

Additional file 4

[illegible]

Conjugative transposons	199	ORF1+2 Tn916	E. faecalis	M37184	61-264, 346-15	5	1,1,1,1,1	aagtggcgcaagctcaagtttccatggttgaagaag	agcgagttgttagcggaatcggaagaatgataaagcggtg	gtggcgcaagttgattacaacggtgatgaagaggtctgtg	ccacatagatttggcgacatacatcttgatacaactatgca	atgctaataatagccatgacgctggaacttaacgacatg	
	213	Excisionase (xis- Tn) Tn916	E. faecalis DS16	U09422	16356-16559	1	1	ctatttgggaagcgtttacatccctaaccattggaagcgtg					
	75	Orf16 Transposon Tn916	E. faecalis	U09422	5193-7640	5	1,1,1,1,1	gccattcgtgcgataaccataatgtagaagatcagagg					
	202	Tyrosine integrase transposon Tn EfcTn1	E. faecium	DQ370176	638-1870	5	1,1,2,1,1	aagtcgtttgggtctacaggtatgttgcgaattgc		agcgcgaccatcgcgaaggttttacagactatgactttgc	tacagtggtcggaacttggttacttccgcacaaggaa	ggagcctttatccgttgatctatgctgattgctattagacc	
	450	Transposon EfcTn1 partial sequence	E. faecium	DQ3217751	1-315	4	1,1,1,2	cgataaactcagcgtcttattcttctgcagcgtttgt		ttctgataaataccaagggaagcgtttatctgcacca	gctttacttaaaagacacgtgattcaaacgaggaaacc	agcatatgactgcttcatggtttccgtacatcagctagt	
	204	Integrase Tn5386	E. faecium	DQ321786	28008-29207	5	1,1,2,1,2	aggaatgacacgcgaatcactatgatatatcagtggaac		tcgcgaataaacggtcaaaagcgacagacagacttta	gacccttcgggaatgatgacattgatagatgcgca	tttagggcctcgcttcatcattggcgatacaaatg	
	208	Excisionase Tn5386	E. faecium	DQ321786	27721-27927	5	1,1,2,1,1	atcggtgcgaatgggtttattatgaaacgcgaataacgt		tatgacgcgaacggttactgataaatacgttccattcca	accattgaggaagcgtcttaataatcatttgcgattg	cgcttgcgaagaataatacgttcggtcgaaatgggt	
	74	hypothetical protein Tn5386	E. faecium	DQ321786	10955-12460_1	5	2,2,1,1,1	tttggcggtcagcggttaactttagaccgcggaanaag		tglagaagacgctgaaagtctggcaatgcacatct	atcgcagaccatattgcagcgtttcacgcgactacga	aatcgtgagaccttgatgaagcgtggcgctttcaa	
	231	responsible for insertion and excision of Tn5397 (I.C. difficile	E. faecalis	AF333235	19045-20646	5	1,1,2,1,2	ggaaatgaaccgaagatctcgtttgcagacacatcgc		cgtaagtgaanaagcagcggaagtgcagaattactca	agaggagaagaatcagagggtacggatgattcttgaac	tgacttgattgattcaattctgattgactgacagaggg	
	452	Integrase Tn1549	E. faecalis	AF192329	32432-33625	5	1,1,1,1,1	gctctgcgtacatatcttgcatttctgcaggttgcaca		agcctcgcgtacatatcttgcatttctgcaggttgcaca	gcaattgcgaacttggcgagctgcgaagcgaactgaa	acagacggtctactccatgacgcggtgatattgat	
SSTe*	454	Excisionase Tn1549	E. faecalis	AF192329	32148-32348	4	1,1,1,2	gacatgcctatttgggaaaaataacacgctgacgattg		clctgcgttcggtcattatgagcgcgaacgcattcca	aaacaattgcgttaatcgttcggcgagaaatccgg		
	39	Rlx-like protein Tn1549	E. faecalis	AF192329	20529-21857	5	1,1,1,1,1	gattgtggacgttggcccttctcaatcaggttagtc		gcttcgctcagtttgttcggcggttctcagtgtag	atccatcgggtlagtggttcttccattgtcagtcagc		
	82	TrsE-like protein Tn1549	E. faecalis	AF192329	6228-8627	5	2,2,1,2,2	tcattgagctgtaaatcgcagatcgtcagtggtgt		tgaattattcggagagcgtaaacccctcgtgcgcctg	gtgtgcgcgtccctgaactgatttaaccaccgtta		
	416	Transposase (InpA) Tn554	S. aureus	X03216	134-1219	5	2,1,1,2,2	aaagtgtcgtacagattctalggaaacagagaggtg		acgacagctctgtaggttggttagatattccttcacg	gggttgtaagaatcgtggtgaagtgttatcgtttagc		
	145	Transposase Tn917	E. faecalis	M11180	2364-5282	5	1,1,1,1,1	tgtagggcatcagcactcatcatcagtggttcttcca		gggaagctactcatcactcgttgatgccttacttaca	acgcagctagaataagatagactcgttcgactgaga		
	146	Transposase Tn1546	E. faecium	M97297	75-3041	5	2,1,1,2,2	tgtgaagtacgcgaatgcatacgcgtctgatacttc		gtgaaagtacgcccggtggtccttttaaccacaacc	tcgaagcgagatggactacaacacatctgtttcgatat		
	214	Putative resolvase (resIpf) pVEF2	E. faecium	AM410096	3130-3747	5	1,2,1,1,1	agcggctcaatcgttgcagcgcgccaataactaagca		tgctcaaaattggttatgcagcgtgtcgatagaaga	aataagggggcacaacccgttcgaatggccttacct		
	216	Resolvase Tn1546 pVEF2	E. faecium	AM410096	15737-16312	5	1,1,1,1,2	gccattcaatccctcagctgttctatccgtaataaga		gccaattcaatccctcagctgttctatccgtaataaga	aatcgtctaacacittttgaagtgtcgcgatacttt		
	223	Resolvase (Tn3 family) pEF1	E. faecium	DQ198088	9180-9752	5	1,1,1,1,1	agatgaatatggtttgacpaagcttgatcgatttgcgtc		cgaaigtgtgacagggcgtgttgatgtgacgaga	gggcacgcatgtaactcttacttcaggttaagttact		
	229	Resolvase Tn917	E. faecalis	M11180	1806-2360	4	1,1,2,2	agccaattgagtggaagtgaatccctactacgtggaaga		actccaacgtctatggaagtgttcttccgagttatgg	cgggcgtccccaagtaaaagtgactgcataactgatt		
