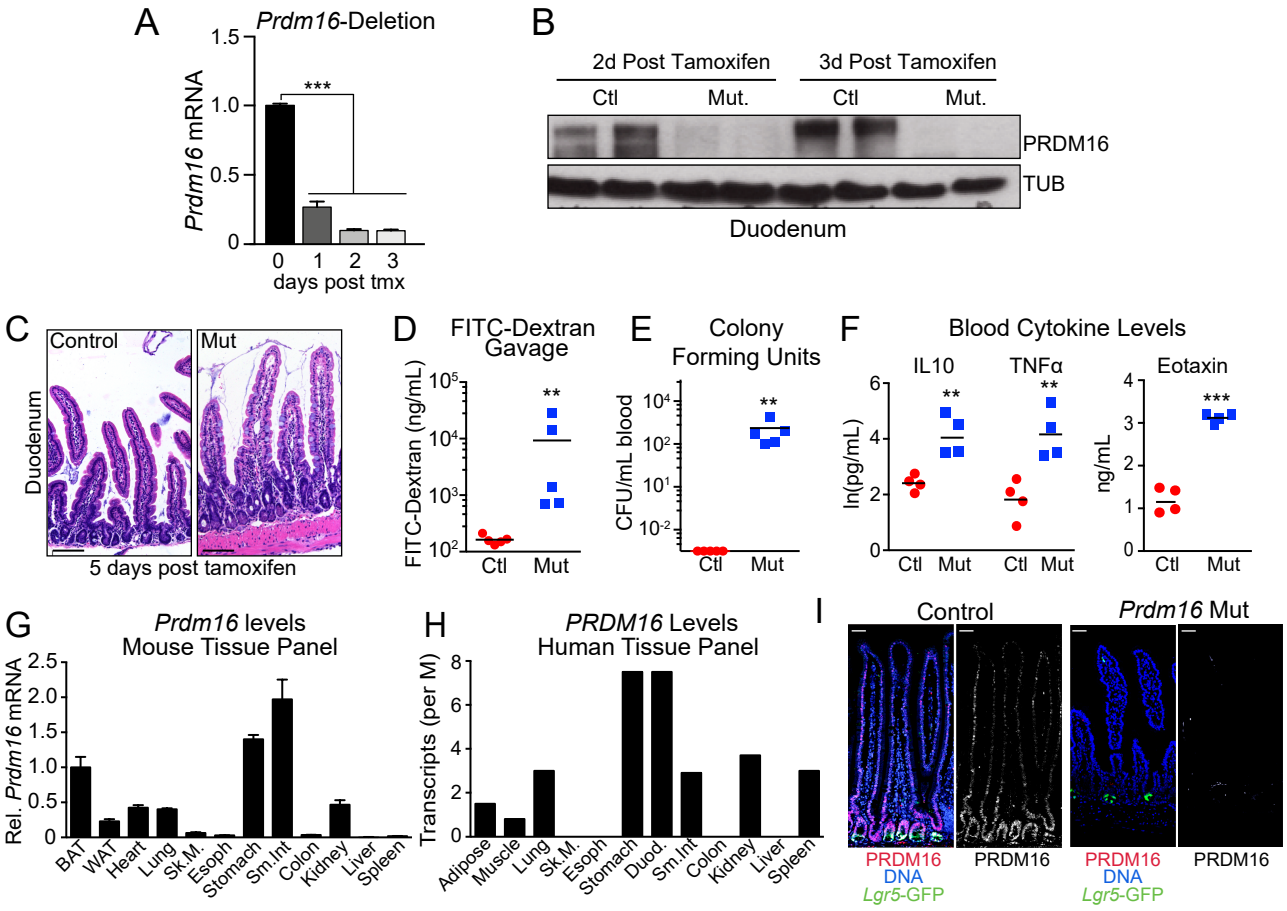


Fig. S1: *Prdm16* is required for small intestine maintenance. (Related to Fig. 1).

A-F) Phenotypes of *Prdm16*$^{loxP/loxP}$ (Control, Ctl) or *R26R*$^{Cre-ERT2}$;*Prdm16*$^{loxP/loxP}$ (Mut) animals after injection with tamoxifen. **A)** Relative *Prdm16* mRNA levels in duodenal crypts at 0, 1, 2, and 3 d post- injection. n=4 mice per group. **B)** Western blot analysis of PRDM16 protein levels in duodenal crypts. n=2 mice/group. **C)** H&E staining of duodenum 5d after tmx injection. **D)** FITC levels in circulation following FITC-Dextran gavage of mice at 6d after tmx injection. n=5 mice per group. **E**) Number of colony forming units (CFU) from whole blood collected 6d after injection. n=5 mice per group. **F**) Cytokine levels measured by Luminex analysis of serum taken 5d after injection. n=4 mice per group. **G)** Relative *Prdm16* mRNA levels across a panel of mouse tissues. n=3 mice. Sk. M= skeletal muscle, Esoph= esophagus, Sm. Int.= small intestine, WAT= white adipose tissue. **H)** *PRDM16* expression in human tissues (from the Human Protein Atlas (https://www.proteinatlas.org)). **I)** α-PRDM16 antibody staining validated by probing *Prdm16* knockout duodenum sections. Compare to Fig. 1E: control is the same image in Fig. 1E. PRDM16 (red), *Lgr5-GFP* (green), DNA (DAPI, blue). PRDM16 only channel in white. All panels show mean ± SEM, *p<0.05, **p<0.01, ***p<0.001. Scale bars: 100 μm (C, I).

