

1 **Supplementary Text:**

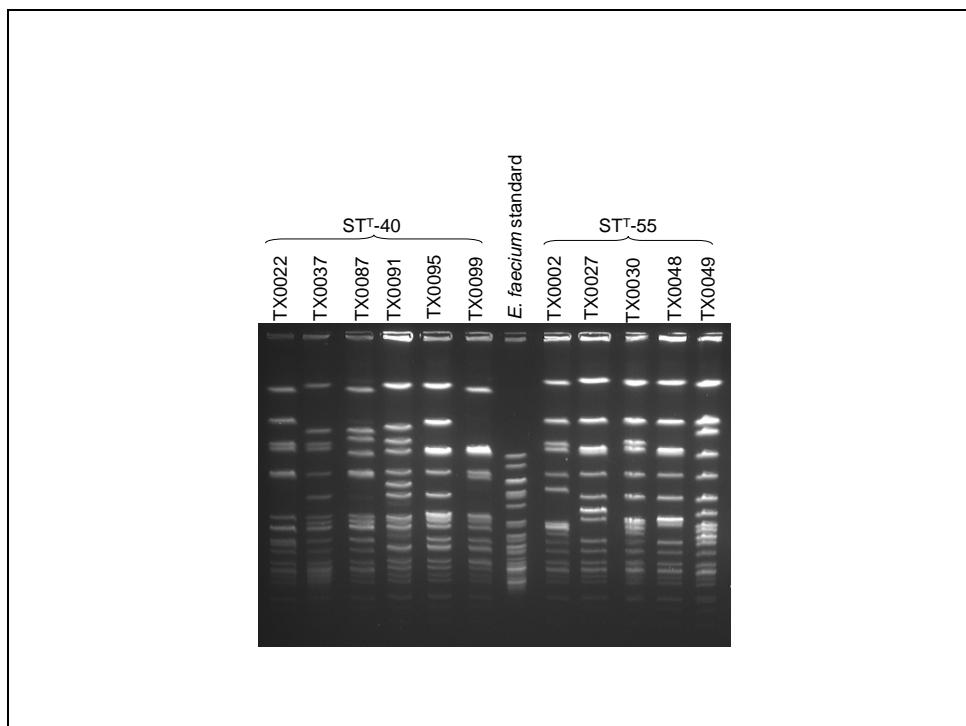
2 A number of the singletons also appear to be rather closely related to isolates in other STs
3 within this collection based on the cladogram in Fig. 1 including ST^T-T517 (n=1), 99.8%
4 identical (SLV differing by four nt in *salA*) to ST^T-T525 (n=2); ST^T-T505 (n=1), 99.9%
5 identical (DLV differing by one nt in *ace* and one nt in *salA*) to ST^T-T509; ST^T-T514
6 (n=1), 99.9% identical (SLV differing by a 6 nt deletion in *lsa*) to ST^T-144 (n=1); ST^T-
7 T507 (n=1), 99.7% identical (SLV differing by 8 nt in *salA*) to ST^T-107 (n=2); ST^T-T504
8 (n=1), 99.7% identical (SLV differing by 6 nt in *salA*) to ST^T-T506 (n=1); and ST^T-T512
9 (n=1), 99.9% identical (SLV differing by one nt in *lsa*) to ST^T-20 (n=4).

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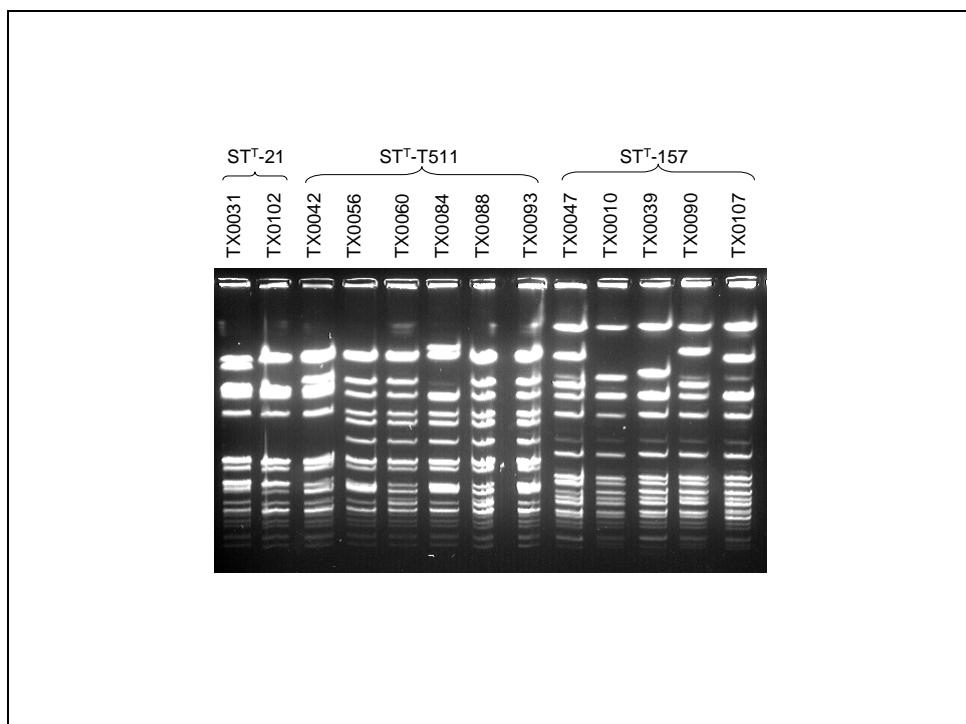
12 **Supplementary Figures:**

