Non-biological synthetic spike-in controls and the AMPtk software pipeline improve fungal high throughput amplicon sequencing data

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Summary:

- High throughput amplicon sequencing (HTAS) of conserved DNA regions is a powerful technique to characterize biological communities from environmental samples. Recently, spike-in mock communities have been used to measure accuracy of sequencing platforms and data analysis pipelines. The fungal internal transcribed spacer (ITS) region is difficult to sequence due to its variability (length and sequence divergence) across the fungal kingdom.
- To assess the ability of sequencing platforms and data processing pipelines using fungal ITS amplicons, we created two ITS spike-in control mock communities composed of single copy plasmid DNA: a biological mock community (BioMock), consisting of cloned ITS sequences, and a synthetic mock community (SynMock), consisting of non-biological ITS-like sequences.
- Using these spike-in controls we show that pre-clustering steps for variable length amplicons are critically important and a major source of bias is attributed to initial PCR reactions. These data suggest HTAS read abundances are not representative of starting values.
- We developed AMPtk (amplicon toolkit), a versatile software solution equipped to deal with variable length amplicons featuring a method to quality filter HTAS data based on spike-in controls. While we describe herein a non-biological (synthetic) mock community for ITS sequences, the concept can be widely applied to any HTAS dataset.

59 **Introduction:**

60 High-throughput amplicon sequencing (HTAS) is a powerful tool that is frequently used
61 for examining community composition of environmental samples. HTAS has proven to be a
62 robust and cost-effective solution due to the ability to multiplex hundreds of samples on a single
63 next-generation sequencing (NGS) run. However, HTAS output from environmental samples
64 requires careful interpretation and appropriate and consistent use of positive and negative
65 controls (Nguyen *et al.*, 2015). One of the major challenges in HTAS is to differentiate
66 sequencing error versus real biological sequence variation. Considerable progress has been
67 made in the last several years through improved quality of sequencing results through
68 manufacturer upgrades to reagents as well as improved quality filtering and "clustering"
69 algorithms. While most algorithm development in HTAS is focused on the prokaryotic
70 microbiome, using the 16S subunit of the rRNA array (e.g. QIIME (Caporaso *et al.*, 2010),
71 Mothur (Schloss *et al.*, 2009), UPARSE (Edgar, 2013), DADA2 (Callahan *et al.*, 2016)), many of
72 these same tools have been adopted for use with other groups of organisms, such as fungi.

73 The internal transcribed spacer (ITS) region of the rRNA array has emerged as the
74 molecular barcode for examining fungal communities in environmental samples (Schoch *et al.*,
75 2012). The ITS region is multi-copy and thus easily amplifiable via PCR even from
76 environmental samples with low quantities of fungal DNA. The ITS region consists of two
77 subunits, ITS1 and ITS2, and is generally conserved within a species yet possess enough
78 variability to differentiate between species in many taxonomic groups. Because of its
79 widespread use, several public databases are rich with reference fungal ITS sequences
80 (Schoch *et al.*, 2012). However, there are several properties of the fungal ITS region that are
81 potentially problematic for HTAS that include: i) fungi have variable cell wall properties making
82 DNA extraction efficiency unequal for different taxa and/or cell types (hyphae, fruiting bodies,
83 spores, etc) (Vesty *et al.*, 2017), ii) the number of nuclei per cell is variable between taxa (Roper
84 *et al.*, 2011), iii) the number of copies of the rRNA array are different between taxa and in some
85 cases isolates of the same taxa (Ganley & Kobayashi, 2007), iv) a single isolate can have
86 multiple ITS sequences (intragenomic variability; (Simon & Weiss, 2008; Lindner & Banik,
87 2011), v) the ITS region is highly variable in length, vi) ITS sequences vary in GC content, and
88 vii) there are a variable number of homopolymer repeats. Additionally, current read lengths of
89 next-generation sequencing platforms (Illumina Miseq currently covers ~ 500 bp (2 x 300) and
90 Ion Torrent is 450 bp) are not long enough to cover the entire length of the ITS region, which is
91 typically longer than 500 bp. However, conserved priming sites exist to amplify either the ITS1
92 region or the ITS2 region, which has been shown to be sufficient for taxonomic identification.

While several studies have used the ITS1 region for HTAS, the ITS1 region contains introns in some taxa and thus to avoid potential bias it has been suggested that ITS2 region should be the preferred region for fungi (Taylor *et al.*, 2016) (Figure 1A).

Sequencing error is a known problem across NGS platforms used for HTAS. To address issues with sequencing error and reliability of results from HTAS, it has become increasingly common practice to use spiked-in "mock" community samples as positive controls for the parameterization and optimization of experimental workflows and data processing. Spike-in mock community controls for fungal ITS have been used (e.g., Amend *et al.*, 2010; Tonge *et al.*, 2014; Nguyen *et al.*, 2015; Taylor *et al.*, 2016; De Filippis *et al.*, 2017), and have consisted of fungal genomic DNA (gDNA) extracted from tissue from fruiting bodies, cultures, or spores of a number of taxa which are then (usually) combined in equimolar amounts. Mock communities composed of fungal gDNA from fruiting bodies, spores, and/or hyphae provide a measure of success of extraction, PCR, and sequencing and thus are useful in the HTAS workflow. However, such mock communities are of limited value if used to validate/parameterize data processing workflows due to intrinsic properties of the ITS region mentioned previously (variable copy number, intraspecific variation, variable length, etc.). Therefore, there is a need for fungal ITS spike-in control mock communities that function to validate laboratory experimental design, validate data processing steps, and compare results between sequencing runs and platforms.

HTAS is cost-effective due to the ability to massively multiplex environmental samples on a single sequencing run. This process depends on the attachment of a unique sequence identifier (referred to as a barcode, an index, or a tag, depending on sequencing platform) to each piece of DNA to be sequenced. In recent years, "index-bleed ("index hopping", "tag jumping", "barcode jumping", "tag switching", or "barcode switching") has been noted to occur on Roche 454 platforms as well as Illumina platforms (Kircher *et al.*, 2011; Carlsen *et al.*, 2012; Degnan & Ochman, 2012; Philippe *et al.*, 2015; Schnell *et al.*, 2015). Index-bleed can lead to over-estimation of diversity in environmental samples (Philippe *et al.*, 2015; Schnell *et al.*, 2015) and mis-assignment of sequences to samples. It has been noted that spike-in mock communities may be useful to help detect index-bleed, and subsequent filters may be applied for use with the HTAS pipeline of choice (Degnan & Ochman, 2012; Philippe *et al.*, 2015).

In this study, we generated a biological mock community (BioMock) composed of cloned ITS sequences (single insert plasmids) from a diverse set of fungal taxa. We show how this BioMock can be used to parameterize a data processing workflow. Subsequently, we found that current "off-the-shelf" software solutions performed poorly with our BioMock community of fungal ITS sequences and thus developed AMPtk (amplicon toolkit), which produces improved

127 results of variable length amplicons from HTAS. We demonstrate that read abundances are an
128 unreliable proxy for measuring relative abundances in fungal communities on both Illumina and
129 Ion Torrent sequencing platforms. Accurate measurement of index-bleed between samples can
130 be accomplished by the use of a non-biological synthetic spike-in mock community consisting of
131 ITS-like sequences (SynMock). Finally, we show how AMPtk paired with SynMock can be used
132 to quality filter HTAS data by detecting and mitigating the effects of index-bleed among
133 multiplexed samples.
134
135 **Materials and Methods:**
136 *Biological mock community (BioMock)*
137 To construct the Biomock we selected 26 identified fungal cultures (Supplementary
138 Table S1) from the Center for Forest Mycology Research (CFMR) culture collection (US Forest
139 Service, Madison, Wisconsin). These cultures were purposefully chosen to represent a
140 taxonomic range of fungi, including paralogs, fungi with GC rich ITS regions, a variety of ITS
141 lengths, and fungi with a variety of homopolymers in the ITS region. To measure the sensitivity
142 of our bioinformatics approach, we also included two ITS sequences from *Leptoporus mollis* that
143 were isolated from the same culture as an example of intragenomic variation in the fungal ITS
144 region. These two sequences are more than 3% divergent (95.9% identical) and thus would
145 typically represent separate operational taxonomic units (OTUs) in a clustering pipeline, despite
146 being from the same fungal isolate. All cultures were grown on cellophane on malt extract agar,
147 and DNA was extracted from pure cultures following (Lindner & Banik, 2008). Following
148 extraction, the genomic DNA was PCR amplified using the fungal ITS specific primers ITS-1F
149 (Gardes & Bruns, 1993) and ITS4 (White *et al.*, 1990). The PCR products were then cloned and
150 Sanger sequenced using the ITS1-F primer following the protocol in (Lindner & Banik, 2011).
151 Sequence identifications were verified via BLAST search and two clones of each isolate were
152 selected and cultured in liquid LB (Luria-Bertani) media and incubated at 37 C for 24 hours.
153 Plasmids were purified from the cultures in LB media using standard alkaline lysis. These
154 plasmids will hereafter be termed “purified plasmids”. The purified plasmids were then Sanger
155 sequenced with vector primers T7 and SP6 to verify the insertion of a single copy of the
156 appropriate ITS fragment. We subsequently quantified the purified plasmid DNA concentration
157 using a Qubit® 2.0 fluorometer and DNA concentrations were equilibrated to 10 nM using DNA-
158 free molecular grade water. Following equilibration, 5 µl of each purified plasmid were combined
159 to make an equimolar “biological mock” community of single-copy purified plasmids (BioMock).

160 PCR has known biases, which are related to different sequence characteristics and are
161 hard to predict in mixed DNA communities of unknown composition. To illustrate the impact of
162 initial PCR bias on the number of reads obtained from each member of a mixed DNA
163 community, we generated individual HTAS-compatible PCR products from each Biomock
164 plasmid which were subsequently mixed (post-PCR) in an equimolar ratio. This was
165 accomplished by PCR amplifying each individual plasmid with the same barcoded primer set.
166 PCR products were purified using E-gel® CloneWell™ 0.8% SYBR® Safe agarose gels
167 (ThermoFisher), quantified using a Qubit® 2.0 fluorometer, and combined into an equimolar
168 mixture post-amplification. This post-PCR combined mock community can be used to examine
169 sequencing error on NGS platforms.
170
171 *Non-biological mock community (SynMock)*
172 We used the well-annotated ribosomal RNA (rRNA) sequence from *Saccharomyces*
173 *cerevisiae* as a starting point to design ITS-like synthetic sequences. The ITS adjacent regions
174 of small subunit (SSU) and large subunit (LSU) of *S. cerevisiae* were chosen as anchoring
175 points because of the presence of conserved priming sites ITS1/ITS1-F and ITS4. A 5.8S
176 sequence was designed using *S. cerevisiae* as a base but nucleotides were altered so it would
177 be compatible with several primers in the 5.8S region, including ITS2, ITS3, and fITS7. Random
178 sequences were generated with constrained GC content and sequence length for the ITS1 and
179 ITS2 regions. Twelve unique sequences were synthesized (Genescript) and cloned into pUC57
180 harboring ampicillin resistance. The SynMock sequences and the script to produce them are
181 available in the OSF repository ((https://osf.io/4xd9r/) as well as packaged into AMPtk
182 distributions. Each plasmid was purified by alkaline lysis, quantified, and an equimolar mixture
183 was created as a template for HTAS library prep.
184
185 *Preparation of HTAS libraries and NGS Sequencing*
186 HTAS libraries were generated using a proofreading polymerase, Pfx50 (ThermoFisher),
187 and thermocycler conditions were as follows: initial denaturation of 94°C for 3 min, followed by
188 11 cycles of [94°C for 30 sec, 60°C for 30 sec (drop 0.5°C per cycle), 68°C for 1 min], then 26
189 cycles of [94°C for 30 sec, 55°C for 30 sec, and 68°C for 1 min], with a final extension of 68°C
190 for 7 minutes. PCR products were cleaned using either E-gel® CloneWell™ 0.8% SYBR® Safe
191 agarose gels (Life Technologies) or Zymo Select-a-size spin columns (Zymo Research). All
192 DNA was quantified using a Qubit® 2.0 fluorometer with the high-sensitivity DNA quantification
193 kit (Life Technologies).