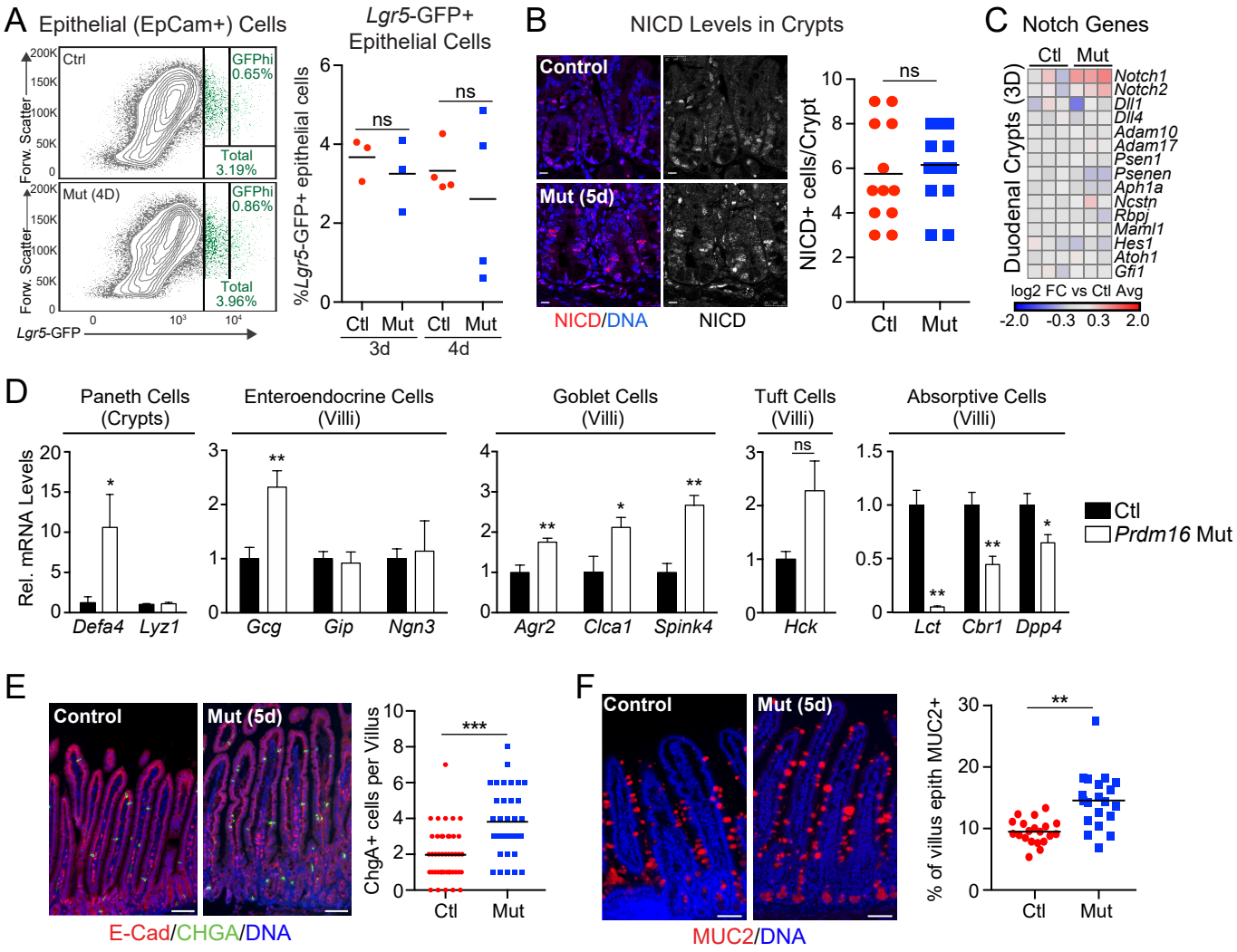


Fig. S2: *Prdm16* deletion leads to apoptosis and altered cell type composition. (Related to Fig. 2).

A) Flow cytometry analysis of GFP (*Lgr5*$^{GFP/CreERT2}$) in epithelial cells from duodenal crypts 3d or 4d after *in vivo* tamoxifen (tmx) injection. n=3-4/group. Control (*Lgr5*$^{GFP/Cre-ERT2}$; *Prdm16*$^{loxP/+}$) or *Prdm16* mutant (*R26R*^{CreERT2}; *Lgr5*$^{GFP/CreERT2}$; *Prdm16*$^{loxP/loxP}$). **B-F)** Analysis of *R26R*^{CreERT2}; *Prdm16*$^{loxP/loxP}$ (Mut) or *Prdm16*$^{loxP/loxP}$ (control) duodenum after tmx injection. **B)** Immunofluorescence staining for the NOTCH intracellular domain (NICD, Red) at 5d post-tmx. DNA (DAPI, blue). n=12-13 crypts from 2 mice/group. **C)** Expression heat map for Notch pathway genes at 3d post tmx. Log_2 fold change (FC) shown relative to mean control expression. **D)** Relative mRNA levels of cell type-specific markers (as indicated) in isolated crypts or villi 5d post-tmx. n=5-7 mice per group. **E**) Immunofluorescence staining for the enteroendocrine cell marker Chromogranin A (CHGA) at 5d post-tmx. Right: Quantification of CHGA+ cells per villus. CHGA (green), E-cadherin (red), DNA (DAPI, blue). n=33-44 villi from 3 mice per condition. **F**) Immunofluorescence staining for the goblet cell marker Mucin 2 (MUC2) at 5d post-tmx. Right: Quantification of the percentage of epithelial cells per villus that were MUC2+. MUC2 (red), DNA (DAPI, blue). n=20 villi from 3 mice per group. Mean ± SEM. *p-value<0.05, **p-value<0.01, ***p-value<0.001, Scale bars: 10 μm (B), 100 μm (E,F).

