Legends to Supplemental Figures

Ramirez-Carrozzi et al.

Supplemental Figure 1. Efficiency of Brg1 and Brm Knockdown by Retroviral shRNA Transduction.

Brg1/Brm knockdown experiments were performed as described in the Experimental Procedures and in Ramirez-Carrozzi et al. (2006). The Brg1 (left panel) and Brm (right panel) Western blots in this figure show the knockdown efficiency at the time of LPS stimulation, which was generally 5 days after retroviral transduction. HMG1 antibodies were included in the Western blots as a loading control. The effects of Brg1/Brm knockdown on gene transcription are shown in Figure 1.

Supplemental Figure 2. Normalized Precursor Transcript Levels for CpG-Island and Non-CpG-Island Genes

The results of two independent experiments are shown (parts A and B) examining relative precursor transcript levels for several LPS-induced genes containing CpG-island (red) or non-CpG-island (black) promoters. Two housekeeping genes, *Gapd* and *Act*, were examined as controls. Real-time RT-PCR signals for the various genes were normalized using genomic DNA. RT-PCR primers (see Suppl. Table 1C) used to examine most genes spanned an exon-intron junction, thereby restricting amplification to precursor transcripts. However, the primers for five of the genes (four Class A genes, *Irf1, Junb, Zfp36, Cxcl1,* and one Class D gene, *Ifnb1*), amplified both precursor transcripts and mature mRNA because no introns exist in these genes therefore over-represent the precursor transcript levels. Primers for two other genes, *Egr1* and *Act*, also amplified both precursor transcripts to the amount of genomic DNA (in ng) required to yield the same signal observed by real-time RT-PCR when analyzing total RNA.

Precursor transcripts were analyzed in unstimulated bone marrow-derived macrophages (top panels) or macrophages stimulated with LPS for 30 min (second panels) or 120 min (third panels). The bottom panel shows the fold-induction at the 30 min and 120 min time-point for each gene relative to the unstimulated value, following normalization to the *Gapd* transcript levels.

Supplemental Figure 3. Changes in RNA Polymerase II Levels at CpG-Island and Non-CpG-Island Promoters Following LPS Stimulation.

ChIP experiments were performed with RNA polymerase II antibodies in bone marrow-derived macrophages left unstimulated (top panel) or stimulated for 30 min (second panel) or 120 min (third panel) with LPS. PCR amplification efficiencies for the various primer pairs were normalized using genomic DNA. In each panel, genes are ordered from lowest to highest RNA polymerase II levels. The bottom panel directly compares the changes in polymerase levels at each gene at each time point. In this panel, the genes are ordered as in the top panel. The results show that polymerase levels change only modestly at most CpG-island promoters following induction, with more dramatic changes at most non-CpG-island promoters and a few CpG-island promoters (e.g. *Cxcl2*). Results are presented as the average values with standard deviations from 3 independent immunoprecipitation experiments using two different chromatin preparations.

Supplemental Figure 4. Modest Changes in Histone H3 Levels Following LPS Stimulation

ChIP experiments were performed with histone H3 antibodies in bone marrow-derived macrophages left unstimulated (top panel) or stimulated for 30 min (second panel) or 120 min (third panel) with LPS. PCR amplification efficiencies for the various primer pairs were normalized using genomic DNA. In each panel, genes are ordered from highest to lowest histone H3 levels. The bottom panel directly compares the change in histone H3 levels at each gene at each time point. In this panel, the genes are ordered as in the top panel. The results

show that, although histone H3 levels decrease considerably at some CpG-island and non-CpG-island genes following induction, the H3 levels remain relatively unchanged at many other genes, with a consistent trend in both unstimulated and stimulated cells toward lower histone H3 levels at CpG-island promoters. Results are presented as the average values with standard deviations from 3 independent immunoprecipitation experiments using two different chromatin preparations.

Supplemental Figure 5. Unusually High DNase I Hypersensitivity Scores at Class A Genes in Resting CD4+ T Cells

(A) Maximum DNase I hypersensitivity scores for the human homologues of 64 of the 67 genes in our dataset are shown from an analysis of quiescent CD4+ T cells (Boyle et al., 2008). Hypersensitivity scores greater than 2.5 are colored red. Scores were obtained from the Duke DNase sig track at the UCSC Genome Browser. The CpG content is shown for the corresponding mouse genes, although the presence or absence of CpG islands was found to be strongly conserved between the mouse and human genomes (data not shown). Expression studies (Wang et al. 2008b) revealed that at least 9 of the Class A genes are induced following activation of human CD4+ T cells. However, this number almost certainly represents an underestimate of the number of Class A genes that are induced in these cells because the studies examined mRNA levels only at late time points, after many Class A genes are known to be downregulated.

(B) Maximum DNase I hypersensitivity scores in unstimulated CD4+ T cells from the Boyle et al. (2008) analysis are shown for 7 non-CpG-island genes that exhibited the strongest induction in CD4+ T cells in mRNA expression analyses (Wang et al. 2008a, 2008b). None of these genes exhibit high scores in unstimulated cells.

Wang, Z., Zang, C., Rosenfeld, J.A., Schones, D.E., Barski, A., Cuddapah S., Cui, K., Roh, T.Y., Peng, W., Zhang, M.Q., and Zhao, K. (2008a). Combinatorial patterns of histone acetylations and methylations in the human genome. Nat. Genet. *40*, 897-903.

Wang, M., Windgassen, D., and Papoutsakis, E.T. (2008b). Comparative analysis of transcriptional profiling of CD3+, CD4+, and CD8+ T cells identifies novel immune response players in T-cell activation. BMC Genomics *9*, 225.

Supplemental Figure 6. Consensus IRF3 Binding Sites are Over-Represented in Class D Promoters

(A) DNA motifs that perfectly match the IRF3 consensus sequence A/TAANNGAAA were identified between -1 and -300 relative to the transcription start site of each of the 67 genes. IRF3 consensus sequences were found in this interval in 6 of the 10 Class D genes, but in only 6 of the remaining 57 genes, two of which exhibited IRF3-dependence (*Cxcl11* and *Gbp2*). Consensus Sp1 and NF- κ B sites are also shown. Although perfect matches to the Sp1 and NF- κ B consensus sequences were identified in only a small number of genes, the factors are thought to regulate many more genes by binding to DNA motifs that diverge from the strict consensus.

(B) The fraction of promoters in each class with consensus IRF3 binding sites between -1 and -300 relative to the main transcription start site (found in the Dbtss database) is shown, along with the consensus sequences used to survey the promoters.

(C) ChIP experiments were performed with antibodies directed against IRF3, as well as GST as a negative control and C/EBP β as a positive control, using chromatin from unstimulated and LPS-stimulated J774 macrophages. Results are presented as a percentage of input values.

Supplemental Figure 7. Fold-Induction Values for Genes Induced by Various Stimuli

The data in Figure 5 of the main manuscript compare mRNA levels for 61 primary and secondary response genes following stimulation of bone marrow-derived macrophages with 5 different stimuli. In Figure 5, mRNA levels are shown as a percentage of the highest level found following induction by any of the stimuli (set at 100%). In this figure, the data are instead presented as fold-inductions at the 30-min, 1-hr, and 2-hr time points relative to the mRNA

levels observed in unstimulated cells. The results show the same trends that are apparent in Figure 5, with preferential activation of Class C and Class D genes by IFN β and preferential activation of Class A genes by TNF α . However, these fold-induction values provide additional insights. For example, although TNF α activates Class A genes more strongly than genes in the other classes, especially when compared to the level of activation observed with the TLR stimuli, it can activate several genes in the other classes several fold above background. However, the expression levels remain very low relative to the levels achieved with the TLR stimuli. Furthermore, TLR2 activates Class D genes to a significant extent above background, despite the fact that TLR2 is known to be incapable of activating IRF3. Nevertheless, the level of induction of these genes achieved by TLR2 remains well below the level of induction achieved by TLR3 and TLR4, whereas genes in the other classes were induced similarly by TLR2, TLR3, and TLR4.









