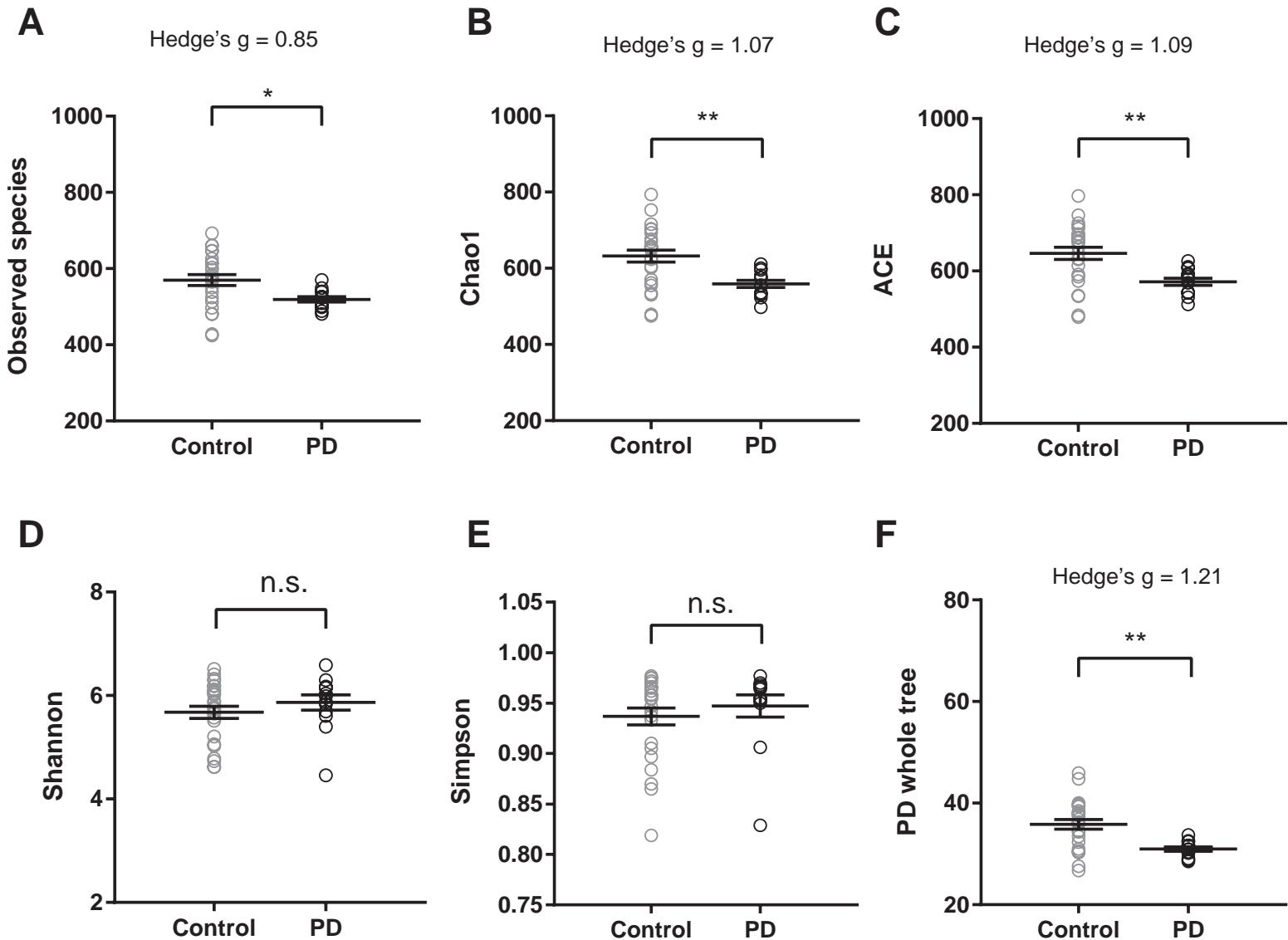
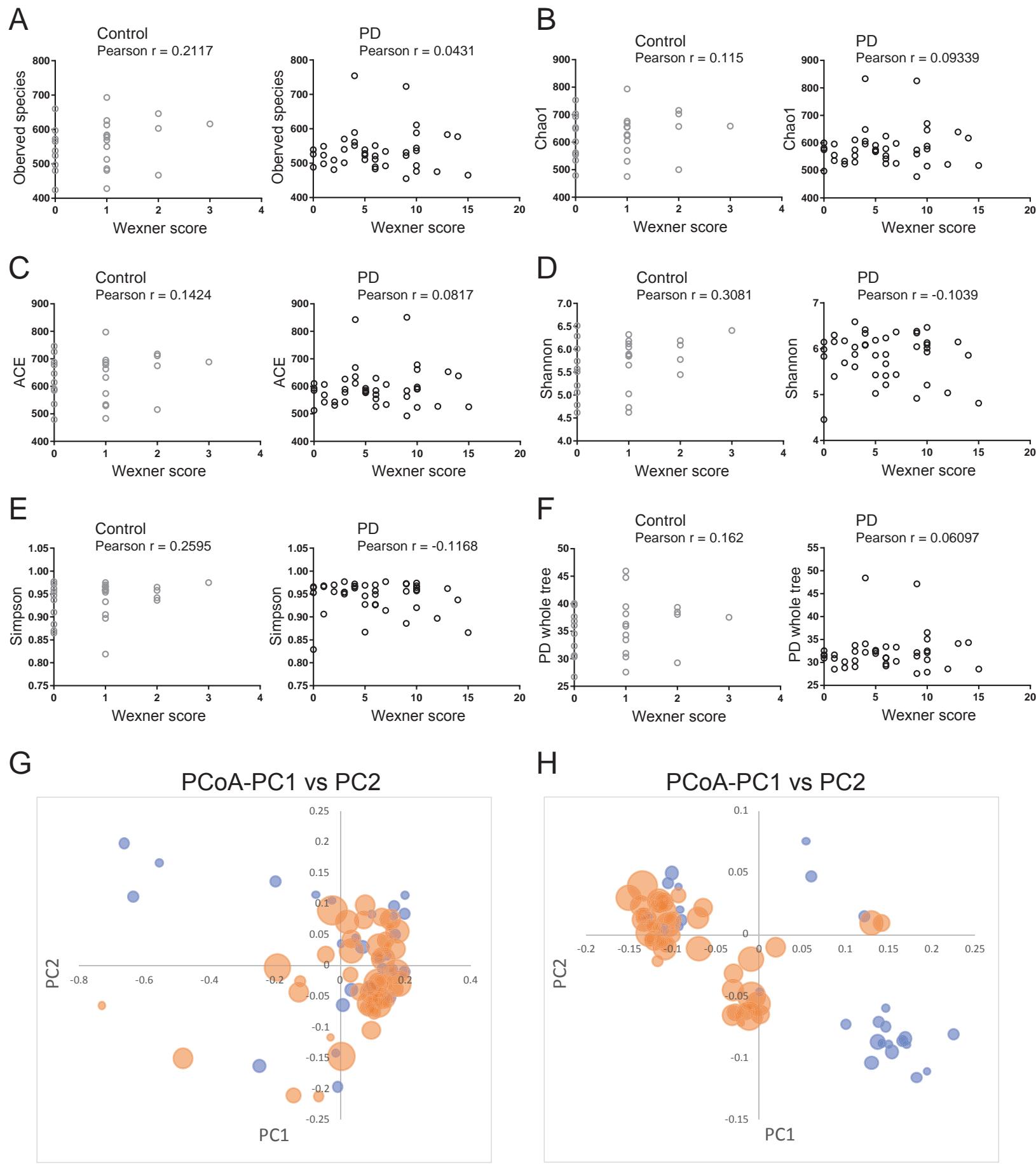


