



**Table S1.** Control quality primer pairs used in the verification of ICESluvan sequence assembly in *E. faecium* MM5-F9a and to confirm different regions of the element in *E. faecalis* OG5-F9a and JH5-F9a, *S. lutetiensis* 5-F9 and NEM760 as well as *S. gallinarum* 4-C11 and 4-G10. + Indicates region confirmed with PCR by other primer combinations.

Primer	Sequence	ICESluvan position	Approximate PCR product size in kb					
			MM5-F9a	OG5-F9a	JH5-F9a	5-F9	NEM 760	4-C11
Q1.forw	gcacttttcaagcattttgtct	Orf2	2	2	2	2		
Q1.rev	tggaatggcgattttagctc	Orf5						
Q2.forw	gaagacagcccagctcatct	Orf5	3.1	+	+			
Q2.rev	gggttagacgatggcagaaa	Orf11/TraG						
Q3.forw	aatgctccacatggaacg	Orf11/TraG	2.7	2.7	2.7	2.7	2.7	-
Q3.rev	ccttgaacggcatagacat	Orf13/VirB6						
Q2.forw	gaagacagcccagctcatct	Orf5	+	5.8	5.8			
Q3.rev	ccttgaacggcatagacat	Orf13/VirB6						
Q4.forw	tttgcccctgttaccattc	Orf13/VirB6	2.6	2.6	2.6	2.6		
Q4.rev	acacggttccaaatctggtc	Orf15/VirB4						
Q5.forw	gaccagatttgaaccgtgt	Orf15/VirB4	2.5	2.5	2.5	2.5	2.5	2.5
Q5.rev	atccgcggtatctgtccat	Orf16/PG hydrolase						
Q6.forw	tttagccttagccaatgga	Orf16/PG hydrolase	2.5	2.5	2.5	+ <sup>a</sup>	2.5	+
Q6.rev	cgatcatcacgtcgaaacac	Orf19/Tn1549 Orf13						
Q7.forw	gctttgatctggccgactat	Orf19/Tn1549 Orf13	2.5	2.5	2.5			
Q7.rev	gtccgacaggtcgatttcat	Orf21-22 intergenic						
Q8.forw	caagtggtaacgcagatga	Orf21-22 intergenic	2.5	2.5	2.5	2.5		
Q8.rev	aaagatagccgtctcgtgt	Orf26/Tn1549 Orf20						
Q9.forw	acacgcagacggctatctt	Orf26/Tn1549 Orf20	2.5	2.5	2.5			
Q9.rev	cgttctctccgacagtg	Orf27/Tn1549 Orf21						
Q10.forw	ccaactgtcggaggaagaac	Orf27/ Tn1549 Orf21	2.5	2.5	2.5			
Q10.rev	cgctgacggcatatagtcg	Orf29/ Tn1549 Orf23						
Q11.forw	ccgtcagcgaaggaagta	Orf29/ Tn1549 Orf23	2.3	+	+			
Q11.rev	gctttcgcatagtctccag	Orf31/ TnpX						
Q12.forw	ctttgcgaggccagacctt	Orf30/ Tn1549 Orf24	2.5	+	+			
Q12.rev	ttagtctgttggtggcgttg	Orf32						
Q13.forw	gcacggcagtatgcagaga	Orf32	2.5	2.5	2.5	2.5		
Q13.rev	gcaagtggctttctctctgc	Orf35-36 intergenic						
Q14.forw	ggaagcgcaggtctatctga	Orf35	2.4	2.4	2.4	2.4		
Q14.rev	ggaagagagcaggtcaacg	Orf37/DNA primase						
Q15.forw	actccggcttgatgtgaaa	Orf37/DNA primase	4.7	4.7	4.7			
Q15.rev	gtctgttccatttggcaag	Orf39 / Tn1549 Orf25						
Q16.forw	gctgttagcgcagttgtcc	Orf39 / Tn1549 Orf25	2.5	2.5	2.5			
Q16.rev	ttcaggctgtccacaatacg	Orf40/ Tn1549 Orf26						
Q17.forw	cgatttcaaagtcacgtca	Orf40/ Tn1549 Orf26	2.5	2.5	2.5			
Q17.rev	ctgaaagcgaagctcaag	Orf43/ Tn1549 Orf28						
Q18.forw	aaacttcccggcttgatct	Orf43/ Tn1549 Orf28	2.6	2.6	2.6			
Q18.rev	cgattacgcggttgcataa	Orf47-48 intergenic						
Q19.forw	ggcaagtggatgatcagaat	Orf47-48 intergenic	2.5	+	+			
Q19.rev	cgattggaatgatagttgc	Orf50/ <i>vanY<sub>B</sub></i>						
Q20.forw	tatcattcaatgcgatca	Orf50/ <i>vanY<sub>B</sub></i>	2.5	2.5	2.5	2.5		+ <sup>b</sup>
Q20.rev	cattcgcatcctaaaagc	Orf52/ <i>vanH<sub>B</sub></i>						+ <sup>b</sup>
Q21.forw	gctttaaaggatgccgaatg	Orf52/ <i>vanH<sub>B</sub></i>	2.5	2.5	2.5	+ <sup>b</sup>	+	+ <sup>b</sup>

