

TABLE S1 Virulence gene targets, their encoded proteins and locations and sequence of the oligonucleotides used in the qPCR microarray

virulence gene targets	proteins encoded	location	GenBank accession number	primer forward / primer reverse
<i>stx</i> - all variants	Shiga toxin	chromosome	NC002695	TTTGTACTGTSACAGCWGAAGC YTTACG / CCCCAGTTCARWGTRAGRTC MAC RTC
<i>stx</i> _{2e}	Shiga toxin 2e variant	chromosome	AB252836	AGGGAGCTACATCGGTATCC / AACATCAAGCCCTCGTATACCT
<i>eae</i>	Intimin	chromosome, LEE (locus of enterocyte effacement) of EHEC O157:H7 (strain EDL933)	Z11541	CATTGATCAGGATTTTTCTGGTGA TA / CTCATGCGGAAATAGCCGTTA
<i>eae</i> -alpha	Intimin-alpha	chromosome, LEE (locus of enterocyte effacement) of EHEC O127:H7 (strain E2348/69)	M58154	GATACGAATGGCTATGCCAAAG / CATCGCTAACACGGGCACTA
<i>eae</i> -beta	Intimin-beta	chromosome, LEE (locus of enterocyte effacement) of EHEC O15:H- (strain RDEC-1)	U60002	GGTGATAATCAGAGTGCGACATA CA / GGAATCAAATAACGTAACCTCGAG TAT
<i>eae</i> -gamma	Intimin-gamma	chromosome, LEE (locus of enterocyte effacement) of EHEC O157:H7 (strain EDL933)	Z11541	GACTGTTAGTGCGACAGTCAGTG A / TTGTTGTCAATTTTCAGTTCATCA AA
<i>eae</i> -epsilon	Intimin-epsilon	chromosome, LEE (locus of enterocyte effacement) of EHEC O103:H2 (strain PMK5)	AF116899	ATACCCAAATTGTGAAAACGGAT A / CACTAACAACAGCATTACCTGCA A
<i>eae</i> -theta	Intimin-theta	chromosome, LEE (locus of enterocyte effacement) of EHEC O111:H- (strain 95NR1)	AF025311	TGTTAAAGCACCTGAGGTTACATT TT / TCACCAGTAACGTTCTTACCAAG AA
<i>iha</i>	Iha, iron regulated gene A homolog, adhesin	chromosome, OI-43, OI-48	AF126104	AGTGGTACGGGTAAAACCG / AGTATCAGCGTGTAACTGGC
<i>terE</i>	tellurite resistant gene	chromosome, OI-43, OI-48	CP003301	GCCGTTACCATCTATGATGC / TGTAACCGCGCATGAAGCTG
<i>ureD</i>	urase transporter	chromosome, OI-43, OI-48	AE005174	GCAATAATTGACTCTGATTGCC /

				GCTGCTGCGGTAAAATTTACT
<i>espV</i>	AvrA family effectors	chromosome, OI-44	AE005174	TCAGGTTCCCTCGTCTGATGCCGC / CTGGTTCAGGCCTGGAGCAGTCC
<i>espK</i>	non-LEE-encoded type III secretion system effectors	chromosome, OI-50	AE005174	GCAGRCATCAAAGCGAAATCAC ACC / TCGTTTGGTAACTGTGGCAGATAC TC
<i>espN</i>	non-LEE-encoded type III secretion system effectors	chromosome, OI-50	AE005174	GACATATTTGTTTATGTCATCAGG AGCGG / CCTCAGGATATGGATGGCCTACT GGC
<i>espX7</i>	non-LEE-encoded type III secretion system effectors	chromosome, OI-50	AE005174	TGCTGAAGAATTGAATTACTCT / TGTATCATCAAGCACTGCTCC
<i>espO1-1</i>	non-LEE-encoded type III secretion system effectors	chromosome, OI -50	AE005174	CATGTTGTTGATGTAAGTATGCAG / AAGTTCACAAGTACATTACCCGG
<i>nleG5</i>	non-LEE-encoded type III secretion system effectors	chromosome, OI -57	AE005174	AGACTATTCGTGGAGAAGCTCAA G / TATTGAAGGCCAATCTGGATG
<i>nleG6-2</i>	non-LEE-encoded type III secretion system effectors	chromosome, OI -57	AE005174	ATATGCTCTCTATATGATAAGGAT G / AAAGTGACATTCGTCTTTTCTCAT A
<i>Z2096</i>	putative gene marker for EHEC	chromosome, OI-57	AE005174	GCCGGGAACGATGAAGGTAAAA / GCTTCTTTGCATGCCTCTCTGA
<i>Z2098</i>	putative gene marker for EHEC	chromosome, OI-57	AE005174	CTGAAAAGAGCCAGAACGTGC/ TGCCTAAGATCATTACCCGGAC
<i>Z2099</i>	putative gene marker for EHEC	chromosome, OI-57	AE005174	TAGCGGGACAATTGTCACGG / GTCTTTCGGAGAAACATTCTGCC
<i>nleA</i>	serine protease	chromosome, OI-71	AE005174	AGATAACYCTAATACTAAATATG CC/ GCCCAACCATTGCRCCGATATGA GG
<i>nleF</i>	non-LEE-encoded type III secretion system effectors	chromosome, OI-71	AE005174	TGAGGTGAGAAATGAAAATACTG ATG / CTATCCCTGTCCTCTATCGTCATT C
<i>nleH1-2</i>	NleH	chromosome, OI-71	AE005174	ACAAGAGAAAGTCATAGTGGTTG / AATCTCYCCCTTAGGCCATCCCA

