

Supplementary Table 1. Updated table of 353 age-related CpG sites with promoter category according to ENCODE ChromHMM

cgID	active promoter in at least 1 from the 9 analyzed cell lines
cgID	weak promoter in at least 1 from the 9 analyzed cell lines

Gene symbol	hypermethylated during aging
Gene symbol	hypomethylated during aging

+	similar methylation pattern as in aging
-	opposite methylation pattern as in aging
nc	no methylation change

CpG marker (cg ID)	Position (GRCh37/hg19)	Gene name	Official Gene Symbol	medianByCpGOld- medianByCpGYoung	Methylation in CRC
cg02489552	chr19:15,121,531-15,121,531	coiled-coil domain containing 105	CCDC105	0,19	+
cg27169020	chr15:83,954,230-83,954,230	basonuclin 1	BNC1	0,16	+
cg22736354	chr6:18,122,719-18,122,719	NHL repeat containing E3 ubiquitin protein ligase 1	NHLRC1	0,159	nc
cg26372517	chr1:36,039,159-36,039,159	transcription factor AP-2 epsilon	TFAP2E	0,12	+
cg13460409	chr21:38,379,571-38,379,571	rippy transcriptional repressor 3	RIPPLY3	0,11	+
cg22809047	chr2:101,618,261-101,618,261	ribosomal protein L31	RPL31	0,11	-
cg26453588	chr22:43,506,021-43,506,021	BCL2 interacting killer	BIK	0,11	nc
cg01353448	chr7:31,726,912-31,726,912	protein phosphatase 1 regulatory subunit 17	PPP1R17	0,1	nc
cg15988232	chr3:47,621,127-47,621,127	chondroitin sulfate proteoglycan 5 (neuroglycan C)	CSPG5	0,1	nc
cg20692569	chr7:72,848,481-72,848,481	frizzled class receptor 9	FZD9	0,1	nc
cg21870884	chr1:200,842,430-200,842,430	G protein-coupled receptor 25	GPR25	0,1	+
cg06493994	chr6:25,652,603-25,652,603	secretagoin, EF-hand calcium binding protein	SCGN	0,092	nc
cg16547529	chr11:75,140,681-75,140,681	kelch-like family member 35	KLHL35	0,08	nc
cg09118625	chr1:68,512,972-68,512,972	DIRAS family GTPase 3	DIRAS3	0,08	nc
cg19945840	chr1:1,168,036-1,168,036	beta-1,3-galactosyltransferase 6	B3GALT6	0,08	nc

cg25148589	chr4:158,141,936-158,141,936	glutamate receptor, ionotropic, AMPA 2	GRIA2	0,08	+
cg12373771	chr22:17,601,382-17,601,382	cat eye syndrome chromosome region, candidate 6	CECR6	0,078	+
cg03760483	chr17:6,899,298-6,899,298	arachidonate 12-lipoxygenase, 12S type	ALOX12	0,07	+
cg06810647	chr16:1,665,094-1,665,094	Crm, cramped-like (Drosophila)	CRAMP1L	0,07	nc
cg05675373	chr1:110,754,257-110,754,257	potassium voltage-gated channel, Shaw-related subfamily, member 4	KCNC4	0,067	+
cg10523019	chr2:227,700,458-227,700,458	rhomboid domain containing 1	RHBDD1	0,064	nc
cg04528819	chr7:130,418,316-130,418,316	Kruppel like factor 14	KLF14	0,063	+
cg06952310	chr19:19,327,990-19,327,990	neurocan	NCAN	0,06	-
cg22901840	chr1:68,512,778-68,512,778	DIRAS family GTPase 3	DIRAS3	0,06	nc
cg25771195	chr16:58,163,815-58,163,815	cilia and flagella associated protein 20	CFAP20	0,06	-
cg08030082	chr2:25,391,839-25,391,839	proopiomelanocortin	POMC	0,06	+
cg17655614	chr16:68,770,945-68,770,945	cadherin 1, type 1, E-cadherin (epithelial)	CDH1	0,06	nc
cg22449114	chr20:590,244-590,244	transcription factor 15 (basic helix-loop-helix)	TCF15	0,06	+
cg07337598	chr1:150,953,943-150,953,943	annexin A9	ANXA9	0,06	nc
cg04084157	chr7:100,809,049-100,809,049	VGF nerve growth factor inducible	VGF	0,054	-
cg02388150	chr8:41,165,700-41,165,700	secreted frizzled related protein 1	SFRP1	0,05	+
cg02654291	chr9:86,572,015-86,572,015	chromosome 9 open reading frame 64	C9orf64	0,05	nc
cg13899108	chr19:18,344,322-18,344,322	phosphodiesterase 4C, cAMP-specific	PDE4C	0,05	+
cg14723032	chr17:6,460,573-6,460,573	PITPNM family member 3	PITPNM3	0,05	+
cg14894144	chr18:21,270,554-21,270,554	laminin, alpha 3	LAMA3	0,05	nc
cg17063929	chr11:89,224,800-89,224,800	NADPH oxidase 4	NOX4	0,05	nc
cg17729667	chr20:25,566,383-25,566,383	ninein-like	NINL	0,05	+
cg21096399	chr11:119,188,145-119,188,145	melanoma cell adhesion molecule	MCAM	0,05	+
cg23517605	chr6:3,228,365-3,228,365	tubulin, beta 2B class IIb	TUBB2B	0,05	+
cg21801378	chr15:72,612,126-72,612,126	CUGBP, Elav-like family member 6	CELF6	0,042	nc
cg12946225	chr19:3,573,752-3,573,752	high mobility group 20B	HMG20B	0,041	-
cg03103192	chr4:52,917,271-52,917,271	spermatogenesis associated 18	SPATA18	0,04	nc
cg12351433	chr2:48,982,957-48,982,957	luteinizing hormone/choriogonadotropin receptor	LHCGR	0,04	+
cg13975369	chr7:130,080,554-130,080,554	centrosomal protein 41kDa	CEP41	0,04	nc
cg25552492	chr8:22,014,000-22,014,000	leucine-rich repeat LGI family, member 3	LGI3	0,04	+
cg01656216	chr10:31,273,710-31,273,710	zinc finger protein 438	ZNF438	0,04	nc
cg08370996	chr15:96,874,032-96,874,032	nuclear receptor subfamily 2, group F, member 2	NR2F2	0,037	-

cg20761322	chr15:78,423,565-78,423,565	calcium and integrin binding family member 2	CIB2	0,037	nc
cg26845300	chr6:158,243,834-158,243,834	sorting nexin 9	SNX9	0,037	nc
cg18573383	chr12:75,603,402-75,603,402	potassium voltage-gated channel, Shaw-related subfamily, member 2	KCNC2	0,034	+
cg26842024	chr19:16,436,123-16,436,123	Kruppel-like factor 2	KLF2	0,032	nc
cg01968178	chr2:86,565,038-86,565,038	receptor accessory protein 1	REEP1	0,031	nc
cg00075967	chr15:74,495,354-74,495,354	stimulated by retinoic acid 6	STRA6	0,03	-
cg00374717	chr17:66,303,145-66,303,145	arylsulfatase G	ARSG	0,03	+
cg02085507	chr19:6,739,193-6,739,193	thyroid hormone receptor interactor 10	TRIP10	0,03	nc
cg03270204	chr6:30,851,639-30,851,639	discoidin domain receptor tyrosine kinase 1	DDR1	0,03	nc
cg05250458	chr19:9,473,566-9,473,566	zinc finger protein 177	ZNF177	0,03	nc
cg05294243	chr19:51,569,106-51,569,106	kallikrein-related peptidase 13	KLK13	0,03	+
cg05755779	chr8:120,079,626-120,079,626	collectin subfamily member 10	COLEC10	0,03	nc
cg09509673	chr17:40,833,697-40,833,697	C-C motif chemokine receptor 10	CCR10	0,03	+
cg14258236	chr6:29,323,330-29,323,330	olfactory receptor, family 5, subfamily V, member 1	OR5V1	0,03	-
cg14329157	chr2:228,736,136-228,736,136	dynein assembly factor with WDR repeat domains 1	DAW1	0,03	nc
cg18440048	chr22:24,093,826-24,093,826	zinc finger protein 70	ZNF70	0,03	+
cg18983672	chr1:47,881,257-47,881,257	forkhead box E3	FOXE3	0,03	nc
cg22289837	chr8:86,350,279-86,350,279	carbonic anhydrase III, muscle specific	CA3	0,03	nc
cg05921699	chr19:42,380,726-42,380,726	CD79a molecule, immunoglobulin-associated alpha	CD79A	0,03	nc
cg02154074	chr2:74,756,234-74,756,234	HtrA serine peptidase 2	HTRA2	0,025	nc
cg08090772	chr8:67,344,641-67,344,641	alcohol dehydrogenase, iron containing, 1	ADHFE1	0,024	+
cg26045434	chr8:21,987,862-21,987,862	hair growth associated	HR	0,023	nc
cg04836038	chr13:99,739,383-99,739,383	dedicator of cytokinesis 9	DOCK9	0,022	nc
cg19167673	chr22:39,640,835-39,640,835	platelet-derived growth factor beta polypeptide	PDGFB	0,022	nc
cg13836627	chr15:30,113,724-30,113,724	tight junction protein 1	TJP1	0,021	nc
cg00945507	chr7:54,827,677-54,827,677	Sec61 translocon gamma subunit	SEC61G	0,02	nc
cg02364642	chr12:58,005,759-58,005,759	Rho guanine nucleotide exchange factor 25	ARHGEF25	0,02	+
cg04126866	chr10:85,932,764-85,932,764	chromosome 10 open reading frame 99	C10orf99	0,02	+
cg05960024	chr4:56,376,021-56,376,021	clock circadian regulator	CLOCK	0,02	-
cg06361108	chr16:2,478,781-2,478,781	cyclin F	CCNF	0,02	nc
cg08251036	chr2:135,008,924-135,008,924	-----	-----	0,02	+
cg08965235	chr11:65,325,158-65,325,158	latent transforming growth factor beta binding protein	LTBP3	0,02	+

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cg10281002	chr12:114,846,400-114,846,400	T-box 5	TBX5	0,02	+
cg10376763	chr2:217,724,364-217,724,364	transition protein 1	TNP1	0,02	nc
cg12768605	chr19:44,324,952-44,324,952	LY6/PLAUR domain containing 5	LYPD5	0,02	+
cg13854874	chr21:37,757,526-37,757,526	chromatin assembly factor 1 subunit B	CHAF1B	0,02	nc
cg18984151	chr3:47,555,476-47,555,476	elongator acetyltransferase complex subunit 6	ELP6	0,02	nc
cg19305227	chr15:45,544,335-45,544,335	solute carrier family 28 member 2	SLC28A2	0,02	nc
cg19692710	chr11:73,661,921-73,661,921	DnaJ (Hsp40) homolog, subfamily B, member 13	DNAJB13	0,02	-
cg20914508	chr3:115,342,333-115,342,333	growth associated protein 43	GAP43	0,02	+
cg24116886	chr20:137,878-137,878	defensin beta 127	DEFB127	0,02	nc
cg06557358	chr17:32,907,002-32,907,002	transmembrane protein 132E	TMEM132E	0,019	+
cg03167275	chr21:18,886,093-18,886,093	coxsackie virus and adenovirus receptor	CXADR	0,017	-
cg09019938	chr10:52,834,499-52,834,499	protein kinase, cGMP-dependent, type I	PRKG1	0,017	nc
cg10486998	chr18:74,961,787-74,961,787	galanin receptor 1	GALR1	0,017	+
cg26005082	chr19:4,769,661-4,769,661	MIR7-3 host gene	MIR7-3HG	0,017	nc
cg13216057	chr11:12,030,643-12,030,643	dickkopf WNT signaling pathway inhibitor 3	DKK3	0,016	+
cg13682722	chr14:90,798,568-90,798,568	NRDE-2, necessary for RNA interference, domain containing	NRDE2	0,016	nc
cg02479575	chr19:4,769,653-4,769,653	MIR7-3 host gene	MIR7-3HG	0,014	nc
cg08434234	chr7:137,531,173-137,531,173	diacylglycerol kinase iota	DGKI	0,014	+
cg19273182	chr2:60,983,417-60,983,417	poly(A) polymerase gamma	PAPOLG	0,014	nc
cg06993413	chr15:65,810,204-65,810,204	dipeptidyl-peptidase 8	DPP8	0,012	nc
cg02827112	chr4:95,129,403-95,129,403	SWI/SNF-related, matrix-associated actin-dependent regulator of chromatin, subfamily a, containing DEAD/H box 1	SMARCA4	0,011	nc
cg14992253	chr1:32,687,567-32,687,567	transmembrane protein 234	TMEM234	0,011	nc
cg01485645	chr17:36,862,200-36,862,200	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 6	MLLT6	0,01	nc
cg02580606	chr17:39,526,726-39,526,726	keratin 33B	KRT33B	0,01	nc
cg03565323	chr17:16,472,866-16,472,866	zinc finger protein 287	ZNF287	0,01	nc
cg04268405	chr10:73,723,222-73,723,222	carbohydrate sulfotransferase 3	CHST3	0,01	nc
cg07455279	chr19:54,605,704-54,605,704	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3, 9kDa	NDUFA3	0,01	nc
cg07595943	chr16:84,224,901-84,224,901	adenosine deaminase domain containing 2	ADAD2	0,01	nc

cg10377274	chr11:125,616,888-125,616,888	prostate and testis expressed 1	PATE1	0,01	-
cg14501253	chr8:12,809,015-12,809,015	KIAA1456	KIAA1456	0,01	nc
cg15381769	chr6:128,841,972-128,841,972	protein tyrosine phosphatase, receptor type, K	PTPRK	0,01	nc
cg15661409	chr14:57,960,976-57,960,976	chromosome 14 open reading frame 105	C14orf105	0,01	nc
cg15974053	chr19:49,339,790-49,339,790	hydroxysteroid (17-beta) dehydrogenase 14	HSD17B14	0,01	nc
cg17338403	chr15:92,395,836-92,395,836	solute carrier organic anion transporter family, member 3A1	SLCO3A1	0,01	+
cg18180783	chr10:75,402,320-75,402,320	myozenin 1	MYOZ1	0,01	nc
cg20795863	chr2:233,896,120-233,896,120	-----	-----	0,01	nc
cg20828084	chr15:81,070,852-81,070,852	cell migration inducing hyaluronan binding protein	CEMIP	0,01	-
cg21378206	chr2:113,817,044-113,817,044	interleukin 36 receptor antagonist	IL36RN	0,01	nc
cg24262469	chr3:156,391,694-156,391,694	TCDD-inducible poly(ADP-ribose) polymerase	TIPARP	0,01	nc
cg27202708	chr1:223,566,710-223,566,710	coiled-coil domain containing 185	CCDC185	0,01	nc
cg26003813	chr16:23,689,802-23,689,802	polo-like kinase 1	PLK1	0,009	+
cg03588357	chr14:91,720,174-91,720,174	G protein-coupled receptor 68	GPR68	0,009	+
cg09191327	chr9:133,540,108-133,540,108	PR domain 12	PRDM12	0,009	+
cg10920957	chr16:87,635,473-87,635,473	junctophilin 3	JPH3	0,009	+
cg27319898	chr7:88,389,004-88,389,004	zinc finger protein 804B	ZNF804B	0,009	+
cg07291563	chr19:48,949,442-48,949,442	glutamate-rich WD repeat containing 1	GRWD1	0,009	nc
cg16494477	chr5:170,847,251-170,847,251	fibroblast growth factor 18	FGF18	0,009	nc
cg26620959	chr6:152,958,489-152,958,489	spectrin repeat containing nuclear envelope protein 1	SYNE1	0,009	+
cg21460081	chr17:46,656,012-46,656,012	homeobox B4	HOXB4	0,008	nc
cg00864867	chr12:80,085,268-80,085,268	pro-apoptotic WT1 regulator	PAWR	0,008	nc
cg01644850	chr19:58,193,232-58,193,232	zinc finger protein 551	ZNF551	0,008	nc
cg02331561	chr16:2,391,081-2,391,081	ATP binding cassette subfamily A member 3	ABCA3	0,008	-
cg15547534	chr7:100,034,411-100,034,411	protein phosphatase 1, regulatory subunit 35	PPP1R35	0,007	nc
cg20524216	chr3:47,555,101-47,555,101	elongator acetyltransferase complex subunit 6	ELP6	0,007	nc
cg06121469	chr15:44,956,099-44,956,099	spastic paraplegia 11 (autosomal recessive)	SPG11	0,007	+
cg19478743	chr17:4,642,647-4,642,647	chemokine (C-X-C motif) ligand 16	CXCL16	0,007	+
cg19514928	chr1:95,583,637-95,583,637	transmembrane protein 56	TMEM56	0,007	nc
cg01027739	chr9:131,842,739-131,842,739	dolichyldiphosphatase 1	DOLPP1	0,007	+
cg06738602	chr14:52,780,635-52,780,635	prostaglandin E receptor 2 (subtype EP2), 53kDa	PTGER2	0,006	nc
cg27092035	chr5:175,792,881-175,792,881	ADP ribosylation factor like GTPase 10	ARL10	0,006	+

