Supplemental Figure Legends

Supplemental Fig. 1

The distribution of the average number of probes that covered (A) a single CGI or (B) a single promoter. 95% (74%) of CGIs (promoters) were covered by multiple probes.

Supplemental Fig. 2

Correlation between the fraction of DNA molecules immunoprecipitated by an anti-5-methylcitidine antibody and individual output values in MeDIP-CGI microarray analysis. The fraction of DNA molecules immunoprecipitated by the anti-5-methylcitidine antibody was calculated from copy numbers obtained by real-time PCR. The signal log ratio did not show linear correlation, and normalization using the Median normalization and the Lowess normalization was not effective. The P[Xbar] value showed a relatively high correlation coefficient. The Me value showed the highest correlation coefficient.

Supplemental Fig. 3

Determination of an appropriate cutoff Me value for methylated (unmethylated) CGIs. Methylation statuses of 113 CGIs were analyzed by qualitative MSP in four cell lines. Sensitivity and specificity for methylated (unmethylated) CGIs were calculated as [# of CGIs assessed as HM (UM) by MeDIP-CGI microarray among CGIs determined as methylated (unmethylated) by MSP] and [# of CGIs assessed as MM and UM (HM and MM) by MeDIP-CGI microarray among CGIs determined as partially methylated and unmethylated (partially methylated and methylated) by MSP], respectively. Arrowheads indicate selected cutoff. (A) Determination of the cutoff Me value for unmethylated CGIs. Cutoff values between 0.2 and 0.7 were tested, and a value of 0.4 was selected as a value of reasonable

sensitivity and specificity. (B) Determination of the cutoff Me value for highly methylated CGIs. Cutoff values between 0.3 and 0.8 were tested, and a value of 0.6 was selected.

Supplemental Fig. 4

Genome-wide methylation analysis of CGIs in four gastric cancer cell lines and normal gastric tissue. (A) Fraction of methylated CGIs according to their relative positions against genes. Promoters were resistant to methylation. (B) Methylation levels in the CGIs spanning both a promoter region and gene body. The average of site Me values was plotted. Promoter was most resistant to methylation. (C, D) Methylation levels according to distances from repetitive sequences, LINE (C) and SINE (D). CGIs closer to repetitive sequences had lower Me values.
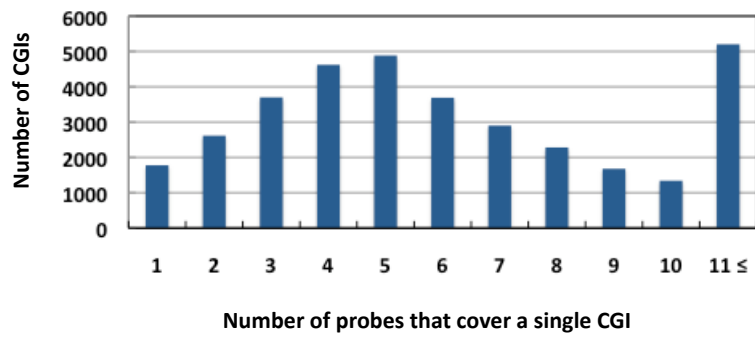
Supplemental Fig. 5

Distribution of methylated CGIs (overall) and promoters on individual chromosomes. AGS and KATOIII had larger numbers of methylated CGIs than HSC39 and HSC57, and this relationship was consistently observed for overall CGIs on all chromosomes. However, when limited to promoters, distorted patterns were observed on some chromosomes, such as chromosome 15, 18, 21 and 22 (with an arrow).
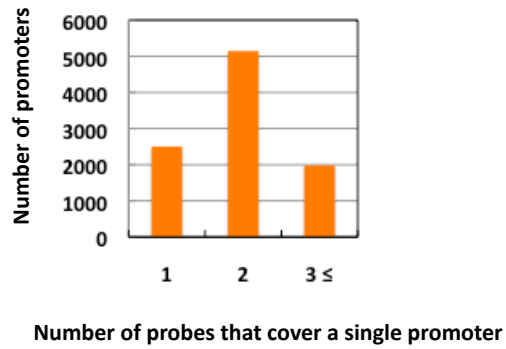
Supplemental Fig. 6

Relationship between expression in normal gastric tissue and methylation in cancer cells. Methylation levels (site Me values) according to gene expression in normal gastric tissues (high or low) at various positions against the TSSs. Solid lines (blue), genes with low expression in normal gastric tissue; and dotted lines (red), genes with high expression in normal gastric tissue. The genes with low expression in normal gastric tissue showed higher

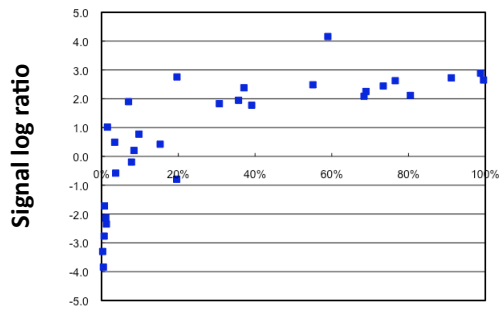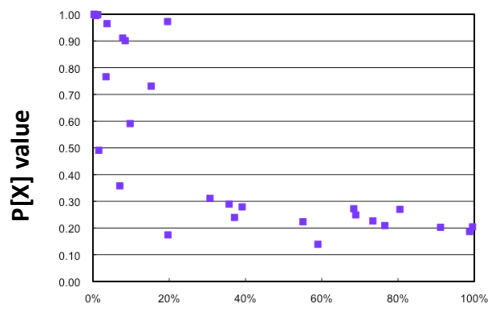methylation levels in cancer cells.

A

Number of probes that cover a single CGI

B

Number of probes that cover a single promoter

Supplemental Fig. 1
Yamashita et al.