194 A single step PCR reaction was used to create Ion Torrent compatible sequencing
195 libraries, and primers were designed according to manufacturer's recommendations. Briefly, the
196 forward primer was composed of the Ion A adapter sequence, followed by the Ion key signal
197 sequence, a unique Ion Xpress Barcode sequence (10-12 bp), a single base-pair linker (A),
198 followed by the fITS7 primer (Ihrmark *et al.*, 2012). The reverse primer was composed of the Ion
199 trP1 adapter sequence followed by the conserved ITS4 primer (White *et al.*, 1990). Sequencing
200 on the Ion Torrent PGM was done according to manufacturer's recommendations using an Ion
201 PGM™ Hi-Q™ OT2 Kit, an Ion PGM™ Hi-Q™ Sequencing Kit, an Ion PGM™ sequencing chip
202 (316v2 or 318v2), and raw data were processed with the Ion Torrent Suite v5.0.3 with the "--
203 disable-all-filters" flag given to the BaseCaller. Libraries for Illumina MiSeq were generated by a
204 two-step dual indexing strategy. All samples were PCR amplified with Illumina-fITS7 and
205 Illumina-ITS4 primers. PCR products were cleaned and then dual-barcoded using an 8 cycle
206 PCR reaction using the Illumina Nextera Kit and subsequently sequenced using 2 x 300 bp
207 sequencing kit on the Illumina MiSeq at the University of Wisconsin Biotechnology Center DNA
208 Sequencing Facility. All primers utilized in this study are available via the OSF repository
209 (https://osf.io/4xd9r/).
210
211 *Data processing using AMPtk*
212 AMPtk is publically available at https://github.com/nextgenusfs/amptk. All primary data
213 and data analysis done in this manuscript is available via the Open Science Framework
214 (https://osf.io/4xd9r/). AMPtk is written in Python and relies on several modules: edlib (Šošic &
215 Šikic, 2017), biopython (Cock *et al.*, 2009), biom-format (McDonald *et al.*, 2012), pandas
216 (McKinney), numpy (van der Walt *et al.*, 2011), and matplotlib modules (Hunter, 2007). External
217 dependencies are USEARCH v9.1.13 (Edgar, 2010) or greater and VSEARCH v2.2.0 (Rognes
218 *et al.*, 2016) or greater. In order to run the DADA2 (Callahan *et al.*, 2016) method R is required
219 along with the shortRead (Morgan *et al.*, 2009) and DADA2 packages. The major steps for
220 processing HTAS data are broken down into i) pre-processing reads, ii) clustering into OTUs, iii)
221 filtering OTU table, and iv) assigning taxonomy.
222
223 *Pre-processing reads* – Data structures from Roche 454 and Ion Torrent are similar where
224 reads are in a single file and have a unique barcode at the 5' end of the read followed by the
225 gene-specific priming site; therefore, AMPtk processes reads from these two platforms very
226 similarly. As a preliminary quality control step, only reads that have a valid barcode and forward
227 primer are retained. Next, reverse primer sequences are removed and reads are trimmed to a

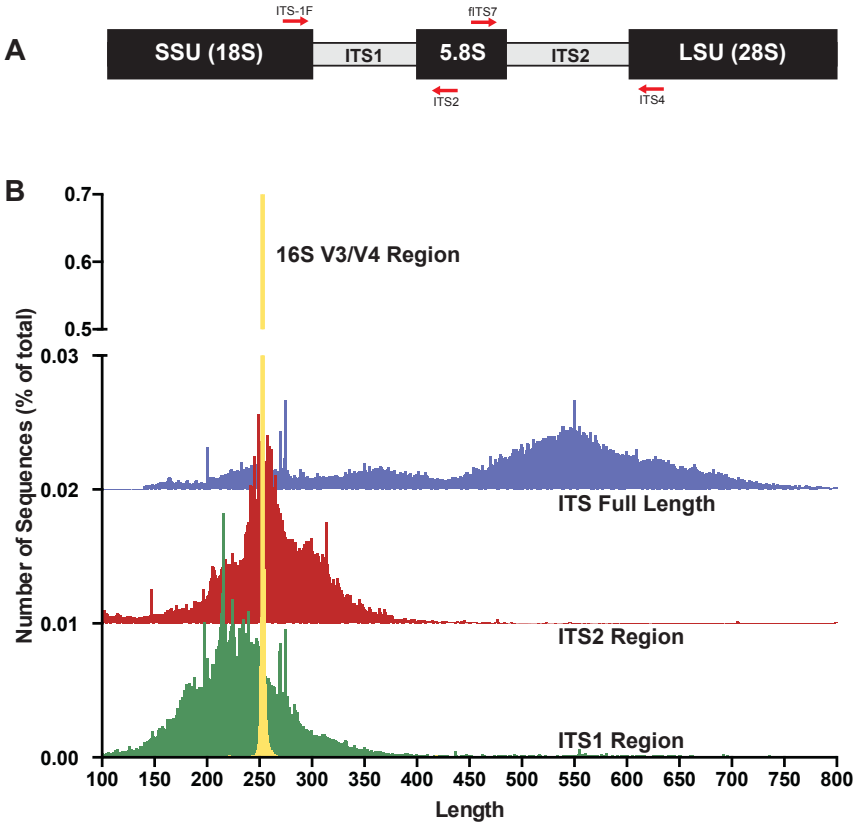
228 user-defined maximum length. Data from Illumina is processed differently because reads are
229 most often paired-end reads and most sequencing centers provide users with de-multiplexed by
230 sample paired-end data (i.e. output of 'bcl2fastq'). AMPtk first merges the paired end reads
231 using USEARCH or VSEARCH, phiX spike-in control is removed with USEARCH, forward and
232 reverse primers are removed if found, and all data are combined into a single file. Pre-
233 processing reads in AMPtk from any of the sequencing platforms results in a single output file
234 that is compatible with all downstream steps.
235
236 *Clustering reads into OTUs* – AMPtk is capable of running several different clustering algorithms
237 including UPARSE, DADA2, UNOISE2, UNOISE3, and reference-based clustering. The
238 algorithms all start with quality filtering using expected errors trimming and are modified slightly
239 in AMPtk to build OTU tables using the original de-multiplexed data; therefore read counts
240 represent what was in the sample prior to quality filtering. This is an important distinction, as
241 expected errors quality trimming (Edgar & Flyvbjerg, 2015) can be rather stringent if long read
242 lengths are used and the amplicons are of variable length.
243
244 *Index-bleed filtering of OTU tables* – Filtering in AMPtk works optimally when a spike-in mock
245 community is sequenced in the dataset. While by default AMPtk is setup to work with the
246 SynMock described herein, any spike-in mock community can be used. AMPtk identifies which
247 OTUs belong to the mock community and calculate index-bleed of that mock community into
248 other samples as well as bleed into the mock community from samples. This calculated index-
249 bleed percentage is then used to filter the OTU table. Filtering is done on a per OTU basis, such
250 that read counts in each OTU that are below the index-bleed threshold are set to zero as they
251 fall within the range of data that could be attributed to index-bleed.
252
253 *Assigning taxonomy* - AMPtk is pre-configured with databases for fungal ITS, fungal LSU,
254 arthropod mtCO1, and prokaryotic 16S; however custom databases are easily created with the
255 'amptk database' command. Several tools are available for taxonomy assignment in AMPtk
256 including remote blast of the NCBI nt database, RDP Classifier (Wang *et al.*, 2007), global
257 alignment to a custom sequence database, UTAX Classifier (RC Edgar,
258 http://drive5.com/usearch/manual9.2/cmd_utax.html), and the SINTAX Classifier (Edgar, 2016).
259 The default method for taxonomy assignment in AMPtk is a "hybrid" approach that uses
260 classification from global alignment, UTAX, and SINTAX. The best taxonomy is then chosen as
261 follows: i) if global alignment percent identity is > 97% then the top hit is retained, ii) if global

262 alignment percent identity is < 97%, then the best confidence score from UTAX or SINTAX is
263 used, iii) if there is disagreement between taxonomy levels assigned by each method then a
264 least common ancestor (LCA) approach is utilized to generate a conservative estimate of
265 taxonomy. AMPtk also can take a QIIME-like mapping file that can contain all the metadata
266 associated with the HTAS study; the output is then a multi-fasta file containing taxonomy in the
267 headers, a classic OTU table with taxonomy appended, and a BIOM file incorporating the OTU
268 table, taxonomy, and metadata. The BIOM output of AMPtk is compatible with several
269 downstream statistical and visualization software packages such as PhyloSeq (McMurdie &
270 Holmes, 2013).
271
272 *Accessory scripts in AMPtk* - AMPtk has several additional features that will aid the user in
273 analyzing HTAS data. For instance, AMPtk contains a script that will prepare data for
274 submission to the NCBI SRA archive by formatting it properly and outputting a ready-to-submit
275 SRA submission file. The FunGuild (Nguyen *et al.*, 2016) package which assigns OTUs to an
276 annotated database of functional guilds is also incorporated directly into AMPtk. Additionally,
277 users can draw a heatmap of an OTU table as well as summarize taxonomy in a stacked
278 histogram.
279
280 **Results:**
281 *In silico analysis of the fungal ITS region*
282 To gain baseline data on potential amplicons of the ITS1 or ITS2 regions, the ITS1 and
283 ITS2 regions were extracted using priming sites specific for each region (ITS1: ITS1-F and
284 ITS2; ITS2: fITS7 and ITS4) from the UNITE+INSD v7.2 database (Abarenkov *et al.*, 2010)
285 consisting of 736,375 ITS sequences. For comparison, the commonly sequenced V3-V4 region
286 was extracted from prokaryotic 16S sequences from the Silva v128 database (Quast *et al.*,
287 2013). A length histogram for each dataset as well as summary statistics were generated
288 (Figure 1B; Table 1), indicating that all three of these molecular barcodes have an average
289 length of ~ 250 bp (Table1); however, there was considerable variation in the lengths of the ITS
290 region in comparison to the V3/V4 region of 16S (Figure 1B). Stretches of homopolymer
291 sequences can also be problematic for some NGS platforms (454 and PGM), and thus the
292 number of sequences in this dataset that contained homopolymer stretches greater than 6
293 nucleotides were calculated (Table 1). Given the small percentage of ITS1 and ITS2 regions
294 that are greater than 450 bp (the current upper limit of the Ion Torrent PGM platform), the
295 number of taxa in the reference database that are unlikely to sequence on the Ion Torrent due

296 to amplicon length is relatively small (Table 1). Illumina MiSeq is now capable of paired end 300
297 bp read lengths (2 x 300); however, reads need to overlap for proper processing in NGS
298 software platforms and thus a ~ 500 bp size limit would also be able to sequence most taxa in
299 the reference database.
300
301 Table 1. Summary statistics of the fungal ITS molecular barcode in comparison to bacterial 16S.

