Supplemental Table 1. Primers used for RT-PCR and ChIP PCR analysis.

Gene ID	Target position	Forward primer (5’→3’)	Reverse Primer (5’→3’)
PFC0060c	ORF	GCATTTAGGTAAGATATC	CCCATCATACTCAGTCA
	Promoter	CAATTTGTAAGACCTGTAA	GTTATATAACATATATGTG
MAL6P1.267	ORF	CGTACATATATTGCATGT	CCCTTTTGATGATTAGTT
	promoter	CTCGAAACGACGGATATC	CCGGCATGAAGTGAAAG
PF07_0019	ORF	CAAACAGCGTGGGGAG	CTCATTAATCTCATATTC
	promoter	CTTGTAATACACCTTGAT	ACATTTTAATCTTCAAAAG
MAL8P1.134	ORF	CCTACATGTACTCCTTGT	CTGAATTGATCCGTTTTG
	promoter	GTGCATTAATCATATGGTC	GTTAATGTACCCTTTTGT
PFI1685w	ORF	GAATTCGTAATTGGTG	GGAATTATGAATGAATAT
	promoter	GTGGTGTAAATTAGGAGA	ACACGTAGCTTTTTTATG
PF11_0362	ORF	TCTGGAAGGCATAACATA	CATCTATTTGTATGACATAC
	Promoter	TGATATGTCAAATCCTTC	CCTGCATGACCATCAATC
PF11_0510	ORF	CAACAACGTTAAGACATG	CCTTCTTTCTTCAATATC
	promoter	GTGTTAGTTTCAGTTGAAT	CTCTAGCAATTTAAAAAGC
PF13_0211	ORF	CCATATTTTGATAGATCC	GATGATCCATCTGTTTCA
	promoter	GAATTTGTAGTGCATCCT	TTCTCAAACGATAGGTAG
PF14_0346	ORF	GTACATTTAGAGCTACCC	CAGTATATATTAACGATG
	promoter	CCTATAATATTACAGCCA	CCTTTTTTTTCTTCAAAG
PF14_0408	ORF	GGCATATTCAATGAAAG	GCTAGTATTGCTATTAAG
	prompter	GAAGTGTGCGCAAAACA	CTTGAGATATACATGTAT
PF14_0602	ORF	GAGAAACTACCTCACGTT	CCATTACCTCAACCACC
	promoter	ATGTGTAGCCATATGTGT	CGTTTAAAGTTTGATCAC
PF08_0054	ORF	CAATTACCAACGACAAAG	TGAGCTTTTAACTCCATA
	promoter	CTCGTTTATAACAAATTG	ATAAGAACTATGGTATTTA
PF08_0131	ORF	TAGATAAGTGGGATATTC	GGATTTAAGAACTCTAAG
	promoter	CATATATATATCATATG	GAATTCTACATACATACTAC
PF14_0081	ORF	CGATATTAGGTTCTCGA	GTTTCTACATCCATAGGA
	promoter	GAGAATTATTTGCACATG	CATATATGACATTGAAGA
PF13_0222	ORF	CGGCATTGTATATCC	GAATCATCATTATGATGA
	promoter	GTATAGCTTATTTAAC	AACAATGGAAATTTTCAC
MAL13P1.134	ORF	GATGATGAAGTTCGTAGTG	GCATACATAAGTAAATAC
	promoter	CATTCCTTTCCTGAAATG	GATATAAACACATCAATC
PF14_0563	ORF	CAGCTTCTGACCTTTTGT	GCTTAGTATCACTTTCAC
	promoter	GTGCGTATATTGATAGG	CAAAACTGCTTAAAAGA

Supplemental Table 2. Down- and up-regulated genes in *P. falciparum* after treatment with anacardic acid (≥2 fold changes at 20 µM)

