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Supplemental Material to:

Francisco Sánchez-Vega, Valer Gotea, Hanna M Petrykowska, Gennady Margolin, Thomas C Krivak, Julie A DeLoia, Daphne W Bell, and Laura Elnitski

Recurrent patterns of DNA methylation in the ZNF154, CASP8, and VHL promoters across a wide spectrum of human solid epithelial tumors and cancer cell lines

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Recurrent patterns of DNA methylation in the *ZNF154*, *CASP8* and *VHL* promoters across a wide spectrum of human solid epithelial tumors and cancer cell lines

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Authors
Francisco Sánchez-Vega[1], Valer Gotea[1], Hanna M. Petrykowska[1], Gennady Margolin[1], Thomas C. Krivak[2], Julie A. DeLoia[3], Daphne W. Bell[4] and Laura Elnitski[1]

[1]Genome Technology Branch and [4] Cancer Genetics Branch, National Human Genome Research Institute, National Institutes of Health, Bethesda, Maryland, [2] Department of Obstetrics, Gynecology and Reproductive Sciences, University of Pittsburgh Medical School, Pittsburgh, Pennsylvania, and [3] School of Public Health and Health Services, The George Washington University, Washington D.C., United States of America.

Supplemental material

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