The files included as Supplementary material help to understand the text BAPS and correlation analysis made of *E. faecium* and *E. faecalis* population structure analysis

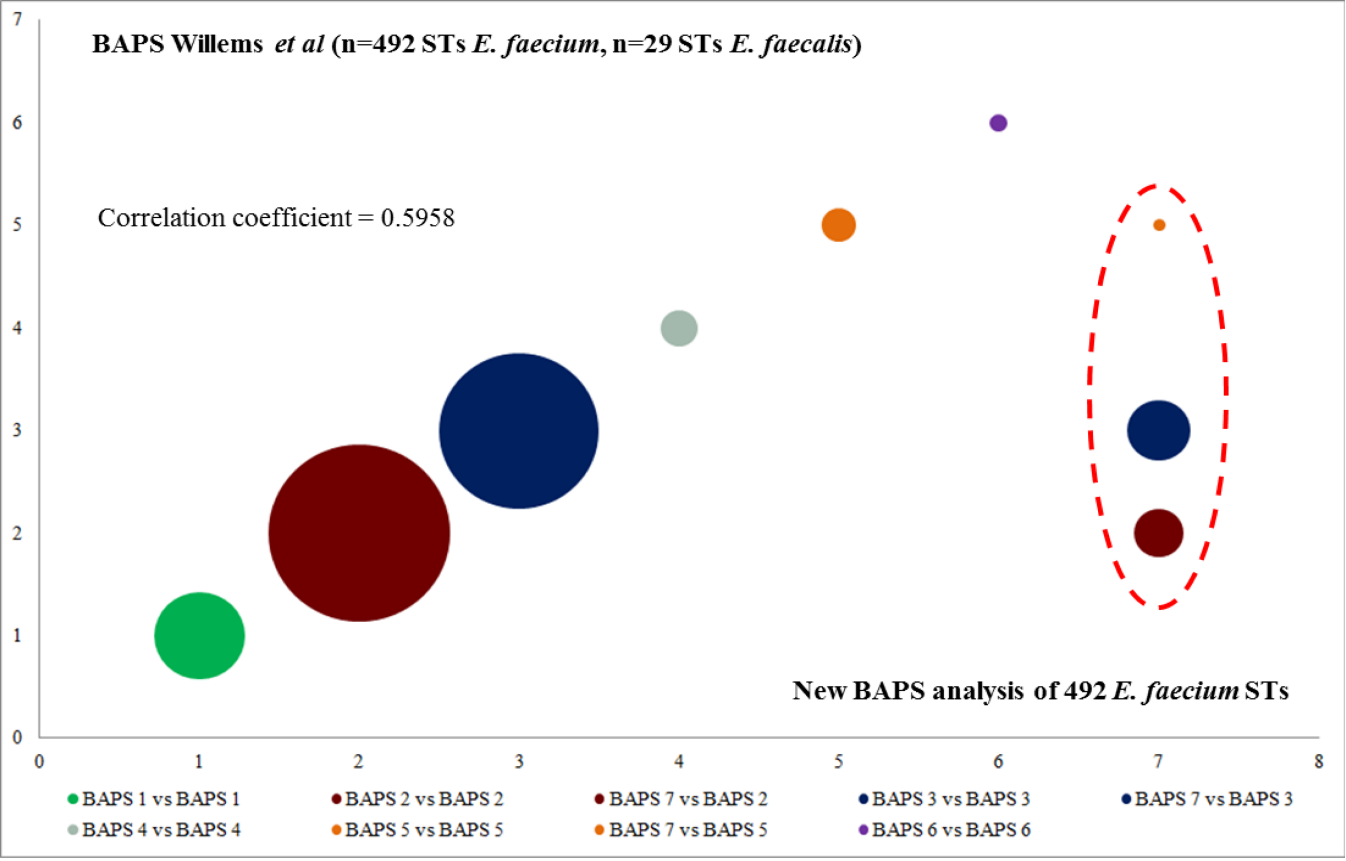


Figure S1. Correlation between the *E. faecium* BAPS groups obtained by Willems *et al* (Willems RJL, Top J, van Schaik W, Leavis H, Bonten M, Sirén J, Hanage WP, Corander J. 2012. Restricted gene flow among hospital subp opulations of *Enterococcus faecium*. MBio **3**:e00151–12) **using a MLST dataset of 492 *E. faecium* STs plus 29 *E. faecalis* (Y) and those obtained by us when using the same 492 *E. faecium* STs but excluding *E. faecalis* STs (X).** The size of each circle represents the population size included in each group. Dotted red line, groups with no correlation.

