Supporting Information

Figure S1. (A) Representative SEM image of BH. (B) Histogram summarizing the length distribution of over 150 BH particles. The mean length was determined as 0.9 ± 0.3 μM.

Figure S2. Latex bead phagocytosis. LPS (0.1 μg/mL)-stimulated RAW 264.7 cells were treated with serum-opsonized fluorescent red latex beads for (A) 6 h or (B) 24 h and analyzed by flow cytometry. Untreated control cell populations (tinted blue) were overlaid with the latex bead treated cell population (tinted orange) to demonstrate the increase in fluorescence upon phagocytosis.

Figure S3. BH phagocytosis. LPS (0.1 μg/mL)-stimulated RAW 264.7 cells were (A) untreated or treated with 0.1 mg/mL serum-opsonized BH for (B) 6 h or (C) 24 h and analyzed by flow cytometry. Consistent with phagocytosis of the Hz, density plots demonstrate that BH treatment markedly increased the side scatter of the total population at both time points.

Figure S4. Effect of HNE on cell death. LPS (0.1 μg/mL)-stimulated RAW 264.7 cells were (A) untreated or (B) treated with 35 μM HNE for 24 h, and stained with apoptosis- and necrosis-specific stains. Three populations were observed by flow cytometric analysis: viable cells, apoptotic cells, and necrotic cells. Viable cells are negative for both Alexa Fluor 488 conjugated annexin V and PI, apoptotic cells are positive for Alexa Fluor 488 conjugated annexin V, and necrotic cells are positive for PI alone or both Alexa Fluor 488 conjugated annexin V and PI. HNE (35 μM) only altered the percentage of apoptotic cells by 3.4% relative to stimulated cells, and the population of necrotic cells was unchanged regardless of HNE treatment, demonstrating that 24 h incubation of 35 μM HNE is well tolerated by RAW 264.7 cells.

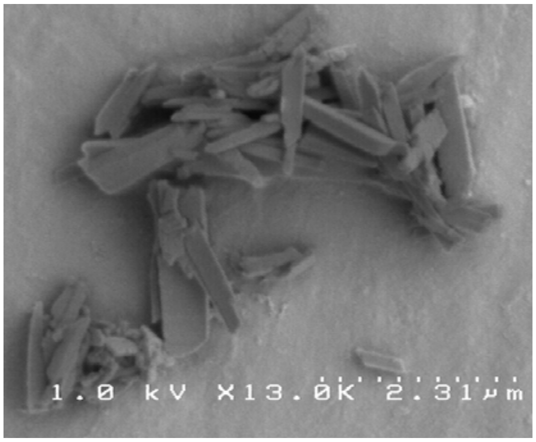

Figure S1(a)

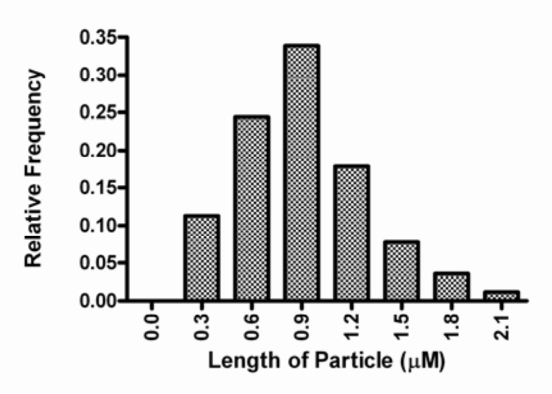

Figure S1(b)

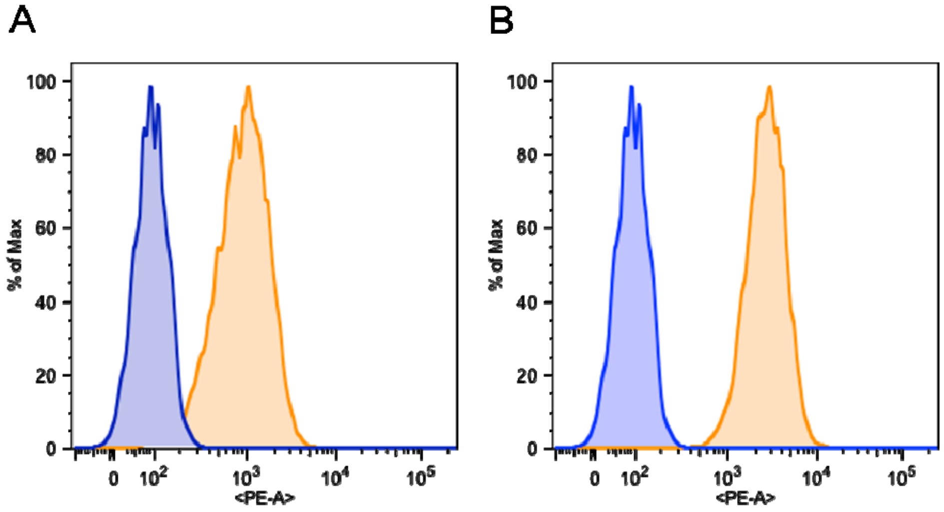

Figure S2.

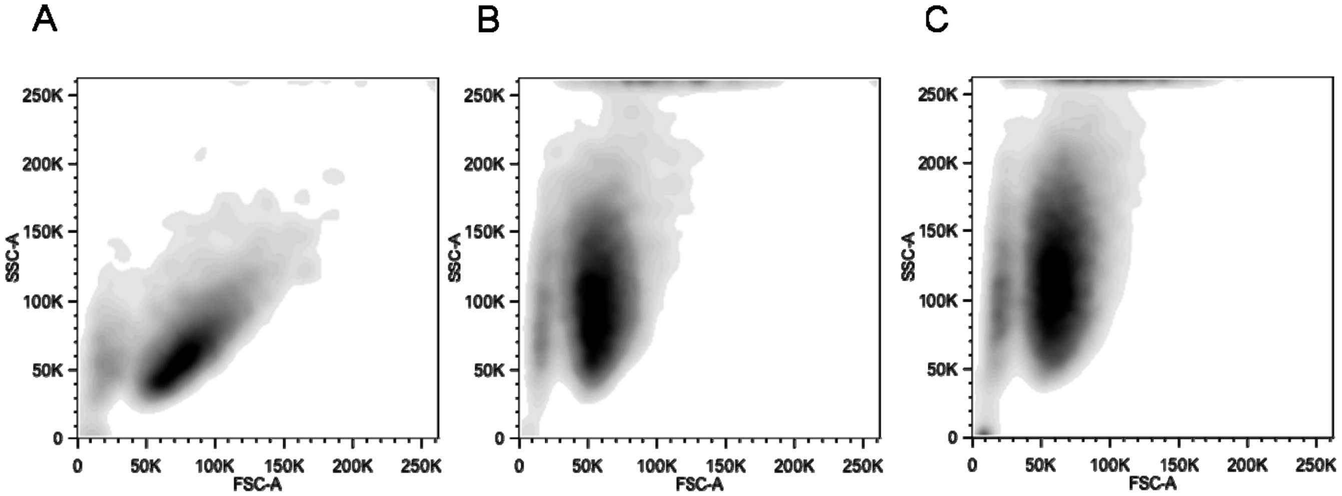

Figure S3

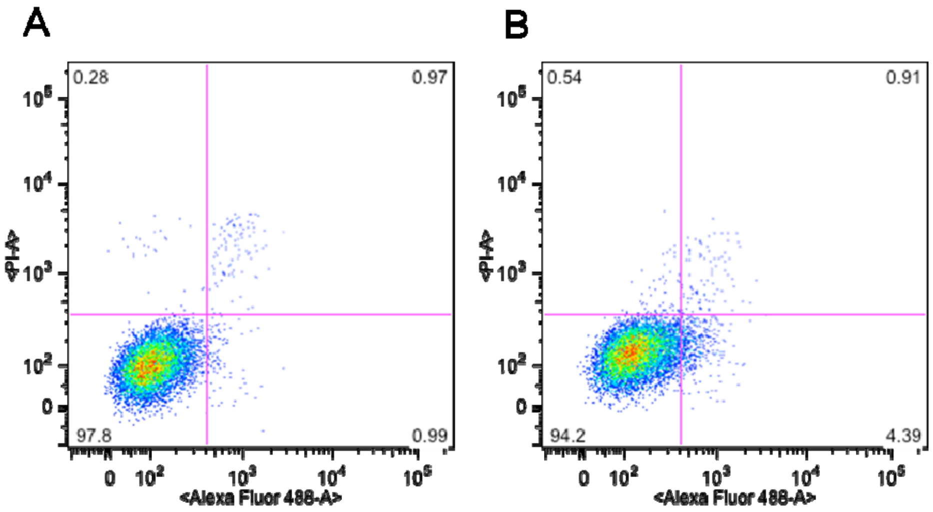

Figure S4

Supporting Information Table 1. Selected Genes Up-Regulated by 35 μM HNE at 6 h[a]

