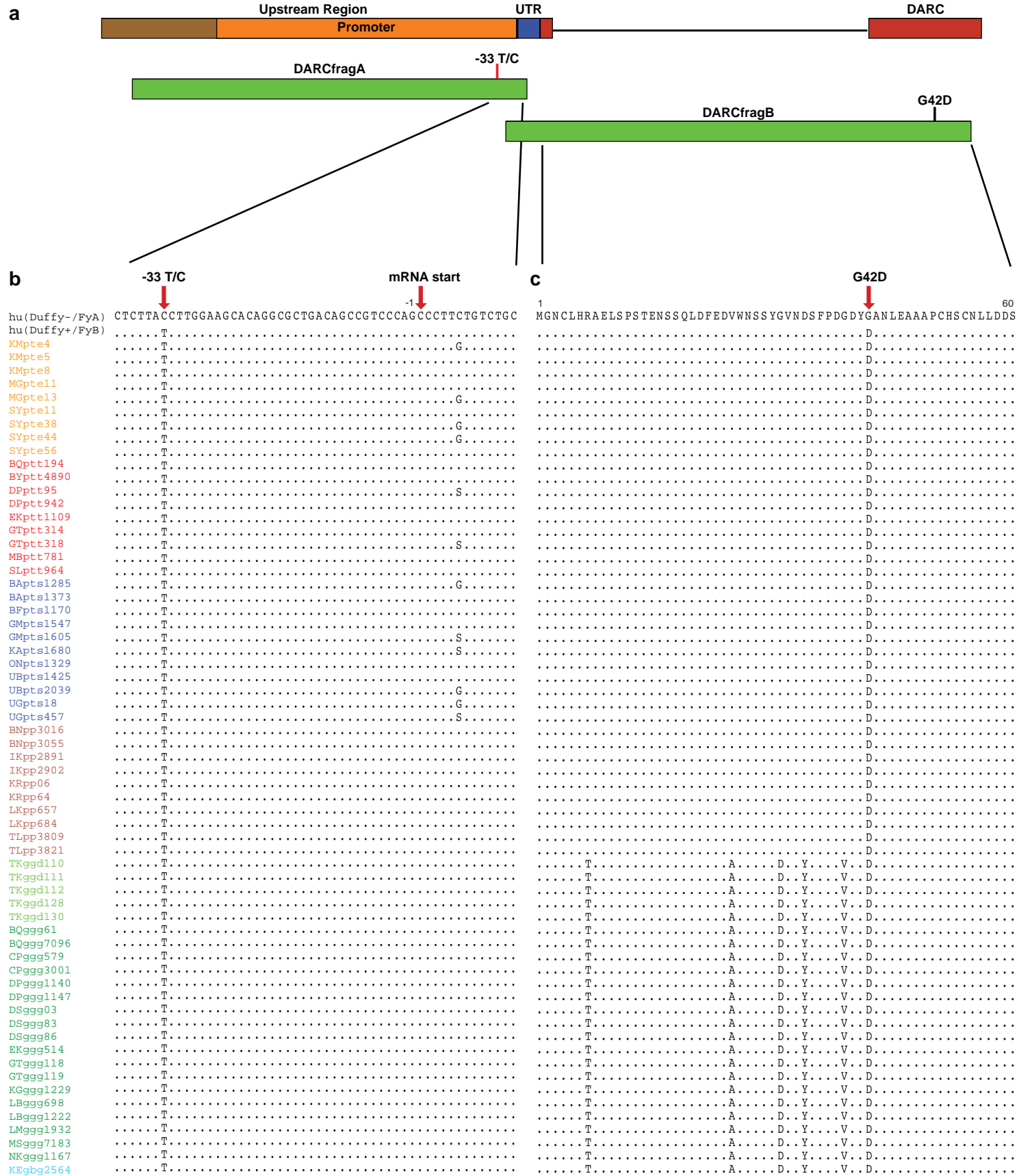


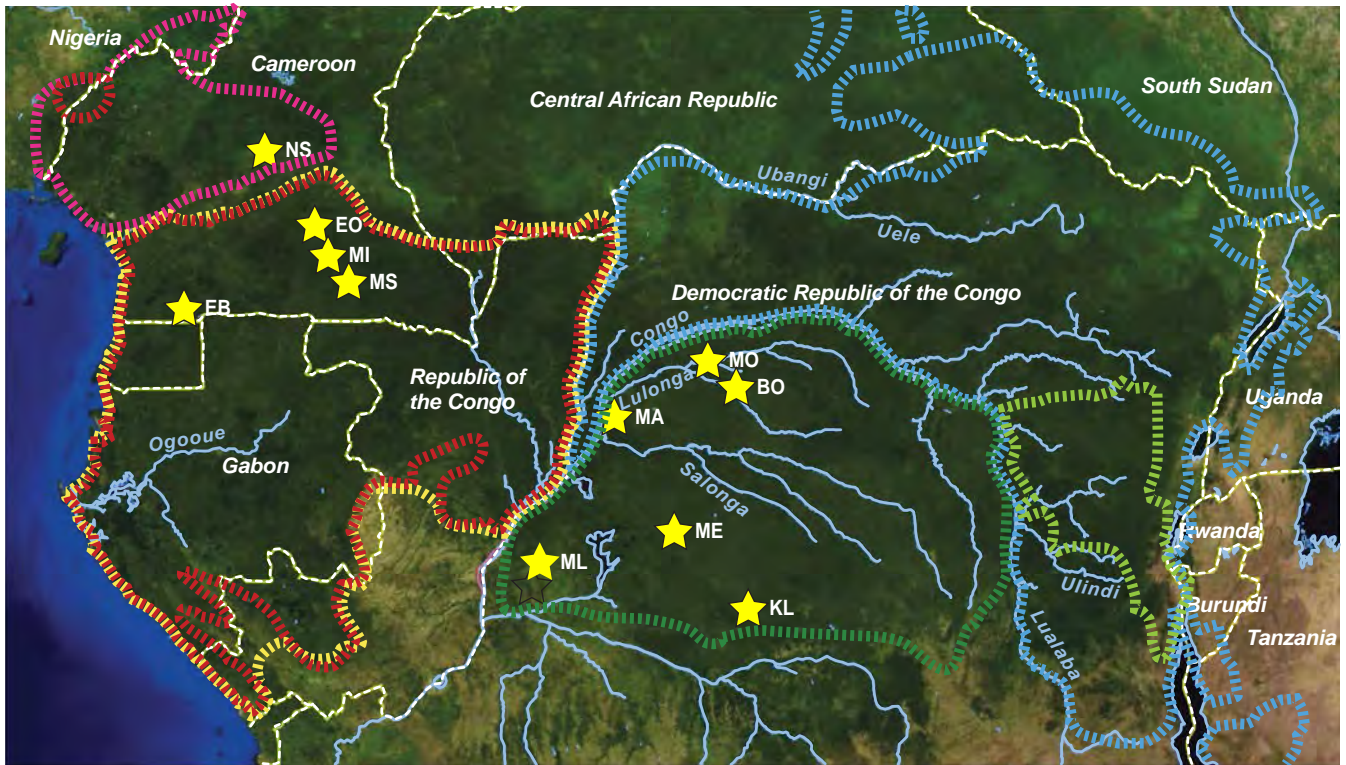
b

	SNV1 (3495)	SNV2 (3849)	SNV3 (5805)	
Salvador I	CACAAGAAAATGTTAACTTAT	TTATTACTACTGTAATGCATC	AAGATATTTTTATTATATG	Human
India VII	
Mauritania I	
North Korean	
Brazil I	
LIpte50577_SGA30.2C.....A.....C.....	Ape
LIpte50579_SGA30.7C.....A.....C.....	
MOpte51058_SGA5.10C.....A.....C.....	
BQptt194_SGA2.12C.....A.....C.....	
BQptt392_SGA5.11C.....A.....C.....	
BYptt4890_SGA2.8C.....A.....C.....	
DGptt540_SGA20.7C.....A.....C.....	
DPptt143_SGA2.6C.....A.....C.....	
MBptt323_SGA5.1C.....A.....C.....	
MOptt51114_SGA20.1C.....A.....C.....	
SYptt1_SGA20.2C.....A.....C.....	
SYptt13_SGA5.12C.....A.....C.....	
SYptt17_SGA5.3C.....A.....C.....	
SYptt31_SGA2.1C.....A.....C.....	
SYptt32_SGA2.1C.....A.....C.....	
SYptt41_SGA2.4C.....A.....C.....	
SYptt43_SGA2.1C.....A.....C.....	
SYptt47_SGA2.9C.....A.....C.....	
BApts1285_SGA2.2C.....A.....C.....	
KApts1680_SGA2.9C.....A.....C.....	
CPggg1426_SGA1.1C.....A.....C.....	
CPggg1444_SGA2.2C.....A.....C.....	
DSggg83_SGA2.1C.....A.....C.....	
DSggg86_SGA2.4C.....A.....C.....	
EKggg514_SGA5.11C.....A.....C.....	
EKggg1179_SGA20.3C.....A.....C.....	
KGggg1246_SGA2.4C.....A.....C.....	
LBggg1222_SGA5.2C.....A.....C.....	
MSggg7183_SGA2.2C.....A.....C.....	
NKggg1167_SGA5.3C.....A.....C.....	

Supplementary Figure 1 Amplification of *P. vivax* mitochondrial sequences. **a**, Schematic representation of the *P. vivax* mitochondrial genome. DNA fragments derived by conventional (diagnostic) PCR (pink) and/or single genome amplification (*cytB*, fragments A-D and S) are shown in relation to cytochrome B (CYTB), cytochrome C oxidase subunit I (COXI) and cytochrome C oxidase subunit III (COXIII) coding regions, respectively. Two single nucleotide variants (SNV2 and SNV3) at positions 3,849 and 5,805, which distinguish all ape- from all human-derived *P. vivax* parasites, are shown. **b**, Alignment of human and ape *P. vivax* sequences surrounding SNVs. Sequences are color-coded, with capital letters indicating the field site (Fig. 1) and lower case letters denoting the species and subspecies origin (pte: *P. t. ellioti*, orange; ppt: *P. t. troglodytes*, red; pts: *P. t. schweinfurthii*, blue; ggg: *G. g. gorilla*, green), followed by sample and SGA amplicon numbers. Sequences of human *P. vivax* reference strains are shown in black (periods denote sequence identity with the Salvador I sequence). The position of SNV2 and SNV3 (arrows) is highlighted. A third previously proposed SNV at position 3,495 (SNV1) was polymorphic in our expanded dataset.

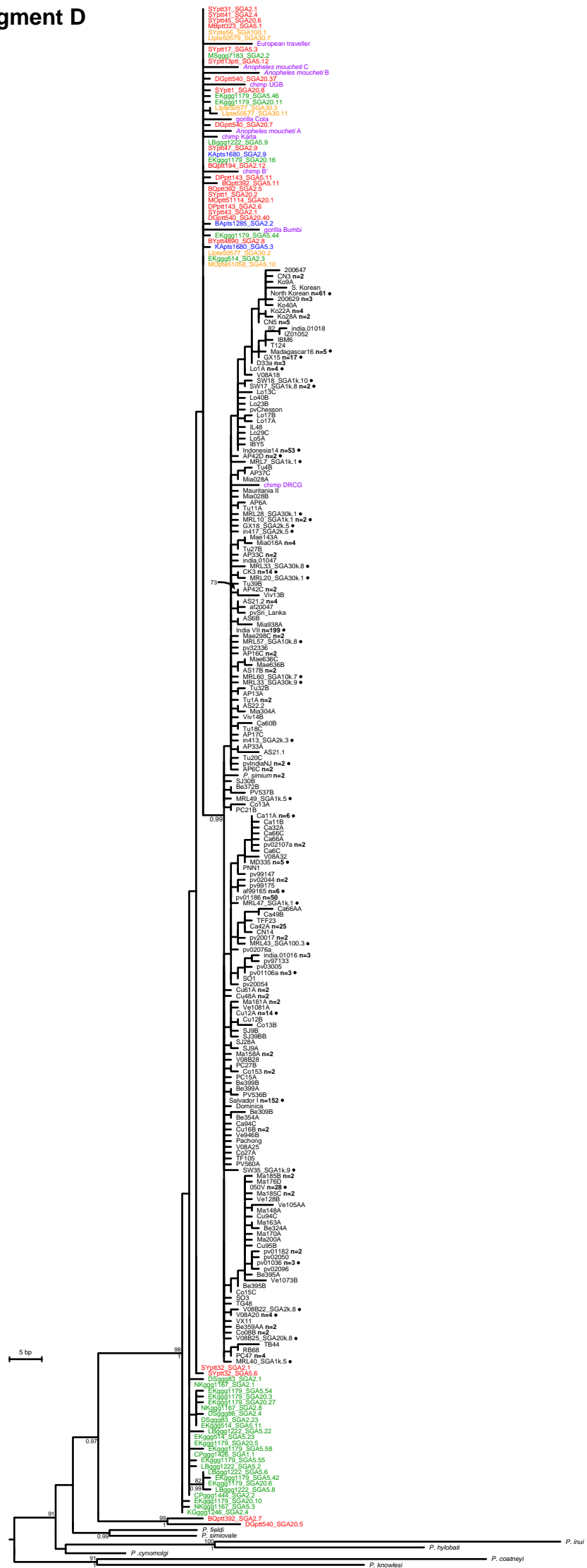


Supplementary Figure 2 Sequence analysis of the DARC promoter and adjacent coding region in African apes. **a**, The relative position of two partially overlapping PCR fragments (DARCfragA and DARCfragB) covering over 1,200 bp of the upstream region (brown) of the DARC gene (including the promoter), an untranslated region (blue) and the first 60 amino acids of the DARC protein (red), is shown. **b,c**, Alignment of human and ape DARC nucleotide (**b**) and deduced protein (**c**) sequences surrounding the GATA-1 transcription factor binding site (-33 T/C) and the Fy antigenic determinant (amino acid position 42), respectively. Sequences are color-coded, with capital letters indicating the field site (Fig. 1) and lower case letters denoting the species and subspecies origin (pte: *P. t. ellioti*, orange; pt: *P. t. troglodytes*, red; pts: *P. t. schweinfurthii*, blue; pp: *Pan paniscus*, brown; ggg: *G. g. gorilla*, dark green; ggd, *G. g. diehli*, light green; gbg: *G. b. graueri*, aqua). PCR amplicons were sequenced directly to differentiate homozygous and heterozygous genotypes (S denotes a mixture of G and C). Ape sequences were aligned to human reference sequences (black) representing Duffy negative/Fy^a (AF100634) and Duffy positive/Fy^b (AF055992) genotypes, respectively (periods denote sequence identity). All ape samples (n=134), including 28 from bonobos, were homozygous for a T at position -33 (Duffy positive phenotype)¹ and encoded an aspartic acid (D) at amino acid position 42 (Fy^b antigen)². Only a subset of sequences is shown (DARC sequences have been deposited in GenBank under accession codes KF618448 - KF618495).

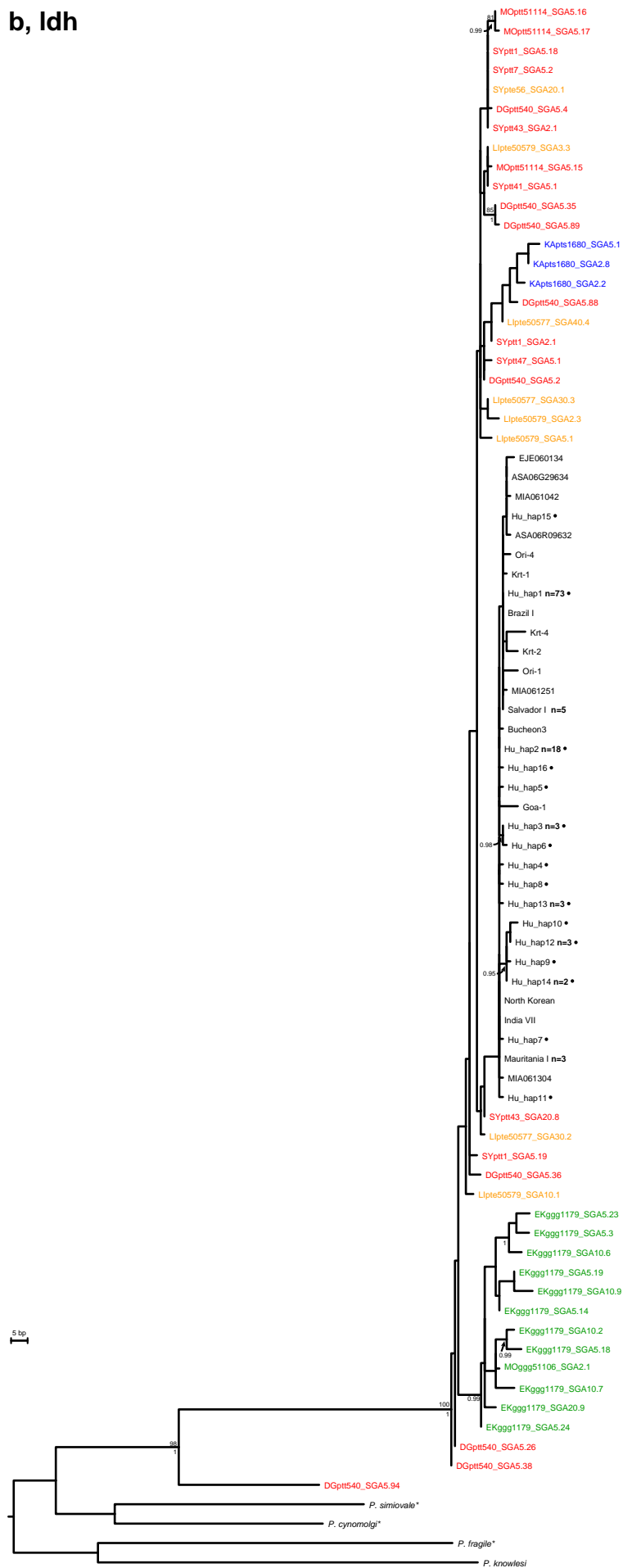


Supplementary Figure 3 Absence of *P. vivax* infection in African monkey species. Blood samples (n=998) were collected from primate bushmeat at 11 different locations in Cameroon and the Democratic Republic of the Congo (EB, Ebolowa; EO, Eboumetoum; MS, Messok; MI, Mindourou; NS, North Sanaga; BO, Boyeka; KL, Kole; ML, Malebo; MO, Mampoko; MA, Mbandaka; ME, Monkoto). Collection sites (yellow stars) are shown in relation to the ranges of chimpanzees (*P. t. ellioti*, magenta; *P. t. troglodytes*, red; and *P. t. schweinfurthii*, blue), western (*Gorilla gorilla*, yellow) and eastern (*Gorilla beringei*, light green) gorillas, as well as bonobos (*Pan paniscus*, green). The EO, MI, MS and EB sites in southern Cameroon overlap areas of high ape *P. vivax* endemicity in sympatric chimpanzee and gorilla populations.

