

**Supplementary Table 1:** Patient's characteristics of methylation profiling cohort

<b>Gender</b>	
male	49 (82%)
female	11 (18%)
<b>Median age (range)</b>	57 (16-78)
<b>Etiology</b>	
HBV	11 (18.3%)
HCV	15 (25.0%)
co-infection	1 (1.7%)
alcohol	14 (23.3%)
cryptogenic	15 (25.0%)
genetic hemochromatosis	2 (3.3%)
others	2 (3.3%)
<b>Grading</b>	
well differentiated HCC	6 (10%)
moderately differentiated HCC	45 (75%)
poorly differentiated HCC	12 (20%)
<b>Tumor size</b>	
< 2.0 cm	2 (3.3%)
2.0 – 5.0 cm	34 (56.7%)
> 5.0 cm	27 (45.0%)
<b>UICC stage</b>	
I	39 (65.0%)
II	19 (31.7%)
III	0 (0%)
IV	2 (3.3%)
<b>Vascular invasion</b>	
present	24 (38.1%)
none	39 (61.9%)
<b>Liver cirrhosis</b>	
present	37 (61.7%)

**Supplementary Table 2:** Primer and siRNA sequences

Per3-fw	5'-CCT CGG ATC CCA GTG AAT AA-3'
Per3-rev	5'-CGA TGT TCC AAT CAG GTC CT-3'
IGFALS-fw	5'-AGC AGA CGT ACC CTC CCT CGC-3'
IGFALS-rev	5'-GTT CCG GGG TCT GCT CCC TCC-3'
PROZ-fw	5'-AGG AAA AGA CTT CTG TGG TGG T-3'
PROZ-rev	5'-CGT GCG TTA TCT TGA TCA TCA-3'
18s-fw	5'- AAA CGG CTA CCA CAT CCA AG-3'
18s-rev	5'-CCT CCA ATG GAT CCT CGT TA-3'
CMV-fw (pDEST vector)	5'-AAT GTC GTA ATA ACC CCG CC-3'
Flag-rev (pDEST vector)	5'-CTT GTC ATC GTC ATC CTT GTA-3'
siPER3	5'-GGU GUA UAA UUG GAU UCA A-dTdT3'
nonsense siRNA (siNS)	5'-UUC UCC GAA CGU GUC ACG U-dTdT3'

**Supplementary Table 3: Antibodies used for Western Immunoblotting**

	<b>species</b>	<b>dilution</b>	<b>Company (order no.)</b>
PER3	polyclonal rabbit	1:500	Acris Antibodies (12550-1-AP)
IGFALS	polyclonal rabbit	1:250	Sigma Aldrich (HPA40692)
PROZ	monoclonal mouse	1:1000	Thermo Scientific (MA5-15533)
β-actin	monoclonal mouse	1:10000	MP Biomedicals

**Supplementary Table 4: Patient's characteristics of TMA cohort**

<b>Gender</b>	
male	59 (78%)
female	17 (22%)
<b>Median age (range)</b>	58 (17-78)
<b>Etiology</b>	
HBV	16 (21.1%)
HCV	25 (32.9%)
co-infection	4 (5.3%)
alcohol	13 (17.1%)
cryptogenic	19 (25.0%)
genetic hemochromatosis	3 (3.9%)
<b>Grading</b>	
well differentiated HCC	13 (17.1%)
moderately differentiated HCC	55 (72.4%)
poorly differentiated HCC	8 (10.5%)
<b>Tumor size</b>	
< 2.0 cm	7 (9.2%)
2.0 – 5.0 cm	39 (51.3%)
> 5.0 cm	30 (39.5%)
<b>UICC stage</b>	
I	35 (46.1%)
II	24 (31.6%)
III	13 (17.1%)
IV	4 (5.3%)
<b>Vascular invasion</b>	
present	27 (35.5%)
none	49 (64.5%)
<b>Liver cirrhosis</b>	
present	46 (60.5%)

**Supplementary Table 5:** List of the differentially methylated genes (median methylation difference  $\geq 0.35$  in HCCs compared to normal samples).

