

1 TITLE

2 Diversity and distribution of *Blastocystis* sp. subtypes in non-human primates

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4 RUNNING TITLE

5 *Blastocystis* subtypes in non-human primates

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49 **ABSTRACT**

50 *Blastocystis* SSU rDNA sequence data from 317 captive and free-living non-human primates
51 (NHPs) representing 30 genera of apes, Old and New World monkeys, and prosimians were
52 analysed to investigate subtype (ST) and allele distribution among hosts. Excluding 20 mixed ST
53 infections, 27% of sequences belonged to ST1, 22% to ST2, 34% to ST3, 1% to ST4, 4% to ST5,
54 11% to ST8, <1% to ST13 and 1% to ST15.

55 The study confirmed cryptic host specificity of ST1 and ST3; conversely, considerable overlap in
56 ST2 alleles exists among humans and NHPs. Subtype distribution in humans and NHPs differs
57 mainly in that ST4 is rarely reported in NHPs while ST5 and ST8 are both unusual in humans.
58 This may be due to host specificity and/or the apparent geographically restricted range of some
59 subtypes.

60 While the distribution of ST1, ST2 and ST3 was independent of NHP group or geographic
61 association, ST5 was seen only in apes and OW monkeys and ST8 primarily in arboreal NHPs
62 and only in species native to Asia or South America.

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64 Keywords: *Blastocystis*, non-human primates, host range, genetic diversity.

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72 INTRODUCTION

73 The most common non-fungal eukaryotic organism in the intestine of humans and possibly non-
74 human primates (NHPs) is *Blastocystis*. This genus comprises many significantly divergent
75 small-subunit ribosomal RNA gene (SSU-rDNA) lineages, termed subtypes (ST), and in humans,
76 NHPs, other mammals and birds, fourteen have already been defined (Fayer *et al.*, 2012; Parkar
77 *et al.*, 2010; Stensvold *et al.*, 2009; Stensvold *et al.*, 2007). In other taxa, *Blastocystis* STs would
78 probably be considered distinct species. There is substantial overlap in the range of *Blastocystis*
79 STs reported from humans and from other mammals and birds, which has prompted some
80 authors to propose that zoonotic transmission is the origin of many human infections (eg. Parkar
81 *et al.*, 2007; Stensvold *et al.*, 2008; Parkar *et al.*, 2010).

82

83 While ST and prevalence data for *Blastocystis* in humans are accumulating quickly from
84 numerous studies, we still know relatively little about the distribution, host specificity and
85 genetic variation in STs found in other hosts, including NHPs. Perhaps not surprisingly, studies
86 have indicated that there is great similarity in the STs infecting humans and NHPs, with ST1,
87 ST2 and ST3 predominating (Parkar *et al.*, 2007; Parkar *et al.*, 2010; Petrášová *et al.*, 2011;
88 Yoshikawa *et al.*, 2009). By studying *Blastocystis* from humans and NHPs on Robundo Island,
89 Tanzania, Petrášová *et al.* (2011) found the same STs in both types of host, but sequence analysis
90 suggested that NHPs did not constitute a reservoir for human infection. Conversely, Yoshikawa
91 *et al.* (2009) concluded that rhesus monkeys might serve as a reservoir for human ST2 infections
92 in Nepal. Apart from this, very little is known about the distribution of STs in NHPs, and
93 whether the potential differences reported among NHPs are linked to host species/genera and/or
94 behaviour/geography.

95
96 Analysis of data obtained by multilocus sequence typing (MLST) of the *Blastocystis*
97 mitochondrial-like organelle genome has shown that many ST3 strains from NHPs are distinct
98 from those found in humans, indicating that cryptic host specificity exists (Stensvold *et al.*,
99 2012), at least in this ST. We also demonstrated that specific polymorphisms in SSU rDNA
100 sequences constitute valid surrogate markers for the intra-ST diversity detected by MLST
101 (Stensvold *et al.*, 2012). In the present study we analyse SSU-rDNAs from NHP *Blastocystis*
102 samples to i) identify the range of STs hosted by NHPs, ii) investigate the existence of any
103 potentially host-specific STs or alleles, and iii) explore whether NHP characteristics (taxon,
104 geography) are linked to STs or alleles. We also compare NHP *Blastocystis* sequences to human
105 *Blastocystis* sequences in order to investigate whether host-specific alleles can be identified in
106 STs other than ST3.

107

108 **Materials and Methods**

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110 Samples

111 Faecal samples for analysis were obtained from NHPs in zoos and sanctuaries in the UK, France,
112 the Netherlands, Germany, and Italy (Supplementary Table). Samples from wild primates were
113 collected in Morocco and St Kitts. For some samples, genomic DNA was extracted directly from
114 fresh or frozen stool using the QIAGEN Mini Stool Kit (QIAGEN, Hilden, Germany) according
115 to the recommendations of the manufacturer. Most samples, however, were subject to short term
116 in vitro culture using Robinson's medium (Clark & Diamond, 2002) prior to DNA extraction,
117 which was carried out as follows: cells were harvested by centrifugation, washed x3 in

118 phosphate-buffered saline, and lysed in 0.25% SDS/0.1 M EDTA (pH 8). DNA was purified
119 from lysates using the Puregene Core Kit A (QIAGEN, Hilden, Germany) according to the
120 recommendations of the manufacturer.

121

122 PCR and sequencing

123 DNAs were submitted to barcoding (Sciicluna *et al.*, 2006). Briefly, the primers RD5 and BhRDr
124 were used to amplify a PCR product of ca. 600 bp. Products were purified using either the
125 GeneJET™ PCR Purification Kit (Fermentas, York, UK) or SureClean (Bioline, London, UK)
126 and analysed on an ABI 3730 capillary sequencer after sequencing with the BhRDr primer and
127 BigDye v. 3.1 sequencing reagents (AppliedBiosystems, Warrington, UK).

128

129 Subtype and allele identification

130 *Blastocystis* SSU-rDNAs from NHPs available in GenBank as of 1st of January 2012 were
131 downloaded and those spanning the barcode region were included in this study (Supplementary
132 Table). Information on host species, species range, location of individual sampled, and GenBank
133 accession no. was recorded where available (Supplementary Table). Current taxonomy and
134 ecological information was obtained from the Primate Info Network
135 (<http://pin.primate.wisc.edu/>). STs and SSU-rDNA alleles were assigned to sequences using
136 BLAST searches of the NCBI GenBank database and the *Blastocystis* Sequence Typing
137 Database (www.pubmlst.org/blastocystis) (Jolley & Maiden, 2010; Stensvold *et al.*, 2012), using
138 the “Sequence Query” algorithm at the latter. The “18S allele” database is not currently part of
139 MLST schemes, but enables discrimination of SSU-rDNA alleles. This offers more resolution
140 than the subtyping system but less resolution than the MLST schemes (Stensvold *et al.*, 2012).

141 Hence, sequences corresponding to 400 bp near the 5'-end of the SSU rDNA are assigned to a
142 ST and an allele in the database; each ST comprises at least two alleles. Importantly, "18S allele"
143 numbers are unique and assigned consecutively as new alleles are discovered irrespective of ST.
144 The vast majority of the sequences met with submission requirements (sequence length and
145 quality) and were submitted to the *Blastocystis* 18S database at www.pubmlst.org/blastocystis.
146
147 In addition to sequences, some ST data for NHPs obtained by other techniques, primarily
148 Sequence Tagged Site (STS) PCR amplification, is also available. This was included to give as
149 complete a picture of the distribution as possible (Supplementary Table).

150

151 **Results and Discussion**

152

153 Subtype distribution

154 Novel data were obtained for *Blastocystis* in 260 NHPs and were combined with 57 NHP
155 *Blastocystis* sequences previously deposited in GenBank. The dataset includes sequences from 6
156 lemurs (Prosimii), 54 New World (NW) Monkeys (Ceboidea), 169 Old World (OW) Monkeys
157 (Cercopithecoidea), 75 apes (Hominoidea) and 13 unidentified NHPs (Supplementary Table).
158 Among the newly generated sample data, 20 sequence traces clearly represented mixed STs.
159 Excluding these mixed ST infections, 79 sequences in the combined dataset belonged to ST1
160 (27%), 65 to ST2 (22%), 101 to ST3 (34%), 3 to ST4 (1%), 13 to ST5 (4%), 32 to ST8 (11%), 1
161 to ST13 (<1%) and 3 to ST15 (1%).

