

Supplemental Information

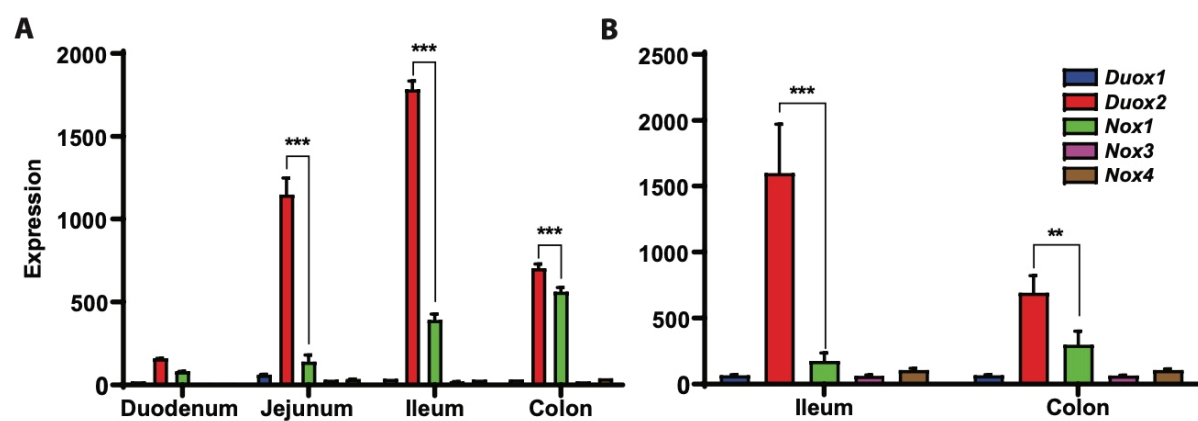


Figure S1: Expression of NOX family members along the mouse intestinal tract and isolated IECs. Expression data for non-fractionated tissue [1] and for isolated IECs [2] were retrieved from published microarray studies and analyzed for NOX family members. ** $p < 0.01$ and *** $p < 0.001$ FDR-corrected p values of moderated t test (for details see the original publications).

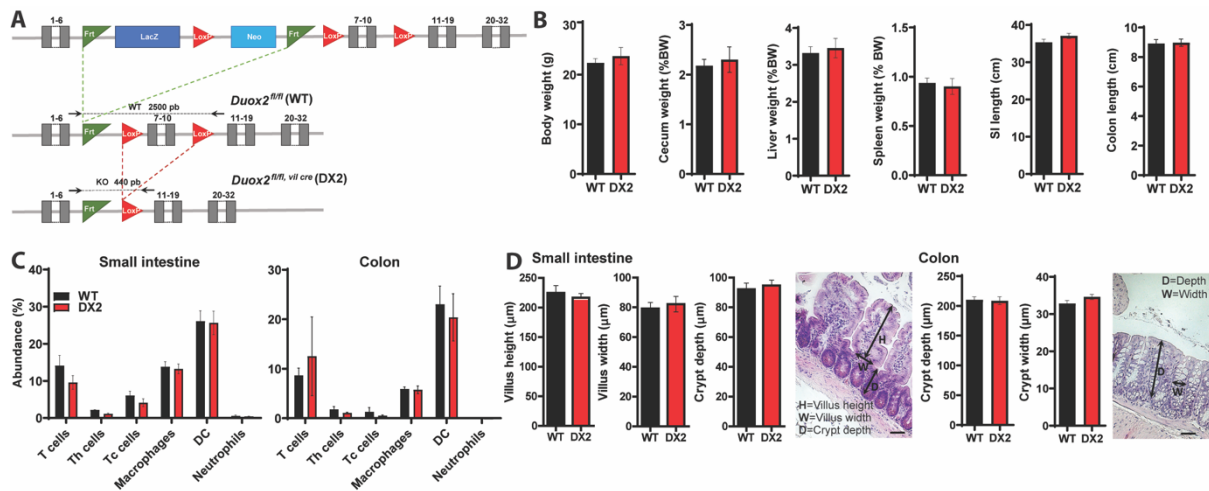


Figure S2: Phenotyping of unchallenged *Duox2*^{ΔIEC} mice. **A)** Strategy for generating *Duox2*^{ΔIEC} mice. IEC-specific DUOX2-deficient mice were generated by crossing *Duox2* floxed (*Duox2*^{fl/fl}) mice with Villin::CRE transgenic mice expressing CRE recombinase under the control of the IEC-specific *Villin1* promoter, resulting in specific conditional deletion of *Duox2* exons 7-10 in IECs and a non-functional DUOX2 protein due to a premature stop codon. **B)** Body and organ measures of *Duox2*^{ΔIEC} and littermate control mice. Deletion of DUOX2 in IECs did not impact any of the observed organs or body weight. BW = body weight, SI = small intestine. **C)** Immune cell profile in lamina propria from small intestine and colon of *Duox2*^{ΔIEC} and littermate control mice. Th = CD4⁺ T helper cells, Tc: CD8⁺ cytotoxic T cells. **D)** Intestinal epithelial architecture of *Duox2*^{ΔIEC} and littermate control mice. Villus height and width along with crypt depth of small intestine samples, and depth and width of colonic crypts were quantified in H&E-stained intestinal sections. The scale bar in the representative images corresponds to 50 μm.

Table S1. List of primers used in this study.

Sequence 5'-->3'	Gene	Organism
Forward -CCCACGTTACCATTTCATCA	<i>Duox1</i>	Mouse
CATCTGCATAGCTGGCTGGA		
ACGCAGCTCTGTGTCAAAGGT	<i>Duox2</i>	Mouse
TGATGAACGAGACTCGACAGC		
ATCCTCACAATTGTTCCATT	<i>Nox1</i>	Mouse
TGACAACCTTGGAATCACGA		
CCCTTTGGTACAGCCAGTGAAGAT	<i>Nox2</i>	Mouse
CAATCCCGGCTCCCACTAACATCA		
CGACGAATTCAAGCAGATTGC	<i>Nox3</i>	Mouse
AAGAGTCTTTGACATGGCTTTGG		
GGATCACAGAAGGTCCCTAGCAG	<i>Nox4</i>	Mouse
GCGGCTACATGCACACCTGAGAA		
GGCTGTATTCCCCTCCATCG	<i>Actb</i>	Mouse
CCAGTTGGTAACAATGCCATGT		

Supplementary References

1. Larsson, E.; Tremaroli, V.; Lee, Y.S.; Koren, O.; Nookaew, I.; Fricker, A.; Nielsen, J.; Ley, R.E.; Bäckhed, F. Analysis of Gut Microbial Regulation of Host Gene Expression along the Length of the Gut and Regulation of Gut Microbial Ecology through MyD88. *Gut* **2012**, *61*, 1124–1131, doi:10.1136/gutjnl-2011-301104.
2. Sommer, F.; Nookaew, I.; Sommer, N.; Fogelstrand, P.; Bäckhed, F. Site-Specific Programming of the Host Epithelial Transcriptome by the Gut Microbiota. *Genome Biol* **2015**, *16*, 62, doi:10.1186/s13059-015-0614-4.