

Eshel A, Sharon I, Nagler A, et al. Origins of bloodstream infections following fecal microbiota transplantation: a strain-level analysis. *Blood Adv.* 2022;6(2):568-573.

The visual abstract and Figure 2 (page 571) included font and/or color changes that were made according to *Blood Advances'* figure rebranding standards. Due to the terms of the copyright license, the images should have been published exactly as supplied by the illustrator. Also, the following copyright line for the visual abstract and Figure 2 should have been included: "Reproduced with permission, copyright © 2022 Elvire Thouvenot." The corrected Figure 2 and its legend are shown below; panel Ai is also the visual abstract. The scientific content of the images is not affected by the changes.

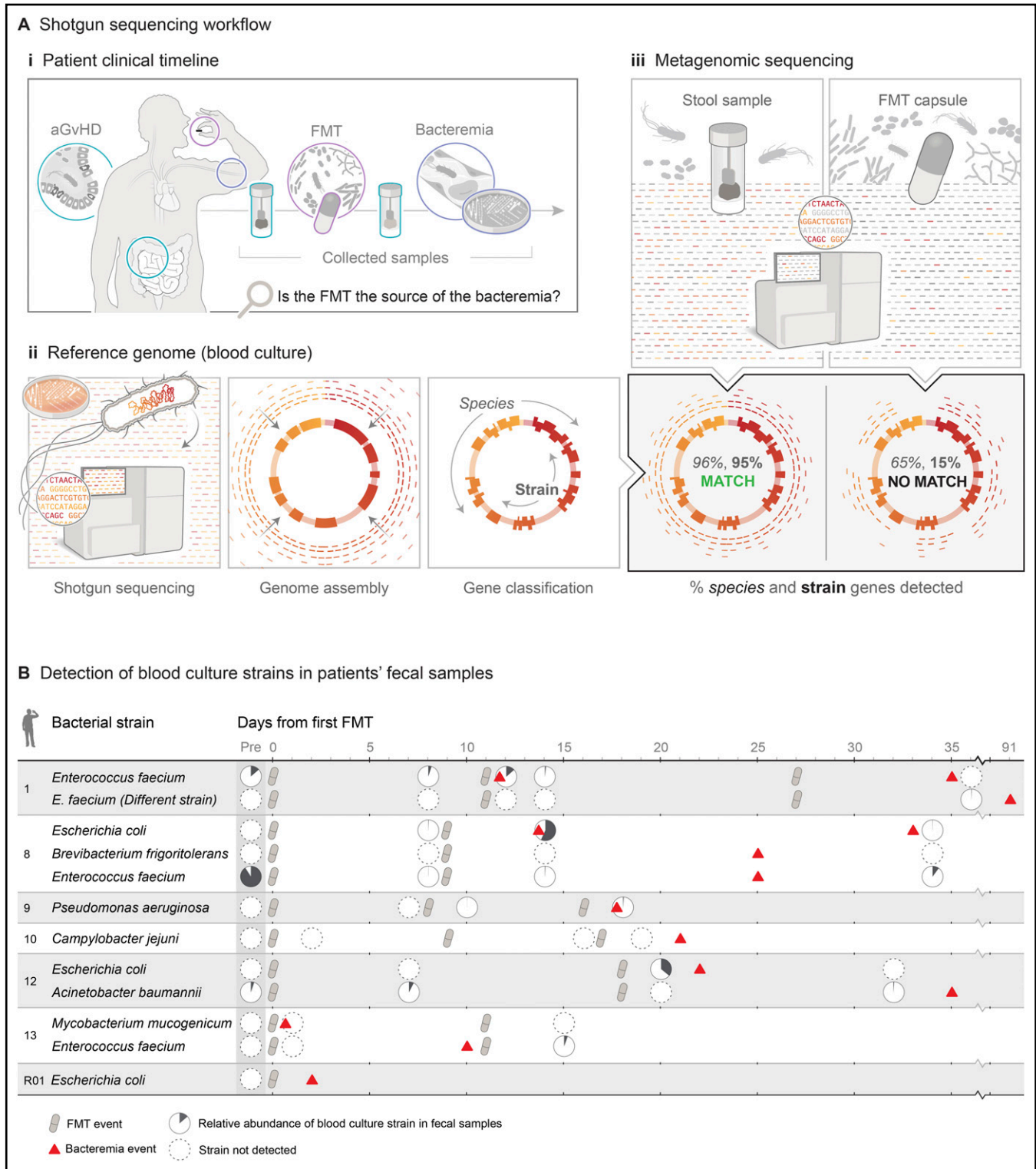


Figure 2. Tracing the source of BSI. (A) Scheme describing the BSI source detection pipeline: collection of relevant biological samples for shotgun sequencing (patient's positive blood cultures, stool samples, and donor-derived fecal microbiota transplant capsules) (i); construction of the reference genomes using sequences of the positive blood culture strains (genome assembly and gene classification into species core genes and strain gene groups) (ii); and identification of BSI strains in the metagenomic samples (searching for species and strain genes identified in the reference genome) (iii). (B) Detection of blood culture strains in fecal samples. Rows are grouped by patients and correspond with bacterial strains detected in the blood cultures. Using the metagenomic bioinformatic pipeline, we searched for BSI-causing strains within donor and recipient stool samples. Offending bacterial strains were absent from fecal microbiota transplant donor capsules. However, they could be detected in a portion of recipients' stool samples at various time points before and after the FMT and BSI event. Source data for the figure are available in the data supplement. aGVHD, acute GVHD. Reproduced with permission, copyright © 2022 Elvire Thouvenot.

The errors have been corrected in the published article.

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