

**Phosphorylation of USP20 on Ser334 by IRAK-1 Promotes IL-1 $\beta$ -evoked Signaling in Vascular Smooth Muscle Cells and Vascular Inflammation**

Lisheng Zhang<sup>‡</sup>, Jiao-Hui Wu<sup>‡</sup>, Pierre-Yves Jean-Charles<sup>‡</sup>, Pavitra Murali<sup>‡</sup>, Wenli Zhang<sup>‡</sup>, Aeva Jazic<sup>‡</sup>, Suneet Kaur<sup>‡</sup>, Igor Nepliouev<sup>‡</sup>, Jonathan A. Stiber<sup>‡</sup>, Kamie Snow<sup>‡</sup>, Neil J. Freedman<sup>‡†1</sup> and Sudha K. Shenoy<sup>‡†2</sup>

From the Departments of <sup>‡</sup>Medicine (Cardiology) and <sup>†</sup>Cell Biology,  
Duke University Medical Center, Durham, North Carolina 27710

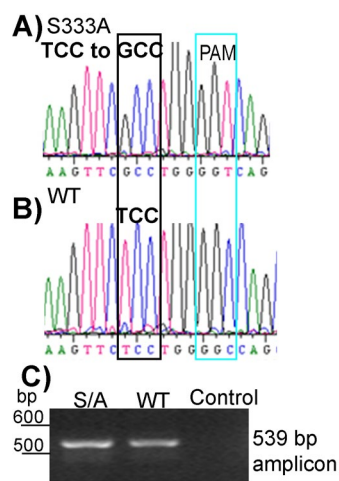
<sup>1</sup>To whom correspondence may be addressed: Box 102150, Duke University Medical Center, Durham, NC 27710. Tel.: 919-684-6873; Fax: 919-681-0718; E-mail: neil.freedman@duke.edu

<sup>2</sup>To whom correspondence may be addressed: Box 103204, Duke University Medical Center, Durham, NC 27710. Tel.: 919-681-5061; Fax: 919-681-7851; E-mail: skshenoy@dm.duke.edu

