

Supplementary Information

Table S1. List of primers used throughout this study.

N° primer	Sequence	Orientation	Restriction site	Vector	Tagged gene	Use
PTPA						
p1	GGATCCGGGTGATGTAAATAGCTTGAGTTA	F	BamHI	pETDuet 1	6-His	PfPTPA recombinant protein
p2	GTCGACTTAAAAGTCTATCAAATTTCCAAATAATATGTG	R	Sall	pETDuet 1	6-His	PfPTPA recombinant protein
p3	CTCGAGATGGGTGATGTAATAGCTTGAG	F	XhoI	pARL	GFP	PfPTPA-GFP episomal construct
p4	GGTACCAAAGTCTATCAAATTTCCAAATAATATGTGTTG	R	KpnI	pARL	GFP	PfPTPA-GFP episomal construct
p5	CTGCAGATGGGTGATGTAATAGCTTGAG	F	PstI	pCAM BSD		KO construct
p6	GGATCCCATTAATAATAGTGTATATACAC	R	BamHI	pCAM BSD		KO construct
p9	GAAAATAATATTAATGTGCTTCC	F				Genotype of transfected parasite
p10	GTAATTTATGGGATAGCGATTTTTTTTACTGTCTG	F				Detection of episomes
p11	CCAAGCGCGCAATTAACCCTCACTAAAG	R				Detection of episomes
p12	GATCTAGCATAATCTGGAACATCATATGGATAG	R				Genotype of transfected parasite
p13	GCACCTTTTCATGCATCATCCCAAATG	F		pETDuet 1	6-His	mutagenesis PfPTPA E272A
p14	CATTTGGGATGATGCATGAAAAGGTGC	R		pETDuet 1	6-His	mutagenesis PfPTPA E272A
p15	GATATATCTGGAGCTGAAACATGGGAA	F		pETDuet 1	6-His	mutagenesis PfPTPA V283A
p16	TTCCCATGTTTCAGCTCCAGATATATC	R		pETDuet 1	6-His	mutagenesis PfPTPA V283A
p17	GAAAAAATATGTAATGCATTACTTAAAATGTAT	F		pETDuet 1	6-His	mutagenesis PfPTPA G292A
p18	ATACATTTTAAGTAATGCATTACATATTTTTTC	R		pETDuet 1	6-His	mutagenesis PfPTPA G292A
p19	TGGATTACTTAAAGCGTATCAAGCTGAAA	F		pETDuet 1	6-His	mutagenesis PfPTPA M296A
p20	TTTCAGCTTGATACGCTTTAAGTAATCCA	R		pETDuet 1	6-His	mutagenesis PfPTPA M296A
p21	TGAAATAATACAAGCGCGACAAATATTAC	F		pETDuet 1	6-His	mutagenesis PfPTPA K304A
p22	GTAATATTGTCTCGCTTGTATTATTCA	R		pETDuet 1	6-His	mutagenesis PfPTPA K304A
PP2A						
p23	GGATCCGGCAAAAGGAGAAGAAAGAAAGTG	F	BamHI	pETDuet 1	6-His	PfPP2A recombinant protein
p24	GTCGACTTATAAGAAGTAGGGTATGGTGGC	R	Sall	pETDuet 1	6-His	PfPP2A recombinant protein
p25	CTCGAGATGGCAAAAGGAGAAGAAAGAAAG	F	XhoI	pARL	GFP	PfPP2A-GFP episomal construct
p26	GGTACCTAAGAAGTAGGGTATGGTGGCC	R	KpnI	pARL	GFP	PfPP2A-GFP episomal construct
p27	CTGCAGATGGCAAAAGGAGAAGAAAGAAAG	F	PstI	pCAM BSD		KO construct
p28	GGATCCCGATAACAATAATTAGGAGCTG	R	BamHI	pCAM BSD		KO construct
p31	AAAATATTCGGCTTTTATATCATTTGG	F				Genotype of transfected parasite

Table S2. List of proteins used in phylogenetic analysis. For *Plasmodium* proteins, accession numbers are from PlasmoDB Database.

