

Table S1. Fold change between *Nfkb1*^{-/-}*Il10*^{-/-} and *Il10*^{-/-} BMDM for all 216 probe sets induced at least 4-fold by LPS.

Affy ID	Symbol	Name	FC	p
1420549_at	Gbp1	guanylate nucleotide binding protein 1	182.13	0.00
1419043_a_at	ligp1	interferon inducible GTPase 1	19.01	0.01
1421008_at	Rsad2	radical S-adenosyl methionine domain containing 2	14.27	0.00
1451905_a_at	Mx1	myxovirus (influenza virus) resistance 1	14.03	0.01
1424339_at	Oasl1	2'-5' oligoadenylate synthetase-like 1	13.77	0.00
1419042_at	ligp1	interferon inducible GTPase 1	13.01	0.01
1422095_a_at	Tyki	thymidylate kinase family LPS-inducible member	12.68	0.01
1449009_at	Tgtp	T-cell specific GTPase	12.30	0.01
1418612_at	Slfn1	schlafen 1	12.23	0.02
1418293_at	lfit2	interferon-induced protein with tetratricopeptide repeats 2	10.68	0.01
1435331_at	AI447904	expressed sequence AI447904	10.44	0.02
1421009_at	Rsad2	radical S-adenosyl methionine domain containing 2	10.40	0.00
1438676_at	Mpa2l	macrophage activation 2 like	10.36	0.00
1449497_at	Il12b	interleukin 12b	10.21	0.00
1418191_at	Usp18	ubiquitin specific peptidase 18	9.97	0.01
1450484_a_at	Tyki	thymidylate kinase family LPS-inducible member	9.67	0.00
1419530_at	Il12b	interleukin 12b	9.13	0.00
1417679_at	Gfi1	growth factor independent 1	8.50	0.00
1418219_at	Il15	interleukin 15	7.25	0.00
1451050_at	Nt5c3	5'-nucleotidase, cytosolic III	7.01	0.00
1419676_at	Mx2	myxovirus (influenza virus) resistance 2	6.90	0.00
1431591_s_at	LOC677168	hypothetical protein LOC677168	6.87	0.01
1428027_at	NA	NA	6.62	0.00
1438716_at	AI451617	expressed sequence AI451617	6.33	0.00
1417793_at	ligp2	interferon inducible GTPase 2	6.30	0.00
1418930_at	Cxcl10	chemokine (C-X-C motif) ligand 10	6.06	0.00
1451537_at	Chi3l1	chitinase 3-like 1	5.82	0.00
1418652_at	Cxcl9	chemokine (C-X-C motif) ligand 9	5.76	0.01
1430005_a_at	Batf2	basic leucine zipper transcription factor, ATF-like 2	5.49	0.00
1425806_a_at	Surb7	SRB7 (suppressor of RNA polymerase B) homolog (S. cerevisiae)	5.38	0.00
1450783_at	lfit1	interferon-induced protein with tetratricopeptide repeats 1	5.16	0.01
1450297_at	Il6	interleukin 6	5.02	0.00
1419026_at	Daxx	Fas death domain-associated protein	4.93	0.00
1453939_x_at	LOC677168	hypothetical protein LOC677168	4.84	0.00
1417292_at	lfi47	interferon gamma inducible protein 47	4.83	0.01
1449227_at	Ch25h	cholesterol 25-hydroxylase	4.83	0.00
1417141_at	Igtp	interferon gamma induced GTPase	4.72	0.00
1436058_at	Rsad2	radical S-adenosyl methionine domain containing 2	4.60	0.01
1425156_at	Gbp6	guanylate binding protein 6	4.55	0.00
1425394_at	BC023105	cDNA sequence BC023105	4.50	0.00
1450403_at	Stat2	signal transducer and activator of transcription 2	4.46	0.01
1419697_at	Cxcl11	chemokine (C-X-C motif) ligand 11	4.38	0.07
1450173_at	Ripk2	receptor (TNFRSF)-interacting serine-threonine kinase 2	4.22	0.00
