Text S1. Supplementary Materials and Methods.

Adhesion properties of selected and unselected parasite lines. The rosette frequency (percentage of IE binding two or more uninfected E) of unselected and HBEC-selected parasite lines was determined by microscopy of ethidium-bromide-stained wet preparations as described (1). The clumping frequency (percentage of IE in clumps of three or more IE in the presence of platelets) was determined by microscopy of ethidium-bromide-stained wet preparations (2) with the clumping assay set up at 1% parasitaemia, 10% haematocrit with 20% platelet-rich plasma and incubated for 60 mins at 10 rpm. Spot binding assays were as described (3) with proteins/concentrations as shown in Table S1 (SI Appendix). The IFA for Knobs was carried out on thin smears fixed with 90% acetone/10% methanol and incubated with 10 μg/ml of mAb 89 to KAHRP (4) or IgG2a isotype control for 1h, followed by 3x washes in PBS and secondary incubation for 45 mins with 1/500 dilution of highly cross-absorbed Alexa Fluor 488 goat anti-mouse IgG with 1 μg/ml of DAPI to stain parasite nuclei. After 3x further washed the slides were mounted with Fluoromount and viewed by fluorescence microscopy. 100 IEs were counted for presence/absence of knobs in four separate areas of each slide to give the mean knob positivity and SEM for each strain.

Microarray hybridizations. HBEC-selected parasites were cultured and synchronized alongside their unselected (non-binding) counterpart. At late schizont stage, HB3-HBEC1 and HB3-Uns1 control cultures (pilot experiment) were Percoll-treated to purify IEs (5), while for all other selections, schizont-IEs were purified on a MACS column (6). Five to seven hours later, after most schizonts had ruptured and parasites were mostly at early-ring stage, cultures were sorbitol-treated (7). Time point 1 of a time-course experiment started 8 hours after the end of the Percoll/MACS

treatment (i.e. 1-3 hours after sorbitol treatment). Samples were processed as described previously (8). Briefly, after RNA extraction, a reference pool was created from each unselected strain by pooling an equal amount of RNA from each time point. After reverse-transcription, each time point sample (from selected and unselected populations) was labelled with Cy5 (red) while the reference pool was labelled with Cy3 (green). Samples were then hybridized overnight. The exception to this was a pilot experiment in which each HB3-HBEC1 time point was hybridised directly with HB3-Uns1 time points rather than using a reference pool.

Microarray data were analysed as described (8). Briefly, each array was normalized with Lowess. Only spots with median intensities greater than the local background plus 2 times the standard deviation of the background were used. For data visualisation, the [HBEC-selected/pool] ratios were divided by the [unselected/pool] ratios to obtain [HBEC-selected/unselected] ratios. Data for HB3-HBEC-2 time point 6 is missing due to a technical problem. Data analysis was carried out using Microsoft Excel, MeV (9), Cluster (http://bonsai.ims.utokyo.ac.jp/~mdehoon/software/cluster/software.htm#ctv) and Jalview (http://jtreeview.sourceforge.net/) for data visualization. All microarray data have been deposited in the GEO repository (GSE32211): http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE32211

Real-Time Quantitative (q)PCR. Transcript levels of the *var* genes from 3D7, IT/FCR3 and HB3 parasite strains and the *rif* genes located head-to-head with the group A *var* gene candidate ligands were determined by real-time qPCR performed on a Rotorgene RG-3000 thermal cycler (Corbett Research) as previously described (10, 11). Primers designed to amplify the *rif* genes of the HB3 strain were as follows: PFHG_03235: forward-tgcgaaaagtcgatagcaga, reverse-agccgctttagtagcagcag; PFHG

_03841: forward-catagtgatgccattccaacat, reverse-ccacctattaatcccaattctgg; PFHG _05051/HB3RifA_081: forward-actgtgggtatgggttaggaagt, reverse-gctttagcaataccttcctggat; PFHG _03670: forward-agtgctatgcccgacaattt, reverse-acaccggttttagcatcagc; PFHG _02275: forward-gatatgttgacataccttcctggt, reverse-agcgtttgaagaattgcaca. Transcript level differences between selected and unselected parasite lines were calculated as ΔΔCt-values and shown as fold changes ($2^{\Delta\Delta Ct}$) (User Bulletin #2: ABI Prism 7700 Sequence Detection System; http://www3.appliedbiosystems.com/cms/groups/mcb_support/documents/generaldocuments/cms_040980.pdf, Applied Biosystems).

Generation of polyclonal antibodies to HB3var3 NTS-DBLα1, HB3var3 di-domain and 3D7 PFD0020c NTS-DBLα1. Recombinant PfEMP1 domains were produced in *E. coli* and purified as described previously (12). The domain boundaries for HB3var3 NTS-DBLα1 were Met1-Pro468, for HB3var3 di-domain were Met1-Arg762 and for 3D7 PFD0020c NTS-DBLα1 were Met1-Pro475. Primers were as follows: HB3var3 NTS-DBLα1 and di-domain forward 5'-aaggatccatggggtcaagcgcatcaaaa-3'; HB3var3 NTS-DBLα1 reverse 5'-aagctagcttatggacatacttggcaataatc-3'; HB3var3 di-domain reverse 5'-aagctagcttagcgctcattcaattgtttgtg-3'; 3D7 PFD0020c forward 5'-aaggatccatggggacaggttcatcaact-3' and reverse 5'-ttgctagcttagggacagggttggcaataatc. Purified proteins with the his-tag removed by TEV protease cleavage (12) were used to immunize rabbits (two per antigen). The rabbits were pre-screened by IFA to exclude animals with heterophilic antibodies that recognise either infected or uninfected Es as described previously (12). All immunizations were carried out by BioGenes GmbH (Berlin, Germany). Rabbits were immunized with 125 μg of protein

on days 0, 7, 14 and 28. An ELISA 50% end titre of at least 1:25,000 was observed for each anti-serum (BioGenes GmbH).

Generation of polyclonal antibodies to HB3var3 DBLδ5 and 3D7 PFD0020c DBLγ6. The HB3var3 DBLδ5 domain was amplified from HB3 genomic DNA by primers LT510 5'-ggatccctgtgaaatcgtggataaaacactgg-3' and LT511 5'-ctgcggccgctacatggagcacagtattctgcatg-3'. The PFD0020c DBLγ6 domain was amplified from 3D7 genomic DNA by primers LT23 5´-cggatccc tgtaatggaattaagacacttcttg-3´and LT24 5´-tgcggccgctcgcactttgtgttggtgctg-3´. The products were cloned and expressed in a baculovirus/insect cell system and recombinant protein purified on a nickel affinity column as described (13). Rabbit antiserum was raised by subcutaneous injection of 10-20 µg protein in complete Freund's adjuvant followed by two boosters of protein in incomplete Freund's adjuvant. Recombinant GammaBind™ G type 2 coupled to Sepharose™ 4B (GE Healthcare) was used to purify IgG according to the manufacturer's instructions.

Flow cytometry with plasma from African children. Isogenic pairs of unselected and HBEC-selected parasites were frozen as trophozoites (14) at 1% parasitaemia. Plasma samples were collected from children attending Kilifi District Hospital between 2006-2010. Ethical approval was granted by the KEMRI Ethical Review Committee (SSC protocol number 1131) and informed consent obtained from the participants parents/guardians. Plasma samples from 10 children admitted with cerebral malaria (*P. falciparum* parasitaemia, fever and Blantyre coma score of ≤2 with other causes of coma excluded) were tested along with their age, blood group and date of admission-matched uncomplicated malaria controls (children seen in outpatients or admitted but with no signs of severe malaria). Acute plasma samples were collected at the time of admission to hospital and convalescent samples collected

3-4 weeks later. Flow cytometry was as described (15). Briefly, 11.5µl of ethidium bromide-stained (10µg/ml) parasite culture suspension (2% haematocrit in PBS/0.5% BSA) was incubated with 1µl test plasma in 96-well U-bottomed plates (Falcon, Becton Dickinson, USA) for 30 mins at room temperature (RT). The cells were washed three times with 200µl of PBS/0.5 % BSA by centrifuging at 1000rpm for 3 mins in a Rotanta 460R centrifuge (Hettich Zentrifugen, Germany). 50µl of FITC-conjugated sheep anti-human IgG-Fc (Binding Site, UK) at a 1:50 dilution in PBS/0.5% BSA was added and incubated for 30 mins at RT in the dark. Following three further washes, the cells were re-suspended in 200µl of PBS/0.5% BSA and 1000 trophozoite-IEs acquired from each well on an FC500 flow cytometer (Beckman Coulter, UK). Analysis was done using Flowjo version 7.6.4.

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Table S1. Proteins, biomolecules and antibodies used in binding assays.