CpG site	Gene	Median difference (HCC - NL)	95% CI		FDR-q-value
cg09053680	UTF1	0.62	0.51	0.69	< 0.001
cg25720804	TLX3	0.60	0.51	0.68	< 0.001
cg26521404	HOXA9	0.60	0.30	0.72	< 0.001
cg04034767	GRASP	0.59	0.33	0.68	< 0.001
cg22881914	NID2	0.57	0.30	0.68	< 0.001
cg18815943	FOXE3	0.54	0.36	0.64	< 0.001
cg22375192	IGF1R	0.54	0.32	0.65	< 0.001
cg08097882	POU4F1	0.52	0.39	0.66	< 0.001
cg02440177	ZNF702	0.52	0.40	0.62	< 0.001
cg18536148	TBX4	0.52	0.24	0.65	< 0.001
cg04797323	SOCS2	0.51	0.22	0.68	< 0.001
cg23391785	DNM3	0.51	0.37	0.63	< 0.001
cg08668790	ZNF154	0.50	0.34	0.65	< 0.001
cg21790626	ZNF154	0.50	0.33	0.65	< 0.001
cg15191648	SALL3	0.50	0.21	0.59	< 0.001
cg13801416	AKR1B1	0.50	0.33	0.61	< 0.001
cg06377278	RUNX3	0.50	0.20	0.63	0.004
cg09099744	CDKN2A	0.49	0.32	0.70	< 0.001
cg00489401	FLT4	0.49	0.30	0.62	< 0.001
cg06291867	HTR7	0.47	0.39	0.55	< 0.001
cg02755525	NETO2	0.47	0.29	0.58	0.003
cg07533148	TRIM58	0.47	0.20	0.61	< 0.001
cg09260089	NKX6-2	0.47	0.33	0.62	< 0.001
cg05684891	DAB2IP	0.47	0.32	0.58	< 0.001
cg21870884	GPR25	0.46	0.32	0.54	< 0.001
cg15520279	HOXD8	0.46	0.28	0.58	< 0.001
cg15433631	IRX2	0.45	0.28	0.57	< 0.001
cg12078929	SERHL	0.44	0.33	0.51	< 0.001
cg00290506	CNIH3	0.44	0.11	0.56	< 0.001
cg03544320	CRMP1	0.44	0.34	0.53	< 0.001
cg08441806	NKX6-2	0.43	0.34	0.51	< 0.001
cg15375239	SPINT2	0.43	0.28	0.54	< 0.001
cg01870826	LOC389458	0.43	0.28	0.56	< 0.001
cg25764191	INA	0.43	0.31	0.52	< 0.001
cg10895543	CDKN2A	0.43	0.28	0.60	< 0.001
cg26609631	GSH1	0.42	0.22	0.53	0.001
cg27009703	HOXA9	0.42	0.31	0.51	< 0.001
cg27409364	KCNC1	0.42	0.34	0.49	< 0.001
cg20616414	WNK2	0.42	0.20	0.54	0.004
cg16076328	TACSTD1	0.42	0.30	0.49	< 0.001

cg01354473	HOXA9	0.42	0.26	0.55	< 0.001
cg03975694	ZNF540	0.42	0.31	0.51	< 0.001
cg03958979	NR2E1	0.42	0.31	0.51	< 0.001
cg04809136	SF3B14	0.41	0.25	0.52	< 0.001
cg17886204	DKFZp434l1020	0.41	0.27	0.51	< 0.001
cg00881370	LOC55908	0.40	0.31	0.46	< 0.001
cg13878010	ADCY5	0.40	0.26	0.51	< 0.001
cg02620013	MLNR	0.40	0.27	0.52	< 0.001
cg25802093	SPAG6	0.40	0.26	0.52	< 0.001
cg12680609	ZFP41	0.40	0.30	0.53	< 0.001
cg25044651	FLJ90650	0.40	0.22	0.51	0.001
cg20449692	CLDN11	0.40	0.11	0.56	0.004
cg18956481	CYP24A1	0.40	0.26	0.47	< 0.001
cg01295203	PRDM14	0.39	0.19	0.54	0.001
cg11935147	PDE4DIP	0.39	0.30	0.47	< 0.001
cg14988503	CDKL2	0.39	0.21	0.50	< 0.001
cg23290344	NEF3	0.39	0.21	0.54	< 0.001
cg18691434	GPC2	0.39	0.28	0.51	< 0.001
cg08260959	HIST1H4F	0.39	0.28	0.50	< 0.001
cg00949442	ABCA3	0.38	0.22	0.48	< 0.001
cg06268694	CELSR1	0.38	0.30	0.46	< 0.001
cg17718302	HIST1H3J	0.38	0.16	0.47	< 0.001
cg25942450	TLX3	0.38	0.27	0.48	< 0.001
cg10210238	CDKN2B	0.38	0.24	0.51	< 0.001
cg23158811	PBX4	0.38	0.24	0.46	< 0.001
cg01725199	GALNT12	0.38	0.14	0.50	0.001
cg01566404	ETNK2	0.38	0.26	0.48	0.001
cg22815110	FOXD3	0.38	0.23	0.53	< 0.001
cg20291049	POU3F3	0.37	0.24	0.48	< 0.001
cg04786857	SPDY1	0.37	0.26	0.48	< 0.001
cg04508649	ANGPTL7	0.37	0.31	0.43	< 0.001
cg19779211	KCNQ1	0.37	0.26	0.46	< 0.001
cg06186808	LOC161247	0.37	0.30	0.43	< 0.001
cg19996355	PBX4	0.37	0.23	0.49	< 0.001
cg21542793	ADRA2B	0.37	0.21	0.50	< 0.001
cg21243096	POU3F1	0.37	0.20	0.48	< 0.001
cg04600618	C6orf206	0.37	0.24	0.47	< 0.001
cg19885761	CPLX2	0.37	0.17	0.47	< 0.001
cg15639951	MAP3K14	0.36	0.19	0.50	< 0.001
cg24432073	CDKL2	0.36	0.23	0.48	< 0.001
cg07752420	CDKN2A	0.36	0.26	0.50	< 0.001
cg26117023	DOK1	0.36	0.11	0.52	< 0.001
cg12874092	VIM	0.36	0.17	0.46	< 0.001
cg23180489	LYNX1	0.36	0.28	0.44	< 0.001
cg14826456	ADRB1	0.36	0.24	0.46	< 0.001
cg04267184	GNRH2	0.36	0.24	0.41	< 0.001

