

1 **First report of foregut microbial community in proboscis**  
2 **monkeys: Are diverse forests a reservoir for diverse**  
3 **microbiomes?**

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- 34

35 **Abstract**

36 Foregut fermentation is well known to occur in a wide range of mammalian species and  
37 in a single bird species. Yet, the foregut microbial community of free-ranging, foregut-  
38 fermenting monkeys, i.e., colobines, has not been investigated so far. We analyzed the  
39 foregut microbiomes in six free-ranging individuals of proboscis monkeys (*Nasalis*  
40 *larvatus*) from two different tropical habitats with varying plant diversity (mangrove  
41 and riverine forests), from a semi-free-ranging setting with supplemental feeding, and  
42 from captivity, using high-throughput sequencing based on 16S ribosomal RNA genes.  
43 We found a decrease in foregut microbial diversity from a diverse natural habitat  
44 (riverine forest) to a low diverse natural habitat (mangrove forest), to human-related  
45 environments. Of a total of 2,700 bacterial operational taxonomic units (OTUs) detected  
46 in all environments, only 153 OTUs were shared across all individuals, dominated by  
47 Firmicutes and Proteobacteria in the relative abundance. This indicates that these OTUs  
48 are candidates that is not influenced by diet or habitat. The relative abundance of the  
49 habitat-specific microbial communities showed a wide range of differences among  
50 living environments, although such bacterial communities appeared to be dominated by  
51 Firmicutes and Bacteroidetes, suggesting that those phyla are key to understanding the  
52 adaptive strategy in proboscis monkeys living in different habitats.

## 53 **Introduction**

54 A variety of mammalian herbivores and a single-known avian herbivore digest plant  
55 material with the help of commensal microbiomes in a forestomach (Stevens and Hume,  
56 1998; Mackie, 2002). Unlike hindgut fermenters, which have enlarged fermentation  
57 compartments in the cecum and/or colon, foregut fermenters have a pregastric  
58 fermentation chamber (Stevens and Hume, 1998). Given recent developments in  
59 sequencing technology, hindgut microbial diversity and community structure based on  
60 large amplicon libraries of 16S ribosomal RNA (rRNA) genes, mostly using fecal DNA,  
61 have been widely investigated in various vertebrate taxa (Ley et al., 2008; Muegge et  
62 al., 2011). Microbiomes of the foregut have been less studied. This is because, although  
63 it is relatively easy to sample feces both in the wild and in captivity, it is difficult to  
64 collect pregastric contents. Nonetheless, several studies have investigated the foregut  
65 microbial community in captive and free-ranging foregut-fermenting animals, revealing  
66 a universal trend in foregut microbial communities at the phylum level: Firmicutes and  
67 Bacteroidetes are generally dominant across different animal taxa such as artiodactyl,  
68 rodents, colobines, sloths, macropod, and avian foregut fermenters (Pope et al., 2010;  
69 Samsudin et al., 2011; Dai et al., 2012; Godoy-Vitorino et al., 2012; Gruninger et al.,  
70 2014; Ishaq and Wright, 2014; Kohl et al., 2014; Li et al., 2014; Roggenbuck et al.,  
71 2014; Zhou et al., 2014; Cersosimo et al., 2015; Henderson et al., 2015; Amato et al.,  
72 2016; Dill-McFarland et al., 2016; Salgado-Flores et al., 2016; Shinohara et al., 2016).  
73 However, the foregut microbial community in free-ranging colobine monkeys has not  
74 been investigated so far.

75 Foregut-fermenting colobine monkeys have complex, multi-chambered  
76 stomachs where the commensal microbiome detoxifies defensive plant chemicals and  
77 digests plant cell walls (Bauchop and Martucci, 1968), thus making an important  
78 contribution to the colobine's digestion. In primates, the distal gut microbiome varies,  
79 even within a species, with diet (Arumugam et al., 2011) and/or living conditions.  
80 Compared with their free-ranging conspecifics, captive primates generally have reduced  
81 gut microbial diversity, which has been associated with gut dysbiosis (Amato et al.,  
82 2013). Additionally, fecal microbiome patterns in captive primates are comparable to  
83 those in humans, most likely as a consequence of artificial ("Western") diets (Amato et  
84 al., 2016; Clayton et al., 2016). Therefore, microbial studies in free-ranging colobine  
85 monkeys living in natural habitats compared with captive monkeys have the potential to  
86 provide a full picture of the microbial diversity in colobine foreguts.