cg14424579	chr2:27,274,310-27,274,310	ATP/GTP binding protein-like 5	AGBL5	0,006	nc
cg06462291	chr12:104,235,480-104,235,480	5'-nucleotidase domain containing 3	NT5DC3	0,006	-
cg19008809	chr3:53,080,682-53,080,682	Scm-like with four mbt domains 1	SFMBT1	0,006	nc
cg16579101	chr12:6,677,158-6,677,158	NOP2 nucleolar protein	NOP2	0,005	nc
cg20305610	chr4:95,373,303-95,373,303	PDZ and LIM domain 5	PDLIM5	0,005	nc
cg25781123	chr3:9,404,599-9,404,599	THUMP domain containing 3	THUMPD3	0,005	nc
cg17853587	chr4:118,954,386-118,954,386	N-deacetylase/N-sulfotransferase (heparan glucosaminy) 3	NDST3	0,004	+
cg22637507	chr11:43,902,408-43,902,408	alkB, alkylation repair homolog 3 (E. coli)	ALKBH3	0,004	nc
cg09722397	chr17:72,855,944-72,855,944	glutamate receptor, ionotropic, N-methyl D-aspartate 2C	GRIN2C	0,004	nc
cg25070637	chr8:97,505,869-97,505,869	syndecan 2	SDC2	0,004	+
cg07663789	chr5:32,711,429-32,711,429	natriuretic peptide receptor 3	NPR3	0,003	+
cg11932564	chr22:42,322,146-42,322,146	tumor necrosis factor receptor superfamily member 13C	TNFRSF13C	0,003	+
cg26723847	chr11:134,095,652-134,095,652	non-SMC condensin II complex, subunit D3	NCAPD3	0,003	nc
cg27413543	chr4:83,812,148-83,812,148	SEC31 homolog A (S. cerevisiae)	SEC31A	0,003	nc
cg27494383	chr15:41,805,868-41,805,868	leukocyte receptor tyrosine kinase	LTK	0,003	+
cg09418283	chr12:80,084,719-80,084,719	pro-apoptotic WT1 regulator	PAWR	0,003	nc
cg22432269	chr15:22,892,697-22,892,697	cytoplasmic FMR1 interacting protein 1	CYFIP1	0,003	nc
cg25683012	chr12:57,030,113-57,030,113	bromodomain adjacent to zinc finger domain, 2A	BAZ2A	0,003	nc
cg09785172	chr4:6,271,658-6,271,658	Wolfram syndrome 1 (wolframin)	WFS1	0,003	nc
cg24834740	chr20:37,434,553-37,434,553	protein phosphatase 1 regulatory subunit 16B	PPP1R16B	0,003	+
cg12616277	chr3:138,153,763-138,153,763	extended synaptotagmin protein 3	ESYT3	0,003	+
cg04121983	chr17:73,511,086-73,511,086	CASK interacting protein 2	CASKIN2	0,002	nc
cg20947775	chr4:83,720,241-83,720,241	stearoyl-CoA desaturase 5	SCD5	0,002	nc
cg20999813	chr16:84,734,015-84,734,015	ubiquitin specific peptidase 10	USP10	0,002	nc
cg22006386	chr19:38,827,378-38,827,378	catsper channel auxiliary subunit gamma	CATSPERG	0,002	nc
cg25505610	chr11:32,605,185-32,605,185	eukaryotic translation initiation factor 3, subunit M	EIF3M	0,002	nc
cg19044674	chr1:43,232,629-43,232,629	leucine proline-enriched proteoglycan (leprecan) 1	LEPRE1	0,002	nc
cg01027805	chr14:21,566,863-21,566,863	zinc finger protein 219	ZNF219	0,001	nc
cg01873645	chr9:74,526,649-74,526,649	chromosome 9 open reading frame 85	C9orf85	0,001	nc
cg04005032	chr3:32,022,767-32,022,767	oxysterol binding protein-like 10	OSBPL10	0,001	nc
cg08771731	chr5:17,216,435-17,216,435	brain abundant, membrane attached signal protein 1	BASP1	0,001	+

cg09885951	chr1:214,776,470-214,776,470	centromere protein F	CENPF	0,001	+
cg11653266	chr17:73,901,339-73,901,339	mitochondrial ribosomal protein L38	MRPL38	0,001	+
cg17408647	chr7:43,769,050-43,769,050	cytochrome c oxidase assembly factor 1 homolog (S. cerevisiae)	COA1	0,001	nc
cg21395782	chr19:19,626,814-19,626,814	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13	NDUFA13	0,001	nc
cg24254120	chr13:34,392,869-34,392,869	replication factor C (activator 1) 3, 38kDa	RFC3	0,001	nc
cg15341340	chr19:12,992,237-12,992,237	deoxyribonuclease II, lysosomal	DNASE2	0,001	nc
cg20295671	chr22:22,090,487-22,090,487	yippee-like 1 (Drosophila)	YPEL1	0,0008	nc
cg04452713	chr6:56,707,687-56,707,687	dystonin	DST	0	nc
cg05903609	chr17:1,587,888-1,587,888	pre-mRNA processing factor 8	PRPF8	0	hypermethylated in CRC
cg06144905	chr17:27,369,780-27,369,780	pipecolic acid and sarcosine oxidase	PIPOX	0	hypomethylated in CRC
cg06688848	chr16:57,220,098-57,220,098	ring finger and SPRY domain containing 1	RSPRY1	0	nc
cg08124722	chr17:32,597,714-32,597,714	C-C motif chemokine ligand 7	CCL7	0	nc
cg08413469	chr1:68,962,941-68,962,941	DEP domain containing 1	DEPDC1	0	nc
cg09869858	chr12:48,120,416-48,120,416	endonuclease, polyU-specific	ENDOU	0	nc
cg12830694	chr19:38,747,797-38,747,797	protein phosphatase 1, regulatory (inhibitor) subunit 14A	PPP1R14A	0	hypermethylated in CRC
cg13319175	chr1:19,746,564-19,746,564	capping protein (actin filament) muscle Z-line, beta	CAPZB	0	nc
cg14060828	chr19:49,926,277-49,926,277	parathyroid hormone 2	PTH2	0	nc
cg14658362	chr8:30,241,662-30,241,662	RNA binding protein with multiple splicing	RBPMS	0	nc
cg15262928	chr1:201,924,573-201,924,573	translocase of inner mitochondrial membrane 17 homolog A (yeast)	TIMM17A	0	nc
cg16150435	chr6:31,080,530-31,080,530	chromosome 6 open reading frame 15	C6orf15	0	hypomethylated in CRC
cg16168311	chr1:156,561,948-156,561,948	apolipoprotein A-I binding protein	APOA1BP	0	hypermethylated in CRC
cg16241714	chr8:48,650,512-48,650,512	CCAAT/enhancer binding protein (C/EBP), delta	CEBPD	0	nc
cg16358826	chr4:46,996,265-46,996,265	gamma-aminobutyric acid (GABA) A receptor, alpha 4	GABRA4	0	hypermethylated in CRC
cg16984944	chr3:99,979,426-99,979,426	TBC1 domain family, member 23	TBC1D23	0	hypomethylated in CRC
cg17099569	chr2:121,549,867-121,549,867	GLI family zinc finger 2	GLI2	0	nc

cg17285325	chr22:50,968,343-50,968,343	thymidine phosphorylase	TYMP	0	nc
cg18055007	chr6:31,698,226-31,698,226	dimethylarginine dimethylaminohydrolase 2	DDAH2	0	nc
cg22190114	chr19:56,459,235-56,459,235	NLR family pyrin domain containing 8	NLRP8	0	hypomethylated in CRC
cg22679120	chr7:2,353,402-2,353,402	sorting nexin 8	SNX8	0	hypermethylated in CRC
cg22920873	chr7:139,025,154-139,025,154	chromosome 7 open reading frame 55	C7orf55	0	nc
cg23662675	chr20:45,985,596-45,985,596	zinc finger, MYND-type containing 8	ZMYND8	0	nc
cg23941599	chr5:114,880,796-114,880,796	fem-1 homolog C	FEM1C	0	nc
cg25657834	chr2:11,810,366-11,810,366	neurotensin receptor 2	NTSR2	0	hypermethylated in CRC
cg26297688	chr12:107,349,093-107,349,093	transmembrane protein 263	TMEM263	0	hypermethylated in CRC
cg27377450	chr19:7,446,302-7,446,302	Rho/Rac guanine nucleotide exchange factor (GEF) 18	ARHGEF18	0	nc
cg26456957	chr19:55,629,364-55,629,364	protein phosphatase 1 regulatory subunit 12C	PPP1R12C	-0,001	nc
cg03286783	chr15:44,580,974-44,580,974	cancer susceptibility candidate 4	CASC4	-0,001	-
cg05847778	chr2:170,336,168-170,336,168	Bardet-Biedl syndrome 5	BBS5	-0,001	nc
cg06926735	chr20:48,732,667-48,732,667	ubiquitin-conjugating enzyme E2 variant 1	UBE2V1	-0,001	nc
cg16408394	chr9:137,219,075-137,219,075	retinoid X receptor, alpha	RXRA	-0,001	nc
cg18956095	chr8:124,287,112-124,287,112	zinc fingers and homeoboxes 1	ZHX1	-0,001	nc
cg20100381	chr16:66,864,409-66,864,409	NEDD8 activating enzyme E1 subunit 1	NAE1	-0,001	nc
cg23786576	chr1:47,133,596-47,133,596	ATP synthase mitochondrial F1 complex assembly factor 1	ATPAF1	-0,001	-
cg25928579	chr17:46,692,535-46,692,535	homeobox B8	HOXB8	-0,001	nc
cg02047577	chr20:62,587,703-62,587,703	uridine-cytidine kinase 1-like 1	UCKL1	-0,0017	nc
cg21950518	chr5:55,290,746-55,290,746	interleukin 6 signal transducer	IL6ST	-0,002	-
cg23092072	chr4:87,927,706-87,927,706	AF4/FMR2 family, member 1	AFF1	-0,002	nc
cg25159610	chr5:57,756,803-57,756,803	polo-like kinase 2	PLK2	-0,002	nc
cg02217159	chr6:62,996,697-62,996,697	KH RNA binding domain containing, signal transduction associated 2	KHDRBS2	-0,002	-
cg02972551	chr2:86,668,068-86,668,068	lysine demethylase 3A	KDM3A	-0,002	nc
cg12985418	chr18:19,320,539-19,320,539	mindbomb E3 ubiquitin protein ligase 1	MIB1	-0,002	nc
cg14408969	chr8:42,396,119-42,396,119	small integral membrane protein 19	SMIM19	-0,002	nc
cg17960516	chr4:3,465,004-3,465,004	docking protein 7	DOK7	-0,002	nc

cg23180365	chr3:33,138,627-33,138,627	galactosidase, beta 1	GLB1	-0,002	nc
cg03947362	chr2:200,820,155-200,820,155	tRNA-γW synthesizing protein 5	TYW5	-0,003	-
cg09441152	chr18:77,712,293-77,712,293	PQ loop repeat containing 1	PQLC1	-0,003	nc
cg10940099	chr6:109,703,938-109,703,938	CD164 molecule, sialomucin	CD164	-0,003	nc
cg15185286	chr6:143,381,675-143,381,675	androgen-induced 1	AIG1	-0,003	nc
cg01262913	chr21:38,580,486-38,580,486	Down syndrome critical region 9 (non-protein coding)	DSCR9	-0,003	nc
cg07849904	chr22:28,197,797-28,197,797	meningioma (disrupted in balanced translocation) 1	MN1	-0,003	nc
cg15703512	chr16:22,012,565-22,012,565	PDZ domain containing 9	PDZD9	-0,003	nc
cg19706682	chr16:84,179,332-84,179,332	dynein, axonemal, assembly factor 1	DNAAF1	-0,003	nc
cg26162695	chr17:12,921,313-12,921,313	elaC ribonuclease Z 2	ELAC2	-0,004	nc
cg08186124	chr3:45,883,677-45,883,677	leucine zipper transcription factor-like 1	LZTFL1	-0,004	nc
cg21211748	chr1:23,858,036-23,858,036	E2F transcription factor 2	E2F2	-0,004	nc
cg21305265	chr8:25,316,572-25,316,572	cell division cycle associated 2	CDCA2	-0,004	nc
cg26043391	chr1:224,302,174-224,302,174	F-box protein 28	FBXO28	-0,004	nc
cg04094160	chr9:37,465,712-37,465,712	zinc finger and BTB domain containing 5	ZBTB5	-0,005	nc
cg06513075	chr11:34,126,714-34,126,714	N-acetyltransferase 10 (GCN5-related)	NAT10	-0,005	nc
cg16419345	chr17:73,976,090-73,976,090	acyl-CoA oxidase 1, palmitoyl	ACOX1	-0,006	nc
cg26824091	chr6:38,670,438-38,670,438	glyoxalase I	GLO1	-0,006	-
cg24081819	chr8:27,348,940-27,348,940	epoxide hydrolase 2, cytoplasmic	EPHX2	-0,006	nc
cg02335441	chr3:130,745,949-130,745,949	asteroid homolog 1 (Drosophila)	ASTE1	-0,008	nc
cg22613010	chr3:184,079,172-184,079,172	chloride channel, voltage-sensitive 2	CLCN2	-0,009	nc
cg03682823	chr7:94,286,953-94,286,953	sarcoglycan, epsilon	SGCE	-0,01	-
cg16034652	chr14:93,798,309-93,798,309	unc-79 homolog (C. elegans)	UNC79	-0,01	-
cg00091693	chr17:39,041,603-39,041,603	keratin 20	KRT20	-0,01	+
cg01584473	chr7:100,663,368-100,663,368	mucin 17, cell surface associated	MUC17	-0,01	+
cg02332492	chr9:139,840,679-139,840,679	complement component 8, gamma polypeptide	C8G	-0,01	+
cg03578041	chr15:71,147,308-71,147,308	La ribonucleoprotein domain family, member 6	LARP6	-0,01	nc
cg06836772	chr1:57,110,404-57,110,404	protein kinase AMP-activated catalytic subunit alpha 2	PRKAA2	-0,01	-
cg10345936	chr5:150,727,813-150,727,813	solute carrier family 36 member 2	SLC36A2	-0,01	+
cg11025793	chr19:13,262,016-13,262,016	syntaxin 10	STX10	-0,01	nc
cg12413566	chr3:39,235,367-39,235,367	xin actin-binding repeat containing 1	XIRP1	-0,01	+
cg13038560	chr2:200,819,113-200,819,113	chromosome 2 open reading frame 47	C2orf47	-0,01	nc
cg14308452	chr19:5,784,185-5,784,185	proline rich 22	PRR22	-0,01	nc