Species	PTPA orthologs	Inhibitor 2 PP2A orthologs	Inhibitor 2 PP1 orthologs	Inhibitor 3 PP1 orthologs
	Accession number	Accession number	Accession number	Accession number
<i>Arabidopsis thaliana</i>	AEE82701.1	AAF27100.1	AED96182.1	NP_565720 INH3
<i>Caenorhabditis elegans</i>	CCD73872.1	NP_001021332.1	NP_498147.1	WBGene00015579
<i>Danio rerio</i>	NP_001003425.2	AAQ97849.1	NP_991231.1	ENSDARP00000052351
<i>Drosophila melanogaster</i>	AAF51115.1	AAF55155.1	NP_524013.1	FBpp0078819
<i>Homo sapiens</i>	CAA60163.1	CAG46847.1	NP_006232.1	ENSP00000407981
<i>Leishmania major</i>	XP_001680923.1	XP_001685161.1	XP_003722091.1	LmjF.07.0743
<i>Mus musculus</i>	AAK62028.1	NP_076360.1	NP_080076.1	ENSMUSP00000047202
<i>Oryza sativa</i>	BAD37240.1	ABR26120.1	NP_001055135.1	NP_001052397
<i>Plasmodium berghei</i>	PBANKA_101460	PBANKA_081990	PBANKA_121850	PBANKA_051550
<i>Plasmodium chabaudi</i>	PCHAS_101540	PCHAS_082020	PCHAS_121920	PCHAS_051560
<i>Plasmodium falciparum</i>	PF3D7_1430100	PF3D7_0919000	PFIT_0320000	PFIT_1031100
<i>Plasmodium knowlesi</i>	PKH_132020	PKH_071620	PKH_082100	PCYB_062600
<i>Plasmodium vivax</i>	PVX_085035	PVX_099365	PVX_095235	PVX_111140
<i>Plasmodium yoelii yoelii</i>	PYYM_1016100	PYYM_0822900	PY06380	PYYM_0516000
<i>Schistosoma mansoni</i>	XP_002579273.1	CCD59858.1	Smp_046160.1	Smp_097560
<i>Tetrahymena thermophila</i>	XP_001010763.2	XP_001022132.2	XP_001024018.2	XP_001014401.1
<i>Theileria parva</i>	EAN33933.1	XP_763467.1	XP_764857.1	XP_764385.1
<i>Toxoplasma gondii</i>	XP_002369121.1	XP_002368303.1	XP_002368145.1	TGME49_226825
<i>Trypanosoma brucei</i>	AEEX79776.1	XP_827991.1	CBH10274.1	Tb927.8.1040
<i>Xenopus laevis (or tropicalis)</i>	NP_001089500.1	NP_001079909.1	NP_001091136.1	NP_001004815.1

Figure S1. Nucleotide and deduced amino acid sequences of PfPTPA cDNA. Nucleotides are numbered to the right of the sequence and amino acids are numbered under the sequence.

