**Supplemental Legends**

**Fig S1. Quantitative PCR of ITS2 and 16S rRNA genes in controlled diet samples.** Each of three independent DNA extraction replicates were analyzed from each diet of each volunteer using ITS2-targeting primers ITS3F-ITS4R (yellow) and 16S rRNA gene-targeting Bact1369F-Prok1492R (blue). The positive standard deviation of the samples is shown. No template controls detected <10 copies of either target.

**Fig S2. Most abundant taxa prior to filtering out plants from ITS2 DNA analysis of stool samples from experimental (1-4) and control (5) volunteers following controlled (A-D) or uncontrolled (U) diets.** Relative abundances of taxa are from an average of one to three samples after rarefaction to 5000 reads/sample.

**Fig S3. Taxa detected by 16S rRNA gene analysis of stool samples from experimental (1-4) and control (5) volunteers following controlled (A-D) or uncontrolled (U) diets**. Samples were rarefied to 9,402 reads/sample. The most abundant taxa are listed, while other and repeated colors represent other taxa.

**Fig S4. Taxa detected by 18S rRNA gene analysis of stool samples from experimental (1-4) and control (5) volunteers following controlled (A-D) or uncontrolled (U) diets**. Samples had 12,600 – 36,250 total reads. Relative abundances for the triplicate samples were averaged and sequences mapping to plants and animals were removed. Samples with >1000 reads remaining were scaled to 1000 reads.

**Fig S5. Comparison of taxa detected by ITS2 analysis of Volunteer 1 stool samples extracted by three different protocols**. Samples had 5,147 – 47,293 reads (median 24,860). Samples were rarefied to 102 reads after sequences mapping to plants were removed.

**Fig S6. Comparison of taxa detected by 18S rRNA gene analysis of Volunteer 1 stool samples extracted by three different protocols**. Samples had 3,922 – 28,096 reads (median 21,610). Samples were rarefied to 149 reads after sequences mapping to plants and animals were removed.

**Fig S7.** **Relative 18S rRNA gene abundance of *Saccharomyces* in stool over time as a *Saccharomyces cerevisiae*-free diet is consumed.** The relative abundance over time of *Saccharomyces* among 18S rRNA gene sequences amplified from stool DNA of a human volunteer. Plant sequences were removed before analysis. Top: stacked bar chart of data rarefied to 456 reads/sample with the most abundant taxa listed. Other colors represent other taxa. Bottom: logarithmic-scaled chart showing just the unrarefied relative abundance of *Saccharomyces* reads over time.

**Table S1. Detection of ITS2 OTUs across longitudinal Human Microbiome Project stool samples.**

**Table S2. Controlled diet experiment information and results.**

**Table S3. Stability of ITS2 RNA and DNA in fungi incubated at different temperatures.**

**Table S4. Bioreactors information and results.**

**Table S5. *Saccharomyces* experiment information and results.**

**Table S7. Fungi detected in Yatsunenko et al. data.**

**Table S8. Primer sequences.**

**Table S9. Fungi in mice.**

**Text S1. Analyzing fungi in the stool of non-Western humans.**

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**Table S6. Comparison of the number of fungi detected in Yatsunenko et al. ribosomal SSU amplicon data from stool collected in different countries.**

**Text S2. Mouse experiment.**