

Supplementary Material

TABLE. S1 No differentially abundant bacterial taxa identified across dietary antioxidant intake tertiles. Taxonomic differential abundance analysis was performed using MaAsLin2. p-values were adjusted for multiple testing to obtain the corresponding q-values (qval). An Excel spreadsheet was generated for each dietary antioxidant, containing all statistical results.

TABLE. S2 Indicator taxa associated with low and high dietary antioxidant intake despite low within-group prevalence. Indicator species were determined using multi-level pattern analysis for all individual dietary antioxidants and combined intake. Bacterial taxa that were identified as significant indicators ($p < 0.05$) but exhibited low prevalence (indicator value (stat) < 0.7) within their respective groups were reported in this table.

Dietary Antioxidant	Intake Group	Bacteria Name (genus-level)	p-value	stat value
Beta-carotene	High	<i>Alloprevotella</i>	0.026	0.370
		<i>Cloacibacillus</i>	0.045	0.403
Vitamin A	High	<i>Acidaminococcus</i>	0.045	0.388
		<i>Anaeroplasma</i>	0.013	0.313
Vitamin C	High	<i>Anaerosporebacter</i>	0.043	0.411
		<i>Intestinimonas</i>	0.044	0.305
		<i>Asteroleplasma</i>	0.015	0.361
	Low	<i>Acidaminococcus</i>	0.022	0.436
		<i>Faecalitalea</i>	0.005	0.379
Vitamin E	High	<i>Victivallaceae</i>	0.036	0.354
		<i>Succinivibrio</i>	0.047	0.256
	Low	<i>[Ruminococcus] gnavus group</i>	0.036	0.424
Combined dietary antioxidants	High	<i>Lachnospiraceae</i>	0.047	0.404
		<i>FCS020 group</i>		
		<i>Solobacterium</i>	0.017	0.347

