

Description of supplementary files

Supplementary Data 1. Sample metadata, relative abundance, and taxonomy at the ASV level. Source data for chi-squared test in Figure 1, alpha-diversity findings in Figures 2A, 2B, and Supplementary Figure 2, and ASV vanishment analysis in Figure 3B and Supplementary Figure 1.

Supplementary Data 2. Sample metadata, relative abundance, and taxonomy at the Genus level. Source data for PCoA plot in Figure 2, microbial relative abundance plot in Figure 3A, and differential abundance analysis in Figure 4 and Supplementary Figures 3 and 4.

Supplementary Data 3. Vanishment analysis results of microbial ASVs in -STH and +STH groups at baseline. This table contains presence and absence counts of microbial ASVs across the dataset, as well as their taxonomic annotation, odds ratios, and corresponding p-values.

Supplementary Data 4. Results of statistical analysis conducted using ALDEx2. This table contains p-values and BH-adjusted p-values for Wilcoxon (wi) paired tests performed based on genus-agglomerated data for comparisons between: **A)** all subjects that were sampled at the follow-up timepoint (sheet 'All'); **B)** subjects with no helminth eggs at baseline (-STH) (sheet 'STH_negative'), **C)** subjects with at least one detected egg of *Ascaris*, *Trichuris* or hookworm (+STH) (sheet 'STH_positive').

Supplementary Data 5. Results of statistical analysis conducted using ALDEx2 with covariates. This table contains p-values and BH-adjusted p-values for Wilcoxon (wi) paired tests performed based on genus-agglomerated data adjusted for egg presence of *Ascaris*, *Trichuris*, and hookworm as covariates. The comparison was performed between all subjects that participated in the follow-up study (sheet 'All').