Protein/molecule/ antibody	Supplier/order number	Type	Diluted in	Concentra-tion used
CD36[a]	R&D Systems: 1955-CD	Recombinant	PBS	25 µg/ml
Chondroitin sulfate A (CSA)[b]	Sigma: C8919	Bovine trachea	PBS	100 µg/ml
E-selectin (CD62E)[c]	R&D Systems: 724-ES	Recombinant	PBS	40 µg/ml
Fibronectin[d]	BD: 354008	Human plasma	BTC[q]	200 µg/ml
Fibronectin	Sigma: F1141	Bovine plasma	BTC[q]	200 µg/ml
Fractalkine/CX3C L1[e]	R&D Systems: 365-FR	Recombinant	PBS	50 µg/ml
gC1qR/HABP1[f]	R&D Systems: 4529-HB	Mouse	PBS	40 µg/ml
Heparan Sulfate Proteoglycan[g]	Sigma: H4777	Purified	PBS	100 µg/ml
Heparin sodium salt	Sigma: H4784	Porcine intestinal mucosa	50mM Tris	50 µg/ml
Hyaluronic acid[h]	Sigma: H1504	Human umbilical cord	2mM $CaCl_2$	100 µg/ml
ICAM1 (CD54)[i]	R&D Systems: 720-IC	Recombinant	PBS	50 µg/ml
Integrin αV β1	Chemicon : CC1092	Purified	PBS	25 µg/ml
Integrin αV β3[j] (CD51)	Chemicon : CC1020	Purified	PBS	25 µg/ml
NCAM (CD56)[k]	Chemicon: AG265	Embryonic chicken brain	PBS	10 µg/ml
PECAM-1 (CD31)[l]	R&D Systems: ADP6	Recombinant	PBS	50 µg/ml
P-Selectin (CD62P)[m]	R&D Systems: 137-PS	Recombinant	PBS	40 µg/ml
Thrombospondin[n]	Calbiochem: 605225	Purified	50mM Tris	50 µg/ml
VCAM-1 (CD106)[c]	R&D Systems: 862-VC	Recombinant	PBS	50 µg/ml
CD36 antibody FA6-152[o]	Beckman Coulter IM2279U	Mouse IgG1 mAb	PBS	10 µg/ml
ICAM-1 antibody 15.2[p]	AbD Serotec MCA1615XZ	Mouse IgG1 mAb	PBS	20 µg/ml
ICAM-1 antibody 15.8	Gift from Prof Alister Craig	Mouse IgG1 mAb	PBS	20 µg/ml

[a] Reference (1, 2)

[b] Reference (3)

[c] Reference (4)

[d] Reference (5)

[e] Reference (6)

[f] Reference (7)

[g] Reference (8)

[h] Reference (9)

[i] Reference (10). Integrin αVβ1 was included as a negative control.

[j] Reference (11)

[k]Reference (12). NCAM was incubated for 2 hours at 37°C with 1U/ml Neuraminidase (Sigma N3001) to digest polysialic acid (PSA) (12).

[l] Reference (13)

[m] Reference (14)

[n] Reference (15)

[o] Reference (16)

[p] Reference (17)

[q] BTC = 50mM Bis-Tris, 100mM NaCl, 25 mM Calcium lactate, 1 mM $MnCl_2$, pH7.4.

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Table S2. Summary of selection and synchronisation methods for time-course experiments.

	HB3-HBEC1	HB3-Uns1	HB3-HBEC2	HB3-HBEC TNF[e]	HB3-Uns2	3D7-HBEC	3D7-Uns	IT-HBEC	IT-Uns	Dd2
Rounds of selection[a]	5	/	5	6	/	7	/	6	/	5[f]
Synchronization method[b]	P + S	P + S	M + S	M + S	M + S	M + S	M + S	M + S	M + S	/
Synchronization window[c]	5 hours	5 hours	7 hours	7 hours	6 hours	7 hours	7 hours	7 hours	5 hours	/
Time between last selection and time-course[d]	13 days	/	12 days	12 days	/	14 days	/	13 days	/	/

[a]Number of rounds of selection on HBEC-5i before the time-course.

[b]P = Percoll, S = Sorbitol, M = MACS. See methods section for details.

[c]Time between the end of MACS treatment and the Sorbitol treatment. The shorter the time, the more tightly synchronised the parasites are.

[d]Number of days elapsed between the last round of selection and the start of the time-course.

[e]HB3 parasites selected on HBEC-5i activated with TNF.

[f]The *P. falciparum* Dd2 strain did not increase its binding ability even after 5 rounds of selection on HBEC-5i.

Table S3. Functional enrichment analysis of down-regulated genes

	Pathway Name	# in Genome	# in Input	# in Pathway	# in Input & Pathway	Direction of deviation from expected	Hypergeometric (to be preferred)	Binomial	Gene List
KEGG pathway testing *	Metabolic pathways	5400	290	259	1	UNDER-representation (expect 13, observe 1)	0.00061	0.00372	PFI1110w
GO pathway testing *	GO:0044267|cellular protein metabolic process	5400	290	759	11	UNDER-representation (expect 40, observe 11)	0	0.00001	MAL8P1.70, PFE0370c, PF07_0043, PFD1175w, PFL1885c, PFI0180w, MAL13P1.260, PFL0190w, PFB0665w, PF14_0224, PF14_0027
	GO:0051701|interaction with host	5400	290	8	4	over-representation (expect 0, observe 4)	0.00048	0.00099	PF13_0197, PF10_0345, PF10_0346, PF11_0344
	GO:0030554|adenyl nucleotide binding	5400	290	368	5	UNDER-representation (expect 19, observe 5)	0.00222	0.00292	PF07_0104, PFD1175w, PFL1885c, PF13_0233, PFB0665w
	GO:0016301|kinase activity	5400	290	292	3	UNDER-representation (expect 15, observe 3)	0.00366	0.00469	PFD1175w, PFL1885c, PFB0665w
	GO:0004175|endopeptidase activity	5400	290	188	3	UNDER-representation (expect 10, observe 3)	0.03094	0.03561	MAL8P1.70, PFE0370c, MAL13P1.260
	GO:0016818|hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	5400	290	165	1	UNDER-representation (expect 8, observe 1)	0.03181	0.03604	PFI0180w
MPM pathway testing*	Functional annotation of merozoite invasion-related proteins	5400	290	60	15	over-representation (expect 3, observe 15)	0	0	PF10_0352, MAL13P1.60, PF10_0351, PF13_0197, PF10_0343, PFL2520w, PFB0570w, PF10_0345, PF10_0281, PFC0110w, PFD1150c, PF10_0346, MAL7P1.176, PF11_0344, PFA0125c
	Subcellular localization of proteins involved in invasion	5400	290	67	12	over-representation (expect 3, observe 12)	0.00019	0.00033	MAL13P1.60, PF10_0351, PF13_0197, PF10_0343, PFL2520w, PF10_0345, PFC0110w, PFD1150c, PF10_0346, MAL7P1.176, PF11_0344, PFA0125c
Testing for Transcription factor*	Transcription Factor								No Transcription Factor(s) are significantly enriched

KEGG: Kyoto Encyclopedia of Genes and Gernomes; GO: Gene Ontology; MPM: Malaria Metabolic Pathway. *(level for statistical significance = 0.05)

Table S4. Pair-wise amino acid identities for HBEC-binding variants (whole protein, extracellular domain, NTS-DBLα, CIDR1, DBLδ and CIDR2)

	HB3var3	ITvar7	ITvar19	PFD0020c
Pair-wise amino acid identities for whole protein				
HB3var3	100	36.2	32.5	34.4
ITvar7		100	33.6	45.7
ITvar19			100	41.9
PFD0020c				100
Pair-wise amino acid identities for extracellular domain encoded by exon 1				
HB3var3	100	34.8	29.6	32.8
ITvar7		100	28.5	39.3
ITvar19			100	37.9
PFD0020c				100
Pair-wise amino acid identities for NTS-DBLα				
HB3var3	100	58.1	42.9	49.5
ITvar7		100	45.9	52.1
ITvar19			100	46.5
PFD0020c				100
Pair-wise amino acid identities for CIDR1				
HB3var3	100	74.4	39.2	40.6
ITvar7		100	42.8	40.2
ITvar19			100	74.2
PFD0020c				100
Pair-wise amino acid identities for DBLδ				
HB3var3	100	36.8	37.7	37.9
ITvar7		100	45.4	48.4
ITvar19			100	47.0
PFD0020c				100
Pair-wise amino acid identities for CIDR2				
HB3var3	100	38.9	42.0	24.2
ITvar7		100	47.8	22.3
ITvar19			100	26.5
PFD0020c				100

Table S5. Pair-wise amino acid identities for DBLβ and DBLγ from HBEC-binding variants

Pair-wise amino acid identities for DBLβ from HBEC-binding variants						
	HB3var3 d2[a]	HB3var3 d5[b]	ITvar7 d2[a]	ITvar7 d3[c]	ITvar19	PFD0020c
HB3var3 d2[a]	100	44.1	52.2	46.4	49.2	49.4
HB3var3 d5[b]		100	41.4	51.0	46.0	47.1
ITvar7 d2[a]			100	45.2	50.2	47.2
ITvar7 d3[c]				100	47.8	46.8
ITvar19					100	58.5
PFD0020c						100
Pair-wise amino acid identities for DBLγ from HBEC-binding variants						
	HB3var3	ITvar7	ITvar19 d3[c]	ITvar19 d5[b]	PFD0020c d3[c]	PFD0020c d4[d]
HB3var3	100	45.0	49.3	38.7	45.6	47.4
ITvar7		100	33.0	42.7	36.0	56.2
ITvar19 d3[c]			100	36.3	52.6	38.9
ITvar19 d5[b]				100	35.7	44.4
PFD0020c d3[c]					100	39.2
PFD0020c d4[d]						100

[a]d2: 2nd DBL domain from the N-terminus
[b]d5: 5th DBL domain from the N-terminus
[c]d3: 3rd DBL domain from the N-terminus
[d]d4: 4th DBL domain from the N-terminus

Supplementary Figure legends.

Figure S1. Adhesion properties of HBEC-selected parasite lines.