cg14654875	chr16:3,493,997-3,493,997	zinc finger protein 597	ZNF597	-0,01	nc
cg14727952	chr11:102,218,359-102,218,359	baculoviral IAP repeat containing 2	BIRC2	-0,01	-
cg17686885	chr17:52,977,770-52,977,770	target of myb1 like 1 membrane trafficking protein	TOM1L1	-0,01	nc
cg24450312	chr1:206,681,158-206,681,158	Ras association (RalGDS/AF-6) domain family member 5	RASSF5	-0,01	nc
cg24580001	chr11:64,106,532-64,106,532	coiled-coil domain containing 88B	CCDC88B	-0,01	nc
cg25166896	chr22:20,009,064-20,009,064	transport and golgi organization 2 homolog	TANGO2	-0,01	nc
cg25411725	chr3:38,306,672-38,306,672	solute carrier family 22 member 13	SLC22A13	-0,01	nc
cg07498421	chr12:94,071,224-94,071,224	CASP2 and RIPK1 domain containing adaptor with death domain	CRADD	-0,011	nc
cg01234063	chr11:126,226,008-126,226,008	ST3 beta-galactoside alpha-2,3-sialyltransferase 4	ST3GAL4	-0,012	nc
cg18031008	chr1:150,266,312-150,266,312	mitochondrial ribosomal protein S21	MRPS21	-0,014	nc
cg27544190	chr21:33,785,434-33,785,434	eva-1 homolog C (C. elegans)	EVA1C	-0,014	nc
cg02275294	chr1:179,262,462-179,262,462	sterol O-acyltransferase 1	SOAT1	-0,016	-
cg13931228	chr7:24,612,418-24,612,418	membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6)	MPP6	-0,017	+
cg11388238	chr2:201,375,098-201,375,098	potassium channel tetramerization domain containing 18	KCTD18	-0,018	-
cg05365729	chr8:23,262,074-23,262,074	lysyl oxidase-like 2	LOXL2	-0,02	-
cg06044899	chr4:91,760,229-91,760,229	coiled-coil serine rich protein 1	CCSER1	-0,02	nc
cg07770222	chr8:144,120,107-144,120,107	chromosome 8 open reading frame 31	C8orf31	-0,02	nc
cg13828047	chr15:75,182,131-75,182,131	mannose phosphate isomerase	MPI	-0,02	+
cg14409958	chr8:120,651,653-120,651,653	ectonucleotide pyrophosphatase/phosphodiesterase 2	ENPP2	-0,02	+
cg14597908	chr20:57,414,960-57,414,960	GNAS complex locus	GNAS	-0,02	-
cg18139769	chr7:94,286,955-94,286,955	sarcoglycan, epsilon	SGCE	-0,02	nc
cg19346193	chr10:127,513,191-127,513,191	uroporphyrinogen III synthase	UROS	-0,02	nc
cg19420968	chr1:32,084,965-32,084,965	hypocretin (orexin) receptor 1	HCRTR1	-0,02	-
cg21370143	chr11:47,374,208-47,374,208	myosin binding protein C, cardiac	MYBPC3	-0,02	nc
cg25101936	chr11:113,929,165-113,929,165	zinc finger and BTB domain containing 16	ZBTB16	-0,02	nc
cg27015931	chr16:22,012,404-22,012,404	PDZ domain containing 9	PDZD9	-0,02	nc
cg01407797	chr22:29,168,514-29,168,514	coiled-coil domain containing 117	CCDC117	-0,022	-
cg03891319	chr3:52,016,839-52,016,839	aminoacylase 1	ACY1	-0,022	nc
cg04999691	chr7:150,027,051-150,027,051	ZBED6 C-terminal like	ZBED6CL	-0,03	-
cg07285276	chr9:134,613,016-134,613,016	Rap guanine nucleotide exchange factor (GEF) 1	RAPGEF1	-0,03	nc

cg01570885	chr6:3,849,273-3,849,273	family with sequence similarity 50 member B	FAM50B	-0,03	-
cg03019000	chr3:51,704,351-51,704,351	testis expressed 264	TEX264	-0,03	+
cg09722555	chr9:34,662,282-34,662,282	chemokine (C-C motif) ligand 27	CCL27	-0,03	nc
cg10045881	chr1:111,770,291-111,770,291	chitinase 3-like 2	CHI3L2	-0,03	+
cg11299964	chr9:128,469,783-128,469,783	mitogen-activated protein kinase associated protein 1	MAPKAP1	-0,03	+
cg13547237	chr11:65,687,878-65,687,878	chromosome 11 open reading frame 68	C11orf68	-0,03	-
cg25564800	chr3:122,234,134-122,234,134	karyopherin alpha 1 (importin alpha 5)	KPNA1	-0,03	nc
cg19046959	chr1:36,565,856-36,565,856	collagen type VIII alpha 2	COL8A2	-0,037	nc
cg22568540	chr19:58,864,847-58,864,847	alpha-1-B glycoprotein	A1BG	-0,04	nc
cg05442902	chr22:21,369,011-21,369,011	purinergic receptor P2X, ligand-gated ion channel, 6	P2RX6	-0,04	-
cg10865119	chr6:170,190,113-170,190,113	long intergenic non-protein coding RNA 574	LINC00574	-0,04	nc
cg14163776	chr3:195,164,581-195,164,581	ArfGAP with coiled-coil, ankyrin repeat and PH domains 2	ACAP2	-0,04	-
cg14423778	chr3:151,985,433-151,985,433	muscleblind-like splicing regulator 1	MBNL1	-0,04	nc
cg16899442	chr16:776,458-776,458	coiled-coil domain containing 78	CCDC78	-0,04	nc
cg17274064	chr21:40,033,893-40,033,893	v-ets avian erythroblastosis virus E26 oncogene homolog	ERG	-0,04	+
cg18328933	chr3:52,008,539-52,008,539	abhydrolase domain containing 14A	ABHD14A	-0,04	nc
cg20240860	chr11:44,087,424-44,087,424	1-aminocyclopropane-1-carboxylate synthase homolog (Arabidopsis)(non-functional)	ACCS	-0,04	-
cg24126851	chr11:6,678,143-6,678,143	dachsous cadherin-related 1	DCHS1	-0,04	-
cg05590257	chr17:17,109,570-17,109,570	phospholipase D family member 6	PLD6	-0,045	nc
cg26394940	chr22:46,449,462-46,449,462	proline rich 34	PRR34	-0,046	nc
cg24899750	chr20:16,710,314-16,710,314	small nuclear ribonucleoprotein polypeptide B	SNRPB2	-0,05	nc
cg00436603	chr10:135,340,740-135,340,740	cytochrome P450, family 2, subfamily E, polypeptide 1	CYP2E1	-0,05	nc
cg01511567	chr11:57,103,631-57,103,631	structure specific recognition protein 1	SSRP1	-0,05	-
cg06117855	chr3:45,067,789-45,067,789	C-type lectin domain family 3 member B	CLEC3B	-0,05	-
cg09133026	chr14:75,388,105-75,388,105	ribosomal protein S6 kinase-like 1	RPS6KL1	-0,05	nc
cg10266490	chr1:55,013,710-55,013,710	acyl-CoA thioesterase 11	ACOT11	-0,05	-
cg13129046	chr10:71,389,697-71,389,697	chromosome 10 open reading frame 35	C10orf35	-0,05	nc
cg14175438	chr7:121,036,729-121,036,729	family with sequence similarity 3, member C	FAM3C	-0,05	-
cg19569684	chr5:138,726,420-138,726,420	marginal zone B and B1 cell-specific protein	MZB1	-0,05	nc
cg13269407	chr22:46,450,107-46,450,107	proline rich 34	PRR34	-0,055	nc
cg00168942	chr10:35,894,431-35,894,431	gap junction protein delta 4	GJD4	-0,06	nc

cg02071305	chr15:41,185,974-41,185,974	VPS18, CORVET/HOPS core subunit	VPS18	-0,06	nc
cg09646392	chr13:108,921,052-108,921,052	tumor necrosis factor (ligand) superfamily, member 13b	TNFSF13B	-0,06	+
cg17324128	chr10:45,455,500-45,455,500	Ras association (RalGDS/AF-6) domain family member 4	RASSF4	-0,06	nc
cg19722847	chr12:30,849,114-30,849,114	importin 8	IPO8	-0,06	-
cg17589341	chr18:43,304,079-43,304,079	solute carrier family 14 (urea transporter), member 1 (Kidd blood group)	SLC14A1	-0,07	+
cg24471894	chr9:2,838,509-2,838,509	pumilio RNA binding family member 3	PUM3	-0,07	nc
cg27016307	chr19:49,658,914-49,658,914	histidine rich calcium binding protein	HRC	-0,07	+
cg04431054	chr5:126,853,025-126,853,025	proline-rich coiled-coil 1	PRRC1	-0,08	nc
cg04474832	chr3:52,008,487-52,008,487	abhydrolase domain containing 14A	ABHD14A	-0,08	nc
cg12941369	chr3:33,839,390-33,839,390	programmed cell death 6 interacting protein	PDCD6IP	-0,08	nc
cg00431549	chr12:15,039,026-15,039,026	matrix Gla protein	MGP	-0,09	+
cg01560871	chr10:72,545,424-72,545,424	thymus, brain and testes associated	TBATA	-0,09	nc
cg07158339	chr9:71,650,238-71,650,238	frataxin	FXN	-0,09	-
cg07730301	chr11:67,777,952-67,777,952	aldehyde dehydrogenase 3 family, member B1	ALDH3B1	-0,09	nc
cg11314684	chr1:244,006,289-244,006,289	AKT serine/threonine kinase 3	AKT3	-0,09	+
cg22171829	chr7:95,225,521-95,225,521	pyruvate dehydrogenase kinase, isozyme 4	PDK4	-0,09	nc
cg01459453	chr1:169,599,213-169,599,213	selectin P (granule membrane protein 140kDa, antigen CD62)	SELP	-0,09	+
cg19724470	chr9:5,450,936-5,450,936	CD274 molecule	CD274	-0,1	-
cg19761273	chr17:80,232,096-80,232,096	casein kinase 1, delta	CSNK1D	-0,1	nc
cg03330058	chr3:127,392,404-127,392,404	ankyrin repeat and BTB (POZ) domain containing 1	ABTB1	-0,11	-
cg22197830	chr5:134,209,785-134,209,785	thioredoxin domain containing 15	TXNDC15	-0,11	nc
cg22947000	chr16:81,272,282-81,272,282	beta-carotene oxygenase 1	BCO1	-0,11	nc
cg15804973	chr6:137,114,513-137,114,513	mitogen-activated protein kinase kinase kinase 5	MAP3K5	-0,12	-
cg07388493	chr1:39,491,460-39,491,460	NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa (NADH-coenzyme Q reductase)	NDUFS5	-0,13	+
cg07408456	chr19:15,590,533-15,590,533	peptidoglycan recognition protein 2	PGLYRP2	-0,13	+
cg24058132	chr14:88,459,866-88,459,866	galactosylceramidase	GALC	-0,13	nc
cg24888049	chr15:91,426,667-91,426,667	FES proto-oncogene, tyrosine kinase	FES	-0,13	nc
cg08331960	chr16:2,076,597-2,076,597	solute carrier family 9, subfamily A (NHE3, cation proton antiporter 3), member 3 regulator 2	SLC9A3R2	-0,14	nc
cg13302154	chr12:15,039,433-15,039,433	matrix Gla protein	MGP	-0,14	nc

cg19853760	chr22:38,071,677-38,071,677	lectin, galactoside-binding, soluble, 1	LGALS1	-0,15	nc
cg25809905	chr17:42,467,728-42,467,728	integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41)	ITGA2B	-0,16	nc
cg26614073	chr3:47,517,820-47,517,820	SREBF chaperone	SCAP	-0,17	nc
cg23124451	chr22:39,548,131-39,548,131	chromobox 7	CBX7	-0,19	nc
cg09809672	chr1:236,557,683-236,557,683	EDAR-associated death domain	EDARADD	-0,2	nc
cg01820374	chr12:6,882,084-6,882,084	lymphocyte activating 3	LAG3	-0,22	nc
cg16744741	chr4:82,126,026-82,126,026	protein kinase, cGMP-dependent, type II	PRKG2	-0,26	+

Supplementary Table 2A. Significantly differentially expressed genes belonging to 353 epigenetic clock CpG sites in CRC vs. normal comparison

Affymetrix probe set ID	Gene Symbol	P value	logFC (CRC-N)
209368_at	EPHX2	5,05655E-15	-2,45
225207_at	PDK4	4,93349E-16	-2,06
213953_at	KRT20	1,61657E-09	-1,95
205049_s_at	CD79A	8,0716E-07	-1,88
237515_at	TMEM56	3,5263E-12	-1,87
205200_at	CLEC3B /// EXOSC7	1,4526E-13	-1,79
205960_at	PDK4	6,82742E-11	-1,74
234980_at	TMEM56	1,18351E-09	-1,72
213501_at	ACOX1	4,31394E-16	-1,60
223565_at	MZB1	0,000108207	-1,58
227962_at	ACOX1	2,3563E-17	-1,51
221286_s_at	MZB1	8,44524E-05	-1,50
207505_at	PRKG2	6,11165E-09	-1,48
202036_s_at	SFRP1	8,65962E-08	-1,47
209600_s_at	ACOX1	1,71823E-17	-1,46
1554938_a_at	ACOT11	1,97586E-11	-1,41
1555779_a_at	CD79A	7,04469E-06	-1,37
217184_s_at	LTK	2,14483E-11	-1,32
213499_at	CLCN2	1,62185E-12	-1,28
230076_at	PITPNM3	3,23452E-07	-1,25
214763_at	ACOT11	4,19894E-13	-1,23
210839_s_at	ENPP2	2,99649E-05	-1,21
202037_s_at	SFRP1	3,97949E-05	-1,11
224728_at	ATPAF1	5,56514E-12	-1,03
221135_s_at	ASTE1	1,65393E-11	-0,96
205697_at	SCGN	3,25519E-05	-0,96
209392_at	ENPP2	0,000295269	-0,90
227892_at	PRKAA2	0,004149339	-0,87

