collection
G4951	EHEC O111:H- ( <i>eae+</i> , <i>stx1+</i> , <i>stx2+</i> )	7
G3105	EHEC O111:H- ( <i>eae+</i> , <i>stx1+</i> , <i>stx2+</i> )	Lab collection
G4955	EHEC O26:H11 ( <i>eae+</i> , <i>stx1+</i> )	4
G4956	EHEC O26:H11 ( <i>eae+</i> , <i>stx1+</i> )	8
G1344	EHEC O26:H11 ( <i>eae+</i> , <i>stx1+</i> )	BfR
G4958	EHEC O26:H- ( <i>eae+</i> , <i>stx1+</i> )	9
G4959	EHEC O26:H- ( <i>eae+</i> , <i>stx1+</i> )	BfR
G1327	EHEC O103:H2 ( <i>eae+</i> , <i>stx1+</i> )	BfR
G1345	EHEC O145:H28 ( <i>eae+</i> , <i>stx1+</i> , <i>stx2+</i> )	BfR
G4963	EHEC O70:H11 ( <i>eae+</i> , <i>stx1+</i> )	10
G4944	EPEC O55:H7 ( <i>eae+</i> )	Aus <sup>‡</sup>
G4945	EPEC O55:H7 ( <i>eae+</i> )	11
G1094	EPEC O127:H- ( <i>eae+</i> )	Aus
G3109	EPEC O127:H- ( <i>eae+</i> )	Lab collection
G1474	EPEC O86:H34 ( <i>eae+</i> )	Aus
G1179	EPEC O114:H2 ( <i>eae+</i> )	BfR
G1679	EPEC O126:H- ( <i>eae+</i> )	Aus
G1095	EPEC O128:H2 ( <i>eae+</i> )	Lab collection
G1098	EPEC O142:H6 ( <i>eae+</i> )	Aus
G1485	EPEC O145:H34 ( <i>eae+</i> )	BfR
G1100	EPEC O145:H34 ( <i>eae+</i> )	Lab collection
<b>Plasmids</b>		
pKD3	Containing a chloramphenicol resistance cassette and the flipase recognition sites, CmR	12
pKD4	Containing a kanamycin resistance cassette and the flipase recognition sites, KmR	12
pKD46	Red recombination plasmid, ApR	12
pCP20	FLP expression plasmid, ApR, CmR	12
pET28a+	T7 expression vector, KmR	Novagen
pWSK29	Expression vector, ApR	13
pTRC99A	Expression vector, ApR	14
pACYC184	Expression vector, CmR, TcR	15
pLW1629	pACYC184 carrying <i>birA</i> from <i>Acinetobacter calcoaceticus</i> (AC), CmR	This work
pLW1693	pWSK29 carrying <i>birA</i> , ApR	This work
pLW1694	pWSK29 carrying <i>fur</i> , ApR	This work
pLW1630	pTRC99A carrying <i>birA</i> , ApR	This work

pLW1633	pTRC99A carrying <i>fur</i> , ApR	This work
pLW1631	pET28a carrying <i>birA</i> , KmR	This work
pLW1634	pET28a carrying <i>fur</i> , KmR	This work
pLW1658	pTRC99A carrying <i>birA</i> -3xFLAG, ApR	This work
pLW1659	pTRC99A carrying <i>fur</i> -3xFLAG, ApR	This work

\* , ATCC, American Type Culture Collection, Manassas, Virginia, USA. † , BfR, Beutin Federal institute for Risk Assessment National Reference Laboratory for *Escherichia coli*, Berlin, Germany. ‡ , Aus, School of Molecular and Microbial Biosciences, University of Sydney, Sydney, Australia.