Supplemental Figure 1. Comparison of dietary intake between PD patients and controls. Unpaired t-test, n=42 for PD, n=23 for control. Data are presented as mean \pm s.e.m.



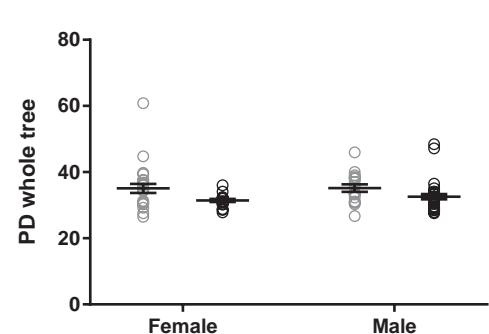
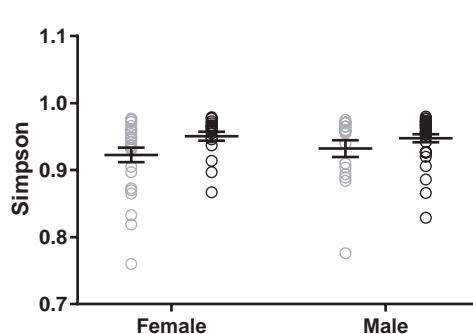
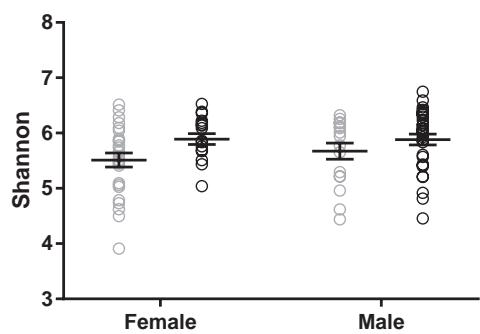
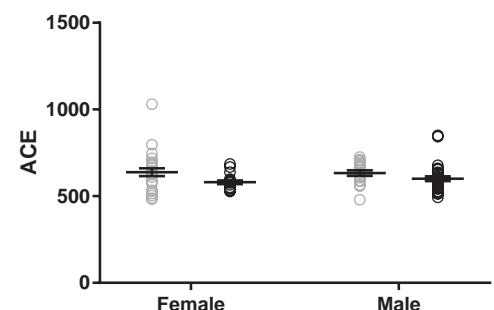
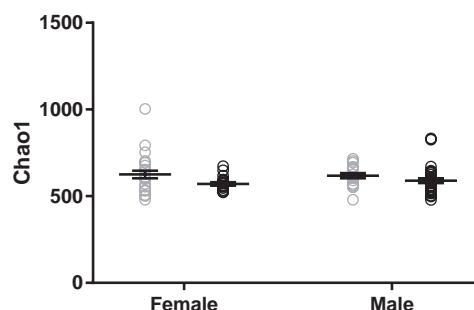
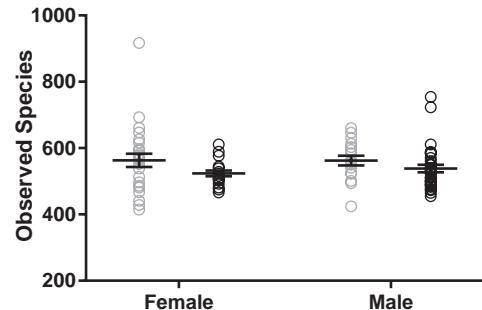
Supplemental Figure 2. Comparison of microbiota richness and diversity indices between PD patients and controls with constipation Wexner score ≤ 3 . A-C: species richness, D-E: α -diversity, F: phylogenetic diversity. n=13 for PD, n=25 for control. Data are presented as mean \pm s.e.m. with individual replicates also shown. *p<0.05, **p<0.01, n.s.: not significant, unpaired t-test.



