Supplemental Material and Methods

Expression Plasmids, siRNA, Cell culture and reagents. The full-length human SETD2 cDNA was cloned into pMSCV-puro/neo to generate SETD2 expression plasmids. SETD2 shRNA sequences are CCGGTGATAGCCATGATAGTATTAACTCGAGTTAATACTATCATGGCTA TCATTTTTG; CCGGCAGGGAGAACAGGCGTAATAACTCGAGTTATTACGCCTGTTC TCCCTGTTTTTG. SSO with 2'-*O*-methoxyethyl (MOE)-phosphorothioate modification was targeted to the 3'-splice site of intron 2 in DVL2 pre-mRNA. SSO sequence is CACCCUUCUAGCUGGUGUCCUC. HCT116, DLD1, RKO and 293T cells were obtained from ATCC and cultured in DMEM with 10% fetal bovine serum. Cells were transfected with siRNA duplexes (60 nM) or Antisense Oligonucleotide (60 nM) by using Lipofectamine 2000 (Invitrogen) or Dharmacon Transfection (Dharmacon) reagents according to manufacturer's instructions. To establish the individual stable cells, retrovirus/lentivirus was used. Cell proliferation assay was performed using CellTiter 96® Non-Radioactive Cell Proliferation Assay (MTT) kit (Promega) based on the manufacturer's instructions. Standard 24-well Boyden invasion chambers (BD Biosciences) were used to assess cell migration abilities following the manufacturer's suggestions. For oncosphere formation assay, cells were suspended in serum-free DMEM-F12 medium containing N-2 Plus Media Supplement (Life Technologies), B-27 Supplement (Life Technologies), 20 ng/ml EGF (PeproTech) and 10 ng/ml FGF (PeproTech) in ultra-low attachment 96-well plate to support growth of oncospheres. Colonies were scored and documented by photomicroscopy 1 week after preparations. For soft-agar colony formation assay, cells were suspended in DMEM containing 0.35% low-melting agar (Invitrogen) and 10% FBS and seeded onto a coating of 0.7% low-melting agar in DMEM containing 10% FBS. Plates were incubated at 37 °C and 5% CO2 and colonies were scored 3 weeks after preparations. Colonies larger than 0.1 mm diameter were scored as positive. All results were calculated based on three independent experiments and statistical significance was determined by One-way ANOVA (Tukey's multiple comparisons test). For Wnt simulation, HCT116 cells were plated in 12-well plates. After 24 hr of culture, Wnt-3a (100 ng/ml, R&D) was added. For Wnt luciferase reporter experiment, HCT116 cells were stimulated for 12 hours of Wnt-3a (100 ng/ml). Luciferase activity was determined with the Promega luciferase assay kit. All values were normalized for

transfection efficiency against *Renilla* activities. Results were quantified based on three independent experiments and statistical significance was determined by two-tailed Student's *t* test. P values less than 0.05 were considered statistically significant.

IECs isolation. IECs from the mice were isolated by isolation buffer (10mM EDTA). In brief, intestines were harvested, and cut into small pieces (4 - 6 mm) in cold PBS and incubated with isolation buffer at 4°C for 30 min. The supernatant was centrifuged to collect the cells for RT-qPCR and ChIP-qPCR assay.

RNA isolation and real-time PCR. Intestines were collected and frozen immediately in liquid nitrogen. RNA was isolated using TRIzol followed by RNeasy Mini kit (Qiagen) cleanup and RQ1 RNase-free DNase Set treatment (Promega) according to the manufacturer's instructions. First strand cDNA was synthesized using Superscript II (Invitrogen) and 2 μg of total RNA was used in each cDNA synthesis reaction. SYBR Green Master Mix reagents (Roche) and primer mixtures (Supplemental Table 2) were used for the real-time PCR. Standard curves were generated by serial dilution of a preparation of total RNA, and all mRNA quantities were normalized against β-actin RNA. Student's t-test was used to statistical analysis of qRT-PCR results and p value less than 0.05 was considered significant.

Histology and immunohistochemistry analysis. Intestines from mice were flushed and fixed in 4% formaldehyde in PBS for 24 h. Samples were then dehydrated and embedded in paraffin, sectioned at 7 μM and processed for H&E staining. The primary antibodies were: SETD2 (Lifespan, LS-C332416, or generated by Ango Technology; Shanghai), H3K36me3 (Abcam, ab9050), Phospho-Histone H3 (Cell Signaling, 9701), Cleaved-caspase3 (Cell Signaling, 9661), β-catenin (Santa Cruz, SC7199), CD44 (BD, 553131), Sox9 (Millipore, AB5535), and Lysozyme (Dako, A0099). Biotinylated secondary antibodies were purchased from Jackson Immunology. Staining was visualized with ABC Kit Vectastain Elite (Vector) or TSA kit (Invitrogen). PAS staining was performed using PAS staining kits (Muto Pure Chemicals, Japan) following the manufacturers' recommendations. An ALP activity assay was performed

using the Alkaline Phosphatase Staining Kit (Sigma-Aldrich) as described in the manufacturer's protocols. RNAscope® in situ hybridization assay was used to examine Olfm4 transcripts on formalin-fixed intestine according the manufacturer's protocol (Advanced Cell Diagnostics).

Organoid culture. The intestine was opened longitudinally, and villus was scraped away. After thorough washing in PBS, the pieces were incubated in 2 mM EDTA/PBS for 10 min and further 15 min at 4 °C. Crypt fractions were isolated and purified by successive centrifugation steps. 100 µl mixture of Matrigel (BD Biosciences) and complete growth medium (at a ratio 2:1) and 5 µl drops of crypt-containing Matrigel were added to pre-warmed wells in a 96-well plate. After polymerization, 100 µl Advanced DMEM/F12 (Invitrogen) containing growth factors (50 ng/ml EGF, PeproTech; 500 ng/ml R-spondin1, PeproTech and 100 ng/ml Noggin; PeproTech) was added and refreshed every two or three days.

