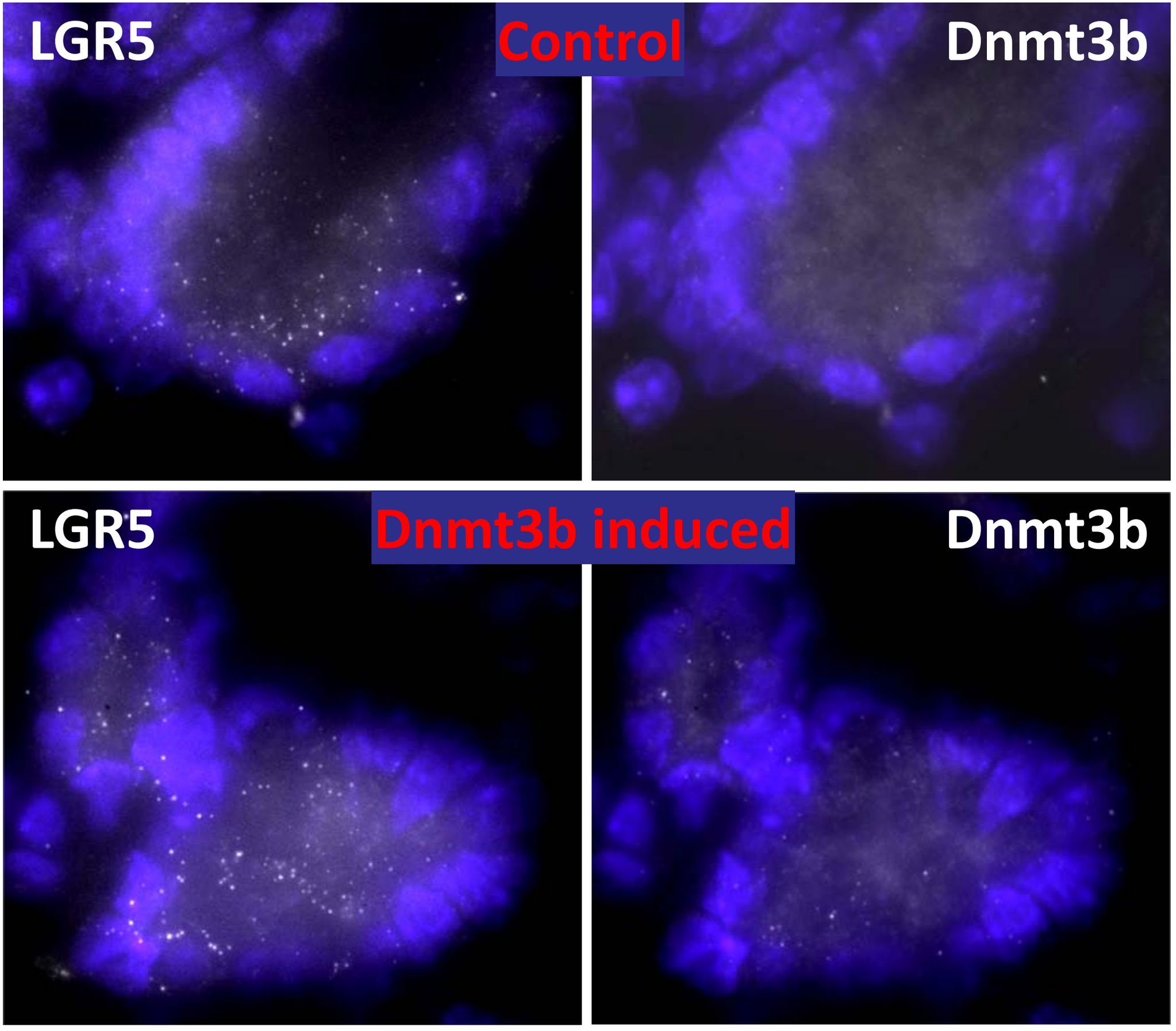
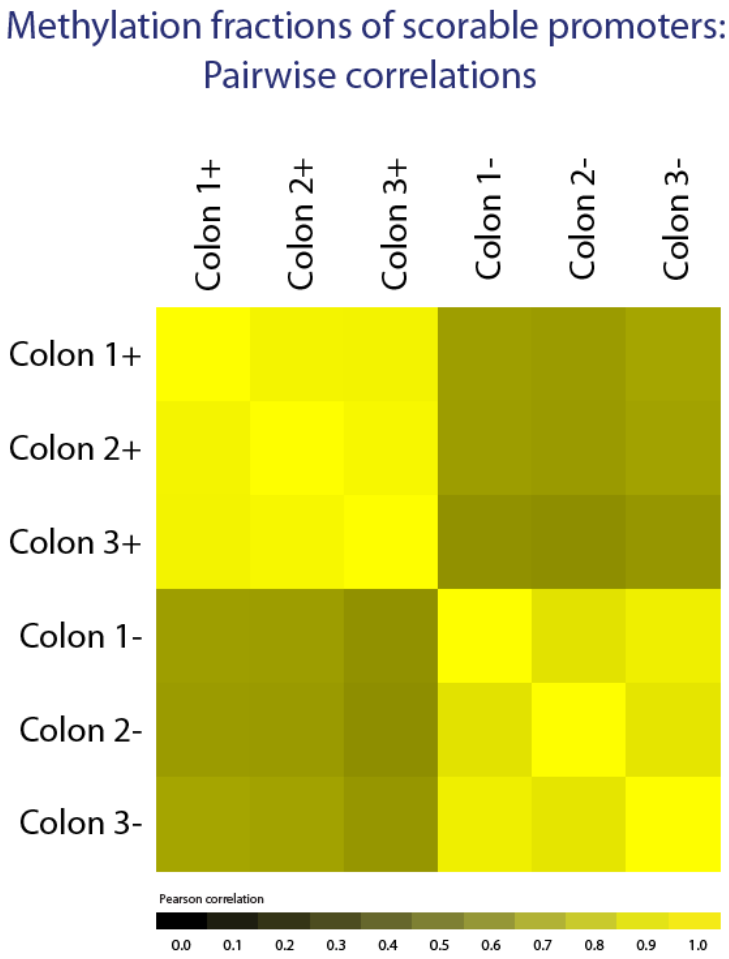
Supplemental Figure 1