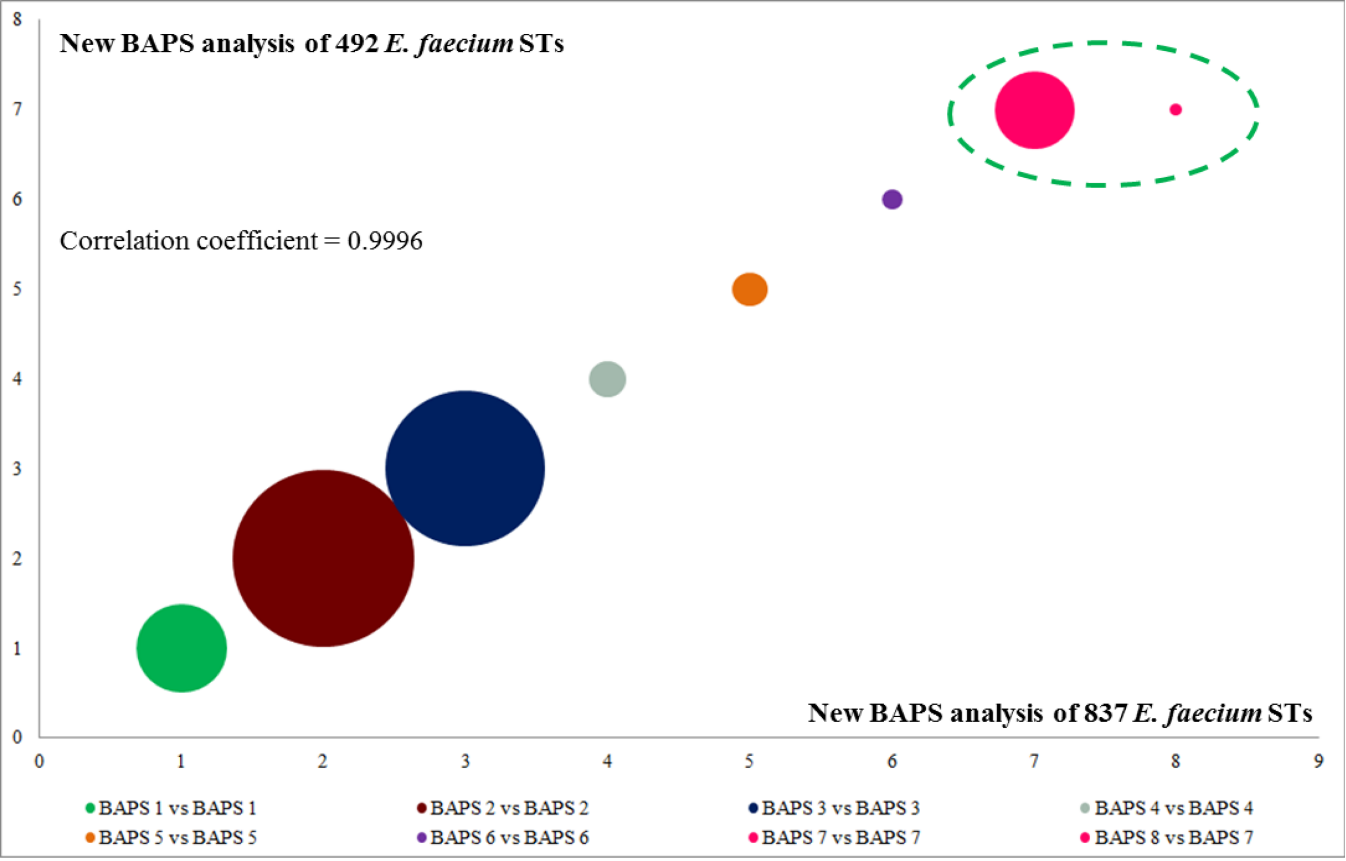
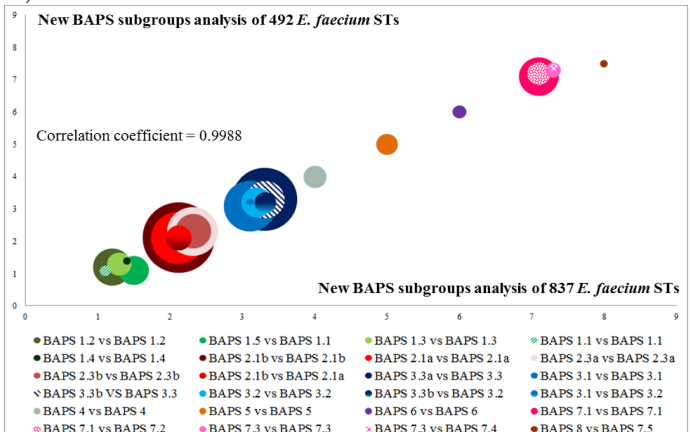


Figure S2. Correlation between the *E. faecium* BAPS groups obtained using the *E. faecium* dataset (492 STs) (Y) or using an updated database (837 STs) (X). The size of each circle represents the population size incl uded in each group. Green line, groups that change with the is increase in size of the population analyzed (**Willems RJL, Top J, van Schaik W, Leavis H, Bonten M, Sirén J, Hanage WP, Corander J**. 2012. Restricted gene flow among hospital subpopulations of *Enterococcus faecium* . MBio **3**:e00151–12).

A)



B)

BAPS Willems *et al*				New BAPS			
Group	**Subgroup**	**No STs**	**%**	**Group**	**Subgroup**	**No STs**	**%**
BAPS 1	-	53	10.77%	**BAPS 1**	**1.1**	2	0.41%
					1.2	25	5.08%
					1.3	10	2.03%
					1.4	1	0.20%
					1.5	15	3.05%
					1.6	0	0.00%
					Total	**53**	**10.77%**
BAPS 2	**2.1**	149	30.28%	**BAPS 2**	**2.1a**	49	9.96%
					2.1b	99	20.12%
					2.3b	1	0.20%
	2.3	63	12.80%		**2.3a**	43	8.74%
					2.3b	20	4.07%
	2.4	15	3.05%	**BAPS 7**	**7.1**	15	3.05%
	2.2	1	0.20%	**BAPS 8**		1	0.20%
	Total	**228**	**46.34%**		**Total**	**228**	**46.34%**
BAPS 3	**3.1**	45	9.15%	**BAPS 3**	**3.1**	45	9.15%
	3.2	17	3.46%		**3.2**	16	3.25%
					3.3b	1	0.20%
	3.3	103	20.93%		**3.3a**	71	14.43%
					3.3b	32	6.50%
	3.4	4	0.81%	**BAPS 7**	**7.3**	4	0.81%
	3.5	21	4.27%		**7.1**	21	4.27%
	Total	**190**	**38.62%**		**Total**	**190**	**38.62%**
BAPS 4		9	1.83%	**BAPS 4**		9	1.83%
BAPS 5		9	1.83%	**BAPS 5**		8	1.63%
				BAPS 7	**7.3**	1	0.20%
					Total	**9**	**1.83%**
BAPS 6		3	0.61%	**BAPS 6**		3	0.61%
	TOTAL	**492**				**492**	

Figure S3. A) Correlation between the *E. faecium* BAPS subgroups obtained using the original *E. faecium* dataset analyzed in previous publications (492 STs) (Y) or using a n updated database (837 STs) (X). The size of each circle represents the population size included in each group. The size of each circle represents the population size included in eac h group. B) Table showing correspondence between BAPS groups/subgroups described in Willems *et al* (**Willems RJL, Top J, van Schaik W, Leavis H, Bonten M, Sirén J, Hanage WP, Corander J** . 2012. Restricted gene flow among hospital subpopulations of *Enterococcus faecium* . MBio **3**:e00151–12) and those described in this study.

