A decade of genomic history for healthcare-associated *Enterococcus faecium* in the United Kingdom and Ireland

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Supplementary Data

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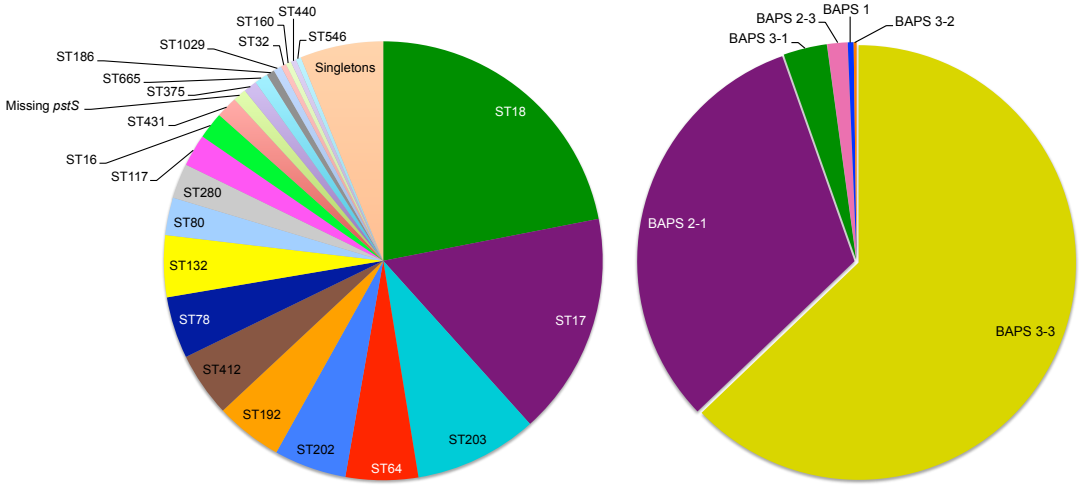
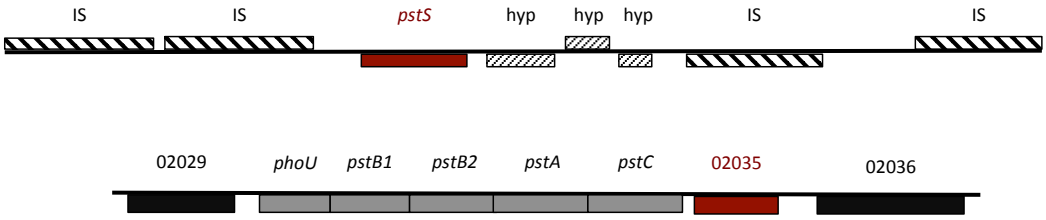
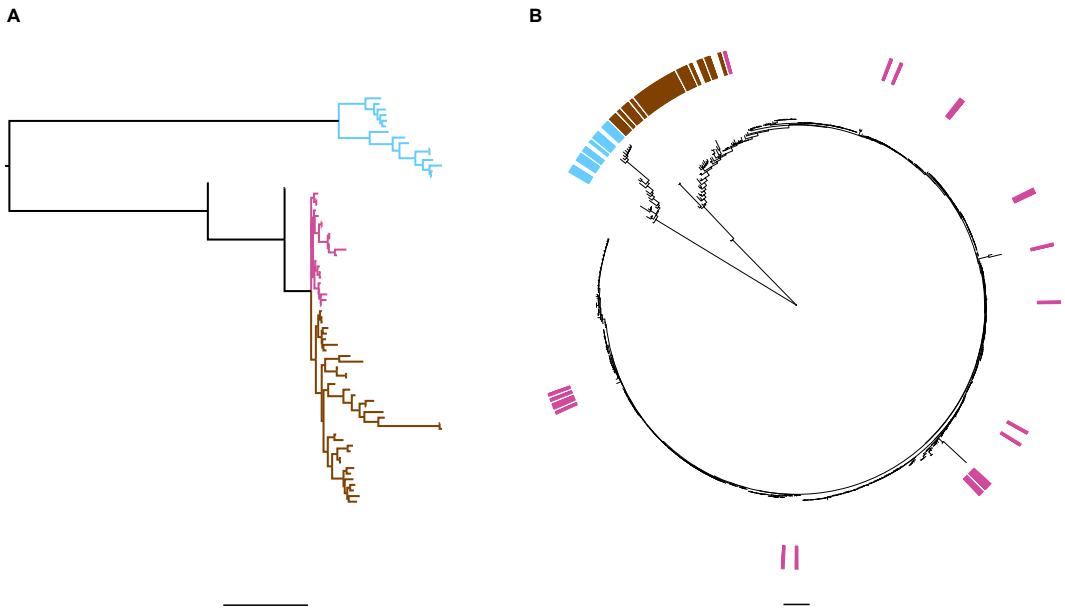