Q21.rev	tccaaatcgcctgtgacaa	Orf55/ Tn1549 Orf7							
Q22.forw	cgtaacgaggccaaaagcta	Orf55/ Tn1549 Orf7	2.5	2.5	2.5				
Q22.rev	gttcatttctgcccttgc	Orf59/ Tn1549 int							
Q23.forw	attatgcacacgccacattc	Orf59/ Tn1549 int	2.5	2.5	+	2.5	+	+	
Q23.rev	atccgctacagcttgttcgt	Orf61/aggl. receptor							
Q24.forw	cgaacaagctgtagcggatt	Orf61/aggl. receptor	2.5	2.5	2.5				
Q24.rev	ggccaagtcccatgaaaga	Orf61/aggl. receptor							
Q25.forw	ccgagggattaaagcagaca	Orf61/aggl. receptor	2.5	2.5	2.5	2.5	-	-	
Q25.rev	ttccactcctcatcaaagtc	Orf64/ helicase							
Q26.forw	gccaccattcctcgtgatag	Orf64/ helicase	2.5	2.5	2.5				
Q26.rev	cgttgtgacactcgttctctg	Orf64/ helicase							
Q27.forw	caccttcacccaatagtcaca	Orf64/ helicase	2.5	+	+				
Q27.rev	gcttgatttctctgagttgctc	Orf64/ helicase							
Q28.forw	ccgatgagtcgtgaaaaaca	Orf64/ helicase	2.5	2.5	2.5	2.5			
Q28.rev	aagttgggcaaccaaatcaa	Orf65							
Q29.forw	ttgatttggtgccaactt	Orf65	0.7	+	0.7				
Q29.rev	catcccatgtattgaaacgaaa	Orf66-67 intergenic							
Q30.forw	tggttacaacaaactgcagaa	Orf66-67 intergenic	2	+	+	2			
Q30.rev	gggaccaaattgatagggta	Orf68							
Q31.forw	gccaagtcacactggacat	Orf68	2.8	+	+				
Q31.rev	tgctcgtatttggtgctcag	Orf70							
Q32.forw	ttggctatacgattggctca	Orf70	2.4	+	2.4	2.4	-	-	
Q32.rev	cgtttaaattgatcctggttctg	Orf74							
Q33.forw	cagaaccagatcaatttaaagc	Orf74	2.5	2.5	2.5	0.5 <sup>c</sup>	-	-	
Q33.rev	gcaaagcttcttgaacatt	Orf77							
Q34.forw	aaaatgtccaagaagctttgc	Orf77	2.5	2.5	2.5	-	-	-	
Q34.rev	ggtatccgtgtaattgtgaca	Orf79/MobC							
Q35.forw	ttgctgaatcccaatagtc	Orf79/MobC	2.4	2.4	2.4	2.5			
Q35.rev	ttgacctgctctagcttctcat	Orf80-81 intergenic							
Q36.forw	gagaagctagagcaggtcaaa	Orf80-81 intergenic	2.5	2.5	2.5				
Q36.rev	agccccagttatgatgatgag	Orf82/ ABC permease							
Q37.forw	cagtttagcaaaaggaaatcca	Orf82/ ABC permease	2.7	2.7	2.7	2.7			
Q37.rev	ccgctcttatacgttgaacc	Orf83/ histidine kinase							
Q38.forw	cgaataaaaatggtgcgaaa	Orf83/ histidine kinase	3.6	+	+	+ <sup>d</sup>	-		
Q38.rev	tctccgctgctattaactcca	Orf86/ resolvase							