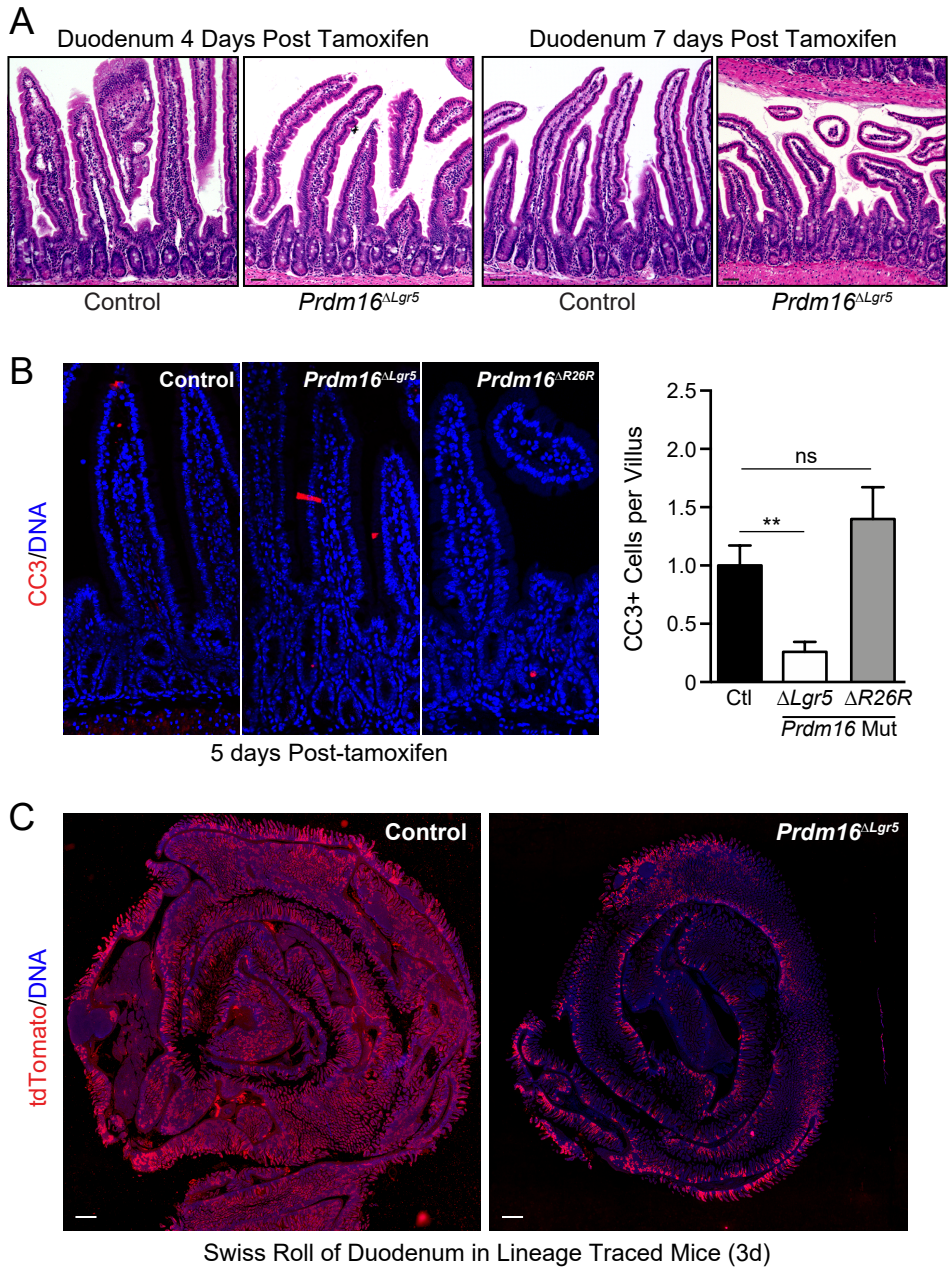


Fig. S3: *Prdm16* deletion causes apoptosis in transit-amplifying cells. (Related to Fig.3).

A) H&E staining of duodenum from *Prdm16*$^{\Delta Lgr5}$ (*Lgr5*$^{GFP/Cre-ERT2}$;*Prdm16*$^{loxP/loxP}$) mice 4d and 7d after injection with tamoxifen (tmx) (*Prdm16*$^{\Delta Lgr5}$) or vehicle (corn oil; Control). **B)** (left) Immunofluorescence staining of Cleaved Caspase 3 (CC3; red) in duodenum from Control (corn oil-treated *Lgr5*$^{GFP/Cre-ERT2}$;*Prdm16*$^{loxP/loxP}$), *Prdm16*$^{\Delta Lgr5}$ (tmx-treated *Lgr5*$^{GFP/Cre-ERT2}$;*Prdm16*$^{loxP/loxP}$) or *Prdm16*$^{\Delta R26R}$ (tmx-treated *R26R*^{CreERT2}; *Lgr5*$^{GFP/CreERT2}$; *Prdm16*$^{loxP/loxP}$) mice 5d after injection. DNA (DAPI, blue). (right) Quantification of CC3+ cells in villi. n=27-53 villi from 3 mice per group. **C)** Immunofluorescence analysis of tdTomato expression (lineage-tracing) in duodenal "Swiss rolls" from Control (*Lgr5*$^{GFP/Cre-ERT2}$; *R26R*$^{lox-stop-lox-tdTomato}$;*Prdm16*$^{loxP/+}$) or mutant (*Prdm16*$^{\Delta Lgr5}$; *Lgr5*$^{GFP/Cre-ERT2}$; *R26R*$^{lox-stop-lox-tdTomato}$;*Prdm16*$^{loxP/loxP}$) animals at 3d post-tamoxifen injection. tdTomato (red), DNA (DAPI, blue). Scale bars: 50 μm (A,B), 1 mm.

