Genomic and transcriptomic evidence for descent from *Plasmodium* and loss of blood schizogony in *Hepatocystis* parasites from naturally infected red colobus monkeys

Eerik Aunin, Ulrike Böhme, Theo Sanderson, Noah D. Simons, Tony L. Goldberg, Nelson Ting, Colin A. Chapman, Chris I. Newbold, Matthew Berriman, Adam J. Reid

1 Parasite Genomics, Wellcome Sanger Institute, Hinxton, Cambridge, United Kingdom, 2 Malaria Biochemistry Laboratory, The Francis Crick Institute, London, United Kingdom, 3 Department of Anthropology and Institute of Ecology and Evolution, University of Oregon, Eugene, Oregon, United States of America, 4 Department of Pathobiological Sciences, School of Veterinary Medicine, University of Wisconsin-Madison, Madison, Wisconsin, United States of America, 5 Department of Anthropology, Center for the Advanced Study of Human Paleobiology, The George Washington University, Washington DC, United States of America, 6 Shaanxi Key Laboratory for Animal Conservation, Northwest University, Xi’an, China, 7 School of Life Sciences, University of KwaZulu-Natal, Scottsville, Pietermaritzburg, South Africa, 8 Weatherall Institute of Molecular Medicine, University of Oxford, John Radcliffe Hospital, Oxford, United Kingdom

*ar11@sanger.ac.uk

Abstract

*Hepatocystis* is a genus of single-celled parasites infecting, amongst other hosts, monkeys, bats and squirrels. Although thought to have descended from malaria parasites (*Plasmodium* spp.), *Hepatocystis* spp. are thought not to undergo replication in the blood—the part of the *Plasmodium* life cycle which causes the symptoms of malaria. Furthermore, *Hepatocystis* is transmitted by biting midges, not mosquitoes. Comparative genomics of *Hepatocystis* and *Plasmodium* species therefore presents an opportunity to better understand some of the most important aspects of malaria parasite biology. We were able to generate a draft genome for *Hepatocystis* sp. using DNA sequencing reads from the blood of a naturally infected red colobus monkey. We provide robust phylogenetic support for *Hepatocystis* as a sister group to *Plasmodium* parasites infecting rodents. We show transcriptomic support for a lack of replication in the blood and genomic support for a complete loss of a family of genes involved in red blood cell invasion. Our analyses highlight the rapid evolution of genes involved in parasite vector stages, revealing genes that may be critical for interactions between malaria parasites and mosquitoes.

Author summary

*Hepatocystis* parasites are single-celled organisms, closely related to the *Plasmodium* species which cause malaria. But *Hepatocystis* are distinct—unlike *Plasmodium* they are thought not to replicate in the blood and cause little or no disease in their mammalian...
and sample accession number ERS3649919. The individual accession numbers for the contigs are: CABPSV010000001-CABPSV010002439. Accession numbers for the apicoplast and the mitochondrion are LR699571-LR699572. Illumina HiSeq 4000 RNA-seq reads, containing a mix of Piliocolobus tephrosceles and Hepatocystis sp. sequences can be found in the European Nucleotide Archive under study accession PRJNA413051. Other data and code are available from our GitHub repository: https://github.com/adamjamesreid/hepatocysts-genome.

Funding: This work was funded by National Institutes of Health (NIH; https://nih.gov/), USA grant TW009237 as part of the joint NIH-NSF Ecology of Infectious Disease program and the UK Economic and Social Research Council (TLG, NT, CAC). National Science Foundation Grant BCS-1540459 (NT, NDS; https://www.nsf.gov/). The Wellcome Sanger Institute is funded by the Wellcome Trust (grant 210918/Z/18/Z). CIN is supported by a Wellcome Trust Sir Henry Wellcome Fellowship (210918/Z/18/Z). AJR is also supported by funding from the UK Medical Research Council (MRC Programme grant #: MR/M003906/1; https://mrc.ukri.org/). TS is supported by a Wellcome Trust Sir Henry Wellcome Fellowship (210918/Z/18/Z). TS is also supported by funding from the Wellcome Trust (grant 206194/Z/17/Z; https://wellcome.ac.uk/). The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

Competing interests: The authors have declared that no competing interests exist.

hosts. They are transmitted from one host to the next, not by mosquitoes, but by biting midges. In this study we generated a genome sequence for Hepatocystis—the first time this data has ever been produced and analysed for this species. We compared genome sequences of Hepatocystis and Plasmodium, confirming that Hepatocystis is descended from Plasmodium. We strengthened support for the absence of replication in the blood and, in line with this finding, discovered that genes involved in interaction with red blood cells have been lost in Hepatocystis. Our analyses revealed rapid evolution of genes which are active when the parasite is in the insect vector, highlighting those which might be important for understanding interaction between malaria parasites and mosquitoes. Hepatocystis has a fascinating evolutionary story and is a powerful comparator for understanding malaria parasite biology.

Introduction

Species of the genus Hepatocystis are single-celled eukaryotic parasites infecting, amongst other hosts, Old World monkeys, fruit bats and squirrels [1]. Phylogenetically, they are thought to reside within a clade containing Plasmodium species, including the parasites causing malaria in humans [2]. They were originally considered distinct from Plasmodium and have remained in a different genus because they lack the defining feature of asexual development in the blood, known as erythrocytic schizogony [3]. The presence of macroscopic exo-erythrocytic schizonts (merocysts) in the liver of the vertebrate host is the most prominent feature of Hepatocystis [3]. Similar to Plasmodium parasites, Hepatocystis merocysts yield many single-celled merozoites. However, unlike Plasmodium, Hepatocystis merocysts appear to be the only replication phase in the vertebrate host [4]. First generation merozoites of Plasmodium spp. are released from liver cells and invade red blood cells, where they multiply asexually, before erupting from red cells as secondary merozoites. These merozoites invade further red blood cells before some develop into stages that can be transmitted to the vector. In contrast, liver merozoites of Hepatocystis spp. are thought to commit to the development of gametocyte transmission stages directly upon invading red blood cells. They are then vectored not by mosquitoes, but by biting midges of the genus Culicoides [5]. After fertilisation, Hepatocystis ookinetes encyst in the head and thorax of the midge between muscle fibres, whereas Plasmodium ookinetes encyst in the midgut wall of mosquitoes. After maturation, oocysts of both Plasmodium and Hepatocystis rupture and release sporozoites that migrate to the salivary glands [1]. These discrete biological differences, in the face of phylogenetic similarity and many shared biological features, make Hepatocystis a potentially powerful comparator for understanding important aspects of malaria parasite biology, such as transmission and host specificity.

A population of red colobus monkeys (Piliocolobus tephrosceles), from Kibale National Park, Uganda were previously shown to host Hepatocystis parasites based on morphological identification of infected red blood cells and DNA sequencing of the cytochrome b gene [6]. In this work we use Hepatocystis sp. genome and transcriptome sequences derived from P. tephrosceles whole blood samples to generate a draft genome sequence and gain insights into Hepatocystis evolution. We go on to use these insights to explore key aspects of malaria parasite biology such as red blood cell invasion, gametocytogenesis and parasite-vector interactions.
Results

Genome assembly and annotation

While examining a published genomic sequence generated from the whole blood of a red colobus monkey (Piliocolobus tephrosceles) in Kibale National Park, Uganda (NCBI assembly ASM277652v1), we noticed the presence of sequences with significant similarity to Plasmodium spp. We hypothesised that this represented genomic material from a bloodborne parasite captured during the sequencing process and for each contig in the assembly we examined the AT-content and sequence similarity to Plasmodium spp. and macaque (Fig 1A). We identified a substantial subset of contigs that appeared to be derived from an apicomplexan parasite. Phylogenetic analysis, using an orthologue of cytochrome b from these contigs, suggested that they represent the first substantial genomic sequence from the genus Hepatocystis (Fig 1B), a parasite previously reported in Kibale National Park that infects at least four species of Old World monkeys [6]. At least four species of Hepatocystis are known to infect African monkeys—H. kochi, H. simiae, H. bouqueti and H. cercopithec i [6]—but with little sequence data currently linked to morphological identification, it was not possible to determine the species. We have thus classified the parasite as Hepatocystis sp. ex Piliocolobus tephrosceles (hereafter Hepatocystis sp.; NCBI Taxonomy ID: 2600580). The extraction of the Hepatocystis sp. sequences from the P. tephrosceles assembly yielded a set of 11,877 scaffolds with a total size of 26.26 Mb and an N50 of 2.4 kb. Automated genome annotation with Companion [7] identified 2,967 genes and 1,432 pseudogenes in these scaffolds. To improve upon this assembly, we isolated putative Hepatocystis sp. reads from the original short read DNA sequencing data. These were assembled into a draft quality nuclear genome assembly of 19.95 Mb, comprising 2,439 contigs with an N50 of 18.3 kb (Table 1). The GC content (22.05%) was identical to that of Plasmodium spp. infecting rodents, and slightly higher than P. falciparum (19.34%). We identified 5,341 genes, compared to 5,441 in P. falciparum and 5,049 in P. berghei, suggesting a largely complete gene set (Table 1; S1 Table). Despite the fragmented nature of the assembly, we were able to identify synteny with P. falciparum around centromeres (S1 Fig) and evidence of clustering of contingency gene families (S2 Fig), as seen in most Plasmodium species.

Phylogenetic position of Hepatocystis sp. ex. Piliocolobus tephrosceles

There is consensus that Hepatocystis spp. are nested within the Plasmodium genus [2,8,9], however their placement within the genus has not been robustly determined. Indeed, our cytochrome b phylogeny confirms that our assembled genome is that of a Hepatocystis species, but it provides little support for the placement of this genus in relation to Plasmodium spp. A phylogeny generated using all mitochondrially encoded protein sequences also provided little support for key nodes (S3 Fig; see GitHub page for all sequence alignment data). The mitochondrial genome is therefore not reliable for determining the species phylogeny. A phylogeny based on 18 apicoplast proteins was more robust and placed Hepatocystis sp. as an outgroup to the Plasmodium species infecting rodents (Vinckeia; S4 Fig). We wanted to reliably place Hepatocystis sp. relative to other Hepatocystis species. Limited sequence data are available for Hepatocystis outside of this study. However, 11 nuclear genes have been sequenced for H. epomophori, a parasite of bats [2]. Based on the sequence of these genes, we found that Hepatocystis sp. forms a sister group to H. epomophori (S5 Fig). Furthermore, the Hepatocystis genus again forms a sister group to the Vinckeia subgenus of Plasmodium, although the tree contains some ambiguous branch points. To improve the robustness of the placement of Hepatocystis sp. within Plasmodium, we used 2673 orthologous nuclear genes from each of 12 species across the Plasmodium genus, which robustly places Hepatocystis sp. as a sister clade to the...
Plasmodium species infecting rodents (subgenus Vinckeia; Fig 2). Interestingly, some Vinckeia species (P. cyclopsi) also infect bats, supporting an earlier suggestion that the ancestor of
Hepatocystis and Vinckeia might have infected bats [10]. However, whole-genome data also suggest that Vinckeia is derived from a group of monkey-infecting parasites [11]. Hepatocystis sp. has a long branch that could indicate rapid evolution after splitting from its ancestor with Vinckeia.

**In vivo transcriptome data supports a lack of erythrocytic schizogony**

Transcriptome sequencing of blood samples from 29 individuals was performed as part of the red colobus monkey genome sequencing project [12]. We found evidence that each of these individuals was infected with the same species of Hepatocystis as found in the genomic reads, consistent with high prevalence of this parasite in Kibale red colobus monkeys [6]. The extremely low SNP density suggested that parasites from different red colobus individuals were highly related (Fig 3A). We identified an average of 1.36 SNPs (standard deviation = 0.47) and 0.43 indels (standard deviation 0.15) per 10 kb of genome when calling variants using RNA-seq reads.

Although it is believed that Hepatocystis spp. do not undergo erythrocytic schizogony [3], this has been challenged by limited microscopic evidence for asexual stages in the blood [13]. To determine whether there was transcriptomic evidence for schizonts in the blood we
deconvoluted the *Hepatocystis* sp. transcriptomes using transcriptome profiles representing different *Plasmodium* life stages. We found no such evidence, but observed varying proportions of cells identified as early blood stages (rings/trophozoites) and mature gametocytes (Fig 3B; S6 Fig; S2 Table). It is thought that chronic infections (of up to 15 months) may be maintained from continual development in the liver [3]. The presence of early blood stages in these individuals may therefore reflect this continual production of new blood forms, rather than recent infection. Proportions of rings and trophozoites were positively correlated and both these forms correlated negatively with female gametocytes (Fig 3C). Interestingly, the inferred proportions of male and female gametocytes were not strongly correlated suggesting there might be variation in commitment rates of gametocytes to male or female development.

**Expanded and novel gene families**

The largest gene family in *Hepatocystis* sp. was a novel family, which we have named *Hepatocystis*-specific family 1 (*hep1*; Table 2). These 12 single-exon genes (plus four pseudogenes) each encode proteins of ~250 amino acids, beginning with a predicted signal peptide (S7A Fig). We could find no significant sequence similarity to genes from any other sequenced genome (using HHblits [14]). However, they contain a repeat region with striking similarity to that in *Plasmodium kahrp*, a gene involved in presenting proteins on the red blood cell surface [15]. Three members were highly expressed in *in vivo* blood stages, with one correlating well with the presence of early stages (S8A Fig; HEP_00211100, Pearson’s r = 0.80 with rings).

