

SUPPLEMENTARY INFORMATION

Telomere damage promotes vascular smooth muscle cell senescence and immune cell recruitment after vessel injury

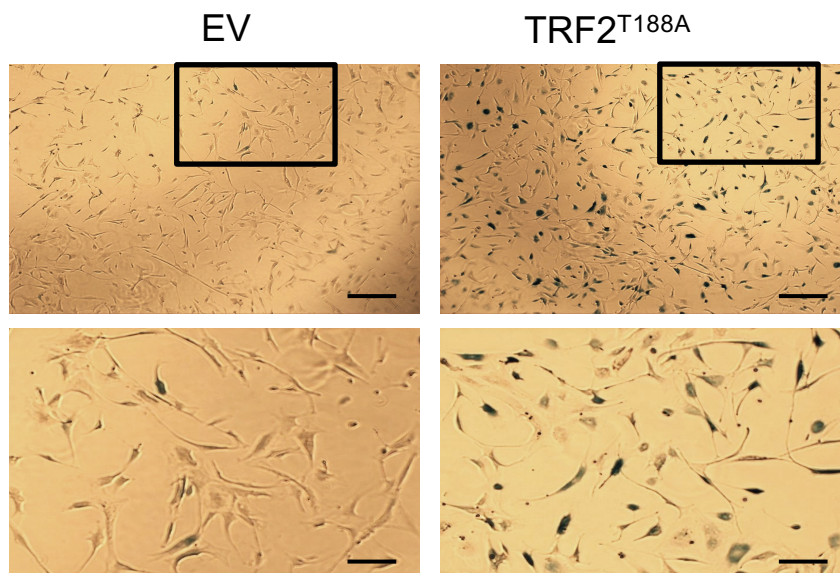
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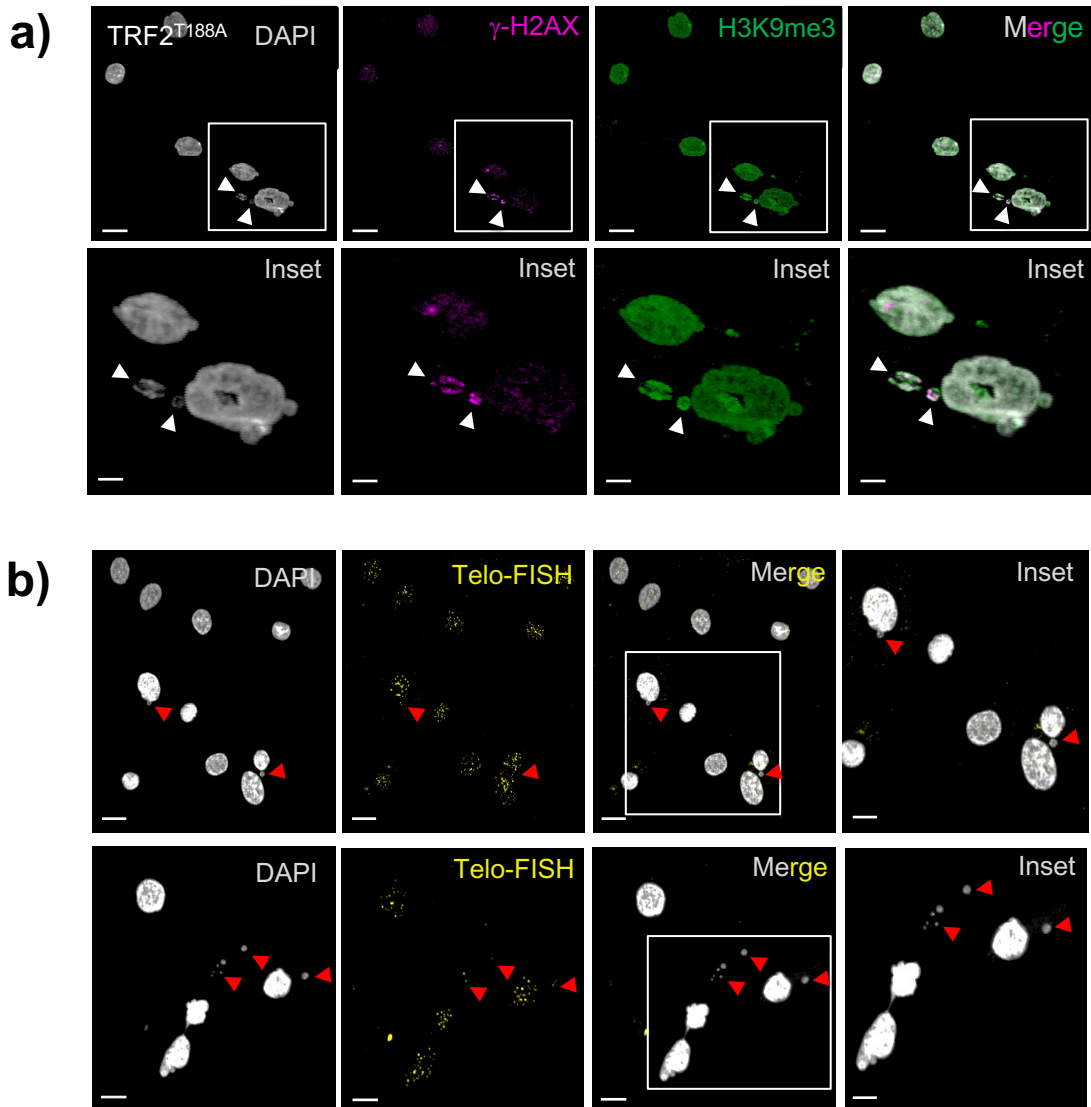
³Istituto di Genetica Molecolare, CNR-Consiglio Nazionale delle Ricerche, Pavia, 2700, Italy

Supplementary Figure 1



Supplementary Figure 1. SAβG activity in human VSMCs expressing an empty vector or TRF2^{T188A}
Human VSMCs infected with an empty vector (EV) or lentivirus expressing TRF2^{T188A}, and analysed for the senescence marker SAβG. Low-power (top, scale bar=150μm) and high-power (bottom, scale bar=50μm) representative images of SAβG-positive cells.

