Supplementary Figure 1. Additional examples of genes within the three groups of TNF-activated genes. 3T3 fibroblasts were stimulated with TNF (10 ng/ml). At indicated times after addition of TNF, mRNA transcripts encoding genes in each group were measured by RT-qPCR and normalized to Rp/32 as described in **Methods**. The results are shown as mean \pm s.d. of triplicate samples and representative of four independent experiments with similar results.

Supplementary Figure 2. Kinetic patterns of TNF-induced gene expression in human dermal primary fibroblasts. Cells were exposed to continual TNF (10 ng/ml) stimulation (TNF; solid diamond), or to 6 hours of TNF followed by medium alone (TNF removal; open square). At indicated times after initial addition of TNF, mRNA transcripts encoding indicated genes were measured by RT-qPCR and normalized to *Rpl32* as described in **Methods**. However, *Rpl32* in these cells was expressed in approximately 100-fold lower amounts than in 3T3 cells. Note that only one time point was taken after removal of TNF so the kinetics of the drop in mRNA concentration are not evident. The results are shown as mean \pm s.d. of triplicate samples from one representative experiment. Numbers in parentheses show the half life of the mRNA, determined by addition to ActD at 6h following TNF stimulation, which is similar to that determined at 0.5h of TNF stimulation for most genes (data not shown)

Supplementary Figure 3. Effect of TNF concentration on gene expression patterns. 3T3 fibroblasts were treated with 10 ng/ml (solid diamond) or 1 ng/ml (open square) TNF and mRNA transcripts encoding indicated genes were measured by qRT-PCR. The data are mean \pm s.d. of triplicate samples and representative of three independent experiments with similar results.

Supplementary Figure 4. Schematic of GFP transgene constructs with various promoters and 3'UTRs.

Supplementary Figure 1



Supplementary Figure 2.





Supplementary Fig. 3





Supplementary Figure 4

promoter	GFP	3' UTR
pCxcl2		3'Fos
pCxcl10		3'Ccl5
pCcl5		

Supplementary Table 1. List of the three groups of genes

			relative			
Gene			basal		TNF	
name	Alias, or sequence description	Accession #	level	fol	d induct	ion
				0.5h	2h	12h
Blood ves	sel regulators					
Ptgs2	Cox-2	M94967	1.59	2.01	-1.46	-2.94
Edn1	endothelin 1	D43775	0.30	3.98	-1.19	1.02
Ereg	epiregulin	NM_007950	1.72	2.12	1.32	-1.08
Cell death,	survival					
Gadd45b	growth arrest and DNA-damage-inducible	41/040400	4.00	0.40	0.00	4.00
		AK010420	1.80	3.16	2.36	1.69
ler2	immediate early response 2	NM_010499	1.20	2.35	-1.18	-1.82
Chemokine	or cytokine					
Cxcl1	Gro1	NM_008176	0.70	28.08	11.98	6.20
Cxcl2	Scyb2	NM_009140	0.02	44.86	9.09	3.59
116	interleukin 6	NM_031168	0.31	14.20	8.40	6.30
Lif	leukemia inhibitory factor	AF065917	0.17	5.69	3.41	2.06
mRNA stab	ility					
Btg2	B-cell translocation gene 2	NM_007570	0.24	3.07	1.22	-2.19
Zfp36	TTP	X14678	0.49	6.65	1.84	-1.04
Signal trans	sduction					
Tnfaip3	A20	NM_009397	1.41	9.71	5.99	2.51
ler3	immediate early response 3	NM_133662.1	5.34	4.08	2.49	1.93
Sqstm1	sequestosome 1	NM_011018	0.36	2.04	1.48	-1.00
Transcriptio	n factors or modulators					
Atf3	activating transcription factor 3	NM_007498	0.38	2.04	1.62	1.95
Axud1	Axud1	BG070296	0.31	2.45	-1.66	-4.62
c-Jun	Jun oncogene	NM_010591	2.69	2.00	1.01	-1.10
c-Fos	FBJ osteosarcoma oncogene	AV026617	0.49	4.71	-1.92	-6.42
lfrd1	interferon-related developmental regulator 1	BB531645	0.15	3.51	1.60	-1.14
Nfkbia	IkBa	NM_010907	1.42	10.03	7.47	3.63
Nfkbiz	IkBzeta	NM_030612	0.62	5.71	3.63	2.00
Irf1	interferon regulatory factor 1	NM_008390	0.77	7.69	5.41	2.86
Junb	Jun-B oncogene	NM_008416	1.44	2.14	1.12	-1.83
Tieg	TGFB inducible early growth response	NM_013692	1.91	2.26	1.18	-1.86
Others						
Slc25a25	solute carrier family 25	BC019978.1	0.28	2.35	1.15	-1.29

Group I genes, (fold>=2.0, p<0.01)

Supplementary Table 1. Continued

		p, p < 0.01 are show	<u> </u>			
0			Relative			
Gene	Comuna Decemination	A	basal	INF falslinskustian		
Name	Sequence Description	Accession #	level			406
Andersteel				0.50	Zn	120
Anti-viral a	ind immune response					
lfi47	interferon gamma inducible protein, 47 kDa	NM_008330	0.02	3.50	37.17	20.91
Tgtp	T-cell specific GTPase	NM_011579	0.03	1.36	24.75	9.73
Blood vesse	el regulators					
Gch	GTP cyclohydrolase 1	NM_008102	0.16	1.24	6.11	5.67
Cell adhesio	on and migration					
lcam1	intercellular adhesion molecule 1	BC008626	0.03	3.09	30.01	22.70
Vcam1	vascular cell adhesion molecule 1	BB250384	1.29	2.34	5.30	4.36
Cell death a	nd survival					
Birc2	baculoviral IAP repeat-containing 2	NM_007464	0.35	1.53	5.25	6.27
Tnfrsf6	Fas	NM_007987	0.50	1.11	3.54	2.66
Chemokine	s or cytokines					
Ccl2	MCP-1, Scya2	AF065933	0.74	9.10	17.44	19.62
Ccl20	MIP-3a, Scya20	AF099052	0.02	100	100	100
Ccl7	MCP-3, Scya7	AF128193	0.34	5.90	10.53	14.09
Cx3cl1	Scyd1, Fractalkine	AF010586	0.88	1.90	4.82	2.62
Cxcl10	IP-10, Scyb10	NM_021274	0.26	10.91	31.91	17.03
Cxcl5	ENA-78, Scyb5	NM_009141	2.87	2.93	3.36	2.72
CSF1	colony stimulating factor 1 (macrophage)	NM_007778	2.53	1.90	3.00	2.10
Ch25h	cholesterol 25-hydroxylase	NM_009890	0.09	7.87	15.15	13.50
Signal trans	sduction					
lfngr2	Interferon gamma receptor 2	BF537076	0.25	1.26	3.01	3.04
p21	cyclin-dependent kinase inhibitor 1A (P21)	NM_007669	0.21	2.46	4.26	1.19
Ripk2	RIP2,	NM_138952.1	0.44	1.62	8.22	2.41
S1pr3	sphingosine-1-phosphate receptor 3	AV238324	0.54	1.37	3.36	3.11
Tlr2	toll-like receptor 2	NM_011905	0.66	2.67	7.30	4.79
Cebpd	CEBP beta	BB831146	1.78	1.22	4.36	1.93
Nfkbie	IkBe	BB820441	0.15	3.03	28.35	20.00
Relb		NM_009046	0.09	2.78	9.40	8.05
Tnfaip2	B94	BB233088	0.72	1.53	3.83	1.95
Npal1	RIKEN cDNA 3830408G10 gene	AK014427	0.23	1.42	3.14	1.24
Rnd1	°	BE852181	0.99	2.67	3.16	3.25
Tmem140	transmembrane protein 140	BC020080.1	0.44	1.04	3.32	2.36
Stx11	RIKEN cDNA 5830405C08 gene	AK017897	0.52	1.82	4.71	2.23

