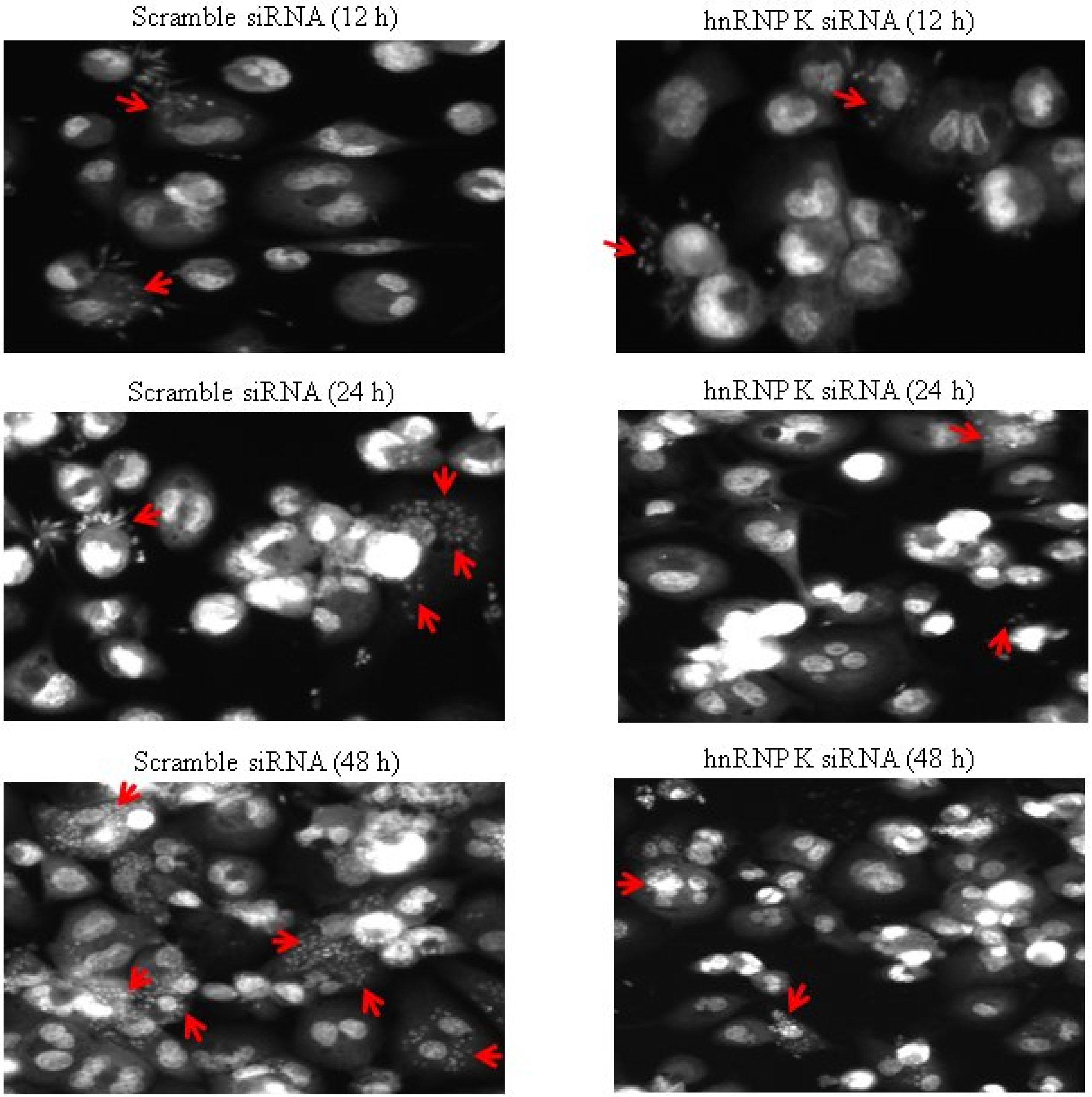
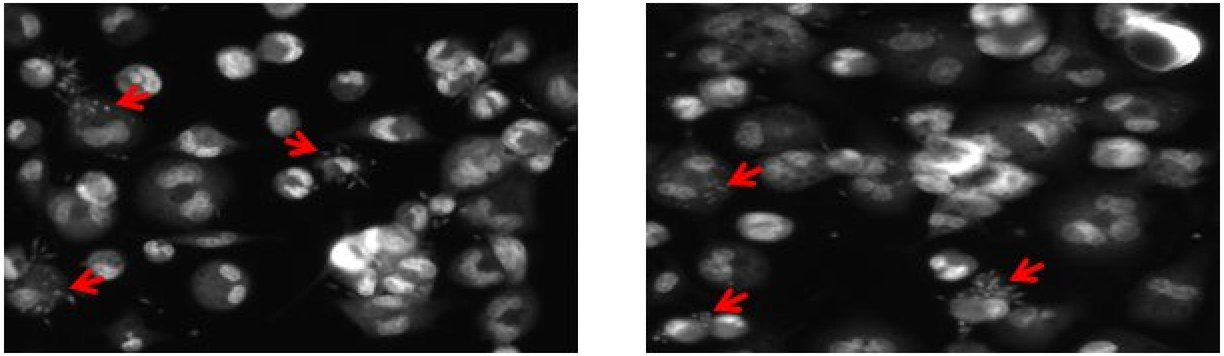
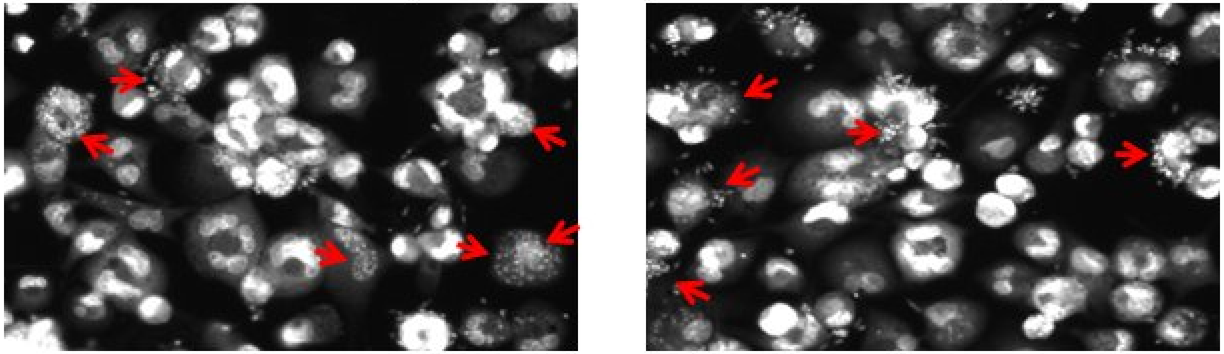


