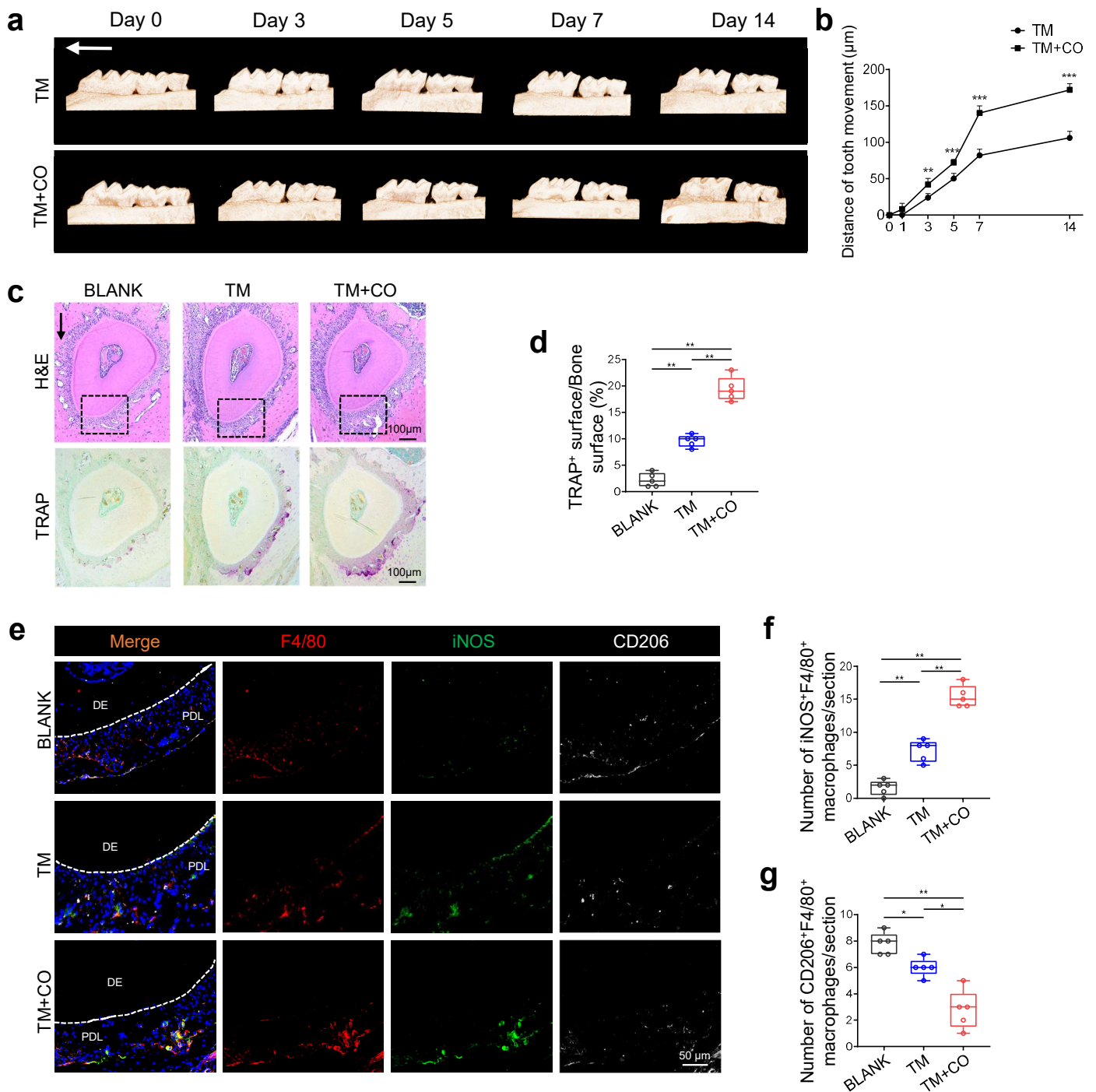


Supplemental Figure 1



Supplemental Figure 1. Corticotomy induces pro-inflammatory macrophage polarization.

(a, b) Representative 3D reconstruction images and statistics of the tooth movement distance from Day 0 to Day 14 in TM and TM+CO groups.

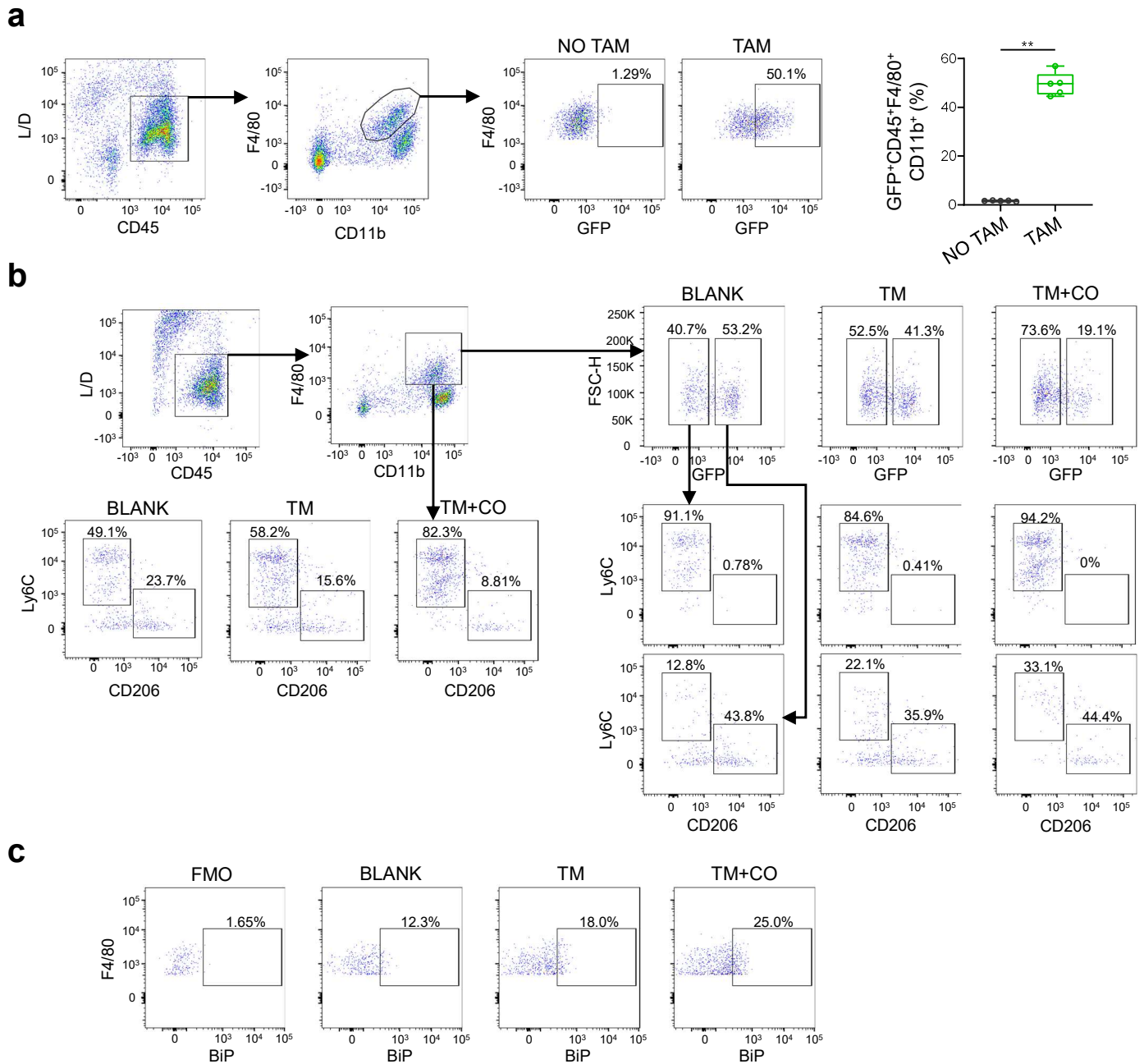
(c) Representative H&E staining and TRAP staining of murine first molar after 7-day application of orthodontic force and corticotomy. Scale bars, 100 μm.

(d) Quantification of surface of osteoclasts relative to the bone surface was shown.