162

163 The 169 OW monkeys (Supplementary Table) include representatives of 12 genera:
164 *Allenopithecus* (n=4), *Cercocebus* (n=3), *Cercopithecus* (n=8), *Chlorocebus* (n=42), *Colobus*
165 (n=21), *Erythrocebus* (n=4), *Lophocebus* (n=4), *Macaca* (n=38), *Mandrillus* (n=29), *Papio*
166 (n=4), *Semnopithecus* (n=6), and *Trachypithecus* (n=6). The natural species range of these NHPs
167 is limited to Africa, apart from *Trachypithecus*, *Semnopithecus* and most *Macaca* species, which
168 are native to Asia. In addition to West Africa, *Chlorocebus sabaenus* is also found on some West
169 Indian Islands. Clear mixed infections were seen in 15/169 (9%) cases. Excluding mixed ST
170 infections, the sequences from the remaining 154 OW monkey *Blastocystis* belonged to ST1
171 (33%), ST2 (21%), ST3 (43%), ST5 (1%), ST8 (1%) and ST13 (1%). Only ST1, ST2 and ST3
172 were seen in mixed infections. Interestingly, all three infections belonging to ST5 and ST8 were
173 from species of *Trachypithecus*, and hence these two STs were not detected in OW monkey
174 species native to the African continent.

175

176 Apes include *Pan troglodytes* (n=27), *Pan paniscus* (n=4), *Gorilla gorilla* (n=11), *Pongo*
177 *pygmaeus* (n=15), *Hylobates* spp. (n=6), *Nomascus* spp. (n=6), and *Symphalangus syndactylus*
178 (n=6). A total of 4/75 apes were positive for more than one ST (Supplementary Table).

179 Excluding these mixed ST infections, sequences from apes belonged to either ST1 (21%), ST2
180 (30%), ST3 (24%), ST5 (15%), ST8 (7%) or ST15 (3%). As for OW monkeys, ST8 was seen
181 only in apes native to SE Asia, namely in *Symphalangus syndactylus* (n=3), *Hylobates lar* (n=1)
182 and *Hylobates lar/agilis* (n=1), all of which are almost exclusively arboreal. Among the more
183 numerous hosts sampled, chimpanzees and orang utans were positive for ST1, ST2, ST3 and
184 ST5, while gorillas were positive for the same STs apart from ST1 (Supplementary Table).

185

186 NW monkeys (Ceboidea) comprise *Alouatta caraya* (n=5), *Ateles* spp. (n=6), *Callithrix jacchus*
187 (n=1), *Lagothrix lagotricha* (n=39), *Leontopithecus rosalia* (n=1), *Pithecia pithecia* (n=1) and
188 *Saguinus labiatus* (n=1). One case of mixed ST infection was detected. Forty-five percent of
189 sequences from the NW monkeys belonged to ST8, while 19% belonged to ST1, 13% to ST2,
190 and 21% to ST3; one ST4 sequence (2%) was seen. Nineteen of 22 ST8 sequences were from *L.*
191 *lagotricha*, and the remaining 3 were from *A. caraya*, the only ST found in the latter host. It is
192 notable that the same allele of ST8 was found in *A. caraya* from zoos in two different countries.

193
194 Only five species of Prosimii and six samples were available for inclusion, and four different STs
195 were seen: a *Hapalemur aureus* had ST1, one *Lemur catta* had ST2 and another ST4, a *Varecia*
196 *rubra* had ST4, a *Varecia variegata* had ST8 and a *Eulemur fulvus rufus* had ST15
197 (Supplementary Table). Few other samples of *Blastocystis* from lemurs have been investigated,
198 but when non-barcode data are included the range of STs is extended to include ST10 also. This
199 range is surprisingly broad yet ST3 is notable by its absence, although the small number of
200 samples precludes any conclusions at this stage. Only studies of samples from wild lemurs in
201 Madagascar can confirm whether all the STs detected are naturally occurring in this host group.

202
203 Humans have been shown to primarily host ST1—ST4; infections with several other STs are
204 suspected of being the result of zoonotic transmission (Stensvold *et al.*, 2009; Stensvold *et al.*,
205 2008). It is perhaps not surprising, therefore, that more than 80% of the NHP *Blastocystis*
206 sequences analysed here belong to ST1—ST3, and that these STs are seen in NHPs from all
207 geographic regions.

208

209 NHP subtypes and alleles

210 Assignment of alleles was possible for 212 sequences; in the remaining cases allele assignment
211 was impossible either due to the data lacking the barcode region (eg. where the sequence data
212 available were from other regions in the SSU rRNA gene), partial sequence data (sequences not
213 covering the whole region necessary for allele assignment), mixed ST infection, or one or more
214 ambiguous/mixed base calls. A total of 36 different alleles were identified across all STs; 6/36
215 alleles were represented by one sequence only and in some cases these represented sequences
216 obtained from cloned DNA. Distinctions may be necessary when comparing allele data obtained
217 by sequencing cloned PCR products versus direct sequencing of the PCR product itself, since the
218 latter sequence will represent the dominant allele in the original sample. Not surprisingly, most
219 variation was seen in ST1—ST3: ST1 exhibited six alleles, ST2 seven, and ST3 a total of 18
220 alleles, a distribution proportional to the number of sequences assigned to each ST. In
221 comparison, only two alleles each were seen in ST5 and ST8.

222

223 Generally, host specificity and ST data generated from material collected from zoo animals
224 should be interpreted with caution since species may be infected with STs to which they are
225 exposed in captivity but which may not be circulating in natural populations. Many of the
226 primates examined in this study are from zoos and so we cannot be sure that the STs and alleles
227 of *Blastocystis* they carry would be found in wild representatives of the same species. Studies
228 using DNA from wild NHPs will be needed to confirm that the STs detected in captive animals
229 are representative. However, the data nevertheless still indicate the subtypes to which the host
230 species are susceptible and are therefore of utility.

231

232 Some findings do suggest that the captive infections reflect the situation in the wild. Of the 42
233 sequences from *Chlorocebus* spp., 10 belonged to *Chlorocebus pygerythrus* and *Chlorocebus*
234 *aethiops* from Tanzania and zoos in the Netherlands, Germany and Japan, while the rest were
235 from *Chlorocebus sabaesus*, which was introduced to St Kitts in the 17th century. Both the wild
236 and captive species host ST1, ST2, and ST3, while allele 14 (ST2) was the most common
237 sequence found in the St Kitts monkeys and was also found in a wild Tanzanian monkey by
238 Petrášová *et al.* (2011). Similarly, in *Macaca sylvanus* from the wild in Morocco and from
239 German and UK zoos only ST1-ST3 were identified, and some of the alleles were present in both
240 wild and captive animals (Supplementary Table).

241
242 ST4 appears to be rare in NHPs (Table 1) as it has been reported only in one woolly monkey
243 (present study) and in captive lemurs (Santín *et al.*, 2011; Stensvold *et al.*, 2009). The woolly
244 monkey ST4 sequence exhibited allele 133. Interestingly, this allele has not previously been
245 reported, yet it was shared by this woolly monkey in the UK and a ruffed lemur from a German
246 zoo. The fact that it is a new allele reduces the possibility of sample mix-up, laboratory
247 contamination or exposure in captivity to this ST. Hence, the finding indicates that these two
248 species may be natural hosts of ST4. It remains to be seen whether ST4 can be found in other
249 NHP hosts and in wild representatives of these species. Previously, only two ST4 alleles have
250 been found in humans (42 and 94), one of which (94) appears to be extremely rare; both also
251 occur in rodents (Stensvold *et al.*, 2012).

252
253 ST5 is seen mainly in African apes, but also in a couple of Asian cercopithecoids (Table 1). It
254 has not been found in NW monkeys, but since ST5 has not been reported in any South American

255 hosts, it is too early to speculate as to whether the absence of ST5 in South American monkeys is
256 due to host specificity or geographic restriction.