215537_x_at	DDAH2	9,09302E-06	-0,82
202262_x_at	DDAH2	1,5549E-05	-0,81
41577_at	PPP1R16B	0,000176236	-0,79
213039_at	ARHGEF18	1,64581E-10	-0,79
212914_at	CBX7	6,87637E-10	-0,79
202472_at	MPI	1,05832E-06	-0,79
210086_at	HR	4,87193E-05	-0,77
201130_s_at	CDH1	0,002955353	-0,76
203726_s_at	LAMA3	0,00337559	-0,76
207106_s_at	LTK	1,9971E-05	-0,75
241355_at	HR	2,45724E-06	-0,72
205008_s_at	CIB2	1,31447E-06	-0,72
226436_at	RASSF4	0,000161062	-0,71
201924_at	AFF1	1,75629E-13	-0,70
205883_at	ZBTB16	0,000105783	-0,67
223213_s_at	ZHX1	8,28026E-06	-0,67
232098_at	DST	0,015512335	-0,66
214909_s_at	DDAH2	1,16313E-05	-0,66
218208_at	PQLC1	7,76537E-10	-0,66
228361_at	E2F2	5,25715E-07	-0,65
202449_s_at	RXRA	3,74323E-11	-0,65
213341_at	FEM1C	1,13636E-07	-0,65
209447_at	SYNE1	4,27084E-05	-0,63
204688_at	SGCE	0,000896466	-0,62
212254_s_at	DST	5,68068E-06	-0,62
241017_at	RPL31 /// TBC1D8	0,001125052	-0,61
215016_x_at	DST	4,89864E-06	-0,60
216103_at	ACOT11	1,15583E-07	-0,59
1552472_a_at	ACAP2	0,001801623	-0,59
217746_s_at	PDCD6IP	1,484E-10	-0,57
212253_x_at	DST	4,7004E-05	-0,55
212196_at	IL6ST	0,00036495	-0,55
228479_at	SOAT1	0,000358777	-0,54
221817_at	DOLPP1	1,33872E-10	-0,54

224729_s_at	ATPAF1	8,59573E-09	-0,52
205856_at	SLC14A1	0,013954673	-0,51
220565_at	CCR10	0,010394658	-0,51
239297_at	KIAA1456 /// LOC101927137	7,81563E-06	-0,50
49306_at	RASSF4	6,95729E-05	-0,50
220939_s_at	DPP8	0,000259144	-0,50
212750_at	PPP1R16B	0,007684144	-0,48
203513_at	SPG11	5,08317E-07	-0,48
206631_at	PTGER2	0,011385957	-0,48
208654_s_at	CD164	3,79354E-05	-0,47
203243_s_at	PDLIM5	0,000152764	-0,47
239155_at	CXADR	0,013493848	-0,47
237144_at	LTBP3	7,32475E-07	-0,46
208405_s_at	CD164	7,90772E-08	-0,46
204417_at	GALC	0,019521165	-0,44
231478_at	LOC729966 /// PDE4C	0,040703311	-0,43
222394_at	PDCD6IP	4,58975E-05	-0,43
213684_s_at	PDLIM5	0,013728273	-0,42
223214_s_at	ZHX1	1,91743E-07	-0,42
201003_x_at	TMEM189 /// TMEM189-UBE2V1 /// UBE2V1 /// UBE2V2	8,38861E-06	-0,42
221593_s_at	RPL31	3,61152E-05	-0,41
219314_s_at	ZNF219	1,15369E-06	-0,41
204863_s_at	IL6ST	0,026656328	-0,41
1555321_at	ACOT11	1,49213E-06	-0,41
227006_at	PPP1R14A	0,036618976	-0,39
226780_s_at	C7orf55	0,000243144	-0,39
212476_at	ACAP2	6,75033E-07	-0,39
220087_at	BCMO1	0,049100494	-0,39
226781_at	C7orf55 /// C7orf55-	0,011495288	-0,38

	LUC7L2 /// LUC7L2		
205007_s_at	CIB2	0,002011713	-0,38
223028_s_at	SNX9	0,000131005	-0,38
208653_s_at	CD164	0,024748418	-0,37
223027_at	SNX9	4,24676E-06	-0,37
208923_at	CYFIP1	3,58564E-09	-0,35
201131_s_at	CDH1	1,87934E-06	-0,34
228788_at	YPEL1	0,001569017	-0,34
227018_at	DPP8	0,001619232	-0,33
223152_at	PPP1R12C	1,31359E-06	-0,32
233609_at	PTPRK	0,017684637	-0,32
209833_at	CRADD	0,002022768	-0,32
212412_at	PDLIM5	1,17755E-06	-0,31
244661_at	SOAT1	0,014943853	-0,31
240261_at	TOM1L1	0,003686186	-0,31
226343_at	DPP8	0,000111342	-0,30
201354_s_at	BAZ2A	0,000167111	-0,30
225534_at	SMIM19	0,001234686	-0,29
208774_at	CSNK1D	1,40195E-05	-0,29
202035_s_at	SFRP1	0,039354066	-0,28
202076_at	BIRC2	1,55179E-05	-0,28
202426_s_at	RXRA	0,01762018	-0,27
212329_at	SCAP	0,000191081	-0,27
212195_at	IL6ST	0,007969961	-0,26
210749_x_at	DDR1 /// MIR4640	0,002281092	-0,26
226493_at	KCTD18	0,009143393	-0,25
225528_at	IPO8	2,41527E-06	-0,25
204485_s_at	TOM1L1	0,03961683	-0,25
210719_s_at	HMG20B	0,011169125	-0,23
238489_at	PRKAA2	0,004670798	-0,22
221578_at	RASSF4	0,000518814	-0,22
207169_x_at	DDR1 /// MIR4640	0,014561975	-0,21
228713_s_at	HSD17B14	0,002156404	-0,21
225121_at	TBC1D23	0,005282247	-0,21

201949_x_at	CAPZB	0,000231716	-0,20
201950_x_at	CAPZB	0,000157893	-0,20
221846_s_at	CASKIN2	0,017700372	-0,19
37012_at	CAPZB	0,000514534	-0,19
202011_at	TJP1	0,009028194	-0,19
227113_at	ADHFE1	0,027735565	-0,19
233164_x_at	RHBDD1	0,001094584	-0,19
217573_at	GRIN2C	0,002833039	-0,19
220163_s_at	HR	0,000784613	-0,19
228264_at	ACCS	0,04619902	-0,18
1007_s_at	DDR1 /// MIR4640	0,038579629	-0,17
206792_x_at	LOC729966 /// PDE4C	0,042300505	-0,17
208779_x_at	DDR1 /// MIR4640	0,028276382	-0,17
225773_at	RSPRY1	0,04122172	-0,15
242377_x_at	THUMPD3	0,007959733	-0,15
205231_s_at	EPM2A	0,044568836	-0,13
235396_at	TANGO2	0,010121013	-0,11
224497_x_at	HSD17B14	0,011042603	-0,10
215451_s_at	AFF1	0,033025241	-0,10
227427_at	ARHGEF25	0,001032262	-0,10
216710_x_at	ZNF287	0,023131131	-0,09
232330_at	COA1	0,003199947	-0,09
217017_at	OSBPL10	0,003994147	-0,07
220600_at	ELP6	0,004081643	-0,07
230856_at	ARSG	0,043593345	-0,05
1553207_at	ARL10	0,045288063	-0,05
214796_at	KIAA1456 /// LOC101927137	0,048750123	-0,04
228296_at	YPEL1	0,001929055	-0,04
1552276_a_at	VPS18	0,012120675	0,05
215041_s_at	DOCK9	0,005829093	0,06
224229_s_at	AKT3	0,015355795	0,07
230542_at	ZNF597	0,036236355	0,11

231656_x_at	OSBPL10	0,006405957	0,11
221701_s_at	STRA6	0,04737003	0,12
200963_x_at	RPL31	0,007000357	0,12
211858_x_at	GNAS	0,026383569	0,13
228436_at	KCNC4	0,034843038	0,13
214795_at	ZMYND8	0,010945036	0,14
229864_at	ELP6	0,002381442	0,16
223656_s_at	TMEM234	0,002233821	0,18
226442_at	ABTB1	0,003925432	0,19
231857_s_at	AGBL5	0,042465882	0,20
211626_x_at	ERG	0,000584179	0,20
201757_at	NDUFS5 /// RPL10	0,016276935	0,20
244752_at	ZNF438	0,03592967	0,20
229092_at	NR2F2	0,00605637	0,21
215238_s_at	DOCK9	0,014271953	0,22
221549_at	GRWD1	0,000644541	0,22
232874_at	DOCK9	0,014442311	0,23
203089_s_at	HTRA2	0,000730778	0,23
207267_s_at	RIPPLY3	0,000477724	0,24
223346_at	VPS18	0,001737362	0,24
209120_at	NR2F2	0,00223297	0,25
213370_s_at	SFMBT1	0,028031266	0,25
220099_s_at	C7orf55-LUC7L2 /// LUC7L2	1,17011E-05	0,26
222839_s_at	PAPOLG	0,014287481	0,26
232810_at	AIG1	0,000948502	0,26
1552632_a_at	ARSG	0,002048595	0,26
207945_s_at	CSNK1D	0,000246743	0,26
229846_s_at	MAPKAP1	0,015535417	0,27
229863_s_at	ELP6	2,1175E-06	0,27
229743_at	ZNF438	0,00801805	0,27
219054_at	NPR3	0,041935604	0,27
224720_at	MIB1	0,010945257	0,27
209137_s_at	USP10	0,001660169	0,28

208075_s_at	CCL7	0,010870354	0,28
236745_at	CCDC78	0,0003382	0,28
205640_at	ALDH3B1	0,029638911	0,29
230533_at	ZMYND8	0,026765029	0,29
201822_at	TIMM17A	0,002875912	0,29
212625_at	STX10	4,13868E-05	0,29
207130_at	ZMYND8	0,032361379	0,29
225628_s_at	MLLT6	0,026416976	0,30
202055_at	KPNA1	0,001729063	0,30
243816_at	LL22NC03-N27C7.1 /// ZNF70	0,003096208	0,30
225730_s_at	THUMP3	0,022720207	0,30
209372_x_at	TUBB2A /// TUBB2B	0,015675076	0,30
211152_s_at	HTRA2	5,42349E-07	0,30
203026_at	ZBTB5	0,000659823	0,31
223834_at	CD274	0,027052238	0,32
224725_at	MIB1	0,036074541	0,32
218892_at	DCHS1	0,0001084	0,32
207034_s_at	GLI2	0,012599702	0,32
215171_s_at	TIMM17A	0,000172282	0,33
228537_at	GLI2	0,005382576	0,33
203836_s_at	MAP3K5	0,009004693	0,33
210542_s_at	SLCO3A1	0,000312675	0,33
39966_at	CSPG5	0,001220481	0,33
229164_s_at	ABTB1	0,021761296	0,33
201939_at	PLK2	0,043539768	0,33
218533_s_at	UCKL1	0,011291941	0,34
235686_at	TYW5	0,026632698	0,34
217842_at	C7orf55-LUC7L2 /// LUC7L2	0,000711596	0,35
226127_at	ALKBH3	0,0063947	0,36
235181_at	TYW5	0,007820525	0,36
236117_at	ZNF597	0,000298275	0,36
207705_s_at	NINL	0,042370602	0,36

202059_s_at	KPNA1	1,62455E-06	0,36
201576_s_at	GLB1 /// TMPPE	7,43856E-05	0,36
231767_at	HOXB4	0,000872592	0,36
232675_s_at	UCKL1	0,017157224	0,37
223197_s_at	SMARCAD1	0,000698197	0,37
201821_s_at	TIMM17A	0,000582409	0,38
230508_at	DKK3	0,000434198	0,38
226945_at	RHBDD1	3,91415E-07	0,38
230697_at	BBS5	0,002583482	0,39
214157_at	GNAS	0,033950664	0,40
209049_s_at	ZMYND8	0,002431098	0,40
209506_s_at	NR2F1 /// NR2F2	0,000511392	0,41
227598_at	ZBED6CL	0,001361102	0,41
202231_at	EIF3M	4,0156E-09	0,42
203837_at	MAP3K5	0,000284982	0,42
225172_at	CRAMP1L	1,13195E-07	0,42
212689_s_at	KDM3A	0,000418135	0,43
222101_s_at	DCHS1	0,012915349	0,44
1555970_at	FBXO28	8,85683E-05	0,44
228231_at	MIR6836 /// SNX8	0,000182453	0,44
201002_s_at	TMEM189 /// TMEM189-UBE2V1 /// UBE2V1 /// UBE2V2	5,43966E-09	0,44
218786_at	NT5DC3	0,000500686	0,45
216061_x_at	PDGFB	4,46864E-07	0,46
221900_at	COL8A2	0,006853466	0,47
225484_at	CEP41	0,014117445	0,47
202268_s_at	NAE1	1,65702E-08	0,48
218437_s_at	LZTFL1	1,69521E-05	0,49
212158_at	SDC2	0,027898974	0,49
227367_at	SLCO3A1	0,000793853	0,49
52651_at	COL8A2	0,000655821	0,49
205330_at	MN1	0,009178707	0,50

214992_s_at	DNASE2	0,000580019	0,50
204775_at	CHAF1B	5,00737E-08	0,50
221605_s_at	PIPOX	0,018804175	0,50
32094_at	CHST3	2,65065E-05	0,51
202232_s_at	EIF3M	3,55819E-08	0,51
202505_at	SNRPB2	8,06936E-09	0,52
1568781_at	UROS	6,48302E-06	0,53
231382_at	FGF18	2,08575E-05	0,54
212157_at	SDC2	0,009776818	0,54
219073_s_at	OSBPL10	5,09807E-07	0,55
209834_at	CHST3	6,59069E-05	0,55
206497_at	COA1	1,92981E-05	0,56
236957_at	CDCA2	0,000427357	0,56
1553611_s_at	KLHL35	0,002023822	0,56
203484_at	SEC61G	1,51904E-13	0,56
225733_at	B3GALT6	1,42545E-06	0,58
210085_s_at	ANXA9	8,37629E-05	0,58
212538_at	DOCK9	7,67198E-09	0,58
200956_s_at	SSRP1	4,55471E-07	0,58
200957_s_at	SSRP1	3,72004E-09	0,59
226434_at	PPP1R35	4,18839E-10	0,59
228843_at	ARL10	0,001680819	0,60
223804_s_at	THUMPD3	3,8948E-08	0,61
222880_at	AKT3	0,002259324	0,61
212609_s_at	AKT3	0,000472201	0,62
229776_at	SLCO3A1	9,11646E-05	0,63
224759_s_at	TMEM263	6,37418E-07	0,63
217497_at	TYMP	0,000916696	0,63
227037_at	FLCN /// PLD6	1,20844E-05	0,63
213741_s_at	KPNA1	1,69204E-05	0,64
241926_s_at	ERG	2,05307E-05	0,64
203973_s_at	CEBPD	3,99439E-09	0,64
212607_at	AKT3	0,000976136	0,64
222632_s_at	LZTFL1	4,67626E-05	0,66