A) The rosette frequency (percentage of IE binding two or more uninfected E) of unselected and HBEC-selected parasite lines was determined by microscopy of ethidium-bromide-stained wet preparations as described (1). The experiment was performed twice for HB3-Uns and HB3-HBEC, once for all other strains. B) The clumping frequency (percentage of IE in clumps of three or more IE in the presence of platelets) was determined by microscopy of ethidium-bromide-stained wet preparations as described (2). The clumping assay was set up at 1% Pt, 10% Ht with 20% platelet-rich plasma and incubated for 60 mins. Data shown are mean and SD from three independent experiments for each strain. There was a significant drop in the clumping frequency after selection for HBEC-binding in all strains (** $p<0.01$ for each strain, paired t test). C) Spot binding assays with HB3 parasite lines. Three µl spots of soluble receptors in PBS were absorbed overnight onto Falcon 351007 plates. The source and concentration of each molecule is shown in Table S1. Spots were removed by suction and the plates blocked with PBS/2% BSA for two hours. Parasite culture suspension in RPMI binding medium (BM)/1% BSA pH 7.1 at 2% Ht, 5% Pt was incubated with the plates for 1 hour, with gentle resuspension every 12 minutes. Plates were washed gently with BM to remove unbound cells. Bound cells were fixed with 1% glutaraldehyde for 1 hour and stained with 5% Giemsa for 20 mins. The number of adherent IEs were counted in at least five fields of each a spot viewed with the 100x objective. PBS was always used as a negative control, CD36 as a positive control. Data shown are the mean and SD from at

least two independent assays, with each assay comprising at least 3 spots for each molecule per plate, and at least two plates. Statistically significant differences between Uns- and HBEC-selected parasites are shown *$p<0.05$ ** $p<0.01$, ***$p<0.001$. D) Spot binding assays with IT parasite lines as for part C. E) Binding inhibition assay of HB3-HBEC parasites on HBEC-5i in the presence of antibodies known to block adhesion to ICAM-1 (15.2 and 15.8) and CD36 (FA6-152). Data shown are the mean and SD from two independent experiments, with at least two wells per antibody in each experiment.

Figure S2. Parasite maturity during the HB3 time-course. Parasites were synchronized as described in the methods/Table S1 to give a five-hour time window. The first sample was collected 3 hours after sorbitol lysis, and samples were then taken 8-hourly throughout the asexual blood stage cycle. The maximum parasite maturity in terms of hours post invasion at each time point is shown in the second column. Samples for RNA extraction were taken from the culture at each time point, mixed with TRIzol reagent and frozen, and a Giemsa-stained thin blood smear was performed to record the developmental stage of the selected and unselected parasites.

Figure S3. Pearson correlation of time points between selected and unselected parasite strains. Gene transcription data from all oligonucleotide probes from one time point in an unselected strain were correlated with data from all oligonucleotide probes of one time point of the selected strain. A Pearson correlation close to 1 shows a strong positive correlation and a value close to -1 shows a strong negative correlation. Here, in almost all cases, the same time point in an unselected strain showed a strong positive

correlation with the same time point in the selected strain (fields with grey background). The largest disparity was found in time point 3 between HB3-HBEC-TNF and HB3-Uns2 (Pearson correlation coefficient 0.34). Gene expression for that time point should therefore be interpreted cautiously. Time point 6 in the IT strain also showed a relatively weak positive correlation (Pearson correlation coefficient 0.51). All other time points and strains showed a strong positive correlation with correlation coefficients of 0.72 or greater, with many being greater than 0.9.

Figure S4. *Var* gene expression profiles determined by reverse transcriptase-PCR in unselected (Uns) and selected (HBEC) parasites. The pie charts represent the frequency of DBLα *var* gene sequence tags detected in each parasite population by reverse transcriptase-PCR with universal primers to DBLα of PfEMP1 (3, 4). 25 to 45 recombinant plasmids containing *var* gene inserts were sequenced for each strain. A) In HB3-HBEC1 and B) HB3-HBEC-TNF, the frequency of *HB3var3* was increased by 14 and 10 fold respectively in selected compared to unselected HB3 ($p < 0.005$, Fisher's exact test). C) The frequency of *PFD0020c* was increased by 16 fold after selection of 3D7 parasites ($p < 0.0001$, Fisher's exact test). D) In IT-HBEC, *ITvar7* was increased nine fold after selection ($p = 0.0184$, Fisher's exact test) while *ITvar19* was detected in 13/45 sequence tags from IT-HBEC in comparison to 0/38 tags from unselected IT ($p = 0.0001$, Fisher's exact test). E) In HB3 selected four times on HDMEC, the frequency of *HB3var3* increased 11-fold after selection ($p = 0.0015$, Fisher's exact test), while for HB3 selected four times on HPMEC, the frequency of *HB3var3* increased nine-fold ($p = 0.0062$, Fisher's exact test). Colour scheme for *var* subgroups: group A genes are in red,

group B in green, group C in blue. Note that *ITvar19*, a group B *var* gene but with group A-like features, is in orange. Nomenclature: A1T= a *var* gene with the A1 upstream sequence found near the telomeres; C1C= a *var* gene with the C1 upstream sequence found near the centromere. T, telomeric; ST, sub-telomeric; C, centromeric; p, pseudogene.

Figure S5. *Rif* and *stevor* genes upregulated in 3D7- and IT-HBEC selected parasites. A) 3D7 *rif* genes (top of panel) and *stevor* genes (bottom of panel) up-regulated by at least three fold in selected parasites. B) IT *rif* genes (top of panel) and *stevor* genes (bottom of panel) up-regulated by at least three fold in selected parasites. Because of the small size of *rif* genes (1-2 kbp) there was only one oligonucleotide probe per gene on the microarray chip. Colour scale as in main text Fig 2.

Figure S6. 15 genes upregulated in selected parasites in at least one time point by two fold or more in all five selections. Data for each gene represents the average of all available oligonucleotide probes. The top 7 genes are proven or predicted to be exported. "ExportPred" = Export prediction score (5). A score of 4.3 or above corresponds to a 95% chance of the protein to be exported. *PF14_0752* (PHISTa) is the only gene to be upregulated by 3 fold in all selections. t, truncated; p, pseudogene. Colour scale as in main text Fig 2.

Figure S7. 58 genes downregulated in selected parasites in at least one time point by two fold or more in all five selections. Data for each gene represents the average of all available oligonucleotide probes. The gene annotation is according to PlasmoDB 6.4. The annotation "INVASION" or "invasion" was added in order to distinguish proteins proven or predicted to be involved in invasion, respectively (6, 7). The top 11 genes are downregulated by at least 3 fold in one or more time point. Colour scale as in main text Fig 2.

Figure S8. Recognition of HBEC-selected and unselected parasites lines by antibodies from African malaria patients. Convalescent plasma samples were collected from 10 cerebral malaria (CM) patients and 10 age- and time of admission-matched uncomplicated malaria patients (UM or uncomp). Surface recognition of HBEC-selected (HBEC) and unselected (uns) parasite lines was tested by flow cytometry. The mean fluorescence intensity (MFI) of the uninfected E population was subtracted from the MFI of the IE population to give the specific MFI of the IE population shown on the y axis. Each data point represents plasma from one patient. A) 3D7 parasites. B) HB3 parasites. C) IT parasites. D) Summary of median MFI, InterQuartile Range (IQR) and P value from Mann Whitney test for all parasite strains.

References.

1. Deans AM & Rowe JA (2006) *Plasmodium falciparum*: Rosettes do not protect merozoites from invasion-inhibitory antibodies. Exp Parasitol 112:269-273.

2. Arman M & Rowe JA (2008) Experimental conditions affect the outcome of *Plasmodium falciparum* platelet-mediated clumping assays. Malar J 7:243.

3. Taylor HM, Kyes SA, Harris D, Kriek N, & Newbold CI (2000) A study of *var* gene transcription in vitro using universal *var* gene primers. Mol Biochem Parasitol 105:13-23.

4. Kyriacou HM*, et al.* (2006) Differential *var* gene transcription in *Plasmodium falciparum* isolates from patients with cerebral malaria compared to hyperparasitaemia. Mol Biochem Parasitol 150:211-218.

5. Sargeant TJ*, et al.* (2006) Lineage-specific expansion of proteins exported to erythrocytes in malaria parasites. Genome Biol 7:R12.

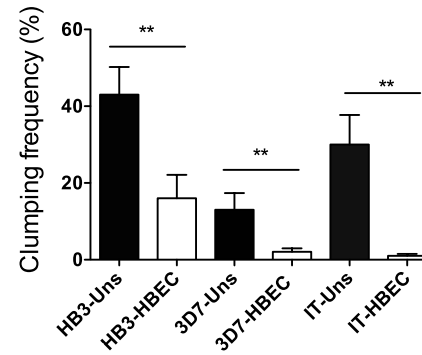
6. Hu G*, et al.* (2010) Transcriptional profiling of growth perturbations of the human malaria parasite *Plasmodium falciparum.* Nat Biotechnol 28:91-98.

7. Haase S*, et al.* (2008) Characterization of a conserved rhoptry-associated leucine zipper-like protein in the malaria parasite *Plasmodium falciparum.* Infect Immun 76:879-887.

