

This document includes Supplementary Information

(Supplementary Table 1 & Supplementary Figures 1-5) to:

Genetic and phenotypic diversity of fecal *Candida albicans* strains in Irritable Bowel Syndrome

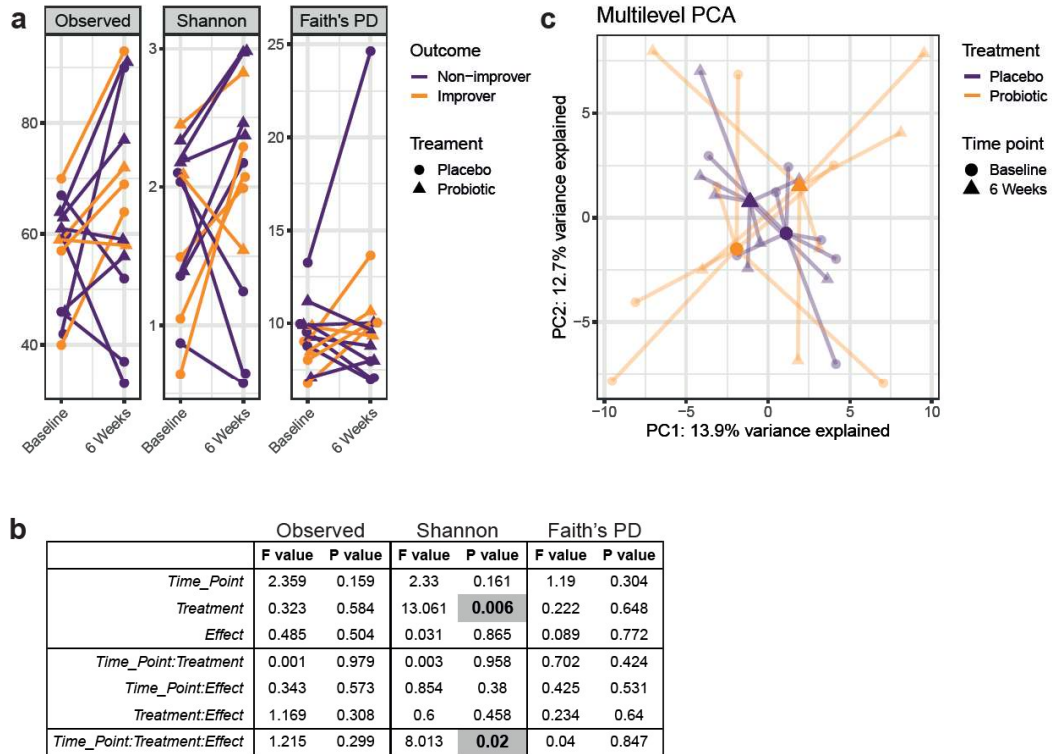
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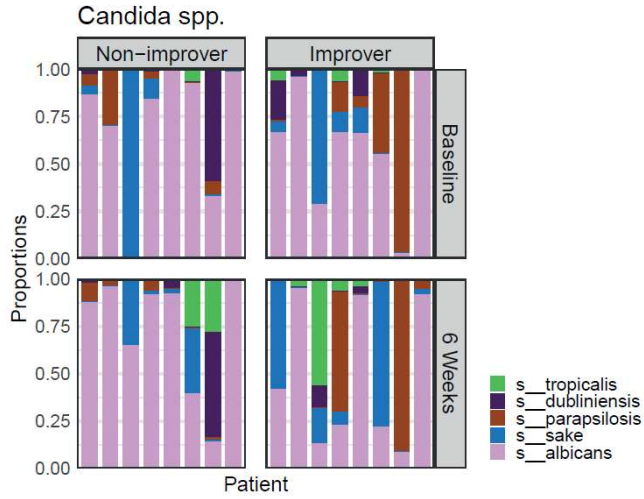
Supplementary Table 1.

Primer sequences for quantitative PCR experiments.