Supplemental Figure 1: Illustration of RNA FISH analysis of Lgr5 (left panel) and Dmnt3b expression (right panel) in colon crypts isolated from a wild-type (top row) and Dmnt3b induced (bottom row) mouse. Particulate signals represent individual LGR5 (left) or Dmnt3b (right) molecules. Nuclei stained with DAPI (purple). Lgr5 was used to identify crypt stem cells and Dmnt3b 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



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		
	Δ meth.	p value	human (references)[#]
Alox15	0.40	< 0.001	6
Apba2	0.58	< 0.001	2
Boll	0.18	< 0.001	3
Cacna1g	0.42	< 0.001	1
Cdkn2a	0.32	< 0.001	5
Efemp1	0.35	< 0.001	3
Gad1	0.50	< 0.001	1
Gata3	0.31	< 0.001	1
Gata4	0.12	< 0.001	1, 2
Gata5	0.51	< 0.001	1
Gnb4	0.47	< 0.001	3
H19.DMR	0.24	< 0.001	9
Hic1	0.39	< 0.001	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

	mouse data		
	Δ meth.	p value	human (references)[#]
Apc	0.00	0.622	1
Bcl2	0.03	< 0.001	1, 2
Brca1	0.00	0.739	7
Cdh1	0.01	0.020	1
Cdkn2b	0.02	< 0.001	1
Chfr	0.00	0.505	1
Dapk1	0.03	0.006	1
Mgmt	0.03	< 0.001	1, 8
Mlh1	0.01	< 0.001	1
Pten	0.00	0.801	1
Rb1	0.03	< 0.001	1
Socs1	0.01	0.127	1
Vhlh	0.01	0.173	1

***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 ≤ 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:

1. Widschwendter, M., Fiegl, H., Egle, D., Mueller-Holzner, E., Spizzo, G., Marth, C., Weisenberger, D. J., Campan, M., Young, J., Jacobs, I., and Laird, P. W. (2007) *Nat Genet* **39**, 157-158
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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	Tgfbr2	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	Erbb2	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., 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 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 $8x10^6$ 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 $8x10^6$ cells were transferred into each of two 100 mm dishes. 12 hours after plating cells were treated with mitomycin C (5µg/ml, incubation 2.5 hours) and washed five times with PBS. Production of culture plates with untreated proliferating cells: For each embryo $2x10^6$ 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 2µg/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 $2.8x10^5$/well and proliferating samples were seeded at $0.7x10^5$/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 10µM 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 Dmnt3b, with Lgr5 coupled to tetramethylrhodamine and Dmnt3b 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 Dmnt3b 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, ß-Actin was used as an endogenous control. Individual data were converted to relative values based on the standard curve and then normalized to the ß-Actin values of the same sample. For Dnmt3b quantification we used primers Dnmt3b forward: GTTCGAGCTGGCAAGACCTT and Dnmt3b reverse: TGGTCCTCCAGTGACTCTCCA and for ß-Actin we used primers ß-Actin forward: TGAACCCTAAGGCCAACCG and ß-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 1ug 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 wit 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 (Ilumina). 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

