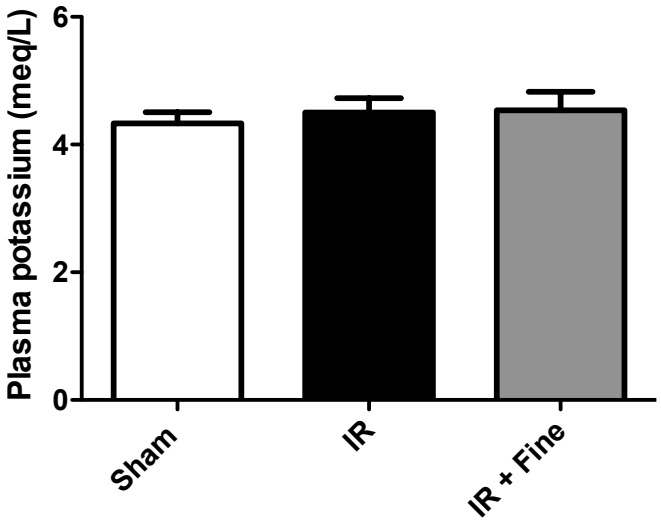
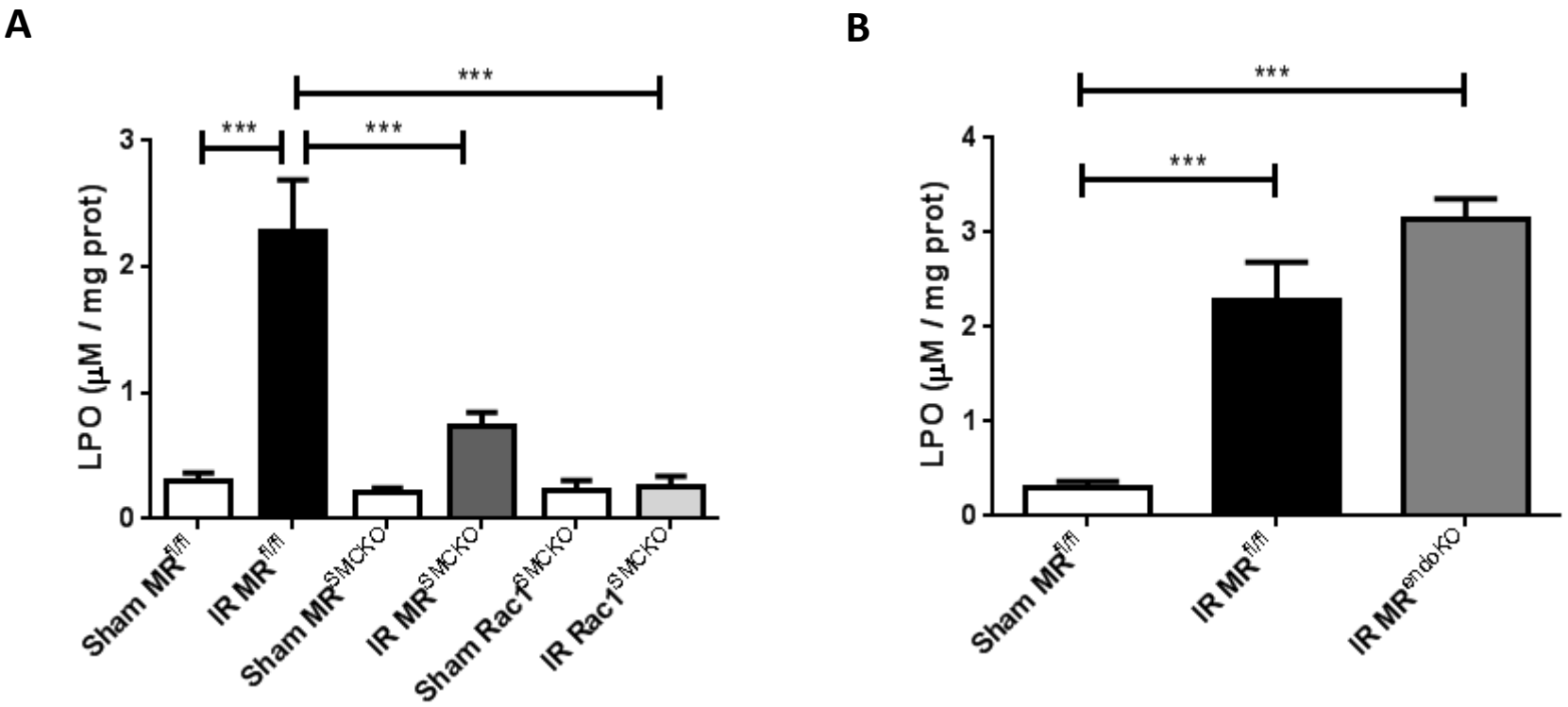
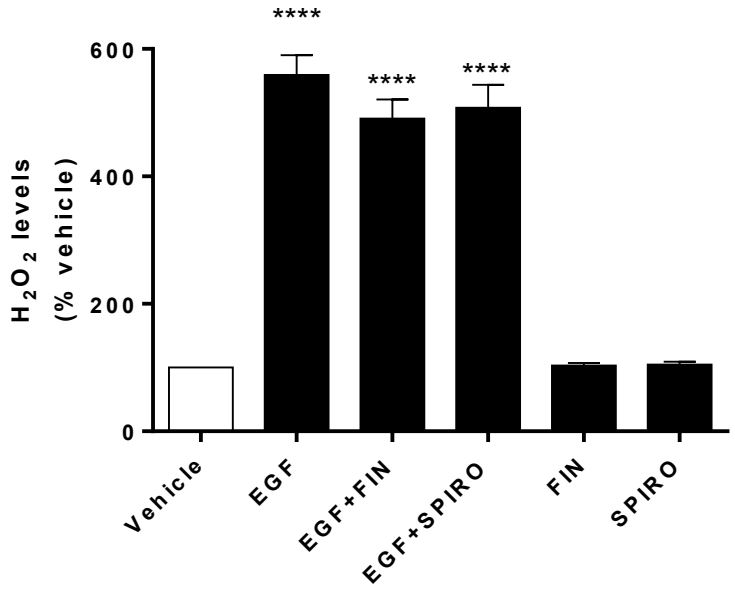