cg12111714	ATP8A2	0.36	0.23	0.48	< 0.001
cg23412850	SOCS2	0.35	0.18	0.48	< 0.001
cg12782180	LEP	0.35	0.28	0.43	< 0.001
cg19850348	PYGO1	0.35	0.16	0.51	0.001
cg15014458	LYPD3	0.35	0.22	0.47	< 0.001
cg10235817	ADRA2C	0.35	0.21	0.46	< 0.001
cg18555440	MYOD1	0.35	0.24	0.44	< 0.001
cg18236477	ATP8A2	0.35	0.20	0.50	< 0.001
cg07711097	GML	-0.35	-0.51	-0.21	< 0.001
cg19841506	ZMYND15	-0.35	-0.50	-0.12	0.001
cg22478614	DEFB4	-0.35	-0.45	-0.26	< 0.001
cg16899306	HLA-DQB2	-0.35	-0.45	-0.24	< 0.001
cg26390526	FLG	-0.35	-0.49	-0.20	< 0.001
cg24423088	KRTAP8-1	-0.35	-0.47	-0.20	< 0.001
cg02442161	PI3	-0.35	-0.47	-0.24	< 0.001
cg18986165	SIGLEC12	-0.36	-0.50	-0.14	< 0.001
cg13928961	K6IRS3	-0.36	-0.49	-0.22	< 0.001
cg12348970	SLC24A2	-0.36	-0.47	-0.24	< 0.001
cg12682367	FLJ46358	-0.36	-0.45	-0.24	< 0.001
cg21003606	CALN1	-0.36	-0.50	-0.20	< 0.001
cg13694749	SCN4A	-0.36	-0.52	-0.21	< 0.001
cg20312687	DEFB118	-0.36	-0.44	-0.27	< 0.001
cg21846488	LCE4A	-0.36	-0.48	-0.24	< 0.001
cg07459489	SLC30A8	-0.36	-0.46	-0.23	< 0.001
cg27513764	EFCAB3	-0.36	-0.46	-0.25	< 0.001
cg03872376	ZP4	-0.36	-0.46	-0.25	< 0.001
cg21991396	CIAS1	-0.36	-0.52	-0.20	< 0.001
cg03602500	FLJ00060	-0.36	-0.46	-0.28	< 0.001
cg23338195	SLC30A8	-0.36	-0.43	-0.28	< 0.001
cg04000821	LAIR2	-0.37	-0.44	-0.26	< 0.001
cg16377872	SLC1A6	-0.37	-0.48	-0.24	< 0.001
cg00152644	SPRR2E	-0.37	-0.53	-0.23	< 0.001
cg07259382	MARCH1	-0.37	-0.49	-0.21	< 0.001
cg14141399	HAS1	-0.37	-0.52	-0.20	< 0.001
cg00679556	TRIM31	-0.37	-0.44	-0.28	< 0.001
cg02202484	SPRR4	-0.37	-0.46	-0.23	< 0.001
cg11750883	C1orf42	-0.37	-0.48	-0.25	< 0.001
cg05440289	IVL	-0.37	-0.50	-0.23	< 0.001
cg22983092	KRT25A	-0.37	-0.51	-0.19	0.001
cg10925082	ARHGDIB	-0.37	-0.45	-0.26	< 0.001
cg04431776	GAGE2	-0.38	-0.46	-0.18	< 0.001
cg23865698	WFDC1	-0.38	-0.46	-0.27	< 0.001
cg17827767	LRRC21	-0.38	-0.49	-0.26	< 0.001
cg24765446	WFDC6	-0.38	-0.47	-0.24	< 0.001
cg18908499	C1orf150	-0.39	-0.46	-0.29	< 0.001
cg27622610	OR1G1	-0.39	-0.47	-0.29	< 0.001