AmpliconNam	GeneName	LeftPrimer	RightPrimer	Chr	targetstart	targetend
SQ00001_Esr1	Esr1	TTTGAGGTAG	TAATACCAAA	chr10	5734091	5734469
SQ00002_Esr1	Esr1	TAAGGTTGTT	TTTTTCAACCA	chr10	5734470	5734729
SQ00003_Esr1	Esr1	GAAGGTTTAT	AAAATAACCT	chr10	5734435	5734861
SQ00004_Esr1	Esr1	TGGATTAGAG	CCTTCTATAA	chr10	5734077	5734439
SQ00005_Myo	Myod1	GTGGTTATTT	AACTCCATAT	chr7	53631705	53632050
SQ00006_Myo	Myod1	GATTTAGGAA	CCTTACAAAC	chr7	53632026	53632340
SQ00007_Myo	Myod1	TTGTTTGTTG	AATATAAAAA	chr7	53632318	53632767
SQ00008_Myo	Myod1	GTTTGAGTAA	TCTAAATATA	chr7	53632404	53632771
SQ00009_Myo	Myod1	GGTTTTAGGA	ACTTTCTTCA	chr7	53632279	53632625
SQ00010_Tus	Tusc1	TTTGTATAAG	TCCTACAACT	chr4	93001296	93001618
SQ00011_Tus	Tusc1	GGAAAGTTTT	AAAACCTCAT	chr4	93002387	93002648
SQ00012_Tus	Tusc1	GGTTAGAGAA	TTACTTCTCTT	chr4	93002223	93002554
SQ00013_Alo	Alox15	GTTTTTAGTA	TAAAAATTTC	chr11	70165895	70166281
SQ00014_Alo	Alox15	GGTAGAAGG	CCATCTTACA	chr11	70165745	70166062
SQ00015_Alo	Alox15	GGTATGGGA	AAAACCCCCA	chr11	70165561	70165919
SQ00016_Alo	Alox15	TTGGATGTTT	AACATCTAAT	chr11	70165417	70165769
SQ00017_Alo	Alox15	GGAGTAAGG	CATCACAAAT	chr11	70165305	70165585
SQ00018_Ter	Tert	GGTTGGAGTA	TACTTAAAAA	chr13	73764004	73764423
SQ00019_Ter	Tert	ATTTTTAGTG	ACCACCAACT	chr13	73764387	73764824
SQ00020_Ter	Tert	GGTGTTATTT	ACAAAAAAAA	chr13	73764798	73765105
SQ00021_Ter	Tert	GAGGTTTGGG	AACCACTAAA	chr13	73764847	73765150
SQ00022_Gad	Gad1	TGTTGAGTGT	ATCACCCCAA	chr2	70399968	70400289
SQ00023_Gad	Gad1	TGTAAGTAAG	ATCACTTCAA	chr2	70400261	70400642
SQ00024_Gad	Gad1	GGTTTTTTTAT	ACTAAAATAA	chr2	70401152	70401534
SQ00025_Gad	Gad1	GTTAATTTTTT	AACAAACACC	chr2	70400790	70401174
SQ00026_Gad	Gad1	GGAGATAGAA	TTCTTTCCAAA	chr2	70400410	70400808
SQ00027_Gad	Gad1	GGAATTTGGA	TACCCTTAATC	chr2	70400054	70400434
SQ00028_Gat	Gata3_01	AGGAGGGAG	CCTAAATAAA	chr2	9795974	9796173
SQ00029_Gat	Gata3_01	AGGATGAGGT	AACATCACAA	chr2	9796154	9796562
SQ00030_Gat	Gata3_01	GGTTAGGTAA	AAAAAATCCT	chr2	9796331	9796538
SQ00031_Gat	Gata3_02	GTTTGTTTTGT	CTAAATAAAC	chr2	9798887	9799190
SQ00032_Gat	Gata3_02	AGATTTTGGT	AAATATACCTA	chr2	9799317	9799512
SQ00033_Gat	Gata3_02	TTAGGAGTTT	ACTCTCCTTTT	chr2	9798875	9799374
SQ00034_Gat	Gata3_03	TAAATAGTTTT	AATTTCAAAA	chr2	9799957	9800187
SQ00035_Gat	Gata3_03	AGGGAATGTA	CTACCTATCCC	chr2	9800164	9800519
SQ00036_Gat	Gata3_03	GGTTGTAGTT	ATCACAAATC	chr2	9800307	9800629
SQ00037_Gat	Gata3_03	TGGAAATTAG	TCCTCAACAC	chr2	9800009	9800331
SQ00038_Hox	Hoxa1	TTAAGGATGG	CTTTAATCCCA	chr6	52108174	52108562
SQ00039_Hox	Hoxa1	TAGAGGATTG	CCCTTCTAAA	chr6	52108942	52109391
SQ00040_Hox	Hoxa1	ATTATTATTAC	AATATACCAA	chr6	52109155	52109435
SQ00041_Hox	Hoxa1	TTTGGAATATT	ACTATACCCC	chr6	52108748	52109185
SQ00042_Hox	Hoxa1	GTAGGAATTA	ACCCAACCCA	chr6	52107892	52108286
SQ00043_Wn	Wnt7a_01	GTTTTTAGTG	CAACCCCACC	chr6	91359590	91360011
SQ00044_Wn	Wnt7a_01	TATTAAAGAT	AAACCTCCCT	chr6	91359997	91360149
SQ00045_Wn	Wnt7a_01	TGGGAAGAAT	CCCCTACTCCA	chr6	91359576	91360017
SQ00046_Wn	Wnt7a_02	TATGTTTAGG	CTCTAAAACA	chr6	91361050	91361265
SQ00047_Wn	Wnt7a_02	GTAGTGGGAC	TCCCTAACTCT	chr6	91361557	91361680