Supplementary Fig. 1: Automated microscopy based images showing effect of knockdown of hnRNP K on infection ratio and intracellular amastigotes at 12 h, 24 h and 48 h respectively.



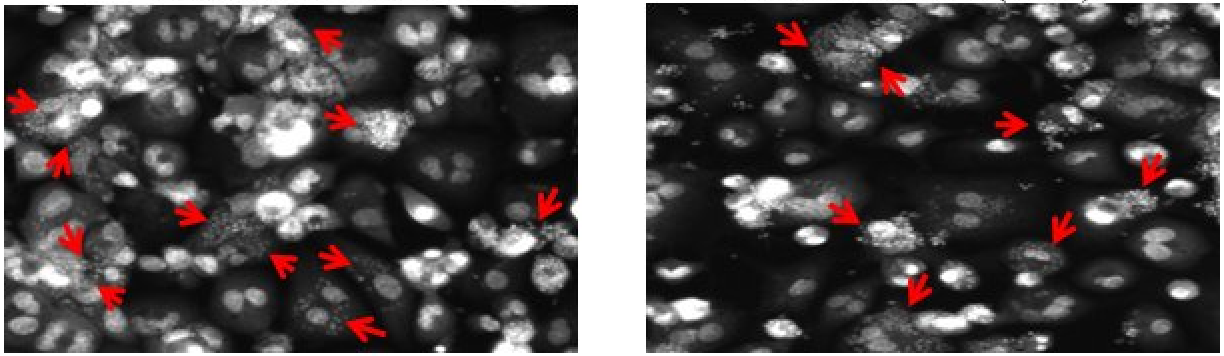
Scramble siRNA (12 h)

MAVS siRNA (12 h)



Scramble siRNA (24 h)

MAVS siRNA (24 h)



Scramble siRNA (48 h)

MAVS siRNA (48 h)

Supplementary Fig. 2: Automated microscopy based images showing effect of knockdown of ARHGEF18 and MAVS on infection ratio and intracellular amastigotes.

Supplementary Table S1: List of iTRAQ labeling reagents used to label the digested peptides originating from different samples used in the study.

Duration of infection	**Experimental Set**	**Sample type**	**iTRAQ label used**
12 h	1/Set A	THP-1 Uninfected	-114
		THP-1 + *L. donovani* (MHOM/IN/80/AG83)-C1	-115
		THP-1 + *L. donovani* (MHOM/IN/80/AG83)-C2	-116
	2/Set B	THP-1 Uninfected	-114
		THP-1 + *L. donovani* (MHOM/IN/80/AG83)-C1	-115
		THP-1 + *L. donovani* (MHOM/IN/80/AG83)-C2	-116
	3/Set C	THP-1 Uninfected	-114
		THP-1 + *L. donovani* (MHOM/IN/80/AG83)-C1	-116
		THP-1 + *L. donovani* (MHOM/IN/80/AG83)-C2	-117
24 h	1/Set D	THP-1 Uninfected	-114
		THP-1 + *L. donovani* (MHOM/IN/80/AG83)-C1	-115
		THP-1 + *L. donovani* (MHOM/IN/80/AG83)-C2	-116
	2/Set E	THP-1 Uninfected	-114
		THP-1 + *L. donovani* (MHOM/IN/80/AG83)-C1	-115
		THP-1 + *L. donovani* (MHOM/IN/80/AG83)-C2	-116
	3/Set F	THP-1 Uninfected	-114
		THP-1 + *L. donovani* (MHOM/IN/80/AG83)-C1	-115
		THP-1 + *L. donovani* (MHOM/IN/80/AG83)-C2	-117
48 h	1/Set G	THP-1 Uninfected	-114
		THP-1 + *L. donovani* (MHOM/IN/80/AG83)-C1	-115
		THP-1 + *L. donovani* (MHOM/IN/80/AG83)-C2	-116
	2/Set H	THP-1 Uninfected	-114
		THP-1 + *L. donovani* (MHOM/IN/80/AG83)-C1	-115
		THP-1 + *L. donovani* (MHOM/IN/80/AG83)-C2	-116
		THP-1 Uninfected	-115

	3/Set I	THP-1 + *L. donovani* (MHOM/IN/80/AG83)-C1	-116
		THP-1 + *L. donovani* (MHOM/IN/80/AG83)-C2	-117

C1: Clone 1; C2: Clone 2

Supplementary Table S2: List of gene IDs, gene names, primer sequences and amplicon size in qRT-PCR based gene expression analyses