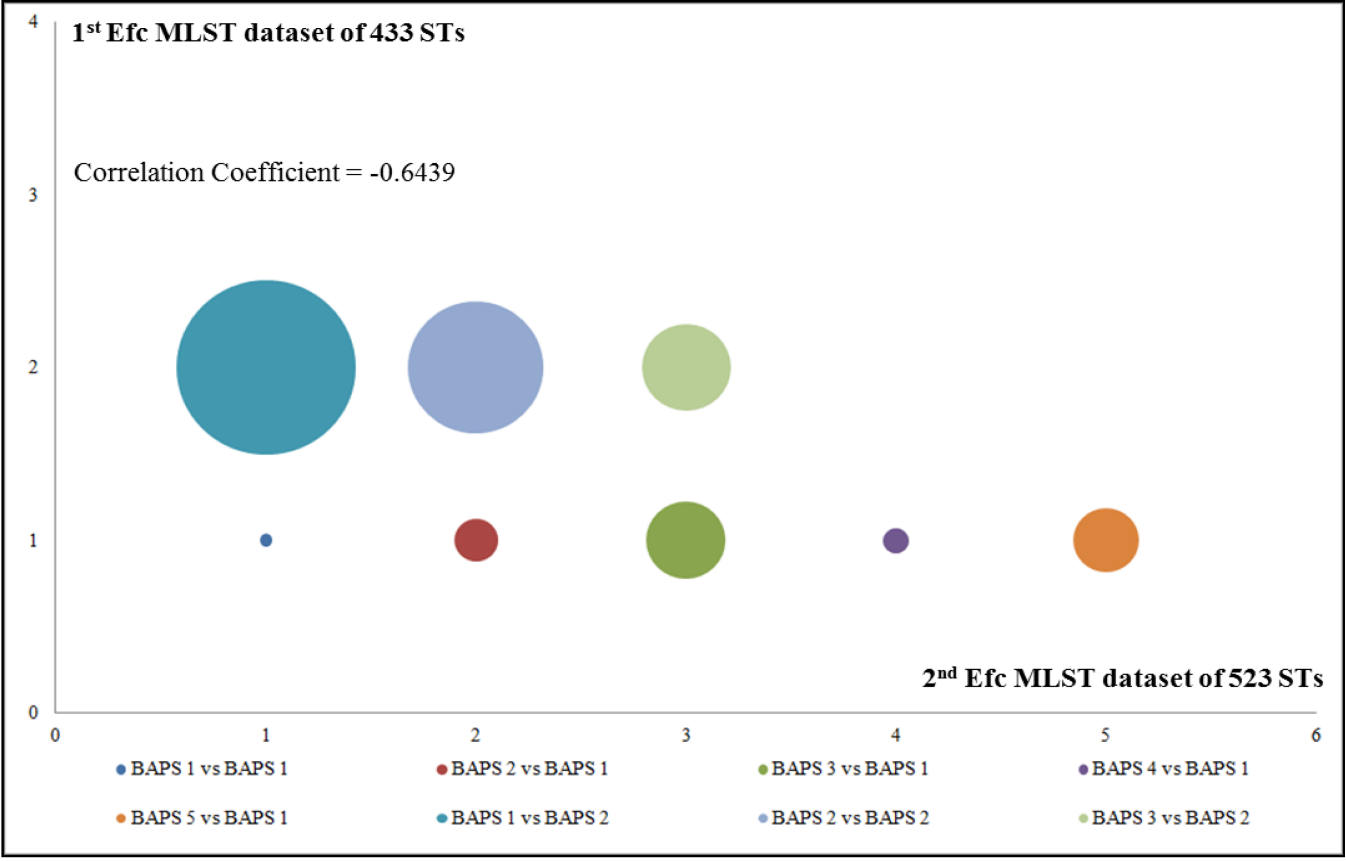


Figure S4. Correlation between the *E. faecalis* BAPS subgroups obtained using the first dataset of 433 STs (Y) and the second dataset of 523 STs (X). The size of each circle represents the population size included in each group.

Table S1. *E. faecium* isolates epidemiological data.