Region	Num Seqs	Avg Length (bp)	% HP[1] > 6	% HP[1] > 8	% > 450 bp
ITS Full Length	696 704	488	55.07%	8.66%	-
ITS1	685 399	247	36.58%	5.60%	3.27%
ITS2	535 200	264	44.19%	5.54%	0.83%
16S (V3/V4)	627 247	253	23.74%	1.02%	-

302 [1] HP: homopolymer stretches



303

304 **Figure 1.** The fungal internal transcribed spacer (ITS) region of the rRNA array is highly variable
305 in length. (A) A schematic of the rRNA array highlights the conserved priming sites commonly
306 used to amplify either the ITS1 or ITS2 region. (B) Size distribution of full length ITS (blue), ITS1
307 (green), ITS2 (red) sequences in the UNITE v7.2 curated databases shown in comparison to the
308 bacterial 16S V3/V4 amplicon from the Silva v128 database. Current sequencing technologies
309 do not have read lengths long enough to capture full-length ITS sequences, and thus ITS1 or
310 ITS2 regions are used for fungal environmental community analysis. 16S V3/V4 in yellow; ITS
311 full length in blue, ITS2 in red, and ITS1 in green.

312 *Creation of a representative artificial fungal mock community (BioMock)*

313 Given the results from analysis of the UNITE datasets, we set out to create a
314 representative ITS mock community to be used as a spike-in sequencing control to determine
315 the quantitative nature of ITS HTAS and to measure the performance between the commonly
316 used Illumina MiSeq platform versus the Ion Torrent PGM. To circumvent the problematic
317 issues associated with the ITS region, we reasoned that cloned ITS sequences in plasmid form
318 would allow for accurate quantification and pooling, thus providing a means to test the accuracy
319 of the sequencer platforms and data processing workflows. Therefore, we cloned known ITS
320 sequences from 26 cultures from the CFMR culture collection that varied in length (237 bp to
321 548 bp), ranged in GC content (43.8% - 68.4%), and contained sequences with homopolymer
322 stretches with one sequence containing two 9 bp stretches (Figure 4). These plasmids were
323 combined into a BioMock and BioMock-standards as described in materials and methods
324 section. The value of the BioMock-standards is that the library was combined after PCR, and
325 thus the standards are free from PCR-induced artifacts that may arise from PCR of a mixed
326 community.
327

328 *Existing data processing workflows perform poorly with fungal ITS sequences*

329 Clustering amplicons into operational taxonomic units (OTUs) is common practice in
330 molecular ecology and there are many software solutions/algorithms (such as QIIME (Caporaso
331 *et al.*, 2010), UPARSE (Edgar, 2013), Mothur (Schloss *et al.*, 2009), and DADA2 (Callahan *et*
332 *al.*, 2016)) that have been developed to deal appropriately with errors associated with next-
333 generation sequencing platforms. Many studies using 16S amplicon data have focused on
334 comparing clustering methods (Edgar, 2013; Callahan *et al.*, 2016), while others have focused
335 on quality filtering reads prior to clustering (Edgar & Flyvbjerg, 2015). Therefore, we chose not
336 to compare the different software algorithms here, but will briefly mention that when we did run
337 our data through QIIME, the number of OTUs was highly over-estimated and the error rates
338 were very high (Table S2). We were unable to run our data through Mothur due to the inability to
339 do a multiple sequence alignment and subsequent distance matrix of the ITS region. The best
340 performing clustering pipeline was UPARSE; however there were several issues with how the
341 reads were pre-processed and quality filtered that lead to suboptimal results (Table S3 and
342 Table S4). It is important to note that all of these software solutions have been built with 16S
343 amplicons in mind and several have been optimized for Illumina data.

344 The major difference in 16S amplicons versus those of ITS1/ITS2 is that the lengths of
345 16S amplicons are nearly identical, while ITS1/ITS2 amplicons vary in length (Figure 1B). This

346 distinguishing feature makes ITS sequences from diverse taxa impossible to align (Schoch *et*
347 *al.*, 2012) and thus represents a major limitation in data processing. To illustrate the importance
348 of properly pre-processing ITS data, we clustered using UPARSE the ITS1 and ITS2 regions
349 using the UNITE reference database (Figure 2). Using the full length ITS1/ITS2 sequences as a
350 benchmark, we then explored the outcome of trimming/truncating the sequences to different
351 length thresholds, a common practice in OTU clustering pipelines. The UPARSE algorithm uses
352 global alignment and as such terminal mismatches count in the alignment (as opposed to local
353 alignment where terminal mismatches are ignored); thus the UPARSE pipeline expects that
354 reads are truncated to a set length. UPARSE achieves this by truncating all reads to a set
355 length threshold and discards reads that are shorter than the length threshold. Therefore real
356 ITS sequences are discarded (Figure 2). We then came up with two potential solutions to fix this
357 unintended outcome: i) truncate reads that were longer than the threshold and keep all shorter
358 reads (full length), and ii) truncate longer reads and pad the shorter reads with N's out to the
359 length threshold (padding). Using the UNITE v7.2 database of curated sequences (general
360 release June 28th, 2017) as input, both "full-length" and "padding" improved UPARSE results
361 with the "full length" method recovering more than 99% of the expected OTUs (Figure 2).
362

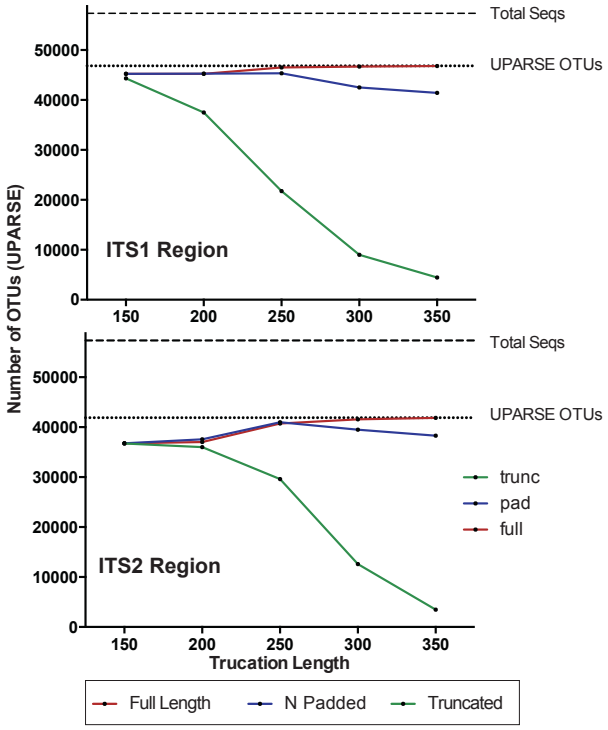
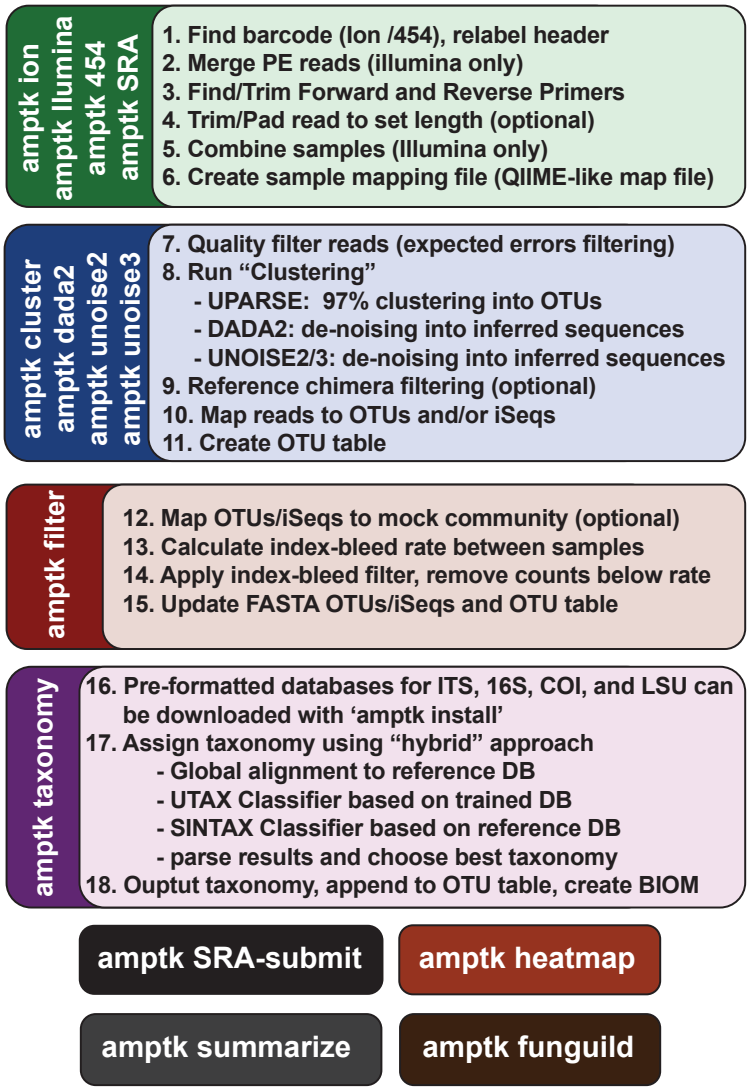


Figure 2. Pre-processing ITS sequences is critically important to accurately recover OTUs using the curated UNITE v7.2 reference database. ITS1 and ITS2 sequences were extracted from the UNITE v7.2 general fasta release database using 'AMPtk database'. Identical sequences were collapsed (dereplication) and remaining sequences were clustering using UPARSE ('cluster_otus) to generate the total number of UPARSE OTUs expected for the ITS1 and ITS2 regions. The data was then processed to five different lengths (150, 200, 250, 300, and 350 bp) and then clustered (UPARSE 'cluster_otus') using i) default UPARSE truncation (longer sequences are truncated and shorter sequences are discarded), ii) padding with ambiguous bases (longer sequences truncated and shorter sequences padded with N's to length threshold), and iii) full-length sequences (longer sequences are truncated and shorter sequences are retained if reverse primer is found). Full-length and padding pre-processing sequences outperforms default UPARSE truncation.

Due to the intrinsic nature of the variable length ITS amplicons, we needed a data processing solution that would be flexible enough to maintain the full length of the reads, trim reads without data loss, prepare sequencing reads for downstream clustering algorithms, and support all major NGS platforms. Using the BioMock artificial communities as a means to validate the results of all data processing steps, we wrote a flexible series of scripts for processing Illumina, Ion Torrent, as well as Roche 454 data that are packaged into AMPtk (amplicon tool kit). A flow diagram of AMPtk is illustrated in Figure 3 and a more thorough description of AMPtk is provided in the material and methods section. A manual for AMPtk is available at http://amptk.readthedocs.io/en/latest/. After data is pre-processed with AMPtk via a

386 platform specific method, AMPtk then functions as a wrapper for several popular algorithms
387 including UPARSE, DADA2, UNOISE2, and UNOISE3. All data presented in this manuscript
388 were processed with AMPtk v1.0.1.
389



390

391 **Figure 3.** Overview of the commands in AMPtk. AMPtk is built to be compatible with multiple
392 sequencing platforms as well as contains several clustering algorithms.