Down-regulated genes

Gene ID*	Functional Description	Fold change (±STD)		
		20 µM	10 µM	5 µM
	Binding			
PFB0640c	WD40 repeats-containing	2.0±0.1	1.4±0.2	1.8±0.4
PFB0935w (GCN5/H3K9ac)	CLAG2	2.5±0.2	2.0±0.4	2.5±0.1
PFC0010c	Rifin	2.5±0.2	2.3±0.5	1.7±0.5
PFC0110w (GCN5/H3K9ac)	CLAG	2.7±0.2	1.7±0.4	1.5±0.3
PFC0160w (H3K9ac)	binding protein, putative	2.1±0.3	1.7±0.4	1.9±0.2
PFC0800w	Band 7-related protein	2.1±0.4	1.4±0.5	1.4±0.4
PFD0030c	Rifin	2.3±0.2	1.7±0.1	1.4±0.4
PFD0135w (GCN5/H3K9ac)	VAR pseudogene	2.2±0.3	2.2±0.4	2.7±0.2
PFD1015c	PfEMP1	2.2±0.2	1.3±0.3	1.3±0.4
PFD1120c (GCN5/H3K9ac)	ETRAMP-like	2.6±0.1	2.1±0.2	2.1±0.3
PFE0400w	ankyrin repeats-containing	2.2±0.6	1.4±0.2	1.8±0.1
PFE1640w	PfEMP1	3.0±0.3	2.0±0.2	2.1±0.3
MAL6P1.315	Rifin	2.1±0.3	1.8±0.3	1.4±0.5
PF07_0101 (GCN5)	Erythrocyte membrane-associated protein 332	2.1±0.1		
PFI0265c	rhoptry protein	2.3±0.2	1.8±0.1	2.4±0.3
PFI1730w	CLAG	2.2±0.1	1.8±0.1	2.0±0.2
PFI1830c	PfEMP1	2.6±0.5	2.2±0.2	2.3±0.2
PF10_0355	PfEMP1-like	2.5±0.1		
PF11_0213	Rifin	2.3±0.3	1.5±0.2	1.7±0.5
PF11_0486	MAEBL	2.5±0.1	1.2±0.2	1.3±0.1
PF11_0512	RESA2	2.9±0.5	2.7±0.2	2.4±0.2
PFL0940c (GCN5/H3K9ac)	VAR fragment, pseudogene	2.2±0.2	1.1±0.4	1.0±0.4
PFL1955w	PfEMP1	2.3±0.3	1.4±0.4	1.7±0.4
PF13_0001	PfEMP1	2.2±0.3	1.3±0.3	1.3±0.4
PF14_0001	PfEMP1	2.8±0.2	1.4±0.3	1.3±0.3
PF14_0513	RNA binding protein	2.7±0.2	1.3±0.2	
	Catalytic/metabolic			
PFA0485w (H3K9ac)	Cytidylyltransferase family	2.0±0.4	1.7±0.4	1.7±0.3
PFB0325c	cysteine protease (SERA)	2.5±0.4	2.8±0.3	2.0±0.2
PFB0335c	cysteine protease (SERA)	2.1±0.3	1.6±0.3	2.0±0.3
PFB0355c	cysteine protease (SERA)	2.3±0.2	1.9±0.3	1.9±0.2
PFB0360c	cysteine protease (SERA)	2.1±0.4	1.4±0.4	2.0±0.3
PFD0085c	ATP-dependent Ac-CoA synthetase	2.1±0.1	0.8±0.3	0.8±0.1
PFD0780w	glutamyl-tRNA amidotransferase subunit A	2.1±0.4	2.1±0.5	1.3±0.5
PFE0835w	ubiquitin carboxyl-terminal hydrolase 2	2.3±0.3	1.6±0.1	2.1±0.3
MAL6P1.278	endonuclease iii homologue	2.1±0.1	1.6±0.1	1.9±0.3
MAL7P1.130	Methyltransferase domain	2.0±0.2	1.7±0.2	1.5±0.4
MAL7P1.29 (GCN5/H3K9ac)	Alpha/beta hydrolase of unknown function	2.1±0.3	1.8±0.1	2.0±0.4