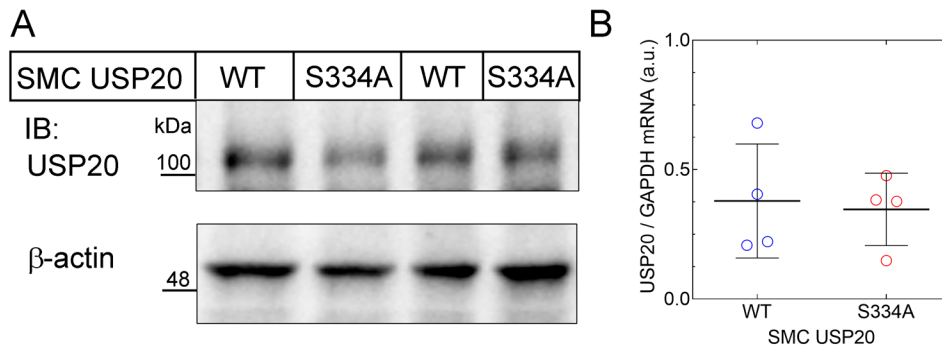
**SUPPLEMENTARY INFORMATION**

**TABLE S1. Primers used for qRT-PCR**

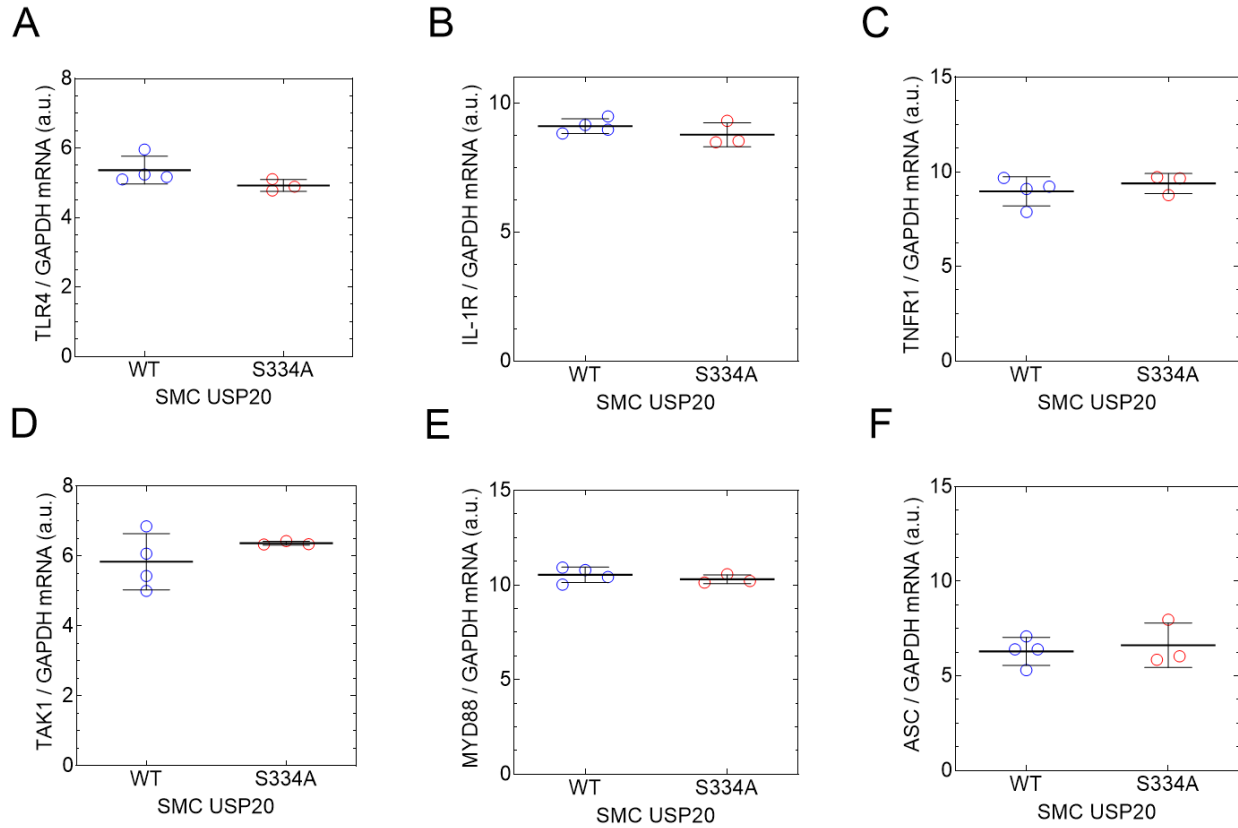
<b>Gene</b>	<b>Forward Primer (5' to 3')</b>	<b>Reverse Primer (5' to 3')</b>
<i>Tlr4</i>	TGCATGGATCAG AAACTCAGC	ATTGTTTCAATTT CACACCTGGA
<i>Il1r</i>	TCATATGCAGGC TTTAAGGAGAA	GGTGTGCGCCGTGC ATTTTAT
<i>Tnfr1</i>	CTAAGTGTCTC CTGGCCAAT	TGGGTTTTCAAGG CGCAGTA
<i>Myd88</i>	TGTTCTTGAACC CTCGGACG	TTCTGGCAGTCCT CCTCGAT
<i>Tak1</i>	TCTGCCAGTGAG ATGATCGAA	TCCATCACAAGA CATACTGGATTC
<i>Asc</i>	TGACAGTGCAAC TGCGAGAA	TGGTCCACAAAG TGTCTGT



