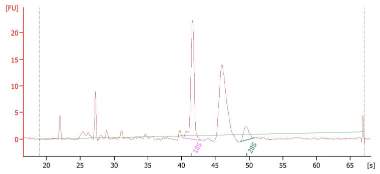
Supplemental data 1: RNA quality

Sample	Nanodrop		Bioanalyzer profil Pico Chip	
	Ratio 260/280	Ratio 260/230	rRNA Ratio [28s/18s]	RIN
01-004	1.98	1.26	0.2	7.6
01-006	2.25	2.3	1.8	8.7
01-013	2.09	0.93	N/A	8.5
01-020	2.26	0.24	N/A	7.5
01-033	2.05	2.13	1.3	7.1
02-002	2.24	2.24	N/A	6.9
02-003	1.89	0.9	1.2	7.2
02-011	2.2	0.42	0.9	8
02-013	2.19	1.96	1.3	7.2
02-016	2.2	1.65	0.6	6.6
02-017	2.22	2.32	1.7	7.3
02-018	1.97	1.35	0.9	9.6
02-025	2.2	1.66	1.1	8.5
02-027	2.21	1.98	0.2	7
02-030	2.19	1.66	N/A	8
02-034	2.22	1.79	0.8	9
03-022	1.73	0.84	0.2	6.6
03-025	2.22	2.09	1.1	9
03-028	2.05	1.58	1.1	6.9
03-030	2.04	0.97	1.0	7.1
03-031	2.11	1.9	1.7	7.4
03-037	2.16	2.34	N/A	7.1
03-051	1.82	1.13	0.7	7.1
03-059	2.12	1.75	1.5	9.7
03-060	2.09	1.68	N/A	7.3
03-075	2.09	0.69	N/A	7.1
03-108	2.02	1.54	1.0	8.1
03-110	2.03	1.71	N/A	6.7
03-113	1.9	1.09	0.3	7.4
03-127	1.97	1.09	0.6	7
03-134	2.11	0.13	0.9	6.8
03-137	1.91	0.15	N/A	6.9
03-140	2.26	2.47	1.6	7.7
03-141	2.21	1.55	1.3	9.7
03-145	1.8	0.75	1.5	7.6
03-153	2.1	1.71	0.9	9.8
03-160	2.09	1.27	3.0	7.8

01-004



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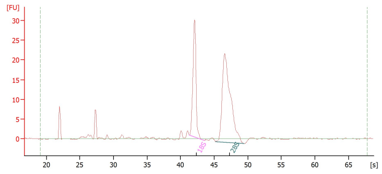

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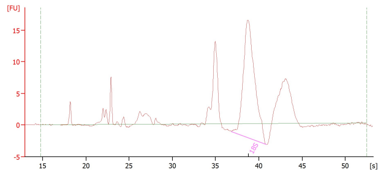

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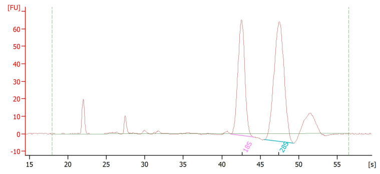

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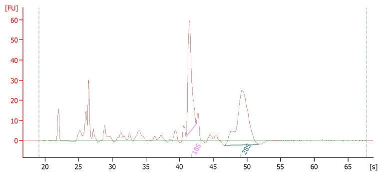

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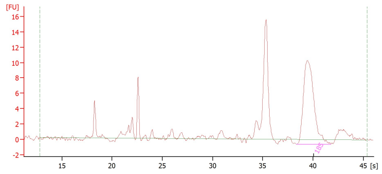

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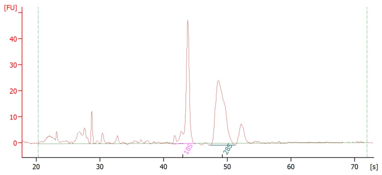

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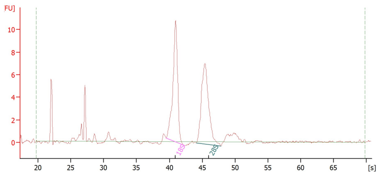

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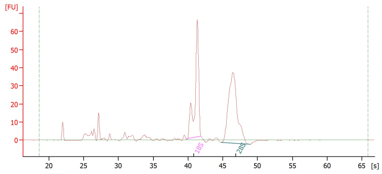

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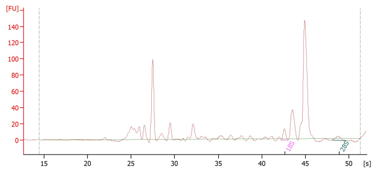

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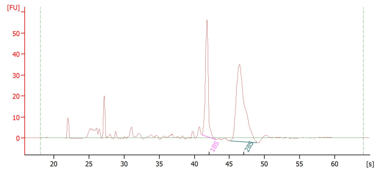

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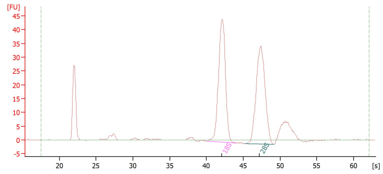