---

**Fig 2. Whole genome phylogeny and key features of the *Hepatocystis* genome.** A whole-genome phylogenetic tree is combined with a graphical overview of key features of *Hepatocystis* and *Plasmodium* species (genome versions from August 2019). The maximum likelihood phylogenetic tree of *Hepatocystis*, *Plasmodium* and *Haemoproteus* species is based on an amino acid alignment of 2673 single copy orthologs encoded by the nuclear genome. Bootstrap support values of all nodes were 100, except for one node where the value was 79. The rooting of the tree at *Hae. tartakovskyi* is based on previously published *Plasmodium* phylogenetic trees [11,45]. TRAP—thrombospondin-related anonymous protein. RBP protein—reticulocyte binding protein.

[Link to original article](https://doi.org/10.1371/journal.ppat.1008717.g002)
Another novel family, hep2, contained N-terminal PEXEL motifs, suggesting it is exported (S7B Fig). Distinct parts of its sequence showed similarity (albeit with low significance) to exported proteins from P. malariae (PmUG01_00051800; probability: 77.88% HHblits) and P. ovale curtisi (PocGH01_00025800; 78.47%) as well as a gene in P. gallinaceum (PGAL8A_00461100; 69.52%). Three or four members were highly expressed in blood stages in vivo, with one member highly correlated with predicted proportions of early blood stages (S8B Fig; HEP_00165500, Pearson’s r = 0.83 with rings; HEP_00480100, Pearson’s r = 0.77 with rings).

The gene encoding Thrombospondin-Related Anonymous Protein (trap) is involved in infection of salivary glands and liver cells by Plasmodium sporozoites. It is found strictly in a single copy in all Plasmodium species sequenced to date. However, it is present in six copies in Hepatocystis sp., suggesting that trap-mediated aspects of sporozoite-host interactions may be

Table 2. Size of known and novel gene families in Hepatocystis sp. in comparison to its relatives.

| Gene Family | Hepatocystis sp. | Plasmodium falciparum 3D7 | P. berghei ANKA | P. vivax P01 | Haemoproteus tartakovskyi |
|-------------|------------------|---------------------------|-----------------|--------------|--------------------------|
| ApiAP2 transcription factors | 27 | 27 | 26 | 27 | 20 |
| Hepatocystis-specific family 1 (hep1) | 16 (includes 4 pseudogenes) | 0 | 0 | 0 | 0 |
| Hepatocystis-specific family 2 (hep2) | 10 (includes 4 pseudogenes) | 0 | 0 | 0 | 0 |
| cpw-wpc | 8 | 9 | 9 | 9 | 8 |
| 6-cysteine proteins | 7 | 14 | 13 | 15 (includes 1 pseudogene) | 22 |
| lcl | 6 | 6 | 6 | 6 | 6 |
| Thrombospondin-Related Anonymous Protein (trap) | 6 | 1 | 1 | 1 | 1 |
| pir | 5 (includes 1 pseudogene) | 0 | 218 (includes 83 pseudogenes) | 1212 (includes 109 pseudogenes) | 0 |
| Serine repeat antigen (SERA) | 5 (1 pseudogene) | 9 | 5 | 13 | 2 |
| early transcribed membrane protein (etramp) | 4 | 15 | 7 | 10 | 1 |
| exported protein 1 (exp1) | 4 (includes 2 pseudogenes) | 1 | 1 | 1 | 0 |
| Tryptophan-rich antigen | 4 | 4 (includes 1 pseudogene) | 11 (includes 4 pseudogenes) | 40 | 0 |
| Lysophospholipase | 2–4 | 6 (includes 1 pseudogene) | 5 (includes 2 pseudogenes) | 7 (includes 1 pseudogene) | 1 |
| Phist domain-containing | 2 | 81 (includes 19 pseudogenes) | 3 | 82 (includes 6 pseudogenes) | 3 |
| fam-a | 1 | 1 | 74 (includes 26 pseudogenes) | 1 | 1 (partial) |
| Reticulocyte binding protein (Rhi/rbp) | 0 | 7 | 15 | 10 | 0 |

https://doi.org/10.1371/journal.ppat.1008717.t002
more complex. None of these genes were highly expressed in blood stage transcriptomes, consistent with their known role in sporozoites. Exported protein 1 (e.g. PF3D7_1121600) is a single copy gene in all Plasmodium species. It encodes a Parasitophorous Vacuolar Membrane (PVM) protein and is important for host-parasite interactions in the liver [16]. In Hepatocystis sp. it is expanded to four copies.

**Missing orthologues tend to be involved in erythrocytic schizontogony**

The genomes of Plasmodium spp. each contain large families of genes known or thought to be involved in host parasite interactions [17]. These include, amongst others the var, rif and stevor genes in the Laverania subgenus, SICAvar genes in P. knowlesi and the pir genes across the genus. We find only four intact pir genes and a single pir pseudogene in Hepatocystis sp., compared to ~200–1000 in Plasmodium spp. infecting rodents. One was particularly highly expressed in the blood stages from most monkeys that were sampled (S8C Fig; HEP_00069900). All of these are most similar to the ancestral pir subfamily, present in single copy in Vinckeia species and in 19 copies in P. vivax P01 (Table 2; S9 Fig). The best described role for pir genes is in Vinckeia parasites, where they are involved in establishing chronic infections in mice [18]. Given that asexual Hepatocystis parasites are not thought to exist in the blood of monkeys or bats, there would be no need for this function of pir genes. However, in Vinckeia, pir genes are expressed in several other stages, including male gametocytes [19], which do feature in the Hepatocystis lifecycle. The function of the ancestral pir gene subfamily is unknown, although it is expressed at multiple stages of the lifecycle in P. berghei [20].

We wanted to determine, more generally, the types of genes that might have been lost in Hepatocystis sp. relative to Plasmodium spp. This is made difficult due to uncertainty in determining missingness in a draft genome. We overcame this problem using clusters of genes identified as having common expression patterns across the lifecycle of the close Hepatocystis relative P. berghei [20]. Cluster 10 (late schizont expression; Fisher’s Exact test odds ratio = 0.09, FDR = 0.0002) tended to contain orthologues shared by P. berghei, P. ovale wallikeri and P. vivax, but not Hepatocystis sp. (Fig 4; S3 Table; S10 Fig). Eleven out of 25 orthologues missing in the late schizont cluster (including two pseudogenes) encoded Reticulocyte Binding Proteins (RBPs). In fact, we could not identify any RBPs in the Hepatocystis sp. genome or Hepatocystis sp. RNA-seq assemblies. Interestingly, counter to previous suggestions [21], we found no evidence for RBP sequences in the Hae. tartakovskyi genome sequence. However, we did find fragmentary sequences with significant sequence similarity to RBPs from malaria parasites with avian hosts in transcriptome assemblies of Leucocytozoon buteonis [22] and Hae. columbae [23] (S11 Fig). Also missing from this cluster was Cdpk5, a kinase that regulates parasite egress from red cells [24]. The other principal gene families involved in erythrocyte binding and invasion by Plasmodium are the erythrocyte binding ligands (eh)/duffy-binding protein (dbp) and the merozoite surface protein (msp) families [25]. These are largely conserved relative to P. berghei. Thus, orthologues missing relative to Plasmodium spp. tend to be involved in erythrocytic schizontogony, the part of the life cycle also absent.

**The most rapidly evolving genes are often involved in vector biology and control of gene expression**

Our whole-genome phylogeny (Fig 2) showed a long Hepatocystis sp. branch, suggesting that some genes have changed extensively in Hepatocystis compared to Plasmodium spp. This might indicate functional changes important for the particular biology of Hepatocystis. We found previously that the ratio of synonymous mutations to synonymous sites (dS) saturates between Plasmodium clades [45] and therefore considered the ratio of non-synonymous
Hepatocystis genome illuminates malaria parasite biology

Fig 4. Hepatocystis sp. orthologues of genes which are highly expressed in late schizont stages in P. berghei tend to be missing from the genome. P. berghei gene expression clusters from the Malaria Cell Atlas were used to determine whether orthologous genes, conserved with P. vivax and P. ovale, but absent in Hepatocystis, tended to be expressed in particular parts of the life cycle. The only significant cluster was cluster 10, which includes genes most highly expressed in late schizont stages (highlighted by a red box). The top panels show the log2 observed/expected ratios for orthologous genes in each cluster which are shared between P. berghei and Hepatocystis and the same ratio for those which are shared between P. berghei, P. vivax and P. ovale, but not Hepatocystis sp. Cluster 1, 18, 19 and 20 were not tested because they contained fewer than 2 expected counts for either ratio. The asterisk indicates a Fisher’s exact test false discovery rate of < 0.05.

https://doi.org/10.1371/journal.ppat.1008717.g004

mutations (dN) rather than the more commonly used dN/dS. We first looked for enrichment of conserved protein domain families in genes with the highest 1% of dN values. There was an enrichment for the AP2 domain (Pfam:PF00847.20; Fisher test with BH correction; p-value = 0.01). Most Plasmodium species possess 27 ApiAP2 transcription factors containing this domain, which are thought to be the key players in control of gene expression and parasite development across the life cycle. AP2-G plays an important role in exiting the cycle of schizogony and commitment to gametocytogenesis in Plasmodium spp. [26,27], whereas, as demonstrated, Hepatocystis sp. lacks erythrocytic schizogony. Hepatocystis spp. also form much larger cysts in the liver (giving the genus its name) and develop in different tissues within a different insect vector compared to Plasmodium spp. Our Hepatocystis sp. assembly contained orthologues of all 27 ApiAP2 genes present in P. falciparum (Table 2). This suggests that life cycle differences between Plasmodium and Hepatocystis spp. are not reflected in gain or loss of these key transcription factors. However, the relatively high rate of non-synonymous mutations suggests there may have been significant adjustment in how these transcription factors act. To determine parts of the life cycle that were enriched for the most rapidly evolving genes, we looked at whether particular gene expression clusters from the Malaria Cell Atlas [19,20] were enriched for genes with high dN (top 5% of values; Table 3; S12A Fig; S4 Table). We found that three clusters (2, 4 and 6) had fewer genes with high dN than expected by chance (Fisher’s exact test with Holm multiple hypothesis testing correction, p-value < 0.05) and that these contained genes expressed across much of the life cycle, especially growth phases. These clusters also tended to contain essential genes expected to be highly conserved in Hepatocystis sp. Although there was not a significant trend for gametocyte-associated genes having higher than average dN, the top 5% of genes ranked by dN contained several putative gametocyte genes (Table 3). Two of these encode putative 6-cysteine proteins P47 and P38, the first required for female gamete fertility [28]. Additionally, Merozoite TRAP-like protein (MTRAP), essential for Plasmodium gamete egress from erythrocytes [29] and two genes (HEP_00254800 and HEP_00195400) with orthologues involved in osmiophilic body formation [30,31] had high dN values. Overall, clusters involved in ookinete (15) and general mosquito stages (16) had significantly higher values than other clusters (Kolmogorov-Smirnov test: Cluster 15 vs all other clusters: D = 0.42, p-value = 1.05e-05. Cluster 16 vs all other clusters: D = 0.52, p-value = 4.50e-12; S12B Fig). This is also reflected in the Hepatocystis sp. genes with the highest dN values, which include oocyst rupture protein 2 (orp2; dN = 1.08), ap2-o, ap2-sp2, secreted ookinete protein (psop7) and osmiophilic body protein (g377). These genes provide clues about changes in the parasite that might relate to its adaptation to transmission by biting midges, rather than mosquitoes.

Discussion

We have taken advantage of parasite reads captured as part of a primate genome sequencing study in order to assemble and annotate a draft quality genome sequence for a species of Hepatocystis. Our nuclear and apicoplast genome phylogenies confirm the recently proposed phylogenetic placement of this genus as an outgroup to the rodent-infecting Vinckeia subgenus of
Plasmodium [2]. However, a distinct branching pattern and low bootstrap support for many nodes in our mitochondrial genome phylogeny highlights why some previous analyses have come to different conclusions about the placement of Hepatocystis. Thus, the use of mitochondrial genes to infer phylogenetic relationships between species within the Haemosporidia should be approached with caution. We found a long branch leading to Hepatocystis sp.,

### Table 3. Top 15 genes with functional annotations ranked by Hepatocystis sp. dN in comparison of Hepatocystis sp., P. berghei ANKA and P. ovale curtisi.