Supplementary Figure 2

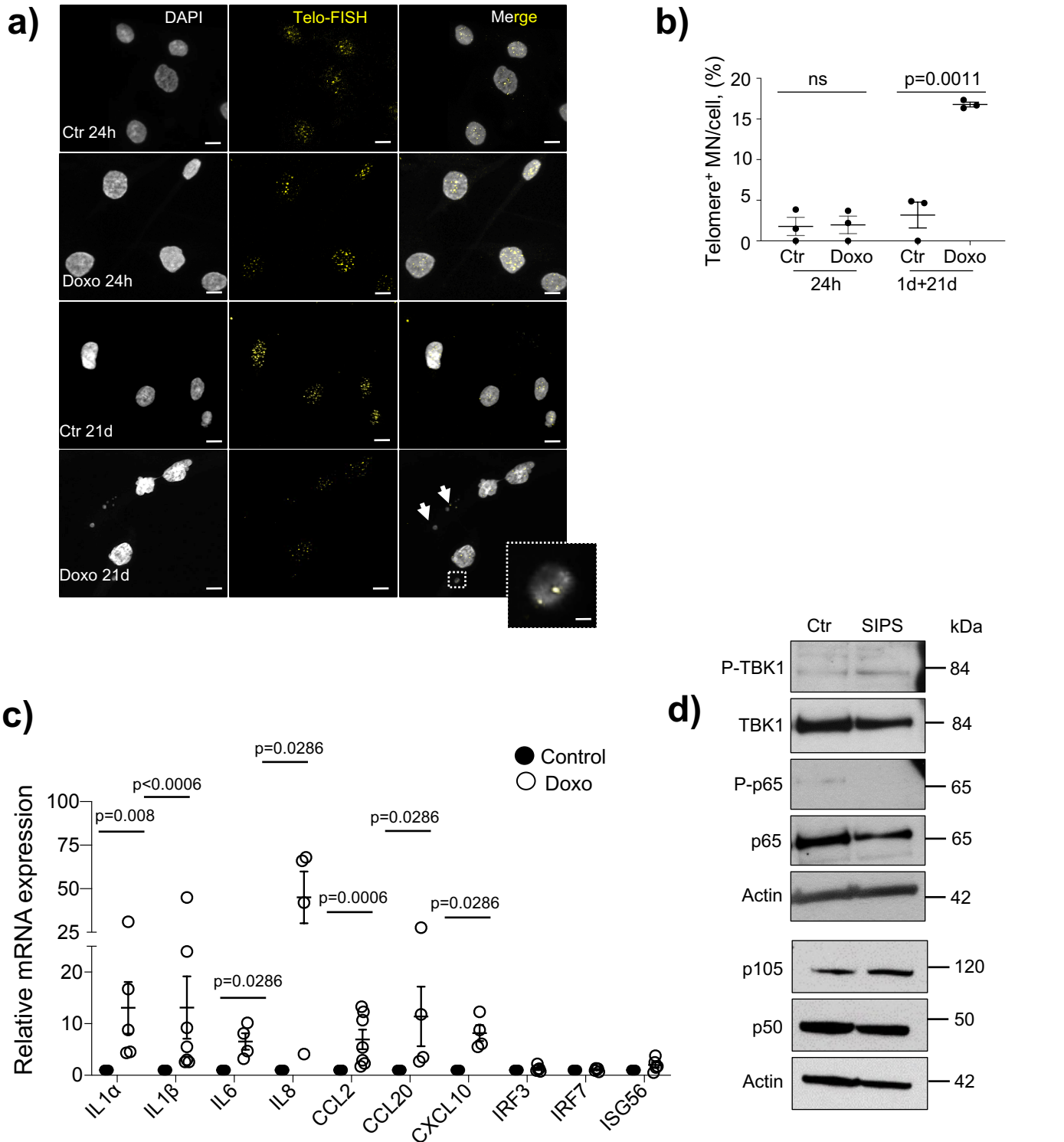


Supplementary Figure 2. Micronuclei in TRF2^{T188A} VSMCs

a) Examples of micronuclei (white arrowheads) seen at low power (upper panels) or high power view of inset image (lower panels) in TRF2^{T188A} VSMCs. Scale bars=20 μ m and 7.5 μ m (insets).

b) Examples of micronuclei containing telomere signals by Telo-FISH in TRF2^{T188A} VSMCs (red arrowheads) . High power view is shown on the right. Scale bars=20 μ m and 12.5 μ m (insets).

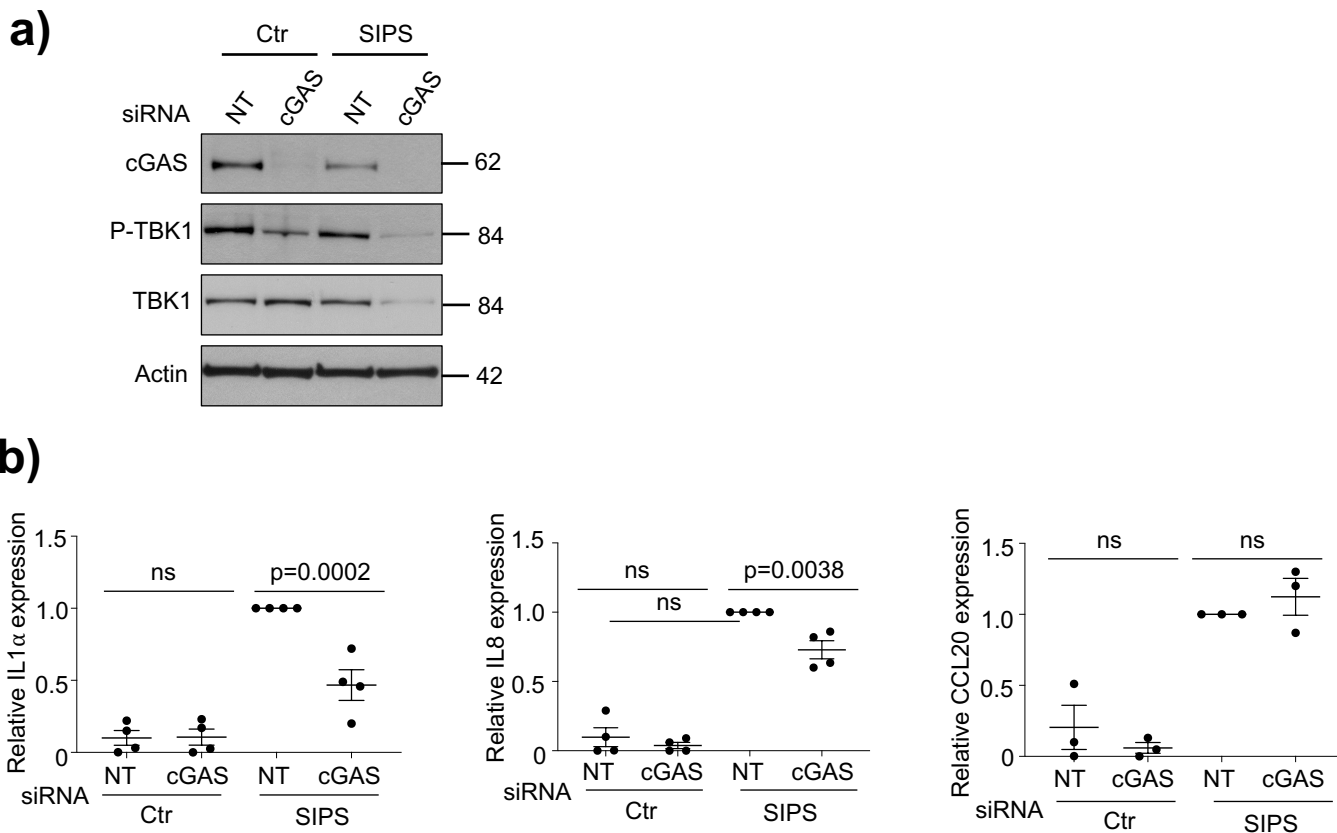
Supplementary Figure 3



Supplementary Figure 3. Doxorubicin-induced premature senescence promotes SASP

a) Telo-FISH and **b)** quantification of Telomere⁺ micronuclei (MN)/cell in control cells or those undergoing doxo24h treatment or doxo-induced SIPS (Doxo1d+21d). DAPI (white) and telo-FISH (yellow). Arrows indicate MN. Scale bars=10 μ m and 1.25 μ m (inset). **c)** Relative mRNA expression of selected cytokines in control hVSMCs or those undergoing doxo-induced SIPS (Doxo1d+21d). n=4-7 independent experiments. **d)** Western blot for TBK1, p65 NF- κ B and their phosphorylated forms and p50 and p105 NF- κ B members in control hVSMCs or those undergoing doxo-induced SIPS. Data shown represent Means \pm SEM, n=3-5 independent experiments, ns-non significant (p>0.05), unpaired, two-tailed Student's t-test or Mann-Whitney U test.