Immunoprecipitation and immunoblotting. For immunoprecipitation assays, cells were pretreated MG132 for 8 hours, and lysed with HEPES lysis buffer (20 mM HEPES, pH 7.2, 50 mM NaCl, 0.5% NP-40, 1 mM NaF and 1 mM dithiothreitol) supplemented with protease-inhibitor cocktail (Roche). Immunoprecipitations were performed using the indicated primary antibody and protein A/G agarose beads (Roche) at 4 °C. Both lysates and immunoprecipitates were examined using anti-Ub primary antibodies (Cell Signaling) and the related secondary antibody followed by detection with the chemiluminescence substrate (Millipore). For immunoblotting, total proteins were extracted from cells following the standard protocol. Cytomembrane free lysate were separated from cells by Native Membrane Protein Extraction Kit (Millipore; 444810). Nuclear and cytoplasmic proteins were separated by Cytoplasmic & Nuclear Extraction Kit (Invent; sc-003). Protein concentration was measured using the BCA protein assay kit (Thermo Scientific; 23225). The primary antibodies used in this study were as follows: H3K36me3 (Abcam, ab9050), H3 (Cell Signaling, 9715), PCNA (Santa Cruz, SC7907), β-catenin (Santa Cruz, SC7199), β-actin (Santa Cruz, SC47778), SETD2 (GeneTex, GTX127905, or homemade), DVL2 (Cell

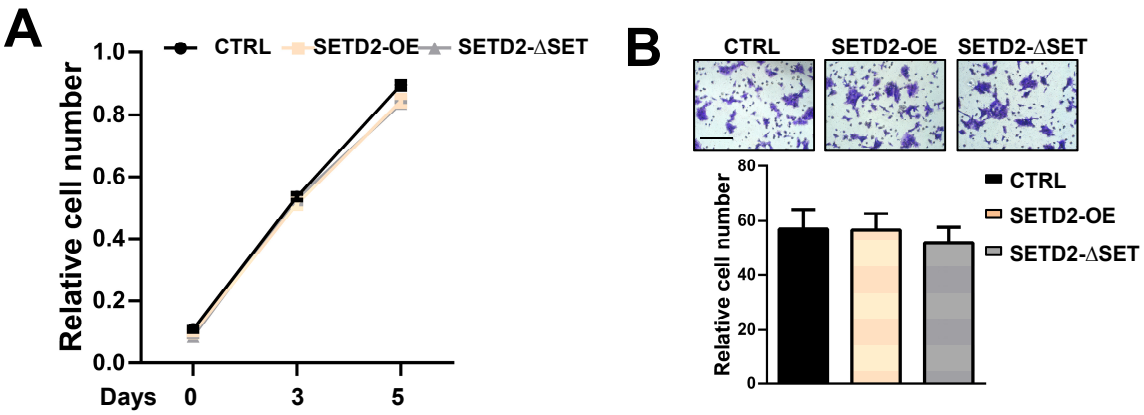
Signaling, 3224), P-LRP6 (Cell Signaling, 2568), LRP6 (Cell Signaling, 3395), Active β-catenin (Cell Signaling, 8814), Cleaved-caspase3 (Cell Signaling, 9661), Caspase 3 (Cell Signaling, 9665), Lamin A/C (Cell Signaling, 2032).

Generation of SETD2 antibody. SETD2 antibody was generated by Ango Technology; Shanghai. In brief, SETD2 truncated protein including 200 amino acids (941 -1140 aa) from the N-terminal coupled with KLH were purified and used as immunogen. Immunogen was diluted with saline, and then mixed with the appropriate adjuvant (mass ratio is1: 1). 4-5 times compulsory immunization was operated by injecting four New Zealand rabbits with emulsion (250 to 500 μg immunogen per animal), and specific column coating different SETD2 protein fragments were used for antibody purification. The specificity was assessed by IB and immunohistochemistry analysis of SETD2 KD cells or Setd2 KO mice.

Immunofluorescence for organoids. Organoids were fixed with warm 4% paraformaldehyde (pH 7.4) for 1 h, permeabilized in PBS containing 1% triton X-100 and blocked with PBS containing 1% BSA, 3% normal goat serum and 0.2% Triton X-100. Primary and secondary antibodies were incubated respectively, then the organoids were mounted and imaged.

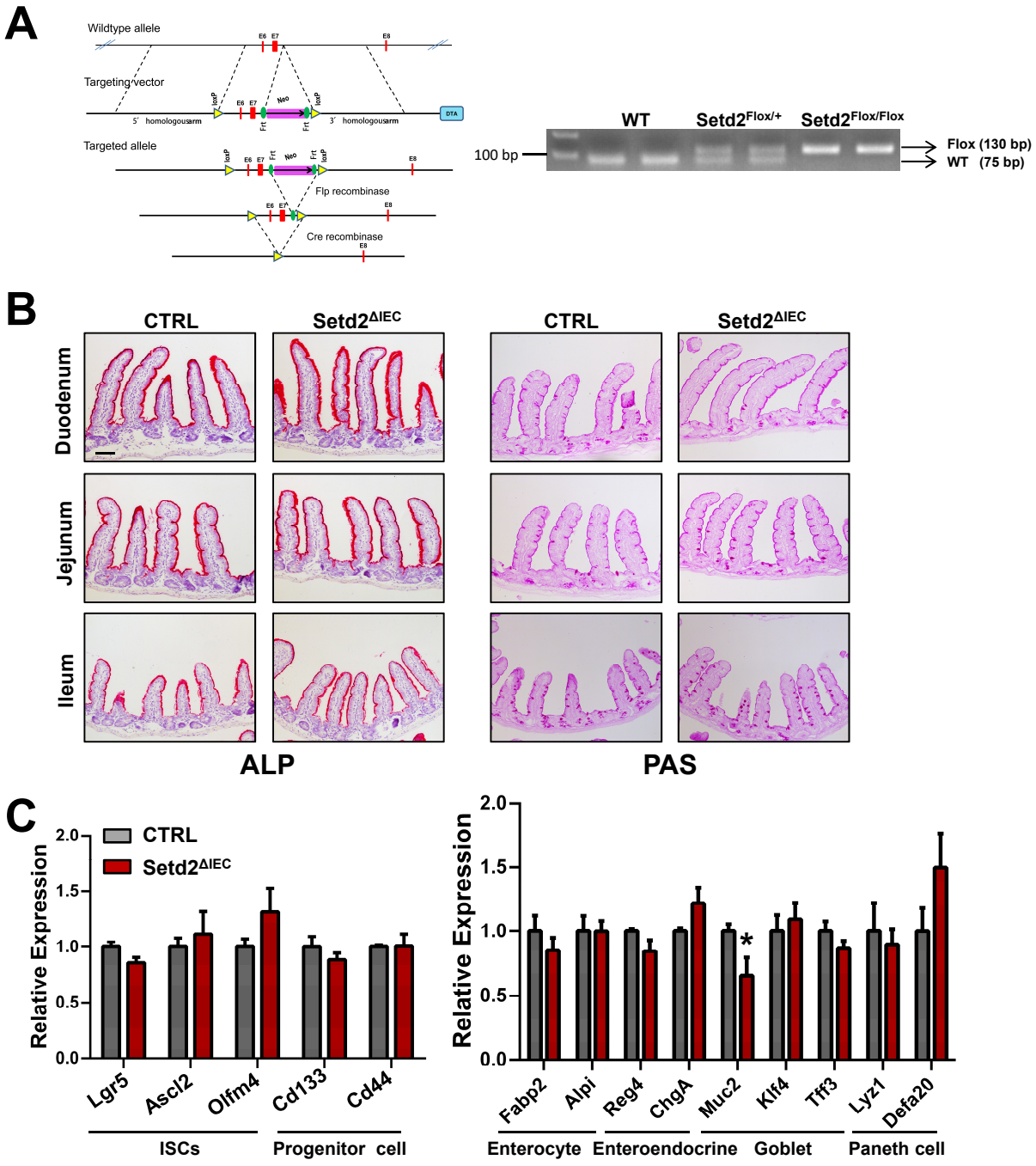
ChIP-qPCR assays. The ChIP assays were performed using Magnetic ChIP kit (Millipore). The procedure was as described in the kit provided by the manufacturer. Briefly, isolated IEC cells were fixed by 1% formaldehyde, fragmented by a combination of MNase and sonication. H3K36me3 (Abcam; ab9050), RNA polymerase II (Abcam; ab817); Ser2-phosphorylated RNA polymerase II (Abcam; ab5095) antibody was then used for immunoprecipitation. After washing and reverse-crosslinking, the precipitated DNA was amplified by primers and quantified by the StepOnePlus real-time-PCR machine (ABI). Primer sequences can be found in the Supplemental Table 3.