MAL8P1.22	dehydrodolichyl diphosphate synthetase	2.2±0.2	1.7±0.3	1.5±0.3
PF08_0011 (GCN5/H3K9ac)	leucine - tRNA ligase	2.1±0.4	1.6±0.4	1.8±0.3
PF08_0066 (GCN5/H3K9ac)	lipoamide dehydrogenase	2.1±0.4	1.5±0.5	1.7±0.2
PFI1180w (H3K9ac)	Patatin-like phospholipase	2.1±0.2	1.5±0.1	1.2±0.2
PF10_0058	Peptidase family M3	2.1±0.4	1.8±0.4	1.8±0.2
PF11_0203	Peptidase family M41	2.0±0.5	1.7±0.4	1.5±0.5
PF11_0412	Vacuolar ATP synthase subunit F	2.2±0.1	1.8±0.3	1.8±0.2
PFL0180w (GCN5/H3K9ac)	cytochrome c1 heme lyase	2.4±0.4	2.2±0.4	
MAL13P1.298	Alpha/beta hydrolase of unknown function	2.9±0.5	2.0±0.4	2.3±0.1
PF13_0066	malonyl coa-acyl carrier protein transacylase	2.4±0.1	1.6±0.6	1.8±0.5
PF13_0336	Endonuclease/Exonuclease/phosphatase family	2.2±0.5	1.4±0.6	1.7±0.2
PF14_0615	ATP synthase (C/AC39) subunit	2.4±0.2	1.9±0.0	2.2±0.4
PF14_0751	fatty acyl coA synthetase-1	2.1±0.1	1.7±0.3	1.2±0.2

Chaperone

PFA0660w	DnaJ domain-containing	2.0±0.4	1.3±0.1	1.4±0.1
PFE0505w	cyclophilin	2.3±0.4	2.1±0.3	2.1±0.3
PFE1170w	DnaJ molecular chaperone homology domain	2.3±0.3	1.6±0.5	1.1±0.5
PF08_0032	DnaJ molecular chaperone homology domain	2.2±0.1	1.5±0.1	1.1±0.2
PFI0355c	ATP-dependent heat shock protein	3.1±0.1	2.8±0.5	2.7±0.4

DNA replication/repair

PFC0765c	PSF2 domain containing	2.1±0.2	1.5±0.4	1.5±0.5
PF08_0126	DNA repair protein rad54	2.3±0.4	1.5±0.1	1.7±0.0
PF13_0102	DNAJ-like Sec63 homologue	2.1±0.1	1.2±0.2	1.9±0.5
PF14_0602 (GCN5/H3K9ac)	DNA polymerase alpha subunit	2.1±0.3	1.6±0.3	1.3±0.4

Motor activity

PFC0770c	kinesin-related protein	2.0±0.4	1.5±0.3	1.6±0.2
PF10_0251 (GCN5/H3K9ac)	dynein heavy chain, N-terminal region 2	2.5±0.3	1.6±0.2	1.4±0.4
PF11_0148	dynein light chain type 2	2.0±0.2	1.3±0.5	0.9±0.2
PF11_0416	myosin heavy chain subunit	2.1±0.5	1.9±0.5	2.0±0.5
PF14_0202	dynein-associated protein	2.1±0.2	1.3±0.1	1.0±0.2

Signal transduction

PFC0060c	Ser/Thr protein kinase	3.9±0.3	3.5±0.5	3.0±0.5
MAL6P1.267	Ser/Thr phosphatases	2.9±0.5	2.9±0.5	2.7±0.3
MAL6P1.41	Protein kinase C conserved region 2	2.3±0.3	2.1±0.5	1.5±0.2
PF07_0019	Ser/Thr phosphatases, family 2C	2.1±0.5	2.0±0.3	1.6±0.3
MAL8P1.134	Protein kinase C conserved region 2	2.5±0.3	2.0±0.3	2.6±0.1
PFI1685w	cAMP-dependent protein kinase catalytic subunit	2.0±0.1	1.7±0.1	1.8±0.2
PFL1110c	cAMP-dependent protein kinase regulatory subunit	2.2±0.2	1.7±0.2	2.2±0.2
PF11_0362	Sigma factor PP2C-like phosphatases	2.6±0.4	1.8±0.1	2.1±0.3
PF11_0510 (GCN5/H3K9ac)	Ser/Thr protein kinase	3.2±0.2	2.8±0.0	2.5±0.0
PF13_0211	calcium-dependent protein kinase	2.3±0.4	1.8±0.2	1.4±0.4
PF14_0346	cGMP-dependent protein kinase 1, beta isozyme	2.4±0.2	1.9±0.1	2.3±0.3
PF14_0408	Ser/Thr protein kinase	2.2±0.6	1.7±0.2	

Structural

PFD0490c	actin-like protein	2.7±0.1	2.2±0.1	2.1±0.1
PFE0255w	actin-related protein	2.3±0.2	1.8±0.0	
PF07_0054 (GCN5/H3K9ac)	histone h2b variant	2.3±0.1	2.1±0.5	2.3±0.5
PFI1635w	delta tubulin	2.3±0.3	1.4±0.1	1.5±0.0