A

Unselected parasites	Rosette frequency	HBEC-selected parasites	Rosette frequency
HB3-Uns	<1%	HB3-HBEC	<1%
HB3-Uns2	<1%	HB3-HBEC-TNF	<1%
3D7-Uns	<1%	3D7-HBEC	<1%
IT-Uns	<1%	IT-HBEC	<1%

B



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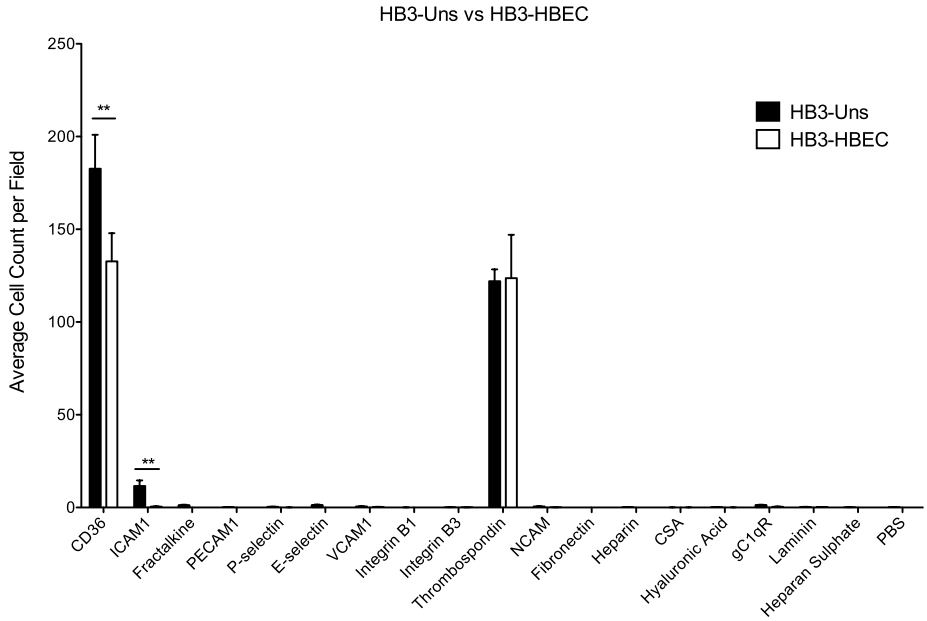

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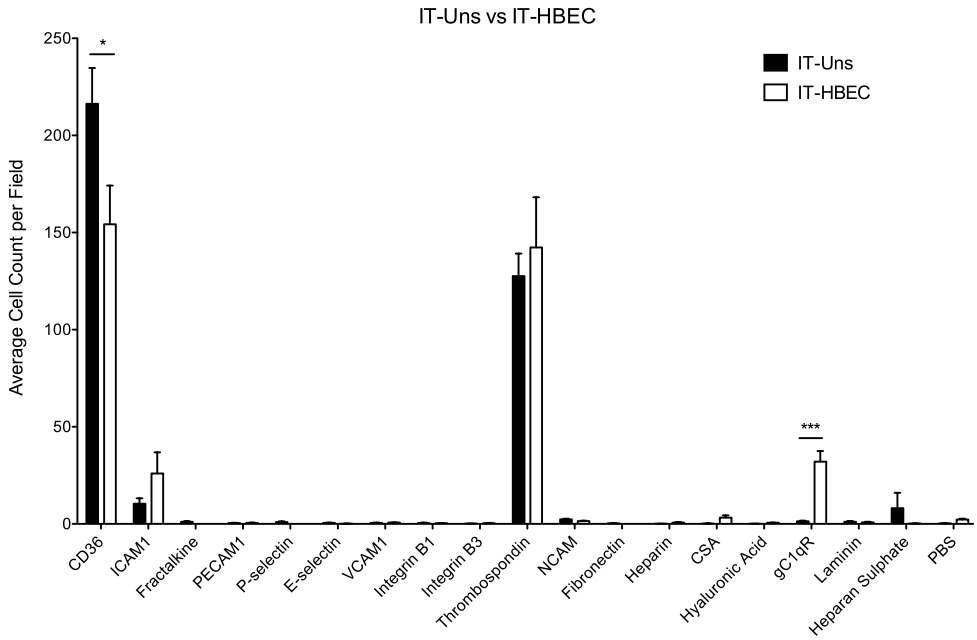

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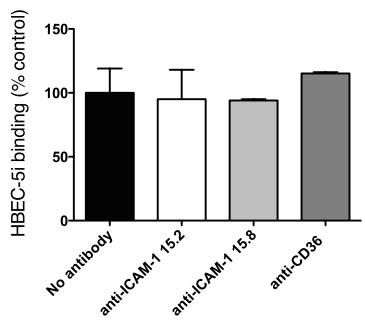


Figure S1

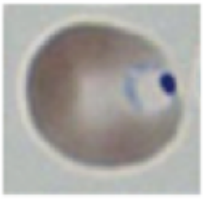
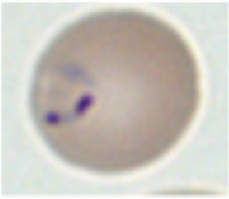
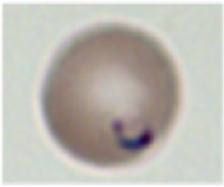
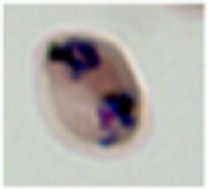
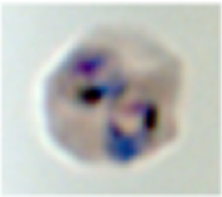
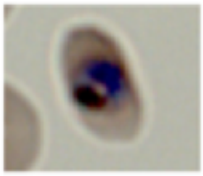
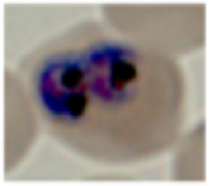
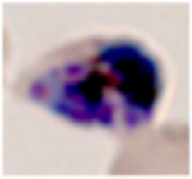
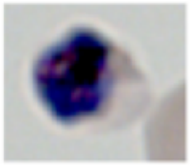
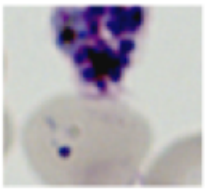
Time-point	Time post invasion	HB3 Unselected	HB3-HBEC Selected
T1 Early ring	8h (range: 3-8h)		
T2 Ring	16h (range: 11-16h)		
T3 Late ring/early troph	24h (range: 19-24h)		
T4 Troph	32h (range: 27-32h)		
T5 Schizont	40h (range: 35-40h)		
T6 Mature schizont	48h (range: 43-48h)		

Figure S2

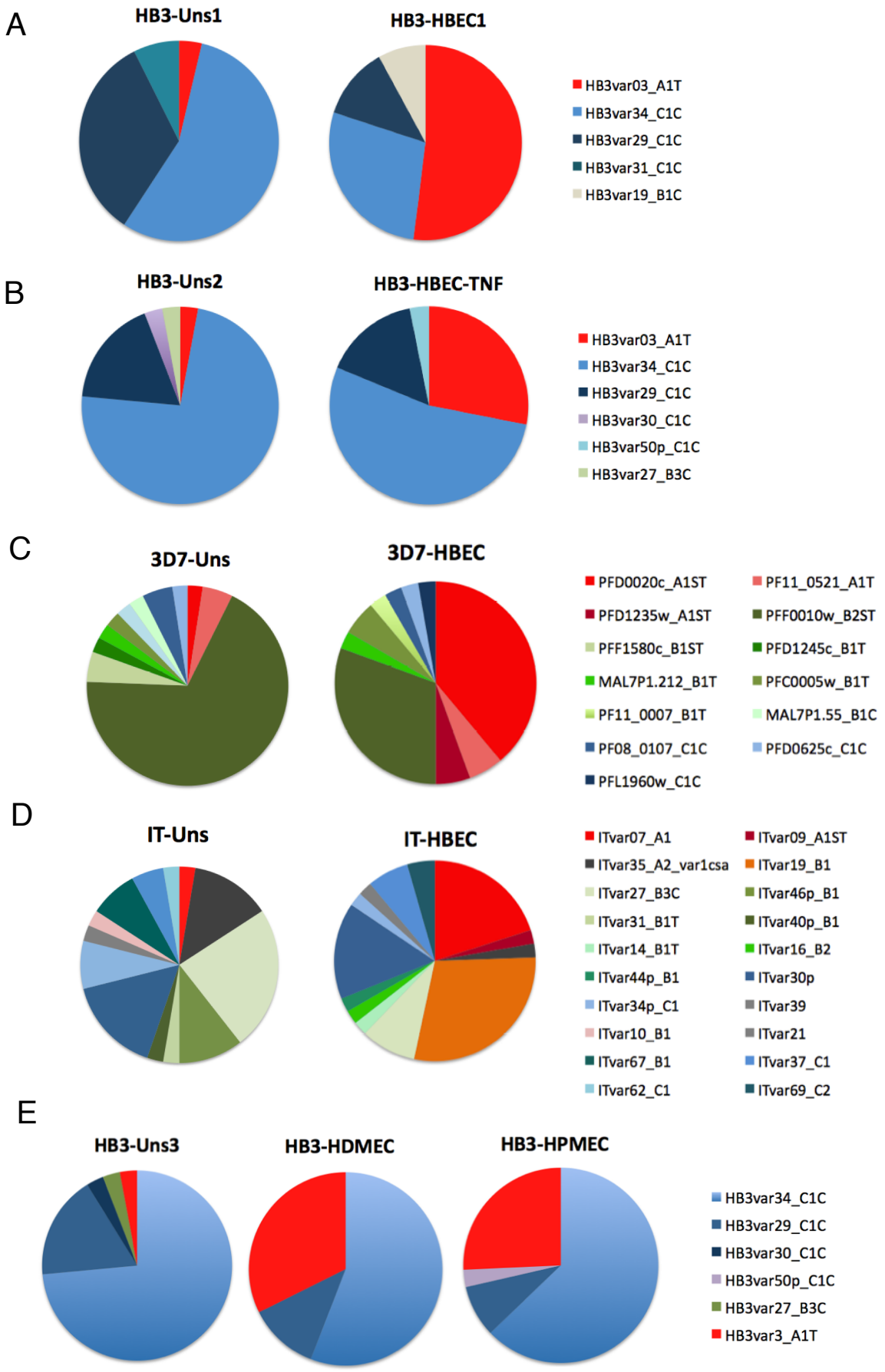
		HB3-Uns2					
		T1	**T2**	**T3**	**T4**	**T5**	**T6**
HB3-HBEC2	**T1**	0.84	0.66	0.12	-0.20	-0.36	N/A
	T2	0.74	0.86	0.29	-0.18	-0.50	N/A
	T3	0.24	0.65	0.78	0.23	-0.35	N/A
	T4	-0.12	0.11	0.71	0.79	0	N/A
	T5	-0.38	-0.54	-0.10	0.56	0.78	N/A
	T6	N/A	N/A	N/A	N/A	N/A	N/A

