

*Supplementary Material*

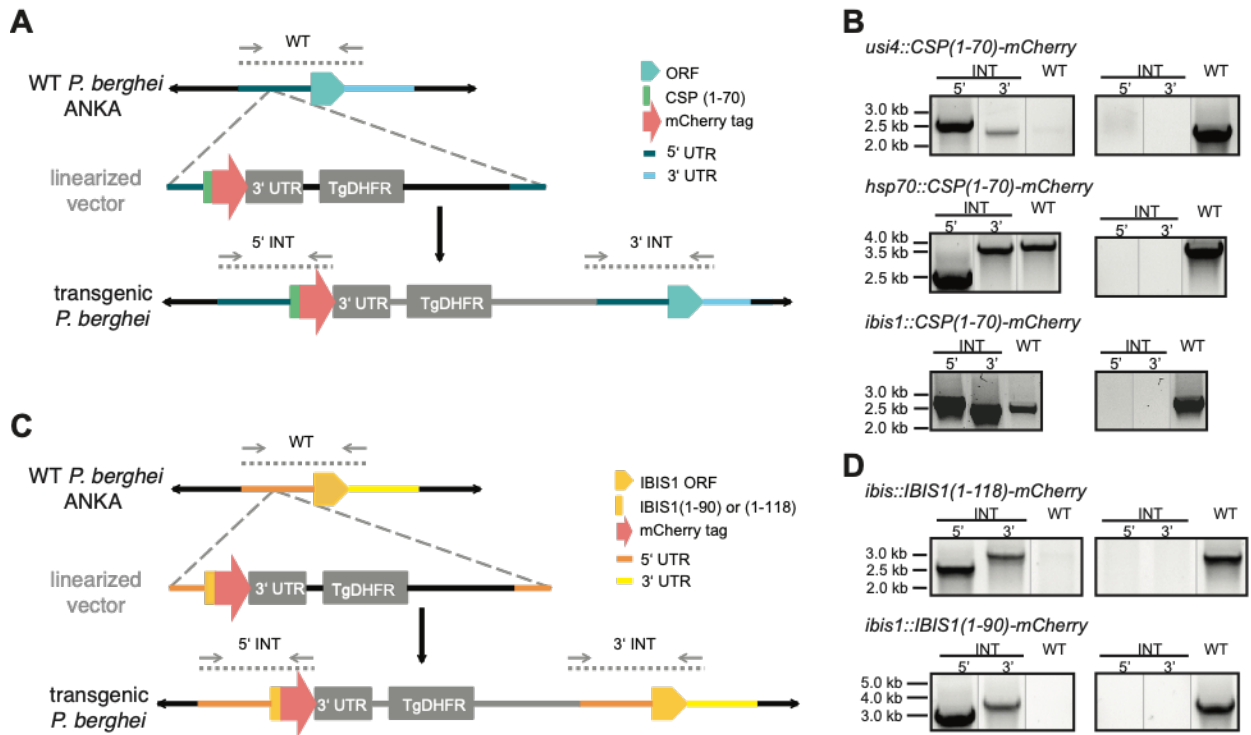
**Absence of PEXEL-dependent protein export in *Plasmodium* liver stages cannot be restored by gain of the HSP101 protein translocon ATPase**

Oriana Kreutzfeld, Josephine Grützke, Alyssa Ingmundson, Katja Müller, Kai Matuschewski

