

Table S1. Additional genomes used in the study, including accessions, geographical location of isolation (Location), continent of isolation, host origin of sample (Type), year of isolates, definitive phage type (DT), multilocus sequence type (ST), membership of Clade A, references for information/genomes, and presence or absence of the virulence plasmid (pSLT).

Isolate	ERS/accession	Location	Continent	Type	Year	DT	ST	CladeA	Reference	pSLT
DT56	ERS007588	United Kingdom	Europe	Human	2009	ND	19	no	(9)	yes
DT99	ERS007596	United Kingdom	Europe	Human	2009	ND	19	no	(9)	yes
U313	ERS007611	United Kingdom	Europe	Human	2008	ND	19	no	(9)	yes
U319	ERS007613	United Kingdom	Europe	Human	2008	ND	19	no	(9)	yes
DT2	HG326213/LN999012	Germany	Europe	Pigeon	1994	2	128	no	(1, 4)	yes
LT2	AE006468/AE006471	United Kingdom	Europe	Human	1948	4	19	no	(1, 8)	yes
DT104	HF937208/HF937209			Human	1988	104	19	no	(2, 7)	yes
SL1344	FQ312003/HE654724/HE654725/HE654726			Cattle	1981	44	19	no	(3, 6)	yes
D23580	FN424405/FN432031	Malawi	Africa	Human	2004	untypable	313	no	(5)	yes
249DRC	ERS004904	DRC	Africa	Human	1991	ND	19	no	(9)	yes
5578	ERS004959	Kenya	Africa	Human	2005	ND	19	no	(9)	yes
5632	ERS004961	Kenya	Africa	Human	2003	ND	19	no	(9)	yes
5912	ERS004963	Kenya	Africa	Human	2005	ND	313	no	(9)	yes
LT6	ERS007492	Sweden	Europe	Pigeon	1946	ND	19	no	(9)	yes
LT8	ERS007494	Denmark	Europe	Mouse	1943	ND	19	no	(9)	yes
LT9	ERS007495	Denmark	Europe	Goose	1946	ND	19	no	(9)	yes
LT10	ERS007496	Chile	South America	Human	1945	ND	19	no	(9)	yes
LT11	ERS007497	Sweden	Europe	Rats	1938	ND	19	no	(9)	yes
SARA1	ERS007499	Mexico	North America	Human	NA	ND	19	no	(9)	yes
SARA2	ERS007500	United Kingdom	Europe	Laboratory strain	1946	ND	19	no	(9)	yes
SARA3	ERS007501	USA-RI	North America	Horse	1987	ND	19	no	(9)	no
SARA4	ERS007502	USA-IN	North America	Rabbit	1986	ND	19	no	(9)	yes
SARA5	ERS007503	Mongolia	Europe	Unspecified	NA	ND	19	no	(9)	yes
SARA9	ERS007507	USA-CA	North America	Parrot	1987	ND	98	no	(9)	yes
SARA10	ERS007508	USA-CA	North America	Opposum	1987	ND	19	no	(9)	yes
SARA11	ERS007509	Thailand	South-East Asia	Unspecified	NA	ND	19	no	(9)	yes
SARA12	ERS007510	USA-LA	North America	Horse	1987	ND	19	no	(9)	yes
DT12	ERS007564	United Kingdom	Europe	Human	2009	ND	19	no	(9)	yes
DT120	ERS007566	United Kingdom	Europe	Human	2009	ND	34	no	(9)	no
DT135	ERS007567	United Kingdom	Europe	Human	2009	ND	19	no	(9)	yes
DT177	ERS007572	United Kingdom	Europe	Human	2008	ND	19	no	(9)	no
DT191A	ERS007574	United Kingdom	Europe	Human	2009	ND	19	no	(9)	yes
DT193	ERS007576	United Kingdom	Europe	Human	2009	ND	34	no	(9)	no
DT195	ERS007578	United Kingdom	Europe	Human	2009	ND	19	no	(9)	yes
DT2B	ERS007580	United Kingdom	Europe	Human	2009	ND	313	no	(9)	yes
DT24	ERS007582	United Kingdom	Europe	Human	2009	ND	19	no	(9)	yes
DT7	ERS007590	United Kingdom	Europe	Human	2009	ND	34	no	(9)	no
DT8	ERS007592	United Kingdom	Europe	Human	2009	ND	19	no	(9)	yes
DT97	ERS007594	United Kingdom	Europe	Human	2008	ND	34	no	(9)	no
DT1	ERS007598	United Kingdom	Europe	Human	2009	ND	19	no	(9)	yes
U276	ERS007600	United Kingdom	Europe	Human	2009	ND	19	no	(9)	yes
U288	ERS007604	United Kingdom	Europe	Human	2009	ND	19	no	(9)	yes