		HB3-Uns2					
		T1	**T2**	**T3**	**T4**	**T5**	**T6**
HB3-HBEC-TNF	**T1**	0.88	0.63	0.12	-0.21	-0.32	0.38
	T2	0.26	0.72	0.83	0.28	-0.50	-0.45
	T3	0.73	0.89	0.34	-0.17	-0.51	0.05
	T4	-0.21	0.11	0.71	0.83	-0.09	-0.55
	T5	-0.46	-0.54	-0.07	0.59	0.76	0.1
	T6	-0.01	-0.46	-0.49	-0.11	0.7	0.72

		3D7-Uns					
		T1	**T2**	**T3**	**T4**	**T5**	**T6**
3D7-HBEC	**T1**	0.75	0.77	0.68	0.39	-0.2	-0.3
	T2	0.71	0.88	0.81	0.39	-0.35	-0.48
	T3	0.52	0.73	0.93	0.68	-0.13	-0.51
	T4	0.19	0.38	0.64	0.94	0.40	-0.37
	T5	-0.39	-0.31	-0.17	0.39	0.96	0.33
	T6	-0.24	-0.45	-0.49	-0.26	0.45	0.92

		IT-Uns					
		T1	**T2**	**T3**	**T4**	**T5**	**T6**
IT-HBEC	**T1**	0.91	0.63	0.17	-0.18	-0.37	0.17
	T2	0.84	0.93	0.43	-0.16	-0.58	-0.1
	T3	0.36	0.7	0.92	0.29	-0.46	-0.39
	T4	-0.19	0.03	0.73	0.89	0.18	-0.34
	T5	-0.5	-0.58	-0.12	0.68	0.89	0.11
	T6	-0.33	-0.58	-0.5	0.1	0.86	0.51

