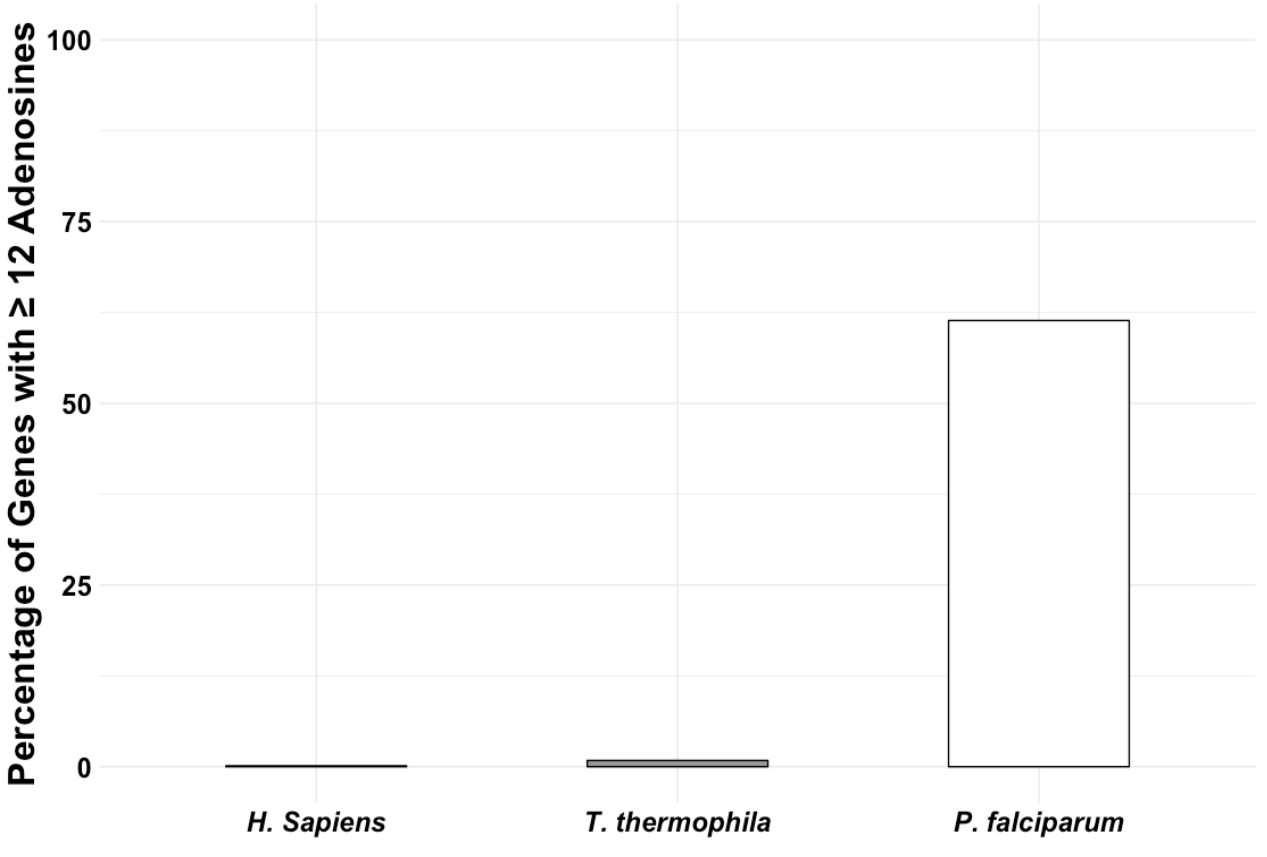
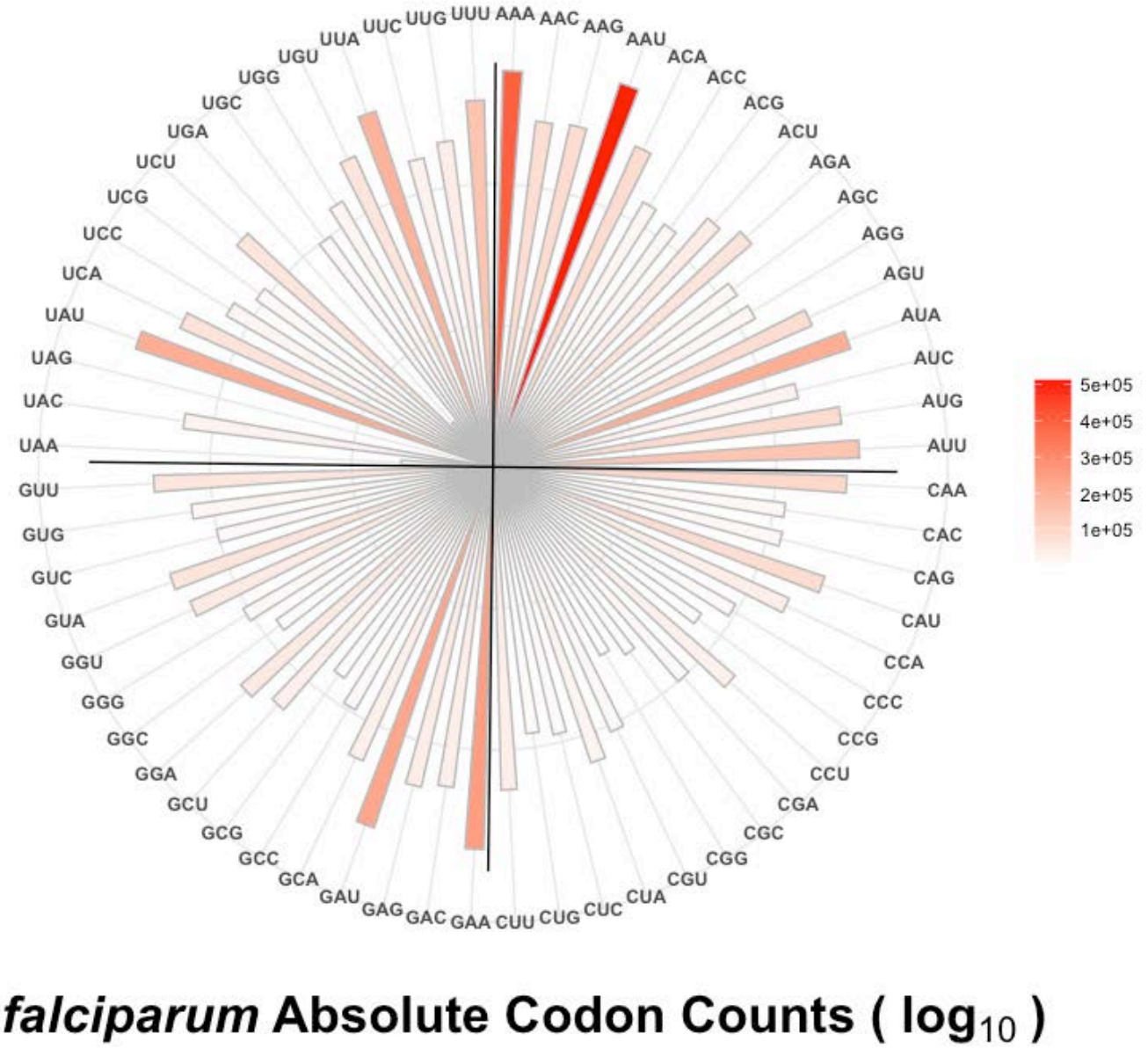
Supplementary Figure 1.



Supplementary Figure 1. Percentage of genes with ≥12 consecutive adenosine nucleotides for each organism. Number of genes was calculated as percentage of total number of genes with ≥12 consecutive adenosine nucleotides over total number of genes for each organism.

Supplementary Figure 2.



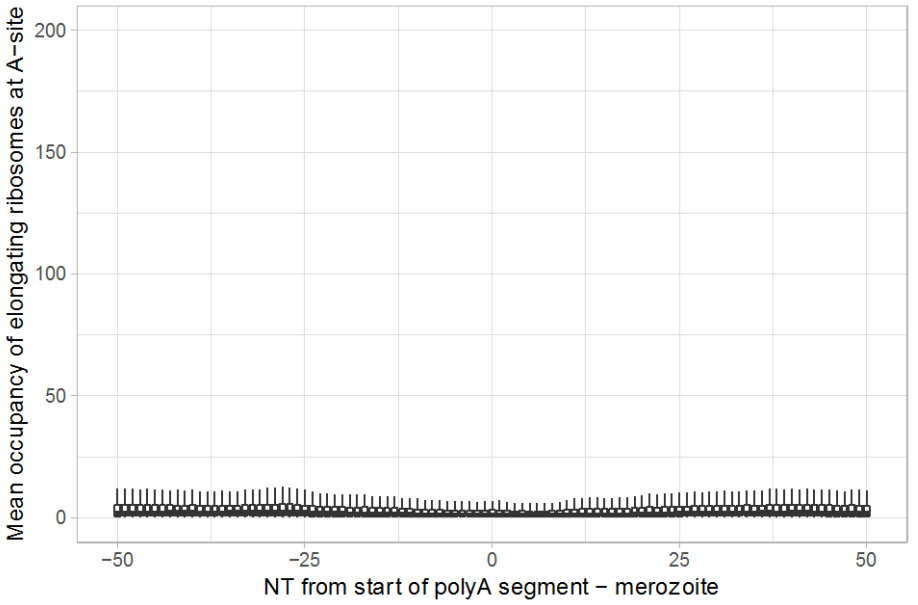
Supplementary Figure 2. Absolute codon usage counts in *P. falciparum* as per Saul and Battistutta 1988 on log10 scale. Lysine AAA and asparagine (AAU) codons show extreme bias over their cognate codons.

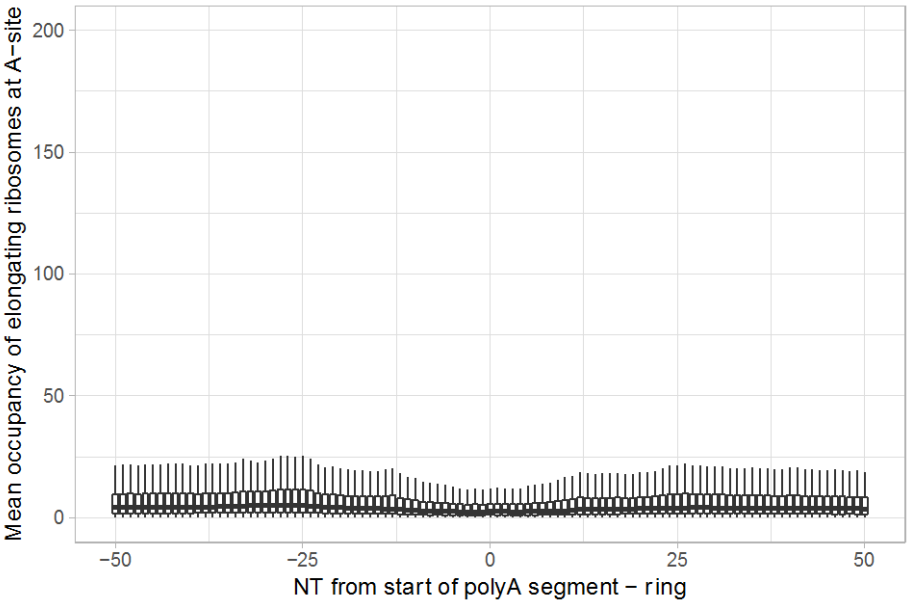
Supplementary Table1.