Supplemental Figure 1



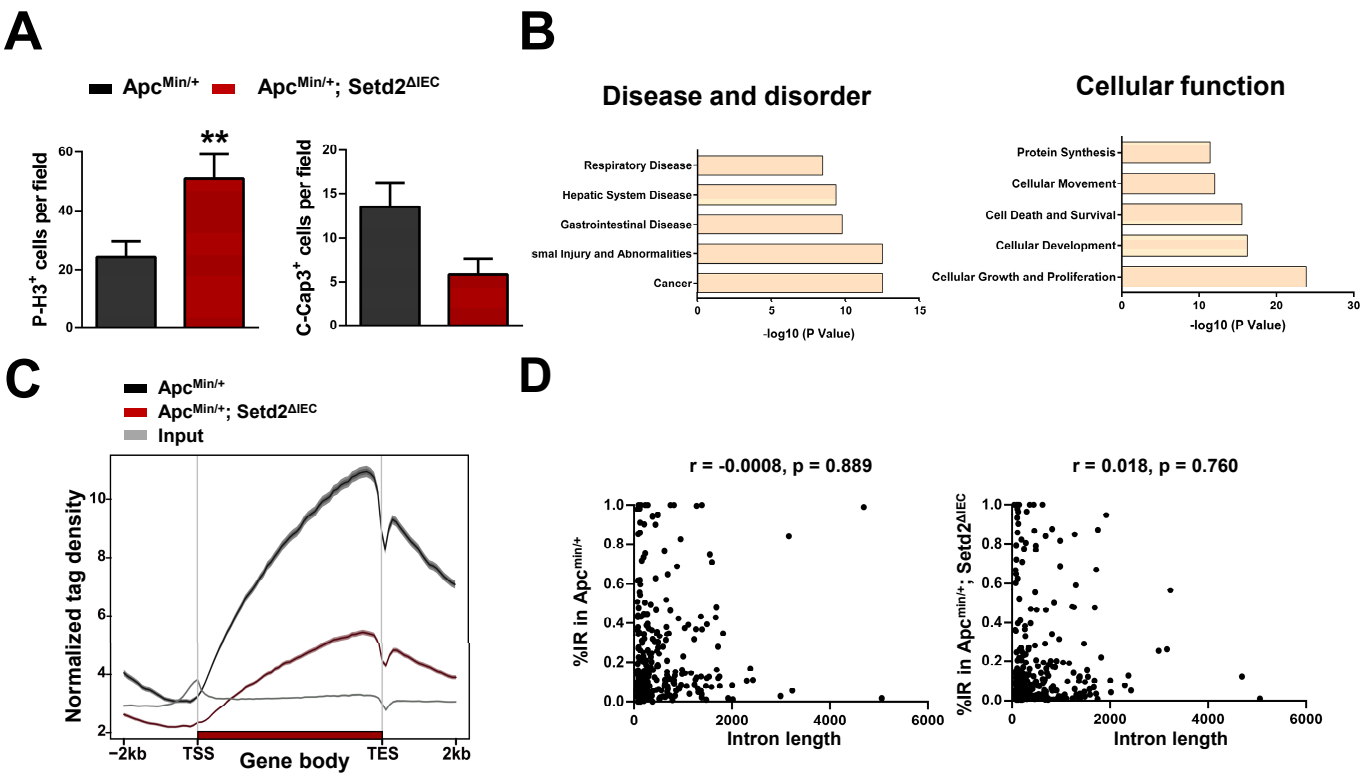
Supplemental Figure 1. SETD2 overexpression does not affect the growth and migration of HCT116 cells. **(A)** MTT analysis of the cell growth in control, wild-type SETD2 or SETD2-ΔSET overexpression HCT116 cells. **(B)** Transwell assays of control, wild-type SETD2 or SETD2-ΔSET overexpression HCT116 cells. The quantitation results are shown in the lower panel. Scale bars: 400 mm (**B**).

