SUPPLEMENTARY MATERIAL

TABLE. S1 Patient samples per condition. Number of samples per condition after filtering steps and removal of samples with usage of multiple medications. Sample number shown before and after alpha rarefaction was conducted at a sampling depth of 5421 nucleotides.

Rarefaction Status	Healthy	PD-untreated	Entacapone	Pramipexole	Rasagiline	Amantadine
Before Rarefaction	103	125	11	22	22	6
After Rarefaction	101	120	11	21	21	5

TABLE. S2 Notable unique taxa indicate dopaminergic therapeutics are associated with a shift towards a healthy gut microbiome. Indicator species analysis shows ASVs which are uniquely associated with the listed treatment group(s). ASVs shown are either genus (g) or family (f) of indicator species with a p-value ≤ 0.05. The degree of correlation between the ASV and the related condition/treatment is shown by the indicator value.

Group	ASV	Characteristic	Indicator Value	*p*-value
Entacapone	(f) Lachnospiraceae	Lower levels of Lachnospiracea are directly related with increased PD disease severity (32)	0.302	0.035
Amantadine	(f) Lachnospiraceae	Lower levels of Lachnospiracea are directly related with increased PD disease severity (32)	0.558	0.005
All except PD-patients	(g) Colidextribacter	Significantly decreased in PD patients: can act as a Possible Biomarker for PD (33)	0.642	0.015

TABLE. S3 Dopaminergic treatments yield more reduced ASVs compared to elevated ASVs. Table showing the number ASVs significantly enriched or depleted in each dopaminergic therapeutic group compared to healthy and PD-untreated groups. Significant results were defined as having an adjusted p-value < 0.01 and |log2FoldChange| > 2.

Therapeutic	Comparison	Number of enriched ASVs	Number of depleted ASVs
Entacapone	vs Healthy	16	25
	vs PD-untreated	9	22
Pramipexole	vs Healthy	13	45
	vs PD-untreated	3	51
Rasagiline	vs Healthy	10	24
	vs PD-untreated	2	31
Amantadine	vs Healthy	2	6
	vs PD-untreated	1	7

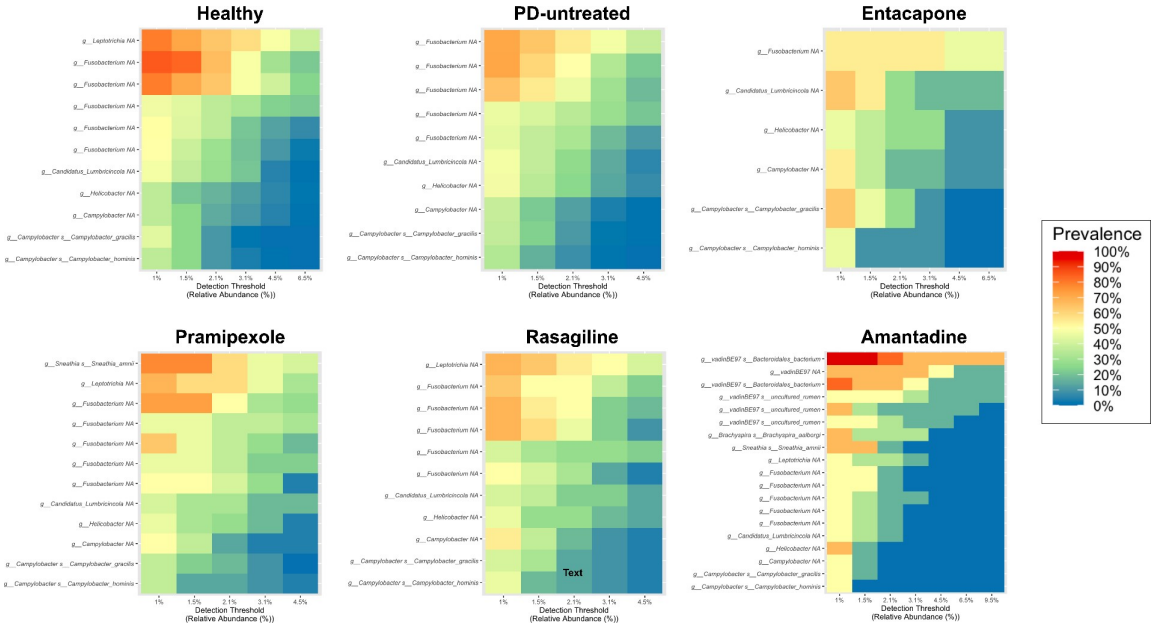

FIG. S1 Prevalence and abundance heat maps for core microbiome analysis. Prevalence heat maps illustrating abundance thresholds for core microbiome analysis across all groups. Each heatmap represents the prevalence of microbial taxa based on different abundance cutoff values to determine core microbiome parameters.