Supplementary Figure 4

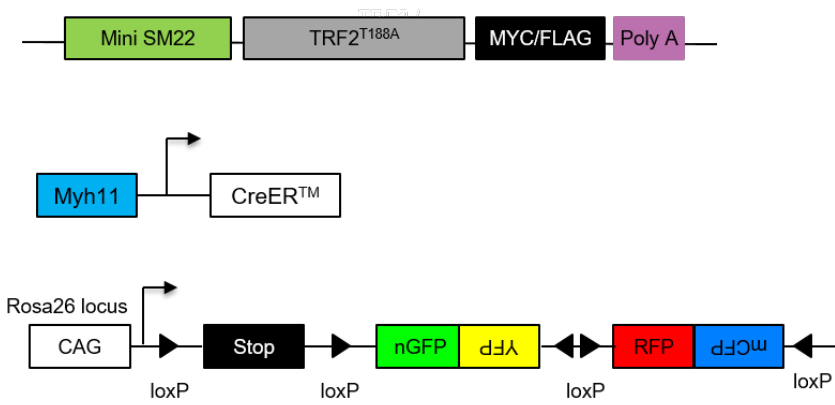


Supplementary Figure 4. Doxorubicin-induced premature senescence promotes SASP through cGAS-STING-TBK1 pathway

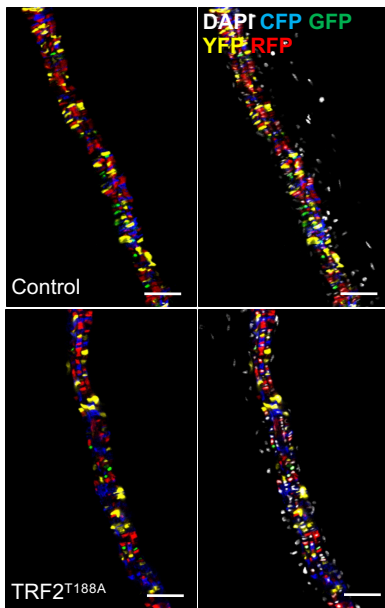
a) Western blot for cGAS, P-TBK1 and TBK1 in control hVSMCs or those undergoing doxo-induced SIPS transfected with non-targeting (NT)- or cGAS-siRNA. **b)** Relative mRNA expression of IL1 α , IL8 and CCL20 in control hVSMCs or those undergoing doxo-induced SIPS transfected with non-targeting (NT)- or cGAS-siRNA. Data shown represent Means \pm SEM, n=3-5 independent experiments, ns-non significant ($p>0.05$), 1-way ANOVA with Bonferroni multiple corrections.

Supplementary Figure 5

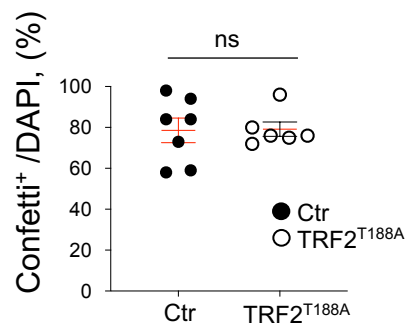
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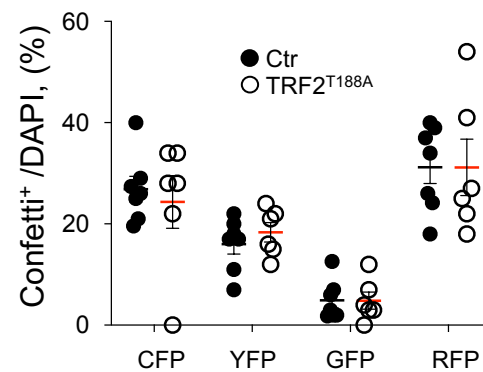
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c)



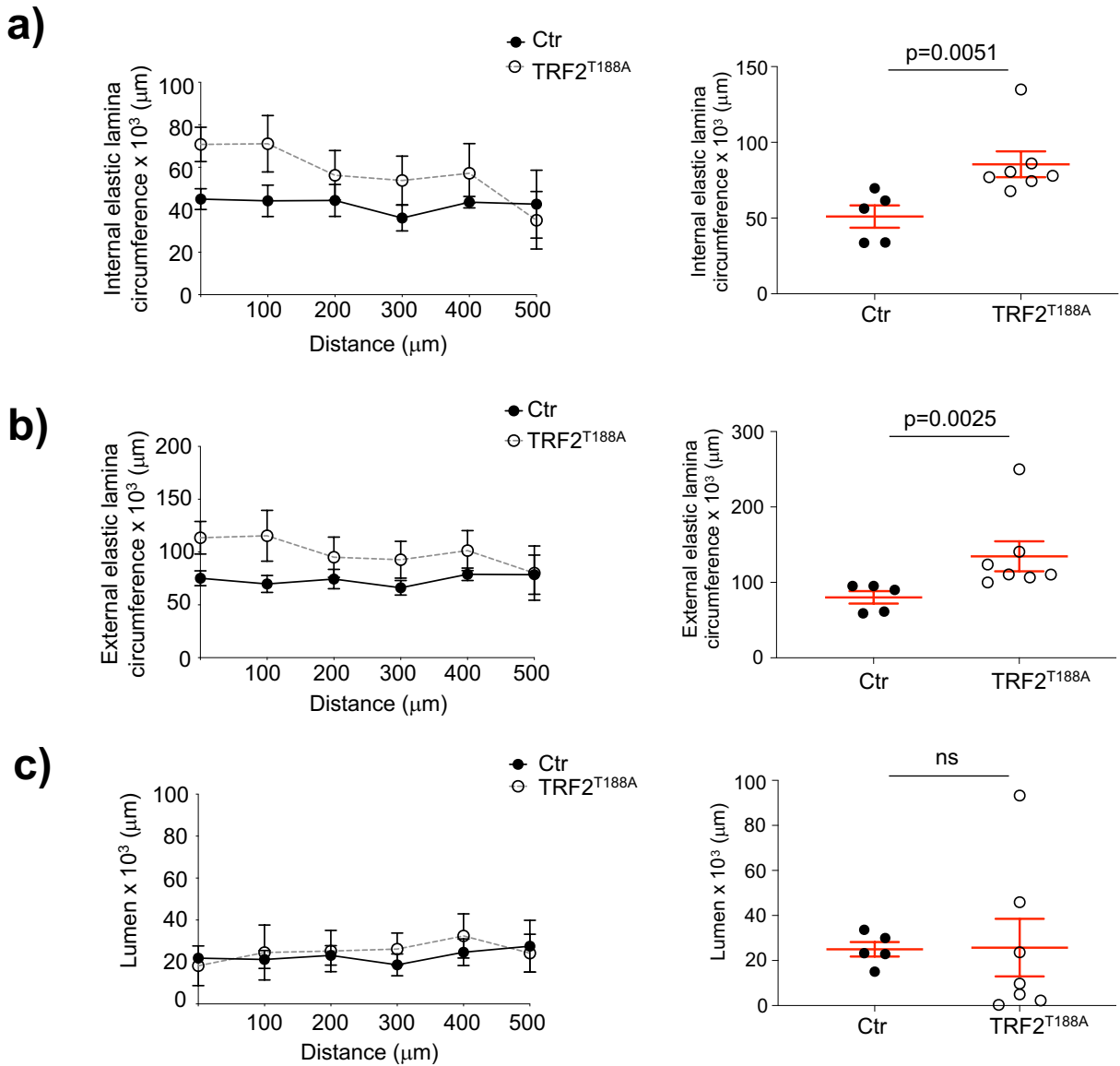
d)



