

Clonal spread of vancomycin resistant *E. faecium* ST80, ST117 and ST203 across Belgian hospitals

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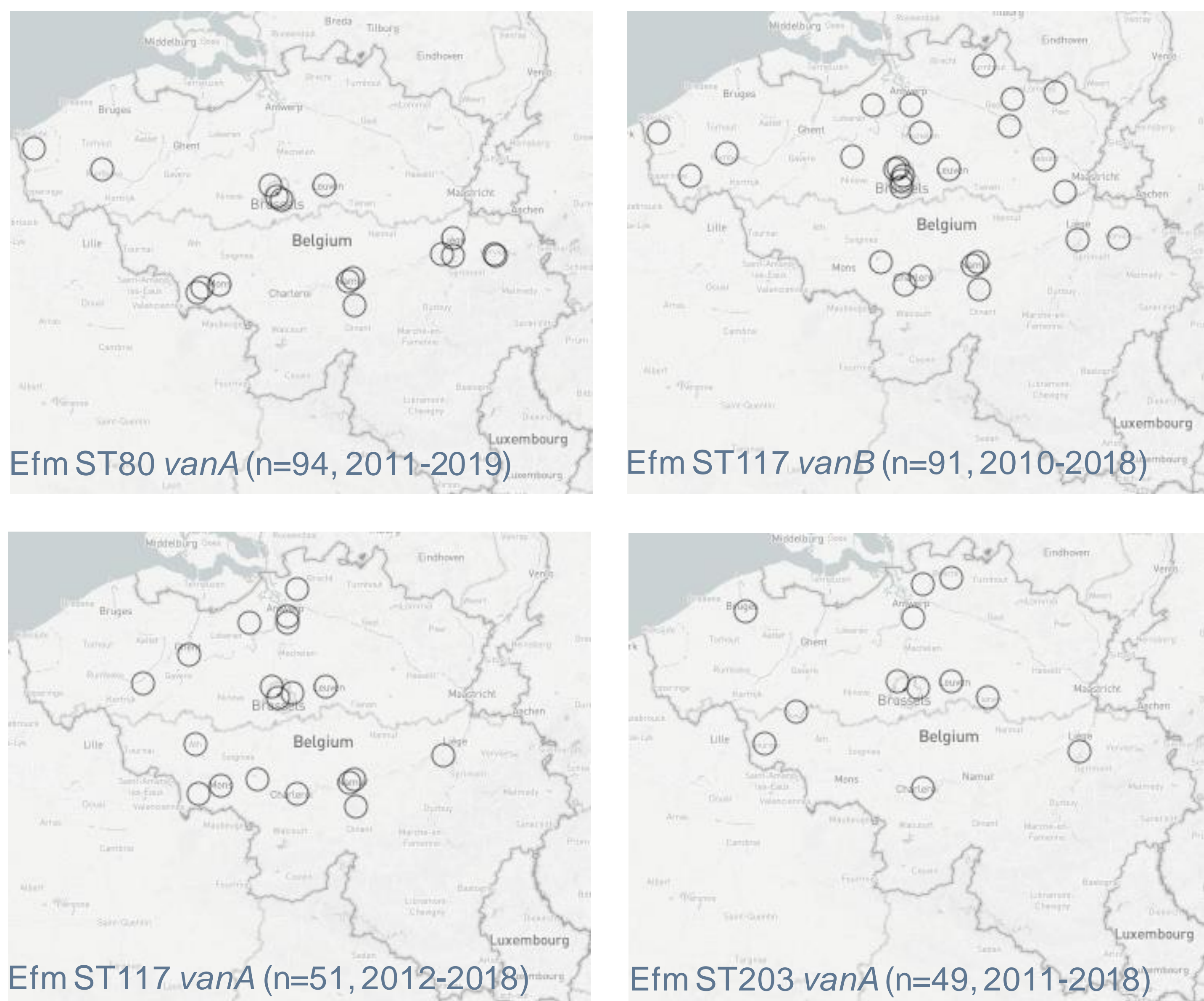
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INTRODUCTION

Since 2014, the Belgian National Reference Centre (NRC) receives an increasing number of vancomycin resistant *E. faecium* (VREfm) strains from infected or colonized patients. Many hospitals reported on outbreaks with VREfm (n=4 in 2012 to ≥ 20 in 2015-2017). The aim of this study was to investigate the molecular epidemiology of VREfm across Belgian hospitals based on whole genome sequencing (WGS).

