**Figure S1. Bayesian phylogeny of 136 complete mtDNA sequences of the *Plasmodium* parasite using our *Chlorocebus* Calibration Model showing only the Asian Plasmodia**

*Plasmodium* phylogeny and divergence dates inferred by Bayesian analysis of 136 complete mtDNA sequences using our *Chlorocebus* calibration model showing only the Asian plasmodia subtree. The first calibration point was set as the most recent common ancestor (MRCA) of *Plasmodium* sp. and *P. gonderi* with a date of 9.18-15.72 million years ago (mya). The MRCA of all Asian plasmodia (node A) was set as the second calibration with a normal distribution and a date range of 3.20-5.90 mya Nodes with Bayesian posterior probabilities greater than 0.50 are indicated by node color. The color legend is on the figure. Some clades are collapsed for visualization with number of sequences belonging to those taxa in parentheses. Capital letters at some nodes indicate divergence dates provided in Table 1. Scale bar at the bottom in one (1) million-year increments.

**Figure S2. Bayesian phylogeny of 136 complete mtDNA sequences of the *Plasmodium* parasites using our *Chlorocebus* Calibration Model showing only *P. hylobati*, *Pongo* 1, *P. inui* and *Pongo* 2 Plasmodia**

*Plasmodium* phylogeny inferred by Bayesian analysis of 136 complete mtDNA sequences using our *Chlorocebus* Calibration Model showing only *P. hylobati*, *P. inui*, *Pongo* 1 and *Pongo* 2 plasmodia with individual sequences making up the *Pongo* 2 and *P. inui* groupings visible. The first calibration point was set to be the MRCA of *Plasmodium* sp. and *P. gonderi* with a date of 9.18-15.72 mya. The most recent common ancestor (MRCA) of all Asian plasmodia (Node A) was set as the calibration with a normal distribution and a date range of 3.20-5.90 mya. Nodes with Bayesian posterior probabilities greater than 0.50 are indicated by node color. The color legend is on the figure. Some clades are collapsed for visualization with number of sequences belonging to those taxa in parentheses. Capital letters at some nodes indicate divergence dates provided in Table 1. Scale bar at the bottom in five-hundred thousand (500,000) year increments.

**Figure S3. Bayesian phylogeny of 136 complete mtDNA sequences of the *Plasmodium* parasites using our *Cercocebus* Calibration Model showing only the Asian Plasmodia**

*Plasmodium* phylogeny inferred by Bayesian analysis of 136 complete mtDNA sequences using our *Cercocebus* Calibration Model showing only the Asian plasmodia region of the tree. The first calibration point was set to be the MRCA of *Plasmodium* sp. and *P. gonderi* with a date of 6.7-11.9 mya. The most recent common ancestor (MRCA) of all Asian plasmodia (Node A) was set as the calibration with a normal distribution and a date range of 3.20-5.90 mya. Some clades are collapsed for visualization with number of sequences belonging to those taxa in parentheses. Capital letters at some nodes indicate divergence dates provided in Table 1. Nodes with Bayesian posterior probabilities greater than 0.50 are indicated by node color. The color legend is on the figure. Scale bar at the bottom in one (1) million-year increments.

**Figure S4. Bayesian phylogeny of 136 complete mtDNA sequences of the *Plasmodium* parasites using our *Cercocebus* Calibration Model showing only *P. hylobati*, *Pongo* 1, *P. inui* and *Pongo* 2 Plasmodia**

*Plasmodium* phylogeny inferred by Bayesian analysis of 136 complete mtDNA sequences using our *Cercocebus* Calibration Model showing only *P. hylobati*, *P. inui*, *Pongo* 1 and *Pongo* 2 plasmodia with individual sequences making up the *Pongo* 2 and *P. inui* groupings visible. The first calibration point was set to be the MRCA of *Plasmodium* sp. and *P. gonderi* with a date of 6.7-11.9 mya. The most recent common ancestor (MRCA) of all Asian plasmodia (Node A) was set as the calibration with a normal distribution and a date range of 3.20-5.90 mya. Nodes with Bayesian posterior probabilities greater than 0.50 are indicated by node color. The color legend is on the figure. Some clades are collapsed for visualization with number of sequences belonging to those taxa in parentheses. Capital letters at some nodes indicate divergence dates provided in Table 1. Scale bar at the bottom in five-hundred thousand (500,000) year increments.

**Figure S5. Maximum Parsimony (MP) phylogeny of 136 complete mtDNA sequences of the *Plasmodium* parasites**

Maximum parsimony phylogeny inferred from a comparison of 136 sequences using the complete mtDNA genome of *Plasmodium* parasites. Only the Asian *Plasmodium* species are shown. The phylogeny was inferred using the subtree-pruning-regrafting (SPR) method with 500 bootstrap repetitions in MEGAX. Bootstrap support values greater than 50 are shown at major nodes in the tree. The color legend is on the figure.

**Figure S6. Maximum Parsimony (MP) phylogeny of 136 complete mtDNA sequences of the *Plasmodium* parasites showing only the Asian primate Plasmodia**

Maximum Parsimony (MP) tree inferred in a comparison of 136 sequences using the complete mtDNA genome of *Plasmodium* sp. parasites. The MP tree was created using the Subtree-Pruning-Regrafting (SPR) method with 500 bootstrap repetitions. This tree only shows the individual sequences that make up the Asian plasmodia clades. Bootstrap support values greater than 50 are shown at major nodes in the tree. Color legend is indicated on the figure.