BAPS		ST		PFGE-type (No)	AREfm	Year	Age Group (No)			Ward (No)		Origin	VF (No isolates)			Anbiotic resistance (No isolates)								
Group	Subgroup (No)	ST (No)*	No PFGE		(No)		I	II	III	Name	Type	(No)	*esp*	*hyl*$_{Efm}$	*acm*	ERY	VAN	TEI	CIP	LEV[l]	STR[l]	GEN	TET	CHL
BAPS 1	1.1 (2)	**39** (1)	1	ASEfm57	-	2009	1			P	M	H	+	-	+	R	S	S	R	ND	ND	S	S	S
		715 (1)	1	ASEfm46	-	2009		1		ER	O	NH	-	-	-	R	S	S	R	ND	ND	S	S	S
	1.2 (27)	**94** (4)	4	ASEfm11-14	-	2009-2010		3	1	PHC	O	NH	+ (2)	-	+ (3)	R	S	S	S	ND	ND	S	R (1)	S
		361 (3)	2[a]	ASEfm30(2) - 31	-	2009	1		2	ER; ID; PHC	O (2); M	NH (2); H	-	-	+	R	S	S	S	ND	ND	S	R (1)	S
		178 (1)	1	ASEfm23	-	2009	1			PHC	O	NH	+	-	+	S	S	S	S	ND	ND	S	S	S
		688 (1)	1	ASEfm15	-	2009	1			PHC	O	NH	-	-	+	R	S	S	S	ND	ND	S	S	S
		691 (1)	1	ASEfm19	-	2009		1		PHC	O	NH	+	-	+	R	S	S	S	ND	ND	S	S	S
		296 (2)	2[b]	ASEfm 21, ASEfm63	-	2009		2		NE; PHC	O; M	NH; H	+ (1)	-	+ (1)	R	S	S	S	ND	ND	S	S	S
		345 (1)	1	ASEfm29	-	2009		1		PHC	O	NH	+	-	+	R	S	S	S	ND	ND	S	S	S
		695 (1)	1	ASEfm22	-	2009	1			PHC	O	NH	-	-	+	R	S	S	S	ND	ND	S	R	S
		583 (2)	2[c]	ASEfm44; ASEfm64	-	2009-2011	1	1		PHC	O	NH; H	-	-	+ (1)	R	S	S	S	ND	ND	S	S	S
		714 (1)	1[c]	ASEfm44	-	2009			1	ER	O	NH	-	-	+	R	S	S	S	ND	ND	S	S	S
		696 (2)	1[d]	ASEfm26	-	2009		2		PHC	O	NH	+ (1)	-	+	R	S	S	S	ND	ND	S	S	S
		620 (1)	1	ASEfm17	-	2009		1		PHC	O	NH	-	-	+	R	S	S	S	ND	ND	S	S	S
		76 (1)	1	ASEfm10	-	2010	1			P	O	NH	+	-	+	S	S	S	S	ND	ND	S	S	S
		684 (1)	1	ASEfm52	-	2009		1		PHC	O	NH	+	-	+	R	S	S	S	ND	ND	S	S	S
		685 (1)	1	ASEfm9	-	2009		1		PHC	O	NH	-	-	-	R	S	S	S	ND	ND	S	S	S
		692 (1)	1	ASEfm20	-	2011	1			P	M	H	-	-	+	R	S	S	S	ND	ND	S	R	S
		693 (1)	1	ASEfm65	-	2010			1	PHC	O	NH	+	-	+	R	S	S	S	ND	ND	S	S	S
		697 (1)	1	ASEfm25	-	2010		1		E	O	NH	-	-	+	R	S	S	S	ND	ND	S	S	S
		717 (1)	1	ASEfm45	-	2010		1		GDS	O	NH	+	-	+	R	S	S	S	ND	ND	S	S	S
	1.5 (2)	**623** (1)	1	ASEfm24	-	2009		1		PHC	O	NH	+	-	+	R	S	S	S	ND	ND	S	S	S
		713 (1)	1	ASEfm62	-	2009		1		PHC	O	NH	-	-	+	S	S	S	S	ND	ND	S	S	S
	1.6 (2)	**686** (1)	NT	NT	-	2009	1			PHC	O	NH	+	+	+	R	S	S	S	ND	ND	S	S	S
		694 (1)	1[b]	ASEfm63.1	-	2009			1	ER	O	NH	-	-	+	R	S	S	R	ND	ND	S	S	S
BAPS 2	2.1a (33)	**117** (25/9)	1[e]	CEfm1	+	2009-2010		8	17	ID (3); IM (3); GDS (3); NP (3); T (3); G (2); UR (2); C; CV; ER; GI; NM; PHC	M (14); I (4); O (4); S (3)	H (21); NH (4)	+ (22)	+ (2)	+	R (23)	S	S	R (24)	R (23)	R (6)	S	S	R (1)
		203 (4/3)	2[k]	CEfm7 (3); CEfm27	+	2009-2010		1	3	IM (2); NM; PS	M (3); S	H	+ (3)	-	+	R (3)	S	S	R (3)	R (3)	R (3)	S	S	R (1)
		80 (1/1)	1	CEfm39	+	2009		1		ID	O	NH	-	-	+	R	S	S	R	R	R	R	ND	ND
		323 (1/1)	1	CEfm18	+	2009		1		G	M	H	+	+	+	R	S	S	R	R	S	S	S	S
		612 (1)	1	CEfm37	+	2011	1			P	M	H	+	+	-	R	S	S	R	R	R	S	ND	ND
		324 (1)	1	ASEfm51	-	2009	1			PHC	O	NH	-	-	+	S	S	S	S	S	S	S	R	S
	2.1b (4)	**704** (1)	1	ASEfm42	-	2009	1			PHC	O	NH	-	-	+	S	S	S	S	ND	ND	S	S	S
		301 (1)	1	ASEfm56	-	2009			1	ER	O	NH	-	-	+	S	S	S	S	ND	ND	S	S	S
		701 (1)	1	ASEfm38	-	2009		1		PHC	O	NH	+	-	-	R	S	S	R	ND	ND	S	R	S
		706 (1)	1	ASEfm54	-	2009		1		PHC	O	NH	-	-	-	S	S	S	S	ND	ND	S	S	S
	2.3a (4)	**92** (1)	1	ASEfm6	-	2009			1	PHC	O	NH	+	-	+	R	S	S	S	ND	ND	S	S	S
		420 (1)	1	CEfm24	-	2009		1		G	M	H	-	-	+	R	S	S	R	ND	ND	S	R	S
		25 (1)	1	CEfm23	+	2009			1	PHC	O	NH	-	-	+	R	S	S	R	S	R	S	R	R
		165 (1)	1	ASEfm34	-	2009		1		G	O	NH	-	-	-	R	S	S	R	S	S	S	S	S
	2.3b (6)	**672** (2/1)	1	Cefm20	+	2009-2011	1	1		P; PHC	M; O	NH; H	+ (1)	+ (1)	+ (1)	R	S	S	R	R (1)	R (1)	S	R (1)	S
		515 (1)	1	ASEfm43	-	2009			1	NE; PHC	M	H	-	-	+	R	S	S	R	ND	ND	S	R	S
		700 (1)	1	ASEfm37	-	2009		1		PHC	O	NH	+	-	+	R	S	S	R	ND	ND	S	S	S
		70 (1)	1	ASEfm40	-	2009		1		ER	O	NH	-	-	+	R	S	S	R	ND	ND	S	S	S
		707 (1)	1	ASEfm49	-	2009			1	ER	O	NH	+	-	-	S	S	S	S	ND	ND	S	S	S
BAPS 3	3.1 (10)	**32** (3/1)	3	ASEfm3; ASEfm59; CEfm32	+ (1)	2009-2010	1	2		PHC	O (2); M	NH (2); H (1)	-	-	+ (2)	R (1)	S	S	R	ND	ND	S	R (1)	S
		22 (3)	3	ASEfm1-2; ASEfm9	-	2009-2011	1	1	1	PHC (2); ER	O	NH	-	-	+	R (2)	S	S	R (1)	ND	ND	S	R (2)	S
		104 (1)	1	ASEfm32	-	2009	1			PHC	O	NH	+	+	+	R	S	S	R	ND	ND	S	S	S
		159 (1)	1	ASEfm33	-	2009		1		P	M	H	-	-	+	R	S	S	R	ND	ND	S	R	S
		682 (1)	1	ASEfm4	-	2009	1			CP	I	H	-	-	+	S	S	S	R	ND	ND	S	R	S
		683 (1)	1	ASEfm5	-	2009	1			P	O	NH	+	-	+	R	S	S	R	ND	ND	S	R	S
	3.2 (1)	**702** (1)	1	ASEfm53	-	2009			1	T	S	H	-	-	+	S	S	S	R	ND	ND	S	R	S