Α					I	Maximum DNasel
		СрО	6 / Expec	ted	DNasel	HS
C	Class	Gene	-200 / 1		HS	Score
		Cd83	2.3		Yes	6.09
		Nr4a1	2.0		Yes	4.99
		Ccrn4l	2.0		Yes	3.62
		lrf1	1.9		Yes	3.96
		NfKDIZ	1.9		Yes	3.32
		Pim1	1.0		Yes	11 45
		Socs3	1.7		Yes	5.06
		Tnfaip3	1.5		Yes	4.68
		Egr1	1.5		Yes	5.60
		Junb	1.5		Yes	2.65
	Λ	Marcksl1	1.4		Yes	1.05
	A	BCI3	1.3		Yes	3.58
		Zfn36	1.3		Yes	2.62
		Tnfsf9	1.1		Yes	1.55
		Nfkbia	1.1		Yes	4.39
		Fosb	1.1		Yes	3.48
		Egr2	1.1		Yes	5.94
S		Fos	1.0		Yes	4.42
Je		NfKDid Btgo2	0.8		Yes	2.79
θĽ		Pigsz Tir2	0.0			2 25
Ğ		Cxcl1	0.7		No	2.25
Ú		Cxc/2	0.6		No	
9e		Tnf	0.6		Yes	1.75
ŝ		Ccrl2	0.5		Yes	1.37
ō		Traf1	0.2		Yes	1.64
ā		Cxcl11	0.2		No	
S		Clec4e	0.2		NO No	
Se	B	Csf2	0.2		No	
		ll23a	0.2		Yes	2.27
N		Cc/3	0.2		No	
al		Gbp2	0.0		Yes	1.75
Ä		Gbp1	0.1		Yes	1.64
L		ll1b Mar 240	0.0		No	0.50
P		Map3k8 Sernine1	1.0		Yes	2.53
		Arhgef3	0.2		Yes	3.06
	~	Vcam1	0.2		No	
	C	Saa3	0.2		Yes	0.91
		Cc/2	0.2		No	
		1110 14640	0.2		NO Voc	2.02
		Peli1	1.0		No	2.02
		lfit2	0.5		Yes	2.04
		Cxcl10	0.4		Yes	0.18
		lfit1	0.2		Yes	2.30
	υ	lfnb1	0.1		No	
		Mmp13	0.1		No	
		LCIS Ifit3	0.0		NO Yos	1 32
		into	0.0		100	1.02
		Tyki	1.4		Yes	3.46
2		Rsad2	0.2		Yes	1.81
ar		lrf7	0.2		Yes	3.76
q		116 11125	0.2		Yes	0.70
L	E	Nos2	0.2		No	
<u> </u>		Lcn2	0.2		No	
90		Marco	0.2		No	
Š		Mx1	0.2		Yes	3.04
~ •		Mx2	0.1		Yes	2.32
		Serpinb3b	0.0		No	

Maximum DNasel HS	' E	B	(
≥ 2.5 < 2.5 CpG / Expec	ted	II2 Ccl4 Ccl3 Cxcl9 Ifng	
0.6 < 0.6		Csf2 Xcl2	

			Maximum DNasel
	CpG	DNasel	HS
Gene	Island	HS	Score
<i>ll</i> 2	No	Yes	1.44
Ccl4	No	No	
Ccl3	No	No	
Cxcl9	No	No	
lfng	No	Yes	0.84
Csf2	No	No	
Xcl2	No	No	





Α

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F

IRF3 A/TAANNGAAA NFxB GGGRNNYYCC Sp1 GGCGGG

C/EBPβ

GST

IRF3

C/EBPβ

GST

IRF3





	% Induction	250 33. 49% 0 - 33%	
% Induction	IRF3-/- w/ CHX	W Cr.X 248 248 248 248 248 248 248 258 258 258 258 258 258 258 25	
% Induction	Brg1/Brm RNAi	Autor 167 167 167 167 167 167 167 167	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
	Induction	2nd highest 3rd highest CpG / Expected 0.6 < 0.6	
	TNFα TNFα 1h 2h	1 1	- 9 - 9 <mark>8 9 - 8 - 7</mark> - 9 - 9 - 9 - 9 - 8 - 9
	TNFα 30'	90 	- 9 - 10 m n
	FNB IFNB 1h 2h	1 1 </td <td>N N N N N N N N N N N N N N N N N N N</td>	N N N N N N N N N N N N N N N N N N N
	1FNβ 1 30'	······································	2 ° ~ ~ ~ ~ ~ ° 7
	84 TLR4 2h	2 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	214 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
	rLR4 TLF 30' 1h	30 31 32 31 32 31 32 31 32 33 34 34 34<	2 ND 12 12 12 10 10 10 10 10 10 10 10 10 10 10 10 10
	TLR3 2h	1 1	22 28 28 28 28 28 28 28 28 28 28 28 28 2
	tLR3 1h		∾ 9 ~ 8 8 8 ∞ ~ ~ ~ ~
	22 TLR3 30'	8 8 9 <td>- 9 - <mark>9</mark> N</td>	- 9 - <mark>9</mark> N
	LR2 TLF 1h 2h	1 1	1 2 2 1 4 2 1 4 4 1 1 2 1 4 4 1 4 4 1 2 1 3 3 1 3 1 3 1 3 1 3 1 3 1 3 1 3 1
q	TLR2 T 30'	<mark>ៜ</mark> ៲៰ ៜ ៰ ৮ ៰ ៰ ៲៰ ៰ ៰ ៰ ៰ ៰ ៰ ៰ ៰ ៰ ៰ ៰ ៰ ៰ ៰	0 2 − 0 − 7 0 − 7 0 − 7
pG / Expecte	-200/-1	4 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
Ū	Gene	Cada3 Inth Inth Inth Socs3 Socs3 Frintip3 Egr1 Frintip3 Egr2 Forb Marcksh Bcr3 Forbid	Rsad2 117 116 116 116 1112b 1115b 11
	Class		J LL]

Primary Response Genes

Secondary

	Gapd	TGGTGAAGGTCGGTGTGAAC	CCATGTAGTTGAGGTCAATGAAGG
ΗK	Actb	AGAGGGAAATCGTGCGTGAC	CAATAGTGATGACCTGGCCGT
	Cd83	CATCCTCAGATGGCAACCTT	TGCTCAAGACCCTGTGTCAG
	Nr4a1	CTGTCCGCTCTGGTCCTCATC	GGTCTCCTGCCACCCTACC
	Ccrn4l	AAGATCCCCCTGATCGTCT	GGICICCIGCCACGGIAGC
	Irf1	TCCAACTCCACCCCACACA	
	Nfkhiz	CECCOCCERCACCOACCAAC	
	Sod2	CCCCCTACCTCAACAATCTC	TGAACTTCACTCCACCTCA
	Pim1	TCAACCACACACTCTACACCC	ACCATCCTACCAATCC
	Soce3		AGCGAIGGIAGCGAAICC
	Tnfain?	GCICCAAAAGCGAGIACCAGC	
	Far1	GGCAGCTGGAATCTCTGAAA	
	Lynh		GCGGAACCCTGATTGTTCTA
	Marckel1		
Δ	Rol2		ACCARCE CONCERNENT
~	BCIS loam1	GCGAAGTAGACGTCCATAACAACC	ACCAAGAGCCGGACCATGT
	10aiii 1 7fm26	TGTCAGCCACTGCCTTGGTA	
	ZIP30	CCCTCTGCAACTCTGGTCTC	GACCACCGGACACTGAACTT
	1111SI9	GCCCCAACACTACAACAG	
	Nikola	CCTGGCCAGTGTAGCAGTCT	AGAGGCTAGGTGCAGACACG
	FOSD Ear2	TGCGGGCCTTTGTTAATATG	
	Egr2		
	ros Nfkhid	GTGCCAGCTGCTATCCAGAAG	GGCTGTGGTTGAAGCTGGAG
	Dtero	GTGACAGCCATCTCCACCA	GTGGGGAGTCCGTAAGGATG
	Ptgs2	CCCCTTCCTGCGAAGTTTA	GAGAAGGCTTCCCAGCTTTT
	1Irz	TTTGCTGGGCTGACTTCTCT	TCGCGGATCGACTTTAGACT
	CXCI1	TGTCAGTGCCTGCAGACCAT	GTGGCTATGACTTCGGTTTGG
	Cxcl2	GCCAAGGGTTGACTTCAAGA	ACTTTTTGACCGCCCTTGAG
	Int	CCCCAAAGGGATGAGAAGTT	TGGGCTACAGGCTTGTCACT
	Ccrl2	TTCCAACATCCTCCTCCTTG	GATGCACGCAACAATACCAC
	Traf1	TGTGTGGCCGGACTGTCA	AGCGCAGGCACAACTTGTAAC
	Cxcl11	AGTAACGGCTGCGACAAAGT	CTGCATTATGAGGCGAGCTT
	Clec4e	CTGTGCCACCATAAGGGACT	TCTGGCATCTCACAAATCCA
D	li1a	AGCAGCCTTATTTCGGGAGT	GTGCAAGTGACTCAGGGTGA
D	Csf2	TTTTGTGCCTGCGTAATGAG	CAGCGTTTTCAGAGGGCTAT
	1123a	GGTGCTTATAAAAAGCCAGACC	AATAATGTGCCCCGTATCCA
	Ccl3	AGATTCCACGCCAATTCATC	CCCAGGTCTCTTTGGAGTCA
	Gbp2	CTCTACCGCACAGGCAAATC	GATGCCCTTGGTGTGAGACT
	Gbp1	ATCATATCCCTTAAACTTCAGGAACAG	GTGGAAACAGGGTAGAGAGCTTTAGI
	li1b	GCTGAAAGCTCTCCACCTCA	AGGCCACAGGTATTTTGTCG
	Map3k8	TCCAAGAAAGTGATCCACCA	CACTCAGGCCAAAATCTACCA
	Serpine1	CCGATCCTTTCTCTTTGTGG	CAAATGAAGGCGTCTCTTCC
	Arhgef3	AAGACCTGCAGGATGGAGAA	ACCGAGTCTGCTACCCACAC
	Vcam1	GCTGTGACCTGTCTGCAAAG	GTCTCCCATGCACAAGTGG
0	Saa3	CCTTCCATTGCCATCATTCT	AGTAGGCTCGCCACATGTCT
U.	Ccl2	GGGCCTGCTGTTCACAGTT	GGGATCATCTTGCTGGTGAA
	1110	AAGGACCAGCTGGACAACAT	TCATTTCCGATAAGGCTTGG
	lrg1	CACAGAGAGCTTTGCTGGTATGA	TGCTCCTCCGAATGATACCAT
	lkbke	AGCTATTCGCAGTGGAGGAA	CGAACGTGTTCTCAGGGTCT
	Cc/12	GTCCGGAAGCTGAAGAGCTA	GGGTCAGCACAGATCTCCTT
	Mmp13	GTTCAAGGAATTCAGTTTCTTTATGGT	GGTAATGGCATCAAGGGATAGG
	Peli1	CTTCCAAAGCCCCAGTAAAA	ACCCAGAGACCAAAATGAGC
	lfit2	AGAAATGCCAGGAAGACAGC	GGTGTGACACATTTCACATGG
	Cxcl10	CCTGCCCACGTGTTGAGAT	GAGTCACAGACCCGTCCCTA
υ	lfit1	TCCATTTCTGGCCATTTCTC	TGAAGCAGATTCTCCATGACC
-	lfnb1	AGCTCCAAGAAAGGACGAACAT	GCCCTGTAGGTGAGGTTGATCT
	Ccl5	GTGCCCACGTCAAGGAGTAT	CCCACTTCTTCTCTGGGTTG
	lfit3	AGTGAGGTCAACCGGGAATCT	TCTAGGTGCTTTATGTAGGCCA
E	Tyki	GGCAATTATCTCGTGGCTTC	GGCCTCCACTCACCTCAGTA
	Rsad2	AACCCCCGTGAGTGTCAACTA	AACCAGCCTGTTTGAGCAGAA
	H28	ATGGTGGCAAAGCTGAAAAA	CCGCTCCTTCTGTAGTGTCC
	Irf7	TCTTCGCTCTCTTCGCTCA	GGTCGTAGGGATCTGGATGA
	116	GTTCTCTGGGAAATCGTGGA	TTTCTGCAAGTGCATCATCG
	ll12b	AGCCACTCACATCTGCTGCT	AACCGTCCGGAGTAATTTGG
F	Nos2	CAGCTGGGCTGTACAAACCTT	CATTGGAAGTGAAGCGTTTCG
-	Lcn2	TTCCGGAGCGATCAGTTCC	TGACCAGGATGGAGGTGACA
	Marco	ATCCTGCTCACGGCAGGTACT	GCACATCTCTAGCATCTGGAGCT
	indi CO		
	Marco Mx1	AAACCTGATCCGACTTCACTTCC	TGATCGTCTTCAAGGTTTCCTTCT
	Mx1 Mx2	AAACCTGATCCGACTTCACTTCC	TGATCGTCTTCAAGGTTTCCTTGT TAGGGCAGTGATGTCCTCCT
	Mx1 Mx2 Serpinb3b	AAACCTGATCCGACTTCACTTCC AGGGTACACGTGTCCTTTCG GCTGTCCTATGTCCCCCCCCAGAA	TGATCGTCTTCAAGGTTTCCTTGT TAGGGCAGTGATGTCCTGGT ATCCCCCCAGAAACCTCAACT