The blank spaces in the columns indicate not examined

<sup>a</sup> Tn5382/Tn1549 left end has been established previously by hybridization (20)

<sup>b</sup> The *vanB2* cluster and link to Tn5382/Tn1549 has been established previously by other PCRs (20)

<sup>c</sup> Sequence identical to 493 bp of ICES<sub>luvan</sub> orf77

<sup>d</sup> Confirmed by end sequencing

1 **Table S2.** Features and predicted functions of ORFs in the ICES<sub>Sluvan</sub> element

ICES <sub>Sluvan</sub>	% G/C content	% aa identity	Size Aa	Product	Homolog	Species	NCBI reference
1	52.4	85	13	C-terminal fragment of 23S rRNA (uracil-5)-methyltransferase RumA	SP70585_1067	<i>S. pneumoniae</i> 70585	CP000918
2	33.3	95	55	Hypothetical protein	SP70585_1068	<i>S. pneumoniae</i> 70585	CP000918
3	36.2	82	57	Hypothetical protein	SP70585_1069	<i>S. pneumoniae</i> 70585	CP000918
4	40.8	94	272	Replication initiator protein	ICES <sub>Sde</sub> 3396_66	<i>S. dysgalactiae</i> subsp. equisimilis NS3396	EU142041
5	44.2	98	451	Cytosine-specific methyltransferase	ICES <sub>Sde</sub> 3396_65	<i>S. dysgalactiae</i> subsp. equisimilis NS3396	EU142041
6	38.2	95	142	Hypothetical protein	ICES <sub>Sde</sub> 3396_64	<i>S. dysgalactiae</i> subsp. equisimilis NS3396	EU142041
7	40.9	97	127	Hypothetical protein	ICES <sub>Sde</sub> 3396_63	<i>S. dysgalactiae</i> subsp. equisimilis NS3396	EU142041
8	36.3	94	79	Hypothetical protein	ICES <sub>Sde</sub> 3396_62	<i>S. dysgalactiae</i> subsp. equisimilis NS3396	EU142041
9	37.8	81	194	CAAX amino terminal protease self- immunity protein	ICES <sub>Sde</sub> 3396_61	<i>S. dysgalactiae</i> subsp. equisimilis NS3396	EU142041
10	39.2	94	174	Hypothetical protein	ICES <sub>Sde</sub> 3396_60	<i>S. dysgalactiae</i> subsp. equisimilis NS3396	EU142041
11	40.8	96	604	Conjugal transfer protein, TraG family coupling protein (pseudogene because of frame shift after codon 465)	ICES <sub>Sde</sub> 3396_59	<i>S. dysgalactiae</i> subsp. equisimilis NS3396	EU142041
12	44.5	96	84	Putative membrane protein	ICES <sub>Sde</sub> 3396_58	<i>S. dysgalactiae</i> subsp. equisimilis NS3396	EU142041
13	41.9	99	284	Putative plasmid conjugal transfer protein, TrbL/VirB6 family	ICES <sub>Sde</sub> 3396_57	<i>S. dysgalactiae</i> subsp. equisimilis NS3396	EU142041
14	39.7	97	151	Hypothetical protein, PrgI family component	SP70585_1080	<i>S. pneumoniae</i> 70585	CP000918
15	40.8	99	776	Putative conjugal transfer protein, VirB4 ATPase	ICES <sub>Sde</sub> 3396_56	<i>S. dysgalactiae</i> subsp. equisimilis NS3396	EU142041
16	43.1	99	933	<i>N</i> -acetylmuramoyl L-alanine amidase, peptidoglycan hydrolase	ICES <sub>Sde</sub> 3396_55	<i>S. dysgalactiae</i> subsp. equisimilis NS3396	EU142041
17	32.6	94	281	Abortive infection protein AbiGII (pseudogene terminated by Tn1549 insertion after codon 251)	ICES <sub>Sde</sub> 3396_54	<i>S. dysgalactiae</i> subsp. equisimilis NS3396	EU142041
18	52.3	100	399	Hypothetical protein	Tn1549 Orf 13	<i>E. faecalis</i> BM4382	AF192329
19	57.3	100	70	Hypothetical protein	Tn1549 Orf 14	<i>E. faecalis</i> BM4382	AF192329
20	53.6	99	160	Hypothetical protein	Tn1549 Orf 15	<i>E. faecalis</i> BM4382	AF192329
21	51.9	99	564	Putative conjugal transfer protein, TraG family coupling protein	Tn1549 Orf 16	<i>E. faecalis</i> BM4382	AF192329
22	57.4	100	82	Putative conjugal transfer protein	HMPREF0348_0460	<i>E. faecalis</i> (TX0104)	ACGL01000032
23	52.3	100	290	Putative conjugal transfer protein	Tn1549 Orf 17	<i>E. faecalis</i> BM4382	AF192329
24	54.1	100	180	Adenine-specific methyltransferase	Tn1549 Orf 18	<i>E. faecalis</i> BM4382	AF192329