	3.3a (20)	**17** (14/6)	13[m]	CEfm3 (2); CEfm6; CEfm11; CEfm13; CEfm14 (2); CEfm16; CEfm25; CEfm30(3); CEfm34; ASEfm50	+ (13)	2009-2010	1	4	9	IM (5); PHC (3); CV (2); GDS; HE; P; UR	M (9); O (2); I (2); S	H (12); NH (2)	+ (10)	+ (13)	+ (12)	R (13)	S	S	R (12)	R (12)	R (3)	R (3)	R (4)	R (2)
		18 (6/2)	6	CEfm8; CEfm10; CEfm15; CEfm28; CEfm35-36	+	2009-2011	2	2	2	ID (2); PHC (2); HE; NE	M (4); O (2)	H (4); NH (2)	-	+ (3)	+	R	S	S	R (3)	R (4)	R (2)	S	R (3)	R (1)
	3.3b (24)	**102**[n] (11)	1[d]	ASEfm7	-	2009-2010	3	6	2	PHC (5); ID (2); ER; G; NE; P	O (9); M (2)	NH (9); H (2)	+ (6)	+ (1)	-	R (6)	S	S	R (9)	ND	ND	S	S	S
		705 (3)	1[g]	ASEfm39	-	2009			1	ER (2); T	O (2); S	NH (2); H	+ (1)	+ (1)	-	R (2)	S	S	R (1)	ND	ND	S	S	S
		709[n] (2)	1[h]	ASEfm7.6	-	2009		2		ER; PHC	O	NH	+ (1)	-	-	R	S	S	S	ND	ND	S	S	S
		708[n] (1)	1[i]	ASEfm7.3'	-	2010		1		PHC	O	NH	-	-	-	S	S	S	S	ND	ND	S	S	S
		710[n] (1)	1[j]	ASEfm7.1	-	2010			1	PHC	O	NH	-	-	-	R	S	S	S	ND	ND	S	S	S
		711 (1)	1	ASEfm8	-	2009	1			PHC	O	NH	-	-	-	S	S	S	R	ND	ND	S	S	S
		513 (1)	1	CEfm41	+	2010			1	PHC	O	NH	-	-	+	R	S	S	R	R	S	S	R	S
		681 (1/1)	1	CEfm33	+	2009	1			P	O	NH	+	-	+	R	S	S	R	ND	ND	S	S	S
		673 (1/1)	1	CEfm31	+	2010			1	PHC	O	NH	-	-	+	R	S	S	S	S	S	S	S	S
		253 (1)	1	ASEfm60	-	2011	1			PHC	O	H	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND
		712 (1)	1	ASEfm58	-	2009			1	IM	M	H	-	-	-	R	S	S	R	ND	ND	S	R	S
BAPS 7	7.1 (8)	**19** (1)	1[k]	CEfm5	+	2009	1	2	1	PHC (2); C; ER	O (3); M	NH (3); H	-	-	+	R	S	S	R	R (2)	R (2)	S	R	R (1)
		687 (1)	1	ASEfm16	-	2011	1			PHC	O	NH	-	-	+	R	S	S	S	ND	ND	S	S	S
		703 (1/1)	1	CEfm38	+	2009			1	GDS	S	H	-	-	-	ND	S	S	ND	ND	ND	ND	ND	ND
		675 (1)	1	ASEfm55	-	2009			1	PHC	O	NH	-	-	-	S	S	S	S	ND	ND	S	S	S
		699 (1)	1	ASEfm35	-	2009			1	PHC	O	NH	-	-	-	S	S	S	S	ND	ND	S	S	S
	7.3 (3)	**718** (1/1)	1	CEfm2	+	2009		1		R	M	H	-	-	-	R	S	S	R	S	S	S	R	S
		716 (1)	1[f]	ASEfm7.5	-	2011	1			PHC	O	NH	+	-	-	S	S	S	S	ND	ND	S	S	S
		59 (1)	1	ASEfm36	-	2009		1		PHC	O	NH	-	-	-	R	S	S	R	ND	ND	S	S	S
BAPS 8	(4)	**698** (2)	2	ASEfm27-28	-	2009	1		1	PHC; T	O; S	NH; H	+	-	+	R (1)	S	S	S	ND	ND	S	S	S
		689 (1)	1	ASEfm61	-	2009			1	PHC	O	NH	-	-	+	S	S	S	S	ND	ND	S	S	S
		690 (1)	1	ASEfm18	-	2009			1	PHC	O	NH	+	-	+	S	S	S	S	ND	ND	S	S	S

*the numbers in after the bar (/) corresponds to the number of AREfm isolates that were only cultured after culture enrichment; PFGE clones were named as CEfm plus the number of the clone, or eventually ASEfm and AREfm to highlight the ampicillin susceptibility or resistance phenotype; [a]two strains have a PFGE pattern that has 3 different bands; [b]PFGE patterns with 1 band of difference; [c]although strains have different STs they have the same PFGE-type; [d]PFGE pattern that has up to 5 bands of difference; [e]3 of the 25 strains that belong to this PFGE-type have 2 bands of difference; [f]PFGE-type with 5 bands of difference regarding ST102-PFGE-type; [g]PFGE-type with 1 band of difference; [h]PFGE-type with 6 bands of difference regarding ST102-PFGE-type; [i]PFGE-type with 3 bands of difference regarding ST102-PFGE-type; [j]PFGE-type with 1 band of difference regarding ST102-PFGE-type; [k]PFGE pattern that has up to 2 bands difference; [l]High level resistance; [m]It is of note that these ST17 strains were among those more frequently detected from samples of patients with bacteremia in our hospital admitted to different wards and locations; [n]Isolates classified as ST102 and its SLVs (ST709, ST708, ST710 and ST711) showed very similar PFGE types (ASEfm7, up to 5 bands difference). Abbreviations: BAPS, Bayesian Analysis of Population Structure; ST, Sequence Type; AREfm, Ampicillin resistance *E. faecium*; VF, Virulence factors; *esp*, Enterococcal Surface Protein; *hyl*$_{Efm}$, Glycosyl Hydrolase; *acm*, Collagen-binding Adhesin Gene ; NH, Non-

Hospital; H, Hospital; O, Outpatient; M, Medical; S, Surgical; I, ICU; ND, Not determined; Group I, 0-19 years old; Group II, 20-59 years old; Group III, ≥60 years old; C, Cardiology; CV, Cardiovascular; CP, Cardiopediatrics; E, Endocrinology; ER, Emergency room; G, Gastroenterology; GDS, General and Digestive Surgery; GI, Gynecology; HE, Hematology; ID, Infectious Diseases; IM, Internal Medicine; NE, Neurology; NM, Neumology; NP, Nephrology; OC, Oncology; OT, Otorhinolaryngology; P, Pediatrics; PS, Plastic Surgery; PHC, Primary health center; R, Rheumatology; T, Traumatology; UR, Urology; AMP, Ampicillin; ERY, Erythromycin; VAN, Vancomycin; TEI, Teicoplanin; CIP, Ciprofloxacin; LEV, Levofloxacin; STR, Streptomycin; GEN, Gentamicin; TET, Tetracycline; CHL, Chloramphenicol.

Table S2. *E. faecalis* isolates epidemiological data.

