

**Table S1.** *Salmonella* spp. that were sequenced and constructed for this research

Strain No.	Strain	Application in the study
SE163A	<i>S. Typhimurium</i> <sup>c</sup>	WGS <sup>a</sup> for SNP <sup>b</sup> analysis (wild type strain)
SE819	<i>S. Heidelberg</i> <sup>c</sup>	WGS for SNP analysis (recipient strain)
SE696A	<i>S. Typhimurium</i> <sup>c</sup>	WGS for SNP analysis
SE710A	<i>S. Typhimurium</i> <sup>c</sup>	WGS for SNP analysis
SE397	<i>S. Typhimurium</i> <sup>c</sup>	WGS for SNP analysis
SE452	<i>S. Typhimurium</i> <sup>c</sup>	WGS for SNP analysis
SE478	<i>S. Typhimurium</i> <sup>c</sup>	WGS for SNP analysis
J53	<i>E. coli</i>	Conjugation (recipient)
J53::IncFIB	Transconjugant	Conjugation (J53 strain containing IncFIB plasmid from donor SE163A strain)
SE819::IncFIB	Transconjugant	Conjugation (SE819 strain containing IncFIB plasmid from donor SE163A strain)

<sup>a</sup> WGS; Whole Genome Sequence

<sup>b</sup> SNP; Single Nucleotide Polymorphism

<sup>c</sup> *Salmonella* serotypes were predicted using SeqSero ([www.denglab.info/SeqSero](http://www.denglab.info/SeqSero))

**Table S2.** Primers employed for qRT-PCR

Gene	Primer sequence (5' to 3')	Amplicon
<i>sitA</i>	<i>sitAF:</i> CTACCAACGTAATGCCGATACT	104 bp
	<i>sitAR:</i> TGACCATCCATCGCTGATT	
<i>iucA</i>	<i>iucAF:</i> TTACGGCTGAAGCGGATTAC	108 bp
	<i>iucAR:</i> CCTGGCAGTCACGGTAAATAA	
<i>iutA</i>	<i>iutAF:</i> AGCGTGGTGGCGAATAAA	114 bp
	<i>iutAR:</i> TCCGGTACTCCAGTCAGTATC	
<i>gmk</i>	<i>gmkF:</i> TTGGCAGGGAGGCGTT	62 bp
	<i>gmkR:</i> GCGCGAAGTGCCGTAGTAAT	