Gene ID	Gene*	Primer Sequence 5’-3’	Amplicon Size (bp)
3190	hnRNP K F	TAAAATCAAAGAACTTCGAGAGAAC	87
	hnRNP K R	AGAACAACTCTGTCAGTGGAATGA	
220988	hnRNP A3 F	TTGTGACTTATTCTTGTGTTGAAGAG	77
	hnRNP A3 R	CACTACACGCCCATCAACCTT	
3184	hnRNP D F	GTTTTGGTGAGGTGGAATCCA	69
	hnRNP D R	AGCAGAACCCACGCCTCTTA	
3309	GRP78 F	CGGCCGCACGTGGAATG	57
	GRP78 R	TTGAACGGCAAGAACTTGATGT	
7431	VIM F	AATGACCGCTTCGCCAACT	59
	VIM R	ATCTTATTCTGCTGCTCCAGGAA	
26827	RNU6A F	CTCGCTTCGGCAGCACATATAC	101
	RNU6A R	AATATGGAACGCTTCACGAATTTG	

*hnRNP K (Heterogeneous nuclear ribonucleoprotein K), hnRNP A3 (Heterogeneous nuclear ribonucleoprotein A3), hnRNP D (Heterogeneous nuclear ribonucleoprotein D), GRP78 (Glucose-regulated protein, 78 kDa), VIM (Vimentin), RNU6A (U6 Small RNA).

F; forward, R; reverse.

Supplementary Table S3: Gene name, accession numbers and Oligo (siRNA) sequences* used in the gene knockdown experiments

Gene Name	Gene ID	Accession Number	siRNA Sequences
hnRNP K	3190	NM_031263	UAAACGCCCUGCAGAAGAU
			GGUCGUGGCUCAUAUGGUG
			UGACAGAGUUGUUCUUAUU
			GCAAGAAUAUUAAGGCUCU
MAVS	57506	NM_020746	AAGUAUAUCUGCCGCAAUU
			CAUCCAAAGUGCCUACUAG
			GCAAUGUGGAUGUUGUAGA
			CAUCCAAAUUGCCCAUCAA
ARHGEF18	23370	NM_015318	UCAGGGCGCUUGAAAGAUA
			GCAGUGACCGGAAUUAUGU
			CACAACGCAUAACCAAAUA
			GGACGCAACUCGGACCAAU

hnRNP K (Heterogeneous nuclear ribonucleoprotein K), MAVS (Mitochondrial anti-viral signaling protein), ARHGEF18 (Rho guanine nucleotide exchange factor 18)

*Pool mixture of 4 siRNA Oligos were used in the study

Supplementary Table S5: List of differentially modulated proteins in THP-1 cells infected with *Leishmania donovani* when compared to uninfected cells at 12 h, 24 h and 48 h after *Leishmania* infection.

				12 h		24 h		48 h	
N	Uniprot ID	Name	Biological Process	Fold (±SD)	R	Fold (±SD)	R	Fold (±SD)	R
Transport, vesicular trafficking, signal transduction, apoptosis, cell death and differentiation, stress related, inflammation and immune response									
Transport and vesicular trafficking									
1	P00918	Carbonic anhydrase 2	bicarbonate transport	0.82 (± 0.08)	3	0.40 (± 0.09)	3	1.03 (± 0.26)	2
2	P02794	Ferritin heavy chain	iron ion transport	0.85 (±0.09)	2	0.59 (±0.11)	2	0.99 (±0.00)	2
3	P22307	Non-specific lipid-transfer protein	lipid transport	0.85 (±0.02)	3	0.58 (±0.26)	3	0.99 (±0.00)	2
4	O00299	Chloride intracellular channel protein 1	regulation of mitochondrial membrane potential	0.99 (± 0)	3	1.07 (± 0.14)	3	0.51 (± 0.36)	3
5	Q14974	Importin subunit beta-1	NLS-bearing substrate import into nucleus	0.98 (± 0.46)	2	0.99 (± 0)	2	0.42 (± 0.12)	2
6	Q13428	Treacle protein	Transport	2.27 (± 0.20)	2	0.94 (± 0.15)	3		
7	P11686	Pulmonary surfactant-associated protein C	respiratory gaseous exchange	9.9 (± 5.87)	2				
8	Q02641	Voltage-dependent L-type calcium channel subunit beta-1	high voltage-gated calcium channel activity			1.76 (± 0.29)	2		
9	Q8IWJ2	GRIP and coiled-coil domain-containing protein 2	late endosome to Golgi transport			0.52 (± 0.02)	2		
10	Q12797	Aspartyl/asparaginyl beta-	activation of store-					0.34	2

		hydroxylase	operated calcium channel activity					(±0.2)	
Signal transduction									
11	Q01518	Adenylyl cyclase-associated protein 1	activation of adenylate cyclase activity	0.93 (± 0.01)	3	0.44 (± 0.21)	3	0.25 (± 0.01)	3
12	P31946	14-3-3 protein beta/alpha	MAPK cascade	1.23 (± 0.05)	3	0.49 (± 0.34)	3	0.61 (± 0.45)	2
13	Q8TEY5	cAMP-responsive element-binding protein 3-like protein 4	positive regulation of transcription from RNA polymerase II promoter	15.3 (± 1.98)	3				
14	P80303	Nucleobindin-2	endoplasmic reticulum-Golgi intermediate compartment	0.99 (± 0)	2			1.96 (± 0.06)	2
15	P63104	14-3-3 protein zeta/delta	intrinsic apoptotic signaling pathway	0.96 (± 0.09)	3	1.5 (± 0.46)	3	0.96 (± 0.01)	3
16	P35613	Basigin	cell surface receptor signaling pathway	0.96 (±0.01)	2	0.65 (±0.01)	2		
17	Q9Y3L3	SH3 domain-binding protein 1	positive regulation of GTPase activity	1.62 (± 0.01)	2				
18	Q9ULV4	Coronin-1C	actin cytoskeleton organization	2.28 (± 1.03)	2			0.84 (± 0.06)	2
19	Q13546	Receptor-interacting serine/threonine-protein kinase 1	TRIF-dependent toll-like receptor signaling pathway			3.06 (± 0.94)	2		
20	Q14160	Protein LAP4	activation of Rac GTPase activity			2.04 (± 0.96)	2		
21	O95294	RasGAP-activating-like protein 1	negative regulation of Ras protein signal transduction			0.56 (±0.14)	2		