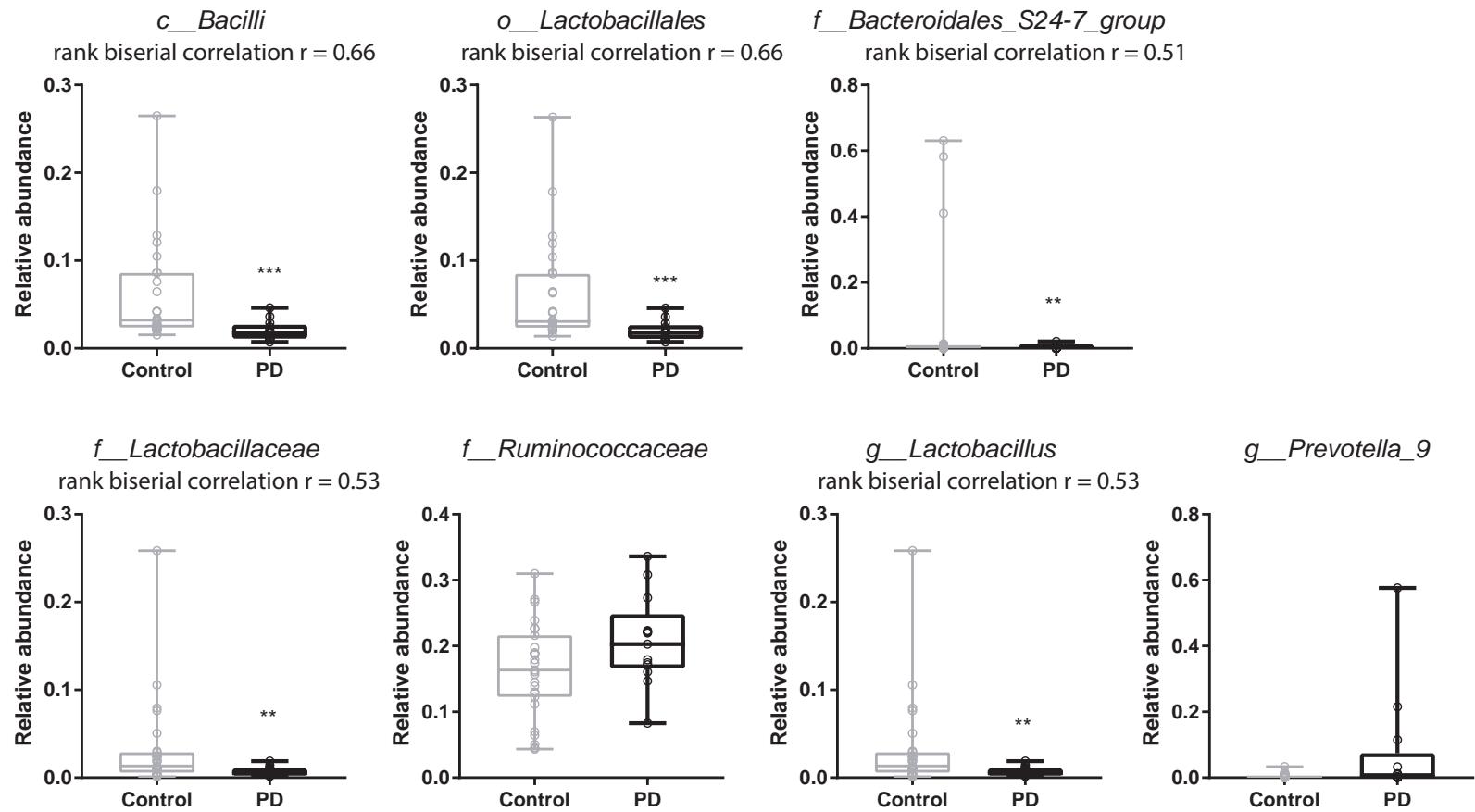
Supplemental Figure 3. Impact of constipation on gut microbiota richness and diversity indices.