SQ00048_Wn	Wnt7a_02	GTTTTGGGAT	TATACCCTCA	chr6	91361229	91361588
SQ00049_Wn	Wnt7a_02	GAAGGATGTT	CTAAACACTA	chr6	91360915	91361254
SQ00050_Wn	Wnt7a_03	GAAGGAAGTT	TCTACTCTTCT	chr6	91344317	91344693
SQ00051_Wn	Wnt7a_03	TGTTTTTGTTA	CAATATCCTCC	chr6	91344316	91344673
SQ00052_Bcl2	Bcl2_01	ATTTTGGATTT	CTTCCAACCTA	chr1	108608894	108609308
SQ00053_Bcl2	Bcl2_01	TGGATTATAG	ACAAAACACA	chr1	108609186	108609584
SQ00054_Bcl2	Bcl2_01	AATTTTTTAGC	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	AAATCCTCTTC	chr1	108610211	108610588
SQ00058_Nr3	Nr3c1	GAGAGGATA	ATTATCAAAT	chr18	39647149	39647472
SQ00059_Nr3	Nr3c1	AGATGATTTA	CCTTAACACC	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_Cld	Cldn5	GGGTTGTTTA	CAAAATAACA	chr16	18777164	18777385
SQ00065_Cld	Cldn5	GGGTTTTGTT	TCCTTTAATTC	chr16	18777912	18778201
SQ00066_Cld	Cldn5	TGTAAGGTGT	CCCTTAAACA	chr16	18777278	18777748
SQ00067_Cld	Cldn5	GATAAGAAGA	TTAAAACAAC	chr16	18777725	18778083
SQ00068_Pte	Pten	TAGTTTAGGG	AACCCATAAA	chr19	32830352	32830616
SQ00069_Pte	Pten	GGTTTTTTGG	CCTAAAACAA	chr19	32830592	32830892
SQ00070_Pte	Pten	GGGGATTAAC	AACCAAACTC	chr19	32830870	32831220
SQ00071_Pte	Pten	GGGGTTTAGT	CAAAAAACAC	chr19	32831189	32831341
SQ00072_Pte	Pten	TTTGTTTAATT	ACCTCAAAAA	chr19	32831317	32831702
SQ00073_Pte	Pten	GGAAGTTGTA	TCCCAACCCTA	chr19	32832123	32832512
SQ00074_Pte	Pten	TTTGTTATTAT	AAACTTCTTCT	chr19	32832488	32832874
SQ00075_Pte	Pten	GAAATTTAGG	ACCTCAAAAA	chr19	32831349	32831702
SQ00076_Pte	Pten	GGAAGGATAA	CTCAACTCTCA	chr19	32831678	32832158
SQ00077_Pte	Pten	GTTTTTTGTTT	CAACCAAAAA	chr19	32831913	32832049
SQ00078_Peg	Peg1	ATATGTTGGG	CAACAAAAAC	chr6	30687764	30688178
SQ00079_Peg	Peg1	TTTATTAGAAT	CAACAAAAAC	chr6	30687835	30688178
SQ00080_Peg	Peg1	TTATTGATGAT	CTAAAACACA	chr6	30688454	30688632
SQ00081_Peg	Peg1	TGAAGAAAGT	TCTTCCAAAAT	chr6	30688569	30688680
SQ00082_Peg	Peg1	GAGTTGTTGT	TAAATTACTTC	chr6	30688154	30688595
SQ00083_Igf2	Igf2r	AGGTTTTAGG	CTAACTTACCT	chr17	12934087	12934299
SQ00084_Igf2	Igf2r	AGATATTTTG	CAAAACACTA	chr17	12934271	12934591
SQ00085_Igf2	Igf2r	GAGGATTTTA	ATCCTCCCCTT	chr17	12934946	12935392
SQ00086_Igf2	Igf2r	GGTGTAAATT	CCTTCATATAC	chr17	12935368	12935676
SQ00087_Igf2	Igf2r	GATAGGAGGA	AACCCCATTAT	chr17	12935619	12935890
SQ00088_Igf2	Igf2r	TTGTAGATAA	CCCAAAATAT	chr17	12935874	12936269
SQ00089_Igf2	Igf2r	GGATTTTGTA	CCCCTCCCTTC	chr17	12934334	12934675
SQ00090_Igf2	Igf2r	GTTAGTAAGA	CCTCCTTATAC	chr17	12934652	12935033
SQ00091_Boll	Boll	TGGAGTTAGG	CTAACTAACCT	chr1	55419136	55419503
SQ00092_Boll	Boll	TAAAGATAAA	ACTAAAACCT	chr1	55419299	55419710
SQ00093_Boll	Boll	GGGAGGGAA	ACTAAAACCT	chr1	55419480	55419710
SQ00094_Boll	Boll	GTTGGAAAGA	ATAAAAACCC	chr1	55419733	55420138
SQ00095_Boll	Boll	GGAAGTTTTT	CTCCAAAATC	chr1	55419260	55419755
SQ00096_Efe	Efemp1	GAAGTAATTG	AAACTCATATT	chr11	28752458	28752781
SQ00097_Efe	Efemp1	TAGTTATAGG	AACACCTAAC	chr11	28752685	28753112