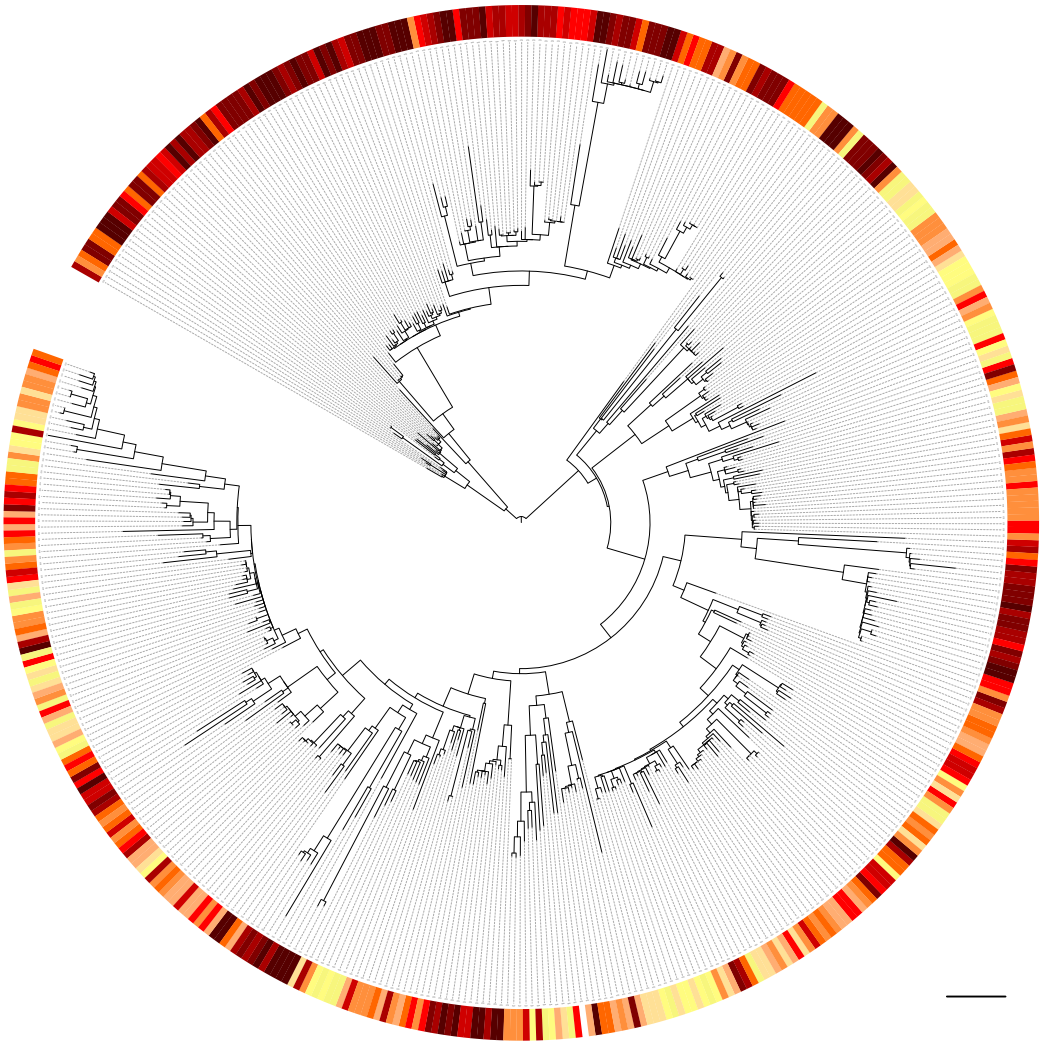
Supplemental Figure S1
Prevalence of STs and BAPs groups in the collection.