Signal log ratio – Background subtraction (r = 0.72)
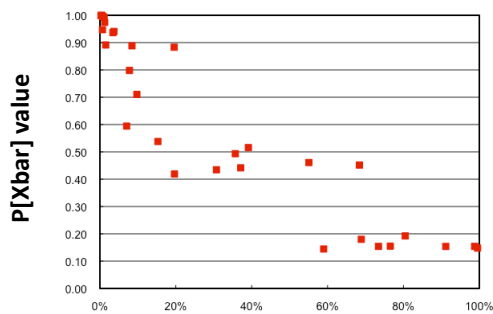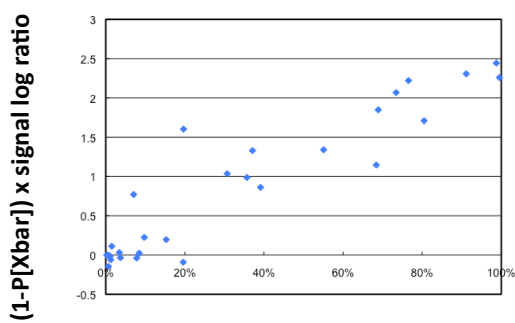
Signal log ratio

Signal ratio (r = 0.63)

Signal ratio

P[X] value (r = -0.79)

P[X] value
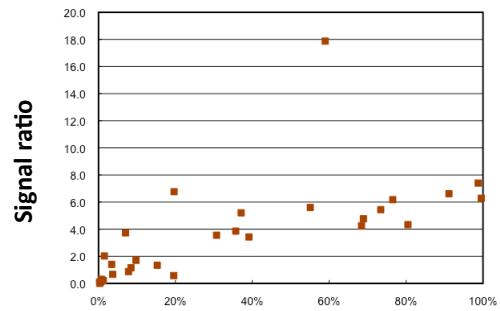
Signal log ratio – Median normalization (r = 0.71)

Signal log ratio

P[Xbar] value (r = -0.91)

P[Xbar] value
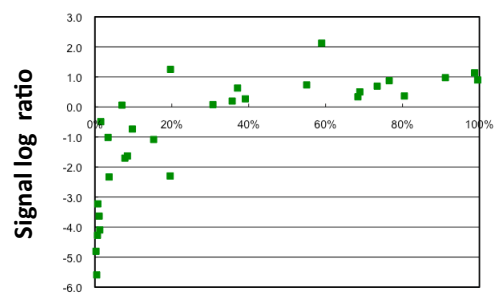
Signal log ratio – Lowess normalization (r = 0.60)

Signal log ratio

(1-P[Xbar]) x signal log ratio (r = 0.93)

(1-P[Xbar]) x signal log ratio

IP/WCE (real-time PCR)
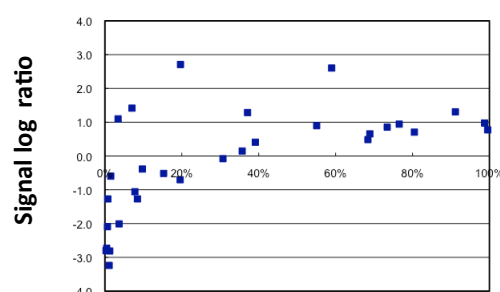
Me value (r = 0.94)

Me Value
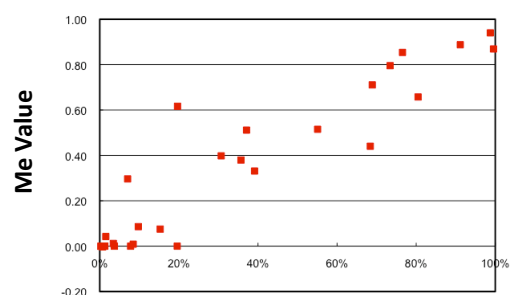
IP/WCE (real-time PCR)