a, mtDNA fragment D

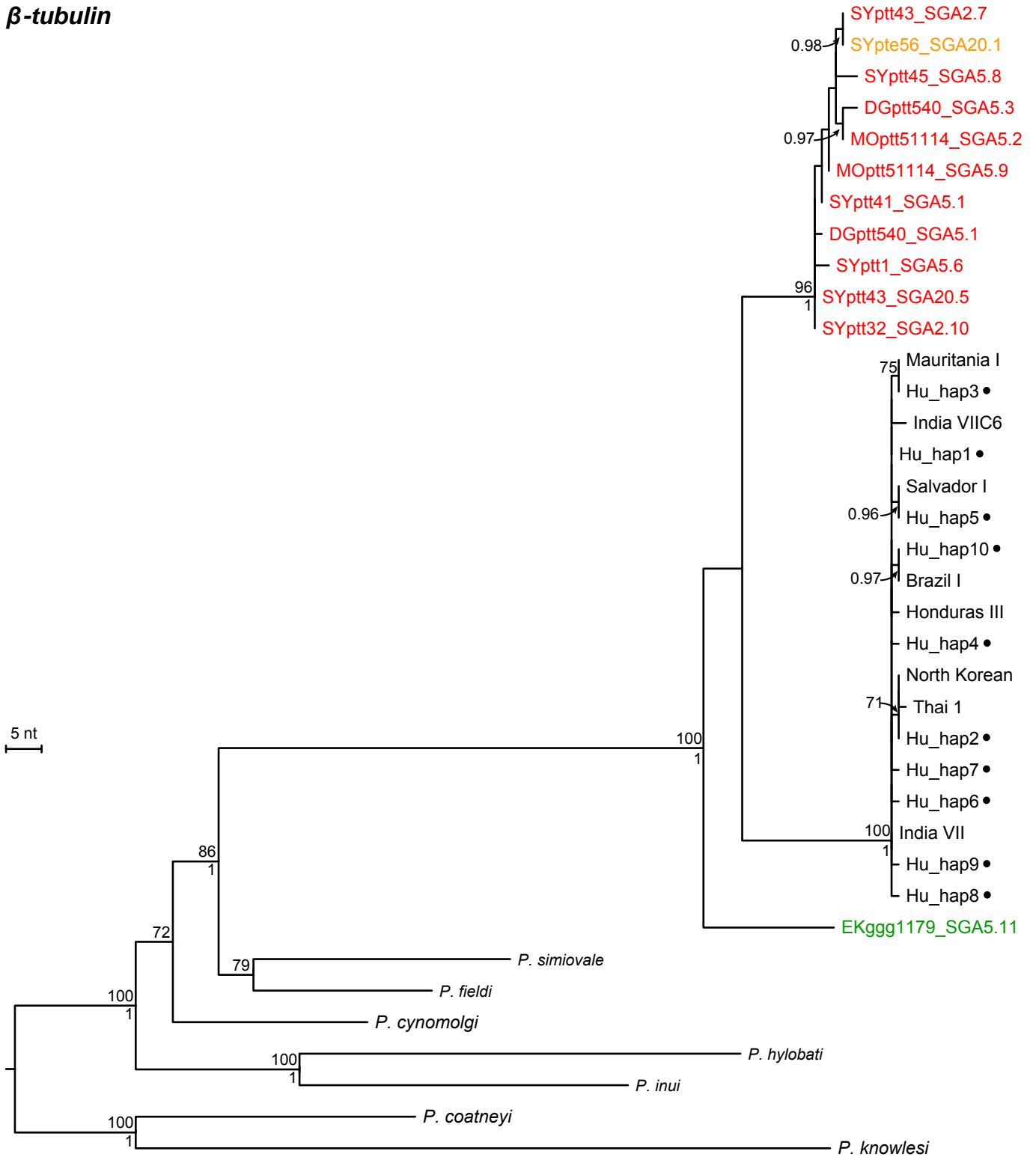


b, *ldh*

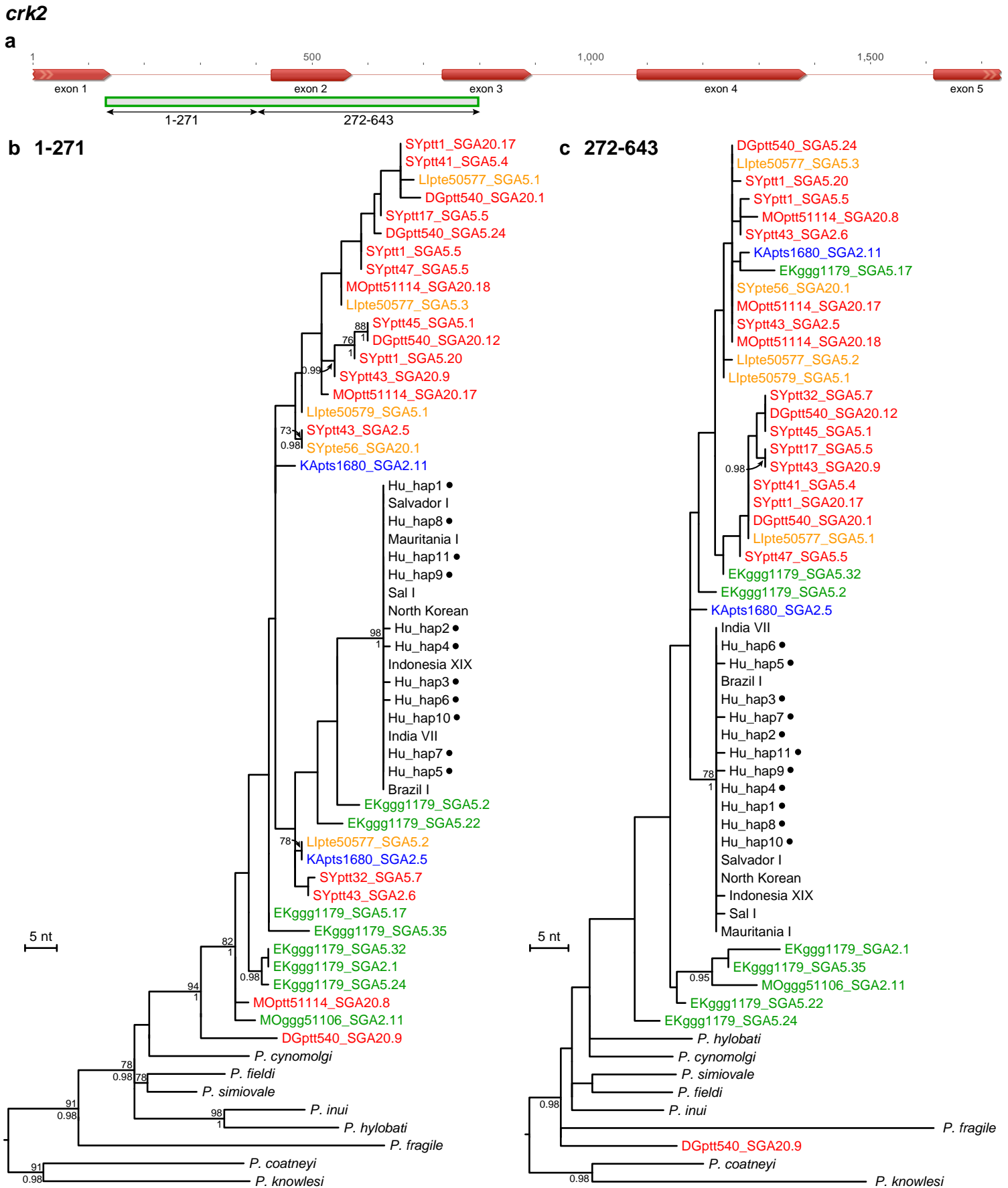


Supplementary Figure 4 Evolutionary relationships of *P. vivax* mitochondrial sequences from African apes. a,b, The phylogenetic positions of (a) mitochondrial fragment D (2,524 bp) and (b) nuclear lactate dehydrogenase (*ldh*) gene (711 bp) sequences from ape and human *P. vivax* parasites are shown in relation to human and simian reference strains (see Supplementary Tables 6-8 for GenBank accession codes). The sequences in the trees are identical to those in Figs. 2 and 3a, except for the inclusion of previously published non-SGA sequences from the database. Sequences from wild apes are color-coded, with capital letters indicating the field site (Fig. 1) and lower case letters denoting species and subspecies origin (ptt: *P. t. troglodytes*, red; pte: *P. t. ellioti*, orange; pts: *P. t. schweinfurthii*, blue; ggg: *G. g. gorilla*, green). SGA numbers are also listed, with the SGA dilution and well position indicated (e.g., EKggg514_SGA2.3 represents an SGA derived sequence amplified from a 1:2 dilution of EKggg514 faecal DNA and identified at position 3 of a plate of multiple PCR reactions). Previously reported mtDNA sequences from captive gorillas (Cola, JX444719; Bumbi, JX444722), wild (UGB, GQ355480) and captive (DRCG, GQ355481, Karla, JX444720, and chimpB', JX444723) chimpanzees, African anopheline mosquitoes (JX444724, JX444725, JX444726), and one European traveller who acquired *P. vivax* infection while working in a central African forest (JX444721), are highlighted in purple. Human and simian sequences are shown in black. Numbers to the right indicate the number of sequences that were identical over the region analysed. Bullets (•) and asterisks (*) denote human and macaque sequences that were obtained by single genome amplification, respectively. Related parasite sequences from chimpanzee samples DGptt540 and BQptt392 likely represents a new *Plasmodium* species. Trees were inferred using maximum likelihood methods³. Numbers above and below nodes indicate bootstrap values ($\geq 70\%$) and Bayesian posterior probabilities (≥ 0.95), respectively (the scale bars represents 5 nucleotide substitutions).

β -tubulin

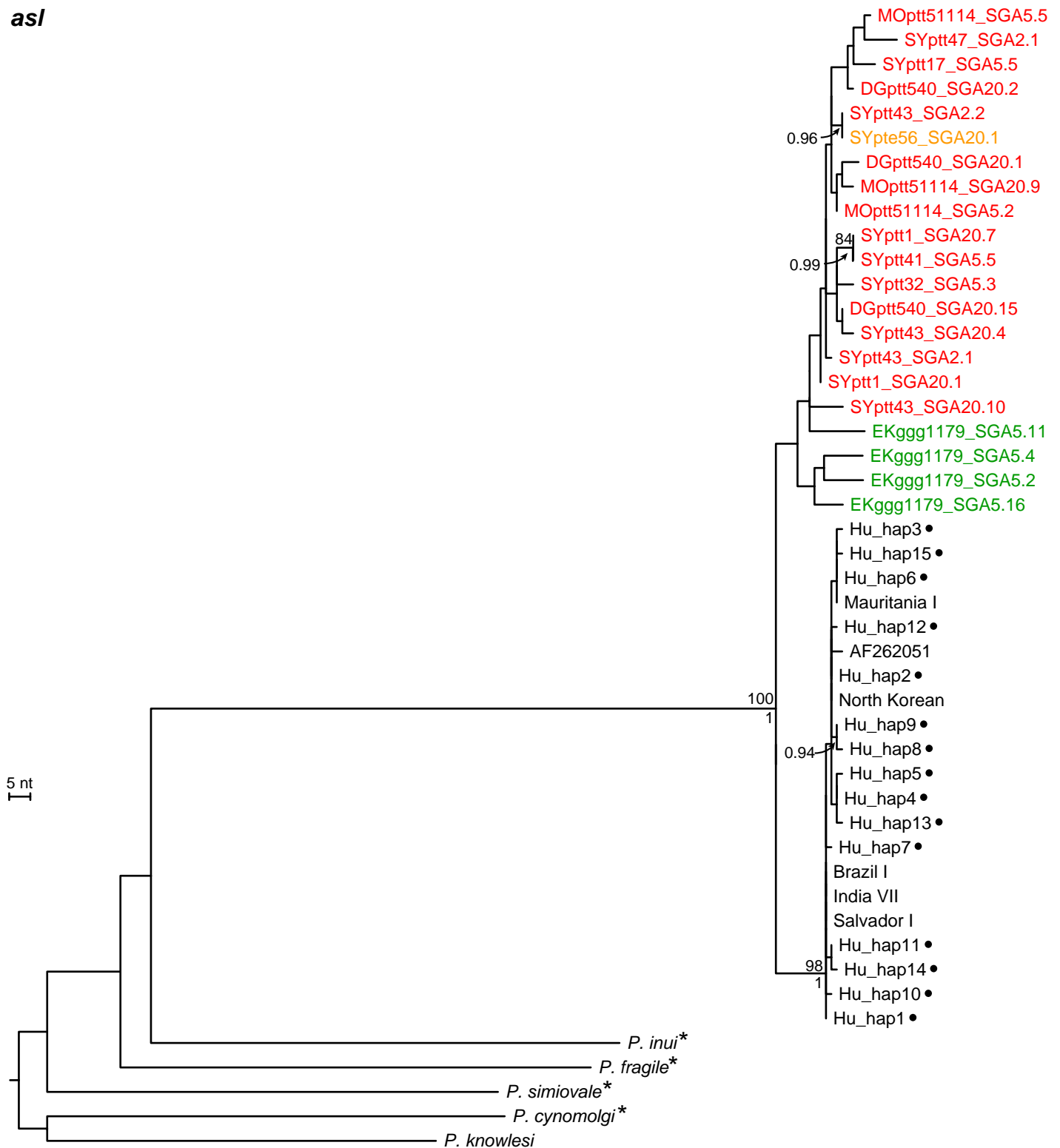


Supplementary Figure 5 Evolutionary relationships of *P. vivax* β -tubulin sequences from African apes. The phylogenetic position of 12 ape-derived nuclear β -tubulin (β -*tub*) sequences (664 bp) is shown in relation to human and simian reference sequences (see Supplementary Tables 6-8 for GenBank accession codes). Newly derived ape *Plasmodium* sequences are labeled and color-coded as in Supplementary Fig. 4. Human and simian reference sequences are shown in black, with SGA-derived human *P. vivax* sequences denoted by bullets (•). The phylogenetic tree was inferred using PhyML³; numbers above nodes indicate bootstrap support $\geq 70\%$; numbers below nodes indicate posterior probabilities ≥ 0.95 . The scale bar represents 5 nucleotide (nt) substitutions.



Supplementary Figure 6 Evolutionary relationships of *P. vivax* *cdc2*-related kinase sequences from African apes. The phylogenetic position of 33 ape-derived nuclear *cdc2*-related kinase 2 (*crk2*) sequences (643 bp) is shown in relation to human and simian reference sequences (see Supplementary Tables 6-8 for GenBank accession codes). **a**, Location of the *crk2* amplicon (green rectangle) in relation to exons and introns of the *crk2* gene. The upper scale indicates nucleotide positions relative to the *crk2* start codon. A single recombination breakpoint (as determined by GARD)⁴ at position 271 is indicated. **b,c**, Maximum likelihood trees of ape and human *P. vivax* sequences spanning nucleotides 1-271 (**b**) and 272-643 (**c**) as shown in (**a**). Newly derived ape *P. vivax* sequences are labeled and color-coded as in Supplementary Fig. 4. Human and simian reference sequences are shown in black, with SGA-derived human *P. vivax* sequences indicated by bullets (•). A related sequence from a chimpanzee sample (DGptt540) likely represents a new *Plasmodium* species. The phylogenetic tree was inferred using PhyML³; numbers above nodes indicate bootstrap support $\geq 70\%$; numbers below nodes indicate posterior probabilities ≥ 0.95 . The scale bar represents 5 nucleotide (nt) substitutions.

asl



Supplementary Figure 7 Evolutionary relationships of *P. vivax* adenylosuccinate lyase sequences from African apes. The phylogenetic position of 21 ape-derived nuclear adenylosuccinate lyase (*asl*) sequences (838 bp) is shown in relation to human and simian reference sequences (see Supplementary Tables 6-8 for GenBank accession codes). Newly derived ape *Plasmodium* sequences are labeled and color-coded as in Supplementary Fig. 4. Human and simian reference sequences are shown in black, with SGA-derived human *P. vivax* sequences designated by bullets (•). Asterisks indicate simian outgroup sequences that were generated by SGA. The phylogenetic tree was inferred using PhyML³; numbers above nodes indicate bootstrap support $\geq 70\%$; numbers below nodes indicate posterior probabilities ≥ 0.95 . The scale bar represents 5 nucleotide (nt) substitutions.