393

394 *Read abundances do not represent community abundances: PCR introduces bias*

395 Next-generation sequencing platforms are quantitative if the library to be sequenced is
396 unbiased, as is typically the case with RNA-sequencing and whole genome sequencing library
397 prep protocols. However, PCR of mixed communities has long been shown to introduce bias in
398 next-generation sequencing workflows (Aird *et al.*, 2011; Pinto & Raskin, 2012; Kebschull &

399 Zador, 2015). For HTAS this is an important caveat, as molecular ecologists are interested in
400 diversity metrics of environmental communities as well as their relative abundance. Through the
401 use of mock communities, several studies have pointed out that read abundance from fungal
402 HTAS are not representative of relative biological abundance (Amend *et al.*, 2010; De Filippis *et*
403 *al.*, 2017). However, it was recently reported that for a fungal ITS mock community of 8
404 members, abundances were meaningful (Taylor *et al.*, 2016) and many studies continue to use
405 abundance-based metrics to analyze HTAS, without giving any consideration to
406 presence/absence-based metrics. We reasoned we could investigate this issue using the ITS
407 BioMock artificial community, which would not suffer from bias associated with DNA extraction,
408 ITS copy numbers, and intraspecific variation. We compared the relative read abundances of
409 BioMock-standards to 3 different combinations of BioMock on both the Ion Torrent PGM and
410 Illumina MiSeq platforms (Figure 4). The BioMock-standards consist of an equimolar mixture of
411 26 PCR products, while the BioMock communities consist of an equimolar mixture of 23 single-
412 copy plasmids. These data show that even in an extreme example of an equally mixed
413 community of cloned ITS sequences, read abundance does not represent actual abundance in
414 the mock community (Figure 4). The majority of the bias is introduced at the initial PCR step, as
415 the pre-PCR combined BioMock-standards result in a more equal distribution of reads, albeit not
416 a perfect distribution. We also tested PCR conditions, DNA concentrations, and sample
417 reproducibility on the Ion Torrent PGM (Supplemental Figure S1). While the bias via PCR is
418 consistent between sequencing platforms, there is no obvious correlation between length of the
419 read, GC content, nor stretches of homopolymers affecting efficient PCR amplification. For
420 example, *Wolfiporia dilatophya* (mock11) contains no homopolymer stretches larger than 5, has
421 GC distribution of 54.6%, and is near the median in length, yet it does not PCR amplify well in
422 the BioMock community (Figure 4). These data also show a size limitation in the Ion Torrent
423 PGM workflow, as *Wolfiporia cocos* (mock 26) sequences very poorly due to its long ITS2
424 region (Figure 5). Three members of the original 26 members of the BioMock community were
425 dropped (mock24, mock25, mock26) due to persistent problems getting them to
426 amplify/sequence in repeated HTAS on the Ion Torrent platform (Supplemental Figure S1).

Species	ITS2 Length	GC Content	HP > 5	ID	Ion Torrent PGM				Illumina MiSeq			
					Stds	Mock A	Mock B1	Mock B2	Stds	Mock A	Mock B1	Mock B2
Phialocephala fusca	237	68.4%	0	mock1	4905	19	6	1	8615	725	329	3337
Ascomycete sp.	238	50.8%	0	mock2	5106	11651	10809	11877	9174	20763	26129	18341
Phialocephala lagerbergii	238	58.8%	0	mock3	4886	13479	12111	13392	8648	28515	29482	21269
Helotiales sp.	239	57.3%	0	mock4	4233	15219	13048	14896	9050	27726	32576	24276
Aspergillus candidus	260	65.8%	3	mock5	2813	31	23	3	8992	147	122	269
Bjerkandera adusta	281	51.2%	0	mock6	3977	8112	7172	7787	13597	13112	13866	15067
Laetiporus caribensis	283	52.7%	0	mock7	3330	7810	6457	6365	9404	15035	16622	16385
Trametes gibbosa	288	50.0%	1	mock8	3637	7281	6914	6865	8137	13819	14579	14787
Laetiporus gilbertsonii	290	54.1%	0	mock9	4066	8831	10401	12638	8751	22860	21680	20682
Gloeoporus pannocinctus	292	43.8%	0	mock10	2603	2922	3025	2567	9718	11150	11792	14265
Wolfiporia dilatohypha	293	54.6%	0	mock11	3957	94	110	109	8775	243	224	194
Schizopora sp.	293	48.1%	0	mock12	4037	6965	7030	6626	8676	12857	13947	14860
Fomitopsis ochracea	295	44.1%	0	mock13	3689	2913	2860	2651	9471	5522	5432	6883
Laetiporus cremeioporus	296	54.7%	0	mock14	3922	10279	11920	12440	8262	16454	16390	16798
Phanerochaete laevis	300	47.7%	1	mock15	3863	6970	7650	6876	9242	15667	15543	18168
Laetiporus cincinnatus	302	54.0%	0	mock16	3133	5699	7645	7505	7675	16819	16157	14608
Punctularia strigosozonata	303	53.1%	0	mock17	4019	8271	7688	8217	7669	10701	11572	11671
Phellinus cinereus	314	49.7%	0	mock18	3672	2937	2985	2597	9807	6314	5953	7496
Antrodiella semisupina	315	43.8%	1	mock19	3089	3047	3406	2741	9297	9356	8990	11593
Leptoporus mollis	315	45.4%	3	mock20	3551	4969	4320	4028	9047	8847	8747	9987
Leptoporus mollis 2	315	45.1%	1	mock21	3776	207	366	249	9250	405	302	414
Mortierellales sp.	353	45.0%	0	mock22	3264	4668	4311	3812	9151	10865	9728	13365
Laetiporus persicinus	379	51.2%	2	mock23	2147	2651	2385	2053	6486	488	421	521
Penicillium nothofagi	260	66.2%	1	mock24	3644	NA	NA	NA	8278	NA	NA	NA
Metapochonia suchlasporia	291	64.6%	1	mock25	1976	NA	NA	NA	2045	NA	NA	NA
Wolfiporia cocos	548	59.7%	0	mock26	7	NA	NA	NA	5979	NA	NA	NA

Figure 4. Read abundance is an unreliable proxy for actual abundance within a mixed community. Using an equimolar mixture of cloned ITS sequences in plasmid form (MockA, MockB1, MockB2) in comparison to equimolar mixture of individual PCR products (Stds) illustrates that the initial PCR reaction during library preparation heavily biases the read abundance obtained after sequencing on both the Ion Torrent PGM and Illumina MiSeq platforms. While read abundances are unreliable, all members of the mock community were recovered. MockA represents a 1:16,000 dilution and MockB1/MockB2 are replicates of a 1:32,000 dilution of the BioMock community. The Ion Torrent PGM platform has a length threshold of approximately 450 bp; therefore longer amplicons like *Wolfiporia cocos* ITS2 sequence very poorly.

In HTAS experiments, considerable effort is made to try to sequence to an equal depth for each sample. However, in practice this rarely works perfectly and thus a typical HTAS dataset has a 2-4X range in number of reads per sample. The depth of sequence range for the HTAS runs presented here is within a range of 2X for each run and the smallest number of

442 reads per sample in any of our sequencing runs was nearly 60,000 (Supplemental Table S5).
443 Unequal sequencing depth has been used as rationale for explaining the lack of correlation
444 between read abundance and actual abundance. Therefore, random subsampling of reads in
445 each sample prior to clustering (also called rarefying) has been widely used in the literature,
446 despite a compelling statistical argument that this method is flawed (McMurdie & Holmes,
447 2014). Randomly subsampling reads for each sample using our BioMock community yielded
448 nearly identical results (Supplemental Figure S2). Sequencing depth has been shown to be an
449 important variable for HTAS experiments (Smith & Peay, 2014), therefore we typically employ a
450 5,000 reads per sample cutoff when processing environmental datasets.
451
452 *A non-biological (synthetic) mock community to measure index-bleed among samples*
453 Index-bleed is a phenomenon that has been described on Roche 454 platform (Carlsen
454 *et al.*, 2012) as well as Illumina platforms (Kircher *et al.*, 2012; Wright & Vetsigian, 2016). A
455 consensus on a mechanism of index-bleed during the sequencing run has yet to be reached.
456 Index-bleed is a significant challenge to overcome as sample crossover has the potential to
457 over-estimate diversity and lead to inaccurate representations of microbial communities,
458 especially considering that read abundance is an unreliable proxy for biological abundance
459 (Figure 4). Using our BioMock sequencing results, we also discovered this phenomenon on both
460 Ion Torrent and Illumina platforms. We calculated the rate of index-bleed in our BioMock Ion
461 Torrent sequencing run to be 0.033% and on Illumina MiSeq between 0.233% and 0.264%. We
462 also confirmed that index-bleed was happening on the Illumina flow-cell by re-running a subset
463 of samples that had shown high index-bleed on different flowcell that did not contain the
464 BioMock (Supplemental Figure S3). One problem that we noticed in measuring index-bleed
465 using a mock community of actual ITS sequences (BioMock) was that these same taxa in the
466 mock community could be present in environmental samples, which would lead to inaccurate
467 estimation of index-bleed. In our environmental data, it was likely that at least one of the
468 BioMock members was present in several of the environmental samples, suggesting the
469 calculated index-bleed could be over-estimated. To overcome this problem, we designed a non-
470 biological (synthetic) mock community composed of ITS-like sequences that contained
471 conserved priming sites (SSU and LSU regions), ITS1 region, 5.8S region, and an ITS2 region
472 (Figure 6). We designed the ITS1 and ITS2 portions of the sequences to be non-biological; that
473 is, no similar sequences are known to occur in nature (based on searches of known databases
474 and based on the infinitesimally low probability that a randomly generated sequence would
475 match something found in nature) and therefore these non-biological sequences can be used to

accurately track index-bleed in HTAS studies. Using the summary statistics from the analysis of the UNITE reference database for guidance, we also varied the length, GC content, and homopolymer stretches to be representative of real ITS sequences.

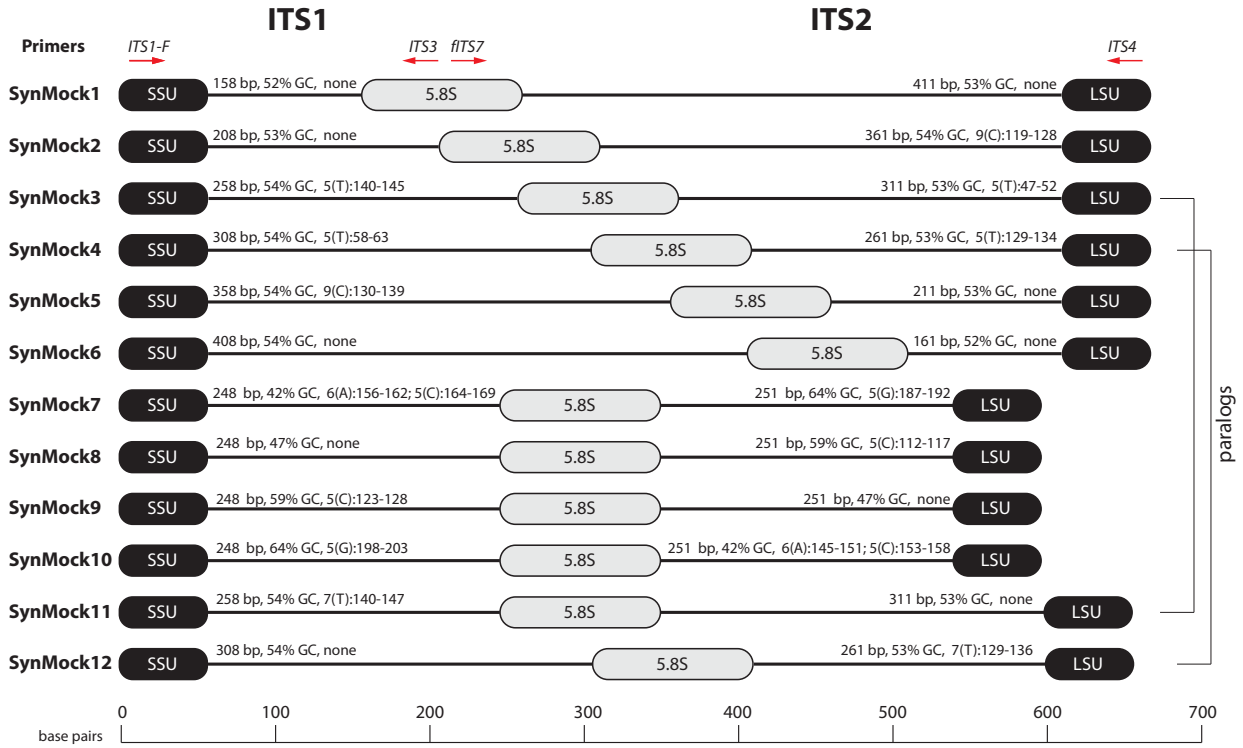


Figure 5. Schematic drawing of the 12-member non-biological synthetic mock community (SynMock). Conserved priming sites for either ITS1 or ITS2 amplicons are retained for versatility. The length distribution, GC content, and homopolymer stretches are representative of curated public databases, however, the sequences are non-biological and thus not found in nature.

