

1 **Matryoshka RNA virus 1: a novel RNA virus associated**
2 **with *Plasmodium* parasites in human malaria**

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32 **Abstract**

33 Parasites of the genus *Plasmodium* cause human malaria. Yet nothing is known about the
34 viruses that infect these divergent eukaryotes. We investigated the *Plasmodium* virome by
35 performing a meta-transcriptomic analysis of blood samples from malaria patients infected
36 with *P. vivax*, *P. falciparum* or *P. knowlesi*. This revealed a novel bi-segmented narna-like
37 RNA virus restricted to *P. vivax* and named Matryoshka RNA virus 1 (MaRNAV-1) to reflect
38 its "Russian doll" nature: a virus, infecting a parasite, infecting an animal. MaRNAV-1 was
39 abundant in geographically diverse *P. vivax* from humans and mosquitoes. Notably, a
40 related virus (MaRNAV-2) was identified in Australian birds infected with a *Leucocytozoon* -
41 eukaryotic parasites that group with *Plasmodium* in the Apicomplexa subclass hematozoa.
42 This is the first report of a *Plasmodium* virus. As well as broadening our understanding of
43 the eukaryotic virosphere, the restriction to *P. vivax* may help understand *P. vivax*-specific
44 biology in humans and mosquitoes.

45 Introduction

46 Viruses are the most abundant biological entities on Earth, replicating in diverse host
47 organisms (*Forterre 2010*). Although there has been an expansion of metagenomic studies
48 dedicated to exploring this immense virosphere (*Angly et al., 2006; Culley et al., 2006;*
49 *Desnues et al., 2008; Paez-Espino et al., 2016; Suttle 2005*), our knowledge of the viral
50 universe remains limited, with only a minute fraction of eukaryotic species sampled to date
51 (*Zhang et al., 2018*). This knowledge gap is especially wide in the case of unicellular
52 eukaryotes (i.e. protists), including those responsible for parasitic disease in humans, on
53 which only a small number of studies have been performed.

54
55 Viral-like particles in parasites were first observed by electron microscopy as early as the
56 1960's in various protozoa from the apicomplexan and kinetoplastid phyla (reviewed in
57 *Miles 1988*). The first molecular evidence for the presence of protozoan viruses was
58 obtained in the late 1980s, resulting in the characterization of double-strand (ds) RNA
59 viruses in the human parasites *Giardia*, *Leishmania*, *Trichomonas* and *Cryptosporidium*
60 (*Khramtsov et al., 1997; Miller et al., 1988; Tarr et al., 1988; Wang and Wang 1985; Wang*
61 *and Wang 1986; Widmer et al., 1989*). More recently, single-stranded narnavirus-like and
62 bunyavirus-like RNA viruses were identified in trypanosomatid parasites, including
63 *Leptomonas seymouri*, *Leptomonas moramango*, *Leptomonas pyrrocoris* and *Crithidia* sp.
64 (*Akopyants et al., 2016; Grybchuk et al. 2018; Lye et al., 2016; Sukla et al., 2017*). However,
65 our knowledge of protozoan viruses is clearly limited, with many of those identified
66 stemming from fortuitous discovery.

67
68 The identification and study of protozoan viruses is also important for our understanding of
69 so-called "Russian doll" ("Matryoshka" in Russian) infections (*Padma 2015*), in which
70 parasites are themselves infected by other microbes. A key question here is whether
71 viruses of parasites can in turn have an impact on aspects of parasite pathogenesis? An
72 increasing number of studies have demonstrated that dsRNA viruses of protozoa can affect
73 key aspects of parasite biology, including their virulence, in a variety of ways (*Gómez-*
74 *Arreaza et al., 2017*). For instance, data from *Leishmania guyanensis* and *Trichomonas*
75 *vaginalis* strongly suggest a link between parasite pathogenesis and the presence of
76 *Leishmania* RNA virus 1 (LRV1) and *Trichomonas vaginalis* virus, respectively (*Fichorova et*
77 *al., 2012; Ito et al., 2015; Ives et al., 2011*). By increasing the inflammatory response in the
78 host these viruses could in theory enhance human pathogenesis (*Brettmann et al., 2016;*
79 *Zangger et al., 2014*). Interestingly, associations have also been observed between LRV1-

80 infected *L. guyanensis* or *L. braziliensis* and treatment failure in patients with leishmaniasis
81 (*Adai et al., 2016; Bourreau et al., 2016*).

82

83 Viral co-infection also has the potential to alter protozoan biology and/or attenuate the
84 mammalian host response, leading to greater replication or persistent protozoan infection,
85 in turn promoting ongoing parasite transmission. Persistence (i.e. avirulent infection) has
86 been proposed in the case of *Cryptosporidium parvum* virus 1 (CSpV1) that infects the
87 apicomplexan *Cryptosporidium* (*Nibert et al., 2009*), and increased *C. parvum* fecundity has
88 been demonstrated in isolates experiencing viral co-infection (*Jenkins et al., 2008*). Viral
89 infections may also have a deleterious effect on parasite biology, adversely impacting such
90 traits as growth and adhesion in the case of axenic cultures of *Giardia lamblia* (*Miller et al.,*
91 *1988*). Clearly, the effects and underlying molecular basis of any consequences that
92 protozoal viruses have on their hosts, including in the context of pathogenesis, requires
93 rigorous investigation. Documenting novel protozoal viruses is an obvious first step in this
94 process.

95

96 Nothing is known about those viruses that infect species of *Plasmodium* (order
97 Haemosporida) - obligate apicomplexan parasites of vertebrates and insects. In vertebrate
98 hosts, these protozoa first infect the liver cells as sporozoites where they mature into
99 schizonts. Resulting merozoites are then released into the bloodstream to undergo asexual
100 multiplication in red blood cells. A portion of these replicating asexual forms can
101 differentiate into gametocytes which, following ingestion by blood-feeding female
102 *Anopheles* mosquitoes, develop into sporozoites and are transmitted to another host via
103 mosquito saliva. The genus *Plasmodium* currently comprises approximately 100 species
104 that infect various mammals, birds and reptile hosts. Among these, six species commonly
105 infect humans and are important causative agents of human malaria: *P. falciparum*, *P. vivax*,
106 *P. malariae*, *P. ovale curtisi*, *P. ovale wallikeri*, and *P. knowlesi*. Despite an early observation
107 of viral-like particles in cytoplasmic vacuoles of simian *P. cynomolgi* sporozoites (*Garnham*
108 *et al., 1962*), no viruses have been discovered in the parasites responsible for malaria.

109

110 With 219 million cases reported in 2017 in 90 countries around the world, malaria continues
111 to be the most important protozoan disease affecting humans (*WHO 2018*). Despite
112 ongoing and considerable global public health efforts, recent progress in reducing the
113 disease burden due to malaria has stalled. Reasons include the emergence of resistance to
114 insecticides in the mosquito vectors, and parasite resistance to antimalarial drugs in

115 humans. In addition, the large number of asymptomatic and/or submicroscopic
116 *Plasmodium* infections in peripheral blood are an important source of transmission, and
117 pose a major challenge to control and eradication strategies (Bousema and Drakeley 2011).
118 This is compounded by the ability of some *Plasmodium* sp., including *P. vivax*, *P. ovale*
119 *curtisi*, and *P. ovale wallikeri*, to form latent liver stages and later relapse. They also illustrate
120 the need for approaches targeting the human parasite reservoir rather than treating only
121 those with clinical disease.

122

123 There is an obvious interest in identifying viruses associated with human *Plasmodium*
124 species from both an evolutionary and clinical perspective. The presence of RNA viruses
125 infecting hematozoa parasites have been largely overlooked, although their divergent
126 position in the eukaryotic phylogeny means that they may constitute a valuable source of
127 information to help understand early events in the evolution of eukaryotic RNA viruses.
128 Knowledge of *Plasmodium*-specific viral infection may also provide insights into parasite
129 biology in humans and mosquitoes, with the potential for identifying preventative or
130 therapeutic strategies.

131

132 **Results**

133

134 ***Plasmodium*-infected human samples**

135 To investigate the virome of *Plasmodium* parasites that infect and cause disease in
136 humans, we performed a meta-transcriptomic study of three species - *P. vivax* (hereby
137 denoted Pv), *P. knowlesi* (Pk) and *P. falciparum* (Pf). These samples were obtained from 7, 6
138 and 5 malaria patients, respectively, at different locations in the state of Sabah, east
139 Malaysia (Table S1) (Grigg *et al.*, 2018). All patients with malaria had uncomplicated
140 disease. An additional library of 6 non-infected patients were also included as a negative
141 control. All infected blood samples were validated for their corresponding *Plasmodium*
142 species (Table S1). Microscopic parasite counts from peripheral blood films revealed similar
143 densities (i.e. no significant differences, p-value=0.7) between the three *Plasmodium*
144 species, with parasitemia centered around 6000-8000/ μ L (Figure S1).

