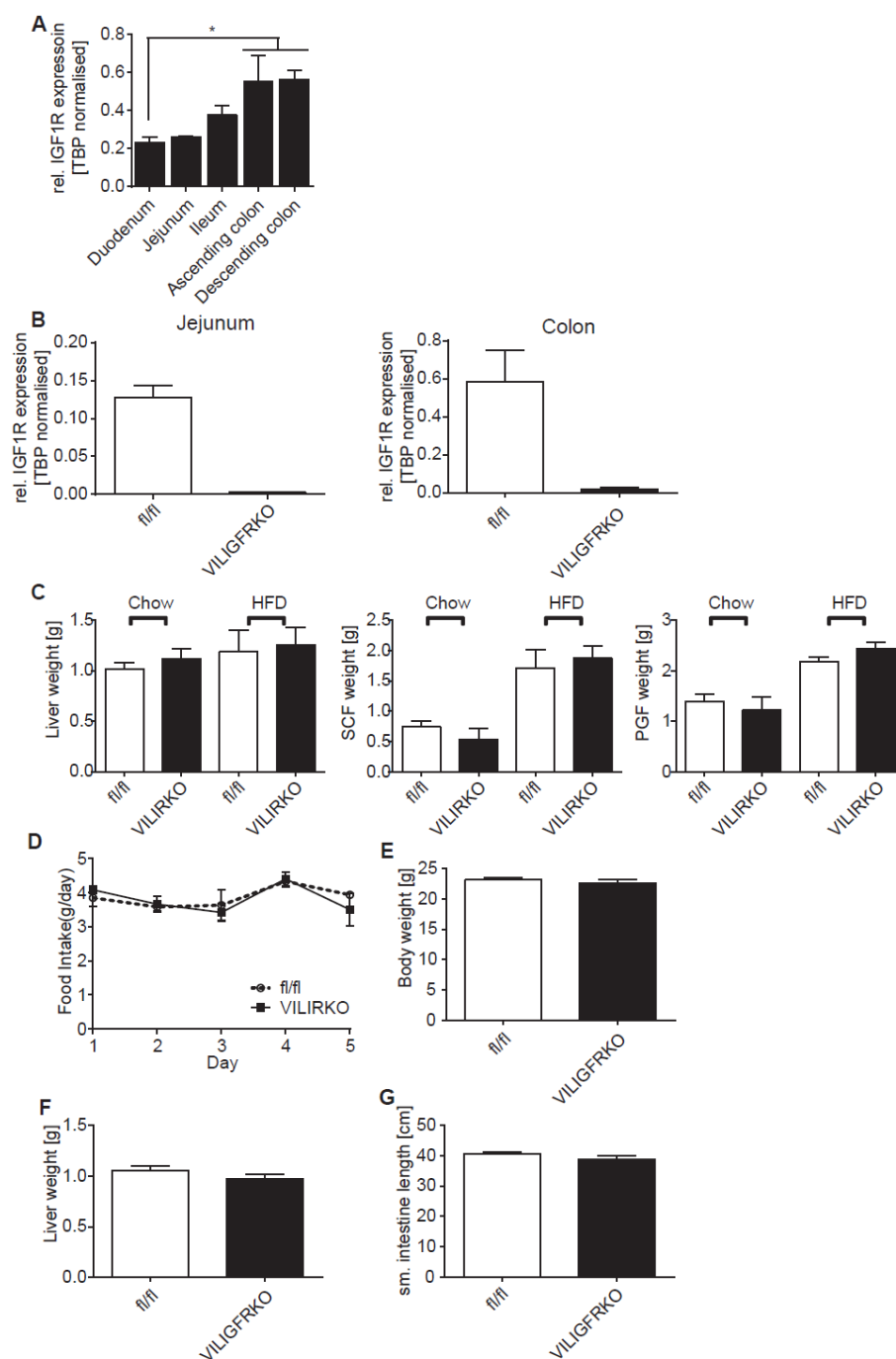


SUPPLEMENTARY DATA

Supplementary Material

Supplementary Figure 1

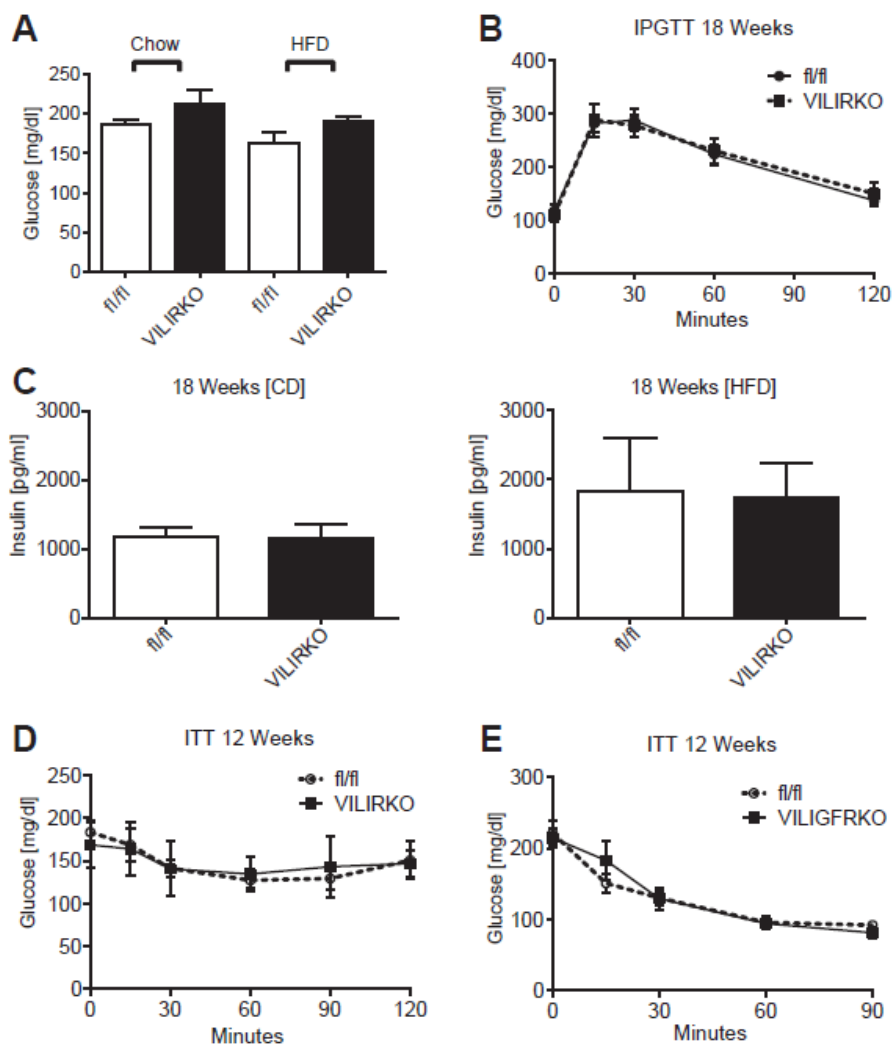
IGF1R qPCR from whole intestinal segments, normalized to TBP (n=3) * = $p < 0.05$ (One-Way ANOVA, Tukey's post-hoc test). **(B)** Expression of IGF1R in isolated epithelial cells of the jejunum and colon of 12 week-old male VILIGFRKO and control (fl/fl) mice on chow diet, n=5 for jejunum, n=4 for colon. **(C)** Liver, subcutaneous fat pad and perigonadal fat pad weights of 18 week-old male VILIRKO and fl/fl mice on chow diet and HFD. **(D)** Food intake of 12 week-old male VILIRKO and fl/fl mice on chow diet, n ≥ 5 . **(E)** Body weight of 12 week-old male VILIGFRKO and fl/fl mice on chow diet, n ≥ 5 . **(F)** Liver weight of 12 week-old male VILIGFRKO and fl/fl mice on chow diet, n ≥ 5 . **(G)** Small intestinal length from 12 week-old male VILIGFRKO and fl/fl mice on chow diet. All data shown as mean \pm SEM, n ≥ 5 .