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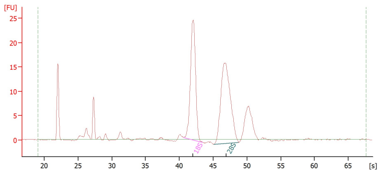

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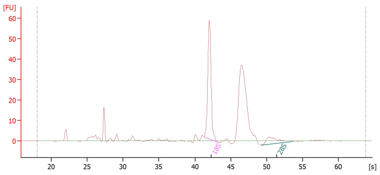

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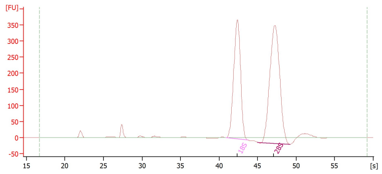

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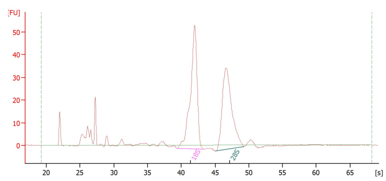

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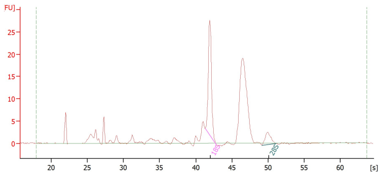

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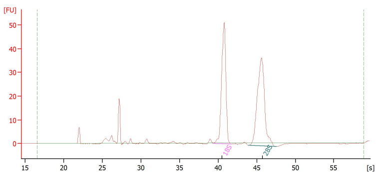

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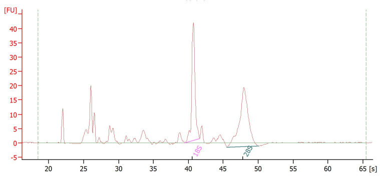

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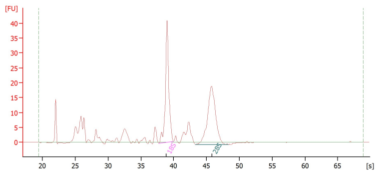

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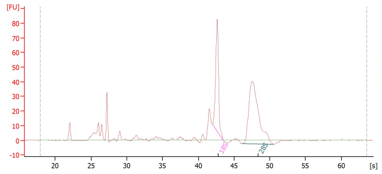

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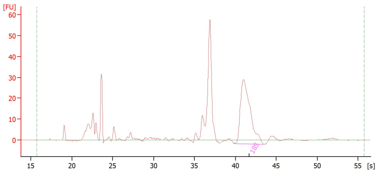

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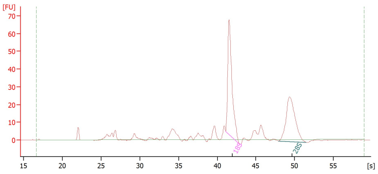

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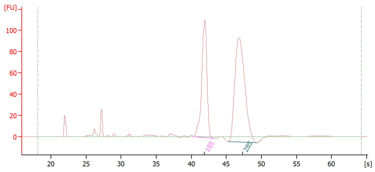

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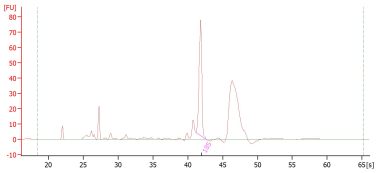

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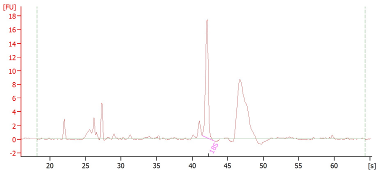

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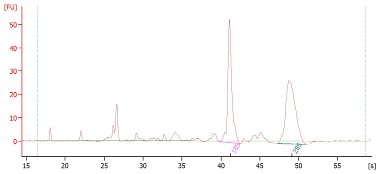

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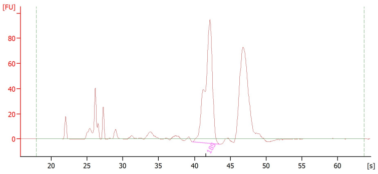

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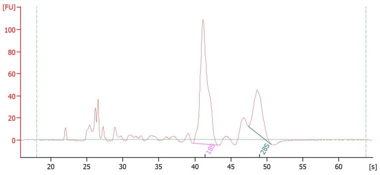

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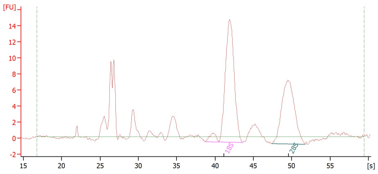

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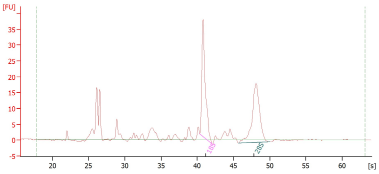

