Isolate	**Serotype**	**SSI typing**	**VirulenceFinder**	**MLST**	**Coverage[i]**	**N50**	**Comment**
Week 1							
C570-12	O157:H-	*eae, vtx1a, vtx2c* Haemolysis, *ehxA* VCA(+)	*astA, eae, ehxA, espA, espB, espF, espJ, espP, etpD, gad, iha, iss, katP, nleA, nleB, nleC, prfB, tir, vtx1a, vtx2c*	ST-11	37x	121635	PFGE.
C541-12	O157:H-	*eae, vtx1a, vtx2c* Haemolysis, *ehxA* VCA(+)	*astA, eae, ehxA, espA, espB, espF, espJ, espP, etpD, gad, iha, iss, katP, nleA, nleB, nleC, prfB, tir, vtx1a*	ST-11	24x	103757	PFGE.
C641-12A	O180:H-	*eae* Haemolysis, *ehxA* VCA(-)	*astA, eae, ehxA, espA, espB, espF, espI, espP, gad, nleB, prfB, tir*	ST-301	47x	73908	From same patient as C641-12B. PFGE.
C641-12B	O180:H-	*eae, (vtx2a)* Haemolysis, *ehxA* VCA(+)	*astA, eae, ehxA, espA, espB, espF, espI, espP, gad, nleB, prfB, tir*	ST-301	110x	77810	From same patient as C641-12A. PFGE.
C696-12	O26:H11	*eae, vtx1a* Haemolysis, *ehxA* VCA(+)	*astA, celb, cif, eae, efa1,ehxA, espA, espB, espF, espJ, espP, gad, iss, katP, lpfA, nleA, nleB, nleC, prfB, tir, toxB, vtx1a*	ST-11	42x	78574	PFGE.
C697-12A	O157:H7	*eae, vtx1a, vtx2c* Haemolysis, *ehxA* VCA(+)	*astA, eae, ehxA, espA, espB, espF, espJ, espP, etpD, gad, iha, iss, katP, nleA, nleB, nleC, prfB, tir, toxB, vtx1a, vtx2c*	ST-11	42x 53x (R)	103670 92026(R)	From same patient as C697-12B. Replicate sequence. PFGE.
C697-12B	O157:H-	*eae, vtx1a, vtx2c* Haemolysis, *ehxA* VCA(+)	*astA, eae, ehxA, espA, espB, espJ, espP, etpD, iha, iss, katP, nleA, nleB, nleC, prfB, tir, toxB, vtx1a, vtx2c*	ST-11	56x	117209	From same patient as C697-12A. PFGE.
Week 2							
C748-12	O128ab:H2	*vtx2b* Haemolysis, *ehxA* VCA(+)	*celb, ehxA, gad, iha, ireA, iss, lpfA, mchB, mchC, mchF, prfB, senB, subA, vtx2b*	ST-25	91x	76452	
C749-12	O55:H12	*vtx1a* *saa* VCA(+)	*cdtB, cnf1, espP, gad, iha, iss, lpfA, prfB,(saa), vtx1a*	ST-101	32x	108930	PFGE.
C750-12	O5:H-	*vtx1c* Haemolysis, *ehxA* VCA(+)	*ehxA, espI, gad, iha, ireA, iss, lpfA, prfB, subA, vtx1c*	ST-447	91x	32602	
C751-12	O117:K1:H7	*vtx1a* VCA(-)	*iha, iroN, iss, prfB, sigA, vtx1a*	ST-504	20x	37148	
Week 3							
C659-12	O117:K1:H7	*vtx1a* VCA(-)	*astA, gad, iha, prfB, senB, sigA, vtx1a*	ST-504	25x	30593	
C757-12	O103:H2	*eae, vtx1a* Haemolysis, *ehxA* VCA(+)	*cif, eae, efa1, ehxA, espA, espB, espF, espJ, etpD, gad, iss, nleA, nleB, prfB, tir, vtx1a*	ST-17	25x	30193	PFGE.
C760-12	O117:K1:H7	*vtx1a* VCA(-)	*astA, celb, iha, prfB, senB, sigA, vtx1a*	ST-504	31x	43540	

C767-12	O145:H34	*eae* VCA(-)	*celb, gad, iha, ireA, iss, lpfA, mchF, prfB, vtx2b*	ST-829	15x	29439	Excluded due to mix-up
C770-12	O27:H30	*vtx2b* Haemolysis VCA(+)	*astA, gad, iha, ireA, iss, mchB, mchC, mchF, prfB, subA, vtx2b*	ST-753	25x 93x(R)	33472 88293(R)	Replicate sequence
Week 4							
C813-12	O103:H-	*eae, vtx1a* Haemolysis, *ehxA* VCA(+)	*cif, eae, efa1,(ehxA,) espA, espB, espI, espJ, espP, gad, katP, nleA, nleB, nleC, prfB, tir, vtx1a*	ST-1967	18x	15964	PFGE.