Supplementary Table 1. *P. vivax* infection rates in wild-living apes

Field site ^a	Country ^b	Chimpanzee/Bonobo (<i>Pan</i>)				Gorilla (<i>Gorilla</i>)			
		Subspecies ^c	Samples tested/positive ^d	Individuals tested/positive ^e	<i>P. vivax</i> parasite rate (%) ^f	Subspecies ^c	Samples tested/positive ^d	Individuals tested/positive ^e	<i>P. vivax</i> parasite rate (%) ^f
Alpicam (AL)	Cameroon					<i>G.g.g.</i>	10/0	--/--	0 (0-45)
Boumba Bek (BB)	Cameroon	<i>P.t.t.</i>	35/1	--/-- ^g	10 (2-33)	<i>G.g.g.</i>	6/0	--/--	0 (0-63)
Bouamir (BM)	Cameroon	<i>P.t.t.</i>	39/0	--/--	0 (0-15)	<i>G.g.g.</i>	1/0	1/0	0 (0-100)
Belgique (BQ)	Cameroon	<i>P.t.t.</i>	94/3	--/--	11 (4-22)	<i>G.g.g.</i>	102/1	--/--	4 (1-13)
Mbam-Bankim (BK)	Cameroon	<i>P.t.e.</i>	1/0	1/0	0 (0-95)				
		<i>P.t.t.</i>	2/0	--/--	0 (0-95)				
Mboy (BY)	Cameroon	<i>P.t.t.</i>	4/1	--/--	90 (22-100)				
Campo Ma'an (CP)	Cameroon	<i>P.t.t.</i>	162/1	--/--	2 (0-8)	<i>G.g.g.</i>	489/5	--/--	4 (2-6)
Deng Deng (DD)	Cameroon	<i>P.t.t.</i>	3/1	--/--	100 (5-100)	<i>G.g.g.</i>	47/2	--/--	15 (4-32)
Diang (DG)	Cameroon	<i>P.t.t.</i>	30/2	--/--	24 (10-51)	<i>G.g.g.</i>	24/1	--/--	15 (3-47)
Djoum (DJ)	Cameroon					<i>G.g.g.</i>	18/0	--/--	0 (0-31)
Doumo Pierre (DP)	Cameroon	<i>P.t.t.</i>	189/4	--/--	8 (4-14)	<i>G.g.g.</i>	15/2	--/--	48 (13-77)
E'kom (EK)	Cameroon	<i>P.t.t.</i>	100/0	--/--	0 (0-6)	<i>G.g.g.</i>	45/2	--/--	16 (4-33)
Gribi (GB)	Cameroon					<i>G.g.g.</i>	15/0	--/--	0 (0-35)
Kagnol (KG)	Cameroon					<i>G.g.g.</i>	15/2	--/--	48 (13-77)
Kika (KK)	Cameroon					<i>G.g.g.</i>	6/0	--/--	0 (0-63)
Kombe (KM)	Cameroon	<i>P.t.e.</i>	9/0	--/--	0 (0-53)				
		<i>P.t.t.</i>	1/0	1/0	0 (0-95)				
Lobéké (LB)	Cameroon	<i>P.t.t.</i>	37/0	--/--	0 (0-15)	<i>G.g.g.</i>	81/5	--/--	22 (11-35)
Liabelem Highlands (LH)	Cameroon	<i>P.t.e.</i>	7/0	--/--	0 (0-63)				
Lomie (LM)	Cameroon	<i>P.t.t.</i>	8/0	--/--	0 (0-53)	<i>G.g.g.</i>	100/3	--/--	11 (4-21)
Manbele (MB)	Cameroon	<i>P.t.t.</i>	141/5	--/--	13 (7-22)	<i>G.g.g.</i>	160/0	--/--	0 (0-4)
Mbam et Djerem (MD)	Cameroon	<i>P.t.e.</i>	2/0	--/--	0 (0-95)				
		<i>P.t.t.</i>	2/0	--/--	0 (0-95)				
Mamfé (MF)	Cameroon	<i>P.t.e.</i>	35/0	--/--	0 (0-16)				
Mont Golep-Bafia (MG)	Cameroon	<i>P.t.e.</i>	10/0	--/--	0 (0-45)				
		<i>P.t.t.</i>	1/0	1/0	0 (0-95)				
Makombe (MK)	Cameroon	<i>P.t.e.</i>	1/0	1/0	0 (0-95)				
		<i>P.t.t.</i>	1/0	1/0	0 (0-95)				
Mengame (MM)	Cameroon	<i>P.t.t.</i>	1/0	1/0	0 (0-95)	<i>G.g.g.</i>	61/1	--/--	6 (1-20)
Mone (MN)	Cameroon					<i>G.g.d.</i>	9/0	--/--	0 (0-53)
Metep (MP)	Cameroon	<i>P.t.e.</i>	12/0	--/--	0 (0-39)				
Messok (MS)	Cameroon					<i>G.g.g.</i>	142/1	--/--	3 (1-9)
Minta (MT)	Cameroon	<i>P.t.t.</i>	56/2	--/--	13 (5-30)				
Nki National Park (NK)	Cameroon	<i>P.t.t.</i>	8/0	--/--	0 (0-53)	<i>G.g.g.</i>	25/1	--/--	14 (3-44)
Nkolomaken (NL)	Cameroon					<i>G.g.g.</i>	7/0	--/--	0 (0-63)
Ngambe Tikar (NT)	Cameroon	<i>P.t.e.</i>	7/0	--/--	0 (0-63)				
		<i>P.t.t.</i>	1/0	1/0	0 (0-95)				
Somalomo (SL)	Cameroon	<i>P.t.t.</i>	44/1	--/--	8 (2-26)				
Takamanda (TK)	Cameroon					<i>G.g.d.</i>	71/0	--/--	0 (0-XX)
Vome (VM)	Cameroon	<i>P.t.e.</i>	3/0	--/--	0 (0-95)				
Wouchaba (WC)	Cameroon	<i>P.t.e.</i>	11/0	--/--	0 (0-45)				
Wassa Emtse (WE)	Cameroon	<i>P.t.e.</i>	19/0	--/--	0 (0-28)				
		<i>P.t.t.</i>	1/0	1/0	0 (0-95)				
Mpem-Ngororo (YB)	Cameroon	<i>P.t.e.</i>	7/0	--/--	0 (0-63)				
		<i>P.t.t.</i>	2/0	--/--	0 (0-95)				
Kagwene (YW)	Cameroon	<i>P.t.e.</i>	2/0	--/--	0 (0-95)				
Dzanga-Sangha (DS)	CAR					<i>G.g.g.</i>	83/2 ^h	--/--	9 (2-19)
Goalougo Triangle (GT)	RC	<i>P.t.t.</i>	168/4	103/4	12 (7-18)	<i>G.g.g.</i>	123/2	--/--	6 (1-13)
Gombe (GM) ⁱ	Tanzania	<i>P.t.s.</i>	170/0	72/0	0 (0-4)				
Ugalla (UG)	Tanzania	<i>P.t.s.</i>	313/4	63/4	20 (11-29)				
Amunyala (AM)	DRC	<i>P.t.s.</i>	37/0	--/--	0 (0-28)				
Ango (AN)	DRC	<i>P.t.s.</i>	15/0	--/--	0 (0-63)				
Azunu (AZ)	DRC	<i>P.t.s.</i>	5/0	3/0	0 (0-63)				
Bafwaboli (BA)	DRC	<i>P.t.s.</i>	300/4	--/--	5 (1-11)				
Bondo-Bili (BD)	DRC	<i>P.t.s.</i>	9/0	--/--	0 (0-78)				
Bafwasende (BF)	DRC	<i>P.t.s.</i>	35/0	--/--	0 (0-31)				
Babingi (BI)	DRC	<i>P.t.s.</i>	60/1	--/--	6 (0-30)				
Bongbola (BL)	DRC	<i>P.t.s.</i>	7/0	--/--	0 (0-78)				
Biruwe (BR)	DRC	<i>P.t.s.</i>	59/0	--/--	0 (0-19)	<i>G.b.g.</i>	6/0	--/--	0 (0-63)
Epulu (EP)	DRC	<i>P.t.s.</i>	11/0	--/--	0 (0-63)				
Gombari (GO)	DRC	<i>P.t.s.</i>	2/0	--/--	0 (0-100)				
Isiro (IS)	DRC	<i>P.t.s.</i>	3/0	--/--	0 (0-95)				
Kabuka (KA)	DRC	<i>P.t.s.</i>	105/3	--/--	10 (3-29)				
Kasese (KE)	DRC					<i>G.b.g.</i>	128/0	--/--	0 (0-5)
Kotakoli (KO)	DRC	<i>P.t.s.</i>	45/1	--/--	8 (1-39)				
Kisangani (KS)	DRC	<i>P.t.s.</i>	5/0	--/--	0 (0-95)				
Lubutu (LU)	DRC	<i>P.t.s.</i>	122/0	--/--	0 (0-10)	<i>G.b.g.</i>	4/0	4/0	0 (0-78)
Munbgera (MU)	DRC	<i>P.t.s.</i>	34/0	--/--	0 (0-31)				
Onga (ON)	DRC	<i>P.t.s.</i>	40/2	--/--	18 (4-55)				
Opienge (OP)	DRC	<i>P.t.s.</i>	36/0	--/--	0 (0-31)	<i>G.b.g.</i>	51/2	--/--	14 (4-32)
Parisi (PA)	DRC	<i>P.t.s.</i>	40/0	--/--	0 (0-28)				
Poko (PO)	DRC	<i>P.t.s.</i>	7/0	--/--	0 (0-78)				
Ubangi (UB)	DRC	<i>P.t.s.</i>	80/2	--/--	9 (2-30)				
Wanie-Rukula (WA)	DRC	<i>P.t.s.</i>	40/1	--/--	9 (1-43)				
Wamba (WB)	DRC	<i>P.t.s.</i>	6/1	--/--	60 (5-100)				
Walikale (WK)	DRC	<i>P.t.s.</i>	11/1	--/--	33 (2-86)				
Walengola (WL)	DRC	<i>P.t.s.</i>	18/0	--/--	0 (0-53)				
Bayandjo (BJ)	DRC	<i>P.p.</i>	2/0	--/--	0 (0-95)				

Balanga (BN)	DRC	<i>P.p.</i>	85/0	--/--	0 (0-7)
Ikela (IK)	DRC	<i>P.p.</i>	52/0	--/--	0 (0-11)
Kokolopori (KR)	DRC	<i>P.p.</i>	69/0	38/0	0 (0-8)
Lomako (LA)	DRC	<i>P.p.</i>	108/0	--/--	0 (0-6)
Lui-Kotal (LK)	DRC	<i>P.p.</i>	38/0	17/0	0 (0-16)
Malebo (ML)	DRC	<i>P.p.</i>	262/0	--/--	0 (0-2)
Tshuapa-Lomami (TL)	DRC	<i>P.p.</i>	138/0	63/0	0 (0-5)

^aField sites are designated by a two letter code (their location is shown in Fig. 1).

^bCAR, Central African Republic; RC, Republic of the Congo; DRC, Democratic Republic of the Congo.

^cSpecies and subspecies origin was confirmed by mitochondrial analysis of host DNA. *P.t.e.*, *Pan troglodytes ellioti*; *P.t.t.*, *P. t. troglodytes*; *P.t.s.*, *P. t. schweinfurthii*; *P.p.*, *Pan paniscus*; *G.g.g.*, *Gorilla gorilla gorilla*; *G.g.d.*, *G. g. diehli*; *G. b. g.*, *G. beringei graueri*.

^dNumber of faecal samples tested/number of faecal samples positive for *P. vivax* mitochondrial sequences by diagnostic PCR; all amplification products were sequenced to confirm *P. vivax* infection.

^eFor a subset of field sites, the number of individual apes was determined by microsatellite analysis; samples were analysed at four to eight polymorphic loci; numbers represent minimum estimates.

^f*P. vivax* infection rates were estimated from the proportion of PCR positive faecal samples, except for field sites where the number of tested individuals was known. Values were corrected for specimen degradation, redundant sampling and the sensitivity of the diagnostic test (see Methods); brackets indicate 95% confidence intervals. Since faecal *P. vivax* detection is an order-of-magnitude less sensitive than blood detection (Supplementary Table 3), the values shown represent minimum estimates.

^g--; samples were derived from an unknown number of individuals.

^hFaecal samples were collected from both habituated (n=26) and non-habituated (n=57) western lowland gorillas.

ⁱAll samples in Gombe National Park were collected from individually known chimpanzees who were habituated to human observers.

Supplementary Table 2. Sensitivity of *P. vivax* detection in chimpanzee blood and faecal samples

ID	Chimpanzees	Subspecies ^a	Blood samples ^b			Faecal samples ^b					
			Sample code	Collection date (mm/dd/yy)	<i>P. vivax</i> PCR ^c	Sample code	Collection date (mm/dd/yy)	<i>P. vivax</i> PCR ^c			
1	Anita	<i>P.t.t.</i>	SYdbs02	04/08/11	neg						
			SYdbs09	04/29/12	neg						
2	Carla	<i>P.t.t.</i>	SYdbs39	09/25/12	neg						
			SYrbc39	09/25/12	neg						
			SYbuf39	09/25/12	neg						
			SYdbs51	01/22/13	neg						
			SYrbc51	01/22/13	neg						
			SYbuf51	01/22/13	neg						
3	Henri	<i>P.t.e.</i>	SYdbs16	06/26/12	neg						
4	Kanoah	<i>P.t.e.</i>	SYdbs44	10/05/12	neg						
			SYrbc44	10/05/12	neg						
			SYbuf44	10/05/12	neg						
5	Margot	<i>P.t.e.</i>	SYdbs22	05/02/12	neg						
			SYdbs23	11/18/11	neg						
			SYdbs36	09/01/12	neg						
			SYwbl36	09/01/12	neg						
6	Nyanga	<i>P.t.e.</i>	SYdbs58	02/02/13	pos						
7	Sambe	<i>P.t.t.</i>	SYdbs26	02/02/12	neg						
			SYdbs59	02/19/13	neg						
			SYrbc59	02/19/13	neg						
			SYbuf59	02/19/13	neg						
8	Selma	<i>P.t.t.</i>	SYdbs07	04/08/11	neg						
9	Aaron	<i>P.t.t.</i>	SYdbs01	04/28/11	pos	SY053	06/17/10	neg			
						SY084	07/25/10	neg			
10	Arvid	<i>P.t.e.</i>	SYdbs38	09/14/12	neg	SY024	06/12/10	neg			
			SYrbc38	09/14/12	neg						
			SYbuf38	09/14/12	neg						
11	Berchi	<i>P.t.t.</i>	SYdbs50	02/14/13	neg	SY055	06/16/10	neg			
			SYrbc50	02/14/13	neg						
			SYbuf50	02/14/13	neg						
12	Bouboul	<i>P.t.e.</i>	SYdbs11	10/19/11	neg	SY110	07/23/10	neg			
						SY042	05/28/10	neg			
13	Baati	<i>P.t.t.</i>	SYdbs10	02/02/12	neg	SY069	07/26/10	neg			
			SYdbs49	02/27/13	neg						
			SYrbc49	02/27/13	neg						
			SYbuf49	02/27/13	neg						
14	Ballas	<i>P.t.t.</i>	SYdbs03	05/05/11	neg	SY049	06/17/10	neg			
			SYdbs04	05/07/11	neg						
15	Caroline	<i>P.t.t.</i>	SYdbs27	07/30/12	neg	SY015	05/28/10	neg			
			SYwbl27	07/30/12	neg	SY092	07/23/10	neg			
16	Cecile	<i>P.t.t.</i>	SYdbs12	06/26/11	neg	SY008	05/29/10	neg			
			SYdbs40	10/08/12	neg	SY087	07/23/10	neg			
			SYrbc40	10/08/12	neg						
			SYbuf40	10/08/12	neg						
17	Charlo	<i>P.t.t.</i>	SYdbs13	04/17/12	pos	SY077	07/05/10	neg			
18	Chouky	<i>P.t.t.</i>	SYdbs28	08/23/12	neg	SY108	07/05/10	neg			
			SYrbc28	08/23/12	neg						
			SYbuf28	08/23/12	neg						
19	Cindy	<i>P.t.t.</i>	SYdbs29	07/20/12	neg	SY004	05/28/10	neg			
			SYwbl29	07/20/12	neg						
			SYdbs52	02/06/13	neg				SY111	07/??/10	neg
			SYrbc52	02/06/13	neg						
20	Coffee	<i>P.t.t.</i>	SYbuf52	02/06/13	neg						
			SYwbl30	08/10/12	neg	SY065	06/15/10	neg			
21	Daniel	<i>P.t.t.</i>	SYdbs14	07/01/12	neg	SY074	07/25/10	neg			
			SYdbs31	07/07/12	pos	SY031	05/25/10	neg			
			SYwbl31	07/07/12	neg						
22	Emma	<i>P.t.t.</i>	SYdbs41	10/22/12	pos	SY018	05/28/10	neg			
			SYrbc41	10/22/12	pos						
			SYbuf41	10/22/12	pos						
			SYrbc53	02/10/13	neg				SY117	07/23/10	neg
			SYbuf53	02/10/13	neg						
23	Foe	<i>P.t.t.</i>	SYdbs15	07/11/12	neg	SY062	06/16/10	neg			
24	Future	<i>P.t.t.</i>	SYdbs32	07/20/12	pos	SY029	05/29/10	neg			
			SYwbl32	07/20/12	pos	SY113	07/23/10	neg			
25	Gabby	<i>P.t.t.</i>	SYdbs42	10/16/12	neg	SY019	05/28/10	neg			
			SYrbc42	10/16/12	neg	SY120	07/23/10	neg			
			SYbuf42	10/16/12	neg						
26	Ginger	<i>P.t.t.</i>	SYdbs54	02/07/13	neg	SY045	05/24/10	neg			
			SYrbc54	02/07/13	neg	SY094	07/26/10	neg			
			SYbuf54	02/07/13	neg						
27	Hope	<i>P.t.t.</i>	SYdbs43	10/19/12	pos	SY098	07/23/10	neg			