22	P27348	14-3-3 protein theta	intrinsic apoptotic signaling pathway			0.55 (± 0.05)	2	1.0 (± 0.07)	2
23	O43572	A kinase anchor protein 10, mitochondrial	termination of G-protein coupled receptor signaling pathway			1.7 (± 0.48)	2		
24	P50395	Rab GDP dissociation inhibitor beta	regulation of small GTPase mediated signal transduction			0.63 (± 0.04)	3	0.50 (± 0.1)	2
25	P29350	Tyrosine-protein phosphatase non-receptor type 6	JAK-STAT cascade involved in growth hormone signaling pathway					0.22 (±0.005)	2
26	P49006	MARCKS-related protein	positive regulation of cell proliferation	1.22 (±1.41)	2	0.82 (±0.29)	3	0.61 (±0.47)	2
Apoptosis, cell death and differentiation									
27	P11021	78 kDa glucose-regulated protein	ER overload response	0.43 (± 0.04)	3	1.03 (± 0.16)	3	1.95 (± 0.38)	3
28	P14625	Endoplasmin	ER-associated protein catabolic process	0.58 (±0.10)	3	1.02 (±0.02)	3	1.17 (±0.14)	3
29	P38646	Stress-70 protein, mitochondrial	ER-associated protein catabolic process	0.58 (±0.07)	3	0.98 (±0.03)	3	1.09 (±0.02)	3
30	P04040	Catalase	hydrogen peroxide catabolic process	0.54 (± 0.05)	3	1.05 (± 0.03)	3	0.98 (± 0.01)	3
31	P61604	10 kDa heat shock protein, mitochondrial	activation of cysteine-type endopeptidase activity involved in apoptotic process	0.59 (± 0.05)	3	0.84 (± 0.12)	3	1.9 (± 0.88)	3
31	P08107	Heat shock 70 kDa protein 1	negative regulation of apoptotic process	1.04 (±0.02)	3	1.07 (±0.10)	3	0.93 (±0.09)	3

33	P06748	Nucleophosmin	CENP-A containing nucleosome assembly at centromere	1.53 (± 0.31)	3	1.09 (± 0.03)	3	1.93 (± 0.16)	3
34	P00441	Superoxide dismutase [Cu-Zn]	hydrogen peroxide biosynthetic process	0.99 (±0.00)	3	0.88 (±0.13)	3	0.7 (±0.01)*	2
35	P04179	Superoxide dismutase [Mn], mitochondrial	hydrogen peroxide biosynthetic process	0.97 (± 0.07)	3	0.57 (± 0.13)	3	2.01 (± 0.22)	3
36	Q9Y2B0	Protein canopy homolog 2	negative regulation of gene expression	0.99 (±0.00)	2	0.60 (±0.01)	2		
37	P08670	Vimentin	cellular component disassembly involved in execution phase of apoptosis	0.58 (± 0.16)	3	1.74 (± 0.55)	3	2.19 (± 0.10)	3
38	P17096	High mobility group protein HMG-I/HMG-Y	DNA unwinding involved in replication	1.56 (± 0.07)	3	3.54 (± 0.1)	3	5.74 (± 0.34)	3
39	Q6ZSZ5	Rho guanine nucleotide exchange factor 18	apoptotic signaling pathway	3.6 (± 0.93)	2				
40	P52926	High mobility group protein HMGI-C	DNA damage response	1.76 (± 0.46)	2	3.32 (± 0.16)	3	9.58 (± 0.12)	3
41	P08758	Annexin A5	negative regulation of apoptotic process			0.34 (± 0.13)	3	0.35 (± 0.12)	2
42	P14222	Perforin-1	apoptotic process			1.75 (± 0.7)	2		
43	Q9UKY	Protein CDV3 homolog	Cell proliferation			1.57 (± 0.62)	2	1 (± 0.05)	2
Stress related proteins, inflammation and immune response									
Cell redox homeostasis									
44	P07237	Protein disulfide-isomerase	cell redox homeostasis	0.46 (± 0.04)	3	1.31 (± 0.31)	3	3.98 (± 2.37)	3

45	P30101	Protein disulfide-isomerase A3	cell redox homeostasis	0.8 (± 0.05)	3	2.43 (± 0.9)	3	1.06 (± 0.08)	3
46	Q15084	Protein disulfide-isomerase A6	activation of signaling protein activity involved in unfolded protein response	0.51 (± 0.05)	3	1.03 (± 0.01)	3	1.01 (± 0.24)	2
47	P13667	Protein disulfide-isomerase A4	cell redox homeostasis	0.52 (± 0.14)	3	1.0 (±0.03)	3	1.15 (± 0.05)	3
48	Q8NBS9	Thioredoxin domain-containing protein 5	cell redox homeostasis	0.99 (± 0)	2	0.4 (± 0.02)	2		
49	Q9BS26	Thioredoxin domain-containing protein 4	cell redox homeostasis	0.82 (±0.12)	2	0.57 (±0.007)	2		
50	O95881	Thioredoxin domain-containing protein 12	cell redox homeostasis	0.99 (± 0)	2	0.29 (± 0.01)	2		
51	Q9H299	SH3 domain-binding glutamic acid-rich-like protein 3	cell redox homeostasis			1.07 (±0.09)	2	0.65 (±0.00)	2
Oxidative stress response									
52	P09211	Glutathione S-transferase P	glutathione metabolic process			1.46 (± 0.5)	3	0.62 (± 0.02)	2
53	Q9Y4L1	Hypoxia up-regulated protein 1	activation of signaling protein activity involved in unfolded protein response	0.62 (±0.02)	3	1.26 (±0.18)	3	0.96 (±0.09)	3
54	P30048	Thioredoxin-dependent peroxide reductase, mitochondrial	hydrogen peroxide catabolic process	0.68 (±0.06)*	3	1.01 (±0.04)	3	0.87 (±0.2)	3
Immune response									
55	Q7Z434	Mitochondrial antiviral-signaling protein	activation of innate immune response	7.86 (± 3.55)	2				

