

Supplemental Table S1. Primers used in this study.

Name	Sequence 5'--3'	Target gene	Samples
long PCR			
clag3.1_long_F*	TGTGCAATATATCAAAGTGACATGC	<i>clag3.1</i>	All
clag3.1_long_R*	TAGAAAATATTAGAATTGCTATTATGTAC	<i>clag3.1</i>	All
clag3.2_long_F*	AATAGTTGAGTACGCACTAATATGTC	<i>clag3.2</i>	All
clag3.2_long_R*	ACACAAATTCTTAATAATTATATAAAACC	<i>clag3.2</i>	All
HVR Sequencing			
seq3.1&3.2B F	ATCAGGCTGTGGCAAGTGC	<i>clag3.1</i> & <i>clag3.2</i>	Field isolates
seq3.1&3.2B R	CTGACGGTTTGCCTTCGTAGG	<i>clag3.1</i> & <i>clag3.2</i>	Field isolates
RT-qPCR			
PF07_0073 F*	AAGTAGCAGGTCATCGTGGTT	<i>seryl</i>	All
PF07_0073 R*	TTCGGCACATTCTCCATAA	<i>seryl</i>	All
rhopH2_qRT_P2F*	TGTTGCTGTCCATATTTAGTTTT	<i>rhopH2</i>	All
rhopH2_qRT_P2R*	AATATATCGCTACATAACTTCGT	<i>rhopH2</i>	All
clag3.1 clag3.2 – 6F*	TAGTAATGAGAATTAGTTGGACA	<i>clag3.1</i> & <i>clag3.2</i>	NF54/3D7, some field isolates
clag3.1 –6R*	ATAAATATTTGGATGCTTCAGCA	<i>clag3.1</i>	NF54/3D7, some field isolates
clag3.2 –6R*	ACAATATGTTTTCTGAACTAGGA	<i>clag3.2</i>	NF54/3D7, some field isolates
BR054_3.1F	TCTGCTAAAAAGGTAGGTCAGT	<i>clag3.1</i>	Some field isolates
BR054_3.1R	GGATTTATATTTACCACTTGCAC	<i>clag3.1</i>	Some field isolates
BR054_3.2R	CGCACTAGGACAAGTTTTCTG	<i>clag3.2</i>	Some field isolates
CRYO947_3.2F	ACACATGCTTTTACAACCTGGAC	<i>clag3.2</i>	Some field isolates
CRYO1000_3.1R	GCTTTTATAGAATTAGTATTAGCG	<i>clag3.1</i>	Some field isolates
CRYO1000_3.2R	TTACAATTAGTAGTAGAACTTGAG	<i>clag3.2</i>	Some field isolates
CRYO1029_3.1R	CTTTTATAGAATTAGTATTAGCGG	<i>clag3.1</i>	Some field isolates
CRYO1029_3.2R	ACAATTAGTAGTAGAACTTGAGG	<i>clag3.2</i>	Some field isolates
CRYO1029_3.1&3.2F	TATCAGGCTGTGGCAAGTGC	<i>clag3.1</i> & <i>clag3.2</i>	Some field isolates
BR044 & BR026_3.1F	GATCCCAAAAGTTGTACTAGTAG	<i>clag3.1</i>	Some field isolates
BR044 & BR026_3.1R	CAGCAAGTGCCTGAGTGAAG	<i>clag3.1</i>	Some field isolates
BR044 & BR026_3.2F	CCTCAAGTTCTACTACTAATTGT	<i>clag3.2</i>	Some field isolates
BR044 & BR026_3.2R	CAGCAAGTCCGTGAGTAAAGA	<i>clag3.2</i>	Some field isolates
clag9_qRT_F2	AATCACTTACCTGAAGAATTGAG	<i>clag9</i>	Field isolates, Selection
clag9_qRT_R2	ACGAAAGGGACAAACCATGAC	<i>clag9</i>	Field isolates, Selection
clag9_qRT_F1*	GTAATCAATGGCAAATCTTGG	<i>clag9</i>	CHMI
clag9_qRT_R1*	CTGGTTGTTGTAATTCTACACC	<i>clag9</i>	CHMI
clag8_qRT_F2	ACGGAAGATACGGATTTTCGAC	<i>clag8</i>	Field isolates, Selection
clag8_qRT_R2	TCGAAAGTATCTTCTCATCCT	<i>clag8</i>	Field isolates, Selection
clag8_qRT_F1*	CATCGGTTTCATGGTTTTACACA	<i>clag8</i>	CHMI
clag8_qRT_R1*	AAGCATATATTTGTGAAAGGCTC	<i>clag8</i>	CHMI
clag2_qRT_F3	GTCATAAGGAAGAAACCAACAC	<i>clag2</i>	Field isolates
clag2_qRT_R3	TGTTTGAATATAGAAATGCCCT	<i>clag2</i>	Field isolates
clag2_qRT_F1*	TTCGTGCATCATATGGTTGGG	<i>clag2</i>	CHMI
clag2_qRT_R1&2*	TATATAGGTGCATCAGATTTCCA	<i>clag2</i>	CHMI, Selection
clag2_qRT_F2	ATCTATCTCTCAGAATTCGTGC	<i>clag2</i>	Selection
Others			
clag9_long_F1	GATTCCAATAATGAAAGGTGATCTTG	<i>clag9</i>	Field isolates
clag9_long_R1	TCATAACGTTTCGTTCTATCTATACC	<i>clag9</i>	Field isolates
clag2_seqF1	GTCTTTTGTGTGAATACCAAGC	<i>clag2</i>	Field isolates
clag2_seqR1	ATGAAGTAGAAAATCCTCCAGG	<i>clag2</i>	Field isolates
clag9_seqF1	AATATCAAGCCATTGGAAGTGC	<i>clag9</i>	Field isolates
clag9_seqR1	TTGCCAATCAACTACTGAACAG	<i>clag9</i>	Field isolates
seqR3.2_BR044 & BR026	TGACGGTTTGCCTTCATACGT	<i>clag3.2</i>	Some field isolates
seqC_R	ATACTTAAATAAGCCTCACGTTCC	<i>clag3.1</i> & <i>clag3.2</i>	Some field isolates

The primers marked with an asterisk have been previously described [1-3]. “Selection” refers to the samples from the selection experiments shown in Figs. 2 and S4. Primers for *clag3* genes were used to analyze *clag3.1* expression in some isolates and to analyze *clag3.2* expression in other isolates. The name of the primer only indicates the isolate and the paralog against which the primer was originally designed. “Others” corresponds to primers used to obtain sequences for the genes indicated to confirm the absence of polymorphism in the regions where the primers for transcriptional analysis were designed.

References.

1. Iriko H, Kaneko O, Otsuki H, et al. Diversity and evolution of the *rhopH1/clag* multigene family of *Plasmodium falciparum*. *Mol Biochem Parasitol* **2008**; 158:11-21.
2. Crowley VM, Rovira-Graells N, de Pouplana LR, Cortés A. Heterochromatin formation in bistable chromatin domains controls the epigenetic repression of clonally variant *Plasmodium falciparum* genes linked to erythrocyte invasion. *Mol Microbiol* **2011**; 80:391-406.
3. Mira-Martínez S, Rovira-Graells N, Crowley VM, Altenhofen LM, Llinás M, Cortés A. Epigenetic switches in *clag3* genes mediate blasticidin S resistance in malaria parasites. *Cell Microbiol* **2013**; 15:1913-23.