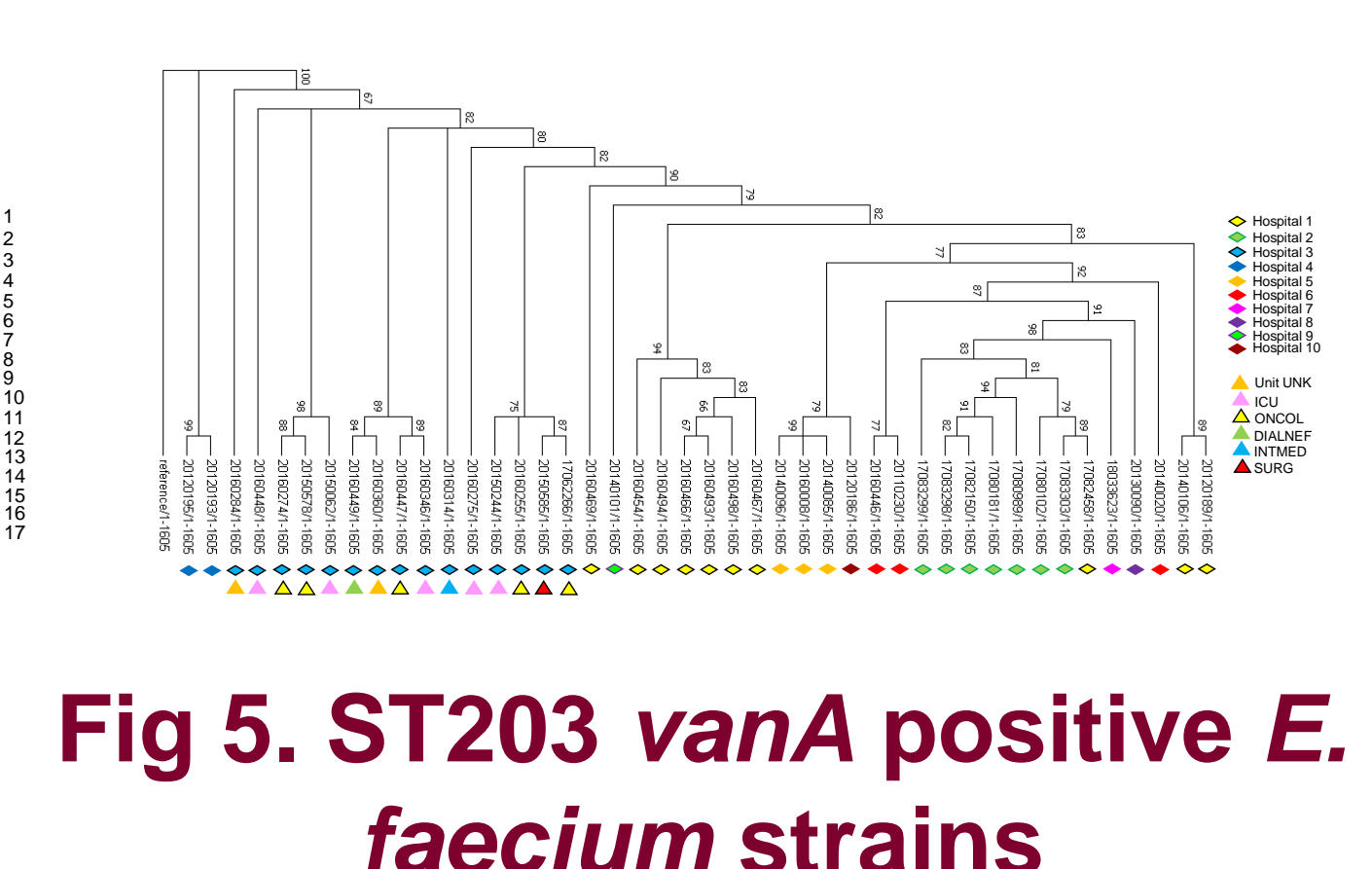
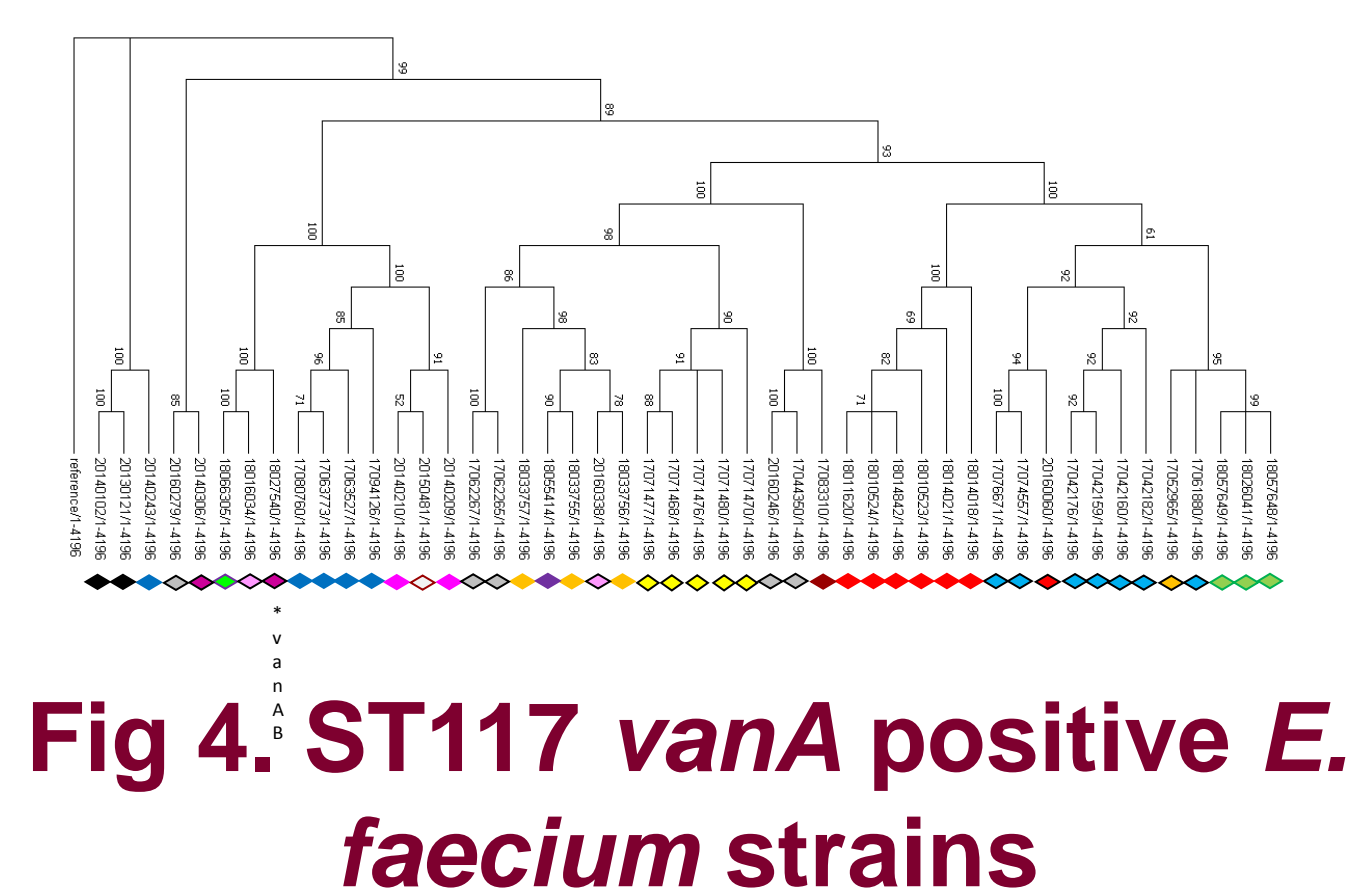