	gene symbol	description	fold change	Affymetrix probeset ID	MGI gene ID	ref
apoptosis (*33*, *34*)	Dap	death-associated protein	1.8	10423498	1918190	
	Dnase2a	deoxyribonuclease II α	1.8	10573461	1329019	
	Sgpl1	sphingosine phosphate lyase 1	1.8	10369413	1261415	
cell cycle (*33*)	Plk2	polo-like kinase 2 (Drosophila)	3.7	10407126	1099790	
	Pdcd4	programmed cell death 4	3.6	10463997	107490	
	Trp53inp1	transformation related protein 53 inducible nuclear pr	3.4	10503259	1926609	
	Plekho1	pleckstrin homology domain containing, family O member 1	2.3	10500295	1914470	
	Ccng1	cyclin G1	2.2	10385271	102890	
	Riok3	RIO kinase 3	1.9	10453900	1914128	
	Nek3	NIMA (never in mitosis gene a)-related expressed kinase 3	1.8	10577492	1344371	
cell-cell signaling (*34*)	Trpv4	transient receptor potential cation channel, subfamily V,	2.0	10532839	1926945	
	Cldn11	claudin 11	1.8	10491313	106925	
defense response (*33*, *34*)	Als2	amyotrophic lateral sclerosis 2 (juvenile) homolog (human)	2.0	10354979	1921268	
	Nlrp10	NLR family, pyrin domain containing 10	1.9	10566709	2444084	
immune response (*33*, *34*)	Procr	protein C receptor, endothelial	4.3	10477717	104596	

	Sqstm1	sequestosome 1	3.2	10385572	107931	
	Il7r	interleukin 7 receptor	3.1	10427628	96562	
	Tnfrsf10b	tumor necrosis factor receptor superfamily, member 10b	2.4	10416230	1341090	
	Pglyrp3	peptidoglycan recognition protein 3	2.1	10493842	2685266	
	Cd300lb	CD300 antigen like family member B	2.0	10392796	2685099	
	Clec4d	C-type lectin domain family 4, member d	1.9	10541614	1298389	
	Cd300a	CD300A antigen	1.9	10382438	2443411	
	Inppl1	inositol polyphosphate phosphatase-like 1	1.9	10565996	1333787	
	Icam1	intercellular adhesion molecule 1	1.8	10583519	96392	
inflammatory response (*33, 34*)	Pla2g7	phospholipase A2, group VII (platelet-activating factor a	3.2	10445293	1351327	
	Lipa	lysosomal acid lipase A	2.9	10467139	96789	
	Ly96	lymphocyte antigen 96	2.3	10344966	1341909	(*30*)
	Nlrc4	NLR family, CARD domain containing 4	2.3	10452879	3036243	
intracellular protein transport (*34*)	Zmat3	zinc finger matrin type 3	2.6	10497673	1195270	
	Chml	choroideremia-like	2.0	10360460	101913	
	Napb	N-ethylmaleimide sensitive fusion protein attachment protei	1.9	10488387	104562	
metabolic process (*33*)	Blvrb	biliverdin reductase B (flavin reductase (NADPH))	3.6	10551347	2385271	(*30*)
	Htatip2	HIV-1 tat interactive protein 2, homolog (human)	3.0	10553403	1859271	
	Hbp1	high mobility group box transcription factor 1	2.9	10399897	894659	
	Camk1d	calcium	2.6	10479852	2442190	
	Pgd	phosphogluconate dehydrogenase	2.4	10518570	97553	(*30*)
	Mocos	molybdenum cofactor sulfurase	2.4	10454353	1915841	
	Alox5ap	arachidonate 5-lipoxygenase activating protein	2.3	10527638	107505	(*30*)
	Crot	carnitine O-octanoyltransferase	2.3	10528102	1921364	
	Pik3cb	phosphatidylinositol 3-kinase, catalytic, β polypeptide	2.3	10595924	1922019	
	Lpin1	lipin 1	2.2	10399478	1891340	
	Gsr	glutathione reductase	2.1	10571274	95804	
	Mtmr10	myotubularin related protein 10	2.1	10553897	2142292	
	Ulk1	Unc-51 like kinase 1 (C.	2.1	10532472	1270126	

		elegans)				
	Calr3	calreticulin 3	2.0	10579691	1920566	
	Atp6v1a	ATPase, H+ transporting, lysosomal V1 subunit A	1.9	10439566	1201780	
	Aldh6a1	aldehyde dehydrogenase family 6, subfamily A1	1.9	10401473	1915077	
	Ephx1	epoxide hydrolase 1, microsomal	1.9	10360684	95405	
	Pgm2l1	phosphoglucomutase 2-like 1	1.9	10555303	1918224	
	Adi1	acireductone dioxygenase 1	1.9	10395058	2144929	
	Pcyox1	prenylcysteine oxidase 1	1.9	10545910	1914131	
	Hsd17b11	hydroxysteroid (17- β) dehydrogenase 11	1.8	10531919	2149821	
	Rpp38	ribonuclease P	1.8	10479749	2443607	
protein folding (*34*)	Dnajb4	DnaJ (Hsp40) homolog, subfamily B, member 4	4.9	10502823	1914285	
	Fkbpl	FK506 binding protein-like	2.0	10444436	1932127	
	Fkbp14	FK506 binding protein 14	1.8	10544885	2387639	
regulation of apoptosis (*34*)	Serpinb9	serine (or cysteine) peptidase inhibitor, clade B, memb	2.5	10404429	106603	
	Bid	BH3 interacting domain death agonist	2.2	10547531	108093	
	Bcl2l11	BCL2-like 11 (apoptosis facilitator)	2.0	10475866	1197519	
regulation of transcription, DNA-dependent (*34*)	Zbtb20	zinc finger and BTB domain containing 20	**3.6**	10435789 10435769	1929213	
	Creg1	cellular repressor of E1A-stimulated genes 1	3.5	10351347	1344382	(*30*)
	Nr1d2	nuclear receptor subfamily 1, group D, member 2	3.2	10417734	2449205	
	Bhlhb3	basic helix-loop-helix domain containing, class B3	3.1	10549276	1930704	
	Eid3	EP300 interacting inhibitor of differentiation 3	2.8	10365286	1913591	
	Phf21a	PHD finger protein 21A	2.4	10474006	2384756	
	Zscan29	zinc finger SCAN domains 29	2.4	10486712	2139317	
	Myst1	MYST histone acetyltransferase 1	2.1	10557831	1915023	
	Nfic	nuclear factor I	1.9	10371176	109591	
	Maf1	MAF1 homolog (S. cerevisiae)	1.9	10424833	1916127	
	Mafg	v-maf musculoaponeurotic fibrosarcoma oncogene family, prot	1.9	10393881	96911	
	Mapk14	mitogen-activated protein	1.8	10443391	1346865	(*30*)

		kinase 14				
	Cep290	centrosomal protein 290	1.8	10366073	2384917	
	Snapc5	small nuclear RNA activating complex, polypeptide 5	1.8	10586176	1914282	
	Rxra	retinoid X receptor α	1.8	10470446	98214	
	Bbx	bobby sox homolog (Drosophila)	1.8	10439854	1917758	
response to stress (*34*)	Srxn1	sulfiredoxin 1 homolog (S. cerevisiae)	10.3	10477061	104971	
	Gclm	glutamate-cysteine ligase , modifier subunit	7.4	10495763	104995	
	Gsta1	glutathione S-transferase, α 1 (Ya)	**6.8**	10587323 10587331	1095417	
	Hmox1	heme oxygenase (decycling) 1	6.0	10572897	96163	(*30, 31*)
	Dnajb4	DnaJ (Hsp40) homolog, subfamily B, member 4	5.3	10502823	1914285	
	Adrb2	adrenergic receptor, β 2	3.9	10459288	87938	
	Prdx1	peroxiredoxin 1	**3.1**	10507328 10436048	99523	(*32*)
	Idh1	isocitrate dehydrogenase 1 (NADP+), soluble	3.1	10355214	96413	
	Hspa1b	heat shock protein 1B	2.6	10450367	99517	
	Hspa4l	heat shock protein 4 like	2.1	10491780	107422	
	Txnrd1	thioredoxin reductase 1	2.1	10365260	1354175	
	Hsph1	heat shock 105kDa/110kDa protein 1	2.1	10535904	10535904	(*30*)
	G6pdx	glucose-6-phosphate dehydrogenase X-linked	2.0	10605338	105979	
	Apex1	apurinic	1.8	10414522	88042	
	Ahsa2	AHA1, activator of heat shock protein ATPase homolog 2 (ye	1.8	10384672	1916133	
signal transduction (*33*)	Kitl	kit ligand	3.9	10366052	96974	
	Rasgrp3	RAS, guanyl releasing protein 3	3.7	10446965	3028579	
	Cebpa	CCAAT	3.4	10552140	99480	
	Olfr26	olfactory receptor 26	3.4	10584470	109309	
	Nrp1	neuropilin 1	3.0	10576639	106206	
	Plekhm1	pleckstrin homology domain containing, family M (with RU	3.0	10391918	2443207	
	Cxcr4	chemokine (C-X-C motif) receptor 4	2.8	10357472	109563	
	Ralgps1	Ral GEF with PH domain and SH3 binding motif 1	2.7	10481804	1922008	
	Olfr933	olfactory receptor 933	2.5	10584479	3030767	
	Rasgef1b	RasGEF domain family, member 1B	2.5	10531610	2443755	
	Nkiras1	NFKB inhibitor interacting Ras-like protein 1	2.5	10412900	1916971	
	Arhgap22	Rho GTPase activating	2.4	10413951	2443418	