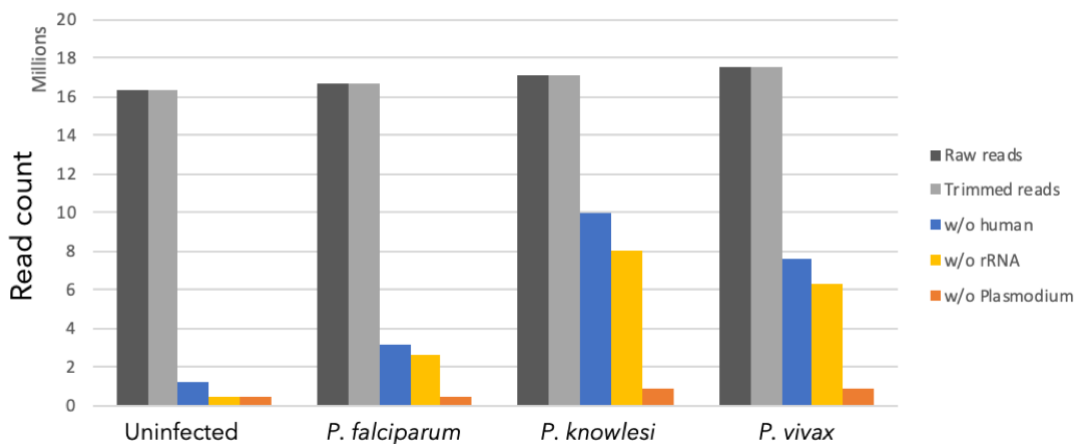
145

146 **Sample processing**

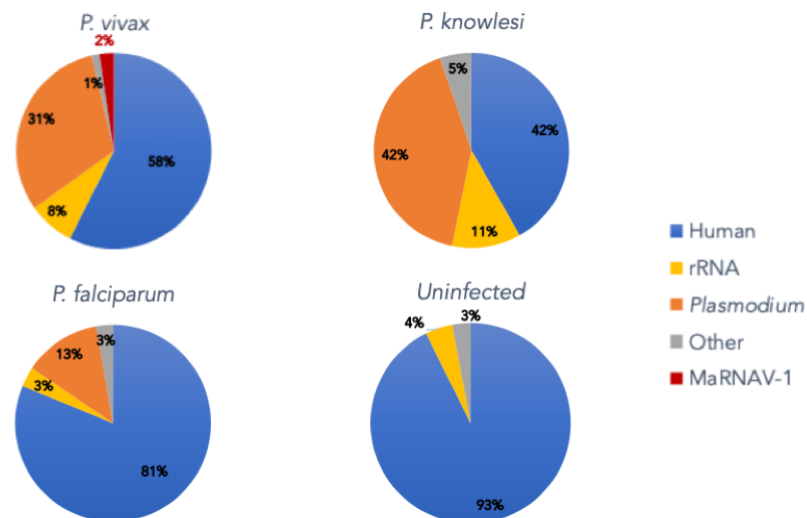
147 Homogenous and equimolar ratios of each of the total RNA samples were used to prepare
148 RNA-Seq libraries. Sequencing depth was similar for all samples, with 17 ± 0.5 million reads
149 obtained (Figure 1.A). The human rRNA read depletion drastically reduced the number of

150 reads in both the non-infected and Pf data sets (93 and 81% of reads filtered, respectively)
151 (Figure 1.B) and to a lesser extent in Pk and Pv (only 42-57% of reads removed). Pf
152 transcripts were less abundant in libraries than those in Pk and Pv. Finally, the contig
153 assemblies performed on each library depleted for rRNA, human and *Plasmodium* reads
154 were almost equally successful for all libraries, with a similar contig length distribution
155 between the data sets (Figure S2).
156

(A)



(B)



157
158 **Figure 1. Host read depletion in RNA-Seq libraries.** Reads were mapped against rRNA
159 SILVAdb (SortMeRNA tool), the human genome, and the genomes of three *Plasmodium*
160 species. (A) Efficiency of read filtering (rRNA and host sorting). (B) Proportion of major host
161 transcripts in each data set. The number of reads mapping to the human genome,
162 *Plasmodium* sp. genomes and MaRNAV-1 are expressed as the percentage of trimmed
163 reads for each library.

164

165 **Virus discovery in *Plasmodium vivax*-infected blood samples**

166 ***Discovery of a bi-segmented RNA Narna-like virus***

167 Ribosomal RNA-depleted data sets were submitted to Blastx against a database containing
 168 all the RNA-dependent RNA polymerase (RdRp) protein sequences available at the NCBI.

169 We focused on this protein as it is the mostly highly conserved among RNA viruses and
 170 hence constitutes the best marker for detecting their presence and performing expansive
 171 phylogenetic analyses. False-positive hits (i.e. non-viral contigs) were discarded by using a
 172 second round Blast against the nr database and removing contigs with non-viral top hits.

173 Notably, true-positive RdRp signals were only found in the Pv library (Table 1).

174

175 **Table 1.** Results of the RdRp Blastx analysis.

Contig query	Length	estimated count	Blastn	Blastx best hit	%ID	e-value	taxID	Virus
Pv_1_DN5867_c0_g1_i1	2924	234605.7	No hit	YP_009388589.1 RdRp	43	1.30E-170	2010280	Wilkie narna-like virus 1
Pv_1_DN5867_c0_g1_i2	3023	77610.78	No hit	YP_009388589.1 RdRp	43	1.10E-170	2010280	Wilkie narna-like virus 1
Pv_1_DN5867_c0_g1_i3	3023	286828.4	No hit	YP_009388589.1 RdRp	43	3.70E-184	2010280	Wilkie narna-like virus 1
Pv_1_DN5867_c0_g1_i4	2141	105799.2	No hit	YP_009388589.1 RdRp	43	1.50E-185	2010280	Wilkie narna-like virus 1
Pv_1_DN5867_c0_g1_i5	3023	1834.39	No hit	YP_009388589.1 RdRp	43	1.10E-170	2010280	Wilkie narna-like virus 1
Pv_1_DN5867_c0_g1_i6	2045	79319.65	No hit	YP_009388589.1 RdRp	43	6.60E-171	2010280	Wilkie narna-like virus 1
Pv_1_DN5867_c0_g1_i7	1496	13751.44	No hit	YP_009388589.1 RdRp	42.8	8.30E-171	2010280	Wilkie narna-like virus 1

176

177 These contigs all correspond to variants of the same gene from the Trinity assemblies, and
 178 all share their highest sequence similarity score (between 42.6 and 42.9% identity, Table 1)
 179 with the RdRp of Wilkie narna-like virus 1, an unclassified virus related to the narnaviruses
 180 recently identified in mosquitoes samples (*Shi et al., 2017*). The mapping of Pv-reads
 181 against this newly-described viral-like genome revealed that the virus-like contig was highly

182 abundant in the Pv library, comprising approximately 1.6% of all the non-rRNA (Figure 1). A
183 more detailed characterization of this virus is presented below. To detect homologs to this
184 newly identified RNA-virus-like contig in the other *Plasmodium* species, DN5867 contigs
185 were used as the reference for another round of Blastx: this analysis revealed no matches
186 in either the Pf or Pk data sets.

187

188 The apparent bias in virus composition between libraries likely reflects differences in their
189 virome composition rather than experimental bias, since the quality of samples, the depth
190 of sequencing, and the contig assembly were similar among the four libraries. However, it is
191 also possible that it in part reflects the limits of Blastn/Blastx sequence-based homology
192 detection methods to identify highly divergent RNA viruses. To help overcome this
193 limitation, and try to identify any highly divergent RNA viruses, we performed a
194 Blastn/Blastx search on the contigs using the nt and nr databases, respectively. All the
195 “orphan” contigs (i.e. those without any match in any of the nt or nr databases) were sorted
196 depending on their length (Figure S3). Assuming that RNA virus-like contigs would be of a
197 certain minimum length, only those larger than 1000 nt were used for further analysis (Table
198 2). To identify remote virus signal from these sequences, a second round of Blastx search
199 was conducted with lower levels of stringency: this revealed no clear hits to RNA viruses.

200

201 Finally, we employed a structural-homology based approach to virus discovery, utilizing
202 information on protein 3D structure rather than primary amino acid sequence, as the former
203 can be safely assumed to be more conserved than the latter (*Illergård et al., 2009*) and is
204 therefore predicted to be better able to reveal distant evolutionary relationships.

205 Accordingly, hypothetical ORFs were predicted from orphan contigs and Hidden Markov
206 model (HMM) searches combined with 3D-structure modelling were performed on the
207 corresponding amino acid sequences using the Phyre2 web portal (*Kelley et al., 2015*).
208 Again, this revealed no reliable signal for the presence of highly divergent viruses in the
209 RNA sequences obtained here.