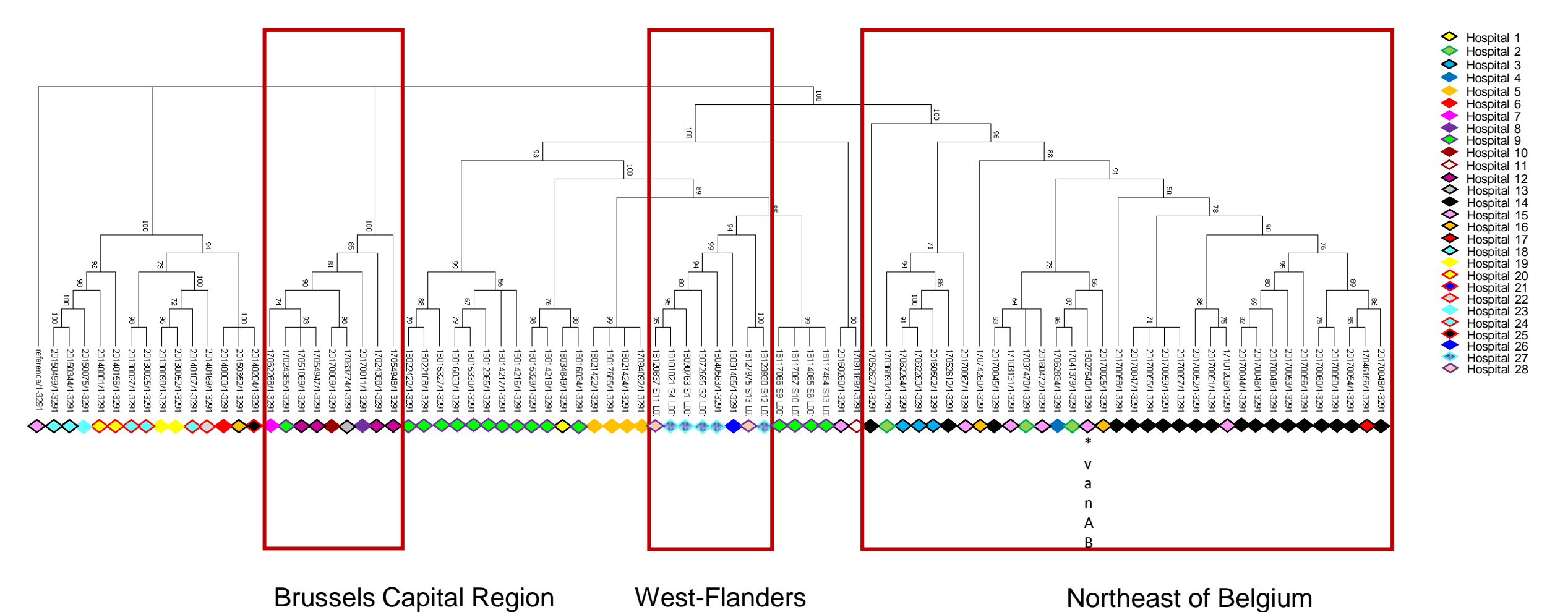