5'	ATGGGTGATGTAATAGCTTGAGTTATAAAATAATTAAACGATGAAAGTATTATAAGATTACGAAAAGTTCTATATATAATGATATAATTGAATTTATTA	100
°	M G D V N S L S Y K I I N D E S I I R F T K S S I Y N D I I E F I	
	1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33	
5'	CGAATTTAAATAAATCAGTTGTCGGTGTGAAATGAAACCTTTAGAAGATTTTAAATTATGTAATGAAATGATATGATTAATAATGACAATTTTATT	200
°	T N L N K S V V G V E M K P L E D F K L C N E N D M I N N D N F L F	
	34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67	
5'	CTTATCAAAAAATGTATATAATATTTTCAATTGATAAAAAATATGAACAAGTGTATTGATTCTTGTCACCTATAAAATCAATCATCTCGATTGGTAAT	300
°	L S K N V Y N I F Q L I K N M N K C I D S C P P I N Q S S R F G N	
	68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100	
5'	AGAGGATTTCAACATTTTGTGATGCATATTATAAGAAGTTGATGAGTATTTACCTCATGCTTTATCAGAATCAAACATACCTAATATATCTGAACATA	400
°	R G F Q H F C D A Y Y K E V D E Y L P H A L S E S N I P N I S E H	
	101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133	
5'	CTTATCAAATATCTTATTATTTAAAGAATTCATTGGAATAAAAAGAGAATAGATTATGGAACCTGGGCATGAATTAATTTTTTGCTTTTCCTCTTTTG	500
°	T Y Q I S Y Y L K N S I G N K K R I D Y G T G H E L N F L L F L F C	
	134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167	
5'	CCTAAATAAAATAAATTTCTTTATTCCTTCGGATTACAAGCACCTCGTCTGTTTTATATCGACAGTATTTAGAAGGAGTAAGAAGAGTGCAGATAATT	600
°	L N K I N F F I P S D Y K H L V L V L Y R Q Y L E G V R R V Q I I	
	168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200	
5'	TACTGTGGAACCTGCAGGTAGTAGAGGGGCATGGGGATTGGATGATTTTCAATTTCTGTTTTCTTTTGGCGCAGCTCAACTTTCTTACAACAGGA	700
°	Y T V E P A G S R G A W G L D D F Q F L V F L F G A A Q L S Y N R	
	201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233	
5'	AAATAAAACCGACGATATTGAAAAAAGAATTGTTGGAATTGTGGGCACCGAAATATTTATATTTTGATGCTCTTAAGTATATATCAATGATAAAACA	800
°	K I K T D D I E K K E L L E L W A P K Y L Y F D A L K Y I S M I K H	
	234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267	
5'	TGCACCTTTTCATGAATCATCCCAATGTTGTATGATATATCTGGAGTTGAAACATGGGAAAAAATATGTAATGGATTACTTAAATGTATCAAGCTGAA	900
°	A P F H E S S Q M L Y D I S G V E T W E K I C N G L L K M Y Q A E	
	268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300	
5'	ATAATACAAAAGCGACAAATATTACAACACATATTATTTGGAATTTGATAGACTTTTAA	
°	I I Q K R Q I L Q H I L F G N L I D F .	
	301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320	

Figure S3. Optimized sequence of PfPTPA 5mut.