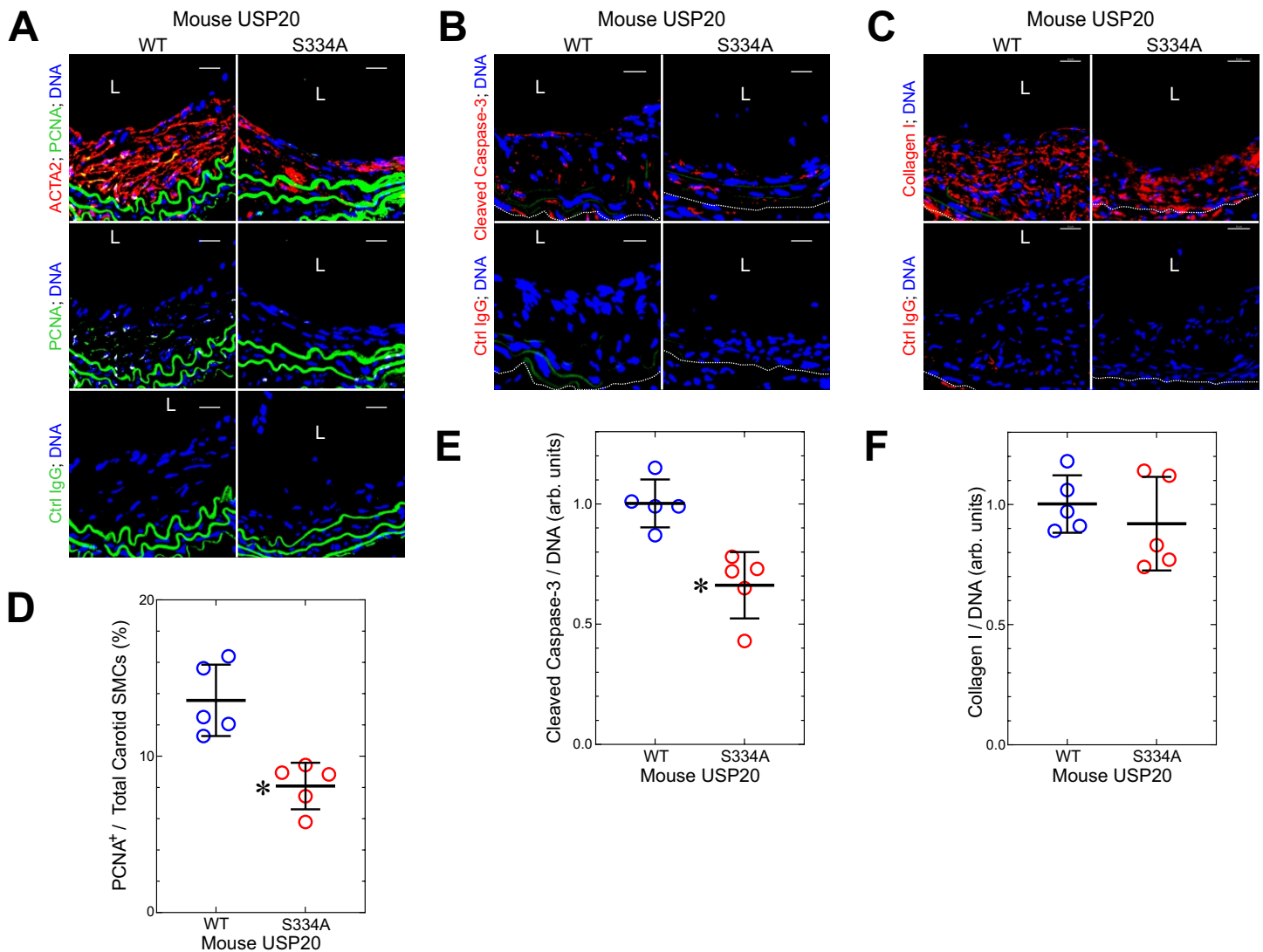
**Figure S1. Creation and characterization of the USP20-S334A mouse.** *A*, CRISPR/Cas9 technology was employed to edit Ser334 (TCC) to Ala334 (GCC). Shown is a sequence chromatogram of the TCC-to-GCC mutation, confirmed by founder analysis and allelic subcloning. *B*, The WT sequence TCC is shown. Panel *A* also shows the engineered silent mutation (GGC to GGT) included in the repair oligo, designed for the purpose of disrupting the Protospacer Adjacent Motif (PAM) sequence. *C*. PCR amplification of no DNA (“control”) or DNA from USP20-S334A (“S/A”) and WT mice was followed by agarose electrophoresis. bp: base pairs.