**Supplemental Fig. 2
Yamashita et al.**

A

Sensibility and specificity

Cutoff of Me value for unmethylated loci

Sensitivity
Specificity

B

Sensibility and specificity

Cutoff of Me value for methylated loci

Sensitivity
Specificity
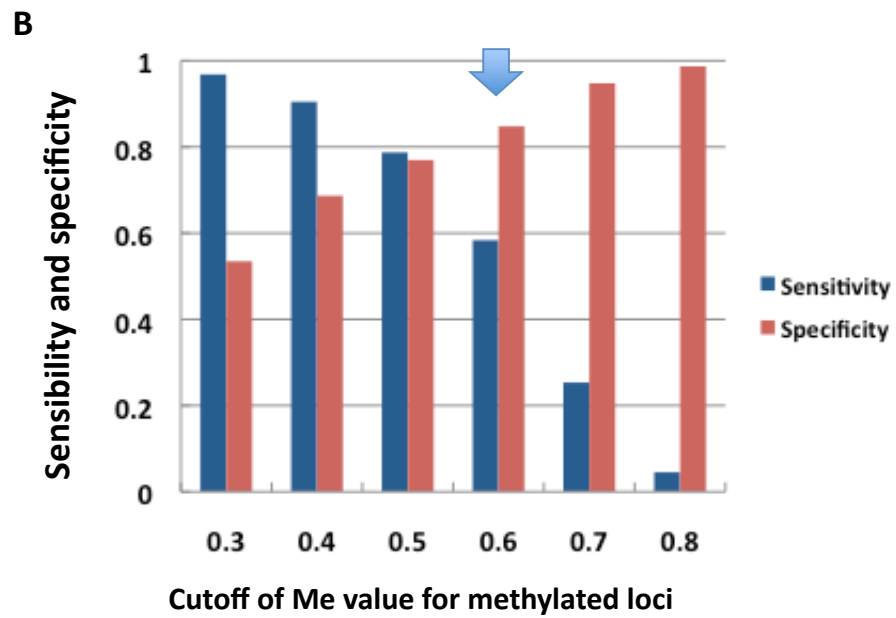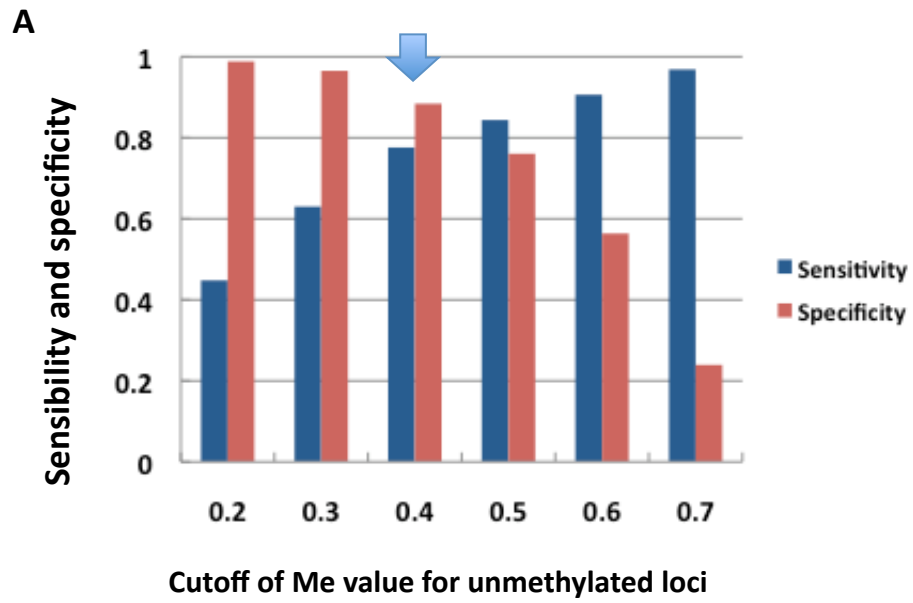
**Supplemental Fig. 3
Yamashita et al.**
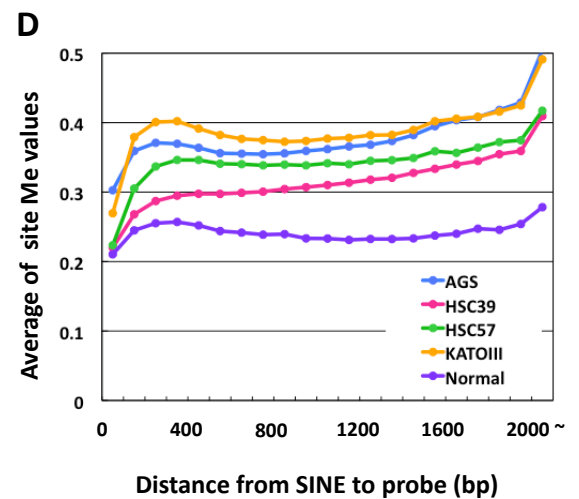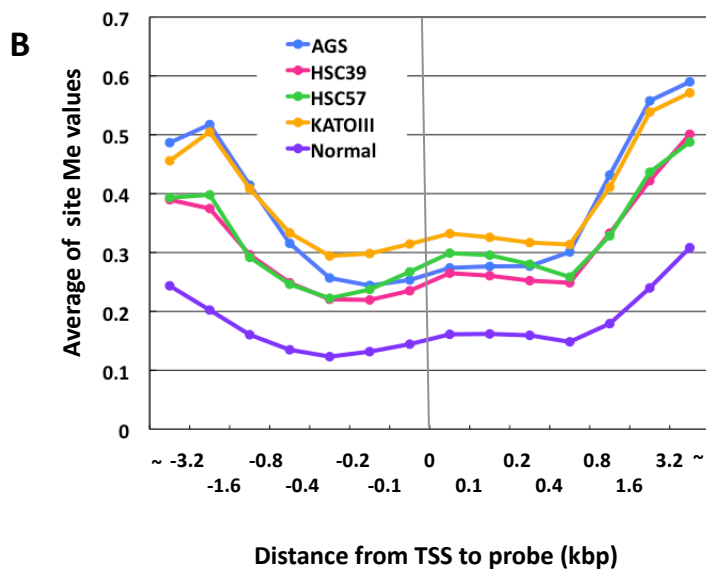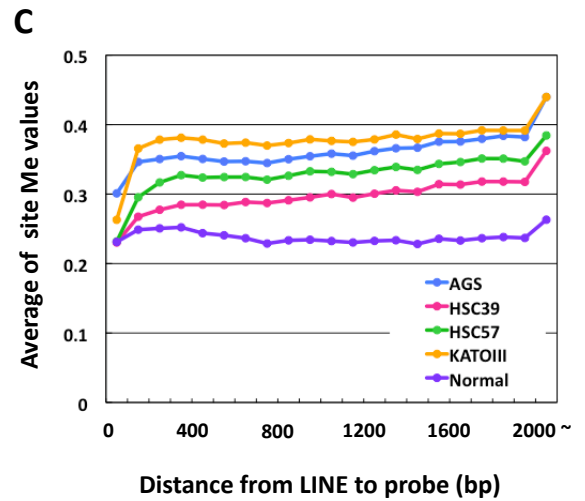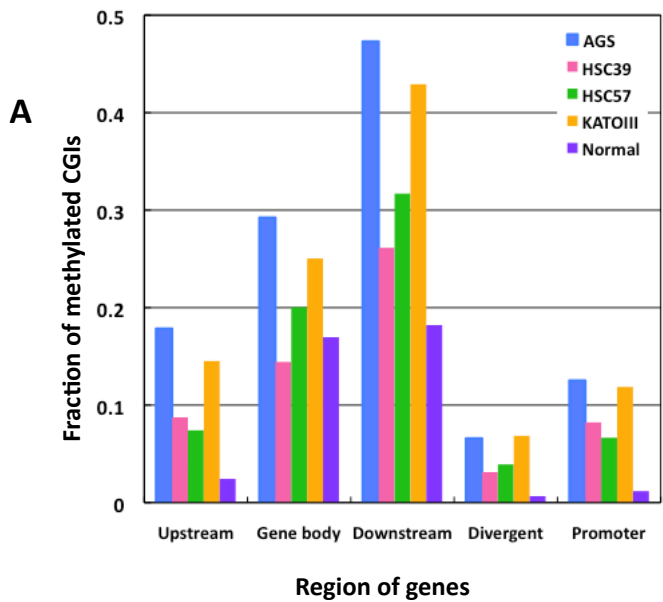
Supplemental Fig. 4
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Promoters

