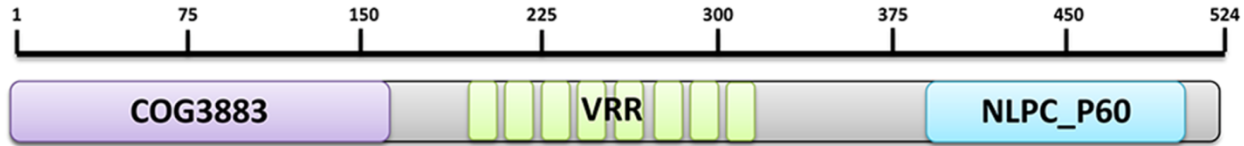
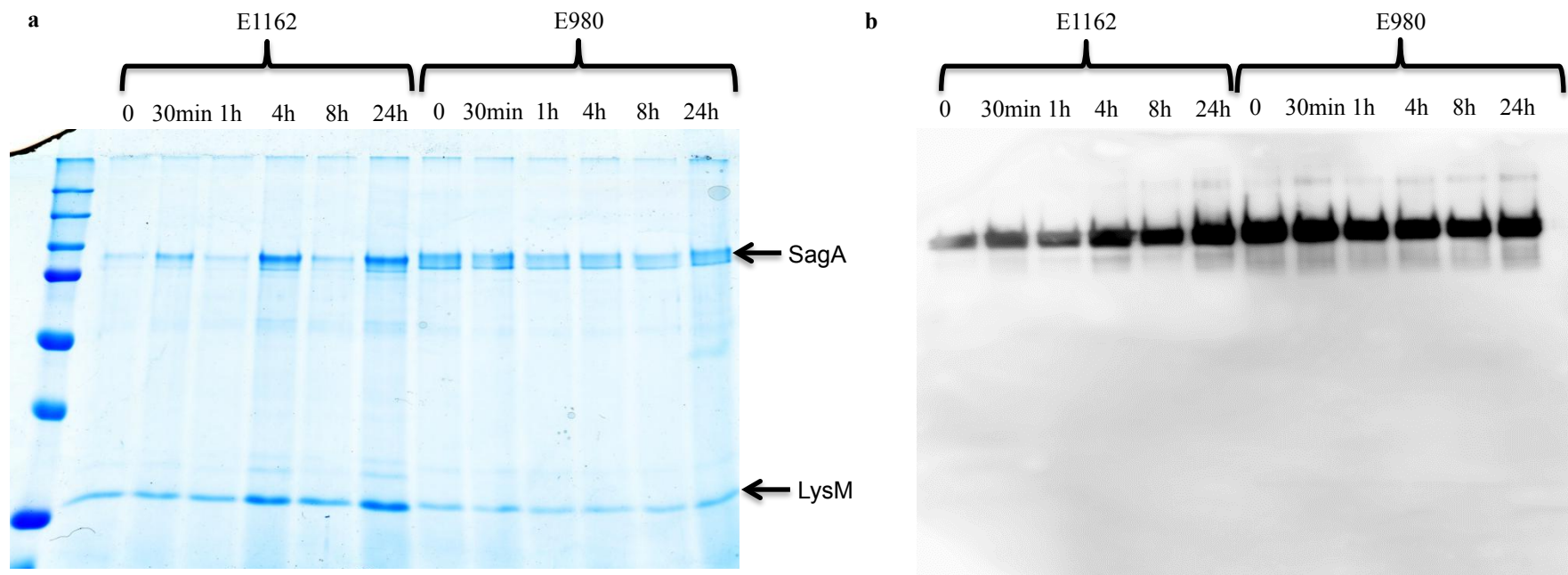


