Legends for Supplemental Figures

Supplemental Fig. S1: Expression profile of various S100 proteins in lung tissues of UG-KO mice and in those of their WT littermates. While the expression of S100A8 and S100A9 in the lungs of the UG-KO mice is markedly elevated, other S100s were not increased. As expected, the expression of brain-specific S100B was not detectable in the lungs of either UG-KO mice or their WT littermates.

Supplemental Fig. S2 Immuno-localization S100A8 and S100A9 in the UGKO lungs and expression of RAGE in the lungs of UGKO mice and in those of their WT littermates. (**A**) Immunohistochemical analyses of UGKO lungs show S100A8/A9 are produced mainly by lung parenchymal cells. Note that the levels of RAGE-mRNA (**B**) and protein (**C**) expression in the lungs of UG-KO mice and their WT littermates are not significantly different.

Supplemental Fig. S3: SiRNA mediated suppression of RAGE expression in B16F10 cells and use of those cells in *in-vitro* invasion and in vivo pulmonary tumor formation through tail vein injection. (A) Suppression of RAGE was confirmed by western blot analysis of RAGE- SiRNA transfected B16F10 cells. (B) In-vitro invasion assay using RAGE SiRNA transfected B16F10 cells showed diminished invasion upon SiRNA mediated inhibition of RAGE expression. Scrambled SiRNA transfected and mock transfected B16F10 cells were used as controls. (C) Number of tumor colonies in the UGKO lungs was found to be less when RAGE SiRNA transfected B16F10 were injected to the tail veins compare to the Scrambled SiRNA transfected B16F10 cells.

Supplemental Fig. S4: Western blot analysis of S100A8/S100A9 levels in the sera of UG-KO mice. Blood samples were collected by canulating pulmonary vein (PV) and tail vein (TV) of UG-KO mice. Note the levels of S100A8 and S100A9 present in the TV serum is appreciably lower than those in sera from PV as evident from the densitometric quantitation provided at the right side of each panel. Albumin was used as loading control. AU, arbitrary unit.

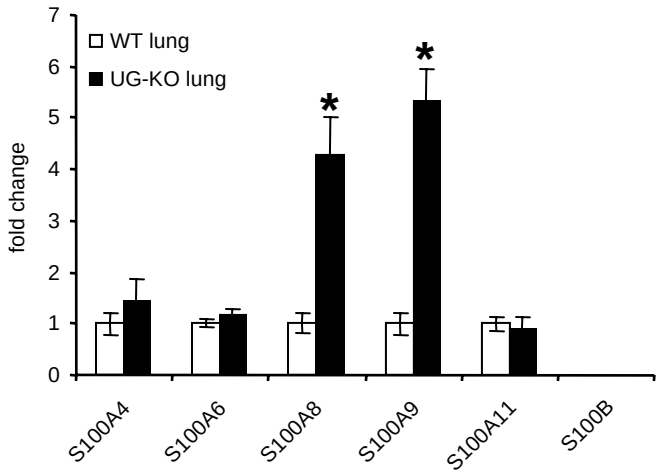
Supplemental Fig. S5: S100A8 and S100A9-stimulated expression of RAGE, MMPs and furin in B16F10 Cells. B16F10 cells were treated with (**1**) 0.2µg/ml of S100A8, (**2**) 0.2µg/ml of S100A9, (**3**) 1.0µg/ml of S100A8, (**4**) 1.0µg/ml of S100A9, (**5**) 2.0µg/ml of S100A8, (**6**) 2.0µg/ml of S100A9, (**7**) 0.2µg/ml of S100A8 + 0.2µg/ml of S100A9 and (**8**) 1.0µg/ml of S100A8 + 1.0µg/ml of S100A9 for 24 hours. The levels of RAGE, MMP2, MMP9, MMP14 and Furin mRNAs in B16F10 cells after treatment with S100A8 and S100A9 (solid bars) were compared against those of the untreated B16F10 cells (clear bars).

Supplemental Fig. S6: Expression profile of various genes associated with inflammation in WT and UG-KO lungs.