The SynMock was tested as a spike-in control on both the Ion Torrent and Illumina MiSeq platforms. The raw data were processed using AMPtk and clustered using UPARSE. These data illustrate that the synthetic sequences are able to be processed simultaneously with real ITS sequences and provide a way to track the level of index-bleed between multiplexed samples (Figure 6). The increased benefit of being able to track the SynMock sequences as they “bleed” out of the sample allows for a more accurate measurement of index-bleed. Using default Illumina de-multiplexing (allowing 1 mismatch in the index sequence), index-bleed using the SynMock community was 0.072% (Figure 6C). To determine if allowing mismatches in the index reads was increasing index-bleed, we reprocessed the data with 0 mismatches and found that index-bleed was reduced to 0.046%. While index-bleed was reduced by nearly half, the tradeoff was that 0 mismatches resulted in approximately 10% fewer reads. For most datasets, a loss of 10% of the sequencing reads should not be problematic, especially if the benefit is to

497 reduce index-bleed in the data. We noted that in our Illumina dual-indexing library prep that
498 there was increased index-bleed on samples that had a shared reverse index (i7), suggesting
499 that errors are increased at later stages of an Illumina sequencing run (Figure 6B). A similar
500 pattern was observed with Ion Torrent PGM data, although not as drastic. Allowing 1 mismatch
501 in the barcode resulted in 0.167% index-bleed while allowing 0 mismatches in the barcode
502 resulted in 0.156% index-bleed (Figure 6C). While these data would suggest that index-bleed is
503 perhaps higher in Ion Torrent PGM datasets, we have subsequently used the SynMock on more
504 than 10 different HTAS Ion Torrent PGM experiments and have since seen much lower levels of
505 index-bleed, occasionally approaching 0% index-bleed.
506 Many environmental samples can contain hundreds of taxa and thus a legitimate
507 concern is that the 12 member SynMock community does not represent a realistic community in
508 terms of diversity in a sample. To test if the SynMock was able to be recovered in a more
509 complex community, we mixed SynMock together with two environmental samples that had
510 more than 200 OTUs in previous sequencing runs. These mixed samples show that SynMock
511 could be recovered from a complex community and the sequences behave like real ITS
512 sequences (Figure 6A). While many studies have set a read count threshold to filter “noisy” data
513 from OTU tables, this threshold has been typically selected arbitrarily, i.e. OTUs with read
514 counts less than 100 or less than 10% of the total, etc. Use of the SynMock spike-in control
515 allowed for data driven thresholds to be measured and moreover for the ability to filter the OTU
516 table based on the calculated index-bleed. The AMPtk filter command calculates index-bleed by
517 mapping the OTUs to the mock community and then provides a way to filter the OTU table
518 based on this calculated value. AMPtk filters across each OTU in the table such that difficult to
519 sequence or “low abundance” OTUs are not indiscriminately dropped. Taken together, these
520 data illustrate the utility of a non-biological mock community in parameterizing data processing
521 steps and importantly providing a method in AMPtk to reduce index-bleed from HTAS datasets.
522 AMPtk provides an easy to use method to accurately process variable length amplicons, cluster
523 them into OTUs or denoise sequences, generate an OTU table, filter the OTU table for index-
524 bleed, and assign taxonomy.

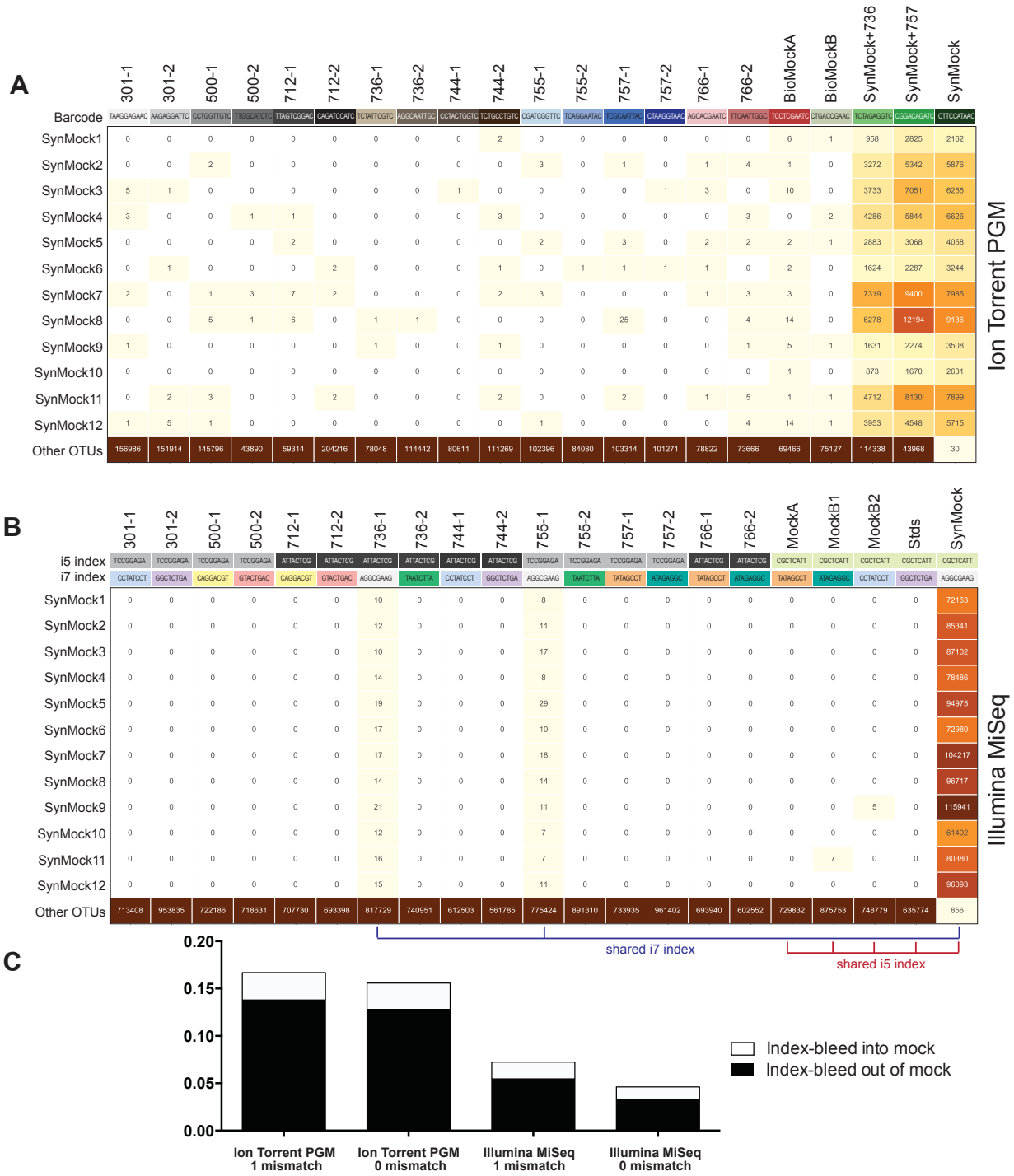


Figure 6. Index-bleed or sample mis-assignment occurs on both Ion Torrent PGM and Illumina Miseq. (A) Read counts from the SynMock community run on the Ion Torrent PGM platform. SynMock reads can be found in environmental samples and reads from the environmental samples are found in the SynMock sample. The data were processed allowing 0 mismatches in the barcode sequence and there is no clear pattern to index-bleed on the Ion Torrent PGM platform. (B) Data processed on the Illumina MiSeq (2x300) allowing 0 mismatches in the index reads show index-bleed in and out of the SynMock sample. Samples that share an index (i5 or i7) show an increase in index-bleed. (C) Index-bleed between samples can be tracked using the

534 SynMock spike-in control, where AMPtk will measure both index-bleed into the SynMock as well
535 as index-bleed into other samples. These calculated values are then used by AMPtk to filter an
536 OTU table to remove read counts that fall below the index-bleed threshold. Index-bleed is
537 reduced if 0 mismatches are allowed in the barcode/index sequence, however, this is still not
538 sufficient to reduce all index-bleed.

539

540 **Discussion**

541 HTAS studies have the goal of measuring environmental diversity; however, there are
542 technical limitations that need to be understood in order to reach justifiable conclusions. Mock
543 communities and negative controls have been shown to have great utility for HTAS studies, and
544 expanding upon this concept, we present a non-biological synthetic mock community of ITS-like
545 sequences for use as a technical spike-in control for fungal biodiversity studies. Additionally, we
546 describe AMPtk, a software tool kit for analyzing variable length amplicons such as the fungal
547 ITS1 or ITS2 molecular barcodes. These two tools can be coupled together to validate data
548 processing pipelines and reduce index-bleed from OTU tables prior to downstream community
549 ecology analyses. The concept of a non-biological synthetic spike-in control can be expanded to
550 many different genes and organisms, including 16S for microbiome studies.

551 The ITS region is widely used as a molecular barcode in fungal biodiversity studies as it
552 is easy to amplify and public reference databases are robust. However, HTAS with the ITS
553 region presents some unique challenges due to variability in sequence characteristics such as
554 length and copy number. Most HTAS software development and optimization has been focused
555 on the 16S molecular barcode, a region that is near uniform in length across prokaryotic taxa.
556 Thus, there is a need for a software solution that can more accurately account for variable
557 length amplicons. We developed a single-copy mock community based on cloned ITS
558 sequences as a tool to validate and compare different NGS platforms and data processing
559 pipelines. Using an artificial single-copy mock community of cloned ITS sequences in plasmids
560 (BioMock), we determined that the core clustering/denoising algorithms work for variable length
561 amplicons; however, pre-processing techniques widely used for uniform length amplicons
562 introduce significant error into the pipelines. Simplifying the pre-processing of sequencing reads
563 (i.e., identifying unique sequence barcodes, forward/reverse primers, and trimming reads to a
564 uniform length without data loss) resulted in large improvement in downstream OTU clustering.
565 The pre-processing of reads prior to quality filtering is critical for variable length amplicons and
566 is implemented in AMPtk.