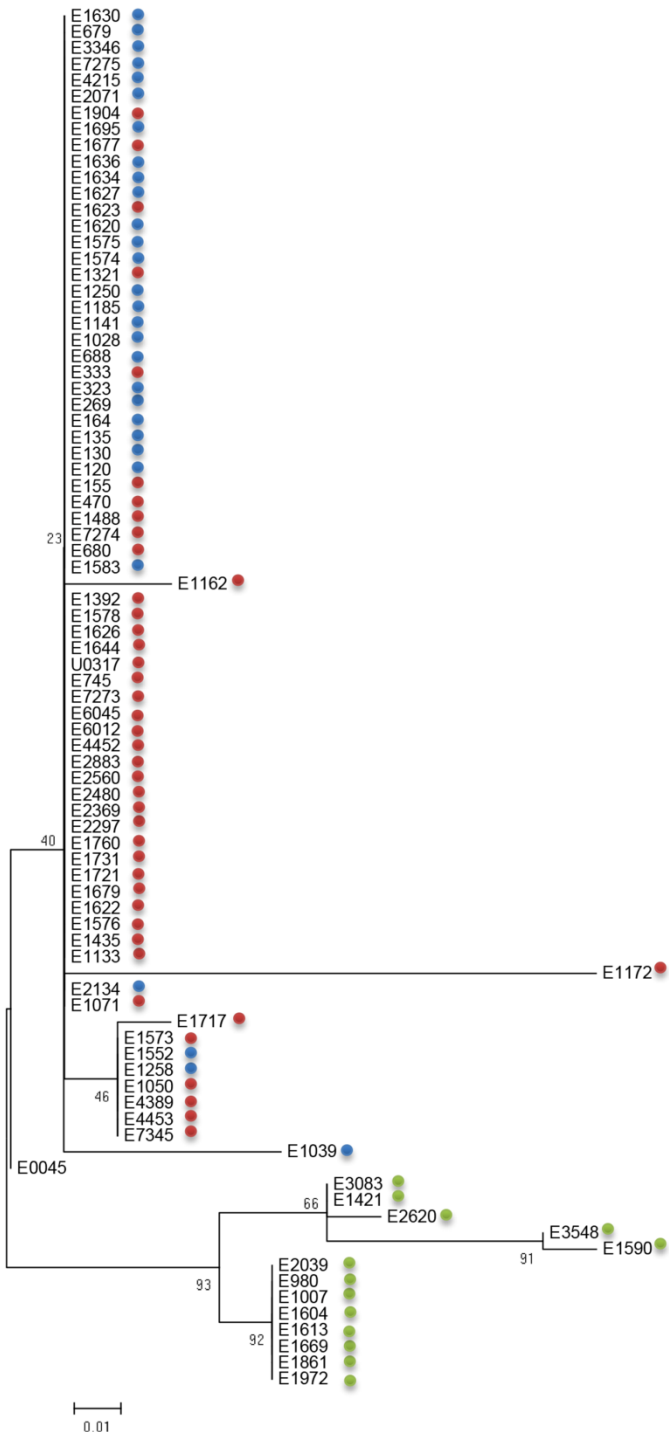
**Figure S1. Confocal microscopy orthoview images depicting biofilm thickness and SagA localization in a semi-static biofilm model.** Biofilms of three clade A1 (a) and three clade B strains (b), were grown for 24 h on poly-L-Lysine coated glass, in TSBg, at 120 rpm, at 37°C. Biofilms were incubated with  $\alpha$ -SagA and goat  $\alpha$ -rabbit Alexa 488 (green). Bacterial membranes were stained with FM 95-5 (red). Pictures were taken at 63x magnification with 2.0 optical zoom.



**Figure S2. Prediction of structural domains of SagA protein sequence.** COG3883 is an uncharacterized conserved domain identified in bacteria. NLPC\_P60 is a conserved domain found in several lipoproteins involved in cell wall biogenesis. The central part of the protein, indicated with green bars, represents the variable repeat region (VRR) with differences between *E. faecium* strains belonging to clade A1 and B and the polyphyletic Intermediate Group (IG).



**Figure S3. Stability of proteins released in the biofilm supernatant.** a. Proteins present in the 24 h biofilm supernatant of hospital-associated (clade A1) *E. faecium* strain E1162 and community (clade B) *E. faecium* strain E980 were equally loaded and separated using a 12.5% SDS page gel and stained with Coomassie blue after incubation at 37°C for 30 min, 1 h, 4 h, 8 h and 24 h. b. Presence of SagA in the biofilm supernatant of *E. faecium* strains after incubation at 37°C, analyzed by Western Blot using rabbit  $\alpha$ -SagA immune sera.



**Figure S4. Phylogenetic tree based on the variable repeat region of SagA.** SagA sequences from 85 *E. faecium* strains were used to build the phylogenetic tree, based on amino acid level of selected variable repeat region by MUSCLE and Mega version 6. Numbers near branches indicate bootstrap values in percentage. Colored circles indicate the clade origin of strains according to core genome-based phylogeny. Clade A1 is indicated in red, IG is indicated in blue, and clade B is indicated in green.