All CGIs

Chromosomes

Fraction of methylated CGIs (%)

Average of site Me values (y-axis)

Distance from TSS to probe (kbp) (x-axis)

AGS

HSC39

HSC57

KATOIII

x-axis labels: ~ -3.2, -1.6, -0.8, -0.4, -0.2, -0.1, 0, 0.1, 0.2, 0.4, 0.8, 1.6, 3.2 ~
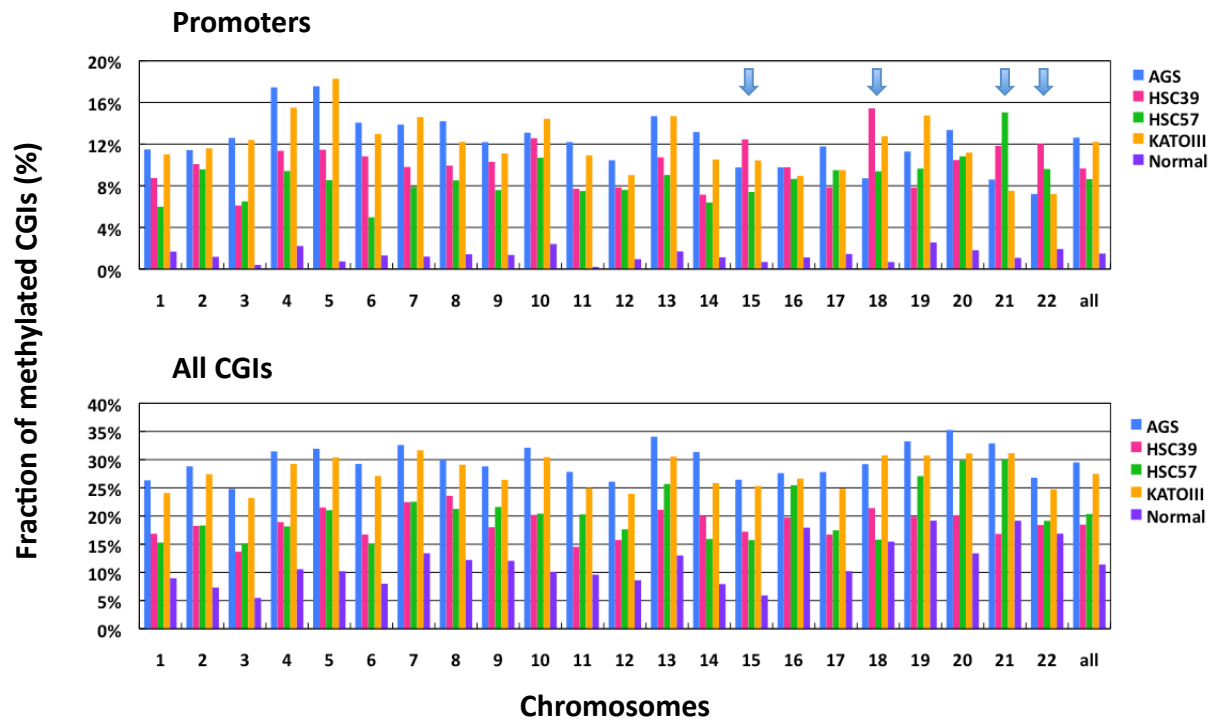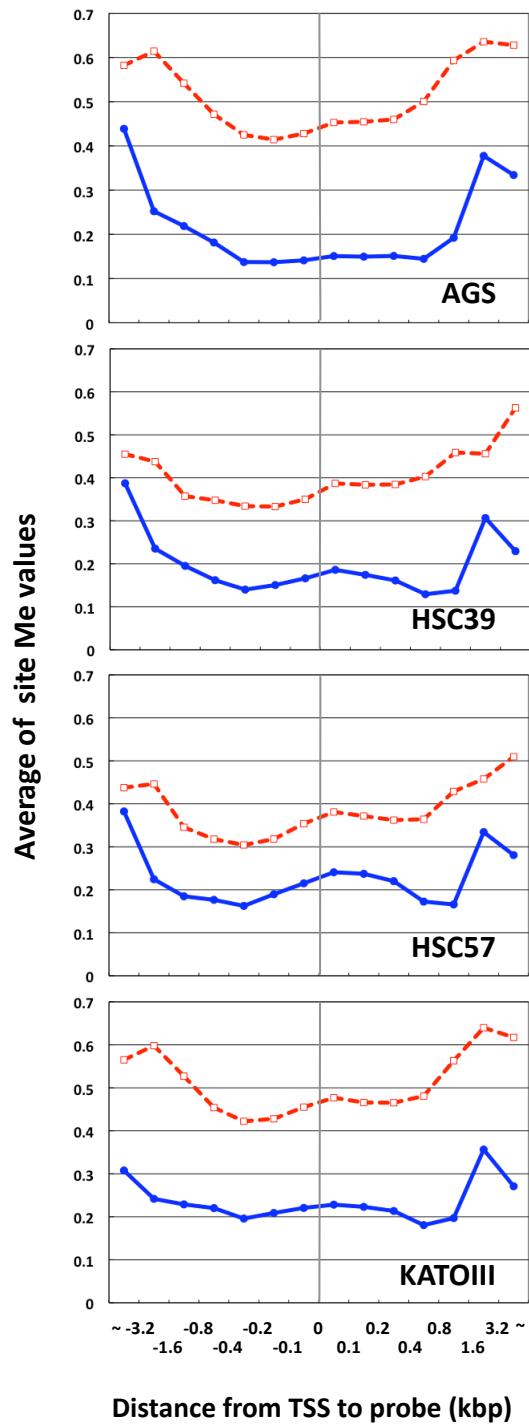
Supplemental Fig. 6
Yamashita et al.