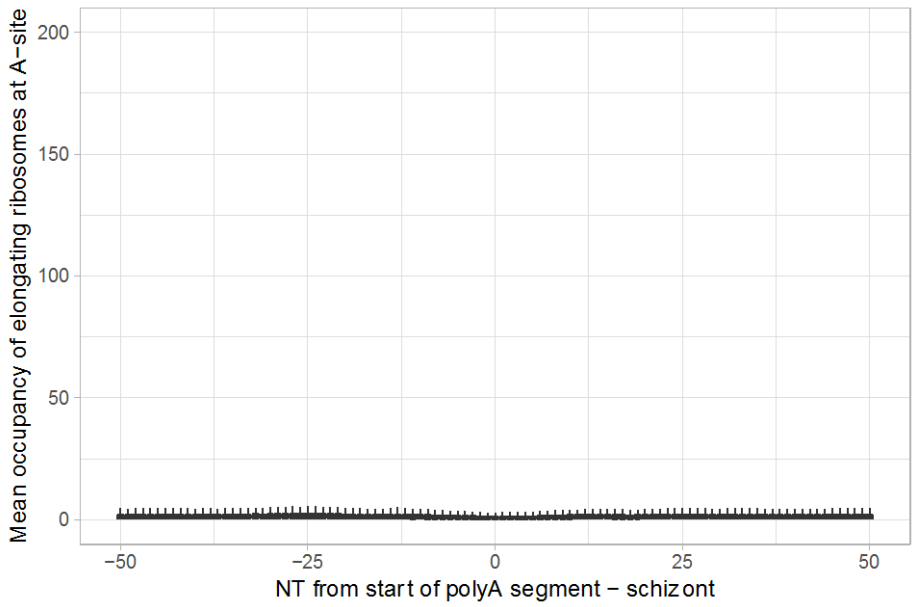
ID	Name	Bgd count	Result count	Pct of bgd	Fold enrichment	Odds ratio	P-value	Benjamini	Bonferroni
GO:0016337	single organismal cell-cell adhesion	57	56	98,2	1,56	33,76	8,98E-11	6,69E-08	1,34E-07
GO:0098602	single organism cell adhesion	57	56	98,2	1,56	33,76	8,98E-11	6,69E-08	1,34E-07
GO:0007155	cell adhesion	77	71	92,2	1,47	7,15	2,66E-09	1,32E-06	3,97E-06
GO:0009405	pathogenesis	101	81	80,2	1,28	2,44	0,00010834	0,04035608	0,16142433

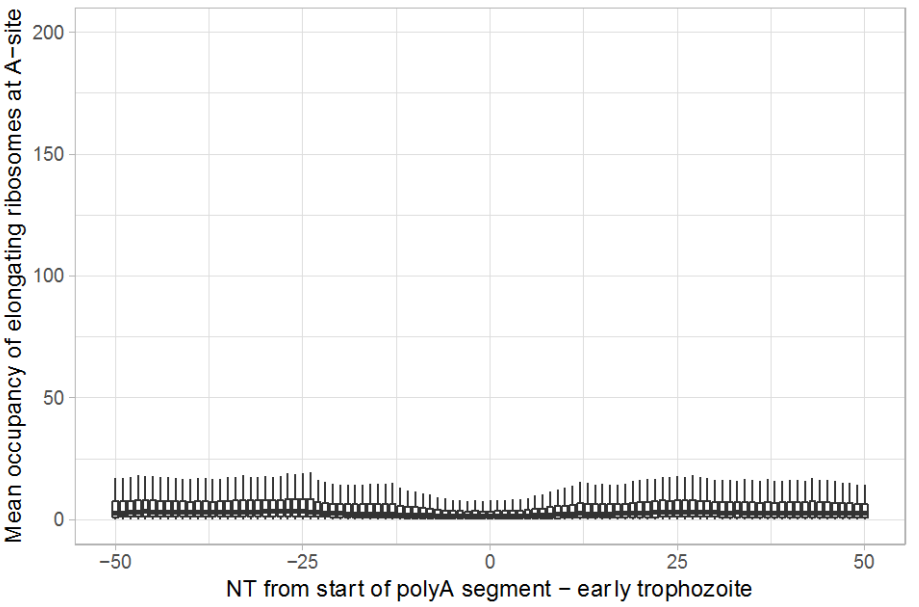
Supplementary Table 1. Highly significant gene ontology terms (GO) from biological process category for polyA-track carrying genes in *Plasmodium falciparum.*

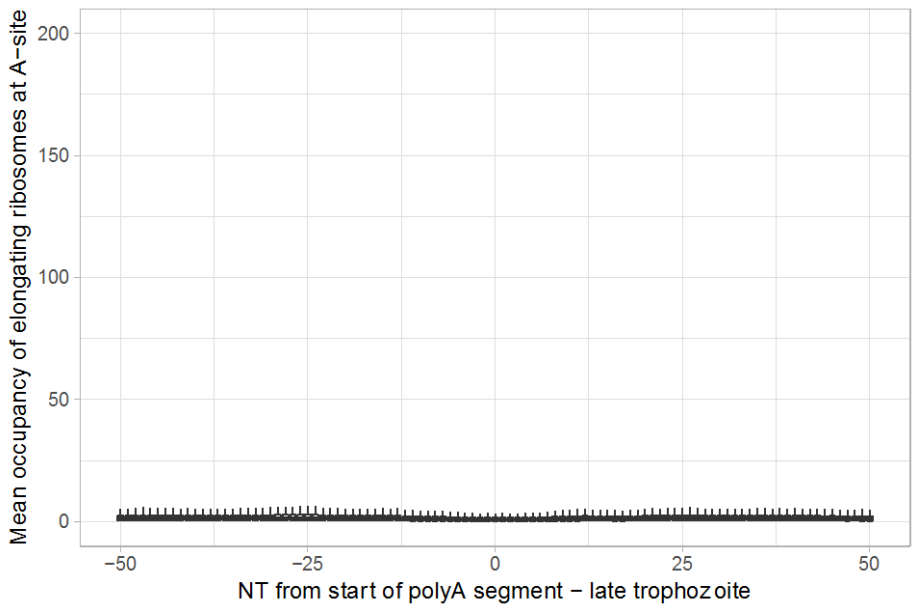
Supplementary Figure 3.