205565_s_at	FXN	9,17553E-05	0,67
211712_s_at	ANXA9	3,70391E-05	0,67
235545_at	DEPDC1	3,80292E-05	0,68
205780_at	BIK	3,84606E-05	0,68
223186_at	TMEM189 /// TMEM189-UBE2V1 /// UBE2V1	5,36855E-09	0,68
201001_s_at	TMEM189 /// TMEM189-UBE2V1 /// UBE2V1 /// UBE2V2	2,40629E-08	0,69
214023_x_at	TUBB2B	0,00264488	0,71
204365_s_at	REEP1	0,001451348	0,71
218651_s_at	LARP6	0,000125835	0,72
211042_x_at	MCAM /// MIR6756	6,6763E-08	0,72
222958_s_at	DEPDC1	0,003176519	0,74
200681_at	GLO1	2,41695E-11	0,74
227458_at	CD274	0,008648902	0,75
221127_s_at	DKK3	1,26148E-07	0,77
213006_at	CEBPD	3,05391E-05	0,79
214247_s_at	DKK3	0,000791552	0,80
229055_at	GPR68	2,37235E-05	0,81
226313_at	C10orf35	1,76111E-12	0,82
220295_x_at	DEPDC1	0,000441344	0,82
209445_x_at	COA1	3,1318E-08	0,82
217884_at	NAT10	1,05262E-09	0,82
202058_s_at	KPNA1	5,47412E-06	0,82
212154_at	SDC2	0,000249321	0,83
223241_at	MIR6836 /// SNX8	1,6863E-08	0,85
219773_at	NOX4	0,000145589	0,85
204858_s_at	TYMP	7,96162E-07	0,86
203712_at	PUM3	7,71728E-09	0,86
202196_s_at	DKK3	0,000174792	0,87
225485_at	CEP41	3,79332E-06	0,89

201105_at	LGALS1	6,60719E-07	0,91
229667_s_at	HOXB8	0,002627011	0,96
1554685_a_at	CEMIP	2,82643E-07	0,96
206049_at	SELP	7,62881E-06	0,97
204364_s_at	REEP1	0,012374264	0,98
204827_s_at	CCNF	1,55044E-08	0,98
202391_at	BASP1	1,2359E-05	1,00
219229_at	SLCO3A1	6,86556E-07	1,00
219371_s_at	KLF2	2,77453E-07	1,00
209487_at	RBPMS	1,50823E-08	1,01
212789_at	NCAPD3	1,56966E-10	1,01
204200_s_at	PDGFB	1,07608E-09	1,04
1555270_a_at	WFS1	8,90493E-08	1,06
213541_s_at	ERG	4,69123E-09	1,08
229845_at	MAPKAP1	9,22665E-09	1,11
214427_at	NOP2	3,42445E-15	1,11
232278_s_at	DEPDC1	0,000296922	1,12
207828_s_at	CENPF	1,41712E-06	1,16
223454_at	CXCL16	3,43937E-13	1,21
226661_at	CDCA2	1,41948E-06	1,25
209488_s_at	RBPMS	1,50152E-12	1,27
209172_s_at	CENPF	1,04885E-09	1,28
205429_s_at	MPP6	3,59642E-07	1,29
1553959_a_at	B3GALT6	2,73384E-16	1,29
202908_at	WFS1	2,1429E-10	1,36
209086_x_at	MCAM /// MIR6756	8,69443E-14	1,40
202997_s_at	LOXL2	5,10345E-10	1,46
204826_at	CCNF	1,43711E-14	1,49
207836_s_at	RBPMS	5,58414E-16	1,58
204127_at	RFC3	1,28326E-11	1,68
202240_at	PLK1	2,19376E-14	1,69
220750_s_at	LEPRE1	1,66433E-17	1,70
236565_s_at	LARP6	3,26992E-10	1,87
204128_s_at	RFC3	3,56642E-09	1,92

202291_s_at	MGP	2,33773E-11	1,97
211340_s_at	MCAM /// MIR6756	2,33157E-16	2,31
202998_s_at	LOXL2	6,19245E-15	2,53
210869_s_at	MCAM /// MIR6756	1,71599E-19	2,58
209087_x_at	MCAM	1,37459E-20	2,71
212942_s_at	CEMIP	5,25376E-25	5,72

Supplementary Table 2B. Significantly differentially expressed genes belonging to 353 epigenetic clock CpG sites in adenoma vs. normal comparison

Affymetrix probe set ID	Gene Symbol	P value	logFC(AD-N)
205200_at	CLEC3B /// EXOSC7	1E-23	-2,44
225207_at	PDK4	2,16E-18	-2,17
204688_at	SGCE	3,82E-16	-1,95
210839_s_at	ENPP2	2,18E-11	-1,84
213499_at	CLCN2	1,08E-26	-1,84
202036_s_at	SFRP1	3,62E-13	-1,79
205960_at	PDK4	1,57E-11	-1,79
213953_at	KRT20	7,74E-18	-1,69
205049_s_at	CD79A	4,83E-09	-1,63
227892_at	PRKAA2	3,7E-08	-1,55
223502_s_at	TNFSF13B	7,71E-10	-1,51
202037_s_at	SFRP1	4,43E-11	-1,48
41577_at	PPP1R16B	1,2E-10	-1,45
207505_at	PRKG2	3,7E-08	-1,43
213501_at	ACOX1	7,4E-14	-1,41
217184_s_at	LTK	7,36E-12	-1,39
209392_at	ENPP2	7,82E-11	-1,36
227006_at	PPP1R14A	2,83E-13	-1,33
223501_at	TNFSF13B	3,75E-10	-1,32
205697_at	SCGN	1,43E-10	-1,32
227962_at	ACOX1	1,22E-18	-1,29
223565_at	MZB1	1,72E-05	-1,28
1555779_a_at	CD79A	2,18E-08	-1,26
209600_s_at	ACOX1	6,25E-16	-1,26

226436_at	RASSF4	8,62E-09	-1,24
223322_at	RASSF5	1,55E-09	-1,22
209447_at	SYNE1	5,76E-15	-1,19
212158_at	SDC2	1,74E-10	-1,17
204863_s_at	IL6ST	3,64E-08	-1,17
213039_at	ARHGEF18	2,64E-20	-1,16
212196_at	IL6ST	2,53E-12	-1,13
212607_at	AKT3	1,17E-11	-1,12
237515_at	TMEM56	8,35E-09	-1,11
221286_s_at	MZB1	1,31E-05	-1,02
228396_at	PRKG1	1,3E-14	-1,02
211000_s_at	IL6ST	3,43E-07	-1,01
1552472_a_at	ACAP2	2,75E-08	-0,99
221135_s_at	ASTE1	4,95E-14	-0,99
234980_at	TMEM56	2,93E-08	-0,99
202262_x_at	DDAH2	8,9E-09	-0,95
215537_x_at	DDAH2	3,27E-09	-0,92
209368_at	EPHX2	4,13E-08	-0,86
49306_at	RASSF4	7,44E-10	-0,86
212195_at	IL6ST	1,24E-14	-0,83
212609_s_at	AKT3	1,57E-09	-0,82
221561_at	SOAT1	9,94E-07	-0,81
212750_at	PPP1R16B	3,28E-07	-0,81
212254_s_at	DST	8,3E-10	-0,81
223213_s_at	ZHX1	1,03E-06	-0,80
205856_at	SLC14A1	1,14E-07	-0,79
201130_s_at	CDH1	0,002186	-0,79
207106_s_at	LTK	3,24E-06	-0,79
223214_s_at	ZHX1	1,02E-10	-0,77

202449_s_at	RXRA	8,27E-19	-0,76
212253_x_at	DST	1,22E-09	-0,76
204864_s_at	IL6ST	0,001921	-0,75
214909_s_at	DDAH2	3,31E-08	-0,74
212914_at	CBX7	9,53E-10	-0,73
215016_x_at	DST	1,88E-09	-0,72
224728_at	ATPAF1	1,11E-07	-0,72
205008_s_at	CIB2	1,76E-06	-0,71
220565_at	CCR10	1,57E-06	-0,71
205883_at	ZBTB16	3,34E-05	-0,70
223028_s_at	SNX9	1,94E-10	-0,70
1554938_a_at	ACOT11	6,6E-05	-0,69
222101_s_at	DCHS1	1,94E-05	-0,69
224901_at	SCD5	0,00529	-0,68
223027_at	SNX9	2,7E-14	-0,68
212157_at	SDC2	2,14E-08	-0,66
214168_s_at	TJP1	0,000605	-0,65
202196_s_at	DKK3	9,82E-05	-0,65
228361_at	E2F2	8,17E-06	-0,65
228479_at	SOAT1	1,6E-05	-0,65
212154_at	SDC2	9,19E-05	-0,64
213341_at	FEM1C	4,03E-08	-0,61
213684_s_at	PDLIM5	0,000434	-0,61
218208_at	PQLC1	7,05E-10	-0,61
231478_at	LOC729966 /// PDE4C	0,00266	-0,55
238441_at	PRKAA2	0,00199	-0,55
217746_s_at	PDCD6IP	1,86E-12	-0,53
221817_at	DOLPP1	2,37E-14	-0,52

214763_at	ACOT11	2,94E-05	-0,52
202426_s_at	RXRA	4,78E-06	-0,51
239297_at	KIAA1456 /// LOC101927137	1,93E-07	-0,51
214247_s_at	DKK3	0,000152	-0,50
212476_at	ACAP2	2,4E-10	-0,49
202472_at	MPI	4,88E-05	-0,49
201924_at	AFF1	4,77E-11	-0,48
203243_s_at	PDLIM5	0,000275	-0,44
225738_at	RAPGEF1	2,46E-06	-0,44
223152_at	PPP1R12C	6,61E-16	-0,43
1554834_a_at	RASSF5	0,011719	-0,43
203242_s_at	PDLIM5	0,018081	-0,43
239155_at	CXADR	0,005489	-0,42
210324_at	C8G	0,027161	-0,41
212412_at	PDLIM5	1,36E-09	-0,41
216804_s_at	PDLIM5	0,012884	-0,40
205007_s_at	CIB2	0,000592	-0,39
225121_at	TBC1D23	5,06E-06	-0,36
227018_at	DPP8	0,000553	-0,35
244661_at	SOAT1	0,001701	-0,35
202011_at	TJP1	3,37E-06	-0,35
201105_at	LGALS1	0,010586	-0,33
201950_x_at	CAPZB	3,67E-08	-0,33
215073_s_at	NR2F2	0,007664	-0,33
202035_s_at	SFRP1	0,015903	-0,32
208653_s_at	CD164	0,046746	-0,31
221846_s_at	CASKIN2	1,46E-05	-0,31
226389_s_at	RAPGEF1	4,72E-10	-0,31

219922_s_at	LTBP3	0,010733	-0,31
201354_s_at	BAZ2A	3,3E-06	-0,31
228713_s_at	HSD17B14	3,6E-06	-0,30
227113_at	ADHFE1	8,52E-06	-0,30
208654_s_at	CD164	0,001089	-0,30
201003_x_at	TMEM189 /// TMEM189-UBE2V1 /// UBE2V1 /// UBE2V2	0,000227	-0,30
222880_at	AKT3	0,005987	-0,29
37012_at	CAPZB	6,25E-10	-0,29
208774_at	CSNK1D	1,94E-07	-0,29
212329_at	SCAP	1,96E-05	-0,28
220939_s_at	DPP8	0,046034	-0,28
202076_at	BIRC2	1,53E-05	-0,27
201131_s_at	CDH1	1,43E-06	-0,27
221578_at	RASSF4	6,78E-05	-0,25
209121_x_at	NR2F2	0,015992	-0,25
201949_x_at	CAPZB	9,81E-07	-0,25
229055_at	GPR68	0,015373	-0,24
201353_s_at	BAZ2A	0,006976	-0,24
235396_at	TANGO2	5,57E-09	-0,23
222394_at	PDCD6IP	0,007145	-0,23
209833_at	CRADD	0,024142	-0,23
226343_at	DPP8	0,000375	-0,23
208405_s_at	CD164	0,000991	-0,21
209120_at	NR2F2	0,012342	-0,21
220495_s_at	TXNDC15	0,024481	-0,20
237144_at	LTBP3	0,010726	-0,20
227873_at	TXNDC15	0,001477	-0,18

208923_at	CYFIP1	0,000225	-0,18
210616_s_at	SEC31A	0,001196	-0,16
225528_at	IPO8	0,000927	-0,16
1555321_at	ACOT11	0,034731	-0,16
224643_at	PRRC1	0,021319	-0,15
225773_at	RSPRY1	0,008991	-0,15
229151_at	SLC14A1	0,001697	-0,14
233164_x_at	RHBDD1	0,022292	-0,14
204543_at	RAPGEF1	0,006714	-0,14
238489_at	PRKAA2	0,011282	-0,14
200945_s_at	SEC31A	0,019612	-0,11
227427_at	ARHGEF25	0,000458	-0,11
224497_x_at	HSD17B14	0,011699	-0,10
232330_at	COA1	0,002844	-0,09
224494_x_at	HSD17B14	0,000705	-0,08
1560078_at	LAMA3	0,031183	-0,07
215506_s_at	DIRAS3	0,006075	-0,07
206986_at	FGF18	0,046658	-0,07
211380_s_at	PRKG1	0,014392	-0,06
219113_x_at	HSD17B14	0,008552	-0,06
222864_s_at	ZNF219	0,047424	-0,06
228848_at	ABTB1	0,042426	0,02
1570529_at	PUM3	0,020839	0,04
232738_at	CCSER1	0,038827	0,05
215041_s_at	DOCK9	0,029816	0,06
234840_s_at	OR5V1	0,048134	0,06
228296_at	YPEL1	0,019654	0,08
221278_at	HOXB8	0,040774	0,08
230542_at	ZNF597	0,003522	0,09

229864_at	ELP6	0,00942	0,09
240633_at	DOK7 /// LOC102724043	0,021039	0,10
231656_x_at	OSBPL10	0,001348	0,10
235212_at	NRDE2	0,014767	0,11
239848_at	EIF3M	0,043418	0,12
230234_at	FXN	0,016732	0,12
214237_x_at	PAWR	0,007508	0,13
237553_at	LZTFL1	0,048517	0,17
225534_at	SMIM19	0,013549	0,18
203484_at	SEC61G	0,002821	0,20
226374_at	CXADR	0,017104	0,20
207267_s_at	RIPPLY3	0,008669	0,20
235181_at	TYW5	0,000274	0,20
233350_s_at	TEX264	0,028744	0,21
223136_at	AIG1	0,037308	0,21
202997_s_at	LOXL2	0,013149	0,22
230697_at	BBS5	0,000276	0,23
201757_at	NDUFS5 /// RPL10	4,98E-05	0,23
211712_s_at	ANXA9	0,004932	0,23
226945_at	RHBDD1	0,000273	0,23
221701_s_at	STRA6	0,007491	0,23
212538_at	DOCK9	0,003569	0,23
209049_s_at	ZMYND8	0,023305	0,24
226442_at	ABTB1	0,000691	0,24
228436_at	KCNC4	0,000159	0,24
236745_at	CCDC78	0,000158	0,24
200000_s_at	PRPF8	0,000145	0,24
212625_at	STX10	0,000373	0,24

223534_s_at	RPS6KL1	0,001232	0,24
227037_at	FLCN /// PLD6	0,002353	0,25
211152_s_at	HTRA2	1,41E-05	0,25
229863_s_at	ELP6	3,1E-05	0,25
218548_x_at	TEX264	0,000487	0,26
243816_at	LL22NC03-N27C7.1 /// ZNF70	0,014433	0,26
209137_s_at	USP10	0,000165	0,26
223277_at	ELP6	2,81E-07	0,27
207130_at	ZMYND8	0,028982	0,27
201821_s_at	TIMM17A	0,003108	0,27
221549_at	GRWD1	6,87E-06	0,27
204485_s_at	TOM1L1	0,008905	0,27
220099_s_at	C7orf55-LUC7L2 /// LUC7L2	5,86E-06	0,28
239054_at	SFMBT1	0,006112	0,28
225103_at	MRPL38	0,000669	0,28
200963_x_at	RPL31	6,61E-14	0,28
232810_at	AIG1	0,000306	0,28
225427_s_at	APOA1BP	4,38E-06	0,29
211721_s_at	ZNF551	0,019254	0,29
215171_s_at	TIMM17A	4,26E-05	0,29
203089_s_at	HTRA2	4,34E-06	0,29
32094_at	CHST3	0,000211	0,31
209831_x_at	DNASE2	2,36E-05	0,31
224720_at	MIB1	0,000464	0,31
224722_at	MIB1	0,000846	0,32
201002_s_at	TMEM189 /// TMEM189-UBE2V1 /// UBE2V1 /// UBE2V2	6,59E-09	0,33
204004_at	PAWR	6,13E-05	0,33
236117_at	ZNF597	1,6E-05	0,34
235467_s_at	KCNC4	4,71E-05	0,34