Group II genes (only those fold>=3. p<0.01 are shown)

Supplementary Table 1. Continued

Cene Name Alias, or Sequence description Accession # TNF tol induction Antigen presentation 1.20 1.75 4.02 H2-D1 histocompatibility 2, K region BC011306 0.37 1.02 2.56 2.68 H2-L histocompatibility 2, L region BC011306 0.37 1.02 2.56 2.56 2.58 H2-L histocompatibility 2, L region M34962 0.23 1.30 1.70 3.66 H a-associated invariant chain BC003476 0.16 1.05 2.49 7.31 Psmb10 protessociated invariant chain BC003476 0.06 1.26 7.69 360.01 Itirt a-associated invariant chain BC003476 0.06 1.26 7.69 360.01 Itirt interferon-induced protein 2 NM_010260 0.06 1.26 7.69 360.01 Itirt interferon-induced protein with tetratraticopaptide repeats 1 NM_007609 0.04 1.66 7.81 18.72 Cdsn comeodesmosin BM231053				relative			
Gene Name Alias, or Sequence description Accession # Ievel fold induction Mattigen presentation 0.5h 2h 12h H2-D1 histocompatibility 2, D region locus 1 M86502 1.29 1.20 1.75 4.02 H2-L histocompatibility 2, Ir region BC011306 0.37 1.02 2.56 29.68 H2-L histocompatibility 2, Ir region M40462 0.23 1.30 1.70 3.66 H Ia-associated invariant chain BC003476 0.16 1.05 2.49 7.31 Psmb10 proteasome subunit, beta type 10 NM.01640 0.81 1.13 2.52 5.02 Gbp2 guanylate nucleotide binding protein 2 NM_010260 0.06 1.26 7.69 36.09 Iffit interferon-induced protein with NM_007609 0.04 1.86 7.81 18.72 Cdsn compelement component 3 SC021053 0.61 1.08 1.65 5.98 Cdf and survival M2 metallothionein 2				basal		TNF	
Antigen presentation 0.5h 2h 12h Antigen presentation histocompatibility 2, D region locus 1 M86502 1.29 1.20 1.75 4.02 H2-K histocompatibility 2, K region BC011306 0.37 1.02 2.56 29.68 H2-L histocompatibility 2, L region M34962 0.23 1.30 1.70 3.66 H2-L histocompatibility 2, L region M34962 0.23 1.30 1.70 3.66 H2-L histocompatibility 2, L region M34962 0.23 1.30 1.70 3.66 H2-D proteasome subunit, beta type 10 NML013640 0.81 1.13 2.52 5.02 Tapbp TAP binding protein AF043943 4.55 1.08 1.74 3.11 Antiviral and immune response C3 complement component 3 M02782 0.07 2.65 6.14 55.51 Call adhesion and migration Casa correodesmosin BM231053 0.61 1.08 1.65 5.89 C	Gene Name	Alias, or Sequence description	Accession #	level	fold	inductio	n
Antigen presentation H2-D1 Inistocompatibility 2, D region locus 1 M86502 1.29 1.75 4.02 H2-L histocompatibility 2, L region BC011306 0.37 1.02 2.56 29.68 H2-L histocompatibility 2, L region M34962 0.23 1.30 1.70 3.66 II Ia-associated invariant chain BC003476 0.16 1.05 2.49 7.31 Parbh 10 proteasome suburit, beta type 10 NM 013640 0.81 1.13 2.52 5.02 Tapbp TAP binding protein AF043943 4.55 1.08 1.74 3.11 Anti-viral and immune response c 0.07 2.65 6.14 55.51 G3 complement component 3 K02782 0.07 2.65 6.14 5.84 Cell adhesion and migration tetratricopeptide repeats 1 NM_008331 0.10 -1.00 2.40 5.84 Caspa caspase 11 NM_007609 0.04 1.86 7.81 18.72 Cds					0.5h	2h	12h
H2-D1 histocompatibility 2, D region locus 1 M86502 1.29 1.20 1.75 4.02 H2-K histocompatibility 2, K region BC011306 0.37 1.02 2.56 29.66 Ii la-associated invariant chain BC003476 0.16 1.05 2.49 7.31 Psmb 10 proteasome subunit, beta type 10 NM_013640 0.81 1.13 2.52 5.02 Anti-viral and immune response TAP binding protein AF043943 4.55 1.08 1.74 3.11 Anti-viral and immune response User trainicopetide repeats 1 NM_012640 0.06 1.26 7.69 36.09 Gbp2 guarylate nucleoide binding protein 2 NM_010260 0.06 1.26 7.69 36.09 Iffit interferon-induced protein with tetratricopetide repeats 1 NM_008331 0.10 -1.08 7.81 8.72 Cdsn conneodesmosin BM231053 0.61 1.08 7.81 8.72 Sod3 superoxide dismutase 3, extracellular NM_013650 0.27	Antigen presen	tation					
H2-K histocompatibility 2, K region BC011306 0.37 1.02 2.56 29.68 H2-L histocompatibility 2, L region M34962 0.23 1.70 3.66 Hi la-associated invariant chain BC003476 0.16 1.05 2.49 7.31 Psmb10 proteasome subunit, beta type 10 NM_013640 0.81 1.13 2.52 5.02 Tapbp TAP binding protein AF043943 4.55 1.08 1.74 3.11 Anti-viral and immune response complement component 3 K02782 0.07 2.65 6.14 55.51 Gbp2 guanylate nucleotide binding protein 2 NM_010260 0.06 1.26 7.69 36.09 lift interferon-induced protein with tetratricopeptide repeats 1 NM_007609 0.04 1.86 7.81 18.72 Cdsn cosmedesmosin BM231053 0.61 1.08 1.65 5.99 M2 metallothionein 2 AA796766 1.35 1.58 3.14 5.24 <t< td=""><td>H2-D1</td><td>histocompatibility 2, D region locus 1</td><td>M86502</td><td>1.29</td><td>1.20</td><td>1.75</td><td>4.02</td></t<>	H2-D1	histocompatibility 2, D region locus 1	M86502	1.29	1.20	1.75	4.02
H2-L histocompatibility 2, L region M34962 0.23 1.30 1.70 3.66 li la-associated invariant chain BC003476 0.16 1.05 2.49 7.31 Psmb10 proteasome subunit, beta type 10 NM_013840 0.81 1.13 2.52 5.02 Tapbp TAP binding protein AF043943 4.55 1.08 1.74 3.11 Anti-viral and immune response C3 complement component 3 K02782 0.07 2.65 6.14 55.51 Gbp2 guanylate nucleotide binding protein 2 NM_010260 0.06 1.26 7.69 36.09 Ifirit interferon-induced protein with tetratricopetide repeats 1 NM_007609 0.04 1.86 7.81 18.72 Casp4 caspase 11 NM_007609 0.04 1.86 7.81 18.72 M2 metallothionein 2 AA796766 1.35 1.58 3.14 5.24 Sod3 superoxide dismutase 3, extracellular NM 014335 0.02 -1.74 3.66 100 Casp4 caspase 1 No NM_023137	H2-K	histocompatibility 2, K region	BC011306	0.37	1.02	2.56	29.68