87 To understand the forestomach microbial patterns of colobines in relation to  
88 their diet and living-environment, we first analyzed the foregut microbiome in  
89 endangered proboscis monkeys (*Nasalis larvatus*) living in multiple natural habitats in  
90 comparison with that of a free-ranging but provisioned individual as well as a captive  
91 specimen. The proboscis monkey is endemic to Borneo, the largest island in Asia. They  
92 are the only colobine species in which an apparent rumination of stomach contents has  
93 been observed under free-range conditions (Matsuda et al., 2011), with a natural diet of  
94 varying proportions of leaves (38%–73%), fruits (11%–50%), and flowers (3%–8%)  
95 (Bennett and Sebastian, 1988; Yeager, 1989; Matsuda et al., 2009; Boonratana, 2013).  
96 They are suitable for the investigation of foregut microbial diversity and community

97 structure in relation to different feeding habits, because they inhabit various forest types  
98 along rivers with great differences in dietary diversity, such as low-diversity mangrove  
99 forests and high-diversity peat swamps and riverine forests (Yeager, 1989; Boonratana,  
100 2003; Matsuda et al., 2009; Feilen and Marshall, 2014). Here, we report the foregut  
101 microbial communities in six proboscis monkeys living in riverine and mangrove  
102 forests, as well as under provision and captive conditions. We expected that foregut  
103 microbial diversity would decrease from a diverse natural habitat (riverine forest) to a  
104 lower diverse natural habitat (mangrove) to captive conditions.

105

## 106 **Results and discussion**

107 We analyzed 16S rRNA gene sequencing-based bacterial composition of the pregastric  
108 contents collected from six adult male proboscis monkeys living in different  
109 environments in Sabah, Borneo, and Malaysia. Two free-ranging monkeys lived in a  
110 riverine forest, another two lived in a mangrove forest, one semi-free-ranging monkey  
111 lived in a mangrove forest where it was provisioned with artificial diet items, and one  
112 monkey was maintained in a zoological collection.

113 **Based on the rarefaction curves**, the number of operational taxonomic units  
114 (OTUs) showed that the species richness of the foregut microbiome of monkeys living  
115 in the riverine forest was about twice as high as that in monkeys living in other  
116 conditions (Table 1, Figure 1A, Figure S1A). In accordance with Shannon's  $H'$  of the  
117 plant diversity of the forests, the number of plant species and plant parts consumed in  
118 the natural habitats of free-ranging monkeys (riverine forest, 188 plant species

119 consumed with  $H'$  4.3; mangrove forest, seven plant species consumed with  $H'$  2.5)  
120 (Table 1), the highest and lowest  $H'$  in microbial diversity were observed in the samples  
121 from riverine ( $H' = 6.0$ ) and mangrove ( $H' = 2.7$ ) forests, respectively. Proboscis  
122 monkeys living in mangrove forest subsist primarily on leaves and unripe fruits of a  
123 single plant species, *Sonneratia caseolaris* (Boonratana, 2003; Matsuda et al., in press),  
124 whereas monkeys living in riverine forest have a more generalist diet. Similarly, three-  
125 toed sloths (*Bradypus variegatus*), which consume primarily only one plant species,  
126 have lower diversity of the foregut microbial community than do two-toed sloths  
127 (*Choloepus hoffmanni*), which consume a broader diet (Dill-McFarland et al., 2016).  
128 These findings support the concept that the variety of nutrients, carbohydrate substrates,  
129 and indigestible compounds derived from a diverse diet can shape a variety of feeding  
130 niches for microbial taxa and/or functional groups, as suggested by the hindgut  
131 microbial diversity of free-ranging howler monkeys (Amato et al., 2013). On the other  
132 hand, proboscis monkeys from the provisioned and captive populations, with a dietary  
133 diversity (in number of individual diet items) and OTU species richness as low as those  
134 in monkeys from the mangrove forest, had relatively high microbial  $H'$  diversity. This is  
135 likely related to the greater variety of nutrient contents in the diet items, which  
136 contained leaves (as in the natural diet) and vegetables raised for human consumption.

