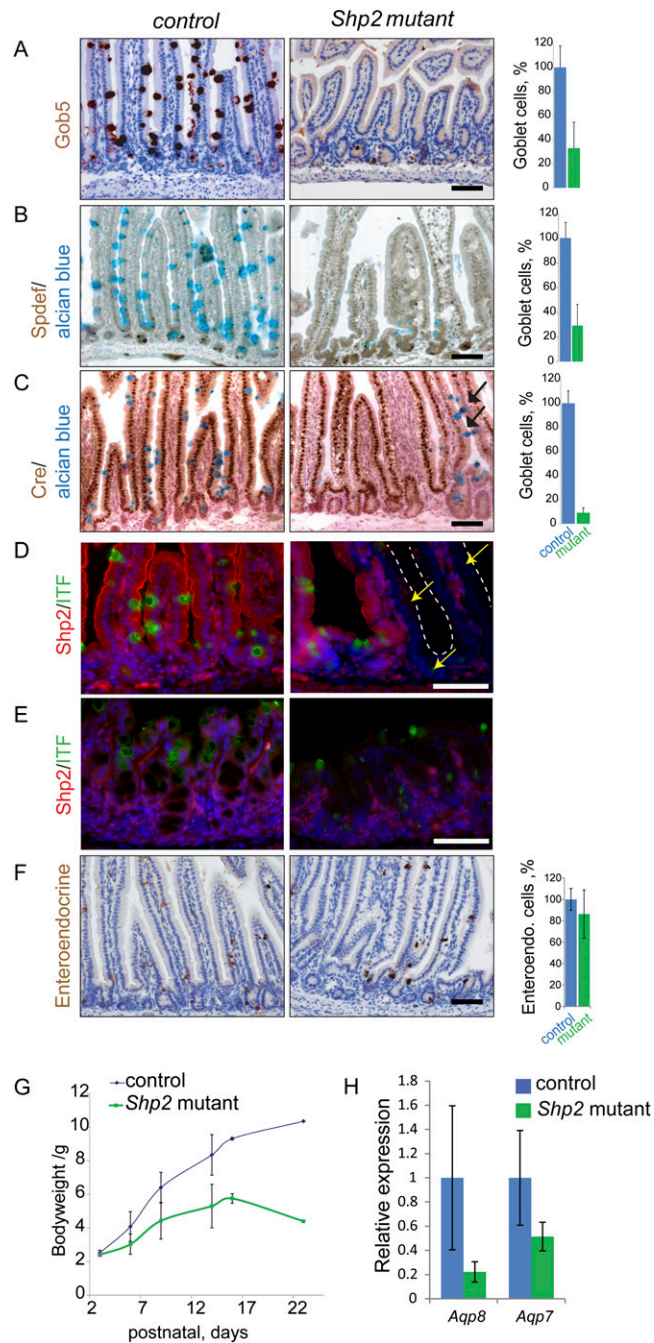
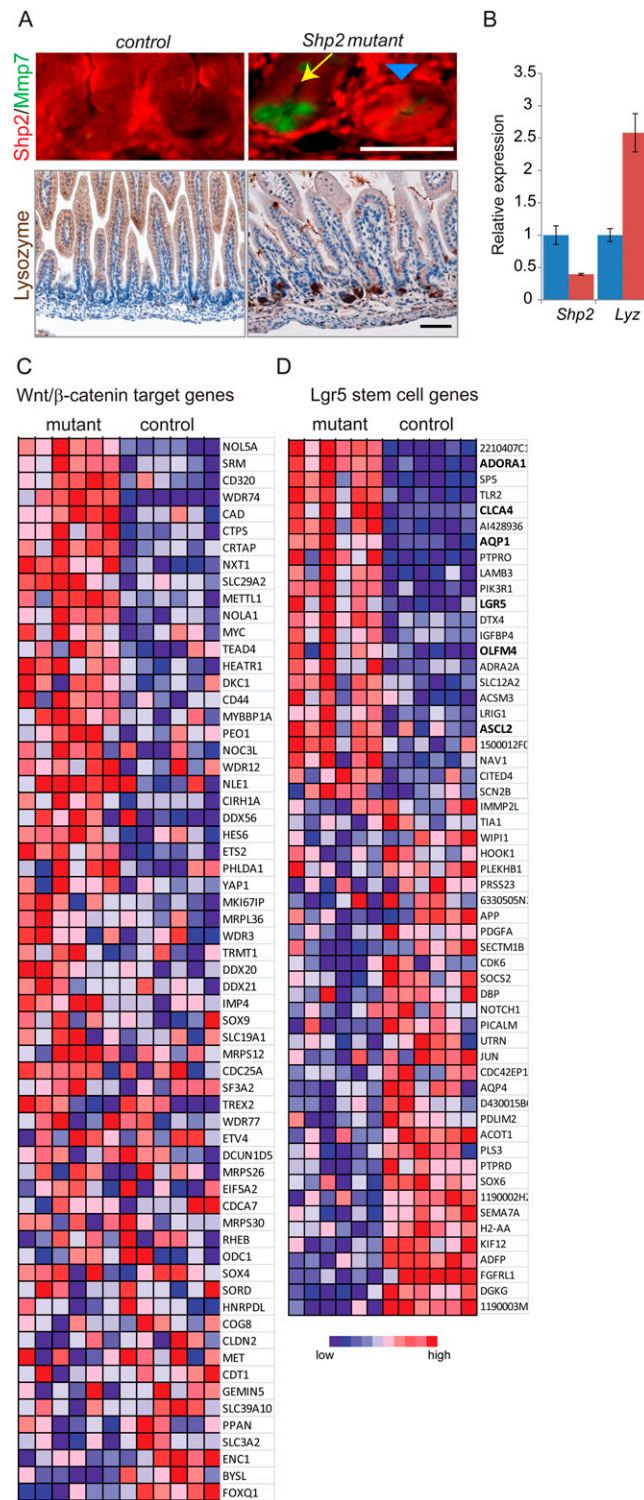