| Gene id          | Hepatocystis dN | P. berghei dN | P. ovale dN | Annotations                                      | Rank | Putative function                                                                 |
|------------------|-----------------|---------------|-------------|--------------------------------------------------|------|----------------------------------------------------------------------------------|
| HEP_00146800     | 1.08            | 0.21          | 0.42        | Oocyst rupture protein 2 (ORP2)                   |      | Sporozoite egress from the oocyst [32]                                          |
| PBANKA_1303400   |                 |               |             |                                                  |      |                                                                                  |
| PocGH01_12075300 |                 |               |             |                                                  |      |                                                                                  |
| HEP_00446500     | 0.71            | 0.19          | 0.34        | Liver specific protein 2 (LISP2)                  | 19   | Involved in liver stage development [33]                                       |
| PBANKA_1003000   |                 |               |             |                                                  |      |                                                                                  |
| PocGH01_03012800 |                 |               |             |                                                  |      |                                                                                  |
| HEP_00295100     | 0.71            | 0.31          | 0.63        | AP2-O                                            | 20   | Essential for morphogenesis in ookinete stage in Plasmodium [34]               |
| PBANKA_0905900   |                 |               |             |                                                  |      |                                                                                  |
| PocGH01_09049300 |                 |               |             |                                                  |      |                                                                                  |
| HEP_00035800     | 0.69            | 0.27          | 0.16        | 6-cysteine protein (p38)                         | 24   | P. berghei p38 is expressed in gametocytes and in asexual blood stages [28]  |
| PBANKA_1107600   |                 |               |             |                                                  |      |                                                                                  |
| PocGH01_10033500 |                 |               |             |                                                  |      |                                                                                  |
| HEP_00213800     | 0.67            | 0.45          | 0.63        | AP2 domain transcription factor AP2-SP2          | 28   | Required for sporozoite production in Plasmodium [35]                           |
| PBANKA_1001800   |                 |               |             |                                                  |      |                                                                                  |
| PocGH01_03011500 |                 |               |             |                                                  |      |                                                                                  |
| HEP_00037100     | 0.62            | 0.36          | 0.42        | AP2 domain transcription factor ApiAP2           | 40   | Involved in blood stage replication [35,36]                                     |
| PBANKA_0112100   |                 |               |             |                                                  |      |                                                                                  |
| PocGH01_11043100 |                 |               |             |                                                  |      |                                                                                  |
| HEP_00456700     | 0.62            | 0.61          | 0.38        | Merozoite TRAP-like protein (MTRAP)               | 42   | Essential for gamete egress from erythrocytes [29]                              |
| PBANKA_0512800   |                 |               |             |                                                  |      |                                                                                  |
| PocGH01_06021700 |                 |               |             |                                                  |      |                                                                                  |
| HEP_00304800     | 0.62            | 0.32          | 0.26        | Secreted ookinete protein (PSOP7)                | 43   | Secreted ookinete proteins are necessary for invasion of the mosquito midgut [37] |
| PBANKA_1353400   |                 |               |             |                                                  |      |                                                                                  |
| PocGH01_12023100 |                 |               |             |                                                  |      |                                                                                  |
| HEP_00254800     | 0.59            | 0.26          | 0.26        | Microgamete surface protein MiGS                | 54   | Plays a critical role in male gametocyte osmiophilic body formation and exflagellation [30] |
| PBANKA_1449000   |                 |               |             |                                                  |      |                                                                                  |
| PocGH01_14060000 |                 |               |             |                                                  |      |                                                                                  |
| HEP_00115700     | 0.55            | 0.41          | 0.15        | Merozoite surface protein 4 (MSP4)               | 62   | Merozoite surface proteins are involved in red blood cell invasion [38]        |
| PBANKA_0304400   |                 |               |             |                                                  |      |                                                                                  |
| PocGH01_04023000 |                 |               |             |                                                  |      |                                                                                  |
| HEP_00166600     | 0.54            | 0.36          | 0.2         | Repetitive organellar protein (ROPE)             | 64   | Localised to the apical end of merozoites, possibly involved in red blood cell invasion [39] |
| PBANKA_0301000   |                 |               |             |                                                  |      |                                                                                  |
| PocGH01_04026800 |                 |               |             |                                                  |      |                                                                                  |
| HEP_00195400     | 0.54            | 0.24          | 0.26        | Osmiophilic body protein (G377)                  | 67   | Female-specific protein, affects the size of the osmiophilic body and female gamete egress efficiency [31] |
| PBANKA_1463000   |                 |               |             |                                                  |      |                                                                                  |
| PocGH01_14074600 |                 |               |             |                                                  |      |                                                                                  |
| HEP_00134000     | 0.53            | 0.17          | 0.11        | Thioredoxin 2 (TRX2)                            | 75   | Part of a protein complex in parasitophorous vacuolar membrane, required for pathogenic protein secretion into host [40], important for maintaining normal blood-stage growth [41] |
| PBANKA_1358000   |                 |               |             |                                                  |      |                                                                                  |
| PocGH01_12018800 |                 |               |             |                                                  |      |                                                                                  |
| HEP_00391300     | 0.52            | 0.49          | 0.27        | Autophagy-related protein 11 (ATG11)            | 76   | Predicted to be involved in cargo selection in selective autophagy [42]        |
| PBANKA_0313400   |                 |               |             |                                                  |      |                                                                                  |
| PocGH01_04013500 |                 |               |             |                                                  |      |                                                                                  |
| HEP_00155500     | 0.52            | 0.18          | 0.17        | Metacaspase-2                                    | 80   | Protease with caspase-like activity [43]                                       |
| PBANKA_1302300   |                 |               |             |                                                  |      |                                                                                  |
| PocGH01_12076400 |                 |               |             |                                                  |      |                                                                                  |

https://doi.org/10.1371/journal.ppat.1008717.t003
suggesting a relatively deep split from the rodent-infecting species. In addition, we showed robustly that *Hepatocystis* sp. clusters, as expected, with *Hepatocystis epomophori*, which infects bats. This finding supports the polyphyly of the *Plasmodium* parasites infecting apes, monkeys and rodents but the monophony of *Hepatocystis* itself. A close relative of rodent-infecting *P. berghei* (*P. cyclops*) has been found in bats [10] and thus the *Hepatocystis/Vinckeia* group represents a relatively labile group with respect to host preference. Indeed, the possibility of cross-species transmission of *Hepatocystis* sp. was reported previously [6].

The paraphyly of *Plasmodium* with respect to *Hepatocystis* exists because *Hepatocystis* spp. lack a defining characteristic of the *Plasmodium* genus, namely erythrocytic schizogony—axial development in the blood. Thus, the very part of the *Plasmodium* life cycle which causes the symptoms of malaria is thought to be absent in *Hepatocystis*. While multiple lines of enquiry have failed to identify these forms (Garnham, 1966) there has remained some doubt, with reports of cells with schizont-like morphology in the blood for some species [13,44]. We were able to take advantage of bulk RNA-seq data collected from blood samples of a number of red colobus monkeys, all apparently infected with very closely related *Hepatocystis* parasites. By comparing to single-cell RNA-seq data from known cell types, we found no evidence for schizont stages in the blood. The apparent lack of schizonts could be due to sequestration of these stages away from the bloodstream. This is seen in some *Plasmodium* species, so we cannot rule out schizogony away from peripheral circulation. However, in its current state, this lack of evidence supports the idea that erythrocytic schizogony has been lost three times: in *Hepatocystis, Polychromophilus* and *Nycteria* [2]. Ancestrally, gametocytogenesis must have been the default developmental pathway, being required for transmission. However, in *Plasmodium*, it seems that erythrocytic schizogony became the default developmental pathway with epigenetic control of the ApiAP2-G transcription factor, required for development into sexual stages [26,27]. Perhaps the simplest explanation for a loss of erythrocytic schizogony would be that ApiAP2-G is no longer under control, but is constitutively expressed in parasites leaving the liver. In line with this idea we find ApiAP2-G present and highly expressed in blood stage *Hepatocystis* sp. Furthermore, all *Plasmodium* ApiAP2 transcription factors are conserved in *Hepatocystis* sp., indicating that changes in its life cycle are not associated with their loss or gain.

The lack of erythrocytic schizogony is supported by a tendency for orthologous genes missing in *Hepatocystis* sp. (relative to *Plasmodium* spp.) to be those expressed in blood schizonts. The most noticeable example is the complete absence of the Reticulocyte Binding Protein (RBP) family, found across all *Plasmodium* spp. examined so far, including those which infect birds [45]. RBP proteins are known to function as essential red blood cell invasion ligands in *Plasmodium falciparum* [46] and multiple copies are thought to provide alternative invasion pathways [25]. However, previous transcriptomic data have suggested that, while *rbp* genes in *P. berghei* are highly expressed in schizonts, they are less abundant or have a distinct repertoire in liver stages [20,47,48]. This implies that RBPs are less important, or at least that distinct invasion pathways are used by first generation merozoites. Also missing were *cdpk5* (involved in schizont egress) and *msp9* (an invasion related gene enriched in blood vs. liver schizonts in Caldelari et al. [47]). Taken together, these results underscore the increasing realisation that first generation merozoites have distinct properties from merozoites that have developed in the blood and suggest the way in which first generation merozoites invade red blood cells may be distinct. Looking more widely across the *Haemosporidia*, we found scant evidence for RBPs outside of the *Plasmodium* genus. There were no matches at all in the draft genome sequence of the relatively close *Plasmodium* outgroup *Haemoproteus tartakovskyi*. However, there were fragmentary matches to RBPs from *Plasmodium* species infecting birds in transcriptome assemblies of *Ha. columbae* and the more distant *Leucocytozoon buteonis*. The *Ha. columbae*
fragment aligned to a conserved region of this divergent family, suggesting it could encode some core function of RBPs. More complete genome sequences from across the haemosporidians will be needed to understand the evolution of this gene family, which seems to be key for understanding the host specificity of Plasmodium parasites [49].

The genomes of Plasmodium spp. each contain large, rapidly evolving gene families that are known, or thought to be involved in host-parasite interactions, principally in asexual blood stages. The reason for their numbers may be due to a bet-hedging strategy, providing the diversity necessary for evading adaptive immune responses or dealing with unpredictable host variation. Although the Hepatocystis sp. genome contains two novel multigene families, we identified only 10–15 copies of each. The largest gene families in the closely related rodent-infecting Plasmodium species (pir and fam-a) are present here only as their ancestral orthologues, also conserved in the monkey-infecting Plasmodium species. We should be cautious in noting a lack of expansion in such families in Hepatocystis sp., as previous draft Plasmodium genome sequences have been shown to under-represent these genes. However, it is perhaps not surprising that pir genes are poorly represented. They are thought to play a role in the maintenance of chronic infections mediated by asexual stages in the blood [18] and Hepatocystis infection does not involve this stage of development. Given that Hepatocystis can sustain long chronic infections [1], presumably from the liver, this parasite may help us to better understand how Plasmodium survives in the liver.

A striking feature of the Hepatocystis life cycle is its vector—a biting midge rather than a mosquito. We found evidence of rapid evolution amongst orthologues of Plasmodium genes involved in mosquito stages of development, suggesting that adaptation to a new insect vector was a major evolutionary force. These rapidly evolving genes provide insights into parasite-vector interactions and may provide avenues for the development of interventions to prevent transmission of the malaria parasite.

Overall, our findings demonstrate the insights that can be gained into malaria parasite biology from relatives of Plasmodium, even with draft-quality genome sequences. In the future, we expect that high-quality genome sequences of Hepatocystis spp., and additional relatives from genera such as Nycteria, Haemoproteus, and Polychromophilus, will be of great value for understanding the evolution and molecular biology of one of humanity’s greatest enemies.

Methods

Ethics statement

All animal research was approved by the Uganda Wildlife Authority (permit number UWA/TDO/33/02), the Uganda National Council for Science and Technology (permit number HS 364), and the University of Wisconsin-Madison Animal Care and Use Committee (V005039) prior to initiation of the study. Biological materials were shipped internationally under CITES permit #002290 (Uganda). The animal was anesthetized with a combination of Ketamine (5 mg/kg) and Xylazine (2 mg/kg) administered intramuscularly using a variable-pressure air rifle (Pneudart, Inc, Williamsport, PA, USA). After sampling, the animal was given a reversal agent (Atipamezole, 0.5 mg/kg), and released after recovery back to its social group. All animal use followed the guidelines of the Weatherall Report on the use of non-human primates in research.

Sample collection and data generation

The sequence data used in this study were part of a project originally designed to generate a reference genome for the red colobus monkey (genus Piliocolobus). Biomaterials used were from wild Ugandan (or Ashy) red colobus monkey (Piliocolobus tephrosceles) individuals from
Kibale National Park, Uganda. These animals reside in a habituated group that has been a focus of long-term studies in health, ecology, and disease [12,50,51]. Red colobus individuals were immobilised in the field as previously described [52]. Whole blood was collected using a modified PreAnalytiX PAXgene Blood RNA System protocol as described in Simons et al. [12]. Additionally, whole blood was collected into BD Vacutainer Plasma Preparation Tubes, blood plasma and cells were separated via centrifugation, and both were subsequently aliquoted into cryovials and stored in liquid nitrogen. Samples were transported to the United States in an IATA-approved liquid nitrogen dry shipper and then transferred to −80 °C for storage until further processing.

Methods for DNA extraction, library preparation, and whole genome sequencing are described in Simons [53]. Briefly, high molecular weight DNA was extracted from the blood cells of one red colobus monkey individual and size selected for fragments larger than 50,000 base pairs. A 10X Genomics Chromium System library preparation was performed and subsequently sequenced on two lanes of a 150 bp paired-end Illumina HiSeqX run as well as two lanes of a 150 bp paired-end Illumina HiSeq 4000 run.

Methods for RNA extraction and library preparation are described in Simons et al. (2019). Briefly, RNA was extracted from 29 red colobus individuals using a modified protocol for the PreAnalytiX PAXgene Blood RNA Kit protocol. Total RNA extracts were concentrated, depleted of alpha and beta globin mRNA, and assessed for integrity (RIN mean: 8.1, range: 6.6–9.2). Sequencing libraries were prepared using the KAPA Biosystems Stranded mRNA-seq Kit and sequenced on four partial lanes of a 150 bp paired-end Illumina HiSeq 4000 run. These data were uploaded to NCBI as part of BioProject PRJNA413051.

**Separation of Hepatocystis and Piliocolobus scaffolds**

The *Piliocolobus tephrosceles* genome assembly (ASM277652v1) was downloaded from the NCBI database. Scaffolds were first sorted by their GC% and Diamond 0.9.22 [54] BLASTX hits against a database of representative apicomplexan and Old World monkey proteomes. The sorting was improved by examining mapping scores of the scaffolds mapped to *Plasmodium* species and *Macaca mulatta* genomes (Mmul_8.0.1, GenBank assembly accession GCA_000772875.3) using Minimap2 2.12 [55]. The separation of scaffolds was further verified and refined by running NCBI BLAST of 960 bp fragments of all scaffolds against the NCBI nt database (Jul 18 2017 version) [56]. To predict genes in the apicomplexan scaffolds, Companion automatic annotation software [7] was run with these scaffolds as input and the *P. vivax* P01 genome as the reference.