137         More than 99.0% of the sequencing reads were assigned at the phylum level.  
138 The five most abundant phyla in the foregut were Bacteroidetes (8.5%–47% of bacterial  
139 reads), Firmicutes (16%–82%), and Proteobacteria (1.5%–68%), followed by  
140 Actinobacteria (1.4%–4.7%) and Spirochaetes (1.0%–3.1%) (Figure 1B), indicating that

141 the foregut microbial community does not deviate substantially from that previously  
142 found in captive colobines (Zhou et al., 2014; Amato et al., 2016) or other foregut  
143 fermenters (Pope et al., 2010; Dai et al., 2012; Godoy-Vitorino et al., 2012; Gruninger et  
144 al., 2014; Ishaq and Wright, 2014; Kohl et al., 2014; Li et al., 2014; Roggenbuck et al.,  
145 2014; Cersosimo et al., 2015; Henderson et al., 2015; Dill-McFarland et al., 2016;  
146 Salgado-Flores et al., 2016; Shinohara et al., 2016). Cyanobacteria reads, possibly  
147 derived from plant chloroplast DNA (Clayton et al., 2016), were generally detected in  
148 the free-ranging individuals in this study (1.8%–5.8%, but 0.4% in the captive  
149 individual). Additionally, many more Tenericutes [reported to include potential human  
150 pathogens (Yildirim et al., 2010)] reads were found in the captive individual (3.7%, but  
151 0.1%–0.5% in free-ranging individuals), possibly related to a more humanized diet or  
152 close contact with humans in captivity. Indeed, the provisioned (semi-free-ranging)  
153 individual showed an intermediate pattern in this respect (1.6%). These tendencies did  
154 not change with polymerase chain reaction (PCR) time or 16S region (Figure S1).

155 A total of 2,700 bacterial OTUs were detected after the individual bacterial  
156 compositions of each environment were subsampled and merged (Dataset S3). Only  
157 153 OTUs were found across all samples from proboscis monkeys (Figure 2A),  
158 indicating that they are the core bacterial community that is not influenced by diet or  
159 habitat. These microbial community members were generally dominated by Firmicutes  
160 and Proteobacteria, though it would be difficult to generalize their patterns across the  
161 different habitats due to the high individual variation even within the individuals living  
162 in the same habitat, e.g., < 60% of the reads of M3 were Proteobacteria while it only



163 comprises < 5% of the reads in M4. On the other hand, 1,081 OTUs were neither shared  
164 among all environments nor specific to particular environments (Figure 2A).  
165 Interestingly, the relative abundance of these OTUs was about one-third in all  
166 individuals (32%–38%) except for the provisioned individual (71%) (Figure 2B),  
167 indicating that much more of the microbiome of the provisioned individual originated  
168 from both free-ranging and captive-like bacteria and that, therefore, it would show an  
169 intermediate pattern in the principal coordinates analysis plot based on the unweighted  
170 distances (Figure S2).

171 Finally, 743 OTUs were found only in samples from free-ranging monkeys  
172 living in riverine forest, 160 only in samples from free-ranging monkeys living in  
173 mangrove forest, 181 only in samples from the semi-free-ranging provisioned monkey,  
174 and 382 only in samples from the captive monkey (Figure 2A). The relative abundance  
175 of the habitat-specific microbial community showed a wide range of differences among  
176 living environments (Figure 2B). The lowest abundance of a specific community (1.1%)  
177 was found in the individuals living in the mangrove forest, indicating that there are  
178 almost no mangrove-specific bacteria, and the highest was found in the captive  
179 individual (38%). The habitat-specific bacterial community consisted mostly of  
180 Firmicutes and Bacteroidetes in the relative abundance, suggesting that OTUs which  
181 belong to these phyla are candidates to understand the adaptive strategy in proboscis  
182 monkeys living in different habitats.

183 Around half of the sequence reads were assigned to known genera. Fifteen of  
184 these genera were commonly observed in some environments (>1%) (Table 2).