		protein 22				
	Spa17	sperm autoantigenic protein 17	2.2	10592336	1333778	
	Bcl6	B-cell leukemia	2.2	10438738	107187	(*30*)
	Raf1	v-raf-leukemia viral oncogene 1	2.2	10547034	97847	
	Tgfbr1	transforming growth factor, β receptor I	2.1	10504817	98728	(*30*)
	Rit1	Ras-like without CAAX 1	2.1	10493309	108053	
	Calcoco1	calcium binding and coiled coil domain 1	2.1	10433057	1914738	
	Arhgap27	Rho GTPase activating protein 27	2.0	10391895	1916903	
	Csf1r	colony stimulating factor 1 receptor	2.0	10456071	1339758	
	Ick	intestinal cell kinase	1.9	10587299	1934157	
	Srpk2	serine	1.9	10528484	1201408	
	Pld2	phospholipase D2	1.9	10377859	892877	
	Cd36	CD36 antigen	1.9	10528207	107899	
	Ptpra	protein tyrosine phosphatase, receptor type, A	1.9	10476163	97808	
	Gnat3	guanine nucleotide binding protein, α transducing 3	1.9	10519905	3588268	
	Mtss1	metastasis suppressor 1	1.8	10428857	2384818	
	Lpar1	lysophosphatidic acid receptor 1	1.8	10513256	108429	
	Tbc1d8b	TBC1 domain family, member 8B	1.8	10602020	1918101	
	Cacna1a	calcium channel, voltage-dependent, P	1.8	10573348	109482	
	Edg5	endothelial differentiation, sphingolipid G-protein-coupled	1.8	10591412	99569	
translation (*33, 34*)	Impact	imprinted and ancient	2.1	10454039	1098233	
	Eif2c3	eukaryotic translation initiation factor 2C, 3	1.8	10516348	2446634	
ubiquitin-dependent protein catabolic process (*33*)	Gclc	glutamate-cysteine ligase, catalytic subunit	8.2	10587266	104990	(*30*)
	Rnf128	ring finger protein 128	4.0	10602009	1914139	
	Fbxl20	F-box and leucine-rich repeat protein 20	2.2	10390574	1919444	
	Herc3	hect domain and RLD 3	2.1	10538658	1921248	
	Map1lc3b	microtubule-associated protein 1 light chain 3 β	2.1	10576056	1914693	
	Fbxo31	F-box protein 31	1.8	10582231	1354708	
	Fbxo30	F-box protein 30	1.8	10361748	1919115	
	Fbxl17	F-box and leucine-rich repeat protein 17	1.8	10452430	1354704	
	Rnf167	ring finger protein 167	1.8	10377927	1917760	
	Ube4b	ubiquitination factor E4B,	1.8	10518642	1927086	

		UFD2 homolog (S. cerevisiae)				
other	Arrdc3	arrestin domain containing 3	7.0	10406407	2145242	
	Zdhhc18	zinc finger, DHHC domain containing 18	2.9	10517070	3527792	(*30*)
	Gabarapl1	γ -aminobutyric acid (GABA(A)) receptor-associated protein-like 1	2.8	10542200	1914980	(*30*)
	Lrrfip2	leucine rich repeat (in FLII) interacting protein 2	1.8	10589723	1918518	

[a] Genes up-regulated ≥1.8-fold ($p \leq 0.01$) at 6 h in HNE-treated RAW 264.7 cells that are associated with (1) specific genes or gene products correlated to malarial infection or HNE exposure (references listed by gene in column 7), or (2) specific overrepresented biological processes in malaria models (references listed with ontology in column 1), are shown in the table. Fold changes (FC) represent the average of three independent biological experiments. **Bold** FC indicate that multiple probes gave analogous results (average FC is shown).

Supporting Information Table 2. Selected Genes Down-Regulated by 35 μM HNE at 6 h[a]

	gene symbol	description	fold change	Affymetrix probeset ID	MGI gene ID	ref
apoptosis (*33, 34*)	Phlda1	pleckstrin homology-like domain, family A, member 1	-2.6	10366346	1096880	
	Bcl2a1c	B-cell leukemia	-2.5	10589884	1278327	
	Ddit4	DNA-damage-inducible transcript 4	-2.5	10369290	1921997	
	Stk17b	serine	-2.4	10354588	2138162	
	Bcl2a1b	B-cell leukemia	**-2.3**	10587683 10587690 10595633	1278326	
	Tnfaip8	tumor necrosis factor, α -induced protein 8	-2.2	10455647	2147191	
	Xaf1	XIAP associated factor 1	-2.1	10378068	3772572	
cell cycle (*33*)	Lif	leukemia inhibitory factor	-11.6	10373918	96787	
	Plk1	polo-like kinase 1 (Drosophila)	-8.6	10557156	97621	
	Kif11	kinesin family member 11	-8.3	10462796	1098231	

Anln	anillin, actin binding protein (scraps homolog, Drosophila)	-7.3	10591781	1920174
Nuf2	NUF2, NDC80 kinetochore complex component, homolog (S. cere	-6.8	10359890	1914227
Kif20b	kinesin family member 20B	-5.8	10462632	2444576
Ccnb1	cyclin B1	**-5.3**	10411739 10562637 10515836	88302
Ccna2	cyclin A2	-5.1	10497831	108069
Sgol2	shugoshin-like 2 (S. pombe)	-4.8	10346365	1098767
Cdca2	cell division cycle associated 2	-4.7	10421029	1919787
Aspm	asp (abnormal spindle)-like, microcephaly associated (Droso	-4.5	10350392	1334448
Ccnf	cyclin F	-4.1	10448506	102551
Nek6	NIMA (never in mitosis gene a)-related expressed kinase 6	-4.1	10471844	1891638
Fbxo5	F-box protein 5	-4.0	10361375	1914391
Mki67	antigen identified by monoclonal antibody Ki 67	-4.0	10568714	106035
Cdc25c	cell division cycle 25 homolog C (S. pombe)	-3.9	10458195	88350
Sgol1	shugoshin-like 1 (S. pombe)	-3.3	10451805	1919665
Nek2	NIMA (never in mitosis gene a)-related expressed kinase 2	-3.2	10352767	109359
Ccng2	cyclin G2	-3.1	10523297	1095734
Spag5	sperm associated antigen 5	-3.1	10379127	1927470
Bub1b	budding uninhibited by benzimidazoles 1 homolog, β (S.	-2.9	10474769	1333889
Smc4	structural maintenance of chromosomes 4	-2.7	10492558	1917349
Gsg2	germ cell-specific gene 2	-2.6	10388234	1194498
Cks2	CDC28 protein kinase regulatory subunit 2	**-2.5**	10353004 10405185 10424779	1913447
Espl1	extra spindle poles-like 1 (S. cerevisiae)	-2.5	10427166	2146156
Ndc80	NDC80 homolog, kinetochore complex component (S. cerevisia	-2.5	10452709	1914302
Birc5	baculoviral IAP repeat-containing 5	-2.4	10382998	1203517
Ercc6l	excision repair cross-complementing rodent repair deficie	-2.4	10606071	2654144
Sass6	spindle assembly 6 homolog (C. elegans)	-2.4	10495574	1920026
Cdkn2d	cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4)	-2.3	10591517	105387
Cenpa	centromere protein A	-2.3	10520521	88375
E2f8	E2F transcription factor 8	-2.3	10563780	1922038
Sesn2	sestrin 2	-2.3	10516932	2651874
Cdc25a	cell division cycle 25 homolog A (S. pombe)	-2.2	10589420	103198