1553611_s_at	KLHL35	0,001369	0,35
225856_at	CLOCK	2,38E-05	0,35
204980_at	CLOCK	0,001081	0,35
205429_s_at	MPP6	0,038031	0,36
226223_at	PAWR	3,37E-05	0,36
207639_at	FZD9	0,000515	0,36
203973_s_at	CEBPD	0,000877	0,36
209086_x_at	MCAM /// MIR6756	0,001436	0,37
223186_at	TMEM189 /// TMEM189-UBE2V1 /// UBE2V1	1,47E-05	0,37
219229_at	SLCO3A1	0,030093	0,39
205640_at	ALDH3B1	0,003681	0,39
228788_at	YPEL1	0,010056	0,39
202058_s_at	KPNA1	0,012266	0,40
213370_s_at	SFMBT1	0,000105	0,41
225730_s_at	THUMPD3	5,95E-05	0,41
213996_at	YPEL1	5,11E-05	0,41
225628_s_at	MLLT6	0,000306	0,41
225484_at	CEP41	0,006611	0,41
238912_x_at	C9orf85	2,64E-05	0,42
204365_s_at	REEP1	0,011283	0,42
217842_at	C7orf55-LUC7L2 /// LUC7L2	2,25E-07	0,42
219073_s_at	OSBPL10	1,15E-06	0,42
225741_at	THUMPD3	2,07E-08	0,42
224725_at	MIB1	0,000374	0,43
201001_s_at	TMEM189 /// TMEM189-UBE2V1 /// UBE2V1 /// UBE2V2	2,42E-07	0,43
204775_at	CHAF1B	6,56E-06	0,43
204005_s_at	PAWR	6,42E-05	0,43
210085_s_at	ANXA9	4,7E-05	0,43

229164_s_at	ABTB1	0,006854	0,44
203031_s_at	UROS	5,65E-06	0,45
231767_at	HOXB4	0,000106	0,45
230723_at	SPATA18	4,41E-05	0,45
231857_s_at	AGBL5	1,1E-07	0,46
204827_s_at	CCNF	0,000156	0,47
224784_at	MLLT6	1,08E-06	0,47
203026_at	ZBTB5	5,51E-09	0,47
236565_s_at	LARP6	0,000344	0,48
226231_at	PAWR	1,58E-07	0,48
202505_at	SNRPB2	7,39E-11	0,48
225172_at	CRAMP1L	9,27E-09	0,48
1568781_at	UROS	1,58E-06	0,49
201767_s_at	ELAC2	8,58E-12	0,49
241017_at	RPL31 /// TBC1D8	0,00375	0,50
227531_at	CLOCK	8,55E-09	0,50
218480_at	AGBL5	1,73E-07	0,50
1555970_at	FBXO28	2,26E-05	0,50
206497_at	COA1	3,17E-07	0,51
223663_at	CCDC88B	0,000215	0,52
218437_s_at	LZTFL1	1,91E-06	0,53
201576_s_at	GLB1 /// TMPPE	9,22E-09	0,54
209834_at	CHST3	1,65E-05	0,55
202268_s_at	NAE1	1,24E-15	0,55
224759_s_at	TMEM263	1,11E-06	0,56
214992_s_at	DNASE2	4,5E-05	0,56
211042_x_at	MCAM /// MIR6756	9,74E-09	0,57
226434_at	PPP1R35	1,43E-11	0,58
223197_s_at	SMARCAD1	3,93E-13	0,60
236957_at	CDCA2	3,01E-06	0,60
225733_at	B3GALT6	1,63E-07	0,60
202231_at	EIF3M	4,04E-23	0,61
231382_at	FGF18	3,48E-07	0,62
227598_at	ZBED6CL	3,79E-07	0,62

203836_s_at	MAP3K5	2,39E-05	0,63
200956_s_at	SSRP1	1,6E-12	0,63
203837_at	MAP3K5	4,91E-07	0,65
200957_s_at	SSRP1	3,83E-14	0,67
202998_s_at	LOXL2	0,001197	0,69
202232_s_at	EIF3M	6,44E-21	0,70
223804_s_at	THUMP3	2,38E-13	0,71
200962_at	RPL31	0,01351	0,72
220750_s_at	LEPRE1	2,05E-08	0,74
210869_s_at	MCAM /// MIR6756	9,37E-05	0,75
218786_at	NT5DC3	6,83E-09	0,76
207417_s_at	ZNF177 /// ZNF559- ZNF177	0,000439	0,78
211340_s_at	MCAM /// MIR6756	2,58E-05	0,78
225485_at	CEP41	7,08E-07	0,79
212789_at	NCAPD3	8,54E-10	0,80
1555270_a_at	WFS1	1,3E-08	0,81
209487_at	RBPMS	1,94E-06	0,84
209445_x_at	COA1	2,97E-12	0,85
200681_at	GLO1	3,8E-22	0,86
217884_at	NAT10	2,72E-15	0,87
235545_at	DEPDC1	7,9E-09	0,89
220295_x_at	DEPDC1	1,3E-05	0,90
210006_at	ABHD14A /// ACY1	8,81E-17	0,96
203712_at	KIAA0020	2,4E-17	0,96
209087_x_at	MCAM	3,61E-06	0,98
226313_at	C10orf35	7,44E-14	0,99
205565_s_at	FXN	3,52E-14	1,01
222632_s_at	LZTFL1	1,83E-11	1,05
209172_s_at	CENPF	2,18E-11	1,05
209488_s_at	RBPMS	5,67E-08	1,06
229845_at	MAPKAP1	6,24E-12	1,08
222958_s_at	DEPDC1	4,78E-07	1,08
207828_s_at	CENPF	2,95E-08	1,11

204127_at	RFC3	6,66E-10	1,12
214427_at	NOP2	1,85E-19	1,12
1554685_a_at	CEMIP	1,71E-11	1,12
1553959_a_at	B3GALT6	8,24E-23	1,13
202240_at	PLK1	2,1E-10	1,17
204128_s_at	RFC3	8,21E-07	1,22
204826_at	CCNF	8,25E-13	1,27
202908_at	WFS1	1,07E-12	1,28
223454_at	CXCL16	2,25E-17	1,34
205780_at	BIK	5,83E-21	1,35
232278_s_at	DEPDC1	1,77E-07	1,37
229667_s_at	HOXB8	3,41E-06	1,42
226661_at	CDCA2	3,77E-10	1,48
207836_s_at	RBPMS	3,61E-11	1,48
229331_at	SPATA18	1,2E-10	1,50
212942_s_at	CEMIP	2,41E-43	6,88

Supplementary Table 2C. Significantly differentially expressed genes belonging to 353 epigenetic clock CpG sites in CRC vs. adenoma comparison

Affymetrix probe Set ID	Gene Symbol	P value	logFC(CRC-AD)
229331_at	SPATA18	0,00000000	-1,73
209368_at	EPHX2	0,00000018	-1,59
207249_s_at	SLC28A2	0,02680453	-1,24
212942_s_at	CEMIP	0,00987622	-1,17
241017_at	RPL31 /// TBC1D8	0,00000220	-1,11
210006_at	ABHD14A /// ACY1	0,00000000	-1,04
210086_at	HR	0,00000957	-0,90
230076_at	PITPNM3	0,00060260	-0,90
241355_at	HR	0,00000094	-0,80
200962_at	RPL31	0,01241559	-0,77
206631_at	PTGER2	0,00099733	-0,77
237515_at	TMEM56	0,00269464	-0,76
234980_at	TMEM56	0,00975307	-0,73
228788_at	YPEL1	0,00003211	-0,72
1554938_a_at	ACOT11	0,00057371	-0,72
214763_at	ACOT11	0,00002633	-0,71
205780_at	BIK	0,00006894	-0,67
207417_s_at	ZNF177 /// ZNF559- ZNF177	0,01968742	-0,63
221593_s_at	RPL31	0,00000030	-0,57
226231_at	PAWR	0,00000589	-0,53
204485_s_at	TOM1L1	0,00015653	-0,52
239054_at	SFMBT1	0,00002631	-0,50
223663_at	CCDC88B	0,00080960	-0,49
204004_at	PAWR	0,00001855	-0,49
233609_at	PTPRK	0,00600135	-0,48
225534_at	SMIM19	0,00000403	-0,47
225856_at	CLOCK	0,00002663	-0,46
218480_at	AGBL5	0,00055195	-0,43

203513_at	SPG11	0,00019905	-0,42
240261_at	TOM1L1	0,00074699	-0,41
216103_at	ACOT11	0,00041290	-0,41
224729_s_at	ATPAF1	0,00000700	-0,41
230723_at	SPATA18	0,00073510	-0,41
201767_s_at	ELAC2	0,00000365	-0,40
213996_at	YPEL1	0,00042181	-0,39
226780_s_at	C7orf55	0,00119510	-0,39
222632_s_at	LZTFL1	0,03462533	-0,39
204980_at	CLOCK	0,00217094	-0,39
226781_at	C7orf55 /// C7orf55- LUC7L2 /// LUC7L2	0,02796880	-0,38
233350_s_at	TEX264	0,00144625	-0,38
238912_x_at	C9orf85	0,00118203	-0,37
226374_at	CXADR	0,00050523	-0,37
224784_at	MLLT6	0,00391978	-0,36
227531_at	CLOCK	0,00011864	-0,35
204005_s_at	PAWR	0,00991909	-0,34
205565_s_at	FXN	0,03327455	-0,34
203031_s_at	UROS	0,00228134	-0,32
226493_at	KCTD18	0,00586814	-0,32
224728_at	ATPAF1	0,04831986	-0,32
203917_at	CXADR	0,00649237	-0,31
218786_at	NT5DC3	0,03354445	-0,31
219314_s_at	ZNF219	0,00065648	-0,30
203038_at	PTPRK	0,00718893	-0,30
205231_s_at	EPM2A	0,00921835	-0,28
220163_s_at	HR	0,00022665	-0,28
226223_at	PAWR	0,01472271	-0,27
207639_at	FZD9	0,01875310	-0,27
231857_s_at	AGBL5	0,01684367	-0,27
237144_at	LTBP3	0,01068685	-0,26
225741_at	THUMPD3	0,00761268	-0,26

210719_s_at	HMG20B	0,00961468	-0,25
225427_s_at	APOA1BP	0,00030187	-0,25
218548_x_at	TEX264	0,00854558	-0,25
1555321_at	ACOT11	0,00254871	-0,25
208405_s_at	CD164	0,00700190	-0,24
235467_s_at	KCNC4	0,01461849	-0,24
200000_s_at	PRPF8	0,00272253	-0,24
223197_s_at	SMARCAD1	0,03705872	-0,23
201924_at	AFF1	0,01930781	-0,22
223277_at	ELP6	0,00074950	-0,21
202231_at	EIF3M	0,01056103	-0,19
223534_s_at	RPS6KL1	0,03624664	-0,19
202232_s_at	EIF3M	0,03246520	-0,19
209831_x_at	DNASE2	0,02938049	-0,19
227775_at	CELF6	0,02306007	-0,18
208923_at	CYFIP1	0,00261950	-0,17
200963_x_at	RPL31	0,00046595	-0,16
224619_at	CASC4	0,02388460	-0,16
230234_at	FXN	0,03293569	-0,11
217573_at	GRIN2C	0,03988940	-0,11
234737_at	NT5DC3	0,02802923	-0,11
228296_at	YPEL1	0,00037649	-0,11
214237_x_at	PAWR	0,03091386	-0,11
220600_at	ELP6	0,00065848	-0,08
224019_at	SCD5	0,01886755	-0,06
230470_at	DSCR9	0,02219213	-0,05
217017_at	OSBPL10	0,02406981	-0,02
224494_x_at	HSD17B14	0,02693087	0,06
224229_s_at	AKT3	0,02689116	0,07
242879_x_at	AKT3	0,03362670	0,09
219393_s_at	AKT3	0,01981404	0,09
214795_at	ZMYND8	0,03250876	0,12
235396_at	TANGO2	0,01401144	0,12

201950_x_at	CAPZB	0,04885291	0,13
227308_x_at	LTBP3	0,03929881	0,14
211626_x_at	ERG	0,04099045	0,14
202734_at	TRIP10	0,03395151	0,16
225774_at	RSPRY1	0,03327248	0,18
1558522_at	MPP6	0,04112270	0,19
229151_at	SLC14A1	0,02726131	0,19
201822_at	TIMM17A	0,04697002	0,21
229743_at	ZNF438	0,04938355	0,21
215238_s_at	DOCK9	0,01489947	0,21
222273_at	PAPOLG	0,01815039	0,23
201889_at	FAM3C	0,01580273	0,24
201001_s_at	TMEM189 /// TMEM189-UBE2V1 /// UBE2V1 /// UBE2V2	0,03673379	0,26
210542_s_at	SLCO3A1	0,01304146	0,26
226389_s_at	RAPGEF1	0,00001591	0,26
212689_s_at	KDM3A	0,03179650	0,27
203973_s_at	CEBPD	0,02272402	0,28
1552632_a_at	ARSG	0,00109988	0,28
202059_s_at	KPNA1	0,00113622	0,29
219054_at	NPR3	0,02237474	0,30
228537_at	GLI2	0,01244155	0,30
218892_at	DCHS1	0,00065405	0,30
223186_at	TMEM189 /// TMEM189-UBE2V1 /// UBE2V1	0,00829019	0,31
208075_s_at	CCL7	0,00491072	0,31
202055_at	KPNA1	0,00072164	0,31
223027_at	SNX9	0,00051373	0,31
207945_s_at	CSNK1D	0,00011834	0,31
223028_s_at	SNX9	0,00646399	0,32
212750_at	PPP1R16B	0,04367836	0,33

207034_s_at	GLI2	0,01021708	0,33
223214_s_at	ZHX1	0,00226080	0,34
212538_at	DOCK9	0,00046299	0,35
230508_at	DKK3	0,00101549	0,36
49306_at	RASSF4	0,00572509	0,36
202056_at	KPNA1	0,00520188	0,36
205697_at	SCGN	0,00269112	0,37
213039_at	ARHGEF18	0,00333436	0,37
203484_at	SEC61G	0,00001363	0,37
226127_at	ALKBH3	0,02809024	0,38
225738_at	RAPGEF1	0,00012794	0,38
227037_at	FLCN /// PLD6	0,01617367	0,38
209121_x_at	NR2F2	0,00152385	0,39
215073_s_at	NR2F2	0,00664390	0,39
213741_s_at	KPNA1	0,00189014	0,40
1552472_a_at	ACAP2	0,03411321	0,41
209506_s_at	NR2F1 /// NR2F2	0,00071571	0,41
216061_x_at	PDGFB	0,00002524	0,41
205330_at	MN1	0,03635339	0,42
202058_s_at	KPNA1	0,01227720	0,43
228231_at	MIR6836 /// SNX8	0,00152640	0,43
201939_at	PLK2	0,02096703	0,44
211712_s_at	ANXA9	0,01348527	0,44
219922_s_at	LTBP3	0,00343928	0,46
214168_s_at	TJP1	0,00805629	0,46
209120_at	NR2F2	0,00001601	0,46
238441_at	PRKAA2	0,02230572	0,48
221561_at	SOAT1	0,02100709	0,49
227367_at	SLCO3A1	0,00555563	0,50
204827_s_at	CCNF	0,00913533	0,51
202240_at	PLK1	0,03112763	0,52
52651_at	COL8A2	0,00026838	0,53
226436_at	RASSF4	0,01228859	0,53
221900_at	COL8A2	0,00194188	0,54