**Contents:**

- **Figures S1 - S6**
- **Tables S1-S2**

Kreutzfeld *et al.*, Figure S1



**Supplementary Figure 1. Generation of reporter parasite lines.**

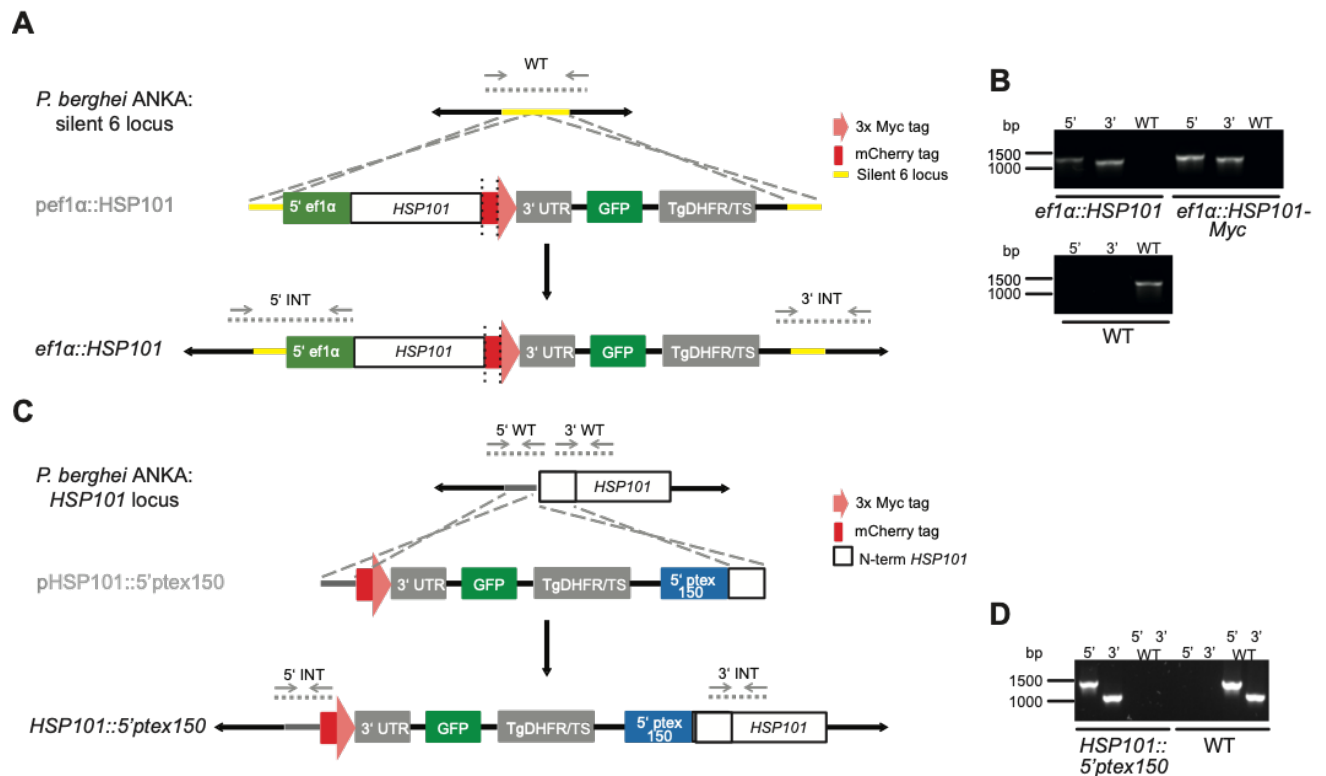
Shown are the (A,C) recombination events and (B,D) diagnostic PCRs to confirm the desired integrations.

(A,C) Integration strategy for the (A) CSP<sub>1-70</sub>-mCherry and (C) IBIS<sub>1-118</sub> reporter proteins. Shown are the WT locus (top), the linearized targeting plasmid (centre) and the recombinant locus (bottom). Diagnostic primers and PCR products are shown as arrows and dotted lines.

(B,D) Diagnostic PCRs show successful integration of the targeting constructs in the recombinant parasites (left) in comparison to WT parasites (right) with the PCR products, as depicted in the schemes.