257

258 ST13 was first reported by Parkar *et al.* (2010) in a quokka (a marsupial) but their sequence
259 lacked the barcode region. A sequence from a wild *Colobus guereza* included in the study by
260 Petrášová *et al.* (2011) was assigned by those authors to ST5, but comparison with a complete
261 ST13 sequence (Alfellani *et al.*, submitted) showed them to be 98-99% identical. This has
262 enabled reassignment of this *Colobus* sequence to ST13 and means that this ST is not restricted
263 to Australia or marsupials.

264

265 ST15 is a newly discovered ST that is quite divergent from the others found in primates
266 (Alfellani *et al.*, submitted). Nevertheless it has been found in both apes and a prosimian, and
267 both African and Asian hosts, suggesting it is quite widespread both geographically and in host
268 range.

269

270 Comparison of human and NHP *Blastocystis*

271 In the total analysis (Table 1), ST1 was the most common ST identified, being found in 136
272 NHPs (excluding mixed infections); this is the second most common ST in humans (Table 1).
273 While allele 4 accounts for over 95% of all human ST1s, non-human primate ST1s belongs to at
274 least 6 alleles (Supplementary Table), with a slight preponderance of alleles 1 and 2 and with, as
275 yet, no apparent link to NHP host species. During the collection of data for this study, we came
276 across two ST1 isolates from zoo keepers (data not shown); one was assigned to allele 2 and
277 another to allele 6, both of which are extremely rare in humans and likely are examples of

278 zoonotic transmission from zoo animals, most likely NHPs. Conversely, human and NHP ST2s
279 appear to be comparable, both being distributed across the same 6-7 alleles.

280

281 The situation in ST3 appears somewhat analogous to ST1. This ST is the most common ST
282 found in studies of human *Blastocystis* (Table 1). We recently demonstrated that while humans
283 and NHPs can host some of the same alleles of ST3, other ST3 alleles appear to be NHP specific
284 (Stensvold *et al.*, 2012). The present study further supports this finding. The most common ST3
285 allele in humans is allele 34 (72%), but this allele accounts for only 24% of NHP ST3. While
286 92% of human ST3 belongs to one of alleles 34, 36, 37, 38, or 128, only 39% of NHP ST3
287 belongs to these five alleles (Figure 1). No single ST3 allele appears to dominate among NHPs
288 or any subset thereof.

289

290 Of the rarer STs, ST6 and ST7 are occasionally found in humans but are generally considered
291 “avian subtypes” and so of zoonotic origin in humans. Interestingly, so far there is no evidence
292 of these STs in NHPs despite the fact that NHPs will certainly be exposed to bird faeces at least
293 as much as humans. In contrast, human ST8 infections are rarely reported except in zookeepers
294 (Scicluna *et al.*, 2006; unpublished observations) but are common in some NHPs (Table 1)
295 suggesting that zoonotic transmission is likely occurring. ST9 has not been reported from NHPs,
296 but as it is very rare in humans any conclusions on host specificity are premature. Three STs
297 have been found in NHPs but not, to date, in humans: ST10, ST13 and ST15. Given that
298 subtyping of human *Blastocystis* in regions where NHPs with these infections are found is
299 limited or absent it would be inappropriate to speculate on the host range of these STs at this
300 stage. However, it is worth noting that ST10 is common in cattle and sheep in several countries

301 where human sampling has been undertaken without any human infections with these STs being
302 detected.

303

304 **Conclusion**

305 This study is the first paper to generate and analyse a large sample of *Blastocystis* STs in NHPs.

306 At first glance it appears that there is a considerable overlap between the range of STs and their

307 relative distribution in humans and NHPs. Study of the more subtle but consistent differences at

308 SSU allele level, however, has enabled us to identify cryptic host specificity of alleles in at least

309 the two most common STs, ST1 and ST3. In addition, some initial suggestions of host restriction

310 of STs and alleles have been obtained but further sampling is needed. NHP to human

311 transmission may occur mainly in zoos and animal sanctuaries as demonstrated in this and a

312 recent study (Stensvold *et al.*, 2012). However, no studies of alleles in humans and NHPs in the

313 same region have been undertaken so the role of NHPs in zoonotic transmission is unresolved.

314 The study of STs and alleles in other host animals is key to completing our understanding of

315 *Blastocystis* epidemiology.

316

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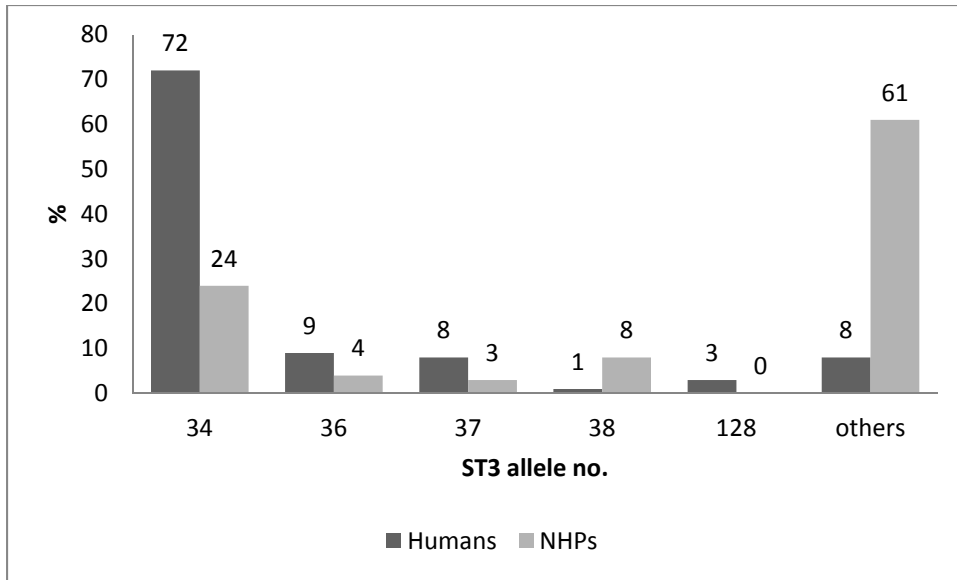
330 Figure Legend:

331 Fig. 1. ST3 SSU allele distribution in humans and non-human primates (NHP). NHP data are
332 from this study, and human data were retrieved from the isolate database available at
333 www.pubmlst.org/blastocystis as of 1st June 2012. While alleles 34, 36, 37, 38, and 128 account
334 for 170/185 (92%) of human ST3 infections, NHP ST3 is assigned to one of these five alleles in
335 only 39% of the samples, and many alleles found in NHPs have not been identified in humans so
336 far.

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339 Figure 1.



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421 Table 1. Overview of *Blastocystis* sp. STs detected in major groups of primates.

Host family/genus	<i>Blastocystis</i> sp.													Total	References ^a
	ST1	ST2	ST3	ST4	ST5	ST6	ST7	ST8	ST9	ST10	ST13	ST15 ^b	Mixed/unknown		
Chimpanzee (including Bonobo (n=4))	24	11	20	-	12	-	-	-	-	-	-	1	3	71	1,2,4,5,12
Gorilla	-	10	2	-	4	-	-	-	-	-	-	-	1	17	1,12
Orang Utan	10	6	5	-	2	-	-	-	-	-	-	-	-	23	1—4, 6— 7,12,13
Gibbons	12	8	3	-	2	-	-	7	-	-	-	1	-	33	1—4, 6— 7,12,13
Non-human Hominoids	46	35	30	-	20	-	-	7	-	-	-	2	4	144	
Baboons	3	-	2	-	-	-	-	-	-	-	-	-	2	7	1, 6,7
Mandrill/drill	19	-	9	-	-	-	-	-	-	-	-	-	5	33	1—4,6,7,13
Macaques	17	19	27	-	-	-	-	-	-	-	-	-	1	64	1—3,6,7-- 10,14

