



Supplementary Fig. 1. Bacterial Sequencing and processing. (A) Around 33.91 Gbases sequences were generated by Illumina NextSeq using 2×150 paired-end reads. (B) Each sample yielded a median of 1.9 Gbases. Sequenced were trimmed and stitched reads mapped to the human genome were removed (42.12%, 0.05%). After quality control, the median number of quality-filtered reads per samples was 10,164,901.