



Figure S1. Schematic representation of the IME containing *tet(M)* in SDSE (SDSE-HUB-4529) compared with different sequences from *E. faecium*, *C. difficile*, *Clostridium innocuum*, *E. faecalis* and *Catenibacterium* sp. This figure shows that the IME structure of SDSE have 100% of identity with the same element of *E. faecium* and *C. difficile*, while the other species have an identity between 98-100% and insertions in the sequence. The shaded areas connect regions with different identity. Each arrow represents a gene. Accession numbers for each sequence are highlighted in boldface.