	Class	Gene	Forward Primer	Reverse Primer
	ЦК	Gapd	GGTCCAAAGAGAGGGAGGAG	GCCCTGCTTATCCAGTCCTA
	IUL	Actb	GAGGGGAGAGGGGGGTAAAA	TCGAGCCATAAAAGGCAACT
		Irf1	TTTCCCCGAAATGATGAGG	GCCGCGAAGAAATCTAAACA
		Nfkbiz	GGCCTTTGAGGTCACAATGA	AGGACTCCTGTCCCAGTGTC
		Pim1	CGTTAGCGACCATTCTGACC	GCTTCAGCCAACCAGAAGAC
		Socs3	CACAGCCTTTCAGTGCAGAG	GGGTATTTACCCGGCCAGT
		Tnfaip3	GCGGGACCTAGGAGTTTCTC	TTGCCAACAGGGGGATTT
		Egr1	GGCCGGTCCTTCCATATTAG	CGAATCGGCCTCTATTTCAA
0		Junb	GTGTGTCTCTGTCTCCACAGC	TCGCGTCACTGTCAGGAA
خ		Zfp36	CGCTACCATCACCTCCAGTT	CATGCAAAATGTGCCTGAAC
		Nfkbia	GCTTCTCAGTGGAGGACGAG	CTGGCAGGGGATTTCTCAG
2		Nfkbid	TACGGTGGTGGAAAGTTGGT	CGAGCGAGCTGGAGAACTAC
)		Fos	GGGCGTAGAGTTGACGACAG	TGGATGGACTTCCTACGTCAC
>		Ptas2	CGCAACTCACTGAAGCAGAG	CCACGTGACGTAGTGGTGAC
)		TIr2	GCTGGAGCATTCCAATAACC	CTCGCCTTTTGGCTGAGTT
		Cxcl1	ACCCTGTACTCCGGGAATTT	GGAGTCTGGAGTGCTGGAAC
2		Cxcl2	CCCCTCTCTCCTTCCTCAT	тесседедестестттате
2		Tnf	GATTCCTTGATCCTGGGTGTC	GACCTTCTCCTCCCTCCCTCT
<u>, </u>		Traf1	ACCACTTCCCTCCTTCACC	СССССТАААСТСТССССААТ
		Cycl11	CCTCACTCCCTTTCACC	CCTACCTTTCTTCCCTCCTC
		Cloc4o	AACCAAAATCCCCCACCAACT	CONCARGENERGCACAC
	B	Cef2		CCALCARGAGAAAIGGCAGAG
5		11229	CCERCERACCCACAACAACCEC	AMAGECCOMCCCARCAMCAMC
		11250	CCCACCCTTCACCACCACCACCTC	
		1110	CCCACCCTTCAGTTTTGTTG	CITGITITCCCTCCCTGTTT
	C	Saa3	CGCAATCTGGGGAAAGAAG	AATGGAGCAATCCCTGTTTG
		Peli1	CCTGACCAGTGAACAGAGATTTGA	GGGCTTTGGAAGGATGATTTTCT
		Cxcl10	TCCAAGTTCATGGGTCACAA	TGATTGGCTGACTTTGGAGA
		lfit1	AGTGCGTCTCCCTGGATAAA	TTAAAGGGCTGGGTGAGCTA
	יין	lfnb1	GCCAGGAGCTTGAATAAAATG	GATGGTCCTTTCTGCCTCAG
		Ccl5	CTGCTACCCTGGCTCCCTAT	TGGGAGATGCATGTGCTGT
		lfit3	GGACTGTCAGGCTGGAGGAAAT	TGTCCTGGCCACAGCATTG
		1		
•	I E	Tyki	GCTGCCTTCACTTTCGTTTC	TTATTAGGGCCATGGGTGTC
,		116	AATGTGGGATTTTCCCATGA	GCTCCAGAGCAGAATGAGCTA
		11126	CCCCACCACCACCATCTTA	Стттстсатсаласссалас
		Nos2	СССПТЕСССААСАСТЕТТСТТП	GCCCCACACTCTCACTCTT
5	I F	L cn2	CCCCACACACCCACACAAAT	
)		Marco	GCACCCTCTTTCCCCAAACTT	СССССТССТССТТАСТСТАС
)		Mx1		GAAACCGTGAAAAAGCCTGA
)		Mx2	CCACCTCCACACTCTCTCTCTC	тессстветаствесстои
				1000010010010111001101
	Class	Gene	Forward Primer	Reverse Primer
	Class	Gene Gapd	Forward Primer	Reverse Primer TCATCCACCTCCCCACAGTA
	Class	Gene Gapd Actb	Forward Primer TGGTGAAGGTCGGTGTGAAC AGAGGGAAATCGTGCGTGAC	Reverse Primer TCATCCACCTCCCCACAGTA CAATAGTGATGACCTGGCCGT
)	Class HK	Gene Gapd Actb Irf1	Forward Primer TGGTGAAGGTCGGTGTGAAC AGAGGGAAATCGTGCGTGAC GTAGGTAGGGTGGGCAGTGA	Reverse Primer TCATCCACCTCCCCACAGTA CAATAGTGATGACCTGGCCGT TGCTGAGTCCATCAGAGAAAGTG
)	Class HK	Gene Gapd Actb Irf1 Nfkbiz Pim1	Forward Primer TGGTGAAGGTCGGTGTGAAC AGAGGGAAATCGTGGCGTGAC GTAGCTAGGGTGGGCAGTGA GTGGCCAGGTAGGCAGGCAGGAAG TCCAACGCCACGTCTGCCCCG	Reverse Primer TCATCCACCTCCCCACAGTA CAATAGTGATGACCTGGCCGT TGCTGAGTCCATCAGAGAAAGTG CAAGCGTGAAAGGACATGAA GCCCCAATGACCTTTACAA
	Class HK	Gene Gapd Actb Irf1 Nfkbiz Pim1 Tnfaip3	Forward Primer TGGTGAAGGTGGGGTGTGAAC AGAGGGAAATCGTGCGTGAC GTAGGTAGGGTGGGCAGTGA GTGCCAGGTAGGCTGGAAG TCAAGGACAACAGTCTACACGG GGCAGCTGGAATCTCTGAAA	Reverse Primer TCATCCACCTCCCCACAGTA CAATAGTGATGACCTGGCCGT TGCTGAGTCCATCAGAGAAAGTG CAAGCGTGAAAGGACATGAA GGCCCAATGACCTTTACAA ATAGGGCTGCCACCACAAAAG
	Class HK	Gene Gapd Actb Irf1 Nfkbiz Pim1 Tnfaip3 Egr1	Forward Primer TGGTGAAGGTCGGTGTGAAC AGAGGGAAATCGTGCGTGAC GTAGGTAGGGTGGCAGTGA GTGGCAGGTAGAGCAGGAAG TCAAGGACACAGTCTACACGG GGCACTGGAATCTCTCAAA GCGCTCTCGGAGCTGCAGTA	Reverse Primer TCATCCACCTCCCCACAGTA CAATAGTGATGACCTGGCCGT TGCTGAGGTCCATCAGAGAAAGTG CAAGCGTGAAAGGACATGA GGCCCAATGACCTTTACAA ATAGGGCTGCCACCACAAAAG GGACCTGCTCCAGTGGCAGA
	Class HK	Gene Gapd Actb Irf1 Nfkbiz Pim1 Tnfaip3 Egr1 Junb	Forward Primer TGGTGAAGGTGGGTGTGGAC AGAGGGAAATCGTGGCGGGAC GTAGGTAGGGTGGCAGTGA GTGGCAGGTAGAGCAGGAAG TCAAGGACACAGTCTACACGG GGCAGCTGGAATCTCTGAAA GCGCTCTCGGAGCTGCAGTA AGCAGGGACCCATGGAAGTT	Reverse Primer TCATCCACCTCCCCACAGTA CAATAGTGATGACCTGGCCGT TGCTGAGTCCATCAGAGAAAGTG CAAGCGTGAAAGGACATGAA GGCCCAATGACCTTTACAA ATAGGGCTGCCACACAAAAG GGACCTGCTCCAGTGGCAGA ATGCACAAGCAAAGGTCATCTTT
	Class HK	Gene Gapd Actb Irf1 Nfkbiz Pim1 Tnfaip3 Egr1 Junb Zfp36	Forward Primer TGGTGAAGGTGGTGTGGAC AGAGGGAAATCGTGCGTGAC GTAGGTAGGGTGGGCAGTGA GTGCCAGGTAGAGCAGGAAG TCAAGGACACAGTCTACACGG GGCAGCTGGAATCTCTGAAA GCGCTCTCGGAGCTGCAGTA AGCAGGGACCCATGGAAGTT CCCTCTGCAACTCTGGTCTC CCTCTGCAACTCTGGTCTC	Reverse Primer TCATCCACCTCCCCACAGTA CAATAGTGATGACCTGGCCGT TGCTGAGTCCATCAGAGAAAGTG CAAGCGTGAAAGGACATGAA GGCCCAATGACCTTTACAA ATAGGGCTGCCCACACAAAAG GGACCTGCTCCAGTGGCAGA ATGCACAAGGACATCTTT GACCACCGGACACTGAACTT
