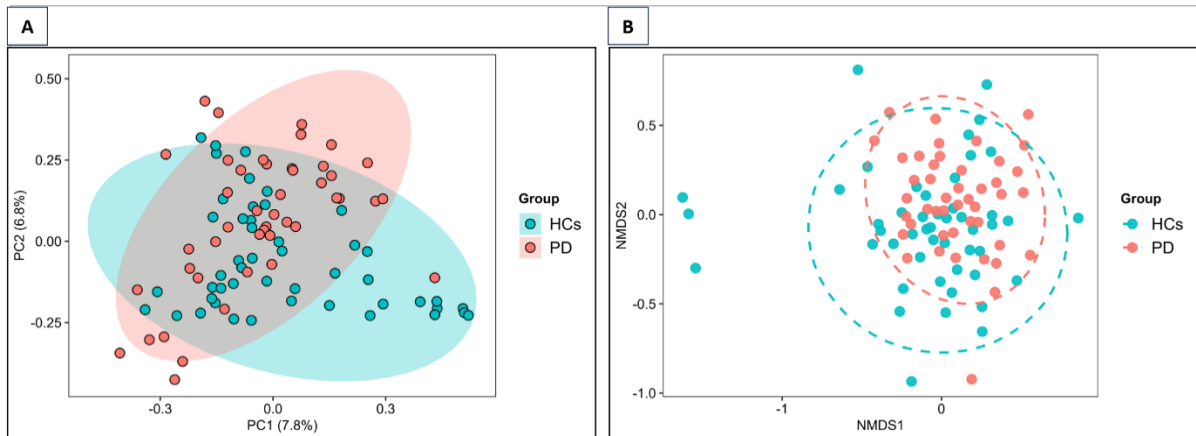
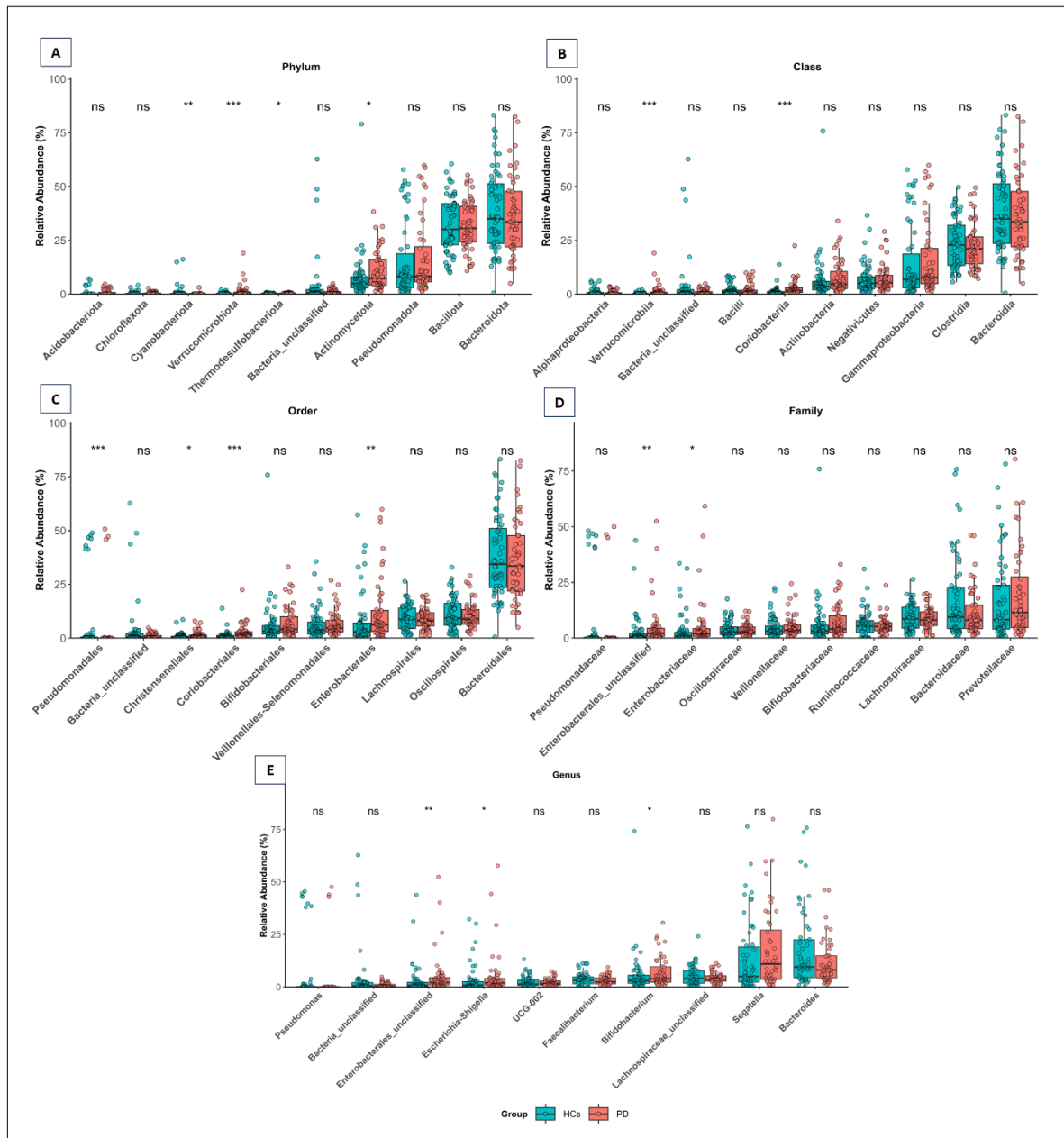


