

## SUPPLEMENTAL MATERIAL

### Supplemental Methods

#### *Femoral artery endothelial denudation:*

Femoral artery endothelial denudation was performed as previously described<sup>28,45-46</sup> on littermate control and TET2-deficient male mice of at least 16 weeks of age. Briefly, the femoral artery was temporarily ligated proximally and distally to the deep muscular branch. The muscular branch was permanently ligated distal to the branch point. An arteriotomy was created between the ligature and the branch point, and a 0.015" guidewire (Cook Medical, C-SF-15-15) was inserted 1cm proximally. The wire was left in place for 60 seconds. Upon wire removal the muscular branch was permanently ligated proximal to the arteriotomy. Injured right femoral arteries and contralateral controls were harvested 21days after surgery.

#### *In vitro cell culture:*

Primary mouse aortic vascular smooth muscle cells (mVSMCs) were isolated by enzymatic dissociation as described<sup>45</sup> (See Supplemental Methods for additional detail). Briefly, aortas were incubated with 175U/ml collagenase II (Thermo, 17101015), 1.25U/ml elastase (Worthington, LS002274) in HBSS (Gibco, 14025092) for 10 minutes at room temperature to facilitate stripping the adventitia. Stripped vessels were then minced with a sterile blade and incubated with 400U/ml collagenase II, 2.5U/ml elastase, and 0.2mg/ml soybean trypsin inhibitor (Cayman, 14502) in HBSS for 1.5 hours in a 37°C water bath with periodic manual vortexing. The cell suspension was triturated, washed with complete medium, filtered through a 75um filter, and allowed to adhere for 3 days before replacing the medium. mVSMCs were propagated in DMEM (Gibco, 11965-092) supplemented with 20% FBS, 100U/ml each penicillin-streptomycin, and 1mM sodium pyruvate (Gibco, 11360070).

Primary human aortic vascular smooth muscle cells (hVSMCs, Lonza) were propagated in 199 medium (Thermo, 11150-067) supplemented with 10% FBS, 100U/ml each penicillin-streptomycin, 2.7ng/ml rhEGF (Biolegend, 713008), and 2ng/ml rhFGF (Biolegend, 71034). hVSMCs were used for experiments at passages 5-7. Cultured VSMCs were treated with recombinant IFN $\gamma$  from the same species (recombinant human IFN $\gamma$  (rh-IFN $\gamma$ ): R&D Systems, 285-IF-100, recombinant mouse IFN $\gamma$  (rm-IFN $\gamma$ ): Biolegend, 714006). In TNF $\alpha$  treatment experiments, mVSMCs were treated with 15ng/ml recombinant murine TNF $\alpha$  (rm-TNF $\alpha$ ; Biolegend, 718004).

Control (++; homozygous wildtype) or *Tet2-deficient* (FF; homozygous floxed) mouse VSMCs were prepared from female littermate mice that harbored one copy of the Rosa26-mTmG mutant allele. Recombination of the floxed region of the *Tet2* gene, and the Rosa locus, was accomplished by treating cultured cells with 200MOI of Cre adenovirus (see Supplemental Methods) + 10ug/ml polybrene for at least two days. Recombination efficiency was monitored microscopically by observing RFP to GFP transition. *TET2* knockdown was accomplished by transfecting hVSMCs with a pool of 4 *TET2*-targeting siRNAs (Dharmacon, L-013776-03-0005), versus a non-targeting siRNA pool (Dharmacon, D-001810-10-5), as per the protocol for Dharmafect 2 (Dharmacon, T-2002-02). In ascorbic acid (AA) *in vitro* experiments, cells were treated with 250uM ascorbic acid dissolved in DPBS and filter sterilized.

ELISA for genomic 5-hmC content (Epigentek, P-1032-96) from cultured cells was performed on 10-20ng/sample denatured genomic DNA. gDNA was isolated using Qiagen or Zymo Research Kits (69504 or D7001, respectively).

#### *Adenovirus preparation:*

Adenoviruses encoding GFP (Vector Biolabs, 1060), TET2b-IRES-GFP (Welgen custom, NM\_017628.4), sh-TET2-IRES-GFP (Welgen custom, shRNA: CAGGTGAAAGCAGTCAACCAAATGTCTCC), and Cre adenovirus as described elsewhere<sup>47</sup>, were amplified in HEK-293A cells (Invitrogen, R70507) as described in the Adeno-X Expression system manual (Clontech, protocol #PT3414-1). Viral titer was determined by Adeno-X Rapid Titer Kit (Clontech, 632250). VSMCs were infected with 200MOI adenovirus in the presence of 10ug/ml polybrene.

#### *Cell viability assay*

Viability was determined by crystal violet staining. Cells were fixed with 4% paraformaldehyde (PFA) in PBS at the indicated time points. 24hours after plating 10-15k cells/well in 24-well cluster plates, cells were collected as a Time=0 control for plating efficiency. Cells were stained with 0.2% crystal violet solution in 90% ethanol, destained with water, dried, solubilized in 10% acetic acid, and the absorbance at 570nm was assessed by spectrophotometer. For each assay type, cells were quiesced in 0.5% FBS medium for 24hr ± AA prior to IFN $\gamma$  or conditioned media (CM) stimulation.

### *Tissue staining*

Coronary artery samples from age-matched control (patients who died from non-cardiovascular diseases) or patients who had received heart transplants (CAV; or kidney transplant (GA)) were preserved in neutral-buffered formalin. Tissues were paraffin embedded and microtome-sectioned at 5µm. Sections were de-paraffinized with Histoclear (National Diagnostics, HS-200) and re-hydrated to PBS prior to immunostaining. Samples were obtained from the Yale Pathology Tissue Service.

Murine graft tissues were prepared by perfusion of the recipient vasculature with PBS containing 40µg/ml sodium nitroprusside, and then with 4% paraformaldehyde (PFA)-PBS. Tissues were excised and further fixed in 4% PFA-PBS at 4°C for 24hours. Tissues were cryopreserved in 30% sucrose-PBS for at least 48hours, then in 50% cryosectioning medium (TissueTek, 4583) plus 15% sucrose-PBS for at least 24hours.

Elastin Van Geison (EVG) staining was performed on 5µm cryosections as described elsewhere<sup>48</sup>. Briefly, sections were stained with Verhoeff's Hematoxylin for 30min, destained with 2% ferric chloride solution, counterstained with Van Gieson's Solution (0.05% acid fuchsin in picric acid) for 65sec, washed with ethanol, cleared with Histoclear, and mounted with DPX mountant (Electron Microscopy Sciences, 13510).

Immunohistochemical staining was performed after heat-induced epitope retrieval in pH6.0 10mM sodium citrate buffer containing 0.05% tween-20 at 95°C for 20-40min. Endogenous peroxidases were quenched with 1-3% H<sub>2</sub>O<sub>2</sub> prior to blocking in 4% normal goat serum-PBS. Sections were incubated with primary antibodies (see Sup. Table 1) for 30min at room temperature. Sections were incubated with biotinylated secondary antibody, and streptavidin conjugated to horseradish peroxidase (HRP) (Vector Laboratories, PK-4001). 3,3'-diaminobenzidine (DAB) was used for chromogenic staining (Vector Labs, SK-4100) and fluorescent tyramides were used for fluorescent staining (Akoya Biosciences, NEL701A001KT/ NEL704A001KT/ NEL705A001KT). Serial staining with multiple rabbit-derived primary antibodies was accomplished by stripping first-round primary antibodies in pH2 glycine-SDS buffer at 50°C<sup>49</sup>. In-direct immunofluorescent staining was performed by incubating sections with primary antibodies at room temperature for 2hr or overnight at 4°C. Fluorescent moiety-conjugated secondary antibodies (see Sup. Table 1) were incubated with sections for 2hr at room temperature. 2µg/ml 4',6-diamidino-2-phenylindole (DAPI) staining was used to visualize nuclei. Slides were mounted with 1x PBS in 90% glycerol containing 0.2% *n*-propyl-gallate as an anti-fade agent. Micrographs of stained tissues were taken on a Nikon 80i epifluorescence microscope, a Nikon spinning disk confocal microscope, or a Leica SP8 laser scanning confocal microscope. Quantification of micrographs was performed in ImageJ. Image quantitation was automated, when possible, and data was performed singly blinded.

*Western blotting:*

Whole cell lysates were prepared using RIPA lysis buffer (Cell Signaling Technologies, 9806) containing 1x protease inhibitor cocktail (Roche, 4693124001) and phosphatase inhibitor cocktail (Roche, 4906845001). Lysates were cleared by centrifugation at  $\geq 14k \times g$ . SDS-PAGE was performed by standard methods; equal amounts of protein were loaded in each lane. Bicinchronic acid assay (Pierce, 23225) was used to quantitate sample protein content. Electrophoresed proteins were transferred to nitrocellulose membranes and blocked with 5% bovine serum albumin or 5% non-fat dry milk in tris-buffered saline. Membranes were probed with primary antibodies, and subsequently with horseradish peroxidase-conjugated secondary antibodies. SuperSignal West chemiluminescent substrate (Thermo, 37069 or 34094) was used as the HRP substrate for detection.