**Identification of Hepatocystis sequences in Piliocolobus RNA-seq data**

Illumina HiSeq 4000 RNA-seq reads from the study PRJNA413051 were downloaded from the European Nucleotide Archive. In order to find out if the RNA-seq data contained apicomplexan sequences, mapping of these reads to apicomplexan scaffolds from *Piliocolobus tephrosceles* genome assembly (ASM277652v1) was done using HISAT2 2.1.0 [57].

**Hepatocystis genome assembly**

**Filtering of reads for assembly.** Minimap2 [55] and Kraken 2.0.8-beta [58] were used to identify the best matching species for each 10x Chromium genomic DNA read (from Illumina HiSeq X and HiSeq4000 platforms). Our Kraken database contained 17 Old World monkey genomes and 19 *Plasmodium* genomes downloaded from NCBI FTP in June 2018 [56]. The Kraken database also included the contigs of the *P. tephrosceles* assembly ASM277652v1, separated into *P. tephrosceles* and *Hepatocystis* sp. *Plasmodium malariae* UG01 (from PlasmoDB...
version 39) and *Macaca mulatta* (Mmul_8.0.1) assemblies were used as reference genomes for the assignment of reads based on Minimap2 mapping scores. Reads that were unambiguously identified as monkey sequences using Kraken and Minimap2 were excluded from subsequent assemblies. The Supernova assembler manual [60] warns against exceeding 56x coverage in assemblies. Reads selected for Supernova assemblies were therefore divided into 34 batches, with ~10 million reads in each batch. Reads were ordered by their barcodes so that those with the same barcode would preferentially occur in the same batch.

**Supernova and SPAdes assemblies.** We generated 34 assemblies with Supernova v2.1.1 with default settings. In addition, two SPAdes v3.11.0 [61] assemblies with default settings were generated with *Hepatoctysis* reads: one with HiSeq X reads and another with HiSeq 4000 reads. Chromium barcodes were removed from the reads before the SPAdes assemblies.

**Deriving the mitochondrial sequence.** *Hepatoctysis* Supernova and SPAdes assembly contigs were mapped to the *P. malariae* UG01 genome from PlasmoDB version 40 with Minimap2. The sequences of contigs that mapped to the *P. malariae* mitochondrion were extracted using SAMTools 0.1.19-44428cd [62] and BEDtools v2.17.0 [63]. The contigs were oriented and then aligned using Clustal Omega 1.2.4 [64]. Consensus sequence of aligned contigs was derived using Jalview 2.10.4b1 [65]. The consensus sequence was circularised with Circlator minimus2 [66].

**Canu assembly.** Scaffolds from the Supernova assemblies were broken into contigs. All contigs from the Supernova and SPAdes assemblies were pooled and used as the input for Canu assembler 1.6 [67] in place of long reads. Canu assembly was done without read correction and trimming stages. The settings for Canu were as follows: assemble genomeSize = 23000k minReadLength = 300 minOverlapLength = 250 corMaxEvidenceE-rate = 0.15 correctedErrorRate = 0.16 stopOnReadQuality = false -nanopore-raw.

**Processing of Canu unassembled sequences file.** Selected contigs from the Canu unassembled sequences output file (*.unassembled.fasta) were recovered and pooled with assembled contigs (*.contigs.fasta). The first step in the filtering of the contigs of the unassembled sequences file was to exclude contigs that had a BLAST match in the assembled sequences output file (with E value cutoff 1e-10). Next, contigs where low complexity sequence content exceeded 50% (detected using Dustmasker 1.0.0 [68]) were removed. Contigs with GC content higher than 50% were also removed. Diamond BLASTX (against a database of *Macaca mulatta*, *P. malariae* UG01, *P. ovale* wallikeri, *P. falciparum* 3D7 and *P. vivax* P0 proteomes) and BLAST (using the nt database from Jul 18 2017 and nr database from Jul 19 2017) were then used to exclude all contigs where the top hits were not an apicomplexan species. In total, 0.34% of contigs from the unassembled sequences file were selected to be included in the assembly.

**Deduplication of contigs.** Initial deduplication of contigs was done using BBTools dedupe [69] (Nov 20, 2017 version) and GAP5 v1.2.14-r3753M [70] autojoin. In addition, BUSCO 3.0.1 [71] was used to detect duplicated core genes with the protists dataset. Two contigs flagged by BUSCO as containing duplicated genes were removed. All vs all BLAST of contigs (with E-value cutoff 1e-20, minimum overlap length 100 bp, minimum identity 85%) was used to find possible cases of remaining duplicated contigs. Contigs yielding BLAST hits were aligned with MAFFT v7.205 [72] and the alignments were manually inspected. Contained contigs were deleted and contigs that had unique overlaps with high identity were merged into consensus sequences using Jalview.

**Removal of contaminants after Canu assembly.** All Canu assembly contigs were checked with Diamond against a database of *Macaca mulatta*, *P. malariae* UG01, *P. ovale* wallikeri, *P. falciparum* 3D7 and *P. vivax* P01 proteomes. The Diamond search did not detect any contaminants. Contigs not identified by Diamond were checked with BLAST against the nt database.
(Jul 18 2017 version). Contigs where the top BLAST hit was a human or monkey sequence were removed from the assembly.

A subset of contigs in the assembly was observed to consist of short sequences with low complexity, high GC% and low frequency of stop codons. These contigs did not match any sequences by BLAST search against nt and nr databases (with E-value cutoff 1e-10). Due to their difference from the rest of the contigs in the assembly, it was assumed that these contigs were contaminants rather than Hepatocystis sequences. In order to programmatically find these contigs, GC%, tandem repeats percentage, percentage of low complexity content and frequency of stop codons were recorded for all contigs in the assembly. Tandem Repeats Finder 4.04 [73] was used to assess tandem repeats percentage and Dustmasker 1.0.0 [68] was used to find low complexity sequence content. PCA and k-means clustering (using R version 3.5.1) showed that the assembly contigs separated into two groups based on these parameters. The group of contigs with low complexity (189 contigs) was removed from the assembly.

**Scaffolding and polishing of Canu assembly contigs.** Before scaffolding, contigs were filtered by size to remove sequences shorter than 200 bp. Hepatocystis RNA-seq reads were extracted from RNA-seq sample SAMN07757854 using Kraken 2. Canu assembly contigs were scaffolded with these reads using P_RNA_scaffolder [74]. To correct scaffolding errors, the scaffolds were processed with REAPR 1.0.18 [75] using 197819014 unbarcoded Hepatocystis DNA read pairs. REAPR was run with the perfectmap option and -break b = 1. Next, the assembly was scaffolded using Scaff10x (https://github.com/wtsi-hpg/Scaff10X) version 3.1, run for 4 iterations with the following settings: -matrix 4000 -edge 1000 -block 10000 -long-read 0 -link 3 -reads 5. 197,819,014 Hepatocystis DNA read pairs were used for Scaff10x scaffolding. After this, P_RNA_scaffolder was run again as above. This was followed by running Tigmint 1.1.2 [76] with 419,652,376 Hepatocystis read pairs to correct misassemblies. fill_gaps_with_gapfiller (https://github.com/sanger-pathogens/assembly_improvement/blob/master/bin/fill_gaps_with_gapfiller) was used to fill gaps in scaffolds, using 197819014 unbarcoded Hepatocystis DNA read pairs. After this, ICORN v0.97 [77] was run for 5 iterations with 4608740 Hepatocystis read pairs. This was followed by polishing the assembly with Pilon 1.19 [78] using 21,794,613 Hepatocystis read pairs. Assembly completeness was assessed with CEGMA v2.5 [79]. *P. berghei* ANKA, *P. ovale curtisi* and *P. falciparum* 3D7 genomes from PlasmoDB release 45 were also assessed with CEGMA with the same settings in order to compare the Hepatocystis assembly with *Plasmodium* assemblies.

**Curation and annotation of the Hepatocystis genome assembly**

The assembly was annotated using Companion [7]. The alignment of reference proteins to target sequence was enabled in the Companion run but all other parameters were left as default. A GTF file derived from mapping of Hepatocystis RNA-seq reads of three biological samples (SAMN07757854, SAMN07757861 and SAMN07757872) to the assembly was used as transcript evidence for Companion. To produce the GTF file, the RNA-seq reads were mapped to the assembly using 2-pass mapping with STAR RNA-seq aligner [80] (as described in the "Variant calling of RNA-seq samples" section) and the mapped reads were processed with Cufflinks [81]. All *Plasmodium* genomes available in the web version of Companion were tested as the reference genome for annotating the Hepatocystis genome, in order to find out which reference genome yields the highest gene density. For the final Companion run the *P. falciparum* 3D7 reference genome (version from June 2015) was used. The Companion output was manually curated using Artemis [82] and ACT [83] version 18.0.2. Manual curation was carried out to correct the overprediction of coding sequences, add missing genes and correct exon-intron boundaries. Altogether 680 gene models were corrected, 546 genes added and 221 genes
deleted. RNA-seq data was used as supporting evidence. Non-coding RNAs were predicted with Rfam [84].

All genes were analysed for the presence of a PEXEL-motif using the updated HMM algorithm ExportPred v2.0 [85]. Distant homology to hep1 and hep2 gene families was sought by using the HHblits webserver with default options [14].

The reference genomes used to produce statistics on features of Plasmodium genomes in Fig 2 and Table 1 were as follows: P. relictum SGS1, P. gallinaceum 8A [45], P. malariae UG01, P. ovale wallikeri, P. ovale curtisi GH01 [11], P. knowlesi H [86], P. vivax P01 [87], P. cynomolgi M [88], P. chabaudi AS [18], P. berghei ANKA [89], P. reichenowi CDC [90], P. falciparum 3D7 [91].

For S1 Table, transmembrane domains of proteins were predicted using TMHMM 2.0 [92]. Conserved domains were detected in proteins using HMMER i1.1rc3 (http://hmmer.org/) and Pfam-A database release 28.0 [93], with E-value cutoff 1e-5. Besides predicting exported proteins with ExportPred 2 [85], matches to PEXEL consensus sequence (RxLxE/Q/D) were counted in protein sequences using string search in Python. Signal peptides were detected using SignalP-5 [94].

Analysis of other Haemosporidian genomes and transcriptomes

Genomes and transcriptomes of other Haemosporidians. A Haemoproteus tartakovskyi genome assembly was downloaded from the Malavi database (http://130.235.244.92/Malavi/Downloads/Haemoproteus_tartakovskyi). The Companion annotation tool [7] was used to automatically annotate the assembly, using the P. falciparum 3D7 genome as the reference. The alignment of reference proteins to target sequence was enabled and the rest of the settings were left as default. The genome annotation was further edited manually using Artemis 18.1.0 [82].

A transcriptome assembly of Haemoproteus columbae [23] was downloaded from GenBank (GenBank ID GGWD00000000.1). Illumina MiSeq reads of Leucocytozoon and its host Buteo buteo were downloaded from the European Nucleotide Archive (study PRJEB5722). The reads from all four samples were processed with Cutadapt 2.7 (http://journal.embnet.org/index.php/embnetjournal/article/view/200) to remove artificial Illumina sequences and then assembled with SPAdes v3.13.1 [95] with the—rna flag. Contigs from the transcripts.fasta and soft_filtered_transcripts.fasta output files of SPAdes were pooled. Leucocytozoon contigs were separated from the contigs of Buteo buteo and bacterial contaminants using Diamond 0.9.24 [54], BLAST and Minimap2 2.17-r941 [55], similarly with how Hepatocystis contigs were isolated from the Pilocolobus assembly ASM277652v1. GAP5 1.2.14-r [70] was used to join the Leucocytozoon assembly contigs by unique overlaps. The Leucocytozoon assembly contigs were then polished using Pilon 1.23 [78] (3 iterations).

The completeness of the Haemoproteus and Leucocytozoon assemblies was assessed using CEGMA 2.5 [79]. The CEGMA completeness statistics for these Haemosporidian assemblies were the following. Haemoproteus tartakovskyi genome assembly: Completeness Complete: 64.52%, Completeness Partial: 68.55%. Haemoproteus columbae transcriptome assembly: Completeness Complete: 37.90%, Completeness Partial: 57.26%. Leucocytozoon buteonis transcriptome assembly: Completeness Complete 25.40%, Completeness Partial 35.08%.

BLAST searches for RBPs. A BLAST database was made from Plasmodium RBPs downloaded from PlasmoDB [96] (release 46). NCBI blastx 2.9.0+ with e-value cutoff 1e-5 was run against this database, using the Plasmodium genome and transcriptome assemblies and the Leucocytozoon transcriptome assembly as queries. The transcripts that yielded BLAST hits were further examined using BLAST against the NCBI nt and nr databases (April 2020 versions) and by sequence alignments with RBPs from PlasmoDB. One of the Haemoproteus transcripts
matched RBPs in the blastx search (the best match was with PRELSG_0
014300: E-value 1.31e-23, score: 89.0) and did not yield non-RBP BLAST hits in searches against
the nt and nr databases. One Leucocytozoon transcript also matched Plasmodium RBPs (top
match: PRELSG_0013000, E-value 1.06e-09, score: 56.2). The sequence of the Haemoproteus
transcript GGWD01016989.1 was translated to amino acids using ExPAsy Translate (April 2020
version) [97] and then aligned with a selection of Plasmodium RBPs from PlasmoDB (release 46)
using MAFFT 7 [98] with default settings. The resulting alignment was cropped in Jalview
2.10.4b1 to include only the region that contained the Haemoproteus sequence [99]. A phylo-
genetic tree was generated from the alignment as described in the next section.