185 *Actinobacillus* (Proteobacteria) was common in both free-ranging and provisioned  
186 individuals (3.8%–25%), whereas *Mitsuokella* (Firmicutes) was only abundant in free-  
187 ranging individuals (28% in riverine forest, 31.7% in mangrove forest). Various  
188 Firmicutes genera were detected in the captive individual, i.e., *Oscillospira* (14%)  
189 followed by [*Eubacterium*], *Bulleidia*, *Lactobacillus*, and *Ruminococcus* (1.7%–5.4%).  
190 Contrary to the finding that both *Prevotella* and *Bacteroides* (Bacteroidetes) are  
191 dominant in the fecal microbiome in humans and captive primates (Clayton et al., 2016;  
192 Hale et al., 2018), *Bacteroides* was rarely found in the foregut microbiome of all  
193 individuals (<0.01%) in this study, although *Prevotella* was broadly found in all  
194 individuals (5.9%–37%). *Prevotella* was higher in the foregut of free-ranging proboscis  
195 monkeys in riverine forest, who had a more diverse (and possibly better) diet than those  
196 living in mangrove forest, consistent with the fact that *Prevotella* increases in the  
197 foregut of cattle fed more energy-rich diets (McCann et al., 2014). A similar foregut  
198 microbial pattern (more *Prevotella* but less *Bacteroides*) has been reported not only in a  
199 captive golden snub-nosed monkey (*Rhinopithecus roxellana*), which is one of the  
200 species phylogenetically closest to the proboscis monkey (Zhou et al., 2014), but also in  
201 other foregut-fermenting animals such as moose (*Alces alces*) (Ishaq and Wright, 2014)  
202 and roe deer (*Capreolus pygargus*) (Li et al., 2014). More metagenomic and functional  
203 analyses of these bacterial groups will help in the understanding of the specialized  
204 physiology of leaf-eating foregut fermenters.

205           To our knowledge, this is the first indication of a relationship among foregut  
206 microbial and diet and habitat diversity in free-ranging, foregut-fermenting animals. Our

207 results may not be representative of the entire proboscis monkey population due to the  
208 small sample size ( $N = 6$ ) with high individual variation within the same environmental  
209 condition. Effects of diet on both foregut and hindgut microbial patterns have  
210 previously been shown in various free-ranging and captive animals (Dill-McFarland et  
211 al., 2016; Borbon-Garcia et al., 2017; Hale et al., 2018), although these results are rarely  
212 shown together with information on the living environment of the animals. The  
213 geographic region Sundaland, which includes our study sites, is a large reservoir of  
214 endemic tropical plant and animal species such as the proboscis monkey (Myers et al.,  
215 2000). Primates of this region have suffered significantly from loss of forest (Wich et  
216 al., 2012; Ancrenaz et al., 2014; Abram et al., 2015; Bernard et al., 2016) due to small-  
217 and large-scale conversion of forest to oil palm plantations (Sodhi et al., 2004;  
218 Woodruff, 2010; Abram et al., 2014). Apart from the response of animals and plants to  
219 such impacts on their environment, the response of microbes is still poorly understood,  
220 with the exception of the effects of conversion of Amazonian rainforest to agricultural  
221 lands on soil bacterial communities (Rodrigues et al., 2013). Thus, there may be the  
222 potential to build upon the preliminary data that we generated for more detailed  
223 investigations testing the novel concept that diverse forests such as riverine forest  
224 provide not only various food sources but also, indirectly, a diverse microbiome for  
225 resident animals. The findings that the loss of microbial diversity in the animal foregut  
226 in this study and in the hindgut in a previous study (Amato et al., 2013) is linked to  
227 forest diversity in some species of endangered primates suggest the expansion of  
228 conservation priorities in biodiversity hotspots. One of the serious problems when

229 primates and other animals are pushed into degraded habitats with lower diversity is  
230 forest destruction (Estrada et al., 2017), which can have dysbiotic effects (Honda and  
231 Littman, 2012) on gastrointestinal microbial patterns that are associated with  
232 gastrointestinal distress (Amato et al., 2016) in threatened primates.

233 Sequencing analysis of this study was according to a previous study  
234 (Hayakawa et al., 2018) and descriptive information of the materials and methods was  
235 available in Supporting Information Appendix S1. The sequencing data have been  
236 deposited in the DDBJ database with accession number DRA006759.

237

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248

## 249 **Author contributions**

250 IM conceptualized the initial idea, SKSSN DJS DARS RS IM performed the sampling,

251 SKSSN DJS DARS RS BG AT arranged the sampling in the wild/zoo, TH AS SF HI  
252 performed the experiment, TH performed and interpreted the statistical analysis and TH  
253 MC IM drafted the manuscript. All authors contributed to the final version of the  
254 manuscript.