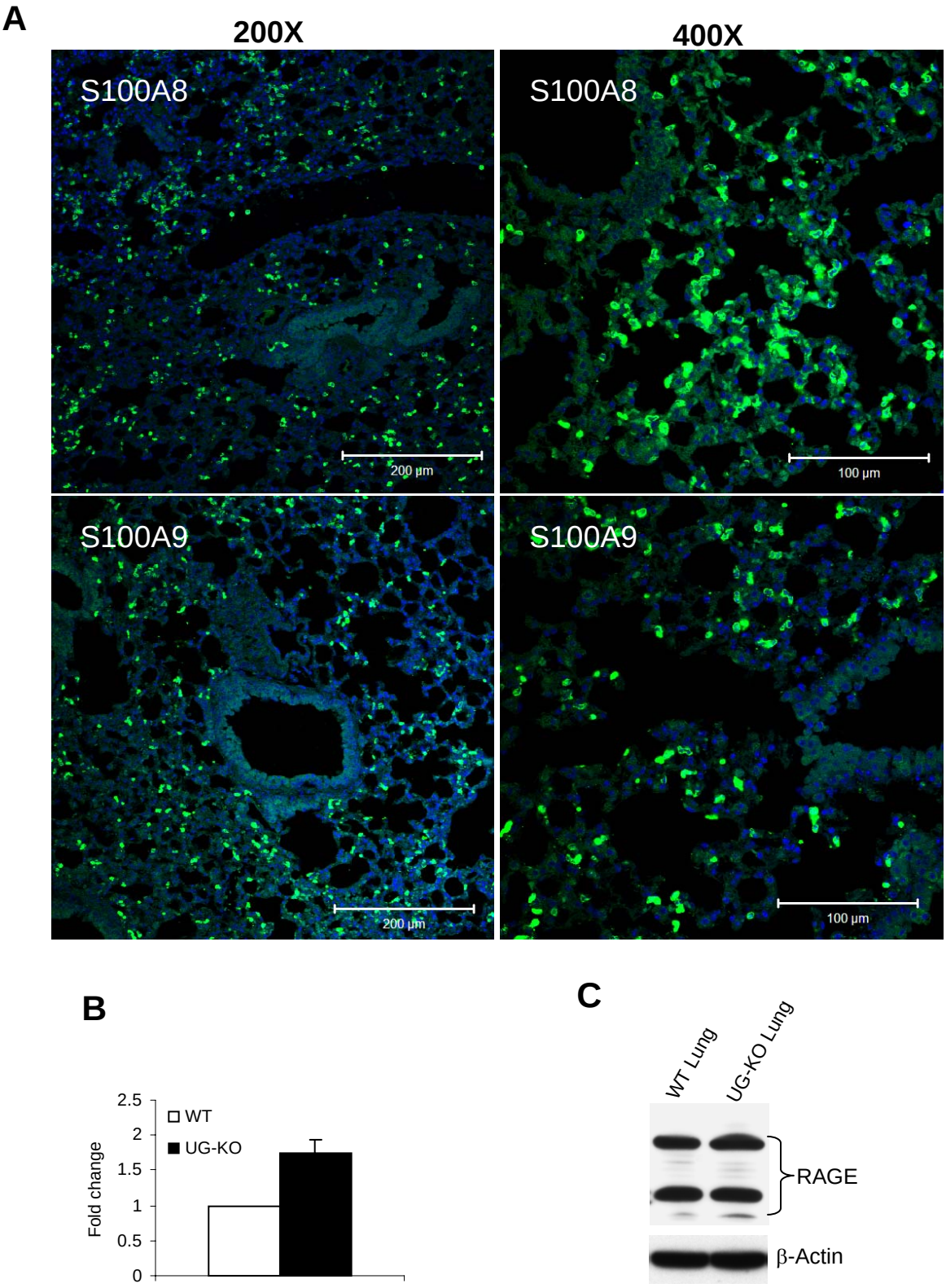
Supplemental Table S1: **Primers used for real-time quantitative RT-PCR**

Name	Forward Primer Sequence (5′ to 3′)	Reverse Primer Sequence (5′ to 3′)
ß-Actin	ACGGCCAGGTCATCACTATTG	TGGAAAAGAGCCTCAGGGC
CARMA1	GATGCGTGCACAAAAGAAGA	TCAGACCATCCTCCATCTCC
Furin	CAGCGAGACCTGAATGTGAA	CAGGGTCATAATTGCCTGCT
GAPDH	GCAGTGGCAAAGTGGAGATT	GAATTTGCCGTGAGTGGAGT
IKKα	TGGCACCTCCTTAAAATTGC	GAGGATGTTCACGGTCTGCT
Maspin	GCTGAATCAGGAAGCAGTCC	TGATTCCCTTTCCCAACAAG
MMP2	CTTCGCTCGTTTCCTTCAAC	AGAGTGAGGAGGGGAACCAT
MMP9	CATTCGCGTGGATAAGGAGT	ATTTTGGAAACTCACACGCC
MMP14	CCGGATAAGTTTGGGACTGA	GCCCACCTTAGGGGTGTAAT
RAGE	TCACAGAAACCGGCGATGA	TAGCGTACCCAGCCCAGACT
RANK	CTAATCCAGCAGGGAAGCAA	CAGTGAAGTCACAGCCCTCA
S100A4	TGGTCTGGTCTCAACGGTTA	TTTGTGGAAGGTGGACACAA
S100A6	CAAGGAAGGTGACAAGCACA	AGATCATCCATCAGCCTTGC
S100A8	GAGTGTCCTCAGTTTGTGCAG	TGCCACACCCACTTTTATCA
S100A9	ATACTCTAGGAAGGAAGGACACC	TCCATGATGTCATTTATGAGGGC
S100A11	AAGTACAGCGGGAAGGATGGA	ATGCGGTCAAGGACACCAG
S100B	TCTGCAGGAAGAATAAGAAGCTG	CCTCTCTGGCTTCAGTGTCC
TGFß	ATTCCTGGCGTTACCTTGG	CCCTGTATTCCGTCTCCTTG
TNFα	TATGGCTCAGGGTCCAACTC	CCCATTTGAGTCCTTGATGG

