The mechanisms underlying the metabolic effects of bariatric surgery are not fully understood. Alterations in gut-derived hormone levels are involved in the beneficial effect of the surgery, but can not alone modulate the potent metabolic effects. Here we analyzed gene transcriptional changes in the full rostrocaudal extent of the gastrointestinal (GI) tract in rats 9, 22 and 60 days after Roux-en-Y gastric bypass (RYGB) as compared to sham and sham weight-matched (WM) controls.

METHODS AND STRATEGY: PREPROHORMONE EXTRACTION
Three cohorts of male diet induced obese (DIO) Sprague-Dawley rats underwent RYGB or sham surgery (SHAM) w/o weight-match (WM) and were terminated at 3 timepoints 9, 22 and 60 days later. Fluorescent immunohistochemistry was used to identify Chromogranin-A positive enteroeocrine cells. For each animal, 5000 cells were sampled using laser capture microdissection from 5 representative regions along the GI tract. Total mRNA of enriched enteroeocrine cells was purified and sequenced to get the full expression profile of each sample.

RESULTS

INTRODUCTION AND AIM
The mechanisms underlying the metabolic effects of bariatric surgeries are not fully understood. Alterations in gut-derived hormone levels are involved in the beneficial effects of the surgery, but cannot alone modulate the potent metabolic effects. Here we analyzed gene transcriptional changes in the full rostrocaudal extent of the gastrointestinal (GI) tract in rats 9, 22 and 60 days after Roux-en-Y gastric bypass (RYGB) as compared to sham and sham weight-matched (WM) controls.

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Figure 1 | Experimental set up and sampling strategy with example of Chromogranin-A positive cells before and after laser capture microdissection.

Sample cluster analysis

Gene regulation overlaps

Table 1 | Regulated preprohormones in RYGB vs. WM 9, 22 and 60 days post surgery in alimentary limb (AL), bilipancreatic limb (BL), proximal common channel (PC), distal common channel (DC) and colon (COL).

Expression profiles of selected genes

CONCLUSION
- RYGB surgery resulted in a sustained body weight loss.
- Different regions of the gastrointestinal tract display distinct gene expression profile.
- Differential gene expression was identified 9, 22 and 60 days after RYGB surgery.
- 60 preprohormone encoding genes were identified which 43 were regulated at 9, 22 and 60 days after surgery.