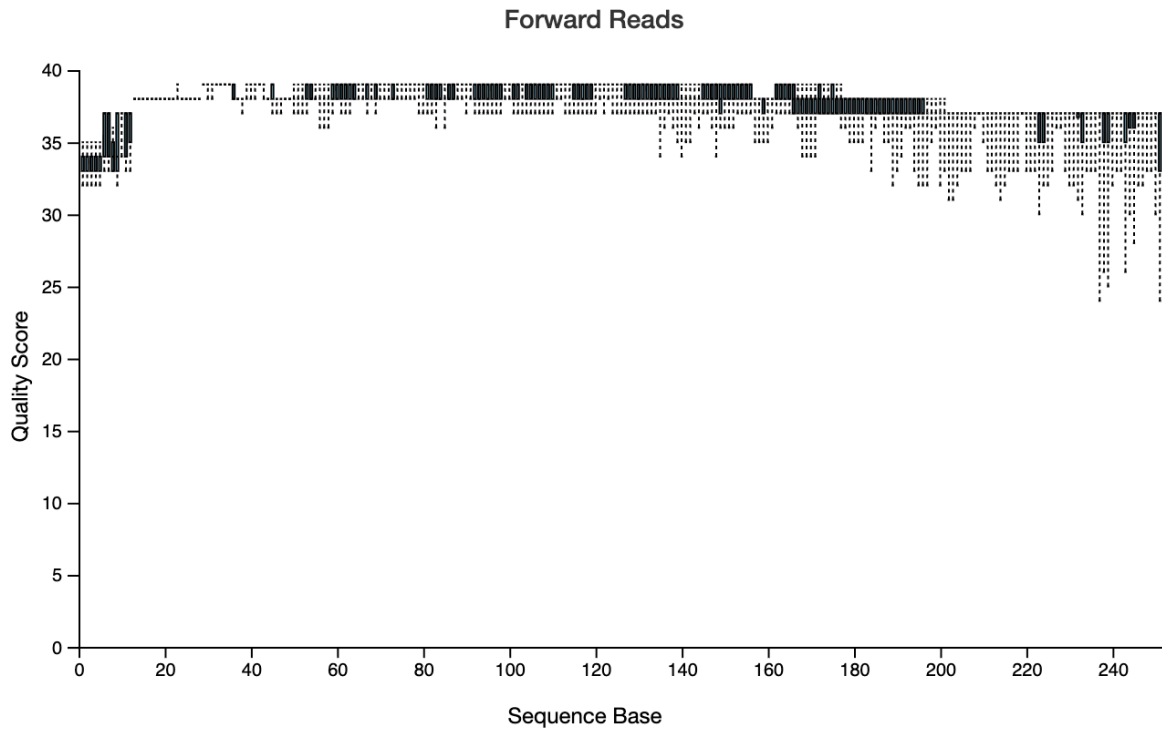


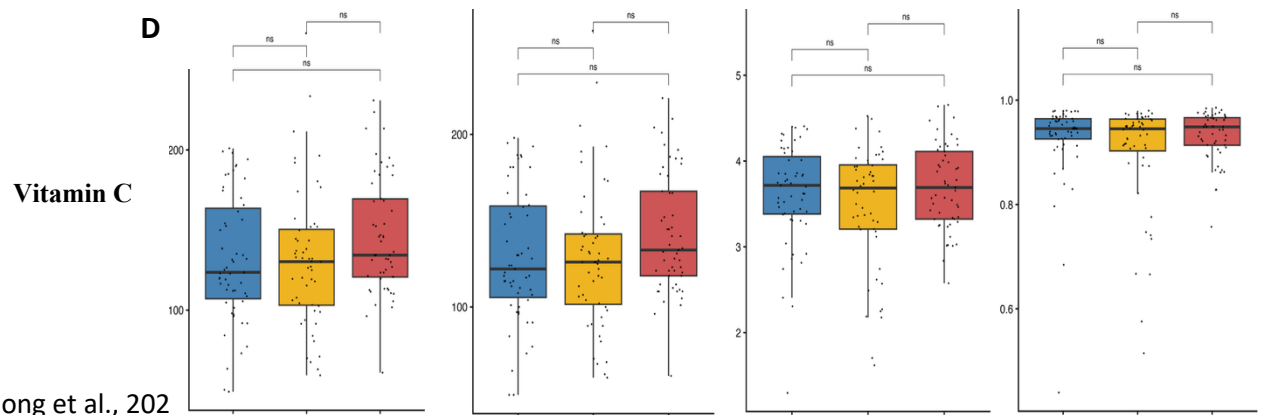
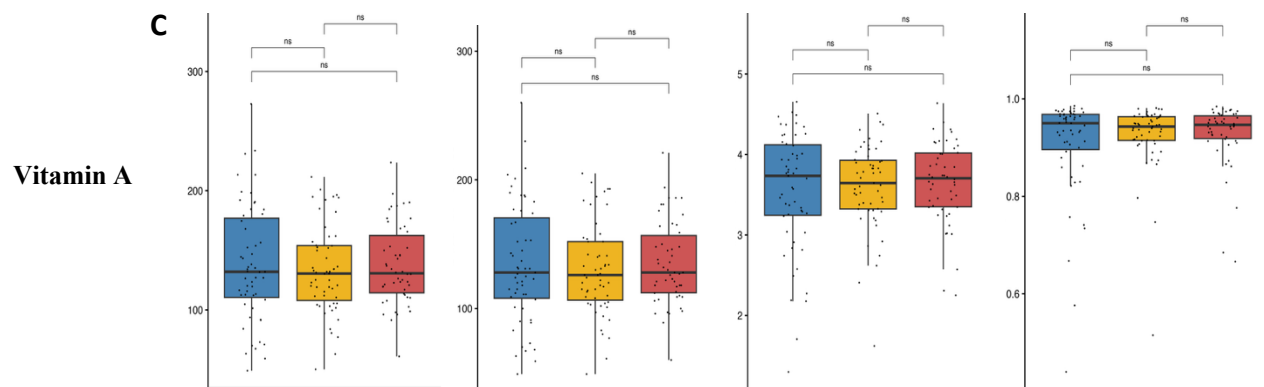
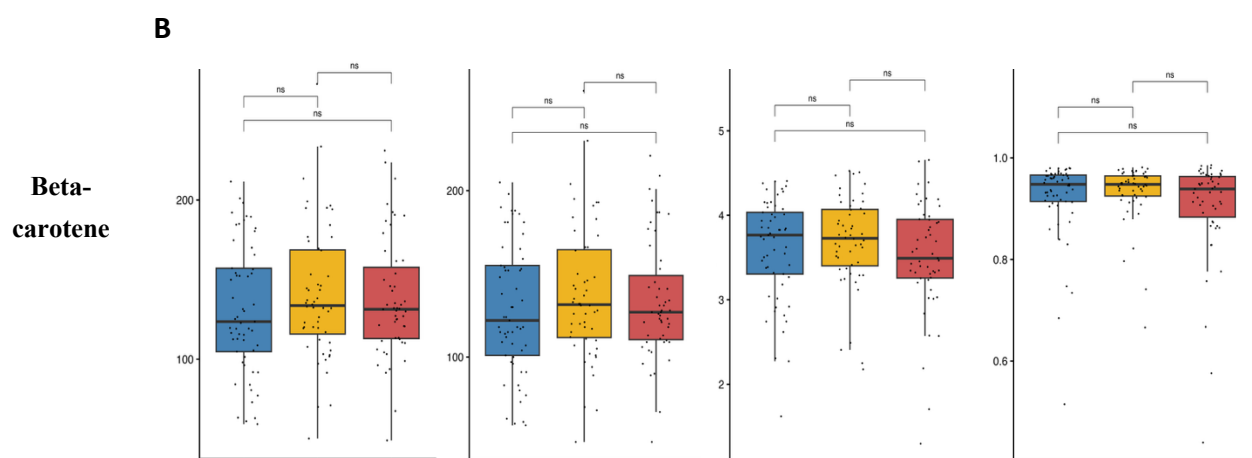
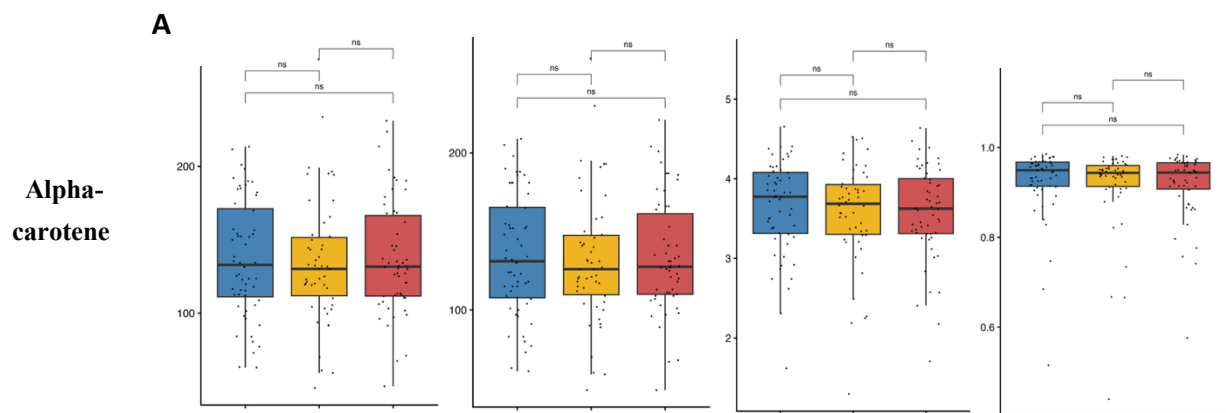
FIG. S1 High sequence quality was maintained across the read length. Quality scores across each base position for forward sequencing reads were visualized using QIIME 2 viewer. The x-axis represents nucleotide position along the read, and the y-axis shows the corresponding Phred quality score of each base.

