

Nrf2 activation protects against lithium-induced nephrogenic diabetes insipidus

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Supplemental Figures:

Suppl. Fig. 1: Effect of 7 consecutive days of LiCl administration through diet on weight, food intake and kidney gene and protein expression. (A) Animal weight as a % of initial weight and (B) 24hr body weight-normalized food intake over 7 days. (●) control chow and (○) 0.17 % LiCl diet. Results plotted as mean ± standard error of 4 (Control) or 6 (LiCl) animals per group and statistical significance assessed by two-way ANOVA with Dunnet correction for multiple comparisons, * denotes p<0.05. C) Full blot image for renal AQP2 expression, re-shown uncropped from Fig. 1C. (D) Nrf2 gene target expression evaluated by RT-PCR; control and LiCl not statistically different by t-test. P<0.05 was considered to be statistically significant.

Suppl. Fig. 2: Li induces NDI and not primary polydipsia. Mice receiving LiCl diet on baseline-clamped water intake develop significant volume depletion with hypernatremia, polycythemia. (A) Experimental design. Water and food intake were measured for 4 days for each animal; beginning at day 4, mice were randomized to control chow or LiCl chow. Mice receiving LiCl were provided their pre-determined baseline water amount daily in small sipper tube. (B) Weight (% Day 0), (C) food intake (g/day), and (D) water intake (mL/24hr). Dark area between dashed lines shows *ad libitum* water intake from LiCl treated animals in Fig. 1. Plasma Na⁺, K⁺, Cl⁻, Hematocrit, spot urine osmolality, plasma iCa⁺⁺, tCO₂, glucose, BUN, anion gap (E-N). Results (B-D) plotted as mean ± standard error of 6 animals per group and statistical significance assessed by two-way ANOVA with Dunnet correction for multiple comparisons. Results (E-N) plotted as mean ± standard error of 6 animals per group, statistical significance assessed by t-test, with p<0.05 considered significant.

Suppl. Fig. 3: Li does not induce renal NQO1 expression. WT (C57BL6 albino) mice fed control chow or 0.17% LiCl chow followed by IF for NQO1, MUC1, actin, DAPI. Two panels of WT-control chow are re-shown from Fig. 1F and Fig. 5A-B, along with additional representative images.

Suppl. Fig. 4: Basal phenotype of Nrf2^{-/-} mice. (A) renal NQO1 expression and quantification. (B) 24-hour metabolic cage urine collection normalized to animal body weight. Statistical analysis by t-test with p<0.05 considered significant.

Suppl. Fig. 5: Keap1 hypomorphism does not induce NDI. (A) Kidney:body mass ratio of WT and Keap1^{hm} mice. (B) Spot urine analysis reveals mild baseline hyposthenuria in Keap1^{hm}. 12-hour water deprivation reveals normal urine concentrating function (C) and appropriate elevation

in plasma renin activity (D). Results are plotted as mean \pm SEM. Statistical analysis by t-test (A-B) or one-way ANOVA with Tukey correction for multiple comparisons (C-D), $p < 0.05$ was considered significant.

Suppl. Fig. 6: (A) Plasma renin activity and (B) blood urea nitrogen (BUN) in WT and Keap1^{hm} mice after 7d Li or chow. Statistical analysis by one-way ANOVA with Tukey correction for multiple comparisons with $p < 0.05$ considered significant.

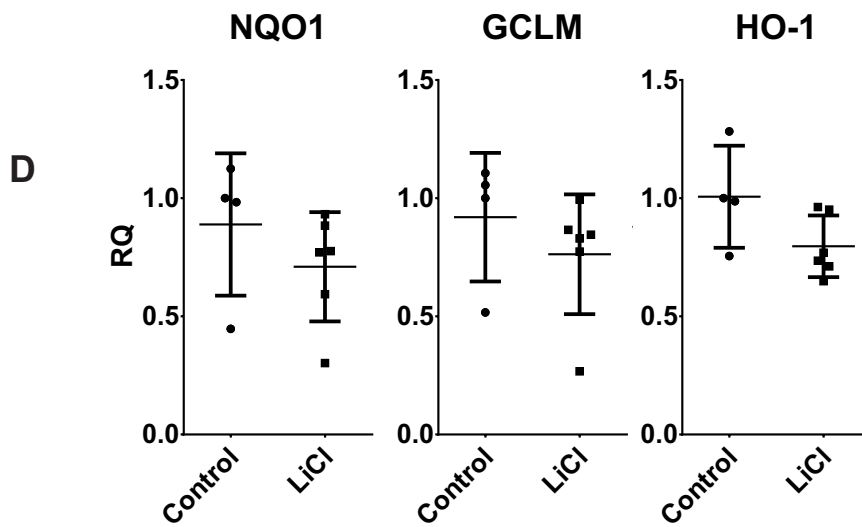
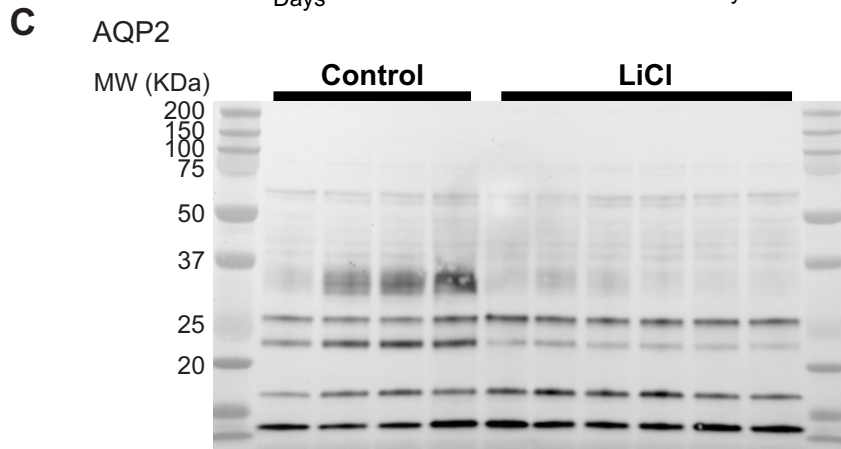
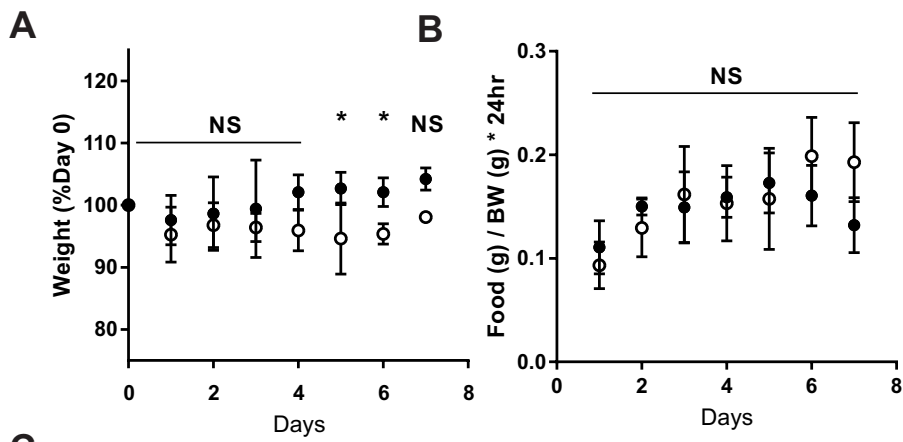
Suppl. Fig. 7: (A-B) Full blot images including molecular weight markers for Fig. 3J. (C) AQP1 expression and quantitation, including full immunoblot with molecular weight markers. Results plotted as mean \pm SEM. Statistical analysis by one-way ANOVA with Tukey correction for multiple comparisons, with $p < 0.05$ considered significant.

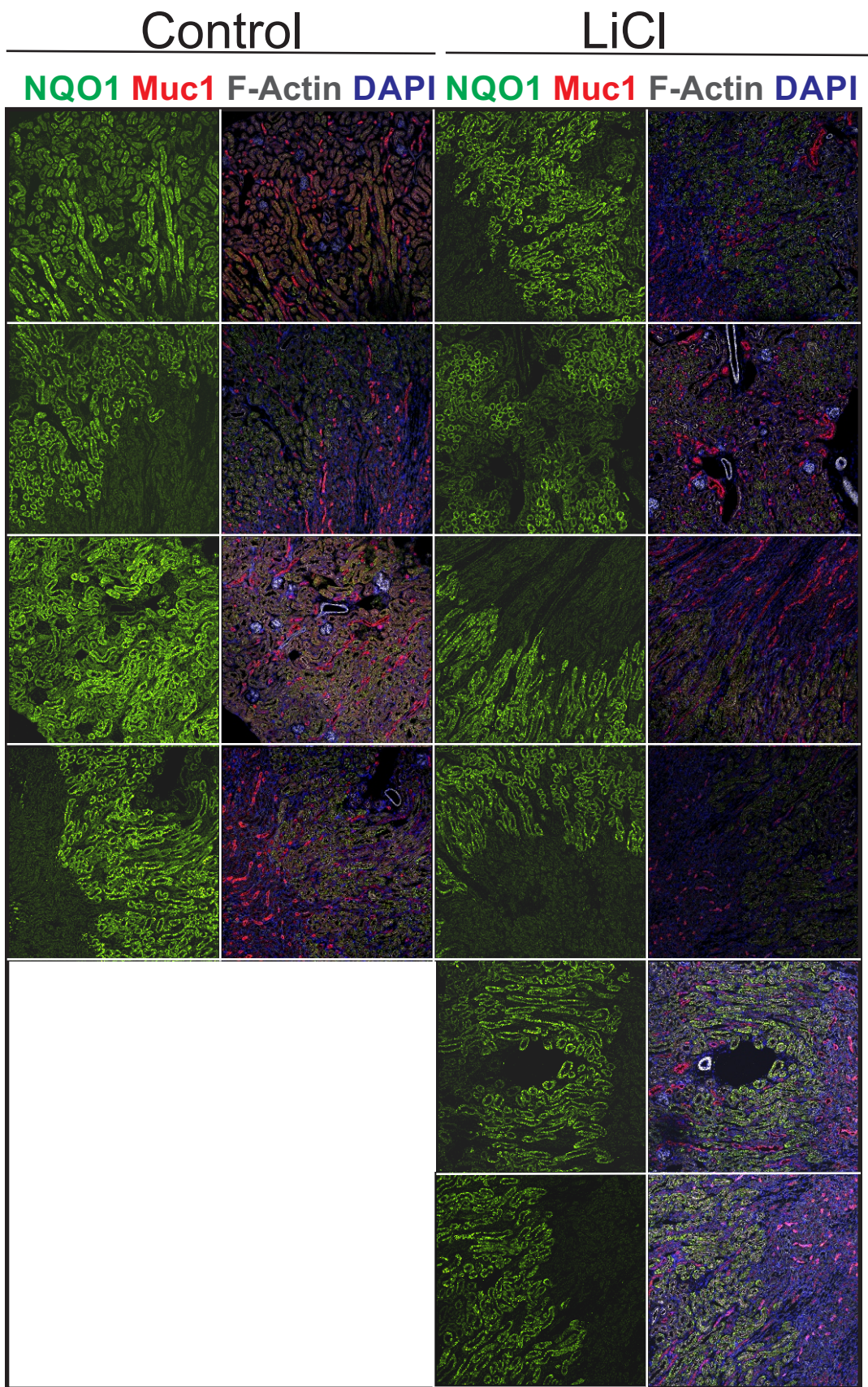
Suppl. Fig. 8: Western blot images. (A-G) Full blots including molecular weight markers for Fig. 4A. (H) Immunoblot and quantitative densitometry of renal ATP6V1B1 protein abundance. Statistical analysis by one-way ANOVA with Tukey correction for multiple comparisons, with $p < 0.05$ considered significant.

Suppl. Fig. 9: Basal ion transporter expression of Keap1^{hm} mice. (A) Immunoblotting and densitometric quantitation of tNCC, NKCC2, and CA-II abundance in Li-naïve WT and Keap1^{hm} mice. Statistical analysis by t-test. (B) tNCC and activating phosphorylation (pNCC, T53) in WT and Keap1^{hm} mice after low sodium (LS) or high sodium (HS) diet.

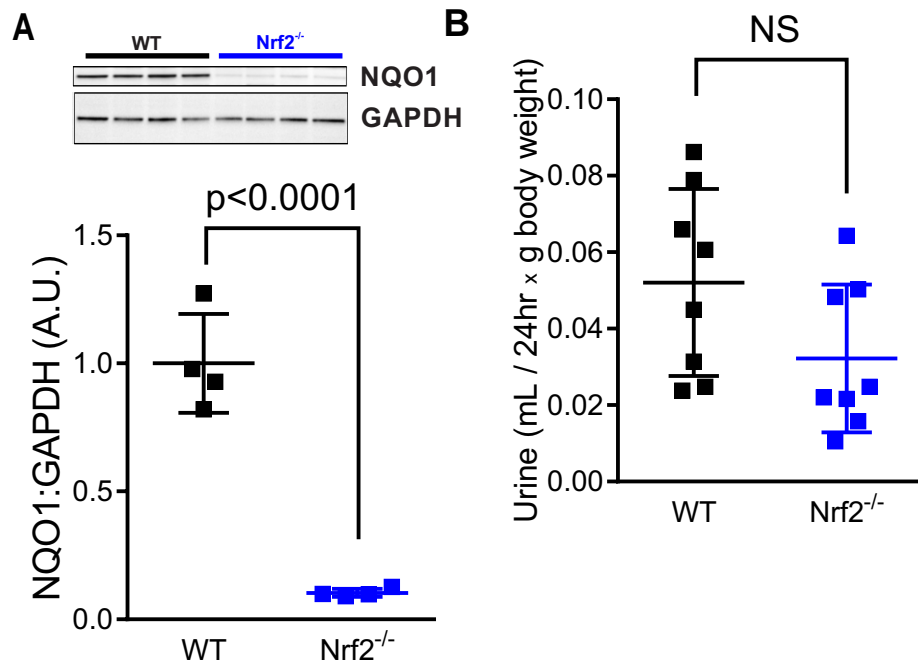
Suppl. Fig. 10: Nrf2 effects on COX expression and PG biosynthesis in Li-naïve mice. (A) Immunoblotting for renal COX-1 and COX-2 expression and corresponding densitometry (B) in Li-naïve WT and Keap1^{hm} mice. (C) COX-1 and COX-2 mRNA transcript abundance is reduced in Keap1^{hm} (D) Immunohistochemistry for COX-2 in kidney sections from WT and Keap1^{hm} mice. (E-F) Immunoblotting and densitometry for COX-1 and COX-2 in kidneys of WT and Nrf2^{-/-} mice. (G) Decreased levels of renal 6-keto-PGF_{1 α} , the stable metabolite of prostacyclin (PGI₂) as assessed by stable isotope-dilution HPLC-MS/MS. Statistical analysis by t-test, $p < 0.05$ considered significant.

Suppl. Fig. 11: Expression of renal ion transporters and COX isoforms in CDDO-Me treated mice. Representative immunoblots and quantitative densitometry; statistical analysis by one-way ANOVA with Tukey correction for multiple comparisons, $p < 0.05$ considered significant.

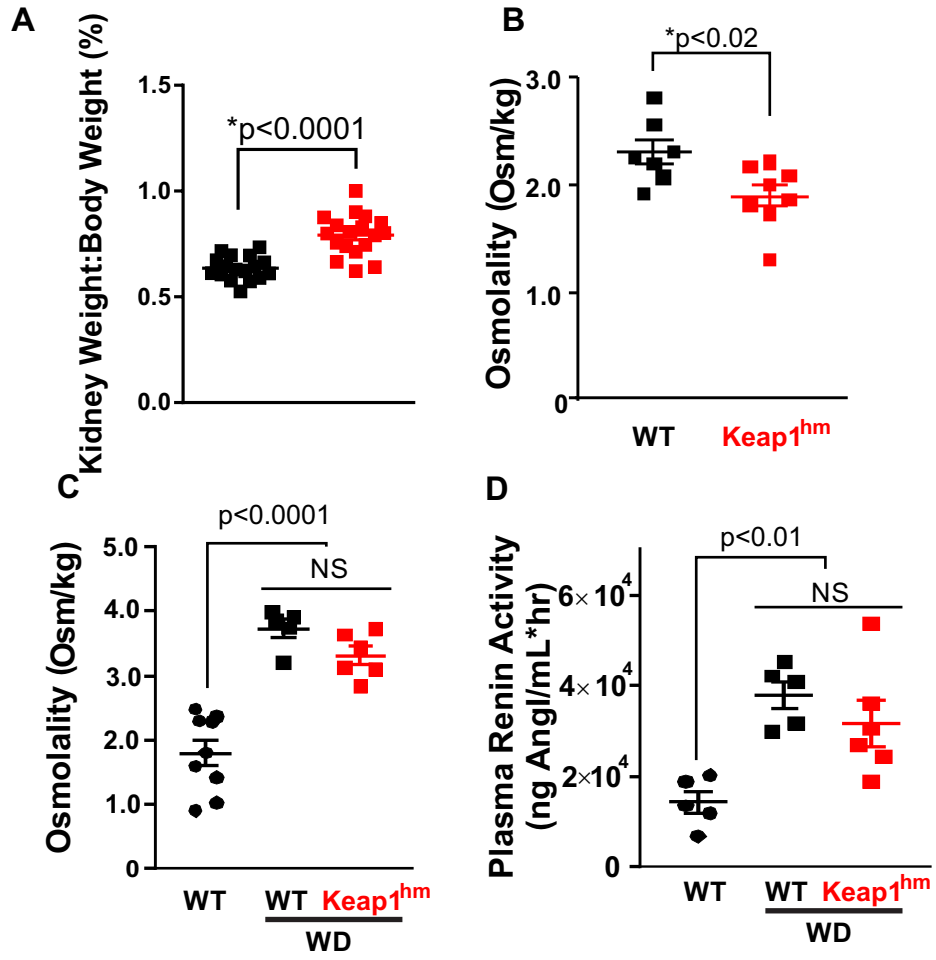




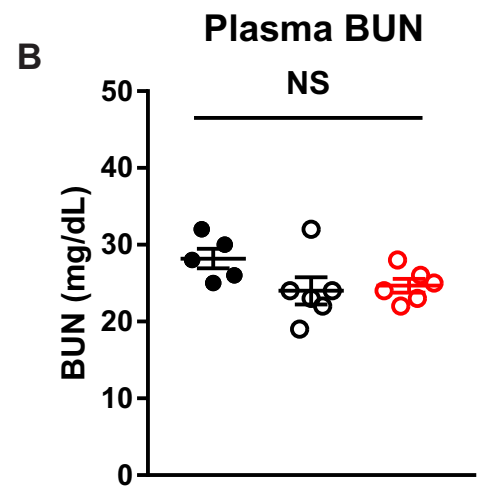
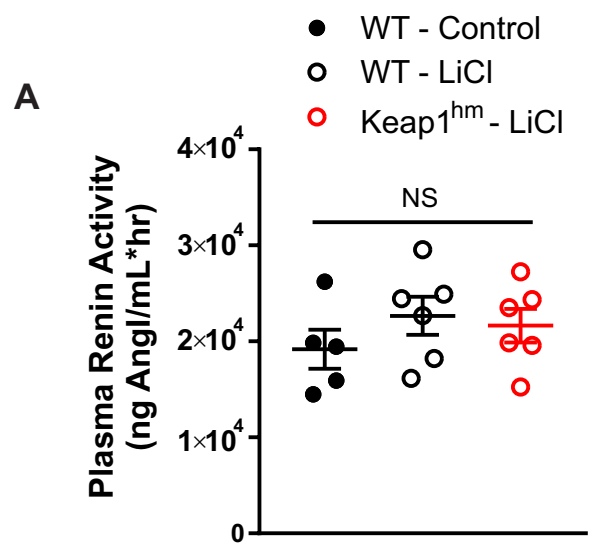
Suppl. Fig. 3



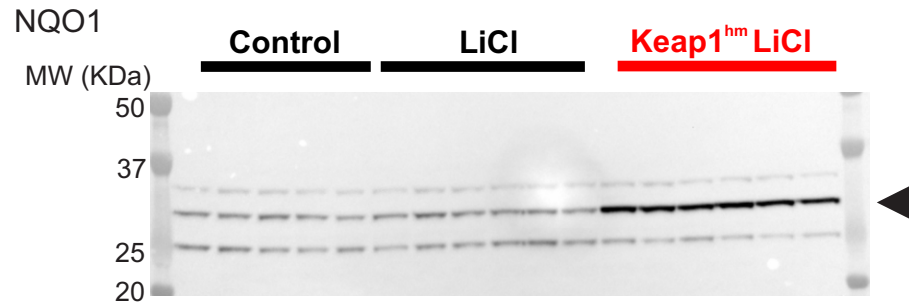
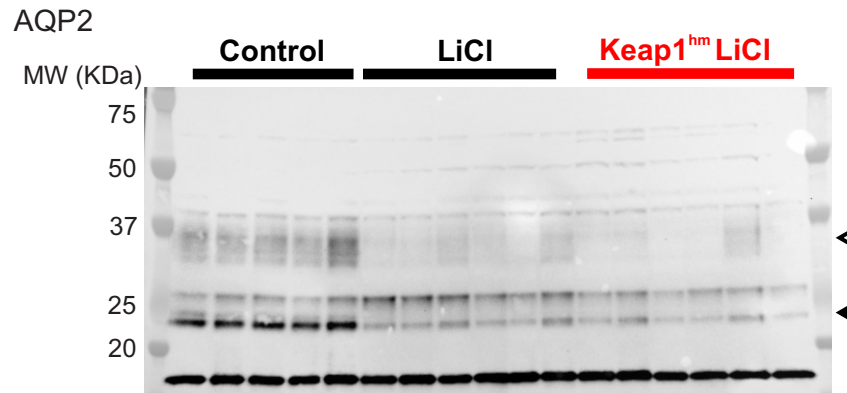
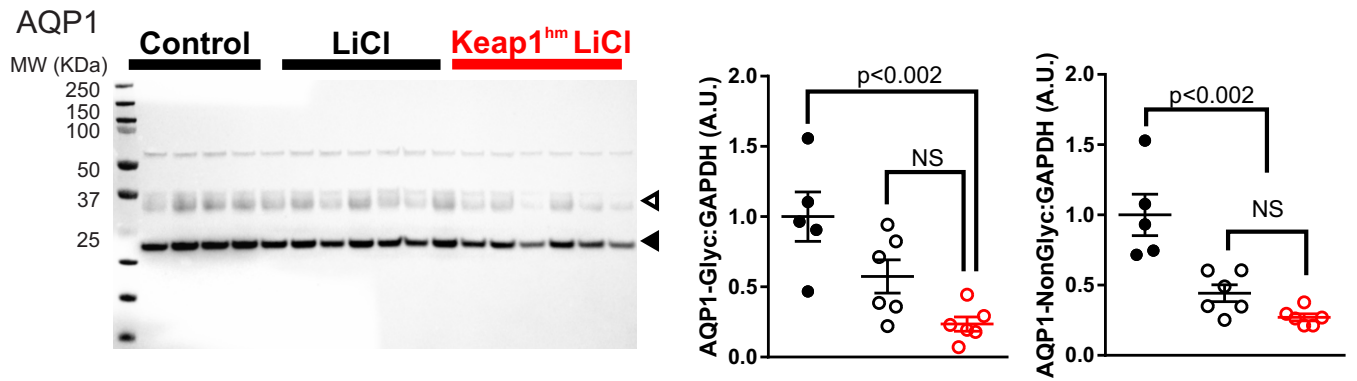
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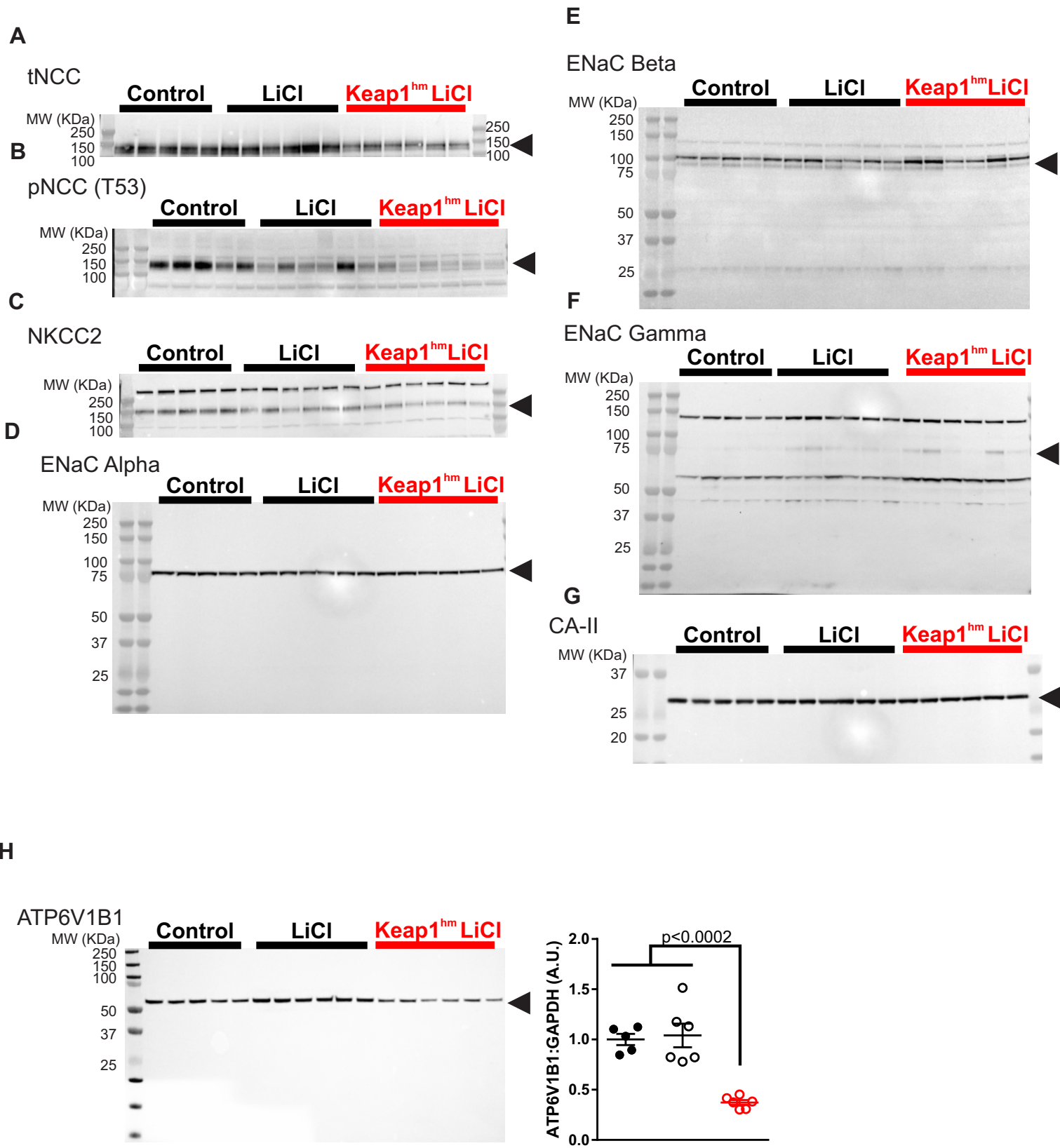