II Ia-associated invariant chain BC003476 0.16 1.05 2.49 7.31 Psmb10 proteasome subunit, beta type 10 NM_013840 0.81 1.13 2.52 5.02 Tapbp TAP binding protein AF043943 4.55 1.08 1.74 3.11 Anti-viral and immune response C3 complement component 3 K02782 0.07 2.65 6.14 5.51 Gbp2 guanylate nucleotide binding protein 2 NM_010260 0.06 1.26 7.69 36.09 Iftit utertarticopeptide repeats 1 NM_00831 0.10 1.00 2.40 5.84 Cell adhesion and migration comeodesmosin BM231053 0.61 1.08 1.55 5.89 Cell death and survival metallothionein 2 AA796766 1.35 1.58 3.14 5.24 Sod3 superoxide dismutase 3, extracellular NM_011435 0.27 1.13 1.67 3.04 Ubd ubiquitin D NM_023137 0.99 -1.08 1.74	H2-L	histocompatibility 2, L region	M34962	0.23	1.30	1.70	3.66
Psmb10 proteasome subunit, beta type 10 NM_013640 0.81 1.13 2.52 5.02 Tapbp TAP binding protein AF043943 4.55 1.08 1.74 3.11 Anti-viral and immune response complement component 3 K02762 0.07 2.65 6.14 55.51 Gbp2 guanylate nucleolide binding protein 2 NM_010260 0.06 1.26 7.69 36.09 Ifirit tetratricopeptide repeats 1 NM_008331 0.10 -1.00 2.40 5.84 Call adhesion and migration compeodesmosin BM231053 0.61 1.08 7.81 18.72 Cdsn comeodesmosin BM231053 0.61 1.08 1.65 5.89 Cell death and survival mtdl metallobinonein 2 AA796766 1.35 1.58 3.14 5.24 Sod3 superoxide dismutase 3, extracellular NM_011435 0.27 1.13 1.67 3.04 Serpin3a serina protease inhibitor 2-1, BC002065 0.06 1.11 2.	li	la-associated invariant chain	BC003476	0.16	1.05	2.49	7.31
Tapbp TAP binding protein AF043943 4.55 1.08 1.74 3.11 Anti-viral and immune response C3 complement component 3 K02782 0.07 2.65 6.14 55.51 Gbp2 guanylate nucleotide binding protein 2 NM_010260 0.06 1.26 7.69 36.09 Ifit interferon-induced protein with tetratricopeptide repeats 1 NM_007609 0.04 1.86 7.81 18.72 Casn cospase 11 NM_007609 0.04 1.86 7.81 18.72 Casn correodesmosin BM231053 0.61 1.08 7.81 18.72 Sod3 superoxide dismutase 3, extracellular NM_011435 0.27 1.13 1.67 3.04 Serpina3g serine protease inhibitor 2-1, BC002065 0.06 1.11 5.65 19.18 Ubd ubiquitin D NM_023137 0.09 -1.08 1.71 9.14 Chemokines and cytokine A9 AF128196 0.24 1.41 2.47 4.11	Psmb10	proteasome subunit, beta type 10	NM_013640	0.81	1.13	2.52	5.02
Anti-viral and immune response C3 complement component 3 K02782 0.07 2.65 6.14 55.51 Gbp2 guanylate nucleotide binding protein 2 NM_010260 0.06 1.26 7.69 36.09 Iff:1 interferon-induced protein with tetratricopeptide repeats 1 NM_00831 0.10 -1.00 2.40 5.84 Cell adhesion and migration caspase 11 NM_007609 0.04 1.86 7.81 18.72 Cdsn corneodesmosin BM231053 0.61 1.08 1.65 5.89 Cell death and survival MZ metallothionein 2 AA796766 1.35 1.58 3.14 5.24 Sod3 superoxide dismutase 3, extracellular NM_011435 0.27 1.13 1.67 3.04 Serpina3g serine protease inhibitor 2-1, BC002065 0.06 1.11 5.65 1.91 Ubd ubiquitin D NM_013653 0.02 -1.74 3.6 100 Carls RANTES, Scya5 NM_013653 0.19 1.02 <td>Tapbp</td> <td>TAP binding protein</td> <td>AF043943</td> <td>4.55</td> <td>1.08</td> <td>1.74</td> <td>3.11</td>	Tapbp	TAP binding protein	AF043943	4.55	1.08	1.74	3.11
C3 complement component 3 K02782 0.07 2.65 6.14 55.51 Gbp2 guanylate nucleotide binding protein 2 NM_010260 0.06 1.26 7.69 36.09 Ifirit interferon-induced protein with NM_008331 0.10 -1.00 2.40 5.84 Cell adhesion and migration Casp.4 caspase 11 NM_007609 0.04 1.86 7.81 18.72 Cdsn comeodesmosin BM231053 0.61 1.08 1.65 5.89 Cell death and survival 3.14 5.24 Sod3 superoxide dismutase 3, extracellular NM_011435 0.27 1.13 1.67 3.04 Serpina3g serine protease inhibitor 2-1, BC002065 0.06 1.11 5.65 19.18 Ubd ubiquitin D NM_013653 0.02 -1.74 3.66 100 Ccl9 small inducible cytokine A9 AF128196 0.24 1.41 2.47 4.11 Lcn2 lipocali	Anti-viral and in	nmune response					
Gbp2 Iffit guanylate nucleotide binding protein 2 Iffit NM_010260 0.06 1.26 7.69 36.09 Iffit interferon-induced protein with tetratricopeptide repeats 1 NM_008331 0.10 -1.00 2.40 5.84 Cell adhesion and migration caspase 11 NM_007609 0.04 1.86 7.81 18.72 Cdsn corneodesmosin BM231053 0.61 1.08 1.65 5.89 Mt2 metallothionein 2 AA796766 1.35 1.58 3.14 5.24 Sod3 superoxide dismutase 3, extracellular NM_011435 0.27 1.13 1.67 3.04 Serpina3g serine protease inhibitor 2-1, B0020265 0.06 1.11 5.65 19.18 Ubd ubiquitin D NM_013653 0.02 -1.74 3.6 100 Ccl5 RANTES, Scya5 NM_013653 0.02 -1.74 3.6 100 Signaling transduction It13 receptor a1 B108103 0.19 1.02 2.17 3.44 <	C3	complement component 3	K02782	0.07	2.65	6.14	55.51
tetratricopeptide repeats 1 NM_008331 0.10 -1.00 2.40 5.84 Cell adhesion and migration Caspa4 caspase 11 NM_007609 0.04 1.86 7.81 18.72 Cdsn corneodesmosin BM231053 0.61 1.08 1.65 5.89 Cell death and survival metallothionein 2 AA796766 1.35 1.58 3.14 5.24 Sod3 superoxide dismutase 3, extracellular NM_011435 0.27 1.13 1.67 3.04 Serpina3g serine protease inhibitor 2-1, BC002065 0.06 1.11 5.65 19.18 Ubd ubiquitin D NM_021337 0.09 -1.08 1.71 9.14 Chemokines and cytokines C/// and and modelse cytokine A9 AF128196 0.24 1.41 2.47 4.11 Lon2 lipocalin 2 X14607 0.16 -1.42 1.01 4.81 Signaling transduction Ill3ra1 IL13 receptor a1 Bl081033 0.19 1.02 2.17 3.44	Gbp2 Ifit1	guanylate nucleotide binding protein 2 interferon-induced protein with	NM_010260	0.06	1.26	7.69	36.09
Call adhesion and migration Casp4 caspase 11 NM_007609 0.04 1.86 7.81 18.72 Casn comeodesmosin BM231053 0.61 1.08 1.65 5.89 Cell death and survival metallothionein 2 AA796766 1.35 1.58 3.14 5.24 Sod3 superoxide dismutase 3, extracellular NM_011435 0.27 1.13 1.67 3.04 Serpina3g serine protease inhibitor 2-1, BC002065 0.06 1.11 5.65 19.18 Ubd ubiquitin D NM_013653 0.02 -1.74 33.6 100 Cc/5 RANTES, Scya5 NM_013653 0.02 -1.74 33.6 100 Call gipaaling transduction intoricible cytokine A9 AF128196 0.24 1.41 2.47 4.11 Lcn2 lipocalin 2 X14607 0.16 -1.42 1.01 4.81 Il13ra1 IL13 receptor a1 Bl081033 0.19 1.02 2.17 3.44<		tetratricopeptide repeats 1	NM_008331	0.10	-1.00	2.40	5.84