	Class HK	Gene Gapd Actb Irf1 Nfkbiz Pim1 Tnfaip3 Egr1 Junb Zfp36 Nfkbia Nfkbia	Forward Primer TGGTGAAGGTCGGTGTGAAC AGAGGGAAATCGTGGCGTGAC GTAGGTAGGGTGGGCAGTGA GTGCCAGGTAGGAGCAGGAAG TCAAGGACACAGTCTACACGG GGCAGCTGGAACTCTGGAAG AGCAGGGACCCATGGATCT CCCTCTGCAACTCTGGCAGCTCT CCCGGCCCAGTGTAGCAGTCT	Reverse Primer TCATCCACCTCCCCACAGTA CAATAGTGATGACCTGGCCGT TGCTGAGTCCATCAGAGAAAGTG CAAGCGTGAAAGGACATGAA GGCCCAATGACCTTTACAA ATAGGGCTGCCCACACAAAAG GGACCTGCTCCAGGAGAACTT GACCACCGGACACTGAACTT TGATGTTTGTGGTTGTCCTCA GGGTGGCTAACCGCCATCTTG
	HK A	Gene Gapd Actb Irf1 Nfkbiz Pim1 Tnfaip3 Egr1 Junb Zfp36 Nfkbia Nfkbia Ptgs2	Forward Primer TGGTGAAGGTCGGTGTGAAC AGAGGGAAATCGTGGCGTGAC GTAGGTAGGGTGGGCAGTGA GTGCCAGGTAGGACAGGAAG TCAAGGACACAGCTCTGAAA GCGCTCTGGAACTCTCGAAA AGCAGGGACCCATGGAAGTT CCCTGGCACGTGTAGCAGTCT TGCGGGCCTTGGTAACAGTTA	Reverse Primer TCATCCACCTCCCCACAGTA CAATAGTGATGACCTGGCCGT TGCTGAGGTCCATCAGAGAAAGTG' CAAGCGTGAAAGGACATGAA GGACCTGACCACCAACAAAA ATAGGGCTGCCACCACAAAAG GGACCTGCTCCAGTGGCAGA ATGCACCAGACACTGACCTT TGATGTTTGTGGTTGTCCTCA GGGTGCTAACAGCCATCTTG TTGGGGTTGGGTTTCTAGTG
	A Class	Gene Gapd Actb Irf1 Nfkbiz Pim1 Tnfaip3 Egr1 Junb Zfp36 Nfkbia Nfkbia Ptgs2 Cxcl1	Forward Primer TGGTGAAGGTGGGGTGTGAAC AGAGGGAAATCGTGGCGGGAG GTAGGTAGGGTGGGCAGTGA GTGGCAGGTAGAGCAGGAAG TCAAGGAACAGGCACAGGAAG GCGCTCTCGGAACTCTCGAAA AGCAGGGACCCATGGAAGTT CCCTCGCCAACTCTGGTCAT TGCGGGCCTTGCTAATATG CCCCTCCCGCAAGTTAA TGTCAGTGCCTCCAGACCAT	Reverse Primer TCATCCACCTCCCCACAGTA CAATAGTGATGACCTGGCCGT TGCTGAGTCCATCAGAGAAAGTG CCAGCGTGAAAGGACATGAA GGCCCAATGACCTTTACAA ATAGGGCTGCCACACAAAG GGACCTGCTCCAGTGGCAGA ATGCACAGGACACTGACTTT GACCACCGGACACTGATCTTG GGGGTCTAGGGTTTGCTCAGTG TTGGGGTTGGGCAGAAGC
	Class HK	Gene Gapd Actb Irf1 Nfkbiz Pim1 Tnfaip3 Egr1 Junb Zfp36 Nfkbia Nfkbia Nfkbia Ptgs2 Cxcl1 Cxcl2	Forward Primer TGGTGAAGGTGGGTGTGGAAC AGAGGGAAATCGTGGCGGTGAC GTGGCAGGTAGGGCGGGAGGAAG GTGGCAGGTAGGACGCAGGAAG GCGCTCTCGGAACTCTCGAAA GCGCTCTCGGAACTCTGGAAGTT CCCTCGCCAGTGTAGCAGTCT TGCGGGCCTTTGTTAATATG CCCCTCCCGCAAGTCAACAGCAT GAACATCCAGAGCTTGAGTGTGA	Reverse Primer TCATCCACCTCCCCACAGTA CAATAGTGATGACCTGGCCGT TGCTGAGTCCATCAGAGAAAGTG CAAGCGTGAAAGGACATGAA GGCCCAATGACCTTTACAA ATAGGGCTGCCACACAAAAG GGACCTGCTCCCAGTGGCAGA ATGCACAGCAAAGGTCATCTTT GACCACGGACACGAGAGTTGTTGTGGGTTGTGTCTCCA GGGTGCTAACAGCCATCTTG TTGGGGTTGGGATTCTAATG AGTCTGGAAGTGGCAGAAGC CATGGCAGAGGCCAATCCAG
	Class HK	Gene Gapd Actb Irf1 Nfkbiz Pim1 Tnfaip3 Egr1 Junb Zfp36 Nfkbia Nfkbid Ptgs2 Cxcl1 Cxcl2 Trf Tref	Forward Primer TGGTGAAGGTCGGGTGGAC AGAGGGAAATCGTGGCGTGAC GTAGGTAGGTAGGCAGGAAG TCAAGGACACAGCTACACGG GGCAGCTGGAACTCTCTGAAA GCGCTCTCGGAGCTCCGAAGTT CCCTCTGCAACTCTGGTCTC CCTGGCCACTCTGGCAGCTT TGCGGCCCTTTGTTAATATG CCCCTTCCTGCGAAGTTTA TGCCGGCCTTGCTTAATATG CCCCTTCCTGCGAAGTTA	Reverse Primer TCATCCACCTCCCCACAGTA CAATAGTGATGACCTGGCCGT TGCTGAGTCCATCAGAGAAAGTG CAAGCGTGAAAGGACATGAA GGCCCAATGACCTTTACAA ATAGGGCTGCCCACACAAAAG GGACCTGCTCCCAGTGGCAGA ATGCACAAGCAAAGGTCATCTT GACACCGGACACTGAACTT TGAGGTTACAGCCATCTTG TTGGGGTTACAGCCATCTGG TTGGGCTACAGGCAGAAGC CATGGCAGAGGCTATCCAG TGGGCTACAGGCTATCCAG
	Class HK A	Gene Gapd Actb Irf1 Nfkbiz Pim1 Junb Zfp36 Nfkbia Nfkbia Nfkbia Qtgs2 Cxcl2 Cxcl2 Trf Traf1 II1b	Forward Primer TGGTGAAGGTCGGTGTGAAC AGAGGGAAATCGTGGCGTGAC GTAGGTAGGGTGGGCAGTGA GTGCCAGGTAGGATCTACACGG GGCAGCTGGAACTCTCGAAA GCCTCTCGGACTCTGCAAA AGCAGGGACCCATGGAAGTT CCCTCTGCAACTCTGGTCT CCTGGCCAGTGTAACAGGTCT TGCGGCCTTGCTAATATG CCCCTTCCTCGCAAGTTAA TGTCAGTGCCCGACTCAT GGGAAGCCTAAAAGGCTCAT TGTTGGCCCGACTGTCA	Reverse Primer TCATCCACCTCCCCACAGTA CAATAGTGATGACCTGGCCGT TGCTGAGTCCATCAGAGAAAGTG CAAGCGTGAAAGGACATGAA GGCCCAATGACCTTTACAA ATAGGGCTGCCCACACAAAAG GGACCTGCTCCAGTGGCAGA ATGCACAAGCAAAGGTCATCTTT GACCACCGGACACTGAACTT TGGAGTTGGGATGGCTGTCACG AGTCTGGAAAGGCCATCTTG TGGGCTACAGGCTATCCAG TGGGCTACAGGCTTGTCACT AGCTGACCAGGCTATCTCG