U302	ERS007606	United Kingdom	Europe	Human	2009	ND	19	no	(9)	yes
U310	ERS007608	United Kingdom	Europe	Human	2009	ND	19	no	(9)	yes
6079U	ERS009038	Uganda	Africa	Human	1998	ND	19	no	(9)	yes
M2815013	ERS009049	Mozambique	Africa	Human	2003	ND	19	no	(9)	yes
A130	ERS007468	Malawi	Africa	Human	1997	56v	313	no	(9)	yes
3299-1997	ERS015626	United Kingdom	Europe	Bird (unspecified)	1997	160	2866	no	(10)	yes
S04698-09	PRJEB10340	United Kingdom	Europe	Cattle	2009	193	34	no	(10)	no
U277	ERS007602	United Kingdom	Europe	Human	2009	ND	568	yes	(9)	no
1164-1995	ERS015624	United Kingdom	Europe	Cattle	1998	141	568	yes	(10)	no
818-1998	ERS015625	United Kingdom	Europe	Chicken	2008	141	568	yes	(10)	no
2610-1998	ERS015627	United Kingdom	Europe	Horse	1998	160	19	yes	(10)	no
S05081-04	ERS015649	United Kingdom	Europe	Horse	2004	40	19	yes	(10)	no
S00060-07	ERS015650	United Kingdom	Europe	Horse	2007	40	19	yes	(10)	no
2087-1997	ERS015654	United Kingdom	Europe	Finch	1997	56	568	yes	(10)	no
S07676-03	ERS015655	United Kingdom	Europe	Bird (wild)	2003	56v	568	yes	(10)	no
S05451-08	ERS015656	United Kingdom	Europe	Dog	2008	56v	568	yes	(10)	no

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Table S2. Primers used to investigate virulence- and fimbriae-associated genes *in silico*.

Gene	Forward primer	Reverse primer	Source
<i>prgH</i>	GCCCGAGCAGCCTGAGAAGTTAGAAA	TGAAATGAGCGCCCCTTGAGCCAGTC	(2)
<i>sopB</i>	CGGACCGCCCAGCAACAAAACAAGAAGAAG	TAGTGATGCCGTTATGCGTCAGTGTATT	(2)
<i>sopE</i>	TCAGTTGGAATTGCTGTGGA	TCCAAAAACAGGAAACCACAC	(2)
<i>invA</i>	CTGGCGGTGGGTTTGTGCTCTCTATT	AGTTTCTCCCCCTCTCATGCGTTACCC	(2)
<i>sitC</i>	CAGTATATGCTCAACCGATGTGGGTCTCC	CGGGGCAAAATAAAGGCTGTGATGAAC	(2)
<i>spiC</i>	CCTGGATAATGACTATTGAT	AGTTTATGGTATTGCGTAT	(2)
<i>sifA</i>	TTTGCCGAACCGGCCACACG	GTTGCCTTTCTTGCCTTCCACCCATCT	(2)
<i>misL</i>	GTCGGCGAATGCCCGAATA	GCGCTGTTAACGCTAATAGT	(2)
<i>orfL</i>	GGAGTATCGATAAAGATGTT	GCGCGTAACGTCAGAACCAA	(2)
<i>pipD</i>	CGGGGATTCATGACTTTGAT	CGTTATCATTGGATCGTAA	(2)
<i>iroN</i>	ACTGGCACGGCTCGCTGCGCTCTAT	CGCTTACCGCCGTTCTGCCACTGC	(2)
<i>pefA</i>	GCGCCGCTCAGCCGAACCAAG	CAGCAGAAGCCCAGGAAACAGTG	(2)
<i>safA</i>	ATGAAAAGCATAAAAAATTGATTATCGC	TTAAGGTTGATATCCCACTACG	This study*
<i>fimA</i>	ATGAAACATAAATTAAATGACC	TTATTCTGATTTCATGATAAAGG	This study*
<i>lpfA</i>	ATGAATTCTGGCTAAAGCAGGG	TCAAGGCCTTGTATTGTTCGG	This study*
<i>bcfA</i>	ATGAAAAAGCCTGTACTAGCATTATGG	TCAGGAATAAACCATGC	This study*
<i>stdA</i>	ATCGCTAATAAAATAACTTGCC	TCACAGGTATTCAGGGTAGG	This study*
<i>stcA</i>	ATGAAACGTTCACTTATTGCTGC	TTAGTCAGTAACAACCGTAAAGTCAGTG	This study*
<i>stfA</i>	ATGAATACAGCAGTAAAGCTCGG	TTACAGATAGCTGATCGTAAGTTACGG	This study*
<i>stbA</i>	ATGTCTATGAAAAAATTTAGC	TTATTATACGAAACGGGTATTGAAGGGTGGC	This study*
<i>sthA</i>	ATGAAACACATAAAGAAATCCGTGTTGGC	CTAGAAATGAACCGGAATCGGGCTCTAAACTCATCCC	This study*
<i>cdtB</i>	ACAACTGTCGCATCTGCCCGTCATT	CAATTGCGTGGGTTCTGTAGGGCGAGT	(4)
<i>lpfC</i>	GCCCCGCCTGAAGCCTGTGTTGC	AGGTCGGCGCTTTGAGGGTGGATA	(4)
<i>msgA</i>	GCCAGGCGCACGCGAAATCATCC	GCGACCAGCCACATATCAGCCTCTCAAAC	(4)
<i>orgA</i>	TTTTGGCAATGCATCAGGAAACA	GGCGAAAGCGGGGACGGTATT	(4)
<i>pagC</i>	CGCCTTTCCGTGGGTATGC	GAAGCCGTTATTTGTAGAGGAGATGTT	(4)
<i>pefA</i>	GCGCCGCTCAGCCGAACCAAG	GCAGCAGAAGCCCAGGAAACAGTG	(4)