25	52.0	100	140	Hypothetical protein	Tn1549 Orf 19	<i>E. faecalis</i> BM4382	AF192329
26	55.1	100	799	Putative conjugal transfer protein, VirB4 APTase	Tn1549 Orf 20	<i>E. faecalis</i> BM4382	AF192329
27	58.6	100	663	DNA-repair protein	Tn1549 Orf 21	<i>E. faecalis</i> BM4382	AF192329
28	52.4	100	83	Hypothetical protein	Tn1549 Orf 22	<i>E. faecalis</i> BM4382	AF192329
29	59.2	100	409	Putative bacteriocin	Tn1549 Orf 23	<i>E. faecalis</i> BM4382	AF192329
30	57.7	99	693	DNA topoisomerase III-like protein (pseudogene terminated by insertion of a 9-kb element after codon 474 )	Tn1549 Orf 24	<i>E. faecalis</i> BM4382	AF192329
31	47.6	83	620	TnpX site-specific recombinase	FAEPRAA2165_00064	<i>F. prausnitzii</i> A2-165	NZ_ACOP02000000
32	55.9	89	98	Hypothetical protein	FAEPRAA2165_00836	<i>F. prausnitzii</i> A2-165	NZ_ACOP02000000
33	39.9	55	350	Transposase (pseudogene because of frame shift after codon 251), IS30 family	LJ0275	<i>Lactobacillus johnsonii</i> NCC 533	AE017198
34	31.7	40	162	Putative VanZ family protein	Pjdr2_3222	<i>Paenibacillus</i> sp. JDR-2	NC_012914
35	59.0	96	108	Hypothetical protein	FAEPRAA2165_00838	<i>F. prausnitzii</i> A2-165	NZ_ACOP02000000
36	56.3	88	502	Putative mobilisation protein	FAEPRAA2165_00070	<i>F. prausnitzii</i> A2-165	NZ_ACOP02000000
37	57.2	93	633	Putative DNA primase	FAEPRAA2165_00840	<i>F. prausnitzii</i> A2-165	NZ_ACOP02000000
38	45.3	70	63	Hypothetical protein	FAEPRAA2165_00072	<i>F. prausnitzii</i> A2-165	NZ_ACOP02000000
39	58.1	100	1306	Hypothetical protein, LtrC family membrane associated enzyme involved in lipid metabolism	Tn1549 Orf 25	<i>E. faecalis</i> BM4382	AF192329
40	56.8	100	314	Hypothetical protein	Tn1549 Orf 26	<i>E. faecalis</i> BM4382	AF192329
41	49.5	100	129	Hypothetical protein	Tn1549 Orf 27	<i>E. faecalis</i> BM4382	AF192329
