**Supplementary information for pathway-centric remodeling of the gut microbiome in constipated Parkinson’s disease: PD-only metagenomic analysis**

**Overview**

All supplementary materials are provided as readable files in the repository. “Supplementary Tables S1–S6” correspond to the items cited in the main manuscript. Additional source files and logs are supplied as supplementary data files to help with reproduction.

**Supplementary tables**

Supplementary Table S1: S1\_alpha\_diversity\_stats.csv

Per-sample α-diversity metrics (Shannon, Gini–Simpson, observed richness), group labels, and Wilcoxon test outputs; source data for Fig. 1.

Supplementary Table S2: S2\_full\_taxa\_differentials.csv

Complete CLR + limma results for *n* = 230 taxa (covariate-adjusted): logFC (case - control), SE, moderated *t*, *P*, *q* (BH FDR), and diagnostics; source data for Fig. 3 and Table 2.

Supplementary Table S3: S3\_full\_pathways\_differentials.csv

Complete voom–limma results for *n* = 510 HUMAnN pathways (covariate-adjusted): log2FC (case - control), SE, moderated *t*, *P*, *q* (BH FDR), and diagnostics; source data for Fig. 4 and Table 3.

Supplementary Table S4: S4\_permanova\_summary.csv and S4\_permdisp\_tests.txt

PERMANOVA summaries (Bray–Curtis and Aitchison; by terms: partial *R*², *F*, *P*, *q*, 999 permutations) and homogeneity-of-dispersion (betadisper/permutest) results; source data for Fig. 2.

Supplementary Table S5: S5\_enterotype\_assignments.csv and S5\_enterotype\_model\_selection.csv

Per-sample enterotype labels (*k* = 2 by BIC) and model-selection diagnostics (mclust BIC for *G* = 1–6; *k*-means average silhouette for centers 2–6); source data for Fig. 5.

Supplementary Table S6: S6\_id\_alignment\_report.csv, S6\_id\_alignment\_report.txt, and S6\_design\_drop\_report.txt

ID-harmonization crosswalk, narrative log (pre/post matching counts, examples of counts-only and metadata-only IDs), and a design-drop audit listing samples removed for missing covariates.

**Supplementary Data (source matrices and manifest)**

Supplementary Data A: S2\_taxa\_full.csv

Species-level relative-abundance matrix (post-filtering; samples × taxa) used for α/β-diversity and taxonomic DA.

Supplementary Data B: S3\_pathways\_full.csv

HUMAnN pathway counts matrix (samples × pathways) used as input to the voom–limma analysis.

Supplementary Data C: Supplement\_index.txt

Index/manifest describing the full set of outputs and on-disk paths.

**Reproducibility notes**

Top-level script: constipation\_pd\_paper\_pipeline.R

Environment: results/tables/session\_info.txt (R 4.4.2; package versions).

Random seed: 42 for ordinations, permutations, and clustering.

Inputs: Copies of the processed derivatives from Wallen et al. (Zenodo record 7246185); raw reads at SRA BioProject PRJNA834801.