SQ00098_Efe	Efemp1	TAGTTATAGG	AATAACTAAA	chr11	28752685	28752827
SQ00099_Efe	Efemp1	TTTGTGAATT	TCCACCTCCA	chr11	28753047	28753449
SQ00100_Gnb	Gnb4	TGGTTTGGGT	AACTTCAAAT	chr3	32515737	32515984
SQ00101_Gnb	Gnb4	GTTTTGTGTG	CCAAACTTTA	chr3	32515594	32516026
SQ00102_Gnb	Gnb4	TGTGGTTTTTT	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	TTTACCAACC	chr11	21901490	21901839
SQ00111_Otx	Otx1	ATTGAGTGAT	TACTAAAACC	chr11	21901702	21902111
SQ00112_Otx	Otx1	TTGGTTGTTTT	AAATAAAACT	chr11	21902130	21902425
SQ00113_Otx	Otx1	GAGGTTAGGT	CTAAAATCCC	chr11	21901735	21902151
SQ00114_Otx	Otx1	GAGGGTAGTA	ATTACAAAAT	chr11	21901484	21901776
SQ00115_Otx	Otx1	GAATATTTTTG	AAATTACTAA	chr11	21900797	21901239
SQ00116_Otx	Otx1	TTTATTAAATT	CACTATAAAA	chr11	21900674	21901091
SQ00117_Irx2	Irx2	GGGTAGTTTT	TCACCCTAAA	chr13	72765605	72765754
SQ00118_Irx2	Irx2	TAGAGGATTG	AAAACCCAAC	chr13	72765634	72765992
SQ00119_Irx2	Irx2	TTGTAGGAGG	CACACTCTCA	chr13	72765805	72766207
SQ00120_Irx2	Irx2	AGTAGGAAAG	CTTTTATTCCT	chr13	72767922	72768326
SQ00121_Irx2	Irx2	GAAGGAGAAT	AAAAACTAAA	chr13	72768288	72768679
SQ00122_Irx2	Irx2	TTTAAGAAAG	ATTAATCCAA	chr13	72769409	72769514
SQ00123_Irx2	Irx2	GTATTGGTTT	AATAACAACT	chr13	72768129	72768367
SQ00124_Irx2	Irx2	TTTGGTTTTTA	TACCCAAACC	chr13	72767725	72768152
SQ00125_Irx2	Irx2	ATAAGGTTAG	AAATTCCCTA	chr13	72767333	72767747
SQ00126_Irx2	Irx2	GGGTTTAAGT	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	ATATCAAAAC	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	GTTTTTATGGT	ACAAAACCTC	chr7	53040894	53041323
SQ00137_Lmt	Lmtk3_01	GGGGAGGAG	ATACCTCCTC	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	TCCCCATAACT	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	GTTTGGAGAT	CCTAACTCTTC	chr7	53050464	53050791
SQ00144_Rbp	Rbp1	GAAGGTTTGA	TAAATTCCAA	chr9	98325069	98325246
SQ00145_Rbp	Rbp1	GGGTTTTGTG	TCCACAAACA	chr9	98325222	98325408
SQ00146_Rbp	Rbp1	AGTTTGTTTTA	CAAACTAACA	chr9	98325384	98325656
SQ00147_Thb	Thbs2	TTAGTATTTTG	CAAAATAAAA	chr17	14831009	14831431

SQ00148_Thb	Thbs2	AGATTGGTTG	ACTAAATTTCT	chr17	14831407	14831846
SQ00149_Thb	Thbs2	GATTGATAGG	CCACTAAACTA	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	AAAACTTCCTT	chr10	85763302	85763724
SQ00154_Tim	Timp3	GTAGAAGGTA	CCCCTATATCA	chr10	85762886	85763327
SQ00155_Tim	Timp3	TTTAGGGTTG	AAAACTTCCTT	chr10	85763302	85763724
SQ00156_Hox	Hoxd1	ATTTAGTTAA	TCCCCTCAAAA	chr2	74601819	74602060
SQ00157_Hox	Hoxd1	GGTGGTTAGC	TCAACCACTTT	chr2	74601412	74601837
SQ00158_Hox	Hoxd1	GGGGATATAC	TAAACTACCTA	chr2	74601047	74601434
SQ00159_Hox	Hoxd1	GGGTTTTGAT	AACCCTTTCAA	chr2	74600812	74601068
SQ00160_Lrp2	Lrp2	GGATAATTTG	ACCAAAACCT	chr2	69423197	69423476
SQ00161_Lrp2	Lrp2	GTTTTGGGTA	CCCTCAAAAC	chr2	69423300	69423648
SQ00162_Lrp2	Lrp2	GTTTTATTTTG	TAACCCCAAA	chr2	69423624	69423772
SQ00163_Lrp2	Lrp2	GGTTTGGTTT	CTACAATCAT	chr2	69423755	69424176
SQ00164_Lrp2	Lrp2	TTGTGTTTTTG	CTCCAAACAA	chr2	69423588	69423789
SQ00165_Lrp2	Lrp2	GGGAATTTAG	CTTACTCCCCT	chr2	69424189	69424673
SQ00166_Lrp2	Lrp2	AGTGATTGAA	TACATAAAAC	chr2	69423497	69423779
SQ00167_mm	mmu_mir_34	GTTGTGAGTA	CCCATACCCA	chr4	148912293	148912450
SQ00168_miR	miR34-a	TGGTTTTATTT	ACAAAAACAT	chr4	149438407	149438825
SQ00169_miR	miR34-a	AAGATTGAGG	CCAAAATAAA	chr4	149438798	149439105
SQ00170_miR	miR34-a	TAGGGGTGTT	CAAAAACTTA	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	AAAATCATTTT	chr4	149440471	149440693
SQ00174_miR	miR34-a	GGTTTTTTTGT	ATAACTCTATC	chr4	149440606	149440824
SQ00175_miR	miR34-a	GTGGGGTTGC	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	TATTGGTTTAC	AACCTAAATTA	chr4	149441633	149441948
SQ00179_miR	miR34-a	GTTGTTTTATA	AACTCTAACA	chr4	149441831	149442116
SQ00180_miR	miR34-a	GATGAGGGTC	ATACAACAATA	chr4	149442099	149442422
SQ00181_miR	miR34-a	GGATGGGGAC	CAACATCCCA	chr4	149442401	149442765
SQ00182_miR	miR34-a	TGGGGAGGTT	ACCAACAAAC	chr4	149442764	149443004
SQ00183_miR	miR34-a	TGTTTATATTT	ACCCTAAACC	chr4	149443005	149443353
SQ001_Cdkn2	Cdkn2a	AGTAAATAGG	CTAAACCAAA	chr4	88765275	88765573
SQ002_Cdkn2	Cdkn2a	GTAAATAGGT	CAAATTCTTAA	chr4	88765276	88765746
SQ003_Cdkn2	Cdkn2a	TTATTTATAAA	CTAAACCCCA	chr4	88766245	88766831
SQ004_Cdkn2	Cdkn2a	TAAGAGAGGC	CCCCTCCCCCA	chr4	88765700	88765446
SQ005_Apba1	Apba1	TTGGAAGATT	ATCCTCTATCC	chr19	23825293	23825663
SQ006_Apba1	Apba1	GTTAGGGATT	CCAAACCTAA	chr19	23825641	23826103
SQ007_Apba1	Apba1	TGGAGAGTAC	TACCACCTCCA	chr19	23826076	23826493
SQ008_Apba1	Apba1	GGGTTTTTTTC	TACCACCTCCA	chr19	23826225	23826493
SQ009_Apba1	Apba1	GATTTTTGGA	ACAACTTTATT	chr19	23826531	23826082
SQ010_Apba1	Apba1	GGTTTGAAAG	AATCCCTAATA	chr19	23825525	23825222
SQ011_Apba2	Apba2	GATTGATTGT	CCCCTTAAAA	chr7	64380395	64380713
SQ012_Apba2	Apba2	TTTAGTTTATT	TTAAAAAATC	chr7	64380675	64380892
SQ013_Apba2	Apba2	TTTTGATTTTT	ATACCCCTCTA	chr7	64380879	64381357
SQ014_Apba2	Apba2	TTTGGGTAGG	CCCCTCAAAA	chr7	64380642	64380426