Chao1

Observed

Shannon

Simpson



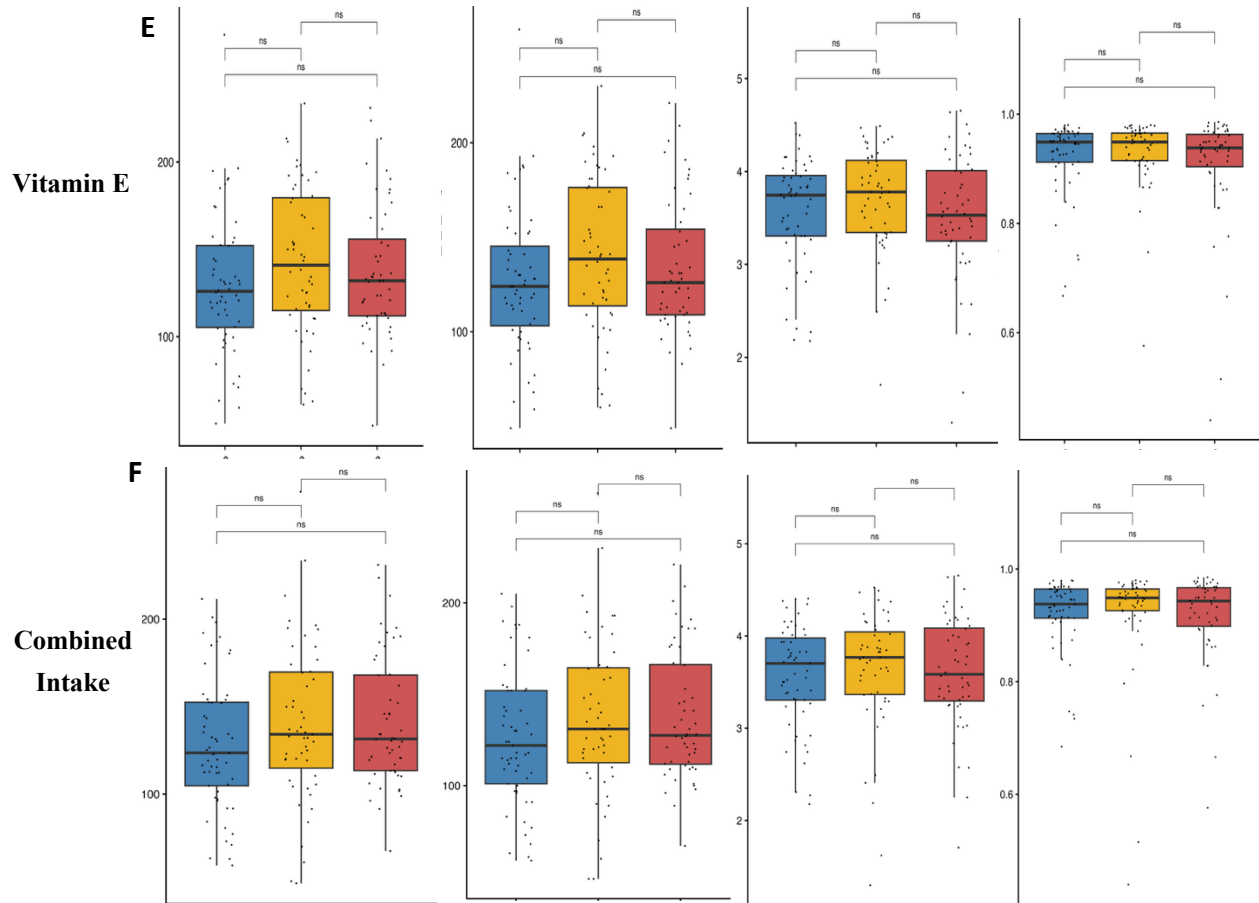


FIG. S2 Alpha diversity did not differ significantly across low, medium, and high tertiles of dietary antioxidants or their combined effects. Alpha diversity was evaluated using Chao1, Observed Species, Shannon, and Simpson indices. Values are shown across low (blue), medium (yellow), and high (red) tertiles of dietary antioxidant intake, including (A) alpha-carotene, (B) beta-carotene, (C) vitamin A, (D) vitamin C, (E) vitamin E, and (F) their synergistic effect. Values are shown across (from left to right) low (blue), medium (yellow), and high (red) tertiles of dietary antioxidant intake, including (A) alpha-carotene, (B) beta-carotene, (C) vitamin A, (D) vitamin C, (E) vitamin E, and (F) their synergistic effect. Boxplots display the median and interquartile range, with individual data points overlaid. Statistical comparisons across tertiles for each individual antioxidant or combined intake were performed using linear regression models adjusted for age, sex, and entacapone use (not significant (ns) = $p > 0.05$). No significant differences in alpha diversity were observed across tertiles for any individual dietary antioxidant or combined intake, suggesting similar microbial richness and evenness among groups.