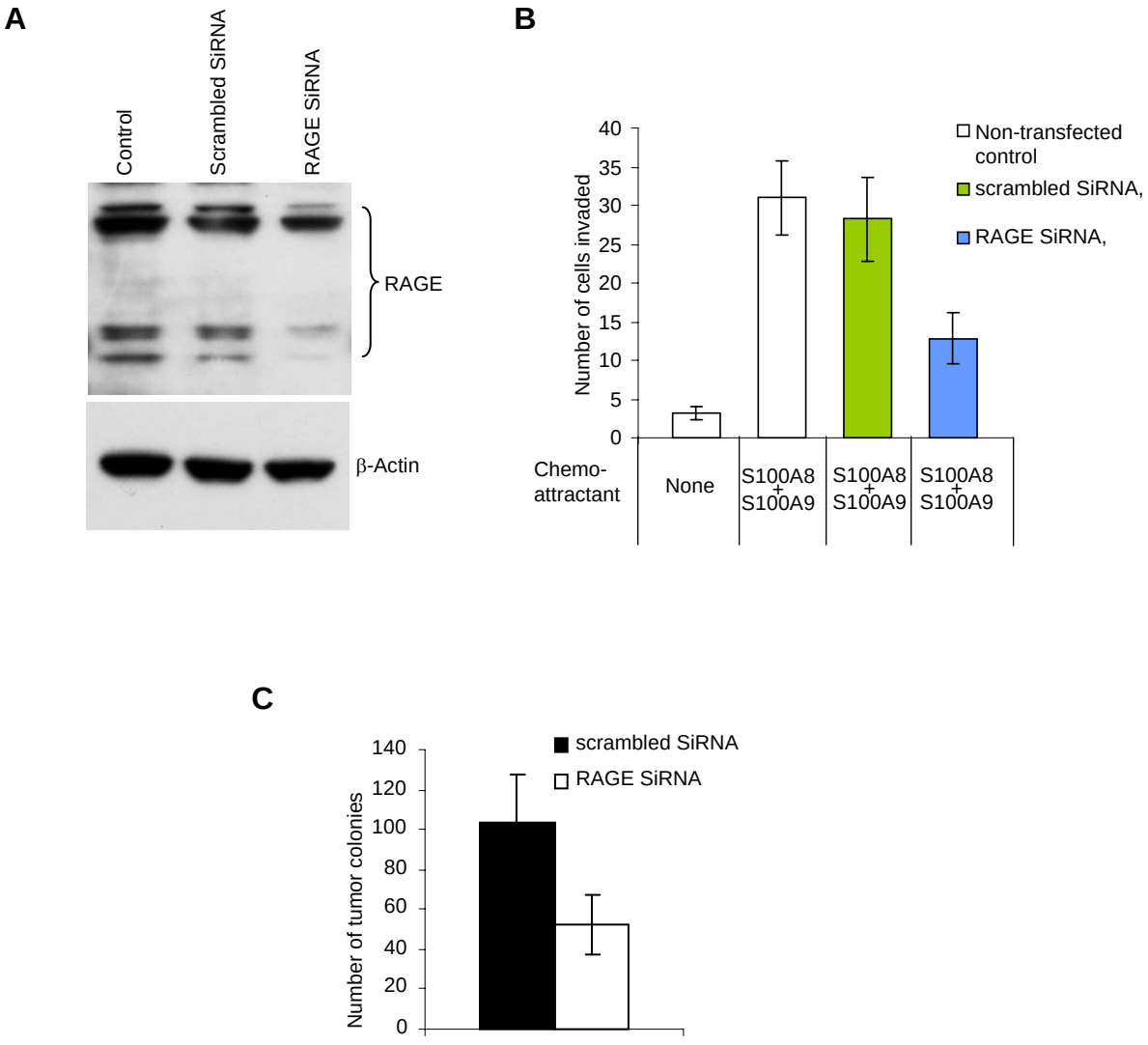
Supplementary Figure S1



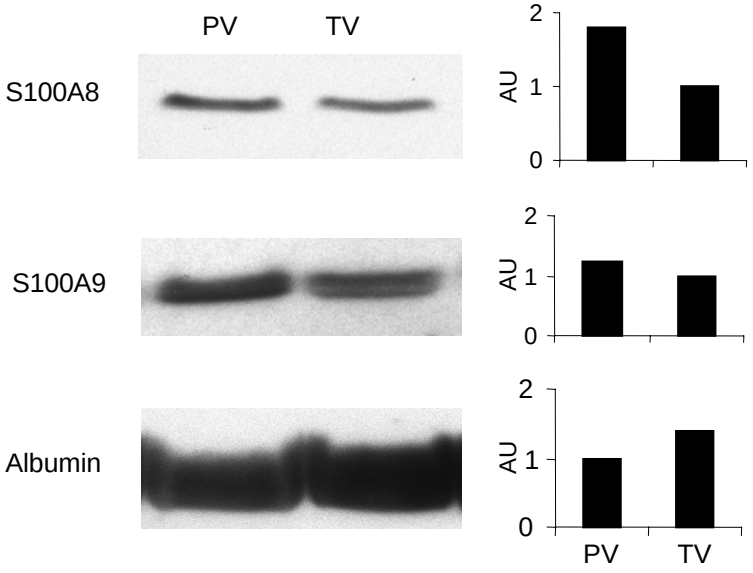
Supplementary Figure S2



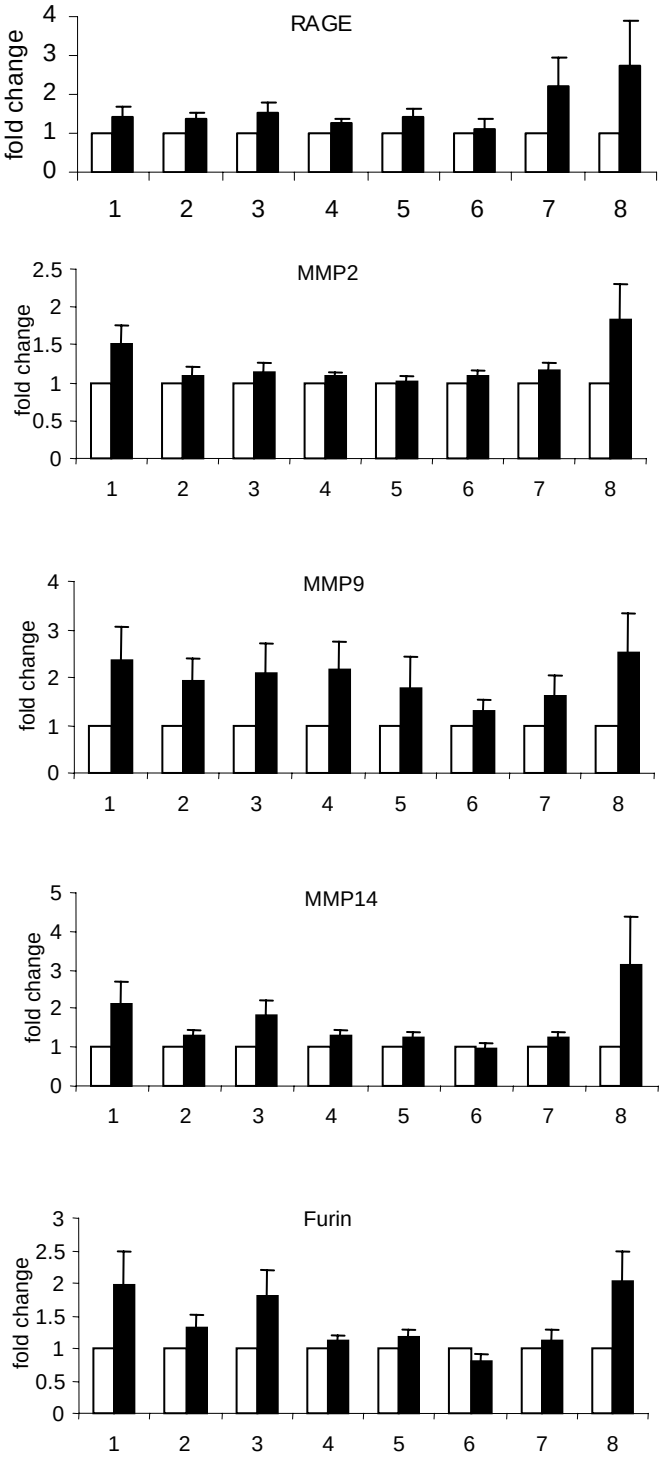
Supplementary Figure S3



Supplementary Figure S4



Supplementary Figure S5



Supplementary Figure S6