Supplementary Materials:



**Supplementary Figure 1.** Heatmap of relative abundance of different genus in the three metagenomes sequenced. Community profile was done with Metaphlan4 and the 40 most abundant genus are shown.



**Supplementary Figure 2.** Normalized gene count of MRGs and ARGs in total assemblies and plasmidic contigs. Gene count was normalized using 16S rRNA count for each metagenomic assembly.



**Supplementary Figure 3.** Transconjugants colonies obtained from 1 of the exogenous plasmids capture assays with BCAA sample. Three colonies with fluorescent phenotype are observed, culture media was supplemented with kanamycin (50 μg/mL) (Km), nalidixic acid (25 μg/mL) (Nal), cycloheximide (10 μg/mL) (Ch) and tetracycline (Tc) (10 μg/mL).