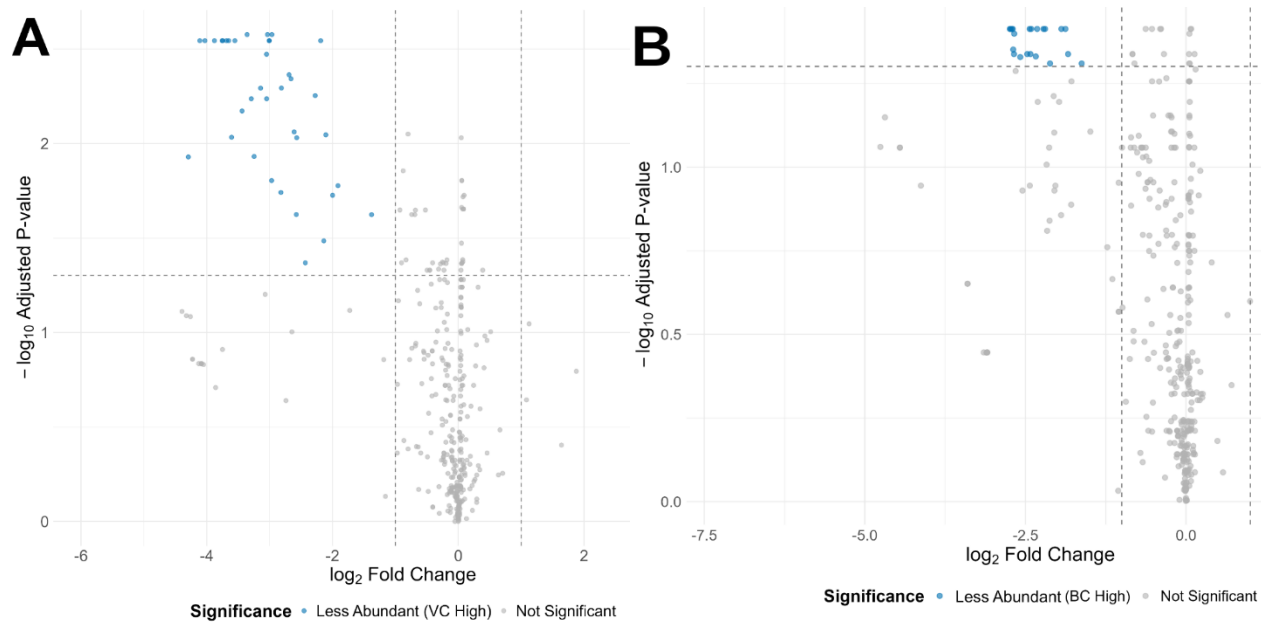


FIG. S3 High beta-carotene and vitamin C dietary antioxidant intake in PD patients drives a global metabolic shift. Functional analysis performed with PICRUST2 and MaAsLin2 revealed high (A) vitamin C (VC) and (B) beta-carotene (BC) intake levels caused predicted functional changes in gut microbial communities.