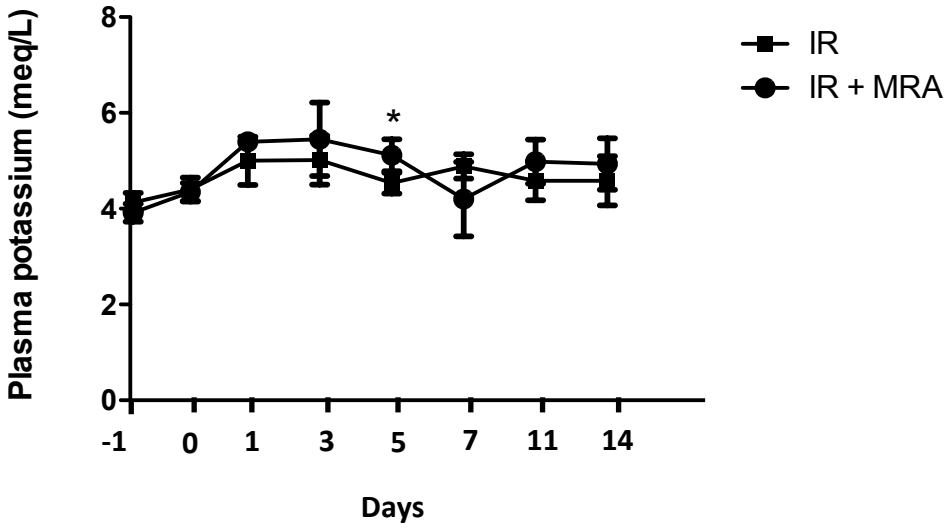
Sup. Fig. 1. Finerenone or IR has no effect on plasma potassium concentration in mice. Plasma potassium levels were determined with a flame photometer. *n = 8* per group.