Vervet monkey	12	24	11	-	2	-	-	-	-	-	-	-	-	49	1,2,3,5,6
Colobus monkey	14	2	6	-	-	-	-	-	-	-	5	-	3	30	1,5,11
Mangabeys	1	1	4	-	-	-	-	-	-	-	-	-	1	7	1,13
Allen's swamp monkey	-	-	4	-	-	-	-	-	-	-	-	-	-	4	1
Guenons	3	1	4	-	-	-	-	-	-	-	-	-	6	14	1—4,13
Patas monkey	1	-	3	-	-	-	-	-	-	-	-	-	-	4	1
Langurs/lutungs	6	1	3	-	2	-	-	1	-	-	-	-	1	14	1—4
Cercopithecoids	76	48	73	-	4	-	-	1	-	-	5	-	19	226	
Woolly monkey	5	5	9	1	-	-	-	19	-	-	-	-	-	39	1,12,14
Howler monkey	-	-	-	-	-	-	-	5	-	-	-	-	-	5	1
Spider monkey	3	2	-	-	-	-	-	-	-	-	-	-	1	6	1
Marmoset	-	-	2	-	-	-	-	-	-	-	-	-	-	2	1,12
Tamarin ^c	1	-	1	-	-	-	-	-	-	-	-	-	-	2	1
Saki monkey	1	-	-	-	-	-	-	-	-	-	-	-	-	1	1
Ceboids	10	7	12	1	-	-	-	24	-	-	-	-	1	55	
Lemurs	4	2	-	4	-	-	-	3	-	2	-	1	-	16	1,2,3,6,7,12,13

NHP primates	136	92	115	5	24	-	-	35	-	2	5	3	24	441	
total	(30.8%)	(20.9%)	(26.1%)	(1.1%)	(5.4%)	-	-	(7.9%)	-	(0.4%)	(1.1%)	(0.7%)	(5.4%)	(100%)	
Humans total	882	343	1399	318	9	89	118	10	3	-	-	-	225	3171 ^d	Alfellani et al.,
	(27.8%)	(10.8%)	(44.1%)	(10.0%)	(0.3%)	(2.8%)	(3.7%)	(0.3%)	(0.1%)	-	-	-	NA	(100%)	submitted.

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a) 'Present study' refers to Supplementary Table and includes data from other studies as well as the sequences generated here. However, in some published studies

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nucleotide sequences for some samples have not been made publically available with only representative sequences being deposited in GenBank. For instance, in the

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study by Petrasova *et al.* (2011), only 12 sequences were submitted to GenBank and were included in Supplementary Table, while the remaining data are included in

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this table as reference no. 5 (see below). In some other studies sequence tag site (STS) primers (Yoshikawa *et al.*, 1998) have been used for ST identification rather

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than sequencing and so are not in Supplementary Table but are included here. References: 1= Present study, 2 = Abe *et al.*, 2003, 3 = Abe, 2004, 4 = Yoshikawa *et*

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al., 2004, 5 = Petrášová *et al.*, 2011, 6 = Parkar *et al.*, 2007, 7 = Parkar *et al.*, 2010, 8 = Yoshikawa *et al.*, 2009, 9 = Yoshikawa *et al.*, 1998, 10 = Yoshikawa *et al.*,

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2003, 11 = Teichroeb *et al.*, 2009, 12 = Stensvold *et al.*, 2009, 13 = Santín *et al.*, 2011, 14 = Scicluna *et al.*, 2006.

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b) Novel ST (Genbank accession no. KC148211; Alfellani et al., in preparation).

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c) Including *Leontopithecus*.

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d) This total does not include mixed/unknown infections.

Supplementary Table. Summary of all *Blastocystis* sp. STs in NHPs identified by sequencing.

Host	Classification	ST	Allele	Geographic		Sample ID	Sample origin	GenBank	Reference
				Region*					
<i>Allenopithecus nigroviridis</i>	Cercopithecoidea	3	23	1		09/1327	UK		Present study
<i>Allenopithecus nigroviridis</i>	Cercopithecoidea	3	23	1		MA252	UK		Present study
<i>Allenopithecus nigroviridis</i>	Cercopithecoidea	3	23	1		MA364	UK		Present study
<i>Allenopithecus nigroviridis</i>	Cercopithecoidea	3	26	1		MA433	UK		Present study
<i>Alouatta caraya</i>	Ceboidea	8	21	2		144	Germany		Present study
<i>Alouatta caraya</i>	Ceboidea	8	NA	2		184	Germany		Present study
<i>Alouatta caraya</i>	Ceboidea	8	21	2		09/1623	UK		Present study
<i>Alouatta caraya</i>	Ceboidea	8	NA	2		MA419	UK		Present study
<i>Alouatta caraya</i>	Ceboidea	8	NA	2		MA423	UK		Present study
<i>Ateles hybridus</i>	Ceboidea	2	11	2		J416	France		Present study
<i>Ateles hybridus</i>	Ceboidea	2	11	2		J445	France		Present study
<i>Ateles hybridus</i>	Ceboidea	mixture	NA	2		38	Germany		Present study
<i>Ateles paniscus</i>	Ceboidea	1	2	2		J398	Netherlands		Present study
<i>Ateles paniscus</i>	Ceboidea	1	2	2		J405	Netherlands		Present study
<i>Ateles paniscus</i>	Ceboidea	1	2	2		J473	Netherlands		Present study
<i>Callithrix jacchus</i>	Ceboidea	3	34	2		MA87	UK		(Stensvold <i>et al.</i> , 2009)
<i>Cercocebus atys</i>	Cercopithecoidea	3	NA	1		PR-13	Spain	HQ641656	(Santín <i>et al.</i> ,

								2011)
<i>Cercocebus torquatus</i>	Cercopithecoidea	3	22	1	09/0805	UK		Present study
<i>Cercopithecus diana</i>	Cercopithecoidea	mixture	NA	1	MA258	UK		Present study
<i>Cercopithecus diana group</i>	Cercopithecoidea	1	NA	1	MA304	UK		Present study
<i>Cercopithecus diana group</i>	Cercopithecoidea	3	NA	1	MA233	UK		Present study
<i>Cercopithecus diana group</i>	Cercopithecoidea	3	NA	1	MA384	UK		Present study
							HQ641642-	(Santín <i>et al.</i> ,
<i>Cercopithecus hamlyni</i>	Cercopithecoidea	1 + 2 + 3	NA	1	PR-4	Spain	HQ641651	2011)
								(Santín <i>et al.</i> ,
<i>Cercopithecus neglectus</i>	Cercopithecoidea	3	NA	1	PR-14	Spain	HQ641657	2011)
<i>Cercopithecus roloway</i>	Cercopithecoidea	1 + 3	NA	1	J461	France		Present study
<i>Cercopithecus roloway</i>	Cercopithecoidea	1 + 3	NA	1	J498	France		Present study
<i>Cercopithecus roloway</i>	Cercopithecoidea	1 + 3	NA	1	J641	France		Present study
<i>Chlorocebus aethiops</i>	Cercopithecoidea	1	2	1	MJ99-568	Japan	AB107968	(Abe, 2004)
<i>Chlorocebus aethiops</i>	Cercopithecoidea	1	1	1	J417	Netherlands		Present study
<i>Chlorocebus aethiops</i>	Cercopithecoidea	1	1	1	J418	Netherlands		Present study
								(Petrašová <i>et al.</i> ,
<i>Chlorocebus pygerythrus</i>	Cercopithecoidea	1	5	1	vervet17	Tanzania	HQ286911	2011)
								(Petrašová <i>et al.</i> ,
<i>Chlorocebus pygerythrus</i>	Cercopithecoidea	1	5	1	vervet14	Tanzania	HQ286913	2011)
<i>Chlorocebus pygerythrus</i>	Cercopithecoidea	1	5	1	vervet13	Tanzania	HQ286912	(Petrašová <i>et al.</i> ,