Figure S3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B
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HB3-HBEC-TNF
HB3var03_A1T
HB3var34_C1C
HB3var29_C1C
HB3var30_C1C
HB3var50p_C1C
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C
3D7-Uns
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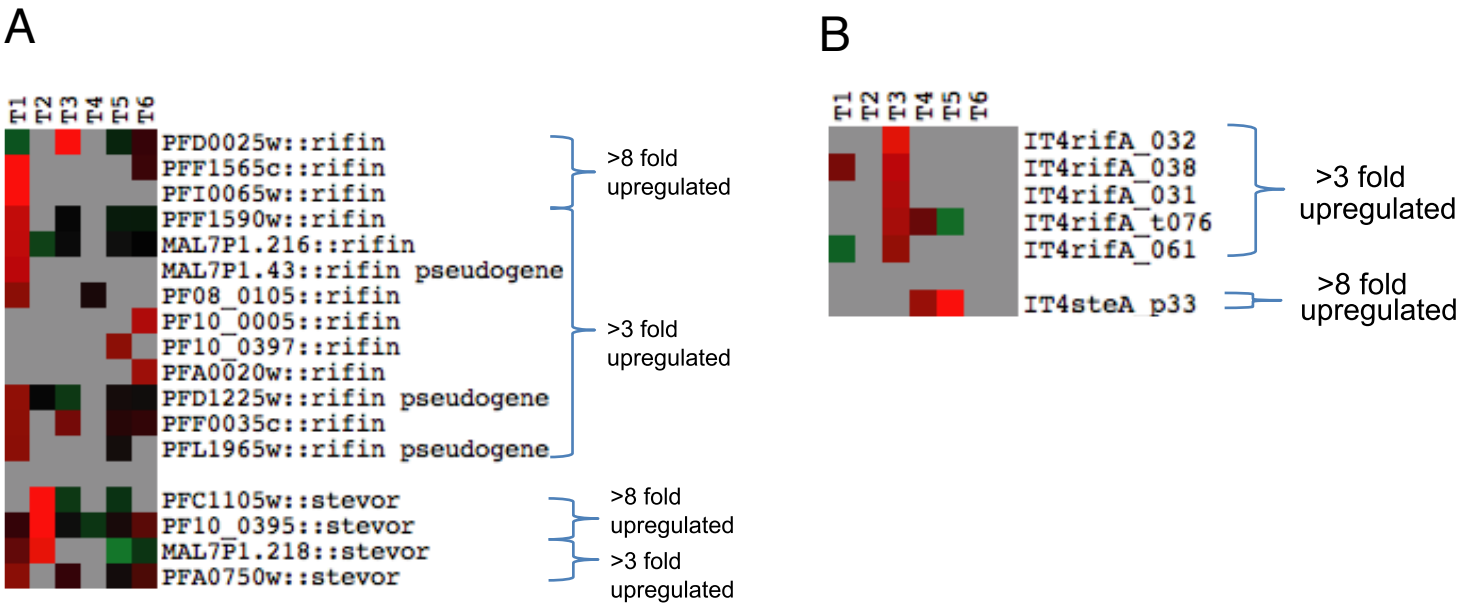
Figure S4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T2
T3
T4
T5
T6
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>3 fold upregulated
>8 fold upregulated
>3 fold upregulated
B
T1
T2
T3
T4
T5
T6
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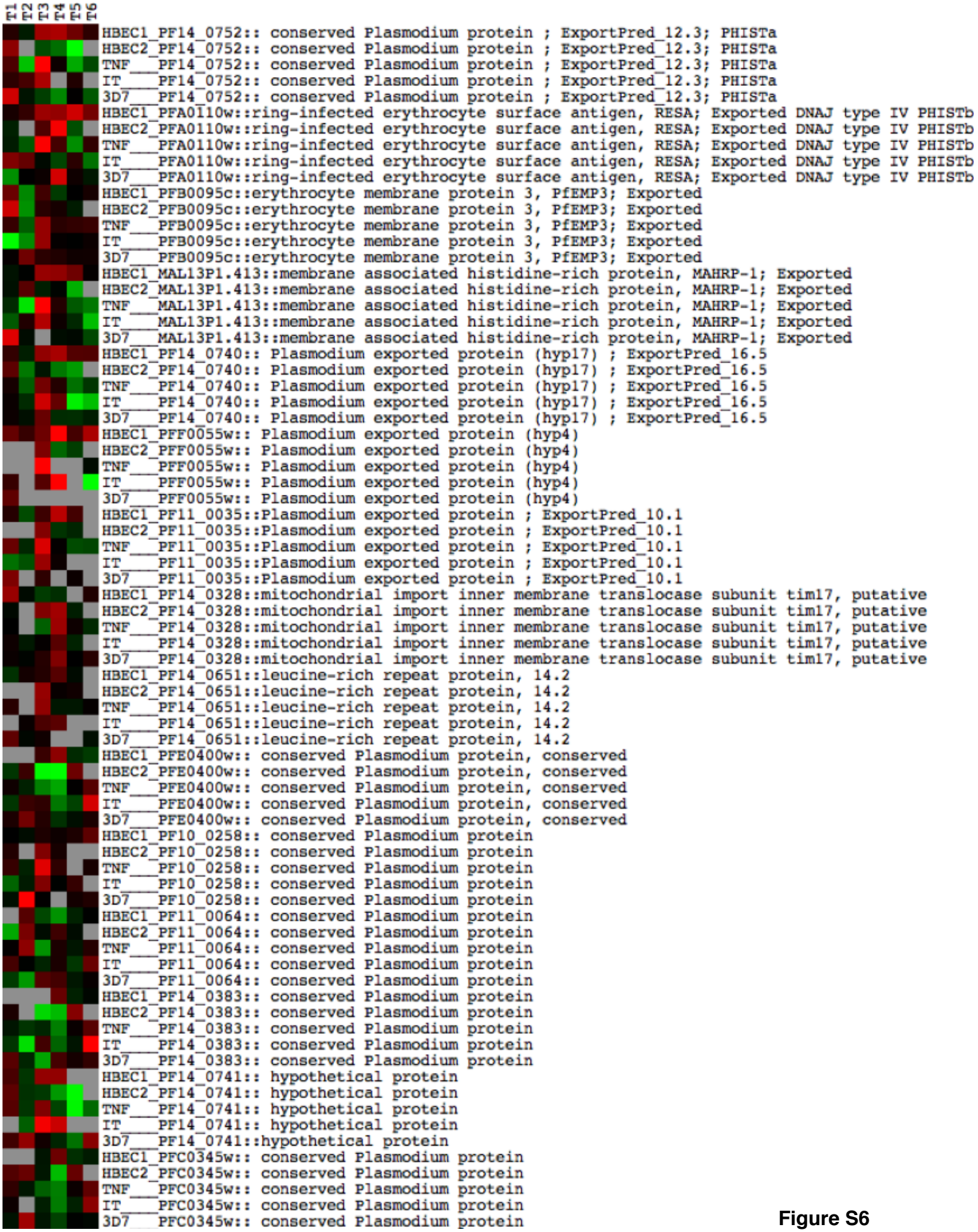
Figure S5.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TNF___PFA0110w::ring-infected erythrocyte surface antigen, RESA; Exported DNAJ type IV PHISTb
IT___PFA0110w::ring-infected erythrocyte surface antigen, RESA; Exported DNAJ type IV PHISTb
3D7___PFA0110w::ring-infected erythrocyte surface antigen, RESA; Exported DNAJ type IV PHISTb
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HBEC2_PFB0095c::erythrocyte membrane protein 3, PfEMP3; Exported
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3D7___PFB0095c::erythrocyte membrane protein 3, PfEMP3; Exported
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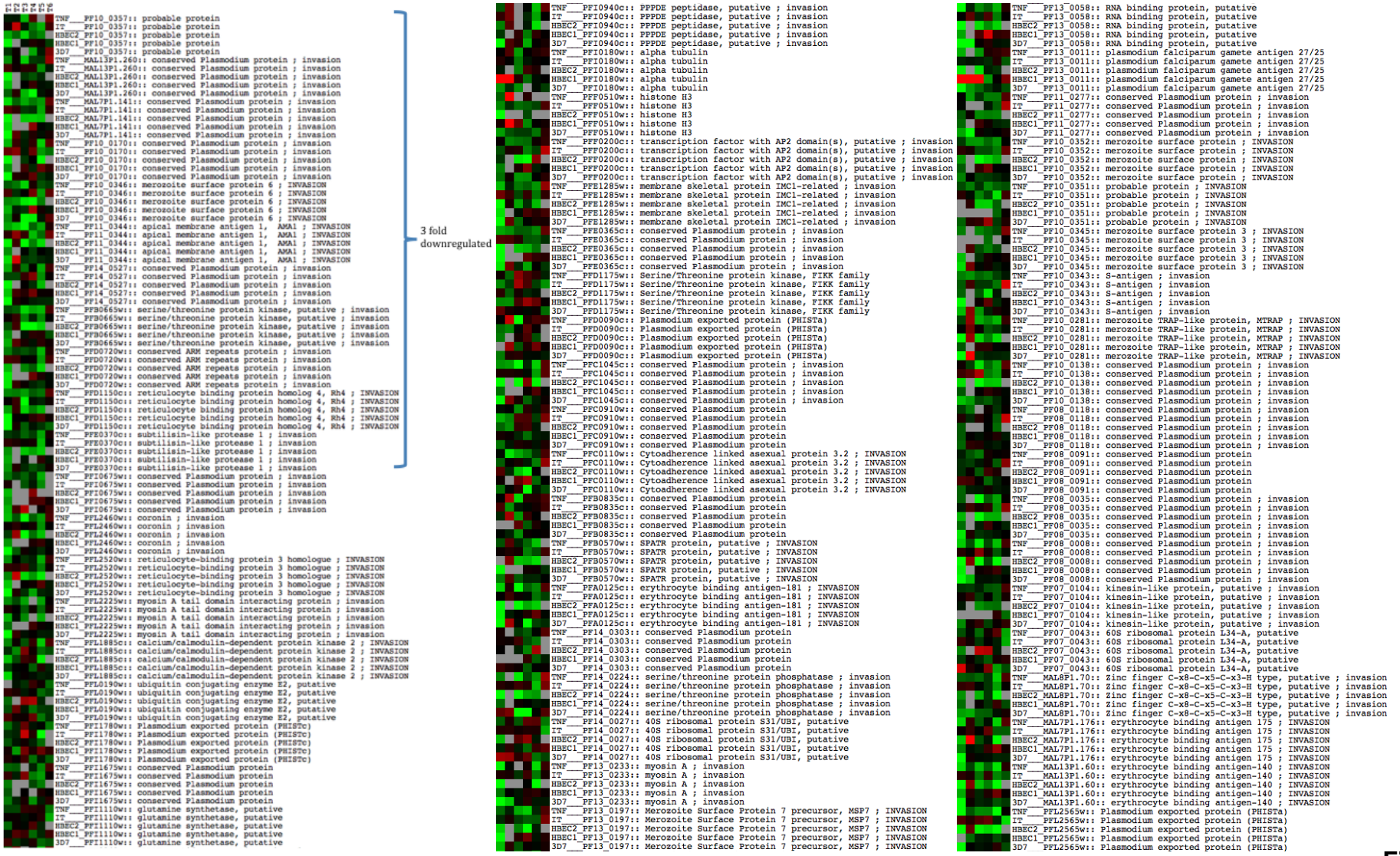
Figure S6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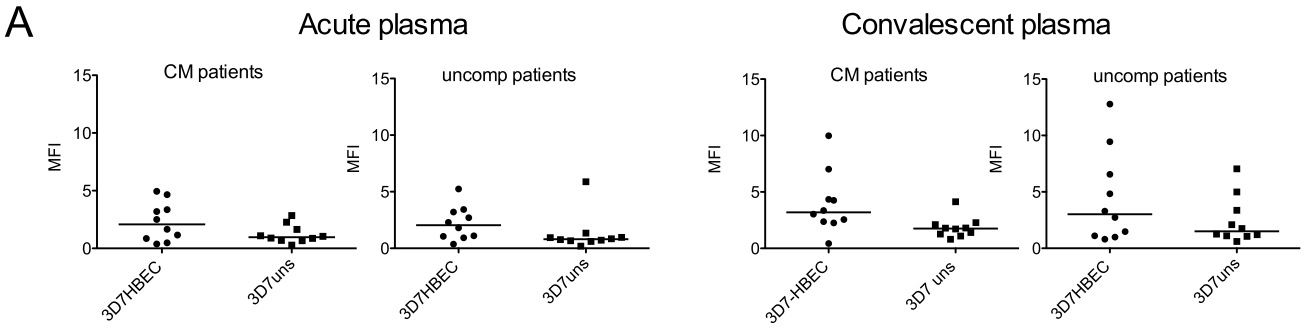
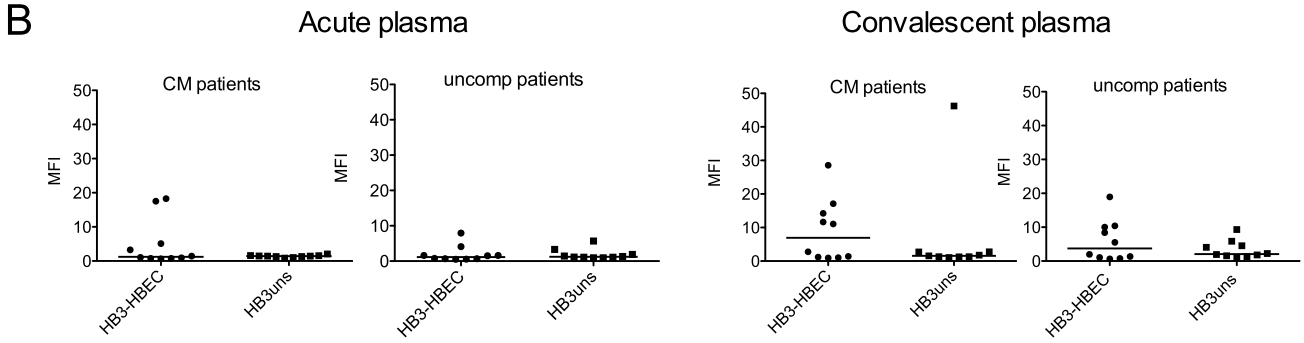
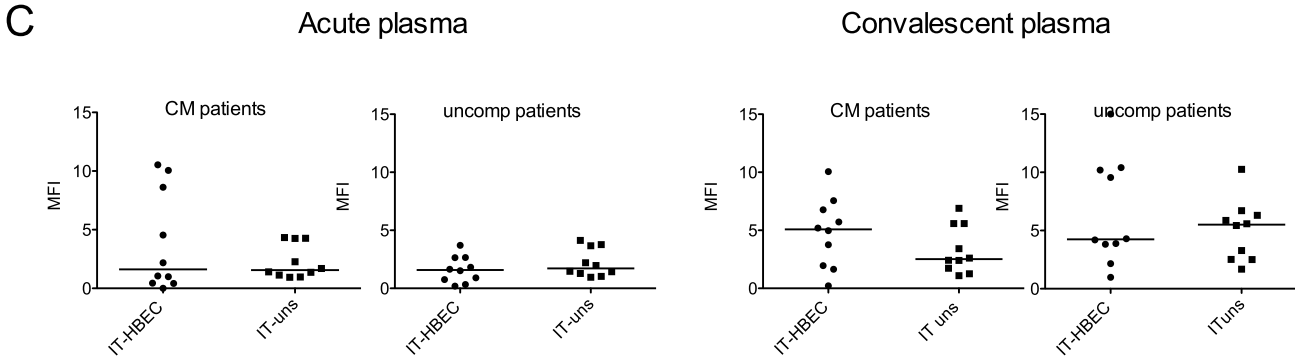
IT___PF11_0344:: apical membrane antigen 1, AMA1 ; INVASION
HBEC2_PF11_0344:: apical membrane antigen 1, AMA1 ; INVASION
HBEC1_PF11_0344:: apical membrane antigen 1, AMA1 ; INVASION
3D7___PF11_0344:: apical membrane antigen 1, AMA1 ; INVASION
TNF___PF14_0527:: conserved Plasmodium protein ; invasion
IT___PF14_0527:: conserved Plasmodium protein ; invasion
HBEC2_PF14_0527:: conserved Plasmodium protein ; invasion
HBEC1_PF14_0527:: conserved Plasmodium protein ; invasion
3D7___PF14_0527:: conserved Plasmodium protein ; invasion
TNF___PFB0665w:: serine/threonine protein kinase, putative ; invasion
IT___PFB0665w:: serine/threonine protein kinase, putative ; invasion
HBEC2_PFB0665w:: serine/threonine protein kinase, putative ; invasion
HBEC1_PFB0665w:: serine/threonine protein kinase, putative ; invasion
3D7___PFB0665w:: serine/threonine protein kinase, putative ; invasion
TNF___PFD0720w:: conserved ARM repeats protein ; invasion
IT___PFD0720w:: conserved ARM repeats protein ; invasion
HBEC2_PFD0720w:: conserved ARM repeats protein ; invasion
HBEC1_PFD0720w:: conserved ARM repeats protein ; invasion
3D7___PFD0720w:: conserved ARM repeats protein ; invasion
TNF___PFD1150c:: reticulocyte binding protein homolog 4, Rh4 ; INVASION
IT___PFD1150c:: reticulocyte binding protein homolog 4, Rh4 ; INVASION
HBEC2_PFD1150c:: reticulocyte binding protein homolog 4, Rh4 ; INVASION
HBEC1_PFD1150c:: reticulocyte binding protein homolog 4, Rh4 ; INVASION
3D7___PFD1150c:: reticulocyte binding protein homolog 4, Rh4 ; INVASION
TNF___PFE0370c:: subtilisin-like protease 1 ; invasion
IT___PFE0370c:: subtilisin-like protease 1 ; invasion
HBEC2_PFE0370c:: subtilisin-like protease 1 ; invasion
HBEC1_PFE0370c:: subtilisin-like protease 1 ; invasion
3D7___PFE0370c:: subtilisin-like protease 1 ; invasion
TNF___PFI0675w:: conserved Plasmodium protein ; invasion
IT___PFI0675w:: conserved Plasmodium protein ; invasion
HBEC2_PFI0675w:: conserved Plasmodium protein ; invasion
HBEC1_PFI0675w:: conserved Plasmodium protein ; invasion
3D7___PFI0675w:: conserved Plasmodium protein ; invasion
TNF___PFL2460w:: coronin ; invasion
IT___PFL2460w:: coronin ; invasion
HBEC2_PFL2460w:: coronin ; invasion
HBEC1_PFL2460w:: coronin ; invasion
3D7___PFL2460w:: coronin ; invasion
TNF___PFL2520w:: reticulocyte-binding protein 3 homologue ; INVASION
IT___PFL2520w:: reticulocyte-binding protein 3 homologue ; INVASION
HBEC2_PFL2520w:: reticulocyte-binding protein 3 homologue ; INVASION
HBEC1_PFL2520w:: reticulocyte-binding protein 3 homologue ; INVASION
3D7___PFL2520w:: reticulocyte-binding protein 3 homologue ; INVASION
TNF___PFL2225w:: myosin A tail domain interacting protein ; invasion
IT___PFL2225w:: myosin A tail domain interacting protein ; invasion
HBEC2_PFL2225w:: myosin A tail domain interacting protein ; invasion
HBEC1_PFL2225w:: myosin A tail domain interacting protein ; invasion
3D7___PFL2225w:: myosin A tail domain interacting protein ; invasion
TNF___PFL1885c:: calcium/calmodulin-dependent protein kinase 2 ; INVASION
IT___PFL1885c:: calcium/calmodulin-dependent protein kinase 2 ; INVASION
HBEC2_PFL1885c:: calcium/calmodulin-dependent protein kinase 2 ; INVASION
HBEC1_PFL1885c:: calcium/calmodulin-dependent protein kinase 2 ; INVASION
3D7___PFL1885c:: calcium/calmodulin-dependent protein kinase 2 ; INVASION
TNF___PFL0190w:: ubiquitin conjugating enzyme E2, putative
IT___PFL0190w:: ubiquitin conjugating enzyme E2, putative
HBEC2_PFL0190w:: ubiquitin conjugating enzyme E2, putative
HBEC1_PFL0190w:: ubiquitin conjugating enzyme E2, putative
3D7___PFL0190w:: ubiquitin conjugating enzyme E2, putative
TNF___PFI1780w:: Plasmodium exported protein (PHISTc)
IT___PFI1780w:: Plasmodium exported protein (PHISTc)
HBEC2_PFI1780w:: Plasmodium exported protein (PHISTc)
HBEC1_PFI1780w:: Plasmodium exported protein (PHISTc)
3D7___PFI1780w:: Plasmodium exported protein (PHISTc)
TNF___PFI1675w:: conserved Plasmodium protein
IT___PFI1675w:: conserved Plasmodium protein
HBEC2_PFI1675w:: conserved Plasmodium protein
HBEC1_PFI1675w:: conserved Plasmodium protein
3D7___PFI1675w:: conserved Plasmodium protein
TNF___PFI1110w:: glutamine synthetase, putative
IT___PFI1110w:: glutamine synthetase, putative
HBEC2_PFI1110w:: glutamine synthetase, putative
HBEC1_PFI1110w:: glutamine synthetase, putative
3D7___PFI1110w:: glutamine synthetase, putative
3 fold downregulated
TNF___PFI0940c:: PPPDE peptidase, putative ; invasion
IT___PFI0940c:: PPPDE peptidase, putative ; invasion
HBEC2_PFI0940c:: PPPDE peptidase, putative ; invasion
HBEC1_PFI0940c:: PPPDE peptidase, putative ; invasion
3D7___PFI0940c:: PPPDE peptidase, putative ; invasion
TNF___PFI0180w:: alpha tubulin
IT___PFI0180w:: alpha tubulin
HBEC2_PFI0180w:: alpha tubulin
HBEC1_PFI0180w:: alpha tubulin
3D7___PFI0180w:: alpha tubulin
TNF___PFF0510w:: histone H3
IT___PFF0510w:: histone H3
HBEC2_PFF0510w:: histone H3
HBEC1_PFF0510w:: histone H3
3D7___PFF0510w:: histone H3
TNF___PFF0200c:: transcription factor with AP2 domain(s), putative ; invasion
IT___PFF0200c:: transcription factor with AP2 domain(s), putative ; invasion
HBEC2_PFF0200c:: transcription factor with AP2 domain(s), putative ; invasion
HBEC1_PFF0200c:: transcription factor with AP2 domain(s), putative ; invasion
3D7___PFF0200c:: transcription factor with AP2 domain(s), putative ; invasion
TNF___PFE1285w:: membrane skeletal protein IMC1-related ; invasion
IT___PFE1285w:: membrane skeletal protein IMC1-related ; invasion
HBEC2_PFE1285w:: membrane skeletal protein IMC1-related ; invasion
HBEC1_PFE1285w:: membrane skeletal protein IMC1-related ; invasion
3D7___PFE1285w:: membrane skeletal protein IMC1-related ; invasion
TNF___PFE0365c:: conserved Plasmodium protein ; invasion
IT___PFE0365c:: conserved Plasmodium protein ; invasion
HBEC2_PFE0365c:: conserved Plasmodium protein ; invasion
HBEC1_PFE0365c:: conserved Plasmodium protein ; invasion
3D7___PFE0365c:: conserved Plasmodium protein ; invasion
TNF___PFD1175w:: Serine/Threonine protein kinase, FIKK family
IT___PFD1175w:: Serine/Threonine protein kinase, FIKK family
HBEC2_PFD1175w:: Serine/Threonine protein kinase, FIKK family
HBEC1_PFD1175w:: Serine/Threonine protein kinase, FIKK family
3D7___PFD1175w:: Serine/Threonine protein kinase, FIKK family
TNF___PFD0090c:: Plasmodium exported protein (PHISTa)
IT___PFD0090c:: Plasmodium exported protein (PHISTa)
HBEC2_PFD0090c:: Plasmodium exported protein (PHISTa)
HBEC1_PFD0090c:: Plasmodium exported protein (PHISTa)
3D7___PFD0090c:: Plasmodium exported protein (PHISTa)
TNF___PFC1045c:: conserved Plasmodium protein ; invasion
IT___PFC1045c:: conserved Plasmodium protein ; invasion
HBEC2_PFC1045c:: conserved Plasmodium protein ; invasion