cg25384595	LILRA1	-0.39	-0.46	-0.31	< 0.001
cg10501065	IGF2AS	-0.40	-0.50	-0.26	< 0.001
cg08763351	SPRR4	-0.40	-0.52	-0.28	< 0.001
cg07592353	GABRA6	-0.40	-0.49	-0.25	< 0.001
cg08878744	LCE1B	-0.41	-0.49	-0.29	< 0.001
cg18675600	PTP4A3	-0.41	-0.49	-0.26	< 0.001
cg23595927	MYL5	-0.41	-0.52	-0.27	< 0.001
cg18780284	SPRR1B	-0.42	-0.51	-0.33	< 0.001
cg15320474	UBD	-0.43	-0.53	-0.32	< 0.001
cg11009736	MARCO	-0.43	-0.51	-0.34	< 0.001
cg17725968	PDHA2	-0.43	-0.54	-0.25	< 0.001
cg04505023	SPRR1A	-0.44	-0.55	-0.30	< 0.001
cg06627364	MGC4677	-0.45	-0.51	-0.36	< 0.001
cg09120035	CYP11B1	-0.46	-0.55	-0.32	< 0.001
cg25856811	SPRR3	-0.46	-0.54	-0.35	< 0.001
cg06806711	MS4A1	-0.46	-0.53	-0.36	< 0.001

**Supplementary Table 6:** Hypermethylated gene enrichment in KEGG pathways.

O is the observed gene number of the pathway. E is the expected number of genes in a specific pathway in a chosen gene set. R represents the ratio of enrichment ( $R=O/E$ ). P defines the p value from hypergeometric testing and FDR-q is the p value adjusted by the multiple test adjustment.

KEGG Pathway	n=	Symbol	Enrichment	FDR-q
<b>Neuroactive ligand-receptor interaction</b>	16	ADORA2A, ADRA2B, ADRA2C, ADRB1, DRD2, DRD5, F2R, GALR3, GPR83, HTR7, LEP, LTB4R2, MLNR, NMBR, PTGDR, VIPR2	O=16;E=2.31;R=6.93; p=2.02e-09	1.47E-07
<b>Retinol metabolism</b>	7	ALDH1A2, CYP1A2, CYP26C1, CYP2A6, CYP2C19, CYP2C8, CYP2C9	O=7;E=0.58;R=12.12; p=1.84e-06	6.72E-05
<b>Drug metabolism - cytochrome P450</b>	7	CYP1A2, CYP2A6, CYP2C19, CYP2C8, CYP2C9, GSTM2, GSTP1	O=7;E=0.65;R=10.78; p=4.11e-06	0.0001
<b>Pathways in cancer</b>	13	BCL2, BMP4, CDKN2A, CDKN2B, FGF19, FLT3, FZD9, GSTP1, IGF1R, LAMA1, RASSF1, WNT2, ZBTB16	O=13;E=2.98;R=4.37; p=1.15e-05	0.0002
<b>Metabolism of xenobiotics by cytochrome P450</b>	6	CYP1A2, CYP2C19, CYP2C8, CYP2C9, GSTM2, GSTP1	O=6;E=0.63;R=9.50; p=4.18e-05	0.0006
<b>Metabolic pathways</b>	24	ABO, ACSL5, AKR1B1, AKR1D1, ALDH1A2, BTD, CKMT2, CYP1A2, CYP2A6, CYP2C19, CYP2C8, CYP2C9, DGKI, ETNK2, FUT6, GALNT12, IL4I1, LDHAL6A, MTHFD2, NDST1, PFKP, SMPD3, ST8SIA5, TDO2	O=24;E=9.96;R=2.41; p=8.12e-05	0.001
<b>Linoleic acid metabolism</b>	4	CYP1A2, CYP2C19, CYP2C8, CYP2C9	O=4;E=0.26;R=15.29; p=0.0001	0.001
<b>Calcium signaling pathway</b>	8	ADORA2A, ADRB1, CALML3, DRD5, F2R, GNA14, HTR7, LTB4R2	O=8;E=1.61;R=4.98; p=0.0002	0.0018
<b>Systemic lupus erythematosus</b>	7	HIST1H2BH, HIST1H3F, HIST1H3G, HIST1H3J, HIST1H4F, HIST3H2A, HIST3H2BB	O=7;E=1.26;R=5.54; p=0.0003	0.0022
<b>Endocytosis</b>	8	ADRB1, DNM3, EHD3, F2R, HSPA2, IGF1R, RAB22A, RAB31	O=8;E=1.69;R=4.74; p=0.0003	0.0022