A-F: Correlation analysis to assess the impact of constipation on species richness, α -diversity and phylogenetic diversity indices. G,H: Impact of constipation on β -diversity. Data shown are the results of Principal Co-ordinates Analysis (PCoA) plotted with weighted Unifrac (G) and unweighted Unifrac (H) in controls (blue bubbles) and PD patients (orange bubbles). The size of the bubbles indicates the severity of the constipation (Wexner score).

○ Control
○ PD



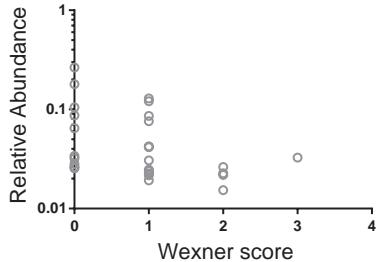
Supplemental Figure 4. Two-way ANOVA analysis to assess the impact of gender and PD on species richness, α -diversity and phylogenetic diversitiy indices.



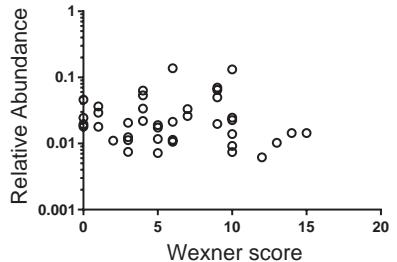
Supplemental Figure 5. Comparison of microbiota abundances between PD patients and controls with constipation Wexner score ≤ 3 . Wilcoxon rank-sum test, n=13 for PD, n=25 for control. ** $p < 0.01$, *** $p < 0.001$, .