Tn3 family	15	IS256 transposase pTEF1	E. faecalis V583	AE016833	50710-51882	5	2,1,1,2,1	ttgtlacggtatattgaaggcgctcttcgaatccatcac		aggtctcttcgcttcgcacctttgaaatcagaag	cgctgcgcattcttggttattcaatcgtctatgatgc		
	96	Transposase IS256 family pVEF1	E. faecium	AM256544	34341-35531	5	2,2,1,1,2	aggaaggttgagtgctgtgattgcgaatcgaatgcg		acaaaagtgctgtctgattgcgtgataaggaactctg	tcocatagccatcgaacagactgttcgatacgaact		
	98	Putative transposase (tnp) gene IS16	E. faecalis	U35366.1	109-1296	5	1,2,1,1,1	aactgctaacggtgatgtgcgactgtttctaatacca		aacgaggtttgttcggtgtaaacacttgctcattctga	gtgtatggcattgattctgatggacgactgacgat		
	102	Putative transposase IS1542	E. faecium	AF114715	101-1273	5	2,2,2,1,1	gaactcgtcgacagcagtaagaatggccttagtcg		gccttcgaaatattggataatgcttcggaagatgc	tgatgtgataatcttcttcgactgccttcgacttgta		
	134	Transposase ISEf1	E. faecalis V583	AE016830	2701329-2702f	5	2,2,2,1,1	tcattcttcaactcgtccggtatagaagaattttcgtc		tcattcttcaactcgtccggtatagaagaattttcgtc	tgcttcgcttccgccatttgaatcagatgcgc		
	154	Transposase IS256	E. faecium	AY971367	2711-3462	5	1,2,2,2,2	ttccttgatcggtatattgaaggcgctcttcgaatcca		agcggccacttaactacgaatcttccgtgactgcgc	ccaatccggtcgaatgatgtccgctgcgtagca		
	157	Transposase IS1310	E. hirae	AF406971	3627-4805	5	1,2,1,1,1	acggcccaacttaactcgaacttccctgagatgcg		acagtcgactgctgtcacaactatgcgctatcttc	cgaatccggtcgaatgatgtctgttcgtagtcaatg		
	104	Putative transposase Tn5382 ISEnfA110	E. faecalis	AF173641	362-1570	5	2,1,1,2,1	aactccagacaactcttccgcgttagctgcctcca		caactccgtaaggagatagcagccttgatgatac	gctcaaacactgttgatcaaggtgaaatccttccgg		
	165	transposase, IS116/IS110/IS902 family	E. faecalis V583	AE016830	1829566-1830f	5	1,1,1,1,2	cgaactccgttaaggagatagcagccttgatgatac		gctcaaacactgttgatcaaggtgaaatccttccgg	agtaggggttccactgattctacattcagatacaaggtgcca		
	IS256	167	Transposase IS116/IS1328/IS1533; transposase	E. faecium DO	NZ_AAAK03000010	2042-3292	5	1,1,1,1,1	gtcacaacactgttgatcaaggtgaaatccttccgg		gtcacaacactgttgatcaaggtgaaatccttccgg	agtaggggttccactgattctacattcagatacaaggtgcca	
109		Putative transposase ISEnfA3	E. faecium	AF469486	755-1393	1	1	agtaggggttccactgattctacattcagatacaaggtgcca		gtcacaacactgttgatcaaggtgaaatccttccgg	agtaggggttccactgattctacattcagatacaaggtgcca		
110		Transposase IS1485	E. faecium	AF029727	76-330_330-12	5	2,1,2,1,1	cgaacttgaagaagtagtgcgtgcgaagaatttaccgcgcg		gtcacaacactgttgatcaaggtgaaatccttccgg	agtaggggttccactgattctacattcagatacaaggtgcca		
143		Transposase IS981 pEF1	E. faecium	DQ198088	1-1101	5	2,1,2,2,1	tgcttcagataagccatattcttccgtcaacctccga		gtggttgattcaccggtcagaagaatgacatccttt	gtggttgattcaccggtcagaagaatgacatccttt		
162		Transposase IS3-like	E. faecium	AY916786	1250-2191	5	1,1,1,1,1	actttgacataggaactgttcggtccgagagattttgat		actttgacataggaactgttcggtccgagagattttgat	cgcttcgcatcttttggttattcaatcgtctatgatgc		
111		Transposase IS6 family pTEF1	E. faecalis V583	AE016833	12615-13304	5	1,1,1,1,2	aataaggaaggggctttatctgtactacaactcgttgt		gcccgaaaaagaagagctgtctttgttcttcgctc	cccgaagggctatcacagacgacttgagaacgttcca		
112		Transposase IS1216 pVEF1	E. faecium	AM296544	36849-37353	5	1,1,1,1,1	atataaggaaggggctttatctgtactacaactcgttgt		cccgaagggctatcacagacgacttgagaacgttcca	aggtcactacaacgcttatccggatccaattaacagcca		
156		Transposase ISEnfA1	E. faecalis	AY884205	509-746	4	1,2,2,2	gcccgaaaaagaagagctgtctttgttcttcgctc		cccgaagggctatcacagacgacttgagaacgttcca	aggtcactacaacgcttatccggatccaattaacagcca		
ISL3		117	Transposase IS1251	E. faecium	L34675	128-1417	5	1,2,1,1,1	cccgaagggctatcacagacgacttgagaacgttcca		aggtcactacaacgcttatccggatccaattaacagcca	tgctatttgcagagaactccggaactgatgatgcg	
		118	Transposase ISL3 family pPPM1000	E. faecium	AY351675	8074-9396	5	1,1,1,1,2	aggtcactacaacgcttatccggatccaattaacagcca		tgctatttgcagagaactccggaactgatgatgcg	tgccaacttcgcaacgacgtccgaattgatgc	
	119	Transposase ISEfa11	E. faecium	JN208887	3241-4536	5	2,2,1,1,2	tgccaacttcgcaacgctccggaactgatgatgcg		tgccaacttcgcaacgctccggaactgatgatgcg	tgccaacttcgcaacgctccggaactgatgatgcg		
	120	Transposase ISL3-like	E. faecium	AF403298	1836-3176	5	1,2,1,1,2	tgccaacttcgcaacgctccggaactgatgatgcg		tgccaacttcgcaacgctccggaactgatgatgcg	tgccaacttcgcaacgctccggaactgatgatgcg		