5'	ATG	GGC	GAC	GTG	AAC	TCC	CTG	AGC	TAC	AAA	ATC	ATC	AAC	GAC	GAA	TCA	ATC	ATC	CGC	TTT	ACC	AAA	66
1	M	G	D	V	N	S	L	S	Y	K	I	I	N	D	E	S	I	I	R	F	T	K	
5'	TCG	AGC	ATC	TAC	AAC	GAC	ATT	ATC	GAA	TTT	ATT	ACC	AAC	CTG	AAT	AAA	AGC	GTG	GTT	GGT	GTC	GAA	132
1	S	S	I	Y	N	D	I	I	E	F	I	T	N	L	N	K	S	V	V	G	V	E	
5'	ATG	AAA	CCG	CTG	GAA	GAT	TTC	AAG	CTG	TGC	AAC	GAA	AAC	GAT	ATG	ATC	AAC	AAC	GAC	AAC	TTT	CTG	198
1	M	K	P	L	E	D	F	K	L	C	N	E	N	D	M	I	N	N	D	N	F	L	
5'	TTC	CTG	TCA	AAG	AAC	GTT	TAC	AAC	ATC	TTC	CAG	CTG	ATC	AAG	AAC	ATG	AAC	AAG	TGC	ATC	GAT	TCG	264
1	F	L	S	K	N	V	Y	N	I	F	Q	L	I	K	N	M	N	K	C	I	D	S	
5'	TGT	CCG	CCG	ATC	AAC	CAG	AGC	TCT	CGT	TTT	GGC	AAT	CGC	ATG	GGT	TTT	CAA	CAT	TTC	TGT	GAT	GCG	330
1	C	P	P	I	N	Q	S	S	R	F	G	N	R	M	G	F	Q	H	F	C	D	A	
5'	TAT	TAC	AAA	GAA	GTG	GAC	GAA	TAT	CTG	CCG	CAT	GCC	CTG	TCA	GAA	TCG	AAC	ATT	CCG	AAT	ATC	TCA	396
1	Y	Y	K	E	V	D	E	Y	L	P	H	A	L	S	E	S	N	I	P	N	I	S	
5'	GAA	CAC	ACC	TAC	CAG	ATT	AGC	TAC	TAC	CTG	AAG	AAC	TCT	ATC	GGC	AAC	AAA	AAG	CGT	ATC	GAT	TAT	462
1	E	H	T	Y	Q	I	S	Y	Y	L	K	N	S	I	G	N	K	K	R	I	D	Y	
5'	GGC	ACG	GGT	CAT	GAA	CTG	AAT	TTT	CTG	CTG	TTT	CTG	TTC	TGC	CTG	AAC	AAA	ATT	AAC	TTT	TTC	ATC	528
1	G	T	G	H	E	L	N	F	L	L	F	L	F	C	L	N	K	I	N	F	F	I	
5'	CCG	TCC	GAC	TAC	AAG	CAC	CTG	GTC	CTG	GTG	CTG	TAT	CGT	CAG	TAC	CTG	GAA	GGT	GTT	CGT	CGC	GTC	594
1	P	S	D	Y	K	H	L	V	L	V	L	Y	R	Q	Y	L	E	G	V	R	R	V	
5'	CAA	ATT	ATC	TAT	ACC	GTG	GAA	CCG	GCA	GGC	AGC	CGC	GGT	GCT	TGG	GGC	CTG	GAT	GAC	TTT	CAG	TTC	660
1	Q	I	I	Y	T	V	E	P	A	G	S	R	G	A	W	G	L	D	D	F	Q	F	
5'	CTG	GTT	TTT	CTG	TTC	GGC	GCG	GCC	CAA	CTG	TCT	TAC	AAC	CGC	AAA	ATT	AAG	ACG	GAT	GAC	ATC	GAA	726
1	L	V	F	L	F	G	A	A	Q	L	S	Y	N	R	K	I	K	T	D	D	I	E	
5'	AAG	AAA	GAA	CTG	CTG	GAA	CTG	TGG	GCG	CCG	AAA	TAT	CTG	TAC	TTT	GAT	GCC	CTG	AAA	TAT	ATT	AGT	792
1	K	K	E	L	L	E	L	W	A	P	K	Y	L	Y	F	D	A	L	K	Y	I	S	
5'	ATG	ATC	AAG	CAT	GCG	CCG	TTC	CAC	GCC	AGT	TCC	CAG	ATG	CTG	TAC	GAC	ATT	TCC	GGT	GCA	GAA	ACG	858
1	M	I	K	H	A	P	F	H	A	S	S	Q	M	L	Y	D	I	S	G	A	E	T	
5'	TGG	GAA	AAA	ATC	TGT	AAT	GCT	CTG	CTG	AAG	GCA	TAT	CAA	GCT	GAA	ATT	ATC	CAA	GCA	CGC	CAA	ATT	924
1	W	E	K	I	C	N	A	L	L	K	A	Y	Q	A	E	I	I	Q	A	R	Q	I	
5'	CTG	CAG	CAC	ATC	CTG	TTC	GGC	AAC	CTG	ATT	GAC	TTC	TGA										
1	L	Q	H	I	L	F	G	N	L	I	D	F	.										

Figure S4. Binding of inactive mutated PfPTPA with XePP2A in oocytes. Co-immunoprecipitation experiment of the PfPTPA-XePP2A complexes was performed with anti-His antibodies (recognizing recombinant wild type and mutated PfPTPA) from microinjected Xenopus oocytes. Immunoprecipitates from Xenopus oocytes microinjected with water, WT or inactive mutated PfPTPA were eluted and separated by SDS-PAGE and transferred to nitrocellulose membrane. Immunoblot analysis was performed with anti-His or anti-PP2A (Abcam) antibodies.