## Supporting data

**Table S1.** Ecological origin and clade assignment of 85 *E. faecium* strains.

Strains	Other name	Clade	ST	Country	Year	Epidemiology	Isolation site	Reference
E0045	EnGen0005	IG	9	GBR	1992	Poultry	Faeces	(1)
E120	EnGen0012	IG	27	NLD	1995	Clinical isolate	Ascites	(1)
E130	E0130	IG	6	NLD	1996	Community	Faeces	This study
E135	E0135	IG	6	NLD	1996	Community	Faeces	This study
E155	E0155	A1	17	USA	1995	Hospital outbreak	Faeces	(2)
E164	EnGen0010	IG	26	NLD	1996	Poultry	Faeces	(1)
E269	EnGen0022	IG	9	NLD	1996	Poultry	Faeces	(1)
E323	E0323	IG	79	FRA	1997	Clinical isolate	Faeces	This study
E333	EnGen0013	IG	80	ISR	1997	Clinical isolate	Blood	(1)
E470	E0470	IG	16	NLD	1999	Hospital outbreak	nd	This study
E679	EnGen0014	IG	150	BEL	1995	Pig	nd	(1)
E680	EnGen0019	IG	151	DEU	1995	Pig	nd	(1)
E688	EnGen0008	IG	5	ESP	1995	Pig	nd	(1)
E980	E0980	B	94	NLD	1998	Community	Faeces	(3)
E1007	EnGen0015	B	61	NLD	1998	Community	Faeces	(1)
E1028	E1028	IG	56	NLD	1998	Community	Faeces	This study

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E1039	E1039	IG	42	NLD	1998	Community	Faeces	(3)
E1050	EnGen0017	A1	92	NLD	1998	Community	Faeces	(1)
E1071	E1071	A1	32	NLD	2000	Clinical isolate	Faeces	(3)
E1133	EnGen0002	A1	117	USA	2001	Clinical isolate	Faeces	(1)
E1141	E1141	IG	123	NLD	1995	Clinical isolate	nd	This study
E1162	E1162	A1	17	FRA	1997	Clinical isolate	Blood	(3)
E1172	E1172	A1	99	POL	1998	Clinical isolate	Urine	This study
E1185	EnGen0011	IG	26	FRA	1998	Clinical isolate	Blood	(1)
E1250	E1250	IG	25	CHE	1997	Clinical isolate	Blood	This study
E1258	EnGen0004	IG	127	ESP	1998	Clinical isolate	Blood	(1)
E1321	EnGen0054	A1	78	ITA	1999	Clinical isolate	Catheter	(1)
E1392	EnGen0016	A1	64	GBR	2000	Clinical isolate	nd	(1)
E1421	E1421	B	100	GBR	2000	Clinical isolate	nd	This study
E1435	E1435	A1	65	GRC	1999	Hospital outbreak	nd	This study
E1488	E1488	A1	32	ESP	2000	Community	Faeces	This study
E1552	EnGen0021	IG	5	NLD	2002	Clinical isolate	Faeces	(1)
E1573	EnGen0009	A1	21	BEL	1994	Bison	Rumen	(1)
E1574	EnGen0020	IG	27	BEL	1995	Dog	nd	(1)
E1575	EnGen0001	IG	158	BEL	1995	Poultry	nd	(1)

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E1576	EnGen0018	A1	159	ZAF	2001	Ostrich	Ceacum	(1)
E1578	EnGen0007	A1	160	DEU	2001	Pig	Faeces	(1)
E1583	E1583	IG	161	BEL	2001	Community	Faeces	This study
E1590	EnGen0003	B	163	IRL	2001	Community	Faeces	(1)
E1604	EnGen0028	B	75	NOR	1956	Cheese	Food	(1)
E1613	EnGen0029	B	77	NOR	1964	Fish burger	Food	(1)
E1620	EnGen0027	IG	67	NLD	1957	Clinical isolate	Blood	(1)
E1622	EnGen0032	A1	104	NLD	1959	Rodent	nd	(1)
E1623	EnGen0031	A1	22	NLD	1960	Clinical isolate	Pus	(1)
E1626	EnGen0025	A1	92	NLD	1965	Clinical isolate	Stomach	(1)
E1627	EnGen0035	IG	66	NLD	1979	Clinical isolate	Gut	(1)
E1630	EnGen0039	IG	69	NLD	1981	Environment	Water	(1)
E1634	EnGen0040	IG	66	NLD	1982	Environment	Water	(1)
E1636	E1636	IG	106	NLD	1961	Clinical isolate	Blood	(3)
E1644	EnGen0051	A1	78	DEU	2002	Hospital outbreak	nd	(1)
E1669	E1669	B	94	BRA	nd	Clinical isolate	nd	This study
E1677	E1677	A1	113	BRA	nd	Clinical isolate	nd	This study
E1679	E1679	A1	114	BRA	1998	Hospital outbreak	Catheter	(3)
E1695	E1695	IG	97	BRA	1998	Clinical isolate	Faeces	This study