Condition medium was concentrated prior to western blotting for extracellular cytochrome C release by trichloroacetic acid (TCA)/deoxycholic acid (DOC) precipitation<sup>49</sup>. Briefly, one volume 50% TCA and one volume 0.1% DOC were added to 6 volumes of conditioned medium. Samples were incubated at 4°C overnight, pelleted at 14,000\* $g$  for 10min at 4°C, and solubilized in 1x Laemmli buffer containing 12% of 2M tris base and 25%  $\beta$ -mercaptoethanol at 95°C for 5min prior to SDS-page and western blotting.

*Apoptosis antibody array:*

Murine VSMC lysates were prepared from ++ or FF mice and treated with Cre virus (see above section on *in vitro* cell culture). Cell lysates were collected 5days after IFN $\gamma$  stimulation as described in the R&D Systems Proteome Profiler manual. 100 $\mu$ g of protein was assayed for each condition by mouse-specific apoptosis antibody array (R&D Systems, ARY031). Immobilon Forte (Millipore, WBLUF0100) was used as the HRP substrate for detection. Densitometry of spots was performed in ImageJ.

*Quantitative Real Time PCR (qPCR):*

Total RNAs were isolated from tissues or cultured cells with one of the following kits: RNeasy (Qiagen,74106) with Qias shredders (79656) for homogenization, MiRNeasy (Qiagen, 217004), or Quick-DNA/RNA (Zymo Research, D7001). Reverse transcription of mRNAs was achieved with All-In-One RT

MasterMix (Applied Biological Materials, G490). qPCR was performed with BrightGreen qPCR MasterMix (Applied Biological Materials, MasterMix-S). qPCR was performed with 300nM primers (see Sup. Table 2) following the manufacturer's thermocycler protocol.

*Hydroxymethylated DNA Immunoprecipitation (hMe-DIP) qPCR:*

Genomic DNA was isolated from cultured control (++) and TET2-deficient (FF) mVSMCs 48hours after treatment with 50nM rapamycin, or vehicle control. hMe-DIP was performed as described previously<sup>23</sup>. Briefly, DNA decorated with 5-hmC was immunoprecipitated with the hydroxymethylated DNA IP kit (Diagenode, C02010031) as per the manufacturer's instructions. Precipitated genomic DNA was quantified by qPCR using SsoFast Supermix (BioRad, 1725200) and primers specific to the proximal promoters of *Cnn1*, and *Myh11* (see Supplemental Table 2 for primer sequences.)

*RNA sequencing and data analysis:*

Total RNAs were isolated from cultured control (++) and TET2-deficient (FF) mTmG-labeled mVSMCs 5days after treatment with 100ng/ml rm-IFN $\gamma$ . RNA sequencing (RNA-seq) was performed at the Yale Center for Genome Analysis. RNA-seq reads were aligned to the *mus musculus* genome build mm10 (Refseq transcripts version 94) using the STAR aligner. Differential expression quantification was performed in Partek Flow by quantifying to a pre-built annotation model (mm10 v94). mRNA reads counts were normalized by fragments per kilobase of transcript per million mapped reads (FPKM) and expressed as FPKM plus 1, Log base 2. Gene set analysis (GSA) and principal component analysis (PCA) were performed on normalized read counts in Partek Flow. Histograms, PCA plot, and differential gene expression filtering were performed in Partek Flow. A gene list was generated based on genes that were upregulated (fold change >2, P<0.01, FDR<0.1) in FF cells, but not similarly upregulated in ++ cells. This gene list was used to perform downstream Ingenuity Pathway Analysis (IPA).

## Supplemental Tables

<b>Primary Antibodies</b>			
Target	Supplier, Catalogue #	Target	Supplier, Catalogue #
5-hmC	Active Motif, 39769	MKI67	Thermo Scientific, MA5-14520
ACTA2	Sigma, A2547	MYH11	Biomedical Technologies, BT-562
ACTA2-660	eBiosciences, 50-9760-82	PDGFRA	CST, 3174
ACTA2-cy3	Sigma, C6198	PDGFRB	CST, 3169
ACTB	Sigma, A2228	phospho-STAT1	CST, 7649
CASP3	CST, 9662	STAT1	CST, 14994
cleaved CASP3	CST, 9661	TAGLN	Abcam, ab10135
CD3	Abcam, ab16669	Mouse-specific TET2	Abcam, ab124297
CNN1	Thermo Scientific, RM-2102-S0	TET1	Genetex, GTX123207
CYCS	Abcam, ab90529	TET2	Abcam, ab94580
GFP	Life Technologies, A11122	TET3	Abcam, ab139805
GFP	Abcam, ab13970		
* CST = Cell Signaling Technologies			
<b>Secondary Antibodies</b>			
Target	Supplier, Catalogue #	Target	Supplier, Catalogue #
$\alpha$ -mouse-HRP	Thermo Scientific, 31450	$\alpha$ -rabbit-alexa546	Invitrogen, A11010
$\alpha$ -rabbit-HRP	Thermo Scientific, 31460	$\alpha$ -rabbit-alexa488	Invitrogen, A11008
$\alpha$ -goat-HRP	Thermo Scientific, 31402	$\alpha$ -chicken-alexa488	Jackson Immuno., 103-545-155
		$\alpha$ -rabbit-HRP IHC kit	Vector Labs, PK-4001

**Supplemental Table I:** Primary and secondary antibodies used in this study.

<b>Human mRNAs</b>		
Target	Forward	Reverse
RNA18SN5	TAACGAACGAGACTCTGGCAT	CGGACATCTAAGGGCATCACAG
TET2	TGGCAAACATTTCAGCAGCAC	TTGCCCTCAACATGGTTGGT
MYOCD	CCACAGCACATCAGTTTGCC	ACTTTGGCCCCACCTTATCA
SRF	TCACCTACCAGGTGTCGGAGTC	GTGCTGTTTGGATGGTGGAGGT
MYH11	CCTTGAGGAGAGGATTAGTGA	TTCCTTCTTTAGCCGCACTTC
KLF4	CATCTCAAGGCACACCTGCGAA	TCGGTCGCATTTTTGGCACTGG
PDGFRA	AACATCGGAGGAGAAGTTTCCCA	GCTCACTTCACTCTCCCAA
PDGFRB	CAAGGACACCATGCGGCTTC	AGCAGGTCAGAACGAAGGTG
CNN1	ATGTCTCTGCTCACTTC	ATACTTCTGGCCAGCTTGTT
ACTA2	CTATGCCTCTGGACGCACAAC	CAGATCCAGACGCATGATGGCA
<b>Mouse mRNAs</b>		
Target	Forward	Reverse
Hprt	TGGATACAGGCCAGACTTTGTT	CAGATTCAACTTGCGCTCATC
Tet2	GGCTGCCCTGTAGGATTTGT	AATGAATCCAGCAGCACCGT
Myocd	GCTGGGCTCAACCCTTGTC	CGTTGGCCCCACCTTGTCAGA
Srf	GCCGCGTGAAGATCAAGATG	GTCAGCGTGGACAGCTCATA
Myh11	GCAACTACAGGCTGAGAGGAAG	TCAGCCGTGACCTTCTCTAGCT
Klf4	CTATGCAGGCTGTGGCAAAC	TTGCGGTAGTGCCTGGTCAGTT
<b>hMe-DIP</b>		
Target	Forward	Reverse
Cnn1	AAGGGGTGGGCTGTATGAGA	CACCCCACACATACTCTGGC
Myh11	GCTGGGATGGTCCAAATCTC	CCTCCCCTTTCCACTCTCAG