*c*__*Bacilli*

Control
Pearson r = -0.3688

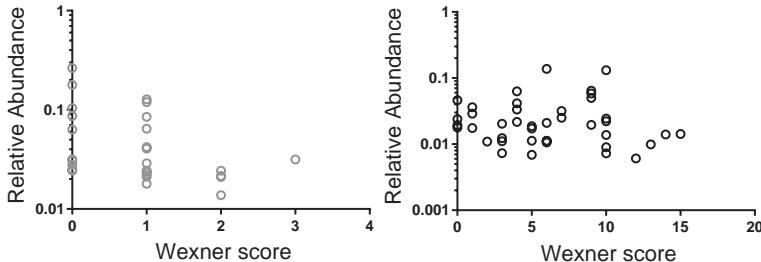


PD
Pearson r = 0.05032

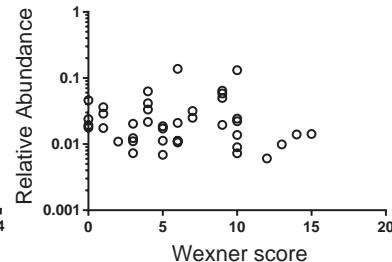


*o*__*Lactobacillales*

Control
Pearson r = -0.3713

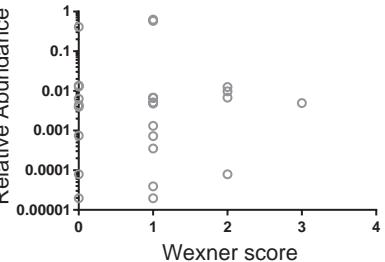


PD
Pearson r = 0.0481

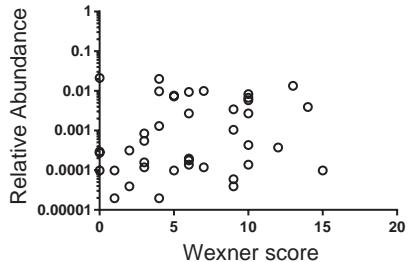


*f*__*Bacteroidales_S24-7_group*

Control
Pearson r = -0.04226

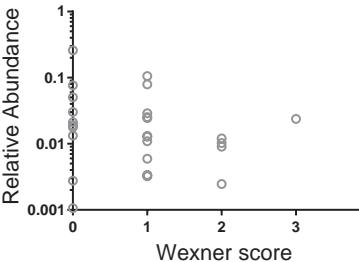


PD
Pearson r = 0.04911

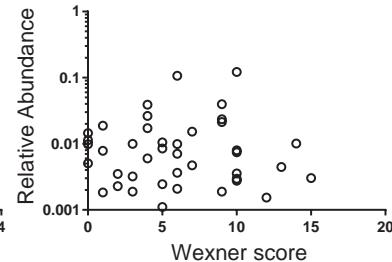


*f*__*Lactobacillaceae*

Control
Pearson r = -0.2537

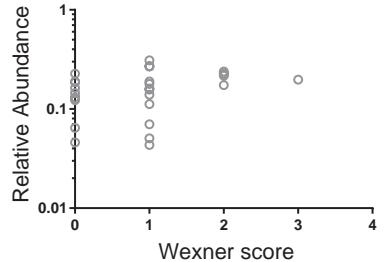


PD
Pearson r = 0.097

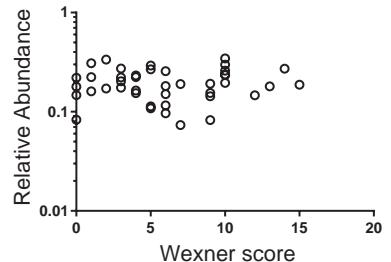


*f*__*Ruminococcaceae*

Control
Pearson r = 0.3326

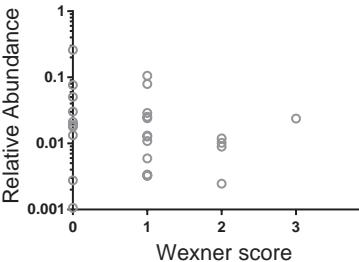


PD
Pearson r = 0.05625

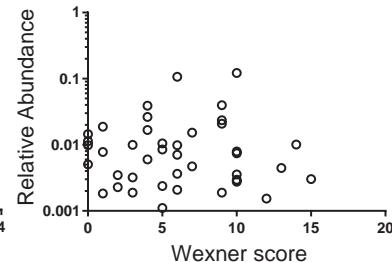


*g*__*Lactobacillus*

Control
Pearson r = -0.2541

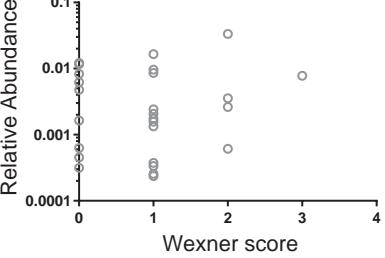


PD
Pearson r = 0.09697

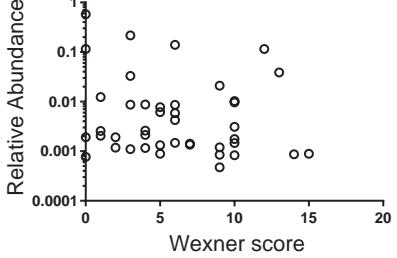


*g*__*Prevotella_9*

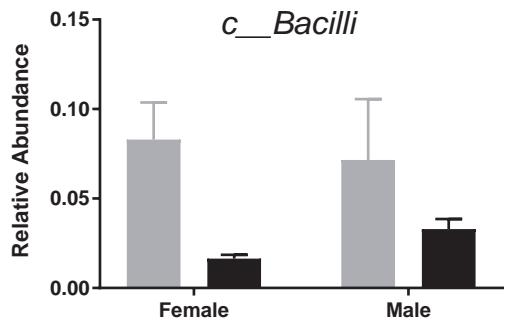
Control
Pearson r = 0.1323



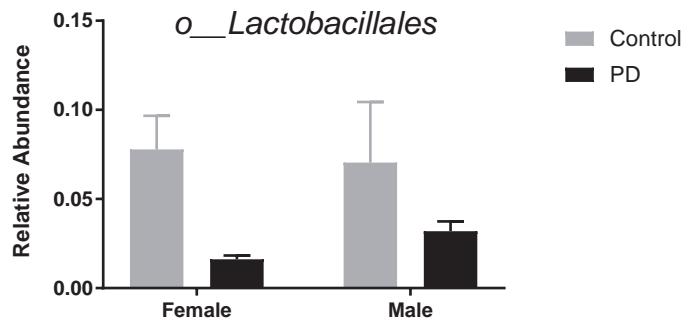
PD
Pearson r = -0.2384



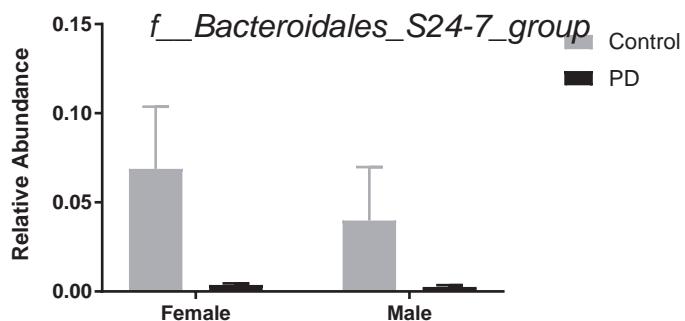
Supplemental Figure 6. Correlation analysis to assess the impact of constipation on the relative abundance of individual taxa. The correlations between the abundances and the Wexner constipation scores are weak, suggesting that the severity of constipation does not have a strong effect on the abundances of these taxa.



