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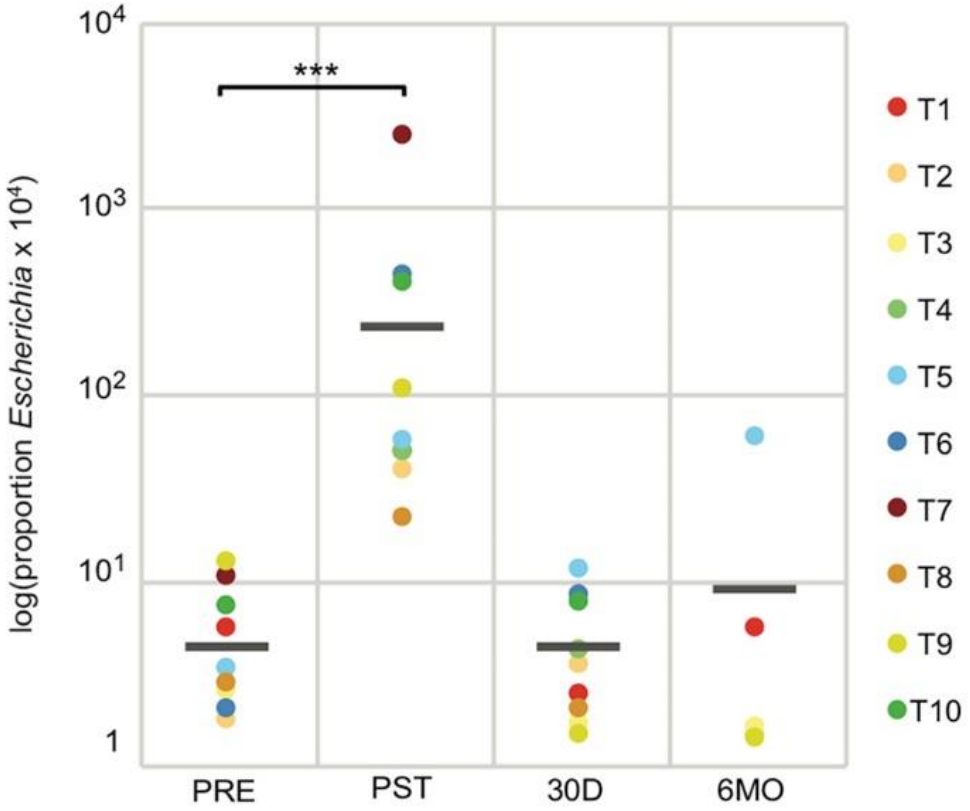
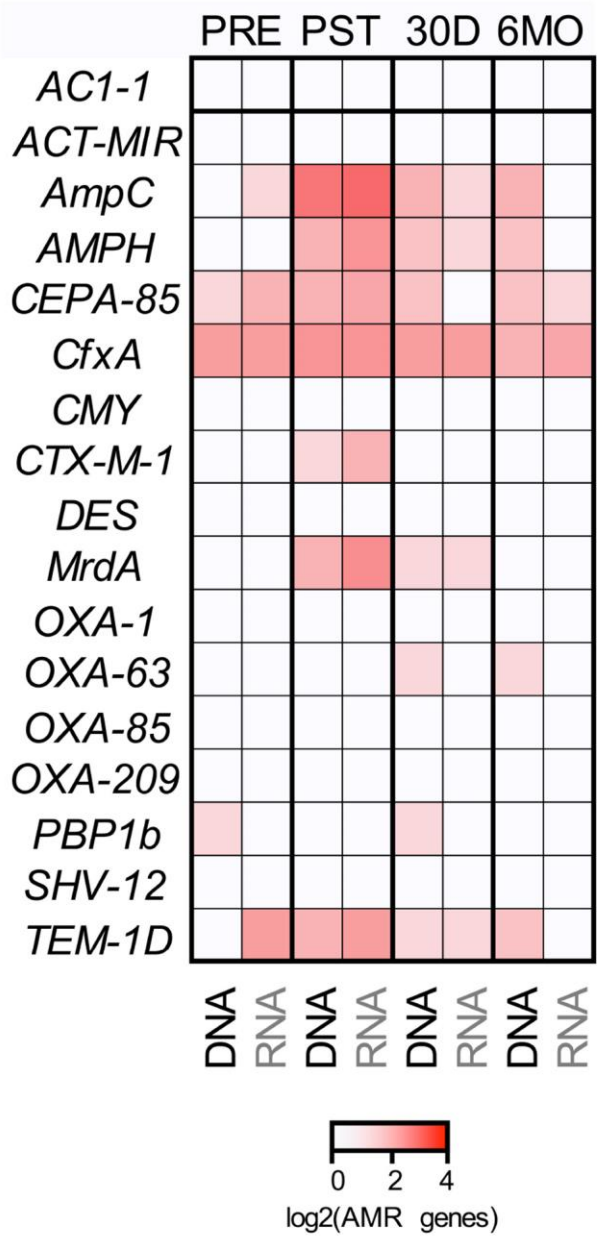
Microbiome and Antimicrobial Resistance Gene Dynamics in International Travelers