Phylogenetic trees

Haemosporidian sequences were downloaded from NCBI FTP and PlasmoDB (release 43).
The phylogenetic tree of cytochrome B and the tree that included 11 Hepatocystis epomophori
genes were based on DNA alignments. The cytochrome B tree also included cytochrome B
sequences from de novo assemblies of Hepatocystis RNA-seq reads derived from Piliocolobus
tephrrodoces blood. The trees of mitochondrial, apicoplast and nuclear proteomes were based
on protein alignments. For apicoplast proteome and nuclear proteome trees, orthologous pro-
teins were identified using OrthoMCL 1.4 [100]. The OrthoMCL run included the Haemopro-
teus tartakovskyi proteome that had been derived from the Haemoproteus tartakovskyi
genome assembly using Companion, as previously described. All vs all BLAST for OrthoMCL
was done using blastall 2.2.25 with E-value cutoff 1e-5. OrthoMCL was run with mode 3. Pro-
teins with single copy orthologs across all the selected species were used for the protein phylo-
genetic trees. Sequences were aligned with MAFFT 7.205 [98] (with—auto flag) and the
alignments were processed using Gblocks 0.91b [101] with default settings. Individual
Gblocks-processed alignments were concatenated into one alignment. The phylogenetic trees
were generated using IQ-TREE multicore version 1.6.5 [102] with default settings and plotted
using FigTree 1.4.4 (https://github.com/rambaut/figtree/releases). Inkscape (https://inkscape.
org) version 0.92 was used to edit text labels of the phylogenetic trees generated with FigTree.

Clustering of pir proteins into subfamilies

Sequences of Plasmodium pir family proteins (including bir, cyir, kir, vir and yir proteins) were
downloaded from PlasmoDB [59] (release 39). The sequences were clustered using MCL
[103], following the procedures described in the section "Clustering similarity graphs encoded
in BLAST results" in clmprotocols (https://micans.org/mcl/man/clmprotocols.html). The
BLAST E-value cutoff used for clustering was 0.01 and the MCL inflation value was 2. The pir
protein counts per subfamily in each species were plotted as a heatmap using the heatmap.2
function in gplots package version 3.0.1.1 in R version 3.5.1.

Mapping and assembly of Hepatocystis sp. RNA-seq data

To separate Hepatocystis reads from Piliocolobus reads, RNA-seq data from the ENA (study
PRJNA413051) were mapped to a FASTA file containing genome assemblies of Hepatocystis
and M. mulatta (NCBI assembly Mmul_8.0.1), using HISAT2 version 2.1.0 [57], with "—rna-
strandness RF". BED files were generated from the mapped reads using BEDTools 2.17.0 [63].
Reads from each technical replicate were merged, resulting in a single set of read counts for
each individual monkey. The BED files were filtered to remove multimapping reads and reads
with mapping quality score lower than 10. Names of reads that specifically mapped to the
Hepatocystis assembly were extracted from the BED file. SeqTK 1.0-r31 (https://github.com/
lh3/seqtk) was used to isolate Hepatocystis FASTQ reads based on the list of reads from the
previous step. The Hepatocystis reads were then mapped to the Hepatocystis genome assembly using HISAT2 2.1.0 with "—rna-strandness RF" flag. The SAM files with mapped reads were converted to sorted BAM files with SamTools 0.1.19-44428cd 62. The EMBL file of Hepatocystis genome annotations was converted to GFF format using Artemis 18.0.1 82. Htsq-count 0.7.1 104 was used to count mapped reads per gene in the GFF file with "-t mRNA -a 0 -s reverse". Htsq-count files of individual RNA-seq runs were merged into a single file.

In order to extract Hepatocystis cytochrome b sequences of each RNA-seq sample, Hepatocystis RNA-seq reads of each sample were isolated from Piliocolobus reads as described above and then assembled with the SPAdes assembler v3.11.0 105 with the "—rna" flag. Hepatocystis cytochrome b contigs were identified in each of the 29 RNA-seq assemblies using BLAST against Hepatocystis cytochrome b from the DNA assembly (E-value cutoff 1e-10).

In addition to assemblies of individual RNA-seq samples, an assembly of all RNA-seq samples pooled was done. The reads for this assembly were sorted by competitive mapping to P. ovale curtisi GH01 (from PlasmoDB release 45) and Macaca mulatta (Mmul_8.0.1, GenBank assembly accession GCA_000772875.3) genomes with Minimap2 (with the "-ax sr" flag). Reads mapping to the Macaca mulatta genome with minimum mapping score 20 were removed and the rest of the reads were assembled with the SPAdes assembler v3.13.1 105 with the "—rna" flag. Hepatocystis contigs were identified by comparison of sequences with Plasmodium and Macaca mulatta reference genomes using Diamond, Minimap2 and BLAST, similarly to what is described in the section "Separation of Hepatocystis and Piliocolobus scaffolds". Further decontamination was done using Diamond and BLAST searches against 19747 sequences from Ascomycota and 165860 bacterial sequences downloaded from UniProt (release 2019_10) 106 and 3 Babesia proteomes from PiroplasmaDB (release 46) 107. Selected contigs were also checked with BLAST against the NCBI nt database. The assembly was deduplicated using BBTools dedupe (Nov 20, 2017 version) and GAP5 v1.2.14-r3753M. Assembly completeness was assessed using CEGMA 2.5. In order to reduce the number of contigs so that they could be used as input for Companion, the assembly was scaffolded with RaGOO Version 1.1 108, using the Hepatocystis DNA assembly as the reference. The assembly was then processed by the Companion annotation software (Glasgow server, November 2019 version, with P. falciparum 3D7 reference genome, with protein evidence enabled and the rest of the settings left as default). In order to detect proteins missed by Companion, EMBOSS Transeq (version 6.3.1) was used to translate the transcriptome assembly in all 6 reading frames. The output of Transeq was then filtered to keep sequences between stop codons with minimum length of 240 amino acids. Protein BLAST with E-value cutoff 1e-20 was used to detect sequences in Transeq output that were not present in the proteins annotated by Companion. These selected Transeq output sequences were checked for contaminants with BLAST similarly to what was described before. The sequences that passed the contaminant check were combined with the set of Hepatocystis RNA-seq assembly proteins that were detected by Companion. OrthoMCL was run with proteins from Hepatocystis RNA-seq assembly (Companion and selected Transeq sequences combined), Hepatocystis DNA assembly proteins, 20 Plasmodium proteomes from PlasmoDB release 43 and P. ovale wallikeri proteome (GenBank GCA_900090025.2). The settings for OrthoMCL were as described in the "Phylogenetic trees" section.

dN analysis

P. berghei ANKA and P. ovale curtisi protein and transcript sequences were retrieved from PlasmoDB 59 (release 45). One-to-one orthologs between Hepatocystis, P. berghei ANKA and P. ovale curtisi were identified using OrthoMCL 100 and a Newick tree of the three species was generated with IQ-TREE 102. The settings for OrthoMCL and IQ-TREE were as
described in the "Phylogenetic trees" section. Transcripts of one-to-one orthologs were aligned using command line version of TranslatorX [109] with "-p F -t T" flags, so that each alignment file contained sequences from three species. Gaps were removed from alignments while retaining the correct reading frame. Alignment regions where the nucleotide sequence surrounded by gaps was shorter than 42 bp were also removed. In addition, the script truncated alignments at the last whole codon if a sequence ended with a partial codon due to a contig break. The alignments and the Newick tree of the 3 species were then used as input for codeml [110] in order to determine the dN and dN/dS of each alignment. The codeml settings that differed from default settings were: seqtype = 1, model = 1. *P. berghei* RNA-seq cluster numbers from Malaria Cell Atlas [20] were assigned to each alignment based on the *P. berghei* gene in the alignment. Transcriptomics-based gametocyte specificity scores of *Plasmodium* genes were taken from an existing study on this topic [111] (transcripts S2 Table of "Transcriptomics_all_-studies" tab). The *P. falciparum* genes in the gametocyte specificity scores table were matched with equivalent *Hepatocystis* genes using OrthoMCL (run with the same settings as when used for phylogenetic trees). Statistical tests with the dN results (Kolmogorov Smirnov test, Fisher test and Spearman correlation) were performed using the *stats* library in R.

**Variant calling of RNA-seq samples**

SNPs and indels were called in *Hepatocystis* RNA-seq reads that had been separated from *Pilio-colobus* reads as described above. Four technical replicates of each RNA-seq sample were pooled. Variant calling followed the "Calling variants in RNAseq" workflow in GATK [112] user guide (https://gatkforums.broadinstitute.org/gatk/discussion/3891/calling-variants-in-rnaseq). First, the reads were mapped to the reference genome using 2-pass mapping with the STAR RNA-seq aligner [80] version 2.5.3a. 2-pass mapping consisted of indexing the genome with genomeGenerate command, aligning the reads with the genome, generating a new index based on splice junction information contained in the output of the first pass and then producing a final alignment using the new index. GATK [112] version 4.0.3.0 was used for the next steps. The mapped reads were processed with GATK MarkDuplicates and SplitNCigarReads commands. GATK HaplotypeCaller was then run with the following settings: -dont-use-soft-clipped-bases—emit-ref-confidence GVCF—sample-ploidy 1—standard-min-confidence-threshold-for-calling 20.0. Joint genotyping of the samples was then done using GATK CombineGVCFs and GenotypeGVCFs commands. This was followed by running VariantFiltration with these settings: -window 35 -cluster 3—filter-name FS -filter 'FS > 30.0'—filter-name QD -filter 'QD < 2.0'. SNPs were separated from indels using GATK SelectVariants. Samples SAMN07757853, SAMN07757863, SAMN07757870 and SAMN07757873 were excluded from further analysis due to their low expression of *Hepatocystis* genes (htseq-count reported below 50,000 reads mapped to the *Hepatocystis* assembly in each of these samples). The average filtered SNP counts per 10 kb of reference genome for each sample were calculated as the number of filtered SNPs divided by (genome size in kb + 10).

**RNA-seq deconvolution**

Deconvolution of a bulk RNA-seq transcriptome sequence aims to determine the relative proportions of different cell types in the original sample. This requires a reference dataset of transcriptomes from “pure” cell types. To create this, we used single-cell *P. berghei* transcriptome sequences from the Malaria Cell Atlas [20]. For each cell type, single-cell transcriptome sequences were combined by summing read counts per gene to generate a set of pseudobulk transcriptome sequences (see our GitHub repository). The aim of summing across cells is to reduce the number of dropouts which are common in individual single-cell transcriptome
sequences. Bulk *Hepatocystis* RNA-seq transcriptome sequences, mapped and counted as above, were summed across replicates and filtered to exclude those with fewer than 100,000 reads. *Hepatocystis* and *P. berghei* pseudobulk read counts were converted to Counts Per Million (CPM) and *Hepatocystis* gene ids were converted to those of *P. berghei* one-to-one orthologues. Genes without one-to-one orthologues (defined by orthoMCL analysis) were excluded. CIBERSORT v1.06 [113] was used to deconvolute the *Hepatocystis* transcriptomes with the MCA pseudobulk as the signature matrix file. To test the accuracy of this deconvolution process we generated mixtures of the pseudobulk resulting in e.g. equal representation of read counts from male gametocyte, female gametocyte, ring, trophozoite and schizont pseudobulk transcriptomes (see our GitHub repository). We also deconvoluted bulk RNA-seq transcriptomes from Otto et al. [89] processed as in Reid et al. [19].

**Enrichment of missing genes in Malaria Cell Atlas gene clusters**

We wanted to determine whether there were functional patterns common to orthologues missing from the *Hepatocystis* genome relative to *Plasmodium* species. To do this we looked for orthologous groups (orthoMCL as above) containing genes from *P. berghei*, *P. ovale wallikeri* and *P. vivax* P01, but not *Hepatocystis*. Genes from *P. berghei* have previously been assigned to 20 clusters based on their gene expression patterns across the whole life cycle [20]. We looked to see whether missing orthologues tended to fall into particular clusters more often than expected by chance (see our GitHub repository). We used Fisher’s exact test with Benjamini-Hochberg correction to control the false discovery rate. We reported clusters with FDR \( > 0.05 \).