Supplementary Figure 5. VSMC labeling efficiency in TRF2^{T188A} mice and littermate controls.

a) Schematic of *SM22 α -TRF2^{T188A}/Myh11-Cre^{ERTM}* and *Rosa26-Confetti* transgenic constructs. b) Right common carotid artery (RCCA) sections derived from TRF2^{T188A} mice and littermate controls. Scale bar=200 μ m. c) Percentage of total confetti⁺ cells and d) each confetti reporter color quantified on longitudinal sections of unligated RCCA of TRF2^{T188A} animals and littermate controls. Data shown in (c-d) represent Means \pm SEM, n \geq 6 mice for each group, ns-non significant (p>0.05), Mann-Whitney U test.

Supplementary Figure 6

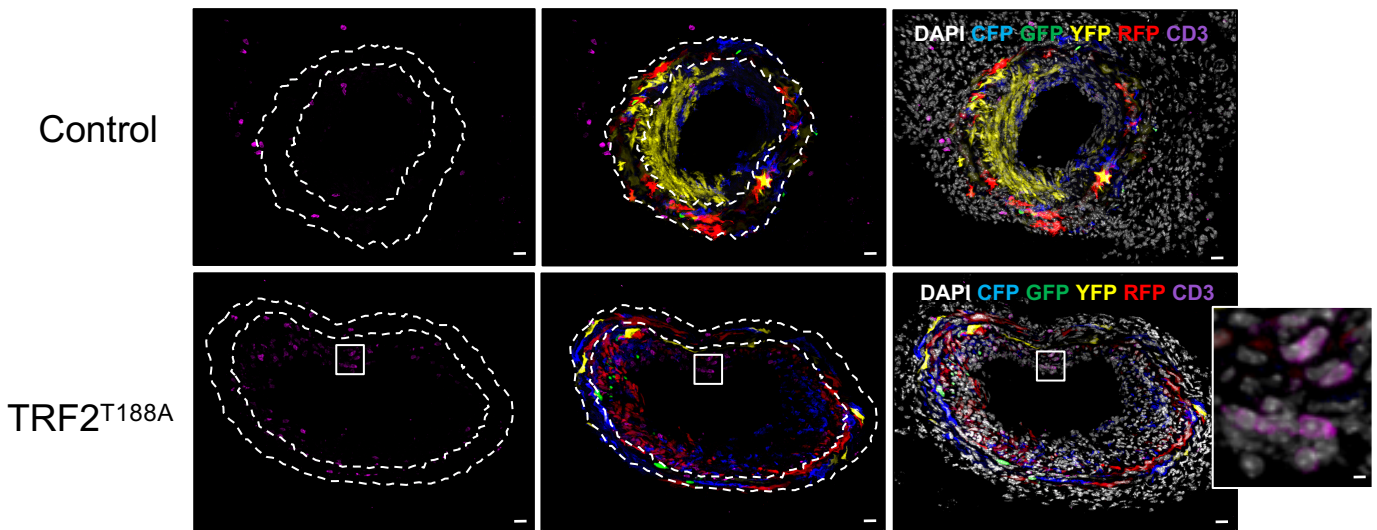


Supplementary Figure 6. $\text{TRF2}^{\text{T188A}}$ promotes outward remodeling in response to injury

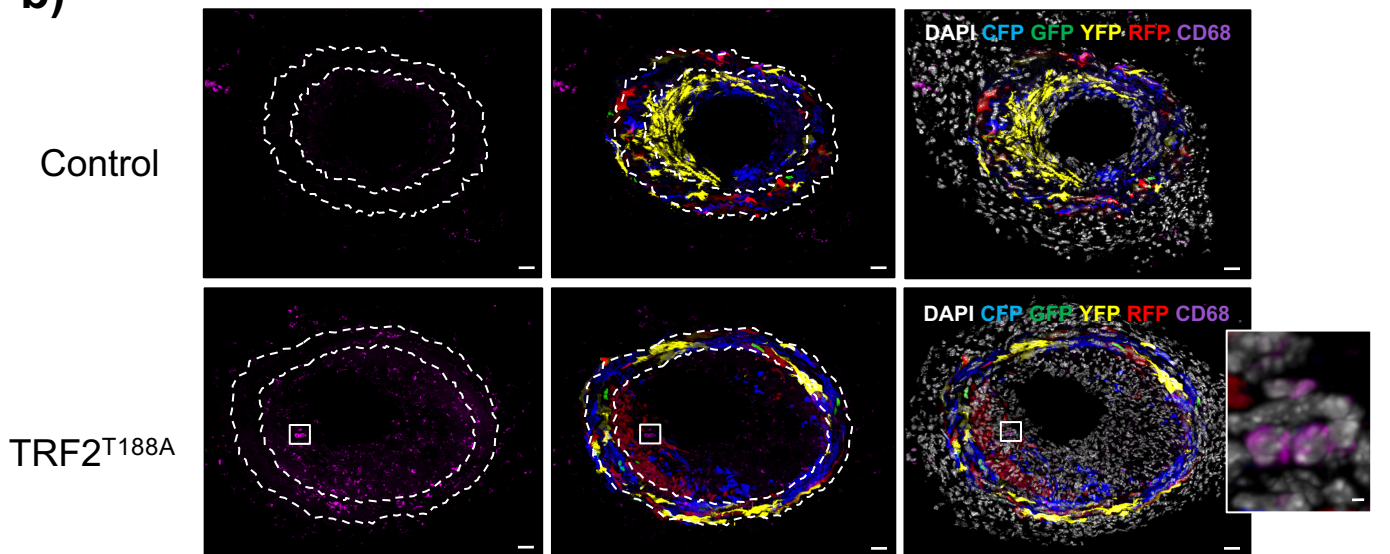
a) Internal elastic lamina, **b)** external elastic lamina and **c)** lumen area of Control (Ctr) or $\text{TRF2}^{\text{T188A}}$ mice using six serial sections 100 μm apart (left panels). Right panels represent maximum area. Data represent Means \pm SEM, $n \geq 5$ mice for group, ns-non significant ($p > 0.05$), Mann-Whitney U test.