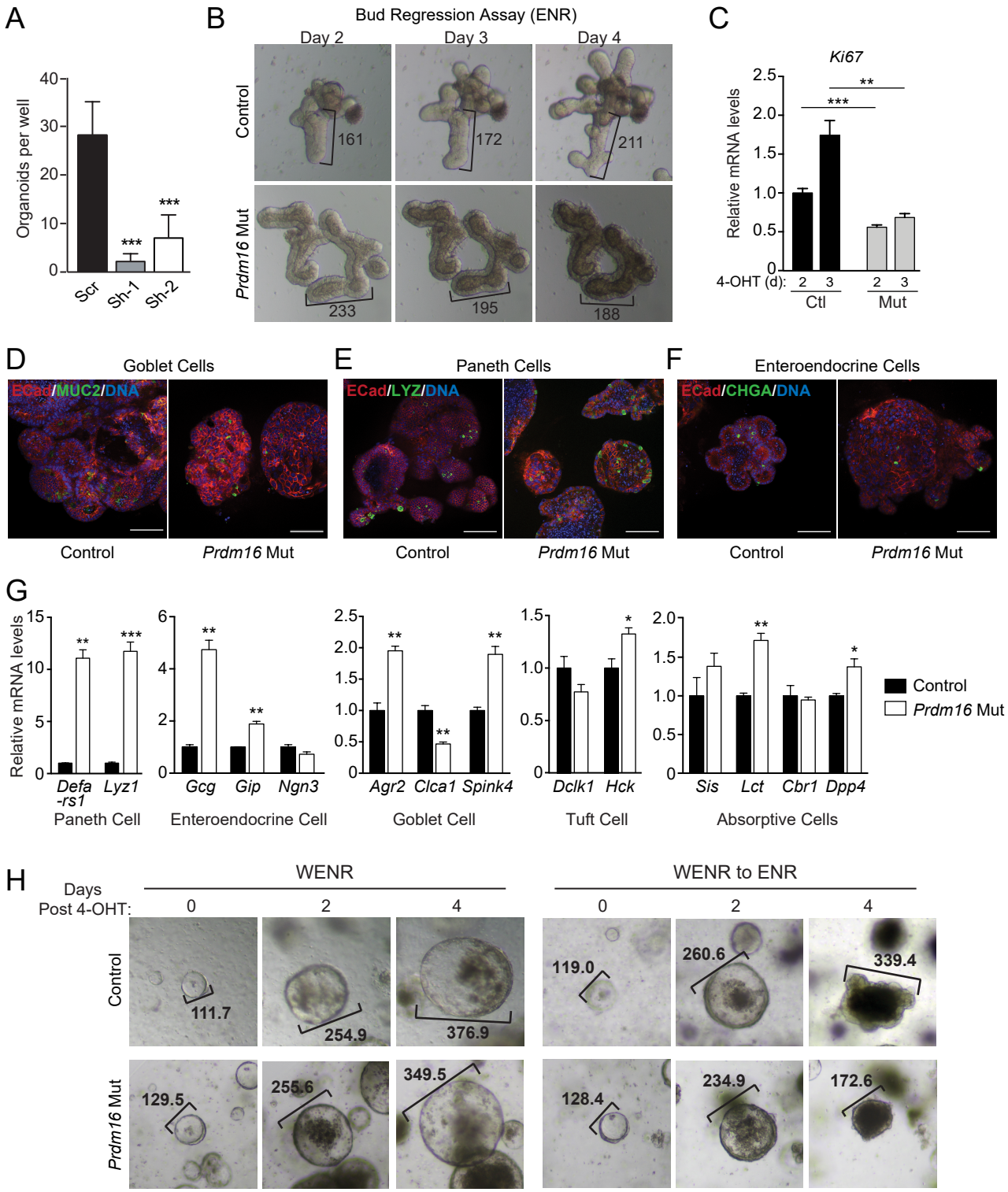
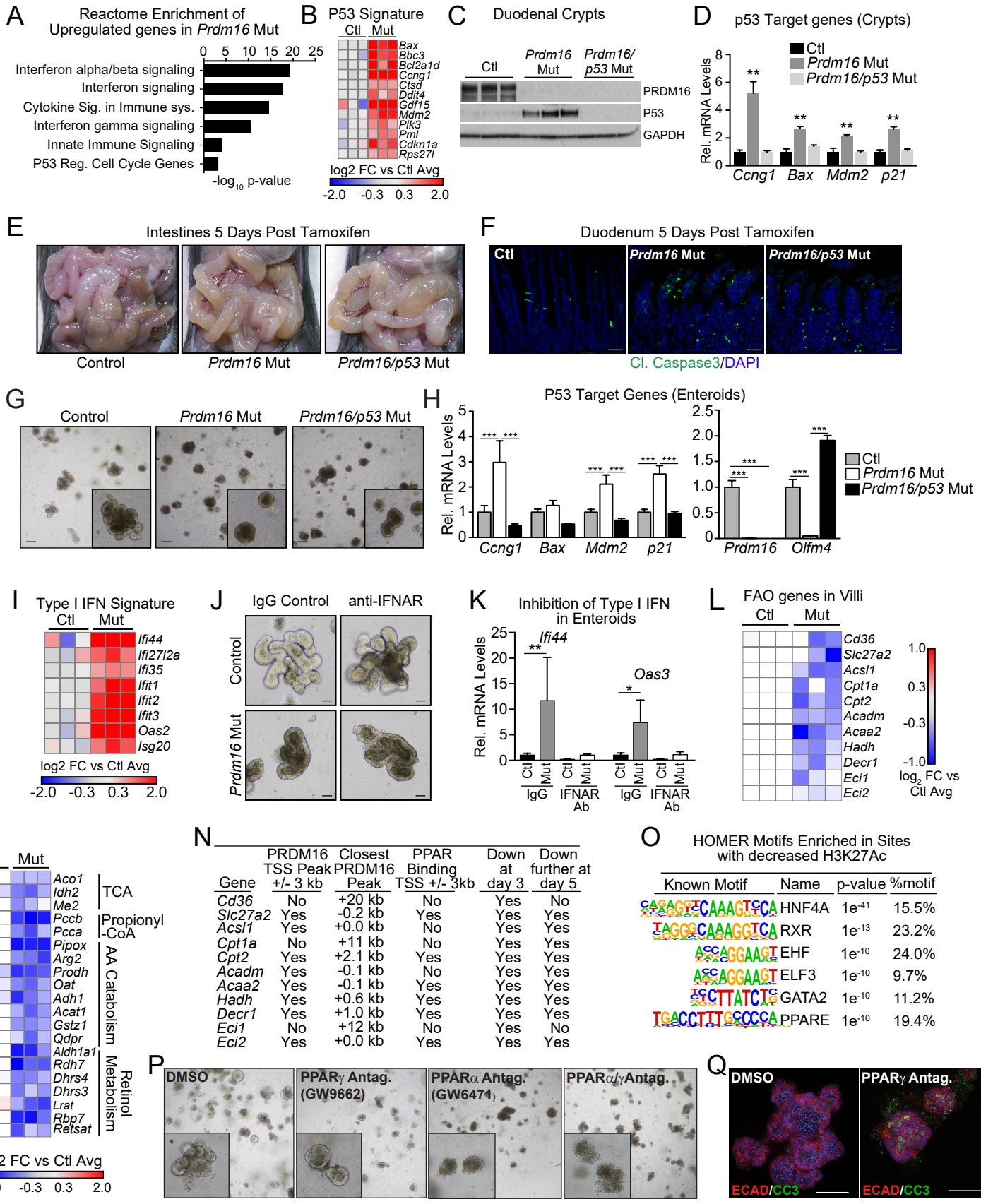


Fig.S4: ***Prdm16* is required for normal budding of duodenal enteroids. (Related to Fig. 4).**

A) Enteroid formation after transduction with lentivirus encoding control (scramble; scr) or *Prdm16 (Sh-1, Sh-2)* shRNAs. n=3 wells per group. **B)** Example of bud regression assay (see Methods) where enteroids were allowed to bud before 4-OHT addition, and then individual enteroid bud size was measured over time. Length is in μm. **C)** Relative *Ki67* mRNA levels in control and *Prdm16* mutant enteroids at 2d and 3d following *ex vivo* 4-OHT treatment. n=4 wells. **D-F)** Immunofluorescence analysis of cell type-selective markers in Control ($Lgr5^{GFP/CreERT2}$; $Prdm16^{loxP/loxP}$) and *Prdm16* mutant ($R26R^{CreERT2}$; $Lgr5^{GFP/CreERT2}$; $Prdm16^{loxP/loxP}$) enteroids at 4d after treatment with 4-OHT (Mut) or vehicle (ethanol, control). E- Cadherin (red), DNA (DAPI, blue). **D)** Mucin2 (MUC2, green); **E)** Lysozyme (LYZ, green); **F)** Chromogranin A (CHGA, green). **G)** Relative mRNA levels of cell type-selective markers (as indicated) in enteroids from control and *Prdm16* mutant mice 4 days after 4OHT treatment in culture. n= 4 wells. **H)** Examples of growth measurements (see Methods) of control and mutant enteroids. Bars show size of enteroids in microns. All panels show Mean ± SEM. *p-value<0.05, **p-value<0.01, ***p-value<0.001, Scale bars: 100 μm (D-F).