(e-g) Representative immunofluorescence staining images (e) and quantification of iNOS⁺ (green) F4/80⁺ (red) cells (f) and CD206⁺ (white) F4/80⁺ (red) cells (g) in murine periodontal tissues from BLANK, TM and TM+CO groups. Scale bars, 50 μm.

Data represent mean $\pm$ SD. N = 5. * P < .05, ** P < .01. TM, tooth movement; TM+CO, corticotomy-assisted orthodontic tooth movement.

Supplemental Figure 2



Supplemental Figure 2. Gating strategies of FACS analysis.

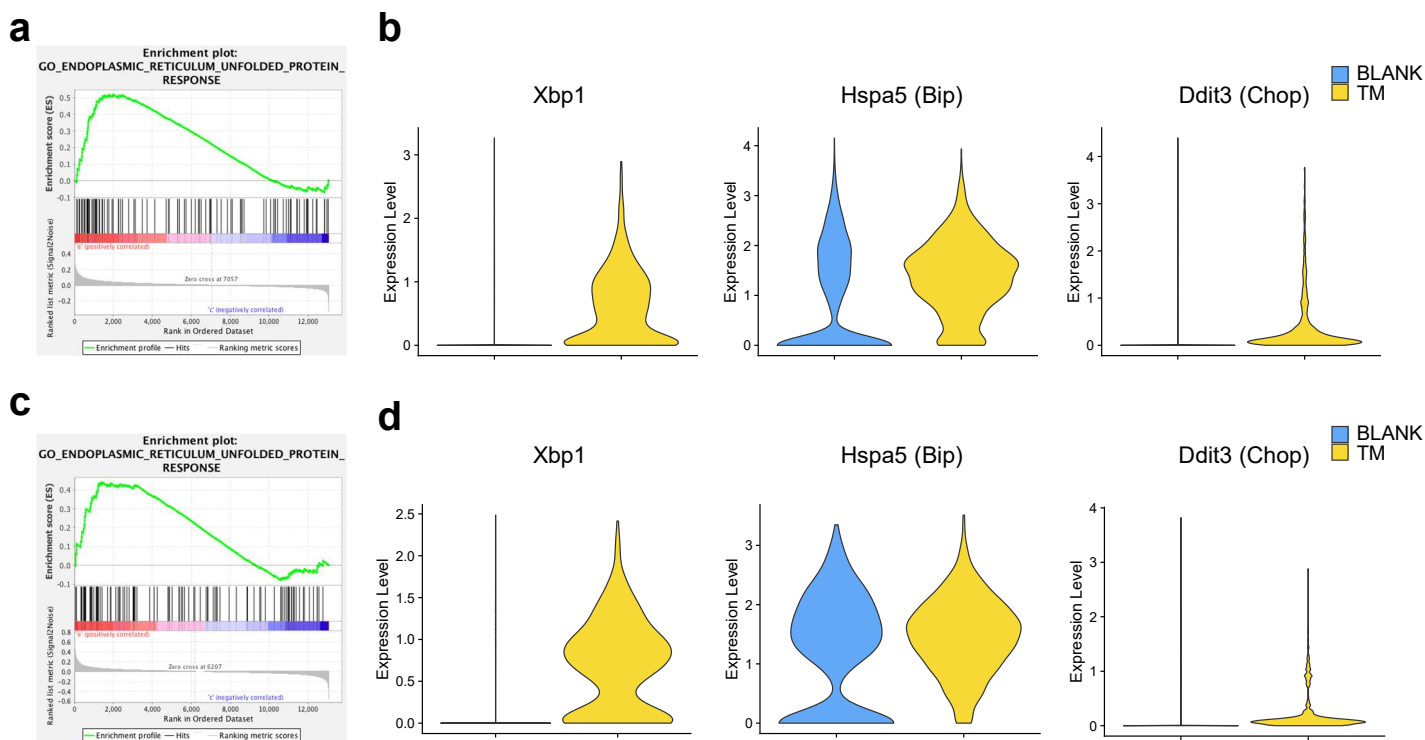
(a) Gating strategies of GFP⁺CD45⁺F4/80⁺CD11b⁺ macrophages in alveolar bone tissues from CX3CR1^{CreERT2}; R26^{GFP} mice with or without tamoxifen injection.

(b) Gating strategies of CD45⁺F4/80⁺CD11b⁺Ly6C⁺ pro-inflammatory and CD45⁺F4/80⁺CD11b⁺CD206⁺ reparative macrophages, GFP-CD45⁺F4/80⁺CD11b⁺ monocyte-derived and GFP⁺CD45⁺F4/80⁺CD11b⁺ resident macrophages from BLANK, TM and TM+CO groups.

(c) Gating strategies of BiP⁺GFP-CD45⁺F4/80⁺CD11b⁺ monocyte-derived macrophages from BLANK, TM and TM+CO groups.

Data represent mean $\pm$ SD. N = 5. ** P < .01.

Supplemental Figure 3



Supplemental Figure 3. UPR is activated in macrophages during orthodontic tooth movement.

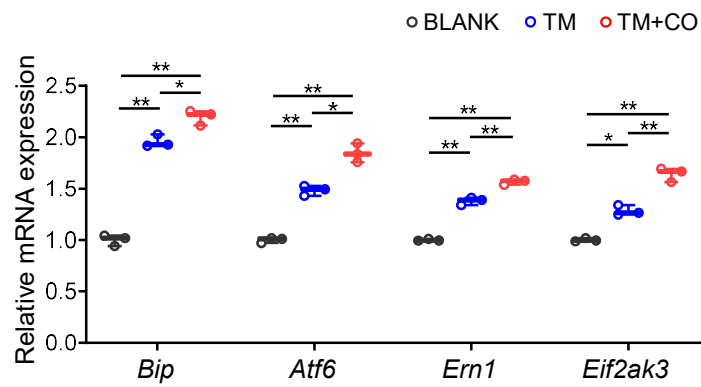
(a) Gene set enrichment analysis (GSEA) of the distribution of genes in Endoplasmic Reticulum Unfolded Protein Response gene sets in total macrophages from BLANK and TM groups.

(b) Violin plots of the expression level of UPR marker genes *Xbp1*, *Hspa5* and *Ddit3* in total macrophages from BLANK and TM groups.

(c) Gene set enrichment analysis (GSEA) of the distribution of genes in Endoplasmic Reticulum Unfolded Protein Response gene sets in CCR2⁺ monocyte-derived macrophages from BLANK and TM groups.

(d) Violin plots of the expression level of UPR marker genes *Xbp1*, *Hspa5* and *Ddit3* in CCR2⁺ monocyte-derived macrophages from BLANK and TM groups.