56	P01584	Interleukin-1 beta	cytokine-mediated signaling pathway	0.75 (± 0.45)	2	0.55 (± 0.03)	2		
57	P09960	Leukotriene A-4 hydrolase	arachidonic acid metabolic process			1.72 (± 0.46)	2		
58	Q13740	CD166 antigen	cell adhesion					1.71 (± 0.12)	2
59	P36222	Chitinase-3-like protein 1	activation of NF-kappaB-inducing kinase activity			0.53 (± 0)	2	0.97 (± 0.04)	2
DNA metabolism (DNA repair, replication and chromatin remodeling)									
Nucleobase, nucleoside and nucleotide metabolism									
60	Q13232	Nucleoside diphosphate kinase 3	CTP biosynthetic process	2.59 (± 0.08)	2				
61	P15531	Nucleoside diphosphate kinase A	CTP biosynthetic process			0.41 (± 0.005)	2	0.94 (± 0.03)	2
62	P19971	Thymidine phosphorylase	pyrimidine nucleobase metabolic process			1.11 (± 0.68)	2	0.54 (± 0.12)	2
Histones and chromatin remodeling									
63	P62805	Histone H4	CENP-A containing nucleosome assembly at centromere	1.62 (± 0.28)	3	5.51 (± 2.94)	3	13.6 (± 3.23)	3
64	Q99880	Histone H2B type 1-L	nucleosome assembly	1.62 (± 0.3)	2	0.94 (± 0.07)	3	19.5 (± 7.56)	2
65	P19338	Nucleolin	Transcription regulation	1.46 (± 0.43)	3	3.23 (± 2.3)	3	1 (± 0.02)	3
66	Q92522	Histone H1x	nucleosome assembly	0.99 (± 0)	2	2.07 (± 0.48)	2	0.9 (± 0.54)	2
67	Q9BTM1	Histone H2A.J	nucleosome assembly	0.93 (± 0.07)	2			6.53 (± 3.18)	2

68	Q93079	Histone H2B type 1-H	nucleosome assembly	2.89 (± 2.49)	2				
69	Q99878	Histone H2A type 1-J	nucleosome assembly	1.23 (± 1.46)	2	4.52 (± 4.33)	2		
70	Q99879	Histone H2B type 1-M	nucleosome assembly			14.5 (± 13.0)	2		
71	P84243	Histone H3.3	nucleosome assembly			1.87 (± 1.32)	3		
72	Q01105	Protein SET	DNA replication			1.96 (± 0.06)	2		
73	O75367	Core histone macro-H2A.1	nucleosome assembly			2.44 (± 1.53)	2	6.07 (± 2.74)	2
74	P05204	Non-histone chromosomal protein HMG-17	chromatin organization			3.6 (± 0.02)	2		
75	Q5SSJ5	Heterochromatin protein 1-binding protein 3	nucleosome assembly			1.68 (± 0.24)	2		
76	Q96L91	E1A-binding protein p400	histone H2A acetylation			1.46 (± 0.34)	2		
77	P04908	Histone H2A type 1-B/E	nucleosome assembly			1.95 (±0.92)	2		
78	P16104	Histone H2A.x	nucleosome assembly			4.23 (±3.34)	2		
79	Q71DI3	Histone H3.2	nucleosome assembly			3.45 (± 1.76)	2		
80	Q6FI13	Histone H2A type 2-A	nucleosome assembly					4 (± 2.24)	2
81	O60814	Histone H2B type 1-K	nucleosome assembly					20.18 (± 6.33)	2

DNA repair and replication									
82	P13010	ATP-dependent DNA helicase 2 subunit 2	DNA recombination	0.89 (± 0.1)	3	3.16 (± 0.61)	2	0.91 (± 0.02)	2
83	Q04837	Single-stranded DNA-binding protein, mitochondrial	DNA replication			0.61 (±0.02)	2		
84	P11387	DNA topoisomerase 1	DNA replication	1.02 (± 0.07)	2	1.72 (± 0.25)	3		
85	Q15233	Non-POU domain-containing octamer-binding protein	DNA recombination	1.17 (± 0.17)	2	1.72 (± 0.88)	3		
86	Q9Y230	RuvB-like 2	DNA recombination			1.45 (± 0.28)*	2		
RNA metabolism (RNA splicing and transcription regulation)									
RNA splicing and processing									
87	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1	RNA transport and mRNA splicing via spliceosome	0.89 (± 0.04)	3	2.96 (± 0.49)	3	1.0 (±0.029)	3
88	P31943	Heterogeneous nuclear ribonucleoprotein H	mRNA splicing via spliceosome	0.98 (± 0.24)	2	2 (± 0.54)	3	0.99 (± 0.108)	3
89	Q14103	Heterogeneous nuclear ribonucleoprotein D0	mRNA splicing via spliceosome	0.71 (± 0.08)	3	3.07 (± 1.64)	3	1.08 (±0.09)	3
90	P09651	Heterogeneous nuclear ribonucleoprotein A1	RNA export from nucleus and mRNA splicing via spliceosome	1.17 (± 0.26)	3	2.57 (± 0.25)	2		
91	P61978	Heterogeneous nuclear ribonucleoprotein K	mRNA splicing via spliceosome	0.46 (± 0.23)	3	2.64 (± 0.34)	3	0.88 (± 0.28)	3
92	Q08211	ATP-dependent RNA helicase A	CRD-mediated mRNA stabilization	1.05 (± 0.42)	2	1.27 (± 0.27)	3	1.76 (± 0.92)	2
93	P07910	Heterogeneous nuclear ribonucleoproteins C1/C2	mRNA splicing via spliceosome	1.13 (± 0.10)	3	2.28 (± 1.04)	3	1.37 ± (0.24)	3

