1	The <i>Plasmodium falciparum</i> rhoptry protein RhopH3
2	plays essential roles in host cell invasion and nutrient
3	uptake
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- 52 Abstract

53	Merozoites of the protozoan parasite responsible for the most virulent form
54	of malaria, Plasmodium falciparum, invade erythrocytes. Invasion involves
55	discharge of rhoptries, specialized secretory organelles. Once intracellular,
56	parasites induce increased nutrient uptake by generating new permeability
57	pathways (NPP) including a <i>Plasmodium</i> surface anion channel (PSAC).
58	RhopH1/Clag3, one member of the three-protein RhopH complex, is
59	important for PSAC/NPP activity. However, the roles of the other members
60	of the RhopH complex in PSAC/NPP establishment are unknown and it is
61	unclear whether any of the RhopH proteins play a role in invasion. Here we
62	demonstrate that RhopH3, the smallest component of the complex, is
63	essential for parasite survival. Conditional truncation of RhopH3
64	substantially reduces invasive capacity. Those mutant parasites that do
65	invade are defective in nutrient import and die. Our results identify a dual
66	role for RhopH3 that links erythrocyte invasion to formation of the
67	PSAC/NPP essential for parasite survival within host erythrocytes.
68	

70 Introduction

71 Parasites of the genus *Plasmodium* are the causative agents of malaria, a 72 disease that claims nearly 600,000 lives each year (1). Of the five 73 *Plasmodium* species that infect humans, *Plasmodium* falciparum is 74 responsible for nearly all the mortality associated with malaria. The disease 75 is the result of asexual replication of the parasite in erythrocytes. For 76 approximately the first half of the 48 h P. falciparum intraerythrocytic life 77 cycle, the parasite exists in a mononuclear trophozoite form (the earliest 78 stages of which are generally referred to as ring stages), during which the 79 parasite grows rapidly. During this phase, P. falciparum-infected 80 erythrocytes gain the capacity to adhere to host vascular endothelium, a 81 process that depends on the export of parasite proteins to form adhesive 82 structures called knobs at the host erythrocyte surface. Nuclear division 83 then commences, initiating differentiation into a schizont (a process called 84 schizogony). This multinucleated form eventually undergoes segmentation 85 to form invasive merozoites that egress upon rupture of the infected 86 erythrocyte to invade new erythrocytes.

87 Egress and erythrocyte invasion involves the regulated discharge of 88 several sets of apical merozoite secretory organelles that are unique to 89 apicomplexan parasites. The largest of these organelles, called rhoptries, 90 contain several proteins involved in adhesion to the host cell. Rhoptries are 91 also thought to mediate formation of the nascent parasitophorous vacuole 92 (PV), a membranous compartment that surrounds the parasite after entry 93 has been completed (2,3). Despite the importance of rhoptries in invasion 94 and subsequent host cell remodeling, a detailed understanding of the

95	function of many rhoptry proteins is lacking. Rhoptries comprise at least two
96	subdomains(3) referred to as the rhoptry neck and the bulb. The contents of
97	these subdomains likely mediate different functions, as reflected by
98	evidence suggesting that they are released sequentially during invasion (4).
99	Proteins of the rhoptry neck are well conserved between Plasmodium spp.
100	and the related apicomplexan parasite Toxoplasma gondii, suggesting
101	conserved functions (3,5). In contrast, proteins of the rhoptry bulb appear
102	to be genus-specific, perhaps reflecting functions unique to each parasite
103	(3). A function for several <i>Plasmodium</i> rhoptry bulb proteins has been
104	proposed, such as a role for a protein called RAMA in transport of proteins
105	to the rhoptry (6), but the inability to produce mutants lacking these
106	proteins has precluded conclusive assignments of function (7). Hence, the
107	molecular functions of most rhoptry proteins remain unknown.
108	One component of the P. falciparum rhoptry bulb that has received
109	particular attention is the so-called high molecular weight (HMW) rhoptry or
110	RhopH complex, which consists of three proteins called RhopH1/Clag,
111	RhopH2, and RhopH3 (8,9). Whilst RhopH2 and RhopH3 are each encoded by
112	single-copy genes, RhopH1/Clag, the largest component of the complex,
113	exists in 5 isotypes encoded by separate genes entitled <i>clag2</i> , <i>clag3.1</i> ,
114	clag3.2, clag8 and clag9 (10,11). RhopH1/Clag3.1 and RhopH1/Clag3.2 are
115	nearly identical proteins that are expressed in a mutually exclusive manner
116	(12-14). Each RhopH complex contains only one form of RhopH1/Clag (11),
117	so each parasite has the potential to produce four different RhopH
118	complexes, differentiated by the particular RhopH1/Clag isotype bound. All
119	members of the RhopH complex are expressed late in the intraerythrocytic

120 cycle (8). The complex is then released during invasion (15) and inserted 121 into the nascent PV membrane (PVM) soon after parasite entry (16,17). 122 Genetic and chemical genetic investigation has revealed a role for 123 the RhopH1/Clag3 proteins in the function of the *Plasmodium* surface anion 124 channel (PSAC), a new permeability pathway (NPP) induced in host 125 erythrocytes following parasite entry and involved in nutrient acquisition by 126 the intracellular parasite (18). Pharmacological inhibition of 127 RhopH1/Clag3.2 function was found to block PSAC/NPP activity, and 128 selection for drug-resistant mutants revealed that part of the protein is 129 exposed at the surface of the erythrocyte and that it may form the channel 130 itself (19,20). However, parasites that do not produce either 131 RhopH1/Clag3.1 or RhopH1/Clag3.2 display only a small growth 132 disadvantage (13) and inhibition of the function of these proteins has only a 133 small effect on parasite growth rates in vitro (21). Parasites lacking 134 RhopH1/Clag9 are viable, and an early report suggested that loss of the 135 clag9 gene resulted in loss of binding to CD36 (22). However, this has been 136 disputed (23), as a subsequent study identified another gene closely linked 137 to the *clag9* gene that is important for CD36 binding (24). Hence, whilst the 138 function of RhopH1/Clag9 remains to be determined, like RhopH1/Clag3.1 139 and RhopH1/Clag 3.2, it is not essential. There are no reports describing a 140 deletion, or attempted deletion, of *clag2* or *clag8*. 141 Much less is known of the function of the RhopH2 and RhopH3 142 components of the complex. There is no report of attempted disruption of 143 the *rhopH2* gene, but the *rhopH3* gene is refractory to deletion in the 144 haploid blood stages (25), suggesting an essential role. Hints that this might

145 include a function in invasion derive from studies showing that antibodies to 146 RhopH3 can inhibit invasion (8,26). However, whether RhopH3 plays other 147 essential roles that involve all forms of the RhopH complex is unknown. 148 Here we use a conditional mutagenesis approach to modify the 149 rhopH3 gene in a manner that blocks formation of the RhopH complex. The 150 resulting mutant parasites show two distinct phenotypes: a significant 151 decrease in the level of erythrocyte invasion and a complete block in 152 intracellular development at the trophozoite stage. Our findings reveal that 153 RhopH3 and the RhopH complex have essential roles in two distinct stages of 154 the erythrocytic lifecycle.

155

156 Results

157 Efficient conditional truncation of the *rhopH3* gene. Previous attempts to 158 disrupt the *P. falciparum rhopH3* gene using conventional genetic 159 techniques were unsuccessful (25), suggesting an indispensable role in 160 asexual blood stages. To gain insights into this role we therefore adopted 161 the DiCre conditional recombinase system recently adapted to P. falciparum 162 (27) to examine the consequences of functional inactivation of RhopH3. For 163 this, we used Cas9-mediated genome editing (28) to introduce synthetic 164 introns containing loxP sites (29) into the rhopH3 gene such that they 165 flanked an internal region spanning exons 4-6, the region of the gene that 166 shows the highest level of conservation across *Plasmodium rhopH3* orthologs 167 (Figure 1A, Figure 1 - figure supplement 1). This genomic modification was 168 made in the DiCre-expressing P. falciparum 1G5DC parasite clone (27) in 169 order that excision of the floxed sequence could be induced by treatment of

the transgenic parasites with rapamycin. DiCre-mediated excision was
predicted to generate an internally-truncated mutant form of *rhopH3*lacking its most highly conserved region.

173 Successful modification of the *rhopH3* gene in the transfected 174 parasite population following introduction of the targeting vector was 175 confirmed by diagnostic PCR (not shown). Subsequent limiting dilution 176 cloning of the modified parasites resulted in the isolation of parasite clones 177 rhopH3-loxP 5F5 and rhopH3-loxP 4B11, which were derived from 178 independent transfections using different guide RNAs. Modification of the 179 native rhopH3 locus in the expected fashion was confirmed in both parasite 180 clones by diagnostic PCR and Southern blot (Figure 1B and Figure 1C). Both 181 clones displayed RhopH3 expression levels and in vitro replication rates 182 indistinguishable from the parental 1G5DC parasites (Figure 1 - figure 183 supplement 2), indicating that the modified *rhopH3* gene generated wild 184 type levels of RhopH3 and that the modifications had no impact on parasite 185 viability. The clones were therefore used for all subsequent experiments. 186 To examine the efficiency of conditional excision of the floxed 187 sequence in the *rhopH3-loxP* clones, tightly synchronized ring stage cultures 188 of both clones were divided into two and treated for 4 h with either 189 rapamycin or DMSO (vehicle control). Following washing and further 190 incubation for ~44 h to allow maturation of the parasites to schizont stage 191 (at which peak expression of RhopH3 occurs (8)), genomic DNA from the 192 clones was examined by PCR and Southern blot. This revealed highly 193 efficient excision of the floxed rhopH3 sequence (Figure 1D and Figure 1E).