	Class HK A B	Gene Gapd Actb Irf1 Nfkbiz Pim1 Junb Zfp36 Nfkbia Nfkbia Nfkbid Ptgs2 Cxcl1 Cxcl2 Trf Traf1 II1b Saa3	Forward Primer TGGTGAAGGTCGGTGTGGAAC AGAGGGAAATCGTGGCGGTGAC GTAGGTAGGGTGGGCAGTGA GTGCCAGGTAGGACGCAGGAAG TCAAGGACACAGTCTCGAAA GCGCTCTGGAACTCTCGAAA GCGCTCTGGAACTCTGGAAGTT CCCTGCAGCCAGGGACTCGGCAGC CCCGCCAGTGTAACAGGCTCT TGCGGGCCTTGCTAATATG CCCCTTCCTCGCAAGTTTA TGCCAGTGCCTGCAGACCAT GAACACCCAAAGCCTCAAT GGGAAGCCTAAAAGGCTCA TGTCCCCTGGACCAAGCCC CAGGATGCAACCCACATG	Reverse Primer TCATCCACCTCCCCACAGTA CAATAGTGATGACCTGGCCGT TGCTGAGTCCATCAGAGAAAGTG' CAAGCGTGAAAGGACATGAA GGACCTGCTCCAGTGGCAGA ATTAGGCTGCCCACAAAAG GGACCTGCTCCAGTGGCAGA ATGCACCGGACACTGAACTT TGATGTTTGTGGTTGTCCTCA GGGTGCTAACAGCCATCTTG TGGGGTTGGGTTGTCTCAGTG AGTCTGGAAGTGGCAGAAGC CATGGCACAGGCATTGTCCACT AGCTGACCTAGCAGGCTGTCACT
	A B C	Gene Gapd Actb Irf1 Nfkbiz Pim1 Junb Zfp36 Nfkbia Nfkbia Nfkbia Nfkbia Th Ptgs2 Cxcl1 Cxcl2 Trf Traf1 II1b Saa3 Ccl2	Forward Primer TGGTGAAGGTCGGTGTGGAAC AGAGGGAAATCGTGGCGTGGAC GTAGGTAAGGCTGGGCAGTGA GTGCCAGGTAGGCTGCAGGAG GGCACCTGGAACCTCTGAAA GCCCTCTGGAACCTCTGAAA AGCAGGACCCATGGAAGTT CCCTGGCACTGTAGCAGTCT TGCGGGCCTTGCTAATATG CCCCTCCCGAAGTTTAA TGTCAGTGCCTGCAAGACTT GAGAACCCCAGGACTCAT GAGAAGCCTAAAAGGCTCAT TGTTGGCCGGACTGTCA TGTTCCCTGACACGACTCC CAGGATGAAGCCTCACAGTT	Reverse Primer TCATCCACCTCCCCACAGTA CAATAGTGATGACCTGGCCGT TGCTGAGTCCATCAGAGAAAGTG CCAGCGTGAAAGGACATGAA GGCCCAATGACCTTTACAA ATAGGCTGCCCACACAAAG GGACCTGCTCCAGTGGCAGA ATGCACAGGACATGGACATCTT GACCACCGGACACTGATCTTG TGGGGTGGAGGCTATCCAG GGGTCTGGAAGTGGCAGAAGC CATGGCCAAGGCTATCCAG TGGGCTACAGGCTATCCAG TGGGCCACAGGTATTTGTCG TCATGAACTGGACCAACTT
	A B C	Gene Gapd Actb Irf1 Nfkbiz Pim1 Tnfaip3 Egr1 Junb Zfp36 Nfkbia Nfkbia Nfkbia Nfkbia Cxcl2 Cxcl2 Trf Traf1 I1b Saa3 Ccl2 Peli1	Forward Primer TGGTGAAGGTCGGGTGGAC GAGAGGAAATCGTGGCGTGAC GTAGGTAGGTGGGCAGGAA GTGCCAGGTAGAGCAGGAAG GCCACCTGCAACAGCTCTCGAAA GCCTCTCGCAACTCTGGACT CCCTCTGCAACTCTGGACT CCCTCTGCAACTCTGGTCC CCGGCCAGTGTAACAGGTCA TGCCGGCCTTGGTCACAGTTA TGTCAGGCCTGAGACGTTAA GGAAGCCTAAAGCCTCAT GGGCCTGCTGACCAGCT CAGGAGAACCCTTCCATG GGGCCTGCTCCCAGACT CCCCTGCCCAGTAAA	Reverse Primer TCATCCACCTCCCCACAGTA CAATAGTGATGACCTGGCCGT TGCTGAGTCCATCAGAGAAAGTG CCAGCGTGAAAGGACATGAA GGCCCAATGACCTTACAA ATAGGGCTGCCACACAAAAG GGACCTGCTCCAGTGGCAGA ATGCACAGGACATCGTGCACAA GGGTGCTAACAGCCATCTTG TGGGGTTGGGACTGGCAGAAGC CATGGCAGAGGCTATCCAG TGGGCTACAGGCTATCCAG TGGGCTACAGGCTATCCAG TGGCCACAGGTATTTGTCG TCATGAACTGGACCTAGCTGT AGCCCACAGGACATCATCT TGCTATCACAATCCACGACAA
	A B C	Gene Gapd Actb Irf1 Nfkbiz Pim1 Tnfaip3 Egr1 Junb Zfp36 Nfkbia Nfkbia Nfkbia Ptgs2 Cxcl2 Trf Traf1 Il1b Saa3 Ccl2 Peli1 Cxcl10	Forward Primer TGGTGAAGGTCGGGTGGAC GAGGGAAATCGTGGCGTGAC GTAGGTAGGTGGGCAGGAAG GTGCCAGGTAGAGCAGGAAG GGCAGCTGGAACTCTCGAAA GCGCTCTCGGAGCTGCAGTA AGCAGGGACCCATGGAAGTT CCCTCTGCAACTCTGGTCTC CCTGGCCAGTGTAGCAGTCT TGCGGCCCTTGGTAACAGG GGCAGCCTTGGTAACAGT CCCCTCCCGCGAAGTTA TGTGGCCGCGCTGCTGAGTGAA GGGAAGCCTAAAAGGCTCAT GGGAAGCCTAAAAGGCTCAT CAGGATGAAGCCTTCCATTG GGGCTGCTGTCCACAGTT CTTCCAAGGCCTCCATTGAAGAT	Reverse Primer TCATCCACCTCCCCACAGTA CAATAGTGATGACCTGGCCGT TGCTGAGTCCATCAGAGAAAGTG CAAGCGTGAAAGGACATGAA GGCCCAATGACCTTTACAA ATAGGGCTGCCACACAAAAG GGACCTGGCTCGAGGAGAGA ATGCACAAGCAAAGGTCATCTT GACCACGGACACGTGGCTGTCACTG GGGTGCTAACAGCCATCTTG TTGGGGTTGGGTT
	A B C D	Gene Gapd Actb Irf1 Nfkbiz Fim1 Tnfaip3 Egr1 Junb Zfp36 Nfkbia Nfkbia Nfkbia Ptgs2 Cxcl2 Cxcl2 Traf1 Il1b Saa3 Ccl2 Peli1 Cxcl10 Ifit1	Forward Primer TGGTGAAGGTCGGTGTGAAC AGAGGGAAATCGTGGCGTGAC GTAGGTAGGGTGGCAGTGA GTGCCAGGTAGGTCGAGCAGGAAG TCAAGGACACAGTCTCGAAA GCGCTCTGGAACTCTGGAAG CCCTCTGGAACTCTGGAAGTT CCCCCTTGGTAACAGGAGCTC CCCGCCAGTGTAACAGGCCCAT GCGGCCCTTGGTAACAGCTC CCCCTCCTCCAGAGCTCA GGGAAGCCTAAAAGGCTCAT GGGCAGCTGCAGACCTCA GGGAAGCCTAAAAGGCTCAT GGGCTGCTGCACGACTCC CAGGATGAACCCTCCATTG GGGCCGCCTTGTCACAGCTC CTTCCAAAGCCTCCATTG GGGCCGCCTGCTGCAAAAA CCTCCCCCCCGCAATAAAGCTCC CAGGATGAACCCCAGTAAAA	Reverse Primer TCATCCACCTCCCCACAGTA CAATAGTGATGACCTGGCCGT TGCTGAGGTCCATCAGAGAAAGTG CCAAGCGTGAAAGGACATGAA GGCCCAATGACCTTTACAA ATAGGGCTGCCACCACAAAAG GGACCTGCTCCAGTGGCAGA ATGCACCAGACATGACCTT TGATGTTGTGGTGTCTCTCA GGGTCCACAGAGTGCCACATCTTG TGGGCTACAGGCTTGTCAGT AGCTGACAGAGGCTTGTCACT AGCTGACCTAGCAGGCTGT AGCGCACAGGCATTTTGTCG TCATGGACTAGCACAGGCCTAT TGCTATCACAATCCACGACCAA ACCCAGAGACCATACCAGACCAA ACCCCAGAGACCCATCCTCT TGCTACCACAGCCCTCTA TGAAGCCAGATCTCCCATGACC