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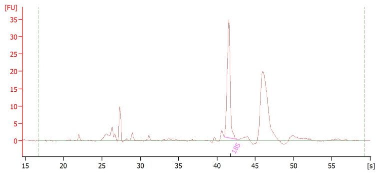

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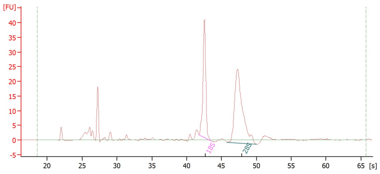

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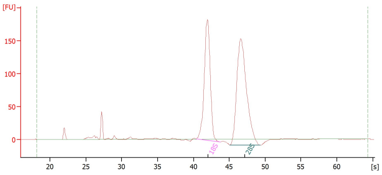

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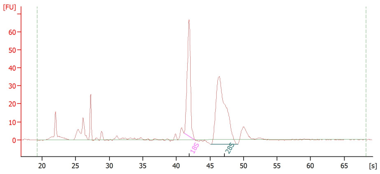

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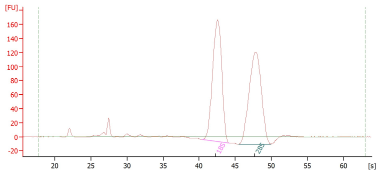

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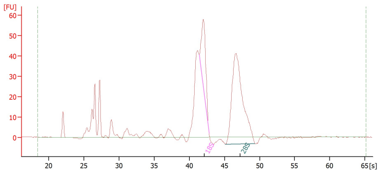


Supplemental data 2: *var* ATS-2 primers

	Primers set	Vardom statistics	VarDB statistics
Forward	cccatccacaaccaactgga ccaattatgaaccaattaga cctatactcaatcaaataaa cctataaccaatcaaataaa	47% (106/226)	13% (196/1517)
Reverse	agatagacatagaratatgtgyga agatagacatagagatatgtgcga agatagacatagagatatgtgtga agatagacatagaaatatgtgtga agatagacatagaaatatgtgcga	68% (154/226)	46% (699/1517)

Supplemental data 3: Mapping statistics

*PE reads aligned concordantly

Sample	Total PE reads	Reads aligned on *P. falciparum**	Reads aligned on human*	% aligned on *P. falciparum*	Included
01-004	29,460,649	25,013,688	1,806,283	84.91	yes
01-006	30,339,991	22,362,568	4,196,159	73.71	yes
01-013	19,726,822	15,530,598	2,581,835	78.72	yes
01-020	24,824,089	22,115,932	367,422	89.09	yes
01-033	24,725,082	842,203	21,956,993	3.41	no
02-002	29,967,330	23,760,342	3,414,561	79.29	yes
02-003	25,691,710	21,589,730	1,440,628	84.03	yes
02-011	20,387,129	13,886,245	3,629,496	68.11	yes
02-013	25,766,867	17,300,223	6,317,238	67.14	yes
02-016	34,260,826	28,218,798	2,673,820	82.36	yes
02-017	22,279,539	18,674,319	1,598,497	83.82	yes
02-018	24,899,632	13,481,147	9,448,237	54.14	yes
02-025	34,465,539	30,214,204	552,149	87.66	yes
02-027	21,078,309	17,703,933	1,482,800	83.99	yes
02-030	18,863,558	14,905,305	1,827,742	79.01	yes
02-034	40,413,108	30,939,185	5,556,226	76.56	yes
03-022	22,443,761	11,821,917	8,357,942	52.67	yes
03-025	22,891,522	19,206,253	1,534,413	83.90	yes
03-028	26,474,232	2,327,672	21,951,661	8.79	no
03-030	40,117,029	931,038	36,233,376	2.32	no
03-031	22,677,427	13,686,139	7,078,106	60.35	yes
03-037	25,984,157	18,574,199	5,313,743	71.48	yes
03-051	27,872,854	367,849	25,725,922	1.32	no
03-059	23,166,613	19,020,322	2,098,601	82.10	yes
03-060	22,842,008	18,788,367	2,057,835	82.25	yes
03-075	17,905,072	13,229,748	2,900,006	73.89	yes
03-108	38,637,117	13,134	34,668,977	0.03	no
03-110	25,517,266	15,103,898	8,062,731	59.19	yes
03-113	23,284,009	4,198,073	16,458,818	18.03	yes
03-127	41,860,202	611,208	36,757,232	1.46	no
03-134	28,279,149	106,671	26,422,856	0.38	no
03-137	36,010,543	27,498,890	4,726,525	76.36	yes
03-140	19,892,897	16,525,296	1,709,248	83.07	yes
03-141	18,449,529	15,826,946	827,848	85.78	yes
03-145	19,143,568	15,935,664	1,057,201	83.24	yes
03-153	18,790,453	11,106,406	5,732,515	59.10	yes
03-160	19,916,399	9,969,847	7,765,547	50.06	yes