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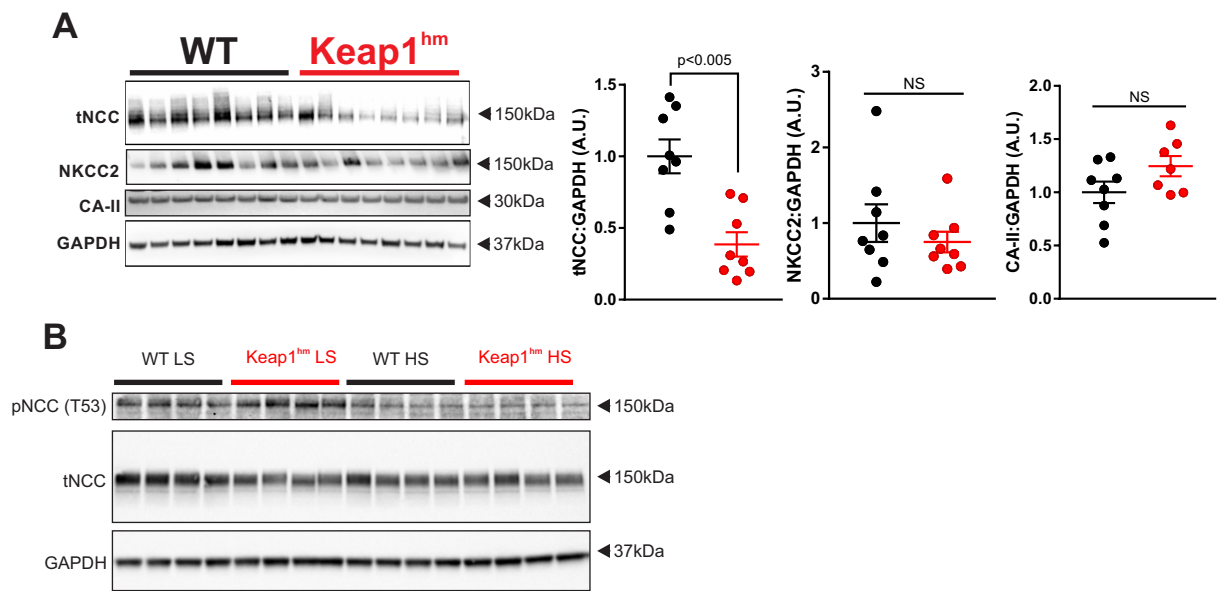