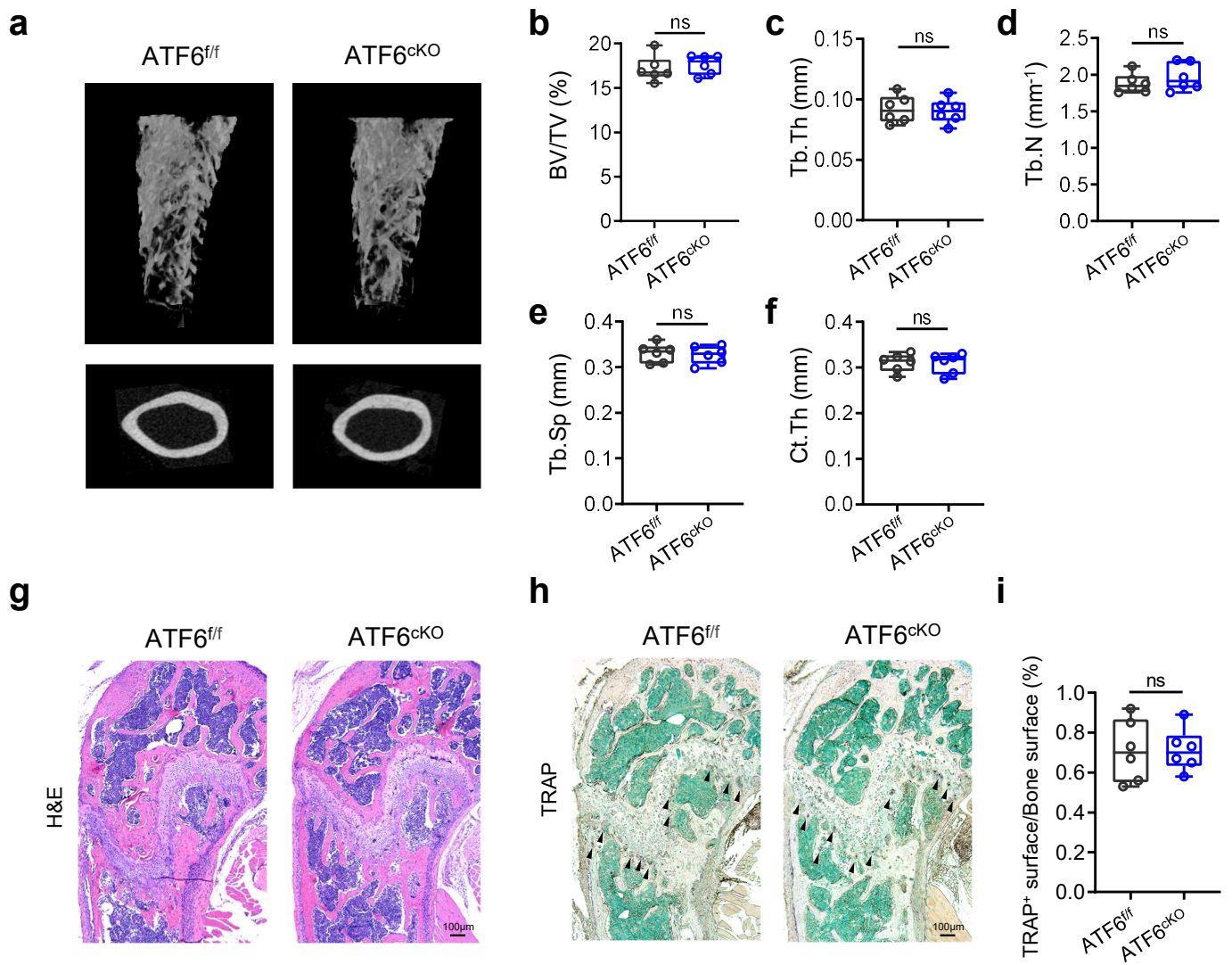
Supplemental Figure 4



Supplemental Figure 4. RT-PCR analysis of *Bip*, *Atf6*, *Ern1* and *Eif2ak3* mRNA expression in BMDMs with stimulation of alveolar bone lysates from Blank, TM and TM+CO mice.

Data represent mean $\pm$ SD. N = 3. * P < .05, ** P < .01. TM, tooth movement; TM+CO, corticotomy-accelerated orthodontic tooth movement.

Supplemental Figure 5



Supplemental Figure 5. Macrophage-specific ATF6 deletion has no significant effect on general bone phenotypes in mice.

(a) Representative 3D reconstruction images of distal femurs in ATF6^{f/f} or ATF6^{cKO} mice.

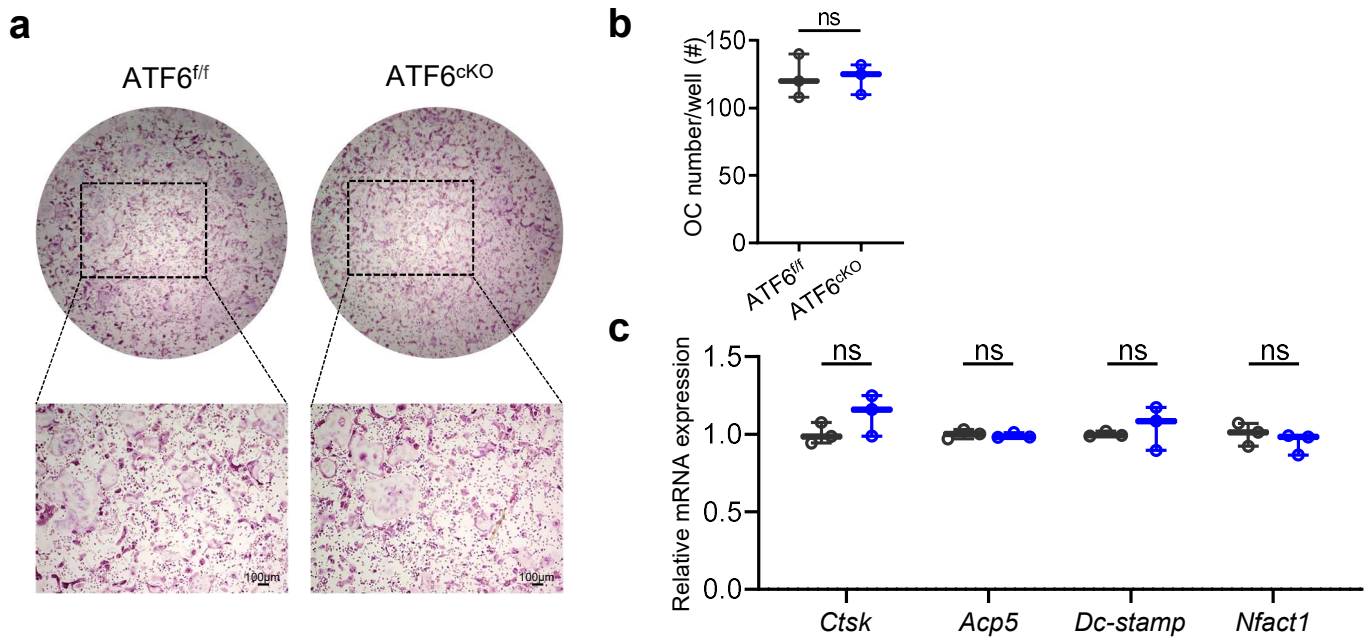
(b-f) Quantitative parameters of micro-CT, including bone volume relative to tissue volume (b), trabecular thickness (c), trabecular number (d), trabecular separation (e) and cortical thickness (f) were shown.

(g, h) Representative H&E (g) and TRAP staining (h) images of distal femurs in ATF6^{f/f} or ATF6^{cKO} mice. Scale bars of H&E staining images and TRAP staining images, 100 μ m.

(i) Quantification of surface of osteoclasts relative to the bone surface was shown.

Data represent mean $\pm$ SD. N = 6. ns, no significance.

Supplemental Figure 6



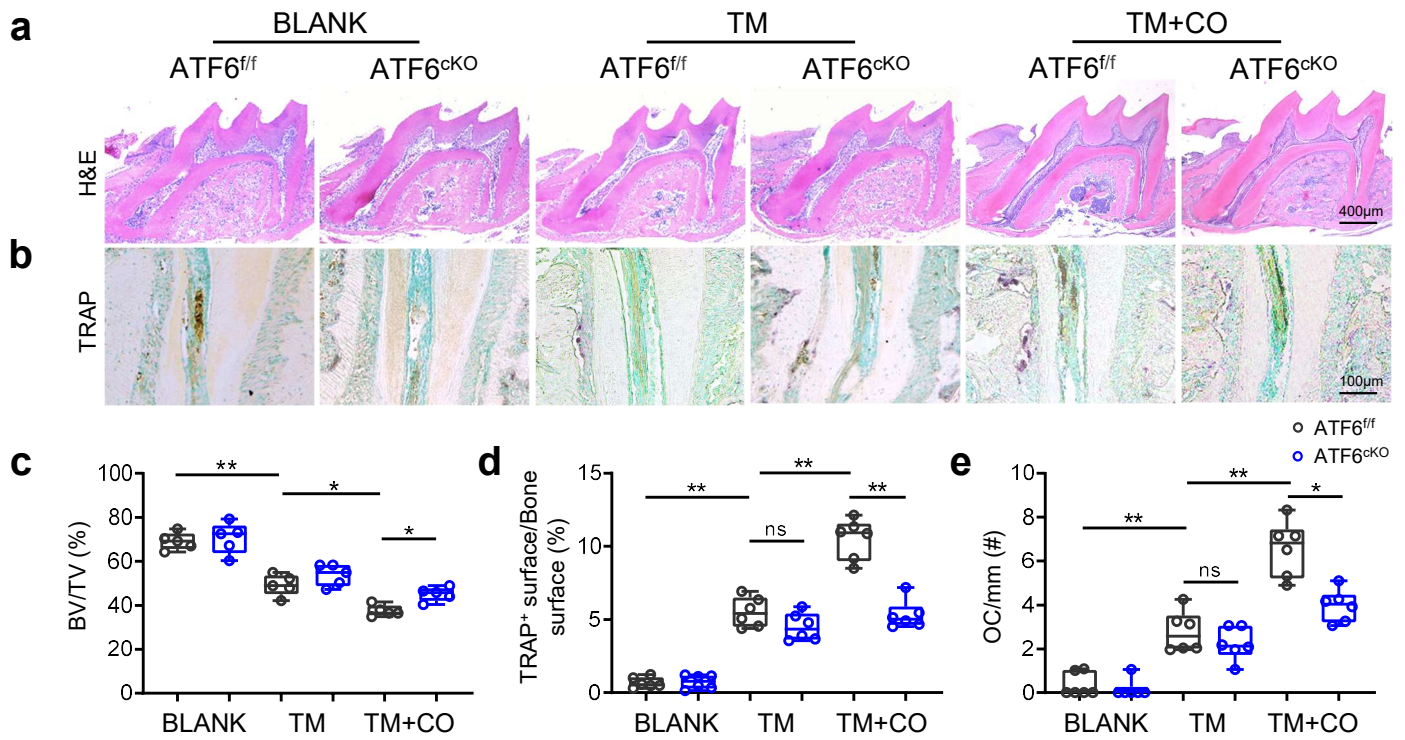
Supplemental Figure 6. Macrophage ATF6 deletion does not affect osteoclast differentiation and function in vitro.