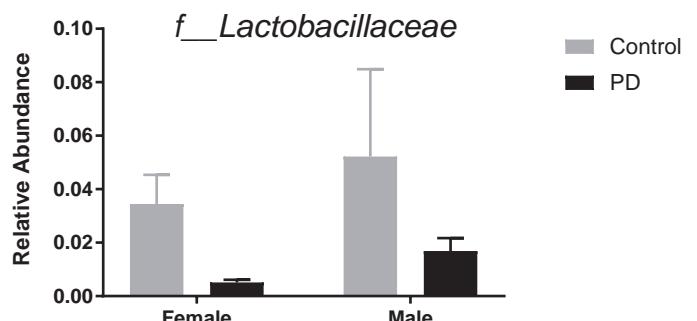
ANOVA table	SS (Type III)	DF	MS	F (DFn, DFd)	P value
Interaction	0.004273	1	0.004273	$F(1, 90) = 0.6149$	$P=0.4350$
Sex	0.0001383	1	0.0001383	$F(1, 90) = 0.0199$	$P=0.8881$
PD vs control	0.06107	1	0.06107	$F(1, 90) = 8.79$	$P=0.0039$
Residual	0.6253	90	0.006948		



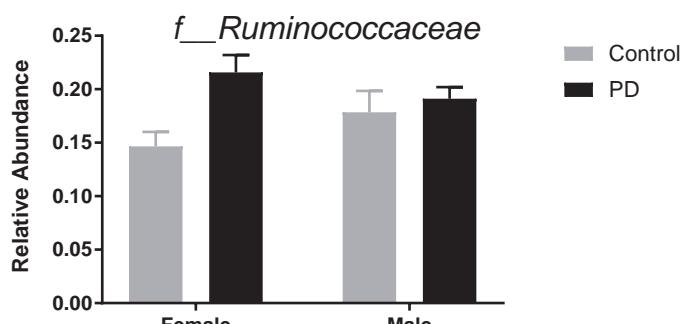
ANOVA table	SS (Type III)	DF	MS	F (DFn, DFd)	P value
Interaction	0.002921	1	0.002921	$F(1, 90) = 0.4577$	$P=0.5004$
Sex	0.0003813	1	0.0003813	$F(1, 90) = 0.05975$	$P=0.8074$
PD vs control	0.05545	1	0.05545	$F(1, 90) = 8.689$	$P=0.0041$
Residual	0.5743	90	0.006381		



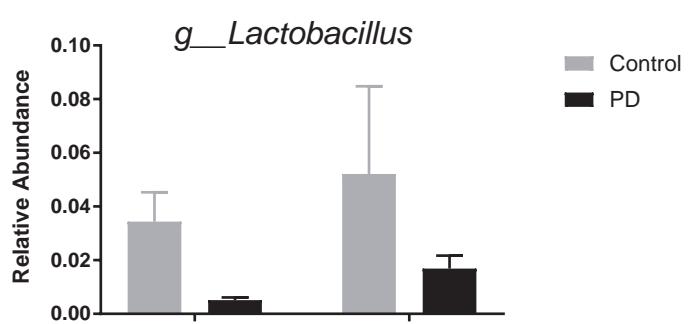
ANOVA table	SS (Type III)	DF	MS	F (DFn, DFd)	P value
Interaction	0.004315	1	0.004315	$F(1, 90) = 0.3744$	$P=0.5422$
Sex	0.004997	1	0.004997	$F(1, 90) = 0.4336$	$P=0.5119$
PD vs control	0.05778	1	0.05778	$F(1, 90) = 5.013$	$P=0.0276$
Residual	1.037	90	0.01152		



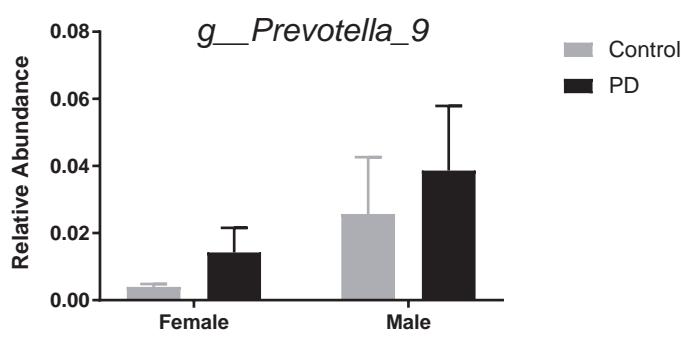
ANOVA table	SS (Type III)	DF	MS	F (DFn, DFd)	P value
Interaction	0.0001958	1	0.0001958	$F(1, 90) = 0.045$	$P=0.8325$
Sex	0.004801	1	0.004801	$F(1, 90) = 1.103$	$P=0.2964$
PD vs control	0.02309	1	0.02309	$F(1, 90) = 5.306$	$P=0.0236$
Residual	0.3917	90	0.004352		