1448940_at	Trim21	tripartite motif protein 21	4.19	0.00
1419149_at	Serpine1	serine (or cysteine) peptidase inhibitor, clade E, member 1	4.11	0.00
1450788_at	Saa1	serum amyloid A 1	4.10	0.00
1449450_at	Ptges	prostaglandin E synthase	4.08	0.00
1418317_at	Lhx2	LIM homeobox protein 2	3.99	0.01
1421679_a_at	Cdkn1a	cyclin-dependent kinase inhibitor 1A (P21)	3.97	0.00
1450446_a_at	Socs1	suppressor of cytokine signaling 1	3.97	0.01
1421911_at	Stat2	signal transducer and activator of transcription 2	3.88	0.00
1418077_at	Trim21	tripartite motif protein 21	3.85	0.00

1421473_at	Il1a	interleukin 1 alpha	3.82	0.00
1419604_at	Zbp1	Z-DNA binding protein 1	3.73	0.02
1419858_at	lfi203	interferon activated gene 203	3.69	0.00
1450639_at	Slc28a2	solute carrier family 28 (sodium-coupled nucleoside transporter), member 2	3.66	0.01
1451340_at	Arid5a	AT rich interactive domain 5A (Mrf1 like)	3.58	0.00
1451567_a_at	lfi203	interferon activated gene 203	3.53	0.01
1436899_at	2700019D07Rik	RIKEN cDNA 2700019D07 gene	3.43	0.00
1449449_at	Ptges	prostaglandin E synthase	3.43	0.00
1452178_at	Plec1	plectin 1	3.34	0.00
1435454_a_at	BC006779	cDNA sequence BC006779	3.34	0.01
1427736_a_at	Ccr1	chemokine (C-C motif) receptor-like 2	3.32	0.00
1434372_at	AW112010	expressed sequence AW112010	3.07	0.05
1421236_at	Ripk2	receptor (TNFRSF)-interacting serine-threonine kinase 2	2.99	0.00
1424698_s_at	Gca	grancalcin	2.97	0.00
1449028_at	Rhou	ras homolog gene family, member U	2.95	0.00
1418392_a_at	Gbp3	guanylate nucleotide binding protein 3	2.94	0.00
1426276_at	lfi1	interferon induced with helicase C domain 1	2.89	0.00
1419282_at	Ccl12	chemokine (C-C motif) ligand 12	2.85	0.09
1434380_at	Gbp6	guanylate binding protein 6	2.83	0.00
1424638_at	Cdkn1a	cyclin-dependent kinase inhibitor 1A (P21)	2.82	0.00
1448436_a_at	lrf1	interferon regulatory factor 1	2.81	0.00
1460415_a_at	Cd40	CD40 antigen	2.78	0.00
1449473_s_at	Cd40	CD40 antigen	2.77	0.00
1429527_a_at	Plscr1	phospholipid scramblase 1	2.76	0.00
1420499_at	Gch1	GTP cyclohydrolase 1	2.73	0.00
1453181_x_at	Plscr1	phospholipid scramblase 1	2.70	0.00
1436172_at	Samd9l	sterile alpha motif domain containing 9-like	2.52	0.02
1450672_a_at	Trex1	three prime repair exonuclease 1	2.48	0.02
1419721_at	Gpr109a	G protein-coupled receptor 109A	2.46	0.01
1417262_at	Ptgs2	prostaglandin-endoperoxide synthase 2	2.33	0.00
1449027_at	Rhou	ras homolog gene family, member U	2.27	0.01
1419714_at	Cd274	CD274 antigen	2.26	0.00
1417851_at	Cxcl13	chemokine (C-X-C motif) ligand 13	2.26	0.34
1455393_at	Cp	ceruloplasmin	2.25	0.09
1443414_at	C78513	EST C78513	2.22	0.00
1450829_at	Tnfaip3	tumor necrosis factor, alpha-induced protein 3	2.17	0.00
1427932_s_at	1200016E24Rik	RIKEN cDNA 1200016E24 gene	2.16	0.00
1419075_s_at	Saa2	serum amyloid A 2	2.10	0.00
1417371_at	Peli1	pellino 1	2.01	0.00
1422924_at	Tnfsf9	tumor necrosis factor (ligand) superfamily, member 9	2.00	0.00