SUPPLEMENTARY DATA

Supplementary Figure 2

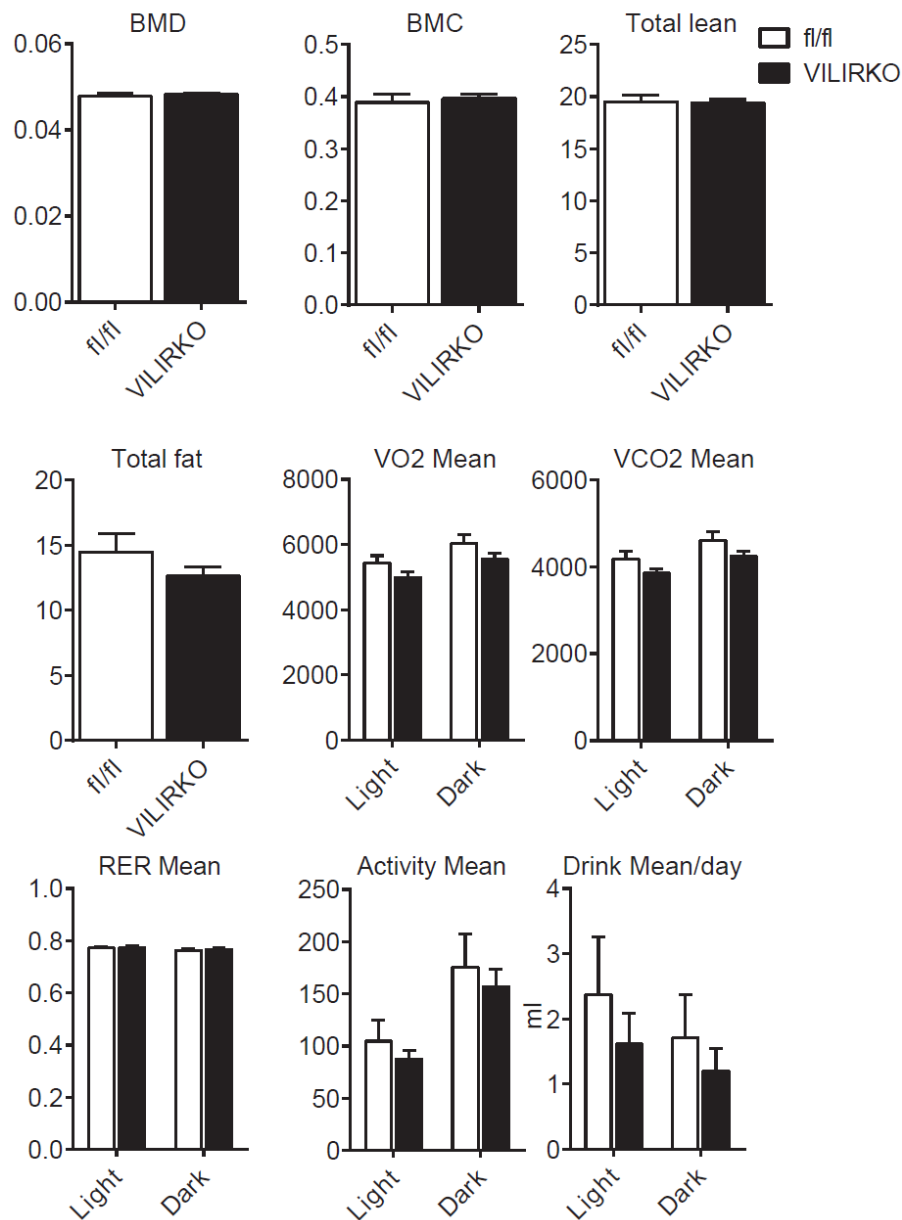
(A) Random fed blood glucose levels of 18 week-old male VILIRKO and fl/fl mice on chow diet and HFD, $n \geq 5$. (B) Intraperitoneal glucose tolerance tests (IPGTT) of 18-week-old male VILIRKO and fl/fl mice on chow diet, $n \geq 5$. (C) Insulin levels of 18-week-old male VILIRKO and fl/fl mice on chow diet and HFD, $n \geq 5$. Insulin tolerance tests of 12 week-old male VILIRKO (D) and VILIGFRKO (E) and fl/fl mice on chow diet. All data are shown as mean \pm SEM, $n \geq 5$.