(a, b) Representative TRAP staining images (a) and quantification (b) of multinuclear osteoclasts from ATF6^{f/f} or ATF6^{cKO} mice at 5 days cultured in M-CSF (25 ng/mL) and RANKL (10 ng/mL). Scale bar, 100 µm.

(c) RT-PCR analysis of *Ctsk*, *Acp5*, *Dc-stamp* and *Nfact1* mRNA expression in osteoclasts from ATF6^{f/f} or ATF6^{cKO} mice at 5 days cultured in M-CSF (25 ng/mL) and RANKL (10 ng/mL).

Data represent mean $\pm$ SD. N = 3. ns, no significance.

Supplemental Figure 7



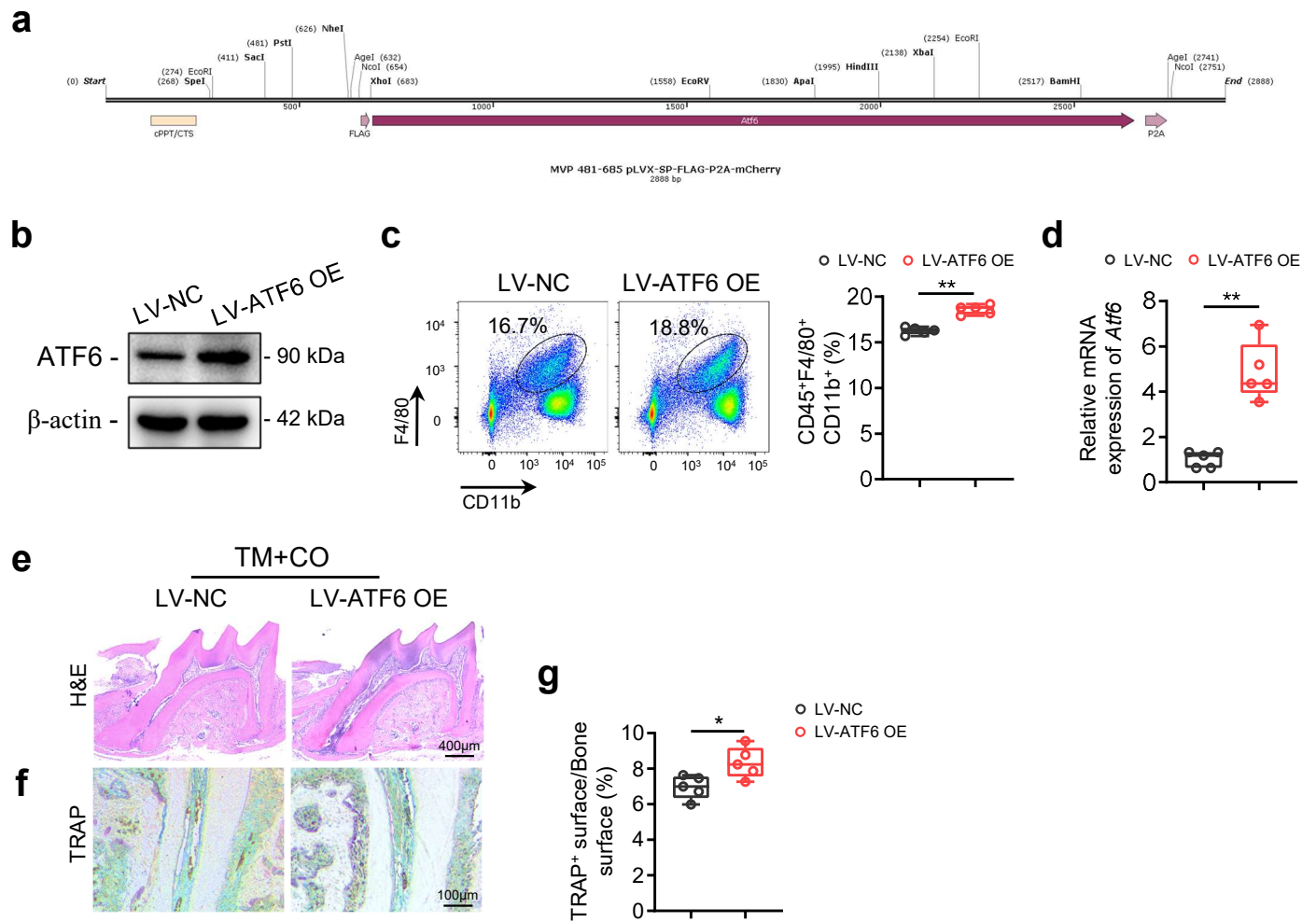
Supplemental Figure 7. Macrophage ATF6 deficiency suppresses orthodontic bone remodeling in corticotomy.

(a, b) Representative H&E (a) and TRAP staining (b) images of murine first molar after 7-day application of orthodontic force and corticotomy in ATF6^{f/f} or ATF6^{cKO} mice. Scale bars of H&E staining images, 400 μ m. Scale bars of TRAP staining images, 100 μ m.

(c-e) Quantification of bone volume relative to tissue volume (c), surface of osteoclasts relative to the bone surface (d) and number of TRAP-positive osteoclasts relative to bone surface (e) were shown.

Data represent mean $\pm$ SD. N = 6. * P < .05, ** P < .01. ns, no significance. TM, tooth movement; TM+CO, corticotomy-accelerated orthodontic tooth movement.