1454070_a_at	Dhdh1	DDHD domain containing 1	1.94	0.01
1425570_at	Slamf1	signaling lymphocytic activation molecule family member 1	1.94	0.00
1417495_x_at	Cp	ceruloplasmin	1.93	0.14
1419607_at	Tnf	tumor necrosis factor	1.91	0.00
1420380_at	Ccl2	chemokine (C-C motif) ligand 2	1.91	0.01
1418992_at	F10	coagulation factor X	1.91	0.10
1418535_at	Rgl1	ral guanine nucleotide dissociation stimulator,-like 1	1.89	0.00
1417494_a_at	Cp	ceruloplasmin	1.86	0.09
1424067_at	Icam1	intercellular adhesion molecule	1.86	0.00
1448734_at	Cp	ceruloplasmin	1.84	0.19
1450698_at	Dusp2	dual specificity phosphatase 2	1.84	0.01
1423006_at	Pim1	proviral integration site 1	1.82	0.03
1448728_a_at	Nfkbiz	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta	1.82	0.02
1448606_at	Edg2	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2	1.81	0.03
1448162_at	Vcam1	vascular cell adhesion molecule 1	1.79	0.01
1420981_a_at	Lmo4	LIM domain only 4	1.76	0.01
1421228_at	Ccl7	chemokine (C-C motif) ligand 7	1.72	0.16

1418240_at	Gbp2	guanylate nucleotide binding protein 2	1.71	0.07
1419212_at	Icosl	icos ligand	1.71	0.01
1416649_at	Ambp	alpha 1 microglobulin/bikunin	1.70	0.00
1419537_at	Tcfec	transcription factor EC	1.70	0.02
1421578_at	Ccl4	chemokine (C-C motif) ligand 4	1.69	0.11
1417143_at	Edg2	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2	1.67	0.04
1451458_at	Tmem2	transmembrane protein 2	1.66	0.06
1425686_at	Cflar	CASP8 and FADD-like apoptosis regulator	1.66	0.01
1435133_at	Ugcg	UDP-glucose ceramide glucosyltransferase	1.65	0.00
1421269_at	Ugcg	UDP-glucose ceramide glucosyltransferase	1.61	0.10
1425412_at	Nlrp3	NLR family, pyrin domain containing 3	1.54	0.03
1421487_a_at	Nck1	non-catalytic region of tyrosine kinase adaptor protein 1	1.53	0.01
1422474_at	Pde4b	phosphodiesterase 4B, cAMP specific	1.51	0.00
1418126_at	Ccl5	chemokine (C-C motif) ligand 5	1.51	0.58
1435906_x_at	Gbp2	guanylate nucleotide binding protein 2	1.50	0.25
1417856_at	Relb	avian reticuloendotheliosis viral (v-rel) oncogene related B	1.50	0.01
1417483_at	Nfkbiz	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta	1.50	0.11
1422473_at	Pde4b	phosphodiesterase 4B, cAMP specific	1.48	0.02
1417496_at	Cp	ceruloplasmin	1.48	0.50
1423602_at	Traf1	Tnf receptor-associated factor 1	1.47	0.02
1460251_at	Fas	Fas (TNF receptor superfamily member)	1.46	0.01
1449984_at	Cxcl2	chemokine (C-X-C motif) ligand 2	1.45	0.01
1450769_s_at	Stard5	StAR-related lipid transfer (START) domain containing 5	1.45	0.01
1449591_at	Casp4	caspace 4, apoptosis-related cysteine peptidase	1.45	0.14
1422822_at	Stard5	StAR-related lipid transfer (START) domain containing 5	1.45	0.01
1416268_at	Ets2	E26 avian leukemia oncogene 2, 3' domain	1.44	0.01
1424711_at	Tmem2	transmembrane protein 2	1.43	0.05
1420331_at	Clec4e	C-type lectin domain family 4, member e	1.42	0.02