	A B C D	Gene Gapd Actb Irf1 Nfkbiz Pim1 Junb Zfp36 Nfkbia Nfkbia Nfkbid Ptgs2 Cxcl2 Cxcl2 Trf Traf1 II1b Saa3 Ccl2 Peli1 Cxcl10 Ifit1 Ifnb1 Ccl5	Forward Primer TGGTGAAGGTCGGTGTGGAAC AGAGGGAAATCGTGGCGTGGAC GTAGGTAAGGTCGGCAGTGA GTGCCAGGTAGGATCACACGG GGCACCTGGAACTCTCGAAA GCCTCTGGAACTCTCGAAA AGCAGGGACCCATGGAAGTT CCCTGCAGCCAGTGGAAGTT CCCCTTCGCAGACTTGGAGTCT TGCGGCCGCTTGCTAGAGTGAA GGGAAGCCTAAAAGGCTCAT GGGAAGCCTAAAAGGCTCA TGTCCCTTGGCCGGACTGTCA TGTCCCTTGACCCAGTT CTTCCCAAGGCCCCAGTAAAA CCTGCCCACTGTCACAGTT CTTCCCAAGACCCCAGTAAAA CCTCCCCACTGTCACAGTT CTCCCAAGACCCAGTACACT CTCCCAAGACCCAGTACACT CTCCCAAGAACCCCAGTAAAA	Reverse Primer TCATCCACCTCCCCACAGTA CAATAGTGATGACCTGGCCGT TGCTGAGTCCATCAGAGAAAGTG CCAGCGTGAAAGGACATGAA GGCCCAATGACCTTTACAA ATAGGGCTGCCACACAAAG GGACCTGCTCCAGTGGCAGA ATGCACAGCAAAGGTCATCTTT GACCACCGGACACTGAACTT GACCACCGGACATGACATCTTG TGGGGTGGGTTGGTACAGTC AGTCTGGAAGTGGCAGAAGC CATGGCCACAGGTAGTCACTT AGCTGACCTAGCATGGCTGT AGGCCACAGGTATTTGTCG TCCATGACCTGGACCATGGCTGT AGCCACAGGTACCCACGACAA ACCCAGAGACCAAAATGAGC GAGTCACAGGACATCATGATGACTA TGAAGCAGATTCTCCATGACC GCCCTGTAGGTGAGGTGAGCC
	A B C D	Gene Gapd Actb Irf1 Nfkbiz Pim1 Junb Zfp36 Nfkbia Nfkbia Nfkbia Nfkbia Nfkbia Nfkbia Traf1 II1b Saa3 Ccl2 Peli1 Cxcl10 Ifit1 Ifitb1 Ccl5	Forward Primer TGGTGAAGGTCGGTGTGGAAC AGAGGGAAATCGTGGCGTGGAC GTAGGTAAGGTCGGCAGTGA GTGCCAGGTAGGACAGCAGAAG TCAAGGACACAGTCTCTGAAA GCGCTCTGGAACTCTCGAAA GCGCTCTGGAACTCTGGAAGTT CCCTGGCAGTGTAGCAGTCT CCTGGCCAGTGTAGCAGTCT GCGGGCCTTTGTTAATATG CCCCTCCCGAAGTTTAA GGGAAGCCTTCAGGACTCAT GGGCAGCTAAAAGCTCAT GGGCAGCTAAAAGCTCAT CTTCCCTAGACCCAGGTCA GGGCCTGCTGTCACAGGTT CTTCCAAGCCTCCCATGG GGGCCGCCCCAGTAGAAA CCTGCCCAGTGTGAGGAT TCCATTCGGCCAGTTGGGAT TCCATTCGGCCAGTTGAGAC CTCCCCAGGAAGGCCAACAT GGGCTGCCAGTGTGAGAGCCAACAT TGCGTCCCAAGAAGGACCAACAT TGGGTACCAAGATGGGTTGG	Reverse Primer TCATCCACCTCCCCACAGTA CAATAGTGATGACCTGGCCGT TGCTGAGTCCATCAGAGAAAGTG CCAGCGTGAAAGGACATGAA GGCCCAATGACCTTTACAA ATAGGCTGCCCACACAAAG GGACCTGCTCCAGTGGCAGAA ATGCACAGGACACTGACTTT GACCACCGGACACTGACTTG TGGGGTTGGTTGGCTGTCAGTG TGGGCTAACAGCCATCTTG TGGGCTACAGGCTATCCAG TGGGCCACAGGTATTTGTCG TCATGAACTGGCCACATCTTT TGCTATCACAATCCACGACAA ACCCAGGACCCAACATCATCA ACCCAGAGCCAAATCCACGACAA ACCCAGAGCCACAGTCATCTT TGATGACTGGACCTATCCACGACAA ACCCAGGACCAAATCCACGACAA ACCCAGGACCCAAATGACC GAGTCACAGGACCCATCATC TCACGACGACCCACATCATCC CTCACCACAGTCATCCCCACACCTA
	A B C D	Gene Gapd Actb Irf1 Nfkbiz Pim1 Tnfaip3 Egr1 Junb Zfp36 Nfkbia Nfkbia Nfkbia Nfkbia Cxcl2 Cxcl2 Trf Traf1 I1b Saa3 Cccl2 Peli1 Cxcl10 Ifit1 Ifnb1 Ccl5	Forward Primer TGGTGAAGGTCGGGTGGAC GAGAGGAAATCGTGGCGTGAC GTAGGTAGGTAGGGCGGGCAGTGA GTGCCAGGTAGAACAGCAGAAG GCCACCTGGAACTCTCGAAA GCCTCTCGCAACTCTGGACT CCCTCTGCAACTCTGGTCC CCTGGCAGTGTAGCAGTCT TGCGGGCCTTGGTCAGCAGTTA TGTCAGGCCTGAGACAT TGTCAGGCCTACTGAGCAT TGTGGCCGGACGTCA GGAAGCCTAAAAGGCTCAT TGTGGCCGGCCTTCCTAGGTCA GGGCATGTCACAGACT CTTCCAAAGCCCCACAGAT CTTCCCAAGACCTTCAGTT CTTCCAAGGCCCATTAAAA CCTGCCCACGTGTGAGAT CCCTTCCTGGCAGTCC TGGGCCGCTGTTCACAGT GGGCCTGTTGGTCAGGT GGGCATTATCCCGGAGATAAA CTGCCCACGACAGAACAT TGGGTATCAAGACGGATGG GGCAATTATCCCGTGGCCTC	Reverse Primer TCATCCACCTCCCCACAGTA CAATAGTGATGACCTGGCCGT TGCTGAGTCCATCAGAGAAAGTG CCAGCGTGAAAGGACATGAA GGCCCAATGACCTTTACAA ATAGGGCTGCCACAAAAG GGACCTGCTCCAGTGGCAGAA ATGCACAAGCATAGGCTATCTTT GACCACCGGACACTGAACTT TGATGTTTGTGGTTGTCTCAC GGGTGCTAACAGCCATCTTG TTGGGGTTGGACTGGCCAGAAGC CATGGCAGAAGGCTATCTAGTG AGCCTACAGGCTATCTAGTG TGCTATCACACGCACATCGTT AGGCCACAGGTATTTTGTCG TCATGAACTGGACCCATCTTT TGCTGTACAGCCACATCATCT ACCCAGAGACCAAAATGAGC GAGTCACAGACCCATCCTCA ACCCAGAGACCAAAATGAGC GAGTCACAGCCACCGTCCCTA TGAAGCAGATCTCCCATGAC GGCCTGTAGGTGAGGTTGATCT CTCACCATCATCCTCCACTGC TTAGGGAGAAGGCATCTTGC TTAGGGAGAAAGGCATCTTGC
	A B C D	Gene Gapd Actb Irf1 Nfkbiz Pim1 Tnfaip3 Egr1 Junb Zfp36 Nfkbia Nfkbia Ptgs2 Cxcl1 Cxcl2 Trf Traf1 Il1b Saa3 Ccl2 Peli1 Cxcl10 Ifint1 Ifnb1 Ccl5	Forward Primer TGGTGAAGGTCGGGTGGAC AGAGGGAAATCGTGGCGTGAC GTAGGTAGGTGGGCGGGCAGTGA GTGCCAGGTAGAGCAGGAAG GGCAGCTGGAACTCTCGAAA GCGCTCTCGGAGCTGCAGTA AGCAGGACCCATGGAGTT CCCTCTGCAACTCTGGTCTC CCTGGCCACTTGGTAGCAGTCT TGCGGCCCTTGGTAATATG CCCCTTCCTGCGAAGTTA TGCCGCCCTTGCTAATATG GGCAAGCCTTAGTAATATG GGCAAGCCTAAAAGGCTCAT TGTTCCCTGCGCAGCTTCA CAGGATGAAGCCTTCCATTG GGGCTGCTGTCACAGTT CTTCCAAGGCCCTCCATTG GGCCTGCTGTCACAGTTA CCTGCCCACGTGTGAAAA CCTGCCCACGTGTGAAAA CCTGCCCACGTGTGAAAA CCTGCCCACGTGTGAGCCAACAT TGGGTATCAAGATGGGTTGG GGCAATTATCTCGTGGCCTCC AACCCCCGTGAGTGCAACTA	Reverse Primer TCATCCACCTCCCCACAGTA CAATAGTGATGACCTGGCCGT TGCTGAGTCCATCAGAGAAAGTG CCAGCGTGAAAGACCTTACAA GGCCCAATGACCTTACAA ATAGGGCTGCCCACACAAAAG GGACCTGCTCCAGTGGCGAGA ATGCACAGCGATGCCATCTTT GACCACCGGACACGTGGTGTCCTCA GGGTGCTACAGCCATCTTG TTGGGGTTGGGACTTGCCAGAGAGC CATGGCAGAGGCTATCCAG TGGGCTACAGGCTATCCAG TGGGCTACAGGCTATCCAG TGGGCTACAGGCTATCTGG TCATGACTGGACCTGGCAGAAGC CATGGCACAGGTATTTTGTCG TCATGACTGGACCTGGCAGAAGC GAGTCACAGGCATCTTT TGCTATCACAATCCACGACAA ACCCCAGAGACCCATCTTT TGCTATCACAATCCACGACAA ACCCCAGAGACCCATCTTC TCATGAACTGGACCGACCCTCT TGAGGCACAGGCATCTCCCAG GAGTCACAGCCACAAATGGACC GCCCTGTAGGTGAGGCTGATCT CTCACCATCATCCCCCTGC TTAGGGGAGAGGCATCTTGC CCAGGAACTTACCAGCCTGT