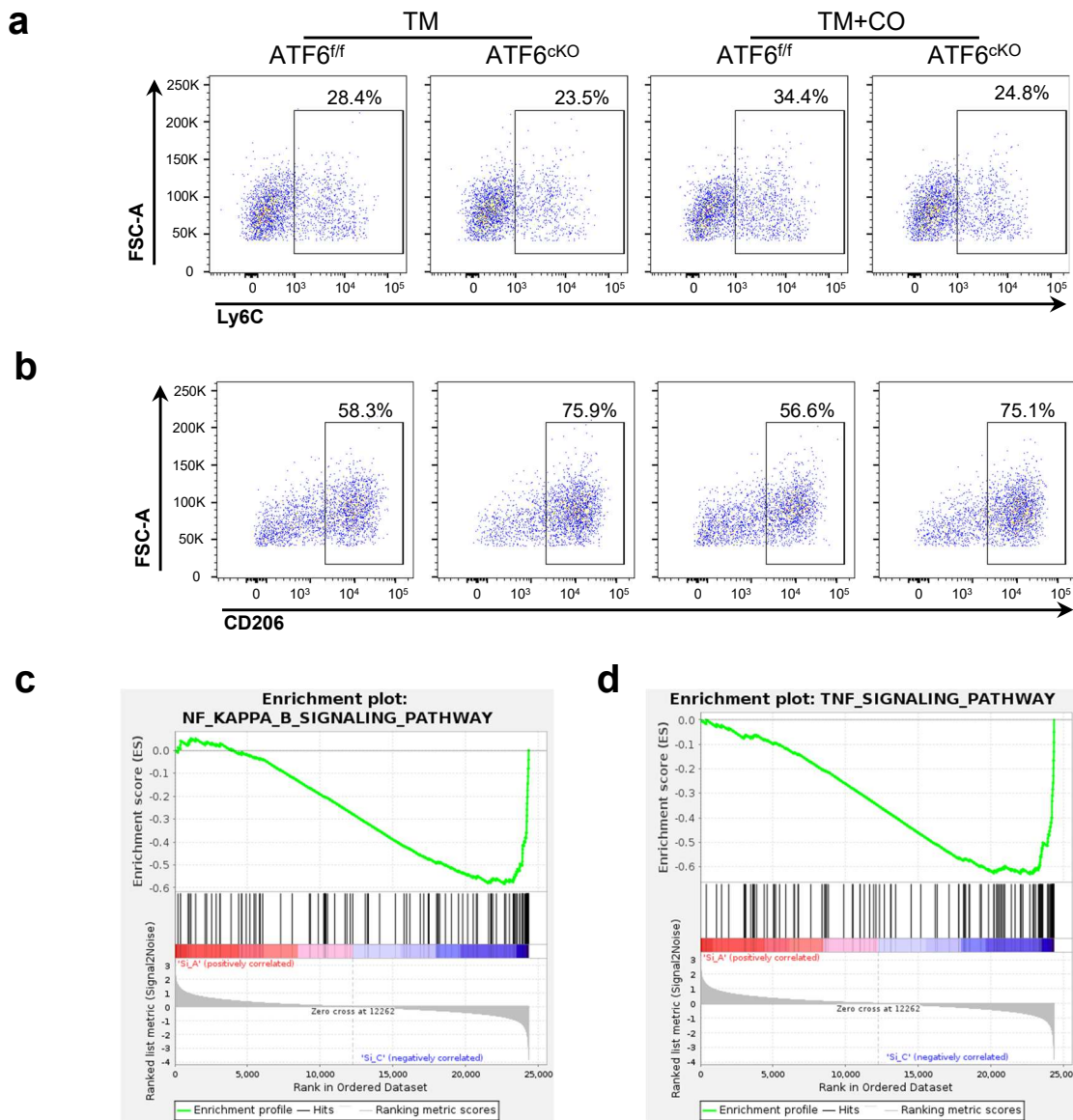
Supplemental Figure 8



Supplemental Figure 8. Confirmation of macrophage-specific *Atf6*-gene overexpressed lentivirus.

- (a) Schematic diagram of vector of macrophage-specific *Atf6*-gene overexpressed lentivirus.
- (b) Representative western blotting of ATF6 expression in BMDMs treated with *Atf6*-gene overexpressed lentivirus or negative control.
- (c) Representative flow plots of the gating scheme used to sort alveolar bone macrophages from mice injected with overexpression lentivirus or negative control.
- (d) RT-PCR analysis of ATF6 mRNA expression in sorted macrophages.
- (e, f) Representative H&E staining(e) and TRAP staining (f) images of murine first molar in TM+CO mice with overexpression lentivirus injection. Scale bars of H&E staining images, 400 μm. Scale bars of TRAP staining images, 100 μm.
- (g) Quantification of surface of osteoclasts relative to the bone surface was shown.
- Data represent mean ± SD. N = 5. * P < .05, ** P < .01. ns, no significance. TM+CO, corticotomy-accelerated orthodontic tooth movement; LV-ATF6 OE, *Atf6*-gene-overexpressed lentivirus; LV-NC, scrambled lentivirus served as a negative control.

Supplemental Figure 9

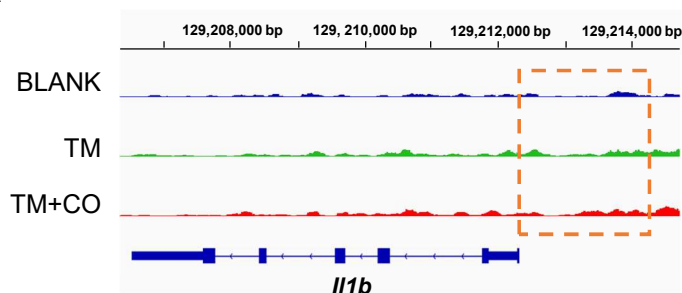


Supplemental Figure 9. ATF6 promotes macrophage pro-inflammatory signals in vitro.

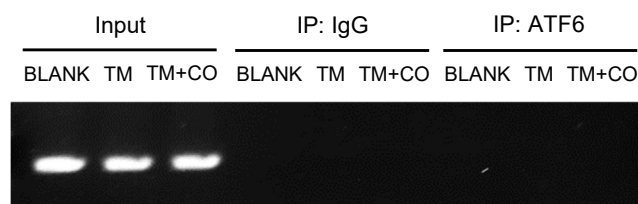
- (a) Gating strategies of $CD45^{+}F4/80^{+}CD11b^{+}Ly6C^{+}$ macrophages in BMDMs from $ATF6^{f/f}$ or $ATF6^{cKO}$ mice upon stimulation of alveolar bone lysates from TM or TM+CO mice.
- (b) Gating strategies of $CD45^{+}F4/80^{+}CD11b^{+}CD206^{+}$ macrophages in BMDMs from $ATF6^{f/f}$ or $ATF6^{cKO}$ mice upon stimulation of alveolar bone lysates from TM or TM+CO mice.
- (c, d) Gene set enrichment analysis (GSEA) of the distribution of genes in the NF- κ B signaling pathway (c) and TNF signaling pathway (d) gene sets of ATF6 knockdown and control groups.

Supplemental Figure 10

a



b



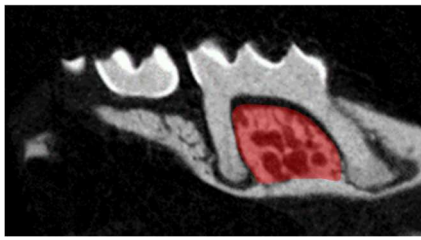
Supplemental Figure 10. ATF6 p50 did not mediate the transcription of *Il1b*.

(a) IGV snapshot of peak values of ATF6 p50 binding on *Il1b* gene in BMDMs from Blank, TM and TM+CO groups.

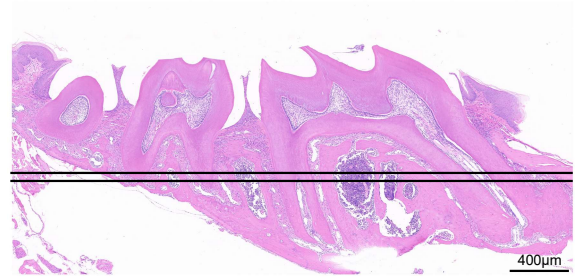
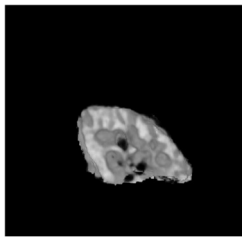
(b) ChIP assay of the binding of ATF6 p50 to *Il1b* promoter in BMDMs treated with tissue suspension from Blank, TM and TM+CO group.

Supplemental Figure 11

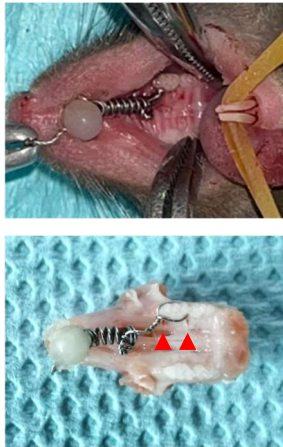
a



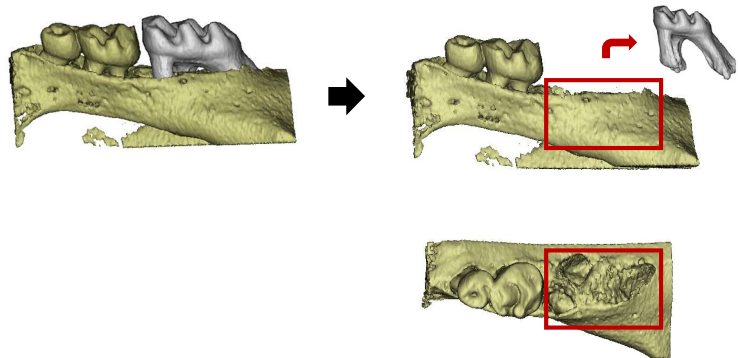
b



c



d



Supplemental Figure 11. Schematic representation of animal models construction, tissue lysates sampling sites, tissue section preparation sites and the region of interest for volumetric measurements.