SQ015_Apba2	Apba2	GGGATTTGGA	CCTTATAAAA	chr7	64381626	64381326
SQ016_Apba2	Apba2	TTTTGTTTTTT	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	TTTATTTTTGA	ACCAAAAACA	chr9	111116592	111117042
SQ022_Mlh1_	Mlh1	TTAGTGTATG	CCACAAAAAC	chr9	111117145	111117335
SQ023_Mlh1_	Mlh1	GTTTTTAGAA	ATTAAACAAC	chr9	111116606	111116452
SQ024_Mlh1_	Mlh1	TGGTATTTATC	TTTCTATCATC	chr9	111116471	111116229
SQ025_Mlh1_	Mlh1	TAATGTTATTA	TAAACCTAAA	chr9	111116254	111115868
SQ026_Cacna	Cacna1g	TTTAGGTTTAT	ACTCAACAAA	chr11	94289358	94289834
SQ027_Cacna	Cacna1g	GGGGGTTTTA	AACCCCTTAA	chr11	94289810	94290160
SQ028_Cacna	Cacna1g	GGTGGGGGTT	ATAACTCTCC	chr11	94290242	94290615
SQ029_Cacna	Cacna1g	TTTAGTTGGTT	ATTCACAATC	chr11	94289723	94289350
SQ030_Cacna	Cacna1g	TTGATTTTTTA	CCCCTACCCTC	chr11	94290162	94289863
SQ031_Cacna	Cacna1g	GTTTGAAGTTC	AAAAAAATCT	chr11	94290494	94290210
SQ032_Neuro	Neurog1	TTTTTGGGTA	ACACCAAACT	chr13	56260860	56261178
SQ033_Neuro	Neurog1	AGGTGGAGGT	AACCAAACCC	chr13	56261428	56261708
SQ034_Neuro	Neurog1	GGGTTGGTTT	CACTTTCTACC	chr13	56261740	56262196
SQ035_Neuro	Neurog1	GTTTTAATTTT	CCCTTTAAAA	chr13	56261154	56261546
SQ036_Neuro	Neurog1	GAGGAGGATT	AATATCTCAA	chr13	56261467	56261109
SQ037_Runx3	Runx3	TGGGTTTGAA	ACTACCACTA	chr4	134393128	134393455
SQ038_Runx3	Runx3	TTTGAGGTTT	AACCAAATAA	chr4	134393475	134393121
SQ039_Socs1_	Socs1	GGAGGATTAG	AAAAAAACCT	chr16	10698797	10699240
SQ040_Socs1_	Socs1	ATTTTTTTATA	AAACCCAAAC	chr16	10699275	10699669
SQ041_Socs1_	Socs1	GAGTGAGTTT	CAAACAACTC	chr16	10699805	10699494
SQ042_Socs1_	Socs1	GATTTTGGTA	CACCTTCCCA	chr16	10699518	10699274
SQ043_Apc_0	Apc	AGGTGAGTAG	CTAAAAAAAC	chr18	34345546	34345904
SQ044_Apc_0	Apc	GGTGGAGTGA	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	AGGGGGAGTA	AAAAAAACCC	chr3	83852187	83851766
SQ050_Sfrp2_	Sfrp2	GGTTGGATGC	AACCCCAACC	chr3	83852806	83852235
SQ051_Sfrp4_	Sfrp4	AGAATTATGG	AACTTTCCTAC	chr13	19630466	19630802
SQ052_Sfrp4_	Sfrp4	GGGTAGTGGA	CACAAACTTTT	chr13	19630815	19630355
SQ053_Rb1_0	Rb1	GTAGAGATGC	AACTACCCCTA	chr14	72059513	72059693
SQ054_Rb1_0	Rb1	GGTTTTTTGGA	AAAACTACCA	chr14	72060333	72060798
SQ055_Rb1_0	Rb1	GGGTTTTTTTC	AAACAAAACT	chr14	72059538	72059151
SQ056_Rb1_0	Rb1	TTTTTTGTTAG	CCAAAATAAA	chr14	72060680	72060314
SQ057_Vhlh_(	Vhlh	TTAATTGTAG	CCTCCTCTAAA	chr6	113589642	113589948
SQ058_Vhlh_(	Vhlh	GGAAGGTAGT	CCTCCAAATTA	chr6	113589925	113590351
SQ059_Vhlh_(	Vhlh	ATAGGTTGGT	ACCCTCTCAA	chr6	113590395	113590025
SQ060_Vhlh_(	Vhlh	GGTTGTAGAA	AAAAAAAACA	chr6	113590050	113589623
SQ061_Brca1_	Brca1	TTTAAGAGAG	CCCACCCTTTA	chr11	101367911	101368267
SQ062_Brca1_	Brca1	GAAGGGGTTG	CTCAAAACTA	chr11	101368218	101367843
SQ063_Gata4_	Gata4	GGGGAATTTT	ATTTTAATACC	chr14	62199249	62199848
SQ064_Gata4_	Gata4	GGAGAGGGTT	TCATCCTTTTA	chr14	62199824	62200077
SQ065_Gata4_	Gata4	GGTTTTAGTG	ACCCTACCTA	chr14	62199849	62199254