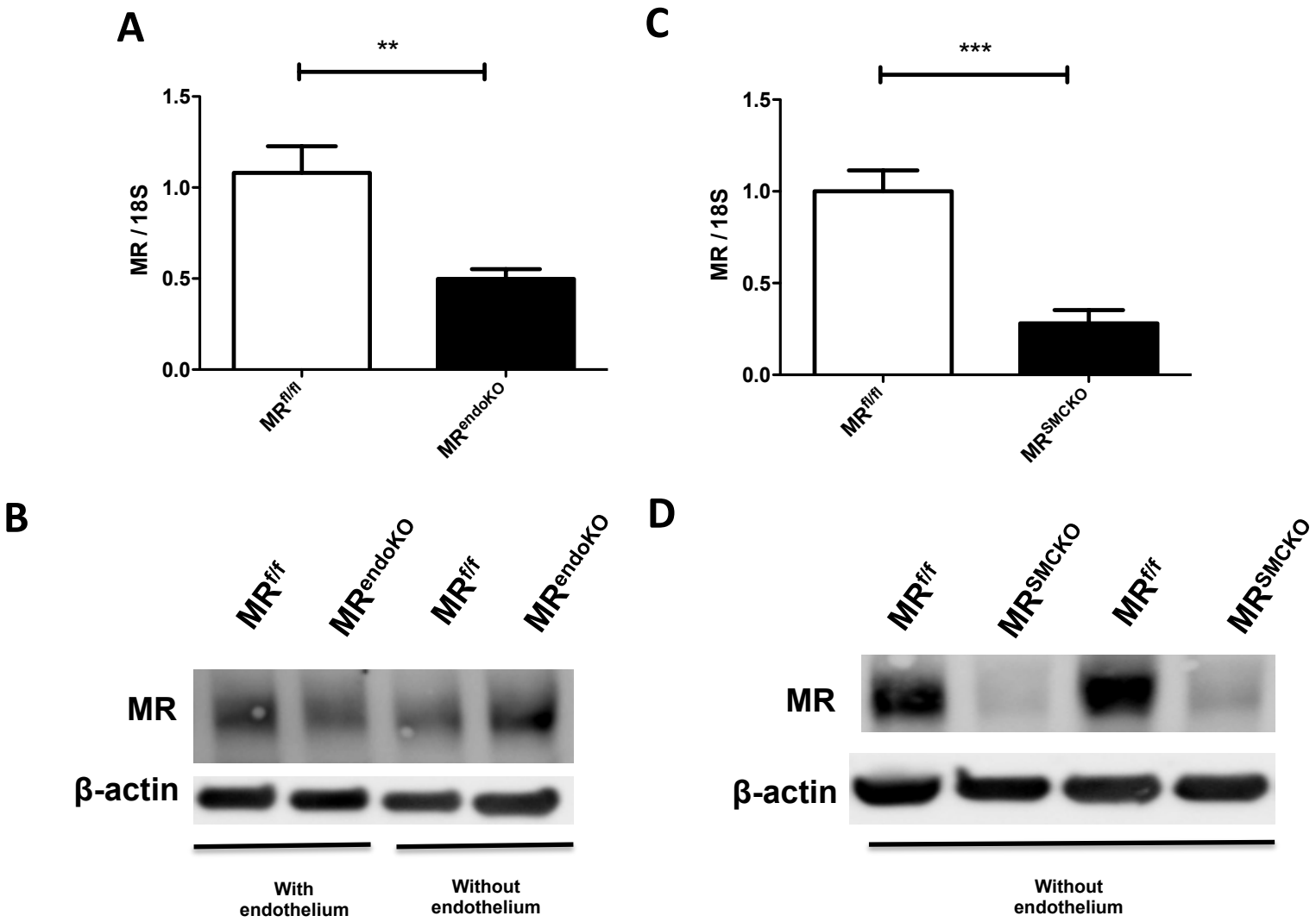
Sup. Fig. 2. Lipid peroxide (LPO) quantification. (A) MR and Rac1 KO in smooth muscle cells prevented LPO increase induced by IR. (B) MR deletion in endothelial cells did not prevent lipid peroxidation induced by IR. LPO levels were quantified in kidney lysates. The data were normalized against the protein concentration of the tissue lysate. *n = 6* per group. Two-way ANOVA was performed. ***p*<0.001 ****p*<0.0001.