Supplemental Table 1   List of primers

gene symbol	CpG island	chromosome	TSS (NCBI)	position	forward primer sequence	position	reverse primer sequence	reference
Primers for MSP (primers for methylated DNA)								
ABHD9	strict	19	15204231	-195	CGTGAGTTATCGTATTCGGTTC	-115	TCCTATACGAAACTTAAAACCG	(1)
ACAA2	strict	18	45593900	-199	GCGCGTTGTGGTTTATTC	-14	ACGCTAAACGACCGCTCG	this study
ACSS3 (FLJ21963)	strict	12	79995940	-232	CGTTTTGGAGTTTGAGCGC	-113	ACAAAAATATCACAACGCCG	(2)
ADFP	strict	9	19117573	-169	GGTCGGGTTTTCGTTCGGTTTC	-36	ACCCGAATATCACCCTCGAACACG	(1)
ADM	strict	11	10283218	-163	TTTTAAAGGAAGTAATGCGC	-69	AACGCACGAATAAAAAAACG	this study
ALDH1A3	strict	15	99237584	-108	TCGGTTTCGTAGTTAATTAGGC	-18	GACTCGACCCGAACACTACGCA	(1)
ANGPTL4 (PGAR)	strict	19	8335011	-499	TTTAGGTTGGAGCGTAATGGC	-298	CAATAACGAAAAAAACGCACG	(3)
ANXA5	strict	4	122837626	-164	TATTTAGGTTCGCGAGATTAGC	-48	CCAAAACCCCAACCGCAAACCG	(1)
AREG	strict	4	75529717	-173	TTTTTAGCGAATTTTTACGTAC	-22	ATAAAACGACGCGCACCTACCG	(1)
BBS10 (FLJ23560)	strict	12	75266338	-276	ATTTGGGGGTAGCGGAC	-139	AAACTAACCCGTTATACGCG	(2)
BDNF	strict	11	27699872	-401	TACGTAAATAGCGAGGTTAGTC	-214	AACTCCGACGAAACTAAATTCG	(1)
BMP7	strict	20	55274708	-227	GTTTTTTCGTTGTTTTTTCGGC	-82	ATACTAACCCCGAACCCCTCG	(1)
BNIP3	strict	10	133645425	-155	TCGTAGGATTCGTTTCGC	-50	AATCTACGACCGCGTCG	(2)
BNIP3	strict	10	133645425	-688	GTTTTTTTTTGCGGGCGGAC	-520	CGCTACGACTCCGAAACG	this study
C1orf115 (FLJ14146)	strict	1	218930285	-168	TTTATTGTGTAGTGCGCGTC	-28	GAAAAATTAAAAAAACCGCAACG	this study
CAV1	relaxed	7	115952075	-80	TTTCGGGACGTTTTCGGTGGT	-6	TAAAAACGTTTCTCCCGCGCTA	(1)
CDH2	strict	18	24011189	-217	TTTATCGGTTAAGGTTTTCGTC	-128	CGTCTACGAATATATAAAAACG	(1)
CDKN2D	strict	19	10540655	-122	GCGGTGTCGTTATATAGTAGC	-15	ACTCTAAACCTACGCCGCCG	(1)
CLDN3	strict	7	72822512	-111	AGGTTTTGGAGAGCGCGGTTTC	-47	ACCCTAAACTAAAACCGATACG	(1)
COL4A1	strict	13	109757459	-117	GCGTCGTTCGCGTATCGTC	2	TTCCAACGCTACGCACCG	(2)
CTSL1	strict	9	89530800	-182	GATTTTATTTTGCGTCGTTTC	-40	ACGCTACGATTAACTATACCG	(1)
CXCR4	relaxed	2	136592195	-290	GAGAGACGCGTTTTTAGTTC	-14	AAAATTTCTAACCGCGACCG	this study
CYP26C1	relaxed	10	94811011	-619	TTTTTTCGTGAGCGCGTC	-544	CCGATTCACACAACGTAACG	(5)
CYR61	strict	1	85819048	-155	GGCGTTTGGTAGTAGTTCGC	-10	CTCGAAAACGCTCTCGCTCG	this study
DAZL	relaxed	3	16622010	-103	GGTATCGGATTTGCGTATAC	-29	AAAAACTACGAAAAACGACG	(2)
DDX43	strict	6	74161192	-91	TATTTTTACGGTTTAGAAAATC	-16	CACTTCGCACTAATTTCACG	this study
DMRTB1	strict	1	53697660	-89	TTCGGGGATATATTGCGAGTC	-2	AACGCTAAAATAAACCGCG	(2)
DNAJC15 (DNAJD1)	strict	13	42495362	-231	GTTGGTGTGATTTATTCGTTTC	-149	CAAAAAAAAAATTATAACCGAATACG	(2)
EID1 (CRI1)	strict	15	46957582	-130	GGAAACGTAGTTTAAAAGGCGAC	-45	CCGCCTCCTACTTAACGCCG	(2)
ERBB2IP	strict	5	65258140	-248	TCGAGGTTCGTCGAGCGTTC	-93	GAAAAACCAACTCCGCGCG	(2)
F2R	strict	5	76047542	-187	TTAGGAGGGTCGAGACGGTAC	-96	TCCTCTAAACACCGTTAATTCG	(1)
FADS1	strict	11	61340886	-234	GTTCGTTTGACGTTAGGAAGTC	-34	GCCCAAAACCAACCGCCTACG	(1)
FAM115A (KIAA0738)	strict	7	143230105	-85	TTAAGTTTTGTAGTTTCGAGTTC	96	AACCCAAACCTCGATCACCG	this study
FBLN2	strict	3	13565625	-82	TTGGGTTTTTGTTCGCGTGC	164	ACGAACACTCCACGCCCG	(2)
FBN2	strict	5	127901634	-412	GGGAATTCGTCGAGTTTTGC	-245	AACCGACAACCCCGAACG	(2)
FERMT2 (PLEKHC1)	strict	14	52487460	-182	AGGGTAGTTTTGCGGGCGGC	-29	GTCCGATTCCTCGACTAACG	this study
FLNC	strict	7	128257719	10	GAGAGAGAGTTAGAGAGCGGTCGAGC	107	GACCACGAAACTCGCTACGCTACG	(3)
FOXO1A	strict	13	40138734	-123	CGTATGTTTATTGGTCGCGC	-33	GACTTACGAAATCTACCGCCG	(2)
FSD1	strict	19	4255691	-159	AGGGTTTTGGGCGAGGTTAGC	-25	AAACTACCTTTACCGCGACCG	(1)
FST	strict	5	52812352	-172	TTTAGATTTAAAGCGCGGTTGC	-47	ACGAATAACTCGAACGAACG	(1)
FSTL1	strict	3	121652515	-226	TCGAAGGGGCGTCGGAC	-102	CTACTACAACGACCCCGCG	(2)
FYN	strict	6	112301320	-228	TCGTACGTATTTTGGGATGTTC	-141	CTACGAACCGCAACCATTAACG	(1)