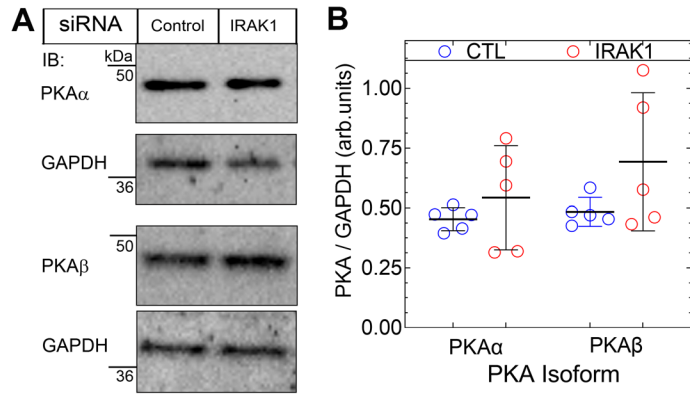
**Figure S2. Expression of USP20 protein is equivalent in SMCs from WT and USP20-S334A mice.** *A*, Primary SMCs were prepared from WT or USP20-S334A mice, and protein extracts (40  $\mu$ g) were separated on 4-12 % gradient gels and serially immunoblotted for USP20 and  $\beta$ -actin. *B*, The intensity of USP20 bands was normalized to cognate  $\beta$ -actin bands and plotted along with means  $\pm$  SD from 4 independently isolated SMC lines of each genotype.



**Figure S3. SMCs from WT and USP20-S334A mice express equivalent levels of pro-inflammatory signaling intermediates.** Total mRNA was isolated from 4 WT and 3 S334A SMC cell lines and analyzed by qRT-PCR for the expression of TLR4 (A), interleukin-1 receptor (IL1-R) (B), TNF receptor-1 (TNFR1) (C), TAK1 (D), MyD88 (E), and ASC (F) using gene-specific primers (see methods). The level of each mRNA was normalized to cognate levels of GAPDH mRNA, and ratios were plotted (with means  $\pm$  SD) as arbitrary units.



**Figure S4. Phosphorylation of UPS20 on Ser334 augments arterial SMC proliferation and apoptosis.** Carotid arteries of female mice from Fig. 2 were serially sectioned and immunostained with IgGs specific for PCNA, cleaved caspase-3, collagen I, or cognate isotype control (“Ctrl”) IgG, and counterstained with Hoechst 33342 (DNA). Confocal fluorescence photomicrographs are shown; scale bars = 20  $\mu$ m. “L” indicates lumen. *A*, PCNA-stained sections were co-stained for ACTA2 as described in Methods. Co-localization of green (PCNA) with either blue (DNA) or red (ACTA2) was performed using Imaris 9.2 software, to yield white or yellow, respectively. Elastic laminae demonstrate green autofluorescence. *B*, *C*, The dotted lines demarcate the external elastic laminae. *D*, Within the neointima and tunica media of each carotid artery cross section, the number of PCNA-positive cells was normalized to total number of cells; these values were plotted for 5 distinct carotid arteries per genetic group, along with means $\pm$ SD. Compared with WT, \*,  $p < 0.01$  (unpaired  $t$  test). *E*, Within the neointima and tunica media of each carotid artery cross section, cleaved caspase-3 immunofluorescence was normalized to DNA fluorescence; these ratios were normalized to the mean value obtained for WT carotid arteries and plotted for 5 distinct carotid arteries per genetic group, along with means $\pm$ SD. Compared with WT, \*,  $p < 0.003$  (unpaired  $t$  test with Welch’s correction). *F*, Within the neointima and tunica media of each carotid artery cross section, collagen I immunofluorescence was normalized to DNA fluorescence; these ratios were normalized to the mean value obtained for WT carotid arteries and plotted for 5 distinct carotid arteries per genetic group, along with means $\pm$ SD.



**Figure S5. IRAK1 knockdown does not affect SMC PKA expression.**

*A.* SMC lysates from experiments included in Figure 9C-E were immunoblotted for PKA $\alpha$  and PKA $\beta$  as indicated, and blots were reprobed for GAPDH. *B* PKA $\alpha$  and PKA $\beta$  band densities were normalized to cognate GAPDH band densities from 5 independent experiments, and ratios were plotted (with means  $\pm$  SD) as arbitrary units.