**Supporting information**

**S1 Fig. Conservation of synteny in the core regions of the assembly.** ACT (Artemis Comparison Tool) screenshot showing a comparison of centromere-proximal regions of *Hepatocystis* scaffold 132, *P. falciparum* 3D7 (Pf3D7) chromosome 4 and *P. vivax* (PvP01) chromosome 5. The red blocks represent sequence similarity (tBLASTx). The centromere is shown in green. Coloured boxes represent genes. The graph shows the GC-content. (TIF)

**S2 Fig. Organization of putative subtelomeric regions of *Hepatocystis* scaffold 67, scaffold 211, *P. knowlesi* H chromosome 4 and *P. falciparum* 3D7 chromosome 9.** Exons are shown in coloured boxes with introns as linking lines. ‘//’ represents a gap. The shaded/grey areas in *P. knowlesi* and *P. falciparum* mark the start of the conserved, syntenic regions to other *Plasmodium* species. The presence of genes that are subtelomeric in *Plasmodium* species, i.e. PHIST proteins, suggests that the *Hepatocystis* scaffolds are also subtelomeric. A complete subtelomere that includes telomeric repeats is missing in our *Hepatocystis* assembly. Thus, whether *Hepatocystis* chromosomes retain the organisation common to most *Plasmodium* species remains unclear. (TIF)

**S3 Fig. Phylogenetic tree of *Haemosporidian* mitochondrial proteins.** *Hepatocystis* sp. ex. *Piliocolobus tephrosceles* (this work, marked with red arrow) appears next to a previously sequenced *Hepatocystis* sample from the flying fox *Pteropus hypomelanus* (NCBI accession FJ168565.1). Branches of the tree have been coloured by bootstrap support values from 45 (red) to 100 (green). Bootstrap values below 100 have also been added to the figure as text. (TIF)
S4 Fig. Phylogenetic tree of 18 apicoplast protein sequences of *Plasmodium* spp. and *Hepatocystis*. Branches of the tree have been coloured by bootstrap support values from 66 (red) to 100 (green). Bootstrap values below 100 have also been added to the figure as text. (TIF)

S5 Fig. Phylogenetic tree of 11 nuclear genes of *Hepatocystis* and *Plasmodium* species. Genes of *Hepatocystis* sp. ex *Piliocolobus tephrosceles* are highly similar to *Hepatocystis epomophori* genes sequenced in a different study [2]. The tree is based on the following genes: splicing factor 3B subunit 1, tubulin gamma chain, DNA polymerase delta catalytic subunit, eukaryotic translation initiation factor 2 gamma subunit, T-complex protein 1 subunit alpha, pantothenate transporter, ribonucleoside-diphosphate reductase large subunit, aminophospholipid-transporting P-ATPase, GCN20, transport protein Sec24A and RuVBLike helicase 3. Branches of the tree have been coloured by bootstrap values from 73 (red) to 100 (green). Bootstrap values below 100 have also been added to the figure as text. The red arrow points to the *Hepatocystis* sample from the current study. (TIF)

S6 Fig. Deconvolution using CIBERSORT and the Malaria Cell Atlas accurately determines the presence and absence of different *Plasmodium* life stages in bulk RNA-seq data. (A) Pre-defined mixtures of pseudobulk RNA-seq data were deconvoluted with very high accuracy. (B) Real samples of *P. berghei* bulk RNA-seq from Otto et al (2014) were deconvoluted showing almost pure mixtures of gametocyte, ookinete or asexual stages as expected. The low proportions of expected parts of the IDC in each asexual sample may result from differences between what the MCA defines as a ring/trophozoite/schizont and what would microscopically be defined as such. (TIF)

S7 Fig. Multiple sequence alignments of two *Hepatocystis*-specific gene families. (A) Alignment of *Hepatocystis*-specific gene family 1 (*hep1*). Pseudogenes (HEP_00099300, HEP_00250500, HEP_00323900) were not included in the alignment. HEP_00353700 is 476 amino acids long and was truncated here. (B) Alignment of *Hepatocystis*-specific gene family 2 (*Hep2*). This gene family contains a PEXEL motif (marked with a black box). Pseudogenes (HEP_00165000, HEP_00165200, HEP_00324000, HEP_00489100) were not included in the alignment. (TIF)

S8 Fig. Heatmaps of *Hepatocystis* gene family expression in the blood of its mammalian host. (A) Expression levels (log vst-normalised) of *hep1* genes across blood samples from multiple red colobus monkeys. The estimated proportions of early blood stages (rings/trophozoites) and mature gametocytes are highlighted above. (B) Expression levels of *hep2* genes (C) Expression levels of *pir* genes. (TIF)

S9 Fig. Heatmap of *pir* protein subfamilies in *Hepatocystis* and *Plasmodium* species. Rows correspond to species and columns correspond to *pir* subfamilies. The columns have been ordered by the number of sequences in each subfamily and the order of rows is approximately based on phylogeny. Colours represent the numbers of proteins belonging to each subfamily for each species. All *Hepatocystis pir* proteins belong to the only subfamily conserved across all these species [114] (indicated with red arrow). (TIF)
S10 Fig. Some orthologues missing in *Hepatocystis* sp. relative to *Plasmodium* species show common gene expression patterns across the *Plasmodium* life cycle. (A) Malaria Cell Atlas (MCA) gene cluster 10 represents genes highly expressed in late schizonts. 25 genes from this cluster were conserved in *P. ovale* wallikeri and *P. vivax*, but were missing from our *Hepatocystis* genome assembly. Genes were clustered here by expression pattern and single-cells were ordered by pseudotime as in [20]. (B) MCA cluster 4 represents genes highly expressed across much of the life cycle—liver stages, trophozoites, female gametocytes and ookinetes/oocysts. 27 genes from this cluster were conserved in *P. ovale* wallikeri and *P. vivax*, but were missing from our *Hepatocystis* genome assembly.

(TIF)

S11 Fig. Alignment of phylogenetic tree of putative RBP-related gene fragment in *Haemoproteus columbae*. (A) Alignment of the translation of a sequence (GGWD01016989.1) from *Haemoproteus columbae* transcriptome assembly (GenBank: GGWD00000000.1) [23] with *Plasmodium* reticulocyte-binding proteins (RBPs) from PlasmoDB [115]. The alignment has been cropped to the length of the *Haemoproteus columbae* sequence. (B) Phylogenetic tree of *Plasmodium* RBPs and the *Haemoproteus columbae* sequence GGWD01016989.1, based on the alignment in panel A. Branch colours indicate bootstrap support values, from 33 (red) to 100 (green).

(TIF)

S12 Fig. Distributions of *Hepatocystis* dN values in Malaria Cell Atlas (MCA) clusters. *Hepatocystis* dN was calculated in 3-way comparison between *Hepatocystis*, *P. berghei* ANKA and *P. ovale* curtisi using codeml. The Malaria Cell Atlas clusters have been described in Fig 2B in the article on Malaria Cell Atlas [20]. (A) *Hepatocystis* genes with dN in the top 5%: observed versus expected ratios for Malaria Cell Atlas clusters. *Hepatocystis* genes that correspond to Malaria Cell Atlas clusters 2, 4 and 6 have less genes with dN rank in the top 5% than expected by chance (Fisher exact test p-value < 0.05). None of the MCA clusters contain significantly more genes ranked in the top 5% of dN than expected by chance, although there is a trend towards clusters 15 and 16 having higher dN. (B) Boxplot of all *Hepatocystis* dN values per each Malaria Cell Atlas cluster. Distribution of values in clusters 15 and 16 differs from the rest of the clusters. Kolmogorov-Smirnov test statistics are the following. Cluster 15 vs all other clusters: D = 0.42, p-value = 1.05e-05. Cluster 16 vs all other clusters: D = 0.52, p-value = 4.50e-12. Clusters 15 and 16 combined vs all other clusters: D = 0.46, p = 2.33e-15.

(TIF)

S1 Table. Summary of gene properties. For each gene in the assembly, the following is listed: annotation, number of exons, gene length (bp), the presence or absence of start and stop codons (reflecting the completeness of the assembly of the gene) and RNA-seq expression level (mean FPKM with standard deviation) in sample SAMN07757854 (RC106R). For the proteins encoded by the genes, the table shows the number of transmembrane segments predicted by TMHMM, ExportPred 2 score, 1 to 1 orthologs in *P. berghei* ANKA and *P. ovale* curtisi GH01 (based on OrthoMCL), PFAM domains, the number of matches to PEXEL motif (RxLxE/Q/D) and SignalP-5 signal peptide prediction.

(XLSX)

S2 Table. Raw and normalised *Hepatocystis* gene expression data.

(XLSX)

S3 Table. *Plasmodium* orthologues missing in the *Hepatocystis* genome assembly. *Plasmodium berghei* genes, which have an orthologue in *P. ovale curtisi* or *P. vivax*, but not the
Hepatocystis sp. DNA (A) or RNA-seq (B) assemblies and are enriched in Malaria Cell Atlas gene clusters.

(S4 Table. Genes with Hepatocystis dN rank in the top 5% in codeml 3-way comparison between Hepatocystis, P. berghei ANKA and P. ovale curtisi GH01. The total number of genes in dN analysis was 4009, out of which 200 correspond to 5%. The table includes Malaria Cell Atlas cluster numbers for each gene.

(Aknowledgments

We would like to thank Alan Tracey for advice on genome assembly and J. Byaruhanga, P. Katurama, A. Mbabazi, A. Nyamwija, J. Rusoke, D. Hyeroba and G. Weny and the staff of Makerere University Biological Field Station for assistance in the field. Manoj Duraisingh provided helpful comments on the manuscript.

Author Contributions

Conceptualization: Theo Sanderson, Adam J. Reid.
Data curation: Eerik Aunin, Ulrike Böhme.
Formal analysis: Eerik Aunin, Adam J. Reid.
Investigation: Eerik Aunin, Ulrike Böhme, Noah D. Simons, Adam J. Reid.
Project administration: Tony L. Goldberg, Nelson Ting, Colin A. Chapman.
Resources: Tony L. Goldberg, Nelson Ting, Colin A. Chapman.
Software: Eerik Aunin, Adam J. Reid.
Supervision: Nelson Ting, Matthew Berriman, Adam J. Reid.
Visualization: Eerik Aunin, Ulrike Böhme, Adam J. Reid.
Writing – original draft: Eerik Aunin, Ulrike Böhme, Theo Sanderson, Adam J. Reid.
Writing – review & editing: Eerik Aunin, Ulrike Böhme, Theo Sanderson, Noah D. Simons, Tony L. Goldberg, Nelson Ting, Colin A. Chapman, Chris I. Newbold, Matthew Berriman, Adam J. Reid.

References

1. Garnham PCC. Malaria parasites and other haemosporidia. Blackwell Scientific; 1966.
2. Galen SC, Borner J, Martinsen ES, Schær J, Austin CC, West CJ, et al. The polyphyly of Plasmodium: comprehensive phylogenetic analyses of the malaria parasites (order Haemosporida) reveal widespread taxonomic conflict. R Soc Open Sci. 2018; 5: 171780. https://doi.org/10.1098/rsos.171780 PMID: 29892372
3. Garnham PCC. The developmental cycle of Hepatocystis (Plasmodium) kochi in the monkey host. Trans R Soc Trop Med Hyg. 1948; 41: 601–616. https://doi.org/10.1016/0035-9203(48)90418-0 PMID: 18912187
4. Perkins SL, Schær J. A Modern Menagerie of Mammalian Malaria. Trends Parasitol. 2016; 32: 772–782. https://doi.org/10.1016/j.pt.2016.06.001 PMID: 27492115
5. Garnham PCC, Heisch RB, Minter DM, Others. The Vector of Hepatocystis (= Plasmodium) kochi; the Successful Conclusion of Observations in Many Parts of Tropical Africa. Trans R Soc Trop Med Hyg. 1961; 55: 497–502. https://doi.org/10.1016/0035-9203(61)90071-2 PMID: 13897017
6. Thurer Mi, Ghai RR, Hyeroba D, Weny G, Turnukunde A, Chapman CA, et al. Co-infection and cross-species transmission of divergent Hepatocystis lineages in a wild African primate community. Int J Parasitol. 2013; 43: 613–619. https://doi.org/10.1016/j.ijpara.2013.03.002 PMID: 23603520

7. Steinbiss S, Silva-Franco F, Brunk B, Foth B, Hertz-Fowler C, Berriman M, et al. Companion: a web server for annotation and analysis of parasite genomes. Nucleic Acids Res. 2016; 44: W29–34. https://doi.org/10.1093/nar/gkw292 PMID: 27105845

8. Boundenga L, Ngoubangoye B, Mombo IM, Tsoubmou TA, Renaud F, Rougeron V, et al. Extensive diversity of malaria parasites circulating in Central African bats and monkeys. Ecol Evol. 2018; 8: 10578–10586. https://doi.org/10.1002/eco3.4539 PMID: 30464829

9. Chang Q, Sun X, Wang J, Yin J, Song J, Peng S, et al. Identification of Hepatocystis species in a macaque monkey in northern Myanmar. Res Rep Trop Med. 2011; 2: 141–146. https://doi.org/10.2147/RRTM.S27182 PMID: 30881188

10. Schauer J, Perkins SL, Decher J, Leendertz FH, Fehr J, Weber N, et al. High diversity of West African bat malaria parasites and a tight link with rodent Plasmodium taxa. Proc Natl Acad Sci U S A. 2013; 110: 17415–17419. https://doi.org/10.1073/pnas.1311016110 PMID: 24101466

11. Rutledge GG, Böhme U, Sanders M, Reid AJ, Cotton JA, Maiga-Ascofare O, et al. Plasmodium malariae and P. ovale genomes provide insights into malaria parasite evolution. Nature. 2017; 542: 101–104. https://doi.org/10.1038/s21038 PMID: 28117441

12. Simons ND, Eick GN, Ruiz-Lopez MJ, Hyeroba D, Omeja PA, Weny G, et al. Genome-Wide Patterns of Gene Expression in a Wild Primate Indicate Species-Specific Mechanisms Associated with Tolerance to Natural Simian Immunodeficiency Virus Infection. Genome Biol Evol. 2019; 11: 1630–1643. https://doi.org/10.1093/gbe/evz099 PMID: 31068820

13. Schaer J, Perkins SL, Ejotre I, Vodzak ME, Matuschewski K, Reeder DM. Epaulleted fruit bats display exceptionally high infections with a Hepatocystis species complex in South Sudan. Sci Rep. 2017; 7: 6928. https://doi.org/10.1038/s41598-017-07093-z PMID: 28761151