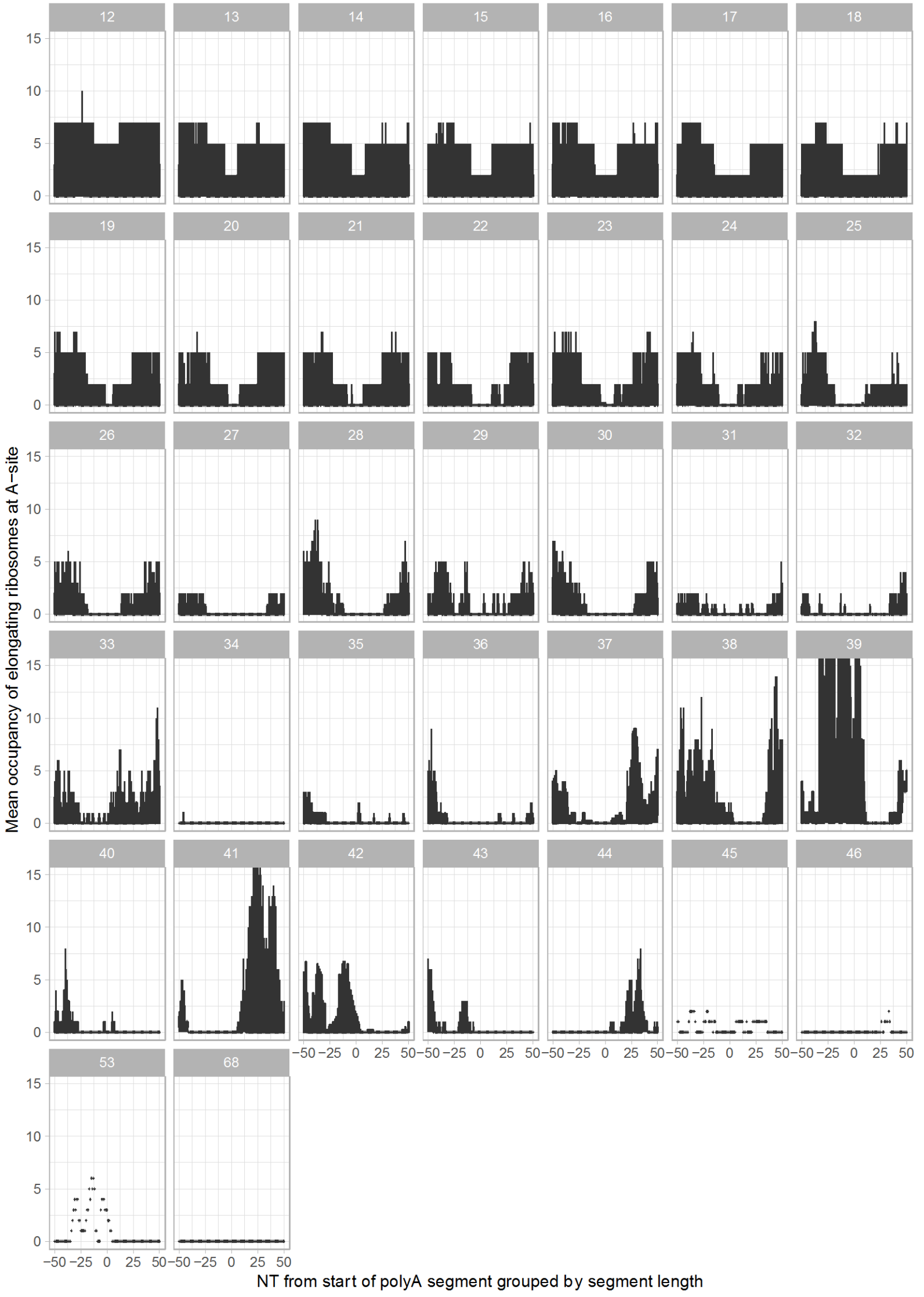






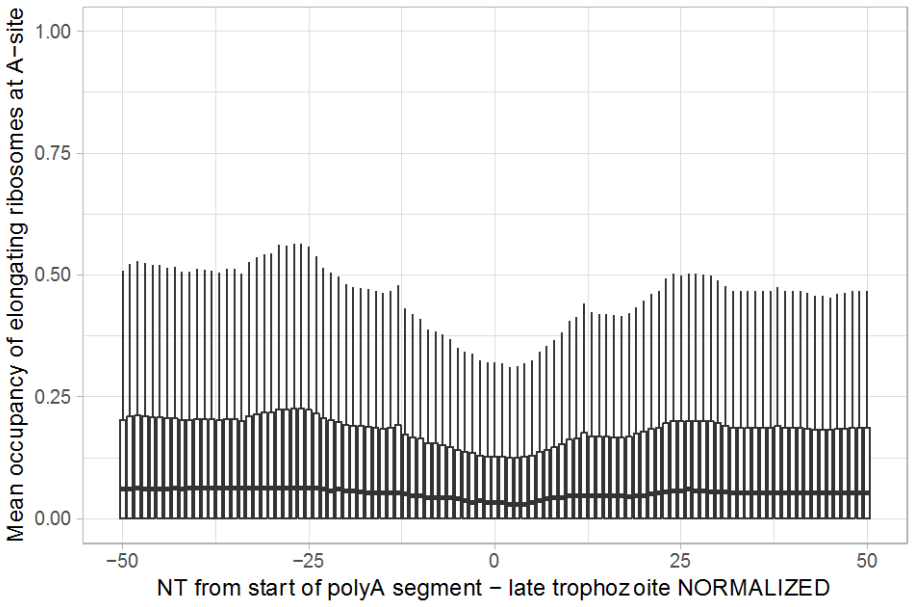
Supplementary Figure 3. Occupancy of elongating ribosomes (mapped to A-site) around start of polyA segment in Plasmodium at different life stages. Scale preserved from the main figures. In all cases, to avoid inclusion of sparsely mapped segments, regions with average occupancy below the mean for the particular dataset were excluded. Gene with segments shorter than 22 adenosine nucleotides were taken into account.

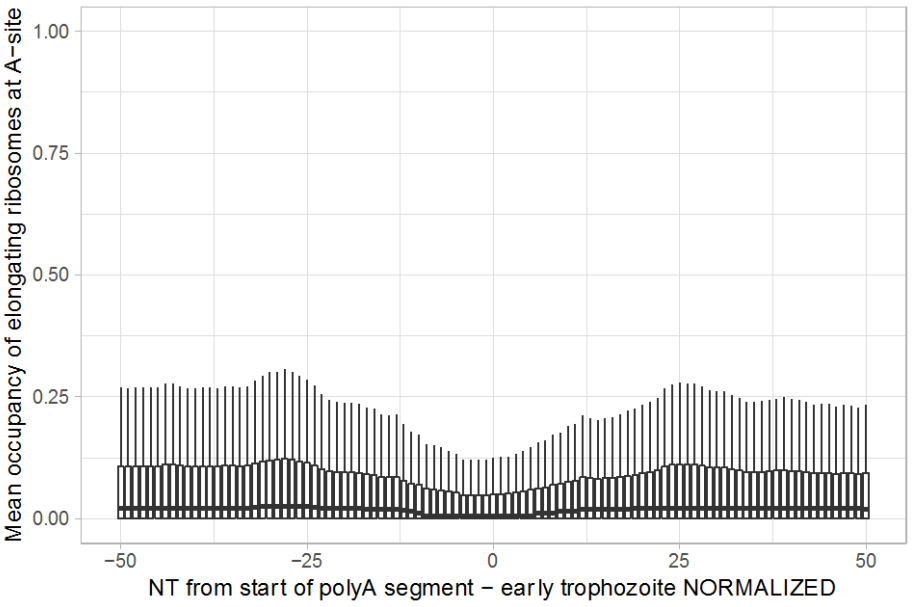
Supplementary Figure 4.

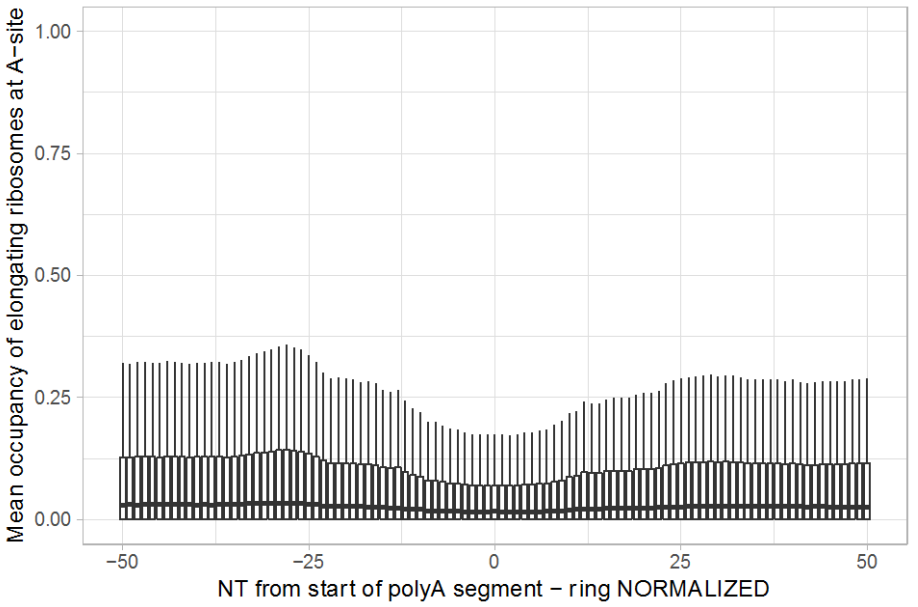


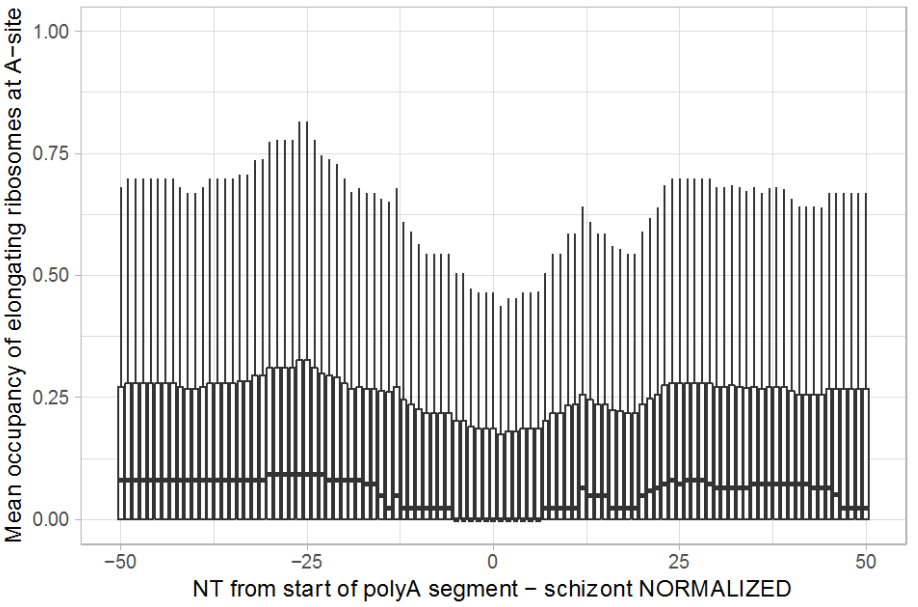
Supplementary Figure 4. Occupancy around polyA segment length (summarized across all life stages) grouped by polyA segment length (12-68 adenosine nucleotides in a row genes are shown).

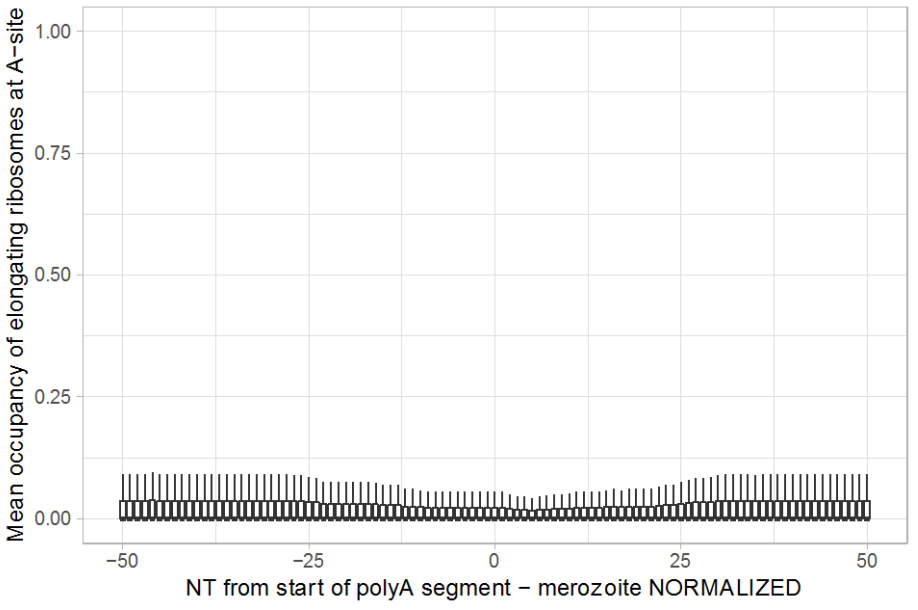
Supplementary Figure 5.





