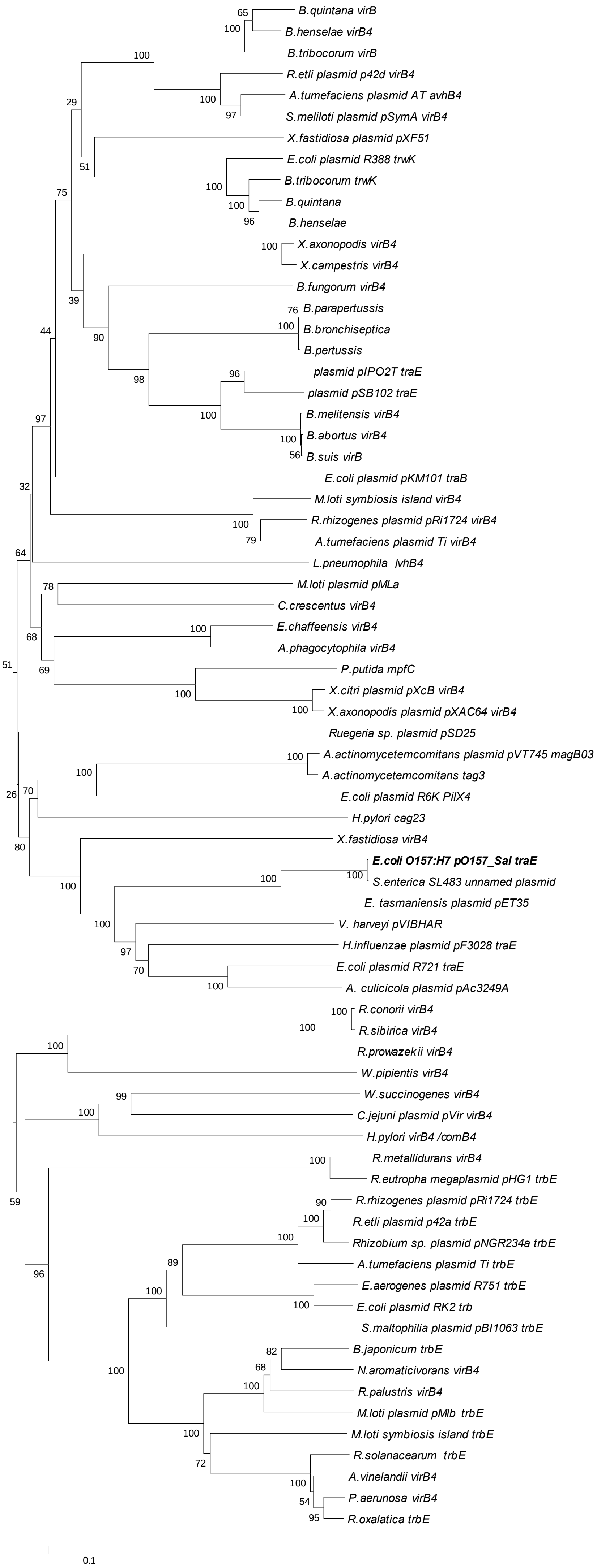
Supplementary table 1. PCR primers for the pO157_Sal plasmid screening.

Primer	Target gene	Sequence (5’-3’)	Amplicon size (bp)
p206-F	*traA*	TGCCCCCTGCGGCGTTAGTA	876
p206-R		TTGCCAACGCAGCCGCTGAT	
p215-F	*traE*	TGATGCGGCAAGTGCGACAA	547
p215-R		AGCGCGGCGAGATGCTTGAG	
p228-F	*mpr*	CCGTCACGTTTTGCGGGGGA	598
p228-R		CGCTAGGTTTCGCCCACGCT	
p247-F	*traL*	AGCGCATCGCTACAAGCACA	481
p247-R		ACGACAACCCCACCGAGGCT	

Supplementary table 2. pO157_Sal genes.