Supplementary Figure 7

a)



b)



Supplementary Figure 7. Enhanced infiltration of lymphocytes and macrophages in *TRF2^{T188A}* mice.

LCCA cryosections of *TRF2^{T188A}* and control mice 28d following carotid ligation stained with a) CD3 (magenta) or b) CD68 (magenta) and counterstained with DAPI (white). Outlined regions show cluster of cells that are CD3⁺ or CD68⁺. Scale bars=30 μ m and 4.8 μ m (inset).

Supplementary Figure 8

Uncropped gels

Fig 1g

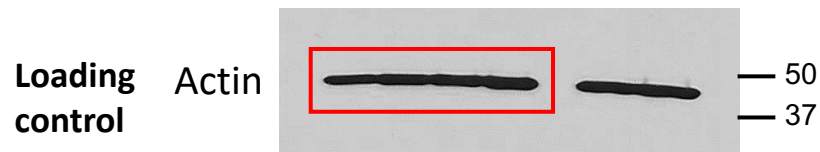
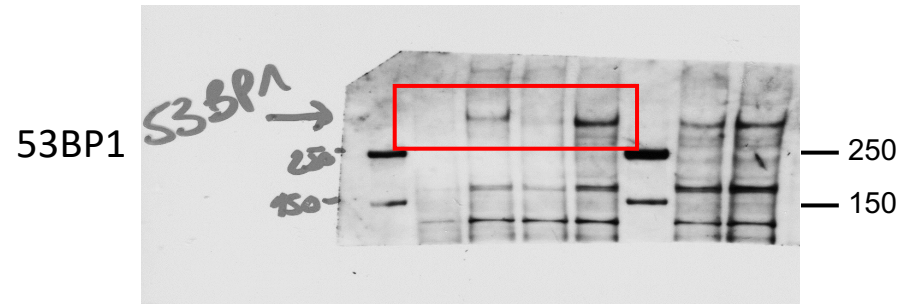
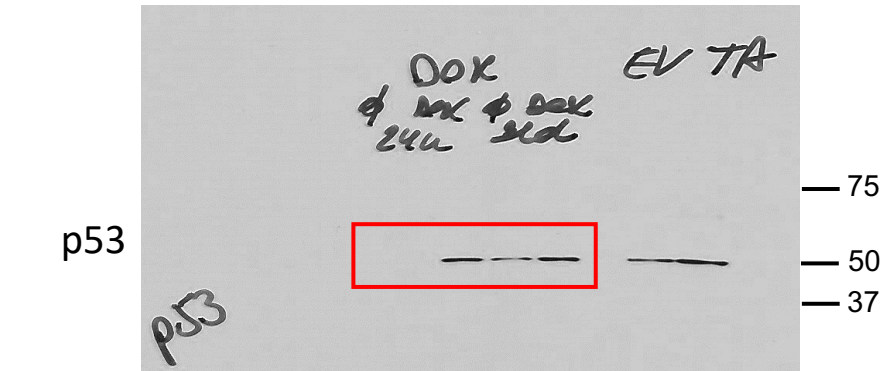
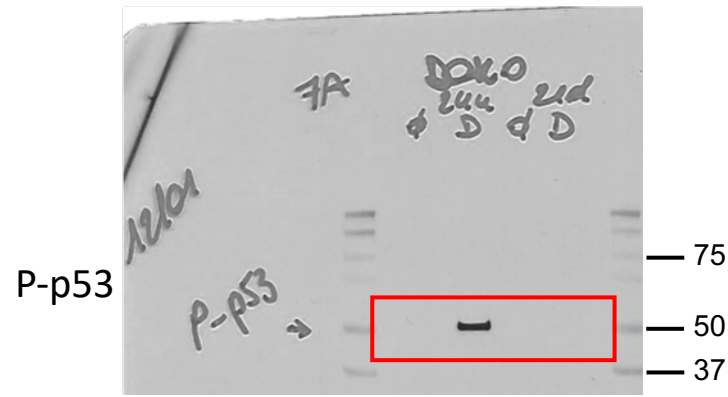
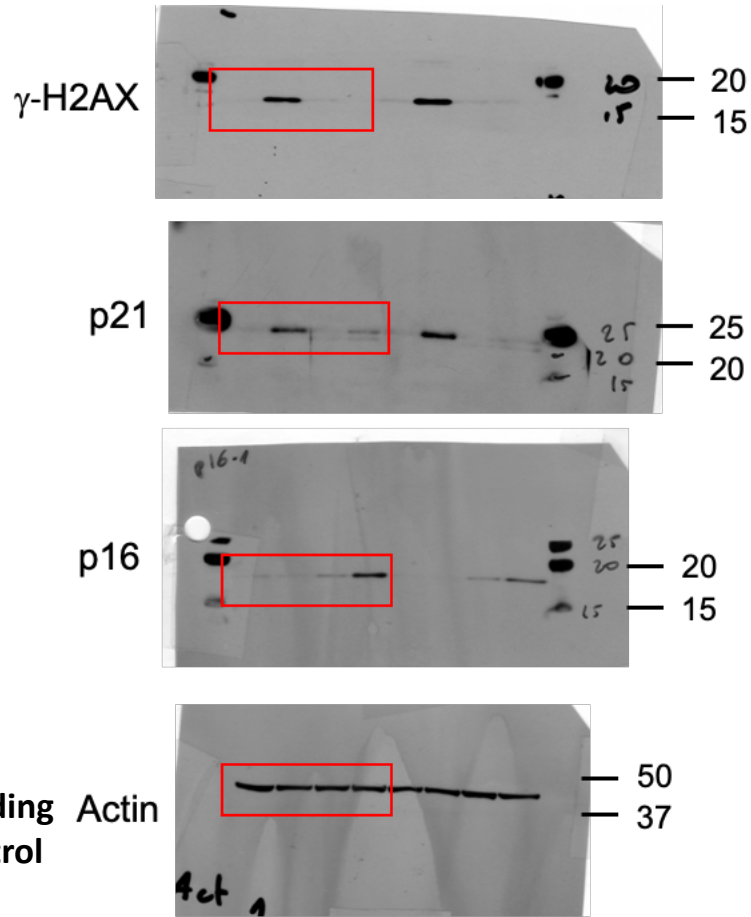


Fig 1j

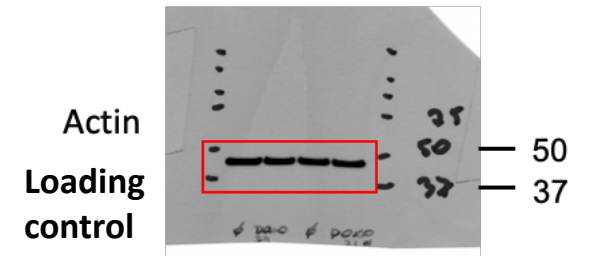
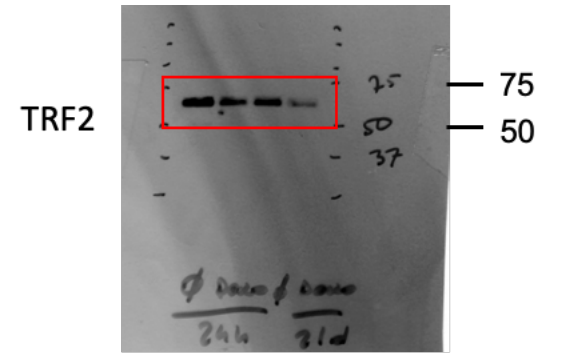