								2011)
								(Petrášová <i>et al.</i> ,
<i>Chlorocebus pygerythrus</i>	Cercopithecoidea	2	14	1	vervet12	Tanzania	HQ286909	2011)
								(Petrášová <i>et al.</i> ,
<i>Chlorocebus pygerythrus</i>	Cercopithecoidea	2	14	1	vervet15	Tanzania	HQ286910	2011)
								(Petrášová <i>et al.</i> ,
<i>Chlorocebus pygerythrus</i>	Cercopithecoidea	3	35	1	vervet1	Tanzania	HQ286908	2011)
<i>Chlorocebus pygerythrus</i>	Cercopithecoidea	3	NA	1	111	Germany		Present study
<i>Chlorocebus sabaesus</i>	Cercopithecoidea	1	4	1**	SK76	Saint Kitts		Present study
<i>Chlorocebus sabaesus</i>	Cercopithecoidea	2	14	1**	SK1	Saint Kitts		Present study
<i>Chlorocebus sabaesus</i>	Cercopithecoidea	2	14	1**	SK3+	Saint Kitts		Present study
<i>Chlorocebus sabaesus</i>	Cercopithecoidea	2	14	1**	SK6	Saint Kitts		Present study
<i>Chlorocebus sabaesus</i>	Cercopithecoidea	2	14	1**	SK14	Saint Kitts		Present study
<i>Chlorocebus sabaesus</i>	Cercopithecoidea	2	14	1**	SK30	Saint Kitts		Present study
<i>Chlorocebus sabaesus</i>	Cercopithecoidea	2	14	1**	SK36	Saint Kitts		Present study
<i>Chlorocebus sabaesus</i>	Cercopithecoidea	2	14	1**	SK44	Saint Kitts		Present study
<i>Chlorocebus sabaesus</i>	Cercopithecoidea	2	14	1**	SK45	Saint Kitts		Present study
<i>Chlorocebus sabaesus</i>	Cercopithecoidea	2	14	1**	SK47	Saint Kitts		Present study
<i>Chlorocebus sabaesus</i>	Cercopithecoidea	2	14	1**	SK53	Saint Kitts		Present study
<i>Chlorocebus sabaesus</i>	Cercopithecoidea	2	14	1**	SK59	Saint Kitts		Present study
<i>Chlorocebus sabaesus</i>	Cercopithecoidea	2	14	1**	SK93	Saint Kitts		Present study

<i>Chlorocebus sabaesus</i>	Cercopithecoidea	2	14	1**	SK94	Saint Kitts		Present study
<i>Chlorocebus sabaesus</i>	Cercopithecoidea	2	14	1**	SK109	Saint Kitts		Present study
<i>Chlorocebus sabaesus</i>	Cercopithecoidea	3	34	1**	SK9F	Saint Kitts		Present study
<i>Chlorocebus sabaesus</i>	Cercopithecoidea	3	34	1**	SK11	Saint Kitts		Present study
<i>Chlorocebus sabaesus</i>	Cercopithecoidea	3	34	1**	SK48	Saint Kitts		Present study
<i>Chlorocebus sabaesus</i>	Cercopithecoidea	3	34	1**	SK81	Saint Kitts		Present study
<i>Chlorocebus sabaesus</i>	Cercopithecoidea	3	34	1**	SK84	Saint Kitts		Present study
<i>Chlorocebus sabaesus</i>	Cercopithecoidea	3	34	1**	SK105	Saint Kitts		Present study
<i>Chlorocebus sabaesus</i>	Cercopithecoidea	3	36	1**	SK8	Saint Kitts		Present study
<i>Chlorocebus sabaesus</i>	Cercopithecoidea	3	36	1**	SK110F	Saint Kitts		Present study
<i>Chlorocebus sabaesus</i>	Cercopithecoidea	2	68	1**	SK35	Saint Kitts		Present study
<i>Chlorocebus sabaesus</i>	Cercopithecoidea	1	NA	1**	SK95	Saint Kitts		Present study
<i>Chlorocebus sabaesus</i>	Cercopithecoidea	2	NA	1**	SK12	Saint Kitts		Present study
<i>Chlorocebus sabaesus</i>	Cercopithecoidea	2	NA	1**	SK25	Saint Kitts		Present study
<i>Chlorocebus sabaesus</i>	Cercopithecoidea	2	NA	1**	SK46C	Saint Kitts		Present study
<i>Chlorocebus sabaesus</i>	Cercopithecoidea	2	NA	1**	SK90	Saint Kitts		Present study
<i>Chlorocebus sabaesus</i>	Cercopithecoidea	2	NA	1**	SK111	Saint Kitts		Present study
<i>Chlorocebus sabaesus</i>	Cercopithecoidea	2	NA	1**	SK115	Saint Kitts		Present study
<i>Chlorocebus sabaesus</i>	Cercopithecoidea	3	NA	1**	SK66F	Saint Kitts		Present study
<i>Colobus guereza</i>	Cercopithecoidea	3	33	1	DMP/08-1043	UK		Present study
<i>Colobus guereza</i>	Cercopithecoidea	2	NA	1	guereza48	Tanzania	HQ286914	(Petrášová <i>et al.</i> ,

								2011)
								(Petrášová <i>et al.</i> ,
<i>Colobus guereza</i>	Cercopithecoidea	3	NA	1	guereza52	Tanzania	HQ286916	2011)
								(Petrášová <i>et al.</i> ,
<i>Colobus guereza</i>	Cercopithecoidea	13	NA	1	guereza49	Tanzania	HQ286915	2011)
<i>Colobus guereza</i>	Cercopithecoidea	1	1	1	J420	France		Present study
<i>Colobus guereza</i>	Cercopithecoidea	1	1	1	J465	France		Present study
<i>Colobus guereza</i>	Cercopithecoidea	1	1	1	J658	France		Present study
<i>Colobus guereza</i>	Cercopithecoidea	1	2	1	J460	France		Present study
<i>Colobus guereza</i>	Cercopithecoidea	1	2	1	J643	France		Present study
<i>Colobus guereza</i>	Cercopithecoidea	3	22	1	J656	France		Present study
<i>Colobus guereza</i>	Cercopithecoidea	1	NA	1	J452	France		Present study
<i>Colobus guereza</i>	Cercopithecoidea	1	NA	1	J459	France		Present study
<i>Colobus guereza</i>	Cercopithecoidea	1 + 3	NA	1	J463	France		Present study
<i>Colobus guereza</i>	Cercopithecoidea	1 + 3	NA	1	J656	France		Present study
<i>Colobus guereza</i>	Cercopithecoidea	1	1	1	1	Germany		Present study
<i>Colobus guereza</i>	Cercopithecoidea	1	1	1	39	Germany		Present study
<i>Colobus guereza</i>	Cercopithecoidea	1	NA	1	96	Germany		Present study
<i>Colobus guereza</i>	Cercopithecoidea	1	NA	1	191	Germany		Present study
<i>Colobus guereza</i>	Cercopithecoidea	3	34	1	MA291	UK		Present study
<i>Colobus guereza</i>	Cercopithecoidea	mixture	NA	1	MA290	UK		Present study

<i>Colobus polykomos</i>	Cercopithecoidea	3	37	1	08/1016	UK		Present study
<i>Erythrocebus patas</i>	Cercopithecoidea	3	38	1	MA399	UK		Present study
<i>Erythrocebus patas</i>	Cercopithecoidea	3	39	1	MA299	UK		Present study
<i>Erythrocebus patas</i>	Cercopithecoidea	1	NA	1	MA318	UK		Present study
<i>Erythrocebus patas</i>	Cercopithecoidea	3	NA	1	MA405	UK		Present study
<i>Eulemur rufus</i>	Prosimii	15	NA	3	MA360	UK		Present study
Gibbon sp.	Hominoidea	15	NA	4	MA7	UK		Present study
<i>Gorilla gorilla</i>	Hominoidea	2	NA	1	J650	France		Present study
<i>Gorilla gorilla</i>	Hominoidea	2	NA	1	49	Germany		Present study
								(Stensvold <i>et al.</i> ,
<i>Gorilla gorilla</i>	Hominoidea	2	12	1	DMP01/594	UK		2009)
<i>Gorilla gorilla</i>	Hominoidea	5	16	1	09/1464	UK		Present study
								(Stensvold <i>et al.</i> ,
<i>Gorilla gorilla</i>	Hominoidea	5	17	1	05/709	UK	DQ462725	2009)
<i>Gorilla gorilla</i>	Hominoidea	3	NA	1	MA223	UK		Present study
<i>Gorilla gorilla</i>	Hominoidea	5	NA	1	MA237	UK		Present study
<i>Gorilla gorilla</i>	Hominoidea	mixed	NA	1	MA77	UK		Present study
							HQ641654-	(Santín <i>et al.</i> ,
<i>Gorilla gorilla</i>	Hominoidea	2	NA	1	PR-11	Spain	HQ641655	2011)
								(Stensvold <i>et al.</i> ,
<i>Gorilla gorilla</i>	Hominoidea	2	12	1	DMP01/590	UK		2009)