14. Remmert M, Biegert A, Hauser A, Söding J. HHblits: lightning-fast iterative protein sequence searching by HMM-HMM alignment. Nat Methods. 2011; 9: 173–175. https://doi.org/10.1038/nmeth.1818 PMID: 22198341

15. Looker O, Blanch AJ, Liu B, Nunez-Iglesias J, McMillan PJ, Tilley L, et al. The knob protein KAHRP assembles into a ring-shaped structure that underpins virulence complex assembly. PLoS Pathog. 2019; 15: e1007761. https://doi.org/10.1371/journal.ppat.1007761 PMID: 31071194

16. Sá E, Cunha C, Nyboer B, Heiss K, Sanches-Vaz M, Fontinha D, Wiedtke E, et al. Plasmodium berghei EXP-1 interacts with host Apolipoprotein H during Plasmodium liver-stage development. Proc Natl Acad Sci U S A. 2017; 114: E1138–E1147. https://doi.org/10.1073/pnas.1606419114 PMID: 28137845

17. Reid AJ. Large, rapidly evolving gene families are at the forefront of host–parasite interactions in Apicomplexa. Parasitology. 2015; 142: S57–S70. https://doi.org/10.1017/S0031182014001528 PMID: 25257746

18. Brugat T, Reid AJ, Lin J, Cunningham D, Turnwine I, Kushinga G, et al. Antibody-independent mechanisms regulate the establishment of chronic Plasmodium infection. Nat Microbiol. 2017; 2: 16276. https://doi.org/10.1038/s41564-016-0052 PMID: 28165471

19. Reid AJ, Talman AM, Bennett HM, Gomes AR, Sanders MJ, Illingworth CJR, et al. Single-cell RNA-seq reveals hidden transcriptional variation in malaria parasites. eLife. 2018; 7. https://doi.org/10.7554/eLife.33105 PMID: 29580379

20. Howick VM, Russell AJC, Andrews T, Heaton H, Reid AJ, Natarajan K, et al. The Malaria Cell Atlas: Single parasite transcriptomes across the complete Plasmodium life cycle. Science. 2019;365. https://doi.org/10.1126/science.aaw2619 PMID: 31497872

21. Bensch S, Carlbäck B, DeBarry JD, Johansson T, Hellgren O, Kissinger JC, et al. The Genome of Haemoproteus tartakovskyi and Its Relationship to Human Malaria Parasites. Genome Biol Evol. 2016; 8: 1361–1373. https://doi.org/10.1093/gbe/evw081 PMID: 27190205

22. Pauli M, Chakarov N, Rupp O, Kalinowski J, Goosemann A, Sorenson MD, et al. De novo assembly of the dual transcriptomes of a polymorphic raptor species and its malarial parasite. BMC Genomics. 2015; 16: 1038. https://doi.org/10.1186/s12864-015-2254-1 PMID: 26645667

23. Toscani Field J, Weinberg J, Bensch S, Matta NE, Valkiūnas G, Sehgal RNM. Delineation of the Genera Haemoproteus and Plasmodium Using RNA-Seq and Multi-gene Phylogenetics. J Mol Evol. 2018; 86: 646–654. https://doi.org/10.1007/s00239-018-9875-3 PMID: 30426144

24. Dvorin JD, Martyn DC, Patel SD, Grimsley JS, Collins CR, Hopp CS, et al. A plant-like kinase in Plasmodium falciparum regulates parasite egress from erythrocytes. Science. 2010; 328: 910–912. https://doi.org/10.1126/science.1186191 PMID: 20466936
25. Wright GJ, Rayner JC. Plasmodium falciparum erythrocyte invasion: combining function with immune evasion. PLoS Pathog. 2014; 10: e1003943. https://doi.org/10.1371/journal.ppat.1003943 PMID: 24651270

26. Sinha A, Hughes KR, Modrzyńska KK, Otto TD, Pfander C, Dickens NJ, et al. A cascade of DNA-binding proteins for sexual commitment and development in Plasmodium. Nature. 2014; 507: 253–257. https://doi.org/10.1038/nature13290 PMID: 24572359

27. Kafsack BFC, Rovira-Graills N, Clark TG, Bancells C, Crowley VM, Campino SG, et al. A transcriptional switch underlies commitment to sexual development in malaria parasites. Nature. 2014; 507: 248–252. https://doi.org/10.1038/nature12920 PMID: 24572369

28. van Dijk MR, van Schaik BCL, Khan SM, van Dooren MW, Ramesar J, Kaczanowski S, et al. Three members of the 6-cys protein family of Plasmodium play a role in gamete fertilization. PLoS Pathog. 2010; 6: e1000853. https://doi.org/10.1371/journal.ppat.1000853 PMID: 20386715

29. Bargen JD, Thibierge S, Tay CL, Carey AF, Rantz A, Hischen G, et al. Plasmodium Merozoite TRAP Family Protein Is Essential for Vacuole Membrane Disruption and Gamete Egress from Erythrocytes. Cell Host Microbe. 2016; 20: 618–630. https://doi.org/10.1016/j.chom.2016.10.015 PMID: 27832590

30. Tachibana M, Ishino T, Takashima E, Tsuboi T, Torii M. A male gametocyte osmiophilic body and microgamete surface protein of the rodent malaria parasite Plasmodium yoelii (PyMiGS) plays a critical role in male osmiophilic body formation and exflagellation. Cell Microbiol. 2018; 20: e12821. https://doi.org/10.1111/cmi.12821 PMID: 29316140

31. Olivieri A, Bertuccini L, Deligiani E, Franke-Fayard B, Currà C, Siden-Kiamos I, et al. Distinct properties of the egress-related osmiophilic bodies in male and female gametocytes of the rodent malaria parasite Plasmodium berghei. Cell Microbiol. 2015; 17: 355–368. https://doi.org/10.1111/cmi.12370 PMID: 25262869

32. Siden-Kiamos I, Pace T, Klonizakis A, Nardini M, Garcia CRS, Currà C. Identification of Plasmodium berghei Oocyst Rupture Protein 2 (ORP2) domains involved in sporozoite egress from the oocyst. Int J Parasitol. 2018; 48: 1127–1136. https://doi.org/10.1016/j.ijpara.2018.09.004 PMID: 30391497

33. Gupta DK, Dembele L, Voorberg-van der Weel A, Roma G, Yip A, Chuenchob V, et al. The Plasmodium liver-specific protein 2 (LISP2) is an early marker of liver stage development. Elife. 2019; 8. https://doi.org/10.7554/eLife.34362 PMID: 31094679

34. Yuda M, Iwanaga S, Shigenobu S, Mair GR, Janse CJ, Waters AP, et al. Identification of a transcription factor in the mosquito-invasive stage of malaria parasites. Mol Microbiol. 2009; 71: 1402–1414. https://doi.org/10.1111/j.1365-2958.2009.06609.x PMID: 19220746

35. Modrzyńska K, Pfander C, Chappell L, Yu L, Suarez C, Dundas K, et al. A Knockout Screen of ApiAP2 Genes Reveals Networks of Interacting Transcriptional Regulators Controlling the Plasmodium Life Cycle. Cell Host Microbe. 2017; 21: 11–22. https://doi.org/10.1016/j.chom.2016.12.003 PMID: 28981440

36. Jeninga MD, Quinn JE, Pettet M. ApiAP2 Transcription Factors in Apicomplexan Pathogens. Pathogens. 2019; 8. https://doi.org/10.3390/pathogens8020047 PMID: 30959972

37. Langer RC, Li F, Vinetz JM. Identification of novel Plasmodium gallinaceum zygote- and ookinete-expressed proteins as targets for blocking malaria transmission. Infect Immun. 2002; 70: 102–106. https://doi.org/10.1128/iai.70.1.102-106.2002 PMID: 11748169

38. Beeson JG, Drew DR, Boyle MJ, Feng G, Fowkes FJI, Richards JS. Merozoite surface proteins in red blood cell invasion, immunity and vaccines against malaria. FEMS Microbiol Rev. 2016; 40: 343–372. https://doi.org/10.1093/femsre/fuw001 PMID: 26833236

39. Werner EB, Taylor WR, Holder AA. A Plasmodium chabaudi protein contains a repetitive region with a predicted spectrin-like structure. Mol Biochem Parasitol. 1998; 94: 185–196. https://doi.org/10.1016/S0166-6851(98)00067-X PMID: 9747969

40. Sharma A, Sharma A, Dixit S, Sharma A. Structural insights into thioredoxin-2: a component of malaria parasite protein secretion machinery. Sci Rep. 2011; 1: 179. https://doi.org/10.1038/srep00179 PMID: 22355694

41. Matthews K, Kalanon M, Chisholm SA, Sturm A, Goodman CD, Dixon MW, et al. The Plasmodium translocon of exported proteins (PTEX) component thioredoxin-2 is important for maintaining normal blood-stage growth. Mol Microbiol. 2013; 89: 1167–1186. https://doi.org/10.1111/mmi.12334 PMID: 23869529

42. Navale R, Atul, Allanki AD, Sijwali PS. Characterization of the autophagy marker protein Atg8 reveals atypical features of autophagy in Plasmodium falciparum. PLoS One. 2014; 9: e113220. https://doi.org/10.1371/journal.pone.0113220 PMID: 25426852

43. Vandan, Singh AP, Singh J, Sharma R, Akhter M, Mishra PK, et al. Biochemical characterization of unusual cysteine protease of P. falciparum, metacaspase-2 (MCA-2). Mol Biochem Parasitol. 2018; 220: 28–41. https://doi.org/10.1016/j.molbiopara.2018.01.001 PMID: 29317266
44. Rodhain J. Plasmodium epomophori n. sp. parasite commun des Rousettes epaulieres au Congo Belge. Bull Soc Pathol Exot Filiales. 1926; 19: 828–838.
45. Böhme U, Otto TD, Cotton JA, Steinbiss S, Sanders M, Oyola SO, et al. Complete avian malaria parasite genomes reveal features associated with lineage-specific evolution in birds and mammals. Genome Res. 2018; 28: 547–560. https://doi.org/10.1101/gr.218123.116 PMID: 29500236
46. Crosnier C, Bustamante LY, Bartholdson SJ, Bei AK, Theron M, Uchikawa M, et al. Basigin is a receptor essential for erythrocyte invasion by Plasmodium falciparum. Nature. 2011; 480: 534–537. https://doi.org/10.1038/nature10606 PMID: 22080952
47. Caldelari R, Dogga S, Schmid MW, Franke-Fayard B, Janse CJ, Soldati-Favre D, et al. Transcriptome analysis of Plasmodium berghei during exo-erythrocytic development. Malar J. 2019; 18: 330. https://doi.org/10.1186/s12936-019-2968-7 PMID: 31551073
48. Preiser PR, Khan S, Costa FTM, Jarra W. Stage-specific transcription of distinct repertoires of a multigene family during Plasmodium life cycle. 2002. Available: https://science.sciencemag.org/content/295/5553/342.short https://doi.org/10.1126/science.1064938 PMID: 11786645
49. Galaway F, Yu R, Constantinou A, Prugnolle F, Wright GJ. Resurrection of the ancestral RH5 invasion ligand provides a molecular explanation for the origin of P. falciparum malaria in humans. PLoS Biol. 2019; 17: e3000490. https://doi.org/10.1371/journal.pbio.3000490 PMID: 31613878
50. Goldberg TL, Sintasath DM, Chapman CA, Cameron KM, Karesh WB, Tang S, et al. Coinfection of Ugandan red colobus (Procolobus [Piliocolobus] rufothorax) with novel, divergent delta-, lent-, and spumaretroviruses. J Virol. 2009; 83: 11318–11329. https://doi.org/10.1128/JVI.02616-08 PMID: 19692478
51. Lauck M, Sibley SD, Hyroba D, Turnukunde A, Weny G, Chapman CA, et al. Exceptional simian hemorrhagic fever virus diversity in a wild African primate community. J Virol. 2011; 87: 688–691. https://doi.org/10.1128/JVI.02433-12 PMID: 23073302
52. Lauck M, Hyroba D, Turnukunde A, Weny G, Lank SM, Chapman CA, et al. Divergent simian hemorrhagic fever viruses in a wild Ugandan red colobus monkey discovered using direct pyrosequencing. PLoS One. 2011; 6: e19056. https://doi.org/10.1371/journal.pone.0019056 PMID: 21544192
53. Simons N. The Role of Gene Regulation in Infectious Disease in the Ugandan Red Colobus Monkey (Piliocolobus tephrosceles). 2018. Available: https://scholarsbank.uoregon.edu/xmlui/handle/1794/23729
54. Buchfink B, Xie C, Huson DH. Fast and sensitive protein alignment using DIAMOND. Nat Methods. 2015; 12: 59–60. https://doi.org/10.1038/nmeth.3176 PMID: 25402007
55. Li H. Minimap2: pairwise alignment for nucleotide sequences. Bioinformatics. 2018; 34: 3094–3100. https://doi.org/10.1093/bioinformatics/bty191 PMID: 29750242
56. Sayers EW, Agarwala R, Bolton EE, Brister JR, Canese K, Clark K, et al. Database resources of the National Center for Biotechnology Information. Nucleic Acids Res. 2019; 47: D23–D28. https://doi.org/10.1093/nar/gky1069 PMID: 30395293
57. Kim D, Langmead B, Salzberg SL. HISAT: a fast spliced aligner with low memory requirements. Nat Methods. 2015; 12: 357–360. https://doi.org/10.1038/nmeth.3317 PMID: 25751142
58. Wood DE, Salzberg SL. Kraken: ultrafast metagenomic sequence classification using exact alignments. Genome Biol. 2014; 15: R46. https://doi.org/10.1186/gb-2014-15-3-r46 PMID: 24580807
59. PlasmoDB: An integrative database of the Plasmodium falciparum genome. Tools for accessing and analyzing finished and unfinished sequence data. The Plasmodium Genome Database Collaborative. Nucleic Acids Res. 2001; 29: 26–69. https://doi.org/10.1093/nar/29.1.66 PMID: 11125051
60. Weisenfeld NL, Kumar V, Shah P, Church DM, Jaffe DB. Direct determination of diploid genome sequences. Genome Res. 2017; 27: 757–767. https://doi.org/10.1101/gr.214874.116 PMID: 28381613
61. Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, et al. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. J Comput Biol. 2012; 19: 455–477. https://doi.org/10.1089/cmb.2012.0021 PMID: 22506599
62. Li H, Handsaker B, Wysoker A, Fennell T, Ruan J, Homer N, et al. The Sequence Alignment/Map format and SAMtools. Bioinformatics. 2009; 25: 2078–2079. https://doi.org/10.1093/bioinformatics/btp352 PMID: 19505943
63. Quinlan AR, Hall IM. BEDTools: a flexible suite of utilities for comparing genomic features. Bioinformatics. 2010; 26: 841–842. https://doi.org/10.1093/bioinformatics/btp033 PMID: 20110278
64. Sievers F, Wilm A, Dineen D, Gibson TJ, Karplus K, Li W, et al. Fast, scalable generation of high-quality protein multiple sequence alignments using Clustal Omega. Mol Syst Biol. 2011; 7: 539. https://doi.org/10.1038/msb.2011.75 PMID: 21988835
65. Waterhouse AM, Procter JB, Martin DMA, Clamp M, Barton GJ. Jalview Version 2—a multiple sequence alignment editor and analysis workbench. Bioinformatics. 2009; 25: 1189–1191. https://doi.org/10.1093/bioinformatics/btp033 PMID: 19151095