HBEC1_PFC1045c:: conserved Plasmodium protein ; invasion
3D7___PFC1045c:: conserved Plasmodium protein ; invasion
TNF___PFC0910w:: conserved Plasmodium protein
IT___PFC0910w:: conserved Plasmodium protein
HBEC2_PFC0910w:: conserved Plasmodium protein
HBEC1_PFC0910w:: conserved Plasmodium protein
3D7___PFC0910w:: conserved Plasmodium protein
TNF___PFC0110w:: Cytoadherence linked asexual protein 3.2 ; INVASION
IT___PFC0110w:: Cytoadherence linked asexual protein 3.2 ; INVASION
HBEC2_PFC0110w:: Cytoadherence linked asexual protein 3.2 ; INVASION
HBEC1_PFC0110w:: Cytoadherence linked asexual protein 3.2 ; INVASION
3D7___PFC0110w:: Cytoadherence linked asexual protein 3.2 ; INVASION
TNF___PFB0835c:: conserved Plasmodium protein
IT___PFB0835c:: conserved Plasmodium protein
HBEC2_PFB0835c:: conserved Plasmodium protein
HBEC1_PFB0835c:: conserved Plasmodium protein
3D7___PFB0835c:: conserved Plasmodium protein
TNF___PFB0570w:: SPATR protein, putative ; INVASION
IT___PFB0570w:: SPATR protein, putative ; INVASION
HBEC2_PFB0570w:: SPATR protein, putative ; INVASION
HBEC1_PFB0570w:: SPATR protein, putative ; INVASION
3D7___PFB0570w:: SPATR protein, putative ; INVASION
TNF___PFA0125c:: erythrocyte binding antigen-181 ; INVASION
IT___PFA0125c:: erythrocyte binding antigen-181 ; INVASION
HBEC2_PFA0125c:: erythrocyte binding antigen-181 ; INVASION
HBEC1_PFA0125c:: erythrocyte binding antigen-181 ; INVASION
3D7___PFA0125c:: erythrocyte binding antigen-181 ; INVASION
TNF___PF14_0303:: conserved Plasmodium protein
IT___PF14_0303:: conserved Plasmodium protein
HBEC2_PF14_0303:: conserved Plasmodium protein
HBEC1_PF14_0303:: conserved Plasmodium protein
3D7___PF14_0303:: conserved Plasmodium protein
TNF___PF14_0224:: serine/threonine protein phosphatase ; invasion
IT___PF14_0224:: serine/threonine protein phosphatase ; invasion
HBEC2_PF14_0224:: serine/threonine protein phosphatase ; invasion
HBEC1_PF14_0224:: serine/threonine protein phosphatase ; invasion
3D7___PF14_0224:: serine/threonine protein phosphatase ; invasion
TNF___PF14_0027:: 40S ribosomal protein S31/UBI, putative
IT___PF14_0027:: 40S ribosomal protein S31/UBI, putative
HBEC2_PF14_0027:: 40S ribosomal protein S31/UBI, putative
HBEC1_PF14_0027:: 40S ribosomal protein S31/UBI, putative
3D7___PF14_0027:: 40S ribosomal protein S31/UBI, putative
TNF___PF13_0233:: myosin A ; invasion
IT___PF13_0233:: myosin A ; invasion
HBEC2_PF13_0233:: myosin A ; invasion
HBEC1_PF13_0233:: myosin A ; invasion
3D7___PF13_0233:: myosin A ; invasion
TNF___PF13_0197:: Merozoite Surface Protein 7 precursor, MSP7 ; INVASION
IT___PF13_0197:: Merozoite Surface Protein 7 precursor, MSP7 ; INVASION
HBEC2_PF13_0197:: Merozoite Surface Protein 7 precursor, MSP7 ; INVASION
HBEC1_PF13_0197:: Merozoite Surface Protein 7 precursor, MSP7 ; INVASION
3D7___PF13_0197:: Merozoite Surface Protein 7 precursor, MSP7 ; INVASION
TNF___PF13_0058:: RNA binding protein, putative
IT___PF13_0058:: RNA binding protein, putative
HBEC2_PF13_0058:: RNA binding protein, putative
HBEC1_PF13_0058:: RNA binding protein, putative
3D7___PF13_0058:: RNA binding protein, putative
TNF___PF13_0011:: plasmodium falciparum gamete antigen 27/25
IT___PF13_0011:: plasmodium falciparum gamete antigen 27/25
HBEC2_PF13_0011:: plasmodium falciparum gamete antigen 27/25
HBEC1_PF13_0011:: plasmodium falciparum gamete antigen 27/25
3D7___PF13_0011:: plasmodium falciparum gamete antigen 27/25
TNF___PF11_0277:: conserved Plasmodium protein ; invasion
IT___PF11_0277:: conserved Plasmodium protein ; invasion
HBEC2_PF11_0277:: conserved Plasmodium protein ; invasion
HBEC1_PF11_0277:: conserved Plasmodium protein ; invasion
3D7___PF11_0277:: conserved Plasmodium protein ; invasion
TNF___PF10_0352:: merozoite surface protein ; INVASION
IT___PF10_0352:: merozoite surface protein ; INVASION
HBEC2_PF10_0352:: merozoite surface protein ; INVASION
HBEC1_PF10_0352:: merozoite surface protein ; INVASION
3D7___PF10_0352:: merozoite surface protein ; INVASION
TNF___PF10_0351:: probable protein ; INVASION
IT___PF10_0351:: probable protein ; INVASION
HBEC2_PF10_0351:: probable protein ; INVASION
HBEC1_PF10_0351:: probable protein ; INVASION
3D7___PF10_0351:: probable protein ; INVASION
TNF___PF10_0345:: merozoite surface protein 3 ; INVASION
IT___PF10_0345:: merozoite surface protein 3 ; INVASION
HBEC2_PF10_0345:: merozoite surface protein 3 ; INVASION
HBEC1_PF10_0345:: merozoite surface protein 3 ; INVASION
3D7___PF10_0345:: merozoite surface protein 3 ; INVASION
TNF___PF10_0343:: S-antigen ; invasion
IT___PF10_0343:: S-antigen ; invasion
HBEC2_PF10_0343:: S-antigen ; invasion
HBEC1_PF10_0343:: S-antigen ; invasion
3D7___PF10_0343:: S-antigen ; invasion
TNF___PF10_0281:: merozoite TRAP-like protein, MTRAP ; INVASION
IT___PF10_0281:: merozoite TRAP-like protein, MTRAP ; INVASION
HBEC2_PF10_0281:: merozoite TRAP-like protein, MTRAP ; INVASION
HBEC1_PF10_0281:: merozoite TRAP-like protein, MTRAP ; INVASION
3D7___PF10_0281:: merozoite TRAP-like protein, MTRAP ; INVASION
TNF___PF10_0138:: conserved Plasmodium protein ; invasion
IT___PF10_0138:: conserved Plasmodium protein ; invasion
HBEC2_PF10_0138:: conserved Plasmodium protein ; invasion
HBEC1_PF10_0138:: conserved Plasmodium protein ; invasion
3D7___PF10_0138:: conserved Plasmodium protein ; invasion
TNF___PF08_0118:: conserved Plasmodium protein ; invasion
IT___PF08_0118:: conserved Plasmodium protein ; invasion
HBEC2_PF08_0118:: conserved Plasmodium protein ; invasion
HBEC1_PF08_0118:: conserved Plasmodium protein ; invasion
3D7___PF08_0118:: conserved Plasmodium protein ; invasion
TNF___PF08_0091:: conserved Plasmodium protein
IT___PF08_0091:: conserved Plasmodium protein
HBEC2_PF08_0091:: conserved Plasmodium protein
HBEC1_PF08_0091:: conserved Plasmodium protein
3D7___PF08_0091:: conserved Plasmodium protein
TNF___PF08_0035:: conserved Plasmodium protein ; invasion
IT___PF08_0035:: conserved Plasmodium protein ; invasion
HBEC2_PF08_0035:: conserved Plasmodium protein ; invasion
HBEC1_PF08_0035:: conserved Plasmodium protein ; invasion
3D7___PF08_0035:: conserved Plasmodium protein ; invasion
TNF___PF08_0008:: conserved Plasmodium protein ; invasion
IT___PF08_0008:: conserved Plasmodium protein ; invasion
HBEC2_PF08_0008:: conserved Plasmodium protein ; invasion
HBEC1_PF08_0008:: conserved Plasmodium protein ; invasion
3D7___PF08_0008:: conserved Plasmodium protein ; invasion
TNF___PF07_0104:: kinesin-like protein, putative ; invasion
IT___PF07_0104:: kinesin-like protein, putative ; invasion
HBEC2_PF07_0104:: kinesin-like protein, putative ; invasion
HBEC1_PF07_0104:: kinesin-like protein, putative ; invasion
3D7___PF07_0104:: kinesin-like protein, putative ; invasion
TNF___PF07_0043:: 60S ribosomal protein L34-A, putative
IT___PF07_0043:: 60S ribosomal protein L34-A, putative
HBEC2_PF07_0043:: 60S ribosomal protein L34-A, putative
HBEC1_PF07_0043:: 60S ribosomal protein L34-A, putative
3D7___PF07_0043:: 60S ribosomal protein L34-A, putative
TNF___MAL8P1.70:: Zinc finger C-x8-C-x5-C-x3-H type, putative ; invasion
IT___MAL8P1.70:: Zinc finger C-x8-C-x5-C-x3-H type, putative ; invasion
HBEC2_MAL8P1.70:: Zinc finger C-x8-C-x5-C-x3-H type, putative ; invasion
HBEC1_MAL8P1.70:: Zinc finger C-x8-C-x5-C-x3-H type, putative ; invasion
3D7___MAL8P1.70:: Zinc finger C-x8-C-x5-C-x3-H type, putative ; invasion
TNF___MAL7P1.176:: erythrocyte binding antigen 175 ; INVASION
IT___MAL7P1.176:: erythrocyte binding antigen 175 ; INVASION
HBEC2_MAL7P1.176:: erythrocyte binding antigen 175 ; INVASION
HBEC1_MAL7P1.176:: erythrocyte binding antigen 175 ; INVASION
3D7___MAL7P1.176:: erythrocyte binding antigen 175 ; INVASION
TNF___MAL13P1.60:: erythrocyte binding antigen-140 ; INVASION
IT___MAL13P1.60:: erythrocyte binding antigen-140 ; INVASION
HBEC2_MAL13P1.60:: erythrocyte binding antigen-140 ; INVASION
HBEC1_MAL13P1.60:: erythrocyte binding antigen-140 ; INVASION
3D7___MAL13P1.60:: erythrocyte binding antigen-140 ; INVASION
TNF___PFL2565w:: Plasmodium exported protein (PHISTa)
IT___PFL2565w:: Plasmodium exported protein (PHISTa)
HBEC2_PFL2565w:: Plasmodium exported protein (PHISTa)
HBEC1_PFL2565w:: Plasmodium exported protein (PHISTa)
3D7___PFL2565w:: Plasmodium exported protein (PHISTa)