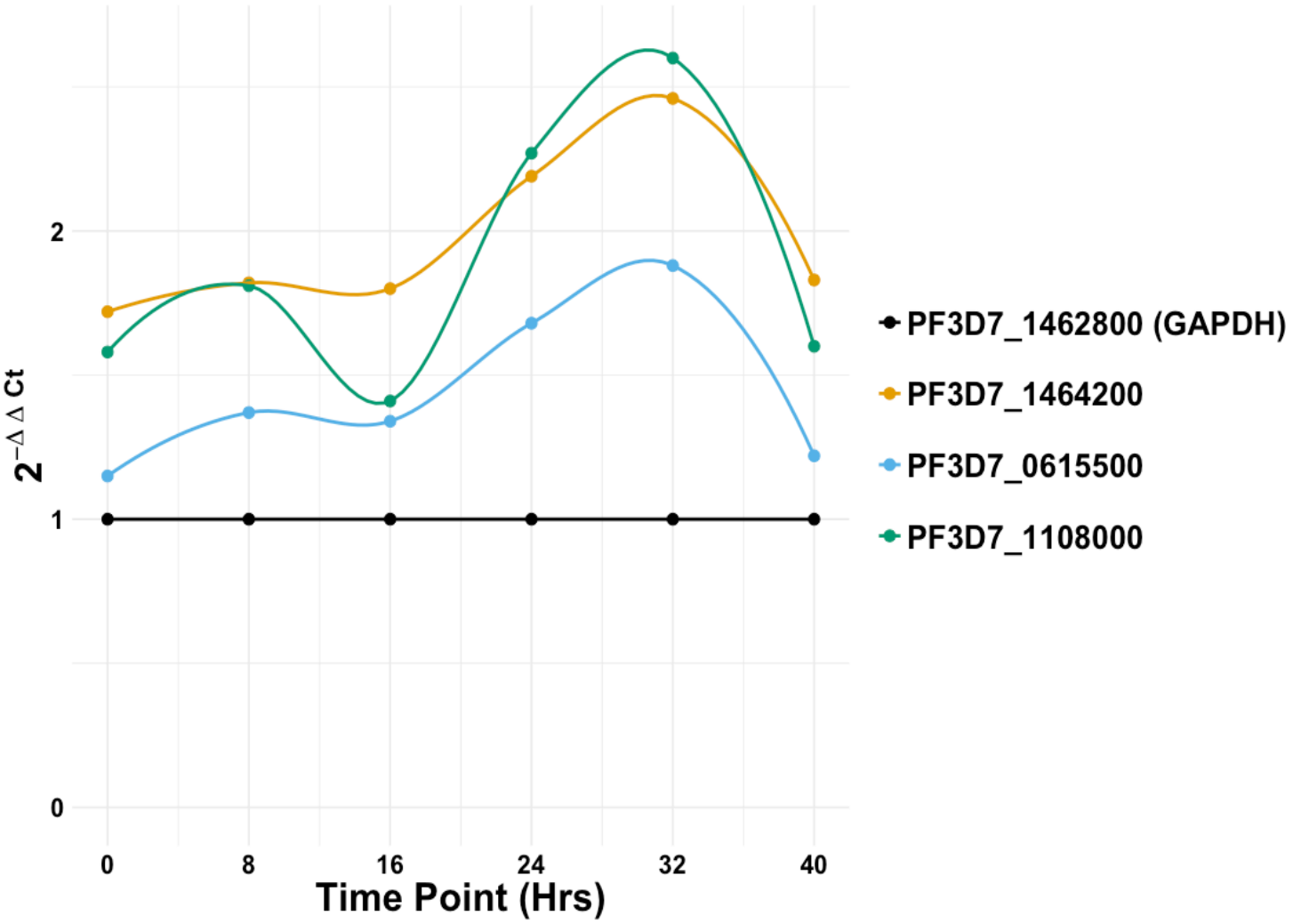






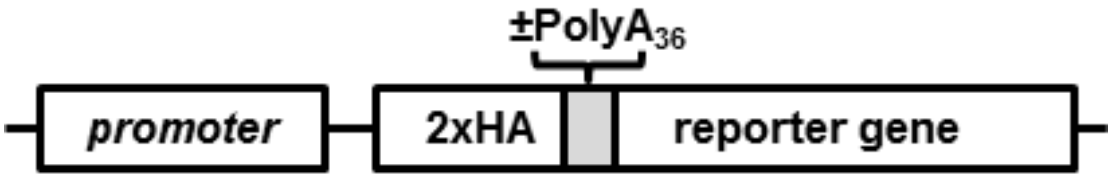
Supplementary Figure 5. Occupancy of elongating ribosomes (mapped to A-site) around start of polyA segment in Plasmodium at different life stages. Scale preserved from the main figures. In all cases, to avoid inclusion of sparsely mapped segments, regions with average occupancy below the mean for the particular dataset were excluded. Genes with segments shorter than 22 adenosine nucleotides were taken into account. In all cases data were normalized by dividing by a mean occupancy of a randomly selected gene segments equally numbered as polyA set from the same dataset.

Supplementary Figure 6.



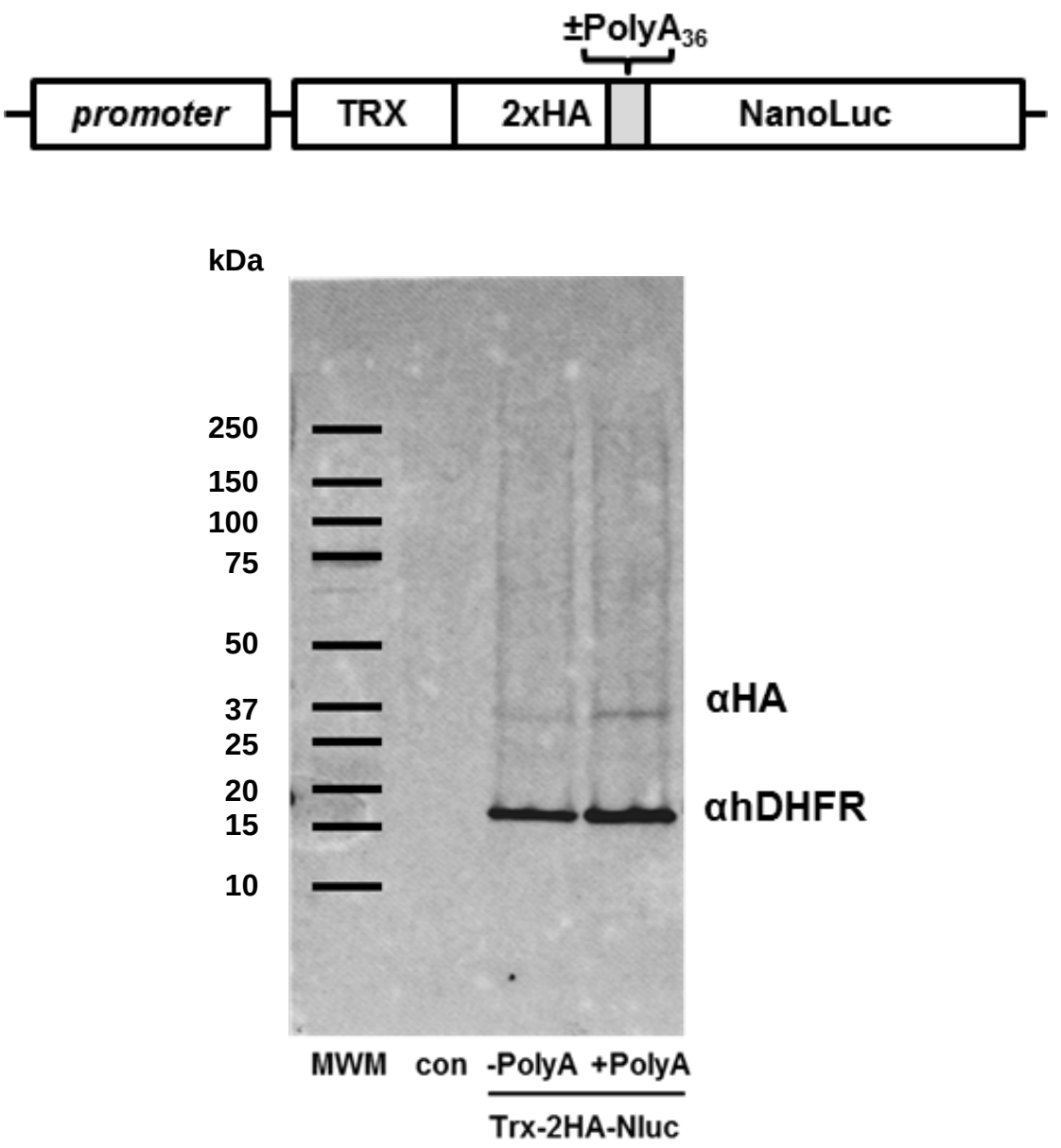
Supplementary Figure 6. Time course mRNA expression analysis of three genes (PF3D7_1464200, PF3D7_0615500, PF3D7_11080000) containing polyA stretches of varying lengths (largest: 20, 21, and 31 adenosines respectively) normalized to GAPDH (PF3D7_1462800) starting with highly synchronized rings at time zero. $2^{-\Delta\Delta Ct}$ values represent mRNA abundance enrichment of genes with polyA stretches over *Pf*GAPDH mRNA levels.

Supplementary Figure 7.



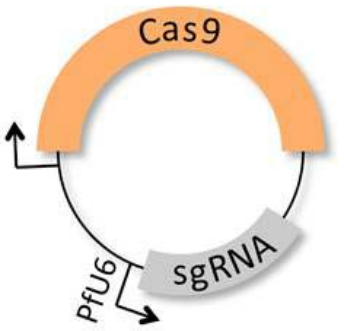
Supplementary Figure 7. Generalized scheme of reporter constructs used for expression in *H. sapiens, T. thermophila, and P. falciparum*.

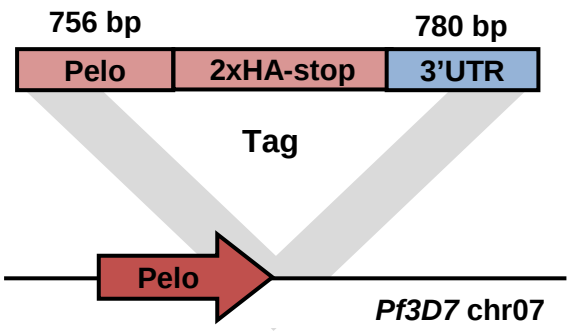
Supplementary Figure 8.



Supplementary Figure 8. Generalized schematic of Thioredoxin fusion NanoLuc reporter construct used for episomal expression in *P. falciparum* cells (Trx-2HA-Nluc). Lower: Western blot analysis of Trx-2HA-Nluc reporter expression in *P. falciparum* without (-polyA36) and with 36 adenosine stretch (+polyA36). Human DHFR (hDHFR) expressed from the same plasmid is used as loading and transfection control. Untransfected *P. falciparum* control cells (con) and Biorad Precision Plus Protein™ molecular weight markers (MWM) are indicated.

Supplementary Figure 9.