			SYrbc43	10/19/12	pos			
			SYbuf43	10/19/12	pos			
28	Jack	P.t.e.	SYwbl33	07/27/12	neg	SY061	06/17/10	neg
						SY082	07/26/10	neg
29	Jimi	P.t.t.	SYdbs17	06/28/11	pos	SY060	06/16/10	neg
			SYdbs34	08/06/12	neg			
			SYwbl34	08/06/12	neg			
			SYdbs55	02/28/13	neg			
			SYrbc55	02/28/13	neg			
30	Kachka	P.t.t.	SYdbs18	02/04/12	neg	SY052	06/15/10	neg
			SYdbs19	07/16/12	neg	SY067	07/24/10	neg
31	Launa	P.t.t.	SYdbs05	05/07/11	neg	SY001	05/23/10	neg
			SYdbs20	02/02/12	neg	SY096	07/23/10	neg
32	Leilah	P.t.t.	SYdbs21	02/03/12	neg	SY040	05/28/10	neg
						SY109	07/23/10	neg
33	Lucy	P.t.t.	SYdbs45	10/20/12	neg	SY014	05/28/10	neg
			SYrbc45	10/20/12	pos	SY112	07/23/10	neg
			SYbuf45	10/20/12	pos			
34	Luky	P.t.t.	SYdbs46	10/18/12	neg	SY047	05/28/10	neg
			SYrbc46	10/18/12	neg	SY093	07/23/10	neg
			SYbuf46	10/18/12	neg			
35	Mannie	P.t.t.	SYdbs35	07/20/12	neg	SY006	05/28/10	neg
			SYwbl35	07/20/12	neg	SY103	07/23/10	neg
36	Mika	P.t.e.	SYdbs56	02/15/13	pos	SY057	06/17/10	neg
			SYrbc56	02/15/13	pos	SY116	07/26/10	neg
			SYbuf56	02/15/13	pos	SY123	07/26/10	neg
						SY032	05/25/10	neg
37	Milou	P.t.t.	SYdbs06	05/27/11	neg	SY121	07/??/10	neg
38	Moabi	P.t.e.	SYwbl37	08/03/12	neg	SY009	05/28/10	neg
			SYdbs57	02/13/13	neg			
			SYrbc57	02/13/13	neg			
39	Moon	P.t.t.	SYdbs24	12/28/11	neg	SY046	05/25/10	neg
						SY107	07/24/10	neg
40	Mowgli	P.t.t.	SYdbs25	12/27/11	neg	SY020	05/28/10	neg
						SY091	07/23/10	neg
41	Niate	P.t.t.	SYdbs47	10/23/12	pos	SY013	05/28/10	pos
			SYrbc47	10/23/12	pos	SY078	07/24/10	neg
			SYbuf47	10/23/12	pos			
42	Shy	P.t.t.	SYdbs60	02/17/13	neg	SY036	05/23/10	neg
			SYrbc60	02/17/13				
			SYbuf60	02/17/13				
43	Simoosa	P.t.t.	SYdbs61	02/20/13	neg	SY066	07/23/10	neg
			SYrbc61	02/20/13	neg			
			SYbuf61	02/20/13	neg			
			SYdbs62	06/14/13	neg			
44	Stanley	P.t.t.	SYdbs48	10/20/12	neg	SY048	05/28/10	neg
			SYrbc48	10/20/12	neg	SY089	07/23/10	neg
			SYbuf48	10/20/12	neg			
45	Tic	P.t.t.	SYdbs63	02/26/13	neg	SY033	05/23/10	neg
			SYrbc63	02/26/13	neg			
46	Tilly	P.t.t.	SYdbs64	02/18/13	neg	SY034	05/23/10	neg
			SYrbc64	02/18/13	neg			
			SYbuf64	02/18/13	neg			
47	Xeko	P.t.t.	SYdbs08	05/19/11	neg	SY037	05/23/10	neg
			SYdbs65	02/08/13	neg	SY073	07/26/10	neg
			SYrbc65	02/08/13	neg			
			SYbuf65	02/08/13	neg			
48	Yoko	P.t.e.	SYdbs66	02/12/13	neg	SY017	05/26/10	neg
			SYrbc66	02/12/13	neg	SY083	07/26/10	neg
			SYbuf66	02/12/13	neg	SY086	07/25/10	neg
						SY088	07/22/10	neg
						SY105	07/26/10	neg
						SY122	07/27/10	neg
49	Akiba	P.t.e.				SY038	05/25/10	neg
50	Alice	P.t.t.				SY080	07/23/10	neg
51	Ava	P.t.t.				SY043	05/25/10	neg
						SY079	07/23/10	neg
52	Bikol	P.t.t.				SY041	05/28/10	neg
						SY068	07/24/10	neg
53	Bouboule	P.t.t.				SY051	06/18/10	neg
54	Bumba	P.t.t.				SY050	06/16/10	neg
55	Gremlin	P.t.t.				SY039	05/27/10	neg
56	Hoaiibi	P.t.e.				SY095	07/23/10	neg
57	Issah	P.t.t.				SY022	05/26/10	neg
						SY101	07/26/10	neg
58	Jacky	P.t.e.				SY030	05/28/10	neg
						SY106	07/23/10	neg
59	Jantan	P.t.e.				SY021	05/28/10	neg

			SY118	07/23/10	neg
60	Jessica	<i>P.t.e.</i>	SY059	06/16/10	neg
			SY100	07/24/10	neg
61	Johnny	<i>P.t.t.</i>	SY003	05/25/10	neg
			SY072	07/26/10	neg
62	Kadei	<i>P.t.t.</i>	SY035	05/25/10	neg
			SY070	07/26/10	neg
63	Karmal	<i>P.t.t.</i>	SY114	07/25/10	neg
64	Karmen	<i>P.t.t.</i>	SY058	06/16/10	neg
65	Katie	<i>P.t.t.</i>	SY075	06/19/10	neg
66	Kenza	<i>P.t.t.</i>	SY012	05/24/10	neg
			SY090	07/26/10	neg
67	Kiki	<i>P.t.t.</i>	SY016	05/28/10	neg
68	Mado	<i>P.t.e.</i>	SY099	07/24/10	neg
69	Massamba	<i>P.t.t.</i>	SY054	06/17/10	neg
			SY085	07/26/10	neg
70	Mintak	<i>P.t.t.</i>	SY010	05/27/10	neg
71	Najabeya	<i>P.t.e.</i>	SY007	05/29/10	neg
			SY104	07/23/10	neg
72	Nama	<i>P.t.t.</i>	SY005	05/28/10	neg
			SY076	07/24/10	neg
73	Robbie	<i>P.t.t.</i>	SY063	06/16/10	neg
			SY081	07/24/10	neg
74	Simon	<i>P.t.t.</i>	SY028	05/28/10	neg
			SY102	07/23/10	neg
75	Tati	<i>P.t.t.</i>	SY064	06/15/10	neg
			SY115	07/25/10	neg
76	Zach	<i>P.t.e.</i>	SY011	05/25/10	neg

^a*P.t.t.*, *Pan troglodytes troglodytes*; *P. t. e.*, *Pan troglodytes ellioti*.

^bBlood samples were collected from chimpanzees housed at the Sanaga Yong Wildlife Rescue Centre as whole blood (wbl), red blood cells (rbc), buffy coats (buf) or dried blood spots (dbs) during annual health examinations or for specific veterinary purposes. Faecal samples were collected from known individuals under direct observation.

^cSamples were tested for *P. vivax* mtDNA sequences by diagnostic PCR (see Methods); all amplicons were sequence confirmed.

65	DSggg83	07/13/08	Faeces	pos					2 (2)	1 (1)				
66	DSggg86	07/13/08	Faeces	pos ^c					1 (1)					
67	EKggg0514	08/09/04	Faeces	pos	7 (2)	6 (4)	1 (1)	2 (1)	3 (3)	2 (1)				
	EKggg1179	08/10/04	Faeces	pos ^c	15 (3)	8 (4)	9 (5)	3 (3)	18 (13)	13 (4)	11 (11)	4 (4)	7 (7)	1 (1)
68	GTggg084	02/10/08	Faeces	pos										
69	GTggg122	05/19/08	Faeces	pos										
70	KGggg1229	07/05/04	Faeces	pos	1 (1)	1 (1)								
71	KGggg1246	02/01/05	Faeces	pos					1 (1)					
72	LBggg0185	03/06/03	Faeces	pos										
73	LBggg0209	06/07/03	Faeces	pos										
74	LBggg1222	04/24/05	Faeces	pos	6 (2)	6 (3)	2 (2)		6 (5)	1 (1)				
75	LBggg2464	07/22/07	Faeces	pos										
76	LBggg710	03/07/03	Faeces	pos										
	LMggg1672	09/28/06	Faeces	pos										
77	LMggg1932	12/01/06	Faeces	pos	1 (1)									
	LMggg1939	12/01/06	Faeces	pos										
78	MMggg1542	07/27/06	Faeces	pos ^c										
79	MSggg7183	10/22/11	Faeces	pos					1 (1)					
80	NKggg1167	04/23/05	Faeces	pos	1 (1)	1 (1)			5 (3)	4 (3)				
81	OPggg2610	10/21/08	Faeces	pos										
	OPggg2612	10/22/08	Faeces	pos										
82	MOggg51106	06/22/06	Blood	pos		1 (1)	1 (1)			2 (1)			1(1)	

^aID, individuals. Blood samples from sanctuary apes were collected from known individuals. Faecal samples from wild-living apes were first subjected to host mitochondrial DNA analysis to identify individuals with different haplotypes. Samples that shared the same mtDNA haplotype were further genotyped at 4 to 8 polymorphic microsatellite loci, and classified as being derived from different individuals if they exhibited mismatches at heterozygous loci.

^bSamples are labeled to indicate their field site of origin (indicated by a two letter code; see Fig. 1 for location) and their species/subspecies of origin (ptt, *P. t. troglodytes*; pte, *P. t. ellioti*; pts, *P. t. schweinfurthii*; ggg (*G. g. gorilla*), followed by a number.

^cThese samples were positive for *P. vivax* mitochondrial *cytb* (BApts1373, EKgor1179, MMgor1452) and 3.4kb (DSgor86) sequences in a previous study⁵.

^dThe location of fragments S, A, B, C, and D within the *P. vivax* mitochondrial genome is shown in Supplementary Fig. 1a.

^eUnk, members of an unknown *Plasmodium* species that were amplified with *P. vivax* primers but are only distantly related to ape and human *P. vivax* (see Figs. 2 and 3; and Supplementary Figs. 4 and 6).

^fThe number of SGA-derived *P. vivax*-like sequences is shown for each sample in the genomic region indicated (parentheses indicate the number of different haplotypes for each sample).

Supplementary Table 4. Failure to detect *P. vivax* in African monkey species

Primate species ^a	Field sites in Cameroon										Field sites in DRC										Total			
	EB ^b		EO		MS		MI		NS		BO		KL		ML		MO		MA		ME		Pv ^c	Hp ^c
	Pv	Hp	Pv	Hp	Pv	Hp	Pv	Hp	Pv	Hp	Pv	Hp	Pv	Hp	Pv	Hp	Pv	Hp	Pv	Hp	Pv	Hp	Pv	Hp
<i>Allenopithecus nigroviridis</i>												0/1	0/1					0/43	34/43	0/2	2/2	0/46	36/46	
<i>Cercocebus agilis</i>			0/35	4/35	0/4	0/4	0/26	6/26										0/3	2/3			0/68	12/68	
<i>Cercocebus torquatus</i>	0/1	0/1																				0/1	0/1	
<i>Cercopithecus ascanius</i>											0/3	3/3	0/87	53/87	0/52	39/52	0/2	2/2	0/36	29/36	0/11	5/11	0/191	131/191
<i>Cercopithecus cephus</i>	0/9	6/9	0/57	52/57	0/2	2/2	0/76	58/76	0/1	0/1												0/145	118/145	
<i>Cercopithecus neglectus</i>			0/6	0/6			0/3	2/3			0/3	0/3	0/5	1/5	0/2	0/2			0/15	6/15	0/11	1/11	0/45	10/45
<i>Cercopithecus nictitans</i>	0/41	8/41	0/35	15/35	0/30	16/30	0/112	40/112	0/1	0/1								0/9	0/9			0/228	79/228	
<i>Cercopithecus pogonias</i>	0/1	0/1	0/13	5/13	0/2	0/2	0/15	4/15														0/31	9/31	
<i>Cercopithecus wolffi</i>											0/1	1/1	0/29	19/29	0/1	1/1	0/5	0/5	0/14	2/14	0/5	4/5	0/55	27/55
<i>Colobus angolensis</i>													0/19	12/19							0/4	2/4	0/23	14/23
<i>Colobus guereza</i>			0/1	0/1	0/3	0/3	0/4	0/4					0/1	0/1				0/1	0/1			0/7	0/7	
<i>Lophocebus albigena</i>			0/2	0/2	0/6	0/6	0/34	1/34	0/1	0/1												0/43	1/43	
<i>Lophocebus aterrimus</i>													0/29	19/29							0/3	0/3	0/32	19/32
<i>Mandrillus sphinx</i>	0/3	0/3																				0/3	0/3	
<i>Miopithecus ogouensis</i>	0/4	1/4																				0/4	1/4	
<i>Ptilocolobus tholloni</i>													0/71	43/71							0/2	1/2	0/73	44/73

^aBlood samples (n=998) were collected from primate bushmeat at 11 different locations (Supplementary Fig. 3) and screened for *P. vivax* using a diagnostic PCR method.

^bSamples are listed by field site and primate species, with the numbers of specimens containing *P. vivax* (Pv) or *Hepaticystis* spp. (Hp) mitochondrial DNA indicated per total number screened.

^cOf 501 blood samples (50.2%) that were PCR positive, all contained *Hepaticystis* spp. mitochondrial DNA as determined by direct amplicon sequencing.

Supplementary Table 5. Single genome amplification of *P. vivax* sequences from infected humans

ID	Sample Code ^a	Country ^b	Region	Year ^c	Mitochondrial genome Fragment D ^d	Apicoplast genome <i>clpC</i> ^e	Nuclear genome ^f			
							<i>ldh</i>	<i>asl</i>	<i>crk2</i>	β - <i>tub</i>
1	MRL31	Africa Overland	Africa	2010	4 (1) ^g	3 (1)	3 (1)	3 (2)	3 (1)	3 (2)
2	MRL19	East Africa	Africa	2009	4 (1)	5 (1)	3 (1)	3 (1)	2 (1)	3 (1)
3	MRL14	Eritrea	Africa	2008	3 (1)	8 (1)	3 (1)	2 (1)	2 (1)	1 (1)
4	MRL6	Eritrea	Africa	2006	3 (1)	3 (1)	3 (1)	3 (1)	4 (1)	3 (1)
5	MRL1	Ethiopia	Africa	2006	3 (1)	5 (1)	3 (1)	3 (1)	4 (1)	2 (1)
6	MRL15	Ethiopia	Africa	2008	3 (1)	4 (2)	2 (1)	2 (1)	1 (1)	
7	MRL16	Ethiopia	Africa	2008	3 (1)	4 (2)	3 (1)		3 (1)	
8	MRL18	Ethiopia	Africa	2009	4 (1)	2 (1)	3 (1)	3 (1)	3 (1)	3 (1)
9	MRL22	Ethiopia	Africa	2009	4 (1)	5 (1)	3 (1)	3 (1)	3 (1)	4 (1)
10	MRL23	Ethiopia	Africa	2010	4 (1)	3 (1)	3 (1)	3 (1)	3 (1)	3 (1)
11	MRL24	Ethiopia	Africa	2010	4 (1)	6 (1)	3 (1)	3 (1)	3 (1)	3 (1)
12	MRL25	Ethiopia	Africa	2010	4 (1)	2 (1)	3 (1)		2 (1)	1 (1)
13	MRL29	Ethiopia	Africa	2010	7 (1)	3 (1)	3 (1)	3 (1)	3 (1)	3 (1)
14	MRL3	Ethiopia	Africa	2006	3 (1)	2 (1)	3 (1)	3 (1)	8 (1)	
15	SW26	Ethiopia	Africa	2003	4 (1)		3 (1)	3 (1)	3 (1)	3 (2)
16	SW38	Ethiopia	Africa	2008	4 (1)		3 (1)	3 (1)	3 (1)	
17	SW9	Ethiopia	Africa	1998					1 (1)	
18	MRL2	Kenya	Africa	2006	3 (1)	7 (1)	3 (1)	3 (1)	4 (2)	4 (1)
19	MRL8	Kenya	Africa	2007	3 (1)	1 (1)	3 (1)	2 (1)	4 (1)	1 (1)
20	MRL9	Mozambique	Africa	2007	3 (1)	3 (1)	3 (1)	2 (1)	3 (1)	3 (1)
21	MRL11	South Africa	Africa	2008	3 (1)	5 (1)	3 (1)	3 (1)	4 (1)	3 (1)
22	MRL10	Sudan	Africa	2007	3 (1)	3 (1)	3 (1)	3 (2)	3 (1)	
23	MRL13	Sudan	Africa	2008	3 (1)	3 (1)	3 (1)	3 (1)	2 (1)	
24	MRL20	Sudan	Africa	2009	5 (1)	3 (1)	3 (1)	3 (1)	2 (1)	
25	MRL21	Sudan	Africa	2009	1 (1)	2 (1)			3 (1)	
26	MRL30	Sudan	Africa	2010	4 (1)	3 (1)	3 (1)	3 (1)	5 (1)	3 (1)
27	MRL4	Sudan	Africa	2006	3 (1)	3 (1)	3 (1)	3 (1)	4 (1)	1 (1)
28	MRL5	Tanzania	Africa	2006	3 (1)	2 (1)	3 (1)	1 (1)	2 (1)	1 (1)
29	SW23	Tanzania	Africa	2001	6 (1)		3 (1)	3 (1)	3 (1)	3 (1)
30	MRL12	Uganda	Africa	2008	3 (1)	5 (1)	3 (1)	3 (1)	2 (1)	2 (1)
31	MRL17	Uganda	Africa	2008	4 (1)	3 (1)	3 (1)	2 (1)	2 (1)	1 (1)
32	MRL26	Uganda	Africa	2010	4 (1)	4 (1)	3 (1)	2 (1)	1 (1)	3 (1)
33	MRL27	Uganda	Africa	2010	4 (1)	5 (1)	3 (1)		3 (1)	2 (1)
34	MRL28	Uganda	Africa	2010	4 (1)	3 (1)	3 (1)	2 (1)	3 (1)	3 (1)
35	MRL7	Uganda	Africa	2007	3 (1)	3 (1)	3 (1)	5 (1)	5 (1)	2 (1)
36	MRL40	Brazil	South/Central America	2007	4 (2)	1 (1)	4 (2)	3 (2)	1 (1)	1 (1)
37	MRL55	Brazil	South/Central America	2011	2 (1)					
38	SW14	Brazil	South/Central America	1999	5 (1)		3 (1)	2 (1)	3 (1)	2 (1)
39	SW34	Brazil	South/Central America	2005	3 (1)	3 (1)		3 (1)	2 (1)	3 (1)
40	SW37	Brazil	South/Central America	2007	4 (1)			1 (1)	3 (1)	
41	SW28	Brazil, Peru, Bolivia	South/Central America	2003	2 (1)		3 (1)	1 (1)	3 (1)	1 (1)
42	SW13	Ecuador	South/Central America	1999	4 (2)					
43	MRL32	French Guiana	South/Central America	2006	1 (1)	3 (1)	3 (1)	3 (1)	3 (1)	3 (1)
44	MRL50	French Guiana	South/Central America	2010	6 (1)	3 (1)	1 (1)	2 (1)	1 (1)	1 (1)
45	SW20	French Guiana	South/Central America	2001	6 (1)	3 (1)	3 (1)	3 (1)	2 (1)	3 (1)
46	MRL37	Guatemala	South/Central America	2006	4 (1)	1 (1)	2 (1)	1 (1)	2 (1)	1 (1)
47	MRL45	Honduras	South/Central America	2009	6 (1)	3 (1)	2 (1)	3 (1)	3 (1)	4 (2)
48	SW15	Nicaragua	South/Central America	1999	6 (1)		3 (1)	3 (1)	3 (1)	3 (1)
49	MRL49	Peru	South/Central America	2009	4 (2)	3 (1)	3 (1)		1 (1)	1 (1)
50	SW27	South America	South/Central America	2003	4 (1)		2 (1)	3 (1)	3 (1)	2 (1)
51	MRL54	Venezuela	South/Central America	2010	1 (1)	3 (1)	3 (1)	3 (1)	1 (1)	3 (1)
52	MRL46	Papua New Guinea	Oceania	2009	5 (1)	3 (1)	3 (1)	1 (1)	3 (1)	1 (1)
53	MRL47	Papua New Guinea	Oceania	2009	5 (1)	3 (1)	1 (1)	3 (1)	1 (1)	1 (1)
54	MRL48	Papua New Guinea	Oceania	2009	2 (1)	3 (1)		1 (1)	2 (1)	1 (1)
55	MRL52	Papua New Guinea	Oceania	2010	6 (1)	3 (1)		2 (1)	1 (1)	1 (1)