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E1717	E1717	A1	18	DNK	nd	Hospital outbreak	nd	This study
E1721	E1721	A1	169	TZA	nd	Clinical isolate	Blood	This study
E1731	EnGen0036	A1	18	TZA	2002	Clinical isolate	Blood	(1)
E1760	E1760	A1	173	AUS	2000	Hospital outbreak	nd	This study
E1861	EnGen0042	B	289	ESP	2001	Clinical isolate	Faeces	(1)
E1904	EnGen0024	A1	210	NLD	2001	Clinical isolate	Urine	(1)
E1972	EnGen0033	B	299	DEU	2000	Clinical isolate	Blood	(1)
E2039	EnGen0026	B	296	DEU	2000	Clinical isolate	K-Spitze	(1)
E2071	EnGen0044	IG	27	DNK	2001	Poultry	nd	(1)
E2134	EnGen0043	IG	12	NLD	2004	Poultry	nd	(1)
E2297	EnGen0034	A1	117	USA	2001	Clinical isolate	Urine	(1)
E2369	EnGen0050	A1	78	HUN	2005	Clinical isolate	Wound	(1)
E2480	C68	A1	16	USA	1996	Hospital outbreak	nd	(1)
E2560	EnGen0046	A1	78	NLD	2006	Clinical isolate	Blood	(1)
E2620	EnGen0038	B	331	NLD	2006	Clinical isolate	Blood	(1)
E2883	EnGen0030	A1	325	NLD	2002	Clinical isolate	Blood	(1)
E3083	EnGen0056	B	327	NLD	2000	Clinical isolate	Blood	(1)
E3346	EnGen0052	IG	332	NLD	2002	Clinical isolate	Blood	(1)
E3548	EnGen0047	B	328	NLD	2004	Clinical isolate	Blood	(1)

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E4215	EnGen0048	IG	310	SWE	2004	Poultry	nd	(1)
E4389	EnGen0057	A1	78	DNK	2008	Dog	Faeces	(1)
E4452	E4452	A1	266	NLD	2008	Dog	Faeces	(4)
E4453	E4453	A1	192	NLD	2008	Dog	Faeces	(4)
E6012	EnGen0045	A1	78	LVA	2010	Clinical isolate	Rectum	(1)
E6045	EnGen0049	A1	78	PRT	2010	Clinical isolate	Rectum	(1)
E7273	E7273	A1	117	ESP	2009	Clinical isolate	Faeces	This study
E7274	E7274	A1	203	ESP	2006	Clinical isolate	Blood	This study
E7275	E7275	IG	nd	ESP	2009	Clinical isolate	Faeces	This study
E7345	AUS0004	A1	17	AUS	1998	Clinical isolate	blood	(5)
E745	E745	A1	16	NLD	2000	Hospital outbreak	Faeces	unpublished
U0317	U0317	A1	78	NLD	2005	Clinical isolate	Urine	(3)

