

Supplementary information

Richer gut microbiota with distinct metabolic profile in HIV infected Elite Controllers

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Supplementary Table 1. Metadata of study subjects

	EC (n=16)	Naive (n=32)	Negative (n=16)
Antibiotics¹	2	6	2
Probiotics	1	2	1
Special diet²	2	0	1
Smoking	6	8	2
Diabetes	1	2	1
Other medication	11	9	4
Travelled abroad³	5	NA	1

¹Within 3 months from inclusion

²Lactose, gluten free, vegan, vegetarian (EC: one lactose/gluten free diet, one vegetarian. Negative: one lactose/gluten free diet)

³More than 4 weeks during the last 12 months before inclusion

NA – not available

Figure S1

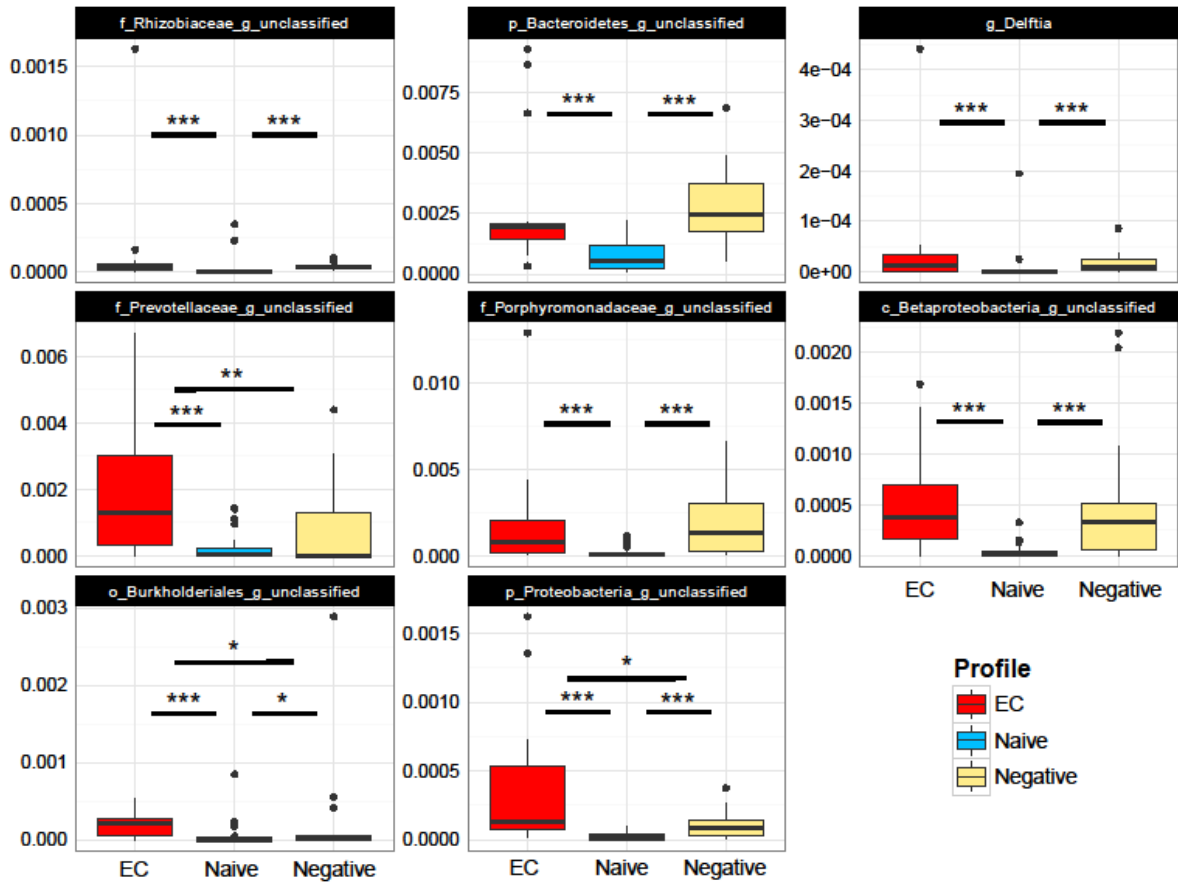
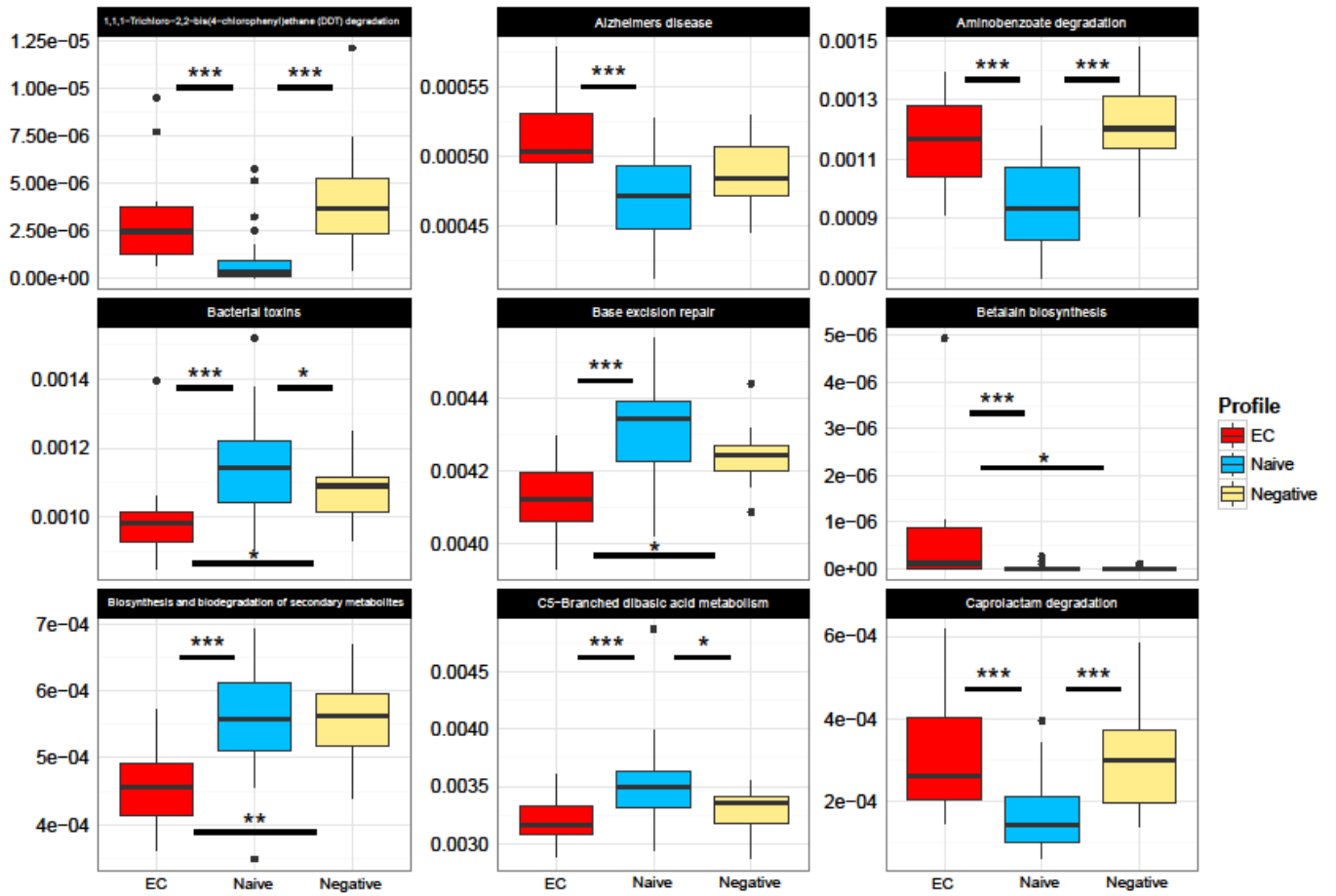
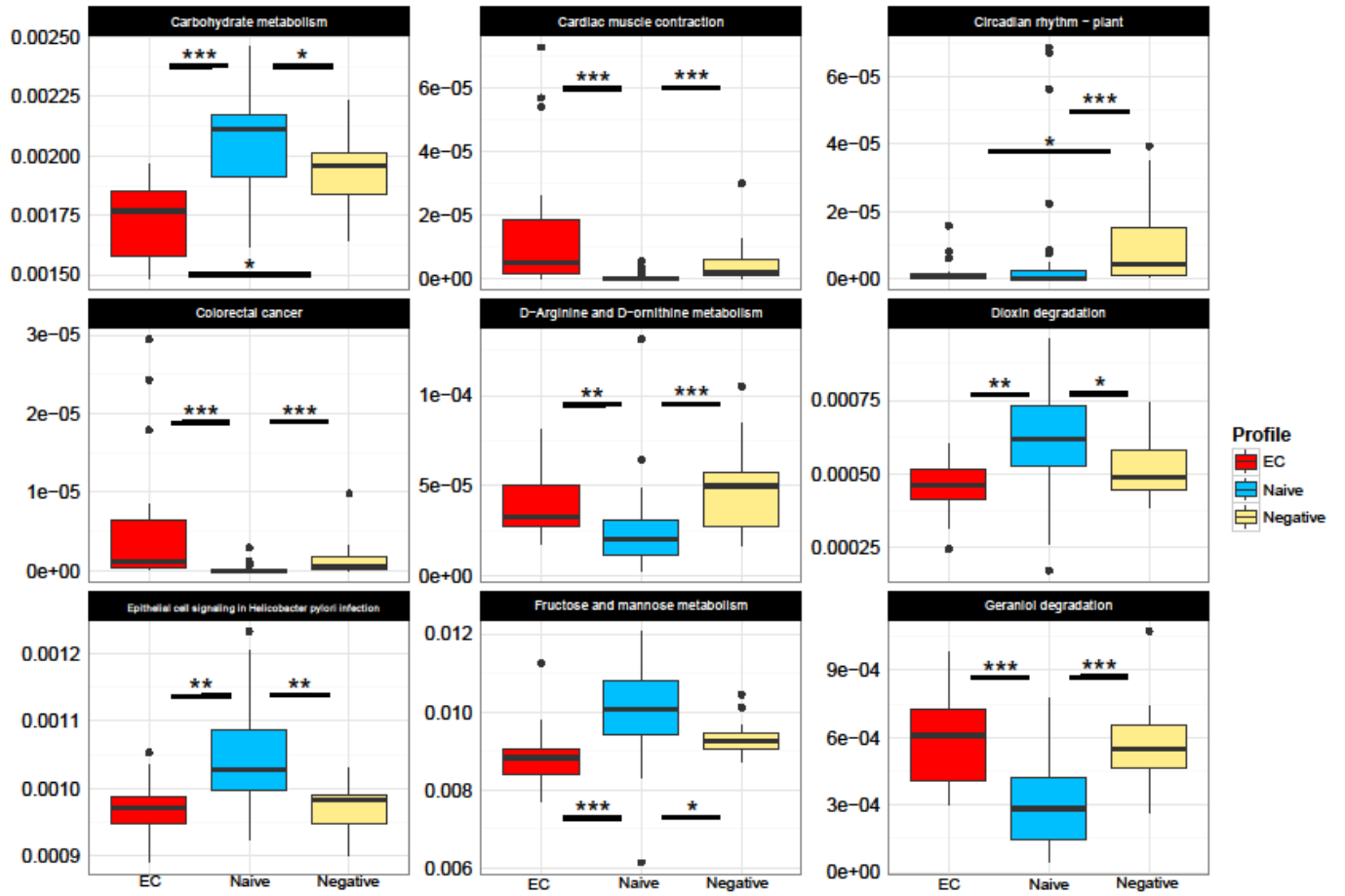
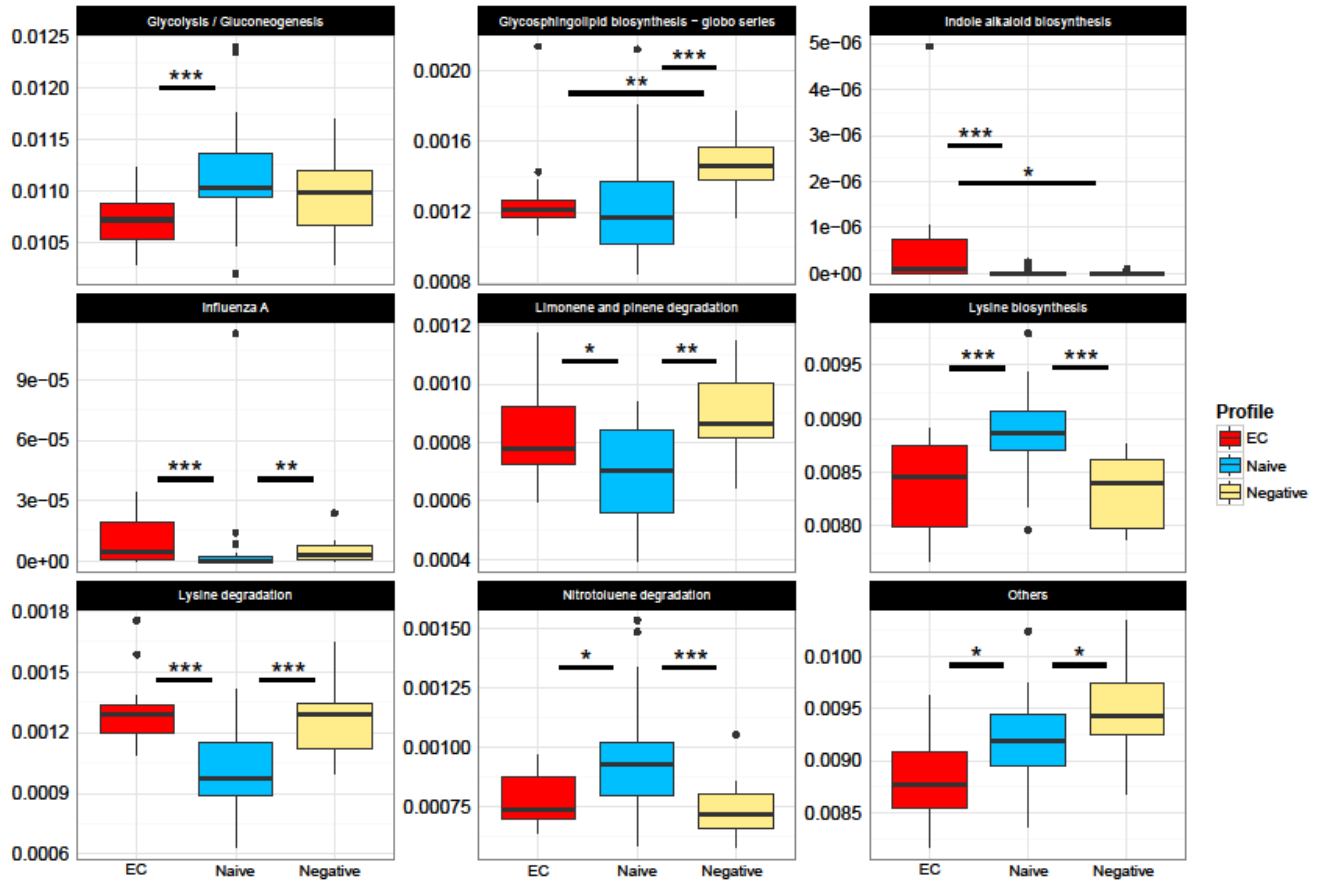