56	MRL56	Papua New Guinea	Oceania	2011	6 (1)	1 (1)	1 (1)	3 (1)	3 (1)	3 (1)
57	SW10	Papua New Guinea	Oceania	1998	6 (1)		3 (1)	4 (2)	3 (1)	3 (1)
58	SW3	Papua New Guinea	Oceania	1996	7 (1)		3 (1)	3 (1)	3 (1)	
59	SW31	Papua New Guinea	Oceania	2004	3 (1)			1 (1)	3 (1)	
60	SW33	Papua New Guinea	Oceania	2005	3 (1)	3 (1)		4 (1)	2 (1)	3 (1)
61	SW39	Papua New Guinea	Oceania	2008	2 (1)				1 (1)	
62	SW5	Papua New Guinea	Oceania	1997	5 (1)			1 (1)	2 (1)	2 (1)
63	SW8	Papua New Guinea	Oceania	1997	5 (1)		2 (1)	2 (1)	3 (1)	3 (1)
64	SW4	Solomon Islands	Oceania	1997	4 (1)		2 (1)	2 (1)	3 (1)	3 (1)
65	MRL38	Afghanistan	Asia	2006	5 (1)	3 (1)	3 (1)	3 (1)	3 (1)	3 (1)
66	MRL57	Afghanistan	Asia	2011	5 (2)	3 (1)	3 (1)	3 (1)	3 (1)	3 (1)
67	MRL35	India	Asia	2006	4 (2)	2 (1)	2 (1)	1 (1)	2 (1)	3 (1)
68	MRL36	India	Asia	2006		3 (1)	3 (1)	1 (1)	1 (1)	1 (1)
69	MRL58	India	Asia	2011	2 (1)			1 (1)	1 (1)	3 (1)
70	MRL61	India	Asia	2011	2 (1)	1 (1)	3 (1)	2 (1)	3 (1)	2 (1)
71	SW2	India	Asia	1996	2 (1)	4 (1)	4 (1)	3 (1)		2 (1)
72	SW32	India	Asia	2004	3 (1)			3 (1)	3 (1)	3 (1)
73	SW36	India	Asia	2007	3 (1)			2 (1)	3 (1)	
74	MRL39	Indonesia	Asia	2006	4 (1)	1 (1)	3 (1)	2 (1)	3 (1)	2 (1)
75	MRL41	Indonesia	Asia	2007	1 (1)	3 (1)	3 (1)	3 (1)	1 (1)	1 (1)
76	MRL44	Indonesia	Asia	2009	4 (1)			1 (1)	3 (1)	1 (1)
77	SW17	Indonesia	Asia	2000	6 (1)	3 (1)	4 (1)	4 (1)	3 (1)	2 (1)
78	SW18	Indonesia	Asia	2000	5 (2)	3 (1)	3 (1)	3 (1)	1 (1)	3 (1)
79	SW21	Indonesia	Asia	2001	6 (1)	3 (1)	2 (2)	4 (1)	3 (1)	3 (2)
80	SW24	Indonesia	Asia	2003	4 (1)			2 (2)	1 (1)	2 (1)
81	SW25	Indonesia	Asia	2003	1 (1)			1 (1)	3 (1)	3 (1)
82	SW30	Indonesia	Asia	2004	2 (1)			1 (1)	1 (1)	
83	MRL33	Pakistan	Asia	2006	2 (2)	1 (1)	2 (2)	3 (1)	3 (1)	3 (1)
84	MRL34	Pakistan	Asia	2006	6 (1)	3 (1)	3 (1)	2 (1)	2 (1)	3 (1)
85	MRL59	Pakistan	Asia	2011	5 (1)			2 (1)	1 (1)	
86	MRL60	Pakistan	Asia	2011	4 (2)	3 (1)	3 (1)	3 (1)	3 (1)	3 (1)
87	SW29	Pakistan	Asia	2003	2 (1)	2 (1)	3 (1)	5 (1)	3 (1)	3 (1)
88	MRL43	Philippines	Asia	2009	2 (1)		1 (1)		2 (1)	
89	MRL51	South Korea	Asia	2010	5 (1)	4 (1)	2 (1)	3 (1)	3 (1)	3 (1)
90	MRL53	South Korea	Asia	2010	4 (1)	3 (1)		2 (1)	2 (1)	1 (1)
91	MRL42	Thailand	Asia	2008	6 (1)			1 (1)	1 (1)	
92	SW11	Thailand	Asia	1998	5 (1)		3 (1)	1 (1)	2 (1)	2 (1)
93	SW12	Thailand	Asia	1999	5 (1)		3 (1)	3 (1)	2 (1)	
94	SW16	Thailand	Asia	2000	6 (1)	3 (1)	4 (1)	1 (1)	3 (1)	2 (1)
95	SW22	Thailand	Asia	2001	1 (1)			1 (1)	3 (1)	
96	SW35	Thailand	Asia	2007	3 (1)			2 (1)	3 (1)	
97	GX11	China	Asia	2006				9 (3)		12 (4)
98	GX12	China	Asia	2006	1 (1)			4 (1)	1 (1)	
99	GX13	China	Asia	2006	2 (1)			12 (1)		12 (1)
100	GX14	China	Asia	2006	1 (1)			4 (1)		3 (2)
101	GX15	China	Asia	2006	1 (1)			5 (1)		6 (1)
102	GX17	China	Asia	2006	9 (1)			3 (1)		3 (1)
103	GX18	China	Asia	2006	9 (2)			5 (1)		5 (1)
104	GX19	China	Asia	2006				10 (2)		9 (1)
105	GX20	China	Asia	2006	10 (1)			10 (1)		11 (1)
106	GX21	China	Asia	2006				3 (1)		3 (1)
107	in0410	India	Asia	2010	16 (1)		3 (1)		6 (2)	
108	in0411	India	Asia	2010					1 (1)	
109	in0413	India	Asia	2010	5 (2)		7 (1)		7 (1)	
110	in0414	India	Asia	2010	6 (1)		12 (1)		10 (1)	
111	in0415	India	Asia	2010	9 (1)		5 (1)		5 (1)	
112	in0416	India	Asia	2010	6 (1)		5 (1)		7 (1)	
113	in0417	India	Asia	2010	6 (2)		11 (1)		11 (1)	
114	in0418	India	Asia	2010	4 (1)		5 (1)		4 (1)	
115	in0419	India	Asia	2010	2 (1)		3 (1)		4 (1)	
116	in0421	India	Asia	2010	6 (1)		12 (1)		11 (1)	

117	PVAR07	Thailand	Asia	2009			2 (1)
118	PVAR08	Thailand	Asia	2009		3 (1)	3 (1)
119	V08B15	Myanmar	Asia	2008	4 (1)	10 (2)	7 (1)
120	V08B17	Myanmar	Asia	2008	4 (1)	14 (1)	12 (1)
121	V08B18	Myanmar	Asia	2008	7 (2)	13 (1)	8 (1)
122	V08B19	Myanmar	Asia	2008	1 (1)	7 (1)	3 (1)
123	V08B20	Myanmar	Asia	2008		4 (1)	3 (1)
124	V08B21	Myanmar	Asia	2008	4 (1)	4 (1)	6 (1)
125	V08B22	Myanmar	Asia	2008	2 (2)	4 (1)	
126	V08B23	Myanmar	Asia	2008	5 (1)	10 (1)	12 (1)
127	V08B24	Myanmar	Asia	2008	5 (1)	10 (1)	10 (1)
128	V08B25	Myanmar	Asia	2008	9 (2)	11 (1)	11 (1)

^aBlood samples designated SW and MRL were collected from travellers who acquired *P. vivax* infection after visiting malaria endemic areas (ID1-98). *P. vivax* infection was identified by microscopy and/or PCR at the Karolinska University Hospital in Stockholm, Sweden (designated SW) or the Malaria Reference Laboratory at the London School of Hygiene and Tropical Medicine, London, UK (designated MRL). The remaining samples (ID 97-128) were from malaria patients who sought treatment in four Asian countries.

^bCountry where *P. vivax* infection is known or believed to have been acquired.

^cYear of sample collection.

^dThe location of fragment D within the *P. vivax* mitochondrial genome is shown in Supplementary Fig. 1a.

^e*clpC*; caseinolytic protease C.

^f*ldh*, lactate dehydrogenase; *asl*, adenylosuccinate lyase gene, *crk2*, cell division cycle 2-related kinase 2; *β-tub*, β-tubulin.

^gThe number of SGA-derived *P. vivax* sequences generated for each sample is indicated, with the number of unique haplotypes shown in parentheses.

Supplementary Table 6. GenBank accession numbers for SGA-derived simian *Plasmodium* sequences^a

Mitochondrial DNA fragments ^b					Apicoplast <i>clpC</i> ^b	Nuclear gene fragments ^b			
D ^c	S ^c	A ^c	B ^c	C ^c		<i>ldh</i> ^c	<i>asf</i> ^c	<i>crk2</i> ^c	β - <i>tub</i> ^c
KF618562	KF618575	KF618504	KF618520	KF618525	KF618410	KF618614	KF618374	KF618438	KF618397
MS7183_SGA2.2	UG18_SGA5.3	GT318_SGA1.1	KA1680_SGA2.6	DG540_SGA20.1	DG540_SGA20.6	SY17_SGA5.2	DG540_SGA20.1	MO51114_SGA20.18	DG540_SGA5.1
LI50577_SGA30.2	DD58_SGA5.12	BQ392_SGA5.4	MO51058_SGA5.12	EK1179_SGA5.5	DP143_SGA2.10	SY1_SGA5.18	KF618376	LI50577_SGA5.3	KF618398
LI50579_SGA30.7	DG540_SGA500.10	DG540_SGA30.4	BQ392_SGA5.22	KF618530	MB323_SGA5.8	SY43_SGA2.1	DG540_SGA20.2	KF618428	DG540_SGA5.3
MO51058_SGA5.10	DP143_SGA5.8	MB323_SGA5.4	DG540_SGA5.4	EK514_SGA5.3	SY56_SGA20.9	SY56_SGA20.1	KF618375	LI50577_SGA5.1	KF618402
SY56_SGA100.1	DP942_SGA5.9	MO51114_SGA5.6	DP143_SGA2.8	EK1179_SGA5.6	SY17_SGA5.2	KF618599	DG540_SGA20.15	KF618423	SY1_SGA5.6
BQ194_SGA2.12	MB323_SGA5.3	KA1680_SGA5.6	MB323_SGA5.4	KF618526	SY47_SGA5.4	LI50577_SGA30.2	KF618389	LI50577_SGA5.2	KF618404
BQ392_SGA2.5	KA1672_SGA5.1	EK514_SGA2.10	SY1_SGA5.1	DG540_SGA20.7	SY43_SGA2.5	KF618600	SY1_SGA20.1	KF618424	SY32_SGA2.10
BY4890_SGA2.8	KA1680_SGA5.8	EK1179_SGA2.1	MO51114_SGA5.2	KF618527	MO51114_SGA5.1	LI50577_SGA30.3	KF618393	LI50579_SGA5.1	KF618405
DG540_SGA20.40	EK514_SGA5.1	LB1222_SGA5.30	EK1179_SGA5.8	DP143_SGA5.9	EK514_SGA5.2	KF618601	SY1_SGA20.7	KF618421	SY41_SGA5.1
DP143_SGA2.6	EK1179_SGA5.12	NK1167_SGA1.1	KF618510	KF618531	EK1179_SGA5.1	LI50577_SGA40.4	SY41_SGA5.5	DG540_SGA5.24	KF618406
MB323_SGA5.1	LB1222_SGA5.6	MO51106_SGA5.1	DG540_SGA5.1	MB323_SGA5.11	LB1222_SGA2.9	KF618602	KF618388	KF618419	SY43_SGA20.5
SY1_SGA20.2	KF618573	KF618496	EK1179_SGA5.6	KF618532	KF618416	LI50579_SGA10.1	SY17_SGA5.5	DG540_SGA20.1	KF618407
SY13_SGA5.12	NK1167_SGA5.9	EK514_SGA2.2	KF618509	SY1_SGA5.1	NK1167_SGA5.8	KF618604	KF618394	KF618420	SY45_SGA5.8
SY17_SGA5.3	EK514_SGA5.7	EK1179_SGA5.11	BQ392_SGA5.5	KF618528	EK1179_SGA5.2	LI50579_SGA3.3	SY32_SGA5.3	DG540_SGA20.9	KF618403
SY31_SGA2.1	EK1179_SGA40.5	LB1222_SGA5.29	KF618508	MO51114_SGA20.1	KF618408	SY41_SGA5.1	KF618395	KF618422	SY43_SGA2.7
SY41_SGA2.4	LB1222_SGA5.1	KC175317	BQ392_SGA5.31	KF618529	BQ392_SGA5.3	KF618605	SY43_SGA20.4	DG540_SGA20.12	SY56_SGA20.1
SY43_SGA2.1	KF618567	EK514_SGA2.6	KF618511	EK1179_SGA5.11	KF618409	LI50579_SGA5.1	KF618396	SY45_SGA5.1	KF618399
SY45_SGA20.6	BQ392_SGA5.1	LB1229_SGA5.2	DG540_SGA5.2		BQ392_SGA5.5	KF618603	SY43_SGA20.10	KF618441	MO51114_SGA5.2
SY47_SGA2.9	KF618568	KF618507	KF618512		KF618417	LI50579_SGA2.3	KF618390	SY1_SGA5.5	KF618400
MO51114_SGA20.1	BQ392_SGA5.4	BQ392_SGA2.8	DP143_SGA2.10		SY56_SGA20.6	KF618576	SY43_SGA2.1	KF618444	MO51114_SGA5.9
KA1680_SGA2.9	KF618570	KF618506	KF618523		KF618418	DG540_SGA5.2	KF618392	SY1_SGA20.17	KF618401
EK514_SGA2.3	KA1680_SGA5.2	BQ392_SGA5.21	MB323_SGA1.1		SY1_SGA5.1	KF618581	SY43_SGA2.2	SY41_SGA5.4	EK1179_SGA5.11
EK1179_SGA20.16	KF618574	KF618505	KF618524		KF618411	DG540_SGA5.4	SY56_SGA20.1	KF618440	
LB1222_SGA5.9	ON1329_SGA5.12	BQ392_SGA5.36	MB323_SGA5.8		DS83_SGA5.8	KF618577	KF618391	SY1_SGA5.20	
KF618536	KF618569	KF618503	KF618514		KF618412	DG540_SGA5.26	SY47_SGA2.1	KF618439	
CP1426_SGA1.1	EK1179_SGA40.6	DG540_SGA30.10	MO51114_SGA5.10		EK1179_SGA5.3	KF618578	KF618378	SY17_SGA5.5	
CP1444_SGA2.2	KF618571	KC175319	KF618519		KF618413	DG540_SGA5.35	MO51114_SGA5.2	KF618445	
EK514_SGA5.23	KG1229_SGA5.12	DG540_SGA40.9	EK514_SGA1.1		EK1179_SGA5.8	KF618579	KF618379	SY32_SGA5.7	
EK1179_SGA20.5	KF618572	KF618501	KF618517		KF618414	DG540_SGA5.36	MO51114_SGA5.5	KF618446	
NK1167_SGA2.1	LM1932_SGA5.2	DP143_SGA2.4	EK1179_SGA5.2		NK1167_SGA2.3	KF618580	KF618377	SY43_SGA20.9	
KF618555		KF618502	KF618518		KF618415	DG540_SGA5.38	MO51114_SGA20.9	KF618447	
EK514_SGA5.11		MB323_SGA5.23	EK1179_SGA5.4		NK1167_SGA2.7	KF618582	KF618382	SY47_SGA5.5	
DS83_SGA2.23		KF618500	KF618515			DG540_SGA5.88	EK1179_SGA5.2	KF618443	
NK1167_SGA2.8		EK514_SGA2.1	EK1179_SGA5.10			KF618583	KF618383	SY43_SGA2.5	
KF618560		KF618499	KF618516			DG540_SGA5.89	EK1179_SGA5.4	SY56_SGA20.1	
LB1222_SGA5.6		EK1179_SGA2.2	EK1179_SGA5.12			KF618584	KF618380	KF618442	
EK1179_SGA20.6		KF618498	KF618521			DG540_SGA5.94	EK1179_SGA5.11	SY43_SGA2.6	
KF618544		EK1179_SGA2.9	LB1222_SGA5.1			KF618615	KF618381	KF618427	
LI50577_SGA30.3		KF618497	KF618522			SY1_SGA2.1	EK1179_SGA5.16	MO51114_SGA20.8	
KF618543		LB1222_SGA5.6	LB1222_SGA5.4			KF618616	KF618384	KF618426	
LI50577_SGA30.11			KF618513			SY1_SGA5.19	Pcyn_SGA50.1	MO51114_SGA20.17	
KF618534			MO51106_SGA5.10			KF618617	KF618385	KF618437	
BQ392_SGA2.7						SY43_SGA20.8	Pfra_SGA50.1	KA1680_SGA2.5	
KF618535						KF618618	KF618386	KF618436	
BQ392_SGA5.11						SY47_SGA5.1	Pinu_SGA5.1	KA1680_SGA2.11	
KF618537						KF618607	KF618387	KF618429	
DG540_SGA20.37						MO51114_SGA5.15	Psim_SGA5.1	EK1179_SGA2.1	
KF618538						KF618608		KF618431	
DG540_SGA20.5						MO51114_SGA5.16		EK1179_SGA5.2	

