

Table S1. Translationally up-regulated mRNAs in 1 h LPS-stimulated RAW264.7 macrophages.

Symbol	Name	Change of translation (d)	mRNA group*
<i>Nfkbid</i>	nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, delta	1.62	3
<i>Nfkbiz</i>	nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, zeta	1.56	1
<i>Nr4a1</i>	nuclear receptor subfamily 4, group A, member 1	1.52	3
<i>Ugt1a6a</i>	UDP glucuronosyltransferase 1 family, polypeptide A6A	1.16	0
<i>ler3</i>	immediate early response 3	0.97	3
<i>Zfp36</i>	zinc finger protein 36	0.83	3
<i>5031414D18Rik</i>	RIKEN cDNA 5031414D18 gene	0.8	2
<i>Impa2</i>	inositol (myo)-1(or 4)-monophosphatase 2	0.79	0
<i>Pank1</i>	pantothenate kinase 1	0.79	2
<i>Tnf</i>	tumor necrosis factor	0.76	3
<i>Arhgef39</i>	Rho guanine nucleotide exchange factor (GEF) 39	0.73	2
<i>Cxcl2</i>	chemokine (C-X-C motif) ligand 2	0.73	1
<i>Snx30</i>	sorting nexin family member 30	0.73	2
<i>Arl10</i>	ADP-ribosylation factor-like 10	0.72	2
<i>Crot</i>	carnitine O-octanoyltransferase	0.68	2
<i>Dusp1</i>	dual specificity phosphatase 1	0.68	3
<i>Il23a</i>	interleukin 23, alpha subunit p19	0.66	1
<i>Cep78</i>	centrosomal protein 78	0.65	2
<i>Plk3</i>	polo-like kinase 3	0.65	3
<i>Fam105a</i>	family with sequence similarity 105, member A	0.64	2
<i>Zc3h12a</i>	zinc finger CCCH type containing 12A	0.64	1
<i>Ppargc1b</i>	peroxisome proliferative activated receptor, gamma, coactivator 1 beta	0.63	2
<i>Ccnb1</i>	cyclin B1	0.62	0
<i>Pif1</i>	PIF1 5'-to-3' DNA helicase homolog (S. cerevisiae)	0.61	0
<i>Tk1</i>	thymidine kinase 1	0.61	2
<i>Wdr67</i>	WD Repeat-Containing Protein 67	0.6	0
<i>Wdyhv1</i>	WDYHV motif containing 1	0.6	0
<i>Abcd2</i>	ATP-binding cassette, sub-family D (ALD), member 2	0.59	2
<i>Fbxo48</i>	F-box protein 48	0.59	0
<i>Gpr155</i>	G protein-coupled receptor 155	0.59	2
<i>Mast1</i>	microtubule associated serine/threonine kinase-like	0.59	2
<i>Usp18</i>	ubiquitin specific peptidase 18	0.59	0
<i>Btbd8</i>	BTB (POZ) domain containing 8	0.58	0
<i>H2-T24</i>	histocompatibility 2, T region locus 24	0.57	0
<i>Zfand2a</i>	zinc finger, AN1-type domain 2A	0.57	1
<i>BC028528</i>	cDNA sequence BC028528	0.56	0
<i>Ttc5</i>	tetratricopeptide repeat domain 5	0.56	0
<i>Zfp36l2</i>	zinc finger protein 36, C3H type-like 2	0.56	2
<i>Chek2</i>	checkpoint kinase 2	0.55	2
<i>Mybl1</i>	myeloblastosis oncogene-like 1	0.55	0
<i>Hoxb6</i>	homeobox B6	0.53	2
<i>Klh30</i>	kelch-like 30	0.53	2
<i>Map3k8</i>	mitogen-activated protein kinase kinase kinase 8	0.53	3
<i>Chd1l</i>	chromodomain helicase DNA binding protein 1-like	0.52	0
<i>Tbc1d2b</i>	TBC1 domain family, member 2B	0.52	2
<i>Fosb</i>	FBJ osteosarcoma oncogene B	0.51	3

