

1 **Selection of appropriate metagenome taxonomic classifiers for ancient microbiome**  
2 **research**

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## 30 **Abstract**

31 Metagenomics enables the study of complex microbial communities from myriad sources,  
32 including the remains of oral and gut microbiota preserved in archaeological dental calculus and  
33 paleofeces, respectively. While accurate taxonomic assignment is essential to this process, DNA  
34 damage, characteristic to ancient samples (*e.g.* reduction in fragment size), may reduce the  
35 accuracy of read taxonomic assignment. Using a set of *in silico*-generated metagenomic datasets  
36 we investigated how the addition of ancient DNA (aDNA) damage patterns influences microbial  
37 taxonomic assignment by five widely-used profilers: QIIME/UCLUST, MetaPhlan2, MIDAS,  
38 CLARK-S, and MALT (BLAST-X-mode). *In silico*-generated datasets were designed to mimic  
39 dental plaque, consisting of 40, 100, and 200 microbial species/strains, both with and without  
40 simulated aDNA damage patterns. Following taxonomic assignment, the profiles were evaluated  
41 for species presence/absence, relative abundance, alpha-diversity, beta-diversity, and specific  
42 taxonomic assignment biases. Unifrac metrics indicated that both MIDAS and MetaPhlan2  
43 provided the most accurate community structure reconstruction. QIIME/UCLUST, CLARK-S,  
44 and MALT had the highest number of inaccurate taxonomic assignments; however, filtering out  
45 species present at <0.1% abundance greatly increased the accuracy of CLARK-S and MALT. All  
46 programs except CLARK-S failed to detect some species from the input file that were in their  
47 databases. Ancient DNA damage resulted in minimal differences in species detection and relative  
48 abundance between simulated ancient and modern datasets for most programs. In conclusion,  
49 taxonomic profiling biases are program-specific rather than damage-dependent, and the choice of  
50 taxonomic classification program to use should be tailored to the research question.

51

## 52 **Importance**

53 Ancient biomolecules from oral and gut microbiome samples have been shown to preserve  
54 in the archaeological record. Studying ancient microbiome communities using metagenomic  
55 techniques offer a unique opportunity to reconstruct the evolutionary trajectories of microbial  
56 communities through time. DNA accumulates specific damage over time, which could potentially  
57 affect taxonomic classification and our ability to reconstruct community assemblages accurately.  
58 It is therefore necessary to assess whether ancient DNA (aDNA) damage patterns affect  
59 metagenomic taxonomic profiling. Here, we assessed biases in community structure, diversity,  
60 species detection, and relative abundance estimates by five popular metagenomic taxonomic

61 classification programs using *in silico*-generated datasets with aDNA damage. Age-related damage  
62 patterns had minimal impact on the taxonomic profiles produced by each program, and biases were  
63 intrinsic to each program. Therefore, an appropriate classification program should be chosen that  
64 minimizes the biases related to the questions being addressed.

65

## 66 **Introduction**

67 Ancient microbiome research offers the possibility of tracing the evolution of the complex  
68 microbial communities that play an integral role in shaping population health and disease.  
69 Palaeomicrobiology uses archaeological material to trace the emergence and spread of  
70 microorganisms throughout history and prehistory. Archaeological dental calculus and palaeofeces  
71 are promising substrates for ancient human microbiome studies, as they have been shown to  
72 preserve DNA (1), proteins (1, 2), and small molecule metabolites (3) from the resident microbes  
73 and the host. During life, these dense microbial communities contain hundreds of species,  
74 predominantly composed of bacteria (4), but also including archaea (4), viruses (5), fungi (6), and  
75 protists (7). Characterizing the microbial ecology of host-associated microbiota through time is a  
76 necessary step in understanding the function of these microbial communities, and further how they  
77 interact with the host.

78 DNA in archaeological samples, including ancient microbial samples, acquires predictable  
79 age-related damage patterns, including short fragment lengths (typically <100 bp) (8) with break-  
80 points coinciding with depurination, and accumulation of cytosine to thymine transitions at the  
81 ends of the molecules (8). The ubiquity and predictability of these damage patterns means that  
82 they are often used to authenticate ancient DNA and estimate modern DNA contamination (9, 10),  
83 and the short fragment lengths of ancient DNA negate the need for shearing during library  
84 construction for high throughput sequencing (HTS). These same properties, however, potentially  
85 affect taxonomic classification of microbial DNA sequence reads more difficult, or less accurate.  
86 Reads that are too short, for example, may not be specific enough for classification at the  
87 taxonomic level desired. Cytosine to thymine transitions may also cause misclassification or  
88 prevent classification, such that reads may be misleadingly assigned to unidentified taxa, thereby  
89 inflating diversity estimates. Additionally, although 16S rRNA gene amplicon sequencing is  
90 popular for profiling complex microbial communities, taxon-specific length polymorphisms in this  
91 gene combined with the relatively long lengths of the hypervariable regions (>150 bp), make it  
92 problematic for sequencing degraded DNA from ancient microbial communities (8). Instead,  
93 shotgun metagenomic sequencing, which is highly compatible with short DNA fragments, is the  
94 preferred analytical approach for ancient microbiome samples (1, 11).

95 Community profiling by DNA shotgun sequencing is currently the most comprehensive  
96 method used to assess microbiome community composition, and a variety of computational tools

97 are available to reconstruct the species present from the millions of short sequences that comprise  
98 HTS datasets. There are several methods for taxonomic assignment available. Popular methods  
99 include matching reads to 16S rRNA gene sequences (QIIME (12), Mothur (13), or to single-copy  
100 gene panels (MetaPhlAn2 (14, 15), MIDAS (16), PhyloSift (17)), k-mer-based whole-genome  
101 matching (Kraken (18), CLARK (19, 20), and hybrid k-mer-based matching and alignment  
102 extension (MALT (21, 22)). While there are several publications comparing the accuracy,  
103 specificity, and precision of various metagenomic classification programs for modern samples  
104 (*e.g.*, (23-25)), no study has yet compared the performance of these approaches on ancient DNA.

105 In order to assess the performance of metagenomic classification systems on ancient DNA,  
106 we performed a comparison of the community profile of six metagenomic classification programs  
107 that use different taxonomic assignment methods (QIIME, DADA2 (26), MetaPhlAn2, MIDAS,  
108 CLARK-S and MALT in BLAST-X-mode). We used *in silico*-generated ancient and modern  
109 metagenome samples to estimate the accuracy of these programs. Our results indicate that the  
110 effect of DNA damage patterns on taxonomic assignments is variable across programs. We show,  
111 however, that most of the programs tested here are robust to misassignment due to DNA damage.  
112 Overall, our results indicate that taxonomic assignment biases are similar between modern and  
113 ancient simulated metagenomic samples.

114

## 115 **Results**

116

### 117 **Description of the datasets**

118 A total of 39 *in silico* generated metagenomic community samples were generated by  
119 independent runs of gargammel (27) (Supplemental Table S1). Three overlapping sets of  
120 genomes were used as input: one set had 40 genomes, the second had 100 genomes, and the third  
121 had 200 genomes. All genomes in the 40 genome set were included in the 100 genome set, and  
122 all genomes in the 100 set were included in the 200 set. Each genome was represented in equal  
123 abundance, where in the 40, 100, and 200 genome datasets each genome comprises 2.5%, 1%,  
124 and 0.5% of the total DNA, respectively. There were 13 independent samples for each set of  
125 genomes, where ten replicates had simulated aDNA damage patterns (ancient dataset) and three  
126 replicates did not have aDNA damage patterns (modern dataset). The estimated copy number of  
127 each genome in each dataset is presented in Supplemental Table S1. We additionally filtered the

128 output profiles to remove species present at <0.1% abundance to understand how filtering low-  
129 abundance, often false-positive, taxa affected diversity metrics. The cut-off of 0.1% was  
130 arbitrarily selected based on (23).

131

### 132 **Community structure is consistent between ancient and modern simulated datasets**

133 We first sought to determine if any of the taxonomic classification programs produced a  
134 community structure that closely resembled the true input files by measuring beta-diversity. We  
135 used both weighted UniFrac (phylogenetic relatedness accounting for relative abundance of  
136 organisms) and unweighted UniFrac metrics (phylogenetic relatedness without accounting for  
137 relative abundance of organisms) on full and filtered (>0.1% abundance) tables. Principal  
138 coordinates analysis (PCoA) of the beta-diversity metrics were plotted to visualize relatedness  
139 between community structure of the input files and community structure as determined by each of  
140 the 5 programs tested (Fig. 1A, B), and demonstrated that classification of replicate samples was  
141 highly consistent by each program, although QIIME showed the greatest variance between  
142 replicates. Filtering low-abundance species did not affect the weighted UniFrac distance, as this  
143 metric accounts for relative abundance of species, and therefore removing low-abundance species  
144 minimally affects the final score. Additionally, there was very little difference in the scores of the  
145 ancient and modern datasets for all programs, although QIIME/UCLUST demonstrated the  
146 greatest age-related difference in beta-diversity. MIDAS-determined community structure  
147 calculated by weighted UniFrac distance was most similar to the input files for 40 and 100-genome  
148 datasets (Fig. 1A). CLARK-S and MALT community structures were more similar to each other  
149 than to any of the other programs for all datasets, while the community structures reconstructed  
150 using QIIME/UCLUST and MetaPhlan2 were each distinct from the other programs and did not  
151 plot near any other programs in the PCoA (Fig. 1A). Using the non-phylogenetic abundance-  
152 weighted Bray-Curtis distance we observed similar PCoA plotting patterns by each group, relative  
153 to the true input, at the species and genus levels (Figs. S2-S4).

154 Plots of beta-diversity by the standard (unweighted) UniFrac metric, which accounts for  
155 species presence/absence but not abundance, were distinct from the weighted UniFrac plots,  
156 demonstrating differences in the ability of the five programs to accurately reflect the species  
157 composition *vs* composition plus abundance (Fig. 1B). Filtering out species present at <0.1%  
158 abundance noticeably altered the relationship of the programs to each other in the PCoA plots.

159 CLARK-S and QIIME/UCLUST exhibited substantial differences in community structure  
160 between ancient and modern datasets. Filtering removed this difference only for CLARK-S, while  
161 QIIME/UCLUST modern and ancient datasets remained distinctly plotted, suggesting that  
162 QIIME/UCLUST reported several taxa not in the input files at higher abundance than the cut-off  
163 of 0.1%. In contrast to the weighted UniFrac PCoA plots, MetaPhlAn2 community structure was  
164 most similar to truth for 40-, 100-, and 200-genome datasets, filtered and full tables, followed by  
165 MIDAS. Filtering output tables reduced the community structure similarity between MIDAS and  
166 the true input, and makes the community structure of CLARK-S and MALT more similar to each  
167 other, suggesting the most abundant species are detected in similar proportions by CLARK-S and  
168 MALT. Using the non-phylogenetic Jaccard distance we observed similar PCoA plotting patterns  
169 by each program, relative to the true input, at the species and genus levels (Figs. S2-S4).

170

### 171 **Community diversity is program-dependent**

172 To understand the differences in community structure we observed in beta-diversity  
173 analyses, we assessed the alpha-diversity of the communities produced by the five taxonomic  
174 classification programs, using several metrics to account for different components of community  
175 diversity. Faith's phylogenetic distance (PD), which determines the community diversity based on  
176 the phylogenetic relatedness of the species present, was estimated to be much lower than the true  
177 PD by all of the programs for the 40-, 100-, and 200-genome datasets, full and filtered tables,  
178 ancient and modern simulations (Figs. 2A, S5A, S6A). QIIME/UCLUST generated the lowest PD,  
179 while MetaPhlAn2 and CLARK-S were both slightly higher than MIDAS and MALT. CLARK-S  
180 was the only program with a slight difference in PD between ancient and modern simulated  
181 datasets, but when the table was filtered the modern and ancient sample diversity was equivalent.

182 The Shannon index, which accounts for species presence/absence and evenness, showed  
183 little difference between ancient and modern simulated datasets per program and was unaffected  
184 by filtering (Figs. 2B, S5B, S6B). As the number of genomes in the input files (truth) increased,  
185 the Shannon index values for each program decrease relative to true value (*i.e.*, in the 40-genome  
186 set QIIME/UCLUST, MIDAS, and CLARK-S are above true value, and in the 200-genome set all  
187 program values are below the true value). This may be caused by the fact that the Shannon index  
188 of communities with dominant species is expected to be lower than those with even abundance  
189 across species, even if the former communities is more species rich.

190 The observed species is the total number of species/subspecies detected by each program  
191 (except QIIME/UCLUST which included all OTUs because it poorly resolves species-level  
192 differences). QIIME/UCLUST, MIDAS, CLARK-S, and MALT always overestimate the total  
193 number of species in the samples (by 1X-150X), and the number of estimated species/subspecies  
194 in ancient simulated samples is much higher than in modern simulated samples for  
195 QIIME/UCLUST and CLARK-S, and to a lesser extent MIDAS (Figs. 2C, S5C, S6C). Filtering  
196 reduced the number of observed species by CLARK-S substantially, by MALT and MIDAS  
197 slightly, and by QIIME/UCLUST minimally. In contrast to the other programs, MetaPhlan2  
198 slightly underestimates the total number of species in all of the datasets, and is consistently closest  
199 to the true number. Chao1 diversity metrics, which include an estimation of undetected species in  
200 the sample, exhibited very similar patterns to observed species for all programs (Figs. 2D, S5D,  
201 S6D).

202

### 203 **Individual program performance and biases**

204 We next assessed how well each program detected the presence and abundance of species  
205 present in both modern and ancient simulated datasets. To do so, we calculated the true and inferred  
206 relative abundance of each input genome for each of the five programs, and determined the percent  
207 over- or under- assignment (Fig. 3, S7-S8). Given the limited species-level resolution afforded by  
208 QIIME/UCLUST, we limited our analysis to genus-level assignments for this program.  
209 MetaPhlan2 does not distinguish between several species (*i.e.* *Streptococcus mitis* and *S. oralis*)  
210 because their marker genes are indistinguishable, and the relative abundance of these in the input  
211 files was likewise combined for calculations. Generally, the species detected/not detected are  
212 consistent between ancient/modern simulated datasets, as is the percent and direction of  
213 over/under-estimation. We have additionally presented as bar charts (Fig. 4, S9-S18) the relative  
214 abundance of each species in the input (labeled If, “Input fastq/a”, and 16f “Input 16S rRNA gene-  
215 identified read fastq/a”) and output profiles from each program. The first output profile bar (labeled  
216 Id, “Input species detected”) excludes the false-positive species not in the input files (grouped  
217 together as “other” assignments). The second output profile bar (labeled Ad, “All species  
218 detected”) includes the “other” assignments to visualize how skewed the proportions of input  
219 species are by assignments to taxa not in the input. Assessment of each of the programs is included  
220 in the program-specific sections below.



221

## 222 *QIIME/UCLUST*

223 QIIME is a highly popular metagenomics analysis program that was developed to analyze  
224 reads generated by 16S rRNA gene amplicon sequencing rather than full metagenome shotgun  
225 sequencing data (12). To accommodate this, we used bowtie2 to select the reads from our *in silico*  
226 communities that matched 16S rRNA genes in the GreenGenes v13.8 database and created new  
227 input fastq files containing only those reads, a protocol that has been previously used to enable  
228 QIIME analysis of ancient metagenomic sequences (8). The taxonomic proportions of the 16S  
229 rRNA gene input files were initially skewed by the bowtie2 identification such that some taxa were  
230 over-represented while others were under-represented relative to the full genome proportions (Fig.  
231 4, S9-S10, bars If vs. 16f, Supplemental Table S3). As the 16S rRNA gene does not provide  
232 species-level resolution for many species, we assessed the accuracy of assignments at the genus  
233 level. QIIME/UCLUST failed to identify 2, 17, and 19 input taxa in the 40-, 100-, and 200-genome  
234 simulated datasets (22 total input taxa comprising 16 genera) (Fig. 3, S7-S8, Supplemental Table  
235 S4), despite the presence of reads derived from these 22 genomes in the bowtie2 16S rRNA gene-  
236 identified reads files. Of the missing taxa, 11 are not included in the GreenGenes v.13.8 database  
237 at the species or genus level.

238 QIIME/UCLUST identified the highest proportion of false-positive taxonomic  
239 assignments (Fig. 4, S9-S10) (“other” in barchart figure), and the proportion of false-positive taxa  
240 was higher in ancient than modern simulated datasets, suggesting that damage patterns decrease  
241 the accuracy of taxonomic identification by this program. Because of the large number of false-  
242 positive taxa identified, as well as the several taxa remaining unidentified, many of the input taxa  
243 were under-represented in the OTU tables produced by QIIME (Fig. 3, 4, S7-S8). Circular trees  
244 generated in metacodeR representing the taxonomy of the OTUs identified in the 40-genome  
245 ancient dataset full and filtered table taxonomic assignments (Fig. 5, S19) show that  
246 QIIME/UCLUST tends to overestimate each phylum in proportion to the original input, except for  
247 poorly characterized taxa such as Candidate divisions TM7 (Candidatus *Saccharibacterium*) and  
248 SR1, *Spirochaetes*, and archaea, and there is a slight bias toward over-assignment of  
249 *Proteobacteria*.

250 We identified several genus-level false-positive taxa with particularly high assignments in  
251 the 40-, 100-, and 200-genome datasets individually, as well as 7 that were shared by all 3 datasets

252 (Supplemental Table S4). Three of the 7 genera, *Bacteriodes*, *Coprococcus*, and *Enterococcus*,  
253 had high numbers of assignments only in the ancient simulated datasets, while *Achromobacter*,  
254 *Actinobacillus*, *Enterobacter*, and *Erwinia* were highly represented in both ancient and modern  
255 simulated datasets. The genomes from which the reads assigned to each of these 7 false-positive  
256 taxa originated were identified (Supplemental Table S4), and we tested if these assignment biases  
257 hold true in real datasets. All reads assigned to the 7 false-positive genera in set of historic calculus  
258 samples from the Radcliffe Infirmary burial ground (ca. 1770-1855; Oxford, England) (3) were  
259 searched against the NCBI nt database using BLASTn to identify the likely species of origin for  
260 the reads. Many of the biases in read assignment observed in the *in silico* datasets were also  
261 observed in the real calculus samples (Table S4), i.e., *in silico*-generated reads assigned to  
262 *Enterococcus* by QIIME were from taxa in the order *Lactobaciales*, and historic calculus reads  
263 assigned to *Enterococcus* by QIIME also had best BLAST hits to the order *Lactobaciales*.

264

#### 265 *DADA2*

266 DADA2 (26) and deblur (28) are new methods for taxonomic assignment of 16S rRNA  
267 gene reads that have been implemented in QIIME v2.0. Rather than using a percent similarity cut-  
268 off for assignment of a read to an operational taxonomic unit, these programs use exact sequence  
269 matches, and rely on Illumina sequencing error models to determine if single nucleotide  
270 polymorphisms in a read are true sequence variation or the product of sequencing error. The  
271 implementation of these programs requires multiple copies of each sequence, which while  
272 common in 16S rRNA gene amplicon datasets, are not likely to occur in a set of ancient reads that  
273 are selected out of a shotgun sequenced metagenomic dataset, such as we performed, due to  
274 insufficient coverage. As a result, we were unable to run DADA2 through to taxonomic assignment  
275 of our 16S rRNA gene-identified reads because each read was represented only once in each of  
276 our datasets. Because 16S rRNA gene amplification from ancient DNA samples has been shown  
277 to produce strong taxonomic biases (8), and because DADA2 is unable to classify the low coverage  
278 reads typical of shotgun metagenomic datasets, we recommend against using QIIME v2.0 for  
279 taxonomic characterization of ancient microbial samples, and any low-coverage non-amplicon  
280 data.

281

## 282 *MetaPhlAn2*

283         MetaPhlAn2 is a fast program that assigns taxonomy based on single-copy marker genes  
284 that are unique to each species in the MetaPhlAn2 database (14, 15). It was shown to be highly  
285 accurate for assigning taxonomy in modern metagenomic samples, and it is implemented in  
286 metaBIT (29), a user-friendly wrapper program that is targeted to ancient metagenomics  
287 researchers. MetaPhlAn2 identified the smallest number of false-positive taxa of the programs  
288 tested (Supplemental Table S5), but had exceptionally skewed proportions of 2 identified taxa,  
289 which may explain why weighted UniFrac distance community structures were so different from  
290 truth, while unweighted UniFrac distance community structures were highly similar to truth, where  
291 truth represents the percent of DNA from a genome rather than the cell count. Circular taxonomic  
292 assignment trees of the ancient dataset demonstrate that MetaPhlan2 does not report high numbers  
293 of false-positive taxa in any phylum (Fig. 5, S19), and although there are 3 more *Proteobacteria*  
294 reported than in the input files, they were identified at low-abundance and removed during  
295 filtering. The only phylum not represented in the MetaPhlAn2 output dataset is Candidate division  
296 SR1, which is not in its database.

297         Candidatus *Saccharibacterium* TM7b was represented at 1500-2000% higher relative  
298 abundance in the output files than the abundance of DNA in the input files in 40-, 100-, and 200-  
299 genome datasets, both ancient and modern (Fig. 3, 4, S7-S8, S11-S12). This may be the result of  
300 the MetaPhlAn2 normalization method, which calculates the proportion of cells from each species  
301 based on single-copy marker genes, rather than reporting the relative abundance of all DNA from  
302 each species detected (14). The TM7 genome is much smaller than the genomes of the other  
303 species we included in our dataset, 0.1 Mb vs. 2.5-3.5 Mb, and because our datasets have the same  
304 number of reads from each species, there must be more copies of the small genome-cells in the  
305 datasets to achieve the same proportion of DNA. We calculated that our datasets have  
306 approximately 7.8 copies of the TM7 genome but on average 0.36 copies of all other species  
307 genomes, which is a difference of ~2000% (Supplemental Table S1). *Desulfobulbus* sp. oral taxon  
308 041 was identified at 200-300% higher relative abundance in all output files, and *Prevotella* sp.  
309 oral taxon 299, present only in the 200-genome datasets, was identified at 200-300% higher  
310 relative abundance in the output files (Figs. 3, 4, S11-S12). Both of these organisms have small  
311 genomes, ~0.7 Mb, and like TM7b they have more cell copies per dataset than the average (1.2 vs.  
312 0.36), which is a difference of ~340%.

313 Twenty-three input taxa were not specifically identified in any of the simulated datasets,  
314 and all were missing from the MetaPhlAn2 database or not present at the appropriate taxonomic  
315 level (Supplemental Table S5). Nine of the missing 22 taxa are subspecies, including four of  
316 *Fusobacterium nucleatum*, one of *Mycobacterium avium*, and 4 of *Salmonella enterica* subsp.  
317 *Enterica* (Supplemental Table S5), and these were identified to the species level (or in the case of  
318 *Salmonella enterica* to subspecies) but not lower. Several species are indistinguishable by the  
319 marker genes used by MetaPhlAn2, and are grouped together, including *Streptococcus*  
320 *mitis/oralis*, *Bordetella bronchiseptica/parapertussis*, and *Mycobacterium tuberculosis* complex  
321 (*tuberculosis/bovis/canetti/africanum*). If a user wishes to specifically identify any of these  
322 species, other programs will need to be used. The 40-genome dataset had 7 false-positive taxa, the  
323 100-genome dataset had 12, and the 200-genome dataset had 14, yet all were low abundance,  
324 suggesting that MetaPhlAn2 may be slightly less accurate making assignments in samples with  
325 higher diversity, and may minimally inflate that diversity. Only one false-positive taxon,  
326 *Streptococcus tigurinus*, was common to the 40-, 100-, and 200-genome datasets, and this may be  
327 because of inconsistencies in naming this *Streptococcus* species, where some NCBI entries use  
328 *tigurinus* as an independent species and others use it as a subspecies of *S. oralis*. The reads assigned  
329 to *S. tigurinus* may be from *S. oralis* subsp. *tigurinis*, which was one of the input genomes we used.

330

### 331 *MIDAS*

332 MIDAS is another fast program that uses a panel of 15 single-copy marker genes present  
333 in all of the species included in its database to perform taxonomic classification (16). It also has  
334 the ability to determine differences in gene presence/absence and detect single nucleotide  
335 polymorphisms (SNPs), although these were not tested in this study. MIDAS has a substantial  
336 database (~31000 genomes) in which related species are grouped together under a single species  
337 identifier number (5952 total identifiers), which we found introduces biases in the species reported  
338 in the output tables. A majority of the species detected in each dataset were found only in ancient  
339 samples (82%, 72%, 64% in the 40-, 100-, and 200-genome datasets, respectively), yet these had  
340 a relative abundance of <0.1%, suggesting that aDNA damage patterns do lead to false assignments  
341 in MIDAS, but only of a small number of reads. *Streptococcus* species were the most common  
342 low-abundance false-positive taxa, and likely indicate a database bias. Biases in reporting  
343 *Firmicutes* and *Proteobacteria*, and to a lesser extent *Actinobacteria*, in ancient datasets can be

344 seen in the circular taxonomic assignment trees (Fig. 5, S19). Filtering low abundance hits removes  
345 many of the false-positive taxa in these phyla, yet several lower-abundance (darker  
346 nodes/branches) false-positive taxa remain in each. MIDAS did not report any archaea, despite  
347 having the input species in the database, nor does it detect Candidate divisions TM7 and SR1,  
348 which are not in the database.

349 In total, MIDAS failed to identify 28 input taxa, the highest number missed of all the  
350 programs we tested, and only 3 of these missed taxa were not in the database (Supplemental Table  
351 6, Figs. 3, S7-S8). Despite missing so many species, MIDAS maintained relative proportions of  
352 the input taxa in even species distribution, and the proportion of false-positive taxa detected was  
353 slightly lower in ancient simulated datasets than modern (Fig. 4, S13-S14). To understand why we  
354 saw certain abundant false-positive taxa, we investigated the origin of the reads assigned to five  
355 false-positive taxa that were highly abundant in the 40-, 100-, and 200-genome datasets. We  
356 determined which, if any, additional species shared the same MIDAS-specific species identifier  
357 number, and the origin of the reads being assigned to these false-positive taxa (Supplemental Table  
358 S6). Reads from several taxa not reported by MIDAS were assigned to false-positive taxa,  
359 explaining both why certain taxa were missed and the high abundance of these false-positive taxa.

360 This phenomenon highlights how grouping related species under a single species identifier  
361 and presenting only one of those species in the output table can result in curious species profiles  
362 from MIDAS. For example, *Phocaeicola abscessus*, which had high abundance in 100 and 200-  
363 genome datasets but was not part of the input files, shares an identifier number with *Bacterioidetes*  
364 oral taxon 272, which was in the input files but was absent from the final species tables MIDAS  
365 produced. By checking the alignment files that MIDAS generates, we determined that the reads  
366 from *Bacterioidetes* oral taxon 272 were assigned to the species identifier shared by these two  
367 organisms. The same was true for other false-positive taxa/missing taxa pairs including  
368 *Actinobaculum* sp. and *Actinobaculum* sp. oral taxon 183, *Bordetella bronchiseptica* and *B.*  
369 *pertussis*/*B. parapertussis*, *Synergistetes* bacterium and *Fretibacterium fastidiosum*,  
370 *Fusobacterium nucleatum* CC53 and *Fusobacterium nucleatum* subsp. *vincentii*, and Candidatus  
371 *Prevotella* and *Prevotella* oral taxon 317 (Supplemental Table S6). Most of these biases are against  
372 oral taxa, which is not surprising for a program developed using non-oral microbiome sources.  
373 MIDAS also has difficulty making assignments to the genera *Neisseria*, *Fusobacterium*, and

374 *Salmonella* (Supplemental Table S6), and slightly overestimates *M. tuberculosis* and *Y. pestis*  
375 (Figs. S7-S8), suggesting a slight bias for potentially human pathogenic organisms.

376

### 377 *CLARK-S*

378 CLARK-S, a version of the CLARK sequence classification system (19, 20), uses spaced  
379 k-mers to match reads to whole genomes in a database, and was developed specifically to classify  
380 reads in metagenomics samples. It performs similarly to Kraken (18), makes assignments only at  
381 the taxonomic level designated by the user (default species), and cannot report strains or sub-  
382 species. As the database size for CLARK-S increases, the amount of memory required to generate  
383 and load the hash table increases substantially, and our database of 16855 genomes required 1TB  
384 of memory (necessitating use of a high-performance computing cluster), yet the program classified  
385 each sample in a few hours. CLARK-S was the only program that detected all of the species in the  
386 input files that were in the database (Supplemental Table S7) (all of the genomes used to create  
387 the input files were deliberately included in the CLARK-S custom database); however, it also  
388 reported the highest number of false-positive taxa (~6000 in each 40-, 100-, and 200-genome  
389 dataset).

390 A majority of the species detected were present only in ancient simulated datasets (80%,  
391 75%, and 69% of species in 40-, 100-, and 200-genome datasets, respectively), and the  
392 overwhelming majority were present at <0.1% abundance. As filtering all species with relative  
393 abundance <0.1% removed most of the low-abundance false-positive taxa but only 1-2% of the  
394 total assigned reads, we recommend filtering all tables generated by CLARK-S. There was no clear  
395 distinction between high and low abundance false-positive taxa, unlike in several other programs  
396 we tested. Instead there was a steady decrease in the abundance of false-positive taxa, with a very  
397 long tail of very low abundance species.

398 Circular taxonomic assignment trees of the CLARK-S unfiltered tables show slight biases  
399 for *Actinobacteria*, but mostly overestimate each phylum in proportion to the original input (Fig.  
400 5, S19). A substantial number of viruses were reported, but were all reported at <0.1% abundance  
401 and removed by filtering. Most of the input species were detected by CLARK-S at proportions  
402 close to those of the input files for 40-, 100-, and 200-genome datasets, both ancient and modern  
403 (Fig. 4, S15-S16), but it was poorly able to detect the genera *Bordetella*, *Burkholderia*,  
404 *Mycobacterium*, and *Yersinia* (Fig. 3, S7-S8). Generally, species overestimation was lower in the

405 modern than ancient samples, but underestimation was not consistently different between ancient  
406 and modern sample sets (Fig. 3, S7-S8).

407

408 *MALT*

409 Like CLARK-S, MALT (21) uses spaced hashes to classify reads to the genomes in a  
410 database, and it is the only program we tested that can align reads to a protein database, done  
411 through BLASTx, which also allows functional characterization of the microbial community. We  
412 ran MALT in BLASTx-mode (22) to assess how translating the ancient simulated metagenomic  
413 reads affected taxonomic profiles, using a database consisting of NCBI RefSeq non-redundant  
414 bacteria, viral, archaeal, and plasmid protein sequences (57435 species/strains). The amount of  
415 memory required to load the hash table into memory was >1TB (again necessitating use of a high-  
416 performance computing cluster), and the program classified samples more slowly than CLARK-  
417 S, requiring several hours longer per sample than CLARK-S. The output files were uploaded to  
418 MEGAN6 (30, 31) and read count and relative abundance tables of only species-level assignments  
419 were exported, although MALT does place reads higher up on the taxonomic tree if they cannot  
420 be assigned to a species with high confidence. Fourteen input taxa were missing from the output  
421 files, 9 of which were not in the database (Supplemental Table S8). However, reads from each of  
422 these taxa were assigned to higher taxonomic levels, and in low numbers to closely-related species  
423 that were not in the input files.

424 MALT overestimated the number of species in all datasets, but the difference in the total  
425 number of assignments between ancient and modern datasets was much smaller than CLARK-S  
426 (Fig. 2C, S5C-S6C). Circular taxonomic assignment trees show a bias for *Proteobacteria* that  
427 remains after filtering (Fig. 5, S19). In the ancient simulated datasets there were 54, 86, and 75  
428 species detected in the 40-, 100-, and 200-genome datasets, respectively, that were not reported in  
429 the modern datasets. The over/underestimation of the relative abundance of each input species was  
430 consistent between modern and ancient samples (Fig. 3, 4, S7-S8, S17-S18). The 40-, 100-, and  
431 200-genome datasets each had 5 false-positive taxa present at >0.1% abundance, while two of  
432 these false-positive taxa were reported in the all 3 genome datasets. We observed that MALT  
433 assigned a low number of reads to a particularly high number of *Neisseria* and *Prevotella* species  
434 that were not in the input files. In the 40-, 100-, and 200-genome datasets, MALT identified 32,  
435 19, and 17 false-positive *Neisseria* species, respectively, and 22, 37, and 34 false-positive

436 *Prevotella* species, respectively, although all of these species were present at <0.1% abundance.  
437 This may be because the number of species in the database from these genera is higher than for  
438 other species in the input files (such as *Actinobacteria* and *Fusobacteria*).

439 One unusual false-positive taxon that was consistent with MIDAS was *Phocaeicola*  
440 *abscessus* in the 100 and 200-genome datasets, both ancient and modern, at a relative abundance  
441 of 0.4-0.9%. The reads assigned to *P. abscessus* were all from the *Bacteroides* sp. oral taxon 272  
442 genome, and *Bacteroides* sp. oral taxon 272 was identified at approximately 10% lower relative  
443 abundance than *P. abscessus* in all samples. Candidatus *Saccharibacterium* oral taxon TM7x had  
444 high numbers of reads assigned to it despite not being in the input file, but it was the only  
445 Candidatus *Saccharibacterium* TM7 species in the database and the reads assigned to it were from  
446 the TM7 genomes included in the input files. MALT classified a very small number of reads per  
447 sample to viruses (<50), but the assignments were not to species level, and were not included in  
448 the output files we analyzed.

449

## 450 **Discussion**

451 Reconstructing microbial community composition and structure from short sequencing  
452 reads is challenging (32), especially from highly damaged ancient DNA data-sets. Here we show  
453 that biases inherent to specific taxonomic assignment programs are more pronounced than biases  
454 arising from ancient DNA damage patterns. Each program we tested has intrinsic, and at times  
455 non-intuitive, assignment biases, and an appreciation of these biases is needed to aid interpretation  
456 and limit inappropriate conclusions.

457 Our study does not show that one program clearly outperforms others, but rather each has  
458 unique advantages and disadvantages. For example, for accurate interpretation of community  
459 structure, MIDAS is an appropriate choice if species relative abundance is critical (ie, by weighted  
460 UniFrac distance), while MetaPhlan2 is more appropriate if relative abundance is not critical (ie,  
461 by standard UniFrac distance). However, taxonomic accuracy in MIDAS is hampered by the way  
462 that the species are reported. For example, while MIDAS reduces potential assignments from tens  
463 of thousands of genomes in its full database to a more manageable 5952 ID clusters that are  
464 actually used at the taxonomic assignment step, and it reports as the identified species for each  
465 query sequence only one representative species per ID cluster, resulting in inappropriate species  
466 profiles despite reads being assigned to an appropriate genome. It may be possible to correct this



467 effect by altering the program to preferentially select a different representative species appropriate  
468 for the sample type under analysis, but this would require alteration of the source code or  
469 substantial reanalysis of the output files.

470 One major difference between the different programs test here lies in the way these  
471 compute relative abundance. By using a set of single-copy marker genes, both MetaPhlAn2 and  
472 MIDAS attempt to report the proportion of cells of each species detected in a sample. This is in  
473 contrast to k-mer-based methods such as CLARK-S and MALT, which report the proportion of  
474 total DNA assigned to each species. This difference may explain why the community structures  
475 (beta-diversity) reported by MetaPhlAn2 and MIDAS were closest to the simulated values.  
476 Genome size can vary substantially between bacterial species, and those with larger genomes may  
477 appear more abundant in a sample because a higher proportion of DNA is from those species, even  
478 though the number of cells may not be higher. Species relative abundance reported by k-mer-based  
479 identification methods can be normalized by predicted genome size in order to approximate cell  
480 copy number even when the exact strain is not known, as genome size is largely consistent within  
481 species. The distinction between the relative abundance reported by cell copy-normalizing  
482 (MetaPhlAn2 and MIDAS) and non-normalizing (CLARK-S, MALT, QIIME) metagenomic  
483 profilers should be kept in mind when considering metagenomic community profiles.

484 For maximizing the number of assigned reads or determining the relative abundance of all  
485 DNA fragments CLARK-S is best (if, for example, one wants to attempt genome assembly from  
486 all reads assigned to a species). Detecting genuine low-abundance species, however, especially  
487 viruses and bacteriophages, cannot be achieved with CLARK-S due to a high rate of false-positive  
488 identification with abundance lower than 0.1%. MALT is unique in that it can provide functional  
489 classification of reads as well as taxonomic classification, but it has difficulty making assignments  
490 when the database used has a high number of closely-related species (discussed below). In  
491 addition, similarly to CLARK-S, MALT has a high rate of false-positive assignment at low  
492 abundance. QIIME/UCLUST provides the least accurate method, which included many false  
493 positives even when low-abundance taxa were filtered out. In addition, our results indicate that it  
494 is the only program whose performance was distinctly different between ancient and modern  
495 samples, and the differences could not be resolved by removing low-abundance taxa.

496 Most of the program-specific biases we observed were due to the database each program  
497 used. Familiarity with the taxa present in modern samples is important to ensure appropriate

498 species representation in the database being used, and to customize the databases when possible.  
499 This will be much more straightforward for relatively well-characterized human body sites such  
500 as the mouth (4), and to a lesser extent the gut (33), but will be more nuanced for poorly  
501 characterized communities such as those from non-model organisms (34-36). For example, the  
502 default RefSeq bacteria database downloaded by CLARK-S does not include any species of  
503 *Actinomyces*, and has very few species of *Prevotella*, both of which are prevalent and highly-  
504 abundant oral genera, and the latter of which is major taxon in the gut microbiota of traditional  
505 societies (37). Restricting the database to RefSeq genomes alone, such as we did for MALT, limits  
506 the genomes to those that have been quality-checked and curated, and most sequenced genomes  
507 have not met these criteria, nor have metagenome-assembled genomes. Finally, the GreenGenes  
508 taxonomy has not been updated since 2013 and contains now-obsolete taxonomic classification  
509 for some organisms, which can confuse results, and more recently updated taxonomic  
510 classification systems (38) should be used.

511         Although ancient dental calculus is highly resistant to taphonomic processes and  
512 infiltration of environmental contaminants, it is not immune from these processes, and palaeofeces  
513 and other non-calcified archaeological specimens (39) are particularly susceptible to  
514 environmental contamination and degradation. Environmental microbes, particularly from soil  
515 burial matrix and skin of individuals handling the samples, may remain associated with  
516 archaeological samples after cleaning and sterilization and contribute to the metagenomic profile  
517 generated by sequencing. Distinguishing environmental signatures from endogenous signatures  
518 will be critical for ensuring accurate reconstruction of host-associated microbial profiles. Although  
519 outside the scope of this discussion, most microbial databases are heavily dominated by human-  
520 associated bacteria, and this may bias the assignment of soil and environmental species.  
521 Approaches for limiting false identification of environmental microbial species as host-associated  
522 species are discussed in Warinner, *et al.* (11).

523         The simulated ancient metagenomic datasets we generated were modeled after data  
524 generated from archaeological dental calculus (3), and we selected 5M reads for the *in silico*  
525 samples because this was the lowest read count in these samples. However, McIntyre, *et al.* 2017  
526 (25) have shown that as read depth increases the performance of metagenomic classifier tools  
527 changes, and this should be kept in mind for studies with higher sequencing depth. We chose not  
528 to normalize the output from each program to a consistent taxonomic level, such as genus, because

529 we wanted to work with data that was as close to the default output as possible. This allowed us to  
530 see the resolution limit of the programs with respect to known species, subspecies, and strains, as  
531 well as the strengths and weaknesses of that resolution. While higher taxonomic classification may  
532 demonstrate broad community level changes, the immense genetic variation in strains of a single  
533 bacterial species, for example *Streptococcus mutans* (40), prevents accurate prediction of changes  
534 in metabolic functional capacity from higher order taxonomy.

535 It is important to note, however, that while community resolution is lost when reads are  
536 assigned to higher levels of taxonomy, this technique may ultimately retain more information.  
537 Community structure may be better estimated at levels of taxonomy higher than species because  
538 reads that do not have species-level resolution can be classified at higher taxonomic levels with  
539 greater confidence. Using an LCA (lowest common ancestor) algorithm, MALT assigns reads to  
540 higher taxonomic levels if they cannot be distinguished between two nearly-genetically identical  
541 species. For example, some species within the genera *Yersinia* (*Y. pestis* and *Y.*  
542 *pseudotuberculosis*) and *Bordetella* (*B. pertussis*, *B. parapertussis*, *B. bronchiseptica*) are highly  
543 genetically similar, and reads that map equally well to multiple species in those genera are usually  
544 assigned at the genus level by the LCA algorithm in MALT. Similarly, QIIME/UCLUST will  
545 classify reads to deeper nodes in the tree by if they cannot be assigned to lower taxonomic levels.  
546 For example, the percent of reads in our dataset assigned to different taxonomic levels were:  
547 species – 17%, genus – 65%, family – 13%, order – 2.4%, and class – 0.7%. Users should be aware  
548 of this behavior in specific programs, and be aware of the node at which reads from those taxa tend  
549 to assign, as this can substantially affect analyses performed only at the species level.

550 Assigning taxonomy to reads below species level is desirable to understand the functional  
551 capacity of the microbial community, but the programs we tested performed this task poorly. The  
552 ability of MIDAS to discriminate strains or subspecies varies considerably by organism. For  
553 example, the 12 strains of *Porphyromonas gingivalis* in the database share the same species ID,  
554 while the 31 strains of *Streptococcus mitis* each have a unique species ID. This resulted in the  
555 MIDAS-produced species profiles containing one strain of *P. gingivalis* in the 100 and 200-  
556 genome datasets (despite there being two and four, respectively), and 29-30 strains of *S. mitis*  
557 across each 40-, 100-, and 200-genome dataset (albeit all very low abundance), despite there being  
558 only one species in all three datasets. To avoid biases of strain-level identification by this program,  
559 we combined all strain-level assignments of the same species into one species-level assignment

560 for all analyses If identifying subspecies or strains present in a sample is desired, programs  
561 specifically designed to perform this function, such as StrainPhlAn (41), Sigma (42), or Platypus  
562 Conquistador (43), are recommended instead. Furthermore, special care should be taken to ensure  
563 results are not false positives or derived from modern environmental contamination by following  
564 guidelines suggested by Warinner *et al.* (11) and Key, *et al.* (44).

565 High proportions of the fecal-associated genera *Coprococcus*, *Enterococcus*, and  
566 *Enterobacter* were identified by QIIME/UCLUST in our *in silico* generated dataset, but they were  
567 not in the input files. Rather, a high number of reads of consistent taxonomy were assigned to these  
568 genera, which we confirmed occurs in real datasets, indicating that these assignments are more  
569 likely an artifact of the taxonomic classification process than an indication of poor hygiene. This  
570 demonstrates how interpreting taxonomic assignment results without understanding the biases and  
571 limitations of the program used could lead to erroneous conclusions about microbial community  
572 profiles, and ultimately human activity.

573 Identifying bacteriophage in ancient metagenomic samples is challenging and new  
574 methods are needed. MetaPhlAn2, CLARK-S, and MALT all detected phages in very low  
575 abundance, below levels of suggested filtering to remove spurious assignments. Active  
576 bacteriophage replication in the oral biofilm is associated with altered host health status (5, 45),  
577 and monitoring phage activity may offer insight into biofilm pathogenicity in oral (45, 46) and gut  
578 (47) sites. Therefore, reliably detecting bacteriophage in host-associated ancient metagenomic  
579 samples may allow us to study phage-mediated biofilm changes and evolution relating to human  
580 disease. While it is unlikely that we will be able to determine if phage-identified sequencing reads  
581 are from viral particles or host-integrated prophages, proteomic characterization of ancient  
582 microbiomes (1) may be able to detect viral proteins indicating free phage particles.

583 Recently, McIntyre, *et al.* (25) assessed performance of a wide selection of metagenomic  
584 taxonomic classification programs built upon a variety of techniques. They reported that the  
585 precision of taxonomic assignment can be improved by combining results of certain programs that  
586 use different assignment methods, including MetaPhlAn2 and CLARK-S. Combining the results  
587 of these taxonomic assignment programs for ancient metagenomics samples may then increase  
588 reliability and confidence in historic community structure and composition, and should be  
589 examined further with *in silico*-generated datasets. Confirming species presence/absence by

590 detection with two independent taxonomic classifiers will assist with ensuring specific program  
591 biases are not reported as true results.

592         There are several factors that we did not test that may influence taxonomic profiling of  
593 ancient DNA. These include environmental contamination (11) (discussed above) sample location-  
594 and age-specific differences in damage patterns (48), and species-specific differential preservation  
595 of bacterial DNA (8). Additional *in silico* dataset testing, such as by using mapDamage profiles  
596 modeled after older archaeological samples, samples from different locations, or based on reads  
597 mapped to different or multiple species, may be warranted to determine if and how strongly these  
598 factors affect taxonomic profiling. Based on our results that age-related damage patterns minimally  
599 affect read taxonomic assignment, however, we do not expect these variables to substantially alter  
600 taxonomic profiles. Nevertheless, location- and age-related biases should be considered in studies  
601 that compare samples across geographic locations and/or time.

602         We have demonstrated that the damage patterns characteristic of ancient DNA do not  
603 substantially affect taxonomic profiling by the five programs we tested. Instead the biases we  
604 detected are inherent to the programs themselves and the database each program uses. This is  
605 promising for comparing ancient microbiome samples with modern samples when using the same  
606 taxonomic classifier, as biases will be shared by both. Our results highlight the importance of  
607 knowing the limitations of the metagenomic classifier being used, and investigating any unusual  
608 results, such as the presence of unexpected taxa and the absence of expected taxa, to ensure  
609 appropriate interpretation of taxonomic profiles.

610

## 611 **Materials and Methods**

### 612 **Simulated ancient and modern metagenomics samples**

613         Simulated ancient and modern metagenomics fastq files were generated with gargammel  
614 (27). Samples of 5 million reads, 99% bacterial and 1% human were generated with 40-genomes,  
615 100-genomes, or 200-genomes, with even genome distribution (equivalent numbers of reads from  
616 each input genome), and both with and without simulated ancient DNA damage patterns, and  
617 sequencing errors were based on Illumina HiSeq2500 150bp paired-end chemistry and default  
618 Illumina adapters. Thirty-nine total metagenomes were simulated as follows: 40-genome even  
619 distribution ancient (10) and modern (3), 100-genome even distribution ancient (10) and modern  
620 (3), and 200-genome even distribution ancient (10) and modern (3). Genomes are listed in

621 Supplemental Table S1, and were selected to resemble dental plaque bacterial communities based  
622 on the species listed in the Human Oral Microbiome Database ([homd.org](http://homd.org)), and relative abundance  
623 was roughly based on dental plaque-derived biofilm composition (Velsko & Shaddox, in review).  
624 Select non-oral bacterial species were added to assess biases in detecting specific “pathogenic”  
625 species. Although the genomes are represented with equal proportions of DNA in each dataset, the  
626 number of cells from each organism is unevenly distributed because of differences in genome size  
627 (Supplemental Table S1).

628 Age-related damage patterns were simulated based on mapDamage (9, 10) base  
629 composition file and misincorporation file generated on analysis of real historic dental calculus  
630 metagenomic samples sequenced on an Illumina HiSeq2500 with 150bp paired-end chemistry,  
631 with bacterial genome damage patterns based on reads mapped to the *Tannerella forsythia* 92A2  
632 genome (assembly GCA\_000238215.1) (Fig. S1) and human genome damage patterns based on  
633 reads mapped to the human genome (assembly GCA\_000001405.26) (Fig. S1), while the fragment  
634 length distribution was based on all reads in sample CS21. Simulations for modern metagenomics  
635 samples did not include damage pattern input files. The command to simulate ancient  
636 metagenomic samples was: `./gargammel.pl --comp 0.99,0,0.01 -n 5000000 --misinc`  
637 `dnacompCS32e.txt --misincb dnacompCS21b.txt -f fragmentlengthCS21.txt -mapdamag`  
638 `ee misincorporationCS32.txt single -mapdamageb misincorporationCS21.txt single -rl 150 -ss HS25`  
639 `-o output/anc40e1 input/`. The command to simulate modern metagenomic samples was:  
640 `./gargammel.pl --comp 0.99,0,0.01 -n 5000000 -l 150 -rl 150 -ss HS25 -o output/mod40e1 input/`.  
641 Damage profiles for human (CS21) and bacterial (CS32) reads came from different calculus  
642 samples because these had the highest number of reads to the human and *T. forsythia* genomes,  
643 respectively, which allows the most accurate assessment of damage profiles (11). Fragment length  
644 distribution for ancient simulated samples was based calculus sample CS21, while read length of  
645 150bp was specified for modern samples. The genome of origin for each read is included in the  
646 read name by a gargammel-generated code (listed in Supplemental Table S1), and the exact  
647 number of reads derived from each genome was determined by counting in each of the 78 input  
648 fastq files.

649

## 650 **Read processing and 16S rRNA gene fragment filtering**

651 Reads were processed following a custom pipeline optimized for ancient DNA  
652 metagenomics samples. AdapterRemoval (49) was used to detect and remove consensus adapter  
653 sequences, quality-trim reads at Q30 and collapse paired reads. Singleton files were discarded and  
654 reads with residual adapters were detected with bowtie2 (50) and filtered from the samples with  
655 filter\_fasta.py in QIIME v1.9 (12). Four final files were generated: collapsed reads, pair 1 reads,  
656 pair2 reads, and truncated collapsed reads, and all 4 files were concatenated to generate a single  
657 input file for taxonomic classification. Reads mapping to the 16S rRNA gene were identified in  
658 the independent final files and collected in separate files for classification as follows. A bowtie2  
659 database was generated from the GreenGenes v13.8 database (51), and the cleaned and collapsed,  
660 pair1, pair2, and collapsed truncated fastq files were searched against this database with bowtie2.  
661 All reads that mapped to 16S rRNA gene reads were filtered from the full fastq files to a separate  
662 file using seqtk (<https://github.com/lh3/seqtk>). All 4 files matching the 16S rRNA gene (collapsed,  
663 pair1, pair2, and collapsed truncated) were concatenated for taxonomic classification  
664 (Supplemental Table S3).

665

## 666 **Taxonomic classification**

667 Reads in all simulated metagenomics samples were classified with 5 taxonomic  
668 identification programs (Supplemental Table S2): QIIME v1.9/UCLUST/GreenGenes v13.8  
669 database (12, 51, 52), MetaPhlan2 (14, 15), MIDAS (16), CLARK-S (20), and MALT (21) run in  
670 BLAST-X mode (22). All options that differed from default are listed in Table S2. Each program  
671 uses a different classification method. QIIME v1.9 was used to bin reads matching the 16S rRNA  
672 gene using UCLUST (52) with pick\_closed\_reference\_otus.py and to assign taxonomic  
673 classification with the GreenGenes v 13.8 database at 97% identity (202421 sequences, 99322  
674 OTUs). Samples were not rarefied to identical OTU counts prior to analysis, as this practice has  
675 been shown to be unnecessary (53). The output biom file was summarized at the species level,  
676 which included all assignment levels kingdom through species. MetaPhlan2 and MIDAS used  
677 their respective default databases (16904 species/strains, 31007 genomes/5952 species groups,  
678 respectively), while CLARK-S was run against a custom database of 16855 genomes, and MALT  
679 was run in BLAST-X mode against a custom database of NCBI RefSeq non-redundant bacteria,  
680 viral, archaeal, and plasmid protein sequences (57435 species/strains). MetaPhlan2 and CLARK-

681 S output were set to species level. The MALT output rma6 files were uploaded to MEGAN6 (31),  
682 and classification tables of species assignments only were exported. Output for each classification  
683 program is unique, with MetaPhlan2 and MIDAS providing relative abundance on a scale of 0-  
684 100 and 0-1, respectfully, QIIME and CLARK-S providing a read count table, and MALT  
685 providing both relative abundance and read counts.

686 Outputs were normalized in 2 ways, generating 2 sets of tables: relative abundance of all  
687 assignments on a scale of 0-100 was calculated based on the number of reads assigned, if provided  
688 (QIIME, CLARK-S, MALT), and pseudo read counts were determined by multiplying the relative  
689 abundance by the total number of reads in the input files for MetaPhlan2 and MIDAS. The true  
690 input tables were also converted to biom format in count read and relative abundance formats. The  
691 NCBI taxonomy ID of each taxonomic assignment in each program was determined and used to  
692 create a single taxonomy file to assign taxonomy to biom files. All output tables, read counts and  
693 relative abundance, were converted to biom format in QIIME v1.9 and taxonomy based on NCBI  
694 taxonomy ID was added to each. To determine if removing very low abundance assignments  
695 improved the profiles, a second set of biom files was generated by removing all assignments  
696 present at less than 0.1% abundance (filtered tables). All biom files were summarized at the  
697 phylum, class, and genus levels in QIIME v1.9 using `summarize_taxa.py`, to allow assessment of  
698 classification biases at different taxonomic levels. Mapping data, including the simulated age of  
699 the sample (ancient or modern) and the taxonomic assignment program, were added to the biom  
700 files in QIIME v1.9.

701 QIIME v1 is no longer being supported with the release of QIIME v2.0, and QIIME v2.0  
702 uses different taxonomic assignment programs from QIIME v1: (DADA2 (26) and `deblur` (28)).  
703 We also tried to include DADA2 in this assessment (Supplemental Table S2), using 16S rRNA  
704 gene-identified reads and the DADA2 R package as follows. `AdapterRemoval` was run on the  
705 simulated samples as before, but `pair1` and `pair2` reads were not collapsed. The reads matching 16S  
706 rRNA genes were identified using `bowtie2` and the GreenGenes v13.8 database as before and  
707 filtered out of the `pair1` and `pair2` files. The `pair1` and `pair2` files of 16S rRNA gene-identified  
708 reads were used as input in DADA2. DADA2 was not able to merge sequences in any file because  
709 all were unique, and this prevented DADA2 from performing the sequence variant calling, and the  
710 program was unable to perform taxonomic assignment. Therefore, we were unable to proceed with  
711 DADA2, and have no results to present.



712

### 713 **Diversity metrics**

714         Alpha-diversity was calculated in QIIME using the metrics Faith's phylogenetic distance,  
715 Shannon index, observed species, and Chao1, using count read and pseudo-count read files, and  
716 graphs were generated using Prism v7. Beta-diversity was calculated on relative abundance biom  
717 files and plotted using the R package phyloseq (54) for the metrics UniFrac (55) (accounts for  
718 phylogenetic relatedness and presence/absence) and weighted UniFrac (56) (accounts for  
719 phylogenetic relatedness, presence/absence and abundance), Bray-Curtis (accounts for  
720 presence/absence and abundance) and binary Jaccard (accounts only for presence/absence). A  
721 newick-formatted phylogenetic tree was generated with phyloT (<http://phylot.biobyte.de>)  
722 including the NCBI taxonomy IDs of all assignments made by each program (9919 total IDs),  
723 using the Internal nodes-Expanded and Polytomy-Yes options.

724

### 725 **Program assignment biases**

726         All output text files were manually inspected for taxonomic assignment biases. When a  
727 species in the input files was not detected by a program, the database of that program was searched  
728 for that species to understand why it was missed. The percent over/under representation of each  
729 genome compared to the input file was calculated (relative abundance in output/relative abundance  
730 in input \* 100) and plotted as a heat map with the R library gplots  
731 (<http://www.rdocumentation.org/packages/gplots>). The percent of each species in the input files  
732 detected by each program as well as the percent of all other species detected but not in the input  
733 file was plotted in R using ggplot2 ([ggplot2.org](http://ggplot2.org)). The R package metacodeR (57) was used to  
734 visualize phylogenetic tree assignment biases in the ancient datasets by each program. Each node  
735 is a taxonomic assignment starting with the root (yellow circle), then kingdoms, phyla, etc  
736 radiating off, to sub-species level at the tips. For programs that did not produce sub-species or  
737 strain-level taxonomic assignments, the species assignment was repeated, so maintain visual  
738 consistency between all trees. The input data for these trees is the species/subspecies level for all  
739 programs except QIIME/UCLUST (which included all levels), so the internal nodes sum the leaves  
740 moving from subspecies back towards the root. The colors and weight of nodes and branches  
741 represent the relative abundance of each taxonomic assignment, where lighter colors with thicker  
742 branches are more abundant (yellows and light blues) and darker, thinner branches are less

743 abundant. The relative abundance is the average of all 10 output files for each program. A ring  
744 circling each tree and color-coding each phylum was added in Inkscape.

745 We tested whether a QIIME/UCLUST false-positive taxa read assignment bias was present  
746 in real ancient metagenomics samples by processing metagenomic data generated from 19th  
747 century dental calculus samples (3) through the same 16S rRNA gene selection and  
748 QIIME/UCLUST OTU-picking, and then filtering out all reads assigned to the designated “false-  
749 positive” genera. These reads were searched against the NCBI nt database with BLAST using  
750 default parameters and the BLAST hits of the reads assigned to each “false-positive” genus were  
751 determined using MEGAN6 and compared to the origin genomes of the false-positive-taxa  
752 assigned reads from the simulated samples.

753

#### 754 **Data sharing and availability**

755 All supplemental figures are available for download on figshare (as a single pdf):

756 <https://doi.org/10.6084/m9.figshare.5811285.v1>

757

758 All supplemental tables are available for download on figshare (seperate tabs in a single excel  
759 spreadsheet): <https://doi.org/10.6084/m9.figshare.5817837.v1>

760

761 All gargammel-generated “raw” sequencing read files (forward and reverse) will be available for  
762 download when we find an appropriate site to host them. They’re big. We’re working on it. Please  
763 until then if you would like the files contact us and we’re happy to share.

764

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774

775

#### 776 **Figure legends**

777 **Fig. 1.** Age-related damage patterns minimally influence reported phylogenetic-based community  
778 structure. (A) Principal coordinates analysis plots of abundance-weighted UniFrac beta-diversity  
779 for datasets made with 40, 100, and 200 genomes for full output tables and tables filtered to remove

780 species present at < 0.1% abundance. (B) Principal coordinates analysis plots of UniFrac beta-  
781 diversity for datasets made with 40, 100, and 200 genomes for full output tables and tables filtered  
782 to remove species present at < 0.1% abundance.

783

784 **Fig. 2.** Age-related damage patterns slightly increase within-sample diversity. Alpha diversity of  
785 40-genome datasets calculated by (A) Faith's phylogenetic distance, (B) Shannon index, (C)  
786 Observed species, and (D) Chao1 for full output tables and tables filtered to remove species present  
787 at < 0.1% abundance. MPA2 - MetaPhlan2, anc – ancient simulated dataset, mod – modern  
788 simulated dataset.

789

790 **Fig. 3.** Species detection and over/under-representation differ by program but not age-related  
791 damage. Heat-map showing for each program tested the species relative abundance under-  
792 represented (blues), over-represented (yellows, oranges, reds), not detected (black), and accurately  
793 represented (white) relative to the true input files for modern and ancient 40-genome datasets.  
794 Where programs were unable to distinguish species, strains, or subspecies a single bar across those  
795 genomes is colored to represent the over/under-representation of the lowest identifiable taxonomic  
796 level. MPA2 - MetaPhlan2, CLK-S - CLARK-S; A – ancient simulated dataset, M – modern  
797 simulated dataset.

798

799 **Fig. 4.** Differences in species relative abundance are program-specific and minimally affected by  
800 age-related damage. Program-specific differences in species detection and relative abundance are  
801 consistent between ancient (top) and modern (bottom) 40-genome simulated datasets. Relative  
802 abundances of each bar represent: If - true input fasta file, Id - input species detected, and Ad - all  
803 species detected. Species other than those included in the input files are grouped together as 'other'  
804 in a gray stripe at the top of the Ad bar. QIIME/UCLUST bars represent genus-level assignments.

805

806 **Fig. 5.** Biases in species detection across the phylogenetic tree are database-dependent. Species  
807 detected by each program represented in a radial phylogenetic tree with the nodes representing  
808 different taxonomic levels, where innermost node is root and the outermost nodes are strains. More  
809 highly represented taxa are lighter in color (yellow to light blue) and have thicker branches/nodes,  
810 while less abundant taxa are darker blues with thinner branches/nodes. The ring encircling each  
811 tree designates the major phyla (those in the input files, plus viruses when distinguishable) by  
812 color. For programs that did not report strains (QIIME/UCLUST, MetaPhlan2, CLARK-S,  
813 MALT) the species was repeated as a strain to maintain consistency with MIDAS.

814

### 815 **Supplemental Tables and Figures**

816 **Table S1.** Details of input metagenomic samples generated *in silico* by gargammel.

817 **Table S2.** Details of the 6 taxonomic classification programs used.

818 **Table S3.** 16S rRNA gene-identified read input file read counts per sample.

819 **Table S4.** QIIME/UCLUST-specific taxonomic assignment biases.

820 **Table S5.** MetaPhlAn2-specific taxonomic assignment biases.

821 **Table S6.** MIDAS-specific taxonomic assignment biases.

822 **Table S7.** CLARK-S-specific taxonomic assignment biases.

823 **Table S8.** MALT-specific taxonomic assignment biases.

824

825 **Fig. S1.** MapDamage plots showing damage patterns applied to bacterial reads (top panels, CS32  
826 *Tannerella forsythia* reads) and to human reads (bottom panels, CS21 human reads). MapDamage  
827 plots are from real ancient dental calculus samples from ref. (3).

828

829 **Fig. S2.** Age-related damage patterns minimally influence reported non-phylogenetic-based  
830 community structure in 40-genome samples. Principal coordinates analysis plots of abundance-  
831 weighted Bray-Curtis distance and un-weighted Jaccard distance beta-diversity for datasets made  
832 with 40-genomes at the species and genus levels for full output tables and tables filtered to remove  
833 species present at < 0.1% abundance.

834

835 **Fig. S3.** Age-related damage patterns minimally influence reported non-phylogenetic-based  
836 community structure in 100-genome samples. Principal coordinates analysis plots of abundance-  
837 weighted Bray-Curtis distance and un-weighted Jaccard distance beta-diversity for datasets made  
838 with 100-genomes at the species and genus levels for full output tables and tables filtered to remove  
839 species present at < 0.1% abundance.

840

841 **Fig. S4.** Age-related damage patterns minimally influence reported non-phylogenetic-based  
842 community structure in 200-genome samples. Principal coordinates analysis plots of abundance-  
843 weighted Bray-Curtis distance and un-weighted Jaccard distance beta-diversity for datasets made  
844 with 200-genomes at the species and genus levels for full output tables and tables filtered to remove  
845 species present at < 0.1% abundance.

846

847 **Fig. S5.** Age-related damage patterns slightly increase within-sample diversity. Alpha diversity of  
848 100-genome datasets calculated by (A) Faith's phylogenetic distance, (B) Shannon index, (C)  
849 Observed species, and (D) Chao1 for full output tables and tables filtered to remove species present  
850 at < 0.1% abundance. MPA2 - MetaPhlAn2, anc – ancient simulated dataset, mod – modern  
851 simulated dataset.

852

853 **Fig. S6.** Age-related damage patterns slightly increase within-sample diversity. Alpha diversity of  
854 200-genome datasets calculated by (A) Faith's phylogenetic distance, (B) Shannon index, (C)  
855 Observed species, and (D) Chao1 for full output tables and tables filtered to remove species present  
856 at < 0.1% abundance. MPA2 - MetaPhlAn2, anc – ancient simulated dataset, mod – modern  
857 simulated dataset.

858

859 **Fig. S7.** Species detection and over/under-representation differ by program not age-related  
860 damage. Heat-map showing for each program tested the species relative abundance under-  
861 represented (blues), over-represented (yellows, oranges, reds), not detected (black), and accurately  
862 represented (white) relative to the true input files for modern and ancient 100-genome datasets.  
863 Where programs were unable to distinguish species, strains, or sub-species a single bar across  
864 those genomes is colored to represent the over/under-representation of the lowest identifiable  
865 taxonomic level. MPA2 - MetaPhlAn2, CLK-S - CLARK-S; A – ancient simulated dataset, M –  
866 modern simulated dataset.

867

868 **Fig. S8.** Species detection and over/under-representation differ by program not age-related  
869 damage. Heat-map showing for each program tested the species relative abundance under-  
870 represented (blues), over-represented (yellows, oranges, reds), not detected (black), and accurately  
871 represented (white) relative to the true input files for modern and ancient 200-genome datasets.  
872 Where programs were unable to distinguish species, strains, or sub-species a single bar across  
873 those genomes is colored to represent the over/under-representation of the lowest identifiable  
874 taxonomic level. MPA2 - MetaPhlAn2, CLK-S - CLARK-S; A – ancient simulated dataset, M –  
875 modern simulated dataset.

876

877 **Fig. S9.** QIIME/UCLUST-specific differences in genus detection and relative abundance are  
878 consistent between ancient and modern 100-genome simulated datasets. Relative abundances of  
879 each bar represent: If - true input fasta file, 16f - 16S rRNA gene-identified read input fasta file  
880 (used for QIIME/UCLUST profiling), Id - input genera detected, and Ad - all genera detected.  
881 Genera other than those included in the input files are grouped together as ‘other’ in a stripe at the  
882 top of the Ad bar.

883

884 **Fig. S10.** QIIME/UCLUST-specific differences in genus detection and relative abundance are  
885 consistent between ancient and modern 200-genome simulated datasets. Relative abundances of  
886 each bar represent: If - true input fasta file, 16f - 16S rRNA gene-identified read input fasta file  
887 (used for QIIME/UCLUST profiling), Id - input genera detected, and Ad - all genera detected.  
888 Genera other than those included in the input files are grouped together as ‘other’ in a stripe at the  
889 top of the Ad bar.

890

891 **Fig. S11.** MetaPhlAn2-specific differences in species detection and relative abundance are  
892 consistent between ancient and modern 100-genome simulated datasets. Relative abundances of  
893 each bar represent: If - true input fasta file, Id - input species detected, and Ad - all species detected.  
894 Species other than those included in the input files are grouped together as ‘other’ in a stripe at the  
895 top of the Ad bar.

896

897 **Fig. S12.** MetaPhlAn2-specific differences in species detection and relative abundance are  
898 consistent between ancient and modern 200-genome simulated datasets. Relative abundances of

899 each bar represent: If - true input fasta file, Id - input species detected, and Ad - all species detected.  
900 Species other than those included in the input files are grouped together as 'other' in a stripe at the  
901 top of the Ad bar.

902

903 **Fig. S13.** MIDAS-specific differences in species detection and relative abundance are consistent  
904 between ancient and modern 100-genome simulated datasets. Relative abundances of each bar  
905 represent: If - true input fasta file, Id - input species detected, and Ad - all species detected. Species  
906 other than those included in the input files are grouped together as 'other' in a stripe at the top of  
907 the Ad bar.

908

909 **Fig. S14.** MIDAS-specific differences in species detection and relative abundance are consistent  
910 between ancient and modern 200-genome simulated datasets. Relative abundances of each bar  
911 represent: If - true input fasta file, Id - input species detected, and Ad - all species detected. Species  
912 other than those included in the input files are grouped together as 'other' in a stripe at the top of  
913 the Ad bar.

914

915 **Fig. S15.** CLARK-S-specific differences in species detection and relative abundance are consistent  
916 between ancient and modern 100-genome simulated datasets. Relative abundances of each bar  
917 represent: If - true input fasta file, Id - input species detected, and Ad - all species detected. Species  
918 other than those included in the input files are grouped together as 'other' in a stripe at the top of  
919 the Ad bar.

920

921 **Fig. S16.** CLARK-S-specific differences in species detection and relative abundance are consistent  
922 between ancient and modern 200-genome simulated datasets. Relative abundances of each bar  
923 represent: If - true input fasta file, Id - input species detected, and Ad - all species detected. Species  
924 other than those included in the input files are grouped together as 'other' in a stripe at the top of  
925 the Ad bar.

926

927 **Fig. S17.** MALT-specific differences in species detection and relative abundance are consistent  
928 between ancient and modern 100-genome simulated datasets. Relative abundances of each bar  
929 represent: If - true input fasta file, Id - input species detected, and Ad - all species detected. Species  
930 other than those included in the input files are grouped together as 'other' in a stripe at the top of  
931 the Ad bar.

932

933 **Fig. S18.** MALT-specific differences in species detection and relative abundance are consistent  
934 between ancient and modern 100-genome simulated datasets. Relative abundances of each bar  
935 represent: If - true input fasta file, Id - input species detected, and Ad - all species detected. Species  
936 other than those included in the input files are grouped together as 'other' in a stripe at the top of  
937 the Ad bar.

938

939 **Fig. S19.** Biases in species detection across the phylogenetic tree are database-dependent. Figure  
940 is identical to Fig. 5, but with a black background to better visualize color gradient and branch/node  
941 sizes of the trees. Species detected by each program represented in a radial phylogenetic tree with  
942 the innermost node as root and the outermost nodes as strains. More highly represented taxa are  
943 lighter in color (yellow to light blue) and have thicker branches/nodes, while less abundant taxa  
944 are darker blues with thinner branches/nodes. The ring encircling each tree designates the major  
945 phyla (those in the input files, plus viruses when distinguishable) by color. For programs that did  
946 not report strains (QIIME/UCLUST, MetaPhlan2, CLARK-S, MALT) the species was repeated  
947 as a strain to maintain consistency with MIDAS.

948

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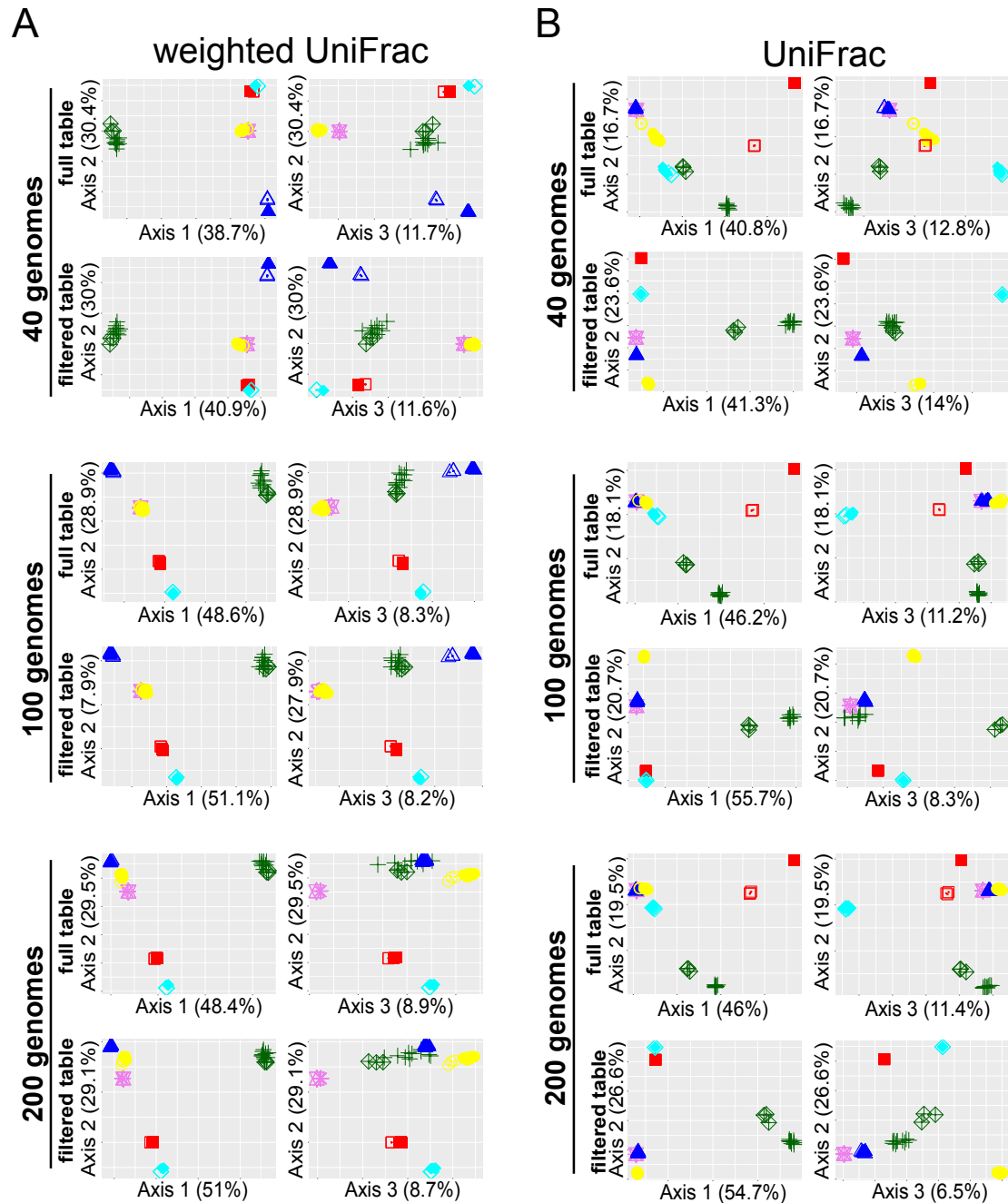
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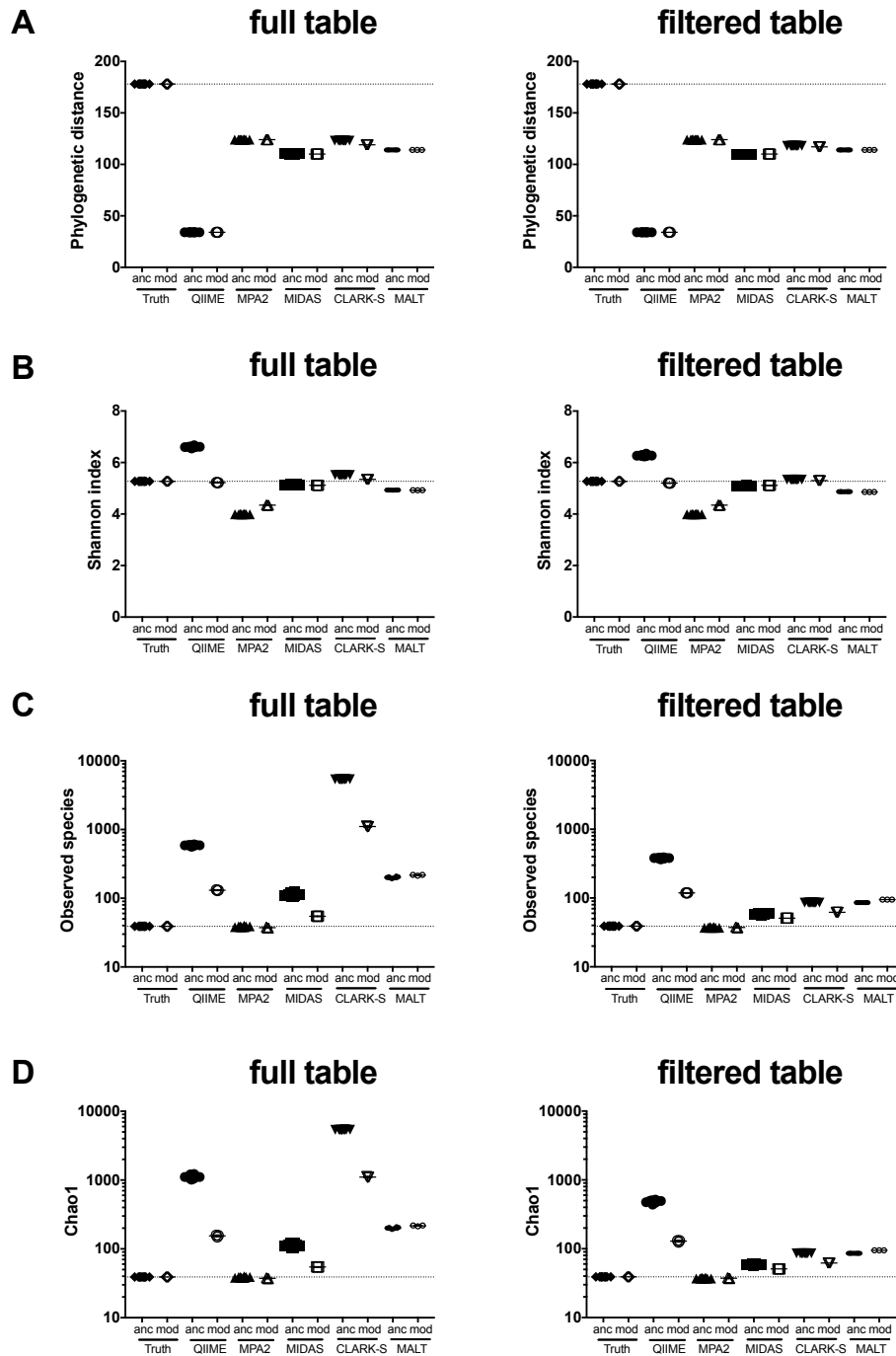
Ancient: \* True + QIIME/UCLUST ◆ MALT ▲ MetaPhlan2 ● MIDAS ■ CLARK-S  
 Modern: \* True ◆ QIIME/UCLUST ◆ MALT ▲ MetaPhlan2 ● MIDAS ■ CLARK-S

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1130 **Figure 1.** Age-related damage patterns minimally influence reported phylogenetic-based  
 1131 community structure. (A) Principal coordinates analysis plots of abundance-weighted UniFrac  
 1132 beta-diversity for datasets made with 40, 100, and 200 genomes for full output tables and tables  
 1133 filtered to remove species present at < 0.1% abundance. (B) Principal coordinates analysis plots  
 1134 of UniFrac beta-diversity for datasets made with 40, 100, and 200 genomes for full output tables  
 1135 and tables filtered to remove species present at < 0.1% abundance.

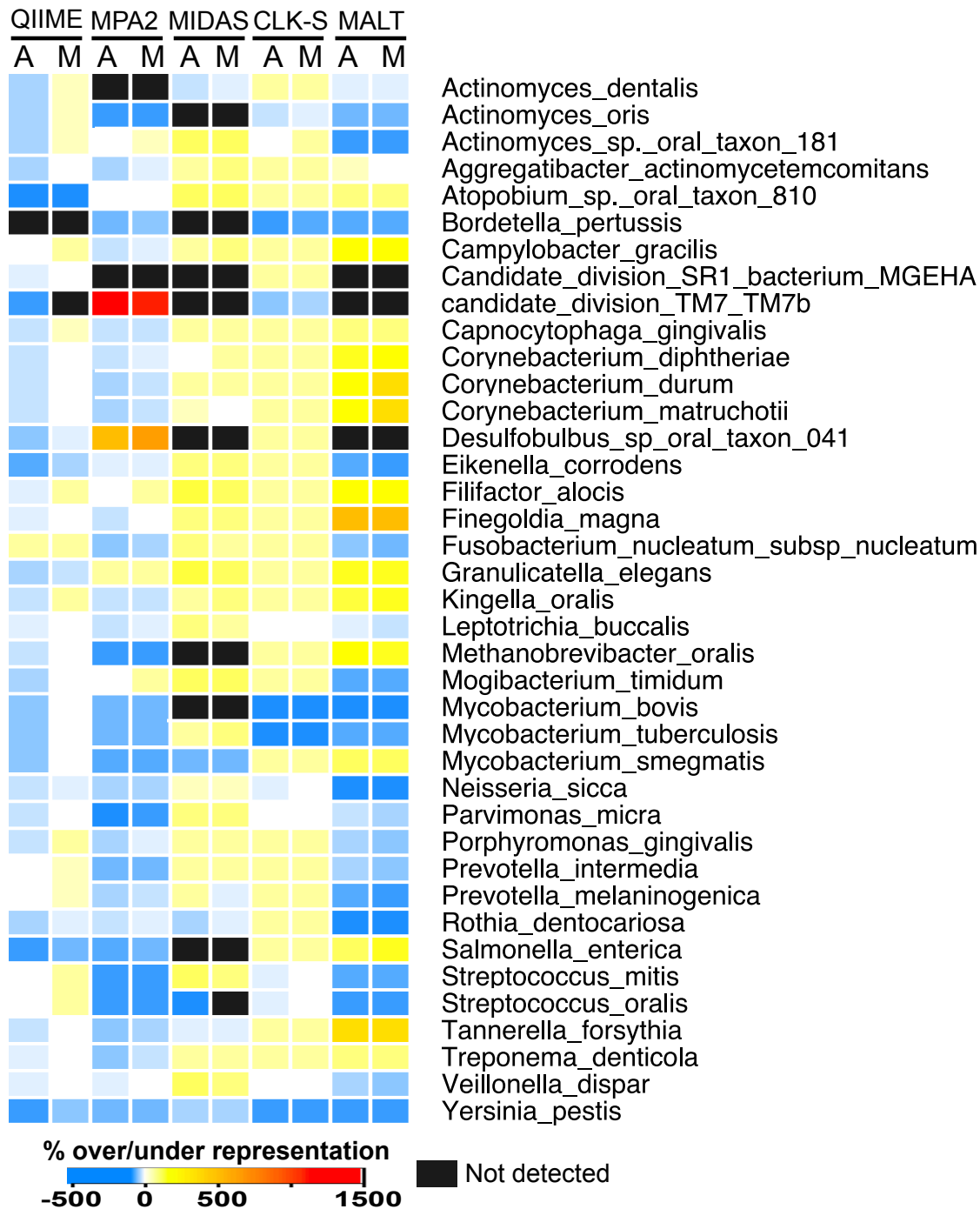
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### 40 genomes



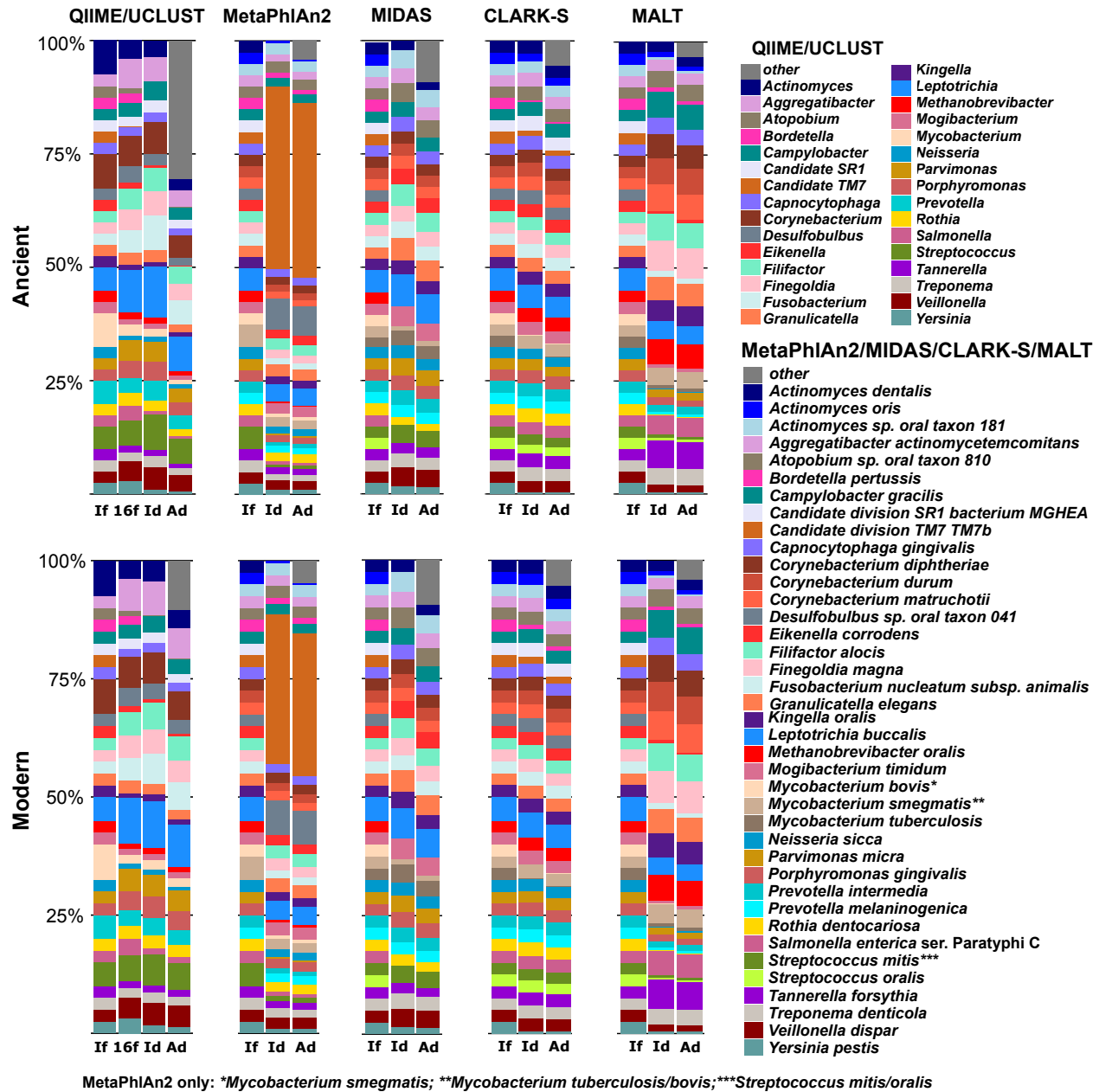
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1139 Figure 2. Age-related damage patterns slightly increase within-sample diversity. Alpha diversity  
1140 of 40-genome datasets calculated by (A) Faith's phylogenetic distance, (B) Shannon index, (C)  
1141 Observed species, and (D) Chao1 for full output tables and tables filtered to remove species present  
1142 at < 0.1% abundance. MPA2 - MetaPhlan2, anc – ancient simulated dataset, mod – modern  
1143 simulated dataset.



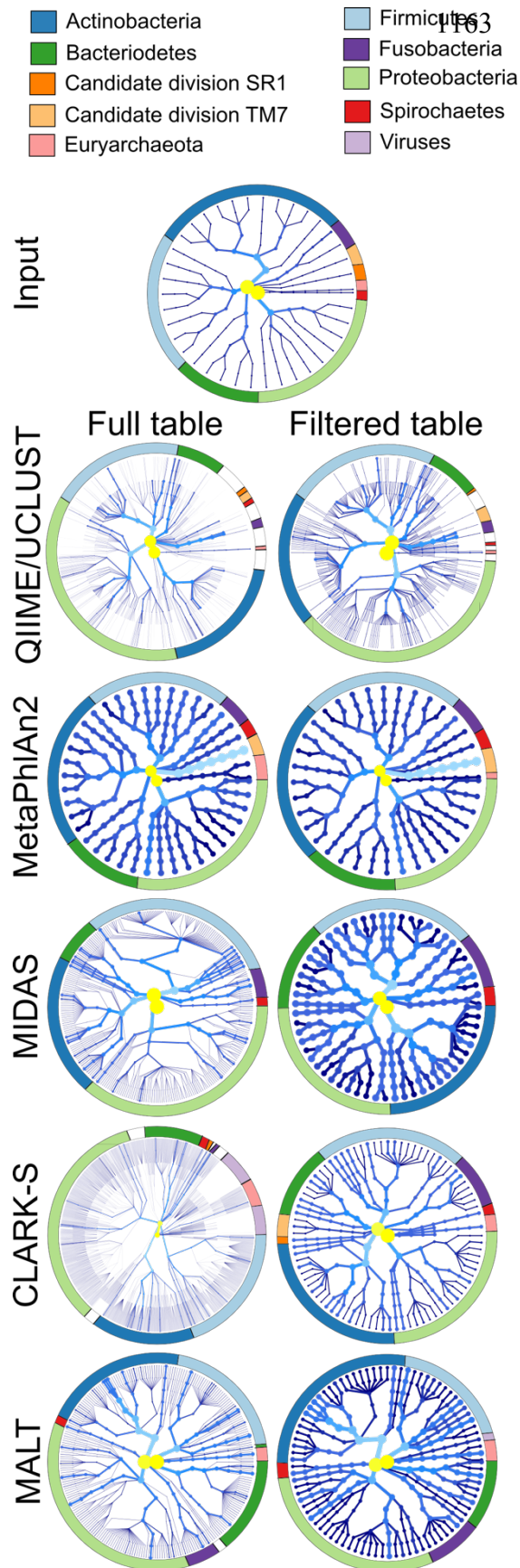
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1146 **Figure 3.** Species detection and over/under-representation differ by program but not age-related  
1147 damage. Heat-map showing for each program tested the species relative abundance under-  
1148 represented (blues), over-represented (yellows, oranges, reds), not detected (black), and accurately  
1149 represented (white) relative to the true input files for modern and ancient 40-genome datasets.  
1150 Where programs were unable to distinguish species, strains, or subspecies a single bar across those  
1151 genomes is colored to represent the over/under-representation of the lowest identifiable taxonomic  
1152 level. MPA2 - MetaPhlan2, CLK-S - CLARK-S; A – ancient simulated dataset, M – modern  
1153 simulated dataset.



**Figure 4.** Differences in species relative abundance are program-specific and minimally affected by age-related damage. Program-specific differences in species detection and relative abundance are consistent between ancient (top) and modern (bottom) 40-genome simulated datasets. Relative abundances of each bar represent: If - true input fasta file, Id - input species detected, and Ad - all species detected. Species other than those included in the input files are grouped together as ‘other’ in a gray stripe at the top of the Ad bar. QIIME/UCLUST bars represent genus-level assignments.





**Figure 5.** Biases in species detection across the phylogenetic tree are database-dependent. Species detected by each program represented in a radial phylogenetic tree with the nodes representing different taxonomic levels, where innermost node is root and the outermost nodes are strains. More highly represented taxa are lighter in color (yellow to light blue) and have thicker branches/nodes, while less abundant taxa are darker blues with thinner branches/nodes. The ring encircling each tree designates the major phyla (those in the input files, plus viruses when distinguishable) by color. For programs that did not report strains (QIIME/UCLUST, MetaPhlan2, CLARK-S, MALT) the species was repeated as a strain to maintain consistency with MIDAS.