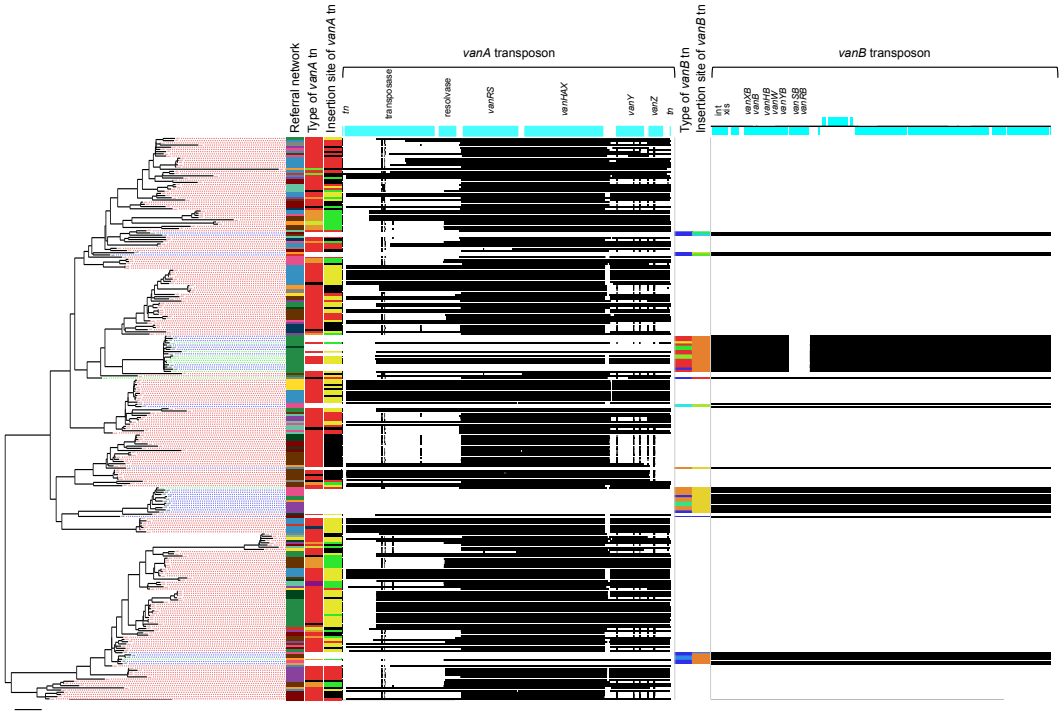
Supplemental Figure S2
Location of the *pstS* gene used in the MLST scheme (top diagram) and its homolog in the Aus0004 reference genome (02035) (bottom diagram). Genes highlighted in grey in the bottom diagram are described as being in the same operon as a phosphate binding protein (*pstS*) and together forming a complex involved in phosphate import. hyp = hypothetical protein.