Gene	PRDM16 TSS Peak +/- 3 kb	Closest PRDM16 Peak	PPAR Binding TSS +/- 3kb	Down at day 3	Down further at day 5
Cd36	No	+20 kb	No	Yes	No
Slc27a2	Yes	-0.2 kb	Yes	Yes	Yes
Acsl1	Yes	+0.0 kb	No	Yes	Yes
Cpt1a	No	+11 kb	No	Yes	Yes
Cpt2	Yes	+2.1 kb	Yes	Yes	Yes
Acadm	Yes	-0.1 kb	No	Yes	Yes
Acaa2	Yes	-0.1 kb	Yes	Yes	Yes
Hadh	Yes	+0.6 kb	Yes	Yes	Yes
Decr1	Yes	+1.0 kb	Yes	Yes	Yes
Eci1	No	+12 kb	No	Yes	No
Eci2	Yes	+0.0 kb	Yes	Yes	Yes

Known Motif	Name	p-value	%motif
	HNF4A	$1e^{-41}$	15.5%
	RXR	$1e^{-13}$	23.2%
	EHF	$1e^{-10}$	24.0%
	ELF3	$1e^{-10}$	9.7%
	GATA2	$1e^{-10}$	11.2%
	PPARE	$1e^{-10}$	19.4%

Fig. S5: The Prdm16 mutant intestinal phenotype does not depend on upregulated P53 and Type I Interferon signaling. (Related to Fig. 5).

A) Pathway enrichment analysis of genes upregulated (FDR<0.05) in mutant duodenal crypts at 3d post-tamoxifen (tmx) injection. *R26R*^{CreERT2}; *Prdm16*$^{loxP/loxP}$ (Mut.) or *Prdm16*$^{loxp/loxP}$ (control).
B) Expression heat map of P53 target gene levels in control and *Prdm16* mutant crypts at 3d after deletion. Log_2 fold change shown relative to mean control expression.
C) Western blot analysis of PRDM16 and P53 protein levels in isolated crypts from control, *Prdm16* mutant, and *Prdm16*/*p53* double mutant (*R26R*^{CreERT2}; *Prdm16*$^{loxP/loxP}$*,p53* $^{loxP/loxP}$) mice at 3d post-tmx injection. Loading control is GAPDH. n=3 mice.
D) Relative mRNA levels of P53 target genes in crypts from control, *Prdm16* mutant, and *Prdm16/p53* mutant mice. n=3 mice.
E) Gross appearance of intestines from control, *Prdm16* mutant, and *Prdm16/p53* mice at 5d post-tmx.
F) Immunofluorescence analysis of Cleaved Caspase 3 in duodenum from control, *Prdm16* mutant, and *Prdm16/P53* mutant mice. Cl. Caspase 3 (green), DNA (DAPI, blue).
G) Images of control, *Prdm16* mutant, and *Prdm16/P53* mutant enteroids after 4-OHT treatment, with magnified detail shown in inset.
H) Relative mRNA levels of P53 target genes, *Prdm16*, and *Olfm4* in control, *Prdm16* mutant, and *Prdm16/P53* mutant enteroids, 5d after *ex vivo* treatment with 4-OHT. n=3 wells.
I) Expression heat map of Type I interferon signaling genes in control and *Prdm16* mutant crypts at 3d post-tmx. Log_2 fold change shown relative to mean control expression.
J-K) Control and *Prdm16* mutant enteroids treated with either IgG (control) or IFNAR neutralizing antibody. (J) Morphology and (K) Relative mRNA levels of Type I interferon-signature genes. n=3-4 wells.
L) Expression heat map of fatty acid oxidation (FAO)-related genes in control and Prdm16 mutant villi 3d post-tmx. Fractionated villi were from the same mice used for crypt analysis in Fig. 5B.
M) Expression heat map of metabolic pathway genes in control and *Prdm16* mutant crypts at 3d post-tmx.
N) Table summarizing PRDM16 regulation of FAO genes. PRDM16 ChIP-seq peak location, both within 3 kb in either direction of transcriptional start site (TSS) and nearest location; presence of a PPAR ChIP-qPCR site, and associated mRNA expression analysis at d3 and d5**.**
O) Enriched transcription factor binding motifs at sites of decreased H3K27Ac following *Prdm16* deletion.
P) Wildtype enteroids treated with vehicle (DMSO), PPARγ antagonist (GW9662, 5μm), PPARα (GW6471, 5 μm), or both antagonists (5 μm for each treatment) for a period of 4 days.
Q) Enteroids treated with PPARγ antagonist (GW9662, 5 μm) for 4 days and stained with Cl. Caspase 3 (green). E-Cad (Red), DNA (DAPI, blue).
All panels show Mean ± SEM. *p-value<0.05, **p-value<0.01, ***p-value<0.001, Scale bars: 100 μm (F,G,P,Q), 50 μm (J).