204864_s_at	IL6ST	0,03891874	0,55
213006_at	CEBPD	0,01168844	0,55
214023_x_at	TUBB2B	0,02370704	0,56
213499_at	CLCN2	0,00047182	0,56
209447_at	SYNE1	0,00029088	0,56
204127_at	RFC3	0,02596003	0,56
212195_at	IL6ST	0,00000120	0,57
212196_at	IL6ST	0,00086144	0,58
229776_at	SLCO3A1	0,00180482	0,58
219229_at	SLCO3A1	0,01173681	0,61
211000_s_at	IL6ST	0,00365517	0,62
228843_at	ARL10	0,00111322	0,62
217497_at	TYMP	0,00081715	0,63
210839_s_at	ENPP2	0,04659594	0,63
41577_at	PPP1R16B	0,00356142	0,65
205200_at	CLEC3B /// EXOSC7	0,00668330	0,66
223241_at	MIR6836 /// SNX8	0,00004691	0,66
227892_at	PRKAA2	0,01995393	0,68
204128_s_at	RFC3	0,04050629	0,70
241926_s_at	ERG	0,00000575	0,71
221127_s_at	DKK3	0,00000065	0,73
204858_s_at	TYMP	0,00016253	0,74
218651_s_at	LARP6	0,00008264	0,74
204863_s_at	IL6ST	0,00096190	0,76
206049_at	SELP	0,00055748	0,80
228396_at	PRKG1	0,00000018	0,80
1554834_a_at	RASSF5	0,00091376	0,83
219773_at	NOX4	0,00014842	0,85
204200_s_at	PDGFB	0,00000165	0,90
222880_at	AKT3	0,00001708	0,90
205429_s_at	MPP6	0,00032226	0,93
227006_at	PPP1R14A	0,00000727	0,94
220750_s_at	LEPRE1	0,00000018	0,96
213541_s_at	ERG	0,00000031	1,02

209086_x_at	MCAM /// MIR6756	0,00000051	1,03
224901_at	SCD5	0,00091342	1,03
229055_at	GPR68	0,00000023	1,05
202391_at	BASP1	0,00022894	1,06
223322_at	RASSF5	0,00000376	1,08
222101_s_at	DCHS1	0,00000029	1,12
227458_at	CD274	0,00042033	1,13
219371_s_at	KLF2	0,00000015	1,14
212157_at	SDC2	0,00000006	1,20
223501_at	TNFSF13B	0,00000015	1,23
202997_s_at	LOXL2	0,00000036	1,24
201105_at	LGALS1	0,00000000	1,24
214247_s_at	DKK3	0,00000039	1,30
204688_at	SGCE	0,00000010	1,33
236565_s_at	LARP6	0,00000847	1,39
212609_s_at	AKT3	0,00000000	1,44
212154_at	SDC2	0,00000002	1,47
223502_s_at	TNFSF13B	0,00000013	1,48
202196_s_at	DKK3	0,00000000	1,51
211340_s_at	MCAM /// MIR6756	0,00000002	1,53
212158_at	SDC2	0,00000000	1,66
209087_x_at	MCAM	0,00000000	1,73
212607_at	AKT3	0,00000000	1,76
210869_s_at	MCAM /// MIR6756	0,00000000	1,83
202998_s_at	LOXL2	0,00000002	1,84
202291_s_at	MGP	0,00000000	2,02

Supplementary Table 2D. Significantly differentially expressed genes belonging to 353 epigenetic clock CpG sites between healthy young and adult samples

Affymetrix probe Set ID	Gene Symbol	P value	logFC (Ch-N)
207505_at	PRKG2	0,021507421	-1,51
237515_at	TMEM56	0,000367571	-1,28
222394_at	PDCD6IP	1,29576E-07	-0,98
213501_at	ACOX1	0,004883092	-0,97
231478_at	LOC729966 /// PDE4C	0,026463942	-0,96
1555716_a_at	CXADR	0,031328727	-0,95
208654_s_at	CD164	5,05917E-06	-0,90
209600_s_at	ACOX1	0,001268357	-0,85
215073_s_at	NR2F2	0,000150953	-0,84
224427_s_at	PAPOLG	0,002740297	-0,82
229667_s_at	HOXB8	0,037343212	-0,80
208405_s_at	CD164	4,85713E-09	-0,79
224725_at	MIB1	0,002421378	-0,79
221561_at	SOAT1	0,001038602	-0,76
226493_at	KCTD18	0,000330525	-0,75
227962_at	ACOX1	0,002364699	-0,73
226374_at	CXADR	7,17412E-06	-0,73
208653_s_at	CD164	0,017788605	-0,72
243135_x_at	SNX8	0,00249727	-0,67
224619_at	CASC4	7,71295E-07	-0,65
212253_x_at	DST	0,006690985	-0,64
202449_s_at	RXRA	3,02965E-06	-0,63
203917_at	CXADR	0,000125174	-0,61
201889_at	FAM3C	0,03739743	-0,61
207306_at	TCF15	0,010311031	-0,60
212689_s_at	KDM3A	0,007774641	-0,59
209368_at	EPHX2	0,010054497	-0,57
212476_at	ACAP2	3,8023E-05	-0,55

241017_at	RPL31 /// TBC1D8	0,024480146	-0,55
216918_s_at	DST	0,003474524	-0,54
1552391_at	CCDC185	0,001799746	-0,53
234980_at	TMEM56	0,045347444	-0,53
229274_at	GNAS	0,039127122	-0,51
223027_at	SNX9	0,001772281	-0,46
225774_at	RSPRY1	0,004568312	-0,45
224726_at	MIB1	0,020223832	-0,44
224728_at	ATPAF1	0,020798161	-0,44
227018_at	DPP8	0,032487883	-0,44
213341_at	FEM1C	0,033510639	-0,42
209833_at	CRADD	0,040327271	-0,41
223214_s_at	ZHX1	0,01112241	-0,41
221593_s_at	RPL31	0,035676532	-0,39
230533_at	ZMYND8	0,0063591	-0,37
225644_at	CCDC117	0,012629814	-0,34
226231_at	PAWR	0,010459673	-0,34
201131_s_at	CDH1	0,000762847	-0,31
209120_at	NR2F2	0,013357831	-0,29
210616_s_at	SEC31A	0,005020509	-0,28
224643_at	PRRC1	0,034263769	-0,27
231857_s_at	AGBL5	0,041787477	-0,27
224729_s_at	ATPAF1	0,020276769	-0,26
229743_at	ZNF438	0,00371976	-0,25
201924_at	AFF1	0,024243458	-0,23
202231_at	EIF3M	0,041616567	-0,16
207639_at	FZD9	0,001064008	0,00
239037_at	GNAS	0,003343109	0,00
237818_at	LARP6	0,003343109	0,00
215710_at	ST3GAL4	0,003343109	0,00
232727_at	UCKL1	0,003343109	0,00
1557223_at	RBPMS	0,012003366	0,00
1552487_a_at	BNC1	0,003343109	0,00
216966_at	ITGA2B	0,003343109	0,00

220621_at	FOXE3	0,000559693	0,00
1553191_at	DST	0,005873221	0,01
220231_at	PPP1R17	0,017466885	0,01
240633_at	DOK7 /// LOC102724043	2,95804E-06	0,01
207331_at	CENPF	0,009141984	0,01
206880_at	P2RX6	0,004309899	0,02
210870_s_at	EPM2A	0,035551957	0,02
215437_x_at	BAZ2A	0,003343109	0,02
1552276_a_at	VPS18	0,035471834	0,02
215097_at	CAPZB	0,005615691	0,04
216670_at	KLK13	0,006529575	0,04
240349_at	PRKAA2	0,011132509	0,06
216803_at	PDLIM5	0,029302171	0,06
231656_x_at	OSBPL10	0,002587602	0,08
211626_x_at	ERG	0,005228406	0,09
226646_at	KLF2	0,008370157	0,16
205720_at	POMC	8,83429E-05	0,17
216755_at	OSBPL10	0,0261775	0,18
226313_at	C10orf35	0,002234619	0,18
227427_at	ARHGEF25	0,024669295	0,19
1552272_a_at	PRR22	0,001702096	0,22
202268_s_at	NAE1	0,04353301	0,23
226389_s_at	RAPGEF1	0,026224636	0,23
201950_x_at	CAPZB	0,001042874	0,24
200780_x_at	GNAS	0,000315993	0,24
212273_x_at	GNAS	0,000335101	0,25
209086_x_at	MCAM /// MIR6756	0,00875904	0,25
227308_x_at	LTBP3	0,002923559	0,25
222864_s_at	ZNF219	0,016378613	0,25
214548_x_at	GNAS	0,000173571	0,26
200981_x_at	GNAS	8,41414E-05	0,26
223834_at	CD274	0,018210986	0,26
226945_at	RHBDD1	0,020724049	0,27

202505_at	SNRPB2	0,00363876	0,27
200681_at	GLO1	0,006086631	0,29
229864_at	ELP6	0,000726359	0,29
211858_x_at	GNAS	5,67999E-06	0,33
201949_x_at	CAPZB	1,74464E-05	0,34
202734_at	TRIP10	0,010944745	0,34
229863_s_at	ELP6	8,56048E-05	0,37
223277_at	ELP6	4,24479E-06	0,39
212329_at	SCAP	0,000246878	0,39
226223_at	PAWR	0,009156798	0,39
225427_s_at	APOA1BP	0,000927364	0,42
204775_at	CHAF1B	1,49233E-05	0,42
217842_at	C7orf55-LUC7L2 /// LUC7L2	0,001926212	0,42
211042_x_at	MCAM /// MIR6756	0,000275682	0,43
214237_x_at	PAWR	1,12686E-10	0,43
202472_at	MPI	0,046741879	0,44
205418_at	FES	0,000186734	0,45
223656_s_at	TMEM234	0,000236942	0,45
229776_at	SLCO3A1	0,022677357	0,45
212609_s_at	AKT3	0,029732963	0,47
221549_at	GRWD1	3,62243E-05	0,47
228843_at	ARL10	0,01302352	0,49
218548_x_at	TEX264	0,005305902	0,49
226434_at	PPP1R35	0,000208771	0,49
61297_at	CASKIN2	0,005477814	0,50
209830_s_at	SLC9A3R2	0,032387985	0,50
200000_s_at	PRPF8	1,77166E-06	0,50
226781_at	C7orf55 /// C7orf55- LUC7L2 /// LUC7L2	0,031113047	0,52
204827_s_at	CCNF	1,37961E-05	0,52
203484_at	SEC61G	7,50862E-07	0,53
207945_s_at	CSNK1D	0,000167009	0,53
235582_at	E2F2	2,34682E-05	0,54

205780_at	BIK	0,016567068	0,54
209445_x_at	COA1	0,012694605	0,54
218563_at	NDUFA3	0,000198058	0,54
201821_s_at	TIMM17A	0,00354123	0,54
217808_s_at	MAPKAP1	0,001350734	0,55
220864_s_at	NDUFA13	3,43156E-06	0,56
201757_at	NDUFS5 /// RPL10	5,71346E-06	0,56
203031_s_at	UROS	0,001742022	0,56
206486_at	LAG3	0,001212687	0,57
203026_at	ZBTB5	3,30792E-05	0,57
233350_s_at	TEX264	0,007799522	0,57
201767_s_at	ELAC2	6,28994E-07	0,57
207705_s_at	NINL	0,005295124	0,58
209113_s_at	HMG20B	9,33987E-05	0,59
220750_s_at	LEPRE1	0,009932977	0,60
213370_s_at	SFMBT1	0,003571916	0,60
232675_s_at	UCKL1	0,000806349	0,60
215171_s_at	TIMM17A	7,50681E-06	0,61
226127_at	ALKBH3	1,62484E-05	0,61
204826_at	CCNF	0,030501946	0,62
229845_at	MAPKAP1	0,019042689	0,62
223804_s_at	THUMP3	0,000277409	0,65
1555270_a_at	WFS1	0,000101846	0,65
223186_at	TMEM189 /// TMEM189-UBE2V1 /// UBE2V1	5,271E-05	0,67
1553959_a_at	B3GALT6	1,07747E-05	0,67
211340_s_at	MCAM /// MIR6756	0,029818696	0,68
213060_s_at	CHI3L2	0,003500308	0,68
228264_at	ACCS	0,011122223	0,68
235940_at	C9orf64	0,024641272	0,69
212789_at	NCAPD3	1,61169E-05	0,70
209087_x_at	MCAM	0,021136598	0,71
214427_at	NOP2	0,000195189	0,71

218533_s_at	UCKL1	1,85125E-06	0,71
202998_s_at	LOXL2	0,028253139	0,75
207836_s_at	RBPMS	0,008930263	0,76
205565_s_at	FXN	0,003710739	0,77
222958_s_at	DEPDC1	0,024977944	0,77
210006_at	ABHD14A /// ACY1	0,000241907	0,77
222997_s_at	MRPS21	6,82031E-05	0,77
210869_s_at	MCAM /// MIR6756	0,006029192	0,79
217884_at	NAT10	8,65958E-07	0,80
200957_s_at	SSRP1	1,34552E-09	0,81
225484_at	CEP41	0,003562203	0,81
209447_at	SYNE1	0,003174479	0,81
209488_s_at	RBPMS	0,008427906	0,82
203973_s_at	CEBPD	0,000123554	0,82
209372_x_at	TUBB2A /// TUBB2B	0,004129186	0,82
203712_at	PUM3	1,04987E-05	0,83
225485_at	CEP41	0,000269175	0,85
219229_at	SLCO3A1	7,3538E-05	0,85
207042_at	E2F2	1,18689E-12	0,87
207828_s_at	CENPF	0,009958979	0,88
214157_at	GNAS	4,75425E-06	0,88
223676_at	TMEM234	2,77144E-11	0,89
227006_at	PPP1R14A	0,004876603	0,90
225103_at	MRPL38	1,28814E-08	0,93
204858_s_at	TYMP	0,000507523	0,93
204127_at	RFC3	0,000109753	0,94
1552719_at	CASC4	3,91529E-06	0,95
222101_s_at	DCHS1	7,40083E-05	0,96
202035_s_at	SFRP1	0,014278422	0,99
205200_at	CLEC3B /// EXOSC7	0,001702251	0,99
223502_s_at	TNFSF13B	0,020571051	1,01
200956_s_at	SSRP1	8,0517E-11	1,02
202908_at	WFS1	1,35473E-05	1,03
204128_s_at	RFC3	0,009252042	1,05

218892_at	DCHS1	8,13905E-17	1,05
219922_s_at	LTBP3	1,51917E-06	1,16
226661_at	CDCA2	0,001709054	1,20
205049_s_at	CD79A	0,014053672	1,21
227188_at	EVA1C	0,001575848	1,23
203759_at	ST3GAL4	0,038781832	1,26
1555779_a_at	CD79A	0,003795007	1,27
204364_s_at	REEP1	0,006543383	1,30
213006_at	CEBPD	4,95513E-05	1,32
202291_s_at	MGP	0,000519223	1,46
228361_at	E2F2	2,24959E-07	1,56
202037_s_at	SFRP1	0,006927184	1,61
202240_at	PLK1	5,29737E-14	1,91
219371_s_at	KLF2	7,13287E-09	2,02
205883_at	ZBTB16	0,000683501	2,22