	Dbf4	DBF4 homolog (S. cerevisiae)	-2.2	10528077	1351328
	Fancd2	Fanconi anemia, complementation group D2	-2.2	10540738	2448480
	Nusap1	nucleolar and spindle associated protein 1	-2.1	10474984	2675669
	Cks1b	CDC28 protein kinase 1b	-1.8	10499639	1889208
	Nsl1	NSL1, MIND kinetochore complex component, homolog (S. cerev	-1.8	10352709	2685830
cell-cell signaling (*34*)	Pxk	PX domain containing serine	-3.3	10412624	1289230
	Agrn	agrin	-2.0	10519270	87961
	Dlg7	discs, large homolog 7 (Drosophila)	-1.9	10419323	2183453
metabolic process (*33*)	Hdc	histidine decarboxylase	-8.8	10487238	96062
	Pbk	PDZ binding kinase	-4.6	10416037	1289156
	Abca1	ATP-binding cassette, sub-family A (ABC1), member 1	-4.5	10512949	99607
	Mmp9	matrix metalloproteinase 9	-4.1	10478633	97011
	Lipg	lipase, endothelial	-3.1	10459772	1341803
	Fgr	Gardner-Rasheed feline sarcoma viral (Fgr) oncogene homolog	-3.0	10508772	95527
	Dgkh	diacylglycerol kinase, eta	-2.2	10421774	2444188
	Neil3	nei like 3 (E. coli)	-2.2	10578690	2384588
	Src	Rous sarcoma oncogene	-2.2	10477970	98397
	Fbxo15	F-box protein 15	-2.0	10457077	1354755
	Fen1	flap structure specific endonuclease 1	-2.0	10465912	102779
	Alpk1	α -kinase 1	**-1.9**	10502042 10502050 10502052	1918731
	Cry2	cryptochrome 2 (photolyase-like)	-1.9	10485170	1270859
	Mthfs	5, 10-methenyltetrahydrofolate synthetase	**-1.9**	10587695 10595630	1340032
	Rara	retinoic acid receptor, α	-1.9	10381082	97856
	Anp32a	acidic (leucine-rich) nuclear phosphoprotein 32 family, m	-1.8	10586064	108447
	Nab2	Ngfi-A binding protein 2	-1.8	10373313	
	Pdss1	prenyl (solanesyl) diphosphate synthase, subunit 1	-1.8	10469712	1889278
	Pgs1	phosphatidylglycerophosphate synthase 1	-1.8	10383012	1921701
	Psmb10	proteasome (prosome, macropain) subunit, β type 10	-1.8	10581378	1096380
	Rad54l	RAD54 like (S. cerevisiae)	-1.7	10515257	894697
cytokine and chemokine mediated signaling pathway (*33*)	Stat1	signal transducer and activator of transcription 1	-2.2	10346191	103063
	Stat5a	signal transducer and activator of transcription 5A	-2.1	10381172	103036
	Stat3	signal transducer and activator	-2.0	10391301	103038

		of transcription 3			
	Jak2	Janus kinase 2	-1.8	10462363	96629
defense response (*33, 34*)	Mx2	myxovirus (influenza virus) resistance 2	-7.9	10437224	97244
	Saa3	serum amyloid A 3	-7.3	10563597	98223
	Ccr1	chemokine (C-C motif) receptor 1	-3.2	10598004	104618
	Sp110	Sp110 nuclear body protein	**-2.6**	10347928 10356278 10582874	1923364
	Hck	hemopoietic cell kinase	-2.3	10477250	96052
	Penk1	preproenkephalin 1	-2.0	10511363	104629
	Sbno2	strawberry notch homolog 2 (Drosophila)	-2.0	10370721	2448490
immune response (*33, 34*)	Il1a	interleukin 1 α	-67.1	10487588	96542
	Il6	interleukin 6	-46.9	10520452	96559
	Il1b	interleukin 1 β	-33.7	10487597	96543
	Il1f6	interleukin 1 family, member 6	-12.8	10469793	1859324
	Cfb	complement factor B	-7.4	10450325	105975
	H28	histocompatibility 28	-6.9	10502801	95975
	Il1rn	interleukin 1 receptor antagonist	-6.9	10469816	96547
	Il27	interleukin 27	-6.5	10567987	2384409
	Gbp5	guanylate nucleotide binding protein 5	-6.3	10496539	2429943
	Il10	interleukin 10	-5.4	10349603	96537
	Oasl2	2'-5' oligoadenylate synthetase-like 2	-5.1	10524621	1344390
	Clec2d	C-type lectin domain family 2, member d	-4.7	10542156	2135589
	Rsad2	radical S-adenosyl methionine domain containing 2	-4.7	10399710	1929628
	Cd40	CD40 antigen	-4.3	10478678	88336
	Il1rl1	interleukin 1 receptor-like 1	-4	10345791	98427
	Cd300lf	CD300 antigen like family member F	-3.9	10392845	2442359
	Gbp3	guanylate nucleotide binding protein 3	-3.8	10496580	1926263
	Ccl6	chemokine (C-C motif) ligand 6	-3.4	10389222	98263
	Irf7	interferon regulatory factor 7	-3.4	10569102	1859212
	Gbp1	guanylate nucleotide binding protein 1	-3.1	10496555	95666
	Il18rap	interleukin 18 receptor accessory protein	-3.0	10345824	1338888
	Il4ra	interleukin 4 receptor, α	-2.9	10557326	105367
	Cxcl14	chemokine (C-X-C motif) ligand 14	-2.8	10409579	1888514
	Clec4n	C-type lectin domain family 4, member n	-2.7	10541605	1861231
	Irf8	interferon regulatory factor 8	-2.5	10576034	96395
	Il18	interleukin 18	-2.3	10585194	107936
	Pou2f2	POU domain, class 2, transcription factor 2	-2.1	10560964	101897

	Clec12a	C-type lectin domain family 12, member a	-2	10542164	3040968
	Clec5a	C-type lectin domain family 5, member a	-1.9	10544273	1345151
	Ercc1	excision repair cross-complementing rodent repair deficien	-1.8	10550650	95412
	Ltb	lymphotoxin B	-1.8	10444752	104796
	Traf3ip2	Traf3 interacting protein 2	-1.8	10362615	2143599
inflammatory response (*33, 34*)	Ccl2	chemokine (C-C motif) ligand 2	-47.2	10379511	98259
	Ccl7	chemokine (C-C motif) ligand 7	-22.6	10379518	99512
	Ccl22	chemokine (C-C motif) ligand 22	-13.0	10574213	1306779
	Fcgr2b	Fc receptor, IgG, low affinity IIb	-7.7	10360028	95499
	Fcgr1	Fc receptor, IgG, high affinity I	-4.4	10500335	
	Cd44	CD44 antigen	-2.7	10485405	88338
	Aoah	acyloxyacyl hydrolase	-2.3	10403871	1350928
	Ccl4	chemokine (C-C motif) ligand 4	-2.2	10379721	98261
	Cd86	CD86 antigen	-1.8	10439312	101773
	Jmjd3	jumonji domain containing 3	-1.8	10387372	2448492
intracellular protein transport (*34*)	Ap1s3	adaptor-related protein complex AP-1, σ 3	-2.2	10355967	1891304
	Tacc3	transforming, acidic coiled-coil containing protein 3	-2.1	10521090	1341163
	Kpna2	karyopherin (importin) α 2	**-2.0**	10392284 10453512 10497503	103561
	Rffl	ring finger and FYVE like domain containing protein	-1.8	10389087	1914588
regulation of apoptosis (*34*)	Csf2	colony stimulating factor 2 (granulocyte-macrophage)	-14.0	10385912	1339752
	Bcl2l1	Bcl2-like 1	-3.7	10488655	88139
	Notch1	Notch gene homolog 1 (Drosophila)	-3.5	10481056	97363
	Casp4	caspase 4, apoptosis-related cysteine peptidase	-2.2	10582997	107700
	Casp7	caspase 7	-2.0	10464128	109383
	Hells	helicase, lymphoid specific	-2.0	10462973	106209
	Ier3	immediate early response 3	-2.0	10444890	104814
regulation of transcription, DNA-dependent (*34*)	Trim30	tripartite motif-containing 30	-7.2	10566358	98178
	Mxd1	MAX dimerization protein 1	-4.7	10545921	96908
	Jdp2	Jun dimerization protein 2	-4.3	10397351	1932093
	Top2a	topoisomerase (DNA) II α	-3.7	10390707	98790
	Nfkbiz	nuclear factor of κ light polypeptide gene enhancer i	-3.4	10439936	1931595
	Nr1d1	nuclear receptor subfamily 1, group D, member 1	-3.4	10390691	2444210
	Axud1	AXIN1 up-regulated 1	-3.0	10597758	2387989
	Bhlhb2	basic helix-loop-helix domain	-3.0	10540472	1097714