<i>Gorilla gorilla</i>	Hominoidea	2	12	1	DMP01/602	UK		(Stensvold <i>et al.</i> , 2009)
<i>Hapalemur aureus</i>	Prosimii	1	NA	3	PR-1	Spain	HQ641637-	(Santín <i>et al.</i> , 2011)
<i>Hylobates lar</i>	Hominoidea	2	12	4	MA253	UK	HQ641641	Present study
<i>Hylobates lar</i>	Hominoidea	8	21	4	MA362	UK		Present study
<i>Hylobates lar/agilis</i> (mixed group)	Hominoidea	8	NA	4	MA68	UK		Present study
<i>Hylobates muelleri</i>	Hominoidea	2	9	4	MA56	UK		Present study
<i>Hylobates pileatus</i>	Hominoidea	5	17	4	MA251	UK		Present study
<i>Lagothrix lagotricha</i>	Ceboidea	1	2	2	J669	Netherlands		Present study
<i>Lagothrix lagotricha</i>	Ceboidea	2	9	2	J403	Netherlands		Present study
<i>Lagothrix lagotricha</i>	Ceboidea	2	11	2	J474	Netherlands		Present study
<i>Lagothrix lagotricha</i>	Ceboidea	1	NA	2	J532	Netherlands		Present study
<i>Lagothrix lagotricha</i>	Ceboidea	1	1	2	09/1625	UK		Present study
<i>Lagothrix lagotricha</i>	Ceboidea	2	15	2	05/543	UK	DQ462719	(Stensvold <i>et al.</i> , 2009)
<i>Lagothrix lagotricha</i>	Ceboidea	8	20	2	09/1256	UK		Present study
<i>Lagothrix lagotricha</i>	Ceboidea	8	20	2	09/1619	UK		Present study
<i>Lagothrix lagotricha</i>	Ceboidea	8	20	2	05/51	UK	DQ462715	(Stensvold <i>et al.</i> , 2009)
<i>Lagothrix lagotricha</i>	Ceboidea	8	20	2	05/243	UK	DQ462720	(Stensvold <i>et al.</i> ,

								2009)
<i>Lagothrix lagotricha</i>	Ceboidea	8	20	2	MA425	UK		Present study
<i>Lagothrix lagotricha</i>	Ceboidea	8	20	2	MA63	UK		Present study
<i>Lagothrix lagotricha</i>	Ceboidea	8	21	2	MA149	UK		Present study
<i>Lagothrix lagotricha</i>	Ceboidea	8	21	2	MA350	UK		Present study
<i>Lagothrix lagotricha</i>	Ceboidea	8	21	2	MA297	UK		Present study
<i>Lagothrix lagotricha</i>	Ceboidea	3	29	2	09/1620	UK		Present study
<i>Lagothrix lagotricha</i>	Ceboidea	3	30	2	09/1624	UK		Present study
<i>Lagothrix lagotricha</i>	Ceboidea	3	30	2	MA429	UK		Present study
								(Stensvold <i>et al.</i> ,
<i>Lagothrix lagotricha</i>	Ceboidea	3	34	2	05/356	UK	DQ462722	2009)
								(Stensvold <i>et al.</i> ,
<i>Lagothrix lagotricha</i>	Ceboidea	3	34	2	05/542	UK	DQ462724	2009)
<i>Lagothrix lagotricha</i>	Ceboidea	3	36	2	MA140	UK		Present study
<i>Lagothrix lagotricha</i>	Ceboidea	4	133	2	MA165	UK		Present study
								(Stensvold <i>et al.</i> ,
<i>Lagothrix lagotricha</i>	Ceboidea	3	NA	2	05/170	UK	DQ462716	2009)
<i>Lagothrix lagotricha</i>	Ceboidea	3	NA	2	MA296	UK		Present study
<i>Lagothrix lagotricha</i>	Ceboidea	8	NA	2	MA103	UK		Present study
<i>Lagothrix lagotricha</i>	Ceboidea	8	NA	2	MA121	UK		Present study
<i>Lagothrix lagotricha</i>	Ceboidea	8	NA	2	MA238	UK		Present study

<i>Lagothrix lagotricha</i>	Ceboidea	8	NA	2	MA241	UK		Present study
<i>Lagothrix lagotricha</i>	Ceboidea	8	NA	2	MA243	UK		Present study
<i>Lagothrix lagotricha</i>	Ceboidea	8	NA	2	MA74	UK		Present study
<i>Lagothrix lagotricha</i>	Ceboidea	8	NA	2	MA293	UK		Present study
<i>Lagothrix lagotricha</i>	Ceboidea	1	1	2	01/893	UK	DQ232800	(Scicluna <i>et al.</i> , 2006)
<i>Lagothrix lagotricha</i>	Ceboidea	1	1	2	01/905	UK	DQ232807	(Scicluna <i>et al.</i> , 2006)
<i>Lagothrix lagotricha</i>	Ceboidea	2	12	2	01/676	UK	DQ232806	(Scicluna <i>et al.</i> , 2006)
<i>Lagothrix lagotricha</i>	Ceboidea	2	15	2	02/521	UK	DQ232799	(Scicluna <i>et al.</i> , 2006)
<i>Lagothrix lagotricha</i>	Ceboidea	8	20	2	02/1003	UK	DQ232783	(Scicluna <i>et al.</i> , 2006)
<i>Lagothrix lagotricha</i>	Ceboidea	8	20	2	02/393	UK	DQ232795	(Scicluna <i>et al.</i> , 2006)
<i>Lagothrix lagotricha</i>	Ceboidea	8	20	2	02/517	UK	DQ232796	(Scicluna <i>et al.</i> , 2006)
<i>Lagothrix lagotricha</i>	Ceboidea	3	24	2	02/1002	UK	DQ232785	(Scicluna <i>et al.</i> , 2006)
<i>Lemur catta</i>	Prosimii	2	NA	3	128	Germany		Present study

<i>Lemur catta</i>	Prosimii	4	NA	3	PR-5	Spain	HQ641652	(Santín <i>et al.</i> , 2011)
<i>Leontopithecus rosalia</i>	Ceboidea	1	1	2	J590(570)	Netherlands		Present study
<i>Lophocebus aterrimus</i>	Cercopithecoidea	1	1	1	J393	Netherlands		Present study
<i>Lophocebus aterrimus</i>	Cercopithecoidea	2	11	1	J408	Netherlands		Present study
<i>Lophocebus aterrimus</i>	Cercopithecoidea	3	23	1	J466	Netherlands		Present study
<i>Lophocebus aterrimus</i>	Cercopithecoidea	1 + 3	NA	1	J467	Netherlands		Present study
<i>Macaca arctoides</i>	Cercopithecoidea	3	NA	4	02/444	UK	DQ232797	(Scicluna <i>et al.</i> , 2006)
<i>Macaca fascicularis</i>	Cercopithecoidea	1	1	4	J668	Netherlands		Present study
<i>Macaca fascicularis</i>	Cercopithecoidea	3	22	4	J653	Netherlands		Present study
<i>Macaca fascicularis</i>	Cercopithecoidea	3	24	4	J667	Netherlands		Present study
<i>Macaca fuscata</i>	Cercopithecoidea	3	34	4	A740	Italy		Present study
<i>Macaca nemestrina</i>	Cercopithecoidea	2	9	4	MJ99-116	Japan	AB107969	(Abe, 2004)
<i>Macaca nigra</i>	Cercopithecoidea	3	22	4	09/0493	UK		Present study
<i>Macaca nigra</i>	Cercopithecoidea	3	23	4	MA380	UK		Present study
<i>Macaca nigra</i>	Cercopithecoidea	3	25	4	MA369	UK		Present study
<i>Macaca nigra</i>	Cercopithecoidea	3	31	4	MA314	UK		Present study
<i>Macaca nigra</i>	Cercopithecoidea	3	NA	4	MA242	UK		Present study
<i>Macaca sylvanus</i>	Cercopithecoidea	1	1	1	102	Germany		Present study
<i>Macaca sylvanus</i>	Cercopithecoidea	3	33	1	103	Germany		Present study