Supplementary Information



Supplementary Figure 1: Beta diversity comparison of gut microbiota between PD and HCs using (A) Principal Component Analysis (PCA) and (B) Non-metric Multidimensional Scaling (NMDS) based on Hellinger-transformed genus-level relative abundance data, illustrating differences in microbial community composition between the two groups.



Supplementary Figure 2: Relative abundance of the top 10 taxa across all taxonomic levels: (A) Phylum, (B) Class, (C) Order, (D) Family, and (E) Genus in PD and HCs. Box plots represent relative abundance distributions, and statistical significance between groups is indicated (ns, not significant; $p < 0.05$ (*), $p < 0.01$ (**), $p < 0.001$ (***)).

Supplementary Data 1

Title 1: Diversity indices for bacterial communities in PD patients and healthy controls.

Legend: This file contains the alpha diversity indices (Chao1, ACE, Shannon, Simpson, Inverse Simpson, and Fisher) calculated from 16S rRNA gene amplicon sequencing data for all study samples. Diversity metrics were used to assess bacterial richness and diversity between Parkinson's disease patients and healthy controls.

Title 2: Statistical analysis of bacterial diversity between PD patients and healthy controls.

Legend: This file contains the statistical results for comparisons of alpha diversity indices (Chao1, ACE, Shannon, Simpson, Inverse Simpson, and Fisher) between PD patients and HCs. Statistical analyses were performed using 16S rRNA gene amplicon sequencing-derived diversity measures.

Supplementary Data 2

Title: Relative abundance of Firmicutes (Bacillota), Bacteroidota, and Proteobacteria (Pseudomonadota), and corresponding Firmicutes/Bacteroidota (F/B), Proteobacteria/Bacteroidota (P/B) and Firmicutes/Proteobacteria (F/P) ratios in PD and HCs.

Legend: This file contains the relative abundances of the major bacterial phyla (Firmicutes (Bacillota), Bacteroidota, and Proteobacteria (Pseudomonadota)) in PD and HCs. The corresponding Firmicutes/Bacteroidota (F/B), Proteobacteria/Bacteroidota (P/B), and Firmicutes/Proteobacteria (F/P) ratios were calculated to compare microbial community composition between the two groups.

Supplementary Data 3

Title: Differentially abundant microbial taxa identified by LEfSe analysis between PD and HCs.

Legend: This file contains microbial taxa identified as significantly differentially abundant between PD and HCs using LEfSe analysis. Taxonomic assignment, enriched group, LDA scores, P values, and adjusted P values are provided.

Supplementary Data 4

Title: Differentially abundant metabolic pathways identified by STAMP analysis between PD and HCs.

Legend: This file contains the significantly altered predicted metabolic pathways identified between PD and HCs using STAMP. Pathway abundances, group means, standard deviations, effect sizes, confidence intervals, and corresponding P values are provided.

Supplementary Data 5

Title: Significant correlations between microbial OTUs and KEGG metabolic pathways identified by SparCC-based network analysis in PD and HCs.

Legend: This file contains significant correlations between microbial OTUs and predicted KEGG metabolic pathways identified using SparCC-based network analysis in PD and HCs. Correlation coefficients, P values, source and target pathways, and corresponding microbial taxa are provided.