		containing, class B2			
	Osm	oncostatin M	-3.0	10373912	104749
	Klf7	Kruppel-like factor 7 (ubiquitous)	-2.6	10355141	1935151
	Foxm1	forkhead box M1	-2.5	10542079	1347487
	Asf1b	ASF1 anti-silencing function 1 homolog B (S. cerevisiae)	-2.4	10573261	1914179
	Foxp1	forkhead box P1	-2.4	10546661	1914004
	Nr4a1	nuclear receptor subfamily 4, group A, member 1	-2.3	10427035	1352454
	Carhsp1	calcium regulated heat stable protein 1	**-2.1**	10437590 10497752	1196368
	Hivep3	human immunodeficiency virus type I enhancer binding prot	-2	10507677	106589
	Id1	inhibitor of DNA binding 1	-2.0	10477169	96396
	Zfp367	zinc finger protein 367	-2.0	10410092	2442266
	Plagl2	pleiomorphic adenoma gene-like 2	-1.9	10488697	1933165
	Zfp36	zinc finger protein 36	-1.9	10561453	99180
	Akna	AT-hook transcription factor	-1.8	10513666	2140340
	Arid5a	AT rich interactive domain 5A (Mrf1 like)	-1.8	10345445	2443039
	Batf2	basic leucine zipper transcription factor, ATF-like 2	-1.8	10460767	1921731
	Hivep2	human immunodeficiency virus type I enhancer binding prot	-1.8	10361807	1338076
	Hlx	H2.0-like homeobox	-1.8	10360834	96109
	Ikzf1	IKAROS family zinc finger 1	-1.8	10374333	1342540
	Nfkb1	nuclear factor of κ light polypeptide gene enhancer in	-1.8	10502299	97312
	Nufip1	nuclear fragile X mental retardation protein interacting	-1.8	10416510	1351474
	Pcgf5	polycomb group ring finger 5	-1.8	10462683	1923505
	Thra	thyroid hormone receptor α	-1.8	10381006	98742
response to stress (*34*)	F3	coagulation factor III	-5.6	10495675	88381
	Gen1	Gen homolog 1, endonuclease (Drosophila)	-5.2	10399391	2443149
	Blm	Bloom syndrome homolog (human)	-3.4	10564978	1328362
	Ifi47	interferon γ inducible protein 47	-3.0	10375515	99448
	Ddx58	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	-2.5	10512067	2442858
	Trip13	thyroid hormone receptor interactor 13	-2.4	10410560	1916966
	Dhx58	DEXH (Asp-Glu-X-His) box polypeptide 58	-2.2	10391207	1931560
	Polq	polymerase (DNA directed), theta	-2.2	10435581	2155399
	Ifih1	interferon induced with helicase C domain 1	-2.0	10483110	1918836
	Eme1	essential meiotic endonuclease 1 homolog 1 (S. pombe)	-1.9	10390050	3576783
	Atad5	ATPase family, AAA domain containing 5	-1.8	10379363	2442925

	Cry1	cryptochrome 1 (photolyase-like)	-1.8	10371400	1270841
	Rad51	RAD51 homolog (S. cerevisiae)	-1.8	10474902	97890
signal transduction (*33*)	Gpr109a	G protein-coupled receptor 109A	-10	10533720	1933383
	Edn1	endothelin 1	-9.2	10404783	95283
	Rnd1	Rho family GTPase 1	-6.7	10432236	2444878
	Adora2b	adenosine A2b receptor	-5.5	10376832	99403
	Ms4a6c	membrane-spanning 4-domains, subfamily A, member 6C	-3.6	10461614	2385644
	Itgal	integrin α L	-3.1	10557591	96606
	Arhgef3	Rho guanine nucleotide exchange factor (GEF) 3	-3.0	10413419	1918954
	Bcar3	breast cancer anti-estrogen resistance 3	-3.0	10495781	1352501
	Cish	cytokine inducible SH2-containing protein	-3.0	10588577	103159
	Rassf2	Ras association (RalGDS	-2.9	10487894	2442060
	Arhgap11a	Rho GTPase activating protein 11A	-2.7	10485963	2444300
	Cysltr1	cysteinyl leukotriene receptor 1	-2.7	10606355	1926218
	Pscd4	pleckstrin homology, Sec7 and coiled	-2.6	10425092	2441702
	Mt2	metallothionein 2	-2.5	10574023	97172
	Itgam	integrin α M	-2.3	10557862	96607
	Ms4a6d	membrane-spanning 4-domains, subfamily A, member 6D	-2.3	10466210	1916024
	Wdr67	WD repeat domain 67	-2.2	10424221	2684931
	P2ry2	purinergic receptor P2Y, G-protein coupled 2	-2.1	10565962	105107
	Pik3cd	phosphatidylinositol 3-kinase catalytic delta polypeptide	-2.1	10518686	1098211
	Bcl3	B-cell leukemia	-2.0	10560685	88140
	Ccl17	chemokine (C-C motif) ligand 17	-2.0	10574226	1329039
	Fpr3	formyl peptide receptor 3	-2.0	10442098	1194495
	Irak3	interleukin-1 receptor-associated kinase 3	-2.0	10372781	1921164
	Eif2ak2	eukaryotic translation initiation factor 2- α kinase	-1.9	10452980	1353449
	Lyn	Yamaguchi sarcoma viral (v-yes-1) oncogene homolog	-1.9	10503098	96892
	Hus1	Hus1 homolog (S. pombe)	-1.8	10384322	1277962
	Per1	period homolog 1 (Drosophila)	-1.8	10377439	1098283
	Ptger4	prostaglandin E receptor 4 (subtype EP4)	-1.8	10427461	104311
translation (*33, 34*)	Denr	density-regulated protein	-2.3	10525657	1915434
	Ppp1r15b	protein phosphatase 1, regulatory (inhibitor) subunit 1	-1.8	10349868	2444211
ubiquitin-dependent protein catabolic process (*33*)	Socs3	suppressor of cytokine signaling 3	**-5.1**	10383010 10393449	1201791

	Usp18	ubiquitin specific peptidase 18	-3.7	10541307	1344364
	Tnfaip3	tumor necrosis factor, α -induced protein 3	-3.0	10368144	1196377
	Herc5	hect domain and RLD 5	-2.5	10538590	1914388
	Cdc20	cell division cycle 20 homolog (S. cerevisiae)	-2.2	10515744	1859866
	Isg15	ISG15 ubiquitin-like modifier	-2.2	10451287	1855694
	Ube2c	ubiquitin-conjugating enzyme E2C	-2.0	10478572	1915862
	Uhrf1	ubiquitin-like, containing PHD and RING finger domains, 1	-1.9	10446074	1338889
	Rabgef1	RAB guanine nucleotide exchange factor (GEF) 1	-1.8	10526133	1929459
	Ube2l6	ubiquitin-conjugating enzyme E2L 6	-1.8	10473356	1914500
	Usp37	ubiquitin specific peptidase 37	-1.8	10355582	2442483
other	Ifit2	interferon-induced protein with tetratricopeptide repeats 2	-6.5	10462613	99449
	Ifi205	interferon activated gene 205	-4.3	10360406	101847
	Ifit1	interferon-induced protein with tetratricopeptide repeats 1	-4.0	10462623	99450
	Ifi202b	interferon activated gene 202B	-3.9	10360398	1347083
	Ifi204	interferon activated gene 204	-3.9	10360382	96429
	Ifit3	interferon-induced protein with tetratricopeptide repeats 3	-3.8	10462618	1101055
	Ifi203	interferon activated gene 203	-3.7	10360391	96428
	Samsn1	SAM domain, SH3 domain and nuclear localization signals, 1	-3.5	10440393	1914992
	Ifitm2	interferon induced transmembrane protein 2	-1.9	10553299	1933382

[a] Genes down-regulated ≤1.8-fold ($p \leq 0.01$) at 6 h in HNE-treated RAW 264.7 cells that are associated with specific overrepresented biological processes in malaria models (references listed with ontology in column 1) are shown in the table. Fold changes (FC) represent the average of three independent biological experiments. **Bold** FC indicate that multiple probes gave analogous results (average FC is shown).