**Supplemental Table II:** Oligonucleotide primers used in this study.

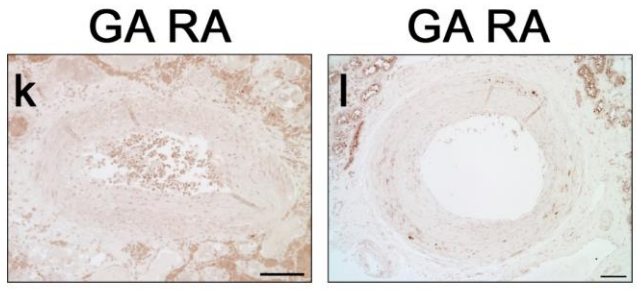
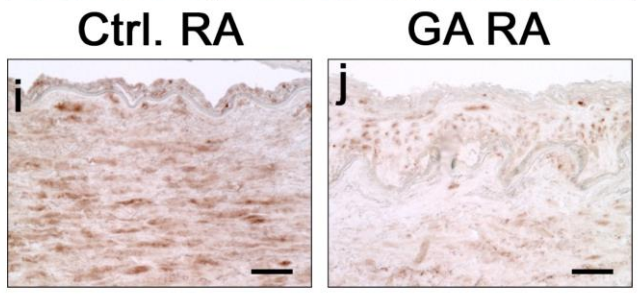
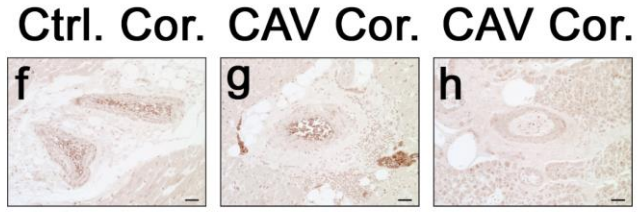
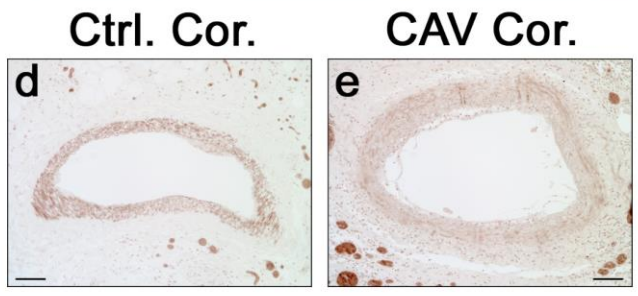
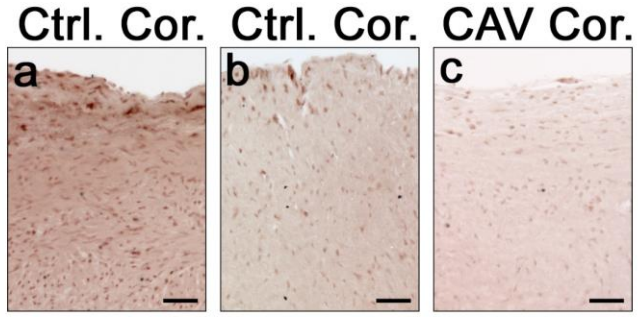
Gene symbol	Transcript ID	Fold change			IPA Pathway Genes
		(1+ Log2)	P-value	FDR step up	
Ifi2712a	NM_029803	4.84	2.78E-04	7.86E-03	TNFR2 Signaling
Tnfaip3	NM_009397	3.25	1.04E-05	5.89E-04	Jun
Apod	NM_001301353	2.79	1.57E-04	5.06E-03	Naip
Cxcl1	NM_008176	2.67	2.05E-03	3.17E-02	Nfkbia
Epha3	NM_010140	2.60	4.13E-05	1.79E-03	Tnfaip3
Luc7l	NM_025881	2.56	5.23E-03	5.94E-02	MIF Regulation of Innate Immunity
Ifi206	NM_001372436	2.54	5.86E-05	2.34E-03	Jun
Trim25	NM_009546	2.50	8.81E-06	5.05E-04	Nfkbia
Foxf1	NM_010426	2.45	1.08E-05	6.06E-04	Nos2
Gdf15	NM_011819	2.39	2.33E-03	3.44E-02	Ptgs2
Il15	NM_008357	2.39	7.63E-05	2.89E-03	TNFR1 Signaling
Fosl1	NM_010235	2.38	3.08E-04	8.46E-03	Jun
4933412E12Rik	NR_038025	2.35	3.05E-04	8.41E-03	Naip
Slc25a25	NM_001290558	2.34	9.87E-03	9.00E-02	Nfkbia
Ptgs2	NM_011198	2.34	5.83E-05	2.33E-03	Tnfaip3
Zc3hav1	NM_001347122	2.33	4.55E-06	2.93E-04	CD40 Signaling
Pml	NM_178087	2.32	4.38E-06	2.83E-04	Jun
Hmga2	NM_010441	2.32	2.04E-06	1.49E-04	Nfkbia
H2-DMb2	NM_010388	2.32	9.95E-05	3.57E-03	Ptgs2
Serpina3f	NM_001168295	2.29	2.00E-06	1.47E-04	Tnfaip3
Parp3	NM_001311150	2.29	5.57E-05	2.24E-03	Role of NFAT in Regulation of the Immune Response
Nos2	NM_010927	2.28	2.00E-06	1.47E-04	Gna13
Prrg4	NM_178695	2.27	6.01E-04	1.38E-02	H2-DMb2
Tgm2	NM_009373	2.23	1.50E-05	7.90E-04	Itpr3
Cavin2	NM_138741	2.23	1.97E-04	6.02E-03	Jun
Tcirg1	NM_016921	2.23	6.14E-06	3.75E-04	Nfkipa
Itpr3	NM_080553	2.22	2.51E-07	2.65E-05	Death Receptor Signaling
Slc2a6	NM_172659	2.20	1.89E-05	9.38E-04	Daxx
P2ry10b	NM_001122596	2.20	9.59E-04	1.90E-02	Naip
9930111J21Rik1	NM_001114679	2.19	1.07E-06	8.90E-05	Nfkbia
Tmcc3	NM_172051	2.17	3.10E-04	8.49E-03	Parp3
Lgals3	NM_001145953	2.15	8.53E-04	1.76E-02	CD28 Signaling in T Helper Cells
Emx2	NM_010132	2.13	2.46E-05	1.18E-03	H2-DMb2
Jun	NM_010591	2.13	7.11E-06	4.19E-04	Itpr3
Rnf14	NM_001361265	2.13	2.67E-03	3.78E-02	Jun
Wipf1	NM_001289722	2.12	2.27E-03	3.39E-02	Nfkbia
Csrnp1	NM_001357561	2.12	3.51E-03	4.52E-02	Induction of Apoptosis by HIV1
Daxx	NM_007829	2.11	6.15E-06	3.75E-04	Daxx
Slco3a1	NM_001038643	2.09	3.72E-05	1.64E-03	Naip
Acot2	NM_134188	2.09	1.84E-05	9.15E-04	Nfkbia
Gdf15	NM_001330687	2.08	4.28E-05	1.83E-03	
Usf1	NM_001305678	2.08	1.61E-04	5.15E-03	
Pnp2	NM_001123371	2.07	3.07E-05	1.40E-03	
Naip2	NM_001126182	2.06	3.33E-05	1.50E-03	
Ido1	NM_001293690	2.06	9.04E-07	7.77E-05	
Csf1	NM_001113529	2.05	1.53E-04	4.97E-03	
Nfkbia	NM_010907	2.05	5.89E-05	2.34E-03	
Tut7	NM_001373964	2.04	2.81E-05	1.31E-03	
Lif	NM_008501	2.04	2.91E-03	4.00E-02	
Prr3	NM_001282013	2.04	6.33E-05	2.49E-03	
Slco3a1	NM_023908	2.04	1.66E-06	1.27E-04	
G3bp2	NM_011816	2.04	2.64E-05	1.24E-03	
Sp100	NM_013673	2.03	1.43E-04	4.71E-03	
Trim26	NM_001286727	2.03	3.85E-05	1.69E-03	
Isoc1	NM_025478	2.02	1.86E-05	9.25E-04	
Zfp429	NM_001080941	2.01	6.61E-05	2.58E-03	
Gna13	NM_010303	2.01	9.02E-08	1.17E-05	
Cyren	NM_001135611	2.01	4.04E-05	1.75E-03	
Ntn1	NM_008744	2.00	1.42E-06	1.13E-04	
E330013P04Rik	NR_026942	2.00	1.56E-06	1.21E-04	



**Supplemental Table III.** Gene Lists from RNA Sequencing. Left) 60 genes found to be induced in iKO mVSMCs by IFN $\gamma$  that were not similarly induced by IFN $\gamma$  in control mVSMCs. Parameters shown include Gene symbols, Ensembl transcript IDs, fold change ( $+1 \log_2$ ), P value, false discovery rate (FDR) step up. Right) Regulated genes from leftward list contributing to significantly regulated pathways in Ingenuity Pathway Analysis (IPA).

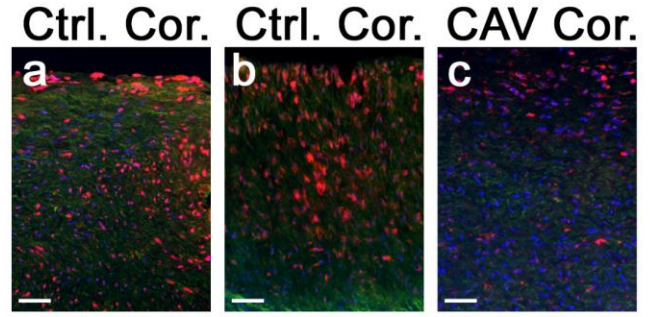
**Supplemental Figures and Figure Legends:**