210

211 Notably, with 122,452 reads mapped to it, the Pv unknown contig retained is highly
212 expressed, possessing a similar level of abundance as the newly-identified Pv RdRp-like
213 contig. Specifically, the abundance of these two contigs were in the same range, with
214 Reads per Kilobase per Million (RPKM) of the Pv RdRp-like and Pv unknown contigs of 2.9
215 and 2.6, respectively (Table 2). Such a similarity in abundance levels supports the existence
216 of a bi-segmented RNA virus. Finally, the 3kb RdRp-segment described in our *P. vivax*

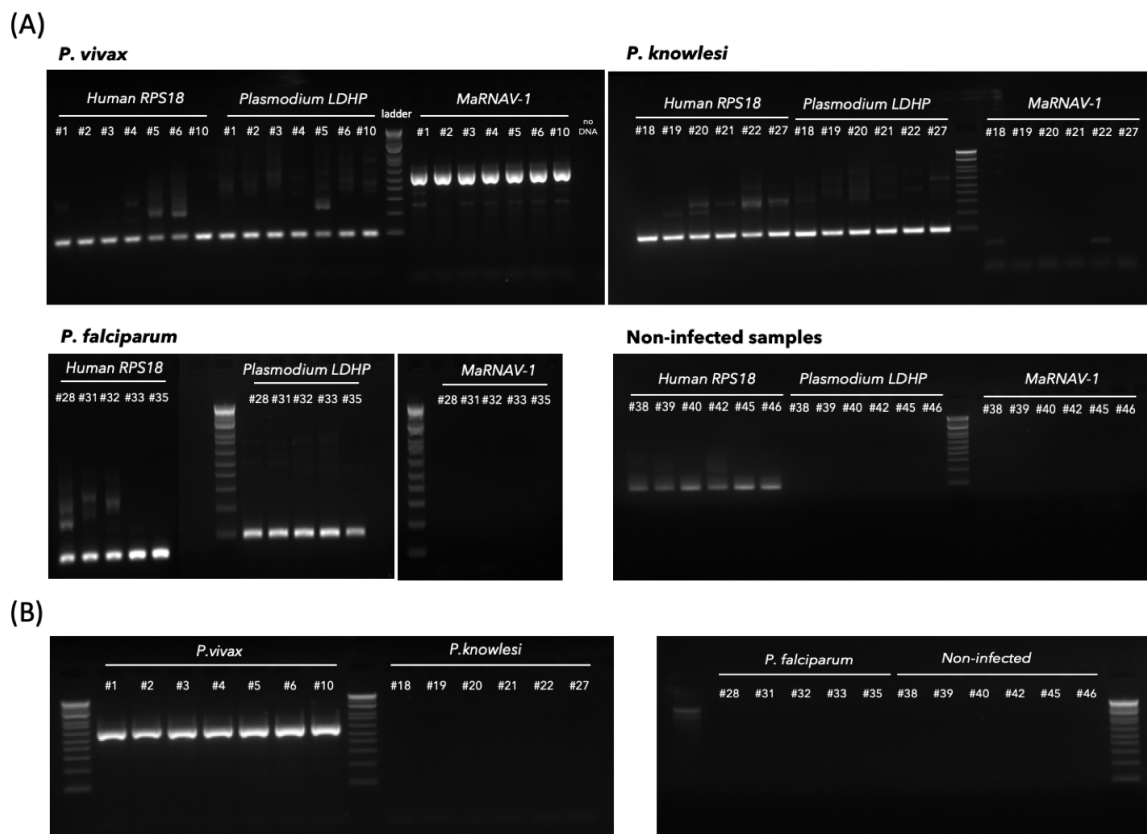
217 samples is also within the range of the genome lengths seen in other members of the
218 *Narnaviridae* (2.3 to 3.6 kb).

219

220 ***Narna-like virus genome and protein annotation***

221 The two segments of our putative narnavirus were both validated by RT-PCR in each of the
222 seven *P. vivax* samples used for this study (Figure 2), but were not found in the *P. knowlesi*,
223 *P. falciparum* and non-infected samples. Corresponding amplicons were then Sanger-
224 sequenced to define both the intra and inter-sample sequence diversity. We named this
225 new virus Matryoshka RNA virus 1 (MaRNAV-1) because of its “Russian doll” composition,
226 reflecting a virus that infects a parasite (protist) that infects an animal.

227



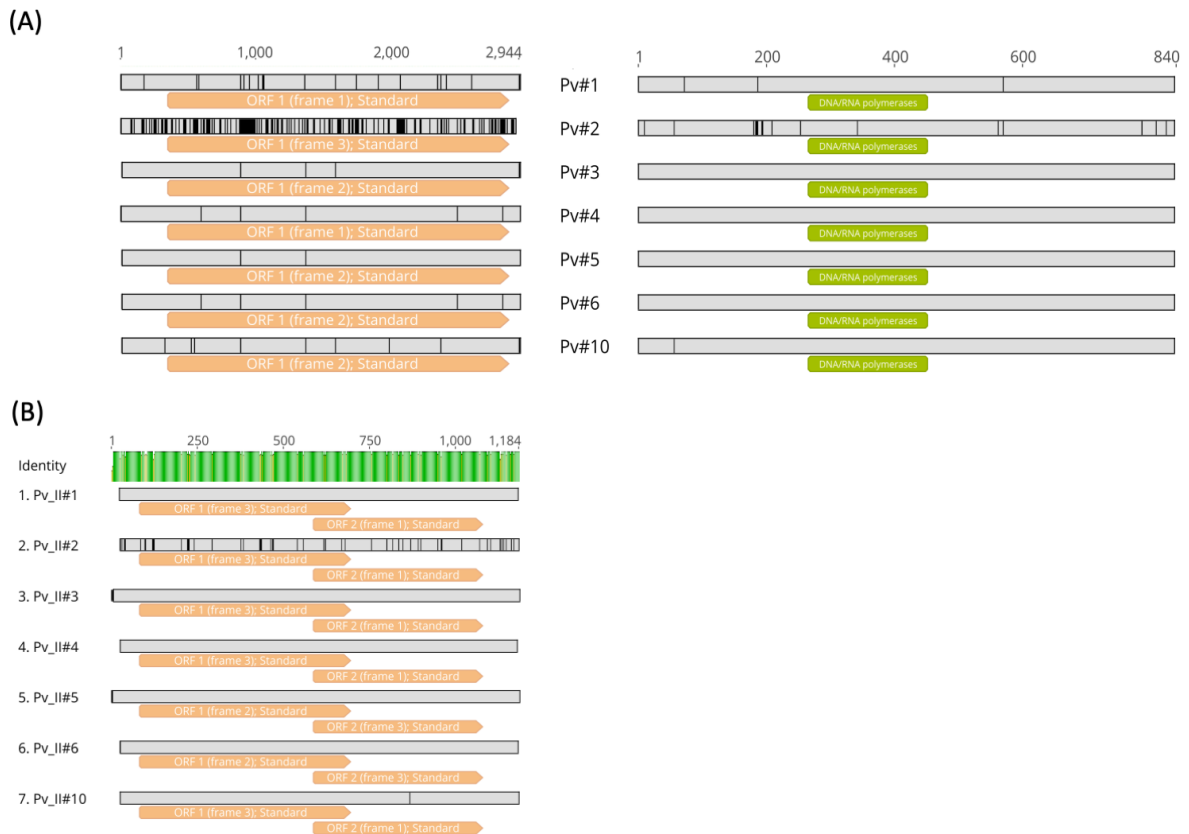
228

229 **Figure 2. RT-PCR confirmation of host and virus-like sequences in all *Plasmodium*-**
230 **infected and non-infected samples used in this study.** (A) RT-PCR of each samples
231 using human RPS18 primers, *Plasmodium* LDHP primers and MaRNAV-1 primers (segment
232 I). (B) Detection of MaRNAV-1 segment II via RT-PCR.

233

234 A very high level of sequence conservation was observed at both the intra and inter-sample
235 scales in the RdRp-encoding segment (“RdRp-segment”; Figure 3A, left). Indeed, very few

236 nucleotide polymorphisms were observed between those viruses collected from samples 1,
 237 3, 4, 5, 6 and 10 (effectively 100%). Across the data set as a whole, only two polymorphic
 238 sites were observed at the intra-sample level and this was restricted to sample #10. In
 239 contrast, the MaRNAV-1 from sample #2 was more distant, with 93% identity to the other
 240 sequences.



241
 242 **Figure 3.** Multiple sequence alignment of MaRNAV-1 from each of the 7 *P. vivax*-infected
 243 blood samples. (A) RdRp-segment analysis. Left: Nucleotide sequence alignment and ORF
 244 prediction (orange boxes). Right: Protein sequence alignment and InterPro domains
 245 predicted (green boxes). Sequence polymorphisms are highlighted in black. (B) Analysis of
 246 segment II. Nucleotide alignment and ORFs predicted from the unknown segment in *P.*
 247 *vivax* samples (top). Distance matrix with percentage of identity at the nucleotide level
 248 (bottom).

249
 250 Virus ORFs were predicted using the ORFinder NCBI tool and corresponding amino acid
 251 sequences were obtained and aligned (Figure 3A, right). This revealed that the nucleotide
 252 polymorphisms described above were also present at the amino acid level, even though
 253 these sequences were still highly conserved (98-100%), especially in the RdRp. An

254 additional attempt at functional annotation was performed, but did not reveal any additional
255 functional motifs or domains aside from the RdRp.