BAPS	ST			PFGE-type (No)	Year	Age Group (No)			Ward (No)		Origin	VF (No)					Anbiotic resistance (No)								
(No)	ST No)	No PFGE	CC (No)			I	II	III	Name	Type	(No)	*asa1*	*gelE*	*esp*	hyl_{Efc}	*cylA*	AMP	VAN	TEI	STR[a]	GEN[a]	LEV	ERI	TET	CHO
BAPS 1 (48)	6 (16)	1[e]	6 (16)	H10	2009-2010	1	4	11	IM (6); NE (3); PHC (2); T (2); CV; ER; P	M (12); O (3); I	H (13); NH (3)	+	+ (13)	+ (6)	-	+ (9)	S	R (5)	R (5)	R	R	R (14)	R	R (15)	R (1)
	513 (6)	1	242 (6)	CEfc35	2009-2010	1	2	3	PHC (4); GDS; ID	O (4); M; I	NH (4); H (2)	+ (2)	+ (1)	+ (1)	-	+ (3)	S	S	ND	R (2)	S	R (1)	R (2)	R (3)	S
	72 (5)	4	72 (5)	CEfc30-33	2009-2011	2	2		ER; P; PHC; R	O (2); M (2)	NH (2); H (2)	+ (2)	+ (3)	-	-	-	S	S	S	S	S	S	S	S	S
	168 (1)	1		CEfc34	2009			1	PHC	O	NH	+	+	-	-	-	S	S	ND	S	S	S	S	R	S
	64 (3)	3	8 (4)	CEfc2-4	2009	2	1		HE; P; PHC	M (2); O (1)	H (2); NH (1)	+	+	-	-	-	S	S	S	S	S	S	R (2)	R (2)	S
	8 (1)	1		CEfc1	2009			1	HE	M	H	+	+	+	-	-	S	S	ND	S	S	S	S	R	S
	34 (2)	1[m]	34 (2)	CEfc21	2009	1	1		G; PHC	O; M	NH; H	+ (1)	+	+ (1)	-	-	S	S	S	S	R (1)	S	R (1)	R (1)	ND
	79 (2)	2	79 (2)	CEfc59-60	2009	2			P; PHC	O; M	NH; H	-	+	-	-	-	S	S	ND	S	S	S	S	S	ND
	81 (1)	1	81 (2)	CEfc55	2010	1			CP	I	H	+	+	-	-	-	S	S	ND	S	S	S	S	S	S
	332 (1)	1	272 (2)	CEfc47	2009	1			PHC	O	NH	+	+	-	-	-	S	S	S	S	S	S	S	S	ND
	517 (1)	1		CEfc48	2009	1			PHC	O	NH	+	+	-	-	-	S	S	ND	S	S	S	S	S	ND
	27 (1)	1	27 (1)	CEfc57	2009			1	PHC	O	NH	+	+	-	-	-	S	S	S	S	S	S	S	S	ND
	82 (1)	1	82 (1)	CEfc69	2009			1	IM	M	H	-	+	-	-	-	S	S	S	S	S	S	S	S	ND
	282 (1)	1	121 (1)	CEfc37	2009		1		G	M	H	-	+	-	-	-	S	S	S	S	S	S	R	S	ND
	241 (1)	1	241 (1)	CEfc43	2009			1	GDS	I	H	-	+	+	-	+	S	S	S	S	S	S	S	S	S
	197 (1)	1	D (1)	CEfc42	2009			1	PHC	O	H	-	-	-	-	-	S	S	S	S	S	S	S	S	ND
	323 (1)	1	D (1)	CEfc56	2009			1	ER	O	NH	-	-	-	-	-	S	S	S	S	S	S	S	S	ND
	515 (2)	2	S (2)	CEfc44-45	2009	2			PHC	O	NH	+	+ (1)	-	-	+ (1)	S	S	ND	S	S	S	S	S	S
	516 (1)	1	S (1)	CEfc46	2009			1	ER	O	NH	-	+	-	-	-	S	S	ND	S	S	S	I	S	S
	520 (1)	1	S (1)	CEfc67	2009			1	PHC	O	NH	-	+	-	-	-	S	S	S	S	S	S	S	S	ND
BAPS 2 (52)	40 (15)	9[c]	40 (17)	CEfc23; CEfc24 (2); CEfc25 (3); CEfc26 (5); CEfc27; CEfc28.5; CEfc52	2009-2011	7	2	6	PHC (7); ER (2); P (2); ID; NP; T; UR	O (10); M (5)	NH (10); H (5)	+ (6)	+ (13)	+ (6)	-	+ (1)	S	S	S	R (1)	S	S	R (7)	R (10)	S
	268 (2)	1[d]		CEfc28	2009-2011	1		1	P; PHC	O; M	NH; H	+ (1)	+	+	-	-	S	S	S	S	S	S	R (1)	R	S
	25 (3)	2	25 (7)	CEfc11; CEfc12 (2)	2009	2		1	GDS; P; PHC	O (2); M	NH (2); H	+ (2)	+	+	-	+ (1)	S	S	S	S	S	S	R (1)	R (1)	S
	97 (1)	1			2009	1			P	M	H	+	+	-	-	-	S	S	ND	S	S	S	S	S	S
	269 (1)	1		CEfc15	2009		1		PHC	O	NH	-	+	+	-	-	S	S	S	S	S	S	S	S	ND
	55 (4)	1[g]	55 (7)	CEfc29	2009-2011	1	1	2	PHC (2); CP; UR	O (2); M; I	NH (2); H (2)	+	+ (1)	+ (3)	-	-	S	S	ND	R (1)	S	S	R (3)	R	S
	285 (1)	1[h]		CEfc29	2011	1			P	M	H	-	-	+	-	-	S	S	ND	S	S	S	R	R	R
	510 (1)	1[i]		CEfc29.1'	2009	1			PHC	O	NH	-	+	+	-	-	S	S	ND	S	S	S	R	R	R
	511 (1)	1[h]		CEfc29	2009		1		ER	O	NH	-	+	+	-	-	S	S	ND	S	S	S	S	R	R
	56 (2)	2	30 (4)	CEfc18-19	2009	1	1		G; PHC	O; M	NH; H	+ (1)	+ (1)	-	-	+	S	S	ND	S	S	S	R (1)	R	S
	30 (1)	1		CEfc17	2009			1	PHC	O	NH	+	+	+	-	-	S	S	ND	S	S	S	S	R	ND
	379 (1)	1		CEfc20	2009		1		ER	O	NH	-	+	+	-	-	S	S	S	R	S	S	R	S	ND