Supplemental data 4: Antibodies anti-*P. falciparum* measurement

- **Quantification of total antibodies against *P. falciparum* iE with indirect fluorescence**

sample	clinical group	Antibody titer	immunological statut
01-004	CM	4096	strongly positive
01-006	CM	4096	strongly positive
01-013	CM	1024	strongly positive
01-020	CM	256	positive
02-002	CM	4096	strongly positive
02-003	CM	256	positive
02-011	CM	4096	strongly positive
02-013	CM	1024	strongly positive
02-016	CM	1024	strongly positive
02-017	CM	256	positive
02-018	CM	1024	strongly positive
02-025	CM	1024	strongly positive
02-027	CM	1024	strongly positive
02-030	CM	256	positive
02-034	CM	4096	strongly positive
03-022	UM	1024	strongly positive
03-025	UM	4096	strongly positive
03-031	UM	4096	strongly positive
03-037	UM	4096	strongly positive
03-039	UM	256	positive
03-060	UM	1024	strongly positive
03-075	UM	1024	strongly positive
03-110	UM	1024	strongly positive
03-113	UM	256	positive
03-137	UM	64	positive
03-140	UM	256	positive
03-141	UM	64	positive
03-145	UM	1024	strongly positive
03-153	UM	256	positive
03-160	UM	1024	strongly positive

- **IgG anti-VSA detection and quantification by flow cytometry**

sample	**clinical group**	**MFI_{iE}**	**$\mathrm{MFI}_{iE} - \mathrm{MFI}_{iE\ goat\ IgG}$**	**$\mathrm{MFI}_{uE} - \mathrm{MFI}_{uE\ goat\ IgG}$**	**MFI**
01-004	CM	44257	42951.5	49897.5	0
01-006	CM	12446	11140.5	25930.5	0
01-013	CM	48585.5	47280	40976	6304
01-020	CM	10500	9194.5	7486	1708.5
02-002	CM	5685	4379.5	15815.5	0
02-003	CM	1920	614,5	5314.5	0
02-011	CM	4924	3618.5	4279	0
02-013	CM	3434.5	2129	9978	0
02-016	CM	2761	1455.5	8378.5	0
02-017	CM	6384.5	5079	3349.5	1729
02-018	CM	2951.5	1646	17533.5	0
02-025	CM	3971.5	2666	33416.5	0
02-027	CM	1534	228.5	2765.5	0
02-030	CM	11035.5	9730	33893.5	0
02-034	CM	5064	3758.5	25153	0
03-022	UM	1117	0	0	0
03-025	UM	5066	3760.5	8818.5	0
03-031	UM	10099	8793.5	96893.5	0
03-037	UM	2136	830.5	0	831
03-059	UM	8330	7024.5	26066	0
03-060	UM	1837	531.5	0	532
03-075	UM	5570.5	4265	3927.5	337
03-110	UM	5115	3809.5	36784	0
03-113	UM	8329	7023.5	9047	0
03-137	UM	2766.5	1461	0	1461
03-140	UM	4381.5	3076	2238	838
03-141	UM	1121	0	0	0
03-145	UM	4230.5	2925	24	2901
03-153	UM	5599	4293.5	12894.5	0
03-160	UM	6506	5200.5	0	5201

MFI_{ie}: patient plasma on iE
MFI_{ue}: patient plasma on uninfected erythrocyte (uE)
$\mathrm{MFI}_{ie\ goat\ IgG}$: goat IgG anti-human on iE
$\mathrm{MFI}_{ue\ goat\ IgG}$: goat IgG anti-human on uE

Supplemental data 5: Parasites developmental blood stages

- **CM samples: microscopy**

Stage **(hpi)**	**Early ring** **(0-16)**	**Late ring + Early trophozoite** **(16-30)**	**Late Trophozoite** **(30-38)**	**Schizont** **38-48**	**Gametocyte**
01-004	Not readable				
01-006	Not readable				
01-013	Not readable				
01-020	0.91	0.09	0	0	0
02-002	1	0	0	0	0
02-003	0.93	0.07	0	0	0
02-011	1	0	0	0	0
02-013	0.93	0.07	0	0	0
02-016	Not readable				
02-017	1	0	0	0	0
02-018	0.94	0.06	0	0	0
02-025	0.96	0.04	0	0	0
02-027	0.98	0.02	0	0	0
02-030	0.55	0.45	0	0	0
02-034	1	0	0	0	0

- **CM samples: computed**

Stage **(hpi)**	**Ring** **(8)**	**Early trophozoite** **(19)**	**Late trophozoite** **(30)**	**Schizont** **(42)**	**Gametocyte**
01-004	0.63	0.37	0	0	0
01-006	0.91	0.09	0	0	0
01-013	0.94	0.06	0	0	0
01-020	1	0	0	0	0
02-002	1	0	0	0	0
02-003	1	0	0	0	0
02-011	1	0	0	0	0
02-013	1	0	0	0	0
02-016	1	0	0	0	0
02-017	1	0	0	0	0
02-018	1	0	0	0	0
02-025	1	0	0	0	0
02-027	0.86	0.14	0	0	0
02-030	0.56	0.41	0.03	0	0
02-034	1	0	0	0	0