SF-I-A

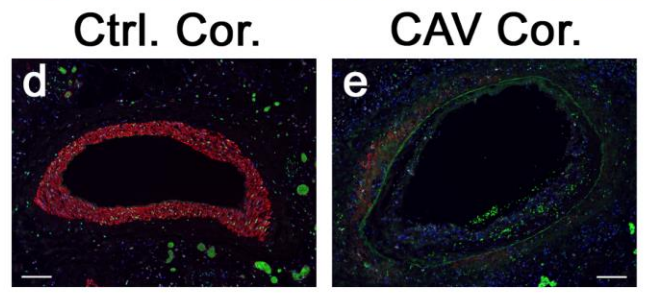


SF-I-B

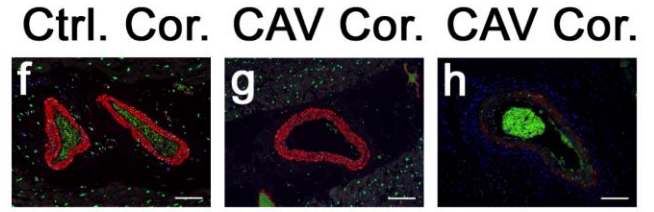
5-hmC  
ACTA2  
DAPI



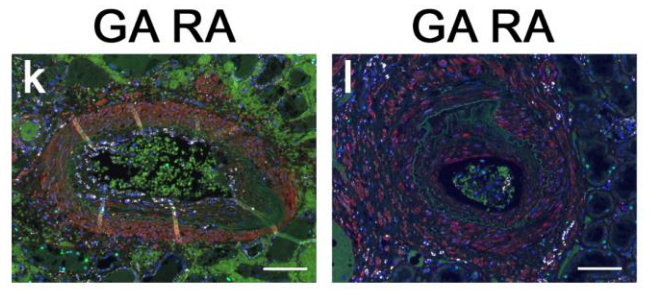
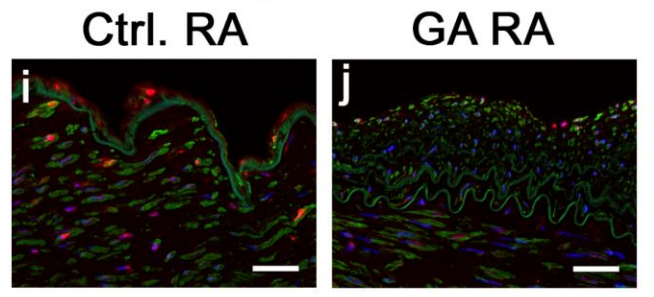
5-hmC  
ACTA2  
DAPI