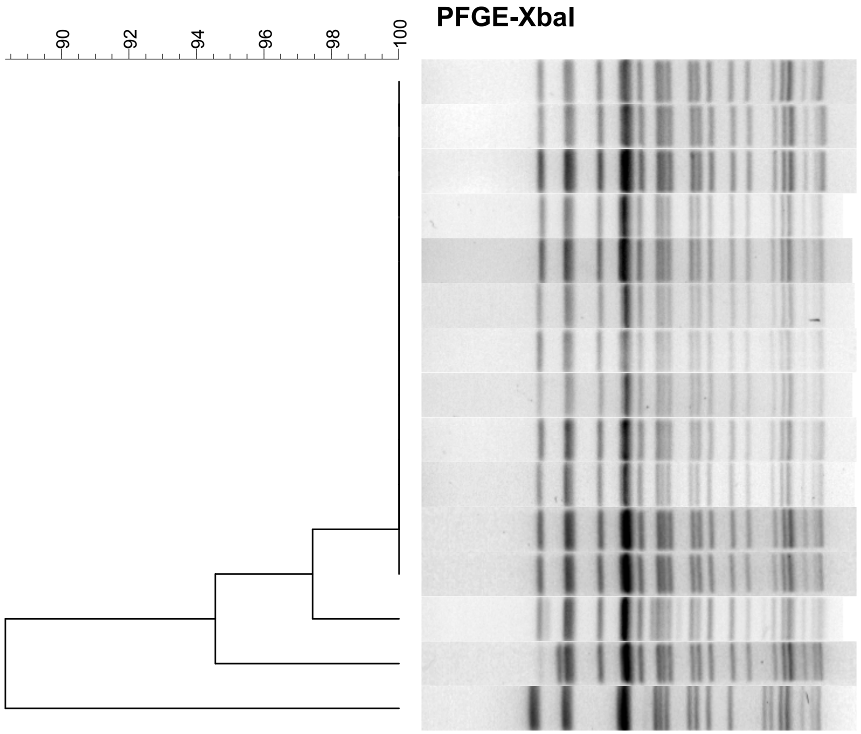
locus_tag	**start**	**end**	**gene name**	**function**	**homology to Salmonella strain SL483 plasmid (% amino acid identity)**
pO157_Sal_01	1	1065	*repA*	plasmid replication protein RepA	97.46
pO157_Sal_02	1066	1569		hypothetical protein	98.80
pO157_Sal_03	1774	2190		hypothetical protein	99.26
pO157_Sal_04	2284	2961	*traB*	Conjugal transfer protein TraB	99.11
pO157_Sal_05	2976	3293	*traC*	conjugal transfer protein TraC	99.05
pO157_Sal_06	3354	3752	*traD*	conjugal transfer protein TraD	100.00
pO157_Sal_07	3697	6240	*traE*	Conjugal transfer protein TraE	99.17
pO157_Sal_08	6008	6904	*traF*	conjugal transfer protein TraF	100.00
pO157_Sal_09	6963	7127		hypothetical protein	100.00
pO157_Sal_10	7129	7920	*traG*	Conjugal transfer protein TraG	97.72
pO157_Sal_11	7941	8729	*traH*	Conjugal transfer protein TraH	100.00
pO157_Sal_12	8722	9948	*traI*	Conjugal transfer protein TraI	98.77
pO157_Sal_13	10025	11086	*traJ*	Conjugal transfer protein TraJ	99.43
pO157_Sal_14	11108	13129	*traK*	Conjugal transfer protein TraK	97.62
pO157_Sal_15	13145	13510	*traR*	conjugal transfer protein TraR	95.04
pO157_Sal_16	13596	13982		hypothetical protein	47.66
pO157_Sal_17	13873	16197	*topB*	DNA topoisomerase III	98.62
pO157_Sal_18	16295	16717	*stpA*	DNA binding protein, nucleoid-associated	97.86
pO157_Sal_19	16730	17074		hypothetical protein	91.07
pO157_Sal_20	17071	17382		hypothetical protein	unique
pO157_Sal_21	17597	18415	*mpr*	zinc metalloproteinase Mpr protein	98.90
pO157_Sal_22	18399	18986		hypothetical protein	94.71
pO157_Sal_23	18997	19200		hypothetical protein	100.00
pO157_Sal_24	19443	19784		hypothetical protein	97.35
pO157_Sal_25	19806	20021		hypothetical protein	97.18
pO157_Sal_26	20021	20521	*yeaA*	nuclease	96.99
pO157_Sal_27	20527	20835		hypothetical protein	96.15
pO157_Sal_28	20961	21248		hypothetical protein	97.89
pO157_Sal_29	21290	21583		hypothetical protein	unique
pO157_Sal_30	21638	22081		hypothetical protein	89.80
pO157_Sal_31	22078	22485		hypothetical protein	74.05
pO157_Sal_32	22486	22689	*hha*	Haemolysin expression modulating family protein	95.52
pO157_Sal_33	22708	23118		hypothetical protein	unique
pO157_Sal_34	23161	23406		hypothetical protein	46.15
pO157_Sal_35	23842	24003		hypothetical protein	98.11
pO157_Sal_36	24245	24457		hypothetical protein	98.57

pO157_Sal_37	28374	24763	*nikB*	relaxase	98.08
pO157_Sal_38	27383	27072	*nikC*	relaxosome accessory protein	98.06
pO157_Sal_39	28807	28349	*nikA*	Relaxosome component	96.12
pO157_Sal_40	29094	29507		hypothetical protein	57.35
pO157_Sal_41	29510	30322	*traL*	Conjugal transfer protein TraL	98.51
pO157_Sal_42	30370	30927		hypothetical protein	100.00
pO157_Sal_43	30960	31313		hypothetical protein	88.03
pO157_Sal_44	31653	31348		hypothetical protein	unique
pO157_Sal_45	32258	31656		hypothetical protein	95.50
pO157_Sal_46	33393	32398		hypothetical protein	100.00
pO157_Sal_47	33842	33516		hypothetical protein	100.00
pO157_Sal_48	34096	33941		hypothetical protein	98.04
pO157_Sal_49	34646	34323		hypothetical protein	98.82
pO157_Sal_50	35259	34678		hypothetical protein	97.93
pO157_Sal_51	36424	35372	*traA*	Conjugal transfer protein TraA	98.86
pO157_Sal_52	36692	36444		hypothetical protein	100.00