C812-12	O157:H7	*eae, vtx1a, vtx2a* Haemolysis, *ehxA* VCA(+)	*astA, eae, ehxA, espA, espB, espJ, espP, etpD, gad, iha, iss, katP, nleA, nleB, nleC, prfB, tir, toxB, vtx1a, vtx2a*	ST-11	45x	111153	PFGE.
Week 5							
C816-12	O145:H-	*eae, vtx2a* Haemolysis, *ehxA* VCA(-)	*astA, cif, eae, ehxA, espA, espB,* espF, *espJ, espP, gad, iha, iss, nleA, nleB, nleC, prfB, tir, toxB, vtx2a*	ST-32	43x	116786	Received later as C884-12. PFGE.
C818-12	O157:H7	*eae, vtx1a, vtx2a* Haemolysis, *ehxA* VCA(+)	*astA, eae, ehxA, espA, espB, espJ, espP, etpD, gad, iha, iss, katP, nleA, nleB, nleC, prfB, tir, toxB, vtx1a, vtx2a*	ST-11	36x	107822	Patient relation to C849-12 and C852-12. PFGE.
C819-12	O157:H7	*eae, vtx1a, vtx2a* Haemolysis, *ehxA* VCA(+)	*astA, eae, ehxA, espA, espB, espJ, espP, etpD, gad, iha, iss, katP, nleA, nleB, nleC, prfB, tir, toxB, vtx1a, vtx2a*	ST-11	54x	142323	Patient relation to C863-12. PFGE.
C820-12	O128abc:H-	*eae, vtx2f* *(bfpA)* VCA(+)	*astA, cba, cif, cma, eae, espA, espB, espF, gad, iss, nleB, nleC, prfB, tir, vtx2f*	ST-20	38x	79409	
C821-12	O121:H19	*eae, vtx2a* Haemolysis, *ehxA* VCA(+)	*astA, eae, efa1, ehxA, espA, espB, espI, espJ, espP, gad, lpfA, nleA, nleB, nleC, prfB, tir, toxB, vtx2a*	ST-655	45x	122181	
C849-12	O157:H7	*eae, vtx1a, vtx2a* Haemolysis, *ehxA* VCA(+)	*astA, eae, ehxA, espA, espB, espF, espJ, espP, etpD, gad, iha, iss, katP, nleA, nleB, nleC, prfB, tir, toxB, vtx1a, vtx2a*	ST-11	38x	117371	Patient relation to C818-12 and C852-12. PFGE.
C848-12	O78:Hbev	VCA(-)	-	-	45x	179879	Excluded *Morganella*
C850-12	O rough:H2	*eae, vtx1a* Haemolysis, *ehxA* VCA(-)	*astA, cif, eae, efa1,ehxA, espA, espB, espJ, etpD, gad, iss, nleA, nleB, prfB, tir, vtx1a*	ST-17	36x	73556	
Week 6							
C852-12	O157:H7	*eae, vtx1a, vtx2a* *Haemolysis, ehxA* VCA(+)	*astA, eae, ehxA, espA, espB, espF, espJ, espP, etpD, gad, iha, iss, katP, nleA, nleB, nleC, prfB, tir, toxB, vtx1a, vtx2a*	ST-11	53x	104244	Patient relation to C818-12 and C849-12
C857-12	O145:H-	*eae, vtx2a* Haemolysis, *ehxA* VCA(+)	*astA, cif, eae, ehxA, espA, espB, espI, espJ, espP, gad, iha, iss, katP, nleA, nleB, nleC, prfB, tir, toxB, vtx2a*	ST-32	65x	97109	PFGE.

C862-12	O128abc:H-	*eae, vtx2f* *(bfpA)* VCA(+)	*astA, cba, cif, cma, eae, espA, espB, espF, gad, iss, nleA, nleB, nleC, prfB, tir, vtx2f*	ST-20	39x	67763	
C863-12	O157:H7	*eae, vtx1a, vtx2a* Haemolysis, *ehxA* VCA(+)	*astA, eae, ehxA, espA, espB, espJ, espP, etpD, gad, iha, iss, katP, nleA, nleB, nleC, prfB, tir, toxB, vtx1a, vtx2a*	ST-11	42x	121712	Patient relation to C819-12. PFGE.