42	56.9	100	118	Hypothetical protein	HMPREF0348_0474	<i>E. faecalis</i> (TX0104)	ACGL01000032
43	52.3	100	442	Putative mobilisation protein, MOB <sub>p</sub> family relaxase	Tn1549 Orf 28	<i>E. faecalis</i> BM4382	AF192329
44	53.0	100	109	Putative mobilisation protein, MobC	Tn1549 Orf 29	<i>E. faecalis</i> BM4382	AF192329
45	51.6	100	123	Hypothetical protein	Tn1549 Orf 30	<i>E. faecalis</i> BM4382	AF192329
46	52.2	100	61	Transposase	HMPREF0348_0478	<i>E. faecalis</i> (TX0104)	ACGL01000032
47	43.5	100	55	Hypothetical protein	HMPREF0348_0479	<i>E. faecalis</i> (TX0104)	ACGL01000032
48	46.5	100	220	Response regulator, VanRB	<i>vanR<sub>B</sub></i>	<i>E. faecalis</i> BM4382	AF192329
49	45.9	99	447	Sensor protein, histidine kinase VanSB	<i>vanS<sub>B</sub></i>	<i>E. faecalis</i> BM4382	AF192329
50	47.0	99	268	Carboxypeptidase VanYB	<i>vanY<sub>B</sub></i>	<i>E. faecalis</i> BM4382	AF192329
51	45.2	100	282	Vancomycin resistance protein VanW	<i>vanW</i>	<i>E. faecalis</i> BM4382	AF192329
52	50.6	100	323	Vancomycin resistance protein VanHB	<i>vanH<sub>B</sub></i>	<i>E. faecalis</i> BM4382	AF192329
53	49.8	100	342	Vancomycin B-type resistance protein VanB2	<i>vanB</i>	<i>E. faecalis</i> BM4382	AF192329
54	47.6	99	202	Vancomycin B-type resistance protein VanXB	<i>vanX<sub>B</sub></i>	<i>E. faecalis</i> BM4382	AF192329
55	51.2	100	258	Hypothetical protein	Tn1549 Orf7	<i>E. faecalis</i> BM4382	AF192329
56	55.6	100	77	Hypothetical protein	Tn1549 Orf8	<i>E. faecalis</i> BM4382	AF192329
57	58.0	100	80	Hypothetical protein	EFXG_01475	<i>E. faecium</i> C68	NZ_GG703717
58	43.3	100	66	Excisionase	Tn1549 xis	<i>E. faecalis</i> BM4382	AF192329
59	48.3	100	424	Integrase	Tn1549 int	<i>E. faecalis</i> BM4382	AF192329