# Supporting Information

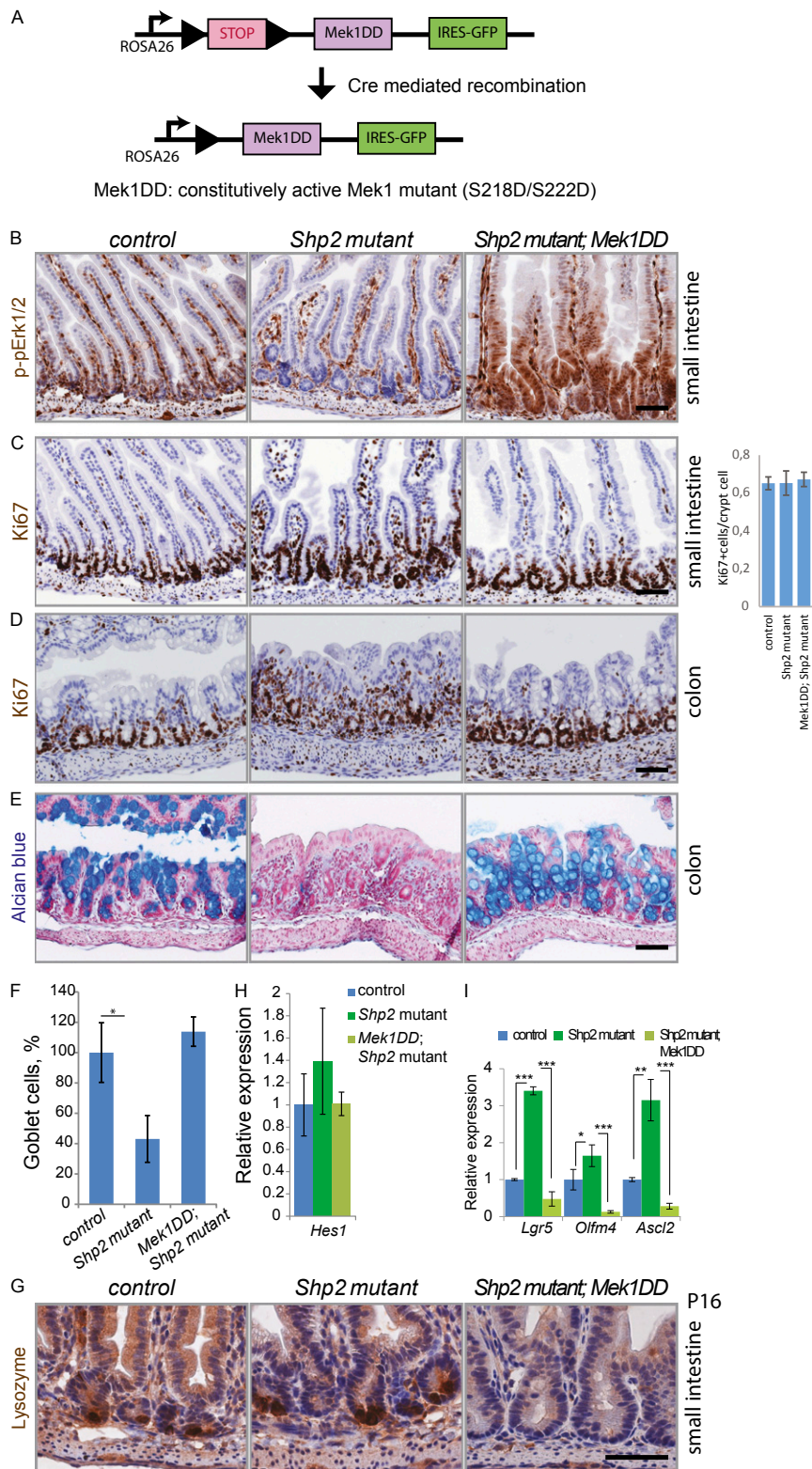
Heuberger et al. 10.1073/pnas.1309342111