Transcription/translation

MAL6P1.183	iswi protein homologue	2.2±0.2	1.1±0.5	1.6±0.3
MAL6P1.49	DNA helicase	2.3±0.2	1.6±0.2	1.6±0.2
MAL7P1.81	eukaryotic translation initiation factor 3	7.5±0.5	9.0±0.2	8.7±0.3
MAL7P1.86	Transcription initiation factor iie, alpha subunit	2.0±0.4	1.8±0.2	1.7±0.2
PF10_0309	DEAD-like helicase superfamily	2.0±0.1	1.4±0.5	1.7±0.3
PF10_0369 (H3K9ac)	helicase	2.1±0.1	1.4±0.3	1.3±0.1
PF13_0229	IRP-like protein	3.4±0.3	2.2±0.2	2.4±0.4
MAL13P1.166	helicase	2.1±0.5	1.6±0.3	2.2±0.1
MAL13P1.248 (GCN5/H3K9ac)	nucleoside diphosphate hydrolase	3.3±0.2	2.2±0.2	2.4±0.5
PF14_0066 (GCN5)	Elp3-like	2.3±0.2	1.9±0.1	2.0±0.2
PF14_0132 (GCN5/H3K9ac)	ribosomal protein S9	2.1±0.1	1.7±0.2	1.8±0.3
PF14_0207	RNA polymerase subunit	2.5±0.4	2.4±0.4	2.3±0.3

Transport

PFC0875w	Transporter, putative	2.3±0.4	2.2±0.3	2.0±0.1
PFL1875w (H3K9ac)	Potassium ion transport	2.1±0.5	3.3±0.4	2.7±0.3
MAL13P1.83	Exportin 1-like protein	2.1±0.4	1.6±0.2	2.2±0.5
PF13_0019	sodium/hydrogen exchanger	2.5±0.2	2.1±0.3	2.2±0.2
PF14_0530	Ferlin like	2.3±0.4	2.1±0.3	2.4±0.4

Unknown

PFA0320w	hypothetical protein	2.1±0.3	1.8±0.4	1.5±0.3
PFA0440w	hypothetical protein	2.2±0.3	1.7±0.4	2.2±0.3
PFB0190c	hypothetical protein	2.2±0.3		2.0±0.4
PFB0775w	hypothetical protein	2.2±0.2	1.3±0.5	1.4±0.1
PFB0800c (GCN5/H3K9ac)	hypothetical protein	4.8±0.5	1.6±0.3	1.2±0.3
PFC0650w	hypothetical protein	2.0±0.3	1.6±0.2	1.2±0.1
PFC0715c	hypothetical protein	2.0±0.2	1.4±0.1	1.4±0.5
PFD0080c	hypothetical protein	2.6±0.1	1.4±0.1	1.7±0.3
PFD0330w	hypothetical protein	2.2±0.2	1.7±0.3	1.6±0.4
PFD0595w (H3K9ac)	hypothetical protein	2.6±0.4	1.9±0.2	2.4±0.4
PFD0900w	hypothetical protein	2.2±0.1	1.2±0.8	1.3±0.3
PFD0945c (H3K9ac)	hypothetical protein	2.3±0.2	1.6±0.3	1.9±0.4
PFD1185w	hypothetical protein	2.9±0.3	2.4±0.2	2.1±0.1
PFE0105c (GCN5/H3K9ac)	hypothetical protein	2.2±0.3	1.7±0.4	1.4±0.5
PFE0325w	hypothetical protein	2.4±0.1	1.5±0.2	1.8±0.1
PFE0940c	hypothetical protein	2.4±0.3	2.1±0.3	2.2±0.3
PFE1550w	hypothetical protein	2.1±0.1	1.7±0.2	1.7±0.4
PFE1555c	hypothetical protein	2.5±0.4	2.5±0.5	2.5±0.3
MAL6P1.147 (H3K9ac)	Hypothetical protein	2.0±0.1	1.2±0.3	2.3±0.5