5-hmC  
ACTA2  
DAPI

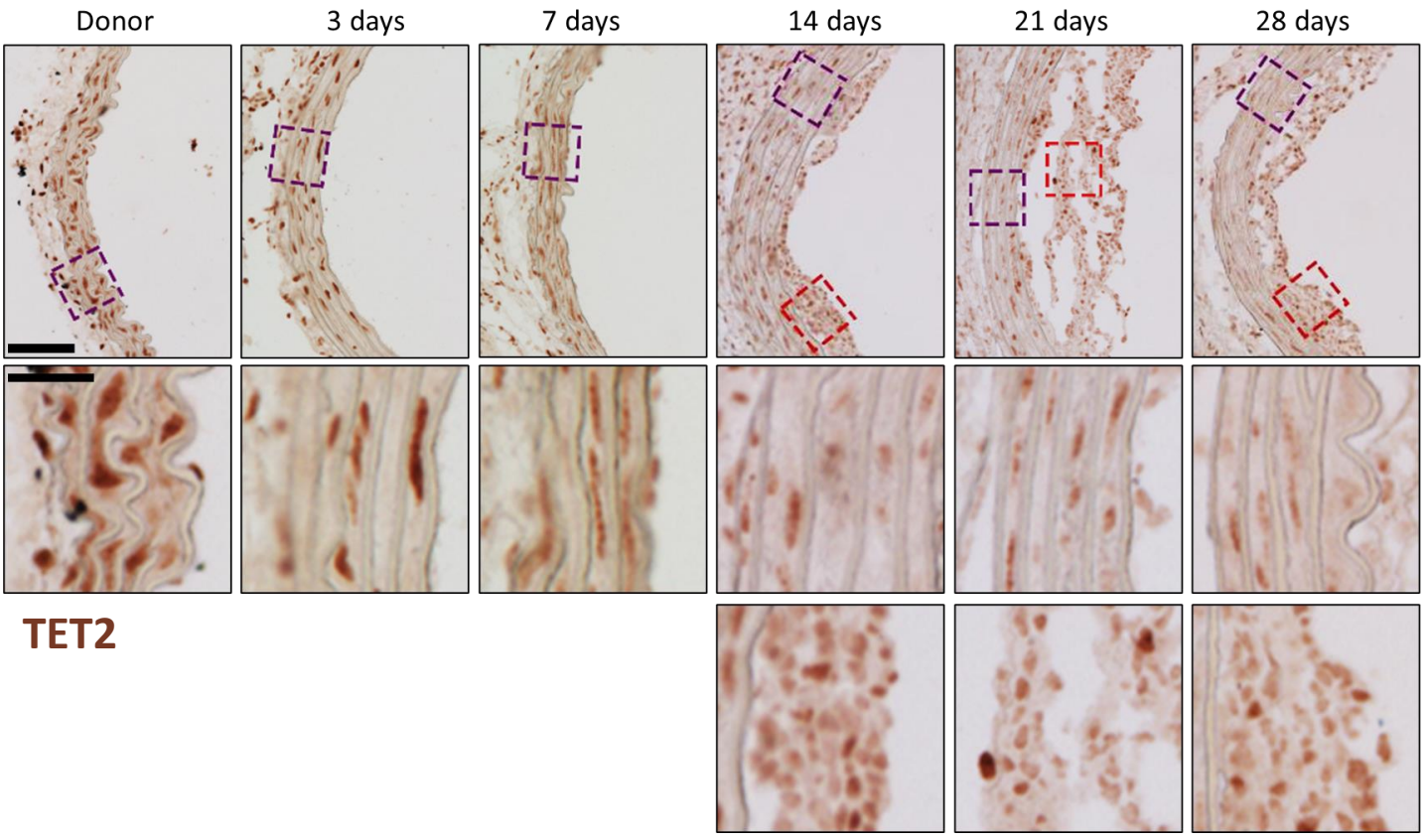


5-hmC  
ACTA2  
DAPI



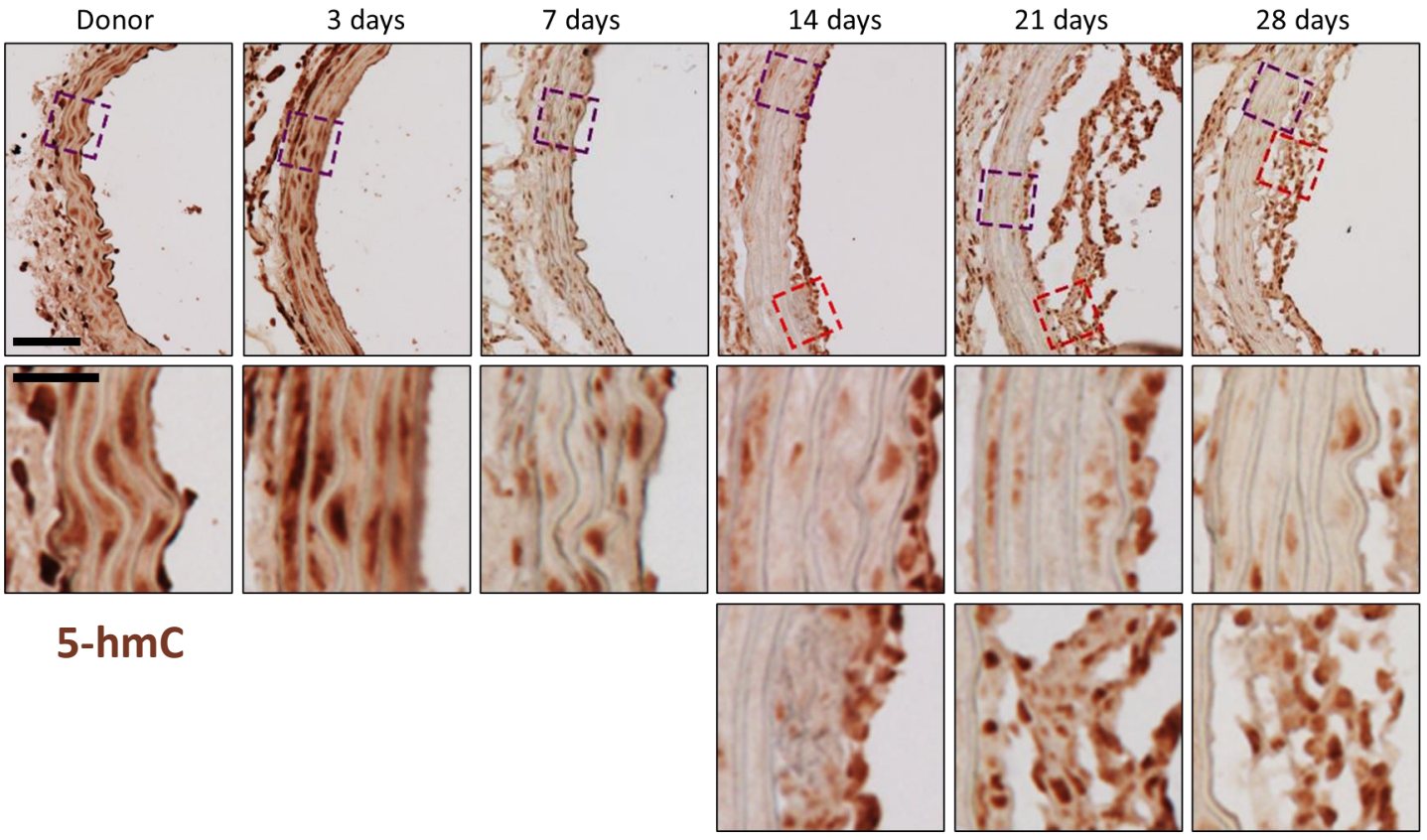


SF-II-A



Media  
Intima

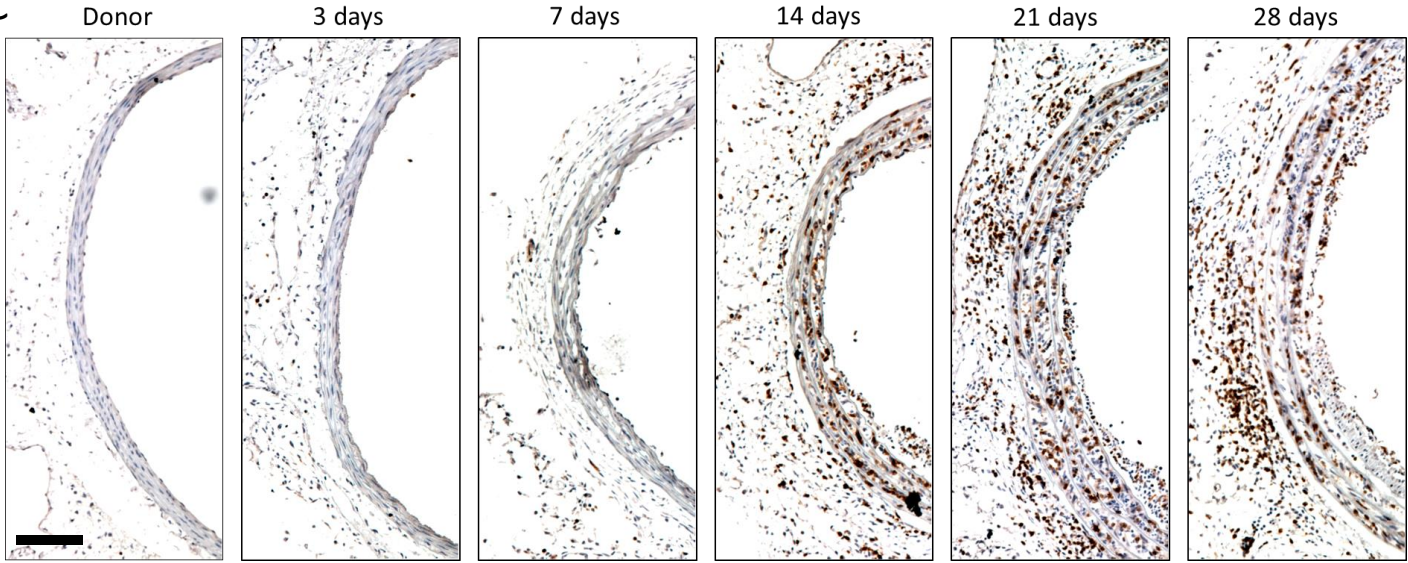
SF-II-B



Media  
Intima

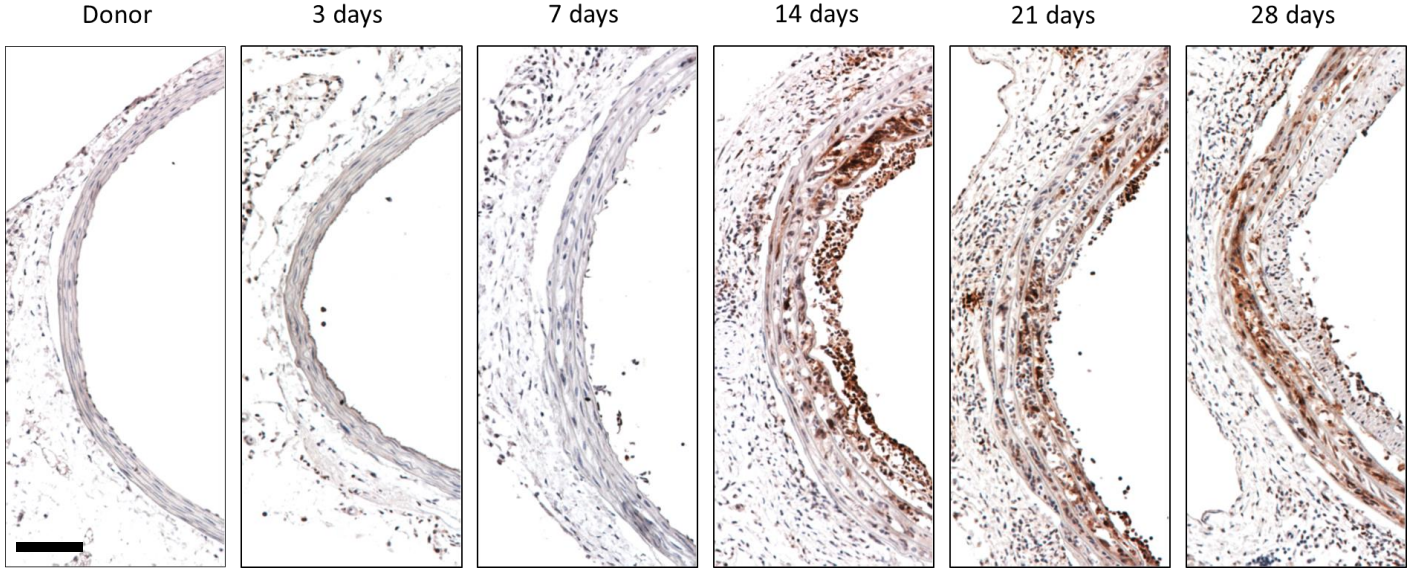