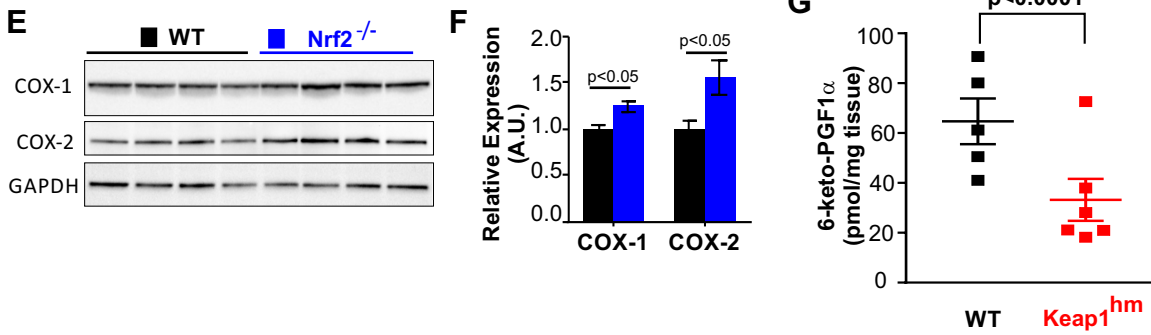
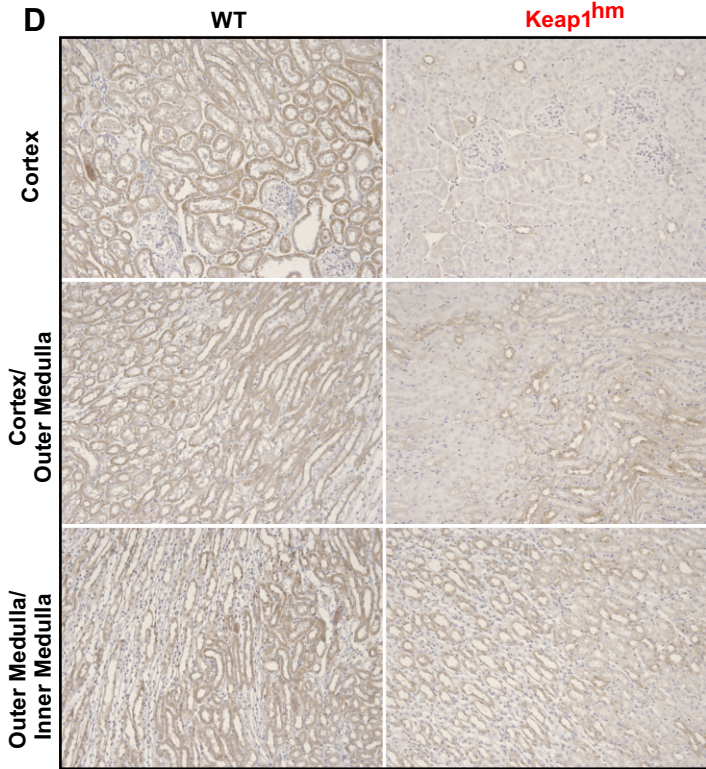
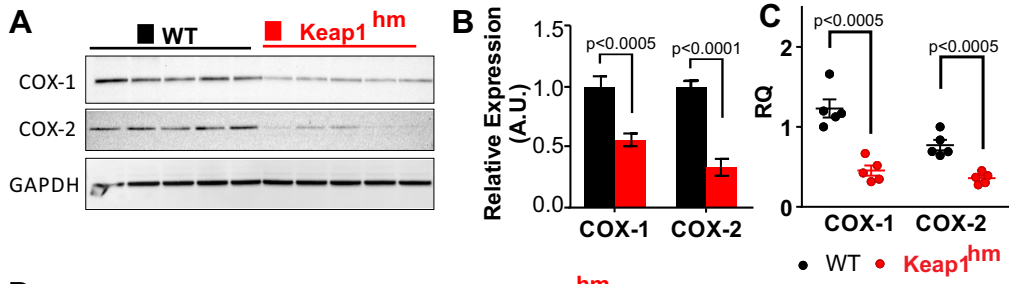
Suppl. Fig. 6

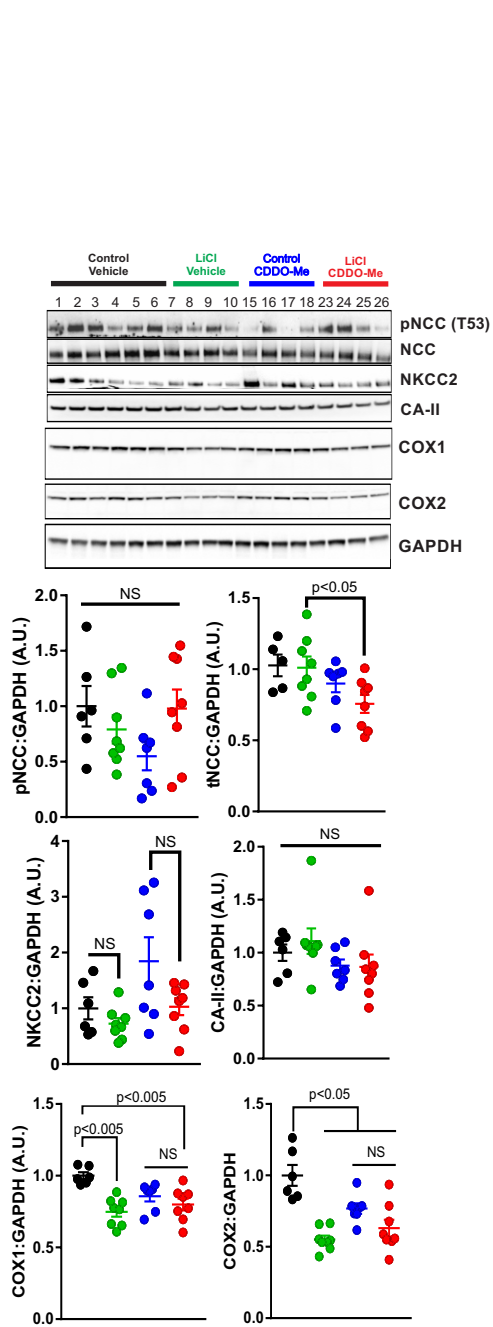
A**B****C**



Suppl. Fig. 8







Suppl. Fig. 11