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gRNA primers

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pelotagRNA1273R
TTCTAGCTCTAAAAC**ATTAGTAATAATAATGTTTT**AATATTATATACTTA

pelotagRNA1314F clone2
TAAGTATATAATATT**GAGCTCTGACCATTTTATAT**GTTTTAGAGCTAGAA
pelotagRNA1314R
TTCTAGCTCTAAAAC**ATATAAAATGGTCAGAGCTC**AATATTATATACTTA

XhoI For Pelota(LH)
gtgacactatagaactcgagGAGCTCTGACCATTTTATATAtGCATAACAAAGTTGTTATATTATAAATATA

cgcgccttaagctca

AflII Pelota For
ATGTGAACCACTTAGATTTATTCAGGTGcttaagCAACAATTATATAAAACAGTTTTTAG

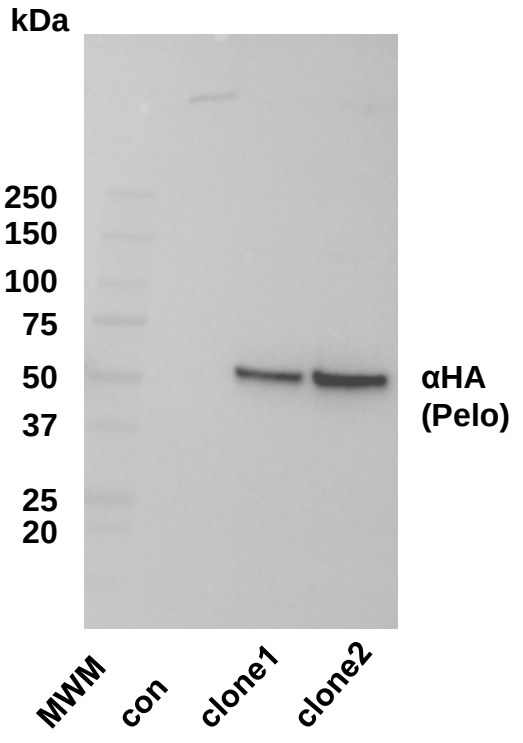
AflII Pelota Rev
CTAAAAACTGTTTTATATAATTGTTGcttaagCACCTGAATAAATCTAAGTGGTTCACAT

AvrIINeonGreen Pelota Rev (RH)
ctccacttcccctaggTATATTTGTCATATGCTCACC

AvrII3xHA Pelota Rev (RH)
CGTACGGGTAcctaggTATATTTGTCATATGCTCACC

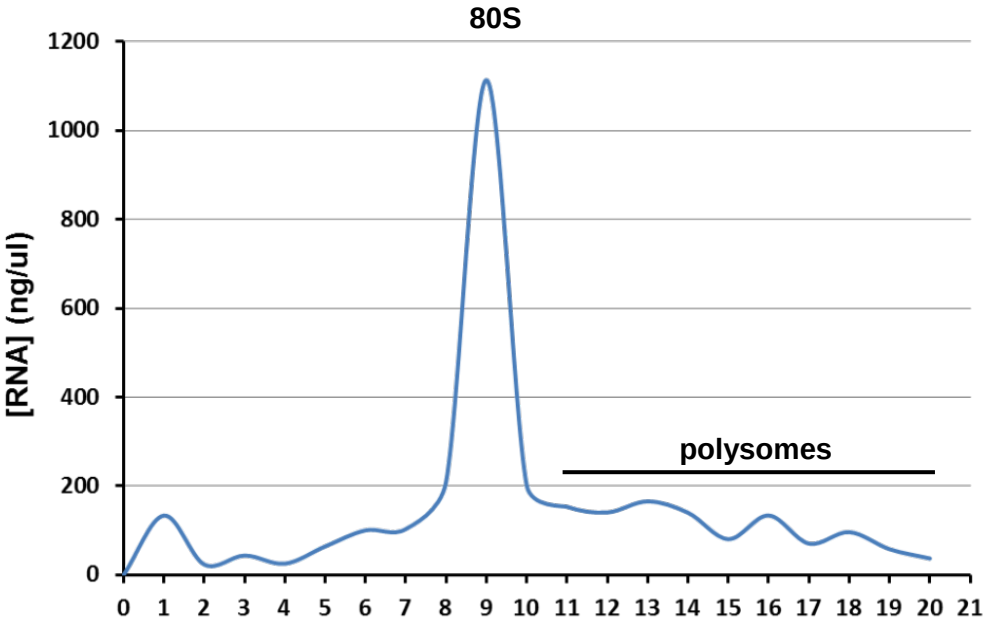
Supplementary Figure 9. Scheme of CRISPR/Cas9 engineering of P. falciparum Pelo (PF3D7_0722100 gene; human Pelo homolog). Two sets of gRNAs creating clone 1 and clone 2(red) were used to create independent clones1 and 2. Recombined sections of *Pf*Pelo gene are indicated in purple and gray, respectively. Primers used for creation of recombinant DNA and target sequences of gRNAs are indicated in teal, yellow and red, respectively.

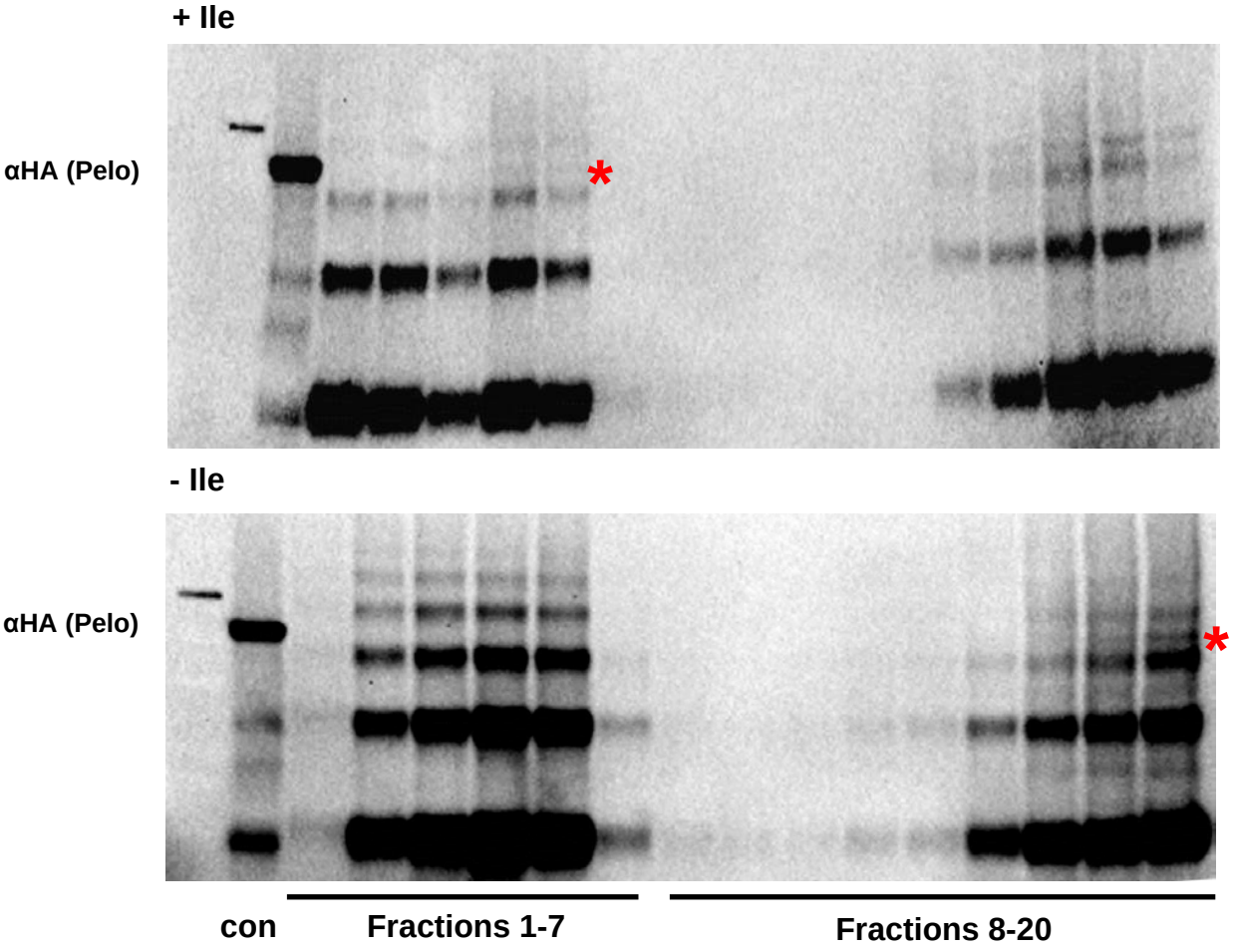
Supplementary Figure 10.



Supplementary Figure 10. Western blot analysis of endogenous HA-tagged *Pf*Pelo protein from two Cas9 engineered clonal lines (Clone 1 and Clone 2) of *P. falciparum Dd2* cells. Control (con) represents non-engineered *P. falciparum Dd2* parent line. Biorad Precision Plus Protein™ molecular weight markers (MWM) are indicated.

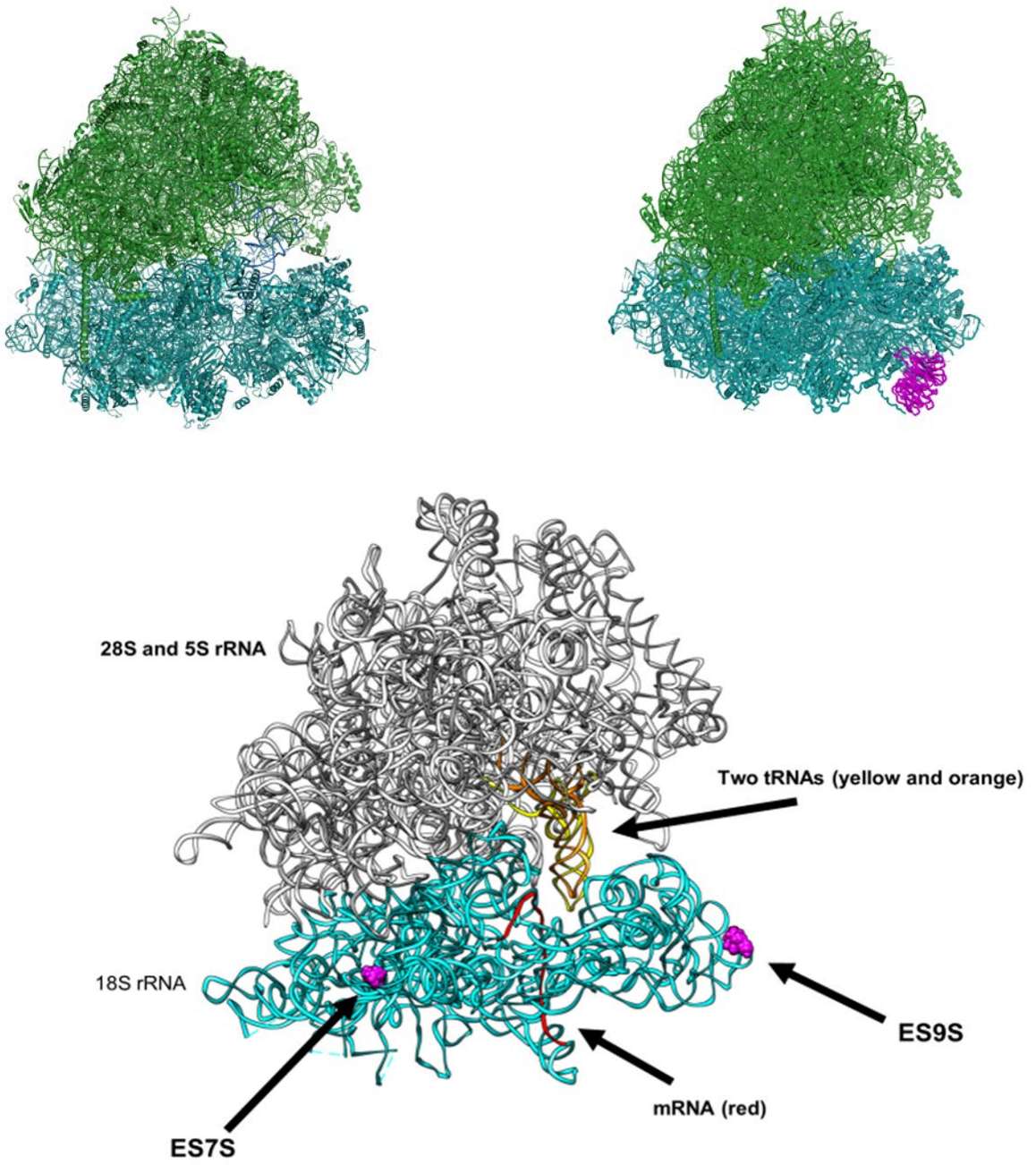
Supplementary Figure 11.