567 Proper pre-processing of variable length amplicons improves clustering results
568 substantially. However, the BioMock results illustrated that read abundances obtained from

569 HTAS are not a reliable proxy for inferring biological relative abundance. These data do support
570 use of presence/absence (binary) metrics as we were able to recover all members of our mock
571 community, even when they were spiked into a diverse environmental sample. We identified the
572 initial PCR reaction (library construction) as the major source of read number bias, a conclusion
573 consistent with the literature (Polz & Cavanaugh, 1998; Wu *et al.*, 2010; Jusino *et al.*, 2017). To
574 reduce PCR artifacts for any assay it is generally accepted that one should use the fewest
575 cycles possible, the most concentrated DNA possible, and it has been suggested to use a
576 proofreading polymerase (Oliver *et al.*, 2015). We have tested DNA concentration and PCR
577 cycle numbers for HTAS library generation and subsequent sequencing on the Ion Torrent PGM
578 platform, and our results were consistent with these general guidelines (Supplemental Figure
579 S1). However, following these guidelines is not sufficient to reduce the bias in read abundance
580 from a mixed community from PCR. The Ion Torrent PGM platform currently has an amplicon
581 size limit of ~ 450 bp, and thus some very large ITS sequences are difficult to sequence.
582 However, there are only a small number of known ITS1 or ITS2 sequences that are longer than
583 450 bp (Table 1) and therefore either platform, Ion Torrent or MiSeq, provided similar results
584 under the conditions tested.
585 Index-bleed has recently been acknowledged by Illumina (https://tinyurl.com/illumina-
586 hopping), although they limit their acknowledgement to a new flow cell on the HiSeq and
587 NovaSeq platforms. Several studies have shown that older instruments/flowcells have also
588 shown index-bleed, albeit at a much lower rate (Kircher *et al.*, 2012; Wright & Vetsigian, 2016)
589 and index-bleed has been identified on Roche 454 (Carlsen *et al.*, 2012). Here we report a low
590 rate of index-bleed on both Ion Torrent and Illumina MiSeq platforms. While the effective rate of
591 index-bleed is low (< 0.2%), coupled with the fact that read number is not a reliable proxy of
592 community abundance, index-bleed in datasets being analyzed by presence-absence metrics is
593 a problematic scenario. To identify and combat index-bleed, we created a non-biological
594 synthetic mock community (SynMock) of ITS-like sequences that behave like real ITS
595 sequences during the HTAS workflow. Because the SynMock sequences are not known to
596 occur in nature, they can be effectively used to measure index-bleed in a sequencing run. A
597 similar approach was recently described for 16S amplicons using synthesized oligonucleotides
598 (Kim *et al.*, 2017). We propose that HTAS studies of fungal ITS communities should employ
599 SynMock or a similar non-biological mock community as a technical control. Additional controls
600 such as a biological mock community of mixed fruiting bodies, spores, hyphae, etc. of taxa of
601 interest are also useful if the experiment is designed to identify the prevalence of particular taxa.

The bioinformatics pipeline presented here, AMPtk, was developed to specifically address the quality issues that we have identified by using spike-in mock communities and to provide the scientific community with a necessary tool to study fungal community diversity. AMPtk is a flexible solution that can be used to study other regions used in HTAS, such as mitochondrial cytochrome oxidase 1 (mtCO1) of insects and the large subunit (LSU) of the rRNA array. The goal of AMPtk is to reduce data processing to a few simple steps and to improve the output of HTAS studies. Due to the inherent properties of HTAS and the ITS molecular barcode, we take the position that studies of this nature should be used as a preliminary survey of which taxa present in an ecosystem and that inferring relative abundance from read numbers should be considered cautiously. To understand relative abundance of particular taxa in a community, additional independent assays such as taxa specific qPCR or digital PCR are warranted.

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Data availability

Raw sequencing reads and data processing scripts are available at the Open Science Framework at https://osf.io/4xd9r/. Data will be deposited in NCBI SRA prior to publication.

Author Contributions

All authors conceived and designed the experiments. MAJ and MTB conducted laboratory experiments. JMP analyzed sequence data and wrote AMPtk. JMP wrote the paper with input from all authors.

Competing financial interests

The authors declare no competing financial interests.

633 **Literature Cited**

634

635 **Abarenkov K, Henrik Nilsson R, Larsson K-H, Alexander IJ, Eberhardt U, Erland S,**
636 **Høiland K, Kjøller R, Larsson E, Pennanen T, et al. 2010.** The UNITE database for
637 molecular identification of fungi--recent updates and future perspectives. *The New*
638 *phytologist* **186**(2): 281-285.
639 **Aird D, Ross MG, Chen W-S, Danielsson M, Fennell T, Russ C, Jaffe DB, Nusbaum C,**
640 **Gnirke A. 2011.** Analyzing and minimizing PCR amplification bias in Illumina
641 sequencing libraries. *Genome Biology* **12**(2): R18.
642 **Amend AS, Seifert KA, Bruns TD. 2010.** Quantifying microbial communities with 454
643 pyrosequencing: does read abundance count? *Molecular Ecology* **19**(24): 5555-5565.
644 **Callahan BJ, McMurdie PJ, Rosen MJ, Han AW, Johnson AJA, Holmes SP. 2016.** DADA2:
645 High-resolution sample inference from Illumina amplicon data. *Nature Methods*.
646 **Caporaso JG, Kuczynski J, Stombaugh J, Bittinger K, Bushman FD, Costello EK, Fierer**
647 **N, Peña AG, Goodrich JK, Gordon JI, et al. 2010.** QIIME allows analysis of high-
648 throughput community sequencing data. *Nature Methods* **7**(5): 335-336.
649 **Carlsen T, Aas AB, Lindner D, Vrålstad T, Schumacher T, Kauserud H. 2012.** Don't make a
650 mista(g)ke: is tag switching an overlooked source of error in amplicon pyrosequencing
651 studies? *Fungal Ecology* **5**(6): 747-749.
652 **Cock PJA, Antao T, Chang JT, Chapman BA, Cox CJ, Dalke A, Friedberg I, Hamelryck T,**
653 **Kauff F, Wilczynski B, et al. 2009.** Biopython: freely available Python tools for
654 computational molecular biology and bioinformatics. *Bioinformatics (Oxford, England)*
655 **25**(11): 1422-1423.
656 **De Filippis F, Laiola M, Blaiotta G, Ercolini D. 2017.** Different amplicon targets for
657 sequencing-based studies of fungal diversity. *Applied and Environmental Microbiology*.
658 **Degnan PH, Ochman H. 2012.** Illumina-based analysis of microbial community diversity. *The*
659 *ISME journal* **6**(1): 183-194.
660 **Edgar R. 2016.** SINTAX: a simple non-Bayesian taxonomy classifier for 16S and ITS
661 sequences. *bioRxiv*: 074161.
662 **Edgar RC. 2010.** Search and clustering orders of magnitude faster than BLAST. *Bioinformatics*
663 **26**(19): 2460-2461.
664 **Edgar RC. 2013.** UPARSE: highly accurate OTU sequences from microbial amplicon reads.
665 *Nature Methods* **10**(10): 996-998.
666 **Edgar RC, Flyvbjerg H. 2015.** Error filtering, pair assembly and error correction for next-
667 generation sequencing reads. *Bioinformatics*.
668 **Ganley ARD, Kobayashi T. 2007.** Highly efficient concerted evolution in the ribosomal DNA
669 repeats: total rDNA repeat variation revealed by whole-genome shotgun sequence data.
670 *Genome Research* **17**(2): 184-191.
671 **Gardes M, Bruns T. 1993.** ITS primers with enhanced specificity for basidiomycetes -
672 application to the identification of mycorrhizae and rusts. *Molecular Ecology* **2**: 113-118.
673 **Hunter JD. 2007.** Matplotlib: A 2D Graphics Environment. *Computing in Science & Engineering*
674 **9**(3): 90-95.
675 **Ihrmark K, Bödeker IT, Cruz-Martinez K, Friberg H, Kubartova A, Schenck J, Strid Y,**
676 **Stenlid J, Brandström-Durling M, Clemmensen KE. 2012.** New primers to amplify the
677 fungal ITS2 region–evaluation by 454-sequencing of artificial and natural communities.
678 *FEMS Microbiology Ecology* **82**(3): 666-677.
679 **Jusino M, Banik M, Palmer J, Wray A, Xiao L, Pelton E, Barber J, Kawahara A, Gratton C,**
680 **Peery M, et al. 2017.** An improved method for utilizing high-throughput amplicon
681 sequencing to determine the diets of insectivorous animals. *PeerJ Preprints* **5**:
682 e3184v3181.

683 **Kebschull JM, Zador AM. 2015.** Sources of PCR-induced distortions in high-throughput
684 sequencing data sets. *Nucleic Acids Research* **43**(21): e143.
685 **Kim D, Hofstaedter CE, Zhao C, Mattei L, Tanes C, Clarke E, Lauder A, Sherrill-Mix S,**
686 **Chehoud C, Kelsen J, et al. 2017.** Optimizing methods and dodging pitfalls in
687 microbiome research. *Microbiome* **5**(1): 52.
688 **Kircher M, Heyn P, Kelso J. 2011.** Addressing challenges in the production and analysis of
689 illumina sequencing data. *BMC Genomics* **12**: 382.
690 **Kircher M, Sawyer S, Meyer M. 2012.** Double indexing overcomes inaccuracies in multiplex
691 sequencing on the Illumina platform. *Nucleic Acids Research* **40**(1): e3.
692 **Lindner DL, Banik MT. 2008.** Molecular phylogeny of Laetiporus and other brown rot polypore
693 genera in North America. *Mycologia* **100**(3): 417-430.
694 **Lindner DL, Banik MT. 2011.** Intragenomic variation in the ITS rDNA region obscures
695 phylogenetic relationships and inflates estimates of operational taxonomic units in genus
696 *Laetiporus*. *Mycologia* **103**(4): 731-740.
697 **McDonald D, Clemente JC, Kuczynski J, Rideout JR, Stombaugh J, Wendel D, Wilke A,**
698 **Huse S, Hufnagle J, Meyer F, et al. 2012.** The Biological Observation Matrix (BIOM)
699 format or: how I learned to stop worrying and love the ome-ome. *Gigascience* **1**(1): 7.
700 **McKinney W** Data structures for statistical computing in Python. *Proceedings of the 9th Python*
701 *in Science Conference*. 51-56.
702 **McMurdie PJ, Holmes S. 2013.** phyloseq: an R package for reproducible interactive analysis
703 and graphics of microbiome census data. *PloS One* **8**(4): e61217.
704 **McMurdie PJ, Holmes S. 2014.** Waste not, want not: why rarefying microbiome data is
705 inadmissible. *PLoS Computational Biology* **10**(4): e1003531.
706 **Morgan M, Anders S, Lawrence M, Aboyoun P, Pagès H, Gentleman R. 2009.** ShortRead: a
707 bioconductor package for input, quality assessment and exploration of high-throughput
708 sequence data. *Bioinformatics (Oxford, England)* **25**(19): 2607-2608.
709 **Nguyen NH, Smith D, Peay K, Kennedy P. 2015.** Parsing ecological signal from noise in next
710 generation amplicon sequencing. *The New phytologist* **205**(4): 1389-1393.
711 **Nguyen NH, Song Z, Bates ST, Branco S, Tedersoo L. 2016.** FUNGuild: An open annotation
712 tool for parsing fungal community datasets by ecological guild - ScienceDirect. *Fungal*
713 *Ecology*.
714 **Oliver AK, Brown SP, Callaham MA, Jumpponen A. 2015.** Polymerase matters: non-
715 proofreading enzymes inflate fungal community richness estimates by up to 15 %.
716 *Fungal Ecology*.
717 **Philippe E, Franck L, Jan P. 2015.** Accurate multiplexing and filtering for high-throughput
718 amplicon-sequencing. *Nucleic Acids Research*: gkv107.
719 **Pinto AJ, Raskin L. 2012.** PCR biases distort bacterial and archaeal community structure in
720 pyrosequencing datasets. *PloS One* **7**(8): e43093.
721 **Polz MF, Cavanaugh CM. 1998.** Bias in template-to-product ratios in multitemplate PCR.
722 *Applied and Environmental Microbiology* **64**(10): 3724-3730.
723 **Quast C, Pruesse E, Yilmaz P, Gerken J, Schweer T, Yarza P, Peplies J, Glockner FO.**
724 **2013.** The SILVA ribosomal RNA gene database project: improved data processing and
725 web-based tools. *Nucleic Acids Research* **41**(Database issue): D590-596.
726 **Rognes T, Flouri T, Nichols B, Quince C, Mahé F. 2016.** VSEARCH: a versatile open source
727 tool for metagenomics. *PeerJ* **4**: e2584.
728 **Roper M, Ellison C, Taylor JW, Glass NL. 2011.** Nuclear and genome dynamics in
729 multinucleate ascomycete fungi. *Current Biology* **21**(18): R786-793.
730 **Schloss PD, Westcott SL, Ryabin T, Hall JR, Hartmann M, Hollister EB, Lesniewski RA,**
731 **Oakley BB, Parks DH, Robinson CJ, et al. 2009.** Introducing mothur: open-source,
732 platform-independent, community-supported software for describing and comparing
733 microbial communities. *Applied and Environmental Microbiology* **75**(23): 7537-7541.

