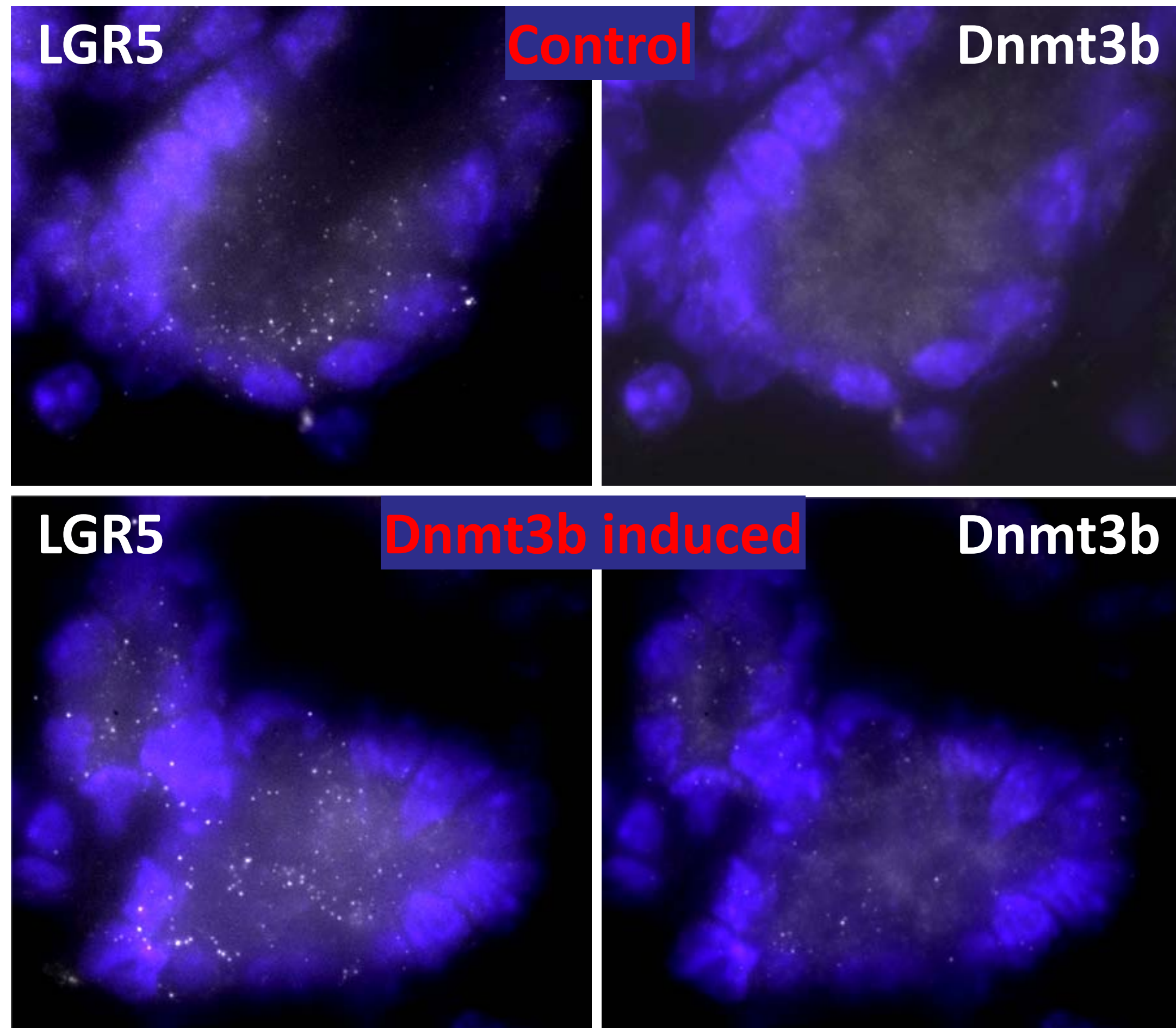
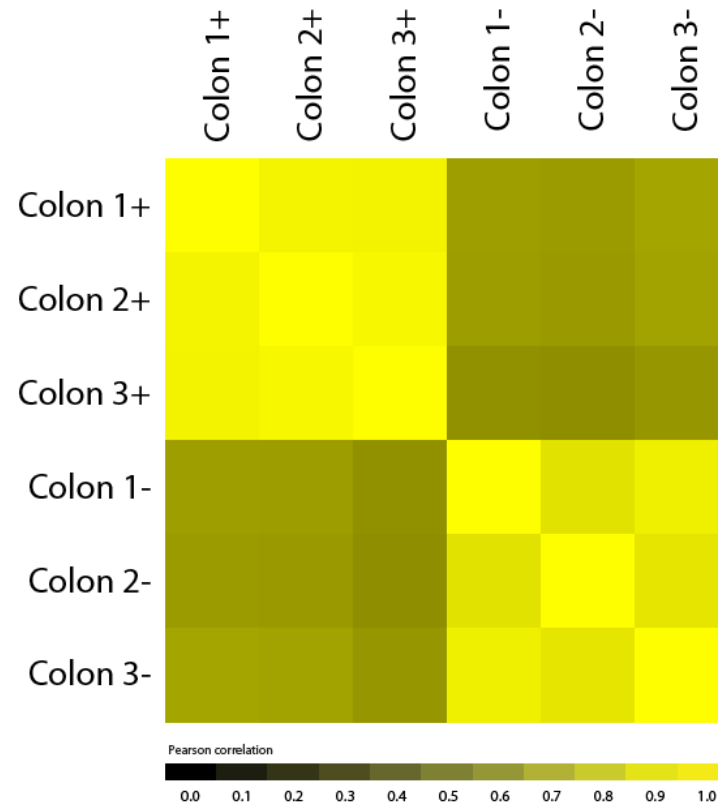




Supplemental Figure 1: Illustration of RNA FISH analysis of Lgr5 (left panel) and Dnmt3b expression (right panel) in colon crypts isolated from a wild-type (top row) and Dnmt3b induced (bottom row) mouse. Particulate signals represent individual Lgr5 (left) or Dnmt3b (right) molecules. Nuclei stained with DAPI (purple). Lgr5 was used to identify crypt stem cells and Dnmt3b expression was quantified in Lgr5 positive cells. Dnmt3b expression in crypt stem cells of the dox induced transgenic mouse was on average ~ 2 fold higher than in the littermate control mouse.

Supplemental Figure 2

Methylation fractions of scorable promoters: Pairwise correlations



Supplemental Figure 2: Pairwise correlation of promoter methylation in colon epithelial cells +/- Dnmt3b transgene expression (+ = Dnmt3b transgene induction, - = no Dnmt3b induction). Promoter methylation fractions were calculated using reduced representation bisulfite sequencing data. The strong correlation of de novo methylation amongst samples with Dnmt3 induction supports the concept that Dnmt3b directly targets certain promoter regions .

Supplemental Table 1*

Comparison of DNA methylation in colon epithelial cells of Dnmt3b overexpressing mice with DNA methylation of human colon cancer

mouse data				mouse data			
	Δ meth.	p value	human (references) [#]		Δ meth.	p value	human (references) [#]
Alox15	0.40	< 0.001	6	Apc	0.00	0.622	1
Apba2	0.58	< 0.001	2	Bcl2	0.03	< 0.001	1, 2
Boll	0.18	< 0.001	3	Brca1	0.00	0.739	7
Cacna1g	0.42	< 0.001	1	Cdh1	0.01	0.020	1
Cdkn2a	0.32	< 0.001	5	Cdkn2b	0.02	< 0.001	1
Efemp1	0.35	< 0.001	3	Chfr	0.00	0.505	1
Gad1	0.50	< 0.001	1	Dapk1	0.03	0.006	1
Gata3	0.31	< 0.001	1	Mgmt	0.03	< 0.001	1, 8
Gata4	0.12	< 0.001	1, 2	MIh1	0.01	< 0.001	1
Gata5	0.51	< 0.001	1	Pten	0.00	0.801	1
Gnb4	0.47	< 0.001	3	Rb1	0.03	< 0.001	1
H19.DMR	0.24	< 0.001	9	Socs1	0.01	0.127	1
Hic1	0.39	< 0.001	1	Vhlh	0.01	0.173	1
Hoxa1	0.15	< 0.001	1				
Hoxd1	0.48	< 0.001	3				
Lrp2	0.50	< 0.001	4				
Myod1	0.39	< 0.001	1, 4				
Neurog1	0.50	< 0.001	1				
Nr3c1	0.32	< 0.001	1, 2				
Otx1	0.19	< 0.001	2				
Rbp1	0.69	< 0.001	1				
Sfrp2	0.48	< 0.001	1				
Sfrp4	0.47	< 0.001	1				
Tert	0.21	< 0.001	1, 4				
Thbs2	0.49	< 0.001	4				
Timp3	0.31	< 0.001	1, 4				