SQ066_Gata4	Gata4	GATTTTGTTTC	CTACCTAACC/	chr14	62199534	62199257
SQ067_Gata5	Gata5	TTTTTGGGTG(	TCAAAAAAAC	chr2	180263947	180264460
SQ068_Gata5	Gata5	GGATTAGGTA	CTCCAACTAA/	chr2	180263103	180263595
SQ069_Gata5	Gata5	TTAGAGTTGT	CTAAACCCCC1	chr2	180264351	180263843
SQ070_Hic1_(	Hic1	TAGGTTGGGT	TACTTCCTACC	chr11	74984019	74984406
SQ071_Hic1_(	Hic1	GGGTTTTTTTT	CCAACTACCT/	chr11	74983031	74983379
SQ072_Hic1_(	Hic1	TTTGGGGTTT	CCCCCAATTTC	chr11	74985083	74984695
SQ073_Hic1_(	Hic1	GTTTTTGTTTT	CAACAACCAC	chr11	74982907	74982345
SQ074_Cdkn2	Cdkn2b	TAGTATTAGA(	AAAAACCATT	chr4	88781798	88782068
SQ075_Cdkn2	Cdkn2b	GGTTTGTGGT	ATTCCAAACT/	chr4	88782046	88782401
SQ076_Cdkn2	Cdkn2b	TTATTGGGTT1	CACACAACCA	chr4	88782132	88781790
SQ077_Cdkn2	Cdkn2b	TTTGTTGAGT(	TCCCCTCTAA/	chr4	88782455	88782112
SQ078_Rassf1	Rassf1	TAGTAGTGGT	CAAAAACAAA	chr9	107412930	107413259
SQ079_Rassf1	Rassf1	GGTTGGAGA/	TAAAAATTAA(	chr9	107412133	107412420
SQ080_Rassf1	Rassf1	TTTTATTTTTT	CCTAAAACAA(	chr9	107413420	107412914
SQ081_Rassf1	Rassf1	AATTGATTATT	CCCAACAAAT/	chr9	107412453	107412068
SQ082_Dapk1	Dapk1	GGGTGTGGG(	CCCCTTCCTA/	chr13	60611909	60612233
SQ083_Dapk1	Dapk1	TTTTTGGGTTT	TCTAAACTAA/	chr13	60611412	60611933
SQ084_Dapk1	Dapk1	TTAGAGAAGG	CCCCAACCTA/	chr13	60612327	60611922
SQ085_Dapk1	Dapk1	AGTTTAGGTT(	AATCCTTAAA1	chr13	60611935	60611410
SQ086_Cdh1_	Cdh1	TTAATTATAG/	CCCTCCACAT/	chr8	109492358	109492683
SQ087_Cdh1_	Cdh1	TGTTTTTGTTG	ACCTTCTACA/	chr8	109492658	109492981
SQ088_Cdh1_	Cdh1	GGATATTTGG	CCTTCTTCCA/	chr8	109493225	109492745
SQ089_Cdh1_	Cdh1	TTTAATTTTTT	CCTACAATTC(	chr8	109492765	109492392
SQ090_Mgmt	Mgmt	AGTTTTAGGT	CAATACCCCA/	chr7	136732674	136733048
SQ091_Mgmt	Mgmt	TGTTTGAGTA	TCTAAAATAA/	chr7	136732981	136732654
SQ092_Chfr_(	Chfr	TTTTGGGTTTT	TTTAAATCCCT	chr5	110376337	110376572
SQ093_Chfr_(	Chfr	GAAGAAGTTT	CAACAAAATA	chr5	110376424	110375991
SQ094_Nespa	Nespas DMR	TTGGATTTTTT	AAAACCTCCA/	chr2	173937600	173937803
SQ095_Nespa	Nespas DMR	GGTGTGAGAC	AACCCCCATA/	chr2	173937934	173938228
SQ096_Nespa	Nespas DMR	TGGGGGTTTT	TAAATCTCAA(	chr2	173938221	173938538
SQ097_Nespa	Nespas DMR	GTGGGTTAGT	ATCTAACATA1	chr2	173938517	173938819
SQ098_Nespa	Nespas DMR	TTTTTTTTAGG	CCCCTCCTCCT	chr2	173938925	173939332
SQ099_Nespa	Nespas DMR	GGGATTTGTA	TTTTCTCAAA/	chr2	173939130	173938926
SQ100_Nespa	Nespas DMR	GGGTATATTG	ACCCCAACCC/	chr2	173938871	173938475
SQ101_Nespa	Nespas DMR	TAGGTTAGTT/	AAAATCCCTA/	chr2	173938497	173938223
SQ102_Nespa	Nespas DMR	GTTAAGGTAA	AAACAAAAAA	chr2	173938253	173937874
SQ103_Nespa	Nespas DMR	GAGAAGGTTT	AAAAAAAACA	chr2	173937744	173937415
SQ104_Peg3.I	Peg3 DMR	GGTGTATGTT(	AAAAACCCTA/	chr7	6334304	6334544
SQ105_Peg3.I	Peg3 DMR	TTTTTTGTTAG	AAACTACATC(	chr7	6334527	6334759
SQ106_Peg3.I	Peg3 DMR	GGGTGTATGT	TCCCCCTTTTC	chr7	6334303	6334730
SQ107_Peg3.I	Peg3 DMR	GGAGAGATG1	ACCTTATCAA1	chr7	6334455	6334202
SQ108_Peg3.I	Peg3 DMR	AGAGGATTTT	CATACTACAA/	chr7	6334545	6334308
SQ109_Peg3.I	Peg3 DMR	GATTTTGTTTC	CCACCAACCC/	chr7	6334717	6334429
SQ110_H19.D	H19 DMR	AGTTTTAAGG	AACTCATAAA	chr7	142389565	142389875
SQ111_H19.D	H19 DMR	TGAAGGAGTT	CCCAAAATCA(	chr7	142389790	142390087
SQ112_H19.D	H19 DMR	TTTTGGGATA	CCAAAAACAA	chr7	142390081	142390403
SQ113_H19.D	H19 DMR	GGGGTTTGAC	TAAAAACACC	chr7	142390505	142390889
SQ114_H19.D	H19 DMR	TTATGATTATC	CCCAAATTCA/	chr7	142391094	142391346
SQ115_H19.D	H19 DMR	ATAAGGGTTA	TTAAAAAATC(	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,ggtcactgaagttcccatta