65
B.quintana virB
100
B.henselae virB4
100
B.tribocorum virB
R.etli plasmid p42d virB4
100
A.tumefaciens plasmid AT avhB4
29
97
S.meliloti plasmid pSymA virB4
X.fastidiosa plasmid pXF51
E.coli plasmid R388 trwK
51
B.tribocorum trwK
100
75
B.quintana
100
96
B.henselae
100
X.axonopodis virB4
X.campestris virB4
B.fungorum virB4
39
B.parapertussis
76
100
B.bronchiseptica
44
90
B.pertussis
96
plasmid pIPO2T traE
98
plasmid pSB102 traE
100
B.melitensis virB4
97
B.abortus virB4
100
56
B.suis virB
E.coli plasmid pKM101 traB
32
M.loti symbiosis island virB4
100
R.rhizogenes plasmid pRi1724 virB4
79
A.tumefaciens plasmid Ti virB4
64
L.pneumophila lvhB4
78
M.loti plasmid pMLa
C.crescentus virB4
100
E.chaffeensis virB4
68
A.phagocytophila virB4
51
69
P.putida mpfC
100
X.citri plasmid pXcB virB4
100
X.axonopodis plasmid pXAC64 virB4
Ruegeria sp. plasmid pSD25
100
A.actinomycetemcomitans plasmid pVT745 magB03
100
A.actinomycetemcomitans tag3
70
26
E.coli plasmid R6K PilX4
H.pylori cag23
X.fastidiosa virB4
80
E.coli O157:H7 pO157_Sal traE
100
100
S.enterica SL483 unnamed plasmid
100
E. tasmaniensis plasmid pET35
100
V. harveyi pVIBHAR
H.influenzae plasmid pF3028 traE
97
70
E.coli plasmid R721 traE
100
A. culicicola plasmid pAc3249A
100
R.conorii virB4
100
R.sibirica virB4
100
R.prowazekii virB4
W.pipientis virB4
99
W.succinogenes virB4
100
C.jejuni plasmid pVir virB4
H.pylori virB4 /comB4
100
R.metallidurans virB4
R.eutropha megaplasmid pHG1 trbE
59
90
R.rhizogenes plasmid pRi1724 trbE
100
R.etli plasmid p42a trbE
100
Rhizobium sp. plasmid pNGR234a trbE
89
A.tumefaciens plasmid Ti trbE
96
E.aerogenes plasmid R751 trbE
100
100
E.coli plasmid RK2 trb
S.maltophilia plasmid pBI1063 trbE
82
B.japonicum trbE
68
N.aromaticivorans virB4
100
100
R.palustris virB4
M.loti plasmid pMlb trbE
100
M.loti symbiosis island trbE
R.solanacearum trbE
72
100
A.vinelandii virB4
54
P.aerunosa virB4
95
R.oxalatica trbE
0.1

Supplementary figure 1. TraE tree

The Genbank accession No. and protein sequences of TraE are described by Frank et al and download from http://www.egs.uu.se/molev/sup_data.html. Other Genbank accession No. are *Erwinia tasmaniensis* plasmid pET35 (YP_001909403), (YP_002268522), *Aeromonas culicicola* plasmid pAc3249A (ABI83640), *Vibrio harveyi* pVIBHAR (YP_001436080).



Strain	PFGE pattern	Location	Year	Source
99A024	EXHX01.0001	Xuzhou	1999	Chicken
99A032	EXHX01.0001	Xuzhou	1999	Porcine
99A038	EXHX01.0001	Xuzhou	1999	Chicken
X119	EXHX01.0001	Xuzhou	1999	Goat
X120	EXHX01.0001	Xuzhou	1999	Bovine
Xuzhou143	EXHX01.0001	Xuzhou	1999	patient(HC)
Xuzhou21	EXHX01.0001	Xuzhou	1999	patient(HUS)
Xuzhou223	EXHX01.0001	Xuzhou	1999	patient(HC)
Xuzhou284	EXHX01.0001	Xuzhou	1999	patient(HUS)
Xuzhou65	EXHX01.0001	Xuzhou	1999	patient
F846	EXHX01.0001	Xuzhou	1999	Fly
F971	EXHX01.0001	Xuzhou	1999	Goat
X114	EXHX01.0115	Xuzhou	1999	Chicken
F828	EXHX01.0173	Xuzhou	1999	Porcine
2063	EXHX01.0175	Xuzhou	1999	Chicken

Supplementary figure 2. Pulsed-field gel electrophoresis (PFGE) type of pO157_Sal positive strains.