<i>espM1</i>	non-LEE-encoded type III secretion system effectors	chromosome, OI-71	AE005174	TCAGCTCTTTTGGTATCA / CGCTAAATTTGTTAACATTAAAG
<i>espM2</i>	IpgM	chromosome, OI-108	AE005174	CAGCACAAAGTTCTATTAATCAT GTRATAATGGGG / ACTTGTCCGCAAGCAAGTTTGCTA TG
<i>nleB</i>	non-LEE-encoded type III secretion system effectors	chromosome, OI-122	AE005174	CATGTTGAAGGCTGGAASTTTGT / CCGCTACAGGGCGATATGTT
<i>nleE</i>	non-LEE-encoded type III secretion system effectors	chromosome, OI-122	AE005174	AGAAGCGTTTGAACCTATTTCCA / TTGGGCGTTTTCCGGATAT
<i>efa1(lifA)</i>	Efa1 EHEC factor for adherence	chromosome, OI-122	AE005174	TTTTACCAGTTCATCATAACAGG / CCATTATAAACATTTGCCAGACC
<i>ent/espL2</i>	enterotoxin	chromosome, OI-122	AE005174	TCCTGGATTATTTTCTGCATTTCA / ACTATTGCCAAGTACGCCACAA
<i>pagC</i>	phoP-activated gene C product (PagC)	chromosome, OI-122	AE005174	GGCTGATAATCATACGCTATCG / ATCGATATTGCAGATTCCTCC
<i>lpfA-O157</i>	long polar fimbriae	chromosome, OI-141, OI-154	AE005174	TACTGTCCGTTGACTCTCAG / ACCAACCGCAGCAAATACAG
<i>lpfA-O113</i>	long polar fimbriae	chromosome, OI-154	AY057066	GCAGCCGTTTCGTTTTGATGGTACA G / CCTGCTGTAAGCGGCGTACCC
<i>lpfA-O26</i>	long polar fimbriae	chromosome	AB161111	GCGCTGACCTCTACTTCCGTA / GGCGTCAACAATCTCACCGGTG
<i>ecs1822</i>	hypothetical protein, putative gene marker for EHEC	chromosome	BA000007	CCGTACAGCGTGATTCATCC / TAGCGAAACGGGCAAGGTC
<i>ecs1763</i>	hypothetical protein, putative gene marker for EHEC	chromosome	BA000007	TACTCTTGACCTTAGTACCGC / TTTTGATTATCAGAACCATATAGC CC
<i>irp2</i>	iron responsible protein 2	chromosome, Yersinia-like high pathogenicity island	CP000468	TGAACTCAAACGCCAGCAGCGC / GGAACGCCCCAGATTGCTGG
<i>fyuA</i>	pectin receptor	chromosome, Yersinia-like high pathogenicity island	AFST01000010	TCAGCGCGCCGGAATTAAGCG / CCGGGCAAGACTCTGGGGAG
<i>ehaA</i>	autotransporter, type V secretion system	chromosome	AE005174	TAAGGGCGCTCACTCCATTAG / TCACTGTCAGAAACCTGAATCAC
<i>hlyA</i>	alpha hemolysin	chromosome	AE014075	CAGTCCTCATTACCCAGCAAC / TCAATGGGTCAAAGACTTGCTTC
<i>paa</i>	porcine attaching and effacing associated adhesin	chromosome or plasmid	U82533	ACCTGGCGTGTGGCTGATAA/ GTTGAAGCAACTTTGCGGGATG
<i>cdtI</i>	cytotoxic distending toxin	chromosome or plasmid	AY365042	CAATAGTCGCCACAGGA/