***Supplemental Table 1:** Comparison of DNA methylation in colon epithelial cells of Dnmt3b overexpressing mice with DNA methylation of human colon cancer. The mouse data show the absolute increase in DNA methylation caused by Dnmt3b overexpression (from 0 to 1) and the corresponding p value (comparison no dox versus plus dox, n = 5 each, t-test). Genes with an absolute increase ≥ 0.1 and $p \leq 0.05$ were defined as methylated and are colored in red, unmethylated genes are colored in blue. The column with human data shows the respective literature reference, red fields indicate genes that were reported as methylated in human colon cancer and blue fields indicate genes that were reported as unmethylated. In the case of Mgmt, labeled yellow, one reference indicates methylation and one reference indicates no methylation. To facilitate the comparison, genes with more than one promoter in human or mouse were not included in the analysis.

References Supplemental Table 1:

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Supplemental Table 2*

Dnmt3b methylates the same genes that are methylated in human colon cancer

Gene Symbol	Dnmt3b	Colon Cancer #	Gene Symbol	Dnmt3b	Colon Cancer #
Gata5	0.69	479	HoxA1	0.00	52
Sfrp5	0.75	443	Chfr	0.02	51
Igf2	0.56	366	Sez6l	0.67	50
Twist1	0.66	284	Mt3	0.08	49
Ebf3	0.51	273	Timp3	0.61	49
Hic1	0.61	266	Neurog1	0.61	44
Sfrp2	0.65	179	Rbp1	0.89	44
Sfrp1	0.60	148	Cdkn1c	0.29	43
Neurod2	0.70	147	Epm2aip1	0.01	42
Gata4	0.45	94	Crabp1	0.63	38
Nr3c1	0.16	93	Bdnf	0.66	36
Gata3	0.22	89	Cdh13	0.53	36
Tert	0.34	89	Socs1	0.17	30
Itga4	0.46	84	Gabra2	0.43	29
Kl	0.67	84	Esr2	0.23	24
Cacna1g	0.51	79	Pgr	0.59	23
Sfrp4	0.60	70	Cyp27B1	0.45	23
Bcl2	0.01	64	Mlh1	0.01	23
Tmeff2	0.67	60	Mgmt	0.19	19
MyoD1	0.50	57	Drd2	0.61	14
Gad1	0.63	54	Gstp1	0.01	13
Gdnf	0.55	52	Thbs1	0.26	10

***Supplemental Table 2:** The table shows a comparison of DNA methylation data from colon epithelial cells of Dnmt3b expressing mice as measured by RRBS with published DNA methylation data of human colon cancer (1). The mouse RRBS data are shown in the column “Dnmt3b” with numbers indicating the absolute methylation gain induced by Dnmt3b expression (0= no methylation, 1= complete methylation). Human colon cancer data are shown in the column “colon cancer” with numbers indicating percent of methylated reference (PMR, 0= no methylation, 100 = methylation equals methylated reference). The supplementary table S1 of Widschwendter et al. (1) lists 77 genes with a significant methylation increase in human colon cancer. For comparison with Dnmt3b data human genes with <0.1 absolute gain in human colon cancer (PMR gain in tumors < 10) or baseline methylation > 100% (PMR>100) were excluded. Based on these criteria 62 genes were eligible for the Dnmt3b/colon cancer comparison. Dnmt3b RRBS data were available for 44/62 eligible human genes. 37/44 (84%) of these genes were methylated both by Dnmt3b and in human colon cancer (red color), only 7/44 (16 %) were methylated in colon cancer and not methylated by Dnmt3b model.

Reference Supplemental Table 2: Widschwendter, M., Fiegl, H., Egle, D., Mueller-Holzner, E., Spizzo, G., Marth, C., Weisenberger, D.J., Campan, M., Young, J., Jacobs, I., et al. 2007. Epigenetic stem cell signature in cancer. *Nat Genet* 39:157-158.

Supplemental Table 3*

Gene Symbol	Dnmt3b	Colon Cancer #	Gene Symbol	Dnmt3b	Colon Cancer #
Smad3	0.001	1.970	Prkar1a	0.003	0.000
Apc	0.003	1.850	Uqcrh	0.000	0.000
Jup	0.000	0.970	Cdk2ap1	0.002	0.000
Rpa3	0.000	0.530	Axin1	0.000	0.000
Grin2b	0.610	0.490	Rb1	0.010	0.000
Smad6	0.050	0.340	Tgfb2	0.002	0.000
Rpa2	0.000	0.320	App	0.001	0.000
Stk11	0.013	0.080	Smad2	0.002	0.000
Xpa	0.018	0.020	Faf1	0.001	0.000
Atm	0.009	0.020	Tnfrsf10b	0.023	0.000
Ercc4	0.001	0.010	Smad9	0.170	0.000
Ctnnb1	0.043	0.010	Xpc	0.000	0.000
Ercc2	0.002	0.000	Rad23A	0.000	0.000
Msh2	0.005	0.000	Xab2	0.010	0.000
Dph1	0.066	0.000	Atr	0.001	-0.010
Stat1	0.003	0.000	Pttg1	0.016	-0.010
Ctsd	0.002	0.000	Ercc6	0.002	-0.020
Cxadr	0.001	0.000	Hsd17b4	0.005	-0.030
Pparg	0.000	0.000	Mbd2	0.000	-0.040
Clic4	0.005	0.000	Vdr	0.002	-0.050
Ncl	0.000	0.000	Ercc5	0.000	-0.070
Ung	0.002	0.000	Ldlr	0.000	-0.090
Mbd4	0.050	0.000	Ccdn1	0.010	-1.030
Ogg1	0.003	0.000	Psen1	0.000	-0.230
Apex1	0.011	0.000	Psat1	0.030	-0.270
Xrcc1	0.060	0.000	Cdkn2b	0.079	-1.130
Parp1	0.005	0.000	Dapk1	0.048	-1.400
Parp2	0.005	0.000	Cdh1	0.004	-1.990
Ercc8	0.003	0.000	Msh4	0.110	-2.340
Ddb1	0.013	0.000	Erb2	0.005	-3.310
Brca2	0.011	0.000	Ptgs2	0.440	-3.510
Pold1	0.020	0.000	Onecut2	0.620	-4.490
Pten	0.000	0.000	Dnajc13	0.001	-5.870
Arpc1b	0.001	0.000	Mthfr	0.267	-6.490
Vhl	0.001	0.000	Sash1	0.001	-10.040
Tgfvbr1	0.002	0.000			

***Supplemental Table 3:** Genes not methylated in human colon cancer are also largely not methylated by Dnmt3b: The table shows a comparison of DNA methylation data from colon epithelial cells of Dnmt3b expressing mice as measured by RRBS with published DNA methylation data of human colon cancer (1). The mouse RRBS data are shown in the column “Dnmt3b” with numbers indicating the absolute methylation gain induced by Dnmt3b expression (0= no methylation, 1= complete methylation). Human colon cancer data are shown in the column “colon cancer” with

numbers indicating percent of methylated reference (PMR, 0= no methylation, 100 = methylation equals methylated reference). The supplementary table S1 of Widschwendter et al. (1) lists 100 genes with no significant methylation increase in human colon cancer. For comparison with Dnmt3b data human genes with baseline methylation > 100% (PMR>100) were excluded. Based on these criteria 94 genes were eligible for the Dnmt3b/colon cancer comparison. Dnmt3b RRBS data were available for 71/94 eligible human genes. 65/71 (92 %) of these genes were not methylated in colon cancer and also not methylated by Dnmt3b (blue color). Only 6/71 (8 %) genes were methylated by Dnmt3b (red) and not methylated in colon cancer.

#Reference Supplemental Table 3:

1. Widschwendter, M., Fiegler, H., Egle, D., Mueller-Holzner, E., Spizzo, G., Marth, C., Weisenberger, D.J., Campan, M., Young, J., Jacobs, I., et al. 2007. Epigenetic stem cell signature in cancer. *Nat Genet* 39:157-158.