Figure S7







D

	Median MFI HBEC	IQR	Median MFI Uns	IQR	P value
3D7 parasites					
Acute plasma CM	2.08	0.77-3.68	0.97	0.69-1.81	0.17
Acute plasma UM	2.05	1.03-3.27	0.81	0.65-1.06	**0.04**
Conv plasma CM	3.20	2.30-5.01	1.76	1.22-2.15	**0.009**
Conv plasma UM	3.02	1.07-7.28	1.50	1.09-3.77	0.44
HB3 parasites					
Acute plasma CM	1.24	0.79-8.22	1.44	1.23-1.57	0.85
Acute plasma UM	1.14	0.64-2.23	1.24	1.06-2.25	0.48
Conv plasma CM	6.92	1.14-14.93	1.57	1.28-2.76	0.60
Conv plasma UM	3.74	0.99-10.12	2.07	4.85	0.74
IT parasites					
Acute plasma CM	1.62	0.44-8.98	1.55	1.09-4.26	1.00
Acute plasma UM	1.58	0.65-2.65	1.72	1.22-3.69	0.35
Conv plasma CM	5.08	1.87-6.96	2.51	1.61-5.58	0.32
Conv plasma UM	4.25	3.41-10.25	5.51	2.52-6.41	0.74

Figure S8