	A B C D	Gene Gapd Actb Irf1 Nfkbiz Pim1 Tnfaip3 Egr1 Junb Zfp36 Nfkbia Nfkbia Nfkbia Ptgs2 Cxcl2 Cxcl2 Cxcl2 Trf Traf1 II1b Saa3 Ccl2 Peli1 Cxcl10 Ifit1 Ifnb1 Ccl5 Tyki Rsad2 H28 III6	Forward Primer TGGTGAAGGTCGGTGGGGGGGGAGCA GGAGGAAATCGTGGCGGGAGGA GTAGGAAGGACAGGAAGGAAGGACAGGAGGAAGGACACAGCAG	Reverse Primer TCATCCACCTCCCCACAGTA CAATAGTGATGACCTGGCCGT TGCTGAGTCCATCAGAGAAAGTG CAAGCGTGAAAGGACATGAA GGACCTGCACAAAGGACATGAA GGACCTGCTCCAGTGGCAGA ATGGCCCACACAAAGG GGACCTGCTCCAGTGGCAGA ATGCACCAGCACATGAACTT TGCACGCACACAGAAGGCCATCTTG TGGGGTCGGTGGTGTCCACTG AGTCTGGAAGTGGCAGAAGC CAGGCACAGGCATGTCCACT AGCTGACCAGGCATGTCCACT AGCCGACCAGGCATGTCCACT TGGCACAGGCATGCCACAA ACCCAGAGACCTGTCCACGACAA ACCCAGAGACCCACCCCCTA TGAAGCCACAGCCATCTTCT TGCTATCACAATCCACGACCAA ACCCAGAGACCCAATCTCCCTA TGAAGCAGATCTCCCATGACC GAGTCACAGCCACATCATGC CCCCTGTAGGGAGAGGCATCTTGC TTAGGGAGAGAGGCATCTTGC CCCAGGAACTTACCAGCCTGT CCCACGACTTACCAGCCTGT CCCACGACTTACCAGCCTGT CCCCGCTCTTCTGTAGTGGCCC
	A B C D	Gene Gapd Actb Irf1 Nfkbiz Pim1 Junb Zfp36 Nfkbia Nfkbia Nfkbia Nfkbia Ptgs2 Cxcl2 Cxcl2 Trf Traf1 II1b Saa3 Ccl2 Peli1 Cxcl1 Cxcl10 Ifit1 Ifnb1 Ccl5 Tyki Rsad2 H28 II6 H28 II12b	Forward Primer TGGTGAAGGTCGGTGTGAAC AGAGGGAAATCGTGGCGTGTGAAC GTAGGTAAGGTGGGCAGTGA GTGCCAGGTAGGTGGCAGGAAG TCAAGGACACAGTCTCGAAA GCGCTTCGGAACTCTCGAAA GCGCTCTGGAACTCTGGAAGTT CCCCTTGGCAACTCTGGTACT GCGGGCCTTTGTAATATG CCCCTTCCTGCGAAGTTAA GCGCAGCTGGAAGCTAATATG GGGAAGCCTAAAAGGCTCAT GGGAAGCCTAAAAGGCTCAT GGGCTGCTGGCGGACTGTCA TGTTCCCAAGACCTCAGAGTT CTTCCCAAGACCCAGACTT CTGCCCAGTGTTCACAGT CTTCCCAAGACCTCCATG GGGCCGCCGCAGTTCA GGGCTGCTGTCACAGTT CTTCCCAAGACCCAGAACT GGGCTGCCGGACTGCA GGCAATTATCTCGGGCTTCC AGGCTGCCGGAGTGGG GGCAATTATCTCGTGGCTCA ATGGTGGCAAAGCTGAAAAA GCCCTCTAGTGGTGCTGACTT	Reverse Primer TCATCCACCTCCCCACAGTA CAATAGTGATGACCTGGCCGT TGCTGAGTCCATCAGAGAAAGTG' CAAGCGTGAAAGGACATGAA GGCCCAATGACCTTTACAA ATAGGGCTGCCACACAAAG GGACCTGCTCCAGTGGCAGA ATGCACAGCACAGGACATGTT GACCACCGGACATGATCTT GACCACCGGACATGATCTTG TGGGGTGGAGTGGCAGAAGC CATGGCCAGAGGCTATCCAG TGGGCTACAGGCTATCCAG TGGGCTACAGGCTATCCAG TGGCCACAGGTATTTTGTCG GACCACAGGACATGGCCATCTT GACCACCAGGACTGTCCACT AGCCACAGGACTGTCCACT AGCCACAGGACTATCCAG TCATGACCTAGCCAGCTGT AGCCACAGGCCACAGCTGT CCCCAGGAGCCACAGCTCTTC TGACGACAGACCCATCTTC TGACGAGAGCCACACTCTCC CCCCGGAGAGCCACACTCTCC TTAGGGGAGAGGCATCTTCC TTAGGGAGAAGGCATCTTCC CCGCTCCTTCCGAGGCCACCTGT CCGCTCCTCCTGTAGTGCCTGT CCGCTCCTTCCGAGGCATCCTCC TTTCGCAAGGCCACCACCTGT
	A B C D F	Gene Gapd Actb Irf1 Nfkbiz Pim1 Tnfaip3 Egr1 Junb Zfp36 Nfkbia Nfkbia Nfkbia Nfkbia Cxcl1 Cxcl2 Traf1 Cxcl2 Peli1 Cxcl10 Ifit1 Ifit1 Cxb1 Cxcl10 Ifit1 Cxb1 Cxb1 Cxcl2 Peli1 Cxcl10 Ifit1 Ifit1 Cxb1 Cxb1 Cxb1 Cxb1 Cxb1 Cxb1 Cxb1 Cxb	Forward Primer TGGTGAAGGTCGGGTGGACCA GAGGGAAATCGTGGCGTGAC GTAGGTAGGTAGGGTGGGCAGTGA GTGCCAGGTAGAACAGCAGAAG GCCACCTGGAACACTCTGAAA GCCTCTCGCAACTCTGGACT CCCTCTGCAACTCTGGACT CCCTCTGCAACTCTGGTCC CCGGCCATTGTTAATATG CCCCTCCTCGCAGCTTAATATG CCCCTCCCGCAGCTTAATATG CCCCTCCCGCAGCTTAATATG GGACATCCAGACCTTAATATG GGACATCCAGACCTTCAGTGTGA GGAAGCCTAAAAGCCTCAT GTGTGGCCGGACGTCA GGGCCTGCTGACAGTT CTTCCAAGCCCTCCAGTT CCCCTCCCCAGACTTCC AGCACGCACTGTTGAGCATT CCCCTCCCCAGCACTC CAGGTGAACCCTTCCATG GGCCTGCTGTCCCAGTT CCCCTCCAGGACGATCT CCCCCCCCGCAGTTAAA CCCCCCGTGTGGGCCTTC AGCCCCAAGACGACATT GGCAATTATCTCGTGGCCTCC AACGCCCAAGACTGAAAA GCCCCCTAGTGGTCCAACTT GGCCACTCCAGGTCTAAAA GCCCCCCAGCAACCTCCT AGCCCCCAAGACTCCAACTT CCCTCTAGTGGTCCAACTA CCCCCCTAGTGGTCCAACTA CCCCCCCAAGACTCCAACTC CAGCTGCCAACCCCCCAACAACCT CCCCCCCAAGCTCCAACCTC CAGCTGCCAACCTCCCACTCC CAGCTGCCAACCCCCCCACTAAAA	Reverse Primer TCATCCACCTCCCCACAGTA CAATAGTGATGACCTGGCCGT TGCTGAGTCCATCAGAGAAAGTC CCAGCGTGAAAGGACATGAA GGCCCAATGACCTTTACAA ATAGGGCTGCCACACAAAG GGACCTGCTCCAGTGGCAGAA ATGCACAGGACATGGATGTTG GACCCCGGACATGATCTTG GACCCCGGACATGGATCTTG TGGGGTTGGAGTGGCAGAAGC CATGGCCAGAGGCTATCCAG TGGGCTACAGGCTATCCAG TGGGCTACAGGCTATCCAG TGGGCCACAGGTATTTGTCG AGCCACAGGTATTTGTCG AGCCACAGGTATTTGTCG TCATGAACTGGACCATGATCT TCATGACCTAGCATGACCATCT TCATGACTGGACCAAATGACC GAGTCACAGGTCATCTTC TCACGACCACAGTATTTGTCG TCACGAGACCCACATCATG TCACGAGACCAAAATGACC GCCCTGTAGGTGAGGCTGATCT CTCACCATCATCCCCACTGC CCGGCCCTTCTGAGTGCCCTTC TTAGGGAGAAGGCATCTTGC CCGCCCTCTTGAGTGCCATCATCG ACTGTCAAGGGGAATGACCACAC
