

Table S1. Relative Levels of -1 and +1 Nucleosome Marks in Relationship to Amount of H3 on *IL1B* in THP1 Cells

		<i>TNF</i>			<i>IL1B</i>		
		0 h	1 h	5h	0 h	1 h	5 h
Nucleosome Mark +1 Nucleosome	H3K4me3	0.19	0.56	0.75	0.02	0.03	0.24
	H3K9ac	0.83	1.61	0.98	0.28	0.31	0.65
	H3K27me3	0.04	0.17	0.08	0.02	0.03	0.06
	H3K36me3	0.21	0.56	0.56	0.02	0.03	0.17
Nucleosome Mark -1 Nucleosome	H3K4me3	0.05	0.13	0.62	0.06	0.09	0.50
	H3K9ac	nd	nd	nd	0.06	0.64	1.33
	H3K27me3	0.05	0.13	0.08	0.06	0.09	0.17
	H3K36me3	0.20	0.25	0.31	0.06	0.09	0.42

Table S2. Antibodies Used For ChIP and Western Blots

EPITOPE	SOURCE	CATALOG NUMBER	AGAROSE IP
RNA Pol II (N-20)	Santa Cruz Biotechnology, Inc.	sc-899	Protein A
RNA Pol II CTD Ser5	Babco-Covance	MMS-134R	Protein M
RNA Pol II CTD Ser2	Babco-Covance	MMS-129R	Protein M
RNA Pol II 8WG16	Babco-Covance	MMS-126R	Protein M
Cdk9 (H-169)	Santa Cruz Biotechnology, Inc.	sc-8338	Protein A
NELF-A (A-20)	Santa Cruz Biotechnology, Inc.	sc-23599	Protein G
PU.1 (H-135)	Santa Cruz Biotechnology, Inc.	sc-22805	Protein A
PU.1/Spi-1 (T-21)	Santa Cruz Biotechnology, Inc.	sc-352	Protein A
TFIID (TBP) (SI-1)	Santa Cruz Biotechnology, Inc.	sc-273	Protein G
TBP	Abcam, Inc.	ab28175	Protein A
C/EBP β (47A1)	Santa Cruz Biotechnology, Inc.	sc-56637	Protein G
H3 (tri methyl K36)	Abcam, Inc.	ab9050	Protein A
H3 (tri methyl K27)	Active Motif	39156	Protein G
H3 (tri acetyl K27)	Abcam, Inc.	ab4729	Protein A
H3 (mono methyl K9)	Millipore	07-450	Protein A
H3 (acetyl K9)	Upstate	07-352	Protein A
H3 (mono methyl K4)	Active Motif	39635	Protein G
H3 (tri methyl K4)	Active Motif	39915	Protein A
Histone H3 (FL-136)	Abcam, Inc.	ab1791	Protein A
BRD4	Abcam	ab84776	Protein A
P300 (N15)	Santa Cruz Biotechnology, Inc.	Sc-584	Protein A/G ⁺
NF κ B p65	Abcam, Inc.	ab7970	Protein A
Anti-proIL-1 β	R&D Systems	MAB6964	(Western Blot)

Table S3. Human *TNF* Primer Sequences

Position	Forward	Reverse
-243	CACAAATCAGTCAGTGGCCAGAA	GGACACACAAGCATCAAGGATACC
-181	GGTATCCTTGATGCTTGTGTGCC	CTGCACCTTCTGTCTCGGTTTCTT
-128	GGAGAAGAAACCGAGACAGAAGGT	CTTCCTTGGTGGAGAAACCCATGA
-98	ACTACCGCTTCCAGATGAG	GGGAAAGAATCATTCAACCAGCGG
-50	CCGCTGGTTGAATGATTCTT	TGTGCCAACAACTGCCTTTA
-15	CCCAGGGACATATAAAGGCAGTTG	TGTCCTTGCTGAGGGAGCGT
+18	TTGGCACACCCAGCCAGCAGA	GGTCTGTAGTTGCTTCTCTCCCTCTT
+57	CCAGCTAAGAGGGAGAGAAGCAACTA	ATGTGGCGTCTGAGGGTTGTTT
+97	AAACAACCCCTCAGACGCCACAT	TATGTGAGAGGAAGAGAACCCTGCC
+145	AGGCAGGTTCTCTCTCTCACAT	TGCTTTCAGTGCATGCTGTCTCT
+214	TGGAAAGGACACCATGAGCACTGA	TGAGGAACAAGCACCGCCT
+293	AGCGGTGCTTGTCTCTCA	TCCAAAGTGCAGCAGGCAGAAGA
+473	TGGGTGAAAGATGTGCGCTGATAG	TTGCCACATCTCTTCTGCATCCC
+1326	ATGTGCTTGGAACTGGAGGGCT	TATCCCACTAAGGCGCTGTCTGTT
+1806	TCAACCTCCTCTGCCATCAAGA	ATAGATGGGCTCACCAGGGCTT
+2014	AGGACGAACATCCAACCTTCCCAA	TTTGAGCCAGAAGAGGTTGAGGGT

