

## Description of Additional Supplementary Files

**File Name:** Supplementary Data 1

**Description:** Summary statistics of the subjectspecific metagenome assemblies.

**File Name:** Supplementary Data 2

**Description:** Summary statistics of the high- and medium-quality MAGs.

**File Name:** Supplementary Data 3

**Description:** TEDDY microbiome species and representative MAGs.

**File Name:** Supplementary Data 4

**Description:** Longitudinal development of human gut microbiota.

**File Name:** Supplementary Data 5

**Description:** Core protein families in the TEDDY microbiomes.

**File Name:** Supplementary Data 6

**Description:** Enrichment analysis for core protein families. Enricher method in clusterProfiler (two-sided), Benjamini-Hochberg adjusted.

**File Name:** Supplementary Data 7

**Description:** Longitudinal development of protein families with KEGG KO annotation.

**File Name:** Supplementary Data 8

**Description:** Core protein families with significant association with seroconversion. Generalized linear mixed modeling (two-sided), Benjamini-Hochberg adjusted.

**File Name:** Supplementary Data 9

**Description:** MAGs with significant association with seroconversion. Fisher's exact test (one-sided), Benjamini-Hochberg adjusted.

**File Name:** Supplementary Data 10

**Description:** Summary of the Seroconversion MAGs in species levels.

**File Name:** Supplementary Data 11

**Description:** GLMM statistics analysis using species abundance in each taxonomy group to test the association with seroconversion. Generalized linear mixed modeling was used (two-sided), without adjustment.

**File Name:** Supplementary Data 12

**Description:** Genomics analysis of LPS biosynthesis pathways comparing between IA-associated Bacteroides MAGs and non-IA-associated Bacteroides MAGs. Wilcoxon test (two-sided) for enrichment analysis and phylogenetic linear modeling (two-sided) for phylogenetic regression analysis, Benjamini-Hochberg adjusted.