Fig 2d

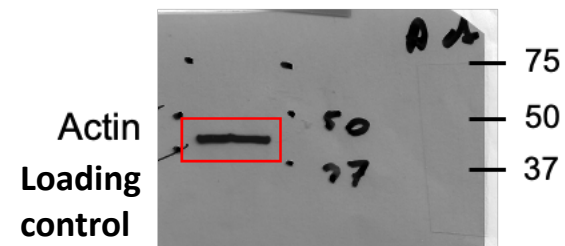
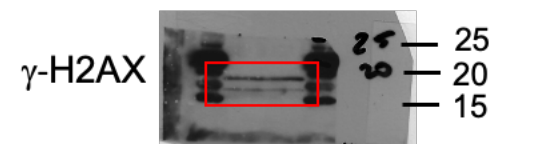
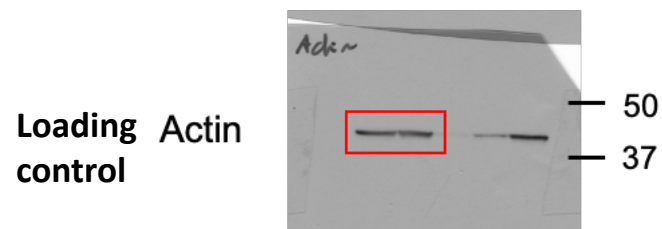
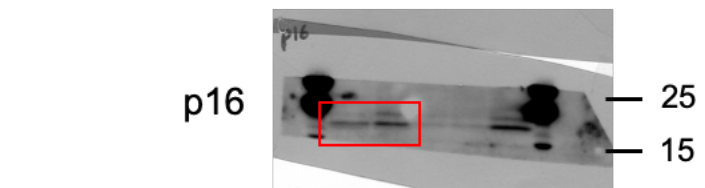
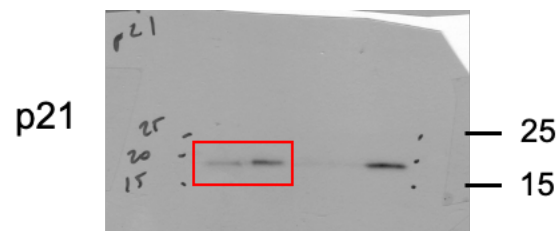
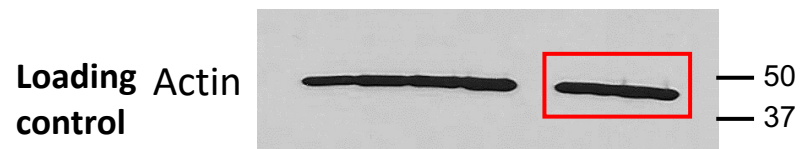
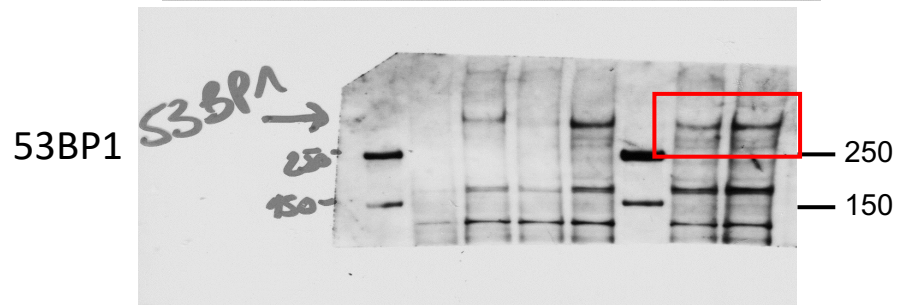
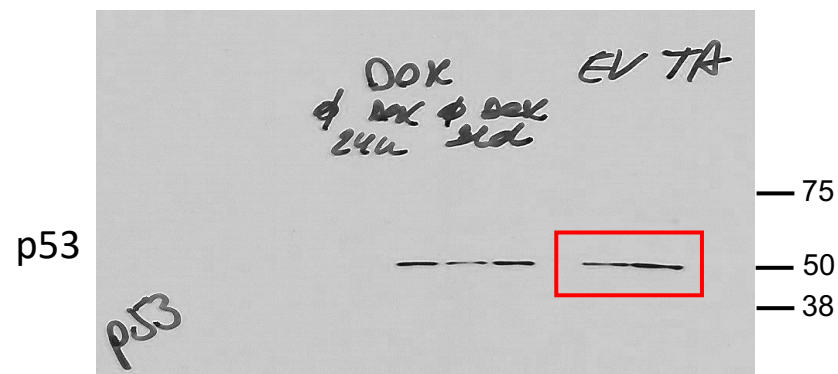