194 DiCre-mediated site-specific recombination between the introduced 195 loxP sites in the modified rhopH3 locus of the rhopH3-loxP parasites was 196 expected to reconstitute a functional, albeit chimeric, intron. Upon splicing 197 of this intron exons 3 and 7 are placed in frame, producing a modified 198 RhopH3 gene product (called RhopH3∆4-6) that retains wild type N-terminal 199 and C-terminal segments but lacking residues encoded by exons 4-6. 200 Extracts of the rapamycin-treated and control parasites were analyzed by 201 immunoblot ~44 h following treatment using antibody anti-Ag-44, which 202 recognizes an epitope within the C-terminal segment of RhopH3 encoded by 203 exon 7 (30). As shown in Figure 1F and Figure 1 - figure supplement 3, 204 rapamycin treatment produced the expected change in mass, converting the 205 ~110 kDa wild-type RhopH3 to a ~70 kDa RhopH3 $\Delta$ 4-6 product. This 206 conversion was highly efficient, with no residual full-length protein 207 detected in the rapamycin-treated schizonts. These results confirmed the 208 excision data and demonstrated essentially complete conditional truncation 209 of RhopH3 within a single erythrocytic cycle in the *rhopH3-loxP* parasite 210 clones. 211 212 Truncation of *rhopH3* leads to mislocalization of other components of the 213 RhopH complex. We next aimed to determine the effects of RhopH3

truncation on its subcellular localization within the parasite, as well as on

215 the trafficking of other members of the RhopH complex.

216 Immunofluorescence analysis (IFA) showed that, as expected, RhopH3

colocalized with the rhoptry marker RAP2 (31,32) in mature schizonts of

218 control *rhopH3-loxP* parasites (Figure 2A). However, in rapamycin-treated

219 (RhopH $3\Delta$ 4-6) parasites, this colocalization was lost, although RAP2 was still 220 detected in a punctate, apically-disposed pattern typical of rhoptries 221 (Figure 2A). To determine the effects of this mistrafficking on localization of 222 the other two RhopH complex proteins, control and rapamycin-treated 223 *rhopH3-loxP* parasites were probed with anti-RAP2 as well as either anti-224 RhopH1/Clag3.1 (11) or anti-RhopH2 antibodies (9). This showed that, as in 225 the case of RhopH3, rhoptry localization of both RhopH1/Clag3.1 and 226 RhopH2 was lost in rapamycin-treated parasites (Figure 2A). These results 227 indicated that truncation of RhopH3 to the RhopH3 $\Delta$ 4-6 form resulted in 228 mistrafficking of at least some components of the RhopH complex. To 229 determine whether the mistrafficked rhoptry proteins all localized to the 230 same parasite compartment, the parasites were co-stained with various 231 combinations of antibodies against two of the three complex proteins. This 232 showed that neither RhopH2 nor RhopH1/Clag3.1 colocalized with 233 RhopH3 $\Delta$ 4-6 in the mutant parasites (Figure 2B). The RhopH2 and 234 RhopH1/Clag3.1 signals were also distinct in the mutant parasites, although 235 in this case some limited colocalization of these proteins was apparent 236 (bottom images, Figure 2B). 237 To better define the fate of the mistrafficked RhopH3∆4-6 in the

mutant parasites, rapamycin-treated mature schizonts were probed with antibodies to the merozoite plasma membrane surface marker MSP1. This indicated that the mutant protein was expressed in a location surrounding (and so likely external to) the plasma membrane of individual segmented intracellular merozoites (Figure 2 - figure supplement 1). In confirmation of this, IFA of naturally released free merozoites showed that the truncated

244 RhopH3 $\Delta$ 4-6 was often largely undetectable in merozoites of the mutant 245 parasites (Figure 2C).

246 One interpretation of these results was that truncation of RhopH3 247 interfered with formation of the RhopH complex. To test this notion, we 248 used a monoclonal antibody (mAb) specific for RhopH2 to 249 immunoprecipitate the complex from extracts of schizonts of rhopH3-loxP 250 clone 5F5. As shown in Figure 2D, both RhopH3 and RhopH1/Clag3.1 were 251 precipitated as expected from lysates of control parasites. In contrast, 252 RhopH $3\Delta$ 4-6 was undetectable in the precipitate from lysates of rapamycin-253 treated parasites, although RhopH1/Clag3.1 could still be detected. This 254 showed that truncation of RhopH3 ablates its association with RhopH2, 255 although it does not appear to affect the interaction between RhopH2 and 256 RhopH1/Clag3.1. Collectively, these results suggested that truncation of 257 RhopH3 caused mistrafficking of other components of the complex, probably 258 due to loss of the association between RhopH3 and these other proteins. 259 260 Loss of the RhopH complex is a lethal event. The above results showed

261 that whilst truncation of RhopH3 affected trafficking of the RhopH complex, 262 it did not prevent schizont development in the erythrocytic growth cycle in 263 which the parasites were treated with rapamycin (henceforth referred to as 264 cycle 1). To evaluate the effects of RhopH3 modification and mistrafficking 265 on longer-term parasite viability, we first exploited a recently developed 266 assay in which parasite replication is assessed in 96-well microplates over a 267 period of 5-7 erythrocytic cycles by visualization of the localized lysis of 268 host erythrocytes in static cultures in 96-well microplates. Under these

269 conditions, successful parasite growth results in formation of 270 microscopically discernible zones of clearance of erythrocytes referred to as 271 plaques (33). As shown in Table 1, in 3 separate assays DMSO-treated 272 rhopH3-loxP parasites seeded at ~10 parasites per well produced plagues in 273 nearly every well, with a mean average of ~8 plaques per well for clone 5F5 274 and  $\sim$ 5 plagues per well for clone 4B11 (Table 1). In contrast, in the plates 275 seeded with an identical density of rapamycin-treated parasites, only  $\sim 10\%$ 276 of the wells contained plagues and no well contained more than one plague 277 (Figure 3A, Table 1). Analysis by diagnostic PCR of several parasite clones 278 isolated from individual plagues that appeared in plates seeded with rapamycin-treated parasites revealed that in all cases they derived from 279 280 parasites that possessed an intact *rhopH3-loxP* gene, indicating that these 281 corresponded to a small subpopulation of parasites in which excision of the 282 floxed sequence had not taken place (Figure 3B). Further analysis by PCR of 283 one of these non-excised clones showed that the DiCre cassette had been 284 lost (Figure 3C) probably due to a genomic rearrangement. This parasite 285 clone (named RhopH3 NE) served as a useful control for subsequent 286 experiments.

To further examine the effects of RhopH3 truncation on long-term parasite viability, low parasitaemia cultures of the *rhopH3-loxP* clones 5F5 and 4B11 were divided equally into two flasks, treated with either DMSO or rapamycin, then the parasites simply maintained in continuous culture, monitoring increase in parasitaemia at 48 h intervals as well taking samples for analysis by diagnostic PCR. Cultures of the parental 1G5DC parasites as well as the DiCre-defective RhopH3 NE clone were similarly treated and

294 monitored in parallel. As shown in Figure 3D, whilst replication of the 295 1G5DC and RhopH3 NE parasites was unaffected by rapamycin treatment, 296 the rapamycin-treated 5F5 and 4B11 clones showed a dramatic decrease in 297 growth rate. However in both clones the appearance of replicating parasites 298 was evident by cycle 3, suggesting that these might correspond to a minor 299 population of normally-replicating non-excised parasites. Diagnostic PCR 300 analysis of the 5F5 culture supported this notion. At the end of cycle 1, PCR 301 using primers that distinguish between the excised and non-excised locus 302 showed the expected highly efficient excision of the floxed rhopH3-loxP 303 sequence in the rapamycin-treated culture, with the non-excised locus 304 undetectable. However, periodic examination of the parasites by diagnostic 305 PCR over the ensuing 6 erythrocytic cycles showed a time-dependent 306 increase in the proportion of non-excised parasites in the rapamycin-treated 307 culture, suggesting that the initially undetectable population of non-excised 308 parasites gradually overgrew the cultures. This occurred likely as a result of 309 a selective advantage conferred on them by the replication defect displayed 310 by the RhopH3 $\Delta$ 4-6 parasites. By cycle 5, the excised locus was hardly 311 detectable in the rapamycin-treated culture (Figure 3E). Together with the 312 results of the plague assay, these results allowed us to conclude that 313 truncation of RhopH3 results in complete loss of long-term parasite viability. 314 315 Loss of the RhopH complex leads to an invasion defect. The severe growth 316 defect displayed in the plague and growth assays could result from an

inability of mutant parasites to egress from the host erythrocyte, a block in

invasion, or a developmental arrest during intracellular growth. We

319 therefore next investigated the capacity of RhopH3 $\Delta$ 4-6 parasites to undergo 320 egress. For this, we used time-lapse differential interference contrast (DIC) 321 microscopy to observe the egress of merozoites from highly mature, 322 synchronized schizonts at the end of cycle 1 (i.e. ~45 h following treatment 323 of ring-stage *rhopH3-loxP* parasites with rapamycin or DMSO). This revealed 324 no gross differences in the efficiency or morphology of egress 325 (Supplementary video 1), indicating that the absence of the RhopH complex 326 from rhoptries does not affect egress.