SUPPLEMENTARY DATA

Supplementary Figure 3

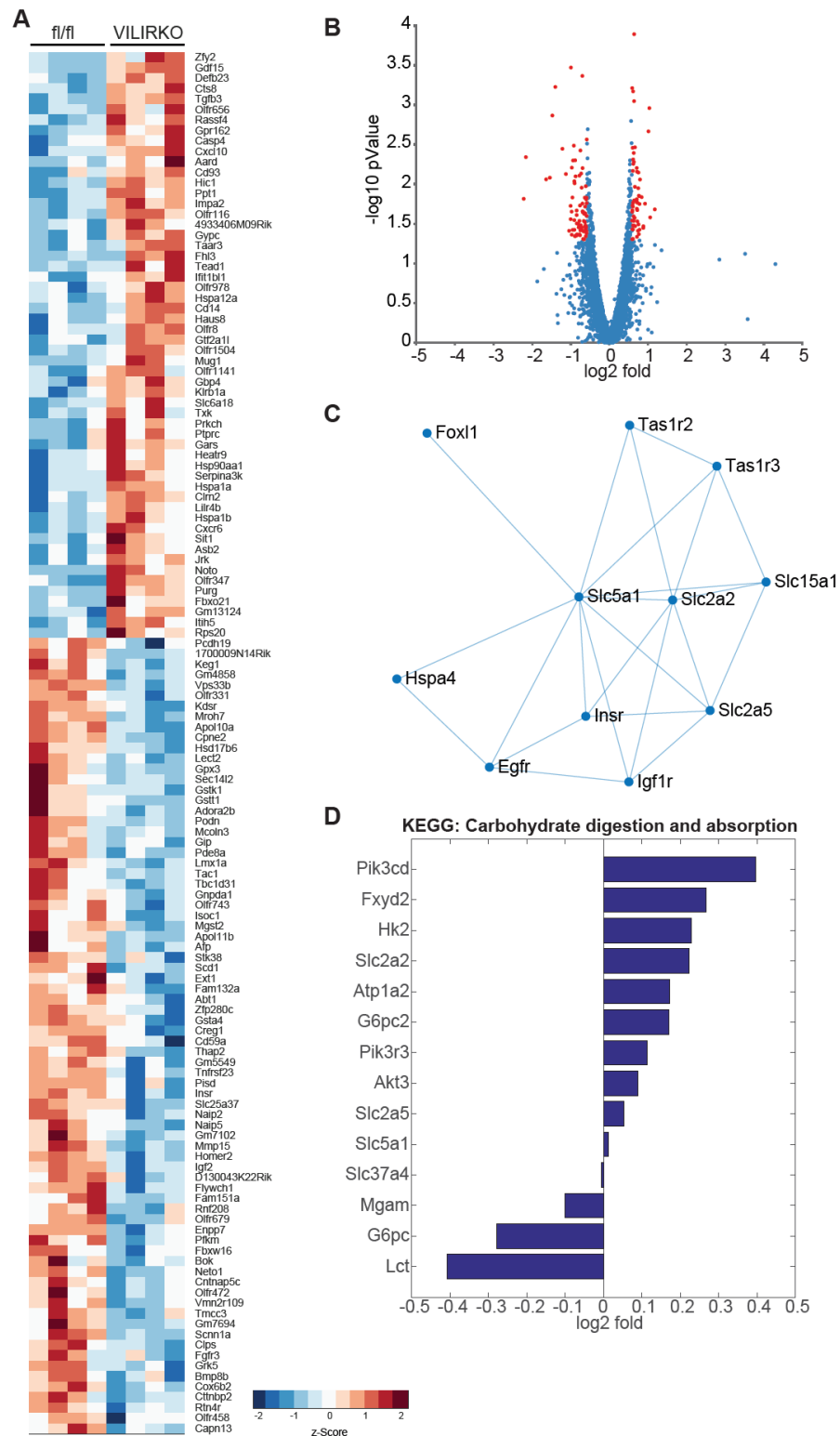
CLAMS and Dexa analysis of 14-week-old male VILIRKO and fl/fl mice on chow diet. Data are shown as mean \pm SEM, n = 6.