94	P51991	Heterogeneous nuclear ribonucleoprotein A3	mRNA splicing via spliceosome	0.69 (± 0.13)	2	2.79 (± 1.16)	3	1.16 ± (0.15)	3
95	O43390	Heterogeneous nuclear ribonucleoprotein R	mRNA splicing via spliceosome	0.99 (± 0)	2	1.5 (± 0.009)	2		
96	P0C7M2	Putative heterogeneous nuclear ribonucleoprotein A1-like protein 3	mRNA splicing via spliceosome	0.53 (± 0.04)	2	0.79 (± 0.507)	2	0.4 (± 0.29)	2
97	Q9BQA1	Methylosome protein 50	ncRNA metabolic process	0.6 (±0.05)	2				
98	P38159	Heterogeneous nuclear ribonucleoprotein G	mRNA splicing via spliceosome			10.6 (± 8.14)	3	1.1 (± 0.46)	2
99	Q92841	Probable ATP-dependent RNA helicase DDX17	RNA processing			1.46 (± 0.009)	2		
100	O43290	U4/U6.U5 tri-snRNP-associated protein 1	RNA processing			1.81 (± 0.59)	2		
101	P35637	RNA-binding protein FUS	mRNA splicing via spliceosome			2.57 (± 0.15)	2	1.13 (± 0.007)	2
102	P62314	Small nuclear ribonucleoprotein Sm D1	ncRNA metabolic process			1.79 (± 0.33)	2		
103	Q9Y333	U6 snRNA-associated Sm-like protein LSm2	exonucleolytic nuclear-transcribed mRNA catabolic process involved in deadenylation-dependent decay			0.56 (±0.04)	2		
104	P52597	Heterogeneous nuclear ribonucleoprotein F	mRNA splicing via spliceosome	0.72 (±0.28)	2	1.09 (±0.21)	3	0.62 (±0.03)	2
Transcription and cell cycle regulation									
105	P53999	Activated RNA polymerase II	regulation of	0.95	2	2.59	3	1.39	2

		transcriptional coactivator p15	transcription from RNA polymerase II promoter	(± 0.03)		(± 1.52)		(± 0.48)	
106	P80723	Brain acid soluble protein 1	negative regulation of transcription	0.64 (± 0.15)	3	5.59 (± 2.63)	3	0.95 (± 0.05)	3
107	Q9UIW0	Ventral anterior homeobox 2	negative regulation of transcription from RNA polymerase II promoter	2.12 (± 0.54)	2				
108	P06454	Prothymosin alpha	transcription, DNA-dependent	1.55 (± 0.3)	2	1.15 (± 0.04)	2	1.05 (± 0.25)	2
109	P14652	Homeobox protein Hox-B2	transcription, DNA-dependent	3.01 (± 0.68)	2				
110	P09874	Poly [ADP-ribose] polymerase 1	DNA damage response			1.58 (± 0.33)	2		
111	Q96AE4	Far upstream element-binding protein 1	positive regulation of gene expression			1.94 (± 0.25)	2	1.01 (± 0.006)	2
112	Q7Z7A1	Centriolin	G2/M transition of mitotic cell cycle			2.24 (± 0.02)	2		
113	Q14814	Myocyte-specific enhancer factor 2D	positive regulation of transcription from RNA polymerase II promoter					1.72 (± 0.02)	2
Protein metabolism (protein folding, modification and synthesis)									
Protein folding									
114	P10809	60 kDa heat shock protein, mitochondrial	'de novo' protein folding	0.53 (± 0.08)	3	0.67 (± 0.03)	3	1.54 (± 0.45)	3
115	P27797	Calreticulin	activation of signaling protein activity involved in unfolded protein response	0.42 (± 0.06)	3	0.93 (± 0.09)	3	0.57 (± 0.29)	3

116	P23284	Peptidyl-prolyl cis-trans isomerase B	protein folding	0.96 (± 0.06)	3	0.55 (± 0.14)	3	1.01 (± 0.09)	3
117	P27824	Calnexin	antigen processing and presentation of exogenous peptide antigen via MHC class II	0.43 (± 0.13)	3	1.05 (± 0.25)	2		
118	P50454	Serpin H1	response to unfolded protein	1.07 (±0.16)	3	0.56 (±0.26)	3	1.28 (±0.26)	3
Protein modification and proteolysis									
119	P22314	Ubiquitin-like modifier-activating enzyme 1	cell death	0.96 (± 0.18)	2	0.43 (± 0.08)	3	0.55 (± 0.36)	3
120	Q14697	Neutral alpha-glucosidase AB	post-translational protein modification	0.56 (±0.08)	3	1.02 (±0.03)	3	1.36 (±0.09)	3
121	P62988	Ubiquitin	Protein turnover	0.69 (±0.09)	3	1.43 (±0.19)	3	0.78 (±0.12)	3
122	O60888	Protein CutA	protein localization	1.14 (± 0.86)	2	1.97 (± 1.72)	2		
123	O75439	Mitochondrial-processing peptidase subunit beta	cellular protein metabolic process					1.82 (± 0.09)	2
124	P49903	Selenide, water dikinase 1	cellular protein modification process					0.51 (± 0.17)	2
Protein synthesis and targeting									
125	P05387	60S acidic ribosomal protein P2	SRP-dependent cotranslational protein targeting to membrane	1.12 (± 0.23)	3	1.75 (± 2.03)	2	5.37 (± 0.45)	2
126	P68104	Elongation factor 1-alpha 1	GTP catabolic process	2.29 (± 0.98)	2	1.55 (± 0.54)	3		
127	P30040	Endoplasmic reticulum protein	intracellular protein	0.94	3	0.23	2	1.49	2