Schnell IB, Bohmann K, Gilbert MTP. 2015. Tag jumps illuminated–reducing sequence-to-sample misidentifications in metabarcoding studies. *Molecular Ecology Resources* **15**(6): 1289-1303.

Schoch CL, Seifert KA, Huhndorf S, Robert V, Spouge JL, Levesque CA, Chen W, Bolchacova E, Voigt K, Crous PW. 2012. Nuclear ribosomal internal transcribed spacer (ITS) region as a universal DNA barcode marker for Fungi. *Proceedings of the National Academy of Sciences* **109**(16): 6241-6246.

Simon UK, Weiss M. 2008. Intragenomic variation of fungal ribosomal genes is higher than previously thought. *Molecular Biology and Evolution* **25**(11): 2251-2254.

Smith DP, Peay KG. 2014. Sequence depth, not PCR replication, improves ecological inference from next generation DNA sequencing. *PloS One* **9**(2): e90234.

Šošic M, Šikic M. 2017. Edlib: a C/C ++ library for fast, exact sequence alignment using edit distance. *Bioinformatics (Oxford, England)* **33**(9): 1394-1395.

Taylor DL, Walters WA, Lennon NJ, Bochicchio J, Krohn A, Caporaso JG, Pennanen T. 2016. Accurate estimation of fungal diversity and abundance through improved lineage-specific primers optimized for Illumina amplicon sequencing. *Applied and Environmental Microbiology* **82**(24): 7217-7226.

Tonge DP, Pashley CH, Gant TW. 2014. Amplicon-based metagenomic analysis of mixed fungal samples using proton release amplicon sequencing. *PloS One* **9**(4): e93849.

van der Walt Sf, Colbert SC, Varoquaux GI. 2011. The NumPy Array: A Structure for Efficient Numerical Computation. *Computing in Science & Engineering* **13**(2): 22-30.

Vesty A, Biswas K, Taylor MW, Gear K, Douglas RG. 2017. Evaluating the impact of DNA extraction method on the representation of human oral bacterial and fungal communities. *PloS One* **12**(1): e0169877.

Wang Q, Garrity GM, Tiedje JM, Cole JR. 2007. Naive Bayesian classifier for rapid assignment of rRNA sequences into the new bacterial taxonomy. *Applied and Environmental Microbiology* **73**(16): 5261-5267.

White T, Bruns TD, Lee S, Taylor J. 1990. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. *PCR protocols: a guide to methods and applications*: 315 - 322.

Wright ES, Vetsigian KH. 2016. Quality filtering of Illumina index reads mitigates sample cross-talk. *BMC Genomics* **17**(1): 876.

Wu J-Y, Jiang X-T, Jiang Y-X, Lu S-Y, Zou F, Zhou H-W. 2010. Effects of polymerase, template dilution and cycle number on PCR based 16 S rRNA diversity analysis using the deep sequencing method. *BMC Microbiology* **10**: 255.

Supplemental Figures

Species	ITS2 Length (bp)	GC Content (%)	Homopolymer stretches > 5	Mock ID	25 Cycles				30 Cycles						37 Cycles								PCR-Stds
					1:20	1:100	1:200	1:2000	1:20	1:100	1:200	1:2000	1:8000	1:32000	1:20	1:100	1:200	1:2000	1:8000	1:32000	1:64000	1:128000	
Phialocephela sp.	237	68.4%	0	mock1	927	1277	895	580	0	0	1	8	0	0	2	0	3	5	1	0	0	0	4583
Ascomycete sp.	238	50.8%	0	mock2	6680	7229	7813	6779	7381	5470	8009	10078	8048	5657	12334	7161	7621	7532	8979	5976	5378	2618	5436
Phialocephala lagerbergii	238	58.8%	0	mock3	8199	7780	8103	6231	9847	6367	10676	9456	8215	6000	15257	7334	8505	7278	9258	5446	6356	2836	4770
Helotiales sp.	239	57.3%	0	mock4	8487	8371	9066	7661	9549	6879	11353	12028	10023	6423	15799	8077	8757	8966	10896	6915	7148	3153	4608
Aspergillus sp.	260	65.8%	3	mock5	780	462	502	328	3	4	8	35	3	1	15	50	53	29	9	0	0	2	3369
Bjerkandera adusta	281	51.2%	0	mock6	4511	5064	4986	5718	4808	4239	5464	6951	6038	4322	8496	4999	5319	5888	6859	5293	4565	2559	4327
Laetiporus caribensis	283	52.7%	0	mock7	2848	3757	3446	3619	3206	2588	3101	5421	3950	3698	5910	2700	3663	3404	4160	3100	3810	1525	2918
Trametes gibbosa	288	50.0%	1	mock8	3862	4620	4296	5075	4431	3697	4319	5817	4972	3747	7421	4599	4665	5006	5311	4305	3966	1709	3902
Laetiporus gilbertsonii	290	54.1%	0	mock9	8004	8675	8203	6420	9503	7279	10708	7268	7758	6967	16289	8715	8860	6438	7270	6902	7910	3734	4222
Gloeoporus pannocinctus	292	43.8%	0	mock10	3002	3751	3413	3483	2673	2492	2026	3141	2763	3120	4868	3323	3023	2488	2959	3458	2868	1400	3137
Wolfiporia dilatohypha	293	54.6%	0	mock11	371	318	310	153	314	229	207	145	137	319	610	359	236	110	190	159	222	81	4025
Trichaptum sp.	293	48.1%	0	mock12	4410	4950	4916	5171	4491	3871	4481	5659	5042	3913	7994	4847	5064	4687	5252	4420	4685	2030	4034
Fomitopsis ochracea	295	44.1%	0	mock13	1846	2299	2201	2568	1744	1550	1424	2488	2172	2186	2798	2144	1847	1947	2095	2160	2057	1086	3802
Laetiporus cremeioporus	296	54.7%	0	mock14	6952	7385	7091	6608	7963	6548	9466	7727	7282	6043	14270	7827	8122	7165	7170	7030	8207	3767	4173
Phanerochaete laevis	300	47.7%	1	mock15	5196	6167	5789	5396	5487	4786	4801	5581	5157	5718	9523	5944	5510	4905	5452	5595	5678	2843	4218
Laetiporus cincinnatus	302	54.0%	0	mock16	5999	6456	5775	4654	6118	5093	5982	4773	4680	5337	10877	6397	6059	4262	4697	4592	5494	10885	3433
Punctularia strigosozonata	303	53.1%	0	mock17	4446	4748	4376	4838	4845	3968	5127	5744	4977	4100	8894	5187	5119	5201	5556	4437	4186	1997	3940
Phellinus cinereus	314	49.7%	0	mock18	1809	2121	2006	2306	1776	1683	1562	2460	1862	1575	3170	2502	1953	2391	2111	2219	1846	826	3724
Junghuhnia lacera	315	43.8%	1	mock19	1883	2011	1833	1944	1572	1493	1114	1452	1456	1873	2622	2055	1646	1299	1568	1667	1617	1267	1985
Leptoporus mollis	315	45.4%	3	mock20	2521	3098	2692	3812	2551	2375	1891	3732	3096	2681	4538	3189	2816	3524	2991	3028	2411	1331	3523
Leptoporus mollis 2	315	45.1%	1	mock21	359	299	305	311	179	177	115	269	166	170	245	513	233	215	166	271	180	57	3622
Mortierellales sp.	353	45.0%	0	mock22	2789	3334	2662	3704	2728	2648	2327	3589	3069	2526	5307	3693	2814	4355	3120	2846	3220	1251	3618
Laetiporus persicinus	379	51.2%	2	mock23	1858	2077	1845	2270	1742	1567	1395	1852	1640	1680	3273	2332	1549	2700	1736	1351	1578	704	2582
Penicillium sp.	260	66.2%	1	mock24	142	103	106	81	0	0	0	3	0	0	0	0	0	0	0	0	0	0	3509
Verticillium sp.	291	64.6%	1	mock25	0	2	0	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1746
Wolfiporia cocos	548	59.7%	0	mock26	3	0	0	1	0	0	0	1	1	0	1	1	1	2	1	1	0	0	1

Figure S1. Read abundances do not correlate with actual abundances even when DNA concentration is high and PCR cycles are low. Creating libraries of the equimolar BioMock community by varying PCR cycles and DNA concentrations for sequencing on the Ion Torrent PGM did little to change read abundances. However, these data are consistent with traditional recommendations to use as few PCR cycles as possible during library prep.