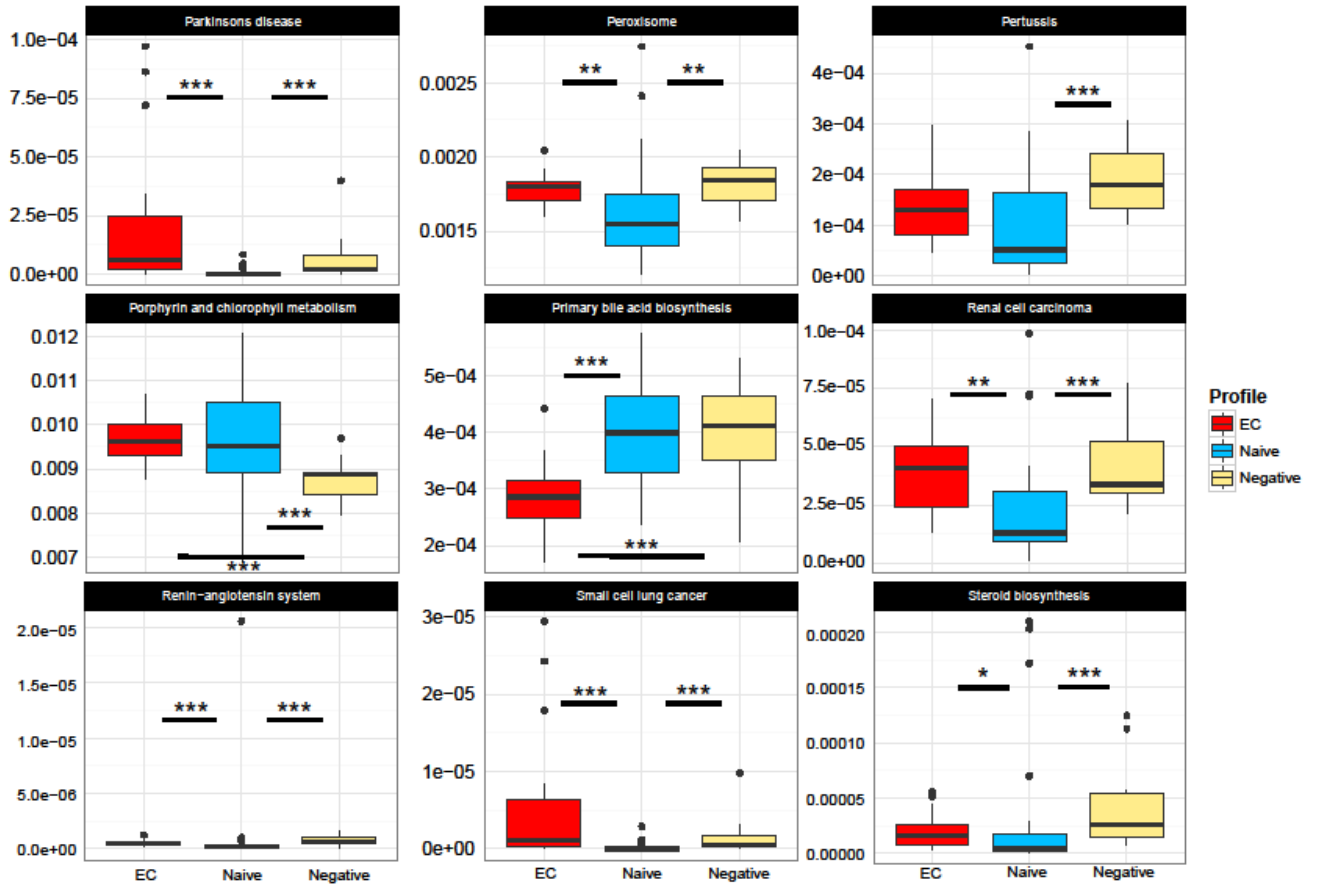
Figure S1. Significant differences in composition of fecal microbiota between EC, naive and negative. The abundance of bacterial taxa at genus level. Differences in taxa abundances were analyzed via Kruskal-Wallis ranked based test and Benjamini-Hochberg was used for correction of multiple testing. Adjusted p-value < 0.01 was considered significant for Kruskal-Wallis. Dunn's post-hoc pairwise analyses: *p<0.05, **p<0.01, ***p<0.001. Box plots represent median (black horizontal line), 25th and 75th quartiles (edge of boxes), upper and lower extremes (whiskers). Outliers are represented by a single data point.