SF-II-C

CD3



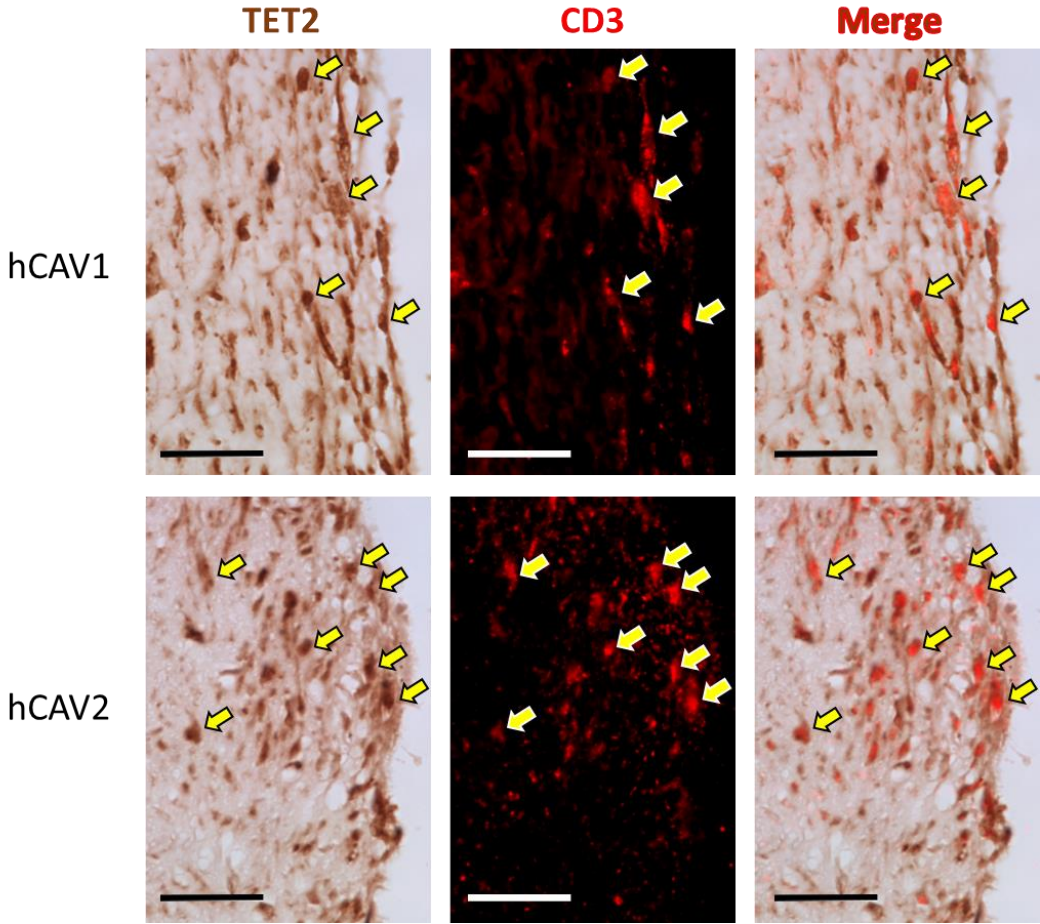
SF-II-D

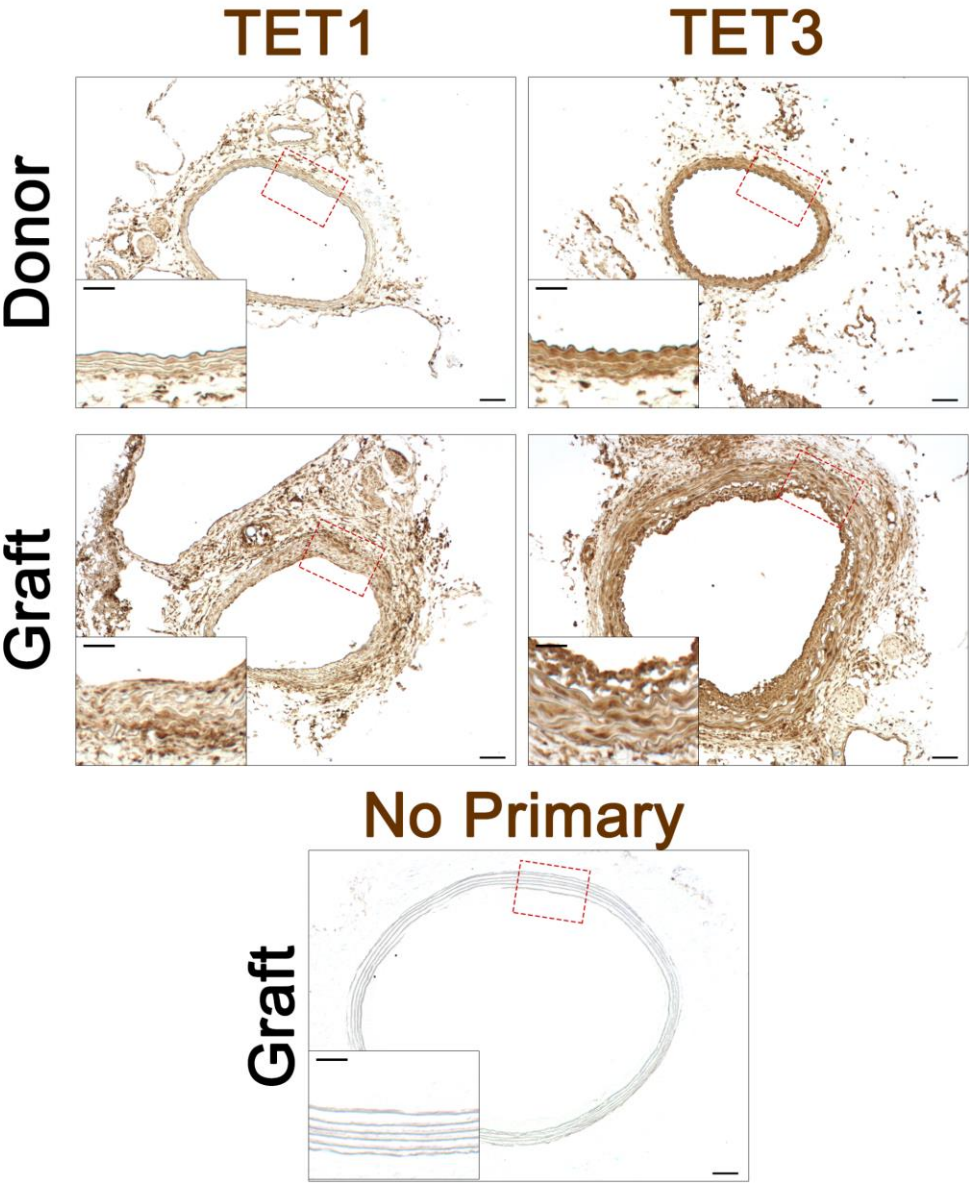
pSTAT1





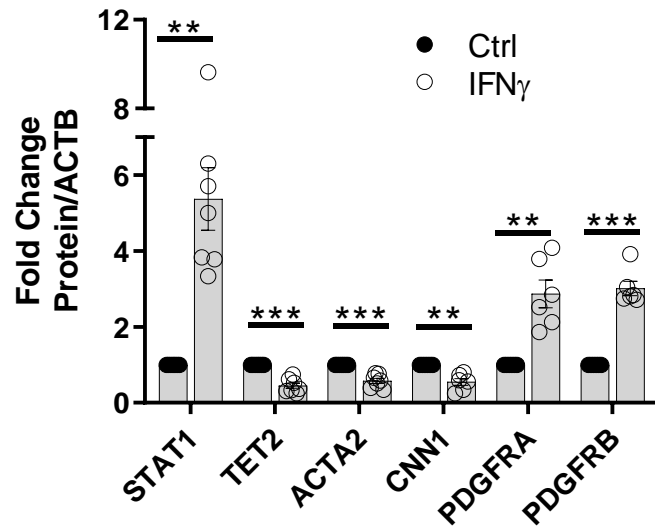
SF-III



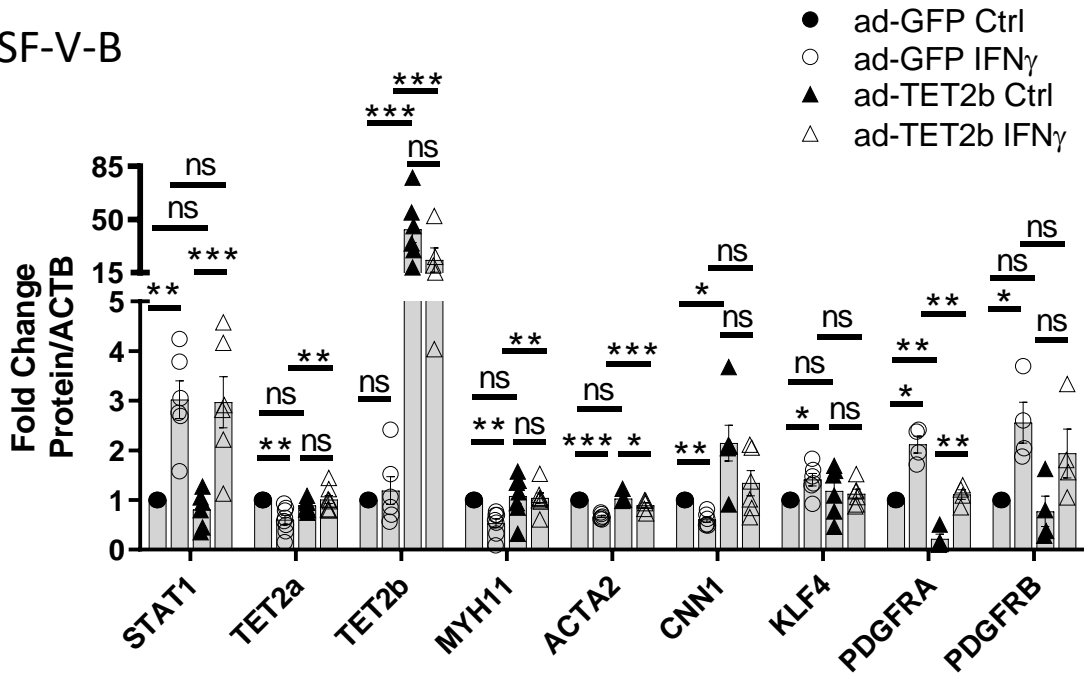




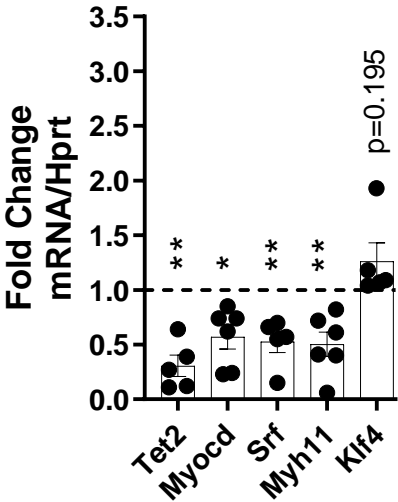