Casp4 caspase 11 NM_007609 0.04 1.86 7.81 18.72 Cdsn corneodesmosin BM231053 0.61 1.08 1.65 5.89 Cell death and survival metallothionein 2 AA796766 1.35 1.58 3.14 5.24 Sod3 superoxide dismutase 3, extracellular NM_011435 0.27 1.13 1.67 3.04 Serpina3g serine protease inhibitor 2-1, BC002065 0.06 1.11 5.65 19.18 Ubd ubiquitin D NM_023137 0.09 -1.08 1.71 9.14 Chemokines and cytokines Ccl5 RANTES, Scya5 NM_013653 0.02 -1.74 33.6 100 Ccl9 small inducible cytokine A9 AF128196 0.24 1.41 2.47 4.11 Lcn2 lipocalin 2 X14607 0.16 -1.42 1.01 4.81 Signaling transduction Ill3ra1 L13 receptor a1 M0.010743 0.88 1.25 2.35 6.13	Cell adhesion a	nd migration					
Cdsn corneodesmosin BM231053 0.61 1.08 1.65 5.89 Cell death and survival Mt2 metallothionein 2 AA796766 1.35 1.58 3.14 5.24 Sod3 superoxide dismutase 3, extracellular NM_011435 0.27 1.13 1.67 3.04 Serpina3g serine protease inhibitor 2-1, BC002065 0.06 1.11 5.65 19.18 Ubd ubiquitin D NM_023137 0.09 -1.08 1.71 9.14 Cells RANTES, Scya5 NM_013653 0.02 -1.74 33.6 100 Carl9 small inducible cytokine A9 AF128196 0.24 1.41 2.47 4.11 Lcn2 lipocalin 2 X14607 0.16 -1.42 1.01 4.81 Signaling transduction II/13ra1 IL13 receptor a1 Bl081033 0.19 1.02 2.17 3.44 I/I1/1 interleukin 1 receptor-like 1 NM_010743 0.88 1.25 2.35 6.13	Casp4	caspase 11	NM_007609	0.04	1.86	7.81	18.72
Cell death and survival MI2 metallothionein 2 AA796766 1.35 1.58 3.14 5.24 Sod3 superoxide dismutase 3, extracellular NM_011435 0.27 1.13 1.67 3.04 Serpina3g serine protease inhibitor 2-1, BC002065 0.06 1.11 5.65 19.18 Ubd ubiquitin D NM_023137 0.09 -1.08 1.71 9.14 Cel5 RANTES, Scya5 NM_013653 0.02 -1.74 33.6 100 Ccl9 small inducible cytokine A9 AF128196 0.24 1.41 2.47 4.11 Lcn2 lipocalin 2 X14607 0.16 -1.42 1.01 4.81 Signaling transduction Ill'3ra1 IL13 receptor a1 BI081033 0.19 1.02 2.17 3.44 Ill'1rl1 interleukin 1 receptor-like 1 NM_010743 0.88 1.25 2.35 6.13 Naf1 Nef-associated factor 1, Abin-1 AJ242777 1.00 1.01 2.41	Cdsn	corneodesmosin	BM231053	0.61	1.08	1.65	5.89
Mf2 metallothionein 2 AA796766 1.35 1.58 3.14 5.24 Sod3 superoxide dismutase 3, extracellular NM_011435 0.27 1.13 1.67 3.04 Serpina3g serine protease inhibitor 2-1, BC002065 0.06 1.11 5.65 19.18 Ubd ubiquitin D NM_023137 0.09 -1.08 1.71 9.14 Chemokines and cytokines 0.02 -1.74 33.6 100 Cc/5 RANTES, Scya5 NM_013653 0.02 -1.74 33.6 100 Cc/9 small inducible cytokine A9 AF128196 0.24 1.41 2.47 4.11 Lcn2 lipocalin 2 X14607 0.16 -1.42 1.01 4.81 Signaling transduction li13ra1 ll-13 receptor a1 BI081033 0.19 1.02 2.17 3.44 I/1/11 interleukin 1 receptor-like 1 NM_010743 0.88 1.25 2.35 6.13 Naf1 Nef-associated	Cell death and s	survival					
Sod3 superoxide dismutase 3, extracellular NM_011435 0.27 1.13 1.67 3.04 Serpina3g serine protease inhibitor 2-1, Ubd BC002065 0.06 1.11 5.65 19.18 Ubd ubiquitin D NM_023137 0.09 -1.08 1.71 9.14 Chemokines and cytokines c/toKines c/toKines 0.02 -1.74 33.6 100 Ccl5 RANTES, Scya5 NM_013653 0.02 -1.74 33.6 100 Ccl9 small inducible cytokine A9 AF128196 0.24 1.41 2.47 4.11 Lcn2 lipocalin 2 X14607 0.16 -1.42 1.01 4.81 Signaling transduction ll13ra 1 ll13ra 1 ll13ra 1 Ndeorta 1 Abin-1 AJ242777 1.00 1.01 2.41 4.30 Naf1 Nef-associated factor 1, Abin-1 AJ242777 1.00 1.08 1.74 13.07 Mmp13 matrix metalloproteinase 13 NM_0008607 0.15 1.53	Mt2	metallothionein 2	AA796766	1.35	1.58	3.14	5.24
Serpina3g serine protease inhibitor 2-1, ubiquitin D BC002065 0.06 1.11 5.65 19.18 Ubd ubiquitin D NM_023137 0.09 -1.08 1.71 9.14 Chemokines and cytokines 1.71 9.14 Ccl5 RANTES, Scya5 NM_013653 0.02 -1.74 3.6 100 Ccl9 small inducible cytokine A9 AF128196 0.24 1.41 2.47 4.11 Lcn2 lipocalin 2 X14607 0.16 -1.42 1.01 4.81 Signaling transduction NM_010743 0.88 1.25 2.35 6.13 Naf1 Nef-associated factor 1, Abin-1 AJ242777 1.00 1.01 2.41 4.30 Tissue remodeling and wound healing Enpp2 ectonucleotide 1.53 4.86 16.48 Mmp13 matrix metalloproteinase 3 NM_010809 1.37 1.20 1.86 6.57 Serpinf1	Sod3	superoxide dismutase 3, extracellular	NM_011435	0.27	1.13	1.67	3.04
Ubd ubiquitin D NM_023137 0.09 -1.08 1.71 9.14 Chemokines and cytokines Col5 RANTES, Scya5 NM_013653 0.02 -1.74 33.6 100 Cc/9 small inducible cytokine A9 AF128196 0.24 1.41 2.47 4.11 Lcn2 lipocalin 2 X14607 0.16 -1.42 1.01 4.81 Signaling transduction II.13 receptor a1 Bl081033 0.19 1.02 2.17 3.44 I/1/11 interleukin 1 receptor-like 1 NM_010743 0.88 1.25 2.35 6.13 Naf1 Nef-associated factor 1, Abin-1 AJ242777 1.00 1.01 2.41 4.30 Tissue remodeling and wound healing pyrophosphatase/phosphodiesterase 2 BC003264 0.30 1.08 1.74 13.07 Mmp3 matrix metalloproteinase 13 NM_01809 1.37 1.20 1.86 6.57 Serpinf1 , PEDF NM_011340 2.18 1.09 1.26 4.08 <t< td=""><td>Serpina3g</td><td>serine protease inhibitor 2-1,</td><td>BC002065</td><td>0.06</td><td>1.11</td><td>5.65</td><td>19.18</td></t<>	Serpina3g	serine protease inhibitor 2-1,	BC002065	0.06	1.11	5.65	19.18
Chemokines and cytokines Cc/5 RANTES, Scya5 NM_013653 0.02 -1.74 33.6 100 Cc/9 small inducible cytokine A9 AF128196 0.24 1.41 2.47 4.11 Lcn2 lipocalin 2 X14607 0.16 -1.42 1.01 4.81 Signaling transduction Ull3ra1 IL13 receptor a1 Bl081033 0.19 1.02 2.17 3.44 <i>Il171</i> interleukin 1 receptor-like 1 NM_010743 0.88 1.25 2.35 6.13 Naf1 Nef-associated factor 1, Abin-1 AJ242777 1.00 1.01 2.41 4.30 Tissue remodeling and wound healing ectonucleotide pyrophosphatase/phosphodiesterase 2 BC003264 0.30 1.08 1.74 13.07 Mmp13 matrix metalloproteinase 13 NM_008607 0.15 1.53 4.86 6.57 Serpinf1 , PEDF NM_011340 2.18 1.09 1.26 4.08 Ppicap peptidylprolyl isomerase C-associated protein	Ubd	ubiquitin D	NM_023137	0.09	-1.08	1.71	9.14