66. Hunt M, Silva ND, Otto TD, Parkhill J, Keane JA, Harris SR. Circlator: automated circularization of genome assemblies using long sequencing reads. Genome Biol. 2015; 16: 294. https://doi.org/10.1186/s13059-015-0849-0 PMID: 26714481

67. Koren S, Walenz BP, Berlin K, Miller JR, Bergman NH, Phillippy AM. Canu: scalable and accurate long-read assembly via adaptive k-mer weighting and repeat separation. Genome Res. 2017; 27: 722–736. https://https://doi.org/10.1101/gr.215087.116 PMID: 28298431

68. Morgulis A, Gertz EM, Schäffer AA, Agarwala R. A fast and symmetric DUST implementation to mask low-complexity DNA sequences. J Comput Biol. 2006; 13: 1028–1040. https://doi.org/10.1089/cmb.2006.13.1028 PMID: 16796549

69. Bushnell B, Rood J, Singer E. BBMerge—Accurate paired shotgun read merging via overlap. PLoS One. 2017; 12: e0185056. https://doi.org/10.1371/journal.pone.0185056 PMID: 29073143

70. Bonfield JK, Whitwham A. Gap5—editing the billion fragment sequence assembly. Bioinformatics. 2010; 26: 1699–1703. https://doi.org/10.1093/bioinformatics/btq068 PMID: 29073143

71. Waterhouse RM, Seppey M, Simão FA, Manni M, Ioannidis P, Kloutchnikov G, et al. BUSCO applications from quality assessments to gene prediction and phylogenomics. Mol Biol Evol. 2017. https://doi.org/10.1093/molbev/msx319 PMID: 29220515

72. Katoh K, Standley DM. MAFFT multiple sequence alignment software version 7: improvements in performance and usability. Mol Biol Evol. 2013; 30: 772–780. https://doi.org/10.1093/molbev/mst010 PMID: 23329690

73. Benson G. Tandem repeats finder: a program to analyze DNA sequences. Nucleic Acids Res. 1999; 27: 573–580. https://doi.org/10.1093/nar/27.2.573 PMID: 9862982

74. Zhu B-H, Xiao J, Xue W, Xu G-C, Sun M-Y, Li J-T. P_RNA_scaffolder: a fast and accurate genome scaffolder using paired-end RNA-sequencing reads. BMC Genomics. 2018; 19: 175. https://doi.org/10.1186/s12864-018-4567-3 PMID: 29499650

75. Hunt M, Kikuchi T, Sanders M, Newbold C, Berriman M, Otto TD. REAPR: a universal tool for genome assembly evaluation. Genome Biol. 2013; 14: R47. https://doi.org/10.1186/gb-2013-14-5-r47 PMID: 23710727

76. Jackman SD, Coombe L, Chu J, Warren RL, Vandervalk BP, Yeo S, et al. Tigmint: correcting assembly errors using linked reads from large molecules. BMC Bioinformatics. 2018; 19: 393. https://doi.org/10.1186/s12859-018-2425-6 PMID: 30367597

77. Otto TD, Sanders M, Berriman M, Newbold C. Iterative Correction of Reference Nucleotides (iCORN) using second generation sequencing technology. Bioinformatics. 2010; 26: 1704–1707. https://doi.org/10.1093/bioinformatics/btq269 PMID: 20562415

78. Walker BJ, Abeel T, Shea T, Priest M, Abouelliel A, Sakthikumar S, et al. Pilon: an integrated tool for comprehensive microbial variant detection and genome assembly improvement. PLoS One. 2014; 9: e112963. https://doi.org/10.1371/journal.pone.0112963 PMID: 25409509

79. Parra G, Bradnam K, Kol I. CEGMA: a pipeline to accurately annotate core genes in eukaryotic genomes. Bioinformatics. 2007; 23: 1061–1067. https://doi.org/10.1093/bioinformatics/btm071 PMID: 17332020

80. Dobin A, Davis CA, Schlesinger F, Drenkow J, Zaleski C, Jha S, et al. STAR: ultrafast universal RNA-seq aligner. Bioinformatics. 2013; 29: 15–21. https://doi.org/10.1093/bioinformatics/bts635 PMID: 23104886

81. Trapnell C, Williams BA, Pertea G, Mortazavi A, Kwan G, van Baren MJ, et al. Transcript assembly and quantification by RNA-Seq reveals unannotated transcripts and isoform switching during cell differentiation. Nat Biotechnol. 2010; 28: 511–515. https://doi.org/10.1038/nbt.1621 PMID: 20436464

82. Carver T, Harris SR, Berriman M, Parkhill J, McQuillan JA. Artemis: an integrated platform for visualization and analysis of high-throughput sequence-based experimental data. Bioinformatics. 2012; 28: 464–469. https://doi.org/10.1093/bioinformatics/btr703 PMID: 22199388

83. Carver TJ, Rutherford KM, Berriman M, Rajandream M-A, Barrell BG, Parkhill J. ACT: the Artemis Comparison Tool. Bioinformatics. 2005; 21: 3422–3423. https://doi.org/10.1093/bioinformatics/bti553 PMID: 15976072

84. Kalvari I, Nawrocki EP, Argasinska J, Quinones-Olvera N, Finn RD, Bateman A, et al. Non-Coding RNA Analysis Using the Rfam Database. Curr Protoc Bioinformatics. 2018; 62: e51. https://doi.org/10.1002/cpbi.51 PMID: 29927072

85. Boddey JA, Carvalho TG, Hodder AN, Sargeant TJ, Sleebs BE, Marapan A, et al. Role of plasmeplin V in export of diverse protein families from the Plasmodium falciparum exportome. Traffic. 2013; 14: 532–550. https://doi.org/10.1111/tra.12053 PMID: 23387285
86. Pain A, Böhme U, Berry AE, Mungall K, Finn RD, Jackson AP, et al. The genome of the simian and human malaria parasite Plasmodium knowlesi. Nature. 2008; 455: 799–803. https://doi.org/10.1038/nature07306 PMID: 18843368

87. Auburn S, Böhme U, Steinbiss S, Trimarzano H, Hostettler J, Sanders M, et al. A new Plasmodium vivax reference sequence with improved assembly of the subtelomeres reveals an abundance of pir genes. Wellcome Open Res. 2016; 1: 4. https://doi.org/10.12688/wellcomeopenres.9876.1 PMID: 28008421

88. Pasini EM, Böhme U, Rutledge GG, Voorberg-Van der Wel A, Sanders M, Berriman M, et al. An improved Plasmodium cynomolgi genome assembly reveals an unexpected methyltransferase gene expansion. Wellcome Open Res. 2017; 2: 42. https://doi.org/10.12688/wellcomeopenres.11864.1 PMID: 28748222

89. Otto TD, Böhme U, Jackson AP, Hunt M, Franke-Fa Yard B, Hoeijmakers WAM, et al. A comprehensive evaluation of rodent malaria parasite genomes and gene expression. BMC Biol. 2014; 12: 86. https://doi.org/10.1186/s12915-014-0086-0 PMID: 25359557

90. Otto TD, Rayner JC, Böhme U, Pain A, Spottiswoode N, Sanders M, et al. Genome sequencing of chimpanzee malaria parasites reveals possible pathways of adaptation to human hosts. Nat Commun. 2014; 5: 4754. https://doi.org/10.1038/ncomms5754 PMID: 25203297

91. Böhme U, Otto TD, Sanders M, Newbold CI, Berriman M. Progression of the canonical reference malaria parasite genome from 2002–2019. Wellcome Open Res. 2019; 4: 58. https://doi.org/10.12688/wellcomeopenres.15194.2 PMID: 31080894

92. Krogh A, Larsson B, von Heijne G, Sonnhammer EL. Predicting transmembrane protein topology with a hidden Markov model: application to complete genomes. J Mol Biol. 2001; 305: 567–580. https://doi.org/10.1006/jmbi.2000.4315 PMID: 11152613

93. El-Gebali S, Mistry J, Bateman A, Eddy SR, Luciani A, Potter SC, et al. The Pfam protein families database in 2019. Nucleic Acids Res. 2019; 47: D427–D432. https://doi.org/10.1093/nar/gky995 PMID: 30357350

94. Almagro Armenteros JJ, Tsirigos KD, Sønderby CK, Peteresen TN, Winther O, Brunak S, et al. SignalP 5.0 improves signal peptide predictions using deep neural networks. Nat Biotechnol. 2019; 37: 420–423. https://doi.org/10.1038/s41587-019-0036-z PMID: 30778233

95. Nurk S, Bankevich A, Antipov D, Gurevich VA, Korobeynikov A, Lapidus A, et al. Assembling single-cell genomes and mini-metagenomes from chimeric MDA products. J Comput Biol. 2013; 20: 714–737. https://doi.org/10.1089/cmb.2013.0084 PMID: 24093227
106. Consortium UniProt. UniProt: a worldwide hub of protein knowledge. Nucleic Acids Res. 2019; 47: D506–D515. https://doi.org/10.1093/nar/gky1049 PMID: 30395287

107. Warrenfeltz S, Basenko EY, Crouch K, Harb OS, Kissinger JC, Roos DS, et al. EuPathDB: The Eukaryotic Pathogen Genomics Database Resource. Methods Mol Biol. 2018; 1757: 69–113. https://doi.org/10.1007/978-1-4939-7737-6_5 PMID: 29761457

108. Alonge M, Soyk S, Ramakrishnan S, Wang X, Goodwin S, Sedlazeck FJ, et al. RaGOO: fast and accurate reference-guided scaffolding of draft genomes. Genome Biol. 2019; 20: 224. https://doi.org/10.1186/s13059-019-1829-6 PMID: 31661016

109. Abascal F, Zardoya R, Telford MJ. TranslatorX: multiple alignment of nucleotide sequences guided by amino acid translations. Nucleic Acids Res. 2010; 38: W7–13. https://doi.org/10.1093/nar/gkq291 PMID: 20435676

110. Yang Z. PAML 4: phylogenetic analysis by maximum likelihood. Mol Biol Evol. 2007; 24: 1586–1591. https://doi.org/10.1093/molbev/msm088 PMID: 17483113

111. Meerstein-Kessel L, van der Lee R, Stone W, Lanke K, Baker DA, Alano P, et al. Probabilistic data integration identifies reliable gametocyte-specific proteins and transcripts in malaria parasites. Sci Rep. 2018; 8: 410. https://doi.org/10.1038/s41598-017-18840-7 PMID: 29323249

112. McKenna A, Hanna M, Banks E, Sivachenko A, Cibulskis K, Kernytsky A, et al. The Genome Analysis Toolkit: a MapReduce framework for analyzing next-generation DNA sequencing data. Genome Res. 2010; 20: 1297–1303. https://doi.org/10.1101/gr.107524.110 PMID: 20644199

113. Newman AM, Liu CL, Green MR, Gentles AJ, Feng W, Xu Y, et al. Robust enumeration of cell subsets from tissue expression profiles. Nat Methods. 2015; 12: 453–457. https://doi.org/10.1038/nmeth.3337 PMID: 25822800

114. Frech C, Chen N. Variant surface antigens of malaria parasites: functional and evolutionary insights from comparative gene family classification and analysis. BMC Genomics. 2013; 14: 427. https://doi.org/10.1186/1471-2164-14-427 PMID: 23805789

115. Bahl A, Brunk B, Crabtree J, Frauenholz MJ, Gajria B, Grant GR, et al. PlasmoDB: the Plasmodium genome resource. A database integrating experimental and computational data. Nucleic Acids Res. 2003; 31: 212–215. https://doi.org/10.1093/nar/gkg081 PMID: 12519984