	All data: Figure 4 from main text								Random sub-sample 100,000 reads per sample							
	Ion Torrent PGM				Illumina MiSeq				Ion Torrent PGM				Illumina MiSeq			
ID	Stds	Mock A	Mock B1	Mock B2	Stds	Mock A	Mock B1	Mock B2	Stds	Mock A	Mock B1	Mock B2	Stds	Mock A	Mock B1	Mock B2
mock1	4905	19	6	1	8615	725	329	3337	4563	8	1	0	3604	231	117	1156
mock2	5106	11651	10809	11877	9174	20763	26129	18341	4726	6072	5711	6016	3833	7253	8834	6319
mock3	4886	13479	12111	13392	8648	28515	29482	21269	4585	7063	6309	6766	3601	10030	9996	7320
mock4	4233	15219	13048	14896	9050	27726	32576	24276	3929	7959	6899	7690	3790	9784	10999	8277
mock5	2813	31	23	3	8992	147	122	269	2599	14	12	1	3810	52	37	88
mock6	3977	8112	7172	7787	13597	13112	13866	15067	3677	4200	3738	4023	5685	4575	4672	5208
mock7	3330	7810	6457	6365	9404	15035	16622	16385	3111	4037	3436	3222	4020	5366	5628	5631
mock8	3637	7281	6914	6865	8137	13819	14579	14787	3400	3881	3628	3457	3454	4917	5052	5110
mock9	4066	8831	10401	12638	8751	22860	21680	20682	3799	4520	5528	6404	3702	8073	7309	7095
mock10	2603	2922	3025	2567	9718	11150	11792	14265	2425	1549	1610	1327	4134	3919	4037	4922
mock11	3957	94	110	109	8775	243	224	194	3667	47	53	45	3719	87	88	64
mock12	4037	6965	7030	6626	8676	12857	13947	14860	3764	3676	3685	3491	3756	4530	4752	5017
mock13	3689	2913	2860	2651	9471	5522	5432	6883	3418	1506	1521	1417	4015	1958	1842	2361
mock14	3922	10279	11920	12440	8262	16454	16390	16798	3650	5442	6324	6285	3501	5780	5557	5723
mock15	3863	6970	7650	6876	9242	15667	15543	18168	3600	3644	4062	3525	3942	5448	5186	6198
mock16	3133	5699	7645	7505	7675	16819	16157	14608	2918	3057	3986	3789	3100	5933	5333	5124
mock17	4019	8271	7688	8217	7669	10701	11572	11671	3734	4327	4049	4204	3203	3756	3903	4080
mock18	3672	2937	2985	2597	9807	6314	5953	7496	3426	1556	1584	1335	4061	2216	2073	2528
mock19	3089	3047	3406	2741	9297	9356	8990	11593	2876	1566	1800	1400	3920	3310	2945	4095
mock20	3551	4969	4320	4028	9047	8847	8747	9987	3303	2605	2230	2049	3807	3124	2896	3560
mock21	3776	207	366	249	9250	405	302	414	3514	116	209	134	3859	158	116	128
mock22	3264	4668	4311	3812	9151	10865	9728	13365	3042	2445	2291	1965	3893	3824	3256	4559
mock23	2147	2651	2385	2053	6486	488	421	521	2003	1368	1283	1055	2704	167	141	221
mock24	3644	NA	NA	NA	8278	NA	NA	NA	3374	NA	NA	NA	3613	NA	NA	NA
mock25	1976	NA	NA	NA	2045	NA	NA	NA	1855	NA	NA	NA	896	NA	NA	NA
mock26	7	NA	NA	NA	5979	NA	NA	NA	7	NA	NA	NA	2567	NA	NA	NA

Figure S2. Random subsampling reads for each sample does not improve accuracy of read abundances. Each sample was randomly sub-sampled to 100,000 reads using 'amptk sample' and then reads were mapped to the BioMock community. Chi-square test for each of these BioMock samples was significant ($p < 0.001$), indicating the read abundances are not equally distributed.

	Illumina MiSeq Run 1										Same Libraries no mocks in run			
	Stds	Mock A	Mock B1	Mock B2	755-1	755-2	744-1	744-2	766-1	766-2	744-1	744-2	766-1	766-2
i5 index	ACTGAGCG	ACTGAGCG	ACTGAGCG	ACTGAGCG	TAGCGCTC	TAGCGCTC	TAGCGCTC	TAGCGCTC	TAGCGCTC	TAGCGCTC	TAGCGCTC	TAGCGCTC	TAGCGCTC	TAGCGCTC
i7 index	GGCTCTGA	TATAGCCT	ATAGAGGC	CCTATCCT	AGGCGAAG	TAATCTTA	CCTATCCT	GGCTCTGA	TATAGCCT	ATAGAGGC	CCTATCCT	GGCTCTGA	TATAGCCT	ATAGAGGC
mock1	8615	725	329	3337	0	0	9	24	2	0	0	0	0	0
mock2	9174	20763	26129	18341	0	0	42	25	57	55	0	0	0	0
mock3	8648	28515	29482	21269	7	4	79	18	306	580	12	4	107	247
mock4	9050	27726	32576	24276	0	0	60	17	54	65	0	0	0	0
mock5	8992	147	122	269	0	0	2	17	0	0	0	0	0	0
mock6	13597	13112	13866	15067	0	1	32	24	27	30	0	0	0	0
mock7	9404	15035	16622	16385	0	0	42	28	32	33	0	0	0	0
mock8	8137	13819	14579	14787	0	0	31	13	26	31	0	0	0	0
mock9	8751	22860	21680	20682	0	0	46	24	55	43	0	0	0	0
mock10	9718	11150	11792	14265	0	0	33	18	22	20	0	0	0	0
mock11	8775	243	224	194	0	0	0	11	1	0	0	0	0	0
mock12	8676	12857	13947	14860	0	0	40	16	23	25	0	0	0	0
mock13	9471	5522	5432	6883	0	0	16	18	7	11	0	0	0	0
mock14	8262	16454	16390	16798	0	0	42	18	42	42	0	0	0	0
mock15	9242	15667	15543	18168	0	0	33	18	35	26	0	0	0	0
mock16	7675	16819	16157	14608	0	0	28	20	32	34	0	0	0	0
mock17	7669	10701	11572	11671	0	0	31	10	19	23	0	0	0	0
mock18	9807	6314	5953	7496	0	2	28	11	16	15	0	0	0	0
mock19	9297	9356	8990	11593	0	0	26	23	14	28	0	0	0	0
mock20	9047	8847	8747	9987	0	0	28	19	18	23	0	0	0	0
mock21	9250	405	302	414	0	0	1	17	1	1	0	0	0	0
mock22	9151	10865	9728	13365	0	0	24	23	9	30	0	0	0	0
mock23	6486	488	421	521	0	0	0	19	0	0	0	0	0	0
mock24	8278	0	0	8	0	0	0	13	0	0	0	0	0	0
mock25	2045	0	0	2	0	0	0	6	0	0	0	0	0	0
mock26	5979	0	0	2	0	0	0	12	0	0	0	0	0	0

Figure S3. Index-bleed on Illumina MiSeq occurs during the sequencing run and is not a result of contamination. Sequencing the BioMock on Illumina MiSeq resulted in elevated levels of apparent index-bleed during our first run. To rule out that this was a result of contamination during library prep/cleanup, the same libraries were sequenced on a second run in the absence of any of the BioMock samples. The index-bleed discovered in the first run then disappeared, however, one of the BioMock members (mock3) was actually found in these environmental samples.

803 **Supplemental Tables**

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805 Table S1. Cultures from the CFMR culture collection used to construct the BioMock community.

Species	Voucher ID	Mock ID	ITS2 Length	% GC	GenBank Accession
Phialocephala fusca	FP-170182	mock1	237	68.35%	KU668953
Ascomycete sp.	FP-170235	mock2	238	50.84%	KU668968
Phialocephala lagerbergii	FP-170134	mock3	238	58.82%	KU668951
Helotiales sp	RF10JR	mock4	239	57.32%	KU668958
Aspergillus candidus	RF1JR	mock5	260	65.77%	KU668969
Bjerkandera adusta	RF3JR	mock6	281	51.25%	KU668970
Laetiporus caribensis	GDL-1	mock7	283	52.65%	KU668960
Trametes gibbosa	RF5JR	mock8	288	50.00%	KU668971
Laetiporus gilbertsonii	OR-2	mock9	290	54.14%	KU668967
Gloeporus pannocinctus	MR5-1	mock10	292	43.84%	KU668965
Wolfiporia dilatohypha	FP-72162	mock11	293	54.61%	KU668959
Schizopora sp.	FP-170198	mock12	293	48.12%	KU668955
Fomitopsis ochracea	FP-170231	mock13	295	44.07%	KU668957
Laetiporus cermeioporus	L34-2	mock14	296	54.73%	KU668963
Phanerochaete laevis	RF9JR	mock15	300	47.67%	KU668973
Laetiporus cincinnatus	DA-37	mock16	302	53.97%	KU668950
Punctularia strigosozonata	RF7JR	mock17	303	53.14%	KU668972
Phellinus cinereus	IN4-1	mock18	314	49.68%	KU668962
Antrodiella semisupina	MR-3	mock19	315	43.81%	KU668966
Leptoporus mollis	TJV-93-174	mock20	315	45.40%	KU668975
Leptoporus mollis 2	RLG-7163	mock21	315	45.08%	KU668974
Mortierellales sp	FP-170186	mock22	353	45.04%	KU668954
Laetiporus persicinus	HHB-9564	mock23	379	51.19%	KU668961
Penicillium nothofagi	FP-170215	mock24	260	66.15%	KU668956
Metapochonia suchlasporia	FP-170177	mock25	291	64.60%	KU668952
Wolfiporia cocos	MD-275	mock26	548	59.67%	KU668964

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814 Table S2. OTU clustering results using default QIIME pre-processing of reads.

Platform	Clustering method	Reads	Total OTUs	Mock OTUs (n = 12)	Error Rate (mismatches / total)
Ion Torrent PGM (400 bp)	UCLUST	2 562 316	97 175	1 347	3.760%
	USEARCH	2 562 316	9 812	560	4.237%
	SWARM	2 562 316	276 403	225	3.517%
	UPARSE	2 562 316	1 609	82	1.100%
Illumina Miseq (2 x 300)	UCLUST	15 696 636	122 802	528	0.131%
	USEARCH	15 696 636	9 785	545	4.694%
	SWARM	15 696 636	614 133	165	4.447%
	UPARSE	15 696 636	2 483	38	0.077%

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817 Table S3. Expected errors quality trimming removes most errors from Ion Torrent PGM data
818 using 12 member SynMock community.[1]

Method	Aligned reads	Subst. errors	Indel errors	UPARSE OTUs	OTUs (chimera filtered)
No Qual Filter	67 185	0.237%	0.342%	26	21
Cutadapt -q 25	73 092	0.152%	0.222%	28	26
Seqtk (Phred)	75 535	0.204%	0.314%	83	79
Sickle –q 25	71 221	0.098%	0.087%	31	30
Exp. Errors < 1	35 810	0.078%	0.100%	18	14

819 [1] Total of 78,525 reads from the SynMock Ion Torrent PGM run demuxed with AMPtk.

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821 Table S4. Expected errors quality trimming removes most errors from Illumina MiSeq data using
822 12 member SynMock community.[1]

Method	Aligned reads	Subst. errors	Indel errors	UPARSE OTUs	OTUs (chimera filtered)
No Qual Filter	1 081 931	0.333%	0.006%	44	27
Cutadapt -q 25	1 148 274	0.253%	0.007%	361	337
Seqtk (Phred)	1 115 657	0.316%	0.007%	173	150
Sickle	1 153 190	0.166%	0.006%	304	285
Exp. Errors < 1	961 458	0.094%	0.006%	45	27

823 [1] Total of 1,167,662 reads from the SynMock Illumina MiSeq run demuxed with AMPtk.

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825 Table S5. Summary statistics for the HTAS runs used in this study.

Run	Platform	Total Reads	Valid Reads	Num Samples	Range reads per sample	Total UPARSE OTUs	Mock Community	Mock Calculated Error Rate	Index-Bleed
Mock3	Ion Torrent PGM	4,332,502	3,029,824	19	107,416 - 217,372	1,010	BioMock	0.086%	0.033%
Mock4a	Illumina Miseq	5,668,955	5,661,700	20	237,035 - 334,455	1,778	BioMock	0.019%	0.264%
Mock4b	Illumina Miseq	659,738	658,730	4	145,405 - 191,095	477	None	NA	NA
Mock4c	Illumina Miseq	6,103,680	6,096,296	20	221,130 - 392,118	1,625	BioMock	0.020%	0.233%
Mock5	Ion Torrent PGM	4,341,392	2,602,544	21	59,394 - 254,269	927	SynMock	0.099%	0.156%
Mock6	Illumina Miseq	18,005,575	17,979,995	21	623,128 - 1,167,662	2,497	SynMock	0.082%	0.046%

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