Cc/5 RANTES, Scya5 NM_013653 0.02 -1.74 33.6 100 Cc/9 small inducible cytokine A9 AF128196 0.24 1.41 2.47 4.11 Lcn2 lipocalin 2 X14607 0.16 -1.42 1.01 4.81 Signaling transduction NM_013653 0.19 1.02 2.17 3.44 I/1/1 interleukin 1 receptor-like 1 NM_010743 0.88 1.25 2.35 6.13 Naf1 Nef-associated factor 1, Abin-1 AJ242777 1.00 1.01 2.41 4.30 Tissue remodeling and wound healing ectonucleotide pyrophosphatase/phosphodiesterase 2 BC003264 0.30 1.08 1.74 13.07 Mmp13 matrix metalloproteinase 13 NM_008607 0.15 1.53 4.86 16.48 Mmp3 matrix metalloproteinase 3 NM_011340 2.18 1.09 1.26 4.08 Ppicap petidylprolyl isomerase C-associated protein NM_011340 2.18 1.09 1.26 <td< td=""><td>Chemokines and</td><td>cytokines</td><td></td><td></td><td></td><td></td><td></td></td<>	Chemokines and	cytokines					
Cc/9 small inducible cytokine A9 AF128196 0.24 1.41 2.47 4.11 Lcn2 lipocalin 2 X14607 0.16 -1.42 1.01 4.81 Signaling transduction N13ra1 IL13 receptor a1 Bl081033 0.19 1.02 2.17 3.44 I/1/1 interleukin 1 receptor-like 1 NM_010743 0.88 1.25 2.35 6.13 Naf1 Nef-associated factor 1, Abin-1 AJ242777 1.00 1.01 2.41 4.30 Tissue remodeling and wound healing pyrophosphatase/phosphodiesterase 2 BC003264 0.30 1.08 1.74 13.07 Mmp13 matrix metalloproteinase 13 NM_008607 0.15 1.53 4.86 16.48 Mmp3 matrix metalloproteinase 3 NM_010809 1.37 1.20 1.86 6.57 Serpinf1 , PEDF NM_011340 2.18 1.09 1.26 4.08 Ppicap peptidylprolyl isomerase C-associated protein NM_011150 0.20 1.	Ccl5	RANTES, Scya5	NM_013653	0.02	-1.74	33.6	100
Lcn2 lipocalin 2 X14607 0.16 -1.42 1.01 4.81 Signaling transduction I/13ra1 IL13 receptor a1 BI081033 0.19 1.02 2.17 3.44 I/111 interleukin 1 receptor-like 1 NM_010743 0.88 1.25 2.35 6.13 Naf1 Nef-associated factor 1, Abin-1 AJ242777 1.00 1.01 2.41 4.30 Tissue remodeling and wound healing Enpp2 ectonucleotide pyrophosphatase/phosphodiesterase 2 BC003264 0.30 1.08 1.74 13.07 Mmp13 matrix metalloproteinase 13 NM_008607 0.15 1.53 4.86 16.48 Mmp3 matrix metalloproteinase 3 NM_010809 1.37 1.20 1.86 6.57 Serpinf1 , PEDF NM_011340 2.18 1.09 1.26 4.08 Ppicap peptidylprolyl isomerase C-associated protein NM_011150 0.20 1.17 1.20 3.07 Others (unknown function) Intoding cassette, sub-family A1 BB144704	Ccl9	small inducible cytokine A9	AF128196	0.24	1.41	2.47	4.11
Signaling transduction I/13ra1 IL13 receptor a1 BI081033 0.19 1.02 2.17 3.44 I/1rl1 interleukin 1 receptor-like 1 NM_010743 0.88 1.25 2.35 6.13 Naf1 Nef-associated factor 1, Abin-1 AJ242777 1.00 1.01 2.41 4.30 Tissue remodeling and wound healing Enpp2 ectonucleotide pyrophosphatase/phosphodiesterase 2 BC003264 0.30 1.08 1.74 13.07 Mmp13 matrix metalloproteinase 13 NM_008607 0.15 1.53 4.86 16.48 Mmp3 matrix metalloproteinase 3 NM_011340 2.18 1.09 1.26 4.08 Ppicap peptidylprolyl isomerase C-associated protein NM_011150 0.20 1.17 1.20 3.07 Others (unknown function) I I 1.004/C05 gene BC010291 3.38 1.24 1.97 3.77 Abca1 ATP-binding cassette, sub-family A1 BB144704 0.07 2.07 2.30	Lcn2	lipocalin 2	X14607	0.16	-1.42	1.01	4.81
II13ra1 IL13 receptor a1 BI081033 0.19 1.02 2.17 3.44 II1rl1 interleukin 1 receptor-like 1 NM_010743 0.88 1.25 2.35 6.13 Naf1 Nef-associated factor 1, Abin-1 AJ242777 1.00 1.01 2.41 4.30 Tissue remodeling and wound healing Enpp2 ectonucleotide pyrophosphatase/phosphodiesterase 2 BC003264 0.30 1.08 1.74 13.07 Mmp13 matrix metalloproteinase 13 NM_008607 0.15 1.53 4.86 16.48 Mmp3 matrix metalloproteinase 3 NM_010809 1.37 1.20 1.86 6.57 Serpinf1 , PEDF NM_011340 2.18 1.09 1.26 4.08 Ppicap peptidylprolyl isomerase C-associated protein NM_011150 0.20 1.17 1.20 3.07 Others (unknown function) 1110004C05 gene BC010291 3.38 1.24 1.97 3.77 Abca1 ATP-binding cassette, sub-family A1 BB144704 0.07 2.07 2.30 7.08 Al/861871 expressed sequence Al561871 <td< td=""><td>Signaling trans</td><td>duction</td><td></td><td></td><td></td><td></td><td></td></td<>	Signaling trans	duction					
II1rl1 interleukin 1 receptor-like 1 NM_010743 0.88 1.25 2.35 6.13 Naf1 Nef-associated factor 1, Abin-1 AJ242777 1.00 1.01 2.41 4.30 Tissue remodeling and wound healing Enpp2 ectonucleotide pyrophosphatase/phosphodiesterase 2 BC003264 0.30 1.08 1.74 13.07 Mmp13 matrix metalloproteinase 13 NM_008607 0.15 1.53 4.86 16.48 Mmp3 matrix metalloproteinase 3 NM_0110809 1.37 1.20 1.86 6.57 Serpinf1 , PEDF NM_011340 2.18 1.09 1.26 4.08 Ppicap peptidylprolyl isomerase C-associated protein NM_011150 0.20 1.17 1.20 3.07 Others (unknown function) 1110004C05 gene BC010291 3.38 1.24 1.97 3.77 Abca1 ATP-binding cassette, sub-family A1 BB144704 0.07 2.07 2.30 7.08 Al561871 expressed sequence Al561871 BI143915 0.17 -1.20 1.51 5.08 Al882074 expressed sequence Al882074 </td <td>ll13ra1</td> <td>IL13 receptor a1</td> <td>BI081033</td> <td>0.19</td> <td>1.02</td> <td>2.17</td> <td>3.44</td>	ll13ra1	IL13 receptor a1	BI081033	0.19	1.02	2.17	3.44
Naf1 Nef-associated factor 1, Abin-1 AJ242777 1.00 1.01 2.41 4.30 Tissue remodeling and wound healing Enpp2 ectonucleotide pyrophosphatase/phosphodiesterase 2 BC003264 0.30 1.08 1.74 13.07 Mmp13 matrix metalloproteinase 13 NM_008607 0.15 1.53 4.86 16.48 Mmp3 matrix metalloproteinase 3 NM_010809 1.37 1.20 1.86 6.57 Serpinf1 , PEDF NM_011340 2.18 1.09 1.26 4.08 Ppicap peptidylprolyl isomerase C-associated protein NM_011150 0.20 1.17 1.20 3.07 Others (unknown function) Ill10004C05 gene BC010291 3.38 1.24 1.97 3.77 Abca1 ATP-binding cassette, sub-family A1 BB144704 0.07 2.07 2.30 7.08 Al561871 expressed sequence Al561871 BI143915 0.17 -1.20 1.51 5.08 Al882074 expressed sequence Al882074 BB730912 0.09 1.29 <td>ll1rl1</td> <td>interleukin 1 receptor-like 1</td> <td>NM_010743</td> <td>0.88</td> <td>1.25</td> <td>2.35</td> <td>6.13</td>	ll1rl1	interleukin 1 receptor-like 1	NM_010743	0.88	1.25	2.35	6.13
