Human body is a breeding ground for antimicrobial resistance genes, shows new study

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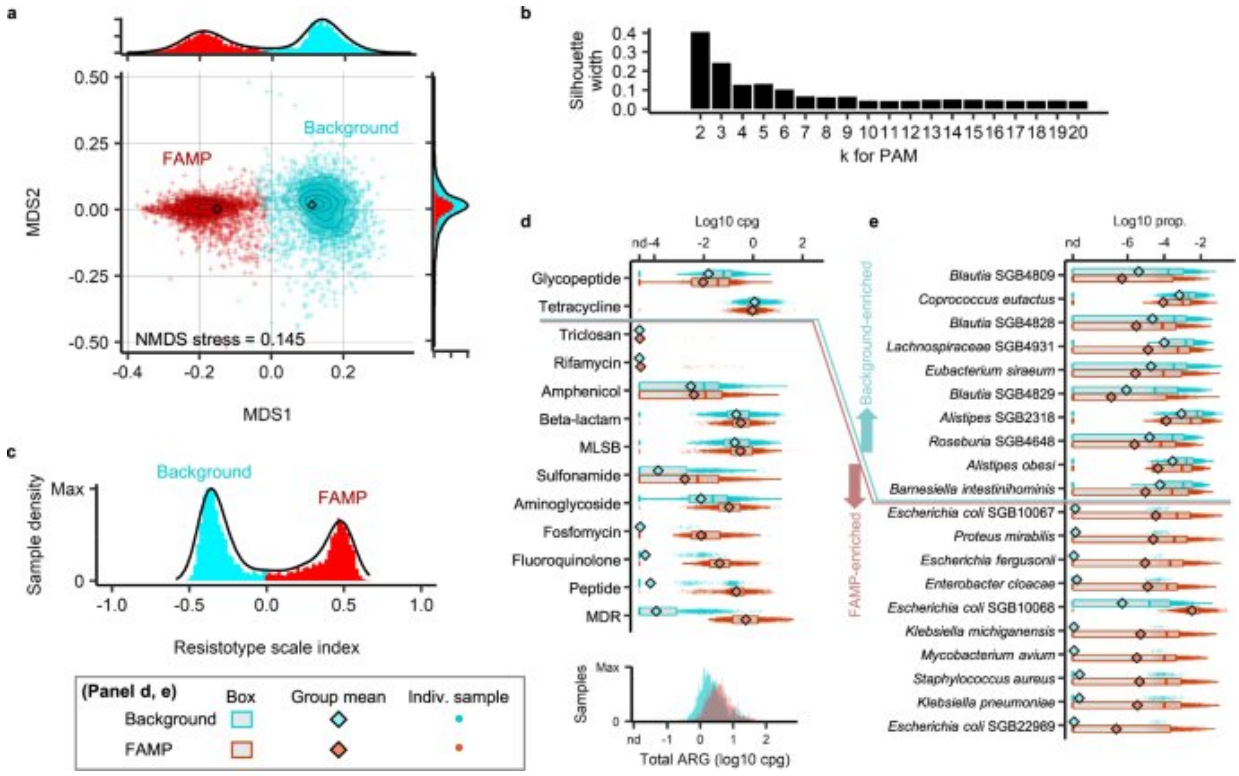

Two distinct clusters apparent in the global landscape of adult gut resistome profiles. a NMDS projection of Bray–Curtis dissimilarities among the log-transformed ARG family profiles (cpg) in adult gut metagenomes (contours estimate sample densities). Samples were colored by cluster assignment (PAM, Bray-Curtis clustering, k=2). b Average silhouette width of PAM Bray-Curtis clusters as a function of cluster number k. c Sample density projecting points onto the line joining cluster medoids using Bray–Curtis dissimilarities. d Box plots of the summed abundance of ARGs in each antibiotic class, separated by

resistotype (`background' or `FAMP') with the distribution of total ARGs (cpg) by resistotype shown at the bottom. e Relative abundances of the ten species with highest mean fold difference between resistotypes and two-sided Mann–Whitney test, Benjamini–Hochberg-adjusted p

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