**Supplementary Table 7:** List of genes known to be silenced by the Polycomb Repressive Complex 2.

CpG site	Median difference	95% CI		FDR-q-value	Gene	Name	Chromosome
cg21243096	0.37	0.20	0.48	< 0.001	POU3F1	POU class 3 homeobox 1	1p34.3
cg11428724	0.07	0.02	0.23	0.004	PAX7	paired box 7	1p36.13
cg02084087	0.12	0.04	0.20	0.004	TNFRSF25	tumor necrosis factor receptor superfamily, member 25	1p36.2
cg23207990	0.13	0.05	0.29	< 0.001	SFRP2	secreted frizzled-related protein 2	4q31.3
cg12629325	0.28	0.10	0.46	0.001	PCDHAC1	protocadherin alpha subfamily C, 1	5q31
cg26252167	0.14	0.04	0.33	0.002	GPR6	G protein-coupled receptor 6	6q21
cg26521404	0.60	0.30	0.72	< 0.001	HOXA9	homeobox A9	7p15.2
cg19172575	0.15	0.05	0.26	0.005	GATA4	GATA binding protein 4	8p23.1-p22
cg13641903	0.15	0.09	0.22	< 0.001	WT1	Wilms tumor 1	11p13
cg18555440	0.35	0.24	0.44	< 0.001	MYOD1	myogenic differentiation 1	11p15
cg22183706	0.11	0.04	0.18	0.002	CALCA	calcitonin-related polypeptide alpha	11p15.2
cg13216057	0.17	0.06	0.30	0.004	DKK3	dickkopf homolog 3 ( <i>Xenopus laevis</i> )	11p15.3
cg19779211	0.37	0.26	0.46	< 0.001	KCNQ1	potassium voltage-gated channel, KQT-like subfamily, member 1	11p15.5
cg23855989	0.15	0.09	0.23	< 0.001	AQP5	aquaporin 5	12q13
cg02055963	0.13	0.03	0.33	0.004	CDX2	caudal type homeobox 2	13q12.2
cg20822579	0.19	0.09	0.30	0.002	RIPK3	receptor-interacting serine-threonine kinase 3	14q12
cg20023231	0.10	0.05	0.16	< 0.001	HS3ST2	heparan sulfate (glucosamine) 3-O-sulfotransferase 2	16p12
cg15439862	0.25	0.11	0.37	0.001	DSC3	desmocollin 3	18q12.1
cg21602520	0.25	0.10	0.35	0.003	BCL2	B-cell CLL/lymphoma 2	18q21.3
cg05488632	0.29	0.14	0.41	< 0.001	ABHD9	epoxide hydrolase 3	19p13.13



**Supplementary Table 8:** List of imprinted genes that show LOI in at least one CpG-site.

CpG site	Median difference	95% CI		FDR-q-value	Gene	Name	Chromosome
cg21808053	-0.25	-0.37	-0.12	< 0.001	DIRAS3	DIRAS family, GTP-binding RAS-like 3	1p31
cg01796223	-0.25	-0.33	-0.17	< 0.001	CPA4	carboxypeptidase A4	7q32
cg00132141	-0.17	-0.26	-0.07	0.003	CTNNA3	catenin (cadherin-associated protein), alpha 3	10q21
cg00041575	-0.28	-0.35	-0.20	< 0.001	TSPAN32	tetraspanin 32	11p15
cg25336198	-0.31	-0.62	-0.16	< 0.001	INS	insulin	11p15.5
cg10501065	-0.40	-0.50	-0.26	< 0.001	IGF2-AS	insulin-like growth factor 2 antisense (non-protein coding)	11p15.5
cg12949760	-0.19	-0.31	-0.08	< 0.001	KCNQ1	potassium voltage-gated channel, KQT-like subfamily, member 1	11p15.5
cg08999895	-0.25	-0.36	-0.14	< 0.001	SLC22A18AS	solute carrier family 22 (organic cation transporter), member 18 antisense	11p15.5
cg02250787	-0.22	-0.28	-0.12	< 0.001	HTR2A	5-hydroxytryptamine (serotonin) receptor 2A	13q14-q21
cg06504820	-0.17	-0.27	-0.09	< 0.001	DLK1	delta-like 1 homolog (Drosophila)	14q32
cg08099701	-0.27	-0.37	-0.17	< 0.001	GABRA5	gamma-aminobutyric acid (GABA) A receptor, alpha 5	15q11-q13
cg27592112	-0.15	-0.27	-0.06	0.001	GABRG3	gamma-aminobutyric acid (GABA) A receptor, gamma 3	15q11-q13
cg03969797	-0.27	-0.37	-0.13	< 0.001	MKRN3	makorin ring finger protein 3	15q11-q13
cg11015241	-0.34	-0.48	-0.14	< 0.001	ATP10A	ATPase, class V, type 10A	15q12
cg19803984	-0.27	-0.35	-0.18	< 0.001	SNRPN	small nuclear ribonucleoprotein polypeptide N	15q12
cg06244906	-0.29	-0.43	-0.17	< 0.001	ZIM2	zinc finger, imprinted 2	19q13.4
cg21988465	-0.25	-0.37	-0.11	< 0.001	GNAS	GNAS complex locus	20q13.2-q13.3