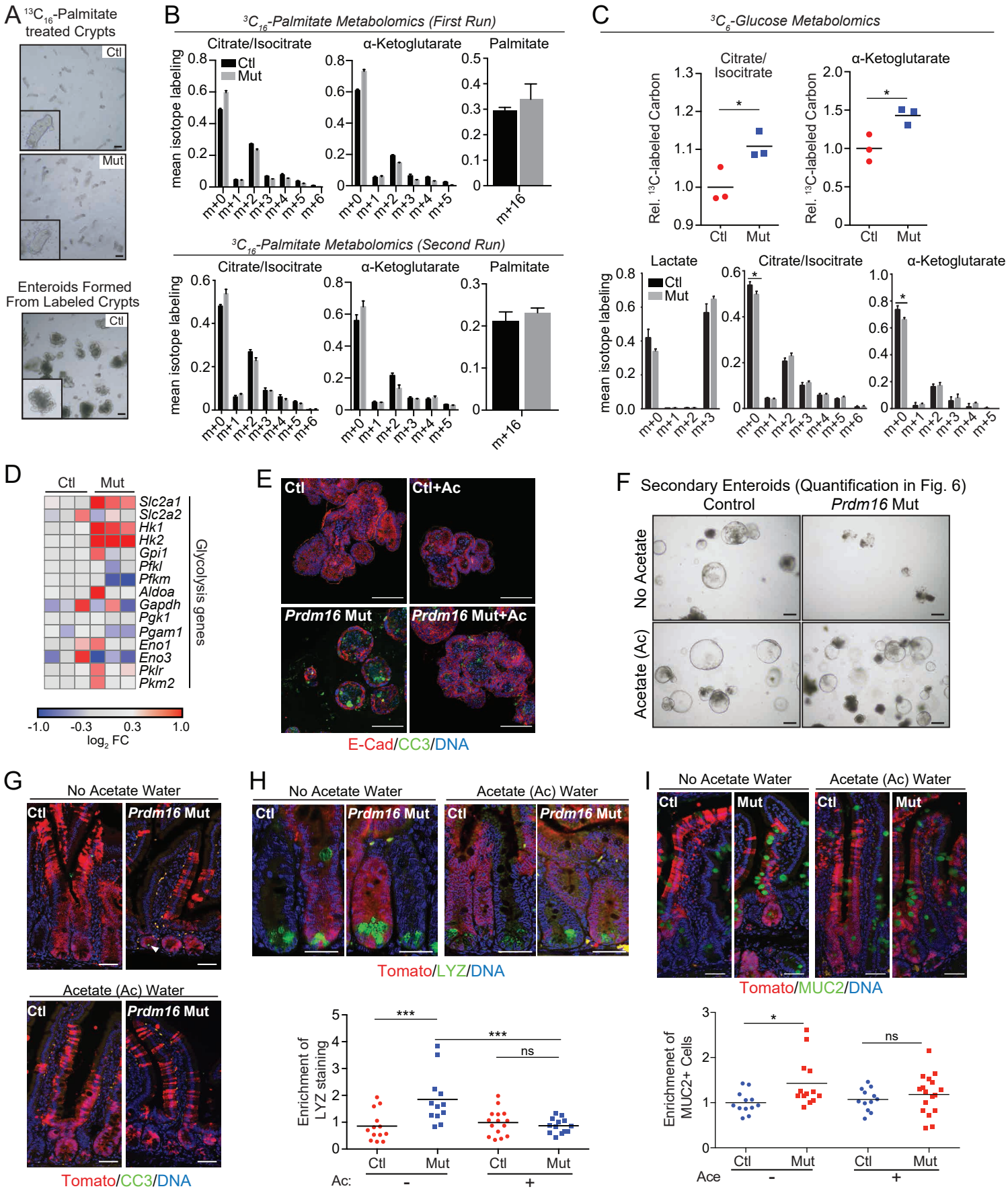

A
$^{13}C_{16}$-Palmitate treated Crypts
Ctl
Mut
Enteroids Formed From Labeled Crypts
Ctl
B
$^{3}C_{16}$-Palmitate Metabolomics (First Run)
Citrate/Isocitrate
α-Ketoglutarate
Palmitate
mean isotope labeling
Ctl
Mut
m+0 m+1 m+2 m+3 m+4 m+5 m+6
m+16
$^{3}C_{16}$-Palmitate Metabolomics (Second Run)
C
$^{3}C_{6}$-Glucose Metabolomics
Citrate/ Isocitrate
α-Ketoglutarate
Rel. ^{13}C-labeled Carbon
Lactate
Citrate/Isocitrate
α-Ketoglutarate
D
Ctl
Mut
Slc2a1
Slc2a2
Hk1
Hk2
Gpi1
Pfkl
Pfkm
Aldoa
Gapdh
Pgk1
Pgam1
Eno1
Eno3
Pklr
Pkm2
Glycolysis genes
-1.0 -0.3 0.3 1.0
log$_2$ FC
E
Ctl
Ctl+Ac
Prdm16 Mut
Prdm16 Mut+Ac
E-Cad/CC3/DNA
F
Secondary Enteroids (Quantification in Fig. 6)
Control
Prdm16 Mut
No Acetate
Acetate (Ac)
G
No Acetate Water
Ctl
Prdm16 Mut
Acetate (Ac) Water
Tomato/CC3/DNA
H
No Acetate Water
Acetate (Ac) Water
Tomato/LYZ/DNA
Enrichment of LYZ staining
Ac:
I
No Acetate Water
Acetate (Ac) Water
Tomato/MUC2/DNA
Enrichmenet of MUC2+ Cells
Ace
ns

Fig. S6: Decreased fatty acid oxidation (FAO) in PRDM16 mutant crypts is partially rescued by supplementation with acetate. (Related to Fig. 6).

A) Crypts retain their structure and viability during palmitate metabolomics. (left) Brightfield images of isolated crypts during $^{13}C_{16}$-palmitate exposure. (right) Enteroids derived from control crypts 4d after exposure to $^{13}C_{16}$-palmitate.

B) Replicate experiments analyzing control and *R26R*^{CreERT2}; *Prdm16*$^{loxP/loxP}$ duodenal crypts at 3d post-tamoxifen. Fractional isotope labeling of citrate/isocitrate, α-ketoglutarate, and palmitate after incubation for 90 minutes in uniformly labeled $^{13}C_{16}$-palmitate. Data from the replicates were combined for final analysis. First run, n=2 for control, n=3 for Mut; Second run, n=2 for control, n=2 for Mut.

C) (Top) Relative ^{13}C label in the citrate and α-ketoglutarate metabolite pools in control vs mutant enteroids 2d after *Prdm16* deletion following incubation with $^{13}C_6$-glucose for 4 hours. n=3 mice per group. ^{13}C-labeling = $\sum$ (% of isotopomer multiplied by labeled carbons in isotopomer) divided by the number of carbons in molecule. (Bottom) Fractional ^{13}C labeling of lactate, citrate, and α-ketoglutarate in duodenal enteroids cultured in $^{13}C_6$ glucose for 4 hours. Experiments were performed 2d after *Prdm16* deletion. Enteroids were from n=3 mice for each condition. n=3 mice.

D) Expression heat map of glycolysis genes in control and mutant crypts, 3d after inducing *Prdm16* deletion. Log_2 fold change shown relative to mean control expression. n=3 mice per group.

E) Staining of Cl. Caspase 3 in control or *Prdm16* mutant enteroids treated with sodium chloride (No Acetate, 5 mM) or sodium acetate (5 mM) 4 days are 4OHT treatment.

F) Secondary enteroids derived from control or *Prdm16* mutant enteroids treated with sodium chloride (No Acetate, 5 mM) or sodium acetate (5 mM).

G-I) Lineage tracing of stem cell progeny in *Prdm16*$^{loxP/+}$ (control) *or Prdm16*$^{loxP/loxP}$ (mutant) tdTomato reporter mice. Animals received drinking water containing either 150 mM NaAc (Ac) or NaCl (No Acetate) 2d before tmx treatment. **G)** Cl. Caspase staining in lineage traced mice (quantification shown in Fig. 6). (Cl. Caspase-3, green; E-Cad, red; DNA, DAPI, Blue). **H)** Lysozyme area was measured in tdTomato positive and tdTomato negative crypts at 4d post tmx treatment. Lysozyme area per crypt in tdTomato positive crypts was normalized to lysozyme area per crypt in tdTomato negative crypts as an internal control for quantification. tdTomato (red), Lysozyme (green) DNA (DAPI, blue). Quantification is shown in graph.

I) Mucin2 positive cells were quantified in tdTomato positive areas of the intestinal epithelium (crypt and villus) at 4d post tmx treatment. Muc2-positive cells per tdTomato positive area are quantified in graph. tdTomato (red), MUC2 (green) DNA (DAPI, blue).

All panels show Mean ± SEM. *p-value<0.05, **p-value<0.01, ***p-value<0.001, Scale bars: 100 μm (A,E-F) 50 μm (G-I).