SUPPLEMENTARY DATA

Supplementary Figure 4

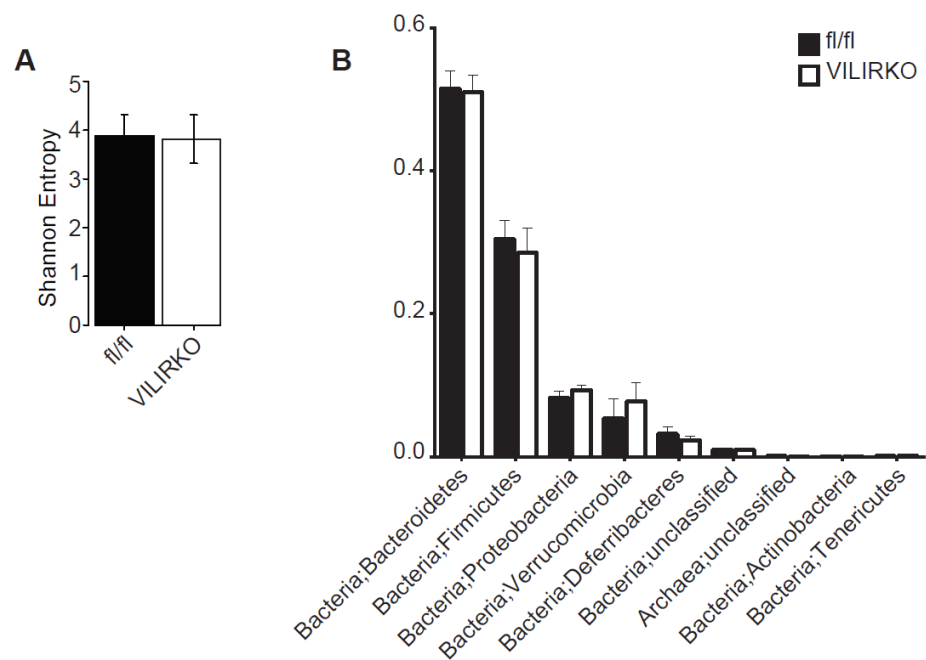
(A) Heatmap of genes significantly differentially regulated in VILIRKO vs. fl/fl mice ($p < 0.05$, $FC > 1.5$). Rows show z-scores of RMA normalized expression values. (B) Volcano plot for all protein coding genes after filtering for low expressed genes with low variance. (C) Protein-protein interaction (PPI) networks. Each edge refers to a validated or predicted PPI. Data taken from STRING DB. (D) Relative expression (log FC) of all expressed genes mapped to the KEGG pathway: Carbohydrate digestion and absorption.



SUPPLEMENTARY DATA

Supplementary Figure 5

A-B: Phylotyping and community structure analyses of the gut microbiota based on sequencing of the V4 region of the 16S rRNA gene from stool of VILIRKO and fl/fl mice, n ≥7.



SUPPLEMENTARY DATA

Supplementary Figure 6

Expression level of GIP, GCG, PYY CHGA, and IR mRNA measured by quantitative real-time PCR (qPCR) of RNA from isolated epithelial cells of the jejunum of 12 week-old male VILIGFRKO and control (fl/fl) mice on chow diet. Data are shown as mean \pm SEM, n =5.