**Supplementary Table 9:** 65 genes commonly altered in HBV-, HCV-, alcohol-induced-, and cryptogenic HCCs.

CpG site	Gene	HBV				HCV				Alcoholic				Cryptogenic			
		median difference (HBV - NL)	95% CI		FDR-q-value	median difference (HCV - NL)	95% CI		FDR-q-value	median difference (Alcoholic - NL)	95% CI		FDR-q-value	median difference (Cryptogenic - NL)	95% CI		FDR-q-value
cg00347904	SCUBE3	0.33	0.15	0.44	< 0.001	0.33	0.15	0.46	0.001	0.31	0.22	0.49	< 0.001	0.26	0.11	0.47	0.001
cg00489401	FLT4	0.48	0.26	0.72	0.003	0.53	0.20	0.63	0.001	0.49	0.29	0.58	< 0.001	0.42	0.27	0.64	0.001
cg00548268	NPTX2	0.25	0.15	0.36	0.001	0.24	0.12	0.33	< 0.001	0.20	0.10	0.28	0.001	0.21	0.10	0.31	0.003
cg00564163	STEAP4	0.36	0.26	0.54	< 0.001	0.36	0.21	0.49	0.001	0.35	0.22	0.50	0.001	0.34	0.19	0.51	0.004
cg00891541	SMPD3	0.26	0.21	0.35	0.002	0.23	0.18	0.30	< 0.001	0.25	0.18	0.31	< 0.001	0.31	0.25	0.36	0.001
cg01830294	WNT2	0.41	0.26	0.55	0.001	0.36	0.20	0.47	< 0.001	0.27	0.11	0.41	0.001	0.30	0.17	0.48	0.003
cg02620013	MLNR	0.46	0.28	0.61	0.002	0.43	0.24	0.55	0.001	0.34	0.20	0.46	< 0.001	0.40	0.22	0.54	0.002
cg03064067	SLC6A15	0.28	0.09	0.60	0.002	0.20	0.11	0.29	< 0.001	0.19	0.10	0.27	< 0.001	0.30	0.13	0.47	0.001
cg03561565	KCNS2	0.22	0.09	0.41	0.004	0.27	0.15	0.37	0.001	0.35	0.24	0.43	< 0.001	0.28	0.16	0.36	< 0.001
cg04034767	GRASP	0.66	0.33	0.73	0.001	0.54	0.16	0.65	0.001	0.59	0.24	0.69	< 0.001	0.64	0.34	0.73	0.005
cg04189838	CYP2C19	0.25	0.19	0.30	< 0.001	0.22	0.15	0.28	< 0.001	0.21	0.13	0.26	< 0.001	0.21	0.09	0.28	0.004
cg04508649	ANGPTL7	0.39	0.31	0.48	0.003	0.38	0.31	0.45	< 0.001	0.36	0.31	0.43	< 0.001	0.34	0.22	0.43	< 0.001
cg04797323	SOCS2	0.74	0.25	0.80	0.004	0.50	0.34	0.73	< 0.001	0.49	0.15	0.65	0.002	0.30	0.14	0.60	0.001
cg05158615	NPY	0.43	0.28	0.58	0.001	0.28	0.19	0.37	0.002	0.30	0.24	0.37	< 0.001	0.34	0.23	0.45	0.001
cg05521696	SLC2A14	0.43	0.18	0.54	0.004	0.28	0.13	0.44	0.001	0.37	0.20	0.54	< 0.001	0.35	0.16	0.49	0.004
cg06186808	LOC161247	0.37	0.25	0.45	0.001	0.37	0.30	0.46	< 0.001	0.39	0.32	0.46	< 0.001	0.34	0.17	0.43	0.003
cg06291867	HTR7	0.58	0.45	0.67	< 0.001	0.46	0.39	0.55	< 0.001	0.43	0.26	0.51	< 0.001	0.44	0.37	0.53	< 0.001
cg06914598	RBAK	0.21	0.10	0.38	0.003	0.19	0.11	0.30	0.001	0.19	0.10	0.28	0.002	0.21	0.12	0.33	0.003
cg07752420	CDKN2A	0.34	0.23	0.59	0.002	0.37	0.20	0.46	< 0.001	0.33	0.25	0.46	< 0.001	0.46	0.25	0.61	0.001
cg08109815	NMBR	0.33	0.19	0.42	0.001	0.21	0.11	0.36	0.002	0.26	0.15	0.36	< 0.001	0.29	0.19	0.40	0.001