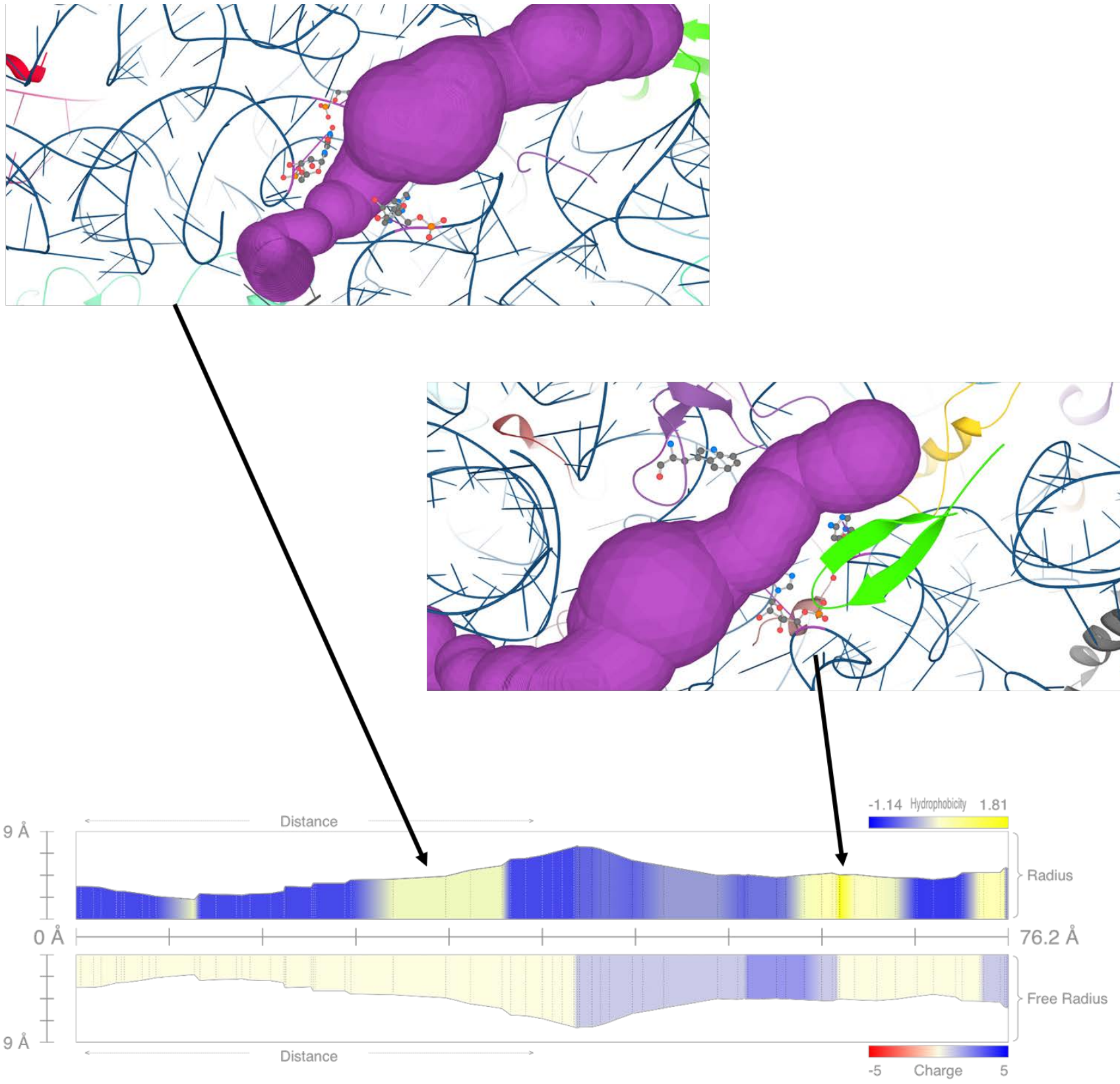
Supplementary Figure 11. Polysome profile analysis of isoleucine starved (-Ile) and control (+Ile) parasites. Star (*) indicates shift in endogenous HA-Pelo distribution into polysome fractions during 48 hour Ile starvation.

Supplementary Figure 12.



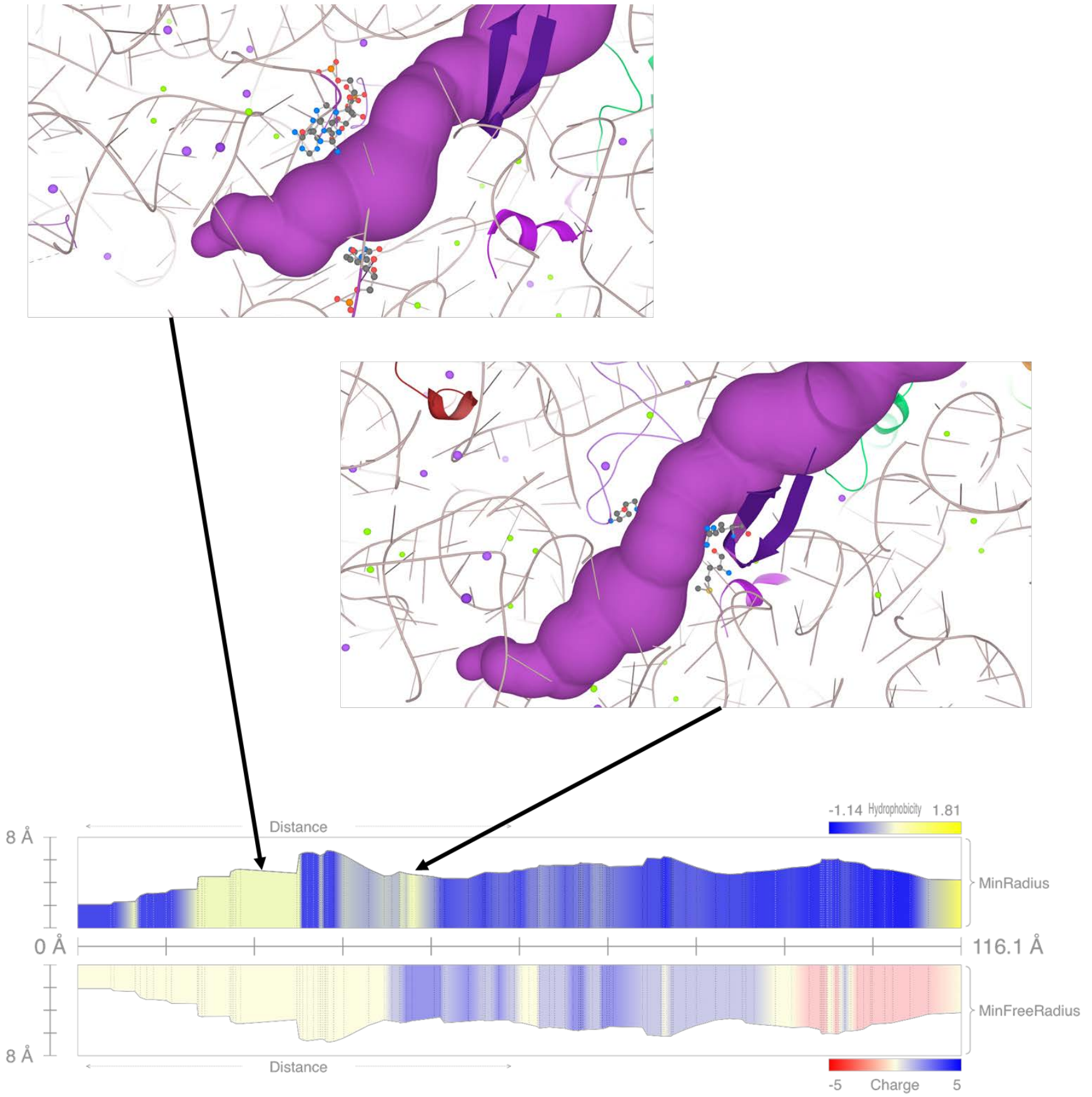
Supplementary Figure 12. Structure of *P. falciparum* (PDB code: 3JBO) and *H. sapiens* (PDB code: 3JAG) ribosomes with receptor for activated kinase C (RACK1) in magenta, previously shown to be absent from *Plasmodium* ribosomes (60S in green, 40S in cyan). Lower: Model of P. falciparum ribosome displaying small subunit ribosomal RNA sequence extensions (28S and 5S rRNAs in gray, 18S rRNA in cyan, tRNAs in yellow and orange, mRNA in red, extended sequences ES7S and ES9S in magenta). The ES7S and ES9S regions distinguish P. falciparum from other organisms. ES7S is located next to the binding pocket for ribosome GTPases and is adjacent to ribosome GTPase center.

Supplementary Figure 13.