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## Reference list

1. **Lebreton F, van Schaik W, McGuire AM, Godfrey P, Griggs A, Mazumdar V, Corander J, Cheng L, Saif S, Young S, Zeng Q, Wortman J, Birren B, Willems RJ, Earl AM, Gilmore MS.** 2013. Emergence of epidemic multidrug-resistant *Enterococcus faecium* from animal and commensal strains. *MBio* **4**:e00534-00513.
2. **de Been M, van Schaik W, Cheng L, Corander J, Willems RJ.** 2013. Recent recombination events in the core genome are associated with adaptive evolution in *Enterococcus faecium*. *Genome Biol Evol* **5**:1524-1535.
3. **van Schaik W, Top J, Riley DR, Boekhorst J, Vrijenhoek JE, Schapendonk CM, Hendrickx AP, Nijman IJ, Bonten MJ, Tettelin H, Willems RJ.** 2010. Pyrosequencing-based comparative genome analysis of the nosocomial pathogen *Enterococcus faecium* and identification of a large transferable pathogenicity island. *BMC Genomics* **11**:239.
4. **de Regt MJ, van Schaik W, van Luit-Asbroek M, Dekker HA, van Duijkeren E, Koning CJ, Bonten MJ, Willems RJ.** 2012. Hospital and community ampicillin-resistant *Enterococcus faecium* are evolutionarily closely linked but have diversified through niche adaptation. *PLoS One* **7**:e30319.
5. **Lam MM, Seemann T, Bulach DM, Gladman SL, Chen H, Haring V, Moore RJ, Ballard S, Grayson ML, Johnson PD, Howden BP, Stinear TP.** 2012. Comparative analysis of the first complete *Enterococcus faecium* genome. *J Bacteriol* **194**:2334-2341.



**Table S3. Proteomics analysis of biofilm supernatant.** Mass spectrometry of the excised protein bands from 24 h biofilm supernatant. Mass spectrometry was performed by matrix-assisted laser desorption/ionization-time of flight (MALDI-TOF) mass spectrometry, using an Ultraflex MALDI-TOF/TOF mass spectrometer (Bruker Daltonics).

Band	Accession	Locus	Mass	Score	Description
75kDa	gi:424797365	ZP_18222963.1	51731	125	NlpC/P60 family protein [ <i>Enterococcus faecium</i> S447]
	gi:314938222	ZP_07845522.1	52950	123	NlpC/P60 family protein [ <i>Enterococcus faecium</i> TX0133a04]
	gi:314992106	ZP_07857556.1	52922	123	NlpC/P60 family protein [ <i>Enterococcus faecium</i> TX0133B]
	gi:424790089	ZP_18216682.1	52977	123	NlpC/P60 family protein [ <i>Enterococcus faecium</i> V689]
	gi:431747447	ZP_19536241.1	53108	123	protein P54 [ <i>Enterococcus faecium</i> E2134]
	gi:289565032	ZP_06445486.1	53894	122	secreted antigen SagA [ <i>Enterococcus faecium</i> D344SRF]
	gi:294623697	ZP_06702530.1	54140	122	SagA [ <i>Enterococcus faecium</i> U0317]
	gi:383329927	YP_005355811.1	54411	122	NlpC/P60 family lipoprotein [ <i>Enterococcus faecium</i> Aus0004]
50kDa	gi:69246939	ZP_00604194.1	80399	74	Sulfatase [ <i>Enterococcus faecium</i> DO]
	gi:257878586	ZP_05658239.1	80411	74	sulfatase [ <i>Enterococcus faecium</i> 1,230,933]
	gi:430835628	ZP_19453617.1	80415	74	sulfatase [ <i>Enterococcus faecium</i> E0680]
	gi:415894466	ZP_11550330.1	71547	57	sulfatase domain protein [ <i>Enterococcus faecium</i> E4453]
	gi:227551868	ZP_03981917.1	80308	56	phosphatidylglycerol--membrane- oligosaccharide glycerophosphotransferase [ <i>Enterococcus faecium</i> TX1330]
	gi:257884281	ZP_05663934.1	80330	56	sulfatase [ <i>Enterococcus faecium</i> 1,231,501]
25kDa	gi:69244843	ZP_00603067.1	21591	96	Peptidoglycan-binding LysM [ <i>Enterococcus faecium</i> DO]
	gi:261208113	ZP_05922788.1	21633	96	peptidoglycan-binding LysM [ <i>Enterococcus faecium</i> TC 6]
	gi:314941298	ZP_07848192.1	21621	96	LysM domain protein [ <i>Enterococcus</i> <i>faecium</i> TX0133C]
	gi:424856196	ZP_18280450.1	21619	96	LysM domain protein [ <i>Enterococcus</i> <i>faecium</i> R499]
	gi:430827476	ZP_19445618.1	21647	96	LysM protein [ <i>Enterococcus faecium</i> E0164]
	gi:431303160	ZP_19508007.1	21018	69	LysM protein [ <i>Enterococcus faecium</i> E1626]