Table S4. Human *JUNB* and *HIST1H4K* Primer Sequences

JUNB

Position	Forward	Reverse
-96	CCGCTGTTTACAAGGACACG	GGAAAGTGGCTCCGATTG
+33	GGCTGGGACCTTGAGAGC	GTGCGCAAAGCCCTGTC
+78	TGACTAGCGCGGTATAAAGCGT	CGATAGCTTCTGCGCTCGTTT
+793	GGACGATCTGCACAAGATGA	TGCTGAGGTTGGTGTAAACG
+1157	CATCAAAGTGGAGCGCAA	TTGAGCGTCTCACCTTGTC
+1969	CCAGCTCAGTGCTGTTGGT	ATCCAACCCTGGAGATCTGG

HIST1H4K

+35	GACTCCTCTTGCTCGTCATGTCTG	CGCCTTTGCCAAGACCCT
+237	GGTGCTGAAGGTGTTCTGCG	CGCTTGGCGTGCTCTGTA
+382	GGTTGAGCGTCCCTTCTATCAACA	TGGGCAAACAAGCATCACGG

Numbers indicate the midpoint of amplicons in relation to the TSS

Table S5. Human *IL1B* Primer Sequences

Position	Forward	Reverse
-3000	CCAAGGAAGTGAACAAGCAGAGA	CCAAGGAAGTGAACAAGCAGAGA
-2876	TCTCCTTGGGAAGACAGGATCTGA	ACCTGGACCCAAATCTGCTACCAT
-2790	ACATGGCAGAAGTGTGGAGACTGT	ATAGCACAGTGTGGTTGAAGCAGC
-2329	TCCCTTCCTGTCACTGGCTTTGAT	TGCATGATCACAGCAGCCTCAAAC
-1520	ATCAGAAGGCTGCTTGGAGAGCAA	TGCATTATCCAAGGGAGTGAGCCT
-800	TAGGCAGAGCTCATCTGGCATTGA	ATTGCAGGAGCCTCTGAGGAGAAA
-279	TGTGTGCTTCCACTTTGTCCAC	CCTGACAATCGTTGTGCAGTTGATG
-223	TGTGGACATCAACTGCACAACG	TTCATGGAAGGGCAAGGAGTAGCA
-155	TTGCTACTCCTTGCCTTCCATGA	GAGTATTGGTGGAAAGCTTCTTAGGG
-91	CCCTAAGAAGCTTCCACCAATACTC	GCAGAAGTAGGAGGCTGAGAAA
-19	CCCTAAGAAGCTTCCACCAATACTC	GCAGAAGTAGGAGGCTGAGAAA
+36	AAACCTCTTCGAGGCACAAG	GAGCAATGAAGATTGGCTGA
+98	CAGCCAATCTTCATTGCTCA	GCATACACACAAAGAGGCAGAG
+160	CTCTGCCTCTTTGTGTATGC	GAGGGAAGGAGAGGGAGAGA
+223	TCTCCCTCTCCTTCCCTCTC	TTCCCAGAATATTTCCCGAGT
+271	GCCAGGTGTAATATAATGCTTATGACTCGG	GACACTAACCTTTAGGGTGTGAGC
+505	TGCACTGGATGCTGAGAGAAA	GGCTGCTTCAGACACCTGTG
+1031	AATCTGCCTTCTGGACTGTTCTGC	AAGAACTGCAACAGCCTGCCTC
+3325	AATCTCCGACCACCACTACAGCAA	AAGGAAAAGAAGGTGCTCAGGTCA
+4000	TCGACACATGGGATAACGAGGCTT	TGGAGGTGGAGAGCTTTCAGTTCA
+5389	ACTGCTGTGCCCTAACCAAGA	TTCACACGCAGGACAGGTACAGA
+6268	TCGCTGCAGAGTGTAGATCCAAA	TGCTTGAGAGGTGCTGATGTACCA
+7192	CCTCATTGCTGAGTGCTGCAAAGT	AGTGCTTCAGCTGATCCTGTCCA