Supplemental Figure S3
A) Maximum likelihood tree based on SNPs in the core genes of 73 isolates reported by Lebreton *et al*. (2013). Colored branches indicate isolates belonging to Clades A1 (pink), A2 (brown) and B (blue), as defined by Lebreton *et al*. (2013). Scale bar, ~15,400 SNPs. B) Maximum likelihood tree based on SNPs in the core genes of the 506 isolates from this study and 73 isolates reported by Lebreton *et al*. (2013), where the definition for core genes was presence in 100% of isolates. Colored ring indicates isolates from Clades A1 (pink), A2 (brown) and B (blue) as defined by Lebreton *et al.* (2013). Scale bar, ~13,400 SNPs.

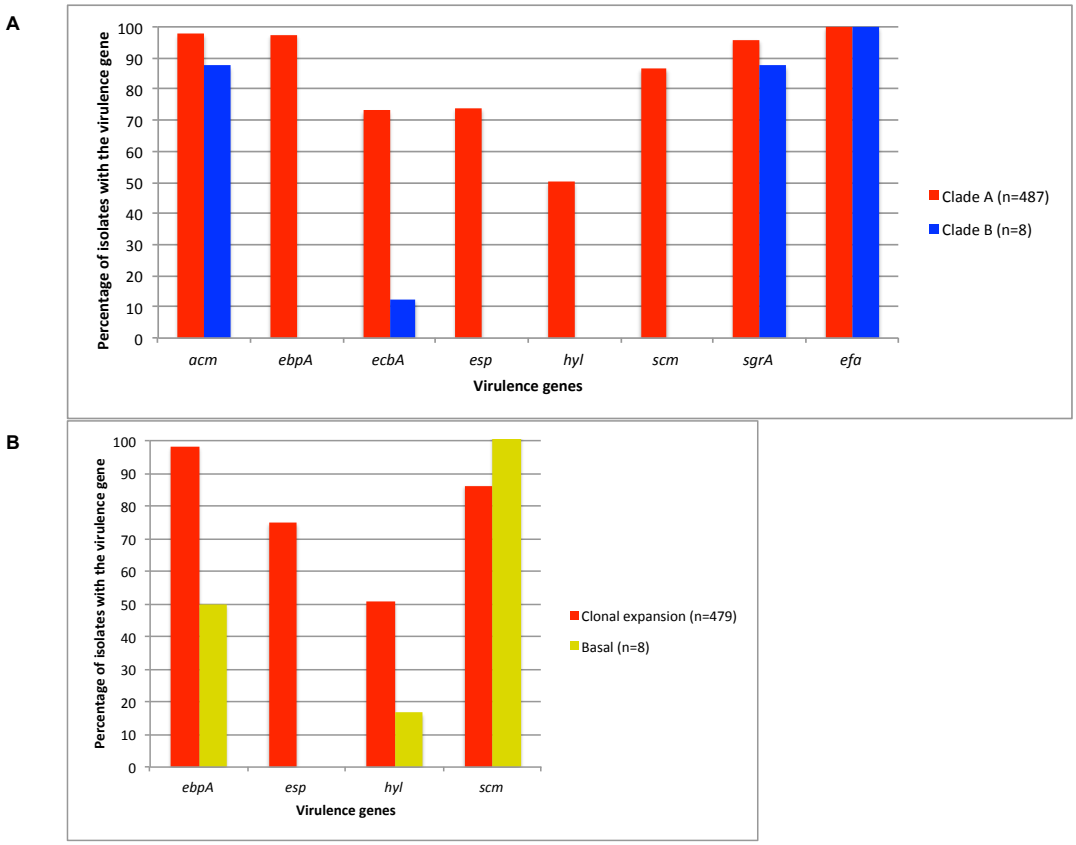


Supplemental Figure S4
Temporal distribution of *E. faecium* lineages across the UK and Ireland. Maximum likelihood tree based on SNPs in the core genome for national isolates belonging to the clonal expansion of Clade A. Colors shown in the circle represent year of isolation grading from 2001 (yellow) to 2011 (dark red). Scale bar, 90 SNPs.