Figure S2









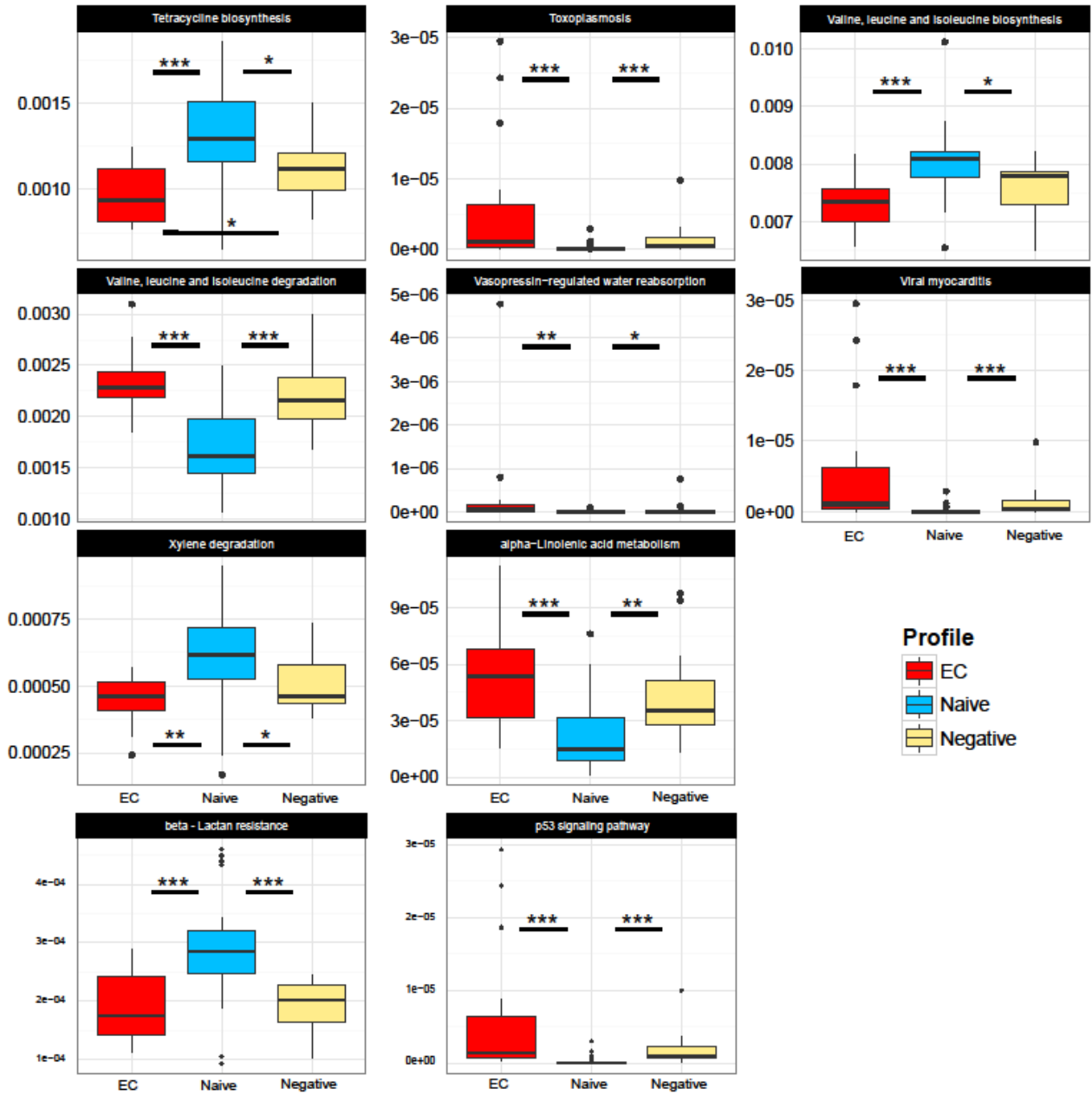


Figure S2. Predicted functional content of gut microbiota reveal significant differences between EC and naive/controls. Microbiome function was inferred using PICRUSt analysis. Differences in predicted gut microbiota functionality are shown in (a) and (b). Kruskal – Wallis rank-based test was applied, and Benjamini – Hochberg correction was used to correct for multiple testing. Adjusted p-value < 0.01 was considered significant for Kruskal-Wallis. Dunn`s post-hoc pairwise analyses: *p<0.05, **p<0.01, ***p<0.001. Box plots represent median (black horizontal line), 25th and 75th quartiles (edge of boxes), upper and lower extremes (whiskers). Outliers are represented by a single data point.