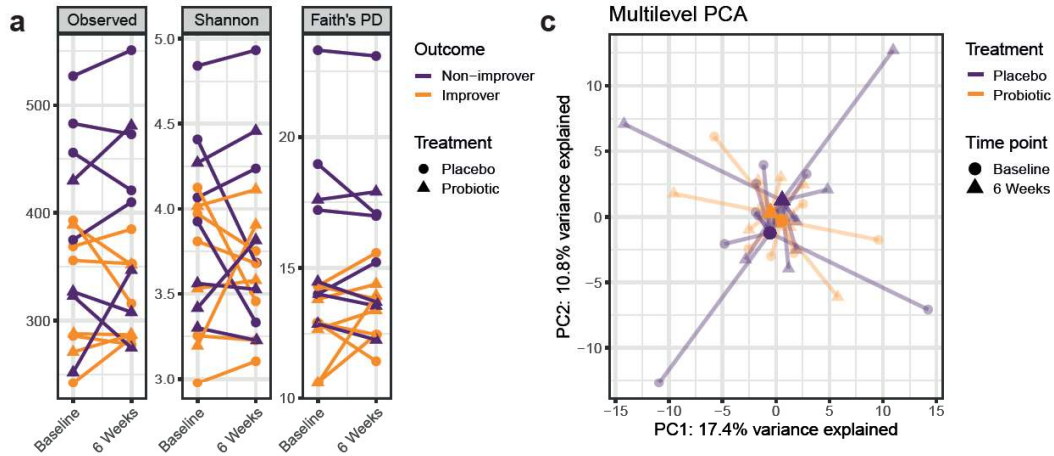
Gene of interest	Identifier	Forward/Reverse	Primer sequences (5'-3')
TDH3 reference	XM_714816.1	Forward	CGGTCCATCCCACAAGGA
		Reverse	AGTGGAAGATGGGATAATGTTACCA
PMA1 reference	XM_712666.2	Forward	TTGCTTATGATAATGCTCCATACGA
		Reverse	TACCCCACAATCTTGGCAAGT
ALS1	XM_712984.2	Forward	CAACAGGCACCTCAGCATCTAC
		Reverse	CTCCACCAGTAACAGATCCACTAGTAA
ALS3	XM_705343.2	Forward	CAACTTGGGTATTGAAACAAAAACA
		Reverse	AGAAACAGAAACCCAAGAACAACCT
NRG1	XM_710106.1	Forward	ACATGTGAAGCCCGTTTGC
		Reverse	CTGTGTTGTTGTCTGTTGCGT
HGC1	XM_713897.2	Forward	GTCAGCTTCCTGCACCTCAT
		Reverse	TTGGTGGTGGTGGTGCATA
SAP2	XM_705955.2	Forward	CCAATGAAGCCGGTGGTAGT
		Reverse	TATTTGTCCCGTGGCAGCAT
SAP4	XM_712961.1	Forward	GCCGATGGTTCTGTTGCAC
		Reverse	ACACCACCAATACCAACGGT
ECE1	XM_706502.1	Forward	CCATCATCCACCATGCTCCA
		Reverse	ACAGTAGGTGCTTGGTCAGC
CDR1	XM_718116.2	Forward	CCATGACTCCTGCTACCGTG
		Reverse	CCATCGAGACCAACCCAACA
MDR1	XM_714072.2	Forward	ACAATTTGGCCACCCCTGAA
		Reverse	CCAACACGGAACCTACCCCAA



Supplementary Figure 1. Mycobiota composition as expressed by Shannon index associates with probiotic treatment and outcome, although no community-based associated was determined. a-b) Alpha diversity as expressed by observed species, Shannon index, and Faith's Phylogenetic Distance of mycobiota samples. Shannon index is significantly different for allocated treatment. Results linear mixed effect models presented in b). c) Mycobiota composition, displayed in a multilevel principle component analysis, is not significantly different after treatment.



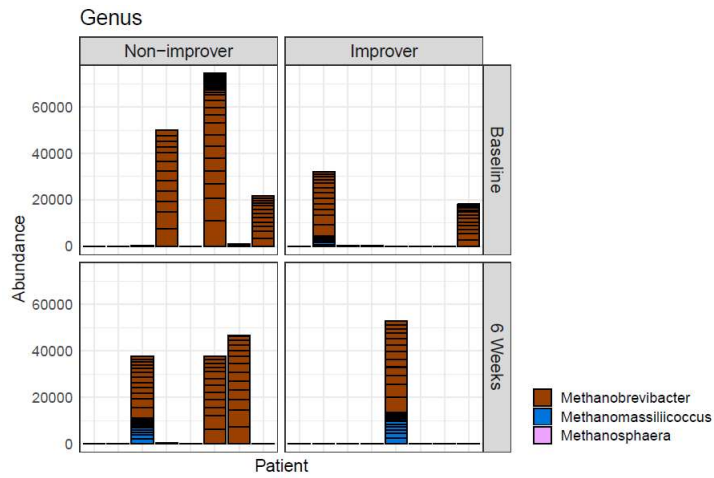
Supplementary Figure 2. Taxonomic analysis of *Candida spp.* reveals *Candida albicans* as most abundant species. Relative abundance of *Candida spp.* in each sample. Each column represents one patient. A minimal abundance threshold of 0.1% was used to remove low-confidence species for enhanced visualization purposes. *C. albicans* is most abundant between all samples, followed by *C. sake* and *C. parapsilosis*.



b

	Observed		Shannon		Faith's PD	
	F value	P value	F value	P value	F value	P value
<i>Time_Point</i>	0.045	0.835	0.014	0.906	0.681	0.425
<i>Treatment</i>	4.674	0.052	0.451	0.515	2.412	0.146
<i>Effect</i>	7.312	0.019	2.001	0.183	7.87	0.016
<i>Time_Point:Treatment</i>	0.103	0.754	5.958	0.031	1.131	0.309
<i>Time_Point:Effect</i>	0.619	0.447	0.5	0.493	3.59	0.082
<i>Treatment:Effect</i>	2.928	0.113	2.357	0.151	2.542	0.137
<i>Time_Point:Treatment:Effect</i>	0.143	0.712	0.058	0.813	1.479	0.247

Supplementary Figure 3. Bacterial microbiome composition is associated with treatment allocation to a limited extent. a-b) Alpha diversity metrics (Observed species, Shannon index, Faith's Phylogenetic distance) as shown for both outcome (improver/non-improver) and allocated treatment (placebo/probiotic). Shannon diversity generally associates with allocated treatment (p=0.031, Linear Mixed Effect Models (LME)). Results linear mixed effects model presented in b). c) Community analysis by multilevel PCA based on Bray-Curtis dissimilarities. Symbol color represents allocated treatment. Composition is associated with treatment (p=0.007, PERMANOVA).



Supplementary Figure 5. Archaeal reads show high inter-individual variability. Archaeal reads counts displayed on genus level. Each column represents one paired sample. Each separated segment indicates individual species. Reads are highly variable between and within patients.