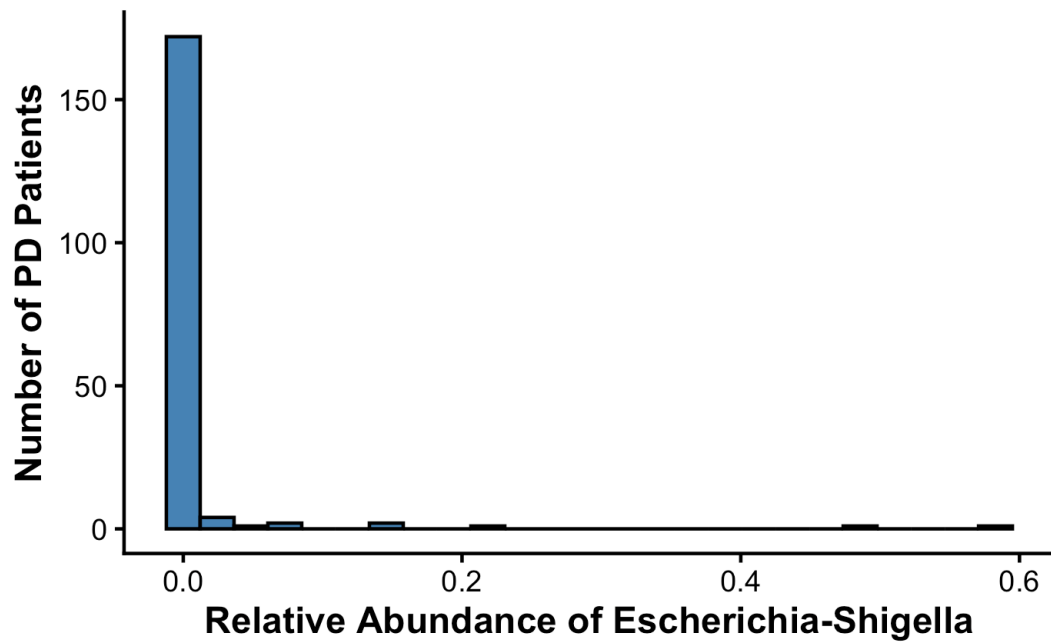


FIG. S4 Distribution of the relative abundance of *Escherichia-Shigella* in PD patients demonstrates a high prevalence of zeros. The distribution of the relative abundance of *Escherichia-Shigella* in PD patients was visualized using a histogram. The histogram shows a highly right-skewed and zero-inflated distribution, with the majority of PD patients exhibiting little to no detectable *Escherichia-Shigella*, and only a small subset displaying elevated relative abundance.

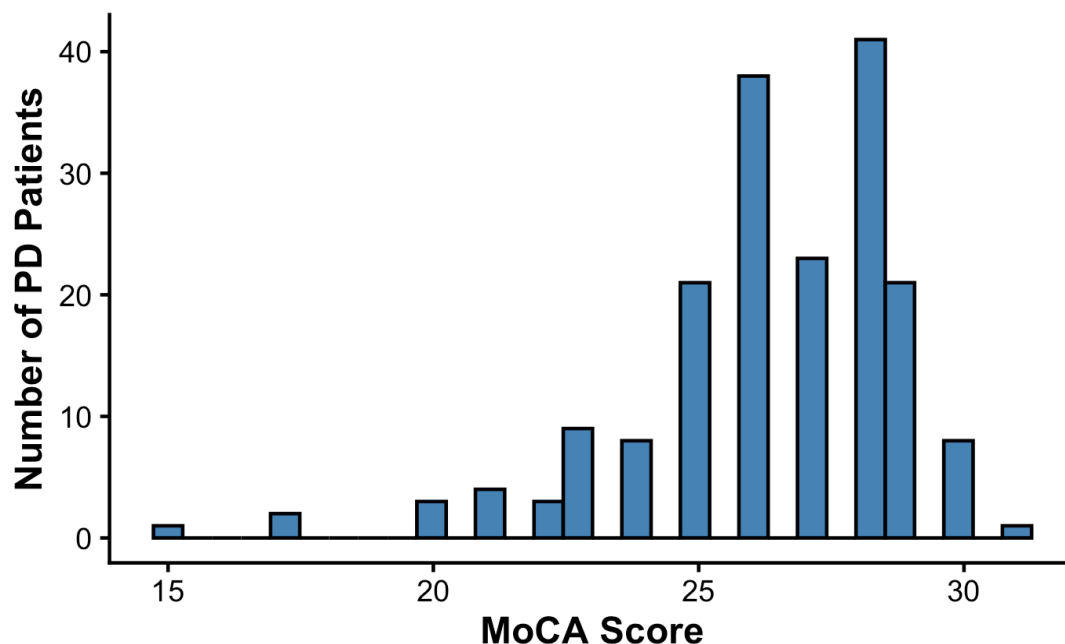


FIG. S5 Distribution of MoCA scores demonstrates limited variability and few cases of severe cognitive impairment in PD patients. The distribution of MoCA scores among PD patients was visualized using a histogram. A score of ≥ 26 is generally considered to reflect normal cognitive function. Approximately 27.7% of PD patients (51 out of 184) were classified as having cognitive impairment.