**Supplementary Table 5. Primers used in this study (5'-3')**

Primers for gene mutation		
<i>birA</i>	F	GTGCATCAGGTGAAGTGAGCGCAGTGGAGACAATTCGTGTAGGCTGGAGCTGCTTC
<i>birA</i>	R	CGCAAATAATTTGCAGGGGAGCTAATGCTCCCTTTTCATGGGAATTAGCCATGGTCC
<i>fur</i>	F	ATGAAGTGAACCGCTTAGTAACAGGACCAGATTCCGCGTGTAGGCTGGAGCTGCTTC
<i>fur</i>	R	GCCAACCCGCAGGTTGGCTTTTCTCGTTCAGACTGGCATGGGAATTAGCCATGGTCC
<i>eae-his</i>	F	TAATGTTAATACTCCAAATGTCTATGCGGTTTGTGTAGAACCACCACCACCACCA CTAATAGGTGTAGGCTGGAGCTGCTTC
<i>eae-his</i>	R	ACTAAAACAATACATATTTTTAGCCGGGGTGGTTATGGAAATGGGAATTAGCCATGGT CC
<i>tir-his</i>	F	TTCGAATAACCCACCAGCGCCGGGATCCCATCGTTTCGTCCACCACCACCACCACCA CTAATAGGTGTAGGCTGGAGCTGCTTC
<i>tir-his</i>	R	CCCCCTCCCTCCCTCTAAATAAAATGATTATGGATATATATGGGAATTAGCCATGGT CC
<i>fur-3</i> ×flag	F	CGATTGCCGCGAAGATGAGCACGCGCACGAAGGCAAAGACTACAAAGACCATGACG GTG
<i>fur-3</i> ×flag	R	GCCAACCCGCAGGTTGGCTTTTCTCGTTCAGACTGGCTTACGCCCCGCCCTGCCACTC A
Primers for gene cloning		
<i>birA</i>	F	CGGGATCCATGAAGGATAACACCGTGCC
<i>birA</i>	R	CCCAAGCTTTTCTTATTTTTCTGCACTACGCA
<i>fur</i>	F	CGGGATCCATGACTGATAACAATACCGCCCT
<i>fur</i>	R	CCCAAGCTTTTATTTGCCTTCGTGCGCGT
<i>birA</i> (AC)	F	CCCAAGCTTGCTAAATTACGAAAAACAGGC
<i>birA</i> (AC)	R	CGGGATCCGTGTTTCCGATATCAAGCCA
Primers for BirA-3×FLAG and Fur-3×FLAG (plasmid)		
<i>birA</i>	F	CATGCCATGGTCATGAAGGATAACACCGTGC
<i>birA</i>	R	CGGAATTCCTTACTATTTATCGTCGTCATCTTTGTAGTCGATATCATGATCTTTATAATC ACCGTCATGGTCTTTGTAGTCTTTTCTGCACTACGCAGGGATAT
<i>fur</i>	F	CATGCCATGGGCATGACTGATAACAATACCG
<i>fur</i>	R	CGGAATTCCTTACTATTTATCGTCGTCATCTTTGTAGTCGATATCATGATCTTTATAATC ACCGTCATGGTCTTTGTAGTCTTTGCCTTCGTGCGCGTGCTCATCT
Primers for qRT-PCR		
<i>rrsH</i>	F	GAAAGCGTGGGGAGCAAAC
<i>rrsH</i>	R	ACATGCTCCACCGCTTGTG
<i>ler</i>	F	CAGGAAGCAAAGCGACTG
<i>ler</i>	R	ACCAGGTCTGCCCTTCTT
<i>eae</i>	F	GACGGTAGTTCCTGGACTTCTT
<i>eae</i>	R	TCGCCACCAATACCTAAACG
<i>escC</i>	F	GACCAAAAATGTTGTCGTCCCA
<i>escC</i>	R	AGGTTACCGCTTCGCTCG
<i>escN</i>	F	AGGTTTTCTTGTTGCCTTTTGA

<i>escN</i>	R	TCTCCATTGGTCTGCCTATGC
<i>escT</i>	F	GCAATAGATGCGGCTGGAC
<i>escT</i>	R	TCGGCTTGTAATGGTAATATCTCG
<i>tir</i>	F	GATGTTCTGGACTTCCTGTAA
<i>tir</i>	R	CAACAGAGGTCTCAACACCATT
<i>espB</i>	F	AAAACCTCTCGCAAGATGG
<i>espB</i>	R	AATAATCCCGCCAACCAAAG
<i>bioA</i>	F	GGATGGTGAATGGGATGAGC
<i>bioA</i>	R	TCTCGTCGGCAATCAGCAA
<i>bioB</i>	F	GGAAGAATCCCCACGAACG
<i>bioB</i>	R	CCTAAACCCACAATGCCACC
<i>bioC</i>	F	AACATCGTATTCAGCCCATCAC
<i>bioC</i>	R	TCACGAACAATCACTCCCAAA
<i>bioD</i>	F	AACGGATACCGAAGTGGG
<i>bioD</i>	R	TGTTGTATCGCCTGTGCC
<i>bioF</i>	F	CGCCATCTTATCTACAGCACCA
<i>bioF</i>	R	GCAGCACCTCCAACAGACG
<i>birA</i>	F	ATGGCGGTAGTGTAAGTGTGCT
<i>birA</i>	R	TCCAGACGCCAGAATCG
<i>accA</i>	F	GCCATCCACAGCGTCCTT
<i>accA</i>	R	TTCTTTGGTTTCACGACCTTTT
<i>accB</i>	F	AAGAATCAGGCATCTCCGAAC
<i>accB</i>	R	CGTTGACTTTCTGACCCACTTC
<i>accC</i>	F	TTGCGTATTCTTCGTGCCTG
<i>accC</i>	R	AGCGTTCAACCTGCTCGG
<i>accD</i>	F	AAAAGCAACATTACTCCCACCC
<i>accD</i>	R	GGCTCAAGCTCGCTACCCA
<i>fur</i>	F	GTATCGTCACCCGCCACAA
<i>fur</i>	R	CGCAGTGACCGTAAAGATAGAGA
Z4332	F	GCATCAGAAGCCCGACTACG
Z4332	R	CATTTGCCAGACCAAGGAGC
Z4971	F	GAGATCGTGGATTACCTTGC
Z4971	R	CGCCCGCTTCAGTGCTAA
Z5225	F	TACAGCCTTTAGTGCGTCG
Z5225	R	TACCAGCGGCAGCATCG
Z2200	F	GCAGCCGAGGGTGATGAA
Z2200	R	GCCAGGCGAGAAGAACGA
Z2203	F	AGAGGCAGACGGCAGTATTCA
Z2203	R	GTCCAGTTTCTTCCAGTCCAT
Z2053	F	TCTGCTCTGGCTATCATTCTGG
Z2053	R	CAGGTCTGGTCAGGTCGTCAA
<i>flhD</i>	F	TAAATGAAGAAATGGCGACAACA
<i>flhD</i>	R	AGATCGTCAACGCGGGAAT