		ERp29	transport	(± 0.15)		(± 0.08)		(± 0.16)	
128	P05386	60S acidic ribosomal protein P1	SRP-dependent cotranslational protein targeting to membrane	1.66 (± 0.82)	3	0.69 (± 0.07)	2	0.98 (± 0.25)	2
129	Q05639	Elongation factor 1-alpha 2	GTP catabolic process	2.27 (± 0.11)	2				
130	Q5VTE0	Putative elongation factor 1-alpha-like 3	GTP catabolic process	0.91 (± 0.04)	2	0.48 (± 0.48)	2	0.98 (± 0.01)	3
131	P23396	40S ribosomal protein S3	SRP-dependent cotranslational protein targeting to membrane	2.33 (± 0.31)	2	4.19 (± 5.3)	2	0.12 (± 0.007)	2
132	P62913	60S ribosomal protein L11	SRP-dependent cotranslational protein targeting to membrane			1.62 (± 0.02)	2		
133	Q02878	60S ribosomal protein L6	SRP-dependent cotranslational protein targeting to membrane			1.9 (± 0.34)	2		
134	P39019	40S ribosomal protein S19	SRP-dependent cotranslational protein targeting to membrane			0.62 (±0.15)	2		
Metabolic pathways									
Carbohydrate metabolism									
Glycolysis									
135	P06733	Alpha-enolase	glycolysis	0.63 (± 0.08)	3	0.4 (± 0.26)	3	0.54 (± 0.05)	3
136	P14618	Pyruvate kinase isozymes M1/M2	glycolysis	0.7 (± 0.02)	3	0.4 (± 0.27)	3	0.54 (± 0.21)	3
137	P04075	Fructose-bisphosphate aldolase A	glycolysis	0.74 (± 0.03)	3	0.32 (± 0.21)	3	0.5 (± 0.03)	3

138	P04406	Glyceraldehyde-3-phosphate dehydrogenase	glycolysis	0.96 (± 0.02)	3	1.66 (± 0.37)	3	0.96 (± 0.04)	3
139	P00558	Phosphoglycerate kinase 1	gluconeogenesis	1 (± 0.04)	3	1.01 (± 0.3)	3	0.42 (± 0.12)	3
140	P60174	Triosephosphate isomerase	gluconeogenesis	0.76 (± 0.02)	3	1.5 (± 0.09)	3	0.96 (± 0.005)	3
141	P18669	Phosphoglycerate mutase 1	gluconeogenesis	0.9 (± 0.01)	2	0.23 (± 0.16)	2		
142	P15259	Phosphoglycerate mutase 2	glycolysis					0.68 (± 0.13)	2
TCA cycle and electron transport chain									
143	P40926	Malate dehydrogenase, mitochondrial	NADH metabolic process	0.51 (± 0.06)	3	0.97 (± 0.04)	3	1.7 (± 0.15)	3
144	O75390	Citrate synthase, mitochondrial	tricarboxylic acid cycle			0.62 (±0.31)	3	1.02 (±0.06)	2
145	P07954	Fumarate hydratase, mitochondrial	tricarboxylic acid cycle	0.99 (± 0)	2	1.77 (± 0.104)	2	1.32 (± 0.04)	2
Beta oxidation of fatty acid and fatty acid metabolism									
146	Q16698	2,4-dienoyl-CoA reductase, mitochondrial	fatty acid beta-oxidation	2.06 (± 0.98)	3	1.13 (± 0.02)	2	1.26 (± 0.46)	2
147	Q6JQN1	Acyl-CoA dehydrogenase family member 10	acyl-CoA dehydrogenase activity	7 (± 2.93)	2				
148	P40939	Trifunctional enzyme subunit alpha, mitochondrial	cardiolipin acyl-chain remodeling			1.56 (± 0.54)	3	0.99 (± 0)	2
Pentose phosphate shunt									
149	P29401	Transketolase	pentose-phosphate shunt	0.86 (± 0.09)	3	1.03 (± 0.03)	3	0.52 (± 0.39)	3
150	P37837	Transaldolase	xylulose biosynthetic process	0.89 (±0.13)	2	1.2 (±0.05)	3		

Energy metabolism									
151	P06576	ATP synthase subunit beta, mitochondrial	ATP hydrolysis coupled proton transport	0.47 (± 0.12)	3	1.24 (± 0.11)	3	3.1 (± 0.89)	3
152	P25705	ATP synthase subunit alpha, mitochondrial	ATP hydrolysis coupled proton transport	1.02 (±0.02)	3	0.58 (±0.20)	3	0.83 (±0.03)	3
153	P13804	Electron transfer flavoprotein subunit alpha, mitochondrial	respiratory electron transport chain	0.66 (±0.08)	3	1.04 (±0.05)	3	0.75 (±0.07)	3
154	P22695	Cytochrome b-c1 complex subunit 2, mitochondrial	oxidative phosphorylation	1.31 (± 0.69)	2	1.71 (± 0.01)	2		
Other metabolic pathways									
155	P23141	Liver carboxylesterase 1	response to toxic substance	0.49 (± 0.08)	3	1.45 (± 0.81)	3	1 (± 0.02)	3
156	P23368	NAD-dependent malic enzyme, mitochondrial	malate metabolic process	1.02 (± 0.05)	2	1.9 (± 0.69)	2		
157	P07686	Beta-hexosaminidase subunit beta	carbohydrate metabolic process			0.64 (±0.06)	2		
158	P22570	NADPH:adrenodoxin oxidoreductase, mitochondrial	NADPH oxidation	3.28 (± 0.25)	2				
159	Q9BZ23	Pantothenate kinase 2, mitochondrial	coenzyme A biosynthetic process			0.54 (± 0.03)	2		
160	Q32M88	Acid trehalase-like protein 1	carbohydrate metabolic process			0.62 (±0.15)	2		
Cytoskeleton									
161	Q13748	Tubulin alpha-3C/D chain	microtubule-based process	6.43 (± 2.13)	2	0.65 (± 0.37)			
162	P07737	Profilin-1	actin cytoskeleton organization	0.85 (± 0.05)	3	1.03 (± 0.09)	3	0.51 (± 0.16)	3
163	P26038	Moesin	leukocyte cell-cell	0.62	3	0.37	3	0.64	3