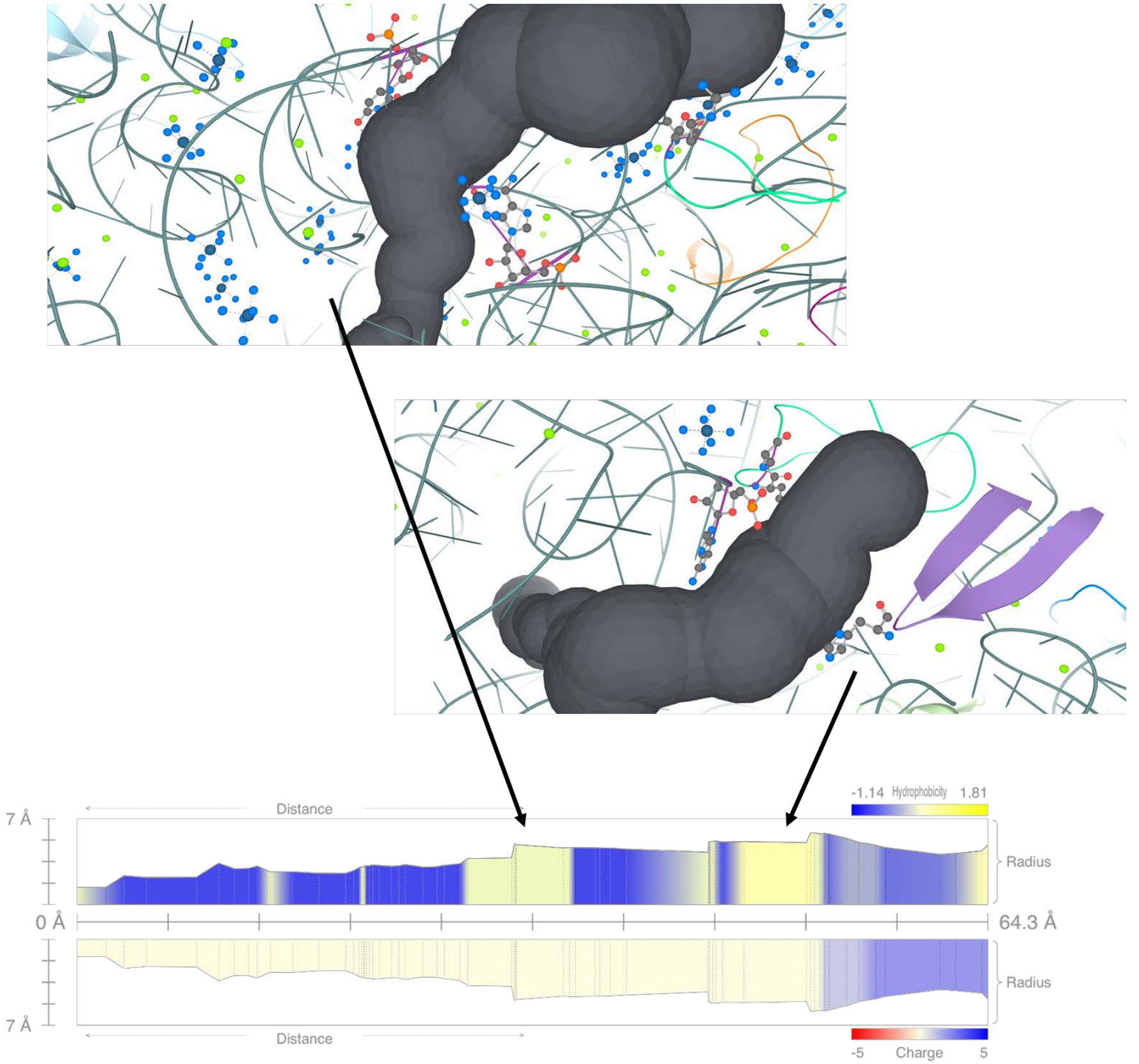
Supplementary Figure 13. Polypeptide exit channel from human ribosome (PDB: 6d90) has two long fragments (over 10 Angstroms) of relatively hydrophobic lining of the tunnel. Two major hydrophobic patches observed in other organisms are rRNA flanked (upper panel, interacting molecules have atoms shown) and L22 and L4 flanked (lower panel).

Supplementary Figure 14.



Supplementary Figure 14. Polypeptide exit channel from Haloarcula marismortui ribosome (PDB: 1jj2) has one long fragment (over 10 Angstroms) of relatively hydrophobic lining of the tunnel. Two major hydrophobic patches observed in other organisms are rRNA flanked (upper panel, interacting molecules have atoms shown) and L22 and L4 flanked (lower panel). .

Supplementary Figure 15.



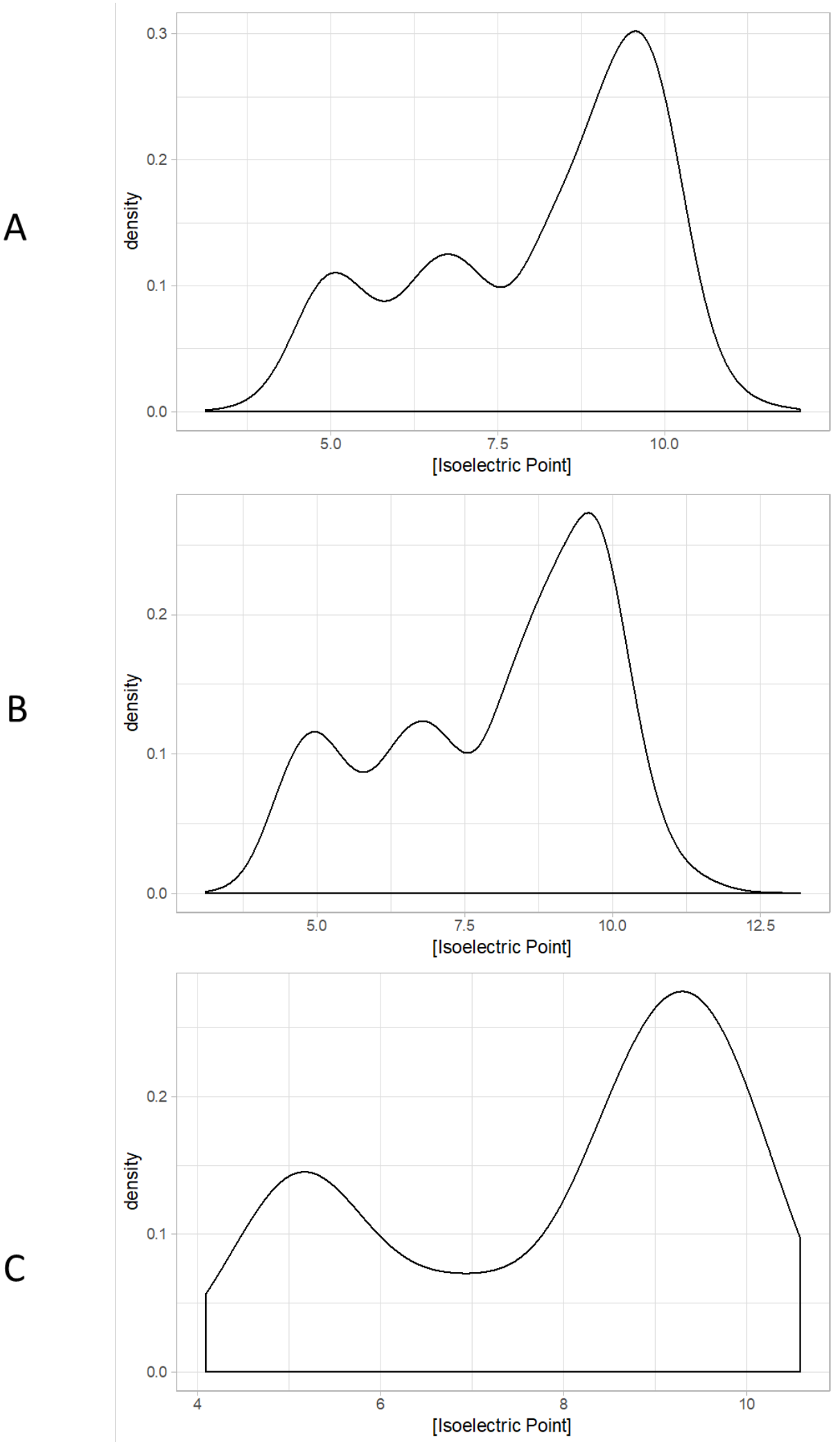
Supplementary Figure 15. Polypeptide exit channel from yeast ribosome (PDB: 5fci) has two long fragments (over 10 Angstroms) of relatively hydrophobic lining of the tunnel. Two major hydrophobic patches observed in other organisms are rRNA flanked (upper panel, interacting molecules have atoms shown) and L22 and L4 flanked (lower panel).

Supplementary Table 2.