	123	Putative transposase IS1476	E. faecium	U63997	140-1414	5	1,1,1,1,1	cacgatcttccatgcagcactcgggttgatcc		cacgatcttccatgcagcactcgggttgatcc	tgccgcaaacgacttccggaactgatgatgcg		
	176	Transposase IS1167	E. faecium DO	NZ_AAAK03000135	3172-3764	5	2,2,2,2,2	tggttcggttgaatagctgtgatggaagcgatttt		tggttcggttgaatagctgtgatggaagcgatttt	tggttcggttgaatagctgtgatggaagcgatttt		
	129	Transposon ISEfm1	E. faecium	AF138282	297-1206	5	1,1,2,1,1	gcaacgcgcatcagtgattgatttgggttatttggggc		gcaacgcgcatcagtgattgatttgggttatttggggc	gcaacgcgcatcagtgattgatttgggttatttggggc		
	138	Transposase ISEfa11	E. faecium	AF516335	12234-12908	5	2,2,1,1,1	ttttgttcggttgaatagctgtgatggaagcgatttt		ttttgttcggttgaatagctgtgatggaagcgatttt	ttttgttcggttgaatagctgtgatggaagcgatttt		
	140	Transposase-like protein A ISEfa4 (similar to putat	E. faecium	AY082011	900-1304	4	2,2,2,1	tgcaaaaaattcatcaatgctctataaagtgccagctcaag		tgcaaaaaattcatcaatgctctataaagtgccagctcaag	tgcaaaaaattcatcaatgctctataaagtgccagctcaag		
	IS200/IS605	142	Putative transposase ISEnfA200	E. faecalis	AF125554	296-766	5	1,1,1,2,1	gcacaatcattgcagcactcgggttgatcc		gcacaatcattgcagcactcgggttgatcc	gcacaatcattgcagcactcgggttgatcc	
166		Transposase IS605	E. faecium DO	NZ_AAAK03000014	6433-7581	5	2,2,1,1,1	tggaagcgcatcgcaatgccccaatattccatattgc		tggaagcgcatcgcaatgccccaatattccatattgc	tggaagcgcatcgcaatgccccaatattccatattgc		
170		Transposase IS200 family	E. faecalis V583	AE016830	575151-57554f	5	2,1,1,2,1	ttggaacgaatccttctgaaattcgagaatggactgtcc		ttggaacgaatccttctgaaattcgagaatggactgtcc	ttggaacgaatccttctgaaattcgagaatggactgtcc		
176		Transposase ISEcp1-like E. casseliflavus plasmid	E. casseliflavus	AY939911	561-1823	5	2,1,1,1,1	tggaacgaatccttctgaaattcgagaatggactgtcc		tggaacgaatccttctgaaattcgagaatggactgtcc	tggaacgaatccttctgaaattcgagaatggactgtcc		
137		Putative transposase IS1678	E. faecium	AY859490	156-1475	5	1,1,1,1,1	gggaattatgttcgaacgggtgagatgacttatcca		gggaattatgttcgaacgggtgagatgacttatcca	gggaattatgttcgaacgggtgagatgacttatcca		
130		Transposase IS1252 ISE6770 homolog pHK701	E. faecium	L38972	665-1624	5	2,1,1,2,1	tcattcagtgctcagatgttgcttgaggtccctgctc		tcattcagtgctcagatgttgcttgaggtccctgctc	tcattcagtgctcagatgttgcttgaggtccctgctc		
133		Putative transposase IS6770	E. faecalis	L28754	97-1056	5	1,1,1,1,2	gttgaatcgcataaccgaatgggtcgctgtatata		gttgaatcgcataaccgaatgggtcgctgtatata	gttgaatcgcataaccgaatgggtcgctgtatata		
136		Transposase IS1062 plasmid	E. faecalis	X96976	2496-3455	5	1,2,1,2,1	tcattaaaaccttttggtgatgtgacaaagactgcg		tcattaaaaccttttggtgatgtgacaaagactgcg	tcattaaaaccttttggtgatgtgacaaagactgcg		
IS4		138	Transposase IS4	E. faecium DO	NZ_AAAK03000061	5880-7001	5	1,1,1,1,1	aattcaactctgcccaacgggtctgactacgtcgc		aattcaactctgcccaacgggtctgactacgtcgc	aattcaactctgcccaacgggtctgactacgtcgc	
		160	Transposase IS21 family	E. faecium	AB105542	105-1343	5	1,1,2,2,1	aaggatttgcaggggatgcacgcctagttaaaaagct		aaggatttgcaggggatgcacgcctagttaaaaagct	aaggatttgcaggggatgcacgcctagttaaaaagct	
	417	Transposon IS21-558 (integrase/resolvase B, 23S	S. aureus	EU598691	1.3006	5	1,2,1,1,1	aaccatttaccgcagatcgttcgctgcgcacagcgc		aaccatttaccgcagatcgttcgctgcgcacagcgc	aaccatttaccgcagatcgttcgctgcgcacagcgc		
	144	Transposase ISEfm3	E. faecium	AY887084	111-1019	4	1,1,2,1,1	tactagccaagagccacgtatagagcggtttgtagc		tactagccaagagccacgtatagagcggtttgtagc	tactagccaagagccacgtatagagcggtttgtagc		
	147	Transposase	E. faecium	AJ223633	3011-3301	3	1,2,1	agattgctttacccttcttgatgacatcgaaagcgtta		agattgctttacccttcttgatgacatcgaaagcgtta	agattgctttacccttcttgatgacatcgaaagcgtta		
	149	Transposase pEF418	E. faecalis	AF408195	12655-13092	5	1,1,1,2,1	tcaatatcattgcagctgtcttccacaacggttcaatgt		tcaatatcattgcagctgtcttccacaacggttcaatgt	tcaatatcattgcagctgtcttccacaacggttcaatgt		
	152	Transposase pAM373	E. faecalis	AE002565	5363-8335	5	1,1,1,2,1	tcagctgtgattgttcgttatcattccacaacgcttcc		tcagctgtgattgttcgttatcattccacaacgcttcc	tcagctgtgattgttcgttatcattccacaacgcttcc		
	153	Transposase Efm DO cyt590	E. faecium	NZ_AAAK03000049	1552-2131	5	2,1,1,1,1	aaatcacaatcgaacgtctgactcgtctgcgcacaa		aaatcacaatcgaacgtctgactcgtctgcgcacaa	aaatcacaatcgaacgtctgactcgtctgcgcacaa		