Fig 4d

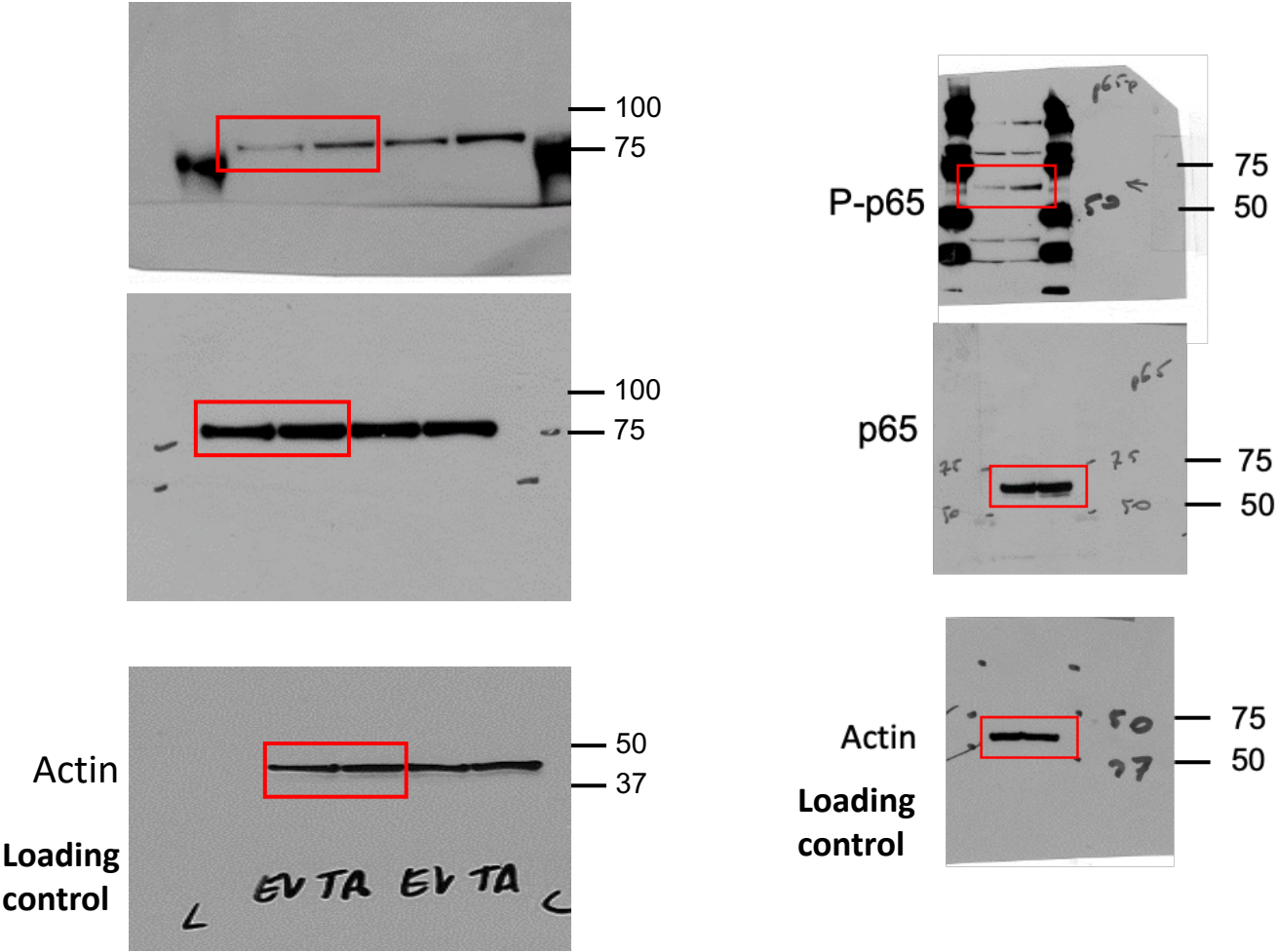
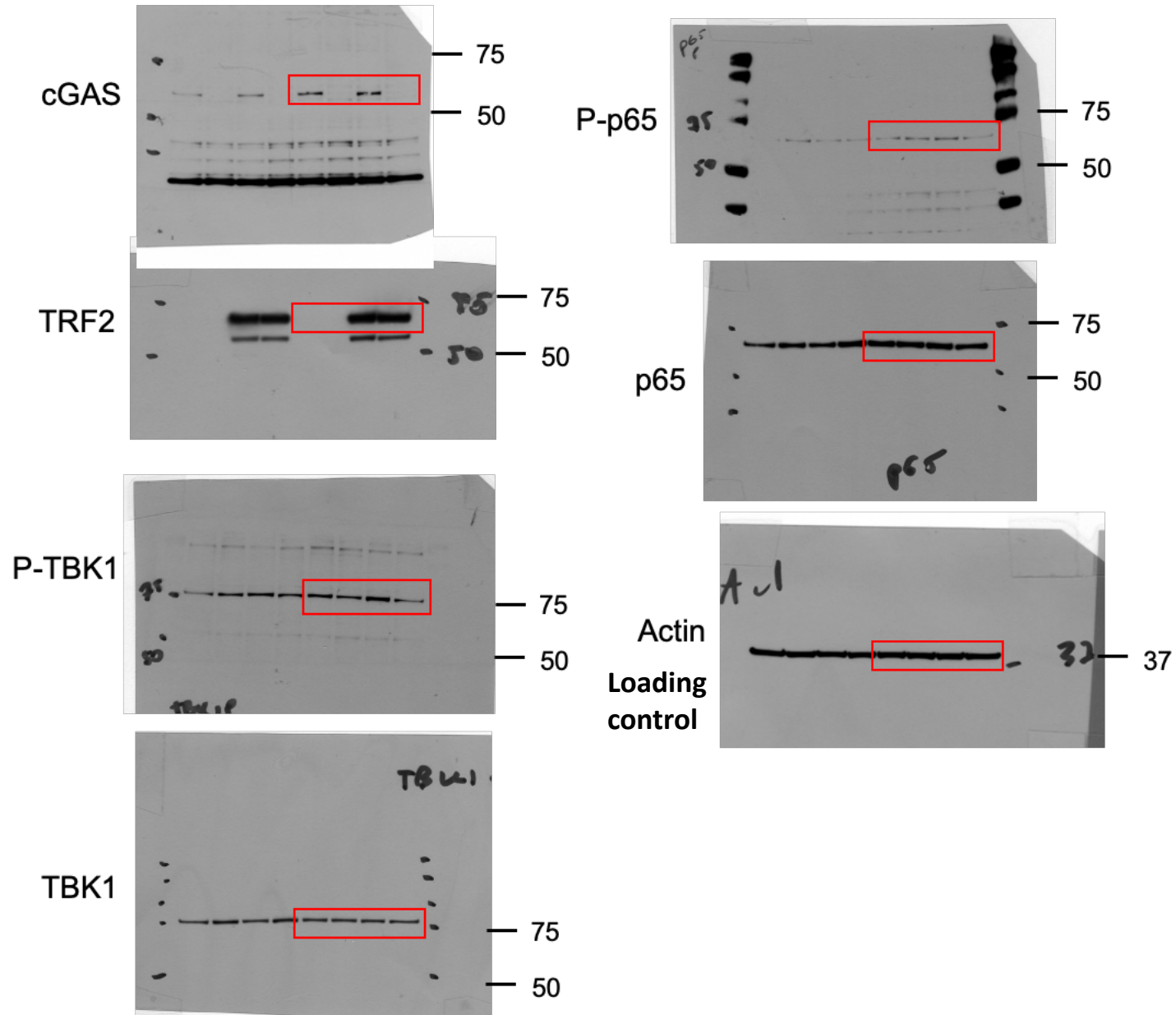
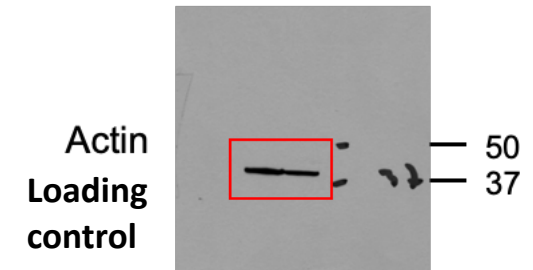
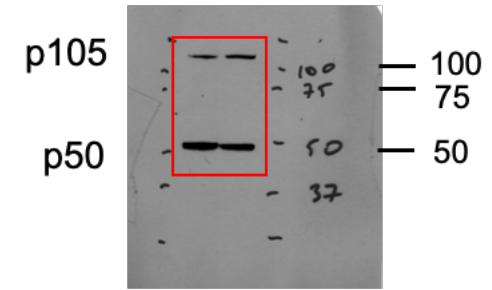
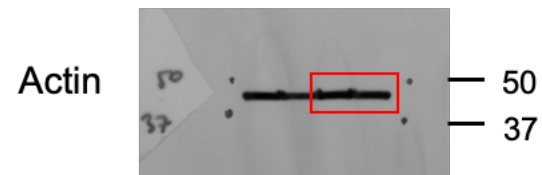
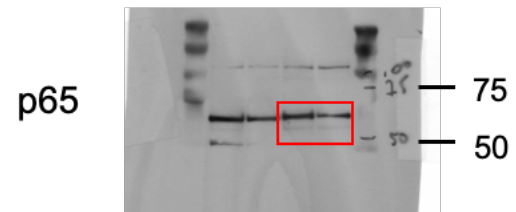
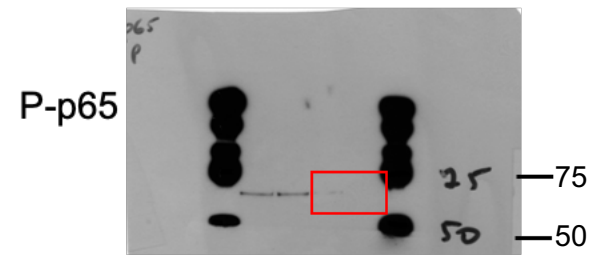
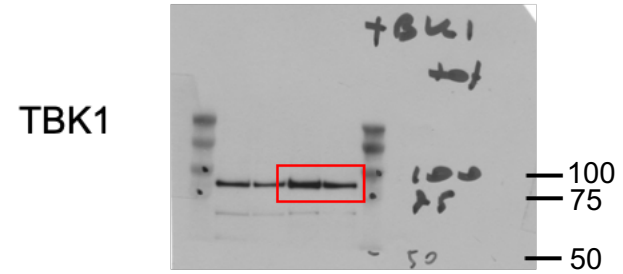
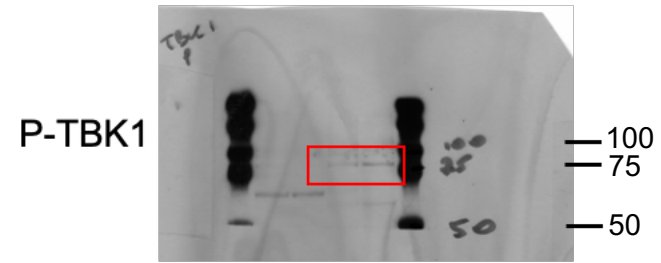