**Figure S7. Maximum Parsimony (MP) phylogeny of 136 complete mtDNA sequences of the *Plasmodium* parasites showing only *P. hylobati*, *Pongo* 1, *P. inui* and *Pongo* 2 Plasmodia**

Maximum Parsimony (MP) tree inferred in a comparison of 136 sequences using the complete mtDNA genome of *Plasmodium* sp. parasites. The MP tree was created using the Subtree-Pruning-Regrafting (SPR) method with 500 bootstrap repetitions. This tree only shows the individual sequences that make up the *P. inui* and *Pongo* 2 *Plasmodium* clades. Bootstrap support values greater than 50 are shown at major nodes in the tree. Color legend is indicated on the figure.

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| **Supplementary Table**  **Table S1.** *Plasmodium* mitochondrial DNA sequences used in this study and GenBank accession numbers (Common names for infected species adapted in part from Muehlenbein *et al*., 2015 Supplemental Table 1 and references therein, as well as sequence information available in GenBank) | | |
| ***Plasmodium* species** | **GenBank Accession Number (*Plasmodium* host source)** | **Host Taxonomic Groups** |
| *Plasmodium cynomolgi* | AB434919, AB444121-AB444131 (Macaques), KJ569865-KJ569868 (Macaques) | Asian Monkeys |
| *Plasmodium knowlesi* | AB444106-AB444108, AY598141, AY722797 (Malayan MRA-487),  EU880467, EU880470 (Humans)  EU880475, EU880484, EU880489 (Long-tailed macaque) | Asian Monkeys and Humans |
| *Plasmodium fieldi* | AB444132-AB444133 (Macaques), KJ569861-KJ569864 (Pig-tailed macaques), AB354574 (Macaques) | Asian Monkeys |
| *Plasmodium* sp. (*P. pygmaeus*) | JQ308530-JQ308534, KJ569804 KJ569833  (Bornean Orangutans) | Orangutans |
| *Plasmodium inui* | KJ569834-KJ569850 (Pig-tailed macaques), GQ355482-leaf monkey (Macaques) | Asian Monkeys |
| *Plasmodium* sp. | KJ569851-KJ569854 (Long-tailed macaques) | Asian Monkeys |
| *Plasmodium* sp. | KJ569855-KJ569860 (Long-tailed macaques) | Asian Monkeys |
| *Plasmodium vivax* | AY598098, AY598107, DQ396547- DQ396548 (Humans) | Humans |
| *Plasmodium simium* | AY800110 | New World Monkeys |
| *Plasmodium simiovale* | AB434920 (Toque macaque), AY800109 (Macaques) | Asian Monkeys |
| *Plasmodium fragile* | AB444136, AB444134 (Macaques and leaf monkeys) | Asian Monkeys |
| *Plasmodium coatneyi* | AB354575 (Long-tailed macaque) | Asian Monkeys |
| *Plasmodium hylobati* | AB354573 (Silvery Gibbon) | Gibbons |
| *Plasmodium sp.* | AY800112 (Mandrill) | African Monkeys |
| *Plasmodium gonderi* | AY800111 (Mangabeys and guenons) | African Monkeys |
| *Plasmodium brasilianum* | GQ355484 (Squirrel monkey) | New World Monkeys |
| *Plasmodium malariae* | AB354570, AB489194 (Humans) | Humans |
| *Plasmodium ovale wallikeri* | HQ712053 (Humans) | Humans |
| *Plasmodium ovale curtisi* | HQ712052 (Humans) | Humans |
| *Plasmodium* sp. A-Lemur | HQ712054 (Eastern lesser bamboo Lemur) | Lemurs |
| *Plasmodium* sp. B-Lemur | HQ712055 (Black and white ruffed Lemur) | Lemurs |
| *Plasmodium* sp. C-Lemur | HQ712056 (Eastern lesser bamboo Lemur) | Lemurs |
| *Plasmodium* sp. D-Lemur | HQ712057 (Indri) | Lemurs |
| *Plasmodium* sp. E-Lemur | JN131536 (Black Lemur) | Lemurs |
| *Plasmodium yoelii* | M29000 (African rats-Genus *Thamnomys*) | Rodents |
| *Plasmodium atheruri* | HQ712051 (African porcupine) | Rodents |
| *Plasmodium chabaudi* | AF014116 (African rats-Genus *Thamnomys*) | Rodents |
| *Plasmodium berghei* | AF014115 (African rats-Genus *Grammomys* sp.) | Rodents |
| *Plasmodium vinckei vinckei* | AB599931 (African rats-Various genera and species) | Rodents |
| *Plasmodium reichenowi* | GQ355476 (Chimpanzee), NC002235 (Chimpanzee) | African Apes |
| *Plasmodium gaboni* | JX893151(Chimpanzee), FJ895307 (Chimpanzee) | African Apes |
| *Plasmodium billcollinsi* | GQ355479 (Chimpanzee) | African Apes |
| *Plasmodium billbrayi* | GQ355468 (Chimpanzee) | African Apes |
| *Plasmodium falciparum* | AY282930 (Humans) | Humans |
| *Plasmodium relictum* | AY733088 (African penguin-Zoo) | Birds |
| *Plasmodium floridense* | NC009961 (Brown Anole) | Lizards |
| *Plasmodium mexicanum* | NC009960 (Western fence lizard) | Lizards |
| *Plasmodium gallinaceum* | NC008288 (Chickens and penguins) | Birds |
| *Plasmodium juxtanucleare* | NC008279 (Chickens and other domestic birds) | Birds |