	Various targets associated with transposable elements	163	Transposase	E. faecium	AJ223633	2127-2975	5	2,1,1,1,1	tgtaaccgtgcaacccaaggtgttccaccaattgac		tgtaaccgtgcaacccaaggtgttccaccaattgac	tgtaaccgtgcaacccaaggtgttccaccaattgac	
		171	Transposase	E. faecium DO	NZ_AAAK03000155	1-218	4	1,2,1,2	tgaattggagaagtgcataatttaagcaacggcgctc		tgaattggagaagtgcataatttaagcaacggcgctc	tgaattggagaagtgcataatttaagcaacggcgctc	
173		Transposase mutator type	E. faecium DO	NZ_AAAK03000050	3310-4500	5	2,1,2,1,2	tccaactctgaacgaacacagcttggttgcagatgcg		tccaactctgaacgaacacagcttggttgcagatgcg	tccaactctgaacgaacacagcttggttgcagatgcg		
177		Transposase	E. faecium DO	NZ_AAAK03000019	25202-25645	5	2,1,1,1,1	ttgttgtagacgtcgtctgttttaccaggagaacca		ttgttgtagacgtcgtctgttttaccaggagaacca	ttgttgtagacgtcgtctgttttaccaggagaacca		
179		Transposase	E. faecium DO	NZ_AAAK03000007	51725-53149	5	1,1,1,1,2	accgcgttcgatccgttactctcgtatttggaaigt		accgcgttcgatccgttactctcgtatttggaaigt	accgcgttcgatccgttactctcgtatttggaaigt		
181		Transposase of IS981J	E. faecium DO	NZ_AAAK03000010	53018-53332	1	2	tgtagcctatccatgatcgtttattagacactttgaggt		tgtagcctatccatgatcgtttattagacactttgaggt	tgtagcctatccatgatcgtttattagacactttgaggt		
188		Transposase ISEfm2	E. faecium E59	AY887085	95-1273	5	1,1,1,2,2	cggacgaatgatcactttagaggagacgctcattcaac		cggacgaatgatcactttagaggagacgctcattcaac	cggacgaatgatcactttagaggagacgctcattcaac		
196		Transposase mutator type	E. faecium DO	AAAK03000007	59056-59637	4	2,1,1,1	tcgcacttcttggtttattcagttatgcggaacactgttc		tcgcacttcttggtttattcagttatgcggaacactgttc	tcgcacttcttggtttattcagttatgcggaacactgttc		
422		ORF480 potential transposase Tn552	S. aureus	X52734	894-2336	5	2,1,1,1,1	ttccagaacccaatgagaatttggcgaacgcgacca		ttccagaacccaatgagaatttggcgaacgcgacca	ttccagaacccaatgagaatttggcgaacgcgacca		
Various targets associated with transposable elements		424	BinL/TnpR Tn552	S. aureus	X52734	2308-2901	5	1,1,2,1,1	gttgtttggagactgcagaaatgcagatgcataagtc		gttgtttggagactgcagaaatgcagatgcataagtc	gttgtttggagactgcagaaatgcagatgcataagtc	
	206	Integrase/recombinase XerD, putative	E. faecalis V583	NC_004668	1492090-1492f	5	2,1,1,2,1	aacgcctgatacaagtaaaacctaggtatgcgga		aacgcctgatacaagtaaaacctaggtatgcgga	aacgcctgatacaagtaaaacctaggtatgcgga		
	212	Excisionase putative PAI	E. faecalis V583	NC_004668	293125-29339f	5	2,1,1,1,1	tttagagaagaatggctgttctaattgcagagacgcg		tttagagaagaatggctgttctaattgcagagacgcg	tttagagaagaatggctgttctaattgcagagacgcg		
	215	Resolvase (res btae) pAMbeta-1	E. faecalis	AF007787	5145-5762	5	1,2,2,2,1	atvgttcgcaacggccacaattacagactatgctta		atvgttcgcaacggccacaattacagactatgctta	atvgttcgcaacggccacaattacagactatgctta		
	219	Resolvase pLW043	S. aureus	AE017171	47565-48122	5	2,1,2,1,2	tggtccaattattgttctgctgtgtcttaccagagaa		tggtccaattattgttctgctgtgtcttaccagagaa	tggtccaattattgttctgctgtgtcttaccagagaa		
	227	Resolvase pk214											

Resistance traits	Glyco-peptides	237	vanA Tn1546	E. faecium	M97297	6979-8010	5	1,1,1,1,1	cgaagccgttatacattggaattacgaaattcggtgtgatgg	gggaaaaacgacaattgctattcagctgtactctgcgcg	gcatgacgtatcggttaaaattcgtaacgagatagccg	acggccgcattgtactgaacgaagtcgaataactctg	gcaggattgcacgtcccgaaactgattgaccgctt	
		238	vanB (D-alanine:D-lactate ligase) Tn1549-like	E. faecium	AY655721	4857-5885	5	1,1,1,1,2	gagccacgggtatcttccgcacatccatcaggaaaacg	attacagttcccgcagacacttccggtcgaggaaacg	ggatggcgccatggttctaataagaggtcgaatacca	gttttacctgacacgcctcaccacgtaagtgtg	tgcatgattgcacagcgtgattacattggcgttaa	
		280	vanE D-alanine,D-serine ligase	E. faecalis	FJ872411.1	39736-40794	5	1,1,1,2,1	agggtaccacccaagaaggtcattggatctatgttaaggg	ccagttttacatggaggttatgtgtgagaaltgtgtgtc	tatgtagttgttggtatcgggactcgagcaaatc	ttgtctgaagcaattgggtgtaaaaagaccacctgatt	ttgctgtgaagcaattgggtgtaaaaagaccacctgatt	
		281	vanG D-Ala-D-Ser ligase	E. faecalis	AY271782	21049-22098	5	1,1,1,2,1	ctatgcacctgttgttgcgttcccaaaatcggttccgt	agggacataactgttgttgcgtcgatcagccattcat	agggacataaaactgttgtgccttgcgggttatctc	tgccacataaactgttgttgcgtcgatcagccattcat	tgccacataaactgttgttgcgtcgatcagccattcat	