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,aagtcaactgatggggtact

11,45,606,tatccataccctcctgatct

12,45,653,atactctgtgctgtctccat

13,45,684,ggtcacctattccaaactct

14,45,714,aggagaagcccttgatcttt

15,45,808,aacttgccatcaccaaacca

16,45,830,tttgtcagcagagatctcag

17,45,865,ttaaagtgctggctgaacag

18,45,887,cagcttattgaaggtagcca

19,45,911,gtacatggccttcctataag

20,45,1063,tgcttcttgttgggtttgag

21,45,1089,gcaccttcgacttattaacc

22,45,1111,aagttcctactgtctgaacg

23,45,1143,ttcgacttttgttctcgcgt

24,45,1170,aagcagcagagtcattggtt

25,45,1206,tatttgtcttgaggcgcttg

26,45,1273,ttggtgacttcagaagccat

27,45,1303,aaacagcggtcttccagatt

28,45,1327,acagggttcttctttccaca

29,45,1398,tgtagaagagctctaggaag

30,45,1420,tgatagccgtcctcatcata

31,45,1488,atctgcagcagcttgtgtta

32,45,1626,tgttccaatctttcctgcgt

33,45,1650,tagtgaagaagtcttgcagg

34,45,1672,aattcttccaggtcaggatc

35,45,1703,aattgctgggtacaacttgg

36,45,1732,actctaatgggcctcctttt

37,45,1761,ccgttgcaattccatcaaac

38,45,1783,aactccttgagcaccaagta

39,45,1813,gaggcaatgtacttttccac

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,ttcatactgaggtccaggta

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,attttgttcagggccaaggt

9,45,599,aaaggcgtagtctgctatgt

10,45,637,ttatggagatgcagaaccac

11,45,670,aagcatttctttcccaggga

12,45,701,atctaaagtctccaggctgt

13,45,733,gtggggaattcatcaaggtt

14,45,755,gttggagagtgtcttgattg

15,45,778,ctgtggaatcctagttcctt

16,45,800,cggtattgacctgatgttgt

17,45,832,ataagagaagggttgcctac

18,45,857,ggggttgtcatagaagtgta

19,45,888,gctgaaaagcagatactcca

20,45,911,cagtgttcttagttcaggca

21,45,942,attcagtaatgtgcgaggca

22,45,987,ttaaagtcagactctccagg

23,45,1009,agagatgagatctttgctcc

24,45,1038,taggtaactgatcacagacg

25,45,1060,gacaaatctagcacttggag

26,45,1083,gtaagtcttcgagtaggttg

27,45,1105,ttttggcagcctgacaaact

28,45,1128,gcctcaggtcaattttctga

29,45,1166,ctgaaaagtgctgcccttaa

30,45,1188,gagatcggaggttaaacaac

31,45,1230,cattggggtgaatgatagca

32,45,1252,agagacggcaacgtagaaaa

33,45,1278,gattggatgataggtccaac

34,45,1314,aaccatgtaacccagtcaca

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,cttgaaataacccagcgtct

43,45,1559,taggaaatcttcaaggtccc

44,45,1581,tcaggtcttcctcaaagtca

45,45,1650,taccaaataggtgctcacag

46,45,1736,agttctgaacacggtcaaag

47,45,1764,gcagctttatggaagagatg

48,45,1793,aatgtccactaccgcgatta