1421268_at	Ugcg	UDP-glucose ceramide glucosyltransferase	1.41	0.23
1449317_at	Cflar	CASP8 and FADD-like apoptosis regulator	1.40	0.09
1448881_at	Hp	haptoglobin	1.39	0.10
1422526_at	Acs1	acyl-CoA synthetase long-chain family member 1	1.36	0.21
1416576_at	Socs3	suppressor of cytokine signaling 3	1.34	0.01
1419354_at	Klf7	Kruppel-like factor 7 (ubiquitous)	1.34	0.05
1421457_a_at	Samsn1	SAM domain, SH3 domain and nuclear localization signals, 1	1.31	0.06
1450918_s_at	Src	Rous sarcoma oncogene	1.30	0.13
1448558_a_at	Pla2g4a	phospholipase A2, group IVA (cytosolic, calcium-dependent)	1.29	0.06
1416572_at	Mmp14	matrix metalloproteinase 14 (membrane-inserted)	1.29	0.58
1420330_at	Clec4e	C-type lectin domain family 4, member e	1.28	0.02
1431843_a_at	Nfkbie	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon	1.25	0.13
1417523_at	Plek	pleckstrin	1.25	0.13
1449399_a_at	Il1b	interleukin 1 beta	1.25	0.45
1418641_at	Lcp2	lymphocyte cytosolic protein 2	1.23	0.15
1420591_at	Gpr84	G protein-coupled receptor 84	1.21	0.44
1450136_at	Cd38	CD38 antigen	1.20	0.74
1419355_at	Klf7	Kruppel-like factor 7 (ubiquitous)	1.19	0.40
1418401_a_at	Dusp16	dual specificity phosphatase 16	1.18	0.11
1450643_s_at	Acs1	acyl-CoA synthetase long-chain family member 1	1.18	0.35
1421065_at	Jak2	Janus kinase 2	1.16	0.34
1427381_at	Irg1	immunoresponsive gene 1	1.16	0.64
1419254_at	Mthfd2	methylenetetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase	1.15	0.73
1419665_a_at	Nupr1	nuclear protein 1	1.14	0.52

1437111_at	Zc3h12c	zinc finger CCCH type containing 12C	1.12	0.30
1418133_at	Bcl3	B-cell leukemia/lymphoma 3	1.11	0.53
1460283_at	Mefv	Mediterranean fever	1.11	0.59
1419666_x_at	Nupr1	nuclear protein 1	1.11	0.60
1418642_at	Lcp2	lymphocyte cytosolic protein 2	1.10	0.55
1423240_at	Src	Rous sarcoma oncogene	1.09	0.72
1449439_at	Klf7	Kruppel-like factor 7 (ubiquitous)	1.08	0.50
1450826_a_at	Saa3	serum amyloid A 3	1.06	0.90
1433741_at	Cd38	CD38 antigen	1.06	0.91
1421066_at	Jak2	Janus kinase 2	1.06	0.57
1455899_x_at	Socs3	suppressor of cytokine signaling 3	1.05	0.79
1417256_at	Mmp13	matrix metalloproteinase 13	1.05	0.90
1448175_at	Ehd1	EH-domain containing 1	1.04	0.82
1456212_x_at	Socs3	suppressor of cytokine signaling 3	1.04	0.85
1418847_at	Arg2	arginase type II	1.04	0.87
1422953_at	Fpr-rs2	formyl peptide receptor, related sequence 2	1.02	0.96
1422018_at	Hivep2	human immunodeficiency virus type I enhancer binding protein 2	1.01	0.93
1416012_at	Ehd1	EH-domain containing 1	1.01	0.95
1438841_s_at	Arg2	arginase type II	-1.05	0.85
1416011_x_at	Ehd1	EH-domain containing 1	-1.06	0.67
1423017_a_at	Il1rn	interleukin 1 receptor antagonist	-1.10	0.81
1423289_a_at	1810029B16Rik	RIKEN cDNA 1810029B16 gene	-1.10	0.68
1437917_at	D530037H12Rik	RIKEN cDNA D530037H12 gene	-1.10	0.57
1416010_a_at	Ehd1	EH-domain containing 1	-1.12	0.40