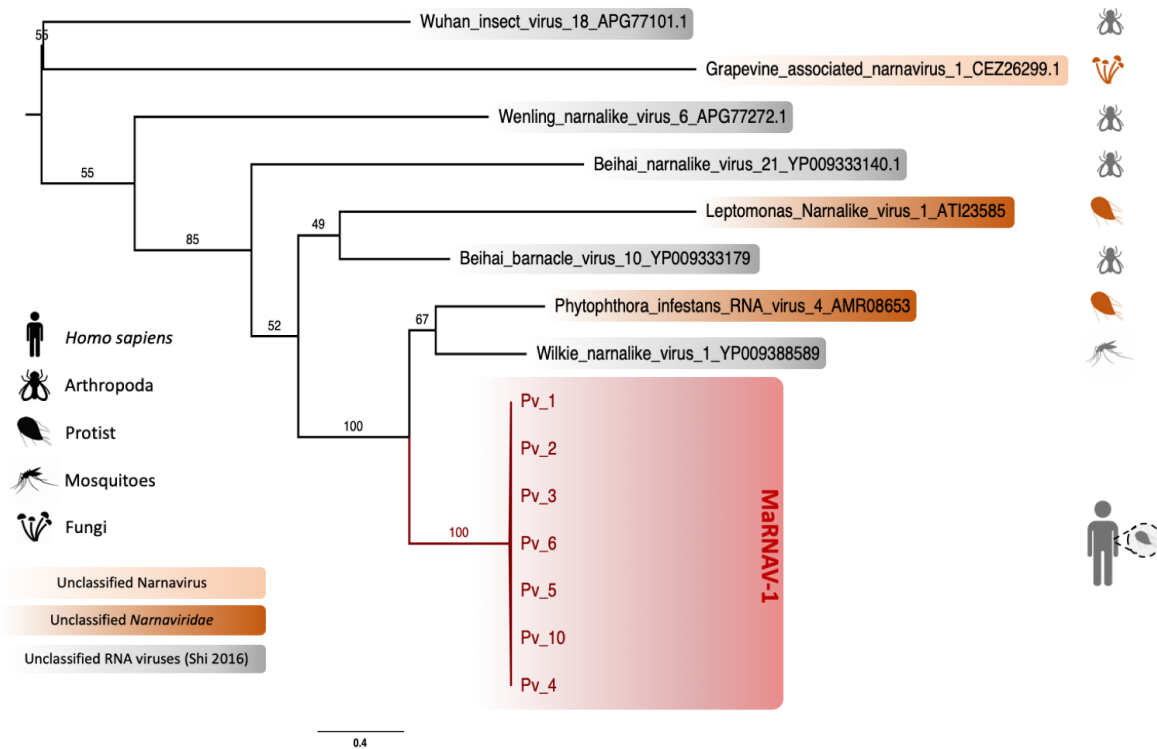
256

257 The second segment, the presence of which distinguishes MaRNAV-1 virus from all other
258 narnaviruses, was also highly conserved between *P. vivax* samples (between 95 and 100%
259 identity at the nucleotide level) and is likely to encode two protein products of 205 and 163
260 amino acids in length through two overlapping ORFs (Figure 3B). Unfortunately, the level of
261 sequence divergence between this second segment and all other sequences available at
262 NCBI meant that no functional annotations were possible.

263

264 ***Phylogenetic analysis of MaRNAV-1***

265 To link the newly-identified *Plasmodium vivax* virus to the diversity of RNA viruses already
266 available, we performed a phylogenetic analysis with the sequence newly acquired here
267 and the closest relatives identified with Blastx (Figure 4). As noted above, this is the first
268 description of a virus infecting *Plasmodium* spp. and few apicomplexan-related dsDNA
269 viruses have been isolated to date. Hence, it is not surprising that only low levels of amino
270 acid sequence similarity (between 15 and 54%) were found in comparisons between
271 MaRNAV-1 and the closest related RNA viruses available at NCBI. Importantly, however,
272 the most closely related viruses were consistently classified as members of the family
273 *Narnaviridae* (genus *Narnavirus*) - a group of single-stranded positive-sense RNA viruses
274 known to infect such host species as fungi, plants and protists (Figure 4). The most closely
275 related virus - Wilkie narna-like virus 1 - was recently identified in a large-scale survey of
276 mosquitoes (*Shi et al., 2017*) and is yet to be formally taxonomically assigned. Although the
277 low abundance of this virus meant that no host could be conclusively assigned, a
278 preliminary study suggested that it was unlikely to be a virus of mosquitoes, such that it
279 could, in theory, infect a protozoan within the mosquitoes. In addition, two of the other
280 narnaviruses most closely related to MaRNAV-1 virus - *Leptomonas seymouri arna-like virus*
281 *1* (LepseyNLV1) and *Phytophthora infestans RNA virus 4* - have been described as infecting
282 unicellular eukaryotes, *Leptomonas seymouri* and *Phytophthora infestans*, respectively.



283

284 **Figure 4.** Phylogenetic analysis of a novel narna-like virus - MaRNAV-1 - associated with
 285 *Plasmodium vivax*. Boxes refer to the newly-described MaRNAV-1 viral sequences obtained
 286 in this study (red) or to RNA viruses classified as members of the *Narnaviridae* (dark
 287 orange), genus *Narnavirus* (light orange) or currently unclassified (grey). Taxa corresponding
 288 to the validated (coloured icons, right) and non-validated (grey icons, right) hosts are
 289 reported on the left part of the tree. Bootstrap values are indicated on each branch. The
 290 tree is mid-point rooted for clarity only.

291

292 The second putative segment found in all the *P. vivax* samples described here also aligned
 293 with the second segment present in *LepseyNLV1* (Lye *et al.*, 2016) which similarly encodes
 294 two overlapping ORFs (KU935605.1), even though they share little sequence identity (only
 295 14-18% identity at the amino acid level for ORF1 and ORF2, respectively). This high
 296 divergence explains why this sequence was not identified in previous Blastx analyses and
 297 precluded more detailed phylogenetic analysis.

298

299 **Virus-host assignment**

300 A major challenge for all metagenomic studies is accurately assigning viruses to hosts as
 301 they could in reality be associated with host diet, the environment surrounding the sampling
 302 site, or a co-infecting micro-organism. In assigning hosts we assumed: (i) that a virus with a

303 high abundance is likely to be infecting a host found also in high abundance, (ii) a virus
304 consistently found in association with one particular host is likely to infect that host, (iii) a
305 virus that is phylogenetically related to those previously identified as infecting a particular
306 host taxa is likely to infect a similar range of host taxa, and (iv) a virus and a host that share
307 identical genetic code and/or similar codon usage or dinucleotide compositions are likely to
308 have adapted and co-evolved, indicative of a host-parasite interaction.

309

310 ***Eukaryotic host read profiling***

311 To initially assess whether MaRNAV-1 is likely to infect *Plasmodium* rather than other intra-
312 host microbes and co-infecting parasites, the host taxonomy of the Blastn/x top hits for
313 each contig of the human and *Plasmodium*-depleted *P. vivax* library were compared to their
314 respective size and abundance. However, this analysis revealed only a small number of
315 short contigs associated with fungi and bacteria (Figure S4). This result is of note as the
316 usual hosts associated with narnaviruses are fungi, and the closest relatives have been
317 found in mosquito samples, although the true host of this virus could in theory be protozoal.
318 Among the Metazoa identified, all the contigs were associated with vertebrates, rather than
319 members of the Arthropoda or Nematoda. Hence, *Plasmodium vivax* appears to be the
320 most likely host of the newly-identified MaRNAV-1 virus.

321

322 ***Comparison of codon usage and dinucleotide composition***

323 Host adaptation can result in specific patterns of codon and dinucleotide usage. We
324 compared the codon usage observed in MaRNAV-1 to those of the potential host
325 organisms. The Codon Adaptation Index (CAI) measures the similarity in synonymous
326 codon usage between a gene and a reference set, and was assessed for MaRNAV-1 using
327 *H. sapiens*, *P. vivax* and *Anopheles* genera mosquitoes (pool of 7 species) as reference data
328 sets. However, as none of the CAI/eCAI values obtained were significant (<1) (Figure S5),
329 no conclusions could be drawn regarding the potential host of MaRNAV-1. In a
330 complementary approach, we compared the dinucleotide composition bias between the
331 newly identified virus and the potential hosts (*Di Giallonardo et al., 2017*). Again, the
332 dinucleotide frequencies in the two potential hosts *An. gambiae* and *P. vivax* revealed
333 strong similarities that prevented us from identifying any signature of viral adaptation
334 (Figure S6).

335

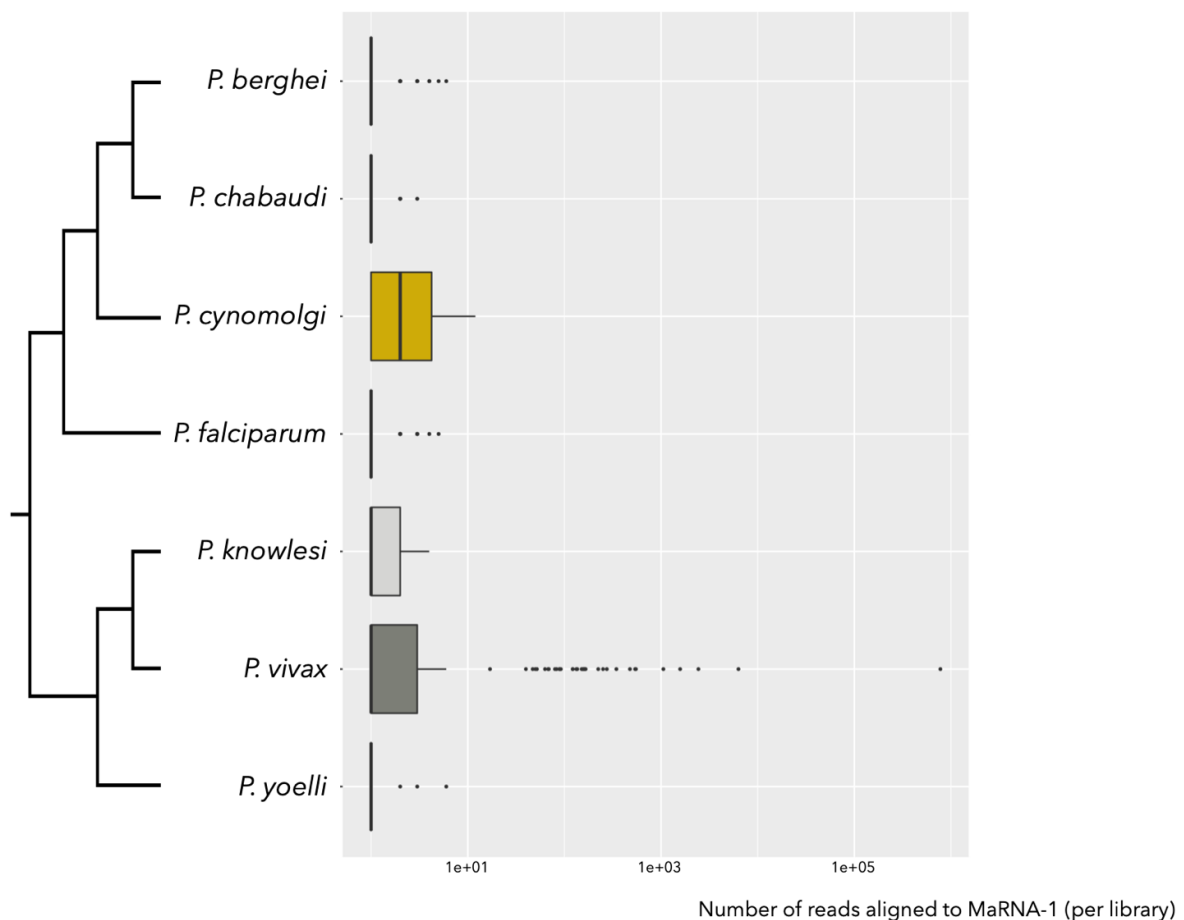
336 ***Investigation of the MaRNAV-1 and Plasmodium sp. association using the Sequence*** 337 ***Read Archive (SRA)***