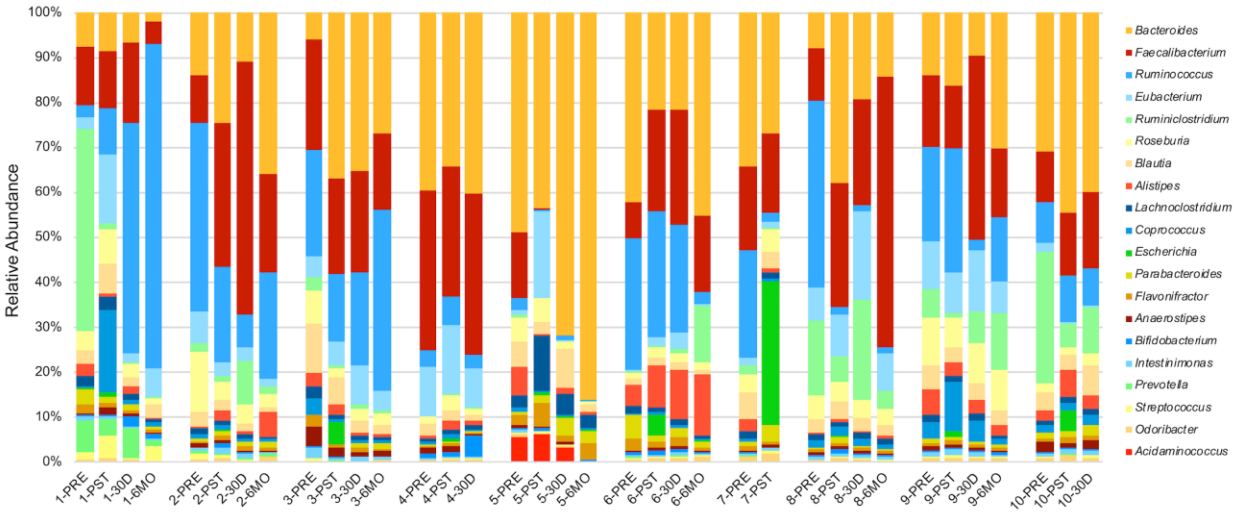
Appendix



Appendix Figure 1. Assessment of relative abundance of *Escherichia* over time, pre- and post-travel, revealed an increase ($p<0.001$ by Wilcoxon Rank Sum) post-travel.



Appendix Figure 2. Relative proportion of the 20 most abundant microbial genera present in the enteric microbiomes of international travelers, assessed longitudinally using shotgun metagenomic DNA sequencing. Participants submitted samples pre-travel (PRE, within 1 week before departure), post-travel (PST, within 1 week after return), 30 days post-travel (30D), and 6 months post-travel (6MO).



Appendix Figure 3**.** Beta-lactamase genes identified in the gut microbiomes of travelers over time, pre- and post-travel. Gradient shading corresponds to gene abundance (average allele sequencing depth per million reads mapped, AdpM).