KF618539	KF618609	KF618430
DG540_SGA20.7	MO51114_SGA5.17	EK1179_SGA5.17
KF618540	KF618596	KF618432
DP143_SGA5.11	KA1680_SGA2.2	EK1179_SGA5.22
KF618564	KF618597	KF618433
SY1_SGA20.8	KA1680_SGA2.8	EK1179_SGA5.24
KF618565	KF618598	KF618434
SY32_SGA2.1	KA1680_SGA5.1	EK1179_SGA5.32
KF618566	KF618595	KF618435
SY32_SGA5.6	EK1179_SGA5.3	EK1179_SGA5.35
KF618533	KF618590	KF618425
BA1285_SGA2.2	EK1179_SGA5.14	MO51106_SGA2.11
KF618556	KF618591	
KA1680_SGA5.3	EK1179_SGA5.18	
KF618541	KF618592	
DS83_SGA2.1	EK1179_SGA5.19	
KF618542	KF618593	
DS86_SGA2.4	EK1179_SGA5.23	
KF618548	KF618594	
EK1179_SGA20.3	EK1179_SGA5.24	
KF618545	KF618585	
EK1179_SGA20.10	EK1179_SGA10.2	
KF618546	KF618586	
EK1179_SGA20.11	EK1179_SGA10.6	
KF618547	KF618587	
EK1179_SGA20.27	EK1179_SGA10.7	
KF618549	KF618588	
EK1179_SGA5.42	EK1179_SGA10.9	
KF618550	KF618589	
EK1179_SGA5.44	EK1179_SGA20.9	
KF618551	KF618606	
EK1179_SGA5.46	MO51106_SGA2.1	
KF618552	KF618610	
EK1179_SGA5.54	Pcyn_SGA200.1	
KF618553	KF618611	
EK1179_SGA5.55	Pfra_SGA200.2	
KF618554	KF618612	
EK1179_SGA5.58	Pinu_SGA200.1	
KF618557	KF618613	
KG1246_SGA2.4	Psim_SGA20.1	
KF618558		
LB1222_SGA5.2		
KF618561		
LB1222_SGA5.8		
KF618559		
LB1222_SGA5.22		
KF618563		
NK1167_SGA5.3		

^aSGA-derived *P. vivax* sequences are color coded according to the host species from which they were derived: red, *P. t. troglodytes*; orange, *P. t. ellioti*; blue, *P. t. schweinfurthii*; green, *G. g. gorilla*. Sequences labeled in black were generated from isolates of *P. cynomolgi* (MRA-350G), *P. fragile* (MRA-352G), *P. inui* (MRA-486F) and *P. simiovale* (MRA-488F) obtained from the Malaria Research and Reference Reagent Resource Center (MR4) of the American Type Culture Collection (catalog numbers in parentheses).

^bThe location of mtDNA fragments S, A, B, C, and D are shown in Supplementary Fig. 1. Amplification conditions and length of these fragments are described in the Methods.

^cIdentical *P. vivax* sequences are listed below their respective GenBank accession number.

Supplementary Table 7. GenBank accession numbers of SGA-derived human *P. vivax* sequences

Mitochondrial fragment D ^a	Accession No ^b	Apicoplast <i>clpC</i> ^c	Accession No ^b	Nuclear <i>ldh</i> ^d	Accession No ^b	Nuclear <i>asf</i> ^e	Accession No ^b	Nuclear <i>crk2</i> ^f	Accession No ^b	Nuclear β - <i>tub</i> ^g	Accession No ^b
Hu_hap1	KF591794	Hu_hap1	KF591777	Hu_hap1	KF591836	Hu_hap1	KF591752	Hu_hap1	KF591782	Hu_hap1	KF591767
	in410_SGA20k.9		MRL1_SGA1k.2		V08B15_SGA400.1		MRL2_SGA10k.1		GX11_SGA200.5		MRL1_SGA10k.2
	in413_SGA2k.2		MRL2_SGA1k.2		V08B17_SGA400.2		MRL3_SGA1k.1		GX12_SGA100.3		MRL2_SGA10k.1
	in414_SGA2k.1		MRL3_SGA1k.11		V08B18_SGA400.6		MRL4_SGA1k.2		GX13_SGA200.1		MRL4_SGA1k.4
	in415_SGA20k.7		MRL5_SGA200.1		V08B19_SGA200.3		MRL7_SGA500.1		GX14_SGA150.9		MRL5_SGA50k.6
	in416_SGA2k.1		MRL6_SGA200.1		V08B20_SGA400.6		MRL11_SGA2k.2		GX15_SGA150.1		MRL7_SGA50k.2
	in417_SGA20k.7		MRL7_SGA1k.2		V08B21_SGA400.3		MRL12_SGA50k.3		GX17_SGA2k.3		MRL8_SGA50k.6
	in418_SGA2k.1		MRL8_SGA1k.4		V08B23_SGA400.1		MRL22_SGA10k.2		GX18_SGA150.6		MRL9_SGA10k.2
	in419_SGA20k.8		MRL9_SGA200.4		V08B25_SGA400.1		MRL23_SGA10k.1		GX19_SGA200.1		MRL12_SGA50k.3
	in421_SGA20k.9		MRL10_SGA1k.4		In410_SGA400.4		MRL26_SGA10k.2		GX20_SGA200.2		MRL14_SGA50k.2
	MRL1_SGA1k.1		MRL11_SGA1k.2		In413_SGA4k.7		MRL28_SGA10k.2		GX21_SGA200.2		MRL17_SGA10k.3
	MRL2_SGA1k.1		MRL12_SGA1k.2		In414_SGA4k.7		MRL29_SGA20k.1		In410_SGA100.1		MRL18_SGA10k.2
	MRL3_SGA40k.1		MRL13_SGA1k.2		In415_SGA400.2		MRL30_SGA10k.3		In411_SGA100.1		MRL19_SGA10k.3
	MRL4_SGA1k.1		MRL14_SGA1k.2		In416_SGA400.4		MRL31_SGA20k.4		In415_SGA200.1		MRL22_SGA10k.2
	MRL5_SGA1k.1		MRL15_SGA1k.2		In417_SGA400.1		MRL32_SGA10k.1		In414_SGA200.1		MRL24_SGA10k.1
	MRL6_SGA1k.1		MRL16_SGA1k.2		In418_SGA400.11		MRL35_SGA10k.7		In415_SGA400.1		MRL25_SGA10k.6
	MRL8_SGA1k.1		MRL18_SGA1k.1		In419_SGA400.2		MRL36_SGA10k.2		In416_SGA150.1		MRL26_SGA10k.1
	MRL11_SGA1k.1		MRL19_SGA1k.1		In421_SGA400.1		MRL42_SGA10k.3		In418_SGA150.4		MRL27_SGA10k.9
	MRL12_SGA1k.1		MRL20_SGA1k.1		PAVR08_SGA400.3		MRL38_SGA10k.1		In421_SGA500.1		MRL28_SGA10k.4
	MRL13_SGA1k.1		MRL21_SGA20.12		MRL2_SGA20.1		MRL39_SGA10k.2		V08B15_SGA1k.1		MRL29_SGA10k.1
	MRL15_SGA1k.1		MRL22_SGA1k.1		MRL3_SGA20.1		MRL40_SGA10k.5		V08B17_SGA200.1		MRL30_SGA10k.3
	MRL16_SGA1k.1		MRL23_SGA1k.1		MRL5_SGA20.1		MRL42_SGA5k.6		V08B18_SGA400.1		MRL31_SGA10k.2
	MRL18_SGA30k.1		MRL24_SGA1k.1		MRL6_SGA20.1		MRL50_SGA10k.10		V08B19_SGA100.1		MRL33_SGA10k.2
	MRL19_SGA30.1		MRL25_SGA1k.1		MRL8_SGA20.1		MRL53_SGA2.5k.6		V08B20_SGA100.2		MRL34_SGA10k.1
	MRL21_SGA5k.2		MRL26_SGA1k.1		MRL9_SGA20.1		MRL54_SGA2k.5		V08B21_SGA400.2		MRL35_SGA5k.3
	MRL22_SGA30k.1		MRL27_SGA1k.1		MRL10_SGA20.1		MRL60_SGA10k.1		V08B23_SGA800.2		MRL36_SGA10k.8
	MRL23_SGA30k.1		MRL28_SGA1k.1		MRL12_SGA20.1		SW14_SGA2k.6		V08B24_SGA800.2		MRL37_SGA10k.5
	MRL24_SGA30k.1		MRL29_SGA1k.1		MRL13_SGA20.1		SW20_SGA1k.1		PVAR07_SGA50.7		MRL38_SGA10k.2
	MRL25_SGA30k.1		MRL30_SGA1k.1		MRL14_SGA20.1		SW21_SGA1k.6		PVAR08_SGA40.5		MRL39_SGA10k.2
	MRL26_SGA30k.1		MRL31_SGA1k.1		MRL15_SGA20.1		SW22_SGA100.4		MRL1_SGA10k.3		MRL44_SGA100.6
	MRL27_SGA30k.1		MRL32_SGA200.1		MRL16_SGA20.1		SW23_SGA1k.3		MRL2_SGA100k.4		MRL45_SGA10k.2
	MRL30_SGA30k.1		MRL33_SGA200.4		MRL17_SGA200.1		SW24_SGA100.7		MRL5_SGA50k.2		MRL46_SGA10k.2
	MRL31_SGA30k.1		MRL34_SGA200.3		MRL18_SGA200.1		SW27_SGA500.3		MRL7_SGA100k.3		MRL47_SGA10k.2
	MRL34_SGA500.7		MRL35_SGA200.2		MRL19_SGA200.1		SW28_SGA1k.3		MRL8_SGA50k.1		MRL49_SGA5k.2
	MRL35_SGA1k.6		MRL36_SGA100.1		MRL20_SGA200.1		SW35_SGA1k.4		MRL9_SGA10k.2		MRL50_SGA10k.2
	MRL38_SGA10k.8		MRL37_SGA200.10		MRL22_SGA200.1		SW37_SGA1k.5		MRL10_SGA10k.2		MRL54_SGA1k.4
	MRL57_SGA10k.7		MRL38_SGA200.1		MRL23_SGA200.1	Hu_hap2	KF591759	MRL12_SGA10k.11	MRL15_SGA5k.9		MRL56_SGA10k.1
	MRL59_SGA100.2		MRL39_SGA100.1		MRL24_SGA200.1		MRL6_SGA20k.2	MRL16_SGA2.5k.1	MRL17_SGA5k.9		MRL57_SGA10k.5
	MRL60_SGA10k.12		MRL40_SGA200.11		MRL25_SGA200.1		MRL13_SGA5k.3	MRL17_SGA2.5k.1	MRL19_SGA10k.5		MRL58_SGA5k.4
	SW2_SGA100.1		MRL45_SGA200.1		MRL26_SGA200.1		MRL14_SGA50k.2	MRL19_SGA10k.1	MRL20_SGA10k.1		MRL60_SGA10k.4
	SW3_SGA1k.11		MRL46_SGA200.1		MRL27_SGA200.1		MRL15_SGA5k.1	MRL20_SGA10k.1	MRL22_SGA10k.1		MRL61_SGA10k.3
	SW21_SGA1k.7		MRL47_SGA200.1		MRL29_SGA200.1		MRL20_SGA5k.2	MRL23_SGA10k.1	MRL24_SGA10k.1		SW2_SGA2k.1
	SW23_SGA1k.7		MRL48_SGA200.2		MRL30_SGA200.1		MRL31_SGA20k.2	MRL25_SGA10k.1	MRL26_SGA10k.1		SW4_SGA50.8
	SW26_SGA1k.9		MRL49_SGA200.7		MRL31_SGA200.1		MRL40_SGA10k.4	MRL27_SGA10k.4	MRL28_SGA10k.4		SW5_SGA500.5
	SW29_SGA1k.10		MRL50_SGA200.7		MRL32_SGA1k.1		MRL41_SGA1k.2	MRL29_SGA10k.2	MRL30_SGA10k.2		SW8_SGA50.8
	SW32_SGA1k.9		MRL51_SGA100.1		MRL34_SGA1k.4		MRL45_SGA10k.2	MRL32_SGA10k.2	MRL33_SGA10k.2		SW11_SGA1k.3
	SW38_SGA1k.9		MRL52_SGA100.2		MRL35_SGA500.1		MRL46_SGA10k.9	MRL34_SGA10k.2	MRL35_SGA10k.2		SW14_SGA2k.2
	V08B17_SGA20k.9		MRL53_SGA100.1		MRL36_SGA500.1		MRL47_SGA2k.1	MRL45_SGA10k.9	MRL36_SGA10k.6		SW15_SGA500.2
	Hu_hap2		MRL54_SGA100.1		MRL37_SGA500.3		MRL48_SGA10k.2	MRL46_SGA10k.2	MRL37_SGA10k.2	Hu_hap2	KF591769
	KF591804		MRL57_SGA200.1		MRL38_SGA500.4		MRL49_SGA10k.3	MRL47_SGA2k.1	MRL38_SGA10k.2		MRL41_SGA10k.5
	MRL37_SGA10k.9		MRL60_SGA200.3		MRL40_SGA1k.1	Hu_hap3	KF591760	MRL48_SGA10k.3	MRL39_SGA10k.2		MRL51_SGA10k.2
	MRL40_SGA1k.2		MRL61_SGA200.3		MRL45_SGA500.2		MRL1_SGA10k.3	MRL49_SGA10k.3	MRL40_SGA10k.2		MRL53_SGA10k.9
	MRL42_SGA500.1		MRL62_SGA20.2		MRL49_SGA500.3		MRL19_SGA10k.1	MRL50_SGA10k.2	MRL45_SGA10k.2		MRL55_SGA10k.1
	MRL45_SGA10k.7		SW2_SGA20.2		MRL50_SGA1k.6		MRL20_SGA5k.2	MRL51_SGA10k.1	MRL46_SGA10k.2		MRL56_SGA10k.1
	MRL49_SGA1k.3		SW16_SGA200.2		MRL54_SGA50.4		MRL31_SGA20k.2	MRL52_SGA5k.6	MRL47_SGA5k.3		MRL57_SGA10k.2
	MRL54_SGA1k.1		SW17_SGA200.2		MRL57_SGA1k.2		MRL42_SGA10k.4	MRL53_SGA5k.2	MRL48_SGA10k.2		MRL58_SGA10k.2
	SW14_SGA200.7		SW18_SGA200.1		MRL60_SGA1k.1		MRL43_SGA10k.4	MRL54_SGA5k.2	MRL49_SGA2.5k.1		MRL59_SGA10k.1
	SW15_SGA1k.8		SW20_SGA200.1		MRL61_SGA1k.2		MRL44_SGA10k.2	MRL55_SGA5k.2	MRL50_SGA10k.7		MRL60_SGA10k.1
	SW27_SGA100.1		SW21_SGA200.1		SW2_SGA20.1		MRL45_SGA10k.3	MRL56_SGA10k.4	MRL51_SGA10k.7		MRL61_SGA10k.1
	SW28_SGA1k.9		SW29_SGA200.2		SW11_SGA20.1		MRL46_SGA10k.3	MRL57_SGA10k.2	MRL52_SGA10k.1	Hu_hap3	KF591770
	SW34_SGA1k.9		SW34_SGA200.1		SW14_SGA20.1		MRL47_SGA2k.1	MRL58_SGA10k.3	MRL53_SGA10k.5		MRL62_SGA10k.3
	SW37_SGA1k.9	Hu_hap2	KF591778		SW15_SGA20.1		MRL48_SGA2k.1	MRL59_SGA10k.4	MRL54_SGA5k.11	Hu_hap4	KF591771
	V08B15_SGA20k.8		MRL4_SGA200.1		SW16_SGA20.1		MRL49_SGA10k.2	MRL60_SGA10k.4	MRL55_SGA5k.11		MRL63_SGA10k.3
	V08B19_SGA2k.1		MRL15_SGA1k.3		SW20_SGA20.1		MRL50_SGA10k.2	MRL61_SGA10k.4	MRL56_SGA10k.6	Hu_hap5	MRL64_SGA10k.3
	V08B23_SGA20k.11		MRL16_SGA1k.1		SW21_SGA20.1		MRL51_SGA10k.2	MRL62_SGA10k.4	MRL57_SGA10k.2		MRL65_SGA10k.3
	V08B24_SGA20k.11	Hu_hap3	KF591779		SW23_SGA20.1		MRL52_SGA10k.1	MRL63_SGA10k.4	MRL58_SGA100.5		MRL66_SGA10k.3
	V08B25_SGA20k.9		MRL17_SGA1k.1		SW26_SGA20.1		MRL53_SGA10k.1	MRL64_SGA10k.4	MRL59_SGA5k.11		MRL67_SGA10k.3
Hu_hap3	KF591815		SW33_SGA200.8		SW27_SGA5.1		MRL54_SGA10k.1	MRL65_SGA10k.4	MRL60_SGA10k.7		MRL68_SGA10k.3
	MRL46_SGA10k.7	Hu_hap4	KF591781		SW27_SGA5.1		MRL55_SGA10k.1	MRL66_SGA10k.4	MRL61_SGA10k.7	Hu_hap3	KF591770
	MRL48_SGA1k.1		MRL41_SGA100.1		SW28_SGA20.1	Hu_hap4	MRL56_SGA10k.2	MRL67_SGA10k.4	MRL62_SGA10k.7		MRL69_SGA10k.1
	MRL56_SGA10k.8	Hu_hap5	KF591780		SW29_SGA20.1		MRL57_SGA10k.2	MRL68_SGA10k.4	MRL63_SGA10k.7	Hu_hap4	KF591771
	SW8_SGA200.8		MRL56_SGA200.1		SW38_SGA200.1		MRL58_SGA10k.3	MRL69_SGA10k.4	MRL64_SGA10k.7		MRL70_SGA10k.1
	SW10_SGA1k.3			Hu_hap2	KF591844		MRL59_SGA500.3	MRL70_SGA10k.4	MRL65_SGA10k.7		MRL71_SGA10k.1
	SW13_SGA10.4				GX11_SGA400.9		MRL60_SGA500.4	MRL71_SGA10k.4	MRL66_SGA10k.7		MRL72_SGA10k.1
	SW25_SGA100.1				GX12_SGA150.11		SW9_SGA100.9	MRL72_SGA100.5	MRL67_SGA10k.7		MRL73_SGA10k.1

	MRL57_SGA10k.8
Hu_hap32	KF591818
	MRL60_SGA10k.7
Hu_hap33	KF591819
	MRL7_SGA1k.1
Hu_hap34	KF591820
	SW18_SGA1k.10
Hu_hap35	KF591821
	SW22_SGA100.1
Hu_hap36	KF591822
	SW31_SGA1k.12
Hu_hap37	KF591823
	SW35_SGA1k.9
Hu_hap38	KF591824
	SW36_SGA1k.9
Hu_hap39	KF591825
	SW4_SGA20.1
Hu_hap40	KF591827
	SW5_SGA200.9
Hu_hap41	KF591828
	V08B18_SGA20k.7
Hu_hap42	KF591829
	V08B22_SGA2k.8
Hu_hap43	KF591830
	V08B25_SGA20k.8

^aGenes were amplified from the human blood samples listed in Supplementary Table 4, sequenced, aligned and classified into different haplotypes.