Supporting Information Table 3. Selected Genes Down-Regulated by 35 μM HNE at 24 h[a]

	gene symbol	description	fold change	ABI probeset ID	MGI gene ID
apoptosis (*33*, *34*)	Sgk	serum/glucocorticoid regulated kinase	-6.6	929684	1340062
	Axud1	AXIN1 up-regulated 1	-1.8	907214	2387989

cell cycle (*33*)	Slfn1	schlafen 1	-15.0	371033	1313259
	Sass6	spindle assembly 6 homolog (C. elegans)	-4.6	881483	1920026
	Nbn	nibrin	-3.4	430613	1351625
	Plekho1	pleckstrin homology domain containing, family O member 1	-2.4	624539	1914470
	Als2cr2	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 2 (human)	-2.3	358886	2144047
	Pols	polymerase (DNA directed) σ	-1.9	732359	2682295
cell-cell signaling (*34*)	Kif1b	kinesin family member 1B	-5.8	744344	108426
	Tsc1	tuberous sclerosis 1	-3.1	550748	1929183
	Gata3	GATA binding protein 3	-2.3	580073	95663
	Ly6e	lymphocyte antigen 6 complex, locus E	-2.3	927958	106651
metabolic process (*33*)	Avil	advillin	-8.1	530983	1333798
	Dio2	deiodinase, iodothyronine, type II	-6.9	738397	1338833
cytokine and chemokine mediated signaling pathway (*33*)	Stat1	signal transducer and activator of transcription 1	-10.8	433757	103063
	Il6st	interleukin 6 signal transducer	-2.7	647028	96560
defense response (*33*, *34*)	(*33*)	myxovirus (influenza virus) resistance 2	-43.4	837469	97244
	Irgm	immunity-related GTPase family, M	-15.0	804608	107567
	Dhx58	DEXH (Asp-Glu-X-His) box polypeptide 58	-7.9	659648	1931560
	B2m	β -2 microglobulin	-2.5	501966	88127
immune response (*33*, *34*)	Irf7	interferon regulatory factor 7	-51.3	345690	1859212
	Ddx58	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	-17.4	439516	2442858
	Ibrdc3	IBR domain containing 3	-2.2	695308	1922484
inflammatory response (*33*, *34*)	Ccl5	chemokine (C-C motif) ligand 5	-22.7	516139	98262
	Fcgr1	Fc receptor, IgG, high affinity I	-13.6	922856	95498
	Il6	interleukin 6	-11.2	924312	96559
	Fcgr2b	Fc receptor, IgG, low affinity IIb	-2.9	930585	95499
	Ccl7	chemokine (C-C motif) ligand 7	-2.3	562485	99512
regulation of apoptosis (*34*)	Ern1	endoplasmic reticulum (ER) to nucleus signalling 1	-12.3	749047	1930134
	Tsc22d3	TSC22 domain family 3	-3.6	700170	1196284
	Traf3	Tnf receptor-associated factor 3	-2.3	613464	108041
	Casp1	caspase 1	-2.0	924714	96544
regulation of transcription, DNA-dependent (*34*)	Gatad2b	GATA zinc finger domain containing 2B	-3.9	332294	2443225
	Ssbp3	single-stranded DNA binding protein 3	-2.7	602705	1919725
	Tspyl2	TSPY-like 2	-2.5	526767	106244
	Usf2	upstream transcription factor 2	-2.1	532994	99961
	Pcgf5	polycomb group ring finger 5	-2.1	315886	1923505
	Zfp30	zinc finger protein 30	-2.0	919271	99178
response to stress (*34*)	Gna13	guanine nucleotide binding protein, α 13	-2.5	576697	95768

	Insig2	insulin induced gene 2	-2.3	603014	1920249
signal transduction (*33*)	Rassf8	Ras association (RalGDS/AF-6) domain family 8	-5.0	704046	1918573
	Rgs1	regulator of G-protein signaling 1	-3.9	923224	1354694
	Nr3c1	nuclear receptor subfamily 3, group C, member 1	-3.0	477364	95824
	Tbc1d12	TBC1D12: TBC1 domain family, member 12	-2.6	360619	2384803
	Spry1	sprouty homolog 1 (Drosophila)	-1.9	404045	1345139
translation (*33, 34*)	Mknk1	MAP kinase-interacting serine/threonine kinase 1	-5.5	679668	894316
	Eif2c2	eukaryotic translation initiation factor 2C, 2	-5.2	526883	2446632
	Impact	imprinted and ancient	-4.4	627739	1098233
	Eif2c3	eukaryotic translation initiation factor 2C, 3	-3.6	526537	2446634
ubiquitin-dependent protein catabolic process (*33*)	Usp18	ubiquitin specific peptidase 18	-100.0	446807	1344364
	Fbxo39	F-box protein 39	-87.4	642750	3505735
	Fem1c	fem-1 homolog c (C.elegans)	-4.1	762818	2444737
	Wsb2	WD repeat and SOCS box-containing 2	-2.6	740571	2144041
	Ube2l6	ubiquitin-conjugating enzyme E2L 6	-2.3	401185	1914500
	Sumo3	SMT3 suppressor of mif two 3 homolog 3 (yeast)	-2.0	463700	1336201
	Fbxl20	F-box and leucine-rich repeat protein 20	-2.0	331560	1919444

[a] Genes down-regulated ≤1.8-fold ($p \leq 0.01$) at 24 h in HNE-treated RAW 264.7 cells that are associated with specific overrepresented biological processes in malaria models (references listed with ontology in column 1) are shown in the table. Fold changes (FC) represent the average of three independent biological experiments.

Supporting Information Table 4. Selected Genes Up-Regulated by 35 μM HNE at 24 h[a]

	gene symbol	description	fold change	ABI probeset ID	MGI gene ID	ref
apoptosis (*33, 34*)	Pdcd8	programmed cell death 8	2.1	26926	1349419	
	Stk3	serine/threonine kinase 3 (Ste20, yeast homolog)	1.9	56274	1928487	
	Tnfaip8	tumor necrosis factor, α -induced protein 8	1.9	106869	2147191	
cell cycle (*33*)	Nek2	NIMA (never in mitosis gene a)-related expressed kinase 2	17.0	18005	109359	
	Psmc3ip	proteasome (prosome,	6.4	19183	1098610	

		macropain) 26S subunit, ATPase 3, interacting protein				
	Zbtb36	zinc finger and BTB domain containing 36	2.3	207259	2443302	
	Atm	ataxia telangiectasia mutated homolog (human)	1.9	11920	107202	(*30*)
cell-cell signaling (*34*)	Dlg7	discs, large homolog 7 (Drosophila)	12.1	218977	2183453	
	Wnt6	wingless-related MMTV integration site 6	4.4	22420	98960	
	Cadps	Ca<2+>dependent activator protein for secretion	2.2	27062	1350922	
	Hprt1	hypoxanthine guanine phosphoribosyl transferase 1	1.9	15452	96217	
metabolic process (*33*)	Asf1b	ASF1 anti-silencing function 1 homolog B (S. cerevisiae)	9.7	66929	1914179	
	Car12	carbonic anyhydrase 12	4.7	76459	1923709	
defense response (*33*, *34*)	Cias1	cold autoinflammatory syndrome 1 homolog (human)	8.3	216799	2653833	
	Ccl17	chemokine (C-C motif) ligand 17	3.1	20295	1329039	
	Fgr	Gardner-Rasheed feline sarcoma viral (Fgr) oncogene homolog	2.8	14191	95527	
immune response (*33*, *34*)	Csf3	colony stimulating factor 3 (granulocyte)	17.5	12985	1339751	
	Tnf	tumor necrosis factor	8.7	21926	104798	(*9*, *10*, *33*, *72*)
	Clec5a	C-type lectin domain family 5, member a	5.0	23845	1345151	
	Raet1e	retinoic acid early transcript 1E	3.8	379043	2675273	
	Il10ra	Interleukin 10 receptor α	3.7	340636	96538	(*31*)
	Cxcl1	chemokine (C-X-C motif) ligand 1	2.7	14825	108068	
	Nfam1	Nfat activating molecule with ITAM motif 1	**2.7**	623312 489525	1921289	
	Tgfb1	transforming growth factor, β 1	2.0	21803	98725	
inflammatory response (*33*, *34*)	Pla2g7	phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma)	10.7	27226	1351327	
	C5r1	Complement component 5, receptor 1	3.4	338868	88232	(*30*, *31*)
	Nlrc4	NLR family, CARD domain containing 4	2.7	268973	3036243	
	Cd14	CD14 antigen	2.2	12475	88318	(*30*)
intracellular protein transport (*34*)	Nup85	nucleoporin 85	3.3	445007	3046173	
	Prdx1	peroxiredoxin 1	**2.9**	18477 545161	99523	(*32*)