Supplemental Methods

Transgenic mice and transgene regulation

All mice used in this study including the tetracycline inducible Dnmt3b transgenic mice and the genotyping protocol were described previously {Linhart, 2007 #227}. Briefly the tetracycline inducible transgene was targeted to the collagen I locus and the tetracycline sensitive transactivator M2-rtTA was targeted to the Rosa locus. Transgene induction was achieved by administering doxycycline (dox) in the drinking water (0.5g/liter). To test the stability of aberrant DNA methylation mice were first induced with dox for five months and a subset was then switched back to regular drinking water without dox for another four months: 5 months dox = On samples, n = 5; 4 months dox withdrawal = On/Off samples, n = 5; control mice with no transgene induction were age matched to On/Off samples (two Dnmt3b +/-, rtTA +/- mice maintained without dox and two Dnmt3b -/-, rtTA +/- mice exposed to dox in analogy to the On/Off samples). For the data shown in figures 1A-C mice were induced for four months.

Tissue harvesting and DNA isolation

Colon tumors from APC^{Min/+} mice were harvested under the dissecting microscope. Colon epithelial cells from tumor free colon samples of APC^{Min/+} mice and APC wild-type mice were harvested as described previously {Fujimoto, 2002 #118}. For DNA isolation tissue samples were digested with proteinase K (10mg/ml) in lysis buffer over night, treated with RNase A, purified twice with Phenol/Chloroform, precipitated with isopropanol, washed in 70% EtOH and resuspended in water.

Mouse embryonic fibroblasts

Double homozygous embryos (Dnmt3b transgene +/+ and Rosa-rtTA +/+) were harvested 12.5 days post conception. Cells were expanded for 12-14 days in culture to generate two fully confluent 150 mm dishes per embryo. Production of gamma-irradiated samples: For each embryo ~ 70 % of two confluent 150 mm dishes with mouse embryonic fibroblasts were gamma-irradiated with 24 Gy. Following irradiation 8×10^6 cells were plated into each of two 100 mm dishes to generate two fully confluent 100 mm culture plates with growth arrested irradiated cells. Medium was replaced 12 hours after plating to remove non adherent cells. Production of mitomycin C treated samples: For each embryo two 150 mm culture plates were harvested and 8×10^6 cells were transferred into each of two 100 mm dishes. 12 hours after plating cells were treated with mitomycin C (5 μ g/ml, incubation 2.5 hours) and washed five times with PBS. Production of culture plates with untreated proliferating cells: For each embryo 2×10^6 untreated cells were transferred to each of two 100 mm plates. Plates with proliferating cells were constantly maintained at ~ 50% - 60% confluency. All cells received fresh medium simultaneously every two days. For transgene induction cells were cultured in the presence of 2 μ g/ml dox final concentration. After 14 days of dox treatment cells were harvested for DNA methylation analysis. Growth arrest by gamma-irradiation and mitomycin C treatment was evaluated by BrdU staining: For each sample cells were seeded into individual wells of a 24 well plate. To simulate the conditions of the experimental plates the seeding density in the 24 well plate was matched to the seeding density of the experimental plates: gamma-irradiated and mitomycin C treated samples were seeded at 2.8×10^5 /well and proliferating samples were seeded at 0.7×10^5 /well. Mitomycin C treatment in the 24 well plate was conducted in analogy to the experimental 100 mm plates. 24 hours after plating cells were incubated with 10 μ M BrdU for 4 hours and then subjected to immunostaining: Cells were fixed for 10 minutes in 4% paraformaldehyde, washed three times in PBS, then treated with 2N HCl for 10 minutes, neutralized in 0.1M borate for 10 minutes at RT, washed three times in PBS and blocked for 1 h with 1% BSA in PBS. Cells were then incubated with the

primary antibody (rat anti BrdU from Axyll h7227, 1:150) for 30 minutes at RT, washed three times in PBS and then incubated with the FITC conjugated secondary antibody for 30 min at RT. Cells were counterstained with DAPI. For analysis of BrdU incorporation at least 100 cells were scored for each sample. Untreated proliferating cells: 32.4% BrdU positive, stdev = 7.04, n=5. Mitomycin C treated cells: 2.9% BrdU positive, stdev = 1.7, n = 3. Irradiated cells: 5.8% BrdU positive, stdev = 0.9, n =2.

Lgr5 and Dnmt3b mRNA quantification by fluorescence in situ hybridization

We used 4 micron sections from frozen circular wrapped colon samples, which were stored on coverglass coated with poly-L-lysine at -80C. The sections were fixed for 10 minutes in 4% formaldehyde at room temperature, followed by 3 washes with PBS. The sections were then permeabilized in 70% EtOH at 4C for at least 4 hours, after which the sections were prehybridized, hybridized and imaged as described {Raj, 2008 #279}. We used probes targeting Lgr5 and Dnmt3b, with Lgr5 coupled to tetramethylrhodamine and Dnmt3b coupled to Cy5. We acquired stacks of images spanning the entire height of the section and then located individual mRNA molecules using the semi-automated method described in {Raj, 2008 #279}. We then manually identified Lgr5 positive cells and found the density of Dnmt3b mRNAs present in those cells in a total of 19 wild-type Lgr5 positive areas and 49 overexpressor Lgr5 positive areas. We obtained errors in the density measurements by bootstrap resampling. To compute the p-value for the difference in density between the two strains, we computed the fraction of the time that the null hypothesis (no difference) would be satisfied given a random resampling of the dataset. A list of probes used for RNA FISH is shown at the end of supplemental methods.

cDNA and quantitative PCR

cDNA production and quantitative PCR was conducted as described previously {Linhart, 2007 #227}. Briefly, cDNA was prepared from total RNA using oligo-dT primers. For each sample, a minus-RT reaction was generated, and pooled minus-RT reactions were used as negative controls for quantitative PCR reactions (SYBR Green, Invitrogen). For quantitation, standard dilution curves were included on each plate. All samples were analyzed in triplicate, β -Actin was used as an endogenous control. Individual data were converted to relative values based on the standard curve and then normalized to the β -Actin values of the same sample. For Dnmt3b quantification we used primers Dnmt3b forward: GTTCGAGCTGGCAAGACCTT and Dnmt3b reverse: TGGTCCTCCAGTGA CTCTCCA and for β -Actin we used primers β -Actin forward: TGAACCCTAAGGCCAACCG and β -Actin reverse: AGGTCTCAAACATGATCTGGGTC

DNA Methylation Analysis (Mass Array Platform)

Genomic DNA sodium bisulfite conversion was performed using EZ-96 DNA Methylation Kit (Zymo Research, Orange County, CA). The manufacturer's protocol was followed using 1 μ g of genomic DNA and the alternative conversion protocol (a two temperature DNA denaturation). Sequenom's MassARRAY platform was used to perform quantitative methylation analysis. This system utilizes matrix-assisted laser desorption ionization time-of-flight (MALDI-TOF) mass spectrometry in combination with RNA base specific cleavage (MassCLEAVE). A detectable pattern is then analyzed for methylation status. PCR primers were designed using Methprimer (www.urogene.org/methprimer/) and Epidesigner (epidesigner.com). When it was feasible, amplicons were designed to cover CpG islands in the same region as the 5'UTR. For each reverse primer an additional T7 promoter tag for *in-*

vitro transcription was added, as well as a 10mer tag on the forward primer to adjust for melting temperature differences. The MassCLEAVE biochemistry was performed as previously described {Ehrich, 2005 #122}. Mass spectra were acquired using a MassARRAY Compact MALDI-TOF (Sequenom, San Diego) and spectra's methylation ratios were generated by the EpiTyper software v1.0 (Sequenom, San Diego). A list of all primers is provided at the end of supplemental methods.