Kreutzfeld *et al.*, Figure S3



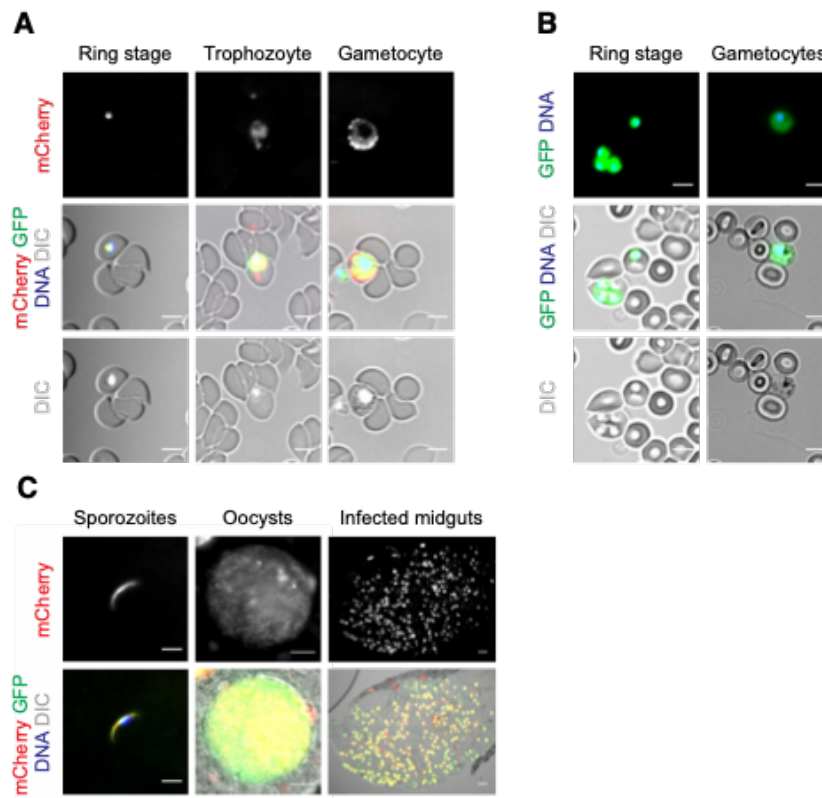
**Supplementary Figure 3. Generation of transgenic *HSP101* parasite lines.**

Shown are the (A,C) recombination events and (B,D) diagnostic PCRs to confirm the desired integrations.

(A,C) Integration strategy for the (A) *ef1α::HSP101* and (C) *HSP101::5'ptex150* parasite lines. Shown are the WT locus (top), the linearized targeting plasmid (centre) and the recombinant locus (bottom). Diagnostic primers and PCR products are shown as arrows and dotted lines.

(B,D) Diagnostic PCRs show successful integration of the targeting constructs in the recombinant parasites in comparison to WT parasites with the PCR products, as depicted in the schemes.

Kreutzfeld *et al.*, Figure S4



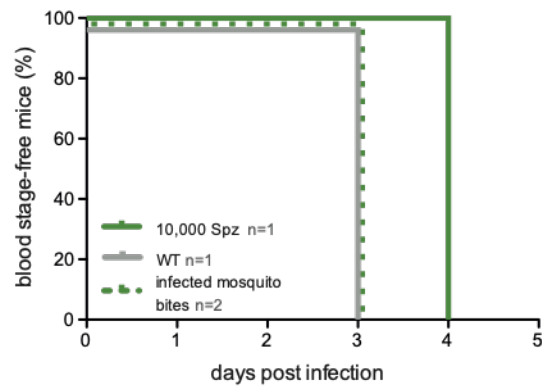
**Supplementary Figure 4. Live imaging of *eflα::HSP101* parasites.**

(A) Asexual (ring stage, trophozoite) and sexual (gametocyte) *eflα::HSP101-mCherry* blood stages from the peripheral blood. Shown are the mCherry signal (top) and merge images (bottom) of mCherry (red), GFP (green), Hoechst 33342 (blue), and DIC images. Bar, 5 μm.

(B) Asexual (ring stage) and sexual (gametocyte) *eflα::HSP101-myc* blood stages from peripheral blood. Shown are the GFP and Hoechst 33342 signal (top) and merge images (bottom), including DIC images. Bar, 5 μm.

(C) Sporozoites, oocysts and infected midguts of *eflα::HSP101-mCherry* parasites. Shown are the mCherry signal (top) and merge images (bottom) of mCherry (red), GFP (green), Hoechst 33342 (blue), and DIC images. Bar, 5 μm.