327 To investigate a potential invasion phenotype resulting from RhopH3 328 truncation, a synchronized culture of *rhopH3-loxP* parasites at early ring 329 stage was divided into two, treated with either DMSO or rapamycin and then 330 allowed to mature to schizont stage before purifying the mature schizonts 331 and adding them to fresh erythrocytes. After incubation for a further 4 h to 332 allow the *rhopH3-loxP* schizonts to undergo merozoite egress and invasion, 333 the percentage of erythrocytes infected with cycle 2 ring-stage parasites 334 was quantified. The results consistently showed that the ring-stage 335 parasitemia values in cultures derived from the rapamycin-treated rhopH3-336 loxP parasites was only ~50% of that in their DMSO-treated counterparts 337 (Figure 3F). Importantly, invasion by the control RhopH3 NE and the 338 parental 1G5DC parasites was unaffected by rapamycin treatment. Taken 339 together with the other results, these data showed that the absence of the 340 RhopH complex from parasite rhoptries significantly affects the ability of 341 the parasite to invade new host cells.

342

343 The RhopH complex is required for intracellular parasite development. 344 Although the results of the above experiments pointed to a severe invasion 345 defect in parasites lacking the RhopH complex, it was unclear whether this 346 could be sufficient to explain the results of the plaque assay, which 347 indicated a complete lack of long-term viability in the RhopH3 $\Delta$ 4-6 mutants. 348 To explore this further, we examined growth and development of the 349 mutants using microscopic examination of Giemsa-stained cultures. This 350 showed that whereas rapamycin-treated *rhopH3-loxP* parasites appeared 351 morphologically normal at the end of the cycle 1 as well as at the ring stage 352 of cycle 2, development of the mutant parasites stalled at trophozoite stage 353 in cycle 2 (Figure 4A) and the parasites did not develop into schizonts. To 354 confirm this developmental block we used flow cytometry to monitor the 355 DNA content of the parasites in cycle 2. This confirmed that rings derived 356 from rapamycin-treated *rhopH3-loxP* parasites did not increase their DNA 357 content during cycle 2 (Figure 4B), i.e. they did not progress to the 358 multinuclear schizont stage. Taken together, these data indicated that the 359 RhopH complex is essential for the trophozoite to schizont developmental 360 transition of the intracellular parasite.

361

362 Protein export occurs normally in the RhopH3∆4-6 mutants. Export of

parasite proteins into the host erythrocyte is important for parasite
virulence and for the uptake of nutrients; blocking export prevents
modification of the erythrocyte surface with the knob structures that play a
role in cytoadhesion, and also prevents development of the parasite beyond
the trophozoite stage (34,35). Since we observed a similar growth

368 phenotype in cycle 2 in the RhopH $_{3\Delta4}$ -6 parasites, we decided to determine 369 whether the developmental arrest was the result of a generalized defect in 370 protein export. To do this, we examined the subcellular localization of 371 KAHRP and MAHRP1, parasite proteins that are established markers for 372 protein export and Maurer's clefts (intraerythrocytic membranous structures 373 of parasite origin) respectively, in cycle 2 trophozoites derived from 374 rapamycin-treated *rhopH3-loxP* parasites (36,37). This revealed no 375 discernible alterations in protein export and Maurer's cleft formation in the 376 RhopH3 $\Delta$ 4-6 mutants (Figure 5A). This conclusion was corroborated by 377 electron microscopy, which revealed the formation of knobs on the surface 378 of erythrocytes infected with rapamycin-treated rhopH3-loxP parasites 379 (Figure 5B). We concluded that protein export from the intracellular 380 parasite can take place normally in the absence of the RhopH complex. 381

382 Import pathways are defective in *rhopH3* mutant parasites. The developmental arrest observed in cycle 2 trophozoites of the RhopH3<sub>4</sub>-6 383 384 parasites was strikingly reminiscent of the effect of isoleucine starvation on 385 P. falciparum (38) Isoleucine is transported into the parasitized cell via the 386 PSAC/NPP, the parasite-induced uptake pathway responsible for enhanced 387 nutrient uptake in parasite-infected erythrocytes (39). The PSAC/NPP is also 388 responsible for the permeability of parasite-infected erythrocytes to the 389 alcohol sugar sorbitol (18), leading to the capacity of sorbitol solutions to 390 mediate osmotic lysis of infected erythrocytes. This lysis can be readily 391 quantified by measuring levels of host cell hemoglobin released following 392 treatment of parasitized cells with a sorbitol solution (40). To determine

393 whether the PSAC/NPP was functional in the RhopH3<sub>4</sub>-6 mutants, their 394 resistance to sorbitol-mediated lysis was assessed. As shown in Figure 6A, 395 erythrocytes infected with parental 1G5DC parasites or the non-excised 396 RhopH3 NE clone displayed the expected sensitivity to sorbitol, as did 397 erythrocytes infected with control (DMSO-treated) rhopH3-loxP parasites. In 398 contrast, erythrocytes infected with cycle 2 rapamycin-treated rhopH3-loxP 399 parasites were insensitive to sorbitol; the amount of hemoglobin released 400 upon sorbitol treatment was not significantly different from the amount 401 released by treatment of the infected erythrocytes with an isotonic control 402 buffer (PBS).

403 To further investigate the activity of the PSAC/NPP in the RhopH3<sub>4</sub>-404 6 mutants, erythrocytes infected with cycle 2 rings were incubated with 5-405 aminolevulinic acid (5-ALA). This compound is excluded from uninfected 406 erythrocytes but is taken up by infected erythrocytes and converted to 407 fluorescent protoporphyrin IX (PPIX) (41). Import of 5-ALA has previously 408 been shown to be sensitive to furosemide, a small molecule inhibitor of 409 PSAC/NPP, and is also blocked upon downregulation of parasite export and 410 PSAC/NPP activity in transgenic P. falciparum (34,41,42). Import of 5-ALA 411 therefore acts as a convenient reporter for PSAC/NPP activity. Examination 412 by fluorescence microscopy (Figure 6B and 6C) and FACS (Figure 6D) showed 413 that erythrocytes infected with DMSO-treated *rhopH3-loxP* clone 5F5 and 414 4B11 parasites readily took up 5-ALA, whereas no fluorescence was observed 415 in erythrocytes infected with rapamycin-treated *rhopH3-loxP* parasites 416 following incubation with 5-ALA. In contrast, rapamycin-treatment had no 417 effect on the capacity of the parental 1G5DC or DiCre-deficient RhopH3 NE

parasites to take up 5-ALA (Figure 6B-D). Combined, these results
convincingly indicate that the PSAC/NPP is defective in the *rhopH3* mutants.

421 Discussion

422 In this study we have shown that RhopH3 plays a central role in the 423 formation of a functional RhopH complex and that mutation of RhopH3 424 results in two severe, but very distinct, phenotypes: 1) a ~50% decrease in 425 host erythrocyte invasion; and 2) a block in the development in the early 426 trophozoite stage of those parasites that do invade. This block in 427 development is a lethal event; no parasites carrying the mutant form of the 428 rhopH3-loxP gene were recovered in a plague assay and parasites with an 429 intact rhopH3-loxP gene quickly outgrew the mutant parasites after 430 rapamycin treatment. These results represent the first published evidence 431 that RhopH3 is essential and mark the first time a rhoptry protein has been 432 shown to have two separate, seemingly unrelated functions at different 433 stages of the erythrocytic life cycle. RhopH3 is also the first rhoptry bulb 434 protein to be directly assigned a role in invasion; other rhoptry proteins 435 previously experimentally implicated in invasion are located in the rhoptry 436 neck. The release of rhoptry neck proteins is considered the step at which 437 the parasite commits to host cell entry (43), so the discovery of an 438 important invasion factor that is presumably released later in the invasion 439 pathway is important.

Whilst it was surprising that loss of the function of the RhopH
complex leads to two different, seemingly unrelated, phenotypes, previous
results had hinted at a role for RhopH3 and the complex in both processes.

443 RhopH3, and proteolytic fragments of RhopH3, can bind to erythrocytes and 444 to liposomes (44,45). This appears to occur even in the absence of other 445 members of the RhopH complex, indicating that, for its role in invasion, 446 RhopH3 may not require the function of the other proteins of the complex. 447 Further supporting a role for RhopH3 in invasion is the finding that anti-448 RhopH3 antibodies can block invasion (26,45). Nonetheless it is curious that 449  $\sim$ 50% of the parasites still enter the erythrocyte in the absence of full-length 450 RhopH3. RhopH3 $\Delta$ 4-6 may retain sufficient activity in 50% of the parasites to 451 allow invasion to take place. Alternatively, these parasites could use a 452 RhopH3-independent pathway. Invasion by P. falciparum relies on several redundant pathways and there is precedent for a partial reduction of 453 454 invasion by mutant parasites (46). It will be of interest to determine 455 whether invasion pathways that are currently thought to be redundant 456 become essential in the absence of wild type RhopH3. A third possibility is 457 that RhopH3 is involved in a post-invasion process. However, the invasion 458 assay used here would detect all intracellular parasites that have completed 459 invasion. We therefore favor the interpretation that the observed decrease 460 in the number of newly invaded *rhopH3-loxP* parasites indicates that the 461 invasion process is not completed in the mutants.