Supplementary Table 3. Demographic and clinical data of samples involved in in silico gene expression analysis

	Sample	Histology	Age	Sex	Dysplasia	TNM	Stage	Grade	Ref
Normal									
	N1024.CEL	normal	47	F					Galamb et al, Dis Markers, 2008
	N1081.CEL	normal	57	F					Galamb et al, Dis Markers, 2008
	N1114.CEL	normal	60	F					Galamb et al, Dis Markers, 2008
	N1122.CEL	normal	45	M					Galamb et al, Dis Markers, 2008
	N1357.CEL	normal	47	M					Galamb et al, Dis Markers, 2008
	N1431.CEL	normal	50	M					Galamb et al, Dis Markers, 2008
	N1440.CEL	normal	44	F					Galamb et al, Dis Markers, 2008
	N1456.CEL	normal	55	M					Galamb et al, Dis Markers, 2008
	N2323.CEL	normal	61	F					Galamb et al, CEBP, 2009
	N2350.CEL	normal	61	M					Galamb et al, CEBP, 2009
	N2378.CEL	normal	45	M					Galamb et al, CEBP, 2009
	N2622.CEL	normal	30	F					Galamb et al, Plos One, 2012
	N2642 .CEL	normal	57	M					Galamb et al, Plos One, 2012
	N2647.CEL	normal	36	M					Galamb et al, Plos One, 2012
	N2664.CEL	normal	49	F					Galamb et al, Plos One, 2012
	N2668.CEL	normal	65	F					Galamb et al, Plos One, 2012
	N2675.CEL	normal	46	F					Galamb et al, Plos One, 2012
	N2689.CEL	normal	54	M					Galamb et al, Plos One, 2012
	N2691.CEL	normal	77	F					Galamb et al, Plos One, 2012
	N2701.CEL	normal	27	M					Galamb et al, Plos One, 2012
	N2770.CEL	normal	82	F					Galamb et al, Plos One, 2012
	N2771.CEL	normal	62	F					Galamb et al, Plos One, 2012
	N2781.CEL	normal	74	M					Galamb et al, Plos One, 2012

	N2785.CEL	normal	71	M					Galamb et al, Plos One, 2012
	N3008.CEL	normal	54	F					Galamb et al, Plos One, 2012
	N3020.CEL	normal	62	F					Galamb et al, Plos One, 2012
	N3035.CEL	normal	22	M					Galamb et al, Plos One, 2012
	N3038.CEL	normal	73	F					Galamb et al, Plos One, 2012
	N3039.CEL	normal	75	F					Galamb et al, Plos One, 2012
	N3040.CEL	normal	41	M					Galamb et al, Plos One, 2012
	N3048.CEL	normal	43	F					Galamb et al, Plos One, 2012
	N3054.CEL	normal	41	M					Galamb et al, Plos One, 2012
	N3057.CEL	normal	30	M					Galamb et al, Plos One, 2012
	N3062.CEL	normal	66	M					Galamb et al, Plos One, 2012
	N3065.CEL	normal	62	F					Galamb et al, Plos One, 2012
	N3069.CEL	normal	61	F					Galamb et al, Plos One, 2012
	N3090.CEL	normal	40	F					Galamb et al, Plos One, 2012
	N3103.CEL	normal	41	M					Galamb et al, Plos One, 2012
	N3106.CEL	normal	47	F					Galamb et al, Plos One, 2012
	N3108.CEL	normal	67	M					Galamb et al, Plos One, 2012
	N3109.CEL	normal	40	F					Galamb et al, Plos One, 2012
	N3112.CEL	normal	44	F					Galamb et al, Plos One, 2012
	N3114.CEL	normal	31	F					Galamb et al, Plos One, 2012
	N3115.CEL	normal	82	F					Galamb et al, Plos One, 2012
	N3118.CEL	normal	33	F					Galamb et al, Plos One, 2012
	N3126.CEL	normal	64	F					Galamb et al, Plos One, 2012
	N3129.CEL	normal	64	F					Galamb et al, Plos One, 2012
	N3140.CEL	normal	45	F					Galamb et al, Plos One, 2012
	N3142.CEL	normal	51	F					Galamb et al, Plos One, 2012
Adenoma									
	AL1138.CEL	tubulovillous	70	M	low-grade				Galamb et al, Dis Markers, 2008
	AL1154.CEL	tubulovillous	73	F	low-grade				Galamb et al, Dis Markers, 2008

	AL1419.CEL	villous	37	F	low-grade			Galamb et al, Dis Markers, 2008
	AL1830.CEL	tubulovillous	70	M	low-grade			Galamb et al, Dis Markers, 2008
	AL2096.CEL	tubulovillous	82	F	low-grade			Galamb et al, CEBP, 2009
	AL2473.CEL	villous	44	F	low-grade			Galamb et al, CEBP, 2009
	AL2586.CEL	villous	84	M	low-grade			Galamb et al, CEBP, 2009
	AL2619.CEL	tubulovillous	51	F	low-grade			Galamb et al, Plos One, 2012
	AL2623.CEL	tubulovillous	61	F	low-grade			Galamb et al, Plos One, 2012
	AL2678.CEL	tubular	71	M	low-grade			Galamb et al, Plos One, 2012
	AL2796.CEL	villous	50	F	low-grade			Galamb et al, Plos One, 2012
	AL2863.CEL	tubulovillous	88	F	low-grade			Galamb et al, Plos One, 2012
	AL2937.CEL	tubular	57	M	low-grade			Galamb et al, Plos One, 2012
	AL2957.CEL	tubular	59	M	low-grade			Galamb et al, Plos One, 2012
	AL2964.CEL	tubular	77	M	low-grade			Galamb et al, Plos One, 2012
	AL2982.CEL	tubular	58	M	low-grade			Galamb et al, Plos One, 2012
	AL2989.CEL	tubular	73	F	low-grade			Galamb et al, Plos One, 2012
	AL3001.CEL	tubulovillous	75	F	low-grade			Galamb et al, Plos One, 2012
	AL3026.CEL	tubular	83	M	low-grade			Galamb et al, Plos One, 2012
	AL3045.CEL	tubulovillous	65	F	low-grade			Galamb et al, Plos One, 2012
	AL3049.CEL	tubular	54	M	low-grade			Galamb et al, Plos One, 2012
	AL3111.CEL	tubulovillous	70	M	low-grade			Galamb et al, Plos One, 2012
	AL3120.CEL	tubulovillous	66	M	low-grade			Galamb et al, Plos One, 2012
	AL980.CEL	tubulovillous	83	F	low-grade			Galamb et al, Dis Markers, 2008
	AL995.CEL	tubulovillous	58	M	low-grade			Galamb et al, Dis Markers, 2008
	AH1115.CEL	tubulovillous	75	F	high-grade			Galamb et al, Dis Markers, 2008
	AH1141.CEL	tubulovillous	63	M	high-grade			Galamb et al, Dis Markers, 2008
	AH1187.CEL	tubulovillous	80	F	high-grade			Galamb et al, Dis Markers, 2008
	AH1312.CEL	villous	93	M	high-grade			Galamb et al, Dis Markers, 2008
	AH1700.CEL	tubulovillous	69	F	high-grade			Galamb et al, Dis Markers, 2008
	AH1748.CEL	villous	78	F	high-grade			Galamb et al, Dis Markers, 2008

	AH1832.CEL	villous	56	M	high-grade				Galamb et al, Dis Markers, 2008
	AH2137.CEL	tubulovillous	82	F	high-grade				Galamb et al, CEBP, 2009
	AH2246.CEL	tubulovillous	73	M	high-grade				Galamb et al, CEBP, 2009
	AH2573.CEL	tubulovillous	59	F	high-grade				Galamb et al, Plos One, 2012
	AH2739.CEL	villous	62	M	high-grade				Galamb et al, Plos One, 2012
	AH2803.CEL	tubular	43	M	high-grade				Galamb et al, Plos One, 2012
	AH2810.CEL	tubulovillous	61	M	high-grade				Galamb et al, Plos One, 2012
	AH2821.CEL	tubular	79	F	high-grade				Galamb et al, Plos One, 2012
	AH2916.CEL	villous	67	M	high-grade				Galamb et al, Plos One, 2012
	AH2945.CEL	tubular	87	F	high-grade				Galamb et al, Plos One, 2012
	AH2952.CEL	tubular	62	M	high-grade				Galamb et al, Plos One, 2012
	AH3051.CEL	tubular	75	F	high-grade				Galamb et al, Plos One, 2012
	AH3059.CEL	tubulovillous	69	M	high-grade				Galamb et al, Plos One, 2012
	AH3139.CEL	tubulovillous	69	M	high-grade				Galamb et al, Plos One, 2012
	AH3147.CEL	tubulovillous	49	F	high-grade				Galamb et al, Plos One, 2012
	AH3151.CEL	villous	78	F	high-grade				Galamb et al, Plos One, 2012
	AH956.CEL	villous	84	F	high-grade				Galamb et al, Dis Markers, 2008
	AH983.CEL	tubulovillous	64	F	high-grade				Galamb et al, Dis Markers, 2008
CRC									
	B1158.CEL	adenocarcinoma	56	M		T3N0M0	B2	G2	Galamb et al, Dis Markers, 2008
	B1293.CEL	adenocarcinoma	88	F		T3N0M0	B2	G3	Galamb et al, Dis Markers, 2008
	B1486.CEL	adenocarcinoma	51	F		T2N0M0	B1	G1	Galamb et al, Dis Markers, 2008
	B1708.CEL	adenocarcinoma	72	F		T3N0M0	B2	G2	Galamb et al, Dis Markers, 2008
	B1739.CEL	adenocarcinoma	76	F		T4N0M0	B3	G1	Galamb et al, Dis Markers, 2008
	B1761.CEL	adenocarcinoma	58	M		T2N0M0	B1	G2	Galamb et al, Dis Markers, 2008
	B1883.CEL	adenocarcinoma	56	M		T3N0M0	B2	G2	Galamb et al, Dis Markers, 2008
	B2237.CEL	adenocarcinoma	64	M			B		Galamb et al, CEBP, 2009
	B2382.CEL	adenocarcinoma	68	M			B	G1	Galamb et al, CEBP, 2009
	B2486.CEL	adenocarcinoma	75	F		T2N0M0	B2	G1	Galamb et al, CEBP, 2009

	B2681.CEL	adenocarcinoma	67	M		T1N0M0	A	G2	Galamb et al, Plos One, 2012
	B2682.CEL	adenocarcinoma	80	F		T3N0M0	B2	G2	Galamb et al, Plos One, 2012
	B2707.CEL	adenocarcinoma	63	F		T3N0M0	B2	G2	Galamb et al, Plos One, 2012
	B2724.CEL	adenocarcinoma	76	F		T3N0M0	B2	G2	Galamb et al, Plos One, 2012
	B2849.CEL	adenocarcinoma	80	F		T3N0M0	B2	G2	Galamb et al, Plos One, 2012
	B2865.CEL	adenocarcinoma	85	M		T2N0M0	B1	G2	Galamb et al, Plos One, 2012
	B2900.CEL	adenocarcinoma	79	M		T3N0M0	B2	G2	Galamb et al, Plos One, 2012
	B2925.CEL	adenocarcinoma	76	F		T3N0M0	B2	G2	Galamb et al, Plos One, 2012
	B2927.CEL	adenocarcinoma	65	F		T2N0M0	B1	G1	Galamb et al, Plos One, 2012
	B2940.CEL	adenocarcinoma	65	F		T3N0M0	B2	G1	Galamb et al, Plos One, 2012
	B2956.CEL	adenocarcinoma	67	F		T3N0M0	B2	G2	Galamb et al, Plos One, 2012
	B2986.CEL	adenocarcinoma	67	F		T2N0M0	B1	G1	Galamb et al, Plos One, 2012
	B2991.CEL	adenocarcinoma	81	F		T3N0M0	B2	G2	Galamb et al, Plos One, 2012
	B3068.CEL	adenocarcinoma	73	M		T3N0M0	B2	G1	Galamb et al, Plos One, 2012
	D1146.CEL	adenocarcinoma	46	M		T2N1M0	C1	G2	Galamb et al, Dis Markers, 2008
	D1316.CEL	adenocarcinoma	85	M		T3N1M1	D	G2	Galamb et al, Dis Markers, 2008
	D1377.CEL	adenocarcinoma	69	F		T4N1M0	C3	G1-2	Galamb et al, Dis Markers, 2008
	D1479.CEL	adenocarcinoma	77	F		T4N0M1	D	G1	Galamb et al, Dis Markers, 2008
	D1494.CEL	adenocarcinoma	73	M		T3N1M1	D	G1	Galamb et al, Dis Markers, 2008
	D1499.CEL	adenocarcinoma	65	M		T3N0M1	D	G1	Galamb et al, Dis Markers, 2008
	D1556.CEL	adenocarcinoma	66	F		T3N1M1	D	G2	Galamb et al, Dis Markers, 2008
	D1651.CEL	adenocarcinoma	59	F		T2N0M1	D	G1	Galamb et al, Dis Markers, 2008
	D2089.CEL	adenocarcinoma	60	M		T3N2M1	D	G1	Galamb et al, CEBP, 2009
	D2171.CEL	adenocarcinoma	78	M		T3N2M1	D	G3	Galamb et al, CEBP, 2009
	D2262.CEL	adenocarcinoma	54	F		T2N1M0	C1	G1	Galamb et al, CEBP, 2009
	D2325.CEL	adenocarcinoma	66	M		T2N0-1?	C (or B?)		Galamb et al, CEBP, 2009
	D2651.CEL	adenocarcinoma	55	F		T3N2M0	C3	G2	Galamb et al, Plos One, 2012
	D2660.CEL	adenocarcinoma	73	F		T3N2M1	D	G2	Galamb et al, Plos One, 2012
	D2662.CEL	adenocarcinoma	78	M		T3N2M1	D	G2	Galamb et al, Plos One, 2012

	D2684.CEL	adenocarcinoma	74	F		T3N1M0	C	G2	Galamb et al, Plos One, 2012
	D2730.CEL	adenocarcinoma	65	M		T2N1M0	C1	G2	Galamb et al, Plos One, 2012
	D2751.CEL	adenocarcinoma	85	F		T3N1M0	C	G2	Galamb et al, Plos One, 2012
	D2765.CEL	adenocarcinoma	48	M		T4N2M0	C3	G2	Galamb et al, Plos One, 2012
	D2842.CEL	adenocarcinoma	66	F		T3N1M0	C	G2	Galamb et al, Plos One, 2012
	D2872.CEL	adenocarcinoma	61	F		T3N1M0	C2	G2	Galamb et al, Plos One, 2012
	D2876.CEL	adenocarcinoma	70	M		T3N1M0	C2	G3	Galamb et al, Plos One, 2012
	D2884.CEL	adenocarcinoma	75	F		T3N1M1	D	G2	Galamb et al, Plos One, 2012
	D2903.CEL	adenocarcinoma	60	M		T3N1M1	D	G2	Galamb et al, Plos One, 2012
	D2936.CEL	adenocarcinoma	40	M		T2N3M1	D	G2	Galamb et al, Plos One, 2012