<i>flhC</i>	F	AGTGCCCGCAAGCAGAAG
<i>flhC</i>	R	TGGTGAGCGTGGGTAATAAAAAT
<i>fliC</i>	F	TGCGAACGGTGTGACGATG
<i>fliC</i>	R	GCCGCATCACCAGCAGAATA
<i>flgM</i>	F	GTATTGATCGCACTTCGCCTCT
<i>flgM</i>	R	ATATCACTGCTGCCGGGTTG
Primers for EMSAs		
<i>P<sub>fur</sub></i>	F	CTTTCTTTAGGGCGGTATTG
<i>P<sub>fur</sub></i>	R	TCAATGCCTGATGTGATGC
<i>bioO</i>	F	GCCCACCAGGACGACATA
<i>bioO</i>	R	GCTTTGCGGGCAGTATTT
Box1	F	GAAGAACTCGCACTCACA
Box1	R	AACAGAAGACTGGTTGCT
Box2	F	TAGTCGATAAACGGCTGAAC
Box2	R	TCCTGGTGTATAGCATGGC
Box3	F	GGATAATCAGTCCACCCAGG
Box3	R	TCCCGTATAGCGAAAGCC
Box4	F	CGATTTTGAAACTACTGGG
Box4	R	GTTGGCGGCATCATTGT
Box5	F	TTGGCAGTAATGATAACAGAAA
Box5	R	GACATTAACTTGATCCTGGC
Box6	F	GAGTCCATCATCAGGCACAT
Box6	R	TTTAAGGTGGTTGTTTGATGAA
<i>P<sub>jepA</sub></i>	F	TGTTTTATTCTGCATTTTTG
<i>P<sub>jepA</sub></i>	R	TTCGTCATTCAGACGCTGC
<i>rpoS</i>	F	CTTCCAGTGTTGCCGCT
<i>rpoS</i>	R	CCCGTACTATTGTTTGCC
Primers for ChIP-qPCR		
Site5	F	TGTATTGGCGTTGCTGTCCG
Site5	R	GGCTTTAGTTCGCTGTGGGT
Site10	F	GCCACGCCTAAATGAAAACC
Site10	R	CGAAATTCTCAATGCCCTGATGT
Site12	F	AAAATTAGCTCGCAACCTTCG
Site12	R	TGGGGCTTCTCCAAAACG
Site16	F	GGCAAGATCCAGCTCCGTC
Site16	R	CGTGCGTGTATTTGGTCAGGT
Site33	F	GGATGTCAGCCGCCGTAT
Site33	R	ATTACTTGCTTGCCAGACGC
Site39	F	TGTGGTCAGGGCTGGAAAA
Site39	R	GGTGAGGGAACCCAATACGT
Site40	F	TTTTCCCGCACACGCTA
Site40	R	GCAGGCCATGCACCAGAG
Site44	F	GAAACTGACGCTGACCTACGC