**Fig. S1.** (A and B) Staining of goblet cells for chloride channel calcium activated 3 (Clca3, also known as Gob5) and SAM pointed domain containing ets transcription factor (Spdef)/alcian blue on sections of control and *Shp2* mutant intestines at P9; quantification of goblet cells is on the right ( $n = 4$ ). (C) Staining for Cre-recombinase (brown, nuclear) and goblet cells (alcian blue) on sections of control and *Shp2* mutant intestines at P9, which show few remaining goblet cells in areas with low Cre expression (see arrows on the *Right*); overall quantification of goblet cells in the majority of high Cre-expressing villi is on the *Right* ( $n = 4$ ). (D and E) Staining for Shp2 (red) and intestinal trefoil factor (ITF)-positive goblet cells (green) on sections of control and *Shp2* mutant small intestines (D) and colons (E). (F) Staining of enteroendocrine cells for ChromograninA on sections of control and *Shp2* mutant intestines at P9; quantification is on the *Right* ( $n = 4$ ). (G) Growth retardation of conditional *Shp2* mutants after birth, compared with controls. (H) Decreased mRNA expression of *Aqp8* and *Aqp7* in *Shp2* mutants, assessed by qRT-PCR ( $n = 5$ ). (Scale bars, 100  $\mu\text{m}$ .)



