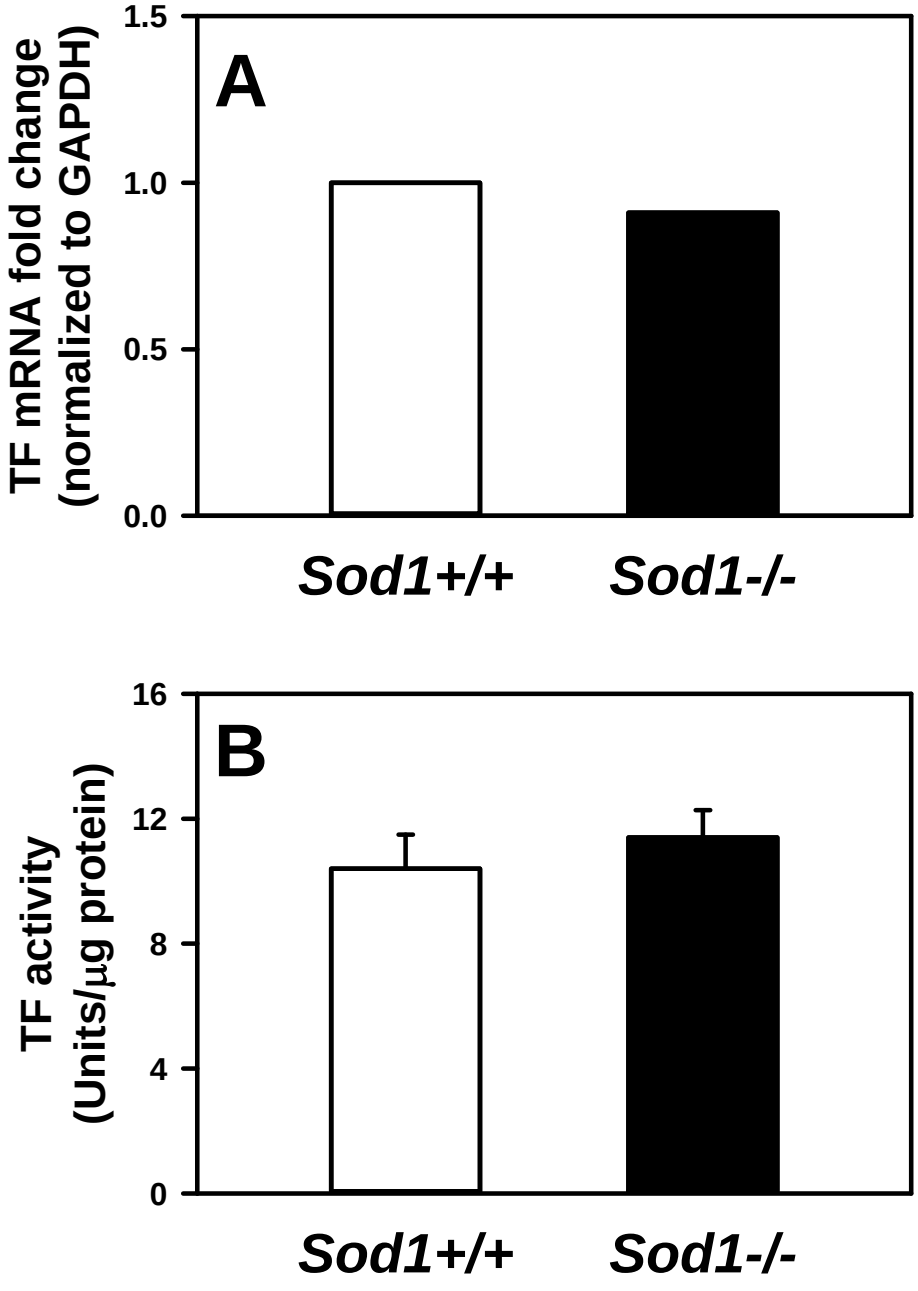
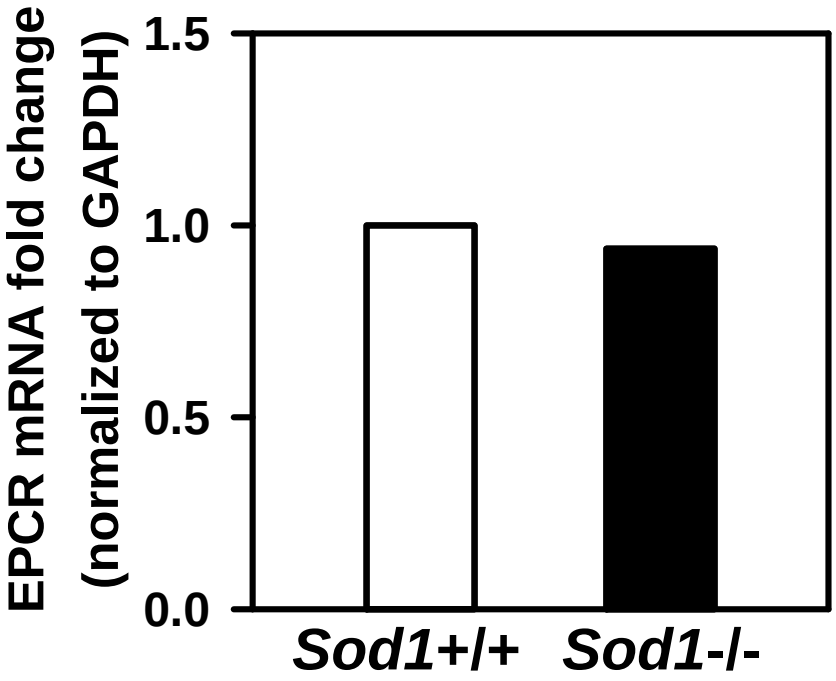
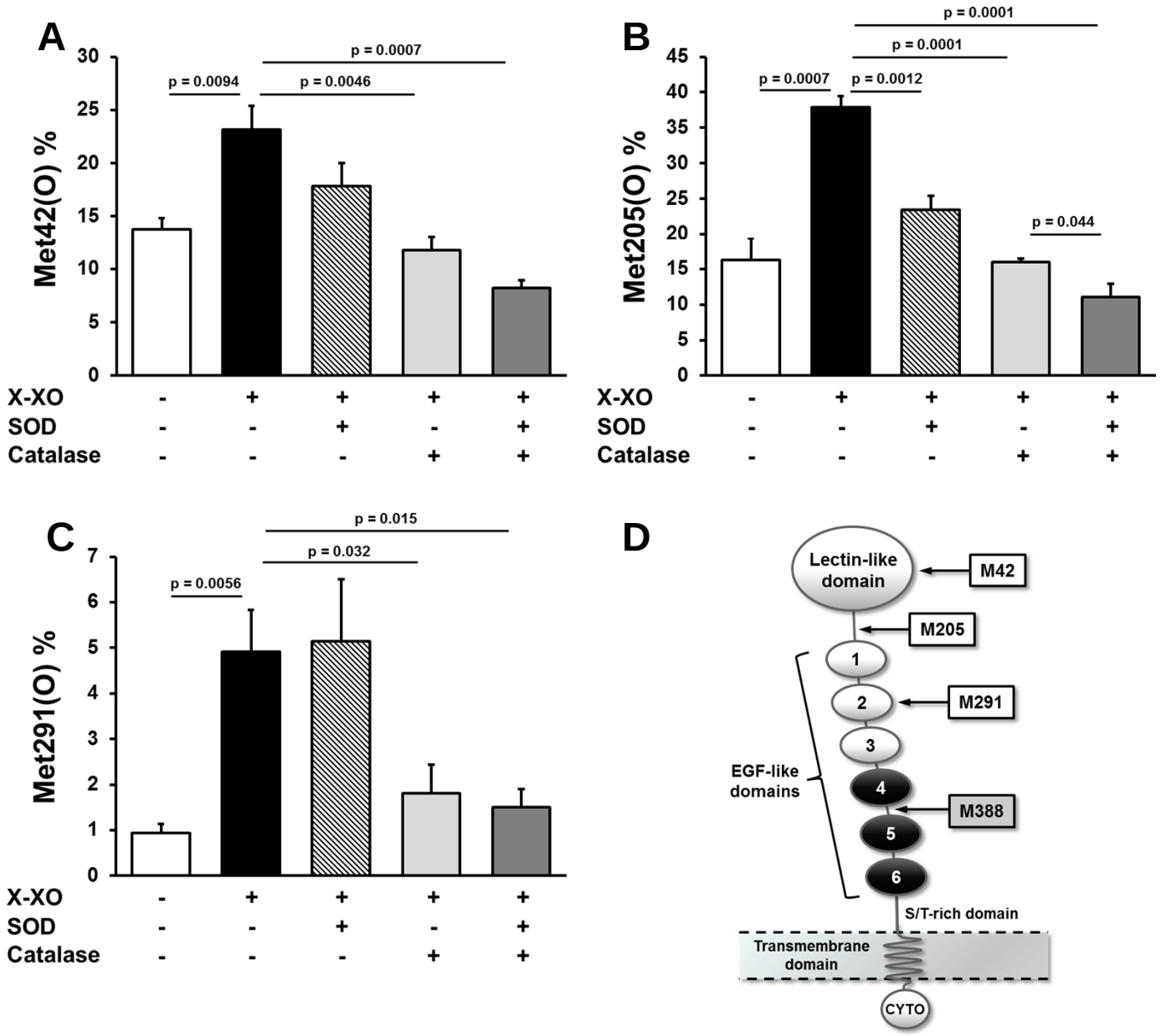


Supplemental Figure I. Deficiency of SOD1 does not influence TF mRNA expression or activity in mice. (A) TF mRNA levels in lung homogenates were determined by qRT-PCR and normalized to GAPDH, and data are displayed as fold-change relative to control (*Sod1*+/+ mice). Comparisons of normalized expression values (ΔCt) employed the conventional ΔΔCt fold change method. Ct values: 24.46 ± 0.09 for *Sod1*+/+ vs. 24.21 ± 0.07 for *Sod1-/-* mice. P = 0.3 vs. *Sod1*+/+ mice (n = 5 to 6 mice per group). **(B)** TF activity in lung homogenates was determined using a TF chromogenic activity assay. Data were quantified based on a TF standard curve. Values are mean ± SEM; P = 0.5 (n = 4 mice per group).