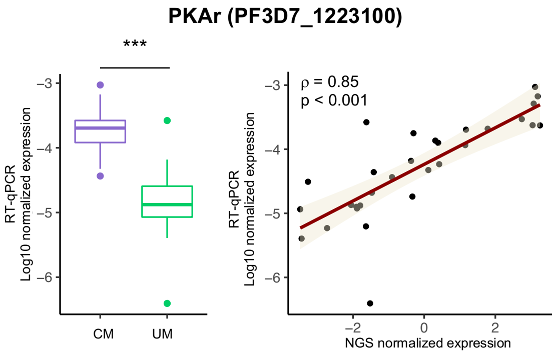
- **UM samples: microscopy**

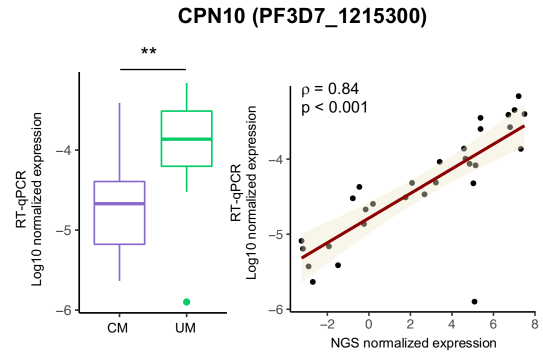
Stage (hpi)	Early ring (0-16)	Late ring + Early trophozoite (16-30)	Late Trophozoite (30-38)	Schizont 38-48	Gametocyte
03-022	0.99	0.01	0	0	0
03-025	-	1	0	0	0
03-031	0.01	0.99	0	0	0
03-037	0.21	0.79	0	0	0
03-059	0.01	0.99	0	0	0
03-060	0.44	0.56	0	0	0
03-075	0.06	0.94	0	0	0
03-110	0.86	0.14	0	0	0
03-113	Not readable				
03-137	0.03	0.97	0	0	0
03-140	-	1	0	0	0
03-141	0.06	0.94	0	0	0
03-145	0.14	0.86	0	0	0
03-153	0.29	0.71	0	0	0
03-160	0.79	0.21	0	0	0

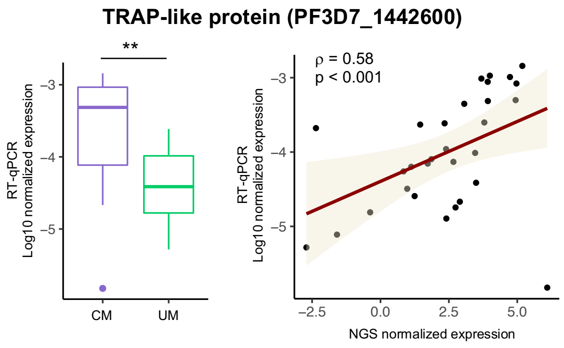
- **UM samples: computed**

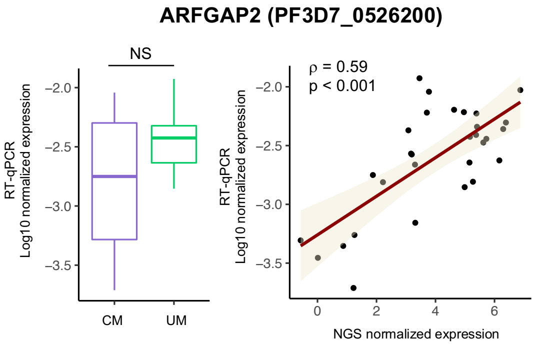
Stage (hpi)	Ring (8)	Early trophozoite (19)	Late trophozoite (30)	Schizont (42)	Gametocyte
03-022	1	0	0	0	0
03-025	0.24	0.73	0	0	0.03
03-031	0.11	0.77	0.02	0	0.1
03-037	0.37	0.58	0	0	0.05
03-059	0.10	0.86	0	0	0.04
03-060	0.77	0.23	0	0	0
03-075	0.13	0.83	0	0	0.04
03-110	0.71	0.29	0	0	0
03-113	1	0	0	0	0
03-137	0.58	0.42	0	0	0
03-140	0.59	0.41	0	0	0
03-141	0.59	0.41	0	0	0
03-145	0.63	0.37	0	0	0
03-153	0.71	0.29	0	0	0
03-160	0.82	0.18	0	0	0

Supplemental data 6: RT-qPCR validations


PKAr (PF3D7_1223100)


CPN10 (PF3D7_1215300)


TRAP-like protein (PF3D7_1442600)


ARFGAP2 (PF3D7_0526200)