60	35.4	89	196	Abortive infection protein AbiGI	ICESde3396_53	<i>S. dysgalactiae</i> subsp. equisimilis NS3396	EU142041
61	41.7	96	1631	Agglutinin receptor precursor	ICESde3396_52	<i>S. dysgalactiae</i> subsp. equisimilis NS3396	EU142041
62	41.7	92	63	Putative Ca <sup>2+</sup> binding protein	ICESde3396_50	<i>S. dysgalactiae</i> subsp. equisimilis NS3396	EU142041
63	38.6	96	183	Hypothetical protein	ICESde3396_49	<i>S. dysgalactiae</i> subsp. equisimilis NS3396	EU142041
64	41.1	95	2276	SNF2-related helicase (pseudogene because of frame shifts after codons 775 and 784)	ICESde3396_48	<i>S. dysgalactiae</i> subsp. equisimilis NS3396	EU142041
65	40.0	83	99	Hypothetical protein	ICESde3396_47	<i>S. dysgalactiae</i> subsp. equisimilis NS3396	EU142041
66	33.3	78	99	Hypothetical protein	ICESde3396_46	<i>S. dysgalactiae</i> subsp. equisimilis NS3396	EU142041
67	29.0	25	401	Putative uncharacterised phage related protein	StrS4_010100015457	<i>Streptomyces</i> sp. S4	NZ_CADY01000120
68	29.1	27	442	Putative uncharacterised phage related protein	StrS4_010100015462	<i>Streptomyces</i> sp. S4	NZ_CADY01000120
69	39.4	93	418	Transposase (pseudogene because of frame shift after codon 33), ISL3 family	SsuiDRAFT_2686	<i>S. suis</i> 89/1591	NZ_AAFA03000023
70	40.0	96	212	Hypothetical protein	ICESde3396_45	<i>S. dysgalactiae</i> subsp. equisimilis NS3396	EU142041
71	38.2	88	258	Putative DNA primase	ICESde3396_44	<i>S. dysgalactiae</i> subsp. equisimilis NS3396	EU142041
72	39.9	97	75	Hypothetical protein	ICESde3396_43	<i>S. dysgalactiae</i> subsp. equisimilis NS3396	EU142041
73	35.4	96	129	Hypothetical protein	ICESde3396_42	<i>S. dysgalactiae</i> subsp. equisimilis NS3396	EU142041
74	34.4	75	96	Hypothetical protein	ICESde3396_41	<i>S. dysgalactiae</i> subsp. equisimilis NS3396	EU142041
75	37.7	100	168	Antidote epsilon protein, zeta toxin regulator	SsuiDRAFT_3902	<i>S. suis</i> 89/1591	NZ_AAFA03000023
76	44.0	99	256	Zeta-toxin/ Signal recognition particle	SsuiDRAFT_3901	<i>S. suis</i> 89/1591	NZ_AAFA03000023
77	29.5	100	835	Hypothetical protein	SsuiDRAFT_3900	<i>S. suis</i> 89/1591	NZ_AAFA03000023
78	38.9	81	119	Hypothetical protein	SsuiDRAFT_3899	<i>S. suis</i> 89/1591	NZ_AAFA03000023
79	35.0	95	121	Putative mobilisation protein, MobC family	SsuiDRAFT_3898	<i>S. suis</i> 89/1591	NZ_AAFA03000023
80	34.7	92	621	Putative relaxase, MOB <sub>p</sub> family	SsuiDRAFT_3897	<i>S. suis</i> 89/1591	NZ_AAFA03000023
81	34.3	82	249	ATPase component, ABC-type antimicrobial peptide transport system	smi_1460	<i>S. mitis</i> B6	FN568063
82	32.5	67	672	ABC transporter permease, ABC-type antimicrobial peptide transport system	smi_1459	<i>S. mitis</i> B6	FN568063
83	27.5	65	524	Histidine kinase	smi_1458	<i>S. mitis</i> B6	FN568063
84	30.5	74	198	Response regulator	smi_1457	<i>S. mitis</i> B6	FN568063
85	30.2	56	73	Transcriptional regulator, Cro/CI family	SsuiDRAFT_3888	<i>S. suis</i> 89/1591	NZ_AAFA03000023
86	33.6	98	579	Site-specific recombinase, resolvase family (lack 1 amino acid compared to SsuiDRAFT_2393)	SsuiDRAFT_2393	<i>S. suis</i> 89/1591	NZ_AAFA03000023