338 To further test for an association between MaRNAV-1 and *Plasmodium* parasites, we
339 performed a wider investigation of the occurrence of this virus in *Plasmodium*-infected
340 samples and other *Plasmodium* species for which RNA-Seq data were available on the
341 SRA. These data sets comprised *P. chabaudi*, *P. cynomolgi*, *P. falciparum*, *P. yoelli*, *P.*
342 *knowlesi* and *P. berghei* (the relevant Bioprojects are listed in Table S2).

343

344 In total, 1682 RNA-Seq data sets from *Plasmodium*-related projects on the SRA were
345 screened for the presence of MaRNAV-1 using Blastx. This analysis identified reads
346 mapping to MaRNAV-1 in 45 libraries, all belonging to *P. vivax* (Figure 5). Among the *P.*
347 *vivax*-related runs (Table S3), none of the 31 non-infected or *P. falciparum*-infected samples
348 contained MaRNAV-1 (Chi-squared test, p-value = 0, Figure S7.A). This pattern is strongly
349 suggestive of a specific association between MaRNAV-1 and *P. vivax*, rather than the result
350 of experimental bias or contamination introduced during RNA extraction or sequencing.
351 Moreover, MaRNAV-1 was found in 43% (13 out of 30) of the *P. vivax*-infected SRA
352 samples investigated here (biological replicates omitted).

353



354

355 **Figure 5.** Number of *Plasmodium* SRA reads aligning with the MaRNAV-1 sequence (RdRp-
356 segment) using Blastx (cut-off $1e-5$).

357

358 Finally, the location of the *P. vivax* isolates from the SRA-based studies (Colombia,
359 Cambodia and Thailand) and the multiple sample types (human blood, mosquito dissected
360 salivary glands or *ex vivo* cultures) were found to be independent of MaRNAV-1 detection
361 (Chi-squared tests, p -values > 0.05 , Figure S7.C and D). Hence, together, these results
362 strongly support a specific association between MaRNAV-1 and *P. vivax*.

363

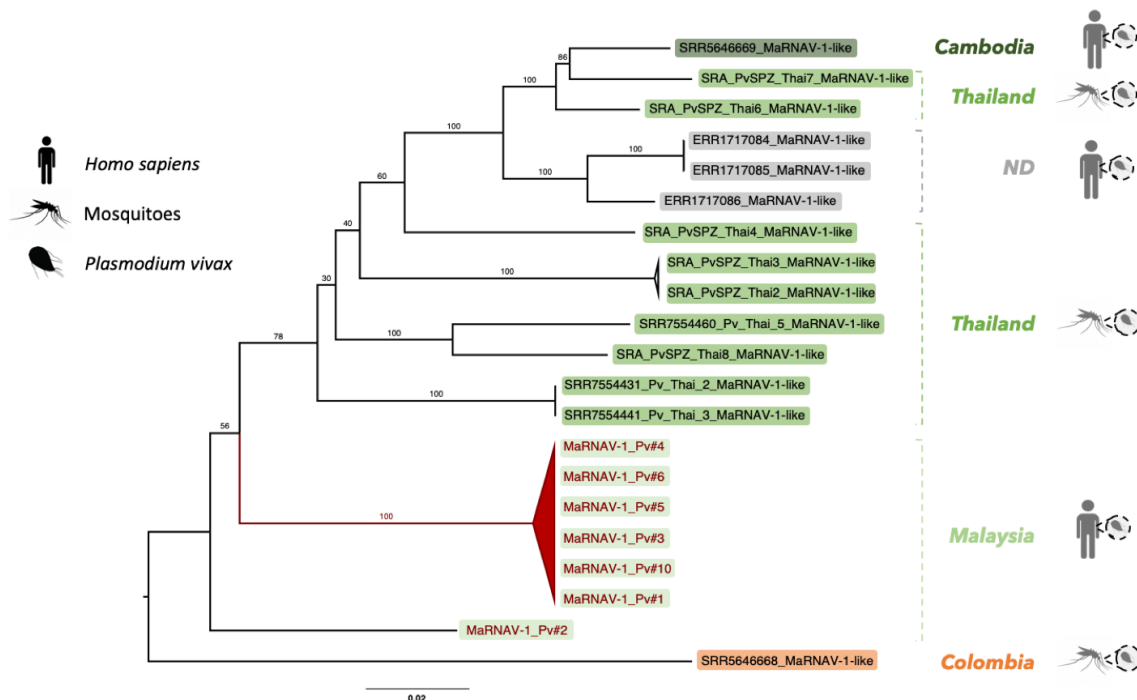
364 **Analysis of SRA-derived MaRNAV-1 virus-like genomes**

365 Narnavirus positive *P. vivax* data sets were further analyzed following the same workflow as
366 described above. Hence, contigs were *de novo* assembled and re-submitted to Blastx to
367 extract full-length contigs corresponding to MaRNAV-1. The genomes obtained were
368 validated and quantified using read mapping and overlapping contigs were merged to
369 obtain full-length viral genomes.

370

371 A phylogenetic analysis of these sequences containing MaRNAV-1 was performed at the
372 nucleotide level (Figure 6). Importantly, phylogenetic position was strongly associated with
373 sampling location rather than the nature of the samples (i.e. human blood or *Anopheles sp.*
374 mosquito salivary glands). This again reinforces the idea that these sequences come from a
375 RNA virus infecting *Plasmodium sp.* rather than human or *Anopheles sp.* hosts. Despite this
376 geographical association, all these newly identified RdRp-encoding sequences shared a
377 high level of sequence nucleotide identity (85-100%). Promisingly, the sequence of the
378 second segment identified in this study is also found in *P. vivax* SRA data sets and is
379 strongly associated ($R > 0.95$) with the presence of the RdRP-encoding segment (Figure
380 S8).

381



382

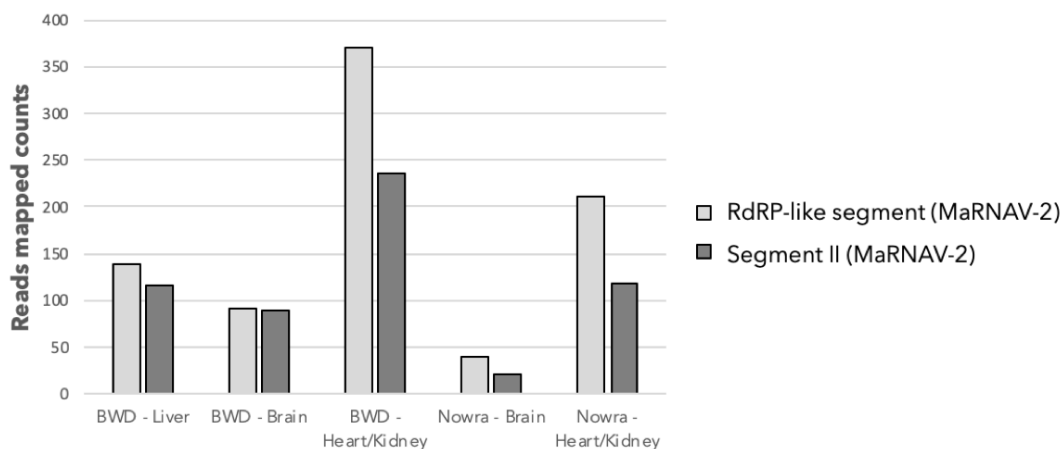
383 **Figure 6. Phylogenetic analysis, based on the RdRp, of the MaRNAV-1 documented**
 384 **here and from the *P. vivax* sequences available on the SRA.** Those viruses obtained in
 385 this study are shown in red while those from the SRA are shown in black. Sampling location
 386 and host characteristics (i.e. human-infected or mosquito-infected samples) are indicated
 387 on the right. Colored boxes indicate the samples collected in Asia (green), in South America
 388 (orange) or from unknown location (grey; ND : non-determined). The tree is mid-point
 389 rooted for clarity only.