Tissue remodeling and wound healing ectonucleotide pyrophosphatase/phosphodiesterase 2 BC003264 0.30 1.08 1.74 13.07 Mmp13 matrix metalloproteinase 13 NM_008607 0.15 1.53 4.86 16.48 Mmp3 matrix metalloproteinase 3 NM_010809 1.37 1.20 1.86 6.57 Serpinf1 , PEDF NM_011340 2.18 1.09 1.26 4.08 Ppicap peptidylprolyl isomerase C-associated protein NM_011150 0.20 1.17 1.20 3.07 Others (unknown function) I110004C055 gene BC010291 3.38 1.24 1.97 3.77 Abca1 ATP-binding cassette, sub-family A1 BB144704 0.07 2.07 2.30 7.08 Al561871 expressed sequence Al561871 BI143915 0.17 -1.20 1.51 5.08 Al882074 expressed sequence Al882074 BB730912 0.09 1.29 3.32 5.91 Arts1 ESTs AV287655 0.10 1.16 1.83	Naf1	Nef-associated factor 1, Abin-1	AJ242777	1.00	1.01	2.41	4.30
Enpp2 ectonucleotide pyrophosphatase/phosphodiesterase 2 BC003264 0.30 1.08 1.74 13.07 Mmp13 matrix metalloproteinase 13 NM_008607 0.15 1.53 4.86 16.48 Mmp3 matrix metalloproteinase 3 NM_010809 1.37 1.20 1.86 6.57 Serpinf1 , PEDF NM_011340 2.18 1.09 1.26 4.08 Ppicap peptidylprolyl isomerase C-associated protein NM_011150 0.20 1.17 1.20 3.07 Others (unknown function) 1110004C05 gene BC010291 3.38 1.24 1.97 3.77 Abca1 ATP-binding cassette, sub-family A1 BB144704 0.07 2.07 2.30 7.08 Al561871 expressed sequence Al561871 BI143915 0.17 -1.20 1.51 5.08 Al882074 expressed sequence Al882074 BB730912 0.09 1.29 3.32 5.91 Arts1 ESTs AV287655 0.10 1.16 1.83 3.59 <t< td=""><td>Tissue remodel</td><td>ing and wound healing</td><td></td><td></td><td></td><td></td><td></td></t<>	Tissue remodel	ing and wound healing					
Mmp13 matrix metalloproteinase 13 NM_008607 0.15 1.53 4.86 16.48 Mmp3 matrix metalloproteinase 3 NM_010809 1.37 1.20 1.86 6.57 Serpinf1 , PEDF NM_011340 2.18 1.09 1.26 4.08 Ppicap peptidylprolyl isomerase C-associated protein NM_011150 0.20 1.17 1.20 3.07 Others (unknown function) 1110004C05 gene BC010291 3.38 1.24 1.97 3.77 Abca1 ATP-binding cassette, sub-family A1 BB144704 0.07 2.07 2.30 7.08 Al561871 expressed sequence Al561871 BI143915 0.17 -1.20 1.51 5.08 Al882074 expressed sequence Al882074 BB730912 0.09 1.29 3.32 5.91 Arts1 ESTs AV287655 0.10 1.16 1.83 3.59 Lhfpl2 lipoma HMGIC fusion partner-like 2 BG917242 0.02 1.82 6.77 23.29	Enpp2	ectonucleotide	BC003264	0.30	1.08	1 74	13 07
Mmp 10 matrix metalloproteinade 10 Mm_2000001 0.10 1.00	Mmn13	matrix metalloproteinase 13	NM 008607	0.00	1.53	4 86	16.07
Serpinf1 , PEDF NM_011340 2.18 1.09 1.26 4.08 Ppicap peptidylprolyl isomerase C-associated protein NM_011150 0.20 1.17 1.20 3.07 Others (unknown function) 1110004C05Rik RIKEN cDNA 1110004C05 gene BC010291 3.38 1.24 1.97 3.77 Abca1 ATP-binding cassette, sub-family A1 BB144704 0.07 2.07 2.30 7.08 Al561871 expressed sequence Al561871 BI143915 0.17 -1.20 1.51 5.08 Al882074 expressed sequence Al882074 BB730912 0.09 1.29 3.32 5.91 Arts1 ESTs AV287655 0.10 1.16 1.83 3.59 Lhfpl2 lipoma HMGIC fusion partner-like 2 BG917242 0.02 1.82 6.77 23.29	Mmp3	matrix metalloproteinase 3	NM 010809	1.37	1.20	1.86	6.57
Ppicap peptidylprolyl isomerase C-associated protein NM_011150 0.20 1.17 1.20 3.07 Others (unknown function) 1110004C05Rik RIKEN cDNA 1110004C05 gene BC010291 3.38 1.24 1.97 3.77 Abca1 ATP-binding cassette, sub-family A1 BB144704 0.07 2.07 2.30 7.08 Al561871 expressed sequence Al561871 BI143915 0.17 -1.20 1.51 5.08 Al882074 expressed sequence Al882074 BB730912 0.09 1.29 3.32 5.91 Arts1 ESTs AV287655 0.10 1.16 1.83 3.59 Lhfpl2 lipoma HMGIC fusion partner-like 2 BG917242 0.02 1.82 6.77 23.29	Serpinf1	. PEDF	NM 011340	2.18	1.09	1.26	4.08
Others (unknown function) BC010291 3.38 1.24 1.97 3.77 Abca1 ATP-binding cassette, sub-family A1 BB144704 0.07 2.07 2.30 7.08 Al561871 expressed sequence Al561871 Bl143915 0.17 -1.20 1.51 5.08 Al882074 expressed sequence Al882074 BB730912 0.09 1.29 3.32 5.91 Arts1 ESTs AV287655 0.10 1.16 1.83 3.59 Lhfpl2 lipoma HMGIC fusion partner-like 2 BG917242 0.02 1.82 6.77 23.29	Ppicap	peptidylprolyl isomerase C-associated protein	NM 011150	0.20	1.17	1.20	3.07
1110004C05Rik RIKEN cDNA 1110004C05 gene BC010291 3.38 1.24 1.97 3.77 Abca1 ATP-binding cassette, sub-family A1 BB144704 0.07 2.07 2.30 7.08 Al561871 expressed sequence Al561871 Bl143915 0.17 -1.20 1.51 5.08 Al882074 expressed sequence Al882074 BB730912 0.09 1.29 3.32 5.91 Arts1 ESTs AV287655 0.10 1.16 1.83 3.59 Lhfpl2 lipoma HMGIC fusion partner-like 2 BG917242 0.02 1.82 6.77 23.29	Others (unknow	In function)		0.20			0.01
Abca1 ATP-binding cassette, sub-family A1 BB144704 0.07 2.07 2.30 7.08 Al561871 expressed sequence Al561871 Bl143915 0.17 -1.20 1.51 5.08 Al882074 expressed sequence Al882074 BB730912 0.09 1.29 3.32 5.91 Arts1 ESTs AV287655 0.10 1.16 1.83 3.59 Lhfpl2 lipoma HMGIC fusion partner-like 2 BG917242 0.02 1.82 6.77 23.29	1110004C05Rik	RIKEN cDNA 1110004C05 gene	BC010291	3.38	1.24	1.97	3.77
Alsolation expressed sequence Alsolation BI143915 0.17 -1.20 1.51 5.08 Alsolation expressed sequence Alsolation BI143915 0.17 -1.20 1.51 5.08 Alsolation expressed sequence Alsolation BB730912 0.09 1.29 3.32 5.91 Arts1 ESTs AV287655 0.10 1.16 1.83 3.59 Lhfpl2 lipoma HMGIC fusion partner-like 2 BG917242 0.02 1.82 6.77 23.29	Abca1	ATP-binding cassette, sub-family A1	BB144704	0.07	2.07	2.30	7.08
Al882074 expressed sequence Al882074 BB730912 0.09 1.29 3.32 5.91 Arts1 ESTs AV287655 0.10 1.16 1.83 3.59 Lhfpl2 lipoma HMGIC fusion partner-like 2 BG917242 0.02 1.82 6.77 23.29	AI561871	expressed sequence AI561871	BI143915	0.17	-1.20	1.51	5.08
Arts1 ESTs AV287655 0.10 1.16 1.83 3.59 Lhfpl2 lipoma HMGIC fusion partner-like 2 BG917242 0.02 1.82 6.77 23.29	AI882074	expressed sequence Al882074	BB730912	0.09	1.29	3.32	5.91
<i>Lhfpl2</i> lipoma HMGIC fusion partner-like 2 BG917242 0.02 1.82 6.77 23.29	Arts1	ESTs	AV287655	0.10	1.16	1.83	3.59
	Lhfpl2	lipoma HMGIC fusion partner-like 2	BG917242	0.02	1.82	6.77	23.29