C864-12	O128ab:H2	*vtx1c, vtx2b* Haemolysis, *ehxA* VCA(+)	*celb, ehxA, gad, iha, iss, lpfA, mchB, mchC, mchF, prfB, vtx1c, vtx2b*	ST-811	45x	68959	
Week 7							
C874-12	O146:H21	*vtx1c, vtx2b* Haemolysis, *ehxA* VCA(+)	*ehxA, gad, ireA, iss, lpfA, mchB, mchC, mchF, prfB, senB, subA, vtx1c, vtx2b*	ST-442	31x	110113	PFGE.
C884-12	O145:H-	*eae, vtx2a* Haemolysis, *ehxA* VCA(-)	*astA, cif, eae, ehxA, espA, espB, espJ, espP, gad, iha, iss, nleA, nleB, nleC, prfB, tir, toxB, vtx2a*	ST-32	39x	135864	Received earlier as C816-12. PFGE.
C885-12A	O146:H21	*eae* VCA(-)	*cif, eae, espA, espF, espJ, gad, lpfA, nleB, prfB, tir*	ST-442	32x	116386	Received later as C896-12B
C885-12B	O115:H-	*eae, vtx2a* Haemolysis, *ehxA* VCA(+)	*astA, eae, ehxA, espA, espF, espI, espJ, espP, gad, lpfA, nleB, prfB, tir, vtx2a*	ST-333	42x	71345	Received later as C896-12A
C886-12	O145:H-	*eae, vtx2a* Haemolysis, *ehxA* VCA(+)	*astA, cif, eae, ehxA, espA, espB, espI, espJ, espP, gad, iha, iss, nleA, nleB, nleC, prfB, tccP, tir, toxB, vtx2a*	ST-32	71x	109186	PFGE.
C887-12	O36:H-	VCA(-)	*astA, gad, lpfA, prfB*	-	30x	168502	
C891-12	O157:H7	*eae, vtx2c* Haemolysis, *ehxA* VCA(+)	*astA, eae, ehxA, espA, espB, espJ, espP, etpD, iha, iss, katP, nleA, nleB, nleC, prfB, tir, vtx2c*	ST-2966	24x	91704	PFGE.
C892-12	OX187:H28	*vtx2d* VCA(-)	*celb, gad, katP, lpfA, prfB, vtx2g*	ST-200	41x	102382	
C893-12	O181:H16	*vtx1a* Haemolysis, *ehxA* VCA(+)	*cba, cma, ehxA, espI, gad, iha, ireA, lpfA, mchB, mchC, mchF, prfB, senB, subA, vtx1c*	-	44x	90784	
C894-12	O157:H7	*eae, vtx2a* Haemolysis, *ehxA* VCA(+)	*astA, eae, ehxA, espA, espB, espJ, espP, etpD, gad, iha, iss, katP, nleA, nleB, nleC, prfB, tir, toxB, vtx2a*	ST-11	71x	105953	PFGE.
C895-12	O rough: -	*vtx2a* Haemolysis VCA(+)	*gad, iha, lpfA, mchC, mchF, pic, prfB, sigA, vtx2a*	ST-678	40x	72589	PFGE.
C896-12A	O115:H-	*eae, vtx2a* Haemolysis, *ehxA* VCA(-)	*astA, eae, ehxA, espA, espF, espI, espJ, espP, nleA, nleB, prfB, tir, vtx2a*	ST-333	60x	72435	Received earlier as C885-12B. PFGE.
C896-12B	O146:H21	*eae* Haemolysis VCA(-)	*cif, eae, espA, espF, espJ, gad, lpfA, nleB, prfB, tir*	ST-442	28x	95889	Received earlier as C885-12A. PFGE.

C904-12A	O76:H-	*vtx1c* Haemolysis, *ehxA* VCA(+)	*celb, ehxA, gad, iha, ireA, lpfA, pic, prfB, subA, vtx1c*	ST-675	56x	54694	PFGE.
C905-12	O165:H-	*eae, vtx1, vtx2* Haemolysis, *ehxA* VCA(+)	*astA, eae, efa1, ehxA, espA, espB, espF, espI, espJ, espP, gad, iss, katP, lpfA, nleA, nleB, nleC, prfB, tir, vtx1a, vtx2a*	ST-119	41x	84914	PFGE.