Gene	**CM** Median [10th-90th percentile]	**UM** Median [10th-90th percentile]	**p-value**
PHISTa - PF3D7_1372000	$1.1*10^{-4}$ [$3.6*10^{-5}$-$5.9*10^{-4}$]	$3.0*10^{-4}$ [$2.0*10^{-4}$-$6.1*10^{-4}$]	< 0.001
PKAr - PF3D7_1223100	$2.0*10^{-4}$ [$5.2*10^{-5}$-$6.1*10^{-4}$]	$1.3*10^{-5}$ [$4.8*10^{-6}$-$5.7*10^{-5}$]	< 0.001
CLAG9 - PF3D7_0935800	$5.5*10^{-4}$ [$1.6*10^{-4}$-$1.5*10^{-3}$]	$9.3*10^{-5}$ [$3.1*10^{-5}$-$1.1*10^{-3}$]	0.02
TRAP-like protein - PF3D7_1442600	$4.9*10^{-4}$ [$3.8*10^{-5}$-$1.0*10^{-3}$]	$3.9*10^{-5}$ [$9.8*10^{-6}$-$2.2*10^{-4}$]	0.002
HSP60 - PF3D7_1015600	$1.6*10^{-3}$ [$5.3*10^{-4}$-$2.1*10^{-2}$]	$2.7*10^{-4}$ [$9.6*10^{-5}$-$6.3*10^{-4}$]	< 0.001
CPN10 - PF3D7_1215300	$2.1*10^{-5}$ [$3.8*10^{-6}$-$7.5*10^{-5}$]	$1.4*10^{-4}$ [$3.5*10^{-5}$-$4.3*10^{-4}$]	0.002
Ppase - PF3D7_0316300	$3.9*10^{-5}$ [$1.4*10^{-5}$-$2.8*10^{-4}$]	$9.6*10^{-4}$ [$1.8*10^{-4}$-$1.8*10^{-3}$]	< 0.001
ARFGAP2 - PF3D7_0526200	$1.8*10^{-3}$ [$3.9*10^{-4}$-$6.1*10^{-3}$]	$3.8*10^{-3}$ [$1.8*10^{-3}$-$8.2*10^{-3}$]	0.09

Supplemental data 7: GSEA – GO biological process and KEGG pathways

- **GO biological process**

GO:0051276	**chromosome organization**
PF3D7_0610400	histone H3
PF3D7_0617800	histone H2A
PF3D7_0617900	histone H3 variant
PF3D7_0509100	structural maintenance of chromosomes protein 4, putative
PF3D7_0414000	structural maintenance of chromosomes protein 3
PF3D7_1318400	structural maintenance of chromosomes protein 2, putative
GO:1902600	**proton transmembrane transport**
PF3D7_1456800	V-type H(+)-translocating pyrophosphatase, putative
PF3D7_1323200	V-type proton ATPase subunit G, putative
PF3D7_0217100	ATP synthase subunit alpha, mitochondrial
PF3D7_1235200	V-type K+-independent H+-translocating inorganic pyrophosphatase
PF3D7_1235700	ATP synthase subunit beta, mitochondrial
GO:0006412	**translation**
PF3D7_1223900	50S ribosomal protein L24, putative
PF3D7_1442800	conserved Plasmodium protein, unknown function
PF3D7_1144000	40S ribosomal protein S21
PF3D7_1414300	60S ribosomal protein L10, putative
PF3D7_0611700	60S ribosomal protein L39
PF3D7_1144300	60S ribosomal protein L41
PF3D7_0710600	60S ribosomal protein L34
PF3D7_1351400	60S ribosomal protein L17, putative
PF3D7_1461300	40S ribosomal protein S28e, putative
PF3D7_0317600	40S ribosomal protein S11, putative
PF3D7_1317800	40S ribosomal protein S19
PF3D7_0316800	40S ribosomal protein S15A, putative
PF3D7_1308300	40S ribosomal protein S27
PF3D7_1408600	40S ribosomal protein S8e, putative
PF3D7_1431700	60S ribosomal protein L14, putative
PF3D7_0415900	60S ribosomal protein L15, putative
PF3D7_0212200	ribosomal protein L12, mitochondrial, putative
PF3D7_0706400	60S ribosomal protein L37
PF3D7_0312800	60S ribosomal protein L26, putative
PF3D7_0304400	60S ribosomal protein L44
PF3D7_1124900	60S ribosomal protein L35, putative
PF3D7_1331800	60S ribosomal protein L23, putative
PF3D7_0814000	60S ribosomal protein L13-2, putative
PF3D7_1242700	40S ribosomal protein S17, putative
PF3D7_0422400	40S ribosomal protein S19
PF3D7_0306900	40S ribosomal protein S23, putative
PF3D7_1003500	40S ribosomal protein S20e, putative
PF3D7_1105400	40S ribosomal protein S4, putative
PF3D7_0307200	60S ribosomal protein L7, putative