cg08260959	HIST1H4F	0.47	0.28	0.60	< 0.001	0.29	0.19	0.43	< 0.001	0.37	0.28	0.52	< 0.001	0.40	0.29	0.52	0.001
cg08441806	NKX6-2	0.42	0.29	0.55	0.002	0.42	0.31	0.51	< 0.001	0.43	0.30	0.53	< 0.001	0.46	0.36	0.54	< 0.001
cg08451957	FOXD4L1	0.27	0.16	0.39	0.003	0.22	0.10	0.32	0.003	0.26	0.14	0.33	0.002	0.23	0.12	0.33	0.003
cg08668790	ZNF154	0.69	0.25	0.75	< 0.001	0.35	0.23	0.48	< 0.001	0.45	0.34	0.62	< 0.001	0.65	0.51	0.75	< 0.001
cg09099744	CDKN2A	0.47	0.17	0.76	< 0.001	0.47	0.40	0.67	< 0.001	0.48	0.32	0.70	< 0.001	0.59	0.32	0.79	< 0.001
cg09313705	HOXB2	0.26	0.18	0.35	< 0.001	0.20	0.13	0.30	0.002	0.17	0.09	0.26	0.005	0.24	0.18	0.29	0.004
cg09509673	CCR10	0.23	0.19	0.28	< 0.001	0.19	0.14	0.24	0.001	0.19	0.14	0.23	0.001	0.22	0.18	0.26	< 0.001
cg10210238	CDKN2B	0.40	0.22	0.56	0.002	0.36	0.18	0.51	0.001	0.35	0.15	0.49	0.001	0.40	0.23	0.57	0.002
cg10895543	CDKN2A	0.44	0.16	0.67	0.003	0.36	0.27	0.55	< 0.001	0.35	0.22	0.63	< 0.001	0.60	0.36	0.69	< 0.001
cg11377136	PKDREJ	0.37	0.23	0.50	0.001	0.30	0.14	0.44	0.003	0.34	0.21	0.45	< 0.001	0.34	0.22	0.46	< 0.001
cg11591325	F2R	0.22	0.12	0.55	0.001	0.27	0.16	0.48	< 0.001	0.29	0.15	0.38	0.001	0.28	0.08	0.42	0.002
cg11653709	CDKN2A	0.32	0.18	0.45	< 0.001	0.27	0.14	0.36	< 0.001	0.29	0.23	0.39	< 0.001	0.41	0.28	0.51	< 0.001
cg11935147	PDE4DIP	0.48	0.37	0.56	< 0.001	0.40	0.27	0.47	0.001	0.33	0.24	0.42	< 0.001	0.37	0.23	0.46	0.003
cg12111714	ATP8A2	0.48	0.37	0.56	< 0.001	0.25	0.14	0.36	< 0.001	0.33	0.16	0.49	0.001	0.34	0.16	0.56	0.003
cg12324629	ULK2	0.23	0.14	0.30	< 0.001	0.21	0.12	0.28	< 0.001	0.20	0.12	0.27	0.001	0.21	0.14	0.28	0.001
cg12680609	ZFP41	0.53	0.25	0.63	0.001	0.37	0.26	0.47	0.002	0.44	0.35	0.54	< 0.001	0.36	0.17	0.54	0.001
cg12782180	LEP	0.40	0.33	0.48	< 0.001	0.33	0.23	0.40	0.002	0.35	0.27	0.44	< 0.001	0.34	0.23	0.46	0.001
cg12840719	CDKN2A	0.34	0.14	0.43	0.001	0.20	0.12	0.28	< 0.001	0.27	0.12	0.45	< 0.001	0.42	0.25	0.51	< 0.001
cg12874092	VIM	0.47	0.35	0.77	< 0.001	0.21	0.08	0.41	0.002	0.38	0.15	0.45	< 0.001	0.26	0.09	0.48	0.002
cg13462129	DLX5	0.43	0.17	0.57	0.003	0.24	0.16	0.32	< 0.001	0.26	0.14	0.39	< 0.001	0.35	0.18	0.54	0.001
cg13899108	PDE4C	0.18	0.11	0.32	0.003	0.19	0.12	0.26	< 0.001	0.20	0.13	0.27	< 0.001	0.25	0.16	0.33	< 0.001
cg14988503	CDKL2	0.55	0.38	0.70	< 0.001	0.39	0.20	0.51	0.001	0.38	0.28	0.49	< 0.001	0.28	0.02	0.49	0.005
cg15105703	NIP	0.43	0.10	0.60	0.001	0.33	0.04	0.43	0.001	0.35	0.10	0.44	< 0.001	0.18	0.07	0.36	< 0.001
cg15191648	SALL3	0.64	0.46	0.77	< 0.001	0.46	0.22	0.56	0.001	0.51	0.09	0.57	0.001	0.44	0.10	0.61	0.001
cg15433631	IRX2	0.56	0.43	0.64	< 0.001	0.33	0.14	0.53	0.003	0.46	0.31	0.55	0.003	0.34	0.16	0.50	0.005
cg15787039	SGNE1	0.33	0.25	0.42	< 0.001	0.31	0.21	0.42	0.001	0.27	0.16	0.39	< 0.001	0.32	0.18	0.44	0.003