The other phenotype displayed by the RhopH3 $\Delta$ 4-6 mutants, the block in development during the early trophozoite stage, is likely the result of a defect in nutrient intake owing to improper trafficking ablating the function of RhopH1/Clag. The loss of sorbitol sensitivity of erythrocytes infected with the RhopH3 $\Delta$ 4-6 mutants and their impermeability to 5-ALA indicate that RhopH1/Clag3.1 (the RhopH1/Clag3 isotype expressed in these 3D7-derived

468	parasites) and RhopH1/Clag3.2 are not functioning at the erythrocyte
469	surface. RhopH1/Clag3 proteins are transported to the erythrocyte surface
470	in a PEXEL-independent manner (34) and are exposed on the surface of the
471	erythrocyte (19), but the mechanism by which these proteins are
472	transported from the rhoptry, beyond the PVM and to the erythrocyte
473	plasma membrane is unknown. RhopH3 and RhopH2 are have been detected
474	in the PVM immediately after invasion, (17)(47), as well as in the
475	erythrocyte at later developmental stages of the intraerythrocytic parasite
476	(34,48). It is likely that mislocalization of RhopH3 $\Delta$ 4-6 in merozoites
477	prevents the proper, or properly timed, release of the complex during
478	invasion and prevents RhopH1/Clag from being delivered to its correct
479	location. As the RhopH1/Clag3.1 and RhopH1/Clag 3.2 in the trophozoite
480	stage parasite derives entirely from protein that is introduced during
481	invasion (15), mislocalization at the merozoite stage likely cannot be
482	corrected by additional subsequent protein synthesis.
483	The complete arrest in development of the RhopH3 ${\scriptstyle\Delta}4$ -6 mutants in
484	the cycle following gene modification (cycle 2) also provides insight into the
485	potential roles of the RhopH1/Clag proteins. Little is known about these
486	proteins other than the importance of the RhopH1/Clag3.1 and RhopH1/Clag
487	3.2 proteins in the PSAC (18). However, chemical inhibition of
488	RhopH1/Clag3.2 function and PSAC activity in parasites cultured in rich
489	medium (RPMI 1640, the same medium used in this study) leads to only a
490	small decrease in parasite viability (21). Similarly, parasites that do not
491	produce RhopH1/Clag3.1 or RhopH1/Clag 3.2 have only a minimal growth
492	disadvantage compared to wildtype parasites in a competition assay (13).

493 Parasites lacking RhopH1/Clag9 have no apparent growth phenotype in vitro 494 (the gene is absent from the D10 and T9-96 laboratory strains that lack part 495 of chromosome 9) (49,50). In contrast, parasites lacking RhopH1/Clag2 or 496 RhopH1/Clag8 have not been reported so the essentiality of these proteins 497 is unknown. We speculate that the RhopH $3\Delta$ 4-6 mutants very likely transport 498 none of the RhopH1/Clag proteins to the erythrocyte surface. If so, the 499 observed growth phenotype is therefore essentially that of a disruption of 500 all the *clag* genes. The striking growth phenotype of this mutant is in stark 501 contrast to the mild phenotype of RhopH1/Clag3.2 inhibition (21) or the 502 absence of both the RhopH1/Clag3 proteins (13) when the parasites are 503 grown in RPMI. This may indicate that RhopH1/Clag2 and RhopH1/Clag8 play 504 important roles in nutrient uptake as well, as previously suggested (21), and 505 that RhopH complexes containing several different RhopH1/Clag proteins 506 together mediate the uptake of the nutrients required for parasite growth in 507 the infected erythrocyte. Interestingly, most *Plasmodium* species encode 508 fewer RhopH1/Clag proteins than *P. falciparum*; some species possess only 509 two *clag* genes, comprising a *clag9* orthologue and a second orthologue more 510 closely related to the other *P. falciparum clag* genes (3,10). In conclusion, 511 our results raise the intriguing possibility that, in *P. falciparum*, 512 RhopH1/Clag proteins in addition to RhopH1/Clag3.1 and RhopH1/Clag3.2 513 function in nutrient import. 514

Together the results presented in this study provide new insights into the role of the rhoptry in the malarial blood stages and reveal that rhoptry proteins can function in multiple, distinct processes. They furthermore show that the functions of rhoptry proteins extend beyond the initial invasion of

the erythrocyte and can affect parasite growth throughout the blood stagelife cycle.

520

521 Materials and methods

522 Reagents and antibodies, Oligonucleotide primers were from Sigma-Aldrich, 523 as was rapamycin (cat# R0395), which was prepared as a 10 µM stock in 524 DMSO. 5-aminoleuvlinic acid (5-ALA) from Sigma-Aldrich (cat# A3785) was 525 prepared as a 1 mM stock in DMSO. Restriction enzymes were from New 526 England Biolabs. The antifolate drug WR99120 (Jacobus Pharmaceuticals, 527 New Jersey, USA), was stored as a 20 µM stock in DMSO. Polyclonal 528 antiserum  $\alpha$ -Ag44, which recognizes the C-terminal 134 amino acid residues 529 of RhopH3 (30), was a kind gift of Ross Coppel (Monash University, 530 Australia). A polyclonal antiserum against *P. falciparum* AMA1 has been 531 previously described (51), as have polyclonal antibodies against P. 532 falciparum MSP1 and the anti-MSP1 mAb 89.1 (52). Other antibodies were 533 kindly provided by Osamu Kaneko, Nagasaki University Japan (rabbit anti-534 RhopH1/Clag3.1A), John Vakonakis, University of Oxford UK (rabbit anti-535 MAHRP1), Ross Coppel at Monash University Australia (anti-KAHRP), Tony 536 Holder, the Francis Crick Institute UK (anti-RhopH2 mAb 61.3). Monoclonal 537 antibody 7.7 (anti-EXP2) was from The European Malaria Reagent 538 Repository, contributed by Jana McBride and the mouse anti-RAP2 mAb 539 MRA-876 was obtained from BEI resources, National Institute of Allergy and 540 Infectious Disease (NIAID), National Institutes of Health (NIH), contributed 541 by Allan Saul. Use of these antibodies in immunoblot and IFA analyses have 542 been described elsewhere (9,11,30,51,53-56).

544 P. falciparum culture, transfection and growth analysis. All P. falciparum 545 transgenesis work described used the 3D7-derived DiCre-expressing clone 546 1G5DiCre (27), here referred to as 1G5DC. Asexual blood stage parasites 547 were continuously cultured in RPMI 1640 medium containing Albumax 548 (Gibco) as a serum substitute and synchronised using established procedures 549 (57). For introduction of transfection plasmids, mature schizonts were 550 enriched using Percoll (GE Healthcare) and electroporated using an Amaxa 551 4D electroporator and P3 Primary cell 4D Nucleofector X Kit L (Lonza) using 552 programme FP158 as described (27). 553 Long-term parasite growth as measured by plaque-forming ability was 554 determined by diluting trophozoite-stage cultures to a density of 10

555 parasites per well in complete medium with human erythrocytes at a

haematocrit of 0.75% and plating 200  $\mu L$  of this suspension into flat

557 bottomed 96 well microplates, as previously described (33). Plates were

incubated for 10 days in gassed humidified sealed modular chambers before

559 plaque formation was assessed by microscopic examination using a Nikon

560 TMS inverted microscope (40x magnification) and documented using a

561 Perfection V750 Pro scanner (Epson).

562 Growth characteristics of mutant parasites were determined by

563 microscopy of Giemsa-stained thin films. Long-term growth was also

measured using flow cytometry of hydroethidine-stained trophozoite-stage

parasites, as described (58). Cultures adjusted to a parasitaemia of 0.1%

566 were monitored every 48 h for up to 7 intraerythrocytic cycles. All

567 experiments were carried out in triplicate, data analysed using GraphPad

Prism and presented as the mean ± standard error of the mean (SE). In
addition, cells 92 h post-rapamycin treatment were fixed in 4%
formaldehyde and 0.1% glutaraldehyde and stained with 2 µM Hoechst 33342
(Invitrogen) before detection of the Hoechst emission (a measure of DNA
replication) by the 355 nm laser of a LSR II (BD Biosciences), through a
440/40 nm bandpass filter. Doublet cells were excluded using a FCS-A versus
FCS-H display. Samples were analysed using FlowJo software.

575 Erythrocyte invasion assays were carried out using a modification of a 576 method described previously (59). Highly synchronous, mature schizonts of 577 the parasite clones under examination were enriched by centrifugation over 578 Percoll cushions then added at a parasitaemia of 1% to fresh erythrocytes. 579 After incubation for 4 h, parasites were stained with SYBR Green-I and the 580 percentage of newly ring-infected erythrocytes was determined by flow 581 cytometry using a BD FACS Calibur flow cytometer (BD Biosciences). SYBR 582 Green-I was excited by a 488 nm 20 mW blue laser and detected by a 583 530/30 filter. BD CellQuest Pro (BD Biosciences, UK) was used to collect 584 100,000 events per sample. Experiments were done in triplicate, data 585 analysed using GraphPad Prism and presented as the mean  $\pm$  SE. 586

587 Generation of *rhopH3-loxP* parasites and conditional RhopH3 truncation.

588 Parasites harbouring a floxed segment of the genomic *rhopH3* gene were

589 generated by Cas9-mediated replacement of *rhopH3* endogenous introns 3

and 6 as well as the intervening sequence. The repair plasmid, called

591 pESS\_R3\_E46\_loxP (synthesised by GENEWIZ) comprised synthetic

592 heterologous *loxP*-containing SERA2 and sub2 introns(29) flanking a

593	recodonized form of <i>rhopH3</i> exons 4-6. The complete native sequences of
594	exons 3 and 7 were included on either side of this central module to act as
595	flanking regions for homology-directed repair. Protospacer Workbench(60)
596	was used to identify 20 bp protospacer sequences specifically targeting
597	rhopH3. To generate pSgRNA plasmids expressing suitable sgRNAs, InFusion-
598	based cloning (Clontech) was used to replace the BtgZI adaptor sequence of
599	pL6-X(28) with annealed oligos encoding a sgRNA targeting <i>rhopH3</i> exon 4
600	(RHOPH3_sgRNA_E4_F and RHOPH3_sgRNA_E4_R, generating pSgRNA1), 5
601	(RHOPH3_sgRNA_E5_F and RHOPH3_sgRNA_E5_R, generating pSgRNA2) or 6
602	(RHOPH3_sgRNA_E6_F and RHOPH3_sgRNA_E6_R, generating pSgRNA3) (see
603	Table 2 for sequences of all oligonucleotide primers used in this study).
604	Schizonts of <i>P. falciparum</i> clone 1G5DC were transfected with 20 $\mu$ g Cas9-
605	expressing pUF(28), 20 $\mu g$ pESS_R3_E46_loxP repair plasmid and 8 $\mu g$ of
606	sgRNA-containing pSgRNA1, pSgRNA2 or pSgRNA3. Twenty-four hours post-
607	transfection, the electroporated parasites were treated with 2.5 $$ nM
608	WR99210 for 48 h to select for transfectants harbouring pUF1 before
609	returning the cultures to medium without drug. Integrant parasites generally
610	reached parasitaemia levels suitable for cryopreservation within 2-5 weeks.
611	Detection of integration of pESS_R3_E46_loxP in the parasite
612	population was performed by diagnostic PCR using primers
613	RHOPH3_exon2_F1 plus RHOPH3_exon5_WT_R (producing a product specific
614	to the wild type <i>rhopH3</i> locus), or RHOPH3_exon2_F1 plus RHOPH3_exon4-
615	6rec_R and RHOPH3_exon4-6rec_F plus RHOPH3_3UTR_R (producing
616	products specific to the <i>rhopH3-loxP</i> modified locus). Integrant parasite
617	clones rhopH3-loxP 5F5 and rhopH3-loxP 4B11 were then isolated by limiting