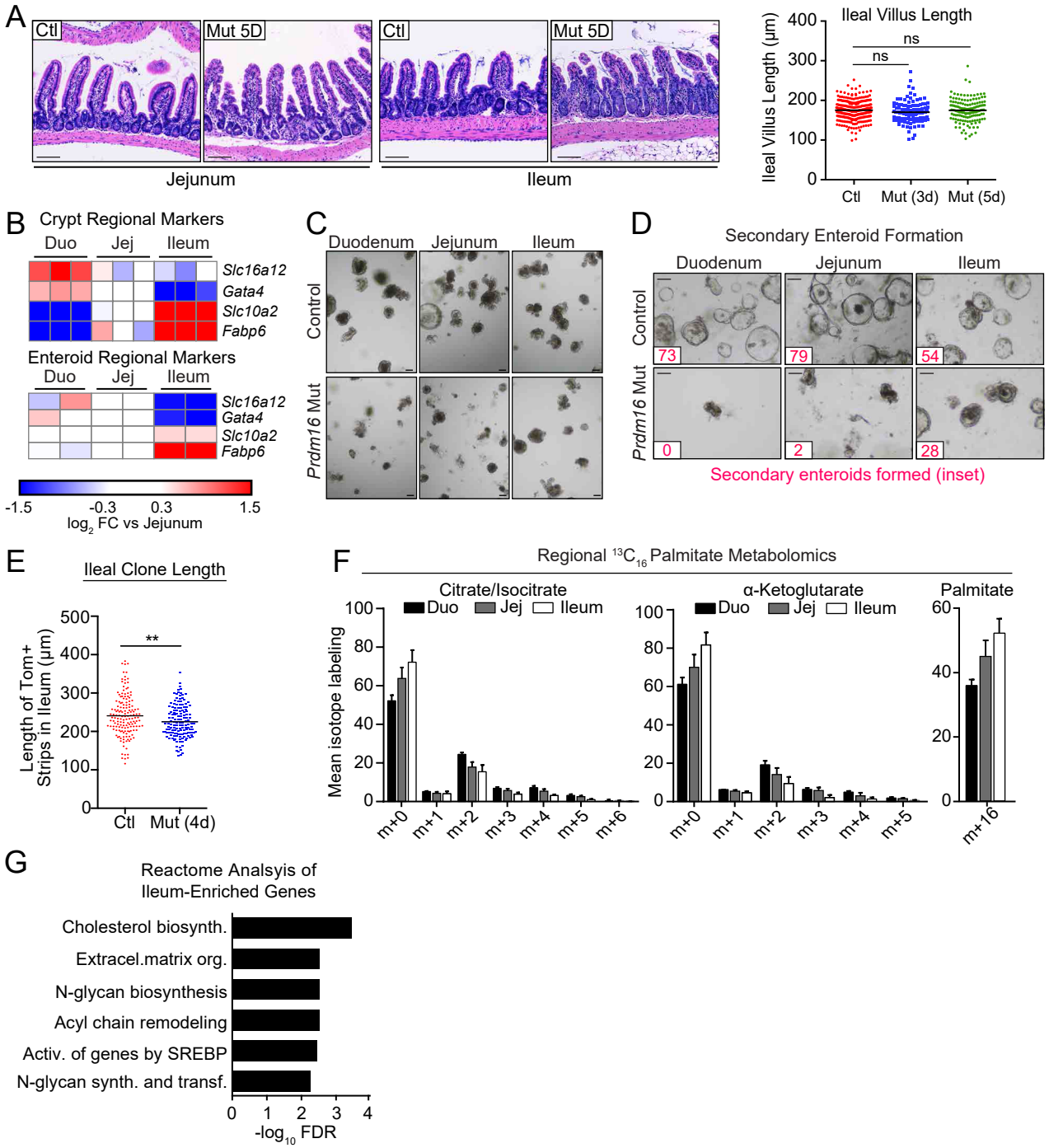


Fig. S7: Regional control of PRDM16 expression and FAO in the small intestine (Related to Fig. 7).

A) H&E histology of control (*Prdm16*$^{loxP/loxP}$) and *Prdm16* mutant (*R26R*^{CreERT2}; *Prdm16*$^{loxP/loxP}$) jejunum and ileum at 5d post tamoxifen (tmx) injection (left). Quantification of ileal villus length at 3d and 5d post-tmx (right). **B)** Expression heat map of regional markers in: crypts from duodenum, jejunum, and ileum; and region-specific derived enteroids. Log_2 fold change shown relative to mean jejunal expression. n=3 mice. **C**) Wide-field view of duodenal, jejunal, and ileal enteroids from control and *Prdm16* mutant animals at 5d after *ex vivo* 4-OHT treatment. **D**) Secondary passaging of duodenal, jejunal, and ileal enteroids from control and *Prdm16* mutant animals at 8d after *ex vivo* 4-OHT treatment. Number (inset) is the number of enteroids recovered per well after passaging. **E)** Length of lineage-traced (tdTomato+) epithelial cell strips in the ileum from control (*Lgr5*$^{GFP/Cre-ERT2}$;*R26R*$^{lox-stop-lox-tdTomato}$;*Prdm16*$^{loxP/+}$) and mutant (*Lgr5*$^{GFP/Cre-ERT2}$;*R26R*$^{lox-stop-lox-tdTomato}$;*Prdm16*$^{loxP/loxP}$) animals at 4d post-tmx. n=146-150, 4 mice per group. **F)** Fractional isotope labeling of citrate/isocitrate, α-ketoglutarate, and palmitate from duodenal, jejunal and ileal crypts incubated for 90 minutes in uniformly labeled $^{13}C_{16}$-palmitate. n=3 mice. **G)** Reactome enrichment analysis of genes with higher expression in ileal versus duodenal crypts. Mean ± SEM. *=p-value<0.05, **p-value<0.01, ***p-value<0.001. Scale bars: 100 µm (A,C,D).