	Pcna	proliferating cell nuclear antigen	2.3	18538	97503	
	Pex7	peroxisome biogenesis factor 7	2.0	18634	1321392	
	Nup210	nucleoporin 210	1.9	54563	1859555	
metabolic process (*33*)	Echdc3	enoyl Coenzyme A hydratase domain containing 3	5.4	67856	1915106	
	Gnaq	guanine nucleotide binding protein, α q polypeptide	3.0	14682	95776	
	Suclg1	succinate-CoA ligase, GDP-forming, α subunit	1.8	56451	1927234	
protein folding (*34*)	Ppid	peptidylprolyl isomerase D (cyclophilin D)	3.3	67738	1914988	
	Ppil1	peptidylprolyl isomerase (cyclophilin)-like 1	2.5	68816	1916066	
regulation of apoptosis (*34*)	Birc5	baculoviral IAP repeat-containing 5	27.4	11799	1203517	
	Mmp9	matrix metalloproteinase 9	5.2	17395	97011	(*30*)
	Igf1	insulin-like growth factor 1	2.1	16000	96432	
regulation of transcription, DNA-dependent (*34*)	Top2a	topoisomerase (DNA) II α	13.2	21973	98790	
	Mcm6	minichromosome maintenance deficient 6 (MIS5 homolog, S. pombe) (S. cerevisiae)	6.0	17219	1298227	
	Tbl1xr1	transducin (β)-like 1X-linked receptor 1	3.5	81004	2441730	
	Bzw1	basic leucine zipper and W2 domains 1	2.9	66882	1914132	
	Hmga2	high mobility group AT-hook 2	2.1	15364	101761	
response to stress (*34*)	Rad51	RAD51 homolog (S. cerevisiae)	16.4	19361	97890	
	Pole	polymerase (DNA directed), ε	15.4	18973	1196391	
	Sod2	superoxide dismutase 2, mitochondrial	9.1	20656	98352	(*30, 31*)
	Tacc3	transforming, acidic coiled-coil containing protein 3	7.3	21335	1341163	
	Trip13	thyroid hormone receptor interactor 13	7.1	69716	1916966	
	Msh5	mutS homolog 5 (E. coli)	6.1	17687	1329021	
signal transduction (*33*)	Pilra	paired immunoglobin-like type 2 receptor α	13.5	640067	2450529	
	Rasgrp3	RAS, guanyl releasing protein 3	4.4	240168	3028579	
	Rab11a	RAB11a, member RAS oncogene family	4.3	53869	1858202	
	Igbp1b	immunoglobulin (CD79A) binding protein 1b	2.8	50540	1354380	
	Gpr183	G protein-coupled receptor 183	2.3	321019	2442034	
translation (*33, 34*)	Eif4e	eukaryotic translation initiation factor 4E	4.2	13684	95305	

	Eif4e2	eukaryotic translation initiation factor 4E member 2	3.4	26987	1914440	
	Pa2g4	proliferation-associated 2G4	2.3	18813	894684	
	Eif5a	eukaryotic translation initiation factor 5A	**1.9**	549097 925942	106248	
	Pet112l	PET112-like (yeast)	1.8	229487	2442496	
ubiquitin-dependent protein catabolic process (*33*)	Ube2t	ubiquitin-conjugating enzyme E2T (putative)	7.1	67196	1914446	
	Fbxo5	F-box only protein 5	4.4	67141	1914391	
	Ggnbp1	gametogenetin binding protein 1	3.5	70772	3055306	
	Fbxo22	F-box only protein 22	3.0	71999	1926014	
	Ube2i	ubiquitin-conjugating enzyme E2I	3.0	22196	107365	
	Ube2d3	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	2.4	66105	1913355	
	Bre	brain and reproductive organ-expressed protein	1.9	107976	1333875	
other	Gsn	Gelsolin	2.5	437857	95851	(*30*)
	Rad23a	RAD23a homolog (S. cerevisiae)	2.2	330310	105126	(*30*)

[a] Genes up-regulated ≥1.8-fold ($p \leq 0.01$) at 24 h in HNE-treated RAW 264.7 cells that are associated with (1) specific genes or gene products correlated to malarial infection or HNE exposure (references listed by gene in column 7), or (2) specific overrepresented biological processes in malaria models (references listed with ontology in column 1) are shown in the table. Fold changes (FC) represent the average of three independent biological experiments. **Bold** FC indicate that multiple probes gave analogous results (average FC is shown).

Table 5. Selected Genes Up-Regulated by 0.1 mg/mL BH at 6 h[a]

	gene symbol	description	fold change	Affymetrix probeset ID	MGI gene ID	ref
cell cycle (*33*)	Rps6ka2	ribosomal protein S6 kinase, polypeptide 2	2.6	10441565	1342290	
	Plk2	polo-like kinase 2 (Drosophila)	2.2	10407126	1099790	
	Plekho1	pleckstrin homology domain containing, family O member 1	1.9	10500295	1914470	
immune response (*33*, *34*)	Fabp3	fatty acid binding protein 3, muscle and heart	**4.2**	10371502 10508614	95476	
	F10	coagulation factor X	2.7	10570291	103107	
	Il7r	interleukin 7 receptor	2.6	10427628	96562	

	Hmox1	heme oxygenase (decycling) 1	2.5	10572897	96163	(*30*, *31*)
	Aadacl1	arylacetamide deacetylase-like 1	1.9	10491083	2443191	
	Eno2	enolase 2, γ neuronal	1.8	10547807	95394	
	Mtmr10	myotubularin related protein 10	1.8	10553897	2142292	
signal transduction (*33*)	Gprc5a	G protein-coupled receptor, family C, group 5, member A	2.3	10542335	1891250	
	Bcar3	breast cancer anti-estrogen resistance 3	1.9	10495781	1352501	
	Plxna2	plexin A2	1.9	10352867	107684	
	Adra1a	adrenergic receptor, α 1a	1.8	10416099	104773	
	Plekhm1	pleckstrin homology domain containing, family M (with RU	1.8	10391918	2443207	
	Gpr176	G protein-coupled receptor 176	1.7	10486102	2685858	
other	Slamf7		3.4	10360173		(*31*)
	Hk3		1.8	10409376		(*30*)

[a] Genes up-regulated $\geq$1.8-fold ($p \leq 0.01$) at 6 h in BH-treated RAW 264.7 cells that are associated with (1) specific genes or gene products correlated to malarial infection or HNE exposure (references listed by gene in column 7), or (2) specific overrepresented biological processes in malaria models (references listed with ontology in column 1) are shown in the table. Fold changes (FC) represent the average of three independent biological experiments. **Bold** FC indicate that multiple probes gave analogous results (average FC is shown).

Supporting Information Table 6. Selected Genes Down-Regulated by 0.1 mg/mL BH at 6 h[a]

	gene symbol	description	fold change	ABI probeset ID	MGI gene ID
immune response (*33*, *34*)	Csf2	colony stimulating factor 2 (granulocyte-macrophage)	-3.0	10385912	1339752
	Il1rl1	interleukin 1 receptor-like 1	-2.0	10345791	98427
metabolic process (*33*)	Dusp2	dual specificity phosphatase 2	-1.8	10475782	101911
	Gfod1	glucose-fructose oxidoreductase domain containing 1	-1.8	10408879	2145304
	Phlda1	pleckstrin homology-like domain, family A, member 1	-1.8	10366346	1096880

[a] Genes down-regulated more than 1.8-fold ($p \leq 0.01$) at 6 h in BH-treated RAW 264.7 cells that are associated with specific overrepresented biological processes in malaria models (references listed with ontology in column 1) are shown in the table. Fold changes (FC) represent the average of three independent biological experiments.