Supplemental Figure 2



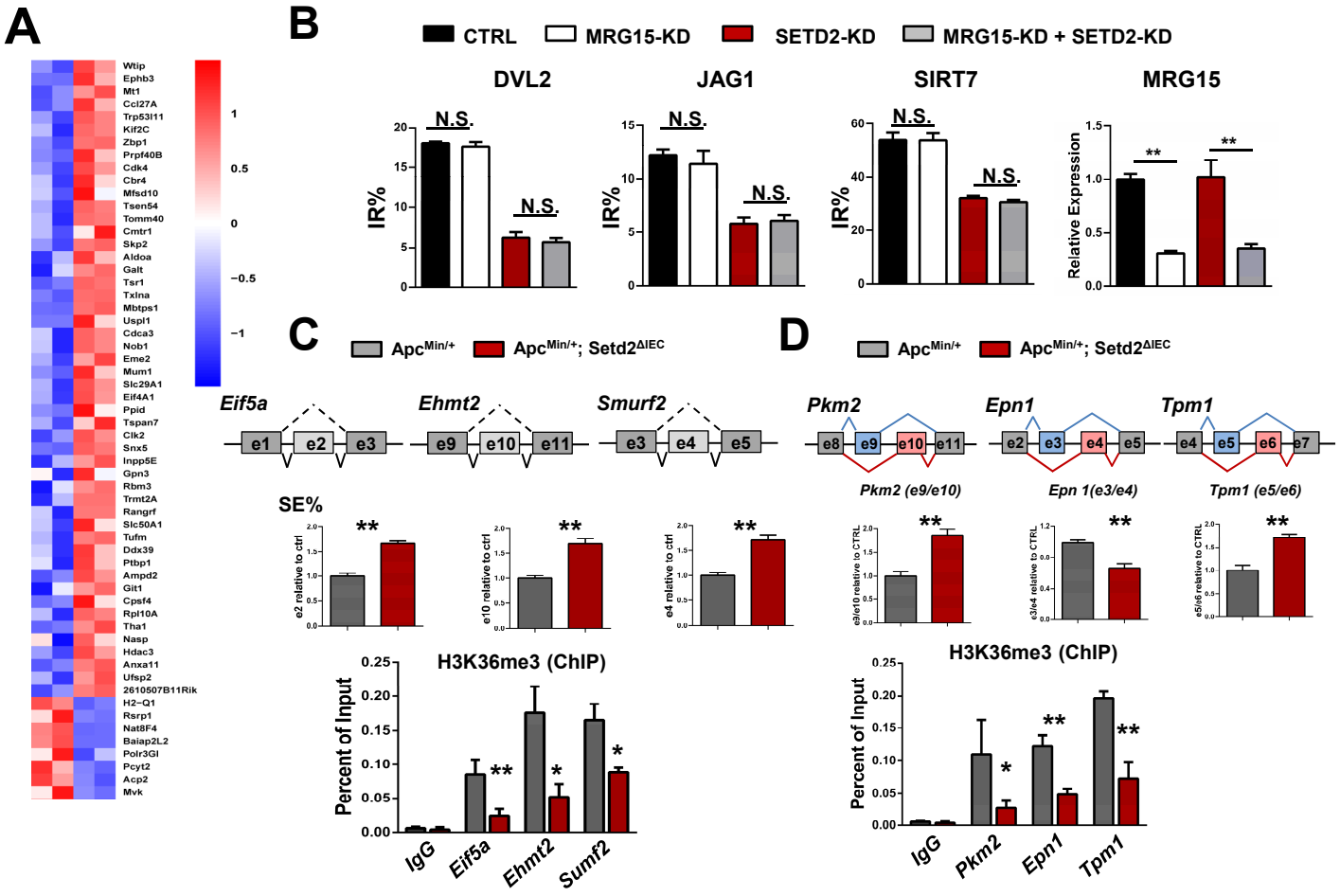
Supplemental Figure 2. SETD2 is dispensable for the self-renewal and differentiation of intestinal epithelial cells under physiological conditions. (A) Schematic generation (left) and genotyping(right) of Setd2 flox mice. **(B)** ALP (Enterocyte) and PAS (Goblet cells) staining of small intestine sections as indicated. **(C)** RT-qPCR analysis of gene expressions in the small intestines of wild-type and SETD2$^{\Delta IEC}$ mice as indicated . ISCs: Intestinal stem cells. *: $p < 0.05$. Scale bars: 50μm (**B**).

Supplemental Figure 3



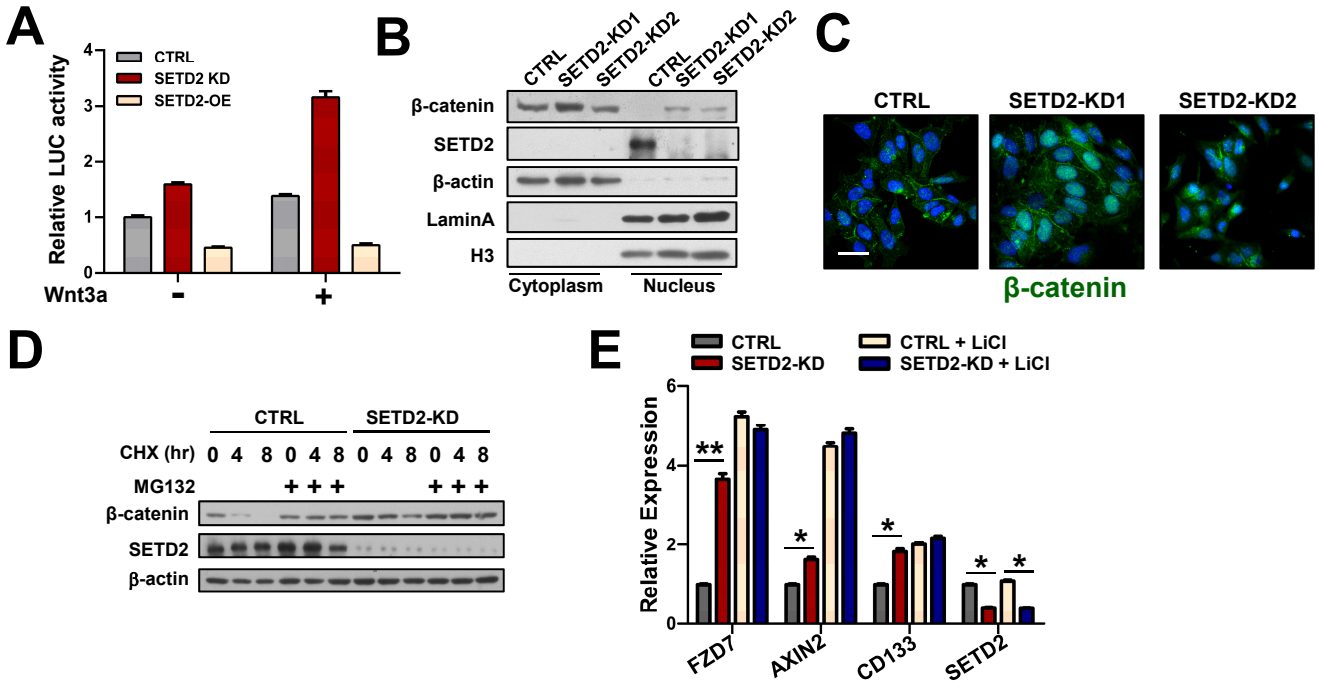
Supplemental Figure 3. Analyses of SETD2 function in intestinal tumorigenesis. (A) The quantitation results of phospho-H3 and cleaved-Caspase 3 positive cells in the intestinal sections of $Apc^{min/+}$ and $Apc^{min/+}$; $Setd2^{\Delta IEC}$ mice (n = 6). **(B)** Ingenuity Pathway Analysis (IPA) of the disease process and cellular function that SETD2 might participate in. **(C)** Tag density profile of H3K36me3 distributions of genes in the intestines of $Apc^{min/+}$ and $Apc^{min/+}$; $Setd2^{\Delta IEC}$ mice (two-month-old). **(D)** The association between intron length and intron retention ratio in the presence or absence of SETD2.