Numbers indicate the midpoint of amplicons in relation to the TSS

Table S6. Murine *Il1b* and *Tnf* ChIP Primer Sequences

Il1b

Position	Forward	Reverse
-408	TGATGGAGAGCACAGAAGCACCAT	ACGTAGATGCACACCCAGAAGTGT
+31	ACAAGTTGGACAACAAACCCTGC	TACTTGCACAAGGAAGCTTGGCTGGA
+1126	AGGGACTCTACAGATGCAATGGT	TGCTCTGGTTGCTCTCTGTTGACT
+3627	AAATCCAATGTTCTTGCCAGCCC	TGCAAGCACTGTGAAGTGAAGCAG
+5169	GCCTTGGCCTCAAAGGAAAGAAT	TAAAGGCAGAGTCTTCGGTGAGCA
+6478	ATAGCCCGCACTGAGGTCTTTCAT	CTCATCAAAGCAATGTGCTGGTGC

Tnf

Position	Forward	Reverse
-404	TATGCACCCAGCTTTCAGAAGCAC	AGGACCCTGAGAACTGAAACCCAT
-79	ACTACCGCTTCTCCACATGAGAT	AGACGGCCGCTTTATAGCCCTT
+15	CTCTTCCCCAAGGGCTATAAAGG	CTTGCTTTTCTGGGAGCTATTTCC
+71	ACTAGCCAGGAGGGAGAACAGAAA	AGTGAGTGAAGGGACAGAACCTG
+797	AAAGAAGCCGTGGGTTGGACAGAT	AGAACTGATGAGAGGGAGGCCATT
+1585	AGCCGATGGGTTGTACCTGTCTA	TGAGATAGCAAATCGGCTGACGGT
+2106	TCTCATGCACCACCATCAAGGACT	ACCACTCTCCCTTTCAGAACTCA
+2937	GTACTGCAGTCTTCCGGCTGTT	TCTGTCTGTTCCAGGGCAGGTTGA

Numbers indicate the midpoint of amplicons in relation to the TSS

Table S7. mRNA Analysis and qPCR Primer Sequences

Gene	Forward	Reverse
18srRNA	TAGAGGGACAAGTGGCGTTC	TCCTCGTTCATGGGGAATAA
hB2M	TGCTGTCTCCATGTTTGATGTATC	TCTCTGCTCCCCACCTCTAAGT
mB2M	GGCCTGTATGCTATCCAGAA	GAAAGACCAGTCTTGCTGA
hIL1B	AATCTCCGACCACCACTACAGCAA	AAGGGAAAAGAGGTGCTCAGGTCA
Splice IL1B	TCTGTACCTGCTCTGCGTGTGAA	GGGCAGACTCAAATCCAGCTTGT
mIL1B	CCCAACTGGTACATCAGCAC	TCTGCTCATTACGAAAAGG
hTNF	AAGCCCTGGTATGAGCCCATCTAT	ATGATCCCAAAGTAGACCTGCCCA
Splice TNF	AGTGACAAGCCTGTAGCCCATGTT	GTTATCTCTCAGCTCCACGCCATT
mTNF	CCCACTCTGACCCCTTACT	TTTGAGTCTTGATGGTGGT
hSPH	CCAGCTCAGATGAGGAGGAG	GCTTGGACGAGAACTGGAAG
hC/EBPA	TGGCCAACCTTCTACTACGAGG	AGAGGAAGTCGTGGTGCTGC
hC/EBPB	TACTACGAGGCGGACTGCTT	CGTAGTCGTGGGAGAAGAGG
p65	GGCGAGAGGAGCACAGATAC	CACTGTCACTGGAAGCAGA
hIRF8	ACGAGGTTACGCTGTGCTTT	CCAGTCTGGAAGGAGCTGAC

Site directed mutagenesis primer sequences

IL1B enhancer I region XT-I (c/g)-Luc primer pairs:

I (c/g) F: 5'CTGTGGAGACTGTTAGGTCAGGGGGCATTGC3'
 I (c/g) R: 5'GCAATGCCCCCTGACCTAACAGTCTCCACAG3'

NF-κB site (-300) mutation

XT-300 F:
 5'AACATTCTTAACGTGTGAAAATACAGTATTTAATGTGGACATC3'
 XT-300 R:
 5'GATGTCCACATTAATACTGTATTTTCACAGTTAGAAGAATGTT3'

I region / NF-κB site (-300) double mutant was engineered by using the XT-I(c/g)-Luc plasmid as a template and the XT-300mut(F)/(R) as primers.

Table S8. Human *IL1B* 3C Primer Sequences

Designation	Position	Sequence
1'	-12369 / -12349	GGGGCCTCCAAATCACTAAGC
2	-2772 / -2750	GCATTGCCCATGGCTCCAAAAT
3'	-482 / -504	TCTTACCTGGGTGCTGTTCTC
4	4605 / 4627	CCGCTGTAACGGGCAAAGTTTC