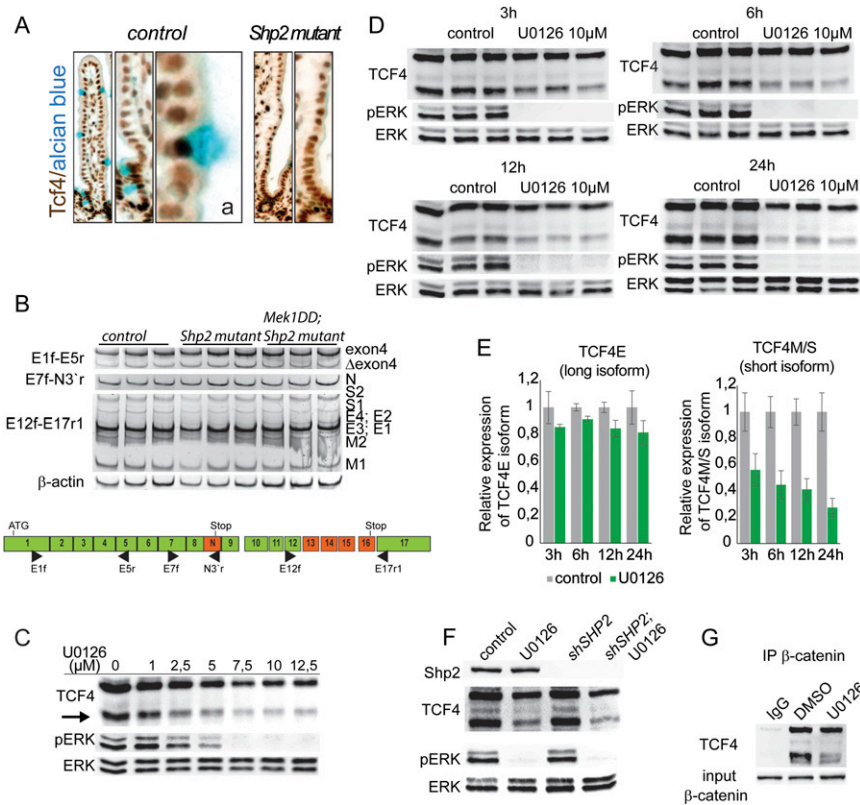
**Fig. S2.** (A) Immunofluorescence of Shp2 and Mmp7-positive paneth cells (Upper, yellow arrow points to Shp2-deficient crypt with paneth cells, blue arrowhead points to nonrecombined crypt without paneth cells) and immunohistology of lysozyme-positive paneth cells (Lower). (B) Expression of *Shp2* and *Lysozyme* mRNAs in control (blue bars) and *Shp2* mutant organoids (red bars) after tamoxifen-induced mutagenesis, assessed by qRT-PCR. (C and D) Gene set enrichment analysis (GSEA) heatmaps of control versus *Shp2* mutants for Wnt/ $\beta$ -catenin target genes and for down-regulated genes of the Lgr5+ stem cell signature.



**Fig. S3.** (A) Scheme of the *Mek1DD* allele. The *ROSA26* allele harbors the cDNA of a gain-of-function variant of Mek1, preceded by a *loxP*-flanked STOP cassette and followed by an eGFP gene under the control of an internal ribosomal entry site (1). *Mek1DD* is expressed upon removal of a translation stop cassette through Cre-mediated recombination. (B) Altered MAPK signaling in the small intestine of *Shp2* mutant and compound *Shp2*; *Mek1DD* mutant mice at P6, assessed by immunohistochemistry for pErk. (C and D) Immunohistochemistry for proliferating cells with anti-Ki67 antibody of P6 sections of small intestines and colon (marked on the Right), *Shp2* and compound *Shp2*; *Mek1DD* mice (quantification is on the Right). (E) Rescue of the goblet cell phenotype in the *Shp2* mutant colon by *Mek1DD*; goblet cells stained with alcian blue. (F) Quantification of goblet cells in *Shp2* mutant and compound *Shp2*; *Mek1DD* mutant small intestines at P6 ( $n = 3$ ). (G) Immunohistochemistry of paneth cells of small intestines at P16 stained for lysozyme. (H) *Hes1* expression in P6 control, *Shp2*, and *Shp2*; *Mek1DD* mice (quantification is on the Right). (I) Relative expression of *Lgr5*, *Olfr4*, and *Ascl2* in P6 control, *Shp2*, and *Shp2*; *Mek1DD* mice (quantification is on the Right). Legend continued on following page