	Amino-glycosides	284	vanG2 D-alanine,D-serine ligase	E. faecalis	FJ872410.1	39328-40377	5	1,1,1,1,1	atttcctgtattgcacggcaagaacggcgagagacg	atttcctgtattgcacggcaagaacggcgagagacg	aatctatttgcagtgattgtcgcagagttgtgggtgt	gcggcttgcgtatagatagactgattgtgcgcgag	gcggcttgcgtatagatagactgattgtgcgcgag	
		313	vanL D-alanine-D-serine ligase	E. faecalis	EU250284	955-2004	5	2,1,1,1,1	tggggtgacgccttcggtctattgttgacaatat	tggggtgacgccttcggtctattgttgacaatat	gaaatgatatacgataaacccagcgaacatttgagggtga	gtgcctctacgctcataattcgcatagaaactgc	aggttactaggcttctcaggactagcacgaattga	
		247	Streptothricin acetyltransferase (sat4) Streptothric	E. faecium	AF330699	927-1469	5	2,1,1,2,1	ttggaaccgctagcttatataagaagatatcgccggtat	ttggaaccgctagcttatataagaagatatcgccggtat	gaaatgatatacgataaacccagcgaacatttgagggtga	gtgcctctacgctcataatatactatagaatgggcaaa	gtgcctctacgctcataatatactatagaatgggcaaa	
		251	aminoglycoside phosphotransferase aph(2')-Ib ger	E. faecium	AF207840	122-1021	5	1,1,1,1,1	actgtgaagctatcttatacaaatccctgcggtagtgtatca	actgtgaagctatcttatacaaatccctgcggtagtgtatca	ttcgaaccaggtagaaaaagccaatagagacagttatactct	ttcgaaccaggtagaaaaagccaatagagacagttatactct	ttcgaaccaggtagaaaaagccaatagagacagttatactct	
		252	Aminoglycoside modifying enzyme (aph(2'')-Id)	E. casseliflavus	AF016483	131-1036	5	2,2,1,1,1	tggaatcccttctgcggctacccgtlaaagctcgaag	tggaatcccttctgcggctacccgtlaaagctcgaag	gaaatgatatacgataaacccaaggaatcgcggtacgacgc	gaaatgatatacgataaacccaaggaatcgcggtacgacgc	gaaatgatatacgataaacccaaggaatcgcggtacgacgc	
		253	Gentamicin resistance protein	E. gallinarum	U51479	196-1116	5	2,2,1,2,1	ttcgaaccaggtatgataaacctcgcgtcagctgcgtt	ttcgaaccaggtatgataaacctcgcgtcagctgcgtt	ttcgaaccaggtatgataaacctcgcgtcagctgcgtt	ttcgaaccaggtatgataaacctcgcgtcagctgcgtt	ttcgaaccaggtatgataaacctcgcgtcagctgcgtt	
		254	Aminoglycoside(6) N-acetyltransferase aac(6'')-li	E. faecium	L12710	169-717	5	1,1,1,1,1	acaacgcggcgagcttttgatcaacgaccttttgga	acaacgcggcgagcttttgatcaacgaccttttgga	ttcgaaccaggtatgataaacctcgcgtcagctgcgtt	ttcgaaccaggtatgataaacctcgcgtcagctgcgtt	ttcgaaccaggtatgataaacctcgcgtcagctgcgtt	
		256	Aminoglycoside-3-adenylyltransferase (aadA) Stre	E. faecalis	AF052459	107-898	5	1,2,1,1,1	ttcgaaccaggtatgataaacctcgcgtcagctgcgtt	ttcgaaccaggtatgataaacctcgcgtcagctgcgtt	ttcgaaccaggtatgataaacctcgcgtcagctgcgtt	ttcgaaccaggtatgataaacctcgcgtcagctgcgtt	ttcgaaccaggtatgataaacctcgcgtcagctgcgtt	
		258	Spectinomycin adenytransferase (aad9) Spectinor	E. faecalis	M69221	271-1038	5	2,2,1,2,2	gcttgatgaacacgacgcgcgagcattgtcgaattg	gcttgatgaacacgacgcgcgagcattgtcgaattg	gcttgatgaacacgacgcgcgagcattgtcgaattg	gcttgatgaacacgacgcgcgagcattgtcgaattg	gcttgatgaacacgacgcgcgagcattgtcgaattg	
		263	Streptomycin-spectinomycin 3' adenytransferase t	S. aureus	AB253625	1-975	5	1,1,1,2,2	cacctatgatgtgggaacgggaaaagacatgatgc	cacctatgatgtgggaacgggaaaagacatgatgc	ttccttggttcgcagactgatgggcccattctcgga	ttccttggttcgcagactgatgggcccattctcgga	ttccttggttcgcagactgatgggcccattctcgga	
		381	aph(3)-IIla aminoglycoside phosphotransferase tyt	E. faecalis	NC_008445	39505-40299	5	1,1,1,1,1	taaltgatgcataaaggccgagagataggaaatttcccac	taaltgatgcataaaggccgagagataggaaatttcccac	acacgcatgatagattgtctatgtctgcgtgaaatcatagttt	acacgcatgatagattgtctatgtctgcgtgaaatcatagttt	acacgcatgatagattgtctatgtctgcgtgaaatcatagttt	
		382	aminoglycoside adenytransferase aadD Kanamyci	S. aureus	AB037420	438-1199	5	2,1,1,2,2	ttccttggttcgcagactgatgggcccattctcgga	ttccttggttcgcagactgatgggcccattctcgga	taaltgatgcataaaggccgagagataggaaatttcccac	taaltgatgcataaaggccgagagataggaaatttcccac	taaltgatgcataaaggccgagagataggaaatttcccac	
		383	ant(6)-Ia or aadE aminoglycoside 6-adenylyltranse	E. faecalis	NC_008445 (X92945.2)	37965-38873	5	1,1,1,2,1	acacgcatgatagattgtctatgtctgcgtgaaatcatagttt	acacgcatgatagattgtctatgtctgcgtgaaatcatagttt	ttccttggttcgcagactgatgggcccattctcgga	ttccttggttcgcagactgatgggcccattctcgga	ttccttggttcgcagactgatgggcccattctcgga	
		384	Spectinomycin adenytransferase (spc) Spectinom	S. sciuri	NC_005076	10755-11537	5	1,1,1,2,1	tgctgttaatgagtttggaggtgtctcaacgtattgtagc	tgctgttaatgagtttggaggtgtctcaacgtattgtagc	gacacttcaaacacctgcgtcttctcggaatgactttaaata	gacacttcaaacacctgcgtcttctcggaatgactttaaata	gacacttcaaacacctgcgtcttctcggaatgactttaaata	
		430	Streptomycin adenytransferase str	E. casseliflavus	AY939931	7990-8724	1	2			tgatgtgtctttgtttatctcaaggggccaacttgaacct	tgatgtgtctttgtttatctcaaggggccaacttgaacct	tgatgtgtctttgtttatctcaaggggccaacttgaacct	tgatgtgtctttgtttatctcaaggggccaacttgaacct
		420	blaZ beta lactamase Tn4002	S. aureus	X16471	142-987	3	1,2,1	aacaacacctatcagccgatttgcgcagagttat	aacaacacctatcagccgatttgcgcagagttat	atcacagcagcaatcggtctcgacaacggcactatc	atcacagcagcaatcggtctcgacaacggcactatc	atcacagcagcaatcggtctcgacaacggcactatc	
473	Low affinity penicillin binding protein pbp5	E. faecium	X84860	523-2559	5	2,1,1,1,2	caggaatcattgtcttattgattgtgctgttattgttgcctt	caggaatcattgtcttattgattgtgctgttattgttgcctt	atcacagcagcaatcggtctcgacaacggcactatc	atcacagcagcaatcggtctcgacaacggcactatc	atcacagcagcaatcggtctcgacaacggcactatc			
Tetracyclines	242	Tetracycline resistance (tetL) efflux pump	E. faecium	AY081910	21-1397	5	1,1,2,2,2	tcgcgtcttcatgatattacgttgattctacgacacagt	tcgcgtcttcatgatattacgttgattctacgacacagt	atcacagcagcaatcggtctcgacaacggcactatc	atcacagcagcaatcggtctcgacaacggcactatc	atcacagcagcaatcggtctcgacaacggcactatc		
	243	Tetracycline resistance (tetM)	E. faecalis	XY9247	214-2133	5	2,1,1,2,1	gcttgatgaacacgacgcgcgagcattgtcgaattg	gcttgatgaacacgacgcgcgagcattgtcgaattg	atcacagcagcaatcggtctcgacaacggcactatc	atcacagcagcaatcggtctcgacaacggcactatc	atcacagcagcaatcggtctcgacaacggcactatc		
	262	Tetracycline efflux protein tet(K) pT181	S. aureus	S67449	1-1380	5	1,1,1,1,1	gtcttctgaagaagcaagtgtccttcggaatgattgtct	gtcttctgaagaagcaagtgtccttcggaatgattgtct	atcacagcagcaatcggtctcgacaacggcactatc	atcacagcagcaatcggtctcgacaacggcactatc	atcacagcagcaatcggtctcgacaacggcactatc		
	385	tetO tetracycline resistance	E. faecalis	AY660532	14-1933	5	1,1,1,1,1	gtctccctattggaagcggaagtgcagatgaagaacga	gtctccctattggaagcggaagtgcagatgaagaacga	atcacagcagcaatcggtctcgacaacggcactatc	atcacagcagcaatcggtctcgacaacggcactatc	atcacagcagcaatcggtctcgacaacggcactatc		
MLS	Chlor-amphenicol	386	tetS tetracyclin resistance	E. faecium	DQ295784	146-2086	5	1,1,1,2,1	agggtgaggtcccaatggaggaaacttgatctctgga	agggtgaggtcccaatggaggaaacttgatctctgga	atcacagcagcaatcggtctcgacaacggcactatc	atcacagcagcaatcggtctcgacaacggcactatc	atcacagcagcaatcggtctcgacaacggcactatc	
		233	msrC protein putative	E. faecalis V583	AE016830	1392319-13937	5	2,2,1,1,2	ttctccaaaagtccggttagaagcaatgattgcaattataga	ttctccaaaagtccggttagaagcaatgattgcaattataga	atcacagcagcaatcggtctcgacaacggcactatc	atcacagcagcaatcggtctcgacaacggcactatc	atcacagcagcaatcggtctcgacaacggcactatc	
		234	Lintosamide nucleotidyltransferase (linB)	E. faecium	AF110130	127-930	5	2,1,1,2,1	ttcatccaactggttgttgtagtagctcgcgtact	ttcatccaactggttgttgtagtagctcgcgtact	atcacagcagcaatcggtctcgacaacggcactatc	atcacagcagcaatcggtctcgacaacggcactatc	atcacagcagcaatcggtctcgacaacggcactatc	
		240	Hydrolase Vgb (inactivates streptogramin B family	S. aureus	AF117258	2869-3768	4	1,2,1,1	ttcacagcaatgattgcagtgaggtgcagcggtttggcg	ttcacagcaatgattgcagtgaggtgcagcggtttggcg	atcacagcagcaatcggtctcgacaacggcactatc	atcacagcagcaatcggtctcgacaacggcactatc	atcacagcagcaatcggtctcgacaacggcactatc	
		260	ermA S-adenosyl-methionine dependent methylas	S. aureus	X03216	4551-5282	5	1,1,2,1,1	gtcgtctcaagaacaatacatagcagtgctacacttggctt	gtcgtctcaagaacaatacatagcagtgctacacttggctt	atcacagcagcaatcggtctcgacaacggcactatc	atcacagcagcaatcggtctcgacaacggcactatc	atcacagcagcaatcggtctcgacaacggcactatc	
		298	erm(2) pBT233	S. pyogenes	X64695	8009-8746	5	1,2,2,1,2	gaacatctgttgtatggcggttgaaatttataagaacatc	gaacatctgttgtatggcggttgaaatttataagaacatc	atcacagcagcaatcggtctcgacaacggcactatc	atcacagcagcaatcggtctcgacaacggcactatc	atcacagcagcaatcggtctcgacaacggcactatc	
		299	msrSA Erythromycin, oleandomycin azithromycin,	S. aureus	AB016613	2005-3471	5	1,2,2,2,1	ccaccaaatagaggaattgattgttctcgaagtgcata	ccaccaaatagaggaattgattgttctcgaagtgcata	atcacagcagcaatcggtctcgacaacggcactatc	atcacagcagcaatcggtctcgacaacggcactatc	atcacagcagcaatcggtctcgacaacggcactatc	
		301	streptograminB lactonase (vgbB) Resistance to str	S. cohnii	AF015628	399-1286	5	1,1,1,1,1	agaggagtttaactgttctattccccgattcaggccca	agaggagtttaactgttctattccccgattcaggccca	atcacagcagcaatcggtctcgacaacggcactatc	atcacagcagcaatcggtctcgacaacggcactatc	atcacagcagcaatcggtctcgacaacggcactatc	