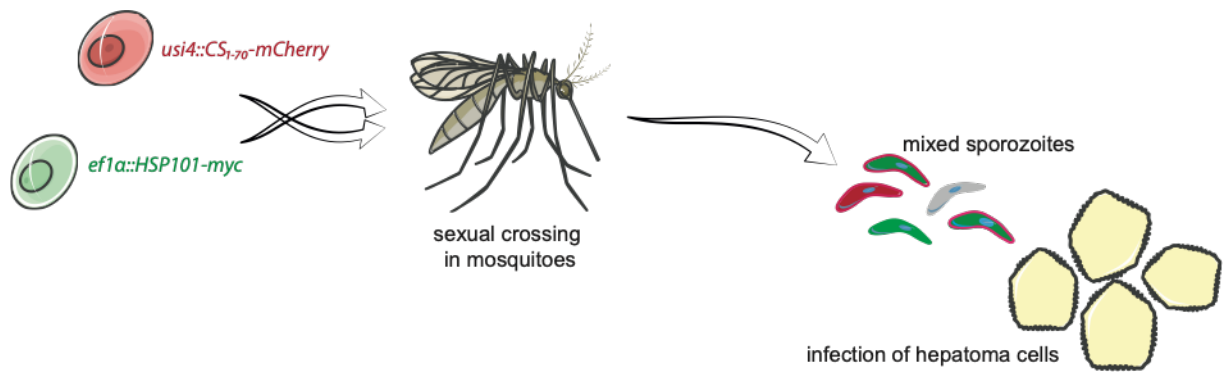
Kreutzfeld *et al.*, Figure S5



**Supplementary Figure 5. Sporozoite-induced blood infection in *ef1a::HSP101-myc* parasites.**

Shown in an exploratory Kaplan-Meier analysis of blood infection over time after intravenous injection of 10,000 sporozoites or exposure to 15 infected mosquitoes. Blood infection was monitored daily by microscopic examination of Giemsa-stained blood films.

Kreutzfeld *et al.*, Figure S6



**Supplementary Figure 6. Genetic crosses by sexual recombination in *Anopheles stephensi* mosquitoes.**

Schematic representation exemplified by coinfection of *ef1a::HSP101-myc* and *UIS4::CSP<sub>1-70</sub>-mCherry* parasites. The progeny was used for hepatoma cell infections and double fluorescent parasites were imaged to monitor protein secretion during liver stage development. Illustrations modified and adapted from Smart Servier Medical Art (Servier).

**Supplementary Table 1.** Midgut oocysts and salivary gland sporozoites from *Anopheles Stephens* mosquitoes infected with WT and transgenic parasite lines

<b>Parasite</b>	<b>% infectivity (d10 midgut oocysts)<sup>a</sup></b>	<b># salivary gland sporozoites per mosquito<sup>b</sup></b>
WT	47 %	17,500 ( $\pm$ 15,600)
<i>ef1<math>\alpha</math>::HSP101-mCherry</i>	50 %	14,300 ( $\pm$ 9,900)
<i>ef1<math>\alpha</math>::HSP101-myc</i>	73 %	11,750 <sup>c</sup>
<u><i>HSP101::5'ptex150</i></u>	70 %	18,400 ( $\pm$ 4,600)