GREM1	strict	15	30797497	-37	CGTCGGTATTTAAACGGGAGAC	63	GAAACTCGACGCGAAATCAACG	(1)
GRHL1 (TFCP2L2)	strict	2	10009273	-205	CGTAATTTCGCGGAACGC	-88	GAAACTAAAAAACCGATCGCG	(2)
HAND1	strict	5	153838017	-259	AATAGTTTAGGGCGTTGGTC	-93	AATTTTACGTCAACCCG	(3)
HAND2	strict	4	174687953	-93	GTCGAGAGTTCGAGGCGTC	-21	ACTACATCTTTAAAACCGCTCG	this study
HDGFL1	strict	6	22677657	-158	TTATTATAAGTATAATCGTTATTC	-89	ACCCGTTAAACCCACCCTCG	this study
HES4	strict	1	925333	-85	TGTGGGAAAGAATGCGGAGTC	-6	GAATCCCGACTCCAAACCCG	this study
HOXB1	relaxed	17	43963271	-94	GTTATGGATTCGAGTTTTAGC	-17	CGTCAAAACCGCAAAAAAATCG	this study
HRASLS	strict	3	194441612	-257	GGGTGTATTTATGATGGGTGTATTC	-95	CAACGCCTACGATCAAAACG	(3)
HS3ST2	strict	16	22733361	-190	CGGTTGTTCGGAGTTTTATC	-38	GTAACGCTACCACGACCACG	(4)
HSPA1A	strict	6	31891316	-153	TGGGGGGGTAGGACGGGAGGC	-27	ACTAACCGTTATCCGAACCG	this study
IGFBP3	strict	7	45927396	-40	TTTCGGTTTTTATATAGCGGTC	23	AAAAAACGACTAATCCTCAACG	(1)
IGFBP7	strict	4	57671296	-195	GGGTCGGTTACGTCGGGTGTTC	-18	GACAAAAACGCGAATAAAACCG	(1)
IL6R	strict	1	152644293	-117	TTTTTATAGCGTAATTTCGTTTAC	78	AACCGAAACGAATAACGCAACA	(1)
INSL6	strict	9	5175618	-122	AGTTTTGGCGACGTTTTTAC	-59	ACTCCCTATCTACGCCTACG	this study
IRS2	strict	13	109236915	-127	GCGGCGTTAATGCGAGGTAGC	-29	TAAATAACACATCGCGCACCG	(1)
KCNA1	strict	12	4889334	-75	TACGTTCGGGTGGGTTAATC	-7	GCTCGATCCATTTCTAAACG	this study
KCTD12	strict	13	76358526	-225	GCGGGTGGGAGTTCGGGC	-19	CGCTCCAAACGAATACCG	this study
KHDC1 (C6orf148)	relaxed	6	74029640	-122	GTTGGGGTTTTTTGCGCGTC	1	ATAACGACGACCCCGCCG	(2)
KISS1R (GPR54)	strict	19	868358	-55	TTATAAACGTTCGGTCGTAGC	92	CAAAATTACGCCTAACACCG	(1)
LAMA1	strict	18	7107813	-333	GGATTGTAGGGTCGCGGC	-139	TAAATCCCGACGACACGCG	(2)
LAYN (LOC143903)	strict	11	110916443	-315	TTTTGGATGTTATTCGCGC	-198	CCAACACGAAAAACGACG	(2)
LOX	strict	5	121441853	-94	GAATAAATAGTTGAGGGGCGGTC	11	GCGACAATCCCGAAAAACG	(3)
MGC42367 (C2orf55)	strict	2	98919110	-193	ATCGTTTTTTCGTTTTTCGC	-46	GCCGCTCAACTCCCCTCG	this study
MLF1	strict	3	159771678	-118	GGGTAGCGGCGTATTGTTTTTC	-16	CTCACTCGCCGCGACGCAAACG	(1)
MLH1	strict	3	37009983	-175	TTTTAGGTAGCGGGTAGTAGTC	-70	GCCATCCAACCCCACCCTTCAACG	this study
MSH4	relaxed	1	76035218	-107	GTTGAGTTTGTTTGCGTTTGC	-39	CAACTACAAAAACTACGCCG	this study
MSX1	strict	4	4912300	-171	CGTCGTTTGGGTTTTGTTTTGC	-11	CCGACTCGCGAACCCTACCG	(1)
MTSS1	strict	8	125809840	-598	TATTTTATTGTAGGATACAGTTTTC	-484	GAAAAAACTACTACCGCTACTACG	this study
MTSS1	strict	8	125809840	-394	AGCGGCGGTGTATTTTTC	-248	ACAAACGACGCTAAACCG	this study
MTSS1	strict	8	125809840	-130	GAGAGCGACGTTTTCGTTTGGC	-32	CGCCTCCTTTTCACTCCTACG	(1)
MX1	strict	21	41720024	-178	GGGTTCGGGTTCGAGAATTTGC	-21	TTCGCCTCTTTCACCCCG	(1)
NAP1L1	strict	12	74764717	-238	AGAGGAGTTTAAGCGCGGC	-94	TTATAATCTCCCAACAACGCG	(2)
NEFL	strict	8	24870043	-112	GTTTTGGTTGTAGTAGCGC	-37	ACCCCTATTTATACGCCG	(5)
NMES1 (C15orf48)	relaxed	15	43510055	-191	GGTAGGTAAGGAAGATCGC	-22	CCGAATAAACCGAACCAACG	this study
NPY	strict	7	24290334	-159	TTTTAAGTCGATATTCGTGC	-45	ATAAAACTTCCTCGCCG	(5)
NT5E	strict	6	86216528	-183	AGTCGATAGTCGCGTTAGGGTC	-36	GAACAACTAAAACCGAAACTCG	(1)
OXT	strict	20	3000266	-171	TAACGCGGTGATTTGATTTC	-13	TAACTAATAACGATCTCTCCG	this study
PAX6	strict	11	31789455	-74	AGGGAGTATTTAATCGGTTGGC	68	CTCCTACGCCTCAAACCAAAACG	(1)
PCDHGC4	relaxed	5	140844925	-161	TTATTAGTAAAAACGGCGC	-12	AAACATTACTACCGCCCG	(5)
PLAGL1	strict	6	144371246	-195	GTTCGGGTTTATTGCGTTAGC	-47	AACCCCTAACGAAAACGTCACG	(1)
PLAU	strict	10	75340941	-177	TTTGTGAGCGTTGCGGAAGTAC	-51	ACGATCTCCGCACTATACTACG	(1)
PPIC	strict	5	122400324	-162	GTTTTTCGTATTCGTTTAAGGC	-33	AAAATAAAAATCGAACAATCCG	(1)
PPP1R14A	strict	19	43439012	-352	GCGGTGAGTCGAGATCGC	-169	CGAAAACGCCTACGCCG	(2)
PRLHR	relaxed	10	120345150	-121	GTATCGAGTATGGTAGAGCGC	48	CTCGATAATCCTCTACCCACG	this study