dilution. Persistence of the integrated DiCre locus in these clones was
confirmed by PCR analysis using primers +27 plus -11 producing a 1900 bp
product specific to the integrated DiCre cassette in 1G5DC parasites, or +27
plus -25 producing an amplicon of 1700 bp specific to the unmodified SERA5
locus.

623 Recombination between the *loxP* sites was induced in tightly 624 synchronised ring-stages of parasite clones rhopH3-loxP 5F5 and rhopH3-625 *loxP* 4B11 by incubation for 4 h in the presence of 100 nM rapamycin in 1% 626 (v/v) DMSO; mock treatment was with 1% (v/v) DMSO only (vehicle control). 627 DiCre-mediated excision of the floxed *rhopH3* exons 4-6 was detected by 628 PCR analysis of schizont stage genomic DNA (harvested ~40 h following mock 629 or rapamycin treatment) using primers RHOPH3\_exon2\_F1 and 630 RHOPH3\_exon7\_R. Truncation of RhopH3 was evaluated by immunoblot 631 analysis of SDS extracts of mature Percoll-enriched schizonts, probing with 632 anti-Ag44 antibodies (or anti-AMA1 as a loading control) followed by 633 horseradish-peroxidase secondary antibodies as described(61). 634 635 **Southern blot**. For Southern blot analysis, a 738 bp probe corresponding to 636 part of *rhopH3* exon 3 was produced by PCR amplification from *P*. 637 falciparum IG5DC genomic DNA with primers RHOPH3\_exon3\_SB\_F and 638 RHOPH3\_exon3\_SB\_R (Table 2). Probe radiolabelling and hybridisation to 639 SacI/BsgI/XmnI-digested gDNA from clones of interest was as previously

640 described (62).

641

642 Immunoprecipitation and immunoblot analysis. For analysis of RhopH 643 complex formation, mature Percoll-enriched schizont-stage parasites (42 h 644 post rapamycin or mock treatment) were harvested and stored at -80°C. 645 Frozen parasite pellets were thawed into 100  $\mu$ L NP-40 lysis buffer (1% 646 Nonidet P-40, 150 mM NaCl, 50 mM Tris-HCL, 5 mM EDTA, 5 mM EGTA pH 647 8.0) containing a complete protease inhibitor cocktail (Roche). Samples 648 were clarified by centrifugation at 14,000 rpm at 4°C and the supernatant 649 passed through a 0.22 µm cellulose acetate Spin-X centrifuge tube filter 650 (Corning). 100 µL Protein G-Sepharose beads (Abcam) were added to the 651 resulting supernatant and pre-clearing carried out at 4°C overnight. 652 Following addition of mAb 61.3 (9), samples were incubated at 4°C overnight 653 before antigen-antibody complexes were precipitated using Protein G-654 Sepharose beads overnight at 4°C. The beads were washed five times in 655 wash buffer I (50 mM Tris-HCl pH 8.2, 5 mM EDTA, 0.5% Nonidet P-40, 1 656 mg/mL bovine serum albumin, 0.5 M NaCl) and twice in wash buffer II (50 657 mM Tris-HCl pH 8.2, 5 mM EDTA, 0.5% Nonidet P-40) before antigen-antibody 658 complexes were eluted using NuPAGE LDS Sample Buffer (Life Technologies) 659 and proteins resolved using precast NuPAGE Novex 3-8% Tris-Acetate protein 660 gels (Life Technologies). Following electrophoresis, samples were evaluated 661 by immunoblot analysis probing with anti-Ag44 or anti-RhopH1/Clag3.1A 662 antibodies followed by horseradish-peroxidase secondary antibodies as 663 described (61). 664

Immunofluorescence microscopy. Immunofluorescence microscopy was
 performed on formaldehyde-fixed thin blood smears, permeabilised with

667	0.1% (v/v) Triton X-100. Monoclonal anti-RAP2 (MRA-876), directly labeled
668	with Alexa Fluor 594 using the Alexa Fluor 594 Antibody Labelling Kit (Life
669	Technologies), was used at a dilution of 1:300. Samples were probed with
670	primary antibodies used at the following dilutions: anti-Ag44 (1:2000), mAb
671	61.3 (1:100), anti-CL3.1A (1:100), anti-MAHRPI (1:2000), anti-KAHRP
672	(1:250), rabbit anti-MSP1 (1:1000), mAb 89.1 (1:1000), and mAb 7.7 (1:100).
673	Bound primary antibodies were detected using Alexa Fluor 488-, 566- or 594-
674	conjugated anti-rabbit or anti-mouse secondary antibodies (Life
675	Technologies), diluted 1:8000. Slides were mounted in ProLong Gold
676	Antifade Mountant with DAPI (Life Technologies) and trophozoite images
677	captured using a Nikon Eclipse Ni-E widefield microscope with a
678	100x/1.45NA objective and a Hamamatsu C11440 digital camera. Schizont
679	stage images were captured with a Zeiss LSM 880 using a $63x/1.4$ NA
680	objective equipped with an Airyscan detector to improve the optical
681	resolution of the scanned images. The DAPI, Alexa Fluor 488 and Alexa Fluor
682	594 channels were imaged sequentially over the axial dimension and
683	processed using the integrated Zeiss software to enhance the optical
684	resolution isometrically ~1.8 fold. All images were processed using either
685	the Zen 2012 or FIJI software packages. For display purposes, linear
686	adjustments were made to the intensity scale of each channel to equalize
687	the intensity output to enhance areas of co-localization. Relative intensities
688	between samples are not comparable.
689	

690 Transmission electron microscopy. Parasite cultures 92 h following

691 rapamycin (or mock) treatment were fixed at 37°C in 8% formaldehyde in

692 0.2 M phosphate buffer pH 7.4 (PB) for 15 min by adding 1 volume of 693 fixative solution to 1 volume of culture. The cells were pelleted, then 694 further incubated in 2.5% glutaraldehyde, 4% formaldehyde in 0.1 M PB at 695 room temperature for a further 30 min. Cells were washed in 0.1 M PB 696 before being embedded in 4% (w/v) low-melting point agarose in distilled water. The agarose-embedded samples were cut into 1 mm<sup>3</sup> blocks, post-697 698 fixed in 1% (w/v)  $OsO_4$  and 1.5% (w/v) potassium ferrocyanide for 60 min at 699  $4^{\circ}$ C then incubated sequentially in 1% (w/v) tannic acid in 0.05 M PB for 45 700 min and 1% (w/v) sodium sulphate in 0.05 M PB for 5 min. The samples were 701 washed in water and dehydrated through a graded series of ethanol before 702 being embedded in Epon resin (Taab 812). Blocks were trimmed and 703 ultrathin 70 nm sections cut using a diamond knife on a UC6 Ultramicrotome 704 (Leica Microsystems), picked up on 150 hexagonal mesh copper grids and 705 post stained with lead citrate before being imaged using a Tecnai G2 Spirit 706 120 kV transmission electron microscope (FEI Company) with an Orius 707 camera (Gatan Inc.).

708

Analysis of erythrocyte membrane permeability. Sorbitol sensitivity of
parasites was determined 72 h following rapamycin or DMSO treatment (i.e.
in cycle 2). Cultures at equal parasitaemia were incubated in osmotic lysis
buffer (280 mM sorbitol, 20 mM Na-HEPES, 0.1 mg/mL BSA, pH 7.4) for 7
min, then hemoglobin release determined by measuring the absorbance of
the cell supernatants at 405 nm, as previously described(63,64).
5-ALA uptake was determined by incubating cultures of synchronous

716 cycle 2 ring-stage parasites overnight in phenol red-free RPMI 1640 medium

717 (K-D Medical) supplemented with 200 µM 5-ALA. Just prior to analysis, 718 parasite nuclei were stained by treatment with 2 µM Hoechst. PPIX and 719 Hoechst fluorescence were captured using a Zeiss LSM 880 equipped with a 720 63x/1.4 NA objective in standard confocal detection mode. Images were 721 captured with the same acquisition setting so that measurements of 722 intensity are directly comparable. Co-occurrence of PPIX and Hoechst was 723 quantified using the MetaMorph software "Cell Scoring" application. Cells 724 were also analyzed on a SORP LSRFortessa, detecting PPIX emission with a 725 532 nm laser through a 605/40 nm bandpass filter and Hoechst emission 726 with the 406 nm laser through a 440/40 nm bandpass filter. Erythrocyte 727 doublets were excluded using a FCS-A versus FCS-H display and data 728 analyzed by BD FACSDiva software.

729

730 Time-lapse video microscopy. P. falciparum egress was imaged as 731 previously described (27,65), using 1 µM (4-[7-[(dimethylamino)methyl]-2-(4-732 fluorphenyl)imidazo[1,2-*a*]pyridine-3-yl]pyrimidin-2-amine (compound 2) to 733 tightly synchronise egress. Following removal of compound 2 by washing, 734 parasites were suspended in fresh pre-warmed medium and introduced into 735 a pre-warmed microscopy chamber on a temperature controlled microscope 736 stage at 37°C. Beginning 6 min after washing off the compound 2, DIC 737 images were collected at 5 s intervals for 30 min using a Nikon Eclipse Ni 738 Microscope fitted with a Hamamatsu C11440 digital camera and converted 739 to QuickTime movies using Nikon NIS-Elements software.

740

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1039 Author contributions

- 1040 E.S.S., M.J.B. and C.v.O. conceived and designed the experiments. E.S.S.
- 1041 performed the experiments and analysed the data. E.K. designed the
- 1042 Southern blotting strategy and J.A.B. assisted with image acquisition.
- 1043 L.H.M., M.J.B. and C.v.O. supervised the project. E.S.S., M.J.B. and C.v.O.
- 1044 wrote the manuscript.
- 1045
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- 1052

Table 1. Conditional truncation of RhopH3 results in decreased parasite survival as determined by plaque assay. 

<sup>a</sup> Plaque assay no.	Treatment	<sup>b</sup> Proportion of wells containing plaques (%)	Mean number of plaques/well
1	DMSO	98.88	7.7
(clone 5F5)			
	Rapamycin	10.56	0.11
2	DMSO	100	9.1
(clone 5F5)			
	Rapamycin	8.89	0.09
3	DMSO	99.44	5.24
(clone 4B11)			
	Rapamycin	9.44	0.1

<sup>a</sup> Three independent plaque assays were set up on different days. <sup>b</sup> A total of 180 wells were used for each treatment (+/-RAP) in each assay. 

# Table 2. Oligonucleotide primers used in this study. Guide sequences shown in bold.

Primer name	Sequence (5'-3')
RHOPH3_sgRNA_E4_F*	taagtatataatattTTCTTCGTTTTTAAAAAAAGgttttagagctagaa
RHOPH3_sgRNA_E4_R*	ttctagctctaaaacCTTTTTTTAAAAACGAAGAAaatattatatactta
RHOPH3_sgRNA_E5_F*	taagtatataatattCACCGATTTTAGCTTTAAAGgttttagagctagaa
RHOPH3_sgRNA_E5_R*	ttctagctctaaaacCTTTAAAGCTAAAATCGGTGaatattatatactta
RHOPH3_sgRNA_E6_F*	taagtatataatattACATTCTTATCATTATATTTgttttagagctagaa
RHOPH3_sgRNA_E6_R*	ttctagctctaaaacACATTCTTATCATTATATTTaatattatatactta
RHOPH3_exon2_F1	AGGAAATGGCCCAGACGC
RHOPH3_exon5_WT_R	TCTTTAAAGCTAAAATCGGTGATATTATGGCTC
RHOPH3_exon4-6rec_R	CAGGAAGTTACCTTTCAGCAGGG
RHOPH3_exon4-6rec_F	CCCTGCTGAAAGGTAACTTCCTG
RHOPH3_3UTR_R	CGAATATGTAATCAGTTGTATTTTTTCTCTAAAAGTTCATAG
+27	CAATATCATTTGAATCAAACAGTGGT
-11	CTTTGCCATCCAGGCTGTTC
-25	CCATTGGACTAGAACCTTCAT
RHOPH3_exon7_R	CATAAAGAACGTCTTGTTTCTGTATCCAATACC
RHOPH3_exon3_SB_F	CAAATATGCTATATGTGTAGGTACTCAATTTAAC
RHOPH3_exon3_SB_R	CATATAACTTTGGAGATGTAGAACCACAAGG

1076 Figure legends

1077 Figure 1 Conditional truncation of the *rhopH3* gene. A) The *rhopH3* gene 1078 comprises seven exons (numbered grey boxes) and six introns (blue lines). 1079 Using Cas9-mediated recombination, the region spanning introns 3 through 6 1080 was replaced with two *loxP*-containing (purple open arrowhead) *P*. 1081 falciparum introns (SERA2 (orange line) and sub2 (green line)) flanking a recodonized and fused version of exons 4 through 6 (exon 4-6, green box). 1082 1083 Integration of this sequence by homologous recombination was promoted by 1084 the addition sequences of exon 3 and 7 to either side of the introns. Colored 1085 arrowheads, primer binding sites. B, S and X, Bsgl, Sacl and Xmnl restriction 1086 sites. Dotted line, probe used for Southern blotting. Rapamycin-induced 1087 site-specific recombination between the loxP sites removes the recodonized 1088 exon 4-6. B) PCR analysis of rhopH3-loxP clones 5F5 and 4B11 confirms the 1089 expected gene modification event. Genomic DNA from parental 1G5DC (WT) 1090 parasites or the clones was used as template for PCR using the indicated 1091 primers (see panel A). Numbers between the arrowheads indicate the 1092 expected size of the amplicon. C) Southern blot analysis of parental 1G5DC 1093 (WT) and the *rhopH3-loxP* parasite clones confirms the expected 1094 modification of the *rhopH3* locus. Genomic DNA was digested with BsgI, SacI 1095 and XmnI and hybridized with a radiolabeled probe that binds to part of 1096 exon 3 (dotted line in panel A). Expected fragment sizes are 3016 bp for the 1097 WT *rhopH3* locus and 3349 bp for the *rhopH3-loxP* locus. D) Efficient 1098 rapamycin-induced truncation of the rhopH3 gene. Clones rhopH3-loxP 5F5 1099 and 4B11 were analyzed by PCR ~44 h after treatment with DMSO (D) or 1100 rapamycin (R) using the indicated primers (see panel A). Excision decreases

1101 the amplicon from 2760 bp to 1755 bp. E) Southern blot showing efficient 1102 rapamycin-induced truncation of the *rhopH3* gene. Genomic DNA extracted 1103 from control or rapamycin-treated *rhopH3-loxP* clones 5F5 and 4B11 was 1104 digested and probed as described in panel C. Expected fragment sizes are 1105 3349 bp for the non-excised locus and 4784 bp for the excised locus. F) 1106 Immunoblot analysis of mature schizonts of *rhopH3-loxP* clone 5F5, 1107 examined ~44 h following treatment at ring stage with DMSO (D) or 1108 rapamycin (R). The blots were probed with an antibody against RhopH3 (left 1109 panel) or the merozoite protein AMA1 (right panel) as a loading control. The 1110 expected molecular masses of WT RhopH3 and RhopH3∆4-6 are 110 kDa and 1111 ~70 kDa, respectively. In panels B-F, positions of relevant molecular mass 1112 markers are indicated.

1113

1114 Figure 2 Truncation of RhopH3 leads to mistrafficking of components of the 1115 RhopH complex and loss of complex formation. A) IFA showing colocalization 1116 of RhopH3, RhopH2 and RhopH1/Clag3.1 with the rhoptry marker RAP2 in 1117 schizonts of control (DMSO) rhopH3-loxP parasites but loss of colocalization 1118 following rapamycin (Rapa) treatment. Parasite nuclei were visualized by 1119 staining with 4,6-diamidino-2-phenylindole (DAPI). Scale bar, 5 µm. B) 1120 Colocalization of the members of the RhopH complex. RhopH3, RhopH2 and 1121 RhopH1/Clag3.1 colocalize in *rhopH3-loxP* parasites treated with DMSO, but 1122 this colocalization is lost in parasites treated with rapamycin. C) 1123 Mislocalisation and reduced levels of RhopH3 in naturally released free 1124 merozoites of *rhopH3-loxP* parasites treated with rapamycin. Samples were 1125 probed with a monoclonal antibody to the merozoite surface marker MSP1

1126 as well as anti-RhopH3 antibodies. Scale bar, 2 µm D) Immunoprecipitation 1127 reveals disruption of the RhopH complex in rapamycin-treated rhopH3-loxP 1128 parasites. RhopH2 was immunoprecipitated from extracts of control or 1129 rapamycin-treated *rhopH3-loxP* parasites. Subsequent immunoblotting with 1130 antibodies against RhopH3 or RhopH1/Clag3.1 revealed the absence of 1131 RhopH3 from the immunoprecipitates derived from the rapamycin-treated 1132 parasites, although RhopH2 and RhopH1/Clag3.1 still showed association. 1133 Arrowheads indicate the expected position of migration of the full-length 1134 (WT) and truncated RhopH3, and RhopH1/Clag3.1. The *rhoph3-loxP* clone 1135 5F5 was used throughout for these experiments.