^bIdentical sequences are listed under their respective haplotype number.

Supplementary Table 8. GenBank accession number of previously published *Plasmodium* sequences

Strain	Mitochondrial	Nuclear Genes*				Apicoplast
	DNA	<i>ldh</i>	<i>asl</i>	<i>crk2</i>	β - <i>tub</i>	<i>clpC</i>
Salvador I	NC_007243 ^a	PVX_116630 ^{zz}	PVX_003765	PVX_114825	PVX_094635	AB649419
India VII	AY791608 ^b	PVIIG_05181	PVIIG_04900	PVIIG_05772	PVIIG_02031	
Mauritania I	AY791526	PVMG_00304 ^{aaa}	PVMG_02711	PVMG_02156	PVMG_00825	JQ437258
North Korean	AY791554 ^c	PVNG_00285	PVNG_01910	PVNG_03742	PVNG_02041	JQ437259
Brazil I	AY791540	PVBG_01369	PVBG_05119	PVBG_01204	PVBG_02787	JQ437257
050V	AY791532 ^d					
200629	JQ240346 ^e					
200647	JQ240352					
af20047	AY791518					
af99165	AY791520 ^f					
<i>Anopheles moucheti</i> A	JX444726					
<i>A. moucheti</i> B	JX444724					
<i>A. moucheti</i> C	JX444725					
AP13A	KC330426					
AP16C	KC330438 ^g					
AP17C	KC330419					
AP33A	KC330409					
AP33C	KC330425 ^h					
AP37C	KC330415					
AP42C	KC330418 ⁱ					
AP42D	KC330414 ^j					
AP6A	KC330407					
AP6C	KC330406 ^k					
ASA06G29634		EU589951				
ASA06R09632		EU589957				
AS17B	KC330398 ^l					
AS21.1	KC330401					
AS21.2	KC330402 ^m					
AS22.2	KC330395					
AS6B	KC330391					
Be309B	KC330619					
Be324A	KC330626					
Be354A	KC330620					
Be359AA	KC330632 ⁿ					
Be372B	KC330621					
Be395A	KC330627					
Be395B	KC330628					
Be399A	KC330615					
Be399B	KC330618					
Bucheon3		JX872280				
Ca11A	KC330522 ^o					
Ca11B	KC330518					
Ca32A	KC330514					
Ca42A	KC330524 ^p					
Ca49B	KC330526					
Ca60B	KC330515					
Ca66A	KC330523					
Ca66AA	KC330527					
Ca66C	KC330520					
Ca6C	KC330521					
Ca94C	KC330530					
Chimpanzee B'	JX444723					
Chimpanzee DRCG	GQ355480					
Chimpanzee Karla	JX444720					
Chimpanzee UGB	GQ355481					
CK3	AY598139 ^q					
Clesson					AY639986	
CN14	AY791591					
CN3	AY791592 ^r					
CN5	AY791593 ^s					
Co08B	KC330385 ^t					
Co13A	KC330380					
Co13B	KC330377					
Co153	KC330384 ^u					
Co15C	KC330381					
Co27A	KC330376					
Cu12A	KC330568 ^v					
Cu12B	KC330570					
Cu16B	KC330567 ^w					
Cu48A	KC330571 ^x					
Cu61A	KC330559 ^y					
Cu94C	KC330577					
Cu95B	KC330579					
D33a	AY791585 ^z					
Dominica	AY791544					
EJE060134		EU589955				
European traveller	JX444721					
Goa-1		JN547223				
Gorilla Bumbi	JX444722					

Gorilla Cola	JX444719	
GX15	JQ240375 ^{aa}	
Honduras III		AY639987
IBM6	AY598103	
IBY5	AY598099	
IL48	AY598108	
india.01016	AY791611 ^{bb}	
india.01018	AY791612	
india.01047	AY791614	
IndonesiaXIX		AY640003
Indonesia14	AY791552	
IZ01052	DQ396547	
Ko22A	KC330506 ^{cc}	
Ko28A	KC330507 ^{dd}	
Ko40A	KC330512	
Ko9A	KC330504	
Krt-1		JN547225
Krt-2		JN547222
Krt-4		JN547224
Lo13C	KC330547	
Lo17A	KC330536	
Lo17B	KC330537	
Lo1A	KC330543 ^{ee}	
Lo23B	KC330553	
Lo29C	KC330542	
Lo40B	KC330557	
Lo5A	KC330551	
Ma148A	KC330592	
Ma158A	KC330587 ^{ff}	
Ma161A	KC330584 ^{gg}	
Ma163A	KC330590	
Ma170A	KC330589	
Ma176D	KC330596	
Ma185B	KC330591 ^{hh}	
Ma185C	KC330593 ⁱⁱ	
Ma200A	KC330595	
Madagascar16	JN788748 ^{jj}	
Mae143A	KC330455	
Mae298C	KC330441 ^{kk}	
Mae636B	KC330463	
Mae636C	KC330464	
Mauritania_II	AY791527	
MD335	JQ240396 ^{ll}	
Mia018A	KC330456 ^{mm}	
Mia028A	KC330443	
Mia028B	KC330440	
MIA061042		EU589954
MIA061251		EU589952
MIA061304		EU589953
Mia304A	KC330460	
Mia938A	KC330454	
Ori-1		JN547221
Ori-4		JN547226
<i>P. simium</i>	AY800110 ⁿⁿ	
Pachong	AY791558	
PC15A	KC330650	
PC21B	KC330658	
PC27B	KC330660	
PC47	AY598084 ^{oo}	
PNN1	AY598119	
pv01036	AY791632 ^{pp}	
pv01106a	AY791633 ^{qq}	
pv01182	AY791635 ^{rr}	
pv01186	AY791636 ^{ss}	
pv02044	AY791682 ^{tt}	
pv02050	AY791643	
pv02076a	AY791644	
pv02096	AY791685	
pv02107a	AY791649 ^{uu}	
pv03005	AY791651	
pv20017	AY791657 ^{vv}	
pv20054	AY791662	
pv32336	AY791525	
PV536B	KC330597	
PV537B	KC330609	
PV560A	KC330612	
pv97133	AY791625	
pv99147	AY791675	
pv99175	AY791678	
pvChesson	AY791690	
pvIndiaNJ	AY791624 ^{ww}	
RB68	AY598093	
Sall		AY640004

S_ Korean	AB550280					
SJ28A	KC330646					
SJ30B	KC330644					
SJ39BB	KC330634					
SJ9A	KC330640					
SJ9B	KC330641					
SO1	AY598116					
SO3	AY598118					
T124	AY598039					
TB44	AY598041					
TF105	AY598060					
TFF23	AY598065					
TG48	AY598070					
Thai-1				AY639992		
Tu11A	KC330495					
Tu18C	KC330487					
Tu1A	KC330485 ^{xx}					
Tu20C	KC330488					
Tu27B	KC330481					
Tu32B	KC330490					
Tu39B	KC330482					
Tu4B	KC330491					
V08A18	JQ240402					
V08A20	JQ240404 ^{yy}					
V08A25	JQ240409					
V08A32	JQ240416					
V08B28	JQ240429					
Ve105AA	KC330677					
Ve1073B	KC330670					
Ve1081A	KC330666					
Ve128B	KC330676					
Ve946B	KC330665					
Viv13B	KC330474					
Viv14B	KC330466					
VX11	AY598126					
Unknown Strain		AF262051				
<i>P. simiovale</i>	AB434920		AY640002	AY639985	AB471881	
<i>P. fieldi</i>	AB354574		AY639996	AY639979	AB471874	
<i>P. coatneyi</i>	AB354575		AY639994	AY639977	AB471872	
<i>P. knowlesi</i>	AY598141	XM_002260056	AF262052	AY640001	AY639984	AB471880
<i>P. fragile</i>	NC_012369			AY639997	AY639980	AB471876
<i>P. cynomolgi</i>	AY800108			AY639995	AY639978	AB471873
<i>P. inui</i>	AB354572			AY640000	AY639983	AB471879
<i>P. hylobati</i>	AB354573			AY639999	AY639982	AB471878

^a Represents a haplotype shared by 151 additional human *P. vivax* sequences: Salvadori (AF055587), T101 (AY598036), T107 (AY598038), TA101 (AY598040), TC22 (AY598048), TC26 (AY598049), TC103 (AY598051), TC137 (AY598054), TC141 (AY598055), TF14 (AY598059), TFF1 (AY598061), TFF20 (AY598064), TG46 (AY598069), TG52 (AY598071), AD80 (AY598074), AD82 (AY598075), AD89 (AY598076), AD90 (AY598077), AD92 (AY598078), PC35 (AY598079), PC38 (AY598080), PC40 (AY598081), PC43 (AY598082), PC44 (AY598083), PC59 (AY598086), BA72 (AY598087), DE75 (AY598088), DE76 (AY598089), BL79 (AY598095), BP1 (AY598096), SG77 (AY598097), BD1 (AY598109), BD2 (AY598110), BD5 (AY598111), BD6 (AY598112), BD8 (AY598113), BD9 (AY598114), BD10 (AY598115), SO2 (AY598117), VX4 (AY598122), VX5 (AY598123), VX6 (AY598124), VX10 (AY598125), 045V (AY791529), 046V (AY791530), 048V (AY791531), 055V (AY791536), Brazil1 (AY791540), NICA (AY791541), Achiote (AY791542), Apastipeque (AY791543), HondurusI (AY791545), HondurusII (AY791546), RioMeta (AY791547), Panamal (AY791548), pv20225 (AY791550), Sall (AY791551), pv97109 (AY791576), Vietnam4 (AY791584), H2 (AY791606), pv02078 (AY791645), pv20004 (AY791654), pv98128 (AY791673), pv2078 (AY791688), pvKamo (AY791691), V08A15 (JQ240399), V08A21 (JQ240405), V08A22 (JQ240406), V08A26 (JQ240410), V08A27 (JQ240411), V08A28 (JQ240412), V08A30 (JQ240414), V08A34 (JQ240418), V08A35 (JQ240419), V08A37 (JQ240421), V08A38 (JQ240422), V08B15 (JQ240423), V08B19 (JQ240426), Co04A (KC330370), Co29A (KC330371), Co05C (KC330372), Co18A (KC330373), Co06B (KC330374), Co17B (KC330375), Co06A (KC330378), Co27B (KC330379), Co18B (KC330382), Co17A (KC330383), Ca27A (KC330528), Ca53A (KC330529), Ca94A (KC330531), Ca53B (KC330532), Cu72A (KC330558), Cu48C (KC330561), Cu72B (KC330562), Cu16A (KC330563), Cu28C (KC330564), Cu29A (KC330565), Cu16C (KC330569), Cu72C (KC330572), Cu64A (KC330573), PV531A (KC330598), PV528B (KC330599), PV536C (KC330600), PV528A (KC330601), PV566A (KC330602), PV559A (KC330603), PV537A (KC330604), PV536A (KC330605), PV537C (KC330606), PV566B (KC330607), PV540B (KC330608), PV533A (KC330610), PV540C (KC330613), PV571A (KC330614), Be372A (KC330616), Be309A (KC330617), Be367C (KC330622), Be359A (KC330631), SJ24B (KC330635), SJ22A (KC330636), SJ24A (KC330643), SJ33A (KC330645), SJ19D (KC330647), SJ19C (KC330648), SJ19B (KC330649), PC25D (KC330651), PPC17B (KC330654), PC23D (KC330655), PC2A (KC330656), PC1A (KC330657), PC27A (KC330659), PC21A (KC330661), PC23F (KC330662), PC22B (KC330663), Ve946A (KC330668), MRL37_FD_SGA_10k.9, MRL40_FD_SGA_1k.2, MRL42_FD_SGA_500.1, MRL45_FD_SGA_10k.7, MRL49_FD_SGA_1k.3, MRL54_FD_SGA_1k.1, SW14_FD_SGA_200.7, SW15_FD_SGA_1k.8, SW27_FD_SGA_100.1, SW28_FD_SGA_1k.9, SW34_FD_SGA_1k.9, SW37_FD_SGA_1k.9, V08B23_FD_SGA_20k.11, V08B24_FD_SGA_20k.11, and V08B25_FD_SGA_20k.9.

^b Represents a haplotype shared by 198 additional human *P. vivax* sequences: IN1 (AY598120), CX4 (AY598131), af97177 (AY791519), pv12105 (AY791521), pv12123 (AY791522), pv205 (AY791523), pv22089 (AY791524), Mauritanial (AY791526), pv02123 (AY791549), MiamiI (AY791553), pv97104 (AY791575), CN74 (AY791594), CN84 (AY791599), CN85 (AY791600), CN89 (AY791601), CN90 (AY791603), CN97 (AY791605), India168 (AY791607), IndiaVII167 (AY791609), IndiaV168 (AY791610), india.01038 (AY791613), india.01123 (AY791615), india.02081 (AY791616), india.20095 (AY791617), india.97097 (AY791618), india.97110 (AY791619), india.97113 (AY791620), india.99143 (AY791621), india.99161 (AY791622), pvBangladesh (AY791623), pv99170 (AY791627), pv02079 (AY791628), pv2003 (AY791629), Angola (JN788737), Madagascar1 (JN788738), Madagascar10 (JN788739), Madagascar11 (JN788740), Madagascar12 (JN788741), Madagascar13a (JN788742), Madagascar13b (JN788743), Madagascar14a (JN788744), Madagascar14b (JN788745), Madagascar15a (JN788746), Madagascar15b (JN788747), Madagascar17 (JN788749), Madagascar17a (JN788750), Madagascar18a (JN788751), Madagascar19a (JN788752), Madagascar19b (JN788753), Madagascar22 (JN788754), Madagascar20 (JN788755), Madagascar3 (JN788756), Madagascar4 (JN788757), Madagascar6a (JN788758), Madagascar6b (JN788759), Madagascar8 (JN788760), Madagascar9 (JN788761), Madagascar9b (JN788762), Niger (JN788763), Rwanda (JN788764),

SaoTome (JN788765), Tanzania (JN788766), Turkey1 (JN788767), Turkey10 (JN788768), Turkey2 (JN788769), Turkey3 (JN788770), Turkey3 (JN788770), Turkey5 (JN788771), Turkey6 (JN788772), Turkey7 (JN788773), Turkey8 (JN788774), Turkey9 (JN788775), Turkey4 (JN788776), 200621 (JQ240342), KoGW5 (JQ240369), GX10 (JQ240370), GX20 (JQ240379), GX21 (JQ240380), GX26 (JQ240384), GX9 (JQ240395), KoPJ6 (JQ240397), V08A17 (JQ240401), AS19A (KC330386), AS19C (KC330387), AS8B (KC330388), AS16C (KC330389), AS16A (KC330390), AS17A (KC330392), AS8A (KC330393), AS6C (KC330394), AS14.4 (KC330397), AS22.1 (KC330399), AS22C (KC330400), AS1.1 (KC330403), AS3A (KC330404), AP6D (KC330408), AP33D (KC330410), AP21D (KC330411), AP27A (KC330412), AP17B (KC330413), AP17D (KC330416), AP17A (KC330417), AP42A (KC330420), AP42B (KC330421), AP37B (KC330422), AP37A (KC330423), AP33B (KC330424), AP21C (KC330427), AP1A (KC330428), AP1B (KC330429), AP1D (KC330430), AP1C (KC330431), AP16D (KC330432), AP21A (KC330434), AP16A (KC330436), AP27C (KC330437), AP27D (KC330439), Mae298B (KC330442), Mae298A (KC330444), Mae636A (KC330445), Mae307C (KC330446), Mae307B (KC330447), Mia028C (KC330448), Mia251B (KC330450), Mia919C (KC330451), Mia310A (KC330452), Mia919B (KC330461), Mia251A (KC330462), Viv5B (KC330467), Viv14D (KC330468), Viv13A (KC330469), Viv16A (KC330470), Viv3.2 (KC330471), Viv16B (KC330473), Viv5.1 (KC330475), Viv3A (KC330476), Viv15A (KC330477), Viv15C (KC330478), Viv13AA (KC330480), Tu18B (KC330483), Tu43A (KC330484), Tu6C (KC330489), Tu4A (KC330492), Tu23A (KC330493), Tu27A (KC330494), Tu39C (KC330496), Ko33A (KC330501), Ko13A (KC330502), Ko16A (KC330503), in410_FD_SGA_20k.9, in413_FD_SGA_2k.2, in414_FD_SGA_2k.1, in415_FD_SGA_20k.7, in416_FD_SGA_2k.1, in417_FD_SGA_20k.7, in418_FD_SGA_2k.1, in419_FD_SGA_20k.8, in421_FD_SGA_20k.9, MRL1 FG_SGA1k.1, MRL11_FD_SGA_1k.1, MRL12_FD_SGA_1k.1, MRL13_FD_SGA_1k.1, MRL14_FD_SGA_1k.1, MRL15_FD_SGA_1k.1, MRL16_FD_SGA_1k.1, MRL18_FD_SGA_30k.1, MRL19_FD_SGA_30.1, MRL2_FD_SGA_1k.1, MRL21_FD_SGA_5k.2, MRL22_FD_SGA_30k.1, MRL23_FD_SGA_30k.1, MRL24_FD_SGA_30k.1, MRL25_FD_SGA_30k.1, MRL26_FD_SGA_30k.1, MRL27_FD_SGA_30k.1, MRL29_FD_SGA_300k.7, MRL3_FD_SGA_40k.1, MRL30_FD_SGA_30k.1, MRL31_FD_SGA_30k.1, MRL34_FD_SGA_500.7, MRL35_FD_SGA_1k.6, MRL38_FD_SGA_10k.8, MRL4_FD_SGA_1k.1, MRL5_FD_SGA_1k.1, MRL51_FD_SGA_1k.1, MRL57_FD_SGA_10k.7, MRL59_FD_SGA_100.2, MRL6_FD_SGA_1k.1, MRL60_FD_SGA_10k.12, MRL8_FD_SGA_1k.1, SW2_FD_SGA_100.1, SW21_FD_SGA_1k.7, SW23_FD_SGA_1k.7, SW26_FD_SGA_1k.9, SW29_FD_SGA_1k.10, SW3_FD_SGA_1k.11, SW32_FD_SGA_1k.9, SW38_FD_SGA_1k.9, and V08B17_FD_SGA_20k.9.