MAL6P1.279	hypothetical protein	2.9±0.3	2.2±0.2	2.5±0.3
MAL6P1.44	hypothetical protein	2.1±0.2	2.2±0.4	2.4±0.5
MAL7P1.118	Hypothetical protein	2.2±0.3	1.8±0.3	1.7±0.4
MAL7P1.134 (H3K9ac)	hypothetical protein	2.1±0.4	1.3±0.2	1.4±0.3
MAL7P1.160 (H3K9ac)	hypothetical protein	2.1±0.2	1.7±0.3	1.6±0.2
MAL7P1.83	hypothetical protein	2.2±0.4	2.0±0.3	
MAL7P1.95	hypothetical protein	2.2±0.2	1.6±0.4	1.8±0.3
PF07_0024	hypothetical protein	2.3±0.2	1.6±0.5	2.1±0.5
MAL8P1.153 (GCN5/H3K9ac)	hypothetical protein	2.6±0.4	2.1±0.3	2.3±0.1
MAL8P1.29	hypothetical protein	2.3±0.3	1.4±0.2	1.5±0.4
MAL8P1.56	hypothetical protein	2.1±0.1	1.7±0.2	1.6±0.3
MAL8P1.73	hypothetical protein	2.3±0.3	1.7±0.2	2.2±0.2
PF08_0008	hypothetical protein	2.2±0.2	1.6±0.3	1.2±0.3
PF08_0013	hypothetical protein	2.7±0.2	2.3±0.1	2.5±0.2
PF08_0047 (GCN5/H3K9ac)	hypothetical protein	3.3±0.5	2.2±0.4	3.0±0.3
PF08_0060	Asn-rich antigen	2.0±0.1	1.3±0.2	1.4±0.3
PFI0210c	hypothetical protein	2.4±0.4	2.2±0.4	2.2±0.3
PFI0410c	hypothetical protein	2.1±0.2	1.9±0.4	2.0±0.3
PFI0665w	hypothetical protein	2.4±0.2		2.0±0.1
PFI0870w (GCN5/H3K9ac)	hypothetical protein	2.2±0.0	1.6±0.3	1.3±0.2
PFI1445w (H3K9ac)	hypothetical protein	2.6±0.4	1.8±0.5	2.8±0.2
PFI1500w	hypothetical protein	2.1±0.5	1.5±0.5	1.5±0.1
PF10_0020	hypothetical protein	2.2±0.1	1.6±0.2	1.9±0.4
PF10_0023 (H3K9ac)	hypothetical protein	2.3±0.1	1.3±0.4	1.3±0.3
PF10_0048 (GCN5/H3K9ac)	hypothetical protein	2.4±0.2	1.9±0.3	1.9±0.2
PF10_0101 (GCN5/H3K9ac)	hypothetical protein	2.0±0.4	1.5±0.2	1.3±0.4
PF10_0107 (H3K9ac)	hypothetical protein	2.1±0.1	1.6±0.2	1.6±0.2
PF10_0189	hypothetical protein	2.1±0.4	1.7±0.5	2.1±0.4
PF10_0206	hypothetical protein	3.3±0.4	1.6±0.4	
PF10_0231 (GCN5/H3K9ac)	hypothetical protein	2.2±0.5		
PF10_0292	hypothetical protein	2.0±0.4	1.5±0.4	1.9±0.2
PF10_0306	hypothetical protein	2.1±0.2	1.5±0.2	1.9±0.3
PF10_0320	hypothetical protein	3.0±0.5	2.7±0.3	2.7±0.3
PF10_0364 (GCN5/H3K9ac)	hypothetical protein	2.1±0.2	1.6±0.1	1.7±0.2
PF11_0063	hypothetical protein	2.5±0.5	2.4±0.4	2.4±0.2
PF11_0131	hypothetical protein	2.1±0.3	1.4±0.2	1.5±0.1
PF11_0135	hypothetical protein	2.1±0.4	1.5±0.5	1.8±0.1
PF11_0143	hypothetical protein	2.9±0.2	2.1±0.1	2.6±0.4
PF11_0146 (GCN5/H3K9ac)	hypothetical protein	2.2±0.1	1.5±0.1	1.6±0.5
PF11_0163	hypothetical protein	2.1±0.1	1.7±0.1	1.6±0.2
PF11_0178	hypothetical protein	2.1±0.3	1.5±0.3	1.7±0.5
PF11_0186 (GCN5/H3K9ac)	hypothetical protein	2.4±0.3	1.7±0.4	1.9±0.4
PF11_0193 (GCN5/H3K9ac)	hypothetical protein	2.3±0.2	1.8±0.2	2.1±0.3
PF11_0243	hypothetical protein	2.2±0.3	1.7±0.2	2.1±0.4
PF11_0261	hypothetical protein	2.1±0.2	1.7±0.3	2.4±0.2
PF11_0262	hypothetical protein	2.6±0.4	2.2±0.3	2.2±0.3
PF11_0300	hypothetical protein	2.2±0.3	1.7±0.1	2.0±0.3