1136

1137 Figure 3 Loss of long-term viability in parasites lacking the RhopH complex. 1138 A) Representative wells seeded with identical concentrations (10 parasitised 1139 cells/well) of DMSO-treated or rapamycin-treated *rhopH3-loxP* clone 5F5 1140 parasites, showing formation of plaques only in the wells seeded with DMSO-1141 treated parasites. Two of the plaques are indicated by white arrowheads. B) 1142 PCR analysis of the *rhopH3-loxP* locus in the small number of clones isolated 1143 from wells seeded with rapamycin-treated *rhopH3-loxP* parasites. The size 1144 of the PCR product indicates excision of the floxed sequence had not taken 1145 place in these seven clones (numbered 1-7), whereas rapamycin induced 1146 efficient excision in the parent 5F5 clone (left-hand two tracks). For PCR 1147 strategy, see Figure 1D. C) PCR analysis of the modified SERA5 locus in 1148 parasite clone RhopH3 NE, showing loss of the DiCre cassette in this clone. 1149 D) Growth curves showing replication of parasites of the indicated clones 1150 over the course of 5 erythrocytic cycles. Data were averaged from 3

1151 biological replicate experiments and presented as the mean  $\pm$  standard error 1152 of the mean. E) Non-excised parasites quickly outgrow RhopH3<sub>4</sub>-6 1153 parasites. The relative abundance of parasites harboring the excised or 1154 intact rhopH3-loxP locus in a population of rapamycin-treated rhopH3-loxP 1155 clone 5F5 parasites was determined by diagnostic PCR over the course of 7 1156 erythrocytic growth cycles (indicated, where cycle 1 indicates that in which 1157 treatment occurred). F) Decreased erythrocyte invasion by rapamycin-1158 treated *rhopH3-loxP* parasites. Parasites of the indicated clones were 1159 treated with DMSO or rapamycin and allowed to invade fresh erythrocytes. 1160 Ring-stage parasitemia levels were determined 4 h later. Data were 1161 averaged from 3 biological replicate experiments. Error bars depict standard 1162 error of the mean. Statistical significance was determined by a two-tailed t-1163 test where  $p \le 0.0001$  (indicated by asterisks) and p > 0.05, non-significant 1164 (ns).

1165

1166 Figure 4 Loss of the RhopH complex results in developmental arrest. A) 1167 Developmental block in rapamycin-treated *rhopH3-loxP* parasites. Giemsa-1168 stained images showing intracellular development of DMSO-treated and 1169 rapamycin-treated rhopH3-loxP clone 5F5 parasites from the end of cycle 1 1170 to the end of cycle 2. A clear developmental block was evident in the 1171 rapamycin-treated parasites in cycle 2. The number of hours following the 1172 beginning of cycle 1 is indicated, as well as its relation to the time point of 1173 rapamycin treatment (indicated in the schematic timeline). B) Flow 1174 cytometry analysis of DMSO-treated and rapamycin-treated rhopH3-loxP 1175 clones 5F5 and 4B11. Analysis was performed at the end of the cycle 2 (92 h

after rapamycin-treatment). The intensity of Hoechst 33342 staining
provides a measure of the DNA content of the parasites, reflecting parasite
development.

1179

1180 Figure 5 Loss of the RhopH complex does not ablate parasite protein export. 1181 Cycle 2 (72 h post rapamycin treatment) DMSO-treated and rapamycin-1182 treated rhopH3-loxP clone 5F5 trophozoite-stage parasites were probed with 1183 antibodies against the parasitophorous vacuole membrane marker EXP2 to 1184 delineate the parasite in the infected erythrocyte, as well as antibodies 1185 specific for either the Maurer's cleft marker MAHRP1 (top panels) or the 1186 export marker KAHRP (bottom panels). Scale bar, 5 µm. B) Transmission 1187 electron micrograph showing a comparison between cycle 2 parasites of 1188 DMSO-treated or rapamycin-treated rhopH3-loxP clone 5F5 parasites ~ 92 h 1189 following rapamycin treatment. The developmental block in the RhopH $_{\Delta4-6}$ 1190 parasite is clearly evident, as is the presence of knobs (arrowed) on the 1191 surface of the erythrocyte in both cases. Components of the mutant parasite 1192 labelled are the digestive vacuole (DV), haemozoin (H), nucleus (N), 1193 parasitophorous vacuole membrane (PVM), cytostomes (C) and parasite 1194 plasma membrane (PPM). The mutant parasites displayed no obvious 1195 ultrastructural differences from wild-type trophozoites at a similar 1196 developmental stage (not shown). Scale bar, 1 µm 1197 1198 Figure 6 Loss of the RhopH complex results in reduced sorbitol sensitivity 1199 and reduced uptake of exogenous small molecules. A) Synchronous cycle 2

1200 parasites of the indicated clone (parasitaemia ~5%) treated 72 h previously

1201 with DMSO or rapamycin in cycle 1 were suspended in osmotic lysis buffer 1202 containing 280 mM sorbitol or in PBS, and the resulting cell lysis determined 1203 by measuring the absorbance of the supernatant at 405 nm. An equal 1204 volume of parasite culture was lysed in 0.15% (w/v) saponin to give a value 1205 for 100% lysis and all other absorbance values normalized to this. Data were 1206 averaged from 3 biological replicate experiments. Statistical significance 1207 was determined by a two-tailed t-test; significance levels are indicated: p≤0.001, \*\*\*; p≤0.01, \*\*; p≤0.05, \*; and p>0.05, non-significant (ns). B) 1208 1209 Uptake of 5-ALA by erythrocytes infected with either DMSO-treated or 1210 rapamycin-treated *rhopH3-loxP* clone 5F5 parasites at cycle 2. Cultures 1211 were incubated overnight with 200 µM 5-ALA and uptake of the compound 1212 and its subsequent conversation to PPIX in infected erythrocytes visualized 1213 by fluorescence microscopy. Infected erythrocytes were visualized by 1214 staining with Hoechst 33342. Top panels show fields of view containing 1215 multiple infected erythrocytes of the indicated strain. Scale bar, 50 µm 1216 Bottom panels show individual infected erythrocytes. Scale bar, 5 µm. C) 1217 Quantitation of the levels of uptake of 5-ALA by infected erythrocytes. For 1218 each condition, a total of 1300 Hoechst-positive cells were analyzed for 1219 intensity of PPIX fluorescence using MetaMorph (Molecular Devices) and a 1220 statistical significance was determined by a two-tailed t-test. Significance 1221 levels are indicated:  $p \le 0.0001$ , \*\*\*\* and p > 0.05, non-significant (ns). D) FACS 1222 analysis of 5-ALA-treated parasites. Uptake of 5-ALA and its subsequent 1223 conversation to PPIX in cycle 2 parasites following treatment in cycle 1 with 1224 rapamycin or DMSO was determined by flow cytometry of Hoechst stained 1225 parasites. Gating was applied to distinguish Hoechst negative cells (red

- 1226 population), Hoechst positive/PPIX negative cells (green population) and
- 1227 Hoechst positive/PPIX-positive cells (purple population). For the 1G5DC
- 1228 parental and RhopH3-loxP NE parasite clones, most of the parasites were
- 1229 positive for both Hoechst and PPIX fluorescence regardless of their
- 1230 treatment with rapamycin or DMSO. In contrast, for rapamycin-treated
- 1231 *rhopH3-loxP* clones 5F5 and 4B11, most of the parasites were Hoechst
- 1232 positive/PPIX negative indicating a defect in 5-ALA uptake.

1234

1236 Supplemental figure legends.

1238	Figure 1 - figure supplement 1. Multiple alignment of predicted primary
1239	sequences of rhopH3 orthologues from P. falciparum (PF3D7_0905400), P.
1240	chabaudi (PCHAS_0416900) and P. vivax (PVX_098712). The portion of the
1241	protein encoded by exon 4-6 in the <i>P. falciparum</i> orthologue is underlined.
1242	Note that this region includes some of the most highly conserved regions of
1243	the protein. Sequence data were obtained from PlasmoDB (1) and aligned
1244	using Clustal Omega (2). '*'indicates positions of identity, ':' indicates
1245	conservation of residues with strongly similar chemical properties  and '.'
1246	indicates conservation of residues of weakly similar properties.
1247	
1248	Figure 1 - figure supplement 2. Modification (floxing) of the rhoph3 gene
1249	does not impact on gene expression or parasite growth. A) Immunoblot
1250	analysis of untreated mature schizonts of <i>rhopH3-loxP</i> clones 5F5 and 4B11,
1251	as well as the RhopH3 NE clone and the parental 1G5DC parasites. The blots
1252	were probed with an antibody against RhopH3 (top), RhopH1/Clag3.1
1253	(middle) or the merozoite protein EBA175 (3) (bottom) as a loading control.
1254	B) Growth curves showing similar replication rates of parasites of the
1255	indicated clones (not treated with rapamycin) over the course of 4
1256	erythrocytic cycles. Data were averaged from 3 biological replicate
1257	experiments and presented as the mean $\pm$ standard error of the mean.
1258	Linear regression analysis showed that all the slopes fall within the same
1259	95% confidence interval range.

1261 Figure 1 - figure supplement 3. Conditional truncation of RhopH3 in both 1262 the 5F5 and 4B11 *rhopH3-loxP* clones. Immunoblot analysis of mature 1263 schizonts of the indicated clones ~44 h following treatment at ring stage 1264 with DMSO (D) or rapamycin (R). The blots were probed with an antibody 1265 against RhopH3 (top) or the mAb 89.1 against the merozoite surface protein 1266 MSP1 (bottom) as a loading control. The expected molecular masses of WT 1267 RhopH3 and RhopH3 $\Delta$ 4-6 are 110 kDa and ~70 kDa, respectively. Positions of 1268 relevant molecular mass markers are indicated.

1269

1270 Figure 2 - figure supplement 1. Truncation of RhopH3 leads to

1271 mistrafficking of components of the RhopH complex. IFA of mature schizonts

1272 of control (DMSO) and rapamycin-treated rhopH3-loxP parasites, probed

1273 with MSP1-specific antibodies (either mAb 89.1 or rabbit polyclonal anti-

1274 MSP1 antibodies; red) and antibodies to the three indicated RhopH

1275 components (green). Mis-localisation of the RhopH proteins was observed in

all cases, and in the case of RhopH3 the protein often appeared to reside

1277 external to the plasma membrane of intracellular merozoites. Parasite

1278 nuclei were visualized by staining with DAPI. Note that, for clarity, the

1279 merge panels do not include the DAPI signal. Scale bar, 5 µm.