			adhesion	(± 0.05)		(± 0.09)		(± 0.14)	
164	P13796	Plastin-2	T cell activation involved in immune response	1.53 (± 0.35)	3	0.73 (± 0.14)	3	0.51 (± 0.11)	3
165	Q9Y490	Talin-1	activation of signaling protein activity involved in unfolded protein response	0.99 (± 0)	2	0.92 (± 0.02)	3	0.5 (± 0.39)	3
166	P40121	Macrophage-capping protein	barbed-end actin filament capping			0.53 (± 0.18)	3	0.99 (± 0.005)	3
167	P68371	Tubulin beta-2C chain	microtubule-based process	4.59 (± 1.69)	3	3.54 (± 0.36)	2		
168	P42167	Lamina-associated polypeptide 2, isoforms beta/gamma	nuclear envelope	0.55 (± 0.39)	2				
169	P60709	Actin, cytoplasmic 1	'de novo' posttranslational protein folding	0.96 (± 0.03)	2			0.28 (± 0.17)	2
170	Q9BQE3	Tubulin alpha-1C chain	cytoskeleton-dependent intracellular transport	5.6 (± 4.12)	3	1.25 (± 0.01)	2		
171	Q5TZA2	Rootletin	centrosome organization	4.5 (± 1.32)	2				
172	P02545	Lamin-A/C	M phase of mitotic cell cycle	1.03 (± 0.08)	3	2.39 (± 0.32)	2	2.47 (± 1.35)	3
173	Q8N3T6	Transmembrane protein 132C	integral to membrane	1.84 (± 0.08)	2				
174	P12109	Collagen alpha-1(VI) chain	cell adhesion	5.87 (± 1.29)	2				
175	P27816	Microtubule-associated protein 4	cell division and establishment of spindle	0.77 (± 0.24)	2			3.92 (± 0.73)	2

			orientation						
176	P04264	Keratin, type II cytoskeletal 1	complement activation			0.1 (± 0.01)	2	2.7 (± 1.48)	3
177	P06753	Tropomyosin alpha-3 chain	muscle filament sliding			0.36 (± 0.34)	3		
178	P35908	Keratin, type II cytoskeletal 2 epidermal	keratinization			0.29 (± 0.34)	2	1.91 (± 0.38)	2
179	Q9Y4G6	Talin-2	cytoskeletal anchoring at plasma membrane			2.0 (± 0.59)	2		
180	Q2KHT4	Germ cell-specific gene 1 protein	integral to membrane			2.08 (± 0.40)	2		
181	Q14019	Coactosin-like protein	defense response to fungus			0.99 (± 0)	2	0.52 (± 0.006)	2
182	P23528	Cofilin-1	Rho protein signal transduction			0.85 (± 0.26)	2	0.52 (± 0.006)	2
183	O43312	Metastasis suppressor protein 1	actin cytoskeleton organization			3.61 (± 1.53)	2		
184	P35527	Keratin, type I cytoskeletal 9	intermediate filament organization			0.91 (± 0.14)	2	3.29 (± 2.0)	3
185	P13645	Keratin, type I cytoskeletal 10	cellular response to calcium ion					4 (± 0.39)	2
186	P04350	Tubulin beta-4 chain	microtubule-based process					0.55 (± 0.03)	2
187	P68363	Tubulin alpha-1B chain	cytoskeleton-dependent intracellular transport					0.55 (± 0.08)	2
188	P05107	Integrin beta-2	cell-cell signaling	0.99 (±0.00)	2	1.03 (±0.03)	2	0.64 (±0.06	2
189	P07437	Tubulin beta chain	cellular component	0.85	2	0.9	3	0.63	3

			movement	(±0.16)		(±0.24)		(±0.33)	
190	P12814	Alpha-actinin-1	actin crosslink formation			1.37 (±0.26)	3	0.66 (±0.02)	3
191	P63261	Actin, cytoplasmic 2	Fc-gamma receptor signaling pathway involved in phagocytosis	0.84 (±0.13)	3	0.78 (±0.08)	3	0.67 (±0.16)	3
192	P06396	Gelsolin	actin filament polymerization	0.84 (±0.13)	3	0.98 (±0.01)	3	0.67 (±0.21)	3
Proteins with unknown function									
193	Q5JR59	Uncharacterized protein KIAA0774		1.54 (± 0.18)	2				
194	Q5TEA3	Uncharacterized protein C20orf194				0.4 (± 0.01)	2		
195	Q5RHP9	Uncharacterized protein C1orf173				2.17 (± 0.89)	2		
196	Q12767	Uncharacterized protein KIAA0195				0.5 (± 0.009)	2		
197	Q8WVS4	WD repeat-containing protein 60				3.1 (± 0.504)	2		
198	Q8NA72	Uncharacterized protein C5orf37		14.3 (± 6.96)	2				
199	Q9H2F9	Coiled-coil domain-containing protein 68		11.2 (±1.31)	2				

The parameters that were used for identification and quantification of differentially modulated proteins included: (1) proteins identified having ≥ 95% confidence (Unused-Prot Score > 1.3); (2) proteins with fold differences ≥ 1.5 or ≤ 0.67 were considered more abundant and less abundant respectively and (3) protein detected in a minimum of two technical replicates.

R: no. of replicate experiment. Fold represents fold abundance (higher/lower) in infected *versus* uninfected THP-1 cells. *nearest fold ratio for threshold cut off.