PF3D7_0317100	6-cysteine protein
PF3D7_0610000	ribosomal protein L19, mitochondrial, putative
PF3D7_0822000	ribosomal protein L4, mitochondrial, putative
GO:0006270	**DNA replication initiation**
PF3D7_1425900	conserved Plasmodium protein, unknown function
PF3D7_1355100	DNA replication licensing factor MCM6
PF3D7_1211700	DNA replication licensing factor MCM5, putative
PF3D7_1317100	DNA replication licensing factor MCM4
PF3D7_1417800	DNA replication licensing factor MCM2
GO:0006260	**DNA replication**
PF3D7_1425900	conserved Plasmodium protein, unknown function
PF3D7_1355100	DNA replication licensing factor MCM6
PF3D7_1463200	replication factor C subunit 3, putative
PF3D7_1334100	conserved protein, unknown function
PF3D7_1111100	replication factor C subunit 5, putative
PF3D7_0411900	DNA polymerase alpha catalytic subunit A
PF3D7_1211700	DNA replication licensing factor MCM5, putative
PF3D7_1317100	DNA replication licensing factor MCM4
PF3D7_1015800	ribonucleoside-diphosphate reductase small chain, putative
GO:0006414	**translational elongation**
PF3D7_1442800	conserved Plasmodium protein, unknown function
PF3D7_0309600	60S acidic ribosomal protein P2
PF3D7_1235400	tetQ family GTPase, putative
PF3D7_0110100	selenocysteine-specific elongation factor, putative
PF3D7_1330600	elongation factor Tu, putative
GO:0007018	**microtubule-based movement**
PF3D7_1020300	cytoplasmic dynein intermediate chain, putative
PF3D7_1122900	dynein heavy chain, putative
PF3D7_1211000	kinesin-X3, putative
PF3D7_0319400	kinesin-8X
PF3D7_1426300	dynein intermediate chain, putative
PF3D7_0729900	dynein heavy chain, putative
GO:0006352	**DNA-templated transcription, initiation**
PF3D7_1404000	DNA-directed RNA polymerase II subunit RPB4, putative
PF3D7_0621000	conserved Plasmodium protein, unknown function
PF3D7_0506200	TATA-box-binding protein
GO:0006333	**chromatin assembly or disassembly**
PF3D7_0610400	histone H3
PF3D7_0320900	histone H2A.Z
PF3D7_1220900	heterochromatin protein 1
GO:0044409	**entry into host**
PF3D7_0404400	6-cysteine protein P36
PF3D7_0309600	60S acidic ribosomal protein P2
PF3D7_1133400	apical membrane antigen 1
PF3D7_1136700	armadillo-interacting protein AIP

PF3D7_1458000	cysteine proteinase falcipain 1
PF3D7_0731500	erythrocyte binding antigen-175
PF3D7_0102500	erythrocyte binding antigen-181
PF3D7_1147800	membrane associated erythrocyte binding-like protein
PF3D7_1430200	plasmepsin IX
PF3D7_0808200	plasmepsin X
PF3D7_1335400	reticulocyte binding protein 2 homologue a
PF3D7_0424200	reticulocyte binding protein homologue 4
PF3D7_1116000	rhoptry neck protein 4
PF3D7_0501600	rhoptry-associated protein 2
GO:0048193	**Golgi vesicle transport**
PF3D7_1437800	trafficking protein particle complex subunit 5, putative
PF3D7_0418500	trafficking protein particle complex subunit 3, putative
GO:0019752	**carboxylic acid metabolic process**
PF3D7_1325200	lactate dehydrogenase, putative
PF3D7_0618500	malate dehydrogenase
GO:0009657	**plastid organization**
PF3D7_1239700	ATP-dependent zinc metalloprotease FTSH 1
PF3D7_1408700	conserved protein, unknown function
PF3D7_0913500	protease, putative
PF3D7_1417800	DNA replication licensing factor MCM2

- **KEGG pathways**

ec00010	**Glycolysis / Gluconeogenesis**
PF3D7_0303700	lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex
PF3D7_1342800	malate dehydrogenase
PF3D7_0922500	ATP-dependent 6-phosphofructokinase
PF3D7_0915400	phosphoglycerate kinase
PF3D7_1325200	lactate dehydrogenase, putative
PF3D7_1446400	phosphoenolpyruvate carboxykinase
PF3D7_0618500	pyruvate dehydrogenase E1 component subunit beta
ec00750	**Vitamin B6 metabolism**
PF3D7_0616000	pyridoxal kinase
PF3D7_1459700	pyridoxal 5'-phosphate synthase, putative
ec00620	**Pyruvate metabolism**
PF3D7_0303700	lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex
PF3D7_0618500	malate dehydrogenase
PF3D7_1325200	lactate dehydrogenase, putative
PF3D7_1342800	phosphoenolpyruvate carboxykinase
PF3D7_1446400	pyruvate dehydrogenase E1 component subunit beta
PF3D7_1450900	acetyl-CoA acetyltransferase, putative