ID	Name	Bgd count	Result count	Pct of bgd	Fold enrich ment	Odds ratio	P-value	Benjamini	Bonferroni
GO:0044419	interspecies interaction between organisms	335	72	21,5	5,36	10,05	1,86E-36	8,28E-35	1,66E-34
GO:0044403	symbiosis, encompassing mutualism through parasitism	335	72	21,5	5,36	10,05	1,86E-36	8,28E-35	1,66E-34
GO:0051704	multi-organism process	381	75	19,7	4,91	9,15	2,44E-35	7,23E-34	2,17E-33
GO:0020013	modulation by symbiont of host erythrocyte aggregation	190	51	26,8	6,69	11,71	4,20E-30	4,68E-29	3,74E-28
GO:0034118	regulation of erythrocyte aggregation	190	51	26,8	6,69	11,71	4,20E-30	4,68E-29	3,74E-28
GO:0034110	regulation of homotypic cell-cell adhesion	190	51	26,8	6,69	11,71	4,20E-30	4,68E-29	3,74E-28
GO:0030155	regulation of cell adhesion	190	51	26,8	6,69	11,71	4,20E-30	4,68E-29	3,74E-28
GO:0022407	regulation of cell-cell adhesion	190	51	26,8	6,69	11,71	4,20E-30	4,68E-29	3,74E-28
GO:0044068	modulation by symbiont of host cellular process	192	51	26,6	6,62	11,54	7,35E-30	7,27E-29	6,54E-28
GO:0044003	modification by symbiont of host morphology or physiology	193	51	26,4	6,58	11,46	9,70E-30	7,84E-29	8,63E-28
GO:0051817	modification of morphology or physiology of other organism involved in symbiotic interaction	193	51	26,4	6,58	11,46	9,70E-30	7,84E-29	8,63E-28
GO:0035821	modification of morphology or physiology of other organism	194	51	26,3	6,55	11,38	1,28E-29	9,47E-29	1,14E-27
GO:0020033	antigenic variation	204	49	24	5,99	9,91	1,93E-26	1,22E-25	1,71E-24
GO:0051809	passive evasion of immune response of other organism involved in symbiotic interaction	204	49	24	5,99	9,91	1,93E-26	1,22E-25	1,71E-24
GO:0043207	response to external biotic stimulus	206	49	23,8	5,93	9,78	3,12E-26	1,26E-25	2,78E-24
GO:0051832	avoidance of defenses of other organism involved in symbiotic interaction	206	49	23,8	5,93	9,78	3,12E-26	1,26E-25	2,78E-24
GO:0051707	response to other organism	206	49	23,8	5,93	9,78	3,12E-26	1,26E-25	2,78E-24
GO:0051834	evasion or tolerance of defenses of other organism involved in symbiotic interaction	206	49	23,8	5,93	9,78	3,12E-26	1,26E-25	2,78E-24
GO:0051807	evasion or tolerance of defense response of other organism involved in symbiotic interaction	206	49	23,8	5,93	9,78	3,12E-26	1,26E-25	2,78E-24
GO:0052173	response to defenses of other organism involved in symbiotic interaction	206	49	23,8	5,93	9,78	3,12E-26	1,26E-25	2,78E-24
GO:0052564	response to immune response of other organism involved in symbiotic interaction	206	49	23,8	5,93	9,78	3,12E-26	1,26E-25	2,78E-24
GO:0051805	evasion or tolerance of immune response of other organism involved in symbiotic interaction	206	49	23,8	5,93	9,78	3,12E-26	1,26E-25	2,78E-24
GO:0009607	response to biotic stimulus	207	49	23,7	5,9	9,71	3,97E-26	1,54E-25	3,53E-24
GO:0009605	response to external stimulus	214	49	22,9	5,71	9,29	2,04E-25	7,55E-25	1,81E-23
GO:0065008	regulation of biological quality	263	51	19,4	4,83	7,55	6,61E-23	2,35E-22	5,88E-21
GO:0051701	interaction with host	285	51	17,9	4,46	6,8	3,10E-21	1,06E-20	2,76E-19
GO:0016337	single organismal cell-cell adhesion	57	23	40,4	10,06	18,32	3,18E-18	1,01E-17	2,83E-16
GO:0098602	single organism cell adhesion	57	23	40,4	10,06	18,32	3,18E-18	1,01E-17	2,83E-16
GO:0007155	cell adhesion	77	23	29,9	7,44	11,48	7,28E-15	2,23E-14	6,48E-13
GO:0009405	pathogenesis	101	25	24,8	6,17	8,93	5,70E-14	1,69E-13	5,07E-12
GO:0044406	adhesion of symbiont to host	165	30	18,2	4,53	6,15	9,42E-13	2,62E-12	8,39E-11
GO:0020035	cytoadherence to microvasculature, mediated by symbiont protein	165	30	18,2	4,53	6,15	9,42E-13	2,62E-12	8,39E-11
GO:0022610	biological adhesion	192	31	16,1	4,02	5,33	1,01E-11	2,72E-11	8,98E-10
GO:0050896	response to stimulus	475	50	10,5	2,62	3,48	4,27E-11	1,12E-10	3,80E-09
GO:0050794	regulation of cellular process	516	51	9,9	2,46	3,24	2,72E-10	6,93E-10	2,43E-08
GO:0050789	regulation of biological process	541	51	9,4	2,35	3,05	1,53E-09	3,78E-09	1,36E-07
GO:0065007	biological regulation	564	51	9	2,25	2,9	6,70E-09	1,61E-08	5,96E-07
GO:0006468	protein phosphorylation	109	10	9,2	2,29	2,5	0,0114981	0,02692976	1

Supplementary Table 1. Highly significant gene ontology terms (GO) from biological process category for exported genes in *Plasmodium falciparum* (197 genes in total).

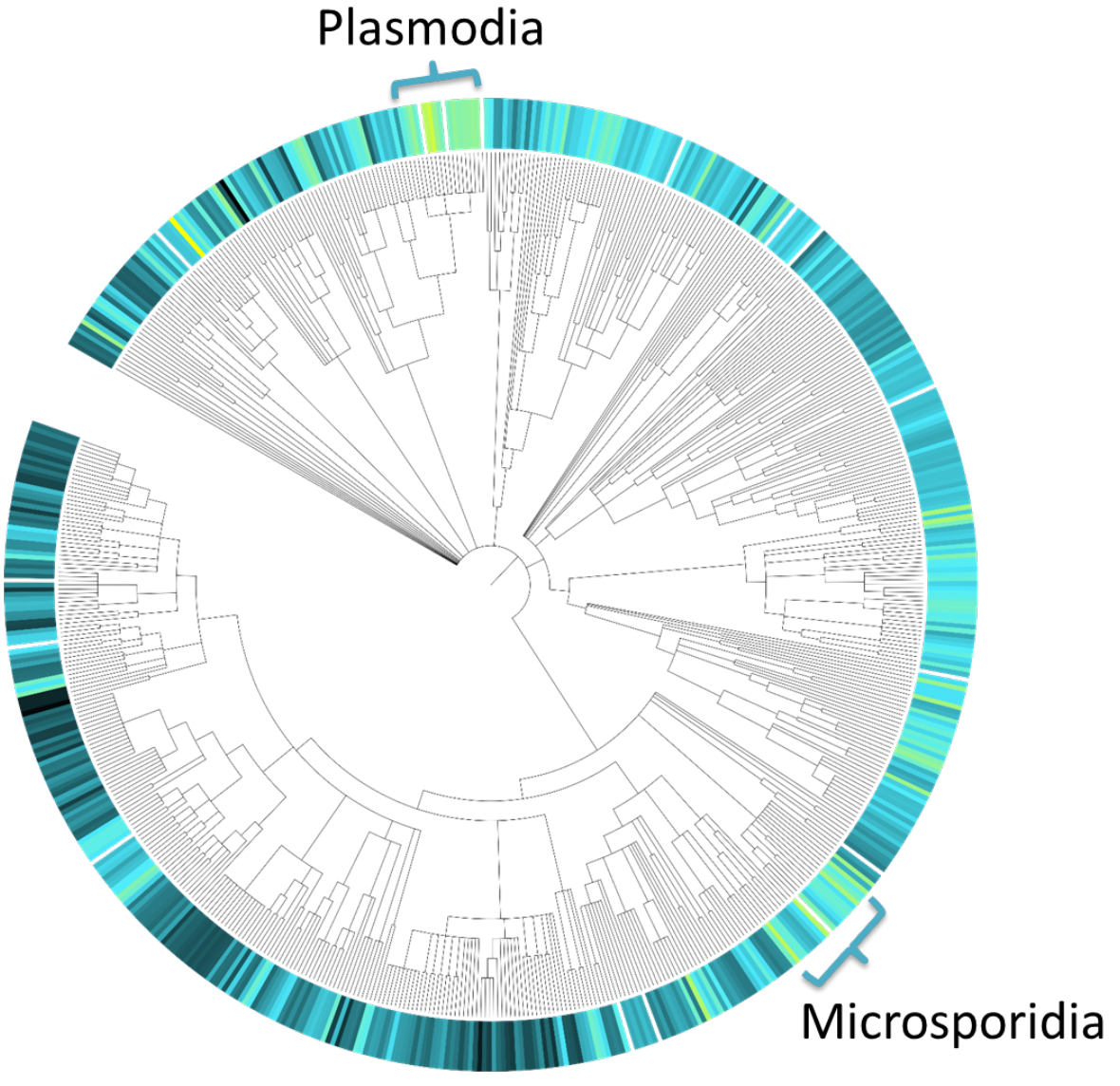
Supplementary Figure 16.



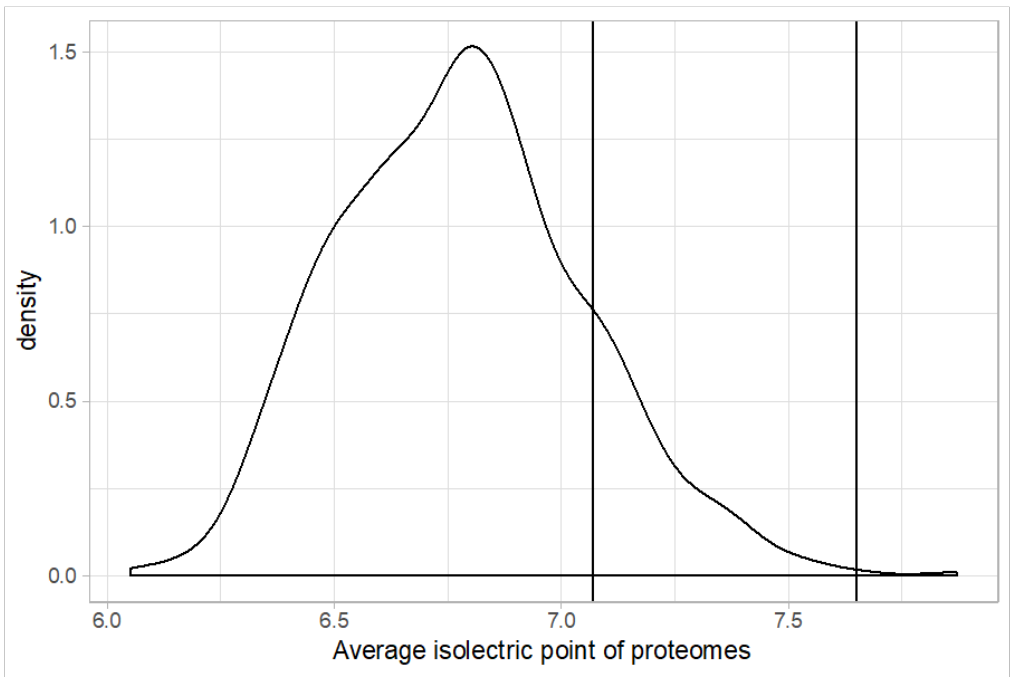
Supplementary Figure 16. Comparison of density plots of isoelectric points of proteins encoded by **A.** polyA-carrying genes in *P. falciparum* (3416 in total), **B.** all *P. falciparum* proteins (5801 in total) and **C.** exported proteins. All distributions do not differ significantly (p-value of Kolmogorov-Smirnov test for comparisons: A-B 0.12, A-C 0.06, B-C 0.23).

Supplementary Figure 17.

A



B



Supplementary Figure 17. A. Distribution of average isoelectric point mapped onto taxonomic tree of eukaryotes. *Plasmodia* and certain *Microsporidia* are the only two taxonomic groups consistently having high mean pI of proteomes. **B.** Density plot of the values from above plot. Range in which fit all *Plasmodium* species marked with vertical lines.