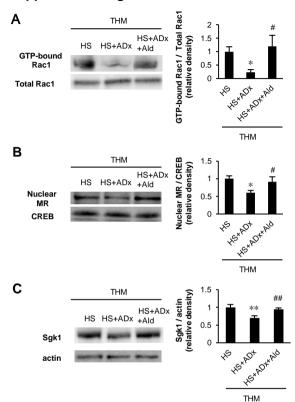
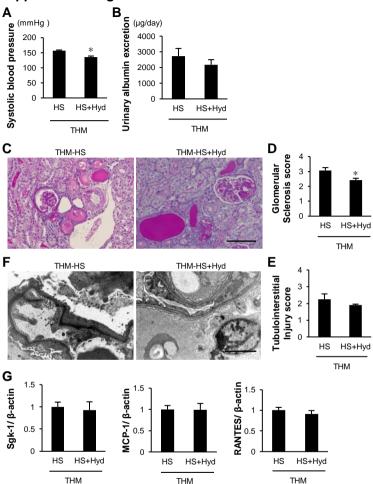


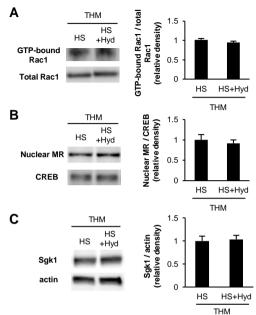
Supplemental Figure 1. Basal renin-angiotensin-aldosterone system components of THM are highly enhanced compared with C57. (A) Plasma renin activity. (B) Plasma angiotensin II. (C) Plasma aldosterone concentration. THM on normal salt diet (n=6) and C57 on normal salt diet (n=6). (D) Plasma aldosterone concentration in C57 (n=12), THM-LS (n=12), THM-HS (n=12), THM-HS+Epl (n=6) and THM-HS+EHT (n=6). Data are expressed as mean ± SEM; * P < 0.05, ** P < 0.01 versus THM-HS.



Supplemental Figure 2. Renal Rac1 and MR activation were suppressed by adrenalectomy in THM-HS. (A) GTP-bound active Rac1 and total Rac1 expressions in the kidneys of THM-HS (n=7), THM-HS+ADx (n=6) and THM-HS+ADx+AId (n=5). (B) Renal MR expressions in the nuclear fraction. CREB was used as a loading control. (C) Renal Sgk1 expressions. Actin was used as a loading reference. Bar graphs show the results of densitometric analysis. Data are expressed as mean \pm SEM; * P < 0.05, ** P < 0.01 versus THM-HS; # P < 0.05, ## P < 0.01 versus THM-HS+ADx.



Supplmental Figure 3. Hydralazine effectively lowered blood pressure but did not suppress salt-induced kidney injury and MR activation in THM-HS. (A) Systolic blood pressure measured by the tail-cuff method in THM-HS (n = 6), THM-HS on 1% NaCl drinking water with hydralazine (THM-HS+Hyd) (n = 5). (B) Urinary albumin excretion. (C) Representative micrographs of PAS—stained kidney sections. Scale bar: 100 µm. (D) Histological analysis of glomerulosclerosis and (E) tubulointerstitial injury by semiquantitative morphometric evaluation. (F) Transmission electron micrographs of podocyte ultrastructure in the kidneys. Scale bar: 1 µm. (G) Gene expression was determined using quantitative real-time RT-PCR. The expression levels were normalized to those of β -actin and expressed relative to THM-HS. Data are expressed as mean \pm SEM;* P < 0.05 versus THM-HS.



Supplemental Figure 4. Hydralazine (Hyd) did not suppress the enhanced Rac1 and MR signaling in the kidneys of salt-loaded THM. (A) GTP-bound active Rac1 and total Rac1 expressions in the kidneys of THM-HS (n=6) and THM-HS+Hyd (n=5). The bar graph represents densitometric analysis of active Rac1. (B) MR expressions in the nuclear fraction of THM-HS and THM-HS+Hyd. CREB was used as a loading control. The bar graph represents densitometric analysis of nuclear MR. (C) Sgk1 expressions in the kidneys of THM-HS and THM-HS+Hyd. Actin was used as a loading reference. The bar graph represents densitometric analysis of Sgk1 expression. Data are expressed as mean \pm SEM; * P < 0.05 versus THM-HS.