Supplementary Data

Supplementary Figures



Supplementary Fig. 1. Wildtype MEFs and *Ikbke*-deficient MEFs were stimulated with TNF for 1 hr, followed by ChIP analysis using the indicated specific and anti-IgG control antibodies. IKKɛ association with the *Icam1* gene promoter region was detected by real-time PCR using specific primers, error bars show standard deviations.





Supplementary Fig. 2. Analysis of phosphorylation-dependent p65 promoter occupancy. p65^{-/-} MEFs stably reconstituted to express p65 and the indicated mutants were stimulated with TNF for 1 and 5 hr. ChIP assays were performed using anti-p65 or anti-IgG control antibodies. Binding of p65 to the indicated promoters was quantified by real-time PCR using specific primers. Experiments were performed in triplicates, error bars display standard deviations. The analyzed promoters are arranged in three groups (A-C) according to the regulation of the target genes by p65 phosphorylation. The amounts of p65-associated DNA are presented as the percentage recovered out of the total input DNA (percent input).

A IKKs hoechst Merge untreated TNF Leptomycin B IKKs hoechst Merge Jose Jose



Supplementary Fig. 3. (A) HeLa cells were incubated for 4 hr with leptomycin B (10 ng/mL) or left untreated prior to TNF stimulation for 30 min. Subcellular localization of endogenous IKKɛ was visualized using an anti-IKKɛ antibody (red). (B) The experiment was done as in (A) with the exception that localization of the endogenous p65 protein was analyzed.

3



Supplementary Fig. 4. (A) HeLa cells were transfected to express the PML-RAR α fusion protein. 36 hr after the transfection, cells were incubated for 4 hr with Leptomycin B or left untreated prior to TNF stimulation for 30 min. Subcellular localization of PML and endogenous IKK ϵ was visualized using an anti-PML (red) and anti-IKK ϵ antibody (green).

Supplementary Materials and methods

Real-time PCR for the quantification of gene expression

The following primers were used to quantify the murine NF-KB target genes:

CSF2_FW 5'-TCCTGGGCATTGTGGTCT-3' CSF2_RV 5'-CGGGTGACAGTGATGGGT-3' VCAM-1_FW 5'-AGTTGGGGATTCGGTTGTTCT-3' VCAM-1_RV 5'-CCCCTCATTCCTTACCACCC-3' CXCL2_FW 5'-AGTGAACTGCGCTGTCAATG-3' CXCL2_RV 5'-CTTCAGGGTCAAGGCAAACT-3' ICAM-1_FW 5'-GGAGACGCAGAGGACCTTAAC-3' ICAM-1_RV 5'-CGCTCAGAAGAACCACCTTC-3' SAA3_FW 5'-CTGTTCAGAAGTTCACGGGAC-3' SAA3_RV 5'-AGCAGGTCGGAAGTGGTT-3' MMP13_FW 5'-ACCTCCACAGTTGACAGGCT-3' MMP3_FW 5'-ACCTATTCCTGGTTGCTG-3' MMP3_RV 5'-GCCTTGGCTGAGTGGTAG-3'

COX-2_FW 5'-TCTCCAACCTCTCCTACTAC-3' COX-2_RV 5'-GCACGTAGTCTTCGATCACT-3' IL6_FW 5'-TGGATGCTACCAAACTGGAT-3' IL6_RV 5'-GGACTCTGGCTTTGTCTTTC-3' IP10_FW 5'-AATCATCCCTGCGAGCCTAT-3' IP10_RV 5'-TTTGGCTAAACGCTTTCATT-3' β -ACTIN_FW 5'-GAGATTACTGCTCTGGCTCCTA-3' β -ACTIN_RV 5'-TCATCGTACTCCTGCTTGCT-3'.

ChIP and re-ChIP assays

The following primers were used to quantify the genomic DNA fragments containing a

NF- κ B binding site.

CSF2_FW 5'-CCTGGCTTCTATACCC-3' CSF2_RV 5'-CTCACAAGTCCACCTCA-3' VCAM-1_FW 5'-TCAGCCCAGAAAGCAGC-3' VCAM-1_RV 5'-AAAGTGTTCAGCCTCCA-3' CXCL2_FW 5'- AGGGCAGGGCAGTAGAATGA -3' CXCL2_RV 5'- TGTGGCTGGAGTCTGGAGTG -3' ICAM-1_FW 5'-AGGGGACTAGGCAGTAGTCAATCAG-3' ICAM-1_RV 5'-GAACGAGGGCTTCGGTATTT-3' SAA3_FW 5'-ATTATGGGTAAGTGGG-3' SAA3_RV 5'-GCTGAGGAGATGTGGC-3' MMP13_FW 5'-ACGTTGTGACTTGGA-3'