1280

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1295		erythrocyte invasion by the malaria parasite. J. Cell Biol. 174, 1023-1033
1296		

- 1298 Supplementary Video 1 Parasite egress is unaffected by loss of the RhopH
- 1299 complex. Synchronized parasites of *rhopH3-loxP* clone 4B11 were treated
- 1300 with DMSO or rapamycin at ring stage, then allowed to mature to schizont
- 1301 stage and further synchronised by incubation for 3-5 h in the presence of 1
- 1302 μM (4-[7-[(dimethylamino)methyl]-2-(4-fluorphenyl)imidazo[1,2-*a*]pyridine-
- 1303 3-yl]pyrimidin-2-amine (compound 2), which reversibly stalls egress. Egress
- 1304 of the parasites was then monitored by time-lapse DIC video microscopy
- 1305 following removal of the compound 2, as described previously<sup>1</sup>. DMSO-
- 1306 treated samples are shown on the left, rapamycin-treated are samples
- 1307 shown on the right.
- 1308

## 1309 Supplementary video reference

1310

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P.falciparum MRSKHLVTLFIITFLSFSTVKVWGKDVFAGFVTKKLKTLLDCNFALYYNFKGNGPDAGSF MPTNSLTKLFLASLSTFSVSQVWGKDYFSGSLNQNLTDILKCNFISYYNSKPGEPDPNAF P.chabaudi MRSKLFVTLFITCLVTLSSVQVLGREYFSGFVNKKLKNLLQCNLAAYYNLRDNGPDPNAF P.vivax \* :: :..\*\*: : ::\* :\* \*:\* \*:\* :.::\*. :\*.\*\*: \*\*\* : \* \* :\* P.falciparum LDFVDEPEQFYWFVEHFLSVKFRVPKHLKDKNIHNFTPCLNRSWVSEFLKEYEEPFVNPV P.chabaudi I.DFVGEPEOFYWFVENYI.SVPFTVPOHI.SSNSGHNWKSCI.KKKWVYEFI.KEYEEPEVSYI. LDFVGEPEOFYWFIEHYLSVPFSIPRNLKNNKSHSYWSCINRSWVSEFLRKYEEPDINEL P.vivax P.falciparum MKFLDKEORLFFTYNFGDVEPOGKYTYFPVKEFHKYCILPPLIKTNIKDGESGEFLKYOL P.chabaudi ASVLDKEORHYYKDTFGDKEPVAKYTIFEVKEFDSYCLLPPFVKTNIRSKNSKENLSFOM MKFLDKEQRVYFSYTFQNIEPVAKYTSFPIKEFHKYCVLPPLIETNIKQKDKGGNLSFQL P.vivax ··\*\*\*\*\* ::· ·\* : \*\* ·\*\*\* \* :\*\*\*·.\*\*:\*\*\*:::\*\*\*: \*.:\*: P.falciparum NKEEYKVFLSSVGSQMTAIKNLYSTVEDEQRKQLLKVIIENESTNDISVQCPTYNIKLHY P.chabaudi DKTDYQTYLEVPDNKYAAMKHLSTNMEYGEKQEIVKAIVESNNENSFQLICPSYYIKIHY P.vivax NQAEYKIYLSSVGTPTSALKNLYLNMEDGERKNIVKTIVENERSNNVFVNCPVYDLKLHY . :\*:\*.\* .:\* :::::\*.\*:\*.\* \*.. : \*\* \* :\*:\*\* :: :\*: :\*. P.falciparum NTECKPNSNILTCIDDYIKNTCIDAVKND-EDPTICDHLLNLFNSLKDFQIESFQKFLTA TKECANSNNILKCIDEFLRKTCEKKTESKHPSADLCEHLQFLFESLKNPYLDNFKKFMTN P.chabaudi NKECGSQPNVLKCLDDYIKHLCERRIAHR-EKGTFCDDLLFLFDALKEPYVENFKKFLSR P.vivax . :\*:.\* \*\*::\*\*: ::.\*:\*\*: ..\*\* . \*:\*.\*:\*:\*:\* P.falciparum SDFTLIKPQSVWNVPIFDIYKPKNYLDSVQNLDTECFKKLNSKNLIFLSFHDDIPNNPYY DELOLTKPRGGWTHPLFHTYSRKDYSNPKMKILPDAFKEFSSENPIFFSFSAEIPEKYSY P.chabaudi P.vivax DDVHLVKPQSVWGIPLFTTYKPRDLKNPKNNVPLNVFKVLNSKNKLFLSFFDEIPKSPYY .:. \* \*\*:. \* \*:\* \*. :: : :: : \*\* :.\*:\* :\*:\*\* :\*\*:. P.falciparum NVELQEIVKLSTYT-YSIFDKLYNFFFVFKKSGAPISPVSVKELSHNITDFSFKEDNSEI P.chabaudi VDNVSIYFKLRNYSSSSVFDTFONIFSVFKKKTPAIAPVSVKEVSODIDNFEFKAPKKPI P.vivax MEESQPLVKLSDFA-SSIFDKLHRFFYVFKKKGNQISPVSVKELSHNISDFSFKHDTSNI : . .\*\* :: \*:\*\*.: .:\* \*\*\*\*. \* : \* \* \* \* \* : \* : \* : \* . \* \* .. \* P.falciparum QCQNVRKSLDLEVDVETMKGIAAEKLCKIIEKFILTKDDAS---K----PEKSDIHRGF QCIGVKKSLDLSIDVDIFKVASVEKICSVIDKYALTEDSDFNKVPTEKKMKKLDKLKKGF P.chabaudi P.vivax ECKKVKKSLNLELEVEVAKGVAAEKICNLIEGFVLTKGKKDKTIR----GEVDDVHKGF :\* \*:\*\*\*:\*.::\*: \* :.\*\*:\*.:\*: : \*\*: . : ..:::\*\* P.falciparum RILCILISTHVEAYNIVRQLLNMESMISLTRYTSLYIHKFFKSVTLLKGNFLYKNNKAIR P.chabaudi HIDCILVSTYVEGYNLIRQFLNLENVLSLIRYTSLYTHKFLKSVTTLKEHFLYGQKNAIG RIQCILIATHVEALNIVRQLLNMESMLSLTRYTSLYLHKFFKSVTALKGSFLYENPSAIR P.vivax \*\*\* : .\*\* P.falciparum YSRACSKASLHVPSVLYRRNIYIPETFLSLYLGLSNLVSSNPSSPFFEYAIIEFLVTYYN YAKSCGSAVLYIPSVMYRRNLYVPETFLSLYLGLSNLVSSNPSSPFFEYSIIDFLITYFN P.chabaudi P.vivax HARACGRAVLHVPAVLYRRNIYLAETFLSLYLGLSNLVSSNPSSPFFEYAIIEFLVSYFN P.falciparum KGSEKFVLYFISIISVLYINEYYYEQLSCFYPKEFELIKSRMIHPNIVDRILKGIDNLMK P.chabaudi KGTKKFLYYFISIISILHINRYYYEQIYCHHNNHFDTLKSKMIHPDIVKGIMKKLRSILN KGSEKFLLYLFSIVSVLYINIYYYEQLYCHHREQFELLRSKMIHPNIADRILENIKTLIK P.vivax \*\*::\*\*: \*::\*:\*:\*:\*: \*:: \*:: ::\*: ::\*: \*::\*: \*:: ::\*: P.falciparum STRYDKMRTMYLDFESSDIFSREKVFTALYNFDSFIKTNEQLKKKNLEEISEIPVQLETS P.chabaudi KPKYSKMMELYKKLESETLFNYDEMAKILFEFDEFAONKDVOEKAOKTIDEEEKPEVNTL NPRYMKMRTFYMKFDNEDMFDKRKVFEVLYSFDEFLSSSDAQQKAKMQDISDESVDLDTT P.vivax . :\* \*\* :\* .::.. :\*. :: \*:.\*\*.\* ...: :\* : .: :::\* P.falciparum NDGIGYRKODVLYETDKPOTMDEASYEETVDEDA--HHV-NEKOHSAHFLDAIAEKDILE EEMANYNE-EWLPKLTRP-----TIPHDPYDEPNPNIKFDENVRSDGNLT P.chabaudi NDGIGLRKEDALFESEQQGSMESIED---IDEGLEGVDP-NQQKKTAEYLKMVPDEDKAN P.vivax :: .: : \* : . ........ : P.falciparum EKTKDQDLEIELYKYMGPLKEQSKSTSAAST-SDEISG-----SEGPSTESTSTGNOG P.chabaudi LADRDKELELSLFKYIGSLPADKTASTTEDHAASTTEDHAASTTEDHAASTTEDHAASTT LTDRNKELELDLYKYIGTLNETSAGVGTVST-HSPATAARMGLNAGGGRAVRPAA---KG P.vivax . :. • P.falciparum EDKTTDNTYKEMEELEEAEGTSNLKKGLEFYKSSLKLDQLDKEKPKKKKSKRKKKRDSSS P.chabaudi ES----QTDLAFDENVKPTDAEEMKT-----ASKEHLNTLDTEDTNNDERRSSYT-----P.vivax LHQRMGQMGKDLK-RMKGKDTSKLRKGVDFYESSTSLNQISPGESATEGKGSST-----\*. \*: :. . .. : :. : :.:::. P.falciparum DRILLEESKTFTSENEL-----P.chabaudi ----NEDDRSEISEPEFQHTAPEFYQDENL -NVSTEG--TSPSET-------P.vivax \* : \*\*





Probed: anti-RhopH3



Probed: anti-EBA175

### Sherling et al. Figure 2



Sherling et al. Figure 2 – supplement 1





Parasites



## Sherling *et al*. Figure 5



В

DMSO

Rapa