Supplemental Figure S5

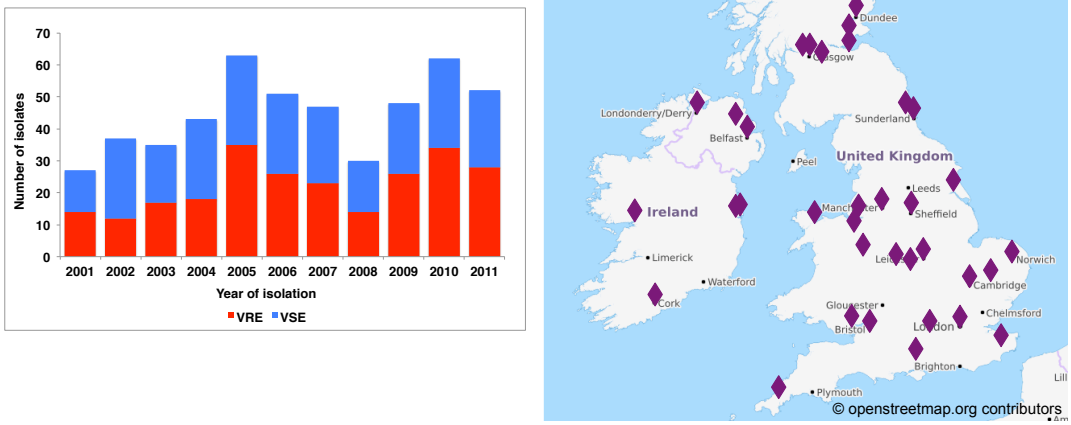
Variants of *vanA* and *vanB* transposons. Left hand side: Maximum likelihood tree of the 257 v*anA* or *vanB* positive BSAC isolates from the clonal expansion of Clade A. Right hand side: Vertical bars indicate referral networks, sequence of the *vanA* and *vanB* transposons (unique sequences = black), and the insertion site of the *vanA* (best matches to pIP816=red, pLG1=yellow, pLG1/pF856/p5753cA/pS177=green; insufficient sequence=black) and *vanB* transposons. Horizontal bars indicate genetic content (present=black, absent=white) of the *vanA* and *vanB* transposons with a map of genes (top, turquoise blocks). Scale bar, 66 SNPs.



Supplemental Figure S6

A) Prevalence of virulence factors in the clinical isolates of Clade A and Clade B.

B) Prevalence of virulence factors in the basal and clonal expansion populations of Clade A, which are absent in Clade B.



Supplemental Figure S7
Geographical and temporal distribution of the BSAC isolates.

Pangenome annotation	Number of vanB positive isolates (n=34)
D-alanine—D-lactate ligase	34
Vancomycin B-type resistance protein VanW	34
D-specific alpha-keto acid dehydrogenase	34
D-alanyl-D-alanine carboxypeptidase	34
D-alanyl-D-alanine dipeptidase	34
integrase	34
Excisionase	34
DNA-directed RNA polymerase specialized sigma subunit	34
Site-specific DNA-methyltransferase (adenine-specific)	34
Relaxase	34
Maff2 family	34
Bacterial mobilization protein (MobC) family protein PcfF	34
DnaG type DNA primase	34
TraG/TraD family protein	34
Type IV secretory pathway C VirB4 components	34
DNA topoisomerase III	34
bacteriocin	33
Helix-turn-helix domain protein	34
Helix-turn-helix domain protein	34
Helix-turn-helix domain protein	34
Protein of unknown function (DUF3801)	34
Hypothetical protein	34
Hypothetical protein	34
Hypothetical protein	34
Hypothetical protein	34
Hypothetical protein	34
Hypothetical protein	34
Hypothetical protein	34
Hypothetical protein	34

Supplemental Table S1
List of genes across the genome specific to *vanB* positive isolates in the study collection.