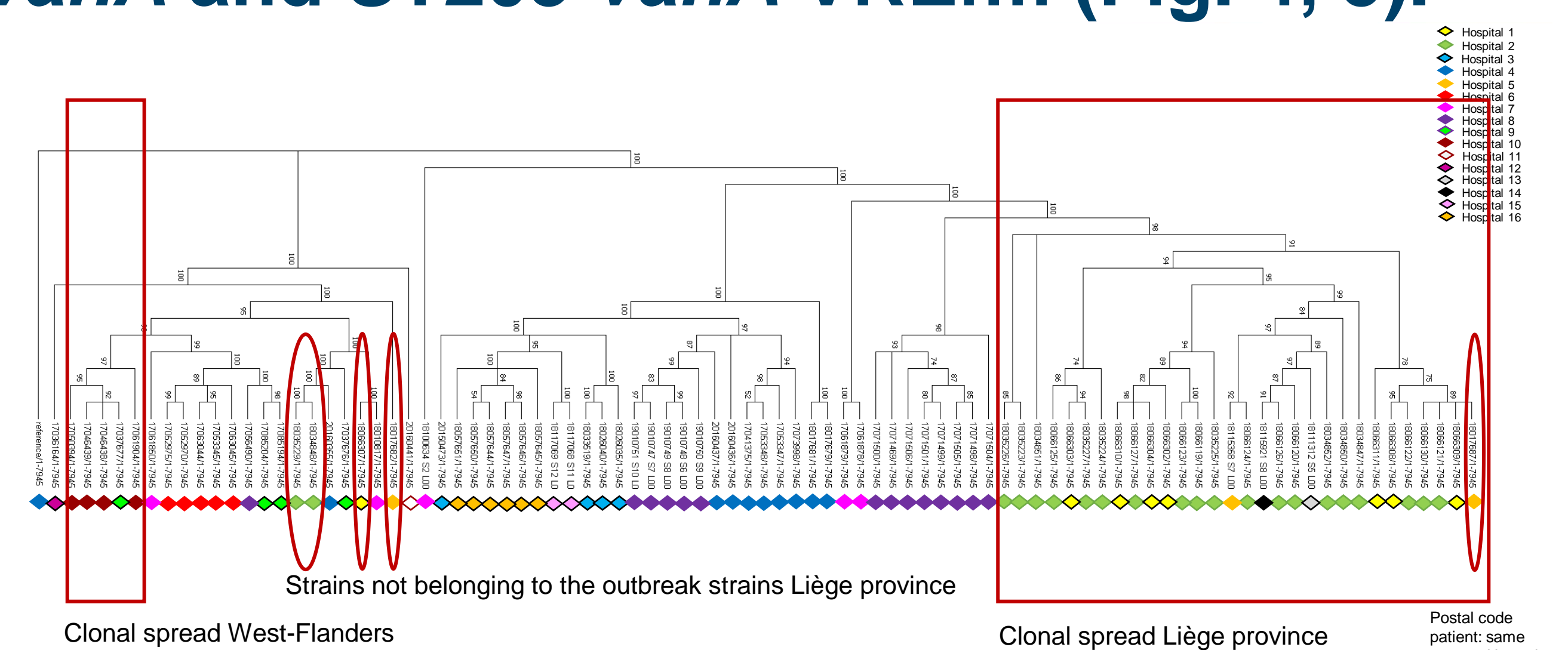
MATERIALS & METHODS