Supplemental Figure 4



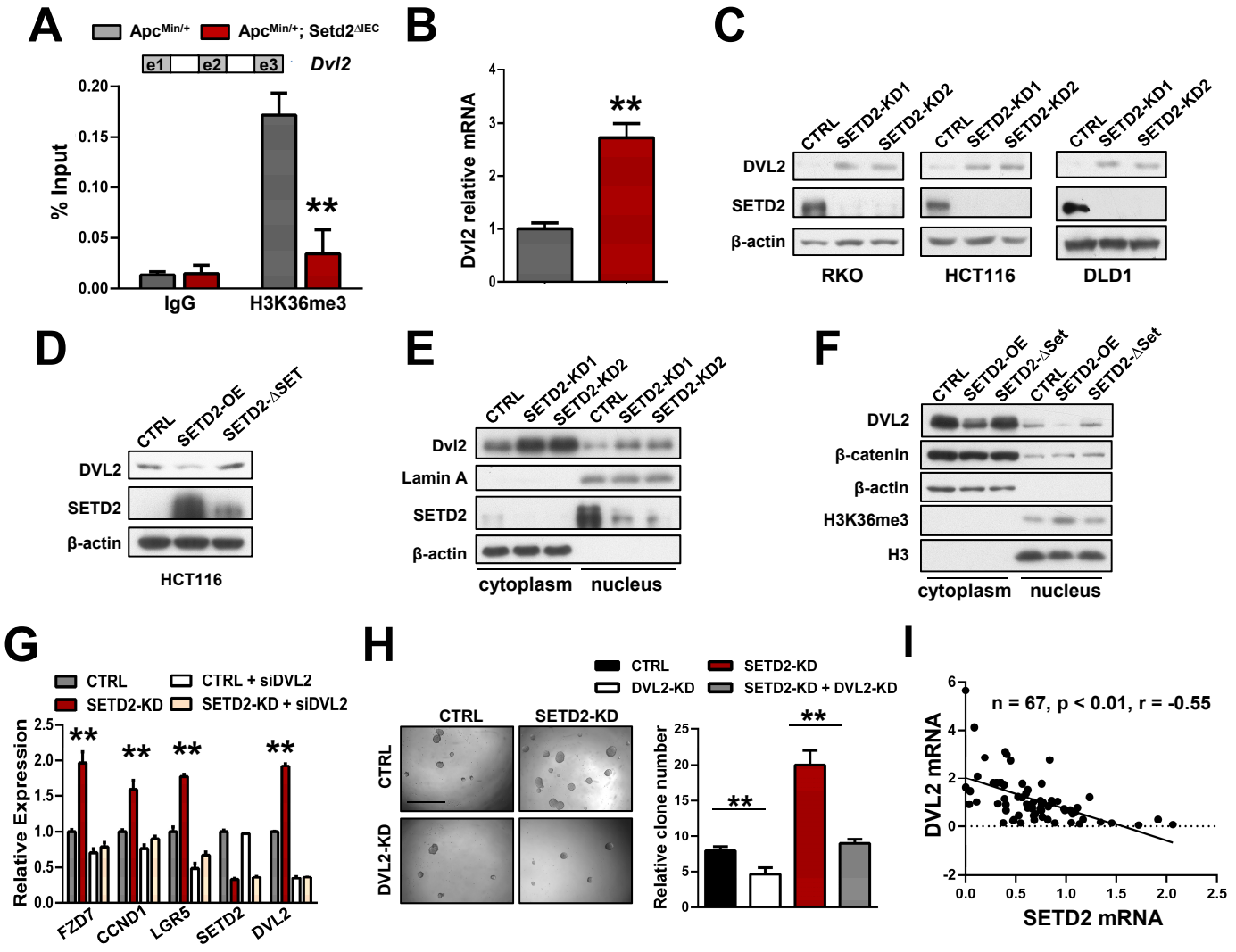
Supplemental Figure 4. SETD2 regulates cancer-associated alternative splicing events. (A) Heatmap summarizes the IR-related genes are largely upregulated in SETD2-deficient IECs. **(B)** The IR% for DVL2, JAG1 and SIRT7 in control and SETD2 depleted HCT116 cells with or without MRG15 knockdown. MRG15 knockdown efficiency is determined by RT-qPCR analysis. Knockout of Setd2 in intestine alteres the ratio of exon skipping (SE%) (**C**; upper panel) and mutually exclusive exon (MXE) (**D**; upper panel). ChIP-qPCR analysis of H3K36me3 occupancies in the areas of ES or MEX genes are shown in bottom panel (**C-D**). Error bars indicate SEM from three experiments. *: $p < 0.05$, **: $p < 0.01$.