	A B C D E	Gene Gapd Actb Irf1 Nfkbiz Pim1 Tnfaip3 Egr1 Junb Zfp36 Nfkbia Nfkbia Pfgs2 Cxcl1 Cxcl2 Traf1 Il1b Saa3 Ccl2 Traf1 Il1b Saa3 Ccl2 Traf1 Il1b Cxcl10 Ifit1 Cxcl10 Ifit1 Cxcl10 Ifit1 Cxcl10 Ifit1 Cxcl2 Tyki Rsad2 H28 Il6 Il12b Nos2 Marco	Forward Primer TGGTGAAGGTCGGGTGGAC GAGGGAAATCGTGGCGTGAC GTAGGTAGGTGGGCAGGAAG GTGCCAGGTAGAGCAGGAAG GGCAGCTGGAACTCTGGAAA GCGCTCTCGGAACTCTGGACT CCCTCTGCAACTCTGGTCTC CCCGCCAGTGTAGCAGACT CCCCTCCTGCGAAGTTA TGCGGCCCTTGGTAATATG CCCCTTCCTGCGAAGTTA TGTCGGCGCAGTGCAGACTTA TGTGGCCGCCTCCTGAGTGTCA GGAAGCCTTAATATG GGGCAGCTGCAGACTCA TGTGGCCGACTTCA TGTGGCCGAGCTTCA TGTGGCCAGGCTTCA TCCATTCCTGGCCAGTTAA CCCCCCCGCGAGTGTAAAA CCCCCCCGCGAGTGTAAAA CCCCCCCGCGAGTGTAAAA CCCCCCCGCGAGTGCAACT TGGGTATCAAGACGCAACAT TGGGTATCAAGATGGGCTTCC AACCCCCGGGAGTGCAACTA ATGGTGGCAAGCCTACATG GGCCACTCACAGCCTACTG GCCCCCTGAGGGCTGCTTCT ACCCCCGGAGTGCCAACTA TGGGTACCACGCCTCCATG GCCCCCTAGTGGCCACCTC ACCCCCGTGAGTGCCACCT ACCCCCCGCACGCCTCCT CAGCTGCCACGCCTCCTGT CAGCTGCCACGCCTCCTGTT ACCCCCCGTAGTGCTCCT CAGCTGCCACGCCCTCCTGCT CAGCTGCCACGCCACCTGCT CAGCTGCCACGCCACCTCC CAGCTGCCCCCGCAGTACTA	Reverse Primer TCATCCACCTCCCCACAGTA CAATAGTGATGACCTGGCCGT TGCTGAGTCCATCAGAGAAAGTGT CCAGCGTGAAAGGACATGAA GGCCCAATGACCTTTACAA ATAGGGCTGCACCACAAAAG GGACCTGCTCCAGTGGCAGAC ATGCACAGCGACACTGAACTT GACCACCGGACACGAACTT GACCACGGACATGGACTGT TGGGGTTACAGGCTATCTTG GGGTGCTACAGGCTATCTGG TGGGCTACAGGCTATCCAG TGGGCTACAGGCTATCCAG TGGGCTACAGGCTATCTGG TCATGGACTGGACCTGGCAGAAGC CATGGCACAGGCTATTTGTCG TCATGACTGGACCTGGCAGAGC GGGTCACAGGCTATTTGTCG TCCATGACTGGACCTGGCAGAGC GGGCCACAGGCTATCCAG TCATGACATGGACCAGCATCTTT TCCATGACTGGACCCATCTTT TCCACCACAGGCATGCCCCTA TGAGGCACAGGCCATCTTCC CCCCCTGTAGTGGAGGCTGTCCCTG CCGCTCCTCTGTAGTGGCC TTAGGGAGAAGGCATCTTCC CCGCTCCTCTGTAGTGGCC ACTGTCAAGGGGGATGGAAT CCTAGCAGGGCCATGACCAG
	A B C D F	Gene Gapd Actb Irf1 Nfkbiz Pim1 Tnfaip3 Egr1 Junb Zfp36 Nfkbia Nfkbia Ptgs2 Cxcl2 Cxcl2 Cxcl2 Trf Traf1 Il1b Saa3 Ccl2 Peli1 Gxcl10 Ifit1 Ifnb1 Cxcl10 Ifit1 Ifnb1 Cxcl2 Tyki Rsad2 H28 II6 Il12b Nos2 Marco	Forward Primer TGGTGAAGGTCGGTGTGAAC AGAGGGAAATCGTGGCGTGAC GTAGGTAGGGTGGCAGGAAG GTGCCAGGTAGGTGGAACTCTGAAA GCGCTCTGGAACTCTGGAAGT CCCTCTGCAACACGGAGTTC CCCTGCCAGTGTAGCAGCATTA TGCGGCCCTTGGTAACAGG GGAAGCCTTAGTAATATG CCCCTCCAGCGAAGTTA TGGTGCCGCAGCTTCA GGGAAGCCTTAGTAACAGG GGGCTGCTTGCCAGAGTT CCAGGCCTGCTTCACAGGTT CCATTCTGGCGCAGCTTCC AGCCCCAGTGTGAAGAAC TCCATTCTGGGCAAGTTA TCGCAGCCTAGATGAGAGT CCAATTCTCGGCAAGTTCC GGGCAATTATCTGGGCAACTA ATGGTGCAAGAGTGAAGCACAT GGCCACTCAGAGGTGCAACAA TGGTGCCAAGAGCTAAAAGGCTTGC GGCCACTCAGAGGTGCAACAA TGGTGCCAAGAGCTGAAAAA GCCCCTCAGTGTGAGGTGCA GGCAATTATCTGGTGCACAACA TGGTGCCAAGTGCAACAA TGGCGCAAGCTGCAACAA TGCCCCGGCAGTGCAACAA TGGCGCAAGCTGCAACACA TGGCGCAAGCTGCAACAACACACACACACACCCCCGCAGGGCTGCACCACACACA	Reverse Primer TCATCCACCTCCCCACAGTA CAATAGTGATGACCTGGCCGT TGCTGAGTCCATCAGAGAAAGTG' CAAGCGTGAAAGGACATGAA GGACCTGCTCCAGTGGCAGA ATAGGGCTGCCACCAACAAAG GGACCTGCTCCAGTGGCCAGA ATGCACAGCACAGAAGGTCATCTTT GACGACCGGACACTGAACTT GGGTGCTAAGGCACATGAGC CAGGCACAGGCTGTCCACTG AGTCTGGAAGTGGCAGAAGC CATGGCACAGGCATTCTAG GGGCCCACAGGCATTCTGG TGGGCTACAGGCTGTCACT AGCCGACAGGCATGCCACT AGCCGACAGGCATGCCACTA AGCCGACAGGCATGCCACTA CCCAGAGACCAGACCCATCTTG TGAGGCAGAGGCATCCTCG CCCCGGTACGCCCTCCACTGC CCCCGGAGGAGAGGCATCTTGC CCCGGCCCTTCTGTAGTGGCCGTC TTAGGGAGAGAGCCATCTTGC CCCGGCCCTCTGTAGTGGCCGTC CCCGGCCCTCTGTAGTGGCCGTC CCCGGCCCTCTGTAGTGCCCTCG CCCTGCAAGGCCATGCCCGCC CCTGCCAGGGGATGGACCCACCG CCTGCCAGAGGCCATGCCCG CCTGCCAGGGCATGCCCCG CCTGCCAGGGGATGGACCCACCG CCTGCCAGGGCATGCACCCG CCTGCCAGGGCATGCACCCG CCTGCCAGGGCATGCCCCG CCTGCCAGGCCCCCGCCCTGGT CCCAGCAGGCCCCGCCCCG CCTGCCAGGCCCCCGCCCCG CCTGCCAGGCCCCCGCCCCG CCTGCCAGGCCCCCCCGCCCCG CCTGCCAGGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC