

Additional figures

Figure S1. PCoA based on Bray-Curtis distances of genus-level abundance profiles of the samples sequenced in the present study using Illumina HiSeq (red) and those from the study of Biagi *et al.* (2015) sequenced by Roche 454 pyrosequencing (yellow). Samples are identified by filled circles. PCoA first and second principal components are plotted.

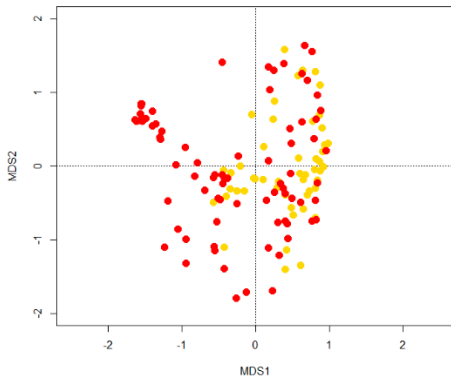


Figure S2. PCoA based on Bray-Curtis distances of genus-level abundance profiles of samples taken from patients aged <2 years (pink), 2-11 years (yellow) and >12 years (green), before HSCT (pre, A), 12-28 days after HSCT (engraftment, B) and >30 days after HSCT (post, C). Samples are identified by filled circles. PCoA first and second principal components are plotted.

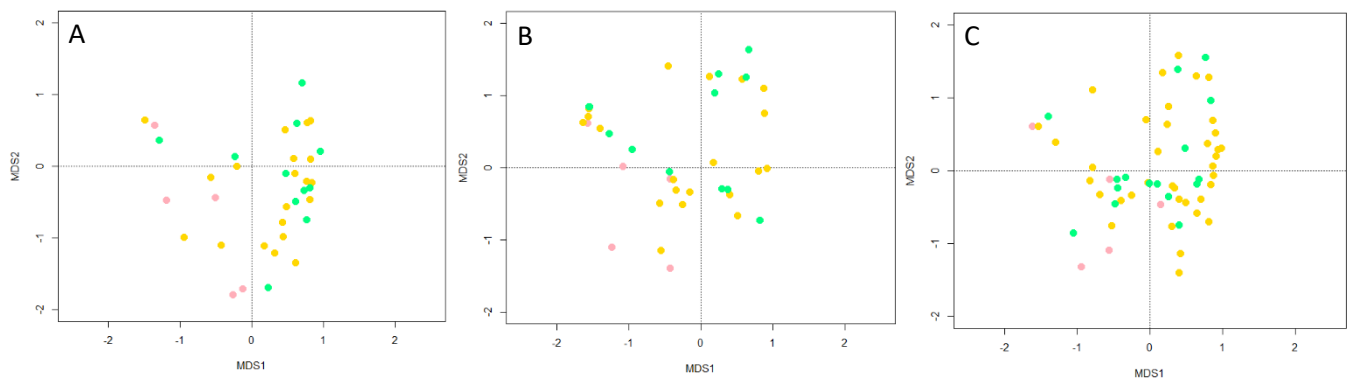


Figure S3. PCoA based on Bray-Curtis distances of genus-level abundance profiles of samples taken from patients hospitalized in the center of Bologna (light blue), Pavia (hotpink), Rome (gold), and Verona (green), before HSCT (pre, A), 12-28 days after HSCT (engraftment, B) and >30 days after HSCT (post, C). Samples are identified by filled circles. PCoA first and second principal components are plotted.

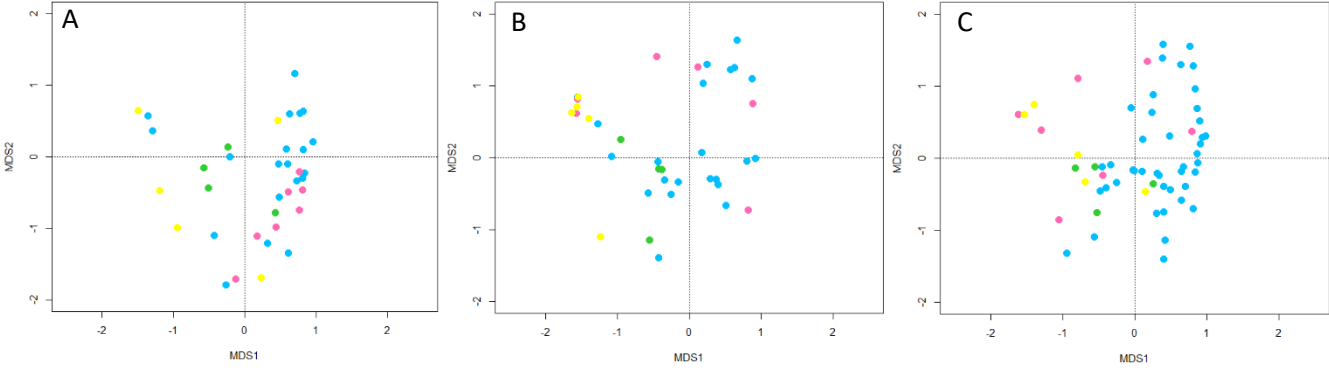


Figure S4. Box and whiskers distribution of the relative abundance (%) of OTUs assigned to the genera *Enterococcus* (A, D, G, L), *Citrobacter* (B, E, H, M) and *Erwinia* (C, F, I, N), in samples grouped as pre-transplantation (PRE, green), engraftment (ENG, orange) and post-transplantation (POST, blue), for the four enrollment centers of Bologna (A, B, C), Pavia (D, E, F), Verona (G, H, I) and Rome (L, M, N) hospitals.

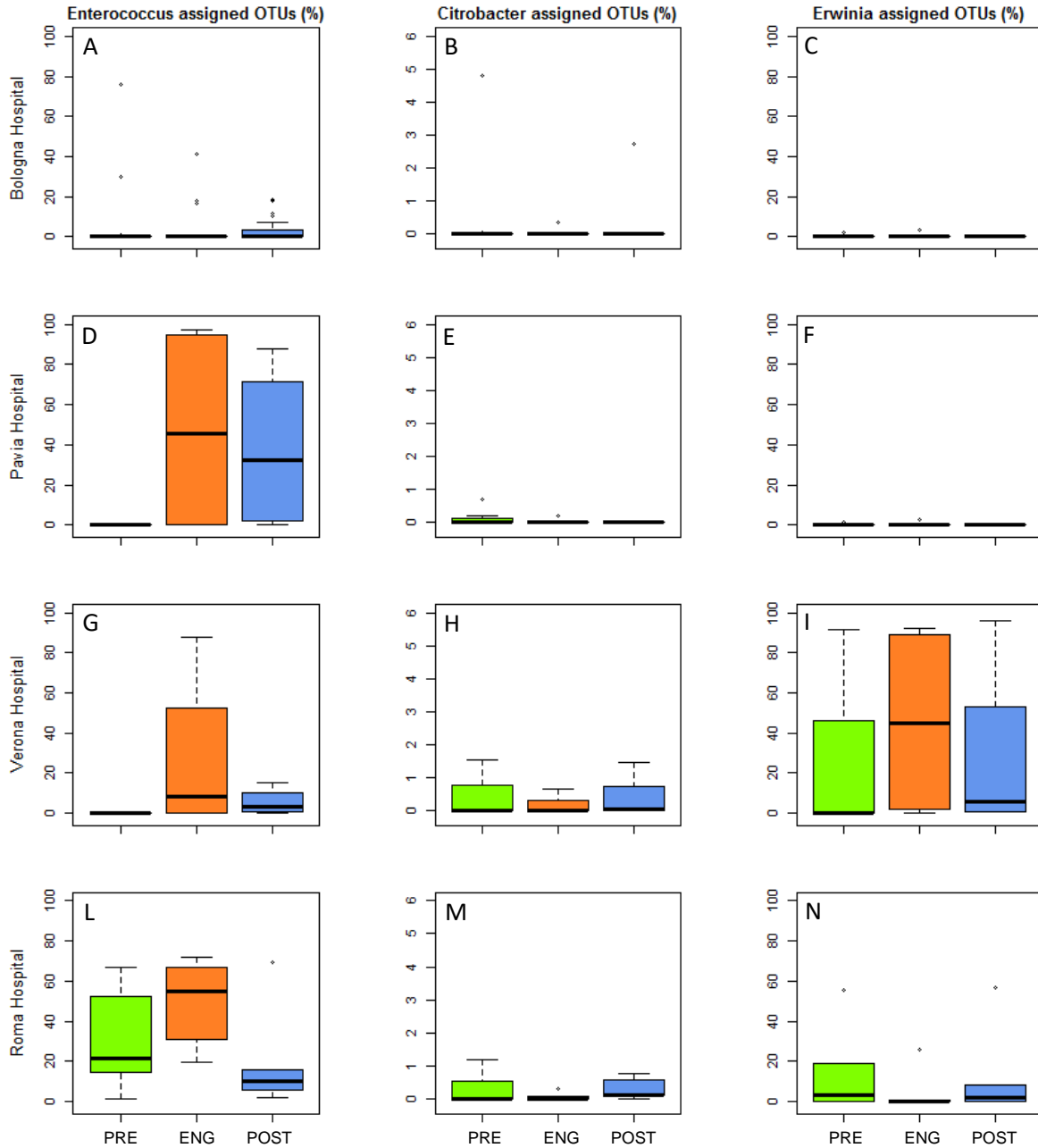


Figure S5. Box and whiskers distribution of the Simpson diversity index calculated for the genus-level microbiota profiles in samples taken before HSCT from subjects who did not develop aGvHD (green), who developed aGvHD (I-II grade) at a skin level (gold), and who developed gastrointestinal aGvHD (II-IV grade) (dark red).

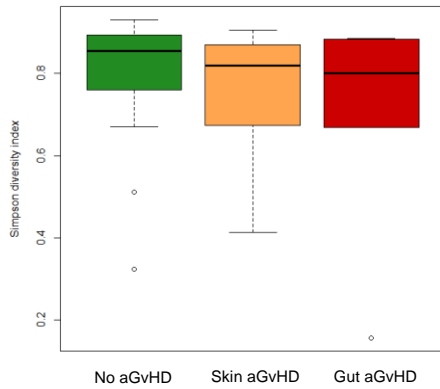


Figure S6. Box and whiskers distribution of the Bray-Curtis distances calculated using the genus-level gut microbiota profiles of samples taken before HSCT from subjects who did not develop aGvHD (green), who developed aGvHD (I-II grade) at a skin level (gold), and who developed gastrointestinal aGvHD (II-IV grade) (dark red).

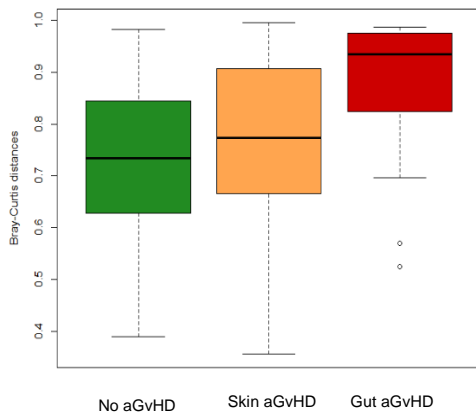


Figure S7. PCoA based on Bray-Curtis distances of genus-level abundance profiles of samples taken >30 days after HSCT from patients who did not develop aGvHD (green), who developed aGvHD (I-II grade) at a skin level (gold), and who developed gastrointestinal aGvHD (II-IV grade) (dark red). Samples are identified by filled circles. First and second principal components (MDS1 and MDS2) are plotted, accounting for 18.4 and 8.9% of variance in the dataset, respectively.