		302	Acetyltransferase (vat) Streptogramin	S. aureus	L07778	258-917	5	1,2,2,2,2	acaatgaccatggacgtcatgcccgaaataattttacgc	acaatgaccatggacgtcatgcccgaaataattttacgc	atcacagcagcaatcggtctcgacaacggcactatc	atcacagcagcaatcggtctcgacaacggcactatc	atcacagcagcaatcggtctcgacaacggcactatc	
		303	Acetyltransferase (vatB) Virginamycin A-like resist	S. aureus	U19459	67-705	5	2,1,1,1,2	ttcattcaatcttcttcggaatgttggggaagaacga	ttcattcaatcttcttcggaatgttggggaagaacga	atcacagcagcaatcggtctcgacaacggcactatc	atcacagcagcaatcggtctcgacaacggcactatc	atcacagcagcaatcggtctcgacaacggcactatc	
	304	StreptograminA acetyltransferase (vatC) Resistant	S. cohnii	AF015628	1307-1945	5	2,1,1,1,2	tgaaatgagcaaaactatagaatgattggctcgaatatacc	tgaaatgagcaaaactatagaatgattggctcgaatatacc	atcacagcagcaatcggtctcgacaacggcactatc	atcacagcagcaatcggtctcgacaacggcactatc	atcacagcagcaatcggtctcgacaacggcactatc		
	305	StreptograminA acetyltransferase (satA) Resistant	E. faecium	L12033	162-791	5	2,1,1,1,1	tgaaatgagcaaaactatagaatgattggctcgaatatacc	tgaaatgagcaaaactatagaatgattggctcgaatatacc	atcacagcagcaatcggtctcgacaacggcactatc	atcacagcagcaatcggtctcgacaacggcactatc	atcacagcagcaatcggtctcgacaacggcactatc		
	306	SatG putative streptogramin acetyltransferase; cor	E. faecium	AF139725	63-707	5	2,1,1,2,1	tgaaacggtgcgaacacccaatgaatgaaggtatttcg	tgaaacggtgcgaacacccaatgaatgaaggtatttcg	atcacagcagcaatcggtctcgacaacggcactatc	atcacagcagcaatcggtctcgacaacggcactatc	atcacagcagcaatcggtctcgacaacggcactatc		
	307	ATP-binding protein (vga)	S. aureus	M90056	909-2477	5	1,1,1,1,2	accacaacaaacttcttgatagtgaagctatagagcggtt	accacaacaaacttcttgatagtgaagctatagagcggtt	atcacagcagcaatcggtctcgacaacggcactatc	atcacagcagcaatcggtctcgacaacggcactatc	atcacagcagcaatcggtctcgacaacggcactatc		
	308	Pristinamycin resistance protein VgaB pIP1633	S. aureus	U82085	629-2287	5	1,1,1,2,1	acaaataaaggttggatttcgttgcgaactgttattgtagcga	acaaataaaggttggatttcgttgcgaactgttattgtagcga	atcacagcagcaatcggtctcgacaacggcactatc	atcacagcagcaatcggtctcgacaacggcactatc	atcacagcagcaatcggtctcgacaacggcactatc		
	309	Macrolide-efflux protein (mef)	S. pyogenes	U70055	314-1531	5	1,1,1,2,2	gctgggtcgggtcttactattgttgccttactatattggag	gctgggtcgggtcttactattgttgccttactatattggag	atcacagcagcaatcggtctcgacaacggcactatc	atcacagcagcaatcggtctcgacaacggcactatc	atcacagcagcaatcggtctcgacaacggcactatc		
	310	Lintosaminide nucleotidyltransferase (linA)	S. aureus	J03947	645-1130	5	1,1,1,1,1	agaagttgattggatgccttcacgtatggaacttaacaa	agaagttgattggatgccttcacgtatggaacttaacaa	atcacagcagcaatcggtctcgacaacggcactatc	atcacagcagcaatcggtctcgacaacggcactatc	atcacagcagcaatcggtctcgacaacggcactatc		
	Oxazolidinone	312	mphBM Marcolide resistance pSR1	S. aureus	AF167161	5665-6564	5	1,1,1,1,1	ccaaaacttacaggtaaaacccgcagccacaaatagat	ccaaaacttacaggtaaaacccgcagccacaaatagat	atcacagcagcaatcggtctcgacaacggcactatc	atcacagcagcaatcggtctcgacaacggcactatc	atcacagcagcaatcggtctcgacaacggcactatc	
		396	ermT erythromycin resistance p121BS	Lactobacillus	NC_004957 (AF310974)	934-1668	2	2,1	acaatgttgttgctattggaagcaacgacacagctttgtg	acaatgttgttgctattggaagcaacgacacagctttgtg	atcacagcagcaatcggtctcgacaacggcactatc	atcacagcagcaatcggtctcg		

E. faecalis phage	334	Putative phage terminase large subunit EfmE1679	E. faecium	NZ_ABS000000000	3672-5339	5	1,1,2,2,1	tcagaagcgcgcatcaacaatcgactgacaaagc	ctccatacatgtgatagcttaatgaaccgcagacga	ttggacatacgccttcacgagtaaacgcgacatc	tgatttaaatgcggactctaaagcggaaagatcgact	tcacgataacgcgcattccaacagcagatgaacc
	336	Phage anti-repressor protein EfmU0317_contig000	E. faecium	NZ_ABSW010000000	51174-51950	5	1,2,2,1,1	gggttattcaaacacgaagaatgtctgttcgcgcg	tcgcgaatcacgacgtcaggtcaatcaagagagat	tttaaacgttgggttaacaagtgagtggtgccagc	tcgatgtccacagagatattgacatgtctccacaac	tcatacaactgagatccgaaagccgatgtgggca
	337	Phage endonuclease EfmU0317_contig00056	E. faecium	NZ_ABSW010000000	62625-62843	4	1,1,2,2	atttatgaaaagagaaggtggcctattgtcagcgggt	ggctcattgtcacgggtgtggcctagttcatatttgg	tttggaaagagagcacacgtccatacattgtacc	tcctacatcattgtacaaacaaagacaacgaactgct	
