SUPPLEMENTARY FIGURE LEGENDS

Suppl. Figure 1. Real-time PCR analysis of the changes in expression of IFN-γ (**A**), iNOS (**B**) , and endothelin 1 (**C**; ET-1) in the small intestine and colon of NHE3-deficient mice. Gene expression was normalized to TATA box–binding protein as an internal control using the ΔΔCt method, with expression values in WT mice used as a calibrator. (**D**) Analysis of NO concentration in the ileal contents of WT and $NHE3^{-/-}$ mice. Asterisks indicate significant differences between WT and $NHE3^{-/-}$ mice (T-test, $p<0.05$).

Suppl. Figure 2. *Expression and activation of Stat1 in the small intestinal mucosa of* $NHE3^{-/-}$ *mice*. (**A**) Representative Western blot of pY701-Stat1, total Stat1, and GAPDH. (**B**) Summary of results of total Stat1 expression (Stat1:GAPDH ratio) and (**C**) Stat1 activation (pY701-Stat1:total Stat1 ratio). Asterisks indicate significant differences between WT and $NHE3^{-/-}$ mice (T-test, $p<0.05$; n=4)

Suppl. Figure 3. **(A)** Cleaved caspase-3 immunostaining in the small intestinal mucosa of WT and $NHE3^{-/-}$ mice. Arrows point to typical apoptotic cells stained with the red chromogen (3-amino-9-ethylcarbazole). (**B**) Graph summary of caspase-3 positive cell count per field of vision calculated in a blinded fashion. No statistically significant differences were observed.

Suppl. Figure 4. *Ki67 staining of proliferating cells in the the small intestinal mucosa of WT and NHE3*$^{-/-}$ *mice.* With the exception of increased number of Ki67-positive mononuclear cells infiltrating the lamina propria, no significant differences were observed for the epithelial cells.

Suppl. Figure 5. **(A)** Histogram depicting the number of genes/probe sets which expression was increased or reduced at $P<0.05$ in NHE3$^{-/-}$ mice relative to their wild-type littermates (Student t-test with Benjamini and Hochberg false discovery rate as multiple testing correction). Increasing stringency of analysis (2-10 fold change on X-axis) demonstrates the magnitude of change in small intestinal gene expression profile in NHE3$^{-/-}$ mice. **(B)** Gene ontology analysis using DAVID Functional Annotation Tool (http://david.abcc.ncifcrf.gov/) of the 1,256 non-duplicated and well annotated genes which indicated >2-fold change at $p<0.05$ (Student t-test with Benjamini and Hochberg false discovery rate as multiple testing correction). Genes categorized based on biological process were grouped and ranked (threshold of 5, $P<0.05$). Categories were sorted according to the EASE score, a modified Fisher exact P value.