(a) Representative 3D reconstruction images of the region of interest for volumetric measurements.

(b) Sections were obtained from the middle part (between the double black bars). Scale bars of H&E staining images, 400 μm .

(c) Representative 3D reconstruction images and pictures of the TM+CO models.

(d) Schematic illustration of tissue lysates sampling sites.

Supplemental Table I. The mouse Atf6 pLV-SP sequence

mAtf6 pLV-SP sequence:

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```

Supplemental Table II. RT-PCR primers used in this study.

Gene Name	Forward primer 5'-3'	Reverse primer 5'-3'
Eif2ak3	GGGAAAACGGTTCTGAGACA	GCTGACCAGCTAGTCTTGGG
Ern1	AACACACCGACCAACCGTATC	AGGGTCCTGGGTAAGGTCTC
Atf6	GAACTTCGAGGCTGGGTTCA	TCCAGGGGAGGCGTAATACA
Bip	CAGATCTTCTCCACGGCT	TGTCACTCGGAGAATACCAT
Tnf α	GTTCTATGGCCCAGACCCTCAC	GGCACCAGTGTGGTTGTCTTTG
Il1 β	TCCAGGATGAGGACATGAGCAC	GAACGTCACACACCAGCAGGTTA
Il6	CCACTTCACAAGTCGGAGGCTTA	GCAAGTGCATCATCGTTGTTTCATAC
Ccl2	AGCAGCAGGTGTCCCAAAGA	GTGCTGAAGACCTTAGGGCAGA
Cd206	CTCTGTTCAGCTATTGGACGC	CGGAATTTCTGGGATTCAGCTTC
Arg1	GCTCAGGTGAATCGGCCTTTT	TGGCTTGCGAGACGTAGAC
Il10	GCCCTTTGCTATGGTGTCTTTTC	TCCCTGGTTTCTCTTCCCAAGAC
Gapdh	AGGTCGGTGTGAACGGATTTG	TGTAGACCATGTAGTTGAGGTCA

Supplemental Table III. The mouse Atf6 sequence

mouse Atf6 sequence: 1971bp

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Supplemental Table IV. The wild-type and mutant Tnfa promoter sequence

mTnfa promoter sequence: 2000bp

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mTnfa-mut promoter sequence: 1990bp

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AAGGGCTATAAAGGCGGCGCTCTGCACAGCCAGCC
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Supplemental Table V. The mutant mouse *Atf6* sequence

mAtf6-299Arg-mut sequence: 1971bp

ATGGAGTCGCCTTTTAGTCCGGTTCTTCCTCATGGACCAGATGAAGACTGGGAGTCTACGTTGTTTGCTGAACTTGGCTATTTACAGACA
CTGATGATGTGCACTTTGATGCAGCACATGAGGCTTATGAAAATAATTTTGATCATCTTAATTTTGATTGGATTGATGCCTTGGGAGTCAG
ACCTATGGAGCCCCGGCAGCCACTTCTGCTCAGACATGAAGGCAGAGCCCCAGCCTCTTTCTCCGGCTTCTCCAGTTGCTCCATCTCC
TCTCCTCGGTCCACAGACTCGTGTTCTTCAACTCAGCACGTTCTGAGGAGTTGGATTGTTGTCTAGTTCTCAGTCCCCCTTTCTTAT
ATGGCGACAGCTGTAATAGCCCCTCCTCTGTAGAGCCACTGAAGGAAGAGAAGCCTGTCACTGGTCCTGGAACAAAACAGAACATGGA
CTGACTCAAAGAAAAAATTCAGATGAGTTCAAAACCTTCAGTTTCAGCCCAAGCCTTTATTACTTCCAGCAGCGCCCAAGACTCAAACCA
ATGCCAGTGTCCCAGCAAAGCCATCATCATTAGACACTACCAGCCCTTATGCCACTGGCAAAGCAGCAGTCGATTATCAGCATACAGCC
TGCGCCACCAAAGGCCAGACTGTTTTGCTCTCTCAGCCGACTGTGGTTCAACTTCAGAGCCCTGCGGTTCTGTCGTCTGCTCAGCCGG
TTCTCGCAGTCACTGGGGGAGCCGCACAGCTGCCAACCATTGGTGAATGTGCTGCCAGCCCTGTGGTGAGCAGCCCGGTGAATGG
AAAACCTCTCCGTGACTAAACCTGTTCTACAAAGTGCCACCAGAAGTATGGGTTTCGGATATCGCTGTGCTGAGGAGACAGCAGGctATGATAA
AGAACCGAGAGTCTGCTTGTGCTGCTGCGCAAGAAGAAGAAAGAGTATATGCTAGGACTGGAGGCCAGGCTCAAGGCTGCCCTCTCAGAG
AATGAGCAGCTGAAGAAGGAGAATGGCTCCCTGAAGCGACAGCTGGACGAGGTGGTGTGAGAGAACCAGAGGCTCAAAGTCCCAAGTC
CAAAGCGAAGAGCTGTCTGTGTGATGATAGTATTAGCATTATAATGCTGAACATATGGGCCCATGAGCATGCTGGAGCAAGAGTCCCGAAG
AGTGAAACCTAGTGTGAGCCCTGCCAATCAGAGGAGGCATCTCTTGAATTTTCAGCGAAAGAAGTTAAAGACACATCCGATGGTGACAA
CCAGAAAGACAGTTACAGCTATGATCACTCTGTGTCCAATGACAAAGCTTTAATGGTGCTAAGTGAAGAGCCATTGCTTTATATGCCTCCAC
CTCCATGTCAACCCCTGATTAAACAGCAGAGTCTCAGGTTGAACCATGAGCTCGAGGCTGGGTGAGGCTGGAAGGA
CCAAATCTAGAAGAATGACAAATAGCCAACAGAAAGCCCGCATTCTCCAGGGTGCTCTGGAACAGGGCTCTAATTCTCAGCTGATGGCTG
TCCAGTACACAGAAACCACTAGCATCAGTAGGAATTCTGGGAGTGAGCTGCAAGTGATTACGCCTCCCCTGGAAGTTACCAAGGCTTCTT
TGACGCCATCCGCAGGAGGGGAGATACGTTTTACGTGGTCTCATTTTGAAGGGATCATCTGCTATTACCAGCTACCACCCACAACAAGAC
CACAAGACCAAAAATGTCAATTGTATTACCAGCAATAAACATAAATGATAATGTGATCAATGGGCAGGACTATGAAGTGATGATGCAGATTGA
CTGTCAGGTGATGGACACCAGGATCCTCCACATCAAAGCTCCTCAGTCCCCCTTATCTCCGGGATCATCAGCGGAACCAAACAGCAC
CTTCTTTGGTTCCCTCCAACAACCACAGAGACGACCCATGTGGTCAGCACCATCCCTGAGTCGTTGCAGTAG

