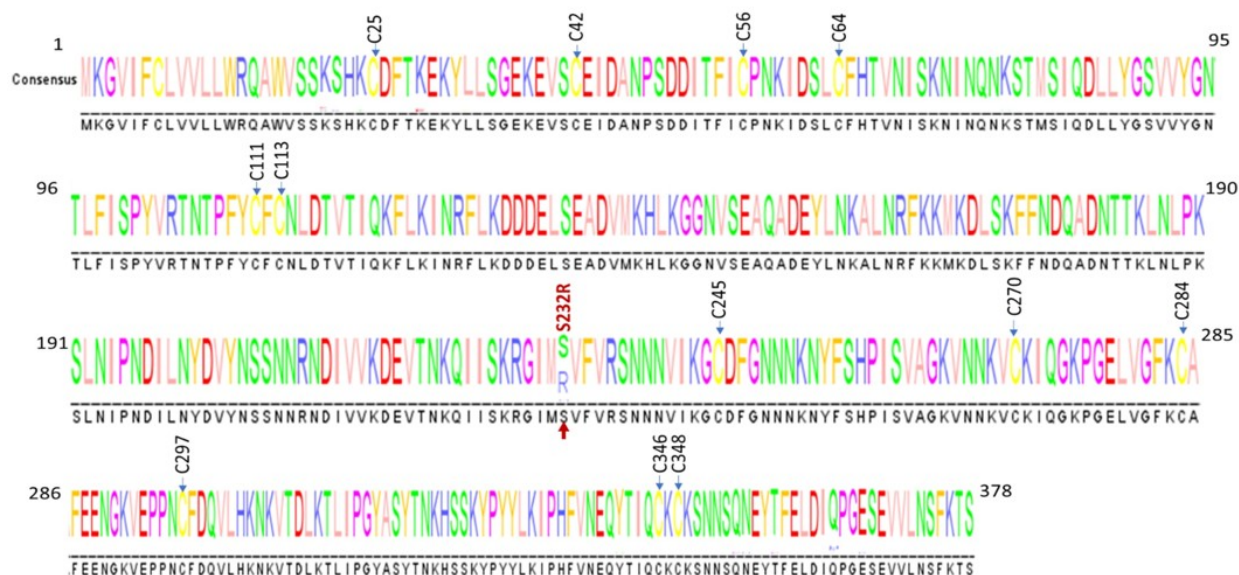




Zappo color legend

Aliphatic/hydrophobic	ILVAM
Aromatic	FWY
Positive	KRH
Negative	DE
Hydrophilic	STNQ
conformationally special	PG
Cysteine	C

Supplementary figure 1: Sequence logo representation of multiple sequence alignment of complete dataset of Pf41 sequences. The x-axis indicates the position of the amino acid and the y-axis shows the probabilities of amino acids across a given sequence set. The residues are colored according to their physico- chemical properties (Zappo color). Conserved cysteine residues C25 - C42 - C56 - C64 - C111 - C113 - C245 - C270 - C284 - C297 - C346 and C348 are shown with arrows. The most representative mutation, S232R, is shown in red

Supplementary table 1: Linkage disequilibrium index of *Pf41*

Gene Domain	ZnS	ZZ	Rm
DI	0,0513	0,0854	1
CD	0,0094	0,0045	0
DII	0,0836	0,0836	2
Over all Gene	0,0443	0,0799	5

Rm =minimum number of recombination events; Zns = statistic representing the average linkage disequilibrium (LD) across all pairwise comparisons of polymorphic sites in dataset; ZZ = difference between two measures of LD

Supplementary table 2: Number of screened samples per site and positivity for the various assays

	Dielmo 2000	Kedougou 2020	Kolda 2020	Tambacounda 2020	Total
Effective	40	25	26	25	116
Positif <i>P. falciparum</i>	35	22	26	25	108
Positif PCR <i>Pf41</i>	34	18	25	24	101
<i>Pf41</i> DNA sequences	29	10	14	20	73