<sup>a</sup> Mean number from three independent experiments

<sup>b</sup> Mean number from six independent experiments

<sup>c</sup> Data from a single experiment only



**Supplementary Table 2.** Primer sequences for generations of plasmids, genotyping and qRT-PCR.

<b>Name</b>	<b>Sequence *</b>
CSPfor	GCATCTAGAAAAGGTAAAATGAAGAAGT
CSP <sub>70</sub> rev	CGGACTAGTCCGATCGGCAAGTA
UIS4-5'for	TGACCGCGGCTTTATGTTTTTTGAAAGATTTAAC
UIS4-5'rev	GATGCGGCCGCTTTATTCAGACGTAATAAT
HSP70-5'for	TGTCCGCGGCATGATTTATTTATTTGC
HSP70-5'rev	GATGCGGCCGCTTTTTTTAATTGTAATTG
IBIS1-5'for	GCATCCGCGGCGTATTTAATCATACTATACGTTTTTCC
IBIS1-5'rev	CGGGCGGCCGCTTTTTAACTAATATGTTTTC
IBIS1 <sub>90</sub> rev	GGACTAGTATCCAACCTCTGATAATATTCTGCTTTTTCC
IBIS1 <sub>118</sub> rev	GGACTAGTTGACATATATGAGGTTGATGCATTTTCAG
5' int B3D rev	GATCCTTACTTGTACAGC
3' int B3D fwd	CTAATACGACTCACTATAGGGC
HSP70 5'int fwd	CCATAATGTTTCGATCGAGCAAATAACTTT
HSP70 3'int rev	CGACTCCATTCACCTTATTCCTTTTTTCAT
UIS4 5'int fwd	CAAATAATTGTGTATGTAATATTTAAGTGTAGAATGGAAT
UIS4 3'int rev	CTCTATAACATTATTTTTCTTTTTCTTACTT
IBIS1 5'int fwd	AAAATAATACATTTAATGAAGGGGAAAAGG
IBIS1 3'int rev	CATTAAAATATAACAATTTTCGATATAATATGTTGATC
HSP101for	CATCTAGAATGGTACGGAACATTGCTAAAAATTATTTATTTG
HSP101rev	GCCCTTGCTCACACCGGTTGACAATGAAAGGTTAATAACAATGTTG
5'EF1a fwd	CATGAGCGCGCGATTTACATGGCGTTTTATGTTTATATG
5'EF1a rev	GCTCATCTAGATTTTATAAAATTTTTATTTATTTATAAGCAAATATA
linker fwd	CGAGTGGCCACGTGGCCACCAGAACCACCACCGGTTTCATG
linker rev	CATGAACCGGTGGTGGTTCTGGTGGCCACGTGGCCACTCG
HSP101-5'-F	AGTACCCCGCGGATAAATAGAATAAGATGCTTGCTTTTCG
HSP101-5'-R	ATCAGGGTTAACTAAATTTATAGTAAATATAGATATAATTTTATCTTCATTC
HSP101_amino_F	CCCGGGGTTTAAACATGGTACGGAACATTGCTAAAAAT
HSP101_amino_R	CCAAAGTTTTAGCTATTACCGC
PTEX150-5'- PrimerF	TTGTCTCCGCGGTATATAAAGTGTTAATAGTGTTTTTTTTTGTGC

Supplementary Material Kreutzfeld *et al.*

PTEX150-5'- PrimerR	CTTGCC <u>GTTAACT</u> TTTATTATTCTAATTTATTATATTTTCGTTTCTTTTG
WT fwd	GACAGCGCATATGATGGATG
WT rev	TTTGAGAAATTGCGTATTCGTA
5' integration fwd efla::hsp101	ATGAAATACCGCTCCATTTTTCC
3' integration rev efla::hsp101	CATCTAGATTTTATAAAAATTTTATTATTATAAGCAAATATA
3' integration fwd hsp101::5'ptex150	GACTGAGGTTGTGTGATGGC
3' integration rev hsp101::5'ptex150	GAGCCAAATTGTTCAATGTTTAAT
5' integration fwd hsp101::5'ptex150	CTATAAATTTAGTAGAAATGGTACGGAAC
5' integration rev hsp101::5'ptex150	GACACTTATATATTTATACTAAGTTTCG
HSP70 fwd qPCR	GCTAACGCAAAAGCAAAGC
HSP70 rev qPCR	TCGGTAAAAGCTACATAGGATG
HSP101 fwd qPCR	TTTGTTATTGTCTGTGCTCAAGG
HSP101 rev qPCR	GCAAAGGTTTAAATTGGTTATGACC
Pb18 fwd	AAGCATTAATAAAGCGAATACATCCTTAC
Pb18 rev	GGAGATTGGTTTTGACGTTTATGTG
mGAPDH fwd	CGTCCCGTAGACAAAATGGT
mGAPDH rev	TTGATGGCAACAATCTCCAC

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\* Restriction sites are underlined