

Supplementary table 1. Official full names of gene symbols (provided by HUGO gene nomenclature committee)

ADAM12	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 5
ADAMTS5	A kinase (PRKA) anchor protein 12
ADHFE1	ADAM metallopeptidase domain 12
AKAP12	alcohol dehydrogenase, iron containing, 1
BOLL	bol, boule-like (Drosophila)
CHL1	cell adhesion molecule with homology to L1CAM (close homolog of L1)
CSMD3	CUB and Sushi multiple domains 3
ECH1	EGF-containing fibulin-like extracellular matrix protein 1
ECHDC3	enoyl CoA hydratase 1, peroxisomal
EFEMP1	enoyl CoA hydratase domain containing 3
EYA4	eyes absent homolog 4 (Drosophila)
FOXD2	forkhead box D2
FRZB	frizzled-related protein
GAS7	GDNF family receptor alpha 1
GDNF	glial cell derived neurotrophic factor
GFRA1	growth arrest specific 7
GUCY1A2	guanylate cyclase 1, soluble, alpha 2
HAND2	heart and neural crest derivatives expressed 2
HMGCL	3-hydroxymethyl-3-methylglutaryl-CoA lyase
HOXA5	homeobox A5
IL10RA	interleukin 10 receptor, alpha
JPH3	junctionophilin 3
KCNQ5	laminin, alpha 1
LAMA1	maelstrom homolog (Drosophila)
MAEL	mal, T-cell differentiation protein
MAL	matrix metallopeptidase 2
MLH1	mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli)
MMP2	myotubularin 1
MTM1	NDRG family member 2
NDRG2	NEL-like 1 (chicken)
NELL1	neuropeptide Y
NPY	orthopedia homeobox
OTP	potassium voltage-gated channel, KQT-like subfamily, member 5
PPP1R3C	PR domain containing 14
PRDM14	protein phosphatase 1, regulatory (inhibitor) subunit 3C
SCNN1B	SFT2 domain containing 3
SFT2D3	slit homolog 2 (Drosophila)
SLC6A15	slit homolog 3 (Drosophila)

SLIT2	sodium channel, nonvoltage-gated 1, beta
SLIT3	solute carrier family 6 (neutral amino acid transporter), member 15
SST	somatostatin
ST3GAL4	ST3 beta-galactoside alpha-2,3-sialyltransferase 4
TAC1	tachykinin, precursor 1
TCEAL2	tissue factor pathway inhibitor 2
TFPI2	transcription elongation factor A (SII)-like 2
TWIST1	twist homolog 1 (Drosophila)
UCHL1	ubiquitin carboxyl-terminal esterase L1
WT1	Wilms tumor 1
ZFHX1B	zinc finger homeobox protein 1b
ZNF447	zinc finger protein 447
ZNF677	zinc finger protein 677

Supplementary table 2. Primers for pyrosequencing analysis

Genes	Forward primer	Reverse primer	Sequencing primer
<i>ADHFE1</i>	GATTGGTTTGAGGTTTAGATAGGT	CTTAAAATCCTCTTCCCTCCT	TTGAGGTTTAGATAGGTGA
<i>BOLL</i>	GGTTGAATGGTAGGTTTTGATTAA	TCCCCCTCTCCTCCACTTAAA	GAGTTTGATTTTAGAATTTT
<i>SLC6A15</i>	TTTGGGGGAATAGGTAGGAAAA	CAAAACAAATTCCTCCAACCATAC	AAATTCCTCCAACCATAC
<i>ADAMTS5</i>	TGGGGGAAGTTTTTTTTTAAGAG	AACCCACTTCCTTTCTTATTTTA	TTGTTATTGTAGGATGGTAT
<i>TFPI2</i>	AAAGTTTGGGAGGTAGGTTTAAT	AAACCTAAAAATAACTAATTCAT	AAAAATAACTAATTCATACA
<i>EYA4</i>	GGGTTGTTTTATAGAAGTAGGTG	ACCCACTCCCTTTTTATTTAACC	TACCTATTATCATAATTTAC
<i>NPY</i>	GTAGATATTTGGGTTTTGGTGTTG	ACTTAAAAAACCCACCCACACC	GGTTTTGGTGTGTTTAG
<i>TWIST1</i>	TTTTTGGGTTGGTATTGTTAGTTG	CTAAACCCTCCTTCCCCTCTA	TGGTATTGTTAGTTGTTAGG
<i>LAMA1</i>	GGGTAGGTAGAGTTTGGGTGGTTT	ATCCCCAACCAAAACCCA	GTTTAGTTTTTGGTAGG
<i>GAS7</i>	TGTTATTAGGTTGTTGGGTTTAGG	CCTCCCAAAAAACCTATCACTA	AAAAAAAAAACTCCCACT
<i>SFT2D3</i>	GGTTTGGGAATAGATTAGGATTGA	CAACACCCTCAACCTACTTCTCTA	CTAACACATCCTTAACTCC
<i>MAEL</i>	TGTAAATTTGAGGGTAAGGAAGAT	AACAACCTAAAATAAAAAATTC	TTTTGTATTGTAAAA

Supplementary table 3. Distribution of aberrant methylation

	Hypermethylation	Hypomethylation	Total
Promoter CpG Y (n=9792) ^a	621	251	872
Promoter CpG N (n=4453) ^b	37	964	1001
N promoter CpG Y (n=9588) ^c	751	112	863
N promoter CpG N (n=3088) ^d	33	717	750
No information about TSS* (n=622)	109	27	136
Total (n=27543)	1551	2071	3622

^a CpG sites are located in promoter region and in CpG islands. ^b CpG sites are located in promoter region but not in CpG islands. ^c CpG sites are located not in promoter region but in CpG islands. ^d CpG sites are located not in promoter region and not in CpG islands.

* transcription start site

Supplementary table 4. Comparison of promoter methylation status with mRNA expression array results

	Promoter methylation status	
	Hypermethylation (N=621)	Hypomethylation (N=251)
mRNA expression (fold change)		
< -0.5	57	21
-0.5 ~ 0.5	413	180
> 0.5	31	24
Not checked	120	26

(p=0.089)