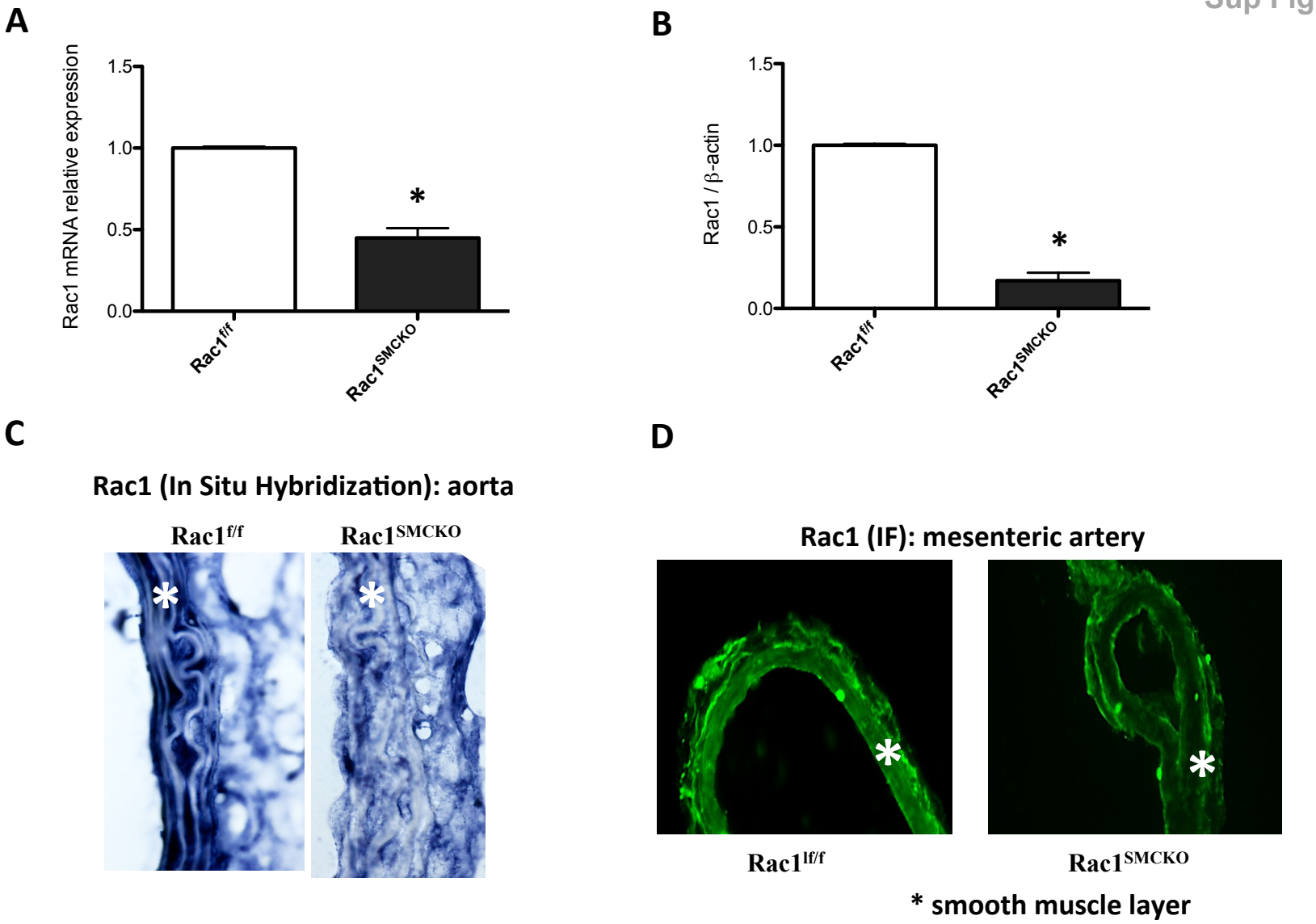
Sup. Fig. 3. Hydrogen peroxide production was quantified in the cell culture medium of rat primary SMC in the presence of EGF, EGF + finerenone or spironolactone and finerenone or spironolactone alone). *n = 5* per group. One-way ANOVA analysis was performed. ****$p<0.0001$.



Sup. Fig. 4. Plasma potassium levels in pigs from the IR and IR + canrenoate groups. *n = 6* per group. Student's *t-test* was performed for each point. **p*<0.01 vs. IR.



Sup. Fig. 5. Characterization of MR-knockout models. We determined mRNA levels for the MR in aortas from (A) MR^{endoKO} mice and (C) MR^{SMCKO} mice. *n = 5* per group. (B) The western blot analysis shows a reduction in MR expression in whole aorta from MR^{endoKO} mice, effect not observed when the endothelium is removed, and (D) a large reduction of MR in aortas from MR^{SMCKO} mice in which the endothelium was removed. Student's *t-test* was performed. $^{**}p<0.001$ $^{***}p<0.0001$.



Sup. Fig. 6. Characterization of Rac1-knockout model. We performed (A) mRNA (n=8) and (B) Western blot (n=4) quantification in aorta, in situ hybridization in aorta (C) and immunofluorescence in mesenteric arteries from Rac1^{SMCKO} mice and control littermates (D). *p<0.05.

Primers for RT-PCR			
Gene	Forward 5'--3'	Reverse 5'--3'	
Mineralocorticoid receptor	CCA GAA GAG GGG ACC ACA TA	GGA ATT GTC GTA GCC TGC AT	
NGAL	GGA CCA GGG CTG TCG CTA CT	GGT GGC CAC TTG CAC ATT GT	
Kim-1	TGT CGA GTG GAG ATT CCT GGA TGG T	GGT CTT CCT GTA GCT GTG GGC C	
Primers for genotyping			
	Forward (1) 5'--3'	Forward (2) 5'--3'	Reverse 5'--3'
Rac 1 KO	CAGAGCTCGAATCCAGAAACTAGTA	GATGCTTCTAGGGGTGAGCC	**TCCAATCTGTGCTGCCCATC**
	Forward 5'--3'	Reverse (1) 5'--3'	Reverse (2) 5'--3'
MR Flox	CTG GAG ATC TGA ACT CCA GGC T	CCT AGA GTT CCT GAG CTG CTG A	TAG AAA CAC TTC GTA AAG TAG AGC T
Cre	GCA CAT GTT CAG CCA TCG CCA GGC G	GCA TAA CCA GTG AAA CAG CAT TGC TG	

Sup. Table 1. Primers sequence.