PF11_0419	hypothetical protein	2.4±0.1	1.7±0.0	2.0±0.3
PF11_0451	hypothetical protein	2.6±0.2	2.2±0.1	2.1±0.1
PF11_0472 (H3K9ac)	hypothetical protein	3.0±0.4	2.8±0.4	2.7±0.3
PF11_0476 (GCN5/H3K9ac)	hypothetical protein	2.2±0.1	1.5±0.4	1.4±0.2
PF11_0481	hypothetical protein	2.3±0.2	2.5±0.2	2.9±0.0
PF11_0528	hypothetical protein	2.0±0.5		2.0±0.3
PFL0250w	hypothetical protein	2.4±0.2	1.9±0.1	1.8±0.1
PFL0370w	hypothetical protein	2.9±0.2	1.1±0.5	0.2±0.2
PFL0875w	hypothetical protein	2.1±0.1		1.3±0.5
PFL1025c	hypothetical protein	2.2±0.1	1.8±0.2	2.0±0.3
PFL1115w	hypothetical protein	2.7±0.2	2.1±0.1	2.2±0.4
PFL1300c	hypothetical protein	2.5±0.2		
PFL1390w	hypothetical protein	2.4±0.1	1.7±0.1	1.7±0.2
PFL1405w	hypothetical protein	2.4±0.4	2.3±0.5	2.2±0.2
PFL1580w (GCN5)	hypothetical protein	2.2±0.3	2.0±0.3	2±0.4
PFL2015w (GCN5/H3K9ac)	Hypothetical protein	2.3±0.1	1.9±0.2	1.7±0.4
PFL2530w	hypothetical protein	2.2±0.4	1.7±0.3	1.3±0.5
MAL13P1.103 (GCN5/H3K9ac)	hypothetical protein	2.1±0.3	1.2±0.2	1.3±0.3
MAL13P1.114	hypothetical protein	2.1±0.2	1.6±0.1	2.2±0.5
MAL13P1.131 (GCN5/H3K9ac)	hypothetical protein	2.1±0.1	1.4±0.1	1.1±0.2
MAL13P1.157	hypothetical protein	2.5±0.5	2.5±0.4	2.1±0.3
MAL13P1.195 (GCN5/)	hypothetical protein	2.6±0.4	2.6±0.3	2.4±0.2
MAL13P1.212	hypothetical protein	2.1±0.5	1.5±0.3	1.6±0.1
MAL13P1.226	hypothetical protein	2.3±0.5	1.9±0.4	1.3±0.4
MAL13P1.247	hypothetical protein	2.6±0.3	2.7±0.3	2.6±0.2
MAL13P1.293	hypothetical protein	2.1±0.4	2.1±0.4	2.0±0.3
MAL13P1.325	hypothetical protein	2.3±0.4	2.1±0.3	1.9±0.2
MAL13P1.78	hypothetical protein	2.1±0.4		2.0±0.3
PF13_0135	hypothetical protein	2.2±0.1	1.6±0.2	1.3±0.2
PF13_0173	hypothetical protein	2.3±0.4	1.8±0.2	2.2±0.5
PF13_0255	hypothetical protein	2.0±0.3	1.7±0.1	2.3±0.2
PF13_0311	hypothetical protein	2.7±0.4	2.5±0.2	2.4±0.3
PF14_0095 (GCN5/H3K9ac)	hypothetical protein	2.1±0.3	1.8±0.5	1.7±0.4
PF14_0217	hypothetical protein	2.0±0.3	1.7±0.2	1.7±0.2
PF14_0291	hypothetical protein	2.2±0.3	1.3±0.8	1.4±0.2
PF14_0325	hypothetical protein	2.1±0.2	1.5±0.4	1.9±0.3
PF14_0404	hypothetical protein	3.0±0.2	2.8±0.4	3.0±0.4
PF14_0468	Hypothetical protein	2.1±0.5	2.0±0.4	2.0±0.3
PF14_0495	hypothetical protein	2.1±0.4	2.0±0.5	2.4±0.3
PF14_0498 (H3K9ac)	hypothetical protein	2.2±0.4	1.5±0.5	
PF14_0506	hypothetical protein	2.1±0.4	1.5±0.5	1.8±0.3
PF14_0657	hypothetical protein	2.1±0.1	1.6±0.1	1.6±0.4
PF14_0701	hypothetical protein	4.0±0.0	2.1±0.5	2.6±0.5
PF14_0712 (H3K9ac)	hypothetical protein	3.0±0.4	1.6±0.1	1.7±0.5
PF14_0714	hypothetical protein	2.0±0.2	1.3±0.2	1.1±0.2
PF14_0757 (H3K9ac)	hypothetical protein	2.4±0.3	1.5±0.3	1.7±0.0