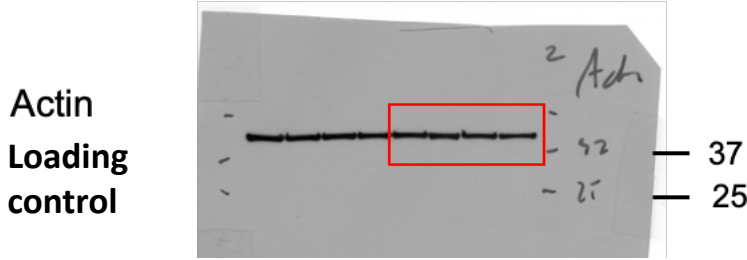
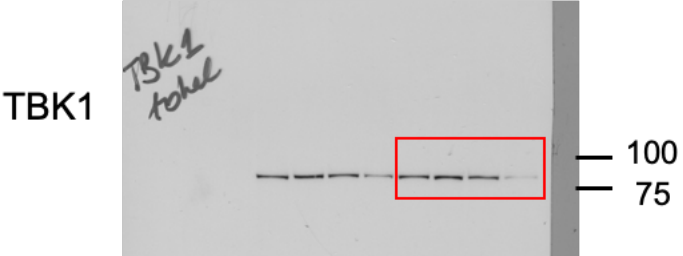
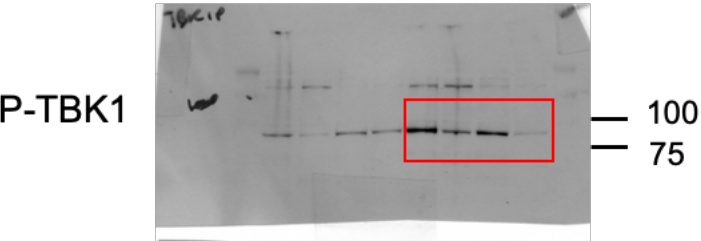
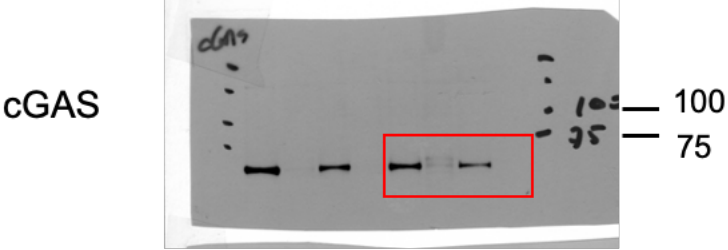
Fig 4f



Supplementary Fig 3d



Supplementary Fig 4a



| Human DNA primers | |
|-------------------|--|
| IL1 α | Fw 5'- ACTGCCCAAGATGAAGACCA -3' Rv 5'- TGGTCTCACTACCTGTGATGG -3' |
| IL1 β | Fw 5'- TCGCCAGTGAAATGATGGCT -3' Rv 5'- TGGAAGGAGCACTTCATCTGTT -3' |
| IL8 | Fw 5'- AGAGAGCTCTGTCTGGACCC -3' Rv 5'- CTCAGCCCTCTTCAAAAATTCT -3' |
| IL6 | Fw 5'- CATCCTCGACGGCATCTCAG -3' Rv 5'- TCACCAGGCAAGTCTCCTCA -3' |
| CCL2 | Fw 5'- CTCAGCCAGATGCAATCAATG -3' Rv 5'- CTTCTTTGGGACACTTGCTGC -3' |
| CCL20 | Fw 5'- AACCATGTGCTGTACCAAGAGT -3' Rv 5'- AAGTTGCTTGCTTCTGATTTCGC -3' |
| CXCL10 | Fw 5'- CCAGAATCGAAGGCCATCAA -3' Rv 5'- CATTTCCTTGCTAACTGCTTTCAG -3' |
| IRF3 | Fw 5'- TCGTGATGGTCAAGGTTGT-3' Rv 5'- AGGTCCACAGTATTCTCCAG-3' |
| IRF7 | Fw 5'- CCTCTCCAGATGCCAGTCCC -3' Rv 5'- AAGGAGCCACTCTCCGAACA -3' |
| ISG56 | Fw 5'- CAAAGGGCAAACGAGGCAG -3' Rv 5'- CCCAGGCATAGTTTCCCCAG -3' |
| p16 | Fw 5'- CATAGATGCCGCGGAAGGT -3' Rv 5'- AAGTTTCCCGAGGTTTCTCAGA -3' |
| p21 | Fw 5'- GACTCTCAGGGTCGAAAACG -3' Rv 5'- GGATTAGGGCTTCCTCTTGG -3' |
| RPL13A | Fw 5'- CGAGGTTGGCTGGAAGTACC -3' Rv 5'- CCGTAGCCTCATGAGCTGTT -3' |
| TeloC (for RT) | Rv 5'- CCCTAACCTAACCTAA -3' |
| TeloG (for RT) | Rv 5'- TAGGGTTAGGGTTAGGG -3' |
| Telo (for qPCR) | Fw 5'- CGGTTTGGTTGGTTGGTTGGTTGCCTTTGCCTTTGGGTT -3' Rv 5'- GGCTTGCCTTACCCTTACCCTTACCCTTACCCTTACCCT -3' |
| RPP0 | Fw 5'- TTCATTGTGGGAGCAGAC -3' |
| RPP0 | Rv 5'- CAGCAGTTTCTCCAGAGC -3' |

Supplementary Table 1

List of QPCR primers