<i>sipB</i>	GGACGCCGCCGGGAAAAACTCTC	ACACTCCCGTCGCCGCCTCACAA	(4)
<i>sopB</i>	CGGACCGGCCAGCAACAAAACAAGAAGAAG	TAGTGATGCCGTTATGCGTGAGTGTATT	(4)
<i>span</i>	AAAAGCCGTGGAATCCGTTAGTGAAGT	CAGCGCTGGGGATTACCGTTTG	(4)
<i>spiA</i>	CCAGGGGTCGTTAGTGTATTGCGTGAGATG	CGCGTAACAAAGAACCCGTAGTGATGGATT	(4)
<i>spvB</i>	CTATCAGCCCCGCACGGAGAGCAGTTTTA	GGAGGGAGGCGGTGGCGGTGGCATCATA	(4)
<i>tolC</i>	TACCCAGGCGAAAAAGAGGCTATC	CCGCGTTATCCAGGTTGTTGC	(4)

* primer sequences based on *Salmonella* Typhimurium LT2 genome sequence (NC_003197, NC_003277) and specificity validated using *in silico* PCR analysis against *S.* Typhimurium LT2 and SL1344 chromosome and plasmids (1, 3).

References

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Table S3. Accession numbers for the raw reads (ERS/SRA) and annotated assemblies used in this study.

Isolate	ERS/SRA	Annotated assemblies
PM1402/06	ERS217356	CYHV01000001-CYHV01000067
XT1456/06	ERS217357	CYIB01000001-CYIB01000076
PM108/01	ERS217358	CYHT01000001-CYHT01000045
PM1422/05	ERS217359	CYID01000001-CYID01000078
PM65/01	ERS217360	CYHZ01000001-CYHZ01000071
PM132/06	ERS217361	CYHX01000001-CYHX01000065
XT062/01	ERS217362	CYIA01000001-CYIA01000075
PM1377/06	ERS217363	CYHU01000001-CYHU01000059
PM100/01	ERS217364	CYIC01000001-CYIC01000080
PM54/01	ERS217365	CYHY01000001-CYHY01000073
PM1356/06	ERS217366	CYHW01000001-CYHW01000070
H144540642	SRR1967749	FKJC01000001-FKJC01000047
H143320447	SRR1969075	FKJF01000001-FKJF01000158
H143540876	SRR1968278	FKJE01000001-FKJE01000079
H142780372	SRR1965151	FKJD01000001-FKJD01000087
H143120429	SRR1969317	FKJB01000001-FKJB01000046

Table S4. The number of intact, incomplete, and questionable prophage sequences found in the assemblies of isolates investigated in this study, along with the number of each intact prophage with associated accession details.

Isolate	No prophage regions	No intact	No incomplete	No questionable	Intact prophage											
	Salmon_ST64B NC_004313	Gifsy_2 NC_010393	Gifsy_1 NC_010392	Entero_ST64T NC_004348	Salmon_Fels_1 NC_010391	EnteropSP3 NC_005340	Plankt_PaV_LD NC_016564	Entero_ST104 NC_005841	Entero_Fels_2 NC_010463	Escher_D108 NC_013594	Entero_186 NC_001317	Edward_FW_3 NC_026611	Pseudo_B3 NC_006548			
H144540642	7	5	2	0	1	1	2	1								
H143320447	7	3	4	0	1	1	1									
H143540876	9	4	4	1	1	1	1	1								
H142780372	6	2	3	1		1										1
H143120429	8	4	3	1	1	1	1								1	
PM1402/06	6	2	3	1	1		1									
XT1456/06	8	3	5	0	1	1	1									
PM108/01	7	4	3	0	1	1	1	1								
PM1422/05	7	2	5	0	1		1									
PM65/01	6	2	4	0	1		1									
PM132/06	5	2	2	1	1		1									
XT062/01	5	2	1	2	1		1									
PM1377/06	7	4	2	1	1	1	1	1								
PM100/01	6	2	3	1	1		1									
PM54/01	7	2	4	1	1		1									
PM1356/06	6	2	4	0	1		1									
D23580	9	7	2	0	1	1	1	1						1		1
DT104	10	6	2	2	1	1	1						1		1	1
LT2	10	5	3	2		1	1		1				1		1	
SL1344	10	5	3	2	1	1	1						1		1	
A130	10	6	3	1	1	1	1	1	1							1
DT2	8	4	2	2	1	1	1						1			

Isolate						Intact prophage					
	No prophage regions	No intact	No incomplete	No questionable		Salmon_ST64B NC_004313	Gifsy_2 NC_010393	Gifsy_1 NC_010392	Shigel_SfII NC_021857	Haemop_HP2 NC_003315	Entero_SfV NC_003444
SO4698-09	11	7	3	1		1	1	1	1	1	2