Supplemental data 8: MCode clusters from PPI network

Cluster 1	
PF3D7_0304400	60S ribosomal protein L44
PF3D7_0306900	40S ribosomal protein S23, putative
PF3D7_0307200	60S ribosomal protein L7, putative
PF3D7_0309600	60S acidic ribosomal protein P2
PF3D7_0312800	60S ribosomal protein L26, putative
PF3D7_0316800	40S ribosomal protein S15A, putative
PF3D7_0317600	40S ribosomal protein S11, putative
PF3D7_0415900	60S ribosomal protein L15, putative
PF3D7_0422400	40S ribosomal protein S19
PF3D7_0611700	60S ribosomal protein L39
PF3D7_0706400	60S ribosomal protein L37
PF3D7_0710600	60S ribosomal protein L34
PF3D7_0814000	60S ribosomal protein L13-2, putative
PF3D7_1003500	40S ribosomal protein S20e, putative
PF3D7_1105400	40S ribosomal protein S4, putative
PF3D7_1124900	60S ribosomal protein L35, putative
PF3D7_1144000	40S ribosomal protein S21
PF3D7_1242700	40S ribosomal protein S17, putative
PF3D7_1308300	40S ribosomal protein S27
PF3D7_1317800	40S ribosomal protein S19
PF3D7_1331800	60S ribosomal protein L23, putative
PF3D7_1351400	60S ribosomal protein L17, putative
PF3D7_1408600	40S ribosomal protein S8e, putative
PF3D7_1414300	60S ribosomal protein L10, putative
PF3D7_1431700	60S ribosomal protein L14, putative
PF3D7_1461300	40S ribosomal protein S28e, putative
Cluster 2	
PF3D7_0508000	6-cysteine protein
PF3D7_1133400	apical membrane antigen 1
PF3D7_0611600	basal complex transmembrane protein 1
PF3D7_1223100	cAMP-dependent protein kinase regulatory subunit
PF3D7_0621100	conserved Plasmodium protein, unknown function
PF3D7_1136200	conserved Plasmodium protein, unknown function
PF3D7_1206300	conserved Plasmodium protein, unknown function
PF3D7_1435600	conserved Plasmodium protein, unknown function
PF3D7_0723300	conserved protein, unknown function
PF3D7_0817600	conserved protein, unknown function
PF3D7_1320700	conserved protein, unknown function
PF3D7_0302500	cytoadherence linked asexual protein 3.1
PF3D7_0302200	cytoadherence linked asexual protein 3.2
PF3D7_0831600	cytoadherence linked asexual protein 8
PF3D7_1035300	glutamate-rich protein GLURP
PF3D7_1345600	inner membrane complex protein

PF3D7_0613900	myosin E, putative
PF3D7_0822900	PhIL1-interacting candidate PIC2
PF3D7_0508900	protein AAP6
PF3D7_1321100	protein kinase domain-containing protein, putative
PF3D7_0932100	protein MAM3, putative
PF3D7_0506900	rhomboid protease ROM4
PF3D7_1463900	rhoptry neck protein 11, putative
PF3D7_1452000	rhoptry neck protein 2
PF3D7_0817700	rhoptry neck protein 5
PF3D7_1410400	rhoptry-associated protein 1
PF3D7_0501600	rhoptry-associated protein 2
PF3D7_0207800	serine repeat antigen 3
PF3D7_1356800	serine/threonine protein kinase ARK3, putative
PF3D7_0704500	serine/threonine protein kinase, putative
PF3D7_0508100	SET domain protein, putative
PF3D7_1235200	V-type K+-independent H+-translocating inorganic pyrophosphatase
Cluster 3	
PF3D7_0102500	erythrocyte binding antigen-181
PF3D7_0203100	protein kinase, putative
PF3D7_0808200	plasmepsin X
PF3D7_1125800	kelch domain-containing protein, putative
PF3D7_1252400	reticulocyte binding protein homologue 3, pseudogene
PF3D7_1332200	conserved protein, unknown function
PF3D7_1335400	reticulocyte binding protein 2 homologue a
Cluster 4	
PF3D7_0316300	inorganic pyrophosphatase
PF3D7_0319400	kinesin-8X
PF3D7_0516800	AP2 domain transcription factor AP2-O2, putative
PF3D7_0707200	conserved Plasmodium protein, unknown function
PF3D7_0717600	inner membrane complex protein, putative
PF3D7_0815500	conserved Plasmodium protein, unknown function
PF3D7_1133200	conserved Plasmodium protein, unknown function
PF3D7_1211700	DNA replication licensing factor MCM5, putative
PF3D7_1239200	AP2 domain transcription factor, putative
PF3D7_1317100	DNA replication licensing factor MCM4
PF3D7_1355100	DNA replication licensing factor MCM6
PF3D7_1417800	DNA replication licensing factor MCM2

Supplemental data 9: *var* genes expression measurement by RT-qPCR

Primers set	**CM** Median [10th-90th percentile]	**UM** Median [10th-90th percentile]	**p-value**
ATS-1	0.004 [0.002-0.008]	0.001 [0.0006-0.003]	<0.001
ATS-2	0.02 [0.01-0.05]	0.01 [0.008-0.02]	<0.001
DBLα	0.1 [0.02-0.9]	0.05 [0.02-0.3]	0.1