*Genes with the microarray oligoes within 500 bp from the putative ATG codon are in blue. Those genes enriched with H3K9ac or PfGCN5 from the ChIP-chip analysis are also indicated.

Up-regulated genes

Binding

PFD0640c	rifin	2.2±0.1	2.3±0.2	2.4±0.2
PF10_0019	early transcribed membrane protein	2.7±0.1	2.4±0.1	1.8±0.4
PF10_0395	stevor	2.2±0.5	2.8±0.4	2.8±0.3
PF14_0532	LCCL domain-containing (G)	2.1±0.4	1.9±0.4	2.2±0.5
PF10_0016	acyl CoA binding protein	2.5±0.3	2.0±0.1	1.9±0.2

Catalytic/Metabolic

PFB0880w	Saccharop-dh domain-containing (G)	2.1±0.4	1.7±0.4	1.9±0.1
PFE0630c	orotate phosphoribosyltransferase	2.0±0.2	1.9±0.0	1.8±0.3
PFE0660c	uridine phosphorylase	2.1±0.1	1.8±0.4	1.9±0.2
PFE1035c	BIS(5'-nucleosyl)-tetraphosphatase	2.0±0.1	1.9±0.5	2.0±0.1
PF08_0131	1-cys peroxidoxin	2.0±0.1	1.9±0.2	1.6±0.4
PF10_0121	hypoxanthine phosphoribosyltransferase	3.7±0.4	2.6±0.2	2.7±0.3
PFL0285w	glyoxalase II family protein	2.3±0.1	2.9±0.1	2.4±0.2
PF13_0269	glycerol kinase (G)	2.3±0.2		2.3±0.4
PF14_0341	glucose-6-phosphate isomerase	2.1±0.5	2.2±0.1	2.0±0.5
PF14_0399	ADP-ribosylation-like factor	2.0±0.3	1.8±0.4	1.8±0.0
PF14_0598	glyceraldehyde-3-phosphate dehydrogenase	2.2±0.5	2.1±0.5	1.9±0.4

Chaperone

PFA0460c	tubulin-specific chaperone a	2.2±0.1	1.9±0.3	1.9±0.3
PFC0975c	cyclophilin	2.3±0.2	1.8±0.2	1.8±0.1
PF08_0054	heat shock 70 kDa protein	2.2±0.2	2.5±0.1	2.0±0.1
PFL0740c	10 kd chaperonin	2.1±0.4	1.9±0.1	2.1±0.1

DNA replication/repair

PF11_0071	RuvB DNA helicase	2.2±0.4	1.2±0.4	1.1±0.1
PF14_0081	DNA repair helicase	1.9±0.2	2.3±0.3	2.1±0.1

Gametocytes specific

PFD0310w	Pfs16 (G)	2.3±0.3	1.9±0.2	1.9±0.2
PF13_0011	Pfs27/25 (G)	2.4±0.1	2.2±0.4	2.1±0.3

Motor activity

PFI0260c	Dynein heavy chain	2.1±0.3	1.9±0.1	1.9±0.1

Signal transduction

MAL6P1.191	protein kinase	2.0±0.3	1.7±0.2	1.9±0.2
MAL13P1.84	protein kinase (G)	2.0±0.2	1.8±0.2	1.7±0.5