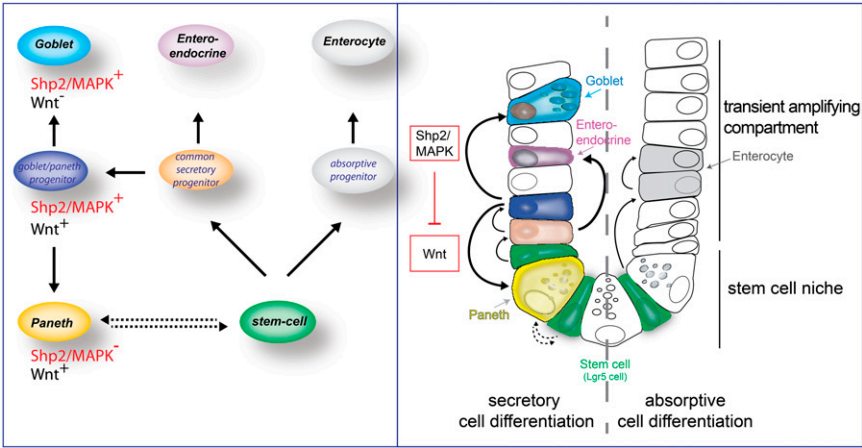
compound *Shp2*; *Mek1DD* mice determined by qRT-PCR ( $n = 3$ ). (I) Rescue of *Lgr5*, *Olfm4*, and *Ascl2* mRNA expression in *Shp2* mutants by *MekDD1*, assessed by qRT-PCR. Significance calculated with  $t$  test; \* $P < 0.05$ , \*\* $P < 0.01$ , \*\*\* $P < 0.001$ . (Scale bars, 100  $\mu\text{m}$ .)

1. Srinivasan L, et al. (2009) PI3 kinase signals BCR-dependent mature B cell survival. *Cell* 139(3):573–586.



**Fig. 54.** (A) Staining for Tcf4 and goblet cells (alcian blue) of control and *Shp2* mutant small intestines. An enlargement (a) of control is also shown. (B, Upper) Analysis of *Tcf4* splice variants on the mRNA level of intestinal organoids of tamoxifen-inducible *Shp2* mutants, *Mek1DD*; *Shp2* double mutants and controls. (Lower) Scheme of exons of *Tcf4* cDNAs with primer binding sites and the classifications of splice variants is based on Weise et al. (1). (C) Dependence of TCF4 isoform changes on the concentration of the MEK1/2 inhibitor UO126 in HT29 cells. (D) Reduction of the short TCF4 splice variants after 3, 6, 12, and 24 h of MEK1/2 inhibition in HT29 cells. Triplicate cell cultures were examined. (E) Quantification of changes of the TCF4 isoforms upon MEK1/2 inhibition by measuring the signal intensities from D; no significant changes of the long TCF4 isoform (diagram on the Left) and decrease of the short TCF4 isoform (diagram on the Right) upon MEK1/2 inhibition (green bars) ( $n = 3$ ). (F) Knockdown of *SHP2* by shRNAs in HT29 has no effect on ERK activity and TCF4 isoform production. (G) Coimmunoprecipitations of TCF4 with  $\beta$ -catenin from nuclear fractions; interaction of  $\beta$ -catenin with TCF4E persists after 6 h of MEK1/2 inhibition.

1. Weise A, et al. (2010) Alternative splicing of *Tcf712* transcripts generates protein variants with differential promoter-binding and transcriptional activation properties at Wnt/ $\beta$ -catenin targets. *Nucleic Acids Res* 38(6):1964–1981.



**Fig. S5.** Schemes of intestinal cell differentiation. (Left) Cell types and intrinsic signaling. Shp2/MAPK activity (red) regulates the differentiation of goblet cells, which are MAPK<sup>+</sup> Wnt<sup>-</sup>, and paneth cells, which are MAPK<sup>-</sup> Wnt<sup>+</sup> after progenitor specification into a common goblet/paneth cell progenitor. Enteroendocrine cells separate earlier, i.e., from a general secretory progenitor in a Shp2/MAPK-independent manner. Shp2/MAPK exerts this function by blocking Wnt/ $\beta$ -catenin signaling. (Right) Cell differentiation in the stem cell niches and in the transient amplifying compartments. The inhibitory effect of Shp2/MAPK on Wnt signaling is shown in red. The common secretory progenitor is marked as +5.