ANOVA table	SS (Type III)	DF	MS	F (DFn, DFd)	P value
Interaction	0.01754	1	0.01754	$F(1, 90) = 3.639$	$P=0.0596$
Sex	0.0003045	1	0.0003045	$F(1, 90) = 0.0632$	$P=0.8021$
PD vs control	0.03713	1	0.03713	$F(1, 90) = 7.707$	$P=0.0067$
Residual	0.4336	90	0.004818		

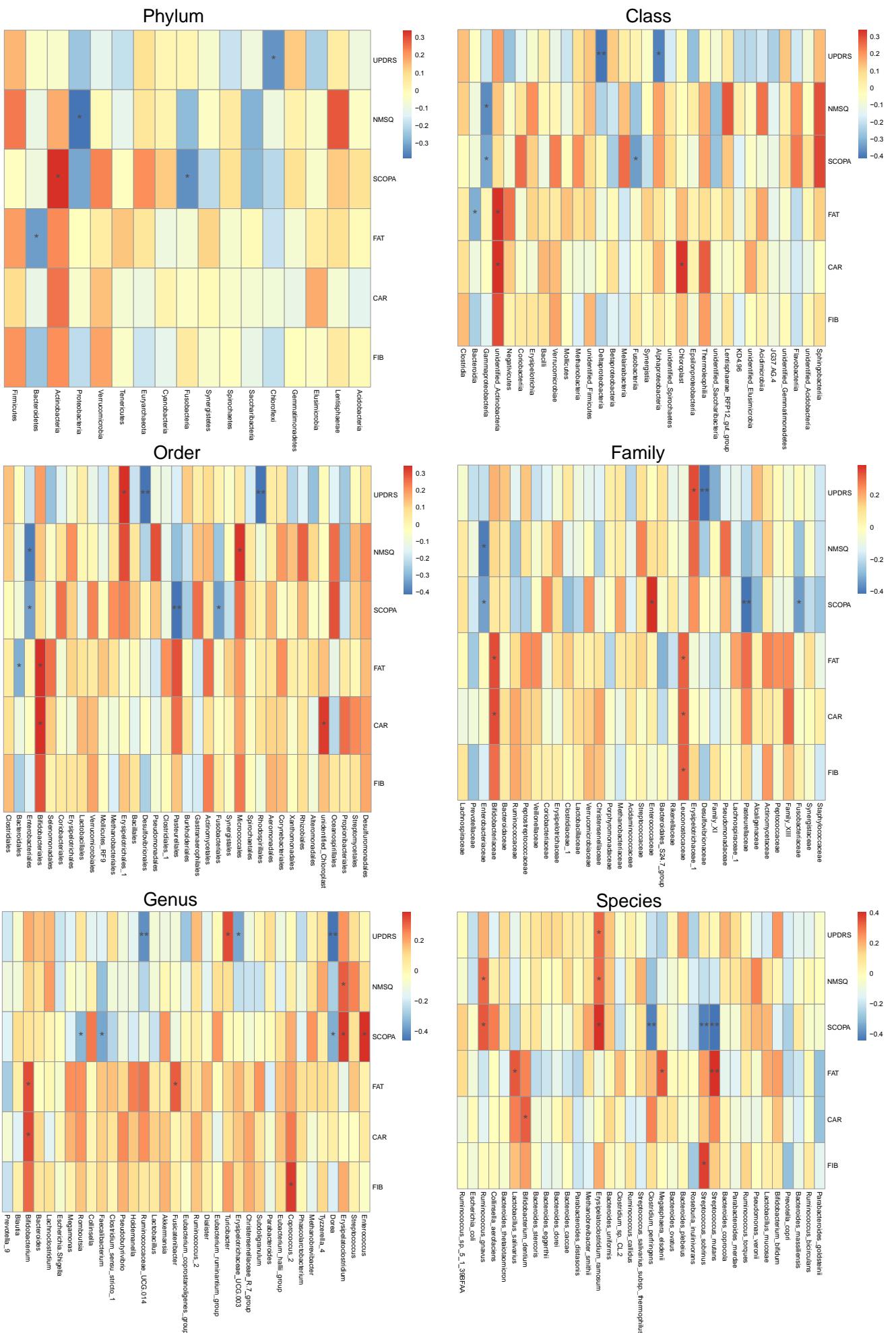


ANOVA table	SS (Type III)	DF	MS	F (DFn, DFd)	P value
Interaction	0.0002024	1	0.0002024	$F(1, 90) = 0.04656$	$P=0.8297$
Sex	0.004815	1	0.004815	$F(1, 90) = 1.108$	$P=0.2954$
PD vs control	0.02301	1	0.02301	$F(1, 90) = 5.293$	$P=0.0237$
Residual	0.3913	90	0.004348		



ANOVA table	SS (Type III)	DF	MS	F (DFn, DFd)	P value
Interaction	0.00003773	1	3.773E-05	$F(1, 90) = 0.007314$	$P=0.9320$
Sex	0.01176	1	0.01176	$F(1, 90) = 2.279$	$P=0.1347$
PD vs control	0.002972	1	0.002972	$F(1, 90) = 0.576$	$P=0.4498$
Residual	0.4643	90	0.005159		

