Figure S2. Detection of ARGs in the two BEAT study subgroups.

A. Prevalence of positive ARG signals in each sample taken at stable (S), exacerbation (E) and recovery (R) stages. Red symbols show ARGs detected per subject (median ± interquartile range) . green and blue symbols show the geometric mean with standard deviation respectively for 16SrDNA and γP:F ratio

B. Proportion of detected positive signals related to antibiotic classes affected. Numbers at column heads denote total number of positive signals

C. Heatmap showing prevalence and abundance of top 90 percent ARGs with positive signals in the main ARGs families in two BEAT study subgroups including High Gammaproteobacteria (HG) and High Firmicutes (HF). Rows represent individual ARGs and columns show individual samples. Name of individual genes are available in the supplimentray (Table S2).

FCA, fluroquinolone, quinolone, florfenicol, chloramphenicol, and amphenicol resistance genes; MLSB, Macrolide-Lincosamide-Streptogramin B resistance