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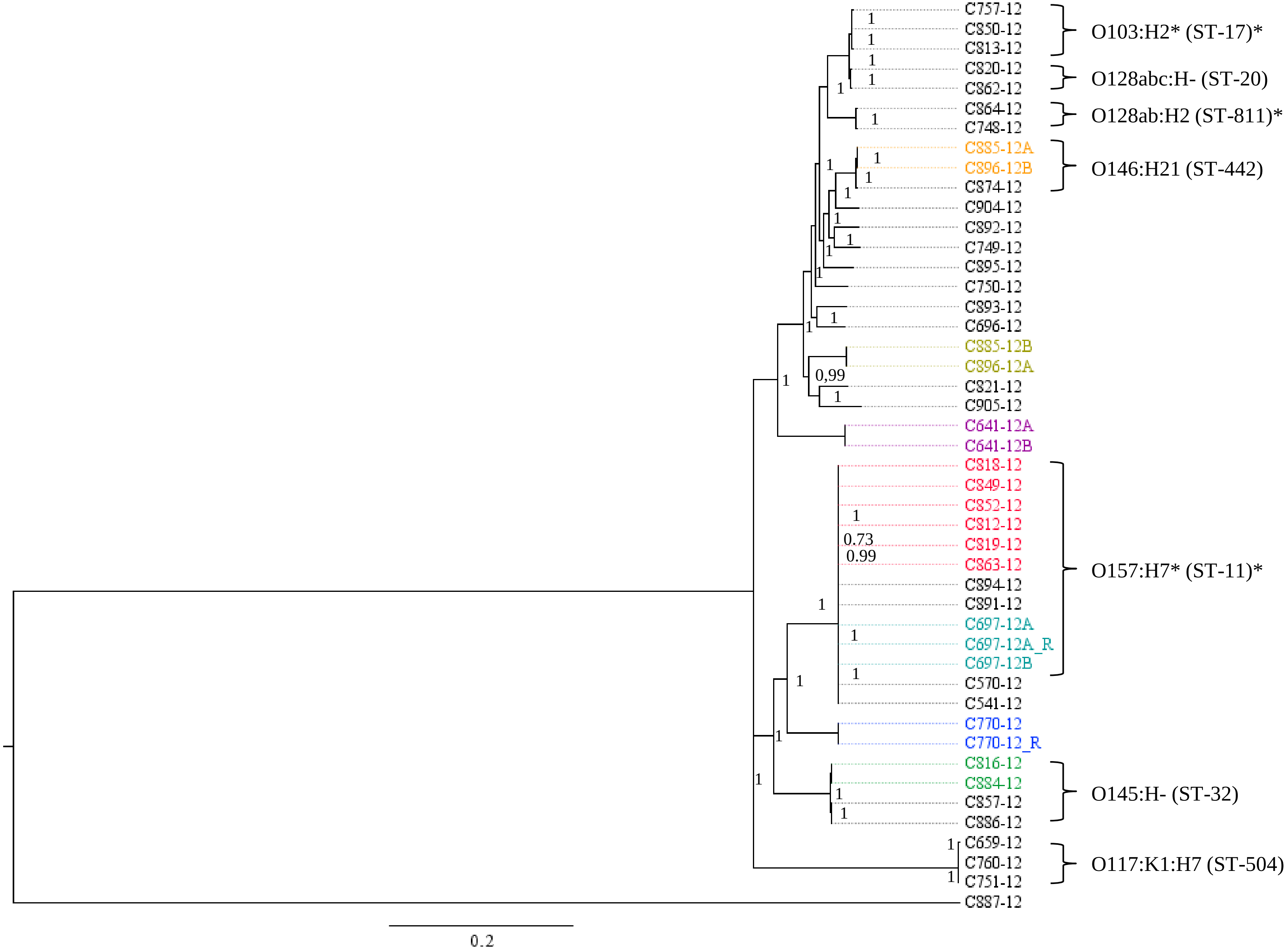
[i] Average coverage was determined using an estimated genome size of 5.5Mb.

Supplementary material 1: Complete set of typing results from routine and WGS typing in this study, including sequence quality and epidemiological information on the isolates.



Supplementary material 4: Phylogeny by NDtree based on positions called in all sequences, using *Fastree* for tree construction. In the ND matrix a Z-score of 1.96 was employed to obtain sufficient resolution. In total, 2476641 positions were called in all strains, and of these 223254 positions were not 100% conserved. Bootstrap values are assigned to each node.