Supporting Information Table 7. Selected Genes Down-Regulated by 0.1 mg/mL BH at 24 h[a]

	gene symbol	description	fold change	ABI probeset ID	MGI gene ID
cell cycle (*33*)	Hectd3	HECT domain containing 3	-70.8	567598	1923858
	Smarcb1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1	-3.0	889629	1328366
	Mre11a	meiotic recombination 11 homolog A (S. cerevisiae)	-2.6	553944	1100512
	Smc4l1	SMC4 structural maintenance of chromosomes 4-like 1 (yeast)	-2.1	789567	1917349
	Camk2g	calcium/calmodulin-dependent protein kinase II γ	-2.0	390021	88259
	Camk2b	calcium/calmodulin-dependent protein kinase II, β	-1.9	868597	88257
cell-cell signaling (*34*)	Rab3a	RAB3A, member RAS oncogene family	-2.1	914789	97843
metabolic process (*33*)	Alas2	aminolevulinic acid synthase 2, erythroid	-9.3	880116	87990
	Rpap1	RNA polymerase II associated protein 1	-7.8	587339	1916175
	Pdgfb	platelet derived growth factor, B polypeptide	-6.0	788848	97528
	Pomt1	protein-O-mannosyltransferase 1	-3.4	914042	2138994
regulation of apoptosis (*34*)	Tnfsf13b	tumor necrosis factor (ligand) superfamily, member 13b	-4.7	386868	1344376
	Bok	Bcl-2-related ovarian killer protein	-4.3	364104	1858494
regulation of transcription, DNA-dependent (*34*)	Setdb1	SET domain, bifurcated 1	-47.8	751594	1934229
	Fos	FBJ osteosarcoma oncogene	-3.6	463565	95574
	Esrra	estrogen related receptor, α	-2.6	923547	1346831

	Yeats2	YEATS domain containing 2	-2.0	654721	2447762
	Asxl2	additional sex combs like 2 (Drosophila)	-1.9	540321	1922552
signal transduction (*33*)	Wfikkn2	WAP, follistatin/kazal, immunoglobulin, kunitz and netrin domain containing 2	-24.5	419373	2669209
	Olfr112	olfactory receptor 112	-6.1	690941	2177495
	Cdgap	Cdc42 GTPase-activating protein	-4.7	827470	1333857
	Ms4a6b	membrane-spanning 4-domains, subfamily A, member 6B	-3.5	920843	1917024
	Dner	delta/notch-like EGF-related receptor	-2.9	618695	2152889
	Frag1	FGF receptor activating protein 1	-1.9	431551	2385286
	Irf3	interferon regulatory factor 3	-1.8	925384	1859179
translation (*33, 34*)	Eif2s3x	eukaryotic translation initiation factor 2, subunit 3, structural gene X-linked	-4.1	772876	1349431
	Pars2	prolyl-tRNA synthetase (mitochondrial)(putative)	-1.9	606179	2386296
ubiquitin-dependent protein catabolic process (*33*)	Pja2	praja 2, RING-H2 motif containing	-50.5	656636	2159342
	Ube2r2	ubiquitin-conjugating enzyme E2R 2	-2.6	546015	1914865

[a] Genes down-regulated more than 1.8-fold ($p \leq 0.01$) at 6 h in HNE-treated RAW 264.7 cells that are associated with specific overrepresented biological processes in malaria models (references listed with ontology in column 1) are shown in the table. Fold changes (FC) represent the average of three independent biological experiments.

Supporting Information Table 8. Selected Genes Up-Regulated by 0.1 mg/mL BH at 24 h[a]

	gene symbol	description	fold change	ABI probeset ID	MGI gene ID	ref
cell cycle (*33*)	Ereg	epiregulin	12.8	593765	107508	
	Cops5	COP9 (constitutive photomorphogenic) homolog, subunit 5 (Arabidopsis thaliana)	1.9	330594	1349415	
metabolic process (*33*)	Pcsk2	proprotein convertase subtilisin/kexin type 2	7.4	732125	97512	
	Ppie	peptidylprolyl isomerase E (cyclophilin E)	3.6	530121	1917118	
	Stard4	StAR-related lipid transfer (START) domain containing 4	3.1	551930	2156764	
	Blvra	biliverdin reductase A	2.2	664457	88170	

	Dusp14	dual specificity phosphatase 14	2.1	928759	1927168	
immune response (*33, 34*)	Il1a	interleukin 1 α	6.0	595893	96542	
	Ccl6	chemokine (C-C motif) ligand 6	5.3	928327	98263	
	Tollip	toll interacting protein	2.5	858428	1891808	
	Il20	interleukin 20	2.4	879278	1890473	
	H2-T23	histocompatibility 2, T region locus 23	2.2	558496	95957	
intracellular protein transport (*34*)	Srp9	signal recognition particle 9	2.1	927925	1350930	
metabolic process	Gpt1	glutamic pyruvic transaminase 1, soluble	2.6	556768	95802	
regulation of transcription, DNA-dependent (*34*)	Irf4	interferon regulatory factor 4	4.6	386166	1096873	
	Taf7	TAF7 RNA polymerase II, TATA box binding protein (TBP)-associated factor	3.4	535868	1346348	
	Rnpc2	RNA-binding region (RNP1, RRM) containing 2	3.0	528719	2157953	
	Rqcd1	rcd1 (required for cell differentiation) homolog 1 (S. pombe)	1.8	686770	1928902	
signal transduction (*33*)	Rab33a	RAB33A, member of RAS oncogene family	2.8	732409	109493	
	Olfr313	olfactory receptor 313	2.2	721885	3030147	
	Gipc1	GIPC PDZ domain containing family, member 1	2.1	794773	1926252	
	Rhebl1	Ras homolog enriched in brain like 1	1.9	456283	1916409	
ubiquitin-dependent protein catabolic process (*33*)	Rbx1	ring-box 1	3.2	494826	1891829	
	Asb1	ankyrin repeat and SOCS box-containing protein 1	2.1	569408	1929735	
	Ube2l3	ubiquitin-conjugating enzyme E2L 3	2.0	336987	109240	
other	Cd2	CD2 antigen	95.7	919536	88320	(*31, 33*)
	Pstpip2	proline-serine-threonine phosphatase-interacting protein 2	6.1	725778	1335088	(*30*)

[a] Genes up-regulated more than 1.8-fold ($p \leq 0.01$) at 6 h in HNE-treated RAW 264.7 cells that are associated with (1) specific genes or gene products correlated to malarial infection or HNE exposure (references listed by gene in column 7), or (2) specific overrepresented biological processes in malaria models (references listed with ontology in column 1) are shown in the table. Fold changes (FC) represent the average of three independent biological experiments.

Supporting Information Table 9. Common Genes Differentially Regulated by 0.1 mg/mL BH and 35 μM HNE[a]

gene symbol	description	probe ID	time (h)	fold change		MGI gene ID
				BH	HNE	
Il1rl1	interleukin 1 receptor-like 1	10345791	6	-2.0	-4.0	98427
Phlda1	pleckstrin homology-like domain, family A, member 1	10366346	6	-1.8	-2.6	1096880
Csf2	colony stimulating factor 2 (granulocyte-macrophage)	10385912	6	-3.0	-14.0	1339752
Cd80	CD80 antigen	10435712	6	-1.8	-2.5	101775
Trem1	triggering receptor expressed on myeloid cells 1	10445746	6	-2.4	4.5	1930005
Dusp2	dual specificity phosphatase 2	10475782	6	-1.8	-2.0	101911
Plekhm1	pleckstrin homology domain containing, family M (with RU	10391918	6	1.8	3.0	2443207
Serpinb9b	serine (or cysteine) peptidase inhibitor, clade B, mem	10404439	6	2.2	2.8	894668
Plk2	polo-like kinase 2 (Drosophila)	10407126	6	2.2	3.7	1099790
Il7r	interleukin 7 receptor	10427628	6	2.6	3.1	96562
Abcc5	ATP-binding cassette, sub-family C (CFTR	10438478	6	2.3	3.0	1351644
Plekho1	pleckstrin homology domain containing, family O member 1	10500295	6	1.9	2.3	1914470
BC004044	cDNA sequence BC004044	10526853	6	1.9	3.6	2136853
Plxna1	plexin A1	10546184	6	1.9	2.4	107685
Mtmr10	myotubularin related protein 10	10553897	6	1.8	2.1	2142292
Hmox1	heme oxygenase (decycling) 1	10572897	6	2.5	6.3	96163
Slc6a8	solute carrier family 6 (neurotransmitter transporter, cr	10600210	6	2.0	2.6	2147834
Centa2	centaurin, α 2	638602	24	-2.6	-3.9	2663075
Ms4a6b	membrane-spanning 4-domains, subfamily A, member 6B	920843	24	-3.5	-4.0	1917024
Olfr112	olfactory receptor 112	690941	24	-6.1	-2.4	2177495
Pdxk	pyridoxal (pyridoxine, vitamin B6) kinase	480631	24	-2.7	-2.7	1351869
Tmem26	transmembrane protein 26	604942	24	-12.3	-2.6	2143537
8030453O22Rik	RIKEN cDNA 8030453O22 gene	769847	24	2.0	2.0	1924459
Blvra	biliverdin reductase A	664457	24	2.2	1.8	88170
Ephx1	epoxide hydrolase 1, microsomal	907012	24	3.6	3.2	95405
Hmgb1	high mobility group box 1	900889	24	2.1	2.7	96113
Metapl1	methionine aminopeptidase-like 1	536468	24	2.8	1.9	1913809
Phb	prohibitin	392862	24	2.2	2.5	97572
Tuba4	tubulin, α 4	509694	24	1.9	2.5	1095410

[a] Genes consistently regulated 1.8-fold up or down ($p \leq 0.01$) at 6 or 24 h in BH- and HNE-treated RAW 264.7 cells. Fold changes (FC) represent the average of three independent biological experiments.