Supplemental Table 1 List of primers (continued)

gene symbol	CpG island	chromosome	TSS (NCBI)	position	forward primer sequence	position	reverse primer sequence	reference
Primers for MSP (primers for methylated DNA)								
PYCARD	strict	16	31121752	-186	CGGGGAATCGCGGAGGTTTC	-36	AATAAAACCCGAAAAAAAACCG	(1)
RAB34	strict	17	24069013	-85	TGGCGAGGGCGGGTAGC	40	AAACCTCGAATCCCACTCCG	(2)
RBP4	strict	10	95350983	-136	TTCGGGTTTCGGTGAGTTAGGGC	-36	CCGCTACTTTATAACGCCG	(1)
RGC32 (C13orf15)	strict	13	40929712	-217	ATCGGGGTTTCGGCGATTTTTC	-33	CCGCGCCCGCCCTACCACCG	this study
RGS2	strict	1	191044794	-184	ACGTTAGTAGCGTTTCGGTTTC	-37	GTCGCAACATTTATAAAACCTCG	(1)
RIF1	strict	2	151974674	-202	ATTTCGGAAGACGTTCGGATC	-40	CAACTCTCCAAACTCCGCCG	(2)
RORA	strict	15	59308794	-213	GGTTGGAGAAGTTTTCGTTAGC	-111	GACGAACGAACAAACAAAAACG	(1)
SCRN1	strict	7	29995902	-106	GAGGGTGGGTTCGCGGTTAC	-14	CTACAATAACGAAAACGACCG	(1)
SLC25A4	strict	4	186301392	-225	TACGGTGTTTTTTGGGTTCGGC	-79	CGCCGCGCATTAACTAAACAAATACG	this study
SNAI1	strict	20	48032934	-299	AGAGGTTTCGTTTCGTTC	-201	CGTAACGATAAAAACCCG	this study
SFRP2	strict	4	154929678	-213	AAATTTTAGGGCGGGCGAGC	4	CCGAAAAAACAAAATAAACCG	this study
SNAI1	strict	20	48032934	-155	ATTTGTTCGGGGAGTGGTTTTC	-91	AAAACGAAACCTTATCTACCACG	(1)
SPAG6	strict	10	22674405	-198	GGTAGTGTAGGGATATTCGAC	-62	ACGTAACGTCACGACCG	(5)
TBX3	strict	12	113606352	-98	TTGGTTCGAAAGCGTTAAAGAG	-22	ACCGAACGTCTACTCGACGACT	(1)
TFAP2C	strict	20	54637765	-146	GCGTTGCGTTAGGTTCGGGTGC	40	CGCGAATATCAAAACCGCTCCG	(1)
TGFBR2	strict	3	30622998	-87	GTAGTTGAAAGTCGGTTAAAGTTTTC	-26	CGACGTCCAACCCCTAACTCTCTCG	(6)
TGFBR2	strict	3	30622998	135	GTATTCGTTCGGGGATAGGAGTC	255	GAACCGACAACGCAAATATACG	(6)
THBD	strict	20	22978301	-849	CGTTCGTTTTTATTCGGCGTC	-750	GCCAAACCCCATCTCATCG	(3)
TNFSF9	strict	19	6482037	-212	GTCGAGTTTGGAAGGTCGGAAAC	-65	AAAAAACCACGCCCCTCCG	(1)
TPM2	strict	9	35680053	-262	GTACGTCGGTTTTTGCGTTC	-97	CGACTAAAAAAACCCCGACG	(2)
TSPYL6	relaxed	2	54336848	-92	CGAGATTGAGGAGTGAGTGTCGC	-14	CCTCGCCCATTTACGCCG	(2)
TUBA1A (TUBA3)	strict	12	47869128	-234	CGGTCGATTGTTTTTGTAC	-20	CGACACATAAACGAATACG	this study
TUBB6	strict	18	12298257	-14	TAATTGCGGGTCGGTTGC	-142	CTACTACAAACCGAACCGCG	(2)
TUSC3	strict	8	15442101	-75	AGTTTCGGGCGGGAGCGTAC	85	TACGAAAAACCCGAACCGCG	(2)
ULBP2	relaxed	6	150304829	-213	TGAGTTTGTCGTGGAAGGAATC	-89	GTCAAACGAATCATAACGTCACG	(1)
UNC5C	strict	4	96689185	-197	TTAGATTTCGGCGTGCGGC	-71	ACTAACGTCTCCCGCGAACG	(2)
WIF1	strict	12	63801356	-131	CGTTCGCGTTTTATTTTTTGC	-27	AACGCGTCGCCTCCCGACCTAA	(1)
WNT4	strict	1	22342106	-79	GCGTTGATAGTTTGGTTCGC	-26	CTCTACCTCCGTATACCTACCG	this study
ZNF177	strict	19	9334696	-119	GTAGGAGTATTTGCGATGTTTC	-12	AAAATAACGAAACGACGAACG	(1)
ZNF559	relaxed	19	9295928	-147	GGTTCGGGAATTCGAGGTTTC	-43	TACCTCAAACGCCAACGAAAACG	(1)
Primers for bisulfite sequencing								
C13orf21 (SERP2)	strict	13	43845978	-45	GGAAAGGGTTTTTTGAGATGAGA	146	AAATACTCCCACCTACAAAAATTC	this study