13 Fig. S1a:
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17 Fig. S1b:



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20 **Supplementary Tables:**21 Table S1: Infective endocarditis *E. faecalis* isolates from the United States collected between 1974-2004

Strain ^a	Isolation Location	Year	ST ^T (<i>ace, salA, lsa</i>)	ST ^{M,b}	CPS type ^c	Reference
TX0104	CT	2002	2 (8, 2, 9)	(2)	5	(1)
TX0011	Houston, TX	1991	6 (3, 8, 13)	6	2	
TX0053	Houston, TX	1991	6 (3, 8, 13)	(6)	2	
TX0052	Springfield, MO	1993	6 (3, 8, 13)	(6)	2	(2,3,4,5)
TX0026	WI	1975	20 (17, 20, 3)	(19)	1	(6)
TX0023	Rochester, MN	1976	20 (17, 20, 3)	(19)	1	
TX0043	ND	1983	20 (17, 20, 3)	19	1	(1)
TX0029	Rochester, MN	1992	20 (17, 20, 3)	(19)	1	
TX0031	Rochester, MN	1992	21 (17, 1, 25)	21	1	(1)
TX0102	Rochester, MN	>1990	21 (17, 1, 25)	21	1	(1)
TX0083	Rochester, MN	>1990	30 (17, 1, 21)	-	5	
TX0109	Houston, TX	2002	33 (6, 25, 23)	59	1	(1)
TX0037	IL	1974	40 (19, 25, 19)	40	1	
TX0022	Rochester, MN	1992	40 (19, 25, 19)	40	1	
TX0087	Rochester, MN	>1990	40 (19, 25, 19)	(40)	1	
TX0091	Rochester, MN	>1990	40 (19, 25, 19)	(40)	1	
TX0095	Rochester, MN	>1990	40 (19, 25, 19)	(40)	1	
TX0099	Rochester, MN	>1990	40 (19, 25, 19)	(40)	1	
TX0007	Houston, TX	1992	44 (28, 14, 18)	(44)	1	
TX0008	Reno, NV	1992	44 (28, 14, 18)	(44)	1	
TX0009	Reno, NV	1992	44 (28, 14, 18)	(44)	1	
TX0101	Rochester, MN	2001	44 (28, 14, 18)	44	1	
TX0027	IA	1975	55 (19, 25, 21)	55	1	(1)
TX0030	IA	1983	55 (19, 25, 21)	(55)	1	
TX0002	New Haven, CT	1993	55 (19, 25, 21)	55	1	
TX0048	Boston, MA	<1980	55 (19, 25, 21)	(55)	1	
TX0049	Boston, MA	<1980	55 (19, 25, 21)	(55)	1	
TX0044	Rochester, MN	1975	62 (6, 1, 30)	62	1	
TX0103	Rochester, MN	>1990	62 (6, 1, 30)	(62)	1	
TX0125	Houston, TX	2004	107 (6, 18, 5)	107	1	
TX0086	Rochester, MN	>1990	107 (6, 18, 5)	(107)	1	
TX0017	Houston, TX	1992	144 (19, 31, 29)	144	1	(1)
TX0010	Columbia, OH	1992	157 (17, 34, 25)	157	1	
TX0039	IL	1975	157 (17, 34, 25)	(157 or 21)	1	
TX0047	Boston, MA	<1980	157 (17, 34, 25)	(157 or 21)	1	(6)
TX0090	Rochester, MN	>1990	157 (17, 34, 25)	(157 or 21)	1	
TX0107	Houston, TX	2002	157 (17, 34, 25)	21	1	
TX0001	New Haven, CT	1993	283 (17, 10, 30)	283	1	(6)
TX0073	Houston, TX	1995	283 (17, 10, 30)	(283)	1	

