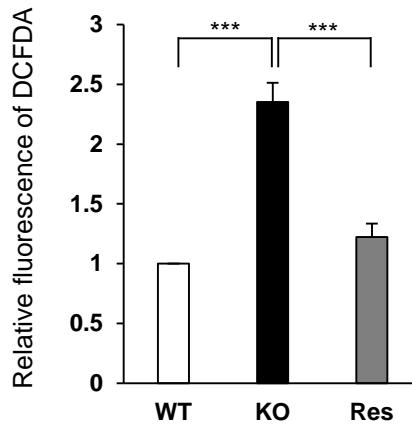
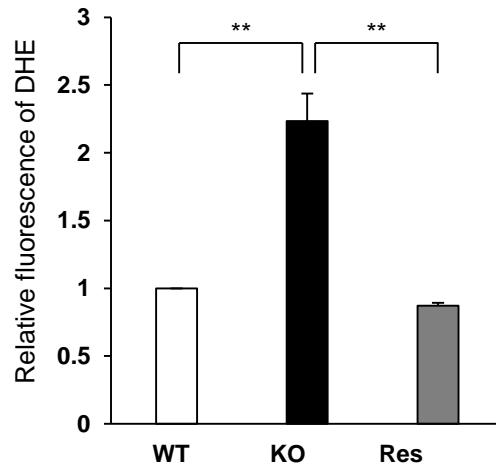
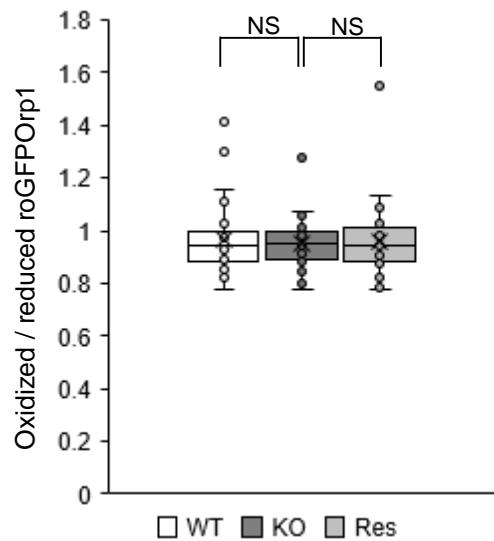
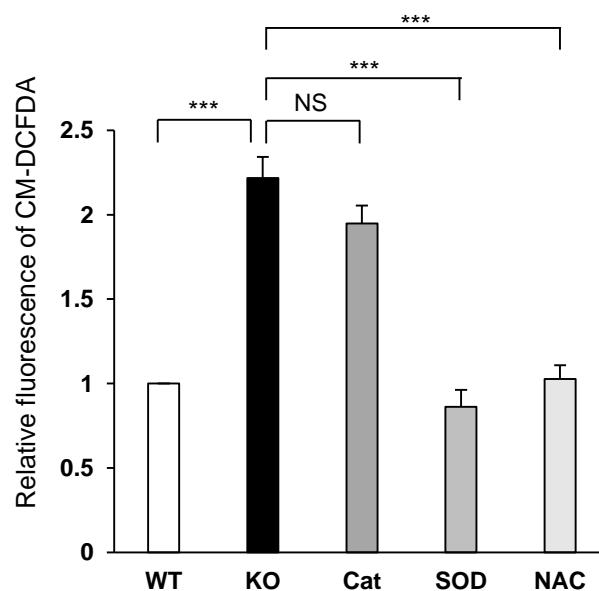


1317

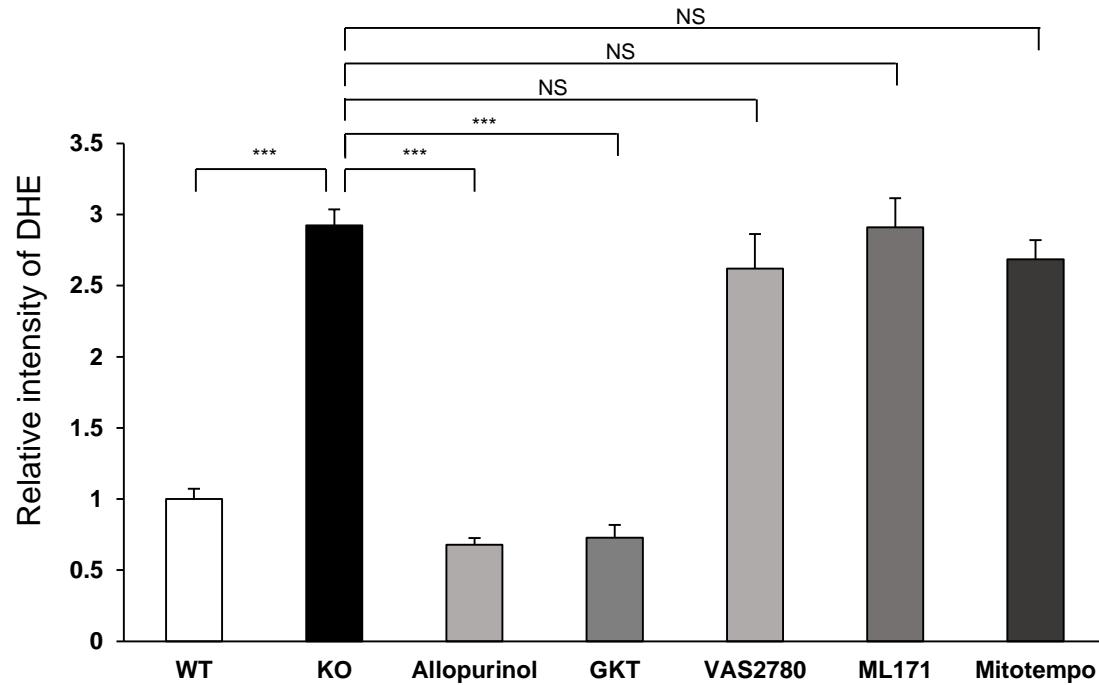
WT	TGGCGAAGATGGCCGCTGTGAGCAAAG <u>CCTGC</u> -GGAAACATGTT <u>CGGCTA</u> ATGCATGGACCTGCCAGAGACGTCAAGTA
KO #1	TGGCGAAGATGGCCGCTGTGAGCAAAG <u>CCTGC</u> -----AACATGTT <u>CGGCTA</u> ATGCATGGACCTGCCAGAGACGTCAAGTA
KO #2	TGGCGAAGATGGCCGCTGTGAGCAAAG <u>CCTGCTT</u> ACATGTT <u>CGGCTA</u> ATGCATGGACCTGCCAGAGACGTCAAGTA
KO #3	TGGCGAAGATGGCCGCTGTGAGCAAAG <u>CCTGC</u> ----GAAACATGTT <u>CGGCTA</u> ATGCATGGACCTGCCAGAGACGTCAAGTA
KO #4	TGGCGAAGATGGCCGCTGTGAGCAAAG <u>CCTG</u> -----
Res	TGGCGAAGATGGCCGCTGTGAGCAAAG <u>ATGT</u> - <b>GGCAAT</b> ATGTT <b>TGGATT</b> GATGCATGGACCTGCCAGAGACGTCAAGTA

WT	AAAAGGGCGGGGTGGGTGCTGTTCCCTGGCCTGAGGGTTCAAGTCTGAGCCTGACACCCATGCCTCCCCCTGCTGGGAGTT
KO #1	AAAAGGGCGGGGTGGGTGCTGTTCCCTGGCCTGAGGGTTCAAGTCTGAGCCTGACACCCATGCCTCCCCCTGCTGGGAGTT
KO #2	AAAAGGGCGGGGTGGGTGCTGTTCCCTGGCCTGAGGGTTCAAGTCTGAGCCTGACACCCATGCCTCCCCCTGCTGGGAGTT
KO #3	AAAAGGGCGGGGTGGGTGCTGTTCCCTGGCCTGAGGGTTCAAGTCTGAGCCTGACACCCATGCCTCCCCCTGCTGGGAGTT
KO #4	-----ACACCCATGCCTCCCC-TGCTGGGAGTT
Res	AAAAGGGCGGGGTGGGTGCTGTTCCCTGGCCTGAGGGTTCAAGTCTGAGCCTGACACCCATGCCTCCCCCTGCTGGGAGTT

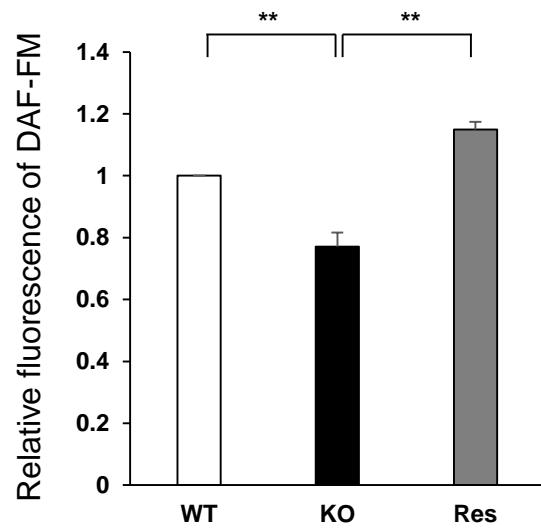
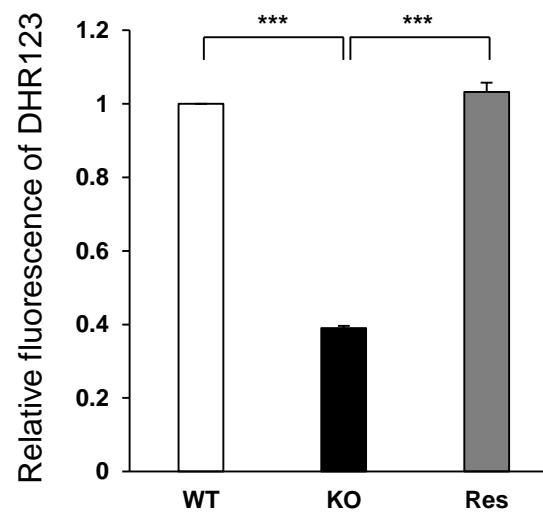
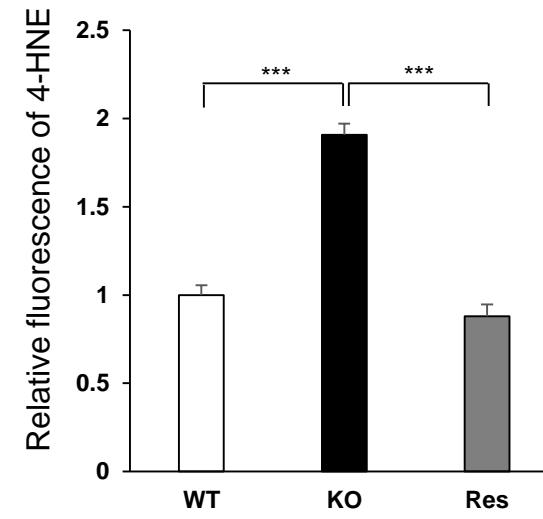
**Figure S1. Sequences of sgRNA, mutations in the knockout cell line (8-22), and rescue constructs.** Genetic information of the cell line used in this study was visualized in an align format of the *Seps1* coding sequence (from 1317). The PAM sequence is underlined. sgRNA is marked with a box. Deletion mutations in the KO cell line are marked as a hyphen, insertions are shown as bold-faced letters, and substitution mutations in rescue are shown in bold-faced red letters.

**A****B****C****D**

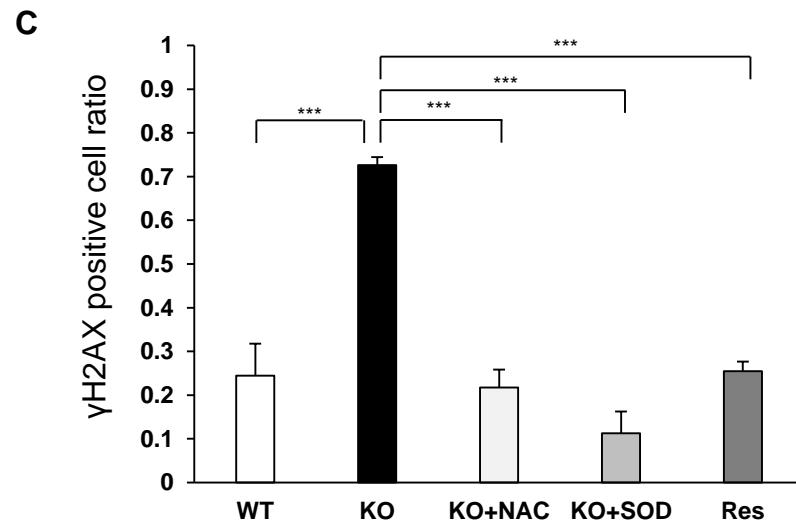
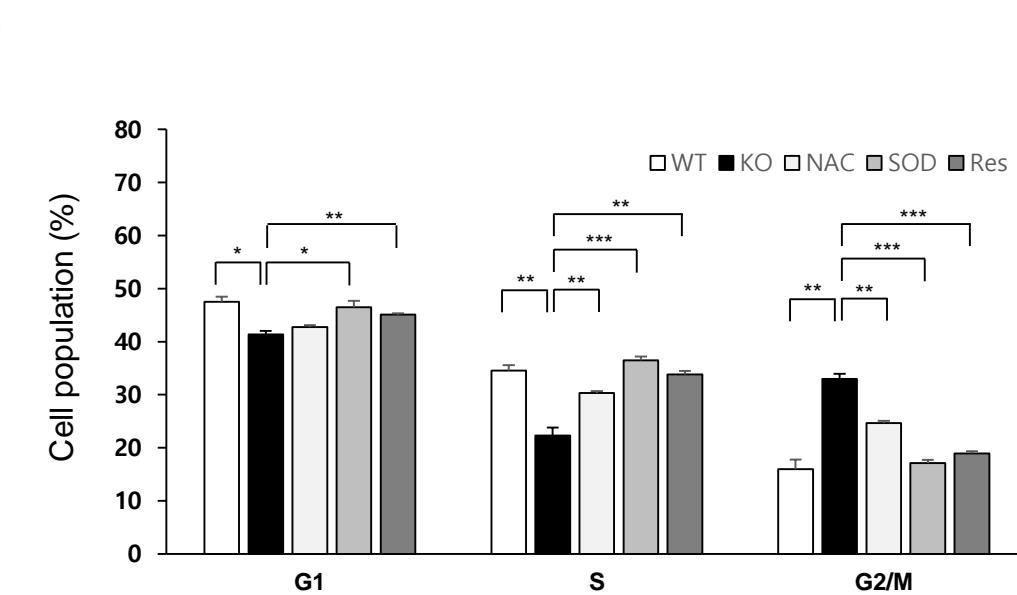
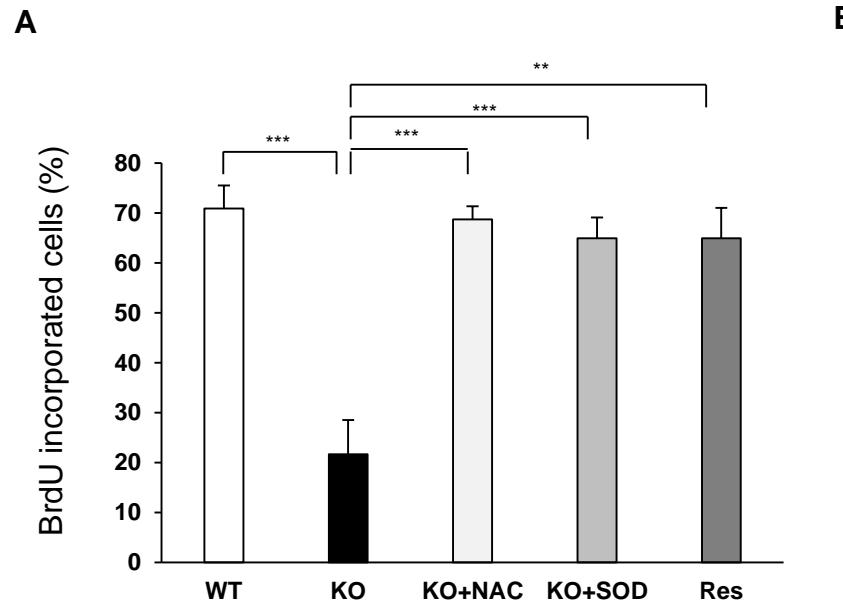
**Figure S2. Quantification of intensity of ROS probes.** **(A)** Quantification of fluorescence intensity of CM-DCFDA. **(B)** Relative intensity of DHE. **(C)** Ratio of oxidized / reduced roGFP-Orp1 probe. **(D)** Fluorescence intensity of CM-DCFDA of ROS scavenger treated knockout cells. \*\* and \*\*\* indicate p-value under 0.01 and 0.001, respectively.



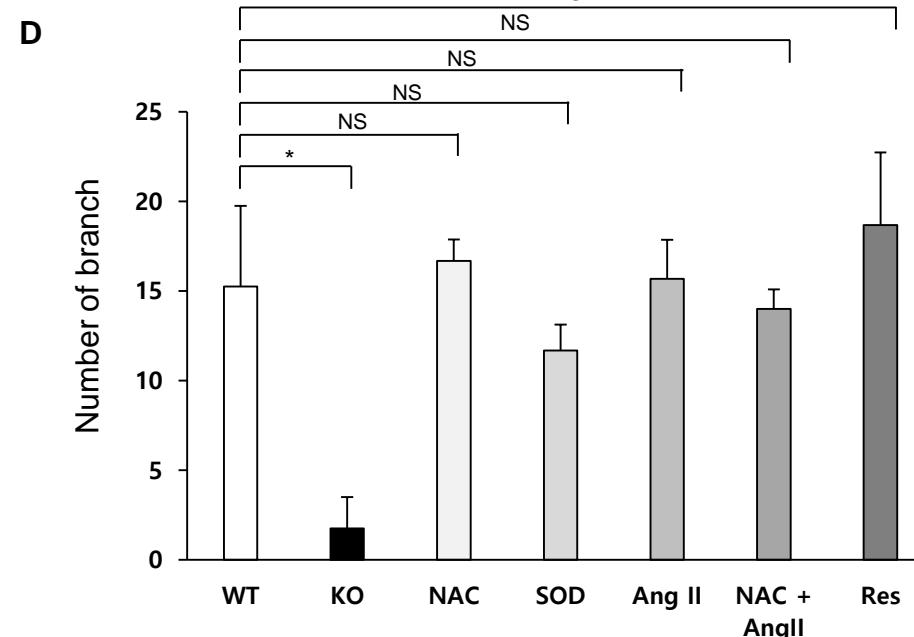
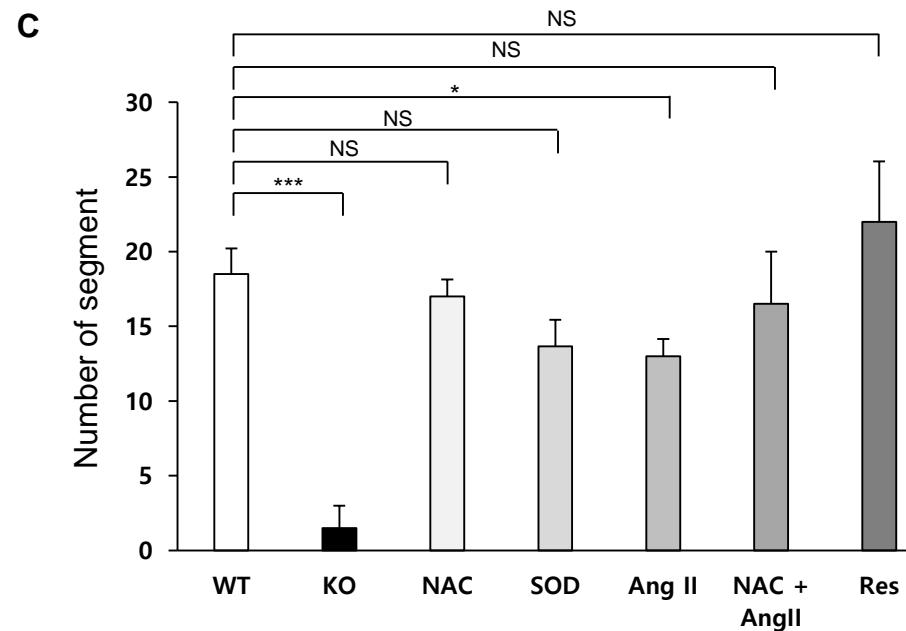
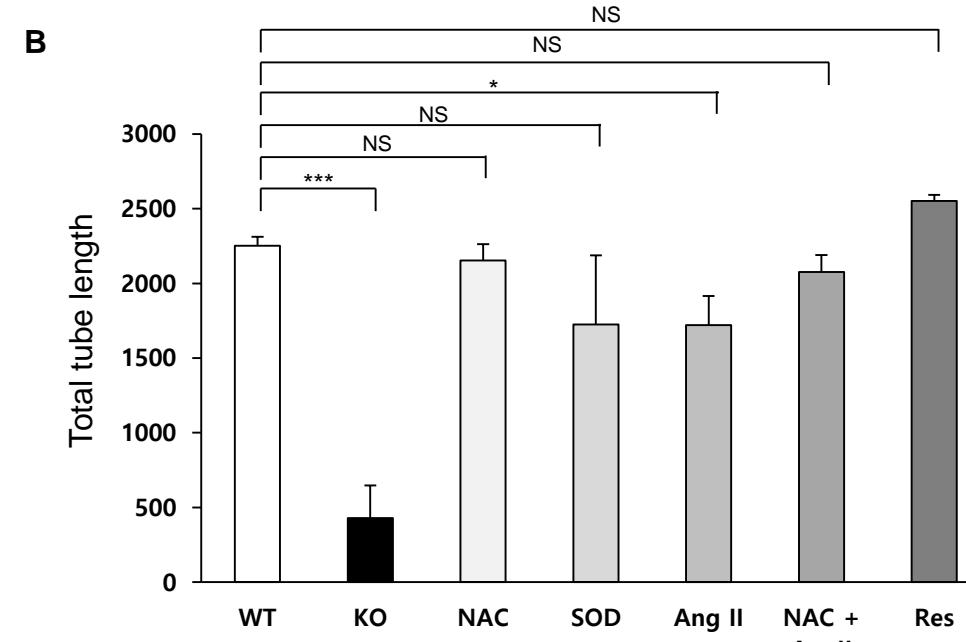
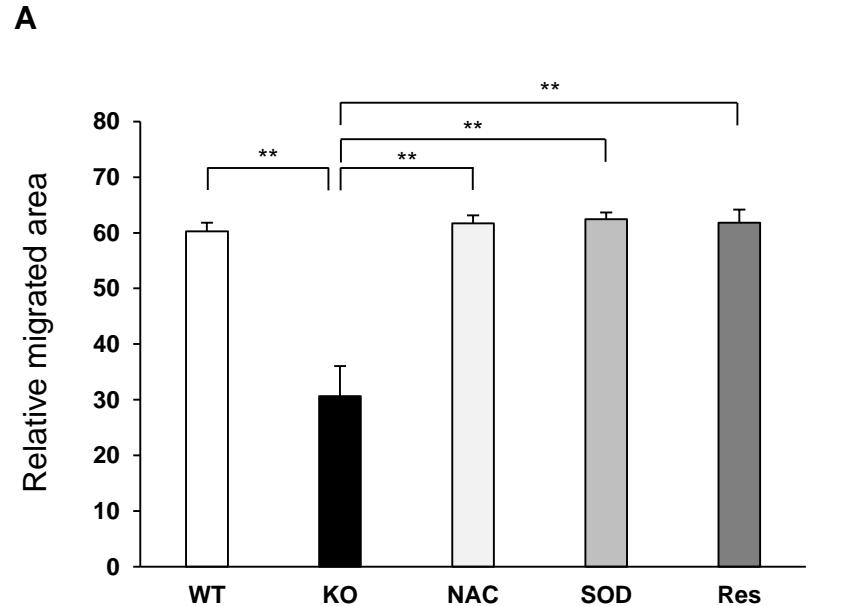
**Figure S3. Quantification of superoxide accumulation in scavenger and selective inhibitor treated cells.** Relative DHE signal intensities. NS and \*\*\* designate non-significant and  $p$ -value  $< 0.001$ , respectively.

**A****B****C**

**Figure S4. Measurement of signal intensities of RNS probe and 4-HNE. (A)** Relative fluorescence intensity of DAF-FM signal. **(B)** Relative fluorescence intensity of DHR123. **(C)** Relative fluorescence intensity of 4-HNE.



**Figure S5. Analysis of cell proliferation. (A)** Percent of BrdU incorporated cells. **(B)** Proportion of cell cycle. **(C)** Relative fluorescence intensity of gamma H2AX. \*, \*\*, \*\*\* indicate p-value under 0.05, 0.01, 0.001, respectively.



**Figure S6. Measurement of cell motility and angiogenesis.** (A) Measuring relative cell migration by wound healing assay. Migrated area was measured by using ImageJ as described in Materials and Methods. (B-D) Number of total tube length (B), segment (C), and branch (D) was measured as described in Materials and Methods. \*, \*\*, \*\*\* designate p-value <0.05, 0.01, 0.001, respectively.

**Table S1. Primer sequences used in this study.**

Primer Name	Sequence (5'-3')
Hprt F	AGTCCCAGCGTCGTGATTAG
Hprt R	GTATCCAACACTTCGAGAGGGTC
Sod1 F	GGAAGCATGGCGATGAAAGC
Sod1 R	AGGTCTCCAACATGCCTCTC
Sod2 F	CAATAATGTTGTGTCGGCGGG
Sod2 R	TCGGTGGCGTTGAGATTGTT
Sod3 F	GATGTTCTCCATGTCCCGG
Sod3 R	GGAAATGGGGTGGCGATAT
Gpx1 F	AGTTCGGACACCAGGAGAATG
Gpx1 R	GAGTGCAGCCAGTAATCACC
Catalase F	CGCTGAGAAGCCTAACGAAACG
Catalase R	CCAGCGTTGATTACAGGTGA
Nox1 F	AGCTTCTGAGTAGGTGTGCATATG
Nox1 R	TTGCAAATGAGCAGGTGCCCT
Nox2 F	AGTGAGCTTCCCTGTGCTT
Nox2 R	TGCCTTCGGTGATGTGCTTA
Nox4 F	GTTGGGCCTAGGATTGTGTT
Nox4 R	CGGCTACATGCACACCTGA
Glrx1 F	GGGGAGCTGATGACTCGGCTGAA
Glrx1 R	AGGGGCACTGGCCATCAG
Prdx1 F	TATCAGATCCCAAGCGCACCC
Prdx1 R	GCTGGACACACTTCACCATG
Gsta4 F	GATGCAAAAGGATGGACACCTG
Gsta4 R	TGGTTGCCAACGAGAAAAGC
Gpx4 F	CGTCTGAGCCGCTTAC
Gpx4 R	CCCATTACACAGATCTTGCT
Nos2 R	CTATGGCCGCTTGATGTGC
Nos2 R	TGGAGCACAGCCACATTGAT
Nos3 F	TGGGTTAGGGCTGTGCGG
Nos3 R	CAATAGCTGCTCAGTGGGTGA
GADD45 $\beta$ F	TTGCCTCTGGGTTCGTATC
GADD45 $\beta$ R	AGCCTCTGCATGCCTGATAC