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1  M L K K K K D Y E N A D L E D C N T K - - - - - E I K G Y S K V G S E K N I - - - - pfmap-
1  M L K K K K E Y S G I E K E E K N T K K K N N A S E C L S M Q N D D S T Y I D S N E E D K S W E Y I pbmap-

34  - K K K M T S I K E S S S R D E E E E D A N V N K N I K K F K E G N K K D N I S K N C N I V E K K N pfmap-
51  N E N T N E N I K N N D D I N K K S G E K E Y N A S E T K K T N N N E K N K N N S N N K T S K I N D pbmap-

83  N K S K E E K I N I K E A I I K N V K V P D N Y E I K H L I G R G S Y G Y V Y L A Y D K N A N K N V pfmap-
101 E K - - - - I N I K E A I I K N V H V P D N Y I I K H L I G R G S Y G Y V Y L A Y D K N T E K N V pbmap-

133 A I K K V N R M F E D L I D C K R I L R E I T I L N R L K S D Y I I R L H D L I I P E D L L K F D E pfmap-
146 A I K K V N R M F E D L I D C K R I L R E I T I L N R L K S D Y I I R L Y D L I I P D D L L K F D E pbmap-

183 I Y I V L E I A D S D L K K L F K T P I F L T E Q H V K T I L Y N L L L G E K F I H E S G I I H R D pfmap-
196 I Y I V L E I A D S D L K K L F K T P I F L T E E H I K T I L Y N L L L G E N F I H E S G I I H R D pbmap-

233 L K P A N C L L N Q D C S V K I C D F G L A R T I N S D K D I H I V N D L E E K E E N E E P G P H N pfmap-
246 L K P A N C L L N Q D C S V K V C D F G L A R T I N S E K D T N I V N D L E - - - E N E E P G P H N pbmap-

283 K N L K K Q L T S H V V V T R W Y R A P E L I L L Q E N Y T N S I D I W S T G C I F A E L L N M M K S pfmap-
293 K N L K K Q L T S H V V V T R W Y R A P E L I L L Q E N Y T K S I D I W S T G C I F A E L L N M L Q S pbmap-

333 H I N N P T N R F P L F P G S S C F P L S P D H N S K K V H E K S N R D Q L N I I F N V I G T P P E pfmap-
343 H I N D P T N R F P L F P G S S C F P L S P D R N S K K V H E K S N R D Q L N I I F N I I G T P T E pbmap-

383 E D L K C I T K Q E V I K Y I K L F P T R D G I D L S K K Y S S I S K E G I D L L E S M L R F N A Q pfmap-
393 D D L K N I N K P E V I K Y I K L F P H R K P I N L K Q K Y P S I S D D G I N L L E S M L K F N P N pbmap-

433 K R I T I D K A L S H P Y L K D V R K E N L E N F S T E K I I L P F D D W M V L S E T Q L R Y I F L pfmap-
443 K R I T I D Q A L D H P Y L K D V R K K K L E N F S T K K I I L P F D D W M V L S E T Q L R Y I F L pbmap-

483 K E I Q S F H A D L I I P A K L N I H Q K S F Y N M . pfmap-
493 K E V Q S F H P E L V I P S V F T I H E N N F Y N N E K P S S . pbmap-

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Fig. 1-SI. Alignment of Pbmap-2 (PlasmoDB identifier Pb_5294-2-125-1861) with Pfmmap-2 (PF11_0147). Boxed areas indicate identical amino acid residues. Boxes highlight the ATP binding glycine triad IGRGSYGYV, the catalytic site HRDLKPANCLL and the atypical activation site TSH, all of which are identical in both sequences. The arrows indicate the boundaries of the fragment used to generate the knock-out construct.

Table 1-SI: Gametocyte numbers in wild-type parasites and Pbmap-2 knock-out mutants.

Genotype	Number of asexuals/10000 RBCs at 24 hpi	Number of gametocytes/10000 RBCs at 30 hpi	Conversion rate	Female: male ratio
NK65 n=2	311.1 ± 14.2	12.3 ± 3.3	3.9%	2.0
a1 (WT) n=2	380.9 ± 13.6	32.7 ± 7.6	8.6 %	1.1
b1 (KO) n=2	393.3 ± 98.5	20.3 ± 9.1	5.2%	1.4
c2 (KO) n=2	241.7 ± 36.5	23.1 ± 6.9	9.6%	1.7

Table 2-SI: Transmissibility to mosquitoes of wild-type parasites and Pbmap-2 knock-out mutants. See Methods for details.

Genotype	Number of oocysts	Percentage infectivity	Number of sporozoites/mosquito
NK65 n=3	42.6 ± 37.39 range 0-92	73.3%	5666 (range 2000-10,000)
a1 (WT) n=2	32.8 ± 28.2 range 8-100	100%	6000 (range 6000)
b1 (KO) n=3	0	0	16 (range 0-50)
c2 (KO) n=3	0	0	0

Table 3-SI: List of primers used in this study.

Name of primer	Sequence
Primer 1	GCGTTTTCCCATACGATCATA
Primer 2	TAGCTATATAGGATAGTATAAAAGGCAC
Primer 3	CGCGGATCCTTGAAAAAAAAAAAAAGAATACTCTG
Primer 4	GGCCCTGGTTCTTCATTTTCTTC
Primer 5	ATGGCACCAAAGCAAAAATAGTAC
Primer 6	GTACCAGCGAAAATATCTTTGTGTC
Primer 7	ATGGAAGAAGTGCATTAGTGC
Primer 8	GAGAAAAGCATAATATGCGGAACC