				ATAATCAAGAACACCACCAC
<i>cdtIII</i>	cytolethal distending toxin	chromosome or plasmid	AY365042	CCGATCAAAGCGGGTGGATAAT/ TGCTCCTGTTGTTGACGGTATG
<i>astA</i>	enteroaggregative <i>E. coli</i> heat stable enterotoxin	chromosome or plasmid	L11241	ATCCGAAGGCCCGCATCCAG / CGGCTTTGTAGTCCTTCCATGAC
<i>estIa</i> (STa)	heat stable toxin	plasmid	M58746	GCAAAATCCGTTTAACTAATCTCA AA / ACAGAAATAAAAATTGCCAACAT TAGC
<i>elt</i> (LT)	heat labile toxin	plasmid	KF733765	AAGCCATTGAAAGGATGAAGGA / CTGATTGCCGCAATTGAATT
<i>sfp</i>	sorbitol-fermenting protein fimbriae	plasmid	AF401292	CTGTTGTCGTTTCTGAAGCG / AGTTTGGTTGCAGAGCCAG
<i>bfp</i>	bundle-forming pilus	plasmid	AB024946	AGGTGTGATGTTTTACTACCAG / TAATTGCAGACGTTGCGCTC
<i>fasA</i> (F6, P987)	F6 fimbrial adhesin	plasmid	U50547	AGCAGTGCTTTCCTCTCTGTTCA / TGCCTGGCTGGTGTGTTT
<i>fedA</i> (F18, F107)	F18 fimbrial adhesin	plasmid	M61713	GGCGGTTGTGCTTCCTTGT / CCGTTACGGTTTTTCAGAGC
<i>fimF_{41a}</i> (F41)	F41 fimbrial adhesin	plasmid	X14354	GCTGCATCAGCGGCAGTAT / AACAGATGGTGATGTAATTTCCAC CAC
<i>cnf2</i>	cytotoxic necrotizing factor	Vir plasmid	U01097	CCTCGCTCGGCTCAACTTATT/ CGGTTTACCTTCTGCCTTCT
<i>orfA</i>	adhesin involved in diffuse adherence (AIDA)	plasmid	X65022	CCGGCTATATCCTGGGAGTATCT/ TTTGCTTGTGCGGTAGACTG
<i>orfB</i>	adhesin involved in diffuse adherence (AIDA)	plasmid	X65022	GGCTATGCTGAGAGCACCATTA/ TACTGGTTTCCGCCGGTATTT
<i>ecf1</i>	enzyme that enhance bacterial membrane structure	plasmid O157	AF043470	TTTGGTGCTGATACGCCCTATG/ CTGTGCTGGCCTGAAGGATATT
<i>ecf2</i>	enzyme that enhance bacterial membrane structure	plasmid O157	AF043470	CAGTCGAAACCCGGTGGGAATAA/ ACATCACCCGTAAGACCAGAAC
<i>ecf3</i>	enzyme that enhance bacterial membrane structure	plasmid O157	AF043470	GTATGTCAGTCCCGCCAAATCT/ CGCAGGGACGGAATGAAGATAA
<i>ecf4</i>	enzyme that enhance bacterial membrane structure	plasmid O157	AF043470	ACCACCGGATTTCTCTGGTTATG/ GCTGGAATGGTCTGGAGATTGT
<i>katP</i>	catalase/peroxidase	plasmid O157	X89017	GAAGTCATATATCGCCGGTTGAA

				/
<i>ehxA</i>	EHEC hemolysin	plasmid O157	AF074613	GTCATTTTCAGGAACGGTGAGATC CGTTAAGGAACAGGAGGTGTCAG TA / ATCATGTTTTCCGCCAATGAG
<i>toxB</i>	potential adhesin for adherence,	plasmid O157	AB011549	AGTATCAGTCACATAAAGTAGAC / GCATTRGGATCAATCCAGAG
<i>etpD</i>	EHEC type II secretion system, transporting protein across the outer membrane	plasmid O157	CP001163	TTGGATGACGGCGAAACTG / AGATGATACGCTGTTGGGAG
<i>stcE</i>	metalloprotease, mucinase	plasmid O157	AF074613	CGGAGGTGGGGGAATTGTTA/ ATCACCATCCCATCCCCAAG
<i>espP</i>	serine protease autotransporter	plasmid O157	CP001163	ATGCCCCGTCAGCATCTG / TCGACCGTCAGCGTATGG
<i>eibG</i>	immunoglobulin binding protein	plasmid O113	AB255744	CGGCAGAACAGACCGTATTG / GCGAGTATTGGACTGAATAGC
<i>epeA</i>	EpeA, serine protease	plasmid O113	AY258503	GAGTCTTTCAGCCTTACCCG / AGAACGCCAGTCAGGTTTCCA
<i>saa</i>	Saa, STEC agglutinating adhesion	plasmid O113	AF399919	ATGAACAGGCTATTGCCGC / ATGTTGTGTATCCCATGAGG
<i>subAB</i>	subtilase cytotoxin	plasmid O113	AF399919	AGTGGCTTCCGCATCGG / ATCATTACCCACTGCCGC
<i>sab</i>	autotransporter	plasmid O113	AF399919	CTGCAGTTGACGCTCCTGTC / CGCGAATACCGGGACTTATG