Group III genes (only those fold >=3, p<0.01 are shown)

LOC677168	cDNA, RIKEN clone:2900034J12,	AK019325	0.25	-1.06	2.32	5.91
AW049765		BC026642.1	0.10	-1.41	2.57	21.95
Prnd	prion protein dublet	AF165166	0.02	1.18	3.38	28.41
U90926	cDNA sequence U90926	NM_020562	0.38	-1.16	1.03	3.72

Supplementary Table 2. Stability of mRNA transcripts measured using two different approaches

	5 (,
	Genes	6h TNF p	retreatment
		TNFa removal	ActD treatment
Group II	Ccl20	1.30 ± 0.12	3.33 ± 1.02
	Ccl2	1.38 ± 0.09	0.82 ± 0.01
	Ccl7	1.56 ± 0.21	1.32 ± 0.06
	Tlr2	1.93 ± 0.25	1.27 ± 0.32
	Nfkbie	1.69 ± 0.07	1.90 ± 0.13
	Cxcl10	1.87 ± 0.05	1.92 ± 0.05
	lcam1	1.66 ± 0.20	2.30 ± 0.56
	CSF1	5.33 ± 2.51	2.60 ± 0.43
	Mmp10	10.5 ± 18.0	stable
Group III	lfit1	stable	1.97 ± 1.22
	Stat1	9.76 ± 18.5	11.7 ± 12.7
	C3	stable	stable
	Ccl5	stable	stable
	Mmp13	stable	stable
	Mmp3	stable	stable
	Saa3	stable	stable

mRNA stability (half life, h, mean \pm s.d., n=3)