	338	Phage prohead protease EfmU0317_contig00056	E. faecium	NZ_ABSW010000000	66354-66923	5	1,1,1,1,1	agcgaagtgattgttctgttggctcattctcaaaagg	ccaatgtgtcaggagacgtacaaagcggaaacccctcg	gaacgtgtgttgaaatcgacgaatgttattccggcac	tggtggactacaattctgaaccaactgtcttcgaacaatcca	cggctacgctgctgtattcaacagctcaaacattt
	339	Phagesite-specific recombinase EfmU0317_ctg00	E. faecium	NZ_ABSW010000000	6735-8087	5	1,1,1,1,1	ctctaagactatctccatgttctgttggctgttcagttga	cttgccttaaatgtttgaccacgtactagctctcgacag	taagcctaaccgaggtttcccgcttactactacc	gicgttctgaatcaatttgggcttccatcagcaa	actgttgcgaatcgaattgttcgcacgtctgagt
	340	Phage terminase small subunit EfmU0317_contigt	E. faecium	NZ_ABSW010000000	21549-22382	5	1,2,1,2,1	agtaacgttactaatcaaggtggcgctcctatttgtt	agcaaaaggaataatgcacgactcttcgcgcagtggtg	acaatttcgtatgatgaagaagaatccaacaagctgaagct	tggaactaatgatgaagaagtcgaacgattgcagca	aattgaagattcattgactcggatagcaaccagttagct
	341	Prophage pi2 protein 43 EfmU0317_contig00121s	E. faecium	NZ_ABSW010000000	33975-34715	4	1,2,1,2	agtgggaagatgcacactcagtaagtggttagatgtcgt	tcctctttgaattacagtcagactcagacatttaagaaga	tccttaaacgcctgtattaaatgagttgttcggagatgc	ctgttttcagctagtcgagtaattgaattgagagacga	
	343	Phage site-specific recombinase EF2955 phage in E. faecalis V583		NC_004668	2828409-28296	5	1,1,1,1,1	aggtgtgcacaaactgcagaaataaccggttatcagct	agttgtcctagcctttacaggttgtcgtgaagagtga	acagcttatataagccaagacogtagcacaagacga	acagcgtcttagcacaacgttctacagctagacaatga	ctcaaatggcgctacaataacacgtagtgactattcca
E. faecalis phage	344	Site-specific recombinase EF2855 phage integras	E. faecalis V583	NC_004668	2735627-27366	5	1,1,1,2,2	agtttaggaatccacattcatagctactgaaacgacgt	cattcggaaaatcgactgacttgaactgattaaacgct	actggtataacgctgtgtgttggaagcttttagcattga	tccctgaagtcagctgtgttggaagcttttagcattga	tctatttggttctatggttttcggcatcaccacgc
	348	Site-specific recombinase EF2043 phage integras	E. faecalis V583	NC_004668	1961337-19624	5	1,1,1,1,1	agcaaacattaaagtagctttcaactcggttaggacaca	agtcctggataccttagccccaagaacattggagtg	gtggcctaaaaattgtaaggaggtattaaacgctgcgg	atcaaatcatctctagcaacacgcttaacagcgttt	cataaccgtacacgcttcaagacatacccatcgaa
	351	Phage integrase EF0303 (pp1)	E. faecalis V583	NC_004668	289354-29053s	5	1,2,1,1,1	cgaaggttcggtgtattgtctcgatattggtatgt	tcctcgggttgactacgtgtgtgcagatgtgaagtc	accaaaacgcattcccgatgtgaaattgagtgtcca	tatagtcgagagataaatgaccacaggaattatcgca	aattacagtcactgactatatacccgagagcttgaa
	353	Site-specific recombinase EF1417 phage integras	E. faecalis V583	NC_004668	1398097-13993	5	2,2,2,2,1	tgccagtcacattgctctagcttcgaactgtgcacgaag	tcctctttctatacaacgcactgcttgcctcaattgtgaga		ttaactgcctcttcgcgaagcctaagtcgaaaatg	cgatagactcctgatagatccacactgtgactcttct
CRISPR-cas	474	csn1 family CRISPR-associated protein	E. faecalis OG1RF	CP002621.1	416527-420540	5	2,2,2,1,1	aaccacggttcacgaaggatggcgaaattctttgg	ttgatagtcctctgtgttgcctatacagtgatttacgcg	ttcctgcgctcctgtgtattaaatgacttgcctaa	agagattgcggtcactcttttcaacattctcagtt	tacgggactgtatgaacacgcagaaagggttgcg
	475	Cas1 CRISPR Associated Protein	E. faecalis OG1RF	CP002621.1	420541-421403	5	2,1,1,2,1	tgcgatgataagcgctttgccaattgtglaaaattttgcc	giagctgttcgaatgacgcacgcggtgtgttggacg	gggctgcgaacggtgagtgattgaaacagactcaa	ttacacttagcgaacagagatcattgcgaagaagcg	ctatgcgctggaattcactgttttgatccagcc
	476	Cas2 CRISPR Associated Protein	E. faecalis OG1RF	CP002621.1	421404-421733	5	2,2,2,2,1	ttgttgatgaatcgtctaataaagcaatgttggctgcgc	tgctgtattattaatgtttgatgtccaaagcacaagc	ttgttgctgccttaaacgagataatcccgaaagag	tggaagacaagacagactgaggttgcattgaatgaagc	caacgcgcgcgcggaagcggttgcagatgttcc
	477	csn2 family CRISPR-associated protein	E. faecalis OG1RF	CP002621.1	421734-422393	5	1,2,2,1,1	atttttaggtctagcgtataattcgcttgcctcagct	ttgccaacgctgaattaaatcatctggggatttagaagca	tttggaaagaatggcatcactgtgcaggaaacttt	gttgctagctatttgacagagatgaagtgcaca	acgattaaagacgttcaaacctttgccactagtga
	478	Conserved CRISPR sequence Repeat pHTbeta	E. faecium	AB183714.1	43550-43717	1	2	gttttgagactatataaaacgacatggttctcaaat	gttttgagactatataaaacgacatggttctcaaat			
479	Conserved CRISPR sequence Repeat	E. faecalis OG1RF	U41084.1	1355-1786	1	2	gttttagactcattgtgttttagaattgtaccaaac					

*SSTE; Site specific transposable element