SUPPLEMENTARY METHODS

**Microbiological analysis**

(1) Methicillin-resistant *Staphylococcus aureus* (MRSA)

Separate nasal, axilla and groin swabs were taken and completed within 6 weeks in all institutions as the estimated mutation rate of one core single nucleotide polymorphism is every 6 weeks. Samples were inoculated to selective chromogenic agar (Oxoid Brillance MRSA2 Agar, Thermo Fisher Scientific, Basingstoke, UK) and incubated aerobically at 35-37◦C for 18-24 hours. Growth of denim blue colonies were referred to matrix-assisted laser desorption ionization-time (MALDI-TOF) mass spectrometry and cefoxitin disc diffusion test for confirmation of microbial identity and methicillin-resistance.

(2) Vancomycin-resistant Enterococci (VRE)

A rectal swab sample was taken from each participant, and stool sample was collected from those who declined rectal swab. Samples were inoculated to ChromID VRE-selective chromogenic medium (bioMérieux, Marcy-l'Étoile, France) and incubated aerobically at 35-37°C for 48 hours. Positive cultures were referred to MALDI-TOF mass spectrometry and VITEK antimicrobial susceptibility testing (bioMérieux, Marcy-l'Étoile, France).

(3) Carbapenemase-producing Enterobacterales (CPE)

Rectal swabs or stool samples were inoculated to ChromID CARBA-selective chromogenic plate (bioMérieux, Marcy-l'Étoile, France). The colonies were confirmed by MALDI-TOF and *Enterobacteriaceae* were further tested for susceptibilities to meropenem and ertapenem using VITEK2 (bioMérieux, Marcy-l'Étoile, France). For sequencing, a single colony was inoculated into Luria-Bertani broth (Gibco) and cultured overnight at 37°C with agitation. Cells were collected by centrifugation and genomic DNA was isolated using the QIAamp DNA mini kit (Qiagen). DNA samples were quantified using a QUBIT 2.0 fluorometer (Invitrogen). Sequencing libraries were prepared with the Nextera XT Library Prep Kit (Illumina) according to the manufacturer’s instructions. The adapters were indexed using either the Nextera XT Index Kit or the Nextera XT Index Kit v2 (Illumina). Finally, 10 nM of each sample DNA sequencing library were pooled together and sequenced on a HiSeq 4000 (Illumina) with a 2×151 run. Resistance genes were called using the SRST2 program (v0.2.0) (PMID 25422674) using the ARG-ANNOT database (PMID 24145532) as provided in the SRST2 distribution. In this study, we focused on β-lactamase genes including blaIMI, blaIMP1, blaKPC1, blaMDM1, and blaOXA48.