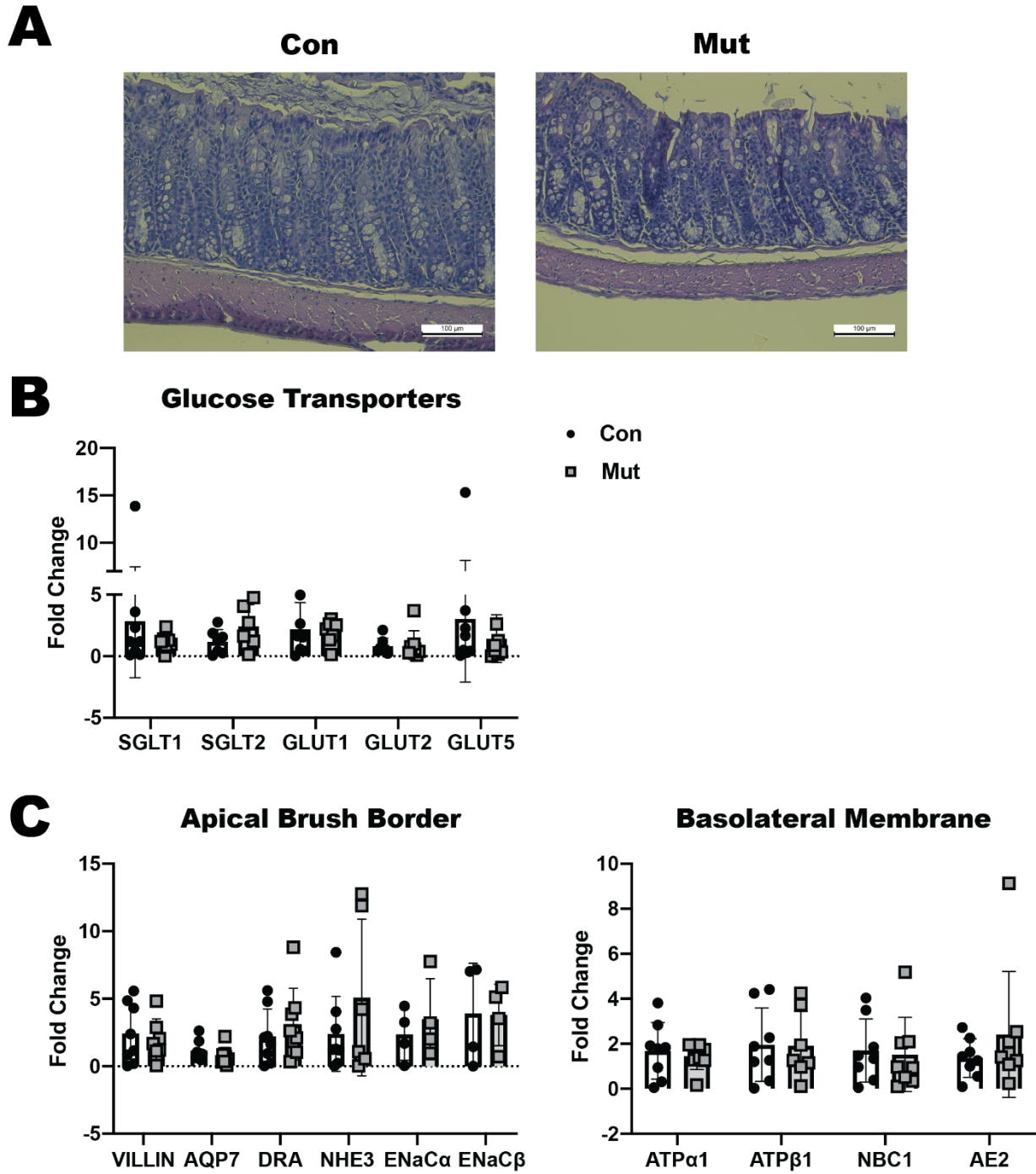
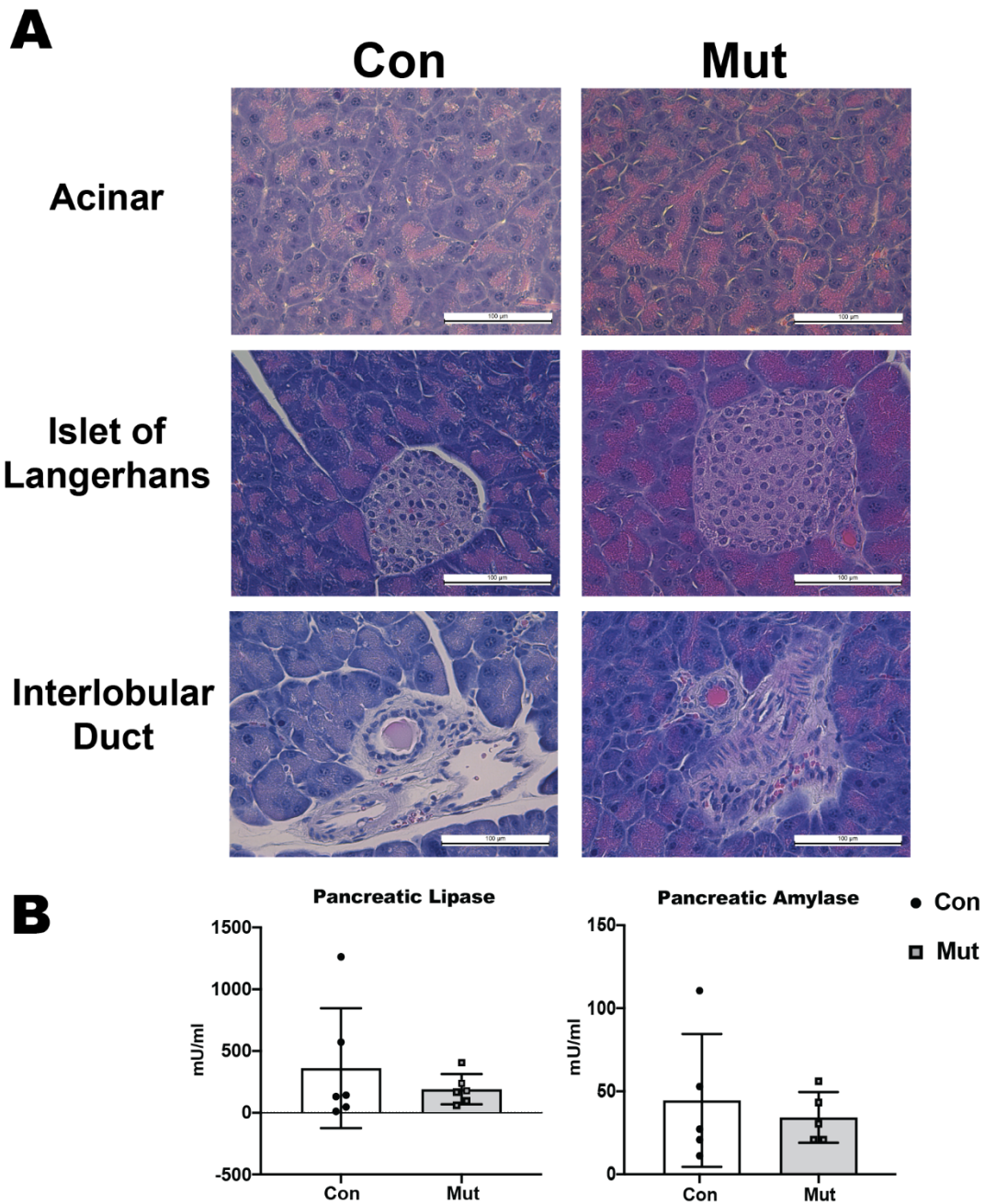


Figure S1



**Supplemental Figure S1: Evaluation of colonic epithelial cell markers in CTE mice** (A) Representative brightfield H&E images of colonic tissue sections from control (Con) and CTE mutant (Mut) mice (n=3). Scale bar denotes 100  $\mu$ m. (B) mRNA expression for glucose transporters (*SGLT1*, *SGLT2*, *GLUT1*, *GLUT2*, *GLUT5*) in colonic tissue lysates from of Con and Mut mice (n=7). (C) mRNA expression for apical brush border markers (*VILLIN*, *AQP7*, *DRA*, *NHE3*) (n=7) and (*ENaC $\alpha$*  and *ENaC $\beta$* ) (n=4) and basolateral membrane markers (*ATPase $\alpha$* , *ATPase $\beta$* , *NBC1*, and *AE2*) (n=7) in colonic tissue lysates from Con and Mut mice in colonic tissue lysates from Con and Mut mice. No statistically significant differences were found for any analyte between Con and Mut.



**Supplemental Figure S2 Evaluation of the pancreas in CTE mice (A)** Representative brightfield H&E images of pancreatic tissue sections showing acinar cells, islet of Langerhans, and interlobular ducts in control (Con) and CTE mutant (Mut) mice (n=3). Scale bar denotes 100  $\mu$ m. **(B)** Pancreatic lipase and amylase activity (n=6) in serum from Con and Mut mice.