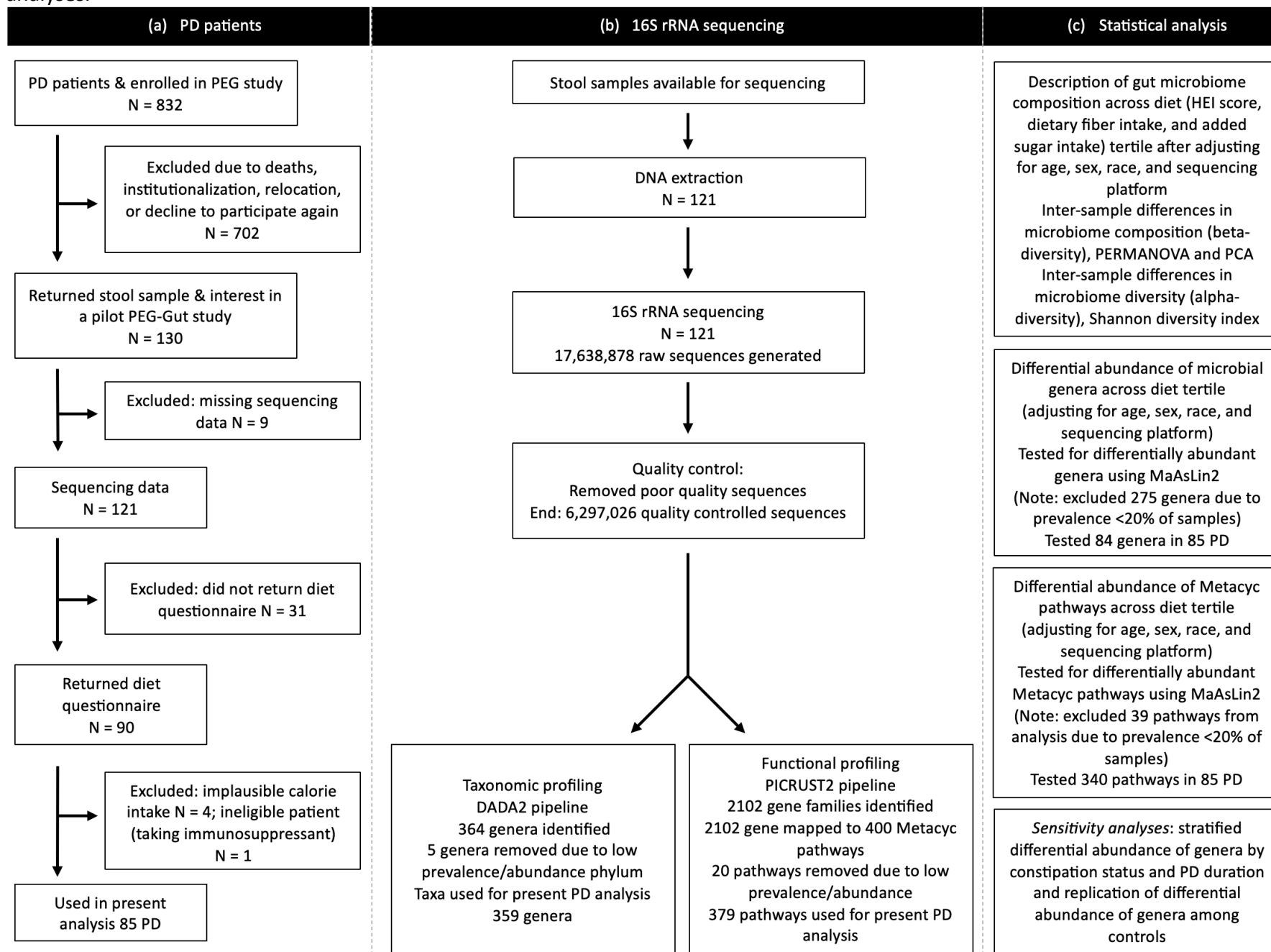


SUPPLEMENTARY MATERIAL

Supplementary Figure 1. The STORMS flowchart. Following reporting guidelines for human microbiome research, we show the step-by-step process by which (a) the study was conducted, enrollment and data collection for PD patients, (b) sequencing and bioinformatics pipeline, and (c) statistical analyses.