TX0041	Rochester, MN	1985	287 (30, 1, 40)	(287)	2	
TX0055	Rochester, MN	1994	287 (30, 1, 40)	(287)	2	
TX0092	Rochester, MN	>1990	287 (30, 1, 40)	287	2	
TX0034	Rochester, MN	1978	317 (12, 33, 34)	(317)	5	(6)
TX0045	Boston, MA	<1980	317 (12, 33, 34)	317	5	(2,3,7)
TX0046	Boston, MA	<1980	317 (12, 33, 34)	(317)	5	(2,3,7)
TX0066	Houston, TX	1994	T501 (3, 1, 21)	-	5	
TX0079	Houston, TX	1996	T502 (4, 7, 35)	-	1	
TX0085	Rochester, MN	>1990	T503 (4, 32, 20)	-	2	
TX0004	New Haven, CT	1993	T504 (6, 18, 42)	-	5	
TX0014	Houston, TX	1992	T505 (6, 34, 21)	-	1	
TX0025	Rochester, MN	1984	T506 (6, 34, 42)	-	2	(6)
TX0036	Rochester, MN	1977	T507 (6, 35, 5)	-	2	
TX0065	Rochester, MN	1994	T508 (6, 36, 44)	-	5	
TX0006	New Haven, CT	1993	T509 (10, 11, 21)	-	1	
TX0003	New Haven, CT	1993	T510 (13, 2, 12)	-	1	
TX0042	Rochester, MN	1992	T511 (17, 1, 36)	21	1	
TX0056	Rochester, MN	1994	T511 (17, 1, 36)	(21)	1	
TX0060	Rochester, MN	1994	T511 (17, 1, 36)	21	1	
TX0084	Rochester, MN	>1990	T511 (17, 1, 36)	21	1	
TX0088	Rochester, MN	>1990	T511 (17, 1, 36)	21	1	
TX0093	Rochester, MN	>1990	T511 (17, 1, 36)	(21)	1	
TX0032	Rochester, MN	1976	T512 (17, 20, 45)	-	5	
TX0012	Houston, TX	1991	T513 (33, 40, 37)	-	1	(1)
TX0063	Rochester, MN	1994	T514 (19, 31, 39)	-	1	
TX0105	TN	2002	T515 (29, 3, 15)	-	5	
TX0013	Houston, TX	1992	T516 (31, 37, 41)	-	1	
TX0098	Rochester, MN	>1990	T517 (34, 42, 32)	-	2	
TX0040	IL	1974	T518 (35, 28, 28)	-	1	
TX0106	TN	2002	T519 (36, 2, 9)	-	5	
TX0020	Houston, TX	1991	T520 (37, 25, 40)	-	5	
TX0035	Rochester, MN	1992	T521 (38, 20, 38)	-	1	
TX0028	Rochester, MN	1992	T522 (39, 38, 47)	-	1	
TX0057	Rochester, MN	1994	T523 (40, 36, 43)	NT	5	
TX0061	Rochester, MN	1994	T523 (40, 36, 43)	(NT)	5	
TX0089	Rochester, MN	>1990	T523 (40, 36, 43)	NT	5	
TX0097	Rochester, MN	>1990	T524 (41, 30, 46)	-	5	
TX0108	Houston, TX	2002	T525 (34, 1, 32)	4	2	
TX0128	Houston, TX	2004	T525 (34, 1, 32)	(4)	2	
TX0018	Houston, TX	1991	T526 (3, 39, 7)		1	
TX0094	Rochester, MN	>1990	T527 (32, 41, 4)		5	
TX0019	Houston, TX	1992	T528 (32, 27, 4)	34	5	

23 ^a Isolates are ordered by ST^T based on intragenic sequences of *ace*, *salA*, and *lsa*. ST^Ts not
24 described previously in isolates typed (5) which had MLST data were assigned, when possible, the same
25 type number as the corresponding ST^M; isolates which did not have MLST data, the ST^M was not in the
26 database, or the ST^M corresponded with another published ST^T allelic profile were assigned an arbitrary
27 number beginning with T500.

28 ^b ST^Ms are per the seven-housekeeping-gene scheme and assigned in accordance with the database
29 at <http://efaecalis.mlst.net/>. Types contained within () were inferred based on identical ST^Ts.
30 NT – a new ST^M not assigned yet in the MLST database (allele types as follows: *gdh*-9, *gyd*-5, *pstS*-4, *gki*-
31 16, *aroE*-1, *xpt*-11, *yqil*-8).