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## 256 **Conflict of Interest**

257 The authors have declared that no competing interests exist.

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387

388 Table 1. Diversity indices in the forestomach commensal microbiome of proboscis

389 monkeys

Habitat	Habitat diversity ( $H'$ )	Plants consumed <sup>a</sup>		Sample ID	V1–V2		V3–V4	
		No. of species	No. of parts		No. of *OTUs	$H'$	No. of OTUs	$H'$
		Riverine forest	4.3 <sup>a</sup>		188	259	R1	1,903
				R2	1,687	3.95	871	3.51
Mangrove forest	2.5 <sup>a</sup>	7	8	M3	778	3.24	501	2.35
				M4	887	2.66	508	2.23
Provisioned		18 <sup>b</sup>	25 <sup>b</sup>	P5	952	4.80	601	4.31
Captive		6	6	C6	782	4.91	610	4.53

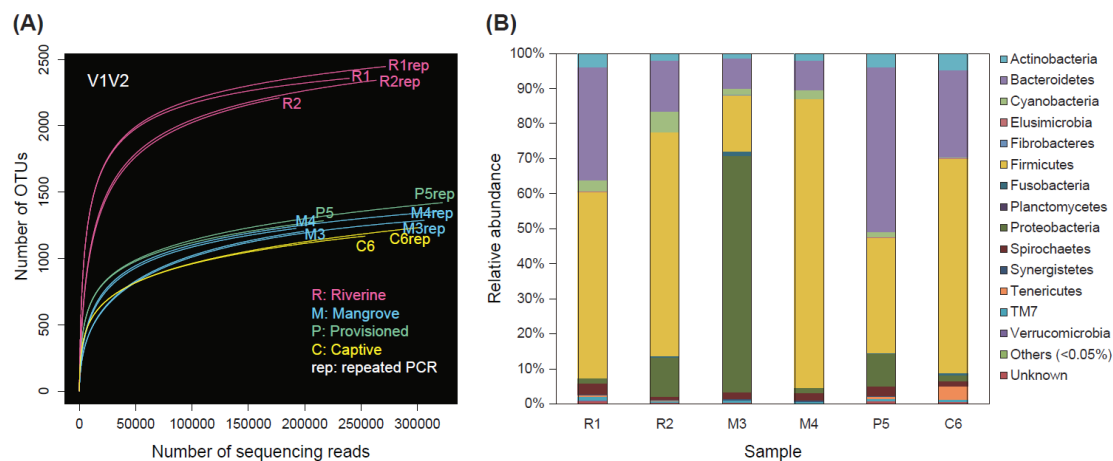
390 <sup>a</sup>Matsuda et al. (in press), <sup>b</sup>Tangah (2012), \*OTU, operational taxonomic unit.

391 Table 2. Relative abundance of commonly observed genera of forestomach commensal  
 392 microbiome of proboscis monkeys

Phylum	Genus	Riverine	Mangrove	Provisioned	Captive
Actinobacteria	<i>Bifidobacterium</i>	3.8%	<b>24.7%</b>	6.3%	–
Bacteroidetes	<i>Prevotella</i>	<b>11.5%</b>	5.9%	<b>37.3%</b>	<b>12.9%</b>
	YRC22	–	–	5.1%	–
Firmicutes	<i>[Eubacterium]</i>	–	–	–	2.6%
	<i>Bulleidia</i>	–	–	–	1.7%
	<i>Butyrivibrio</i>	–	–	1.3%	–
	<i>Lactobacillus</i>	–	–	–	2.9%
	<i>Mitsuokella</i>	<b>28.2%</b>	<b>31.7%</b>	–	–
	<i>Oscillospira</i>	–	–	–	<b>14.4%</b>
	RFN20	3.0%	1.7%	–	–
	<i>Ruminococcus</i>	1.2%	–	–	5.4%
Proteobacteria	<i>Actinobacillus</i>	3.8%	<b>24.7%</b>	6.3%	–
Spirochaetes	<i>Treponema</i>	1.6%	1.3%	2.5%	1.2%