390

391 **Detection of MaRNAV-2 in *Leucocytozoon* parasites infecting birds**

392 To investigate whether these narna-like sequences might infect a wider taxonomic
 393 distribution of hosts, we performed a complementary analysis of bird samples infected by
 394 members of the genus *Leucocytozoon*: apicomplexan parasites that belong to the same
 395 hematozoa subclass (of the Apicomplexa) as *Plasmodium*. These complementary studies
 396 were conducted on available RNA-Seq data previously obtained from liver, brain, heart and
 397 kidney tissues from Australian Magpie, Pied currawong and Raven birds collected at
 398 various time points in New South Wales, Australia (Table S4). Using the newly-discovered
 399 MaRNAV-1 viral segments as references, a Blastx analysis was performed on RNA-Seq
 400 data previously obtained for these samples. A first segment encoding a single predicted
 401 ORF of 859 amino acid long and containing the RdRp domain motif was retrieved and
 402 compared to the *P. vivax* MaRNAV-1 sequences (Figure S9A). A relatively high level of
 403 sequence similarity (73% identity at the amino acid level) was observed between the

404 *Leucocytozoon*-infected birds and the viral sequences found in the *P. vivax* infected-
405 humans. A second segment was also extracted from these avian libraries that exhibited
406 strong similarities in terms of length, genome organization and sequence identity with the
407 prediction of two overlapping ORFs, denoted ORF1 and ORF2, that encode proteins of 246
408 and 198 amino acids, respectively, and that share 48-52% amino acid identity with the
409 MaRNAV-1 segment II ORFs (Figure S9.B). The relative abundance of the *Leucocytozoon*
410 and MaRNAV-1 like transcripts were assessed and showed a strong correlation in all the
411 five RNA-Seq libraries (Figure 7).
412



413
414 **Figure 7.** Comparative abundance of MaRNAV-2 in *Leucocytozoon*-infected avian RNA-
415 Seq libraries.

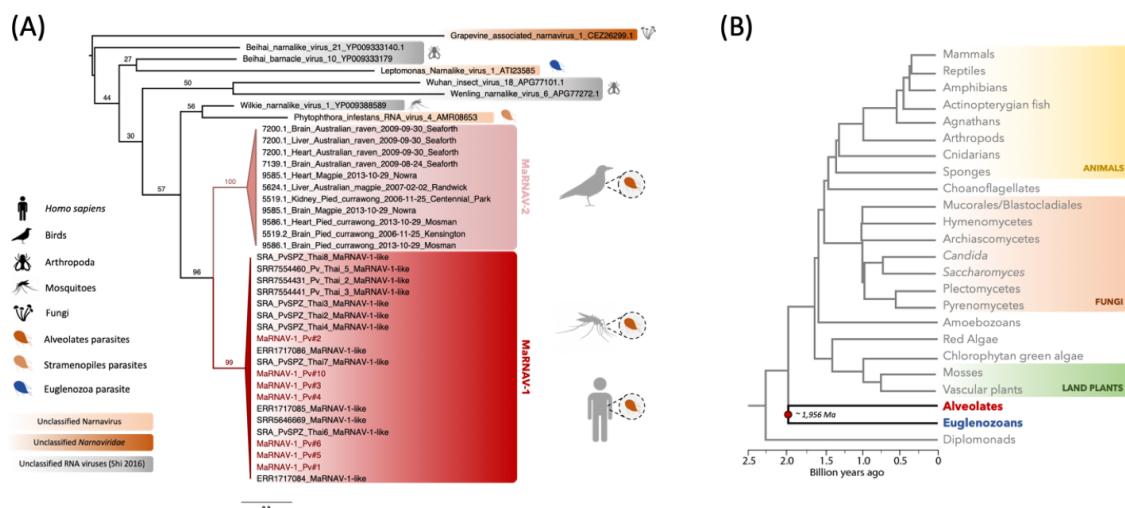
416
417 We also explored the association between the presence of the *Leucocytozoon* parasites
418 and the MaRNAV-1 virus homologs by performing RT-PCR on each individual sample
419 previously used to perform RNA-Seq. First, the two viral segments were always found as
420 both-present or both-absent for all of the 12 avian samples analyzed (Table S4, Figure S10).
421 In addition, in the majority of samples (25 of 27), the presence of the viral segments was
422 directly linked to the presence of the parasite: that is, the virus was present only when the
423 parasite was detected and absent in parasite-free samples (Table S4). This supports the
424 idea that the viral sequences screened are infecting the *Leucocytozoon* parasite rather than
425 the bird carrying it. Because of its similarity to *P. vivax* MaRNAV-1, we term this
426 *Leucocytozoon* parasite MaRNAV-2.

427
428 MaRNAV-2 sequences were highly prevalent and detected in 6 of the 7 individual birds
429 carrying the *Leucocytozoon*, independently of the tissue, date of sampling or bird species

430 collected (Table S4). Interestingly, the only *Leucocytozoon* parasites free of MaRNAV-2
 431 (sample 9585.3 collected from an Australian Magpie) may belong to a different
 432 *Leucocytozoon* species as it is phylogenetically distinct from the cluster formed by all the
 433 other *Leucocytozoon* populations in an analysis of the cytB gene (Figure S11.A).

434
 435 A phylogenetic analysis of the *Leucocytozoon* MaRNAV-2 amino acid sequences revealed a
 436 strong clustering of the RdRp-segment with the *P. vivax*-infecting MaRNAV-1 viruses
 437 (Figure 8). Together, these *Plasmodium* and *Leucocytozoon*-associated viruses appear to
 438 belong to a newly-described viral clade infecting haematozoa parasites. In addition, for
 439 both segment I (Figure S11.B) and segment II (Figure S11.C), the viral sequence variability
 440 between samples reflects the bird species rather than the location or the date of sampling.
 441 Interestingly, the overall level of divergence is similar between the two putative segments
 442 (between 86 and 100% identical nucleotide sites).

443



444
 445 **Figure 8. Evolutionary relationships of the newly-identified hematozoa viral sequences**
 446 **(MaRNAV-1 and MaRNAV-2).** (A) Phylogeny of all the newly-identified viral sequences.
 447 Red box: *P. vivax* viruses MaRNAV-1 (human or mosquitoes infection stage). Pink box:
 448 *Leucocytozoon sp.* MaRNAV-2 (bird infection stage). MaRNAV-1 viruses identified from *P.*
 449 *vivax* samples from this study are highlighted in red. Putative protozoan hosts are coloured
 450 depending on their belonging to the Alveolates (orange dark), Stramenopiles (light orange)
 451 and Euglenozoa (blue) major eukaryotic groups. Numbers indicate the branch support from
 452 1000 bootstrap replicates. The virus tree is mid-point rooted for clarity only. (B) Eukaryotic
 453 host evolution and timescale, adapted from (Hedges et al., 2004). The two major groups

454 Alveolates (red) and Euglenozoa (blue) are basal and their separation potentially occurred
455 approximately two billion years ago (*Hedges et al., 2004*).

456

457 **Discussion**

458 Our meta-transcriptomic study of human blood samples infected with three major
459 *Plasmodium* species revealed the presence of a highly abundant and geographically
460 dispersed bi-segmented RNA virus in *P. vivax* that we named Matryoshka RNA virus 1
461 (MaRNAV-1). To the best of our knowledge this is the first documented RNA virus in the
462 genus *Plasmodium*, and more broadly in parasites of the Apicomplexa subclass
463 hematozoa. An additional investigation of complementary data sets from the SRA similarly
464 provided strong evidence for the presence of MaRNAV-1 in *P. vivax*, but not in any of the
465 other *Plasmodium* species analyzed. Notably, MaRNAV-1 is both highly conserved and at
466 high prevalence in *P. vivax* populations from both South East Asia and South America.
467 Finally, we documented closely related-viral sequences - MaRNAV-2 - in avian samples
468 infected with *Plasmodium*-related *Leucocytozoon* parasites. The divergent nature of the
469 *Plasmodium* and *Leucocytozoon* viruses identified here, including the unique presence of a
470 second genome segment, raises the possibility that they should be classified as a new
471 genus or family, although this may require additional sampling.