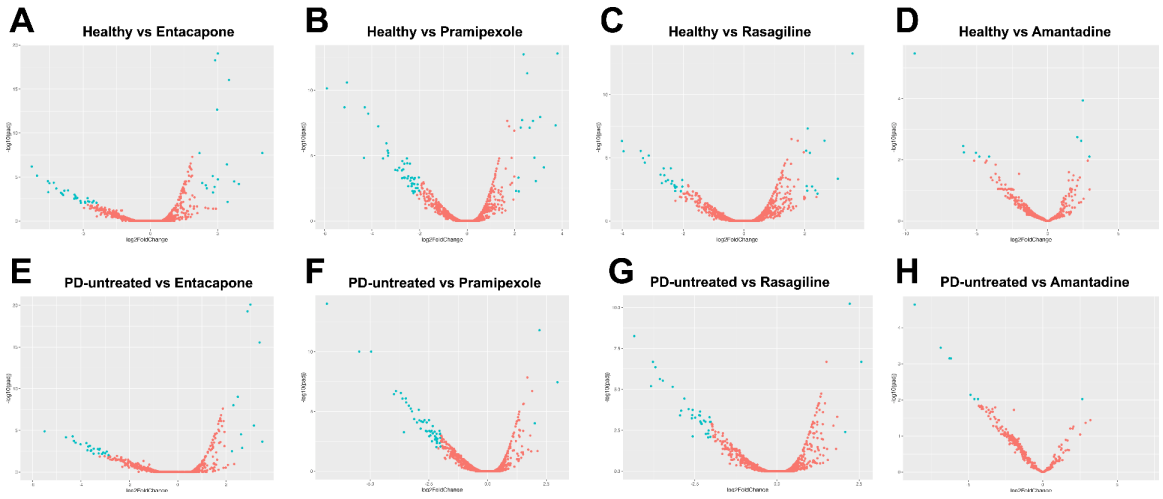

FIG. S2 Dopaminergic therapeutics are associated with differential abundances of some but not all ASVs compared to healthy controls and PD-untreated patients. Volcano plots display all changes in ASV abundances associated with each dopaminergic treatment. Differential abundance analysis was performed, with the healthy group serving as a reference for comparison to the **(A)** entacapone, **(B)** pramipexole, **(C)** rasagiline, and **(D)** amantadine treatment groups. The PD-untreated group was also used as a reference for identifying elevated and reduced ASVs in the **(E)** entacapone, **(F)** pramipexole, **(G)** rasagiline, and **(H)** amantadine treatment groups. Significant changes in abdundance are represented as blue dots, while insignificant changes are shown as red dots. Significance was defined with an adjusted p-value < 0.01 and |log2FoldChange| > 2.

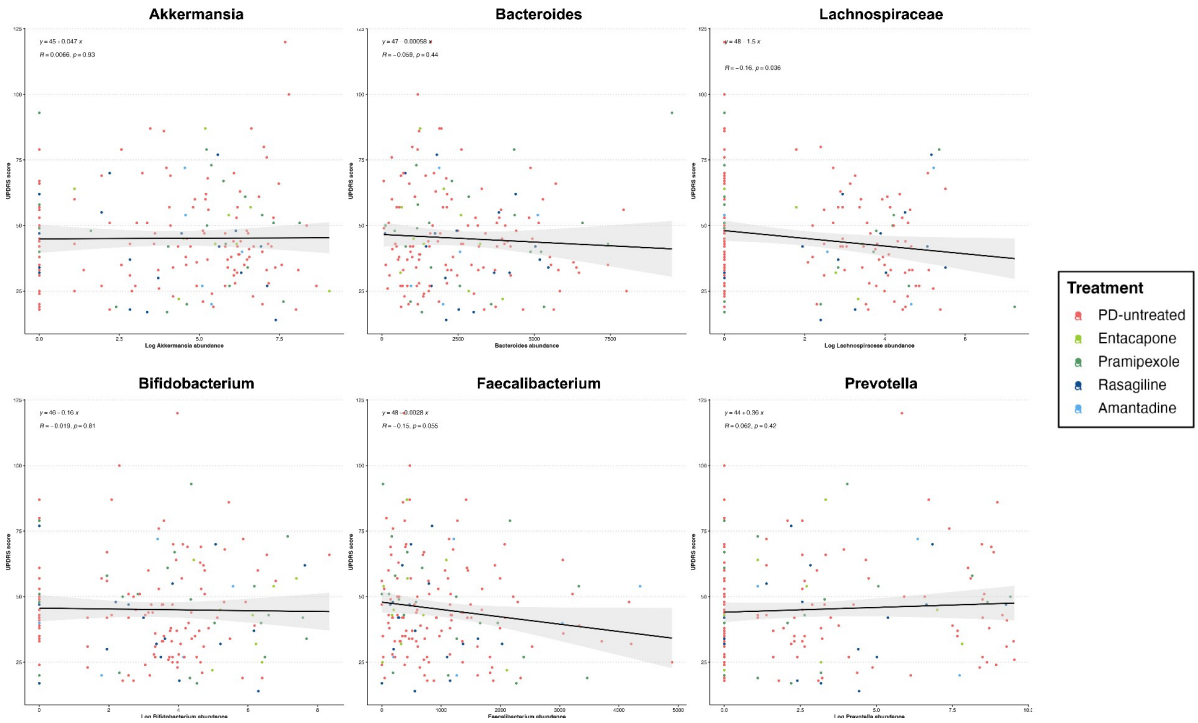

FIG. S3 Linear regression analysis of bacterial abundance and UPDRS score. Linear regression analysis examining the relationship between Unified Parkinson's Rating Scale (UPDRS) scores and bacterial abundance from genera of interest. The X-axis of each plot specifies log(x+1) transformation of abundance. Corresponding correlational coefficient, regression line and p-values are denoted on the graph.