SF-V-A



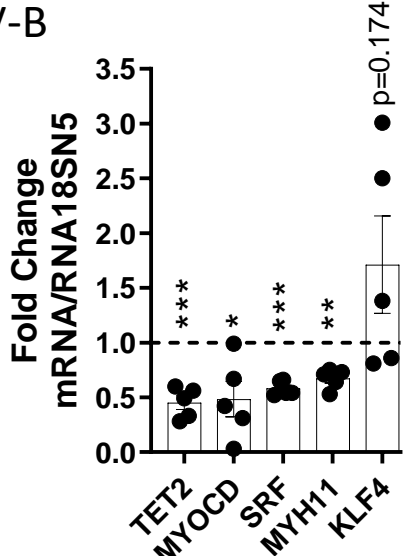
SF-V-B



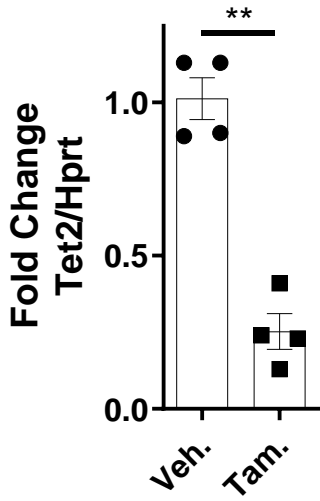
SF-VI-A



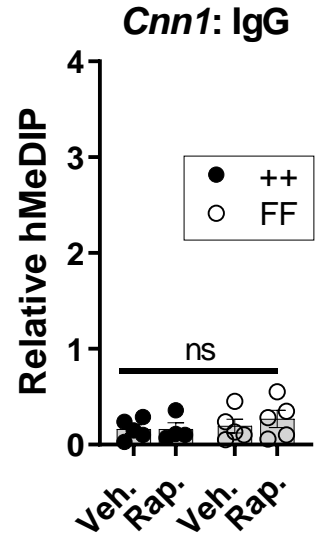
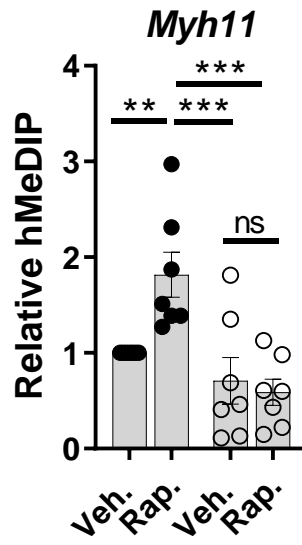
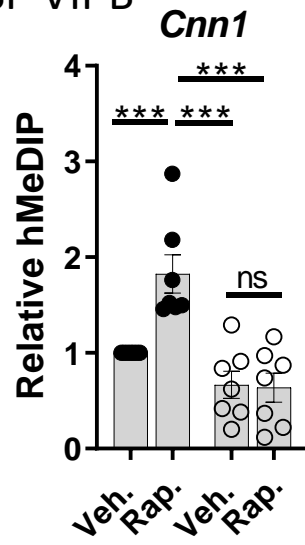
SF-V-B