32 ^cThe *cps* gene locus types were designated as follows: type 1 (corresponding to serotype A & B)
33 possesses *cpsA* and *cpsB* only; type 2 (corresponding to serotype C) possesses *cpsA-cpsK*; type 5
34 (corresponding to serotype D) possesses *cpsA-cpsK* except *cpsF* (8, 9,10).

35

Table S2: Additional *ace* locus allele types

^a The position of each variable site within the sequenced fragment is shown in the numbers above the nucleotide, read vertically.

Table S3: Additional *salA* locus allele types

<i>salA</i> Alleles	# bases varied	Nucleotide variations with reference to <i>E. faecalis</i> OG1RF at positions: ^a																																																									
		47	82	83	108	155	291	317	320	347	353	363	383	416	443	444	449	456	464	488	491	494	527	548	557	558	559	584	605	614	627	628	638	650	661	662	675	682	689	699	712	716	730	734	737	754	762	763	768	778	794	815	830	842	848	852	853	854	855
1		T	C	G	G	A	G	T	C	C	C	C	T	A	G	A	T	C	G	G	T	G	G	C	G	G	A	C	G	C	A	C	C	C	C	A	C	C	T	G	C	T	A	A	*	*	*	-	-	-									
28	5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	*	*	*	-	-	-																	
29 ^c	4	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	*	*	*	-	-	-																			
30	5	-	-	-	-	-	-	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	*	*	*	-	-	-																			
31	11	-	-	-	-	-	-	A	C	-	-	-	-	-	-	-	-	A	A	T	T	-	-	-	-	-	-	-	-	-	-	-	-	-	*	*	*	-	-	T																			
32	7	-	-	-	-	-	-	-	C	-	-	-	-	T	-	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	*	*	*	-	-	-																				
33	8	-	-	-	-	-	-	T	-	T	-	-	-	T	-	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	*	*	*	-	-	-																					
34	4	-	-	-	-	-	-	-	-	-	-	-	-	T	-	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	*	*	*	-	-	-																						
35	5	-	-	-	-	-	-	-	-	-	-	-	-	T	-	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	*	*	*	-	-	-																						
36	4+3	-	-	-	-	-	-	-	-	-	-	-	-	-	A	-	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	G	T	G	-	-	-																					
37	8+3	A	-	-	-	-	-	-	-	-	-	-	-	G	-	A	-	A	-	G	-	-	-	T	A	T	-	-	-	-	-	-	G	T	G	-	-	-																					
38	5+3	-	-	-	-	-	-	-	C	-	-	-	-	A	-	-	A	-	-	-	-	-	-	T	-	-	C	-	-	-	-	G	T	G	-	-	-																						
39	6+3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	T	-	-	C	-	-	-	T	-	-	-	G	G	-	G	T	G	-	T	-	-	-																				
40	4+3	-	-	-	-	-	-	-	T	-	-	-	-	-	-	-	-	T	-	-	C	-	-	-	T	-	-	-	-	-	G	T	G	-	-	-	-	-	-																				
41	6+3	-	-	T	-	-	-	-	-	A	-	-	-	C	A	-	-	-	-	-	-	-	-	A	-	-	-	C	-	-	-	G	T	G	-	-	-	-	-	-																			
42	1+3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	C	-	-	-	G	T	G	-	-	-	-	-	-																			

^a The position of each variable site within the sequenced fragment is shown in the numbers above the nucleotide, read vertically.

^b The * represents a base deletion (a total of 3 bases deleted, in frame).

^c Allele type 29 not found among 81 isolates in this study.

Table S4: Additional *lsa* locus allele types

^a The position of each variable site within the sequenced fragment is shown in the numbers above the nucleotide, read vertically.

^b Allele type 39 has a 6 bp deletion of AGA AAA from position 592-597.

42 **Supplementary Figure Legends:**

43 Fig. S1a - PFGE of isolates within ST^T-40 (n=6) and ST^T-55 (n=5) clonal lineages.

44 Black brackets group isolates with an identical ST^T. Strains are listed vertically above

45 their corresponding lanes. *E. faecium* TX0016 (DO) was used as a standard.

46

47 Fig. S1b - PFGE of isolates within CC21 (n = 13). CC21 contains isolates within ST^T-21

48 (n=2), ST^T-T511 (n=6), and ST^T-157 (n=5) clonal lineages. Black brackets group

49 isolates with an identical ST^T. Strains are listed vertically above their corresponding

50 lanes.

51

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