mAtf6-302Lys-mut sequence: 1971bp

ATGGAGTCGCCTTTTAGTCCGGTTCTTCCTCATGGACCAGATGAAGACTGGGAGTCTACGTTGTTTGCTGAACTTGGCTATTTACAGACA
CTGATGATGTGCACTTTGATGCAGCACATGAGGCTTATGAAAATAATTTTGATCATCTTAATTTTGATTGGATTGATGCCTTGGGAGTCAG
ACCTATGGAGCCCCGGCAGCCACTTCTGCTCAGACATGAAGGCAGAGCCCCAGCCTCTTTCTCCGGCTTCTCCAGTTGCTCCATCTCC
TCTCCTCGGTCCACAGACTCGTGTTCTTCAACTCAGCACGTTCTGAGGAGTTGGATTGTTGTCTAGTTCTCAGTCCCCCTTTCTTAT
ATGGCGACAGCTGTAATAGCCCCTCCTCTGTAGAGCCACTGAAGGAAGAGAAGCCTGTCACTGGTCCTGGAACAAAACAGAACATGGA
CTGACTCAAAGAAAAAATTCAGATGAGTTCAAAACCTTCAGTTTCAGCCCAAGCCTTTATTACTTCCAGCAGCGCCCAAGACTCAAACCA
ATGCCAGTGTCCCAGCAAAGCCATCATCATTAGACACTACCAGCCCTTATGCCACTGGCAAAGCAGCAGTCGATTATCAGCATACAGCC
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GAATGAGCAGCTGAAGAAGGAGAATGGCTCCCTGAAGCGACAGCTGGACGAGGTGGTGTGAGAGAACCAGAGGCTCAAAGTCCCAAGT
CCAAAGCGAAGAGCTGTCTGTGTGATGATAGTATTAGCATTATAATGCTGAACATATGGGCCCATGAGCATGCTGGAGCAAGAGTCCCGAA
GAGTGAAACCTAGTGTGAGCCCTGCCAATCAGAGGAGGCATCTCTTGAATTTTCAGCGAAAGAAGTTAAAGACACATCCGATGGTGACA
ACCAGAAAGACAGTTACAGCTATGATCACTCTGTGTCCAATGACAAAGCTTTAATGGTGCTAAGTGAAGAGCCATTGCTTTATATGCCTCCA
CCTCCATGTCAACCCCTGATTAAACAGCAGAGTCTCAGGTTGAACCATGAACTTCGAGGCTGGGTTTCATAGACATGAAGTGGAAGG
ACCAATCTAGAAGAATGACAAATAGCCAACAGAAAGCCCGCATTCTCCAGGGTGCTCTGGAACAGGGCTCTAATTCTCAGCTGATGGCT
GTCCAGTACACAGAAACCACTAGCATCAGTAGGAATTCTGGGAGTGAGCTGCAAGTGATTACGCCTCCCCTGGAAGTTACCAAGGCTTC
TTTGACGCCATCCGCAGGAGGGGAGATACGTTTTACGTGGTCTCATTTTGAAGGGATCATCTGCTATTACCAGCTACCACCCACAACAAGA
CCACAAGACCAAAAATGTCAATTGTATTACCAGCAATAAACATAAATGATAATGTGATCAATGGGCAGGACTATGAAGTGATGATGCAGATTG
ACTGTCAGGTGATGGACACCAGGATCCTCCACATCAAAGCTCCTCAGTCCCCCTTATCTCCGGGATCATCAGCGGAACCAAACAGCA
CCTTCTTTGGTTCCCTCCAACAACCACAGAGACGACCCATGTGGTCAGCACCATCCCTGAGTCGTTGCAGTAG

mAtf6-303Asn-mut sequence: 1971bp

ATGGAGTCGCCTTTTAGTCCGGTTCTTCCTCATGGACCAGATGAAGACTGGGAGTCTACGTTGTTTGCTGAACTTGGCTATTTACAGACA
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ACCTATGGAGCCCCGGCAGCCACTTCTGCTCAGACATGAAGGCAGAGCCCCAGCCTCTTTCTCCGGCTTCTCCAGTTGCTCCATCTCC
TCTCCTCGGTCCACAGACTCGTGTTCTTCAACTCAGCACGTTCTGAGGAGTTGGATTGTTGTCTAGTTCTCAGTCCCCCTTTCTTAT
ATGGCGACAGCTGTAATAGCCCCTCCTCTGTAGAGCCACTGAAGGAAGAGAAGCCTGTCACTGGTCCTGGAACAAAACAGAACATGGA
CTGACTCAAAGAAAAAATTCAGATGAGTTCAAAACCTTCAGTTTCAGCCCAAGCCTTTATTACTTCCAGCAGCGCCCAAGACTCAAACCA
ATGCCAGTGTCCCAGCAAAGCCATCATCATTAGACACTACCAGCCCTTATGCCACTGGCAAAGCAGCAGTCGATTATCAGCATACAGCC
TGCGCCACCAAAGGCCAGACTGTTTTGCTCTCTCAGCCGACTGTGGTTCAACTTCAGAGCCCTGCGGTTCTGTCGTCTGCTCAGCCGG
TTCTCGCAGTCACTGGGGGAGCCGCACAGCTGCCAACCATTGGTGAATGTGCTGCCAGCCCTGTGGTGAGCAGCCCGGTGAATGG
AAAACCTCTCCGTGACTAAACCTGTTCTACAAAGTGCCACCAGAAGTATGGGTTTCGGATATCGCTGTGCTGAGGAGACAGCAGCGGATGAT
AAAGgtCAGAGAGTCTGCTTGTGCTGCTGCGCAAGAAGAAGAAAGAGTATATGCTAGGACTGGAGGCCAGGCTCAAGGCTGCCCTCTCAGA
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CCAAAGCGAAGAGCTGTCTGTGTGATGATAGTATTAGCATTATAATGCTGAACATATGGGCCCATGAGCATGCTGGAGCAAGAGTCCCGAA
GAGTGAAACCTAGTGTGAGCCCTGCCAATCAGAGGAGGCATCTCTTGAATTTTCAGCGAAAGAAGTTAAAGACACATCCGATGGTGACA
ACCAGAAAGACAGTTACAGCTATGATCACTCTGTGTCCAATGACAAAGCTTTAATGGTGCTAAGTGAAGAGCCATTGCTTTATATGCCTCCA
CCTCCATGTCAACCCCTGATTAAACAGCAGAGTCTCAGGTTGAACCATGAACTTCGAGGCTGGGTTTCATAGACATGAAGTGGAAGG
ACCAATCTAGAAGAATGACAAATAGCCAACAGAAAGCCCGCATTCTCCAGGGTGCTCTGGAACAGGGCTCTAATTCTCAGCTGATGGCT
GTCCAGTACACAGAAACCACTAGCATCAGTAGGAATTCTGGGAGTGAGCTGCAAGTGATTACGCCTCCCCTGGAAGTTACCAAGGCTTC
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CCACAAGACCAAAAATGTCAATTGTATTACCAGCAATAAACATAAATGATAATGTGATCAATGGGCAGGACTATGAAGTGATGATGCAGATTG
ACTGTCAGGTGATGGACACCAGGATCCTCCACATCAAAGCTCCTCAGTCCCCCTTATCTCCGGGATCATCAGCGGAACCAAACAGCA
CCTTCTTTGGTTCCCTCCAACAACCACAGAGACGACCCATGTGGTCAGCACCATCCCTGAGTCGTTGCAGTAG