Site44	R	GACGATAGTGCCTTCACCAAAC
Site45	F	ACGATGCCGAAATGCTGTC
Site45	R	CGCAAGGTACTCGCCATAAAA
<i>rpoS</i>	F	GTTATCGCAGGGAGCCACA
<i>rpoS</i>	R	TTTTACCACCAGACGCAAGTTA
Box1	F	CGAAGAACTCGCACTCACATTA
Box1	R	AACAGAAGACTGGTTGCTGGAG
Box2	F	CACGTAGTCGATAAACGGCTGA
Box2	R	TTAATTGGTTTTCTTTGGCTGTG
Box3	F	TAATCAGTCCACCCAGGTACGA
Box3	R	GGTGCCAAGAGTTATTCCCGTA
Box4	F	CACGATTTTGAAACTACTGGG
Box4	R	TGTTGGCGGCATCATTGTA
Box5	F	GCTGTGAGCCAATGGTCATT
Box5	R	CATTAAACTTGATCCTGGCGAG
Box6	F	CGCAGTCGCTTTGCTTCC
Box6	R	GGTCCTTCCTGATAAGGTCGC
<i>P<sub>hms</sub></i>	F	AGCATTTCTTCCAGCGTTCA
<i>P<sub>hms</sub></i>	R	GCGGCACAAAATAAAGAACAAT
<i>P<sub>fepA</sub></i>	F	CATCAACACGACGCATCCC
<i>P<sub>fepA</sub></i>	R	GACCTCAAACATTTTCGTCATTCA
<i>P<sub>fis</sub></i>	F	TGGTATCTCCAGGAACACGCT
<i>P<sub>fis</sub></i>	R	TTAACCGAGTCACGCAGGG
<i>P<sub>ihfA</sub></i>	F	CATTTGGCGACGGTAGCG
<i>P<sub>ihfA</sub></i>	R	GTAAGGGTGTTCGCGAGGG
<i>P<sub>ihfB</sub></i>	F	GGTTTCGTCTGTAAATCAAGCA
<i>P<sub>ihfB</sub></i>	R	TGGGTGGCAAGTCTTTCTATCA
<i>P<sub>grlR/A</sub></i>	F	AAGCAATATCAAGAATAATGGAGACC
<i>P<sub>grlR/A</sub></i>	R	AAAACAATCGGAAGCATAACAGTAA
<i>P<sub>grvA</sub></i>	F	TTACTCAGAAAATAAAGGCAAGAACA
<i>P<sub>grvA</sub></i>	R	CCTATAACGGGGATACGCAGTT
<i>P<sub>qseA</sub></i>	F	GAGCAGGCGTTATTATTTTCAGC
<i>P<sub>qseA</sub></i>	R	GCGTTTTAGTCGTTCCATTATTCA
<i>P<sub>hha</sub></i>	F	CCTGACTTCCGCCATTTCTG
<i>P<sub>hha</sub></i>	R	TGAGCATATTGCGACCTTCG
<i>P<sub>gadE</sub></i>	F	TATGGAGTGCGTGATGGATAAAT
<i>P<sub>gadE</sub></i>	R	ACTGCCAAAAGCCCTGTAAAA
<i>P<sub>hfq</sub></i>	F	TACAGGTTGTTGGTGCTATCGC
<i>P<sub>hfq</sub></i>	R	GATTGCCCTTAGCCATTCTC
<i>P<sub>etrA</sub></i>	F	CTATTCCCTCAACGTTAAGCAAAT
<i>P<sub>etrA</sub></i>	R	GTGAAGTAGACATCACTGGAAAAGAC
<i>P<sub>eivF</sub></i>	F	TTTCCCCGTAAGAACCACATTT
<i>P<sub>eivF</sub></i>	R	TGGACAGGATGACGTACTAGTGTAAG

<i>P<sub>rpoS</sub></i>	F	CAGAAATGTTGGCAAGAATGGA
<i>P<sub>rpoS</sub></i>	R	GGTATCGCCGCAGCAAGTAT
<i>P<sub>rpoN</sub></i>	F	AAACGCATCATTGAGCACCTG
<i>P<sub>rpoN</sub></i>	R	ACGTCGCAAACCTTCTACCCTATC
Primers for EHEC/ EPEC identification		
<i>mdh</i>	F	AGGCGCTTGCACTACTGTTA
<i>mdh</i>	R	AGCGCGTCTGTTCAAAATG
<i>eae</i>	F	ATTATGGAACGGCAGAGGTTAAT
<i>eae</i>	R	ATCCCCATCGTCACCAGAGG
<i>stx1A</i>	F	CATTCGCTCTGCAATAGGTA
<i>stx1A</i>	R	AACTCGCGATGCATGATGA
<i>stx2A</i>	F	TATCTGGCGTTAATGGAGTT
<i>stx2A</i>	R	CCTGTCGCCAGTTATCTGAC

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