	191 (2)	2	191 (3)	CEfc39-40	2009-2010	1		1	PHC	O	NH	+ (1)	+	+	-	-	S	S	ND	S	S	R (1)	R (1)	R	ND
	514 (1)	1		CEfc41	2009			1	PHC	O	NH	+	+	+	-	-	S	S	ND	S	S	S	S	S	ND
	19 (2)	1[l]	19 (2)	CEfc7	2009		1	1	PHC	O	NH	+ (1)	+ (1)	+	-	-	S	S	S	S	S	S	S	R	S
	21 (2)	2	21 (2)	CEfc8-9	2009-2010	1	1		HE; PHC	O; M	NH; H	+ (1)	+	+	-	-	S	S	ND	S	S	S	S	R (1)	S
	512 (1)	1		CEfc22	2009			1	PHC	O	NH	+	+	-	-	-	S	S	ND	S	S	S	R	S	ND
	116 (2)	1[g]	116 (2)	CEfc36	2009		1	1	ER; PHC	O	NH	-	+	-	-	-	S	S	S	R (1)	S	S	R	R (1)	ND
	509 (1)	1	26 (1)	CEfc16	2009	1			PHC	O	NH	-	+	+	-	-	S	S	ND	S	S	S	S	R	ND
	41 (1)	1	41 (1)	CEf21	2009		1		PHC	O	NH	-	+	+	-	-	S	S	ND	R	S	S	S	R	ND
	74 (1)	1	73 (1)	CEfc58	2010			1	PHC	O	NH	-	-	-	-	-	S	S	ND	S	S	S	S	S	S
	508 (1)	1	206 (1)	CEfc51	2009		1		PHC	O	NH	+	+	-	-	+	S	S	ND	S	S	S	S	R	S
	86 (2)	1	S (2)	CEfc61	2009		2		G; NP	M	H	+	+	+	-	+	S	S	S	S	R (1)	R (1)	R	R	ND
	147 (1)	1	S (1)	CEfc62	2009		1		PHC	O	NH	-	-	-	-	-	S	S	S	S	S	S	S	S	ND
	321 (1)	1	S (1)	CEfc64	2009	1			P	M	H	+	+	+	-	+	S	S	S	S	S	S	R	S	ND
	322 (1)	1	S (1)	CEfc65	2009	1			P	M	H	+	-	+	-	-	S	S	S	R	S	S	S	S	ND
BAPS 3 (30)	179 (11)	1[a]	16 (18)	EFC11	2009-2011	5	5	1	PHC (3); P (3); ER (2); G; IM; OT	O (7); M (3); I	NH (7); H (4)	+	+ (8)	+ (9)	-	+ (4)	S	S	S	S	S	S	R (4)	R (8)	S
	16 (7)	4[b]		CEfc5 (4); CEfc6; CEfc50; Degraded	2009-2011	1	4	2	PHC (4); ER; OC; P	O (5); M (2)	NH (5); H (2)	+ (6)	+ (3)	+ (5)	-	+ (6)	S	S	S	R (3)	R (3)	R (2)	R (6)	R (6)	R (4)
	62 (2)	2[f]		CEfc12.5; CEfc13	2009	2			P; PHC	O; M	NH; H	+ (1)	+	+	-	-	S	S	ND	S	S	S	S	R	S
	333 (1)	1[j]	28 (3)	CEfc49.4	2009			1	IM	M	H	+	+	+	-	+	S	S	S	R	R	R	R	R	ND
	518 (1)	1		CEfc49	2009		1		CV	I	H	+	+	+	-	+	S	S	ND	R	R	S	R	R	ND
	519 (1)	1[k]		CEfc49	2009		1		CV	I	H	+	+	+	-	+	S	S	ND	R	R	R	R	R	S
	35 (1)	1	35 (1)	CEfc22	2010			1	PHC	O	NH	-	+	-	-	-	S	S	ND	S	S	R	R	R	S
	320 (1)	1	58 (1)	CEfc53	2009			1	PHC	O	NH	-	+	-	-	-	S	S	S	S	S	S	S	S	ND
	141 (1)	1	141 (1)	CEfc38	2009	1			PHC	O	NH	-	+	-	-	-	S	S	S	S	S	S	S	S	ND
	225 (1)	1	S (1)	CEfc63	2009		1		ID	M	H	-	+	-	-	-	S	S	ND	S	S	S	R	S	ND
	330 (1)	1	S (1)	CEfc66	2009		1	1	IM; ID	O; M	NH; H	+ (1)	+	+	-	-	S	S	S	R	S	R	R	R (1)	ND
	521 (1)	1	S (1)	CEfc68	2009			1	ER	O	NH	-	-	-	-	-	S	S	ND	S	S	S	S	S	S

PFGE clones were named CEfc plus the number of the clone; [a]CEfc5 has up to 5 bands of difference; [b]up to 3 bands of difference; [c]Several PFGE-types here prevalent. Among this PFGE-types there are up to 5 bands of difference; [d]5 bands of difference compared with ST40- CEfc28; [e]up to 6 bands of difference when comparing to V583; [f]5 bands of difference to ST25-CEfc12; [g]up to 2 bands of difference; [h]1 band of difference regarding ST50-CEfc29; [i]the same PFGE type as ST50-CEfc29; [j]the same PFGE as ST518; [k]4 bands of difference regarding ST518; [l]up to 6 bands of difference; [m]up to 1 bands of difference; [n]High level resistance. Abbreviations: BAPS - Bayesian Analysis of Population Structure; MLST – Multilocus Sequence Typing; CC – Clonal Complex; ST - Sequence Type; VR - Virulence factors; *esp* - Enterococcal Surface Protein; hyl_{Efc} -

Glycosyl Hydrolase; *cylA* - cytolysin/haemolysin; *gelE* - gelatinase; *asa1* - aggregation substance; NH - Non-Hospital; H -Hospital; O - Outpatient; M - Medical; S - Surgical; I - ICU; ND - Not determined; Group I - 0-19 years old; Group II - 20-59 years old; Group III - ≥60 years old; CV - Cardiovascular; CP - Cardiopediatrics; ER - Emergency room; G - Gastroenterology; GDS - General and Digestive Surgery; HE - Hematology; ID - Infectious Diseases; IM - Internal Medicine; NE – Neurology; NP - Nephrology; OC - Oncology; OT - Otorhinolaryngology; P - Pediatrics; PHC - Primary health center; R - Rheumatology; T - Traumatology; UR – Urology; AMP - Ampicillin; ERY - Erythromycin; VAN - Vancomycin; TEI - Teicoplanin; CIP - Ciprofloxacin; LEV - Levofloxacin; STR - Streptomycin; GEN - Gentamicin; TET - Tetracycline; CHL – Chloramphenicol.

Table S3. ORs analysis of *E. faecium* BAPS groups/subgroups regarding the origin of isolates.