Supplementary Table 1. Association of beta diversity of predicted bacterial functional genes with diet. Parameters are from Bray-Curtis distance with continuous diet as the predictor, adjusting for age, sex, race, and platform. Trend tests across tertile are done by entering the tertile midpoints into the model as continuous term.

Bray-Curtis distance	Categorical tertile		Continuous	
	R2	p-trend	R2	p-value
HEI	0.03182	0.0298	0.02272	0.0744
Dietary fiber	0.02074	0.0912	0.02599	0.0497
Added sugar	0.01589	0.1598	0.01425	0.1981

Supplementary Table 2. Association of gut microbial beta diversity with diet stratified by constipation. Parameters are from Bray-Curtis distance with continuous diet as the predictor, adjusting for age, sex, race, and platform. Trend tests across tertile are done by entering the tertile midpoints into the model as continuous term.

Bray-Curtis distance	Constipation (n = 50)				No constipation (n = 35)			
	Categorical tertile		Continuous		Categorical tertile		Continuous	
	R2	p-trend	R2	p-value	R2	p-trend	R2	p-value
HEI	0.02357	0.1898	0.02341	0.2043	0.03361	0.2098	0.03804	0.0870
Dietary fiber	0.02927	0.0289	0.02820	0.0395	0.02150	0.9193	0.03598	0.1259
Added sugar	0.02676	0.0694	0.02584	0.0956	0.03956	0.0575	0.02143	0.9218

Supplementary Table 3. Table presenting results of changes of gut microbiota compositions associated with Parkinson’s disease and diet. ↑ and color coded blue indicate higher abundance associated with increased diet or PD. ↓ and color coded orange indicate lower abundance associated with increased diet or PD. Empty cells indicate that no significant changes. Putative anti-inflammatory bacteria are marked in green. Putative pro-inflammatory bacteria are marked in yellow. PD = Parkinson’s disease, HEI = healthy eating index.

Genus	Changes associated with PD (previously reported in literature)		Changes with diet in PD patients (observed in this study)		
	PD vs. healthy controls	Associated clinical characteristics	HEI	Fiber	Added sugar
<i>Adlercreutzia</i>				↑	
<i>Butyricicoccus</i>	↓ ^{1,2}	↓ Patients with RBD and early PD ²	↑	↑	↓
<i>Coprococcus 1</i>	↓ ³⁻⁵		↑	↑	↓
<i>Hydrogenoanaerobacterium</i>		↓ Patients with lower MoCA scores ⁶		↑	
<i>Negativibacillus</i>			↑	↑	
<i>Romboutsia</i>		↓ PD patients with worsening cognitive function and depressive symptoms ⁷			↓
<i>Ruminococcaceae NK4A214 group</i>	↓ ⁸⁻¹⁰	↓ PD patients with tremor dominant phenotype ⁹ ; use of COMT inhibitors ¹⁰		↑	
<i>Ruminococcaceae UCG-003</i>	↓ ⁸⁻¹⁰	↓ PD patients with tremor dominant phenotype ⁹ ; use of COMT inhibitors ¹⁰	↑		
<i>Subdoligranulum</i>			↑		
<i>Turicibacter</i>	↑ ¹¹		↑		
<i>Tyzzereella 4</i>		↓ Patients with cognitive impairment ¹²	↑	↑	↓
<i>Veillonella</i>	↑ ^{13,14}				↓
<i>Bacteroides</i>	↑ ^{5,8,15,16}	↑ PD patients with tremors ¹³ , postural instability and gait disability phenotypes ¹⁶ , and severe motor symptoms ¹³		↓	
<i>Eggerthella</i>	↑ ¹⁷		↓		
<i>Faecalitalea</i>			↓		
<i>Klebsiella</i>	↑ ^{15,18}				↑
<i>Lachnospiraceae NK4A136 group</i>	↓ ^{2,5,14,18-22}	↓ Patients with RBD and early PD ²	↓		
<i>Parabacteroides</i>	↑ ^{13,20}		↓	↓	
<i>Tyzzereella</i>			↓	↓	↑
<i>UC5-1-2E3</i> (Lachnospiraceae family genus)			↓	↓	
<i>Butyricimonas</i>	↑ ¹³		↓	↑	

Intestinimonas

↑¹⁹

↓

↑

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