FLNC	strict	7	128257719	-1	GTTTTGGAGGGAGAGAGAGTTAGAG	308	TATATTCTACTAAATCTTCTTCCAC	this study
FSD1	relaxed	19	4255691	-543	GTTGGATTTAGATATTTTTAGTTT	-168	CCCAAAACCCTCACATCCAA	this study
HAND1	strict	5	153838017	-651	TTTGTTTGAGGTTGGGTTAGAATTG	-442	ATTCCAACAATTCCCAATCCC	this study
IGF2	strict	11	2127409	-5928	AGATGGGTAGGAAGTGGGGAGTT	-6318	AAAACCTAAAACTAAAATCCAAAC	this study
STX5	strict	11	62356136	-240	AGAAATTTTATTTTTTGGAGGTTG	-507	AAAATAAAAATAAACTCAAAAACC	this study
NKX2-8	strict	14	36121537	-1547	TGGAAGTATTTGTTTTAGTTAAGA	-1771	CAACCAAATCATTTCAATTTAATC	this study
Primers for copy number analysis of DNA								
DMRTB1	strict	1	53697660	126	AGGGACACGCGGGCAAAT	186	ATGATCTTCTGGCGCTCGGAG	this study
CYP26C1	relaxed	10	94811011	-190	CTGCAGTCTTTCACCGTCCGTC	-96	GCAGTGCTCACCTGTTCCGTC	this study
HOXB1	relaxed	17	43963271	-182	CATTGGCCTGGGAGAGATCACAT	-56	CCCTCTTGCCCTACAACCTTT	this study
DNAJC15 (DNAJD1)	strict	13	42495362	-137	GGGGTGGAGTAAGCAAAT	-57	GCCTTTCTTCCCACTCTCAACT	this study
COL4A1	strict	13	109757459	321	GTCCCTGTAGGCTACGATCGC	386	CCGGAGGAATTCCTTAACTC	this study
FSTL1	strict	3	121652515	-58	GGGGAAGGAGAGGTCTTAAGG	17	CGAGCTGTAAGCGGAGGT	this study
NPY	strict	7	24290334	-100	GGGAAGTGGCGGGTGGGAGTCA	5	GAGGGGTGAGAGCCAGCGGATG	this study
HAND1	strict	5	153838017	-584	TCCAGAAAGGGCCGATGACTA	-517	AAGACAGGATAGGCCGCTAAC	this study
FSD1	strict	19	4255691	-448	TTCAGTTGTGACATAGGGACA	-341	CAGGTTATCCGTTGCTACT	this study
ANXA5	strict	4	122837626	-874	GGCCACGCTTCTGTCTACCACA	-794	CAAACGCGAAGGAGTCAAGA	this study
MTSS1	strict	8	125809840	-614	ACTTTATCGAACTCGGCATCC	-507	TTCTGAGAAGACGCCCATTC	this study
BNIP3	strict	10	133645425	805	CCGTGCAGCACTCAGTCGT	869	GATGGTCTTGCGAATCTAGC	this study
PAX6	strict	11	31789455	239	CCCTCACCCACACTCTTTATC	350	TTTTCTCCACGGATGTTG	this study
TBX3	strict	12	113606352	-196	CGTGCTGCGACGTTACAGTT	-122	TGTTGCTGCATAGGCGTGGTT	this study
TFAP2C	strict	20	54637765	-361	CGTCTTTTGGAGGAACGAGTGAA	-281	GTAAACACACCTGAGATTGGC	this study
HRASLS	strict	3	194441612	-223	TGGGCTCAACAAAACCGATTA	-165	CCGCAGCCAACGTTTAGG	this study
TUBB6	strict	18	12298257	-20	CGCAGTTGCCGCTGTCGTC	98	GCCCACCTTGGTGCCGATCTG	this study
ZNF559	relaxed	19	9295928	-452	CAATGGGAAAATTCTAGGA	-361	TTTGTTGAAAACGAAAGCATA	this study
TGFBR2	strict	3	30622998	-76	TCGGCCAAAGCTCTCGGAG	-21	TCGACGTCCAGCCCCTAGCTC	this study
MLH1	strict	3	37009983	-177	CCTTCTAGGTAGCGGGCAGTA	-88	GCGGCAGCTATTGATTGGACA	this study
SNAI1	strict	20	48032934	76	GCGCTCTTTCCTCGTCAG	124	AGTCCTGCAGCTCGCTGTAG	this study

(1) Yamashita, S. *et al.* (2006) Cancer Sci, 97, 64-71.
(2) Moriguchi, K. *et al.* (2007) Cancer Lett, 249, 178-187.
(3) Kaneda, A. *et al.* (2002) Cancer Res, 62, 6645-6650.
(4) Abe, M. *et al.* (2008) Oncology, 74, 50-60.
(5) Miyamoto, K *et al.* (2003) Oncogene, 22, 274-280.
(6) Yamashita, S. et al. (2008) Cancer Res, 68, 2112-2121.