Structural

PF11_0062	histone H2B	2.2±0.5	2.0±0.3	1.6±0.1

Translation/transcription

PFC0400w	60S acidic ribosomal protein P2	2.0±0.3	1.7±0.1	1.7±0.4
MAL7P1.151	DNA methylase	2.4±0.3	2.5±0.4	2.1±0.3
PF08_0037	MED7 protein homologue	2.2±0.2	2.0±0.1	2.4±0.2
PF11_0260	ribosomal protein L35	2.0±0.3	1.9±0.5	1.8±0.5
PFL2475w	DEAD/DEAH box helicase	2.0±0.2	2.3±0.3	1.6±0.1
MAL13P1.209	60S ribosomal subunit porotein L18	2.1±0.0	2.0±0.2	1.6±0.1
PF14_0141	ribosomal protein L10	2.1±0.4	2.0±0.4	1.9±0.5
PF14_0448	ribosomal protein S2	2.1±0.2	2.1±0.3	1.8±0.3

Transport

PF13_0358	mitochondrial import inner membrane translocase	2.1±0.5	1.8±0.5	1.8±0.4
PF13_0252	nucleoside transporter 1	2.0±0.4	1.9±0.5	2.1±0.5

Unknown

PFA0490w	hypothetical protein (G)	2.2±0.5	2.0±0.3	2.0±0.1
PFB0985c	hypothetical protein	2.5±0.0	2.2±0.1	2.0±0.4
PFD0440w	hypothetical protein	2.6±0.3	3.6±0.3	3.1±0.3
PFD0820w	hypothetical protein	2.1±0.2	2.0±0.5	2.2±0.3
PFE0060w	hypothetical protein	2.2±0.2	2.3±0.4	2.2±0.3
PFE0680w	hypothetical protein (G)	2.2±0.4	2.5±0.1	2.5±0.1
PFE0685w	hypothetical protein (G)	2.8±0.4	2.8±0.1	2.8±0.1
PFE0875c	hypothetical protein (G)	5.3±0.4	6.1±0.4	1.8±0.1
PFE1395c	hypothetical protein	2.4±0.2	1.6±0.5	1.2±0.5
MAL6P1.15	hypothetical protein	2.3±0.1	2.5±0.4	2.0±0.1
MAL6P1.214	hypothetical protein	2.1±0.2	1.9±0.1	1.9±0.2
PF07_0094	hypothetical protein (G)	2.2±0.0	2.1±0.1	2.2±0.1
MAL8P1.49	hypothetical protein	2.3±0.5	2.0±0.4	2.2±0.2
PFI1405c	hypothetical protein	2.3±0.2		2.1±0.2
PFI1785w	hypothetical protein	2.5±0.2	1.8±0.3	1.3±0.2
PF10_0164	hypothetical protein	2.6±0.2	2.1±0.2	2.0±0.3
PF11_0014	hypothetical protein	2.4±0.3	2.3±0.1	2.5±0.5
PF14_0290	hypothetical protein (G)	2.7±0.3	2.1±0.3	2.4±0.1
PFL0715w	hypothetical protein	2.7±0.1	2.3±0.1	2.6±0.4
PFL0795c	hypothetical protein (G)	2.9±0.3	2.3±0.1	2.8±0.2
PFL1585c	hypothetical protein	3.0±0.2	2.8±0.3	2.1±0.3
MAL13P1.340	hypothetical protein (G)	2.1±0.4		
MAL13P1.350	hypothetical protein (G)	2.4±0.4	2.2±0.2	
PF13_0075	hypothetical protein	2.1±0.4	1.8±0.1	1.4±0.5
PF13_0076	hypothetical protein	2.0±0.1	1.8±0.2	1.8±0.3
PF14_0744	hypothetical protein	2.2±0.1	2.1±0.1	2.0±0.2

(G): Gametocyte-specific genes according to published data (Young et al. 2005. The *Plasmodium falciparum* sexual development transcriptome: a microarray analysis using ontology-based pattern identification. Mol Biochem Parasitol. 143:67-79.)

Supplemental Fig.1. Cluster analysis of genes with ≥2-fold down- or up-regulation after 12 h of 20 μM of AA treatment. Based on their expression profiles, the genes were roughly divided into seven groups. Two vertical arrows and lines are used to illustrate the expression status of the genes at the time of addition of AA (18 h) and of microarray analysis (30 h).