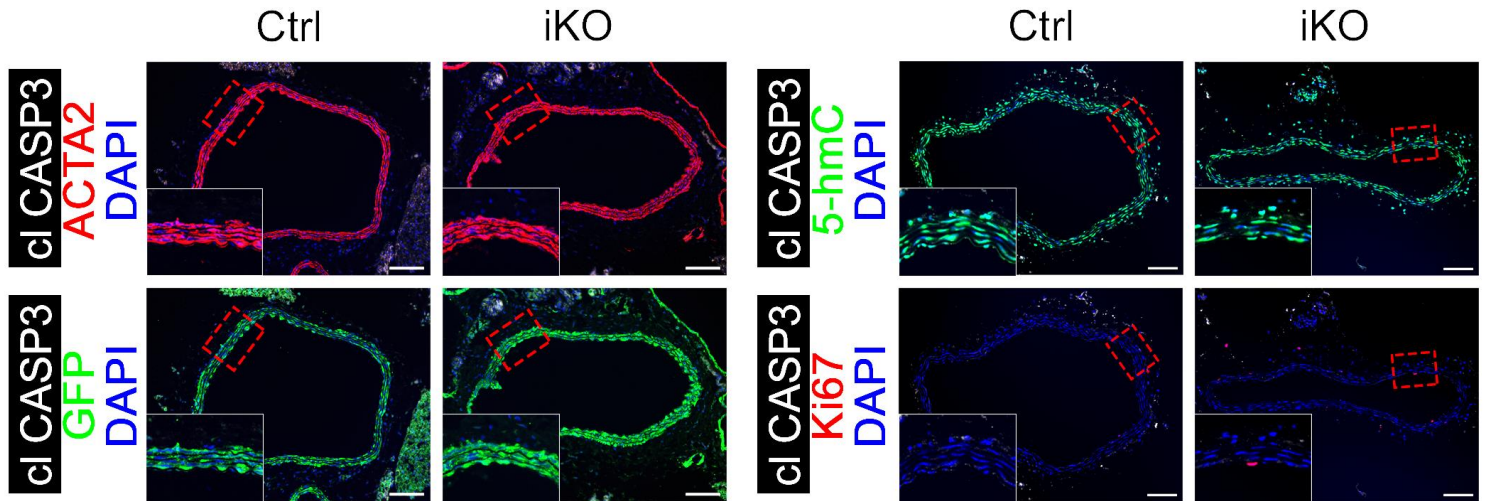
SF-VII-A



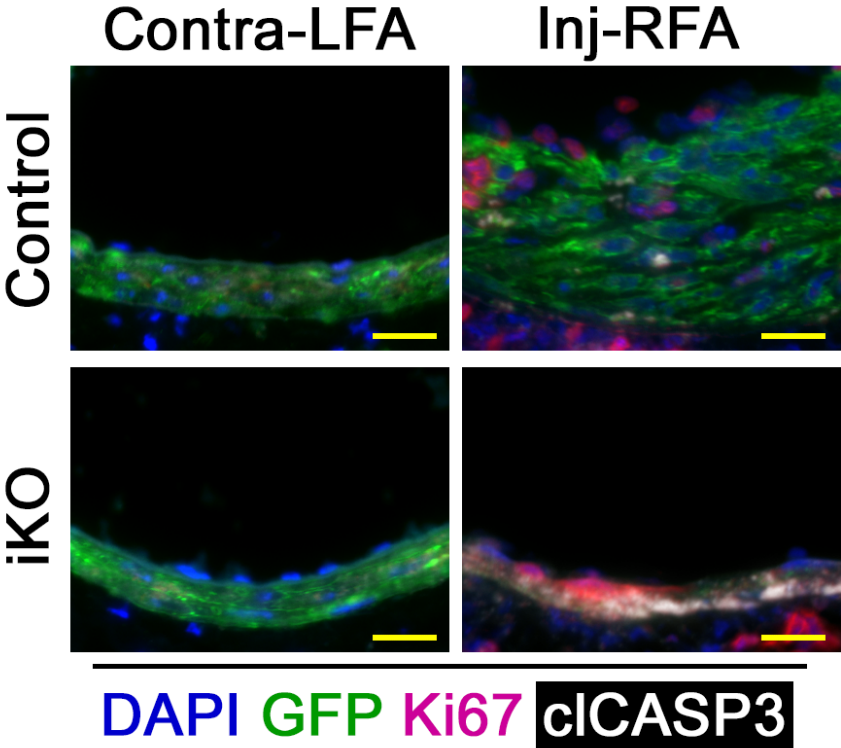
SF-VII-B



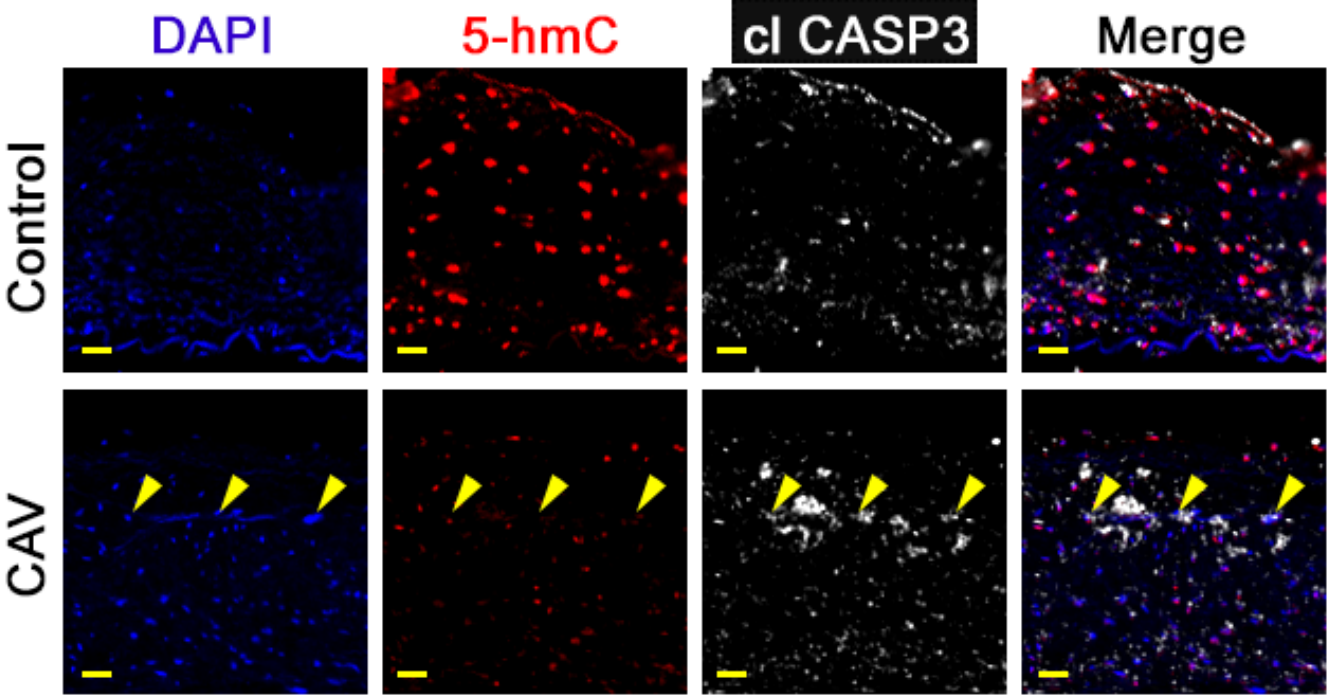
SF-VII-C



SF-VIII

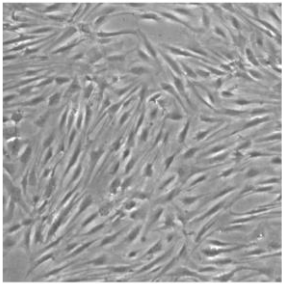


SF-IX

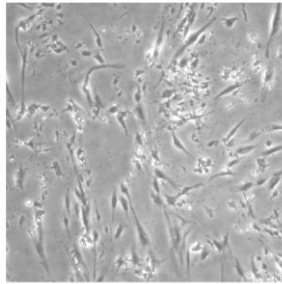


SF-X-A

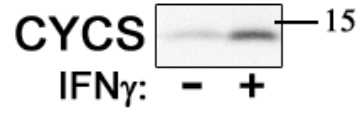
Ctrl



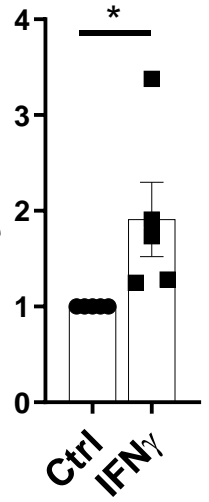
IFN $\gamma$



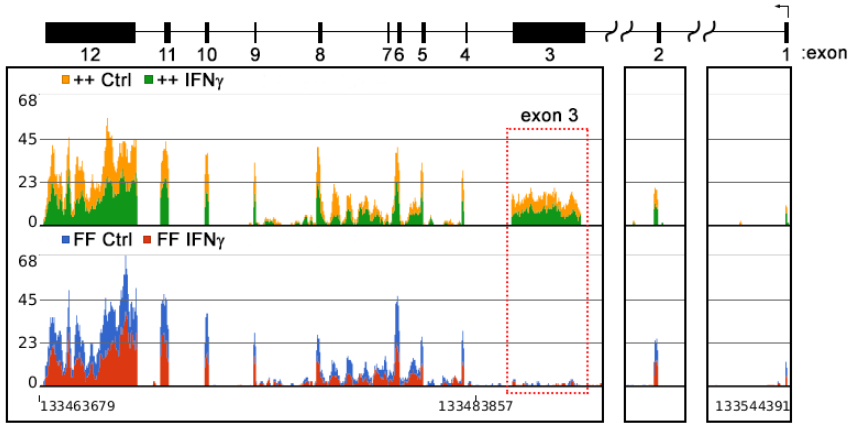
SF-X-B



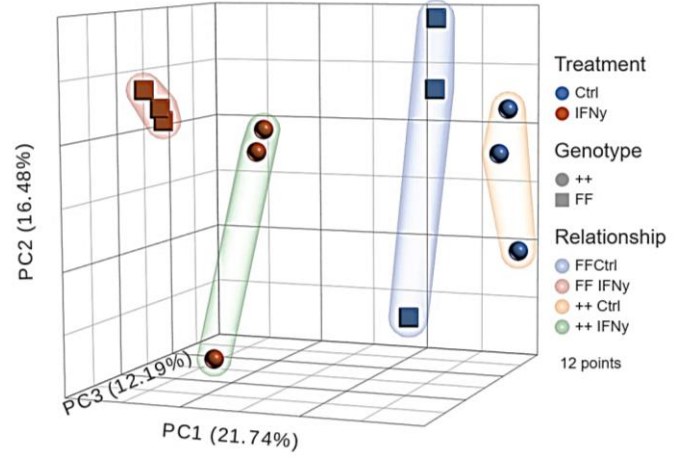
Relative Cytochrome C



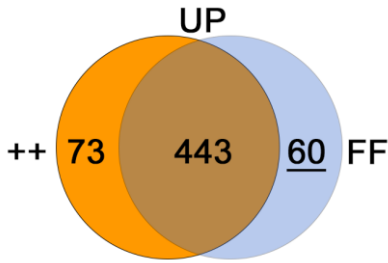
### SF-XI-A



### SF-XI-B

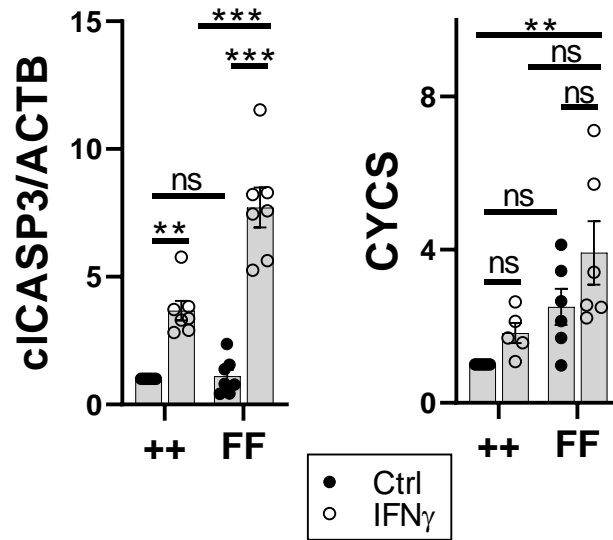
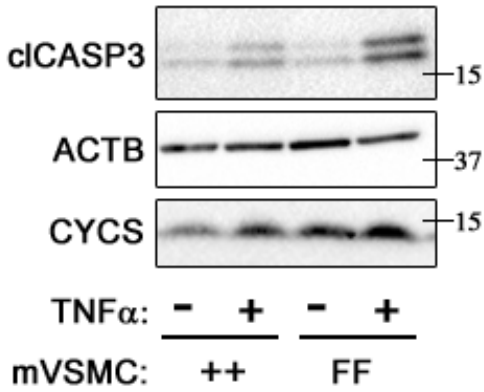


### SF-XI-C

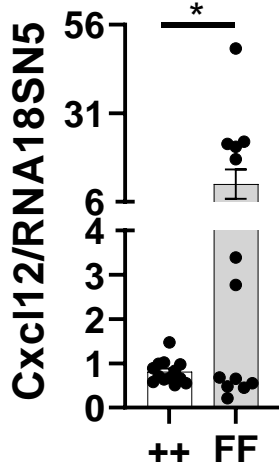


IPA Canonical Pathways	$-\log(p\text{-value})$
TNFR2 Signaling	6.26
MIF Regulation of Innate Immunity	5.66
TNFR1 Signaling	5.35
CD40 Signaling	4.9
Role of NFAT in Regulation of the Immune Response	4.32
Death Receptor Signaling	4.32
CD28 Signaling in T Helper Cells	3.85
Induction of Apoptosis by HIV1	3.48

### SF-XI-D



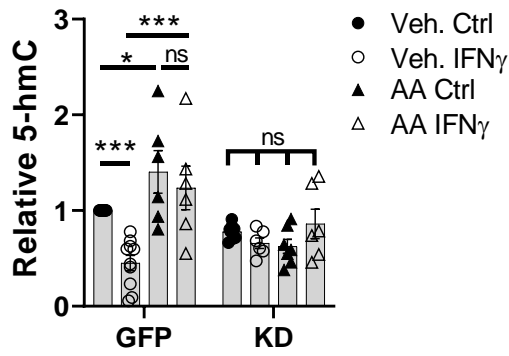
### SF-XI-E



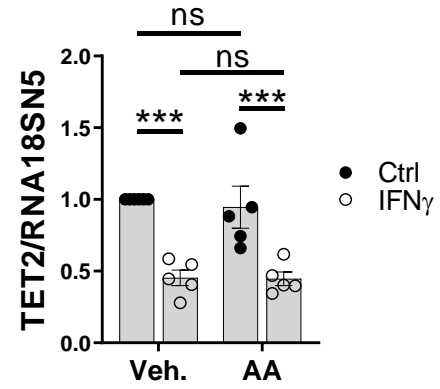




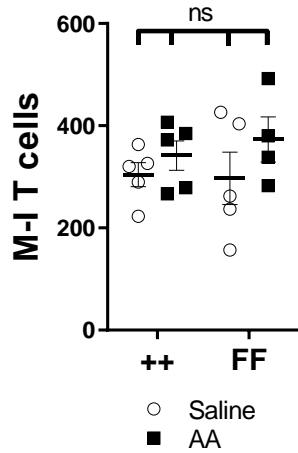
### SF-XII-A



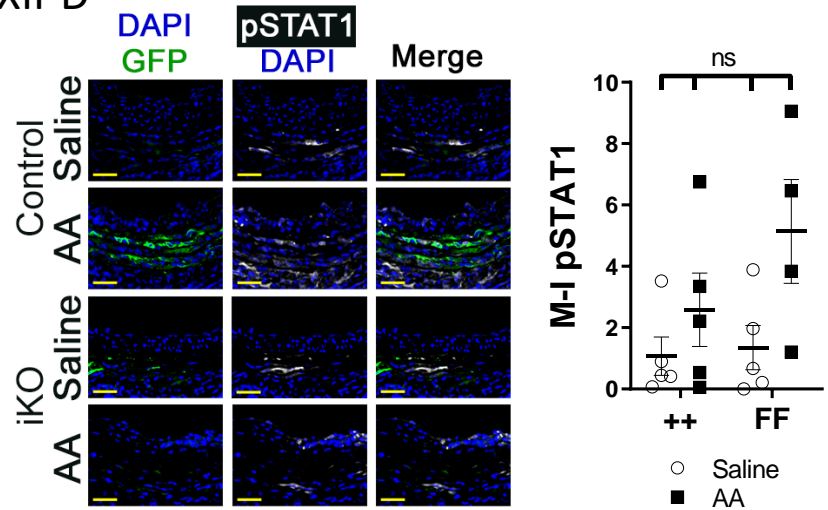
### SF-XII-B



### SF-XII-C



### SF-XII-D



### SF-XII-E