<i>Macaca sylvanus</i>	Cercopithecoidea	3	135	1	94	Germany	Present study
<i>Macaca sylvanus</i>	Cercopithecoidea	3	135	1	95	Germany	Present study
<i>Macaca sylvanus</i>	Cercopithecoidea	3	135	1	99	Germany	Present study
<i>Macaca sylvanus</i>	Cercopithecoidea	3	NA	1	98	Germany	Present study
<i>Macaca sylvanus</i>	Cercopithecoidea	3	NA	1	101	Germany	Present study
<i>Macaca sylvanus</i>	Cercopithecoidea	3	32	1	A796	Italy	Present study
<i>Macaca sylvanus</i>	Cercopithecoidea	1	1	1	MR46	Morocco	Present study
<i>Macaca sylvanus</i>	Cercopithecoidea	1	4	1	MR14	Morocco	Present study
<i>Macaca sylvanus</i>	Cercopithecoidea	1	4	1	MR15	Morocco	Present study
<i>Macaca sylvanus</i>	Cercopithecoidea	1	4	1	MR24	Morocco	Present study
<i>Macaca sylvanus</i>	Cercopithecoidea	3	33	1	MR26	Morocco	Present study
<i>Macaca sylvanus</i>	Cercopithecoidea	2	68	1	MR22	Morocco	Present study
<i>Macaca sylvanus</i>	Cercopithecoidea	2	68	1	MR23	Morocco	Present study
<i>Macaca sylvanus</i>	Cercopithecoidea	2	68	1	MR35	Morocco	Present study
<i>Macaca sylvanus</i>	Cercopithecoidea	2	68	1	MR36	Morocco	Present study
<i>Macaca sylvanus</i>	Cercopithecoidea	1	NA	1	MR25	Morocco	Present study
<i>Macaca sylvanus</i>	Cercopithecoidea	2	NA	1	MR1	Morocco	Present study
<i>Macaca sylvanus</i>	Cercopithecoidea	2	NA	1	MR8	Morocco	Present study
<i>Macaca sylvanus</i>	Cercopithecoidea	3	NA	1	MR9	Morocco	Present study
<i>Macaca sylvanus</i>	Cercopithecoidea	3	NA	1	MR32	Morocco	Present study
<i>Macaca sylvanus</i>	Cercopithecoidea	3	29	1	MA119	UK	Present study

<i>Macaca sylvanus</i>	Cercopithecoidea	3	30	1	09/1070	UK	Present study
<i>Macaca sylvanus</i>	Cercopithecoidea	3	30	1	MA320	UK	Present study
<i>Macaca sylvanus</i>	Cercopithecoidea	3	30	1	MA358	UK	Present study
<i>Macaca sylvanus</i>	Cercopithecoidea	3	38	1	MA372	UK	Present study
<i>Mandrillus leucophaeus</i>	Cercopithecoidea	1	1	1	33	Germany	Present study
<i>Mandrillus leucophaeus</i>	Cercopithecoidea	1	1	1	34	Germany	Present study
<i>Mandrillus leucophaeus</i>	Cercopithecoidea	1	1	1	48	Germany	Present study
<i>Mandrillus leucophaeus</i>	Cercopithecoidea	1	1	1	82	Germany	Present study
<i>Mandrillus leucophaeus</i>	Cercopithecoidea	1	1	1	88	Germany	Present study
<i>Mandrillus leucophaeus</i>	Cercopithecoidea	1	1	1	90	Germany	Present study
<i>Mandrillus leucophaeus</i>	Cercopithecoidea	1	1	1	162	Germany	Present study
<i>Mandrillus leucophaeus</i>	Cercopithecoidea	1	2	1	15	Germany	Present study
<i>Mandrillus leucophaeus</i>	Cercopithecoidea	1	2	1	32	Germany	Present study
<i>Mandrillus leucophaeus</i>	Cercopithecoidea	1	2	1	89	Germany	Present study
<i>Mandrillus leucophaeus</i>	Cercopithecoidea	1	2	1	160	Germany	Present study
<i>Mandrillus leucophaeus</i>	Cercopithecoidea	1	2	1	182	Germany	Present study
<i>Mandrillus leucophaeus</i>	Cercopithecoidea	3	22	1	86	Germany	Present study
<i>Mandrillus leucophaeus</i>	Cercopithecoidea	3	31	1	177	Germany	Present study
<i>Mandrillus leucophaeus</i>	Cercopithecoidea	mixture	NA	1	66	Germany	Present study
<i>Mandrillus leucophaeus</i>	Cercopithecoidea	3	NA	1	69	Germany	Present study
<i>Mandrillus leucophaeus</i>	Cercopithecoidea	mixture	NA	1	70	Germany	Present study

<i>Mandrillus leucophaeus</i>	Cercopithecoidea	3	NA	1	71	Germany		Present study
<i>Mandrillus leucophaeus</i>	Cercopithecoidea	3	NA	1	145	Germany		Present study
<i>Mandrillus leucophaeus</i>	Cercopithecoidea	3	NA	1	155	Germany		Present study
<i>Mandrillus leucophaeus</i>	Cercopithecoidea	mixture	NA	1	156	Germany		Present study
<i>Mandrillus leucophaeus</i>	Cercopithecoidea	mixture	NA	1	165	Germany		Present study
<i>Mandrillus leucophaeus</i>	Cercopithecoidea	3	NA	1	176	Germany		Present study
<i>Mandrillus leucophaeus</i>	Cercopithecoidea	3	NA	1	PR-9	Spain	HQ641653	(Santín <i>et al.</i> , 2011)
<i>Mandrillus sphinx</i>	Cercopithecoidea	1	1	1	104	Germany		Present study
<i>Mandrillus sphinx</i>	Cercopithecoidea	1	2	1	105	Germany		Present study
<i>Mandrillus sphinx</i>	Cercopithecoidea	1	NA	1	MA255	UK		Present study
<i>Mandrillus sphinx</i>	Cercopithecoidea	1	NA	1	MA289	UK		Present study
<i>Mandrillus sphinx</i>	Cercopithecoidea	1	NA	1	MA316	UK		Present study
<i>Nomascus gabriellae</i>	Hominoidea	3	34	4	MA141	UK		Present study
<i>Nomascus gabriellae</i>	Hominoidea	1	NA	4	05/521	UK	DQ462723	Present study
<i>Nomascus leucogenys</i>	Hominoidea	1	6	4	9	Germany		Present study
<i>Nomascus siki</i>	Hominoidea	2	11	4	J421	France		Present study
<i>Nomascus siki</i>	Hominoidea	2	11	4	J464	France		Present study
<i>Nomascus siki</i>	Hominoidea	2	11	4	J483	France		Present study
<i>Pan paniscus</i>	Hominoidea	3	38	1	40	Germany		Present study
<i>Pan paniscus</i>	Hominoidea	3	38	1	83	Germany		Present study

<i>Pan paniscus</i>	Hominoidea	3	38	1	85	Germany		Present study
<i>Pan paniscus</i>	Hominoidea	3	39	1	141	Germany		Present study
<i>Pan troglodytes</i>	Hominoidea	1	6	1	chimp40	Tanzania	HQ286904	(Petrašová <i>et al.</i> , 2011)
<i>Pan troglodytes</i>	Hominoidea	1	8	1	chimp23	Tanzania	HQ286905	(Petrašová <i>et al.</i> , 2011)
<i>Pan troglodytes</i>	Hominoidea	1	8	1	chimp17	Tanzania	HQ286906	(Petrašová <i>et al.</i> , 2011)
<i>Pan troglodytes</i>	Hominoidea	1	8	1	chimp44	Tanzania	HQ286907	(Petrašová <i>et al.</i> , 2011)
<i>Pan troglodytes</i>	Hominoidea	2	12	1	05/345	UK	DQ462718	(Stensvold <i>et al.</i> , 2009)
<i>Pan troglodytes</i>	Hominoidea	2	12	1	MA352	UK		Present study
<i>Pan troglodytes</i>	Hominoidea	2	12	1	MA381	UK		Present study
<i>Pan troglodytes</i>	Hominoidea	2	12	1	MA6	UK		Present study
<i>Pan troglodytes</i>	Hominoidea	2	15	1	DMP01/592	UK		(Stensvold <i>et al.</i> , 2009)
<i>Pan troglodytes</i>	Hominoidea	5	16	1	DMP01/585	UK		(Stensvold <i>et al.</i> , 2009)
<i>Pan troglodytes</i>	Hominoidea	5	16	1	DMP01/591	UK		(Stensvold <i>et al.</i> , 2009)

