

Figure S1. Biological processes modulated by NF- κ B in various vascular cells under inflammatory conditions.

- a) Heatmap showing the pairwise correlation of RNA-seq signals between WT and *RelA*^{-/-} vascular cells under basal condition and upon TNF α treatment. Pearson correlation coefficient (R) is presented to the right.
- b) Western blot analysis of RelA protein levels in WT VECs, VSMCs and MSCs under basal condition (n=3). The number below represents the relative expression of RelA in various vascular cells. β -Actin was used as a loading control.
- c) Ki67 immunostaining of WT MSCs infected with shCLEC11A viruses. shGL2 viruses were used as a negative control. DNA was labeled by Hoechst 33342. ***p< 0.001. Scale bar, 30 μ m.
- d) GO enrichment analysis of upregulated genes only in WT VECs upon TNF α treatment. Enriched top 10 GO biological processes are presented with dots. The area of dot represents the count of genes in the terms.
- e) GO enrichment analysis of upregulated genes upon TNF α treatment only in WT VSMCs.
- f) GO enrichment analysis of upregulated genes upon TNF α treatment only in WT MSCs.
- g) GO enrichment analysis of upregulated genes upon TNF α induction among WT but not *RelA*^{-/-} VECs, VSMCs and MSCs.

Figure S2. RNA-seq analysis identified I κ B α -regulated genes in vascular cells.

- a) Correlation analysis of RNA-seq replicates of WT and *I κ B α* ^{-/-} VECs, VSMCs, and MSCs under basal and TNF α -treated conditions. Pearson correlation coefficient (R) is presented.
- b) Overlapping of upregulated (left) and downregulated (right) genes in *I κ B α* ^{-/-} VECs, VSMCs, and MSCs under basal condition.
- c) GO enrichment analysis of differentially expressed genes between WT and *I κ B α* ^{-/-} in VECs under basal condition. Enriched GO terms of upregulated and downregulated genes are marked in red and green color, respectively.
- d) GO enrichment analysis of differentially expressed genes between WT and *I κ B α* ^{-/-} in VSMCs under basal condition.
- e) GO enrichment analysis of differentially expressed genes between WT and *I κ B α* ^{-/-} in MSCs under basal condition.