472

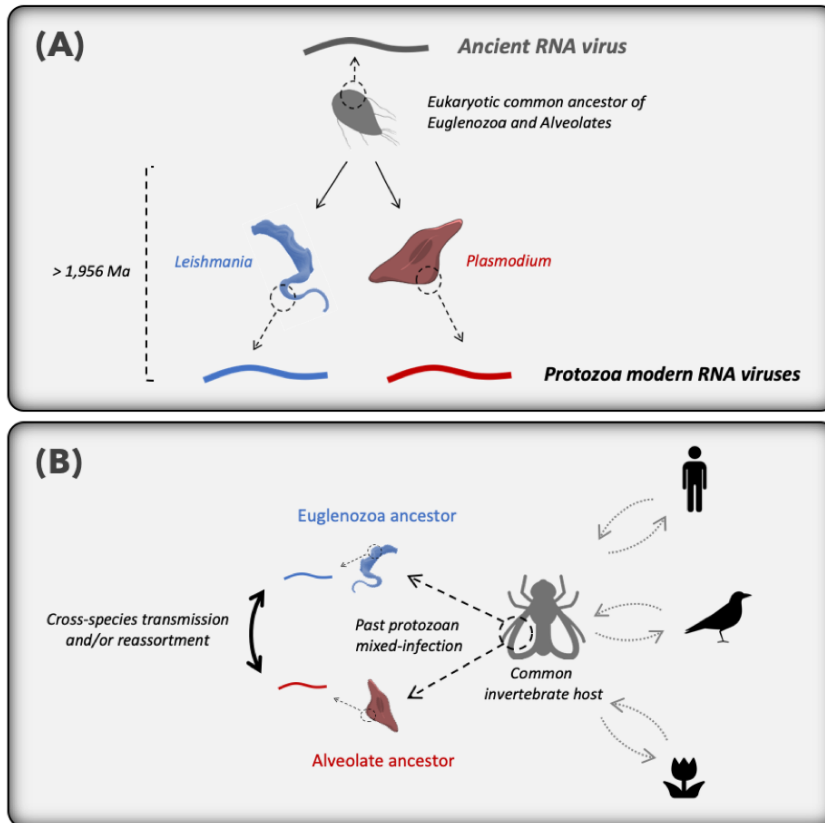
473 The first segment of MaRNAV-1 encodes a single ORF containing the conserved RdRp-
474 motif that is related to those found in the *Narnaviridae*, while the second segment, which is
475 not characteristic of narnaviruses, encodes two overlapping ORFs of unknown function.
476 The family *Narnaviridae* comprises a capsid-less viral family that infects plants, fungi and
477 protists. Interestingly, no sequences associated with fungi were observed in our samples,
478 suggesting that this virus is indeed likely to infect *Plasmodium*. In addition, the closest RNA
479 virus homologs were also observed in protozoans, or in arthropods that could conceivably
480 be infected by protozoan parasites (*Shi et al., 2016; Shi et al., 2017*). Such a strong virus-
481 protist association evidence was reinforced by the consistent link between this virus and *P.*
482 *vivax*, rather than to the metazoan hosts (mosquitoes and human) from which the samples
483 were extracted, or the other *Plasmodium* species.

484

485 The evolutionary origin of these novel *Plasmodium* and *Leucocytozoon* viruses is less clear,
486 but can be framed as two hypotheses: (i) an ancient virus-host co-divergence between the
487 Euglenozoa (e.g. *Leptomonas*) and Alveolate (including the hematozoa) groups of
488 eukaryotes at almost two billion years ago (*Hedges et al., 2004*) (Figure 9A), or (ii) horizontal

489 virus transfer events between either a secondary (likely invertebrate) host and protozoan
490 parasites, or among two protozoan parasites co-infecting the same secondary host, over
491 an unknown time-scale (Figure 9B). Given the very high rates of evolutionary change in RNA
492 viruses (*Duffy et al., 2008*), the recognizable sequence similarity between the narna-like
493 RNA viruses from *Plasmodium* (Alveolates, Apicomplexa) and *Leptomonas* (Euglenozoa,
494 kinetoplastids) suggests that they are unlikely to have arisen from a common ancestor that
495 lived approximately two billion years ago (Figure 8.B, Figure 9). Some Euglenozoa and
496 Alveolates independently evolved a parasitic lifestyle by infecting invertebrates and, more
497 recently, vertebrate hosts. Hence, it is more likely that the protozoan narnavirus-like
498 similarities reflects viral cross-species transmission between two protozoan parasites
499 during mixed-infection in either vertebrate or invertebrate hosts (Figure 9B). The wide
500 distribution and prevalence of MaRNAV-1 in *P. vivax* populations, as well as in the different
501 species of *Leishmania* parasites investigated previously, supports the idea that this host
502 jumping event is relatively ancient, although the exact time-scale is difficult to determine. As
503 previously demonstrated, invertebrates play a key role in RNA virus evolution by feeding on
504 many different hosts and transmitting viruses, fungi and protozoa among both plants and
505 vertebrates (*Li et al., 2015; Shi et al., 2016*). This may also explain why narnaviruses or
506 closely related RNA virus have been able to spread to such a diverse range of eukaryotes,
507 including Fungi, Stramenopiles, Alveolates and Euglenozoa. Moreover, the recent
508 characterization of a narnavirus in the plant-infecting trypanosomatid *Phytomonas serpens*
509 (*Akopyants et al., 2016*) suggests that vertebrates are not likely to be the hosts where the
510 horizontal virus transfer occurred.

511



512

513 **Figure 9. Hypothetical scenarios for the origin and evolution of MaRNAV-1 and**
514 **MaRNAV-2 and relatives among parasites belonging to the Alveolates and**
515 **Euglenozoa.**

516

517 The RdRp segment of MaRNAV-1 documented here is clearly related to the narnavirus
518 RdRp, although we are unable to identify a clear homolog for the second, divergent
519 segment. Hence, as previously hypothesized for the tri-segmented plant RNA virus
520 ourmiaviruses that combine a *Narnaviridae*-like RdRp and *Tombusviridae*-like movement
521 and capsid proteins (Rastgou *et al.*, 2009), our newly-described viruses may have evolved
522 by reassortment of different RNA viruses during co-infection, resulting in the combination of
523 RdRp from Narnavirus and another two ORFs from an undescribed yet RNA virus family or
524 families (Figure 9B). Further investigation of the origins and functions of these hypothetical
525 proteins clearly need to be conducted, for both the understanding of the virus biological
526 cycle and its evolutionary history. Indeed, capsid-less elements cannot exist in an
527 extracellular state and are necessarily transmitted via intracellular mode (cell division or cell
528 mating) (Dolja and Koonin 2012; Hillman and Cai 2013).

529

530 *Narnaviridae* comprise some of the simplest viruses described to date, containing a single
531 segment encoding a single replicase. Despite this, they are still able to impact their hosts in
532 profound ways. For example, a reduction in host virulence (hypovirulence) has been
533 documented in the case of mitoviruses (a genus of *Narnaviridae* infecting Fungi) (Hillman
534 and Cai 2013). Combined with the previously reported impacts of dsRNA viral infections on
535 the biology, pathogenesis and treatment response of the human parasite *Leishmania*
536 (Gómez-Arreaza *et al.*, 2017), investigating the effects of newly discovered viruses on *P.*
537 *vivax* biology and pathogenesis is clearly an area of interest. Intuitively, the biological
538 consequences of the high prevalence of this virus in *P. vivax*-infected individuals must
539 represent an important avenue for future research. More broadly, the characterization of the
540 viral cycle of MaRNAV-1, their biology, and interactions with its host may also help to better
541 understand the biology and life-cycle of *P. vivax* parasites, as well as the modulation of host
542 and parasite responses leading to immunoevasion, pathogenesis and transmission. In
543 particular, future work should focus on the impact of virus infection on the hypnozoite liver
544 stage of *P. vivax*, which is not present among the other, virus-negative, *Plasmodium*
545 species assessed in this study, and is responsible for *P. vivax* infection relapses in human
546 hosts and ongoing transmission in the absence of specific liver treatment. Similarly, it will
547 be important to determine whether MaRNAV-1 or a related virus infects the other human
548 *Plasmodium spp.* with the hypnozoite life-cycle stage - *P. ovale curtisi* and *P. ovale wallikeri*
549 (White 2016) - as well as the possible role of viral infection in promoting immunoevasion,
550 such as asymptomatic infection (Pava *et al.*, 2016) or pathogenesis (Barber *et al.*, 2015).

551

552 **Materials and Methods**

553

554 **Ethics statement**

555 The study was approved by the ethics committees of the Malaysian Ministry of Health
556 (NMRR-10-754-6684) and Menzies School of Health Research (HREC 2010-1431).

557

558 **Biological samples**

559 Whole blood samples (1 ml) were collected at district hospitals from healthy and
560 *Plasmodium*-infected patients in the state of Sabah, east Malaysia in 2013-14. Patients had
561 a clinical illness consistent with malaria, with blood collected prior to antimalarial treatment.
562 Parasite density was quantified by research microscopy using pre-treatment slides and
563 reported as the number of parasites per 200 leukocytes from thick blood film. This was
564 converted into the number of parasites per microliter using the patient's leukocyte count

565 from their hospital automated hematology result. Remaining blood samples were stored in
566 RNeasy and conserved at -80°C until RNA extraction. Sampling locations, sampling dates,
567 *Plasmodium* species validation and parasite counts are reported in Table S1.

568

569 PCR validation for *P. vivax* and *P. falciparum* were conducted following Padley *et al.* (2003).
570 A single-round PCR was performed using one single reverse primer in combination with
571 species-specific forward primers (Table S5). The *P. knowlesi*-infected sample validation
572 were conducted following Imwong *et al.* (2009) using a nested-PCR strategy with two
573 primer couples: rPLU3 and rPLU4 for the first PCR, and PkF1140 and PkR1150 for the
574 nested PCR (see Table S5 for the corresponding sequences).

575

576 **Total RNA extraction and RNA sequencing**

577 Total RNAs were extracted from blood samples using the Qiagen® RNeasy Plus Universal
578 MIDI kit and following manufacturer's instructions. Importantly, randomized and serial
579 extractions were conducted to prevent potential experimental biases and to facilitate the
580 detection of kit, columns, reagents or extraction-specific contamination from the
581 corresponding meta-transcriptomic data.

582

583 Total RNA samples were grouped by *Plasmodium* species and pooled in equimolar ratios
584 into a single sample. Quality assessments were then conducted and four TruSeq stranded
585 libraries were synthesized by the Australian Genome Research facility (AGRF), including a
586 rRNA and globin mRNA depletion using RiboZero and globin depletion kit from Illumina®.
587 Resulting libraries were run on HiSeq2500 (paired-end, 100bp) from the AGRF platform
588 (RNA samples quality and the features of each library are described in Table S6).

589

590 **rRNA and host read depletion**

591 Raw reads were first trimmed using the Trimmomatic software (Bolger *et al.*, 2014) to
592 remove Illumina adapters and low-quality bases. Human, ribosomal RNA (rRNA) and
593 *Plasmodium* associated reads were removed from the data sets by successively mapping
594 the trimmed reads to the latest versions of each corresponding reference sequence
595 databases (see Table S7 for more details) with either SortmeRNA (Kopylova *et al.*, 2012) or
596 Bowtie2 software and by applying local and very-sensitive options for the alignment
597 (Langmead and Salzberg 2012). All corresponding databases and the software used for the
598 host analyses and rRNA depletions are summarized in Table S7.

599

600 **Contig assembly and counting**

601 Depleted read data sets were assembled into longer contigs using the Trinity software
602 (*Grabherr et al., 2011*). The resulting contig abundances were estimated using the RSEM
603 software (*Li and Dewey 2011*).

604

605 **Virus discovery**

606 A global sequence-based homology detection was performed using Blastn and Diamond
607 Blastx (*Buchfink et al., 2015*) against the entire non-redundant nucleotide (nt) or protein (nr)
608 databases with using e-values of 1e-10 and 1e-5, respectively. Profiling plots were
609 obtained by clustering contigs based on the taxonomy of their best Blastn and/or Blastx
610 hits (highest Blast score) and plotting their respective length and abundance using ggplot2
611 (*Wickham 2009*).

612

613 In parallel, a RNA virus-specific sequence-based homology detection was conducted by
614 first aligning our data sets to a viral RdRp database using Diamond Blastx. To ensure the
615 removal of false-positives, a second Blastx round using exhaustive hits output parameters
616 was performed on each RdRP-matched contigs to discard contigs which are more likely
617 from a non-viral source. True-positive viral contigs were merged when possible and further
618 analysed using Geneious 11.1.4 software (*Kearse et al., 2012*).

619

620 “Unknown contigs” (i.e. contigs with no Blastx hit) longer than 1kb were retained and
621 submitted to a second round of Blastx using low-stringent cut-off of 1e-4. HMM-profile and
622 structural-based homology searches were also performed on these unknown contigs using
623 the normal mode search of the Protein Homology/analogy Recognition Engine v 2.0
624 (Phyre2) web portal (*Kearse et al., 2012; Kelley et al., 2015*). Briefly, the amino acid
625 sequences of predicted ORFs were first compared to a curated non-redundant nr20 data
626 set (comprising only sequences with <20% mutual identity) using HHblits (*Remmert et al.,*
627 *2012*). Secondary structures were predicted from the multiple sequence alignment and this
628 information was converted into a Hidden Markov model (HMM). This HMM was then used
629 as a query against a HMM database built from proteins of known 3D-structures and using
630 HHsearch (*Söding 2005*). Finally, a 3D-structure modelling step was performed using
631 HHsearch hits as templates, following the method described in *Remmert et al. (2012)*.

632

633 Virus-like sequences were further experimentally confirmed in total RNA samples by
634 performing cDNA synthesis using the SuperScript™ IV reverse transcriptase (Invitrogen™,

635 Catalog number: 11756500) and PCR amplification with virus candidate specific primers
636 using the Platinum™ SuperFi™ DNA polymerase (Invitrogen™, Catalog number:
637 12359010). Amplified products were Sanger sequenced using intermediary primers
638 enabling a full-length coverage (all primers are listed in Table S5).

639

640 **Host-virus assignment**

641 To help assign a virus to a specific host (i.e. determining which host organism these viruses
642 likely infect), we analyzed both codon usage bias and genomic dinucleotide composition (*Di*
643 *Giallonardo et al., 2017; Su et al., 2009*). Accordingly, the average codon usage of *H.*
644 *sapiens* and *P. vivax* were retrieved from the Codon Usage Database (available at
645 <http://www.kazusa.or.jp/codon/>) and the codon adaptation index (CAI) and associated
646 expected-CAI (eCAI) were determined using the CAIcal web-server, available at
647 <http://genomes.urv.es/CAIcal/E-CAI/> (*Puigbò et al., 2008*). The most prevalent *Anopheles*
648 mosquito vector in the Sabah region of Malaysia (*Anopheles balabacensis*) did not have a
649 codon usage table available. Hence, in this case we retrieved the codon usage from seven
650 other *Anopheles* species (*A. dirus*, *A. minimus*, *A. cracens*, *A. gambiae*, *A. culicifacies*, *A.*
651 *merus* and *A. stephensi*) which included major vectors of malaria in South East Asia.

652

653 As well as codon bias, we determined the dinucleotide composition of MaRNAV-1 and
654 compared to that of *Anopheles gambiae* (RefSeq | GCF_000005575.2) and *P. vivax* (RefSeq
655 | GCF_000002415.2). The match between host and virus was then calculated using the
656 method described in *Di Giallonardo et al. (2017)* by calculating the f/ffratio from the
657 MaRNAV-1 sequences obtained by Sanger sequencing (see above).

658

659 **Virus genome characterization**

660 Validated virus-like genomes were further characterized using both genome/protein
661 annotation programs, including InterProScan for protein domain, Sigcleave and Fuzzpro
662 from EMBOSS package for signal cleavage sites and motifs, and TMHMM for
663 transmembrane regions (*Krogh et al., 2001; Mulder and Apweiler 2007*).

664

665 **Mining of the Sequence Read Archive (SRA)**

666 To identify homologs of MaRNAV-1, the newly identified Narna-like virus sequence was
667 used as a reference in both Magic-blast blastn (default parameters) (*Boratyn et al., 2018*)
668 and Diamond blastx (cut-off 1e-5) (*Buchfink et al., 2015*) analyses of several RNA-seq data
669 sets obtained from *Plasmodium sp.* available on the NCBI SRA using the NCBI SRA toolkit

670 v2.9.2. The list of the corresponding BioProjects, runs and references are provided in Table
671 S2.

672
673 *P. vivax* SRA library information (i.e. host, location and biological replicates) was manually
674 retrieved from the corresponding papers (Table S3). When possible, this information was
675 used to assess whether such variables were associated with the detection of narna-like
676 viruses by performing Chi-squared tests using the SPSS Statistics software (IBM®). SRA
677 runs positive for homologs to MaRNAV-1 (number of read blast hits >100) were imported
678 locally and assembled following the same workflow as previously used to extract
679 homologous full-length contigs and to calculate their relative abundance in the samples.

680
681 To further assess host assignments, the same SRA data sets were subjected to Magic-
682 Blast using *Plasmodium* and mosquito and human specific housekeeping gene transcripts
683 (LDH-P gb|M93720.1 and RSP-7 gb|L20837.1, respectively). This large-scale analysis may
684 necessarily result in false-negative results because of the idiosyncrasies of the experimental
685 procedures used, such as the depletion of human reads or *Plasmodium* RNA enrichment,
686 both of which can bias such host read counting. Moreover, some samples come from the
687 same biological replicate and hence cannot be counted as independent. Such potential
688 biases forced us to manually retrieve all information for each *P. vivax* SRA library using
689 related publications (Table S3).

690

691 **Phylogenetic analysis**

692 Predicted ORFs containing the viral RNA-dependent (RdRp) domain from both the SRA and
693 human blood and bird associated sequences (see below) were translated and aligned using
694 the E-INS-I algorithm in MAFFT v7.309 (Kato and Standley 2013). To place the newly
695 identified viruses into a more expansive phylogeny of RNA viruses, reference protein
696 sequences of the closest homologous viral families or genera were retrieved from NCBI and
697 incorporated to the amino acid sequence alignment. The alignments were then trimmed
698 with Gblocks under the lowest stringency parameters (Castresana 2000). The best-fit amino
699 acid substitution models were then inferred from each curated protein alignment using
700 either the Smart model selection (SMS) (Lefort et al., 2017) or ModelFinder
701 (Kalyaanamoorthy et al., 2017), and maximum likelihood phylogenetic trees were then
702 estimated with either PhyML (Guindon et al., 2009) or IQ-tree (Nguyen et al., 2015) with
703 bootstrapping (1000 replicates) used to assess node support. For clarity, all phylogenetic
704 trees were midpoint rooted.

705

706 **Analysis of avian meta-transcriptomic libraries**

707 To supplement our analysis of human *Plasmodium* samples, we analyzed four meta-
708 transcriptomic libraries sampled from four bird species (*Gymnorhina tibicen*, *Strepera*
709 *graculina*, *Corvus coronoides* and *Grallina cyanoleuca*) in New South Wales, Australia.
710 Sampling details are reported in Table S4. The RNA-Seq data analysis and the Blastx
711 detection of MaRNAV-1 homologs from bird sample data sets were conducted as
712 described above.

713

714 The PCR-based detection of both Narna-like viruses and *Leucocytozoon* parasites were
715 conducted using newly-designed primers corresponding to the *Leucocytozoon* homologs
716 of the MaRNAV-1 RdRp and segment II (primers are described in Table S5), and following
717 the same PCR protocol as described above. PCR-based *Leucocytozoon* detections were
718 performed using primers targeting the *Leucocytozoon* mitochondrial cytochrome B oxidase
719 gene as described in (*Pacheco et al., 2018*). All additional analyses of the bird data sets
720 were performed utilizing the software and tools described above.

721

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