- Species identification by MaldiTof (Bruker)
- Confirmation of *vanA/vanB* by monoPCR (Depardieu et al. 2004) and duplex real-time PCR (in-house)
- Strains: 368 VREfm, (2002-2019), blood isolates and outbreak strains
- WGS:
 - MasterPure complete DNA and RNA purification kit (Epicentre)
 - Nextera XT (2x250bp paired end sequencing) and MiSeq (Illumina)
 - Bacpipe pipeline (Xavier et al., under revision),
 - Comparative genome analysis (Mauve) and CLC genomics Workbench v9,5,3 (clcbio, Denmark)
 - Core genome phylogenetic analysis by ParSNP
 - Gene by gene analysis by Chewbbacca (<https://github.com/EUMMI/chewBBACA>)
 - Microreact (<http://microreact.org>)



RESULTS

- The majority of the VREfm strains belong to ST80, ST117 and ST203.
- Clonal spread of ST80 *vanA* VREfm across several hospitals in Liège province (Fig. 2).
- Clonal spread of ST117 *vanB* VREfm across several hospitals in 3 regions (Fig. 3).
- No clear geographical clonal spread of ST117 *vanA* and ST203 *vanA* VREfm (Fig. 4, 5).



CONCLUSIONS

- Belgian *E. faecium* ST80, ST117 and ST203 isolates can be divided into distinct (sub)clusters.
- Clonal spread of *E. faecium* ST80 *vanA* over at least 5 hospitals within the Liège province.
- Clonal spread of *E. faecium* ST117 *vanB* over 3 hospitals in West-Flanders, 6 hospitals in Brussels Capital region, and 7 hospitals in the North-east of Belgium.
- Typing of *E. faecium* is critical to monitor further spread of dominant clones.
- If patients are transferred from one hospital to another, information on VRE- carriage status should be provided.