Table S3. Oligonucleotide sequences, Related to STAR Methods

Gene	Forward Primer	Reverse Primer
Prdm16	CAGCACGGTGAAGCCATTC	GCGTGCATCCGCTTGTG
Cd36	AAAGTTGCCATAATTGAGTCCT	TCCGAACACAGCGTAGATAGA
Slc27a2	TCCTCCAAGATGTGCGGTACT	TAGGTGAGCGTCTCGTCTCG
Acsl1	TGCCAGAGCTGATTGACATTC	GGCATACCAGAAGGTGGTGAG
Cpt1a	CTCCGCCTGAGCCATGAAG	CACCAGTGATGATGCCATTCT
Cpt2	GCTCCGAGGCATTTGTC	CATCGCTGCTTCTTTGGT
Acadm	AGGGTTTAGTTTTGAGTTGACGG	CCCCGCTTTTGTCATATTCCG
Acaa2	CCTCAGTTCTTGTCTGTTCAG	AGGTGTGCGGTGATTCTG
Hadh	AGGCTACACGAGCGAGGCGA	ACGGACCCATGGGATACCCAGC
Eci1/Dci	GCAGGGGTTGCAGTGATGAA	GATGACACCTCGGATGCTCTT
Eci2/Peci	TGCTCCTCTTACACGTTTCCG	CGTTGACTGCGTAGAGCTTTTC
Decr1	ACCGTGGTCTTCCACTTGTC	TGCCCCTTTTTGTTTTTCAC
Pparg	TGTGAGACCAACAGCCTGAC	GCATGGTGCCTTCGCTGA
Ppara	GCGTACGGCAATGGCTTTAT	GAACGGCTTCCTCAGGTTCTT
Gata4	TGGAAGACACCCCAATCTCG	AGGTAGTGTCCCGTCCCATC
Slc16a12	TGCTTCCTTGTTACCATCTGC	CATGCTGTTTGGGAGTAATCCT
Fabp6	CTTCCAGGAGACGTGATTGAAA	CCTCCGAAGTCTGGTGATAGTTG
Ppard	TCCATCGTCAACAAAGACGGG	ACTTGGGCTCAATGATGTCAC
Ppargc1a	CCCTGCCATTGTTAAGACC	TGCTGCTGTTCCTGTTTTC
Acaca	ATGGGCGGAATGGTCTCTTTC	TGGGGACCTTGTCTTCATCAT
Fasn	CCCGAGTCAGAGAACCTACA	GATCCTTCAGCTTTCCAGACC
Scd1	GAGGCGAGCAACTGACTATC	TCACCTTCTCTCGTTCATTTCC
Slc10a2	GTCTGTCCCCCAAATGCAACT	CACCCCATAGAAAACATCACCA
Olfm4	TGAAGGAGATGCAAAAACTGG	CTCCAGCTTCTCTACCAAGAGG
Lgr5	TAAAGACGACGGCAACAGTG	GCCTTCAGGTCTTCCTCAAA
Ascl2	CCTCTCTCGGACCCTCTCTCAG	CAGTCAAGGTGTGCTTCCATGC
Sis	CGTTTCCGGTTCAAGCTCACA	CCTGATGACTTTGATGCTGAACG
Chga	CAGCTCGTCCACTCTTTCCG	CCTCTCGTCTCCTTGGAGGG
Reg4	CTGAGCTGGAGTGTCAGTCAT	GTCCACTGCCATAATTGCTTCT
Dclk1	GGGTGAGAACCATCTACACCATC	CCAGCTTCTTAAAGGGCTCGAT
KI67	CCTTTGCTGTCCCCGAAGA	GGCTTCTCATCTGTTGCTTCCT
Ifi44	ATACTATTAGATGAGAAAGCTGTGATTG	TACTATGTAACACAGCAATGCCT
Oas3	CTCTGGGGTCGCTAAACATCA	CTGAGTGACAGGTCTTCTGGT
Ccng1	ACAACTGACTCTCAGAAACTGC	CATTATCATGGGCCGACTCAAT
Bax	TGAAGACAGGGGCCTTTTTG	AATTCGCCGGAGACACTCG
Mdm2	TGTCTGTGTCTACCGAGGGTG	TCCAACGGACTTTAACAACTTCA
P21	CCTGGTGATGTCCGACCTG	CCATGAGCGCATCGCAATC
Tff3	TTGCTGGGTCCTCTGGGATAG	TACACTGCTCCGATGTGACAG
Mmp7	AGGAAGCTGGAGATGTGAGC	TCTGCATTTCCTTGAGGTTG
Defa4	CCAGGCTGATCCTATCCAAA	ATTCCACAAGTCCCACGAAC
Defa-rs1	GCACAGAAGGCTCTGCTCTT	ACCCAGATTCCACATTCAGC
Lyz1	GGAATGGATGGCTACCGTGG	CATGCCACCCATGCTCGAAT
Lct	CTGTCATGGGCACAACTTCTC	TGTGGCATAATCAGCAAAGAGG
Cbr1	TCAATGACGACACCCCCTTC	CCTCTGTGATGGTCTCGCTTC
Spink4	TGCAGTCACATAGCTCACAAG	CCATGCCAAGGAGGGGAA
Agr2	TGTCCCCAGAATTGTGTTTGTAGA	TGTCAGAAGGTTCATAAGCGTAGA
Clca1	ACCAAAAGATCACCGCAAACC	CTCTCCAACTGTCATGTCCGA
Gcg	CTTCCCAGAAGAAGTCGCCA	GTGACTGGCACGAGATGTTG

Gip	AACTGTTGGCTAGGGGACAC	TGATGAAAGTCCCCTCTGCG
Hck	TCCTCCGAGATGGAAGCG	ACAGTGCGACCACAATGGTAT
Ngn3	TCTCAAGCATCTCGCCTCTTC	ACAGCAAGGGTACCGATGAGA
ChIP qPCR Primers	**Forward**	**Reverse**
Decr1 -2kb (Neg Control	CATCCTTCTCTTTCCTCCACTC	CAGCGATATTCCTATGGAACTGA
Hadh +2.6 kb (Neg Con)	ACAGACTCTCCACTGACTTAGA	CTCGAAGTAGCATCAGGGTTAC
Slc27a2 -0.2 kb	TGCGGTGCGTTTATAAGGT	CGTGGTGCTGTGGTTAGTTA
Acsl1 -0.7 kb	CGTCCTTGAGCAACGACTAA	GGAATACAGGACTTCCGCAATA
Cpt1a +2kb	CACGCGACTTTCCTGTACTT	TCGGGCCTACCGGTAAATA
Cpt2 -0.2kb	TGTAACTCTGAAGCTAACCTCTTT	GTCTGCCAAATGCCAAGTTT
Acaa2 -0.25kb	AGTGGTTCTCAAATTCCCAGAG	CTCGGGAAGACCAAGGTTAC
Hadh +0.8kb	ACAGAAGCCGATCAGAGATTAG	CTGAAATCTGCGTGCTTGTC
Eci2 -0.2kb	GGACAGCTCCCAGAATGTTTA	CAGGAGCACTCTTGTCCATATAA
Decr1 +0.7kb	CCTTGTGGAGGATTCCTTTCT	GAGAGGGAAAGACACAGCTAAT
shRNA	**Sequence**	
Prdm16 shRNA A	GCATGGTATGAAAGAGGAAAT	
Prdm16 shRNA C	GCTCCTGTCTACATTCCTGAA	