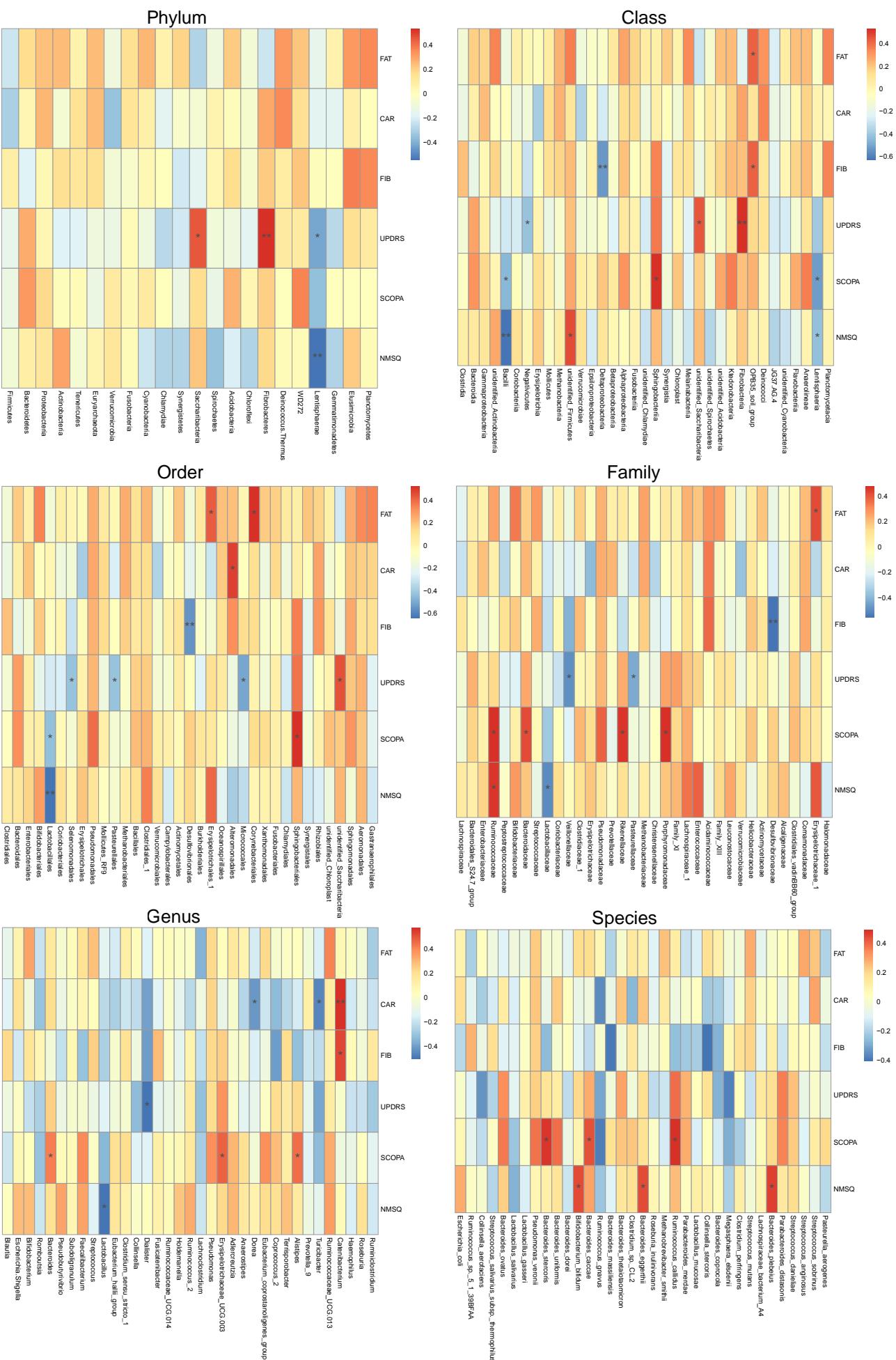
Supplemental Figure 7. Two-way ANOVA analysis to assess the impact of gender and PD on gut microbiota taxa identified by LDA scores>4 in LEfSe analysis.



Supplemental Figure 8. Correlations between environmental factors and gut microbiota in PD patients.

Correlation heatmaps showing the relationship between environmental factors and gut microbiota at different taxonomic ranks. Each row in the heatmap represents an environmental factor. Each column represents a taxon.

The color temperature encodes Spearman correlation coefficient r . $n=42$, * $p < 0.05$, ** $p < 0.01$.



Supplemental Figure 9. Correlations between clinical and dietary factors and gut microbiota in healthy controls.
 Correlation heatmaps showing the relationship between clinical and dietary factors and gut microbiota at different taxonomic ranks. Each row in the heatmap represents a clinical or dietary factor. Each column represents a taxon. The color temperature encodes Spearman correlation coefficient r . $n=23$, $*p < 0.05$, $**p < 0.01$.