BAPS		Hospitalized patients						Non-hospitalized patients						Animal						Environmental		Food		Others	
Group	**Subgroup**	**No**	**%**	**OR[a]**	**p**	**95% CI**		**No**	**%**	**OR[a]**	**p**	**95% CI**		**No**	**%**	**OR[a]**	**p**	**95% CI**		**No**	**%**	**No**	**%**	**No**	**%**
BAPS 1	**1.1**	3	0.20%	ND				1	0.07%	ND				0	0.00%	ND				1	0.07%	0	0.00%	6	0.40%
	1.2	37	2.45%	0.0386	<0.01	0.0232	0.0640	33	2.19%	35.1080	<0.01	17.0839	72.1480	3	0.20%	1.2816	0.698	0.3667	4.4793	13	0.86%	4	0.27%	10	0.66%
	1.3	2	0.13%	0.0109	<0.01	0.0024	0.0492	1	0.07%	ND				4	0.27%	ND				1	0.07%	2	0.13%	6	0.40%
	1.4	1	0.07%	ND				0	0.00%	ND				1	0.07%	ND				0	0.00%	0	0.00%	0	0.00%
	1.5	14	0.93%	0.0394	<0.01	0.0194	0.0802	7	0.46%	ND				6	0.40%	7.1036	<0.01	2.6186	19.2698	1	0.07%	0	0.00%	13	0.86%
	1.6	1	0.07%	ND				2	0.13%	ND				1	0.07%	ND				0	0.00%	0	0.00%	2	0.13%
BAPS 2	**2.1a**	479	31.74%	0.3672	<0.01	0.2551	0.5289	15	0.99%	1.7320	0.165	0.7978	3.7625	56	3.71%	4.4539	<0.01	2.5256	7.8547	4	0.27%	0	0.00%	23	1.52%
	2.1b	60	3.98%	0.0174	<0.01	0.0116	0.0262	24	1.59%	4.9073	<0.01	2.3729	10.1485	182	12.06%	54.2563	<0.01	31.5295	93.3649	15	0.99%	10	0.66%	30	1.99%
	2.3a	72	4.77%	0.0844	<0.01	0.0539	0 .1320	17	1.13%	8.5132	<0.01	4.3025	20.2869	20	1.33%	7.2065	<0.01	3.6271	14.3184	9	0.60%	0	0.00%	17	1.13%
	2.3b	13	0.86%	0.0275	<0.01	0.0136	0 .0552	8	0.53%	ND				22	1.46%	33.7639	<0.01	15.9460	71.4912	3	0.20%	2	0.13%	1	0.07%
BAPS 3	**3.1**	67	4.44%	0.0927	<0.01	0.0584	0.1471	15	0.99%	8.5132	<0.01	3.8086	19.0289	21	1.39%	8.6157	<0.01	4.3507	17.0619	5	0.33%	2	0.13%	12	0.80%
	3.2	16	1.06%	0.0283	<0.01	0.0148	0.0539	12	0.80%	ND				20	1.33%	21.2500	<0.01	10.2157	44.2028	3	0.20%	0	0.00%	8	0.53%
	3.3a	630	41.75%	#	#	#	#	12	0.80%	#	#	#	#	16	1.06%	#	#	#		4	0.27%	1	0.07%	16	1.06%
	3.3b	29	1.92%	0.0333	<0.01	0.0195	0.0567	24	1.59%	22.6594	<0.01	10.6789	48.0809	25	1.66%	15.4618	<0.01	7.8651	30.3956	3	0.20%	3	0.20%	8	0.53%
BAPS 4		6	0.40%	ND				2	0.13%	ND				0	0.00%	ND				1	0.07%	0	0.00%	2	0.13%
BAPS 5		14	0.93%	0.2130	<0.01	0.0736	0.6163	0	0.00%	ND				3	0.20%	ND				1	0.07%	0	0.00%	1	0.07%
BAPS 6		9	0.60%	ND				0	0.00%	ND				0	0.00%	ND				0	0.00%	0	0.00%	0	0.00%
BAPS 7	**7.1**	41	2.72%	0.0395	<0.01	0.0245	0.0637	7	0.46%	3.7619	<0.01	1.4284	9.9075	54	3.58%	33.9034	<0.01	18.3744	62.5597	2	0.13%	7	0.46%	9	0.60%
	7.2	3	0.20%	ND				0	0.00%	ND				0	0.00%	ND				0	0.00%	0	0.00%	3	0.20%
	7.3	4	0.27%	ND				6	0.40%	ND				3	0.20%	ND				1	0.07%	0	0.00%	0	0.00%
	7.4	2	0.13%	ND				0	0.00%	ND				0	0.00%	ND				0	0.00%	0	0.00%	0	0.00%
BAPS 8		6	0.40%	ND				3	0.20%	ND				0	0.00%	ND				1	0.07%	0	0.00%	1	0.07%
TOTAL		**1509**						**189**						**437**						**68**		**31**		**168**	

[a]using BAPS 3.3a as a reference group

Table S4. *E. faecalis* BAPS analysis data.

	BAPS		
Group	**No STs**	**% STs**	**No isolates**
BAPS 1	234	44.74%	576
BAPS 2	144	27.53%	417
BAPS 3	108	20.65%	270
BAPS 4	5	0.96%	5
BAPS 5	32	6.12%	42
TOTAL	**523**		**1310**

Table S5. ORs analysis of *E. faecalis* BAPS groups regarding the origin of isolates.

BAPS	Hospitalized patients						Non-hospitalized patients						Animal						Environmental		Food		Others	
	No	%	OR[a]	p	95% CI		No	%	OR[a]	p	95% CI		No	%	OR[a]	p	95% CI		No	%	No	%	No	%
BAPS 1	316	45,01%	#	#	#	#	70	36,27%	#	#	#	#	114	47,11%	#	#	#	#	10	47,62%	31	40,26%	35	46,67%
BAPS 2	206	29,34%	0,8033	0,089	0,6240	1,0341	85	44,04%	1,8507	<0,01	1,3103	2,6139	43	17,77%	0,4659	<0,01	0,3198	0,6788	7	33,33%	43	55,84%	33	44,00%
BAPS 3	155	22,08%	1,1090	0,487	0,8284	1,4847	34	17,62%	1,0414	0,856	0,6721	1,6136	69	28,51%	1,3912	0,058	0,9885	1,9580	4	19,05%	2	2,60%	6	8,00%
BAPS 4	3	0,43%	ND				0	0,00%	ND				1	0,41%	ND				0	0,00%	1	1,30%	0	0,00%
BAPS 5	22	3,13%	0,9051	0,755	0,4833	1,6949	4	2,07%	ND				15	6,20%	ND				0	0,00%	0	0,00%	1	1,33%
TOTAL	**702**						**193**						**242**						**21**		**77**		**75**	

[a]using BAPS 1 as a reference group