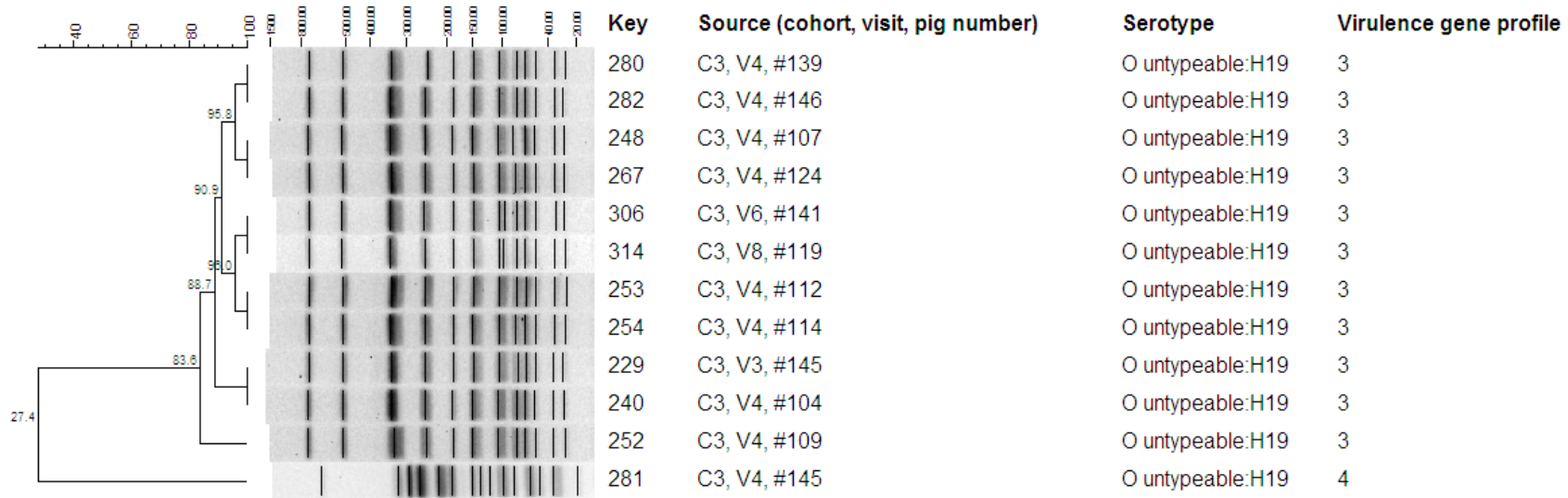


FIG S1 PFGE analysis of swine O untypeable:H19 STEC strains. Key represents strain numbers. Source represents the strain from a pig in which cohort, which time of the eight farm visits, and the individual pig number.

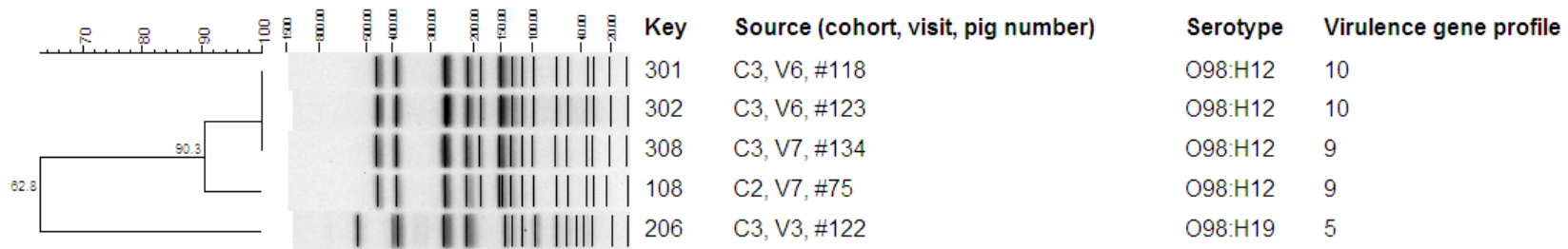


FIG S2 PFGE analysis of swine O98 STEC strains. Key represents strain numbers. Source represents the strain from a pig in which cohort, which time of the eight farm visits, and the individual pig number.