mAtf6-304Arg-mut sequence: 1971bp

ATGGAGTCGCCTTTTAGTCCGGTTCTTCCTCATGGACCAGATGAAGACTGGGAGTCTACGTTGTTTGCTGAACTTGGCTATTTACAGACA
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ACCTATGGAGCCCCGGCAGCCACTTCTGCTCAGACATGAAGGCAGAGCCCCAGCCTCTTTCTCCGGCTTCTCCAGTTGCTCCATCTCC
TCTCCTCGGTCCACAGACTCGTGTTCTTCAACTCAGCACGTTTCTGAGGAGTTGGATTTGTTGTCTAGTTCTCAGTCCCCCTTTCTTAT
ATGGCGACAGCTGTAATAGCCCCCTCTCTGTAGAGCCACTGAAGGAAGAGAAGCCTGTCACTGGTCTGGAACAAAACAGAACATGGA
CTGACTCCAAAGAAAAAATTCAGATGAGTTCAAACCTTCAGTTGAGCCAAAGCCTTTATTACTTCCAGCAGCGCCCAAGACTCAAACCA
ATGCCAGTGTCCCAGCAAAAGCCATCATCATTCAGACACTACCAGCCCTTATGCCACTGGCAAAGCAGCAGTCGATTATCAGCATACAGCC
TGCGCCCACCAAAGGCCAGACTGTTTTGCTCTCTCAGCCGACTGTGGTTCAACTTCAGAGCCCTGCGGTTCTGTCGTCTGCTCAGCCGG
TTCTCGCAGTCACTGGGGGAGCCGCACAGCTGCCTAACCATGTGGTGAATGTGCTGCCAGCCCTGTGGTGAGCAGCCCGGTGAATGG
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AAAGAACgctGAGTCTGCTTGTGAGTCGCGCAAGAAGAAGAAAGAGTATATGCTAGGACTGGAGGCCAGGCTCAAGGCTGCCCTCTCAGA
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CCAAAGCGAAGAGCTGTCTGTGTGATGATAGTATTAGCATTATAATGCTGAACATGGGCCCATGAGCATGCTGGAGCAAGAGTCCCCGA
GAGTGAAACCTAGTGTGAGCCCTGCCAATCAGAGGAGGCATCTCTTGGAAATTTTCAGCGAAAGAAGTTAAAGACACATCCGATGGTGACA
ACCAGAAAGACAGTTACAGCTATGATCACTCTGTGTCCAATGACAAAGCTTTAATGGTGCTAAGTGAAGAGCCATTGCTTTATATGCCTCCA
CCTCCATGTCAACCCCTGATTAACACGACAGAGTCTCTCAGGTTGAACCATGAACCTCGAGGCTGGGTTCATAGACATGAAGTGGAAGG
ACCAAATCTAGAAGAATGACAAATAGCCAACAGAAAGCCCGCATTCTCCAGGGTGCTCTGGAACAGGGCTCTAATTCTCAGCTGATGGCT
GTCCAGTACACAGAAACCACTAGCATCAGTAGGAATTCTGGGAGTGAGCTGCAAGTGATTACGCCTCCCCTGGAAGTTACCAAGGCTTC
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CCACAAGACCAAAAATGTCAATTGTATTACCAGCAATAAACATAAATGATAATGTGATCAATGGGCAGGACTATGAAGTGATGATGCAGATTG
ACTGTCAGGTGATGGACACCAGGATCCTCCACATCAAAAGCTCCTCAGTCCCCCTTATCTCCGGGATCATCAGCGGAACCAACACAGCA
CCTTCTTTGGTTCCCCTCCAACAACCACAGAGACGACCCATGTGGTCAGCACCATCCCTGAGTCGTTGCAGTAG

mAtf6-311Arg-mut sequence: 1971bp

ATGGAGTCGCCTTTTAGTCCGGTTCTTCCTCATGGACCAGATGAAGACTGGGAGTCTACGTTGTTTGCTGAACTTGGCTATTTACAGACA
CTGATGATGTGCACTTTGATGCAGCACATGAGGCTTATGAAAATAATTTTGATCATCTTAATTTTGATTTGGATTTGATGCCTTGGGAGTCAG
ACCTATGGAGCCCCGGCAGCCACTTCTGCTCAGACATGAAGGCAGAGCCCCAGCCTCTTTCTCCGGCTTCTCCAGTTGCTCCATCTCC
TCTCCTCGGTCCACAGACTCGTGTTCTTCAACTCAGCACGTTTCTGAGGAGTTGGATTTGTTGTCTAGTTCTCAGTCCCCCTTTCTTAT
ATGGCGACAGCTGTAATAGCCCCCTCTCTGTAGAGCCACTGAAGGAAGAGAAGCCTGTCACTGGTCTGGAACAAAACAGAACATGGA
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TTCTCGCAGTCACTGGGGGAGCCGCACAGCTGCCTAACCATGTGGTGAATGTGCTGCCAGCCCTGTGGTGAGCAGCCCGGTGAATGG
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AAAGAACCGAGAGTCTGCTTGTGAGTCGgctAAGAAGAAGAAGAGTATATGCTAGGACTGGAGGCCAGGCTCAAGGCTGCCCTCTCAGA
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ACCAGAAAGACAGTTACAGCTATGATCACTCTGTGTCCAATGACAAAGCTTTAATGGTGCTAAGTGAAGAGCCATTGCTTTATATGCCTCCA
CCTCCATGTCAACCCCTGATTAACACGACAGAGTCTCTCAGGTTGAACCATGAACCTCGAGGCTGGGTTCATAGACATGAAGTGGAAGG
ACCAAATCTAGAAGAATGACAAATAGCCAACAGAAAGCCCGCATTCTCCAGGGTGCTCTGGAACAGGGCTCTAATTCTCAGCTGATGGCT
GTCCAGTACACAGAAACCACTAGCATCAGTAGGAATTCTGGGAGTGAGCTGCAAGTGATTACGCCTCCCCTGGAAGTTACCAAGGCTTC
TTTGACGCCATCCGCAGGAGGGGAGATACGTTTTACGTGGTCTCATTTTGAAGGGATCATCTGCTATTACCAGCTACCACCCACAACAAGA
CCACAAGACCAAAAATGTCAATTGTATTACCAGCAATAAACATAAATGATAATGTGATCAATGGGCAGGACTATGAAGTGATGATGCAGATTG
ACTGTCAGGTGATGGACACCAGGATCCTCCACATCAAAAGCTCCTCAGTCCCCCTTATCTCCGGGATCATCAGCGGAACCAACACAGCA
CCTTCTTTGGTTCCCCTCCAACAACCACAGAGACGACCCATGTGGTCAGCACCATCCCTGAGTCGTTGCAGTAG

mAtf6-315Lys-mut sequence: 1971bp

ATGGAGTCGCCTTTTAGTCCGGTTCTTCCTCATGGACCAGATGAAGACTGGGAGTCTACGTTGTTTGCTGAACTTGGCTATTTACAGACA
CTGATGATGTGCACTTTGATGCAGCACATGAGGCTTATGAAAATAATTTTGATCATCTTAATTTTGATTTGGATTTGATGCCTTGGGAGTCAG
ACCTATGGAGCCCCGGCAGCCACTTCTGCTCAGACATGAAGGCAGAGCCCCAGCCTCTTTCTCCGGCTTCTCCAGTTGCTCCATCTCC
TCTCCTCGGTCCACAGACTCGTGTTCTTCAACTCAGCACGTTTCTGAGGAGTTGGATTTGTTGTCTAGTTCTCAGTCCCCCTTTCTTAT
ATGGCGACAGCTGTAATAGCCCCCTCTCTGTAGAGCCACTGAAGGAAGAGAAGCCTGTCACTGGTCTGGAACAAAACAGAACATGGA
CTGACTCCAAAGAAAAAATTCAGATGAGTTCAAACCTTCAGTTGAGCCCAAGCCTTTATTACTTCCAGCAGCGCCCAAGACTCAAACCA
ATGCCAGTGTCCCAGCAAAAGCCATCATCATTCAGACACTACCAGCCCTTATGCCACTGGCAAAGCAGCAGTCGATTATCAGCATACAGCC
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AAAGAACCGAGAGTCTGCTTGTGAGTCGCGCAAGAAGAAGgctGAGTATATGCTAGGACTGGAGGCCAGGCTCAAGGCTGCCCTCTCAGA
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GAGTGAAACCTAGTGTGAGCCCTGCCAATCAGAGGAGGCATCTCTTGGAAATTTTCAGCGAAAGAAGTTAAAGACACATCCGATGGTGACA
ACCAGAAAGACAGTTACAGCTATGATCACTCTGTGTCCAATGACAAAGCTTTAATGGTGCTAAGTGAAGAGCCATTGCTTTATATGCCTCCA
CCTCCATGTCAACCCCTGATTAACACGACAGAGTCTCTCAGGTTGAACCATGAACCTCGAGGCTGGGTTCATAGACATGAAGTGGAAGG
ACCAAATCTAGAAGAATGACAAATAGCCAACAGAAAGCCCGCATTCTCCAGGGTGCTCTGGAACAGGGCTCTAATTCTCAGCTGATGGCT
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TTTGACGCCATCCGCAGGAGGGGAGATACGTTTTACGTGGTCTCATTTTGAAGGGATCATCTGCTATTACCAGCTACCACCCACAACAAGA
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CCTTCTTTGGTTCCCCTCCAACAACCACAGAGACGACCCATGTGGTCAGCACCATCCCTGAGTCGTTGCAGTAG