<i>Pan troglodytes</i>	Hominoidea	5	16	1	DMP01/599	UK	(Stensvold <i>et al.</i> , 2009)
<i>Pan troglodytes</i>	Hominoidea	5	16	1	MA40	UK	Present study
<i>Pan troglodytes</i>	Hominoidea	3	29	1	MA65	UK	Present study
<i>Pan troglodytes</i>	Hominoidea	3	34	1	DMP01/185	UK	(Stensvold <i>et al.</i> , 2009)
<i>Pan troglodytes</i>	Hominoidea	3	34	1	DMP01/596	UK	(Stensvold <i>et al.</i> , 2009)
<i>Pan troglodytes</i>	Hominoidea	3	38	1	MA116	UK	Present study
<i>Pan troglodytes</i>	Hominoidea	2	NA	1	MA224	UK	Present study
<i>Pan troglodytes</i>	Hominoidea	3	NA	1	MA26	UK	Present study
<i>Pan troglodytes</i>	Hominoidea	3	NA	1	MA64	UK	Present study
<i>Pan troglodytes</i>	Hominoidea	3	NA	1	MA127	UK	Present study
<i>Pan troglodytes</i>	Hominoidea	5	NA	1	MA106	UK	Present study
<i>Pan troglodytes</i>	Hominoidea	15	NA	1	MA359	UK	Present study
<i>Pan troglodytes</i>	Hominoidea	2 + 3	NA	1	DMP01/595	UK	(Stensvold <i>et al.</i> , 2009)
<i>Pan troglodytes</i>	Hominoidea	2 + 5	NA	1	DMP01/588	UK	(Stensvold <i>et al.</i> , 2009)
<i>Pan troglodytes</i>	Hominoidea	2 + 3	NA	1	MA198	UK	Present study
<i>Pan troglodytes</i>	Hominoidea	3	34	1	DMP01/571	UK	(Stensvold <i>et al.</i> ,

								2009)
<i>Papio anubis</i>	Cercopithecoidea	1 + 3	NA	1	J671	Netherlands		Present study
<i>Papio hamadryas</i>	Cercopithecoidea	mixture	NA	1#	2	Germany		Present study
<i>Papio hamadryas</i>	Cercopithecoidea	3	22	1#	DMP/08-1040	UK		Present study
<i>Papio hamadryas</i>	Cercopithecoidea	3	22	1#	MA257	UK		Present study
<i>Pithecia pithecia</i>	Ceboidea	1	6	2	J647	France		Present study
<i>Pongo pygmaeus</i>	Hominoidea	1	4	4	MJ99-424	Japan	AB107967	(Abe, 2004)
<i>Pongo pygmaeus</i>	Hominoidea	3	37	4	187	Germany		Present study
<i>Pongo pygmaeus</i>	Hominoidea	1	1	4	08/1350	UK		Present study
								(Stensvold <i>et al.</i> ,
<i>Pongo pygmaeus</i>	Hominoidea	1	1	4	05/259	UK	DQ462717	2009)
<i>Pongo pygmaeus</i>	Hominoidea	1	4	4	MA385	UK		Present study
<i>Pongo pygmaeus</i>	Hominoidea	2	12	4	MA199	UK		Present study
<i>Pongo pygmaeus</i>	Hominoidea	2	12	4	MA379	UK		Present study
<i>Pongo pygmaeus</i>	Hominoidea	2	12	4	MA434	UK		Present study
<i>Pongo pygmaeus</i>	Hominoidea	5	17	4	MA361	UK		Present study
<i>Pongo pygmaeus</i>	Hominoidea	3	34	4	MA47	UK		Present study
<i>Pongo pygmaeus</i>	Hominoidea	1	NA	4	MA260	UK		Present study
<i>Pongo pygmaeus</i>	Hominoidea	1	NA	4	MA288	UK		Present study
<i>Pongo pygmaeus</i>	Hominoidea	2	NA	4	MA330	UK		Present study
<i>Pongo pygmaeus</i>	Hominoidea	3	NA	4	MA213	UK		Present study

<i>Pongo pygmaeus</i>	Hominoidea	5	NA	4	MA292	UK		Present study
<i>Saguinus labiatus</i>	Ceboidea	3	22	2	J259	Netherlands		Present study
<i>Semnopithecus entellus</i>	Cercopithecoidea	1	6	4	91	Germany		Present study
<i>Semnopithecus entellus</i>	Cercopithecoidea	1	6	4	92	Germany		Present study
<i>Semnopithecus entellus</i>	Cercopithecoidea	1	6	4	93	Germany		Present study
<i>Semnopithecus entellus</i>	Cercopithecoidea	1	6	4	139	Germany		Present study
<i>Semnopithecus entellus</i>	Cercopithecoidea	1	6	4	140	Germany		Present study
<i>Semnopithecus entellus</i>	Cercopithecoidea	2	NA	4	138	Germany		Present study
<i>Symphalangus syndactylus</i>	Hominoidea	1	1	4	MA143	UK		Present study
<i>Symphalangus syndactylus</i>	Hominoidea	1	4	4	MA71	UK		Present study
<i>Symphalangus syndactylus</i>	Hominoidea	8	21	4	MA133	UK		Present study
<i>Symphalangus syndactylus</i>	Hominoidea	8	21	4	MA334	UK		Present study
								(Stensvold <i>et al.</i> ,
<i>Symphalangus syndactylus</i>	Hominoidea	1	NA	4	06/258	UK	DQ462721	2009)
<i>Symphalangus syndactylus</i>	Hominoidea	8	NA	4	MA33	UK		Present study
<i>Trachypithecus auratus</i>	Cercopithecoidea	3	30	4	MA426	UK		Present study
<i>Trachypithecus cristatus/auratus (mix)</i>	Cercopithecoidea	5	16	4	09/1248	UK		Present study
<i>Trachypithecus francoisi</i>	Cercopithecoidea	3	30	4	09/1259	UK		Present study
<i>Trachypithecus francoisi</i>	Cercopithecoidea	3	30	4	MA424	UK		Present study
<i>Trachypithecus obscurus</i>	Cercopithecoidea	5	NA	4	09/1245	UK		Present study
<i>Trachypithecus phayrei</i>	Cercopithecoidea	8	NA	4	MA427	UK		Present study

<i>Varecia rubra</i>	Prosimii	4	133	3	8	Germany		Present study
<i>Varecia variegata</i>	Prosimii	8	21	3	MJ99-132	Japan	AB107970	(Abe, 2004)
Unidentified primate		2	13		JM92-2	Japan	AB070997	(Arisue <i>et al.</i> , 2003)
Unidentified primate		3	34		DMP00/879	UK		(Stensvold <i>et al.</i> , 2009)
Unidentified primate		1	4		M2	Philippines	EU445488	(Rivera, 2008)
Unidentified primate		1	4		M9	Philippines	EU445490	(Rivera, 2008)
Unidentified primate		2	9		M24	Philippines	EU445491	(Rivera, 2008)
Unidentified primate		3	58		M5	Philippines	EU445489	(Rivera, 2008)
Unidentified primate		8	21		00/1009	UK	DQ232842	(Scicluna <i>et al.</i> , 2006)
Unidentified primate		3	24		02/029	UK	DQ232790	(Scicluna <i>et al.</i> , 2006)
Unidentified primate		3	33		02/027	UK	DQ232788	(Scicluna <i>et al.</i> , 2006)
Unidentified primate		3	33		02/030	UK	DQ232791	(Scicluna <i>et al.</i> , 2006)
Unidentified primate		2	NA		00/1005	UK	DQ232845	(Scicluna <i>et al.</i> , 2006)
Unidentified primate		3	NA		02/028	UK	DQ232789	(Scicluna <i>et al.</i> , 2006)

						2006)
						(Scicluna <i>et al.</i> ,
Unidentified primate	3	NA	02/033	UK	DQ232792	2006)

* = Geographic ranges are identified as follows: 1=Africa, 2=South America, 3=Madagascar, 4=Asia

** = Native to West Africa but transplanted to some West Indian islands

= Found in Northeast Africa and the Arabian Peninsula

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