<i>Gem</i>	GTP binding protein (gene overexpressed in skeletal muscle)	0.51	3
<i>Tnfsf9</i>	tumor necrosis factor (ligand) superfamily, member 9	0.51	1
<i>Uevld</i>	UEV and lactate/malate dehydrogenase domains	0.51	0
<i>Acadm</i>	acyl-Coenzyme A dehydrogenase, medium chain	0.5	0
<i>Nusap1</i>	nucleolar and spindle associated protein 1	0.5	0
<i>Slc25a40</i>	solute carrier family 25, member 40	0.5	0
<i>Tada2a</i>	transcriptional adaptor 2A	0.49	2
<i>Casp7</i>	caspase 7	0.48	0
<i>Clec4a3</i>	C-type lectin domain family 4, member a3	0.48	0
<i>Dusp2</i>	dual specificity phosphatase 2	0.48	3
<i>Iffo1</i>	intermediate filament family orphan 1	0.48	2
<i>Il15ra</i>	interleukin 15 receptor, alpha chain	0.48	2
<i>Mtss1</i>	metastasis suppressor 1	0.48	0
<i>Rhebl1</i>	Ras homolog enriched in brain like 1	0.48	2
<i>Hps3</i>	Hermansky-Pudlak syndrome 3 homolog (human)	0.47	0
<i>Prc1</i>	protein regulator of cytokinesis 1	0.47	0
<i>Marveld1</i>	MARVEL (membrane-associating) domain containing 1	0.46	2
<i>Acad12</i>	acyl-Coenzyme A dehydrogenase family, member 12	0.45	0
<i>Fos</i>	FBJ osteosarcoma oncogene	0.45	3
<i>Racgap1</i>	Rac GTPase-activating protein 1	0.45	0
<i>Sgol2</i>	shugoshin-like 2 (S. pombe)	0.45	0
<i>Sgsh</i>	N-sulfoglucosamine sulfohydrolase (sulfamidase)	0.45	2
<i>Abcd1</i>	ATP-binding cassette, sub-family D (ALD), member 1	0.44	0
<i>Fgd4</i>	FYVE, RhoGEF and PH domain containing 4	0.44	2
<i>Junb</i>	Jun-B oncogene	0.43	3
<i>Ptk2b</i>	PTK2 protein tyrosine kinase 2 beta	0.42	0
<i>Rasa3</i>	RAS p21 protein activator 3	0.42	2
<i>Sipa1</i>	signal-induced proliferation associated gene 1	0.42	2
<i>Slco2b1</i>	solute carrier organic anion transporter family, member 2b1	0.42	0
<i>Bora</i>	bora, aurora kinase A activator	0.41	0
<i>Inpp5d</i>	inositol polyphosphate-5-phosphatase D	0.41	0
<i>Ttk</i>	Ttk protein kinase	0.41	0
<i>Alox5</i>	arachidonate 5-lipoxygenase	0.4	0
<i>Aurkb</i>	aurora kinase B	0.39	0
<i>Fbxo9</i>	f-box protein 9	0.39	0
<i>Kbtbd11</i>	kelch repeat and BTB (POZ) domain containing 11	0.39	2
<i>Kif20a</i>	kinesin family member 20A	0.39	0
<i>Pus10</i>	pseudouridylate synthase 10	0.39	0
<i>Rgs14</i>	regulator of G-protein signaling 14	0.39	2
<i>Traf3ip3</i>	TRAF3 interacting protein 3	0.39	2
<i>Troap</i>	trophinin associated protein	0.39	1
<i>Accs</i>	1-aminocyclopropane-1-carboxylate synthase (non-functional)	0.36	2
<i>Cep55</i>	centrosomal protein 55	0.36	0
<i>Appl2</i>	adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 2	0.35	0

* Group 0, all mRNAs with no significant change in expression levels during 2h stimulation of RAW264.7 macrophages with LPS; Group 1, mRNAs with a significant maximum at or after 1h; Group 2, mRNAs with a significant minimum at or after 1h; Group 3, mRNAs with a significant maximum before 1h; Group 4, mRNAs with a significant minimum before 1h.