^c Represents a haplotype shared by 60 additional human *P. vivax* sequences: S.KoreaB2 (AB550276), S.KoreaB3 (AB550277), S.KoreaB4 (AB550278), S.KoreaB5 (AB550279), CX1 (AY598128), CX2 (AY598129), CX3 (AY598130), CX7 (AY598134), CX8 (AY598135), CX10 (AY598137), CK1 (AY598138), CN1 (AY791588), CN75 (AY791595), CN76 (AY791596), CN78 (AY791597), CN81 (AY791598), CN9 (AY791602), CN96 (AY791604), 200601 (JQ240331), 200603 (JQ240332), 200604 (JQ240333), 200606 (JQ240334), 200608 (JQ240335), 200611 (JQ240336), 200616 (JQ240337), 200617 (JQ240338), 200618 (JQ240339), 200619 (JQ240340), 200620 (JQ240341), 200622 (JQ240343), 200626 (JQ240344), 200627 (JQ240345), 200632 (JQ240347), 200633 (JQ240348), 200639 (JQ240349), 200644 (JQ240350), 200646 (JQ240352), 200649 (JQ240354), 200652 (JQ240355), 200657 (JQ240356), 200659 (JQ240357), 200665 (JQ240358), 200666 (JQ240359), 200667 (JQ240360), 200669 (JQ240361), 200672 (JQ240362), 200674 (JQ240363), 200676 (JQ240364), 200677 (JQ240365), 200678 (JQ240366), GX11 (JQ240371), GX12 (JQ240372), GX13 (JQ240373), GX14 (JQ240374), GX22 (JQ240381), GX6 (JQ240392), KoPJ7 (JQ240398), Ko2A (KC330511), Ko37A (KC330513), and MRL53_FD_SGA1k.1.

^d Represents a haplotype shared by 27 additional human *P. vivax* sequences: RB61 (AY598090), RB69 (AY598094), 051V (AY791533), 052V (AY791534), 054V (AY791535), belem1 (AY791537), belem2 (AY791538), belem3 (AY791539), pvThai.NYU (AY791559), pvThai9.6.00 (AY791560), Cu94B (KC330574), Cu95A (KC330575), Cu6A (KC330576), Cu94A (KC330578), Ma176A (KC330588), Ma170B (KC330594), Be344C (KC330623), Be334B (KC330624), Be334A (KC330625), Be344A (KC330629), Be344B (KC330630), Ve119A (KC330669), Ve139B (KC330671), Ve1082A (KC330672), Ve128AA (KC330674), Ve113A (KC330678), and MRL32_FD_SGA50k.4.

^e Represents a haplotype shared by two additional human *P. vivax* sequences: 200645 (JQ240351) and KoGW3 (JQ240367).

^f Represents a haplotype shared by five additional human *P. vivax* sequences: pv02108 (AY791650), pv20195 (AY791669), pv2108 (AY791689), pv02137 (AY791692), and MRL52_FD_SGA500.7.

^g Represents a haplotype shared by one additional human *P. vivax* sequence: Mia133B (KC330453).

^h Represents a haplotype shared by one additional human *P. vivax* sequence: AP49C (KC330433).

ⁱ Represents a haplotype shared by one additional human *P. vivax* sequence: Mia304B (KC330449).

^j Represents a haplotype shared by one additional human *P. vivax* sequence: AP49A (KC330435).

^k Represents a haplotype shared by one additional human *P. vivax* sequence: AS3.2 (KC330396).

^l Represents a haplotype shared by one additional human *P. vivax* sequence: Viv3B (KC330479).

^m Represents a haplotype shared by three additional human *P. vivax* sequences: AS9.3 (KC3304050), MRL61_FD_SGA1k.5, and SW11_FD_SGA1k.9.

ⁿ Represents a haplotype shared by one additional human *P. vivax* sequence: MA148B (KC330581).

^o Represents a haplotype shared by five additional human *P. vivax* sequences: TFF128 (AY598067), V08A31 (JQ240415), Ca56C (KC330517), Ca56B (KC330519), and SW22_FD_SGA100.1.

^p Represents a haplotype shared by 24 additional human *P. vivax* sequences: T077 (AY598035), T131 (AY598037), TB66 (AY598042), TB98 (AY598043), TB103 (AY598044), TB128 (AY598045), TC19 (AY598046), TC20 (AY598047), TC106 (AY598052), TC126 (AY598053), TD29 (AY598056), TE26 (AY598057), TF4 (AY598058), TFF5 (AY598062), TFF30 (AY598066), TG57 (AY598072), VX12 (AY598127), V08A17 (JQ240401), V08A19 (JQ240403), V08A24 (JQ240408), V08A33 (JQ240417), V08A36 (JQ240420), V08B18 (JQ240425), and Ca42B (KC330525).

^q Represents a haplotype shared by 13 additional human *P. vivax* sequences: S.KoreaA1 (AB550270), S.KoreaA2 (AB550271), S.KoreaA3 (AB550272), S.KoreaA4 (AB550273), S.KoreaA5 (AB550274), S.KoreaB1 (AB550275), CX5 (AY598132), CX6 (AY598133), pv01100 (AY791561), Ko18C (KC330497), Ko5A (KC330498), Ko18A (KC330499), and Ko5C (KC330500).

^r Represents a haplotype shared by one additional human *P. vivax* sequence: CN12 (AY791590).

^s Represents a haplotype shared by two additional human *P. vivax* sequences: CN10 (AY791589) and KoGW4 (JQ240368).

^t Represents a haplotype shared by one additional human *P. vivax* sequence: PV533C (KC330611).

^u Represents a haplotype shared by one additional human *P. vivax* sequence: Cu15.1 (KC330580).

^v Represents a haplotype shared by 13 additional human *P. vivax* sequences: Ma166C (KC330582), Ma148C (KC330583), Ma161A (KC330584), Ma165A (KC330585), Ma166A (KC330586), SJ39B (KC330633), SJ2B (KC330637), SJ39A (KC330638), PC26C (KC330653), Ve1080A (KC330667), MRL50_FD_SGA500.7, MRL55_FD_SGA100.1, and SW20_FD_SGA1k.7.

^w Represents a haplotype shared by one additional human *P. vivax* sequence: Cu29B (KC330566).

^x Represents a haplotype shared by one additional human *P. vivax* sequence: Ve945B (KC330664).

^y Represents a haplotype shared by one additional human *P. vivax* sequence: Cu64B (KC330560).

^z Represents a haplotype shared by two additional human *P. vivax* sequences: D33b (AY791586) and D33c (AY791587).

^{aa} Represents a haplotype shared by 16 additional human *P. vivax* sequences: KH20703 (DQ396548), GX17 (JQ240376), GX18 (JQ240377), GX19 (JQ240378), GX23 (JQ240382), GX24 (JQ240383), GX27 (JQ240385), GX28 (JQ240386), GX29 (JQ240387), GX3 (JQ240388), GX30 (JQ240389), GX4 (JQ240390), GX5 (JQ240391), GX7 (JQ240393), GX8 (JQ240394), and SW16_FD_SGA100.1.

^{bb} Represents a haplotype shared by two additional human *P. vivax* sequences: TG42 (AY598068) and V08A23 (JQ240407).

^{cc} Represents a haplotype shared by three additional human *P. vivax* sequences: Ko28C (KC330505), Ko35B (KC330509), and Ko35C (KC330510).

^{dd} Represents a haplotype shared by one additional human *P. vivax* sequence: Ko35A (KC330508).

^{ee} Represents a haplotype shared by three additional human *P. vivax* sequences: pv01006 (AY791631), MRL9_FD_SGA1k.1, and SW30_FD_SGA100.5.

- ^{ff} Represents a haplotype shared by one additional human *P. vivax* sequence: SJ34A (KC330642).
- ^{gg} Represents a haplotype shared by one additional human *P. vivax* sequence: PC26E (KC330652).
- ^{hh} Represents a haplotype shared by one additional human *P. vivax* sequence: Ve105A (KC330673).
- ⁱⁱ Represents a haplotype shared by one additional human *P. vivax* sequence: Ve128A (KC330675).
- ^{jj} Represents a haplotype shared by four additional human *P. vivax* sequences: V08A29 (JQ240413), Viv2B (KC330465), MRL35_FD_SGA1k.1, and MRL58_FD_SGA100.1.
- ^{kk} Represents a haplotype shared by one additional human *P. vivax* sequence: Viv4A (KC330672).
- ^{ll} Represents a haplotype shared by four additional human *P. vivax* sequences: V08A16 (JQ240400), V08B18_FD_SGA2k.2, SW12_FD_SGA200.1, and SW13_FD_SGA10.6.
- ^{mmm} Represents a haplotype shared by three additional human *P. vivax* sequences: Mia042C (KC330457), Mia018C (KC330458), Mia042B (KC330459).
- ⁿⁿ Represents a haplotype shared by one additional sequence: *P. simium* (NC_007233).
- ^{oo} Represents a haplotype shared by three additional human *P. vivax* sequences: PC51 (AY598085), RB66 (AY598091), and RB67 (AY598092).
- ^{pp} Represents a haplotype shared by two additional human *P. vivax* sequences: pv02097 (AY791647) and SW31_FD_SGA1k.12.
- ^{qq} Represents a haplotype shared by two additional human *P. vivax* sequences: pv01106b (AY791634) and SW4_FD_SGA20.1.
- ^{rr} Represents a haplotype shared by one additional human *P. vivax* sequence: pv20005 (AY791655).
- ^{ss} Represents a haplotype shared by 49 additional human *P. vivax* sequences: pvFKB (AY791555), pv02121 (AY791564), pv03001 (AY791565), pv3002 (AY791566), pv20096 (AY791568), pv20097 (AY791569), pv20129 (AY791570), pv20134 (AY791571), pv20242 (AY791574), pv97137 (AY791626), pv2112 (AY791630), pv01188a (AY791637), pv01188b (AY791638), pv01193a (AY791639), pv01193b (AY791640), pv02088 (AY791646), pv02098a (AY791648), pv1024 (AY791652), pv20002 (AY791653), pv20013 (AY791656), pv20029 (AY791658), pv20031 (AY791659), pv20033 (AY791660), pv20043 (AY791661), pv20115 (AY791663), pv20120 (AY791664), pv20127 (AY791665), pv20186 (AY791667), pv20191 (AY791668), pv97105 (AY791670), pv97114 (AY791671), pv97126 (AY791672), pv99110 (AY791674), pv99157 (AY791676), pv99166 (AY791677), pv99110 (AY791679), pv99190 (AY791680), pv99215 (AY791681), pv02084 (AY791684), pv02098b (AY791686), MRL46_FD_SGA10k.7, MRL48_FD_SGA1k.1, MRL56_FD_SGA10k.8, SW10_FD_SGA1k.3, SW13_FD_SGA10.4, SW25_FD_SGA100.1, SW33_FD_SGA1k.9, SW39_FD_SGA1k.7, and SW8_FD_SGA200.8.
- ^{tt} Represents a haplotype shared by two additional human *P. vivax* sequences: pv02044a (AY791641) and pv02044b_AY791642.
- ^{uu} Represents a haplotype shared by one additional human *P. vivax* sequence: pv02107b (AY791687).
- ^{vv} Represents a haplotype shared by one additional human *P. vivax* sequence: SW5_FD_SGA200.9.
- ^{ww} Represents a haplotype shared by one additional human *P. vivax* sequence: SW36_FD_SGA1k.9.
- ^{xx} Represents a haplotype shared by one additional human *P. vivax* sequence: Tu1B (KC330486).
- ^{yy} Represents a haplotype shared by three additional human *P. vivax* sequences: V08B20 (JQ240427), V08B21 (JQ240428), and V08B22_FD_SGA2k.6.
- ^{zz} Represents a haplotype shared by four additional human *P. vivax* sequences: Belem (DQ060151), Gwalior (EU262038), Hainan (FJ527750) and Sal1 (XM_001615570).
- ^{aaa} Represents a haplotype shared by two additional human *P. vivax* sequences: ASA06R09623 (EU589956) and Anhui (GU078391).

Supplementary Table 9. *P. vivax* specific primers

Genes	Genome	Amplicon (bp)	First round primers		Second round primers	
diagnostic fragment	mtDNA	297	Pv2768p Pv3287n	GTATGGATCGAATCTTACTTATTC AATACCAGATACTAAAAGACCAACAATGATA	Pv2870p Pv3185n	TTGCAATCATAAAACTTTAGGTC TCCTCCAAATTCTGCTGCTGTAGATAAAATG
fragment S	mtDNA	799	Pv2768p Pv4818n	GTATGGATCGAATCTTACTTATTC CAATACATAATGCTACAAAAGGAAG	Pv2870p Pv3689n	TTGCAATCATAAAACTTTAGGTC AGCCCATACAACACTTCTAATATAGCA
fragment A	mtDNA	1922	Pv2768p Pv5033n	GTATGGATCGAATCTTACTTATTC ATTGGTGAACATATGTATTAATAAT	Pv2870p Pv4818n	TTGCAATCATAAAACTTTAGGTC CAATACATAATGCTACAAAAGGAAG
fragment B	mtDNA	2982	Pv4431p Pv1720n	GCAAGTCGTTACTCCAGAAATATCT GGATATTGTATAAATGATGCTATATCT	Pv4615p Pv1607n	GGATATCAGGATTAATCATATTTGCAT TGAAATGTATGATACTAATAGTAA
fragment C	mtDNA	2134	Pv936p Pv3287n	ATGACGCTATCAATTTGACAAGGCA AATACCAGATACTAAAAGACCAACAATGATA	Pv985p Pv3185n	AACGTTTCATCCTCCATACATAA TCCTCCAAATTCTGCTGCTGTAGATAAAATG
fragment D	mtDNA	2536	Pv2768p Pv5739n	GTATGGATCGAATCTTACTTATTC AATATCTATAAACCAATAAAGTKAAACCAATT	Pv2856p Pv5434n	CTTATTACAAATTGCAATCATAAAACTTTAGGT TTCAGAGATATCGTCTTATCGTAGC
<i>ldh</i>	Nuclear	713	PvLdhF1 PvLdhR1	AACCCAAAATTGTGCTCGTCGG TCCTTTTAGTCTCCGCAACTGC	PvLdhF2 PvLdhR2	AATGTGATGGCTTATCCAATTGC TCGTGCAACTGGTCTTCTCCTCGG
<i>ldh^a</i>	Nuclear	724	PkvLdhF1 PkvLdhR1	ATGRCGCCRAAACCCAAAATYGTSC GCCTTCATYCTTTTRGYTCCGC	PkvLdhF2 PkvLdhR2	ATACRTCYCACTCSAATGTGATGGC TCGTCRAACTGGYCTTYCCTC
<i>asl</i>	Nuclear	838	PvAslF1 PvAslR4	ATGGAGCACCTGAAGAATCTC ATGAGGCAATAGGCAAGGGAGCTT	PvAslF2 PvAslR5	ATCGACGGGCGGTACAAAAGGC ATTGGGTTGACCTTATGTGGCAT
<i>crk2</i>	Nuclear	666	PvCdc2F1 PvCdc2R1	TGGAGAAGGTACATATGGTGTAGT ACCACTTTGCGTAAGACCTACCT	PvCdc2F2 PvCdc2R2	AAAGGAGGATGAAGGCATTCCG GGTGCAGCACTCTGTGTTTCATG
<i>β-tub</i>	Nuclear	684	PvBtubF1 PvBtubR1	TGTGGGAACCAGATAGGTGCGAA ACCTGCCACCRGTTGCTTCATTG	PvBtubF2 PvBtubR2	GACGAGCACGGCATAGATCCA GTARGETCACTGYTCTCTGTAGGT
<i>clpC</i>	Apicoplast	574	PvclpCF6 clpCR2	TAAAAATATAAATTCCTATAATA GTTAATCTATTTARTAATTCHGGTTTAA	PvclpCF7 PvclpCR2	AATACAATTTAGAATATTTAAATACT GTCTTTAAGTCTATATCAGATAAGT

^aDegenerate primers designed to amplify more divergent macaque *Plasmodium* species.

Supplementary References

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