cg17264618	ENTPD3	0.37	0.21	0.48	0.002	0.26	0.14	0.37	0.001	0.27	0.11	0.42	0.002	0.33	0.25	0.42	0.001
cg17718302	HIST1H3J	0.39	0.15	0.84	0.001	0.39	0.17	0.46	< 0.001	0.41	0.21	0.52	< 0.001	0.24	0.04	0.45	0.003
cg18236477	ATP8A2	0.54	0.36	0.63	0.001	0.28	0.10	0.44	0.002	0.27	0.10	0.48	0.002	0.33	0.15	0.50	0.005
cg19779211	KCNQ1	0.37	0.18	0.54	0.001	0.41	0.33	0.48	< 0.001	0.32	0.18	0.39	< 0.001	0.36	0.14	0.53	0.001
cg20322977	CYP26C1	0.34	0.21	0.41	< 0.001	0.26	0.18	0.35	< 0.001	0.26	0.15	0.35	< 0.001	0.27	0.15	0.35	< 0.001
cg21243096	POU3F1	0.47	0.24	0.59	< 0.001	0.37	0.16	0.45	< 0.001	0.28	0.13	0.47	0.001	0.32	0.15	0.48	0.002
cg21460081	HOXB4	0.42	0.26	0.52	< 0.001	0.21	0.11	0.33	< 0.001	0.24	0.16	0.33	< 0.001	0.22	0.13	0.37	< 0.001
cg21790626	ZNF154	0.61	0.31	0.69	0.001	0.42	0.28	0.58	0.001	0.46	0.27	0.57	< 0.001	0.67	0.41	0.76	< 0.001
cg22680204	CRMP1	0.34	0.25	0.49	< 0.001	0.31	0.15	0.42	< 0.001	0.30	0.19	0.41	< 0.001	0.21	0.15	0.34	< 0.001
cg23180489	LYNX1	0.38	0.30	0.48	< 0.001	0.41	0.31	0.48	< 0.001	0.38	0.29	0.46	< 0.001	0.28	0.12	0.38	0.003
cg23391785	DNM3	0.53	0.37	0.70	< 0.001	0.53	0.35	0.65	< 0.001	0.52	0.33	0.69	0.001	0.49	0.30	0.67	0.001
cg24432073	CDKL2	0.38	0.19	0.55	0.003	0.33	0.18	0.45	0.001	0.37	0.19	0.50	0.002	0.39	0.23	0.53	0.003
cg25340403	LYPD3	0.26	0.16	0.37	0.001	0.25	0.19	0.34	< 0.001	0.26	0.17	0.34	< 0.001	0.22	0.11	0.33	0.005
cg25484904	FLJ21511	0.43	0.28	0.54	< 0.001	0.30	0.21	0.40	0.001	0.25	0.11	0.32	0.001	0.34	0.19	0.42	0.003
cg25720804	TLX3	0.62	0.52	0.73	< 0.001	0.55	0.41	0.65	< 0.001	0.62	0.54	0.69	< 0.001	0.62	0.44	0.73	0.001
cg25764191	INA	0.49	0.30	0.62	0.001	0.34	0.22	0.48	0.001	0.46	0.33	0.55	< 0.001	0.44	0.31	0.53	< 0.001
cg25802093	SPAG6	0.45	0.30	0.60	0.001	0.42	0.26	0.55	< 0.001	0.40	0.23	0.52	< 0.001	0.35	0.19	0.56	0.001
cg25902889	FSD1	0.25	0.17	0.33	< 0.001	0.22	0.11	0.31	0.001	0.18	0.10	0.29	0.002	0.24	0.13	0.33	0.003
cg27409364	KCNC1	0.43	0.30	0.55	< 0.001	0.42	0.33	0.49	< 0.001	0.43	0.36	0.48	< 0.001	0.42	0.31	0.52	< 0.001