Supplemental Figure II. Deficiency of SOD1 does not alter mRNA levels of EPCR. EPCR mRNA levels in lung were determined by qRT-PCR. Levels of mRNA were normalized to GAPDH, and data are displayed as fold-change relative to control (*Sod1*+/+ mice). Comparisons of normalized expression values (ΔCt) employed the conventional ΔΔCt fold change method. The Ct values for EPCR were 24.34 ± 0.14 in *Sod1*+/+ vs. 24.16 ± 0.28 in *Sod1-/-* mice. P = 0.6 vs. *Sod1*+/+ mice (n = 5 to 6 mice per group).



Supplemental Figure III. Superoxide-induced oxidation of TM Met42, Met 205, and Met291. Recombinant human TM was incubated with or without 5 mU/ml xanthine oxidase and 1 mM hypoxanthine (X-XO) in the presence or absence of 50 U/ml PEG-SOD and/or 250 U/ml PEG-catalase. The content of **(A)** Met42(O), **(B)** Met205(O), and **(C)** Met291(O) was determined by nano-LC-MS/MS (n=4). *P < 0.05 vs. untreated control, † P < 0.05 vs. X-XO treatment, # P < 0.05 vs. PEG-catalase only**. (D)** Schematic representation of TM domain structure. The extracellular portion of TM contains a lectin-like domain, six epidermal growth factor (EGF)-like domains, and a serine/threonine (S/T)-rich domain. The region of TM involved in thrombin binding and protein C activation are EGF-like domains 4, 5, and 6. The location of the four extracellular methionine residues are indicated (arrows) with the redox active regulatory methionine 388 (M388) highlighted. TM also contains a transmembrane domain and a cytoplasmic tail (CYTO).