1451798_at	Il1rn	interleukin 1 receptor antagonist	-1.14	0.47
1419561_at	Ccl3	chemokine (C-C motif) ligand 3	-1.16	0.55
1416701_at	Rnd3	Rho family GTPase 3	-1.22	0.57
1449222_at	Ebi3	Epstein-Barr virus induced gene 3	-1.23	0.19
1425663_at	Il1rn	interleukin 1 receptor antagonist	-1.23	0.21
1419356_at	Klf7	Kruppel-like factor 7 (ubiquitous)	-1.25	0.20
1416700_at	Rnd3	Rho family GTPase 3	-1.26	0.28
1419684_at	Ccl8	chemokine (C-C motif) ligand 8	-1.35	0.54
1422868_s_at	Gda	guanine deaminase	-1.48	0.11
1421720_a_at	Dtx2	deltex 2 homolog (Drosophila)	-1.51	0.00
1427035_at	Slc39a14	solute carrier family 39 (zinc transporter), member 14	-1.55	0.01
1423996_a_at	Il4ra	interleukin 4 receptor, alpha	-1.57	0.03
1450214_at	Adora2b	adenosine A2b receptor	-1.57	0.01
1426600_at	Slc2a1	solute carrier family 2 (facilitated glucose transporter), member 1	-1.58	0.02
1437992_x_at	Gja1	gap junction membrane channel protein alpha 1	-1.58	0.06
1415800_at	Gja1	gap junction membrane channel protein alpha 1	-1.60	0.10
1438650_x_at	Gja1	gap junction membrane channel protein alpha 1	-1.65	0.02
1419209_at	Cxcl1	chemokine (C-X-C motif) ligand 1	-1.65	0.09
1426599_a_at	Slc2a1	solute carrier family 2 (facilitated glucose transporter), member 1	-1.71	0.00
1438945_x_at	Gja1	gap junction membrane channel protein alpha 1	-1.73	0.05
1450808_at	Fpr1	formyl peptide receptor 1	-1.74	0.21
1419410_at	Batf	basic leucine zipper transcription factor, ATF-like	-1.87	0.00
1425503_at	Gcnt2	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme	-1.89	0.01
1428306_at	Ddit4	DNA-damage-inducible transcript 4	-2.12	0.03
1423594_a_at	Ednrb	endothelin receptor type B	-2.45	0.00
1428942_at	Mt2	metallothionein 2	-2.53	0.06
1416432_at	Pfkfb3	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3	-2.68	0.00
1437308_s_at	F2r	coagulation factor II (thrombin) receptor	-2.78	0.01
1452408_at	Trex1	three prime repair exonuclease 1	-3.64	0.02
1460197_a_at	Steap4	STEAP family member 4	-3.99	0.00
1419082_at	Serpinb2	serine (or cysteine) peptidase inhibitor, clade B, member 2	-4.23	0.00

FC refers to expression in *Nfkb1*^{-/-}*Il10*^{-/-} BMDM divided by expression in *Il10*^{-/-} BMDM following stimulation with LPS in the presence of exogenous IL-10. p refers to the P-value between genotypes calculated using the Benjamini-Hochberg correction for multiple comparison testing. All listed genes were induced at least 4 fold by LPS in either *Il10*^{-/-} or *Nfkb1*^{-/-}*Il10*^{-/-} BMDM. Duplicates, ESTs, and hypothetical genes have been removed.

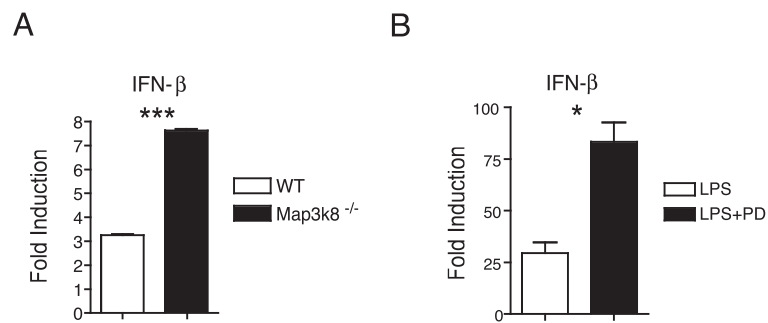


Figure S1. Increased IFN- β expression in the absence of Tpl-2/ERK signaling. A) Fold-induction of IFN- β mRNA in WT and *Map3k8*^{-/-} BMDM 9 hours after stimulation with LPS (10 ng/ml). B) Fold-induction of *Ifnb1* mRNA in WT BMDM stimulated for 4h with LPS in the presence or absence of PD184352 (PD).