Supplementary Table 3. Sequneces of qPCR primers

name	alias	species	primer name	sequence
Tnfaip3	A20	mouse	A20_(1)_F	GAACAGCGATCAGGCCAGG
			A20_(1)_R	GGACAGTTGGGTGTCTCACATT
actb	β-actin	mouse	actin_F	AGGTGTGCACCTTTTATTGGTCTCAA
			actin_R	TGTATGAAGGTTTGGTCTCCCT
C3	Complement 3	mouse	C3_(2)_F	CTGAGAAGCGTCTCCATCAAG
			C3_(2)_R	ACGGGCAGTAGGTTGTTGTC
Ccl2	MCP-1	mouse	Ccl2_F	CTGAAGACCTTAGGGCAGAT
			Ccl2_R	AAGGAATGGGTCCAGACATAC
Ccl20	MIP-3α	mouse	CCL20_F	GCCTCTCGTACATACAGACGC
			CCL20_R	CCAGTTCTGCTTTGGATCAGC
Ccl5	Rantes	mouse	Ccl5_(1)_F	GCTGCTTTGCCTACCTCTCC
			Ccl5_(1)_F	TCGAGTGACAAACACGACTGC
Ccl7	MCP-3	mouse	CCL7_(1)_F	GCTGCTTTCAGCATCCAAGTG
			CCL7_(1)_R	CCAGGGACACCGACTACTG
Ptgs2	COX-2	mouse	COX-2_F	TGAGCAACTATTCCAAACCAGC
			COX-2_R	GCACGTAGTCTTCGATCACTATC
CSF1	M-CSF	mouse	CSF1_(2)_F	AGTCAACAGAGCAACCAAACC
			CSF1_(2)_R	CAAAAATCCCTCACTAGCCTCTC
Cxcl1	KC	mouse	Cxcl1_(1)_F	CTGGGATTCACCTCAAGAACATC
			Cxcl1_(1)_R	CAGGGTCAAGGCAAGCCTC
Cxcl10	IP-10	mouse	Cxcl10_F	AGGACGGTCCGCTGCAA
			Cxcl10_R	CATICICACIGGCCCGICAI
Cxcl2	MIP-2	mouse	Cxcl2_(1)_F	CCCICAACGGAAGAACCAAAG
			Cxcl2_(1)_R	
Edn1	endotnelln-1	mouse	EI-1_(1)_F	GLALLGGAGLTGAGAATGG
F	а Г аа		EI-1_(1)_K	GIGGLAGAAGIAGACACACIC
FOS	C-FOS	mouse	FOS_(2)_F	
loom1		mouloo	FOS_(Z)_K	
ICalli	ICAIVIT	mouse		
lfi+1	lfi+1	mouro	ICAWIT_R	
Inti	111(1	mouse	liit1_(1)_F	CTGAGATGTCACTTCACATGGAA
Nfkhia	lkBa	mouse	lkBa F	
NIKBIA	INDU	mouse	IkBa_I	
Nfkhie	lkΒε	mouse	IkBe (1) F	TGGACCTCCAACTGAAGAACT
NINOIO	in Bo	medee	IkBe (1) R	TTCCTCTGCAATGTGGCAATG
ll1b	interleukin-1ß	mouse	IL-1b (1) F	GCAACTGTTCCTGAACTCAACT
	interiounin ip		IL-1b (1) R	ATCTTTTGGGGTCCGTCAACT
11.6	interleukin 6	mouse	II6 F	TAGTCCTTCCTACCCCAATTTCC
			IL6 R	TTGGTCCTTAGCCACTCCTTC
lrf1	lrf1	mouse	IRF1 (2) F	AGGCCGATACAAAGCAGGAGA
			IRF1 (2) R	GCTGCCCTTGTTCCTACTCTG
Jun	c-Jun	mouse	Jun (2) F	ACTCGGACCTTCTCACGTC
			Jun (2) R	CGGTGTAGTGGTGATGTGCC
Rpl32	L32	mouse	L32 F	AAGCGAAACTGGCGGAAAC
,			 L32_R	TAACCGATGTTGGGCATCAG
Mmp10	MMP-10	mouse		AACACGGAGACTTTTACCCTTTT
	-		MMP-10_(2)_R	GGTGCAAGTGTCCATTTCTCAT
Mmp13	MMP-13	mouse	MMP-13_(2)_F	ACCTCCACAGTTGACAGGCT
-			MMP-13_(2)_R	AGGCACTCCACATCTTGGTTT

Supplementary Table 3. Continued

name	alias	species	primer name	sequence
Mmp3	MMP-3	mouse	MMP-3_(2)_F	TGTCCCGTTTCCATCTCTCTC
			MMP-3_(2)_R	TGGTGATGTCTCAGGTTCCAG
Saa3	Saa3	mouse	Saa3_(1)_F	TGCCATCATTCTTTGCATCTTGA
			Saa3_(1)_R	CCGTGAACTTCTGAACAGCCT
Serpina3g	Spi2A	mouse	Spi2A_(1)_F	CTTCCCAACGGCTGGAATCTA
			Spi2A_(1)_R	ACTGTCCAATCAGGCATAGCG
TLR2	TLR2	mouse	TLR2_(3)_F	CCAGACACTGGGGGTAACATC
			TLR2_(3)_R	CGGATCGACTTTAGACTTTGGG
Tnf	ΤΝFα	mouse	TNF_F	CTACTCCCAGGTTCTCTTCAA
			TNF_R	GCAGAGAGGAGGTTGACTTTC
Vcam1	Vcam1	mouse	Vcam1_(1)_F	AGTTGGGGATTCGGTTGTTCT
			Vcam1_(1)_R	CCCCTCATTCCTTACCACCC
Zfp36	TTP	mouse	Zfp36_(1)_F	TCTCTGCCATCTACGAGAGCC
			Zfp36_(1)_R	CCAGTCAGGCGAGAGGTGA
Zfp36	TTP	mouse	Zfp36_(2)_F	TCGAAGAGACCCTAACCAGGC
			Zfp36_(2)_R	GCGTAGTCATCAGGATCGGA
C3	C3	human	hC3_(1)_F	CCTGCTACTAACCCACCTCC
			hC3_(1)_R	AACAGTGACTGGAACATCCCC
CCL2	MCP-1	human	hCCL2_(1)_F	CAGCCAGATGCAATCAATGCC
			hCCL2_(1)_R	TGGAATCCTGAACCCACTTCT
CCL5	Rantes	human	hCCL5_F	CCCAGCAGTCGTCTTTGTCA
			hCCL5_R	TCCCGAACCCATTTCTTCTCT
CXCL1	CXCL1	human	hCXCL1_F	CTGCGCTGCCAGTGCTTGCA
			hCXCL1_R	TGTGGCTATGACTTCGGTTTG
CXCL10	IP-10	human	hCXCL10_(1)_F	GTGGCATTCAAGGAGTACCTC
			hCXCL10_(1)_R	GCCTTCGATTCTGGATTCAGACA
FOS	c-FOS	human	hFOS_(3)_F	GGGCAAGGTGGAACAGTTATC
			hFOS_(3)_R	CCGCTTGGAGTGTATCAGTCA
GAPDH	GAPDH	human	hGAPDH_F	AACAGCGACACCCACTCCTC
			hGAPDH_R	CATACCAGGAAATGAGCTTGACAA
ICAM1	ICAM1	human	hICAM1_(1)_F	TCTGTGTCCCCCTCAAAAGTC
			hICAM1_(1)_R	GGGGTCTCTATGCCCAACAA
NFKBIA	ΙκΒα	human	hlkBa_(1)_F	CICCGAGACITICGAGGAAATAC
			hlkBa_(1)_R	GCCATIGIAGIIGGIAGCCIICA
IL6	Interleukin6	human	hIL-6_(1)_F	AAATTCGGTACATCCTCGACGG
D /00	D 100		hIL-6_(1)_R	GGAAGGIICAGGIIGIIIICIGC
Kpl32	RpI32	human	nL32_F	AGUICUUAAAAAIAGAUGUAU
	055		hL32_R	
GFP	GFP		GFP_(BMC)_F	GGAGCGCACGATCTTCTTCA
050			GFP_(BMC)_R	AGGGIGICGCCCICGAA
GFP	GFP			
			GFP_(6)_R	IGGGIGCICAGGIAGIGGIIG