Supplemental Figure 5



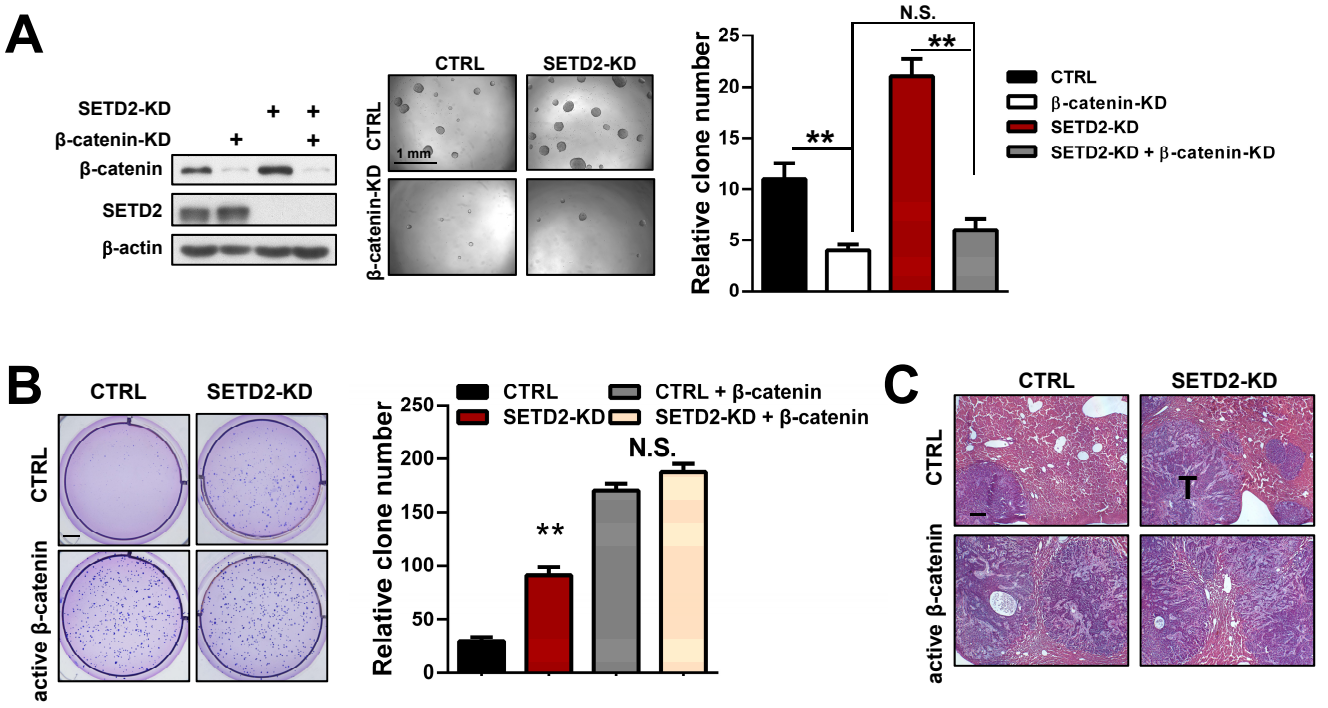
Supplemental Figure 5 . SETD2 modulates Wnt signaling. (A) TOP/FOP luciferase reporter ratio of SETD2 knockdown and overexpression in HCT116 with or without the treatment of Wnt3a. **(B-C)** SETD2 knockdown induces nuclear localization of β-catenin in HCT116 cells. **(D)** IB analysis of control and SETD2 knockdown HCT116 cells with or without MG132 treatment for the indicated duration of time. **(E)** RT-qPCR analysis of Wnt target gene expressions in control and SETD2-KD HCT116 cells treated with or without LiCl. Scale bar: 20 μm (**C**).

Supplemental Figure 6



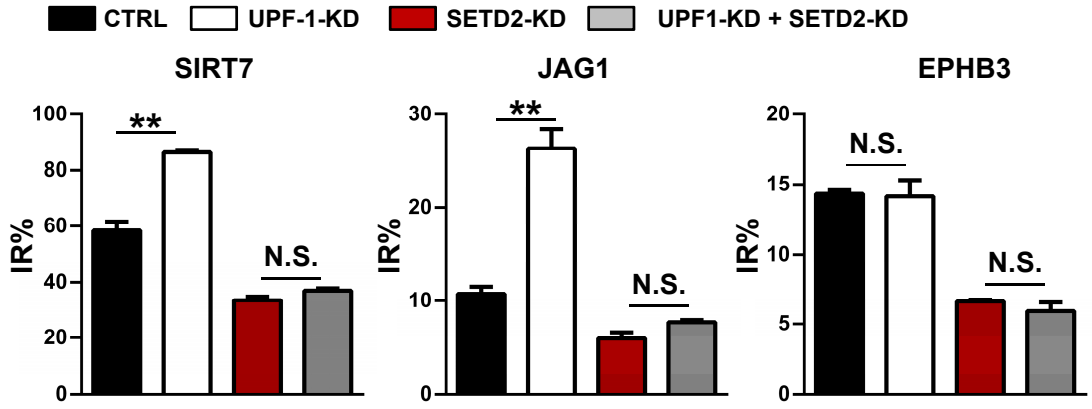
Supplemental Figure 6. SETD2 modulate DVL2 expression to modulate intestinal tumorigenesis. (A) ChIP-qPCR analysis of H3K36me3 codes in the IR area of *Dvl2* gene locus. **(B)** Dvl2 mRNA level in IECs isolated from $Apc^{min/+}$ and $Apc^{min/+}$; $Setd2^{\Delta IEC}$ mice is shown. **(C)** IB analysis of DVL2 protein in control and SETD2-depleted RKO, HCT116 and DLD1 cells. Blot images are derived from replicate samples run on parallel gels. **(D)** Western blotting analysis of DVL2 expression in control, wild-type SETD2 or SETD2-ΔSET overexpression HCT116 cells. **(E)** SETD2 knockdown induces DVL2 nuclear localization in HCT116 cells. **(F)** IB analysis of β-catenin and DVL2 nuclear accumulations in control and wild-type SETD2 or SETD2-ΔSET overexpression HCT116 cells. **(G)** RT-qPCR analysis of Wnt target genes in control and SETD2 knockdown HCT116 cells with or without DVL2 knockdown. **(H)** Oncosphere formations of SETD2-KD HCT116 cells with or without DVL2 depletion. The quantitation results are shown in the right panel. **(I)** RT-qPCR analysis of DVL2 and SETD2 mRNA levels in colorectal tumors (n = 67). Scale bars: 1mm **(H)**, *: $p < 0.05$, **: $p < 0.01$.

Supplemental Figure 7



Supplemental Figure 7. SETD2 depletion promotes liver metastasis dependent on activation of Wnt/β-catenin signaling. (A) Western blotting analysis and oncosphere formations of SETD2-KD HCT116 cells with or without β-catenin depletion. The quantitation results are shown in the right panel. **(B)** Soft agar formations of SETD2-KD HCT116 cells with or without active β-catenin overexpression (left panel). The quantitation results are shown in the right panel. **(C)** H&E staining of tumor metastatic lesions in livers in control and SETD2-KD HCT116 cells with or without active β-catenin overexpression. T: tumor. Scale bars: 1 mm (**A**), 5 mm (**B**), 100 μm (**C**). *: $p < 0.05$, **: $p < 0.01$

Supplemental Figure 8



Supplemental Figure 8. Analysis of intron retention related genes affected by NMD. RT-qPCR analysis of IR% in control and SETD2-depleted HCT116 cell with or without UPF1 knockdown. **: $p < 0.01$

Supplemental Table 1: Univariate and Multivariate Analysis of Prognostic Parameters including SETD2 for Patients Survival in the TMA dataset (n = 146)

Variable	Univariate Analysis		Multivariate Analysis	
	HR (95% CI)	p value	HR (95% CI)	p value
Gender (male versus female)	1.239 (0.688-2.231)	0.474	*N.A.*	*N.A.*
Stage (I or II versus III or IV)	3.992 (1.688-9.437)	0.001	0.631 (0.11-3.8)	0.615
pT status (T1 or T2 versus T3 or T4)	2.065 (0.64-6.665)	0.215	*N.A.*	*N.A.*
pN status (N0 versus N1, N2 or N3)	3.163 (1.471-6.799)	0.002	1.671 (0.387-7.215)	0.491
pM status (M0 versus M1)	9.092 (4.776-17.309)	<0.001	8.432 (3.786-18.782)	< 0.001
Differentiation (low versus high)	0.585 (0.322-1.062)	0.075	*N.A.*	*N.A.*
SETD2 expression (≤4 versus ≥6)	0.306 (0.208-0.680)	0.001	0.439 (0.198-0.973)	0.043

Supplemental Table 2: The primers for RT-qPCR analysis.

qRT-PCR primer

Human gene	
SETD2	TGCTTCTAGTCGATTTTTGCCC, AGGGTTTGGAGTATCACTTTGC
AXIN2	AGTGTGAGGTCCACGGAAAC, CTTCACACTGCGATGCATTT
CD133	CTGGGGCTGCTGTTTATTATTCTG, ACGCCTTGTCCTTGGTAGTGTTG
CD44	TGGCACCCGCTATGTCGAG, GTAGCAGGGATTCTGTCTG
LGR5	CTTCCAACCTCAGCGTCTTC, TTTCCCGCAAGACGTAACTC
CTNNB1	AAAGCGGCTGTTAGTCACTGG, CGAGTCATTGCATACTGTCCAT
β-actin	AGAGCTACGAGCTGCCTGAC, AGCACTGTGTTGGCGTACAG
DVL2	TCAGCAGCGTCACAGATTCC, GTCTCCCCGCTCATTGCTC
DVL2-IR	AGCCTTCTCCTTCTGGAGTCT, CACCAGCTAGAAGGGTGCAA

Murine gene	
Setd2	TAAGGGCTGCTAAGGATCTTCC, GTGGCATCTATTATCTCGTCATTTT
Axin2	CTCCCCACCTTGAATGAAGA, ACTGGGTCGCTTCTCTTGAA
Cd133	TTGGTGCAAATGTGGAAAAG, ATTGCCATTGTTCCTTGAGC
Cd44	AGAAAAATGGCCGCTACAGTATC, TGCATGTTTCAAAACCCTTGC
Lgr5	CCTACTCGAAGACTTACCCAGT, GCATTGGGGTGAATGATAGCA
Ctnnb1	CCCAGTCCTTCACGCAAGAG, CATCTAGCGTCTCAGGGAACA
Fzd6	ATGGAAAGGTCCCCGTTTCTG, GGGAAGAACGTCATGTTGTAAGT
Fzd7	CGGGGCCTCAAGGAGAGAA, GTCCCCTAAACCGAGCCAG
Apcdd1	GAAAGAGGTTGGGGTGAGACT, GAAGCCGAATCAAGCTGGTAA
Myc	GATGGAGATGAGCCCGACT, CCTAGTGCTGCATGAGGAGAC
Ccnd1	GCGTACCCTGACACCAATCTC, CTCCTCTTCGCACTTCTGCTC
Ki67	GATGGAAGCATTGTGAGAACCA, CCTGCTCTTCCACAGATTCAAG
Lrp5	AAGGGTGCTGTGTACTGGAC, AGAAGAGAACCTTACGGGACG
Ephb2	GCGGCTACGACGAGAACAT, GGCTAAGTCAAAATCAGCCTCA
Sox9	AGTACCCGCATCTGCACAAC, ACGAAGGGTCTCTTCTCGCT
Ascl2	GCCTACTCGTCGGAGGAA, CCAACTGGAAAAGTCAAGCA
Olfm4	AGTGACCTTGTGCCTGCC, CACGCCACCATGACTACA
Alpl	GGCCATCTAGGACCGGAGA,TGTCCACGTTGTATGTCTTGG
Fabp2	CACACACAGCTGAGATCATGG, GGGAAAGTTTACACCGAGCTC
Muc2	TCCACCATGGGGCTGCCACT, GGCCCGAGAGTAGACCTTGG
Clca3	TCTTCCTCTTGATCCTCCACC, GCCCTCATAGCCGTTGTTGT
Klf4	GGCGAGTCTGACATGGCTG, GCTGGACGCAGTGTCTTCTC
Tff3	CTTTGACTCCAGTATCCCAAATG, TGGCTGTGAGGTCTTTATTCTTC
ChgA	CCAAGGTGATGAAGTGCGTC, GGTGTCGCAGGATAGAGAGGA
Reg4	GGCGTGCGGCTACTCTTAC, GAAGTACCCATAGCAGTGGGA
Lyz1	GAGACCGAAGCACCGACTATG, CGGTTTTGACATTGTGTTCGC
Defa20	TGTAGAAAAGGAGGCTGCAATAG, AGAACAAAAGTCGTCCTGAGC
β-actin	GGCTGTATTCCCCTCCATCG, CCAGTTGGTAACAATGCCATGT

Supplemental Table 3: The primers for AS and ChIP-qPCR analysis.

RT-qPCR primer(Alternative splicing)

Dvl2	TGTCGTCAGATACCCCACAG, CTGGATACATTAGGGTGGAAGGA
Dvl2-IR	CCTCTTCCTATAGCCTCCCGTA, TGTGGGGTATCTGACGACAC
Ephb3	CATGGACACGAAATGGGTGAC, GCGGATAGGATTCATGGCTTCA
Ephb3-IR	AACTTATCCGCAATGCTGCC, AGGATCTTCTTCTGGTGCCC
Sirt7	AGCATCACCCGTTTGCATGA, GGCAGTACGCTCAGTCACAT
Sirt7-IR	TGGGGAGAGGGGGACATTAG, TTCCCATGGAGTTTCAGGGC
Jag1	ATGCAGAACGTGAATGGAGAG, GCGGGACTGATACTCCTTGAG
Jag1-IR	CCAGCCAGTGAAGACCAAGT, AGTGAGCTGTTTCCATCCCG
Cdk4	ATGGCTGCCACTCGATATGAA, TGCTCCTCCATTAGGAACTCTC
Cdk4-IR	GTGGAGCGTTGGCTGTATCT, AACCATATAGGCATGCCCTGG, R:CAGTCGTCTTCTGGAGGCAAT
β-actin	GGCTGTATTCCCCTCCATCG, CCAGTTGGTAACAATGCCATGT
β-actin-IR	TGAGGCTCTTTTCCAGCCTTC, GCAGCTCAGTAACAGTCCGC
Eif5a	CCTTCCCAATGCAGTGCTCA, AAGGTCCTCTCGTACCTCCC
Eif5a-ES	TGGAGCTCATCCCTCAGTCT, TGCCAACCAGATGGACCTTG
Ehmt2	CAAGATTGACCGCATCAGCG, AAGCGGTGAGCTACACGAAA
Ehmt2-ES	TCAGGGCCCAGTGAGTACAT, AGGAGCTCTCCATCCACACT
Smurf2	CAGAGACCGAATAGGCACGG, GGATTCTTCCCGAGGCAGTC
Smurf2-ES	CAAGAGTCCTGCTCGCTCA, TTGAGGCGGTTGATGGCATT
Pkm2-MXE-E9	GTGATGTGGCCAATGCAGTC, TCAAACAGCAGACGGTGGAA
Pkm2-MXE-E10	GTGATGTGGCCAATGCAGTC, CAAGTGGTAGATGGCAGCCT
Tpm1-MXE-E5	AGCCGAGCCCAAAAAGATGA, TTCCAGCTGTCGAACTTGGC
Tpm1-MXE-E6	GATCCAGCTGAAAGAGGCCA, TGAGCCTCCAGTGACTTCAA
Epn1-MXE-E3	GACACCACTACTGGGCACAA, TCTGACATGAGGGAGCTGGA
Epn1-MXE-E4	CAAGGAGAAGCTGGCACAGA, CCTCCTCCTTGCTCATAGCC

ChIP-qPCR Primer

Dvl2	CCCTGACCACTTCCACCTCCAAA, ACCAGAGCCCACTTCATCCCAAA
Ephb3	CCTGGACTCCTTTCTACGGGTAA, GACTATGAATAGGGTTTCTGACTTGG
Sirt7	GCGTACTGCCCTTCACCGACACCT, AGCCAGCAACATGCTCAATCCAC
Jag1	CGCTTGATGGTGACTCAGGGTAT, ACTTCGGTGGCTCAGGATTAGGA
Cdk4	TGGCTGCTTGTCTTACTGTGCTA, GTATGAACTGGGTAGGCTGGATG
eif5a	GGGAAACTGAGGGCGATTGGACT, GGAAGGCACTGGCATGGTGAAGA
Ehmt2	CCTCTGTCCCTATCCACCCTTTC, TCCTCCTCCTCCTCCTCACTCAA
Smurf2	GAAGTGAAATCTACAAGAGTCCTGCTC, GCACTGTCAAGGCTGATAGACCA
Pkm2	GGAACAAACACCCAGTTTCACCG, CTACAAATCCAGACATTCGCCTAC
Tpm1	ATGTGATGTGGATGAGCCGTGAG, CTGTCTGGGATGCAGTTAAACCT
Epn1	GCTGTCTTTGTCCGTGCTTAGAG, GTGTTCCACTTTGTTATCACCCTA
Dvl2-1 (Pol II)	GTGGTGTAGGCGAGACGAAG, TCTAGCATACCCACCGTCCT
Dvl2-2(Pol II)	AGTTTCTTCTCGTACACCGCT, ACCTCAGGCTGTGGGGTATC
Dvl2-3(Pol II)	ATGGAGAGGGTGAGGGTTCTT, AGGATGAGGTCTACAGCGGG
Dvl2-4(Pol II)	GGTCTCTCCTATCAGGCTGC, TGGGATGGTGATCTTGAGCC
Ephb3-1 (Pol II)	CCTGTTCCAGGTGCCTTCTTA, CACACCTGATACGTGCGGATA
Ephb3-2(Pol II)	AGCTCATGCTGGACTGTTGG, CATGGAGCTAGGGAGTAGGGT
Ephb3-3(Pol II)	GGGTAGAAGGGAGGGACTGAG, CGTTGGAGCTGAGTGTCAGA
Jag1-1 (Pol II)	AGAAGCTGAGTCCCTCACCAA, CAGGTGGACAGATACAGCGAT
Jag1-2(Pol II)	CTTGTGAGCCTTTTATTTCATCCA, TTCGCTGCAAATGTGTTCGG
Jag1-3(Pol II)	ACCAGCTTCTGGCAATAGTGAA, AGTAGAAGGCTGTCACCAAGC
Sirt7-1 (Pol II)	ACACAGCTGCTCACTGTTAGA, AATCTGGGATAGAAGCTGCCT
Sirt7-2(Pol II)	GACTGAGCGTACTGCCCTTC, CAAGCCAGCAACATGCTCAAT
Sirt7-3(Pol II)	CCTGCCTGATGCTGCTTTTC, CCTCCTAGGATAGGGGGAGC
Cdk4-1 (Pol II)	AGTTTCCGGTGTTCTGTGCTT, AAAGTCAGCCAGCTTGACGG
Cdk4-2(Pol II)	AACCATATAGGCATGCCCTGG, TCGGCTTCAGAGTTTCCACA
Cdk4-3(Pol II)	CAGGCTGTAGTTGTCACTGCT, GGCAGAGATTCGCTTATGTGG
Cdk16-1 (Pol II)	CCATGCAACCTCACAGCATCT, TTCCCGGATAGCAGTACAGG
Cdk16-2(Pol II)	CTTCCCATTGACTCCTCAGCA, AGCTGGAATGAGGAGGTTGTG
Cdk16-3(Pol II)	GTCGCAATCGGATCTCTGCT, GGTATGGCACAAACCAGCAC