Figure S1

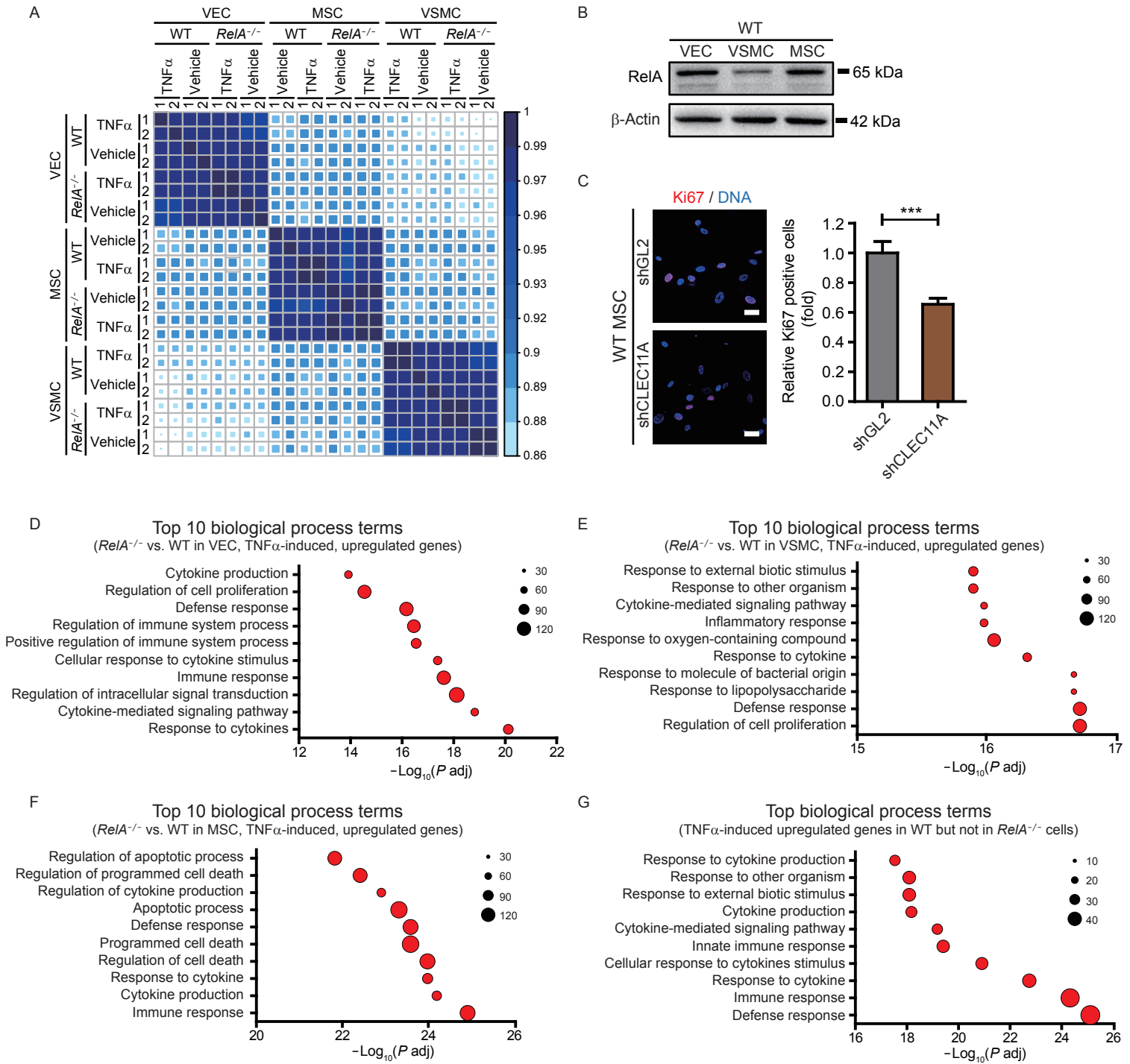
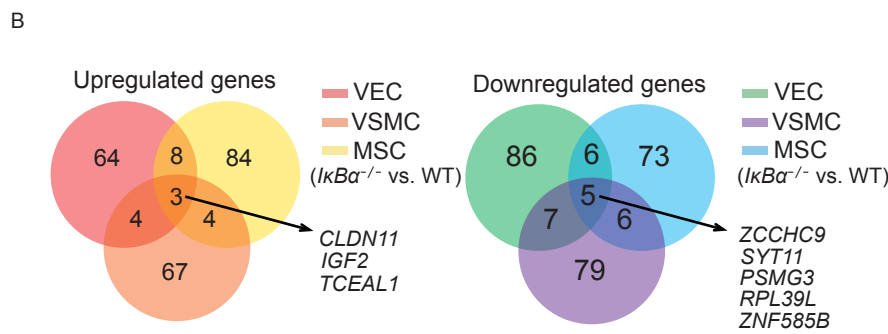
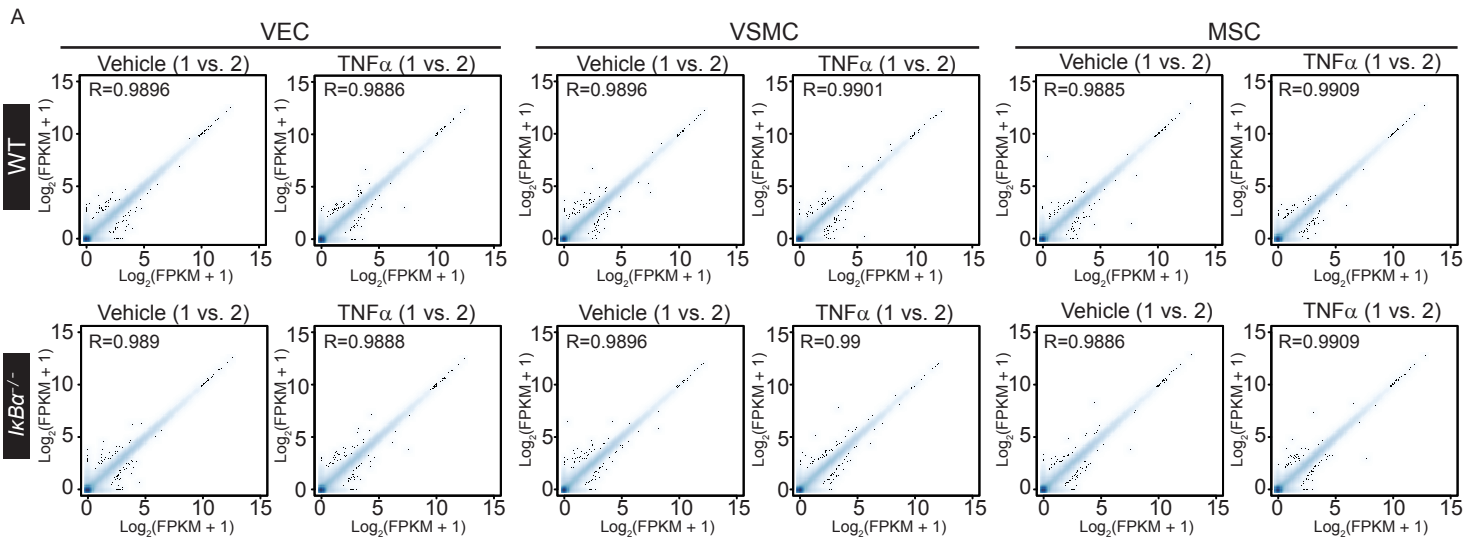


Figure S2



C

Top GO terms of biological process in VEC (*IkBa^{-/-}* vs. WT, vehicle)

Biological process	P value (adj)
Extracellular matrix organization (14)	1.59E-7
Positive regulation of leukocyte migration (7)	4.94E-4
Positive regulation of chemotaxis (7)	4.94E-4
Collagen biosynthetic process (5)	4.94E-4
Integrin-mediated signaling pathway (9)	6.01E-6
Endothelial cell differentiation (7)	1.56E-3
Smooth muscle cell migration (6)	2.35E-3
Endothelium development (7)	2.35E-3

D

Top GO terms of biological process in VSMC (*IkBa^{-/-}* vs. WT, vehicle)

Biological process	P value (adj)
Extracellular matrix organization (12)	9.02E-6
Response to muscle stretch (5)	6.86E-5
Tube morphogenesis (12)	1.21E-4
Response to TGF β (10)	1.21E-4
Epithelial tube morphogenesis(11)	1.47E-4

E

Top GO terms of biological process in MSC (*IkBa^{-/-}* vs. WT, vehicle)

Biological process	P value (adj)
Angiogenesis (18)	7.68E-8
Positive regulation of locomotion (16)	3.71E-6
Response to lipopolysaccharide (13)	3.71E-6
Chemokine-mediated signaling pathway (8)	3.71E-6
Extracellular matrix organization (11)	6.92E-7