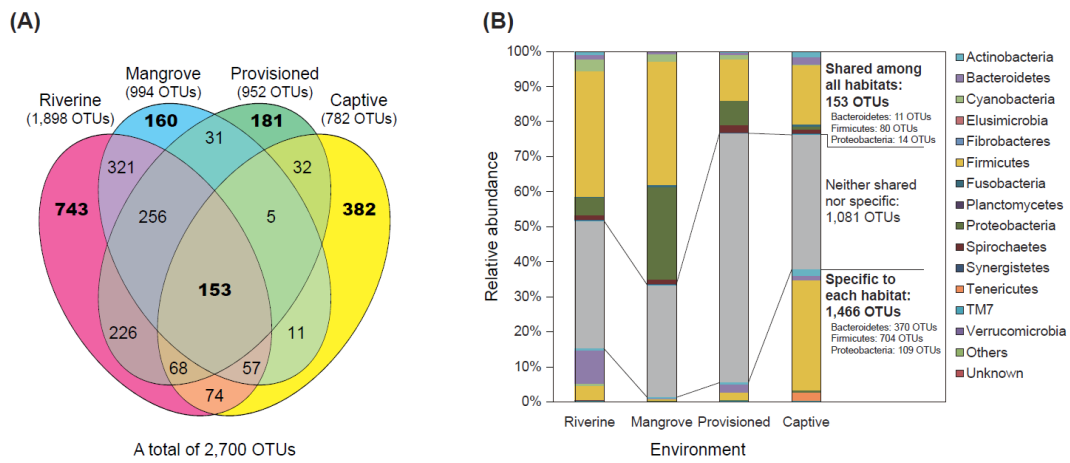
393 Only genera with >1% relative abundance are shown. Values >10% are highlighted in  
 394 bold.

395



396

397 Figure 1. (A) Rarefaction curve of operational taxonomic units and (B) relative  
 398 abundance of microbial flora and taxonomic assignments at the phylum level from  
 399 proboscis monkeys living in different environments based on the V1–V2 region of the  
 400 16S rRNA gene. Phyla represented by less than 0.05% in any samples were merged in  
 401 the category “Others.”



402

403 Figure 2. (A) Venn diagram of the detected bacterial operational taxonomic units  
 404 (OTUs) in forestomach contents collected from proboscis monkeys living in four  
 405 different environments (riverine, mangrove, provisioned, and captive) and (B) the  
 406 relative abundance of their microbial flora and taxonomic assignments with degree of  
 407 sharing of bacterial species. The number of OTUs that belongs to each category is also  
 408 shown.

409

410 **Electronic supplementary material**

411 Appendix S1 Descriptive information regarding the methods used within this study.

412

413 Dataset S1. Operational taxonomic units (OTUs), assigned taxa, nucleotide sequences,  
414 and number of sequencing reads based on the 16S V1–V2 region.

415 Attached different data file.

416

417 Dataset S2 Operational taxonomic units (OTUs), assigned taxa, nucleotide sequences,  
418 and number of sequencing reads based on the 16S V3–V4 region.

419 Attached different data file.

420

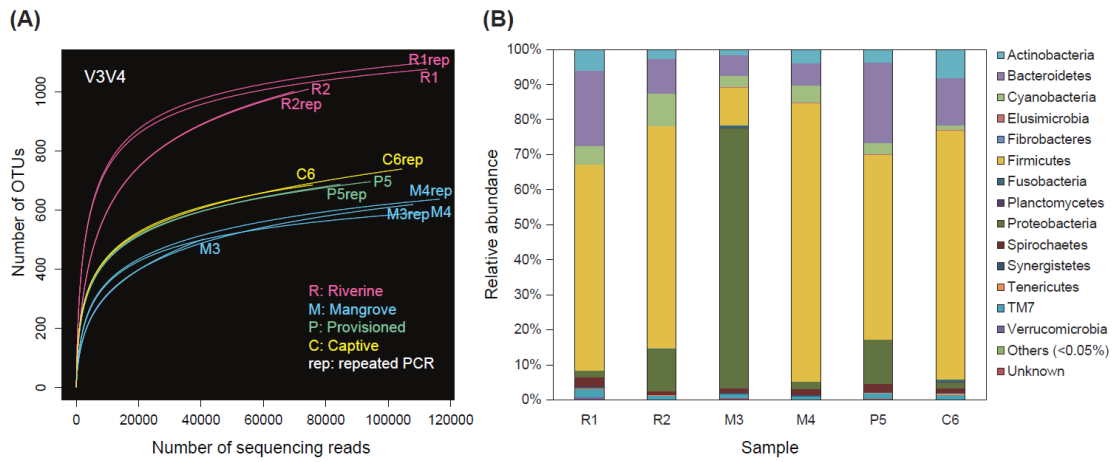
421 Dataset S3 Operational taxonomic units (OTUs), assigned taxa, nucleotide sequences,  
422 and number of subsampled and merged sequencing reads based on the 16S V1–V2

423 region.

424

425 Attached different data file.

426

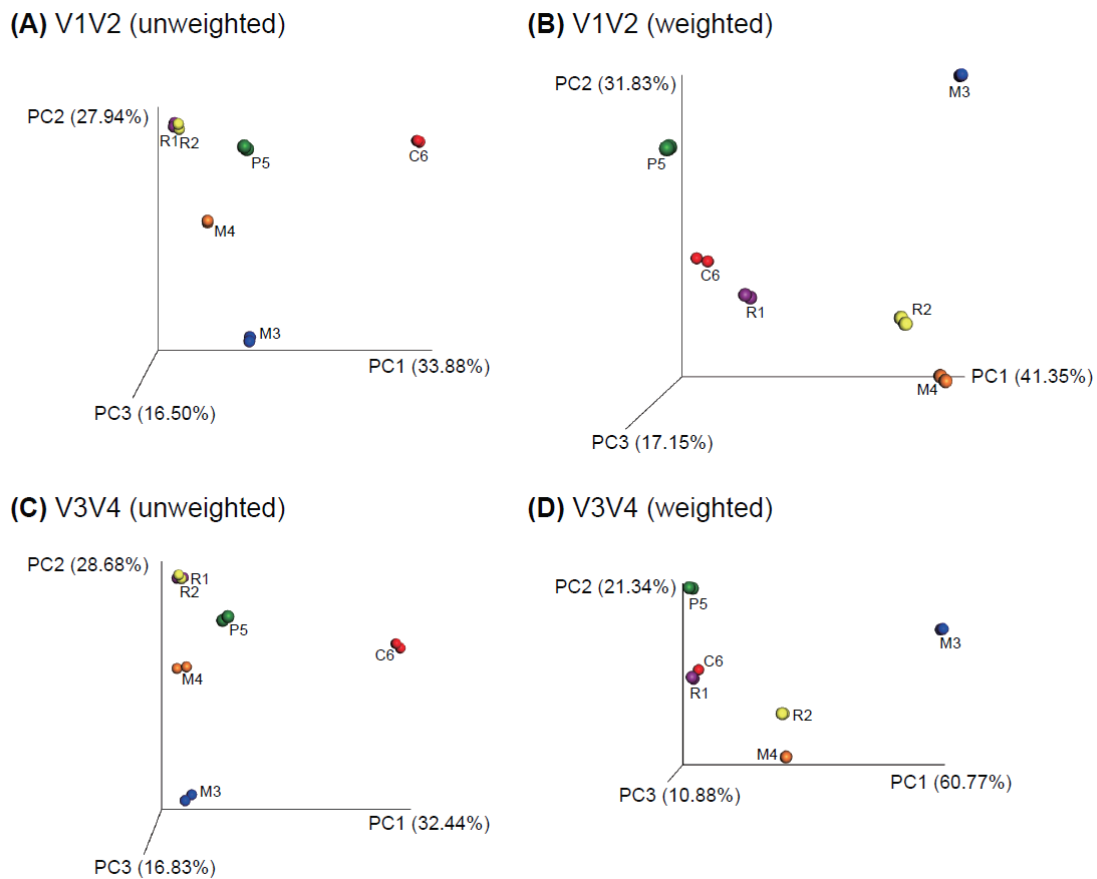


427

428 Figure S1. (A) Rarefaction curve of operational taxonomic units (OTUs) and (B)  
429 relative abundance of microbial flora and taxonomic assignments at the phylum level  
430 from proboscis monkeys living in different environments based on the V3–V4 region of  
431 the 16S rRNA gene. Phyla represented by less than 0.05% in any samples were merged  
432 in the category “Others.”

433

434



435

436 Figure S2. Principal coordinates analysis plots using UniFrac distances. Two circles of  
 437 the same color indicate the first and repeated polymerase chain reaction results from the  
 438 same sample. Note that P5 (a provisioned individual) was located between free-ranging  
 439 individuals (R1, R2, M3, M4) and a captive individual (C6) in the plots based on the  
 440 unweighted distances, indicating that P5 had an intermediate pattern of microbial  
 441 community. (A) Based on the unweighted distances in the 16S V1–V2 region. (B)  
 442 Based on the weighted distances in the 16S V1–V2 region. (C) Based on the  
 443 unweighted distances in the 16S V3–V4 region. (D) Based on the weighted distances in  
 444 the 16S V3–V4 region.

445