DNA Methylation Analysis (Reduced Representation Bisulphite Sequencing)

RRBS methylation analysis was conducted as described previously {Meissner, 2008 #272}. The library was constructed with the DNA sample kit (Illumina, IP-102-1001). Mouse genomic DNA was digested with MspI. A small and a large size fragment band were isolated from a 3% Nusieve gel, 40-120bp and 120-220bp fragments respectively. Isolated and phenol:chloroform purified DNA was end-repaired and adenylated. The fragments were ligated to the 3'T-overhang methylated-cytosine-containing adapters. After adapter ligation DNA was bisulfite treated with Qiagen's EpiTect bisulfite kit with modification of the manufacturers' protocol by adding two additional bisulfite conversion cycles. After bisulfite treatment DNA was PCR amplified for 24 cycles. Small and large library fragments (with adapters) were size selected on a 3% Nusieve gel, 120-220 and 220-310 bp respectively. Libraries were sequenced on the genome Analyzer II (Illumina). For sequence analysis the mouse genome (NCBI Build 37) was *in silico* digested with MspI and fractionated into fragments with ranges of 40-120 ("short") or 120-220 nt ("long"). Tags representing 36 nt at both ends of each fragment were extracted and every C was converted to T to generate the RRBS library. A bisulphite-aware short-read aligner {Gu, #308} was used to align each set of Illumina 36 nt reads to the appropriate RRBS library, allowing up to 2 mismatches. Reads mapped to a library were intersected with genome locations representing promoters (defined

as 2 kb up- and downstream of the transcription start site) derived from NCBI Refseq transcripts (with coordinates from UCSC Bioinformatics) for further analysis. A CpG was defined as scorable if it was assayed by at least 5 reads, and a promoter with least 5 scorable CpGs was itself defined as scorable. In each sample, the methylation fraction of a promoter was calculated as the mean of scorable CpGs. After grouping methylation fractions for short and long fragment sets, differential methylation was assayed by a moderated t-test as implemented in the R package "limma".

List of primers used for MALDI-TOF methylation analysis

AmpliconName	GeneName	LeftPrimer	RightPrimer	Chr	targetstart	targetend
SQ00001	Esr1	TTTGAGGTAG	TAATACCAAA	chr10	5734091	5734469
SQ00002	Esr1	TAAGGTTGTT	TTTTTCAACCA	chr10	5734470	5734729
SQ00003	Esr1	GAAGGTTTAT	AAAATAACCT	chr10	5734435	5734861
SQ00004	Esr1	TGGATTAGAG	CCTTCTATAA	chr10	5734077	5734439
SQ00005	Myo1	GTGGTTATTT	AACTCCATAT	chr7	53631705	53632050
SQ00006	Myo1	GATTTAGGAA	CCTTACAAAC	chr7	53632026	53632340
SQ00007	Myo1	TTGTTTGTGT	AATATAAAAA	chr7	53632318	53632767
SQ00008	Myo1	GTTTGAGTAA	TCTAAATATA	chr7	53632404	53632771
SQ00009	Myo1	GGTTTTAGGA	ACTTCTTCAC	chr7	53632279	53632625
SQ00010	Tus	TTTGATAAGT	TCCTACAAC	chr4	93001296	93001618
SQ00011	Tus	GGAAAGTTTT	AAAACCTCAT	chr4	93002387	93002648
SQ00012	Tus	GGTTAGAGAA	TTACTTCTCT	chr4	93002223	93002554
SQ00013	Alox15	GTTTTTAGTA	TAAAAATTTCT	chr11	70165895	70166281
SQ00014	Alox15	GGTAGAAGG	CCATCTTACA	chr11	70165745	70166062
SQ00015	Alox15	GGTATGGGA	AAAACCCCCA	chr11	70165561	70165919
SQ00016	Alox15	TTGGATGTTT	AACATCTAAT	chr11	70165417	70165769
SQ00017	Alox15	GGAGTAAGG	CATCACAAAT	chr11	70165305	70165585
SQ00018	Tert	GGTTGGAGTA	TACTTAAAAA	chr13	73764004	73764423
SQ00019	Tert	ATTTTTAGTG	ACCACCAACT	chr13	73764387	73764824
SQ00020	Tert	GGTGTATTTT	ACAAAAAAA	chr13	73764798	73765105
SQ00021	Tert	GAGGTTTGGC	AACCACTAAA	chr13	73764847	73765150
SQ00022	Gad1	TGTTGAGTGT	ATCACCCCAA	chr2	70399968	70400289
SQ00023	Gad1	TGTAAGTAAG	ATCACTTCAA	chr2	70400261	70400642
SQ00024	Gad1	GGTTTTTTTAT	ACTAAAATAA	chr2	70401152	70401534
SQ00025	Gad1	GTTAATTTTT	AACAAACACC	chr2	70400790	70401174
SQ00026	Gad1	GGAGATAGA	TTCTTTCCAA	chr2	70400410	70400808
SQ00027	Gad1	GGAATTTGGA	TACCTTAATC	chr2	70400054	70400434
SQ00028	Gata3_01	AGGAGGGAG	CCTAAATAAA	chr2	9795974	9796173
SQ00029	Gata3_01	AGGATGAGG	AACATCACAA	chr2	9796154	9796562
SQ00030	Gata3_01	GGTTAGGTAA	AAAAAATCCT	chr2	9796331	9796538
SQ00031	Gata3_02	GTTTGTTTTGT	CTAAATAAAC	chr2	9798887	9799190
SQ00032	Gata3_02	AGATTTTGGT	AAATATACCT	chr2	9799317	9799512
SQ00033	Gata3_02	TTAGGAGTTT	ACTCTCTTTT	chr2	9798875	9799374
SQ00034	Gata3_03	TAAATAGTTT	AATTTCAAAA	chr2	9799957	9800187
SQ00035	Gata3_03	AGGGAATGTA	CTACCTATCCC	chr2	9800164	9800519
SQ00036	Gata3_03	GGTTGTAGTT	ATCACAAATC	chr2	9800307	9800629
SQ00037	Gata3_03	TGGAAATTAG	TCCTCAACAC	chr2	9800009	9800331
SQ00038	Hoxa1	TTAAGGATGG	CTTTAATCCC	chr6	52108174	52108562
SQ00039	Hoxa1	TAGAGGATTG	CCCTTCTAAA	chr6	52108942	52109391
SQ00040	Hoxa1	ATTATTATTAC	AATATACCA	chr6	52109155	52109435
SQ00041	Hoxa1	TTTGGAATAT	ACTATACCCC	chr6	52108748	52109185
SQ00042	Hoxa1	GTAGGAATTA	ACCCAACCCA	chr6	52107892	52108286
SQ00043	Wnt7a_01	GTTTTTAGTG	CAACCCCACC	chr6	91359590	91360011
SQ00044	Wnt7a_01	TATTAAAGAT	AAACCTCCCT	chr6	91359997	91360149
SQ00045	Wnt7a_01	TGGGAAGAAT	CCCCTACTCC	chr6	91359576	91360017
SQ00046	Wnt7a_02	TATGTTTAGG	CTCTAAAACA	chr6	91361050	91361265
SQ00047	Wnt7a_02	GTAGTGGGAC	TCCCTAACTCT	chr6	91361557	91361680

SQ00048_Wn Wnt7a_02	GTTTTGGGAT.TATACCCTCA/ chr6	91361229	91361588
SQ00049_Wn Wnt7a_02	GAAGGATGTT CTAACACTA/ chr6	91360915	91361254
SQ00050_Wn Wnt7a_03	GAAGGAAGTTTCTACTCTTCT chr6	91344317	91344693
SQ00051_Wn Wnt7a_03	TGTTTTGTTA CAATATCCTC/ chr6	91344316	91344673
SQ00052_Bcl2 Bcl2_01	ATTTTGGATT/CTTCCAACCT/ chr1	108608894	108609308
SQ00053_Bcl2 Bcl2_01	TGGATTATAG ACAAACACA chr1	108609186	108609584
SQ00054_Bcl2 Bcl2_01	AATTTTTTAG/ AACCTTAAAA/ chr1	108609435	108609660
SQ00055_Bcl2 Bcl2_02	TTGTAAATGT/ AATTTCCAAA/ chr1	108610741	108610891
SQ00056_Bcl2 Bcl2_02	TAGTTATTTTT TCAATCCAAC/ chr1	108610389	108610758
SQ00057_Bcl2 Bcl2_02	GAGGTGTTTA AAATCCTCTT/ chr1	108610211	108610588
SQ00058_Nr3 Nr3c1	GAGAGGATA/ ATTATCAAA/ chr18	39647149	39647472
SQ00059_Nr3 Nr3c1	AGATGATTTA/ CCTTAACACCT/ chr18	39646730	39647143
SQ00060_Nr3 Nr3c1	GGGGAATGA/ TCAACAAATC/ chr18	39646334	39646695
SQ00061_Nr3 Nr3c1	GGATTTGTAT/ CTATAAATAA/ chr18	39646070	39646358
SQ00062_Nr3 Nr3c1	GAATTATTTTT AAAACCTTAA/ chr18	39645838	39646114
SQ00063_Nr3 Nr3c1	TAGAGAGGA/ AATAAAAAAC chr18	39645580	39645912
SQ00064_Cld1 Cldn5	GGGTGTTTA/ CAAAATAACA. chr16	18777164	18777385
SQ00065_Cld1 Cldn5	GGGTTTTGTT/ TCCTTTAATTC chr16	18777912	18778201
SQ00066_Cld1 Cldn5	TGTAAGGTGT CCCTTAAACA/ chr16	18777278	18777748
SQ00067_Cld1 Cldn5	GATAAGAAG/ TTAATAACA/ chr16	18777725	18778083
SQ00068_Pte1 Pten	TAGTTTAGGG AACCCATAAA. chr19	32830352	32830616
SQ00069_Pte1 Pten	GGTTTTTTGG/ CCTAAAACAA. chr19	32830592	32830892
SQ00070_Pte1 Pten	GGGGATTAA/ AACCAAACCT/ chr19	32830870	32831220
SQ00071_Pte1 Pten	GGGGTTTAGT CAAAAAACAC chr19	32831189	32831341
SQ00072_Pte1 Pten	TTTGTTTAATT ACCTCAAAAA/ chr19	32831317	32831702
SQ00073_Pte1 Pten	GGAAGTTGTA TCCCAACCT/ chr19	32832123	32832512
SQ00074_Pte1 Pten	TTTGTTATTAT AAACCTCTTCT chr19	32832488	32832874
SQ00075_Pte1 Pten	GAAATTTAGG ACCTCAAAAA/ chr19	32831349	32831702
SQ00076_Pte1 Pten	GGAAGGATA/ CTCAACTCTC/ chr19	32831678	32832158
SQ00077_Pte1 Pten	GTTTTTTGTTT CAACCAAAAA chr19	32831913	32832049
SQ00078_Peg Peg1	ATATGTTGGG CAACAAAAAC chr6	30687764	30688178
SQ00079_Peg Peg1	TTTATTAGAA/ CAACAAAAAC chr6	30687835	30688178
SQ00080_Peg Peg1	TTATTGATGA/ CTAATAACACA/ chr6	30688454	30688632
SQ00081_Peg Peg1	TGAAGAAAGT TCTTCAAAAA/ chr6	30688569	30688680
SQ00082_Peg Peg1	GAGTTGTTGT TAAATTACTT/ chr6	30688154	30688595
SQ00083_Igf2 Igf2r	AGGTTTTAGG CTAACCTACCT/ chr17	12934087	12934299
SQ00084_Igf2 Igf2r	AGATATTTTG/ CAAAAACTA. chr17	12934271	12934591
SQ00085_Igf2 Igf2r	GAGGATTTTA ATCCTCCCCTT chr17	12934946	12935392
SQ00086_Igf2 Igf2r	GGTGTAATTT CCTTCATATAC/ chr17	12935368	12935676
SQ00087_Igf2 Igf2r	GATAGGAGG/ AACCCCATTA/ chr17	12935619	12935890
SQ00088_Igf2 Igf2r	TTGTAGATAA/ CCAAAAATAT/ chr17	12935874	12936269
SQ00089_Igf2 Igf2r	GGATTTTGTA/ CCCCTCCCTTC chr17	12934334	12934675
SQ00090_Igf2 Igf2r	GTTAGTAAGA CCTCCTTATAC chr17	12934652	12935033
SQ00091_Boll Boll	TGGAGTTAGG CTAACCTAACCT/ chr1	55419136	55419503
SQ00092_Boll Boll	TAAAGATAAA ACTAAAACCT/ chr1	55419299	55419710
SQ00093_Boll Boll	GGGAGGGAA/ ACTAAAACCT/ chr1	55419480	55419710
SQ00094_Boll Boll	GTTGGAAAGA ATAAAAACCT/ chr1	55419733	55420138
SQ00095_Boll Boll	GGAAGTTTTT/ CTCAAAAATC/ chr1	55419260	55419755
SQ00096_Efe1 Efemp1	GAAGTAATTG AAACCTCATAT/ chr11	28752458	28752781
SQ00097_Efe1 Efemp1	TAGTTATAGG. AACACCTAAC/ chr11	28752685	28753112

SQ00098_EfeI Efemp1	TAGTTATAGG.AATAACTAAA\chr11	28752685	28752827
SQ00099_EfeI Efemp1	TTTGTGAATT\TCCACCTCCA\chr11	28753047	28753449
SQ00100_Gnl Gnb4	TGGTTTGGGT AACTTCAAA\chr3	32515737	32515984
SQ00101_Gnl Gnb4	GTTTTGTGTG\CCAAACTTTA\chr3	32515594	32516026
SQ00102_Gnl Gnb4	TGTGGTTTTT\ACCACACCCA\chr3	32515093	32515589
SQ00103_Dlk: Dlk1-Gtl2	ATAGGTTTTT\ACTCCATAAT\chr12	110764758	110765207
SQ00104_Dlk: Dlk1-Gtl2	TTTATTAGGG\CACCTAACCT\chr12	110765178	110765559
SQ00105_Dlk: Dlk1-Gtl2	TTATGGTATA\ACATCCATAT\chr12	110765494	110765662
SQ00106_Dlk: Dlk1-Gtl2	ATAGTATTGG\CCATAACATA\chr12	110765635	110766063
SQ00107_Dlk: Dlk1-Gtl2	TTTGGTATAG\CCACAACACT\chr12	110765970	110766419
SQ00108_Dlk: Dlk1-Gtl2	GATGTGTTGT\ATCCCCTATA\chr12	110766349	110766776
SQ00109_Dlk: Dlk1-Gtl2	GGAGAATGTT\TCCACAATCT\chr12	110766752	110767126
SQ00110_Otx Otx1	GGTAGGGATT\TTTACCAACCT\chr11	21901490	21901839
SQ00111_Otx Otx1	ATTGAGTGAT.TACTAAAACCT\chr11	21901702	21902111
SQ00112_Otx Otx1	TTGGTTGTTT\AAATAAAACT.\chr11	21902130	21902425
SQ00113_Otx Otx1	GAGGTTAGGT\CTAAAATCCC\chr11	21901735	21902151
SQ00114_Otx Otx1	GAGGGTAGT\ATTACAAAAT\chr11	21901484	21901776
SQ00115_Otx Otx1	GAATATTTTT\AAATTACTAA\chr11	21900797	21901239
SQ00116_Otx Otx1	TTTATTAAATT\CACTATAAAA\chr11	21900674	21901091
SQ00117_Irx2 Irx2	GGGTAGTTTT.TCACCTAAA\chr13	72765605	72765754
SQ00118_Irx2 Irx2	TAGAGGATTG\AAAACCCAAC\chr13	72765634	72765992
SQ00119_Irx2 Irx2	TTGTAGGAGG\CACTCTCA\chr13	72765805	72766207
SQ00120_Irx2 Irx2	AGTAGGAAAG\CTTTTATTCCT\chr13	72767922	72768326
SQ00121_Irx2 Irx2	GAAGGAGAA\AAAAACTAAA\chr13	72768288	72768679
SQ00122_Irx2 Irx2	TTTAAGAAAG\ATTAATCCAA\chr13	72769409	72769514
SQ00123_Irx2 Irx2	GTATTGGTTT\AATAACAAC\chr13	72768129	72768367
SQ00124_Irx2 Irx2	TTTGGTTTTT\TACCCAAACC\chr13	72767725	72768152
SQ00125_Irx2 Irx2	ATAAGGTTAG\AAATTCCTA\chr13	72767333	72767747
SQ00126_Irx2 Irx2	GGGTTAAGT\AATACCCCTA\chr13	72766110	72766549
SQ00127_Irx2 Irx2	GTTTGTAGTG\AACCTCAAAC\chr13	72765817	72766135
SQ00128_Irx2 Irx2	GTAGTTAGGA\CCCAATTTAA\chr13	72768926	72769236
SQ00129_Irx2 Irx2	GAGTAGGTTG\TTCCTCAACTC\chr13	72768797	72768951
SQ00130_Irx2 Irx2	GTGTTGGTGA\CCCACCAACC\chr13	72768342	72768816
SQ00131_Ghs Ghsr	GGAGGATTTT\CCACCAACAT\chr3	27270662	27270917
SQ00132_Ghs Ghsr	GGTTAAGGTG\ATATCAAAA\chr3	27271165	27271522
SQ00133_Ghs Ghsr	TTTTATATGTT\CAATAAATCA\chr3	27271432	27271658
SQ00134_Ghs Ghsr	TTGATAAATT\CTAAAAAAAC\chr3	27271075	27271499
SQ00135_Ghs Ghsr	TTTTTATTGTT\TCTACAAACT\chr3	27270656	27271099
SQ00136_Lmt Lmtk3_01	GTTTTTATGG\ACAAAACCTC\chr7	53040894	53041323
SQ00137_Lmt Lmtk3_01	GGGGAGGAG\ATACCTCCTCA\chr7	53040926	53041357
SQ00138_Lmt Lmtk3_01	GGGGTTGTTT.CCCCTCCAAA\chr7	53040638	53040967
SQ00139_Lmt Lmtk3_01	GTATTTTGTTT\AATATCAAAA\chr7	53040489	53040662
SQ00140_Lmt Lmtk3_01	ATTTGAGGGA\TCCCCATAAC\chr7	53040126	53040573
SQ00141_Lmt Lmtk3_02	AGAGTTTTGG\AACTAACCAA\chr7	53050199	53050488
SQ00142_Lmt Lmtk3_02	GGGTTTTGAG\CTCCTCTATTA\chr7	53050305	53050734
SQ00143_Lmt Lmtk3_02	GTTTGAGAT\CTAACTCTTC\chr7	53050464	53050791
SQ00144_Rbp Rbp1	GAAGGTTTGA\TAAATTCCAA\chr9	98325069	98325246
SQ00145_Rbp Rbp1	GGGTTTTGTG\TCCACAAACA\chr9	98325222	98325408
SQ00146_Rbp Rbp1	AGTTTGTTTT\CAAACCTAAC\chr9	98325384	98325656
SQ00147_Thb Thbs2	TTAGTATTTTC\CAAAATAAAA\chr17	14831009	14831431

SQ00148_Thb Thbs2	AGATTGGTTG ACTAAATTTCT chr17	14831407	14831846
SQ00149_Thb Thbs2	GATTGATAGG CCACTAAACT/ chr17	14831538	14831830
SQ00150_Thb Thbs2	TGGGGAGTTT CAAAAAACCT. chr17	14831268	14831554
SQ00151_Tim Timp3	TTATTATGATT CTACAAAACA' chr10	85763594	85763782
SQ00152_Tim Timp3	TTTTATAGGG/ TCTTACTCCCT chr10	85763473	85763773
SQ00153_Tim Timp3	TTTAGGGTTG' AAAACTTCCT' chr10	85763302	85763724
SQ00154_Tim Timp3	GTAGAAGGTA CCCCTATATCA' chr10	85762886	85763327
SQ00155_Tim Timp3	TTTAGGGTTG' AAAACTTCCT' chr10	85763302	85763724
SQ00156_Hox Hoxd1	ATTTAGTTAA/ TCCCCTCAAA/ chr2	74601819	74602060
SQ00157_Hox Hoxd1	GGTGGTTAGG TCAACCACTT' chr2	74601412	74601837
SQ00158_Hox Hoxd1	GGGGATATAG TAAACTACCT/ chr2	74601047	74601434
SQ00159_Hox Hoxd1	GGGTTTTGAT' AACCTTTTCA/ chr2	74600812	74601068
SQ00160_Lrp1 Lrp2	GGATAATTTG. ACCAAAACCT' chr2	69423197	69423476
SQ00161_Lrp1 Lrp2	GTTTTGGGTA/ CCCTCAAAAC' chr2	69423300	69423648
SQ00162_Lrp1 Lrp2	GTTTTATTTTG TAACCCCAAA/ chr2	69423624	69423772
SQ00163_Lrp1 Lrp2	GGTTTGGTTT/ CTACAATCAT(chr2	69423755	69424176
SQ00164_Lrp1 Lrp2	TTGTGTTTTTG CTCCAACAA' chr2	69423588	69423789
SQ00165_Lrp1 Lrp2	GGAATTTAG CTTACTCCCCT chr2	69424189	69424673
SQ00166_Lrp1 Lrp2	AGTGATTGAA TACATAAAAC(chr2	69423497	69423779
SQ00167_mm mmu_mir_34	GTTGTGAGTA CCCATACCCA(chr4	148912293	148912450
SQ00168_miR miR34-a	TGGTTTTATT ACAAAAACAT chr4	149438407	149438825
SQ00169_miR miR34-a	AAGATTGAGG CCAAAATAAA chr4	149438798	149439105
SQ00170_miR miR34-a	TAGGGGTGTT CAAAACTTA/ chr4	149439534	149439935
SQ00171_miR miR34-a	GTTTAAGATG. AATCACCTAA(chr4	149439850	149440188
SQ00172_miR miR34-a	GTGTTAATAG CAACCTAAAC' chr4	149440153	149440491
SQ00173_miR miR34-a	TTAGGGATTA. AAAATCATTT(chr4	149440471	149440693
SQ00174_miR miR34-a	GGTTTTTTTG ATAACCTCTAT(chr4	149440606	149440824
SQ00175_miR miR34-a	GTGGGGTTG(CAAAATCCCA(chr4	149440800	149441072
SQ00176_miR miR34-a	TGAGTTTAGG AACAAAAAAA chr4	149441208	149441462
SQ00177_miR miR34-a	TGAGAGATGT AAATCCTTCA(chr4	149441431	149441662
SQ00178_miR miR34-a	TATTGGTTTA(AACCTAAATT/ chr4	149441633	149441948
SQ00179_miR miR34-a	GTTGTTTTATA' AACTCTAACA(chr4	149441831	149442116
SQ00180_miR miR34-a	GATGAGGGT(ATACAACAAT/ chr4	149442099	149442422
SQ00181_miR miR34-a	GGATGGGGA(CAACATCCCA' chr4	149442401	149442765
SQ00182_miR miR34-a	TGGGGAGGT' ACCAACAAAC chr4	149442764	149443004
SQ00183_miR miR34-a	TGTTTATATT ACCCTAAACC(chr4	149443005	149443353
SQ001_Cdkn2 Cdkn2a	AGTAAATAGG CTAAACCAAA' chr4	88765275	88765573
SQ002_Cdkn2 Cdkn2a	GTAAATAGGT CAAATTCTTA/ chr4	88765276	88765746
SQ003_Cdkn2 Cdkn2a	TTATTTATAAA' CTAACCCCA/ chr4	88766245	88766831
SQ004_Cdkn2 Cdkn2a	TAAGAGAGG(CCCCTCCCCA' chr4	88765700	88765446
SQ005_Apba1 Apba1	TTGGAAGATT ATCCTCTATCC chr19	23825293	23825663
SQ006_Apba1 Apba1	GTTAGGGATT CCAAACCTAA/ chr19	23825641	23826103
SQ007_Apba1 Apba1	TGGAGAGTAC TACCACCTCC/ chr19	23826076	23826493
SQ008_Apba1 Apba1	GGGTTTTTTT(TACCACCTCC/ chr19	23826225	23826493
SQ009_Apba1 Apba1	GATTTTGGTA/ ACAACTTTAT' chr19	23826531	23826082
SQ010_Apba1 Apba1	GGTTTGAAAG AATCCCTAAT/ chr19	23825525	23825222
SQ011_Apba2 Apba2	GATTGATTGT(CCCCTTAAAA/ chr7	64380395	64380713
SQ012_Apba2 Apba2	TTTAGTTTATT TTAATAAATC/ chr7	64380675	64380892
SQ013_Apba2 Apba2	TTTTGATTTT ATACCCCTCTA' chr7	64380879	64381357
SQ014_Apba2 Apba2	TTTGGGTAGG CCCCTCAAAA/ chr7	64380642	64380426

SQ015_Apba2 Apba2	GGGATTTGGA CCTTATAAAA(chr7	64381626	64381326
SQ016_Apba2 Apba2	TTTTGTTTTT AAATCCCTTA/ chr7	64381351	64380874
SQ017_Apba2 Apba2	TTTAAAGAGA CCAAAAACCC(chr7	64380904	64380750
SQ018_Mlh1_Mlh1	AATTTAGAAG CCAAACTAAT` chr9	111115814	111116092
SQ019_Mlh1_Mlh1	AATTTAGAAG CCAAACTAAT` chr9	111115814	111116092
SQ020_Mlh1_Mlh1	GGTAAGTGTT TTCCCTCAACT chr9	111116441	111116614
SQ021_Mlh1_Mlh1	TTTATTTTGA ACCAAAAACA chr9	111116592	111117042
SQ022_Mlh1_Mlh1	TTAGTGTATG(CCACAAAAAC chr9	111117145	111117335
SQ023_Mlh1_Mlh1	GTTTTTAGAA/ ATTAACAAC/ chr9	111116606	111116452
SQ024_Mlh1_Mlh1	TGGTATTTAT(TTTCTATCATC chr9	111116471	111116229
SQ025_Mlh1_Mlh1	TAATGTTATT/ TAAACCTAAA/ chr9	111116254	111115868
SQ026_Cacna Cacna1g	TTTAGGTTTA1ACTCAACAAA/ chr11	94289358	94289834
SQ027_Cacna Cacna1g	GGGGGTTTTA AACCCCTTAA/ chr11	94289810	94290160
SQ028_Cacna Cacna1g	GGTGGGGGT1ATAACTCTCCC(chr11	94290242	94290615
SQ029_Cacna Cacna1g	TTTAGTTGGT1 ATTCACAATC(chr11	94289723	94289350
SQ030_Cacna Cacna1g	TTGATTTTTTA CCCCTACCCT(chr11	94290162	94289863
SQ031_Cacna Cacna1g	GTTTGAAGTT(AAAAAAATCT(chr11	94290494	94290210
SQ032_Neuro Neurog1	TTTTTGGGTA(ACACCAAAC1(chr13	56260860	56261178
SQ033_Neuro Neurog1	AGGTGGAGG1 AACCAAACCC(chr13	56261428	56261708
SQ034_Neuro Neurog1	GGGTTGGTTT CACTTTCTACC chr13	56261740	56262196
SQ035_Neuro Neurog1	GTTTAAATTTT CCCTTTAAAA/ chr13	56261154	56261546
SQ036_Neuro Neurog1	GAGGAGGAT1AATATCTCAA(chr13	56261467	56261109
SQ037_Runx3 Runx3	TGGGTTTGAA ACTACCACTA1 chr4	134393128	134393455
SQ038_Runx3 Runx3	TTTGAGGTTT/ AACCAAATAA(chr4	134393475	134393121
SQ039_Socs1_Socs1	GGAGGATTAC AAAAAAACCT chr16	10698797	10699240
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SQ041_Socs1_Socs1	GAGTGAGTTT CAAACAAC1(chr16	10699805	10699494
SQ042_Socs1_Socs1	GATTTTGGTA(CACCTTCCCA(chr16	10699518	10699274
SQ043_Apc_0 Apc	AGGTGAGTAC CTAAAAAAAC chr18	34345546	34345904
SQ044_Apc_0 Apc	GGTGGAGTG/ CAAACAATCC` chr18	34345879	34346416
SQ045_Apc_0 Apc	TTGGAAGGGT AAAATCTACC/ chr18	34345904	34345511
SQ047_Sfrp2_Sfrp2	TGGTTGGGTT ACTCCAACAC(chr3	83852229	83852691
SQ048_Sfrp2_Sfrp2	GTAGTGTTGA CCAACCAAAA` chr3	83851828	83852235
SQ049_Sfrp2_Sfrp2	AGGGGGAGT/ AAAAAAACCC chr3	83852187	83851766
SQ050_Sfrp2_Sfrp2	GGTTGGATGC AACCCCAACC` chr3	83852806	83852235
SQ051_Sfrp4_Sfrp4	AGAATTATGG AACTTTCCTAC(chr13	19630466	19630802
SQ052_Sfrp4_Sfrp4	GGGTAGTGG/ CACAACTTT1 chr13	19630815	19630355
SQ053_Rb1_0 Rb1	GTAGAGATGC AACTACCCCT/ chr14	72059513	72059693
SQ054_Rb1_0 Rb1	GGTTTTTTGG/ AAAACTACCA` chr14	72060333	72060798
SQ055_Rb1_0 Rb1	GGGTTTTTTT(AAACAAAAC1 chr14	72059538	72059151
SQ056_Rb1_0 Rb1	TTTTTTGTTAG CCAAAATAAA(chr14	72060680	72060314
SQ057_Vhlh_(Vhlh	TTAATTGTAG(CCTCCTCTAA/ chr6	113589642	113589948
SQ058_Vhlh_(Vhlh	GGAAGGTAG1 CCTCCAAATT/ chr6	113589925	113590351
SQ059_Vhlh_(Vhlh	ATAGGTTGGT ACCCTCTCAA/ chr6	113590395	113590025
SQ060_Vhlh_(Vhlh	GGTTGTAGAA AAAAAAACA chr6	113590050	113589623
SQ061_Brca1_Brca1	TTTAAGAGAG CCCACCTTTA chr11	101367911	101368267
SQ062_Brca1_Brca1	GAAGGGGTT(CTCAAAACTA` chr11	101368218	101367843
SQ063_Gata4_Gata4	GGGGAATTTT ATTTTAATACC chr14	62199249	62199848
SQ064_Gata4_Gata4	GGAGAGGGT1 TCATCCTTTTA chr14	62199824	62200077
SQ065_Gata4_Gata4	GGTTTTAGTG` ACCCTACCTA/ chr14	62199849	62199254

SQ066_Gata4_Gata4	GATTTTGTTC CTACCTAACCT/chr14	62199534	62199257
SQ067_Gata5_Gata5	TTTTTGGGTG(TCAAAAAAAC chr2	180263947	180264460
SQ068_Gata5_Gata5	GGATTAGGTA CTCCAACCTAA/chr2	180263103	180263595
SQ069_Gata5_Gata5	TTAGAGTTGT CTAAACCCCCC chr2	180264351	180263843
SQ070_Hic1_(Hic1	TAGGTTGGGT TACTTCCTACC chr11	74984019	74984406
SQ071_Hic1_(Hic1	GGGTTTTTTTT CCAACTACCT/chr11	74983031	74983379
SQ072_Hic1_(Hic1	TTTGGGGTTT CCCCCAATTT chr11	74985083	74984695
SQ073_Hic1_(Hic1	GTTTTTGTTC CAACAACCAC chr11	74982907	74982345
SQ074_Cdkn2_Cdkn2b	TAGTATTAGA(AAAAAACCTT chr4	88781798	88782068
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SQ076_Cdkn2_Cdkn2b	TTATTGGGTT CACACAACCA chr4	88782132	88781790
SQ077_Cdkn2_Cdkn2b	TTTGTTGAGT(TCCCTCTAA/chr4	88782455	88782112
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SQ079_Rassf1_Rassf1	GGTTGGAGA TAAAAATTAA chr9	107412133	107412420
SQ080_Rassf1_Rassf1	TTTTATTTTT CCTAAAAACA chr9	107413420	107412914
SQ081_Rassf1_Rassf1	AATTGATTAT CCAACAAAT/chr9	107412453	107412068
SQ082_Dapk1_Dapk1	GGGTGTGGG(CCCCTTCTAA/chr13	60611909	60612233
SQ083_Dapk1_Dapk1	TTTTTGGGTT TCTAAACTAA/chr13	60611412	60611933
SQ084_Dapk1_Dapk1	TTAGAGAAGG CCAACCTA/chr13	60612327	60611922
SQ085_Dapk1_Dapk1	AGTTTAGGTT(AATCCTTAA/chr13	60611935	60611410
SQ086_Cdh1_Cdh1	TTAATTATAG/CCCTCCACAT/chr8	109492358	109492683
SQ087_Cdh1_Cdh1	TGTTTTGTTC ACCTTCTACA/chr8	109492658	109492981
SQ088_Cdh1_Cdh1	GGATATTTGG CTTCTTCCAA chr8	109493225	109492745
SQ089_Cdh1_Cdh1	TTTAATTTTT CCTACAATTCC chr8	109492765	109492392
SQ090_Mgmt_Mgmt	AGTTTAGGT CAATACCCCA/chr7	136732674	136733048
SQ091_Mgmt_Mgmt	TGTTGAGTA TCTAAATAA/chr7	136732981	136732654
SQ092_Chfr_(Chfr	TTTTGGGTTTT TTTAAATCCCT chr5	110376337	110376572
SQ093_Chfr_(Chfr	GAAGAAGTTT CAACAAAATA chr5	110376424	110375991
SQ094_Nespa_Nespas DMR	TTGGATTTTT AAAACCTCCA/chr2	173937600	173937803
SQ095_Nespa_Nespas DMR	GGTGTGAGAC AACCCCATA/chr2	173937934	173938228
SQ096_Nespa_Nespas DMR	TGGGGGTTTT TAAATCTCAA(chr2	173938221	173938538
SQ097_Nespa_Nespas DMR	GTGGGTTAGT ATCTAACATA/chr2	173938517	173938819
SQ098_Nespa_Nespas DMR	TTTTTTTAGG CCCCTCTCCT chr2	173938925	173939332
SQ099_Nespa_Nespas DMR	GGGATTTGTA TTTTCTCAAAA chr2	173939130	173938926
SQ100_Nespa_Nespas DMR	GGGTATATTG ACCCAACCC/chr2	173938871	173938475
SQ101_Nespa_Nespas DMR	TAGGTTAGTT(AAAATCCCTA/chr2	173938497	173938223
SQ102_Nespa_Nespas DMR	GTAAAGGTAA AAACAAAAAA chr2	173938253	173937874
SQ103_Nespa_Nespas DMR	GAGAAGGTTT AAAAAAACA chr2	173937744	173937415
SQ104_Peg3.I Peg3 DMR	GGTGTATGTT(AAAAACCCTA chr7	6334304	6334544
SQ105_Peg3.I Peg3 DMR	TTTTTTGTTAG AAACCTACATC chr7	6334527	6334759
SQ106_Peg3.I Peg3 DMR	GGGTGTATGT TCCCCCTTTC chr7	6334303	6334730
SQ107_Peg3.I Peg3 DMR	GGAGAGATGT ACCTTATCAA/chr7	6334455	6334202
SQ108_Peg3.I Peg3 DMR	AGAGGATTTT CATACTACAA/chr7	6334545	6334308
SQ109_Peg3.I Peg3 DMR	GATTTTGTTC CCACCAACCC/chr7	6334717	6334429
SQ110_H19.D H19 DMR	AGTTTAAAGG AACTCATAAA chr7	142389565	142389875
SQ111_H19.D H19 DMR	TGAAGGAGTT CCCAAATCA/chr7	142389790	142390087
SQ112_H19.D H19 DMR	TTTTGGGATA CAAAAACAA chr7	142390081	142390403
SQ113_H19.D H19 DMR	GGGGTTTGAG TAAAAACACC chr7	142390505	142390889
SQ114_H19.D H19 DMR	TTATGATTAT CCAAAATTC/chr7	142391094	142391346
SQ115_H19.D H19 DMR	ATAAGGGTTA TAAAAAATC chr7	142389838	142389559

SQ116_H19.D H19 DMR	GAGGGGGTTT CAAAAATACA chr7	142390265	142390034
SQ117_H19.D H19 DMR	GTGGTAGGAT AACCCCCTCC/ chr7	142390656	142390257
SQ118_H19.D H19 DMR	TTGGAATTTA` CATAAACCCC` chr7	142391378	142391070
SQ119_H19.D H19 DMR	TAAGGAGATT AAAAAAACTC. chr7	142391503	142391126

List of probes used for RNA FISH analysis of Dnmt3b mRNA expression

Probes are numbered according to their position on the Dnmt3b mRNA starting at the 5' position.

The second number indicates the CG content of the probe in %.

The third number indicates the position of the probe on the target mRNA.

1,45,8,attcagatgtctgctgtctc

2,45,46,ataatgcactcctcataccc

3,45,69,ggtcactgaagttccatta

4,45,208,taattcagaaggctggagac

5,45,245,atcatctctgtctccatctc

6,45,267,agccattcccatcatctact

7,45,293,ggtgagctttggcattagaa

8,45,492,ttgctgaagatgatgctcga

9,45,538,acttcttccatgaagtcgac

10,45,574,aagtcaactgatgggtact

11,45,606,tatccataccctcctgatct

12,45,653,atactctgtgctgtctccat

13,45,684,ggtcacctattccaaactct

14,45,714,aggagaagcccttgatcttt

15,45,808,aacttgccatcaccaaacca

16,45,830,ttgtcagcagagatctcag

17,45,865,ttaaagtgtggctgaacag

18,45,887,cagcttattgaaggtagcca

19,45,911,gtacatggccttcctataag

20,45,1063,tgcttctgttggttgag

21,45,1089,gcaccttcgacttattaacc

22,45,1111,aagttcctactgtctgaacg

23,45,1143,ttcgactttgttctcgct

24,45,1170,aagcagcagagtcattgggtt

25,45,1206,tatttgccttgaggcgcttg
26,45,1273,ttggtgacttcagaagccat
27,45,1303,aaacagcggtcttccagatt
28,45,1327,acagggttcttcttccaca
29,45,1398,tgtagaagagctctaggaag
30,45,1420,tgatagccgtcctcatcata
31,45,1488,atctgcagcagcttgtgtta
32,45,1626,tgtccaatcttctcctgcgt
33,45,1650,tagtgaagaagtcttcagg
34,45,1672,aattcttccaggtcaggatc
35,45,1703,aattgctgggtacaacttgg
36,45,1732,actctaattgggcctcctttt
37,45,1761,ccgttgcaattccatcaaac
38,45,1783,aactccttgagcaccaagta
39,45,1813,gaggcaatgtactttccac
40,45,1852,ttaacagttcccacagcgat
41,45,1889,ccggacgtcattgacatatt
42,45,1923,ggccccactcttcaatattt
43,45,1965,agagatcattgcatgggctt
44,45,1997,atataaacctttgcgggcag
45,45,2027,aaactcgaagaagagccttc
46,45,2049,gggtataattcagcaagtgg
47,45,2086,atccagaagaatggacggtt
48,45,2110,ttcatggccacaacattctc

List of probes used for RNA FISH analysis of Lgr5 mRNA expression

Probes are numbered according to their position on the LGr5 mRNA starting at the 5' position.

The second number indicates the CG content of the probe in %.

The third number indicates the position of the probe on the target mRNA.

1,45,208,ttcatactgaggtccaggt
2,45,265,aactcttctaggaagcagag
3,45,287,caaagcatttccagcaagac
4,45,338,aagcactttgaggctgtgaa
5,45,391,aaattctgtagcgcttcctc
6,45,497,attgtcatctagccacaggt
7,45,534,aacttctgaaagcctggaca
8,45,574,attttgttcaggccaaggt
9,45,599,aaaggcgtagtctgctatgt
10,45,637,ttatggagatgcagaaccac
11,45,670,aagcatttcttcccaggga
12,45,701,atctaaagtctccaggctgt
13,45,733,gtggggaattcatcaagggt
14,45,755,gttgagagtgtcttgattg
15,45,778,ctgtggaatcctagttcctt
16,45,800,cggtattgacctgatgttgt
17,45,832,ataagagaagggtgcctac
18,45,857,ggggttgtcatagaagtga
19,45,888,gctgaaaagcagatactcca
20,45,911,cagtgttcttagttcaggca
21,45,942,attcagtaatgtgcaggca
22,45,987,ttaaagtcagactctccagg
23,45,1009,agagatgagatctttgctcc

24,45,1038,taggtaactgatcacagacg
25,45,1060,gacaaatctagcacttgag
26,45,1083,gtaagtcttcgagtaggttg
27,45,1105,tttggcagcctgacaaact
28,45,1128,gcctcaggtcaattttctga
29,45,1166,ctgaaaagtgtgcccttaa
30,45,1188,gagatcggaggttaaacaac
31,45,1230,cattggggtgaatgatagca
32,45,1252,agagacggcaacgtagaaaa
33,45,1278,gattggatgataggtccaac
34,45,1314,aacctgtaaccagtcaca
35,45,1345,gctcggttccctgttaattt
36,45,1367,agatggtatcaggctctgta
37,45,1389,tcttgagctctgggaagttt
38,45,1413,ggtaagcagatggcatttct
39,45,1449,tatagacattctcacacccc
40,45,1479,cgtcgtctttattccattgg
41,45,1504,ttatgaaggtcgtccacact
42,45,1527,cttgaaataaccagcgtct
43,45,1559,taggaaatcttcaaggtccc
44,45,1581,tcaggtcttctcaaagtca
45,45,1650,taccaaataaggtgtcacag
46,45,1736,agttctgaacacggtcaaag
47,45,1764,gcagctttatggaagagatg
48,45,1793,aatgtccactaccgcgatta