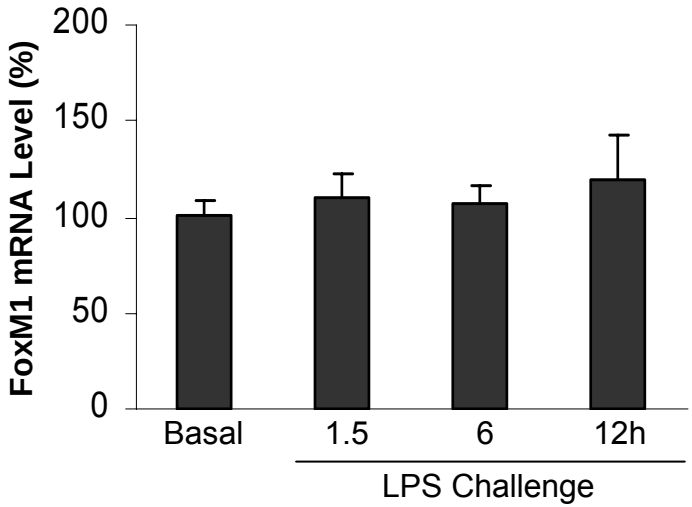
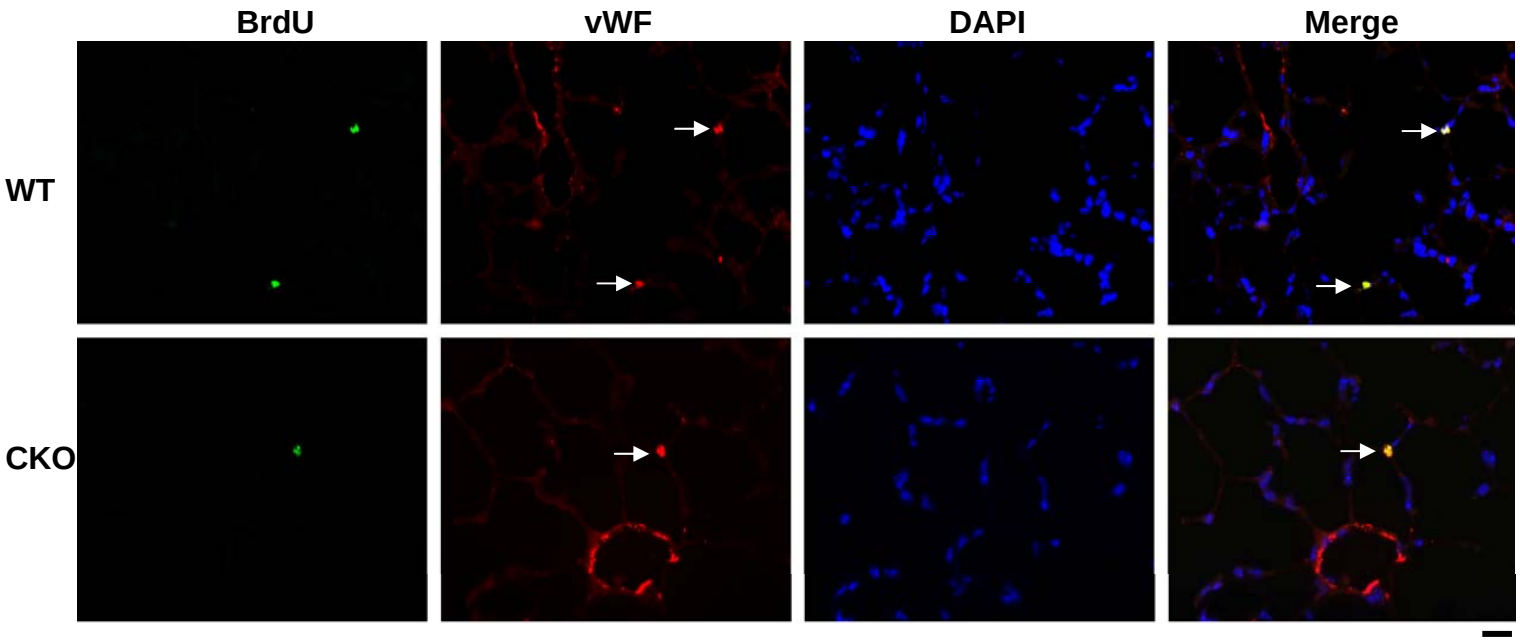
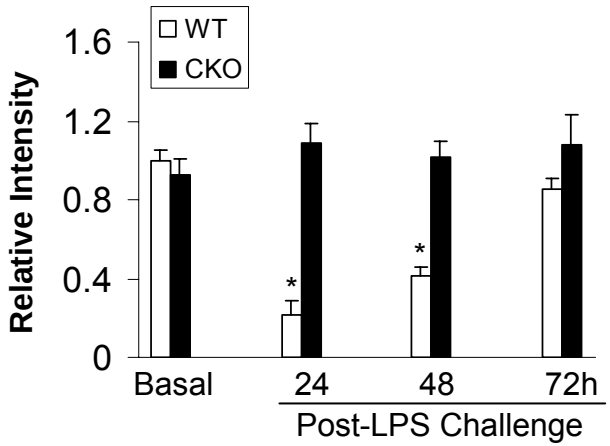



**Supplemental Figure 1**




**Supplemental Figure 2**




**Supplemental Figure 3**

**Supplemental Figure 1. Quantitative analysis of FoxM1 mRNA expression in lungs following LPS challenge.** Lungs were collected at the indicated time points following LPS challenge (5 mg/kg BW) and RNA was isolated for QRT-PCR. FoxM1 mRNA levels were normalized to cyclophilin. Data are expressed as mean ± 1SD (n=3/group). There is no induction of FoxM1 expression at the earlier time points following LPS challenge.

**Supplemental Figure 2. Representative micrographs of immunostaining.** Cryosections of lungs were stained with both anti-BrdU and anti-vWF to identify proliferating endothelial cells. Nuclei were counterstained with DAPI. Arrows indicate $BrdU^{+}vWF^{+}$ cells. Scale bar, 25 μm.

**Supplemental Figure 3. Graphic representation of $p27^{Kip1}$ expression in WT and *FoxM1* CKO lungs.** Total protein (50 μg) from mouse lungs collected at basal or indicated time points following LPS challenge (5mg/kg BW) was loaded/lane, the gel was electrophoresed and proteins were transferred to PVDF, and probed with monoclonal antibody against $p27^{Kip1}$. The same membrane was re-probed with a rabbit polyclonal antibody against β-actin as a loading control. The experiment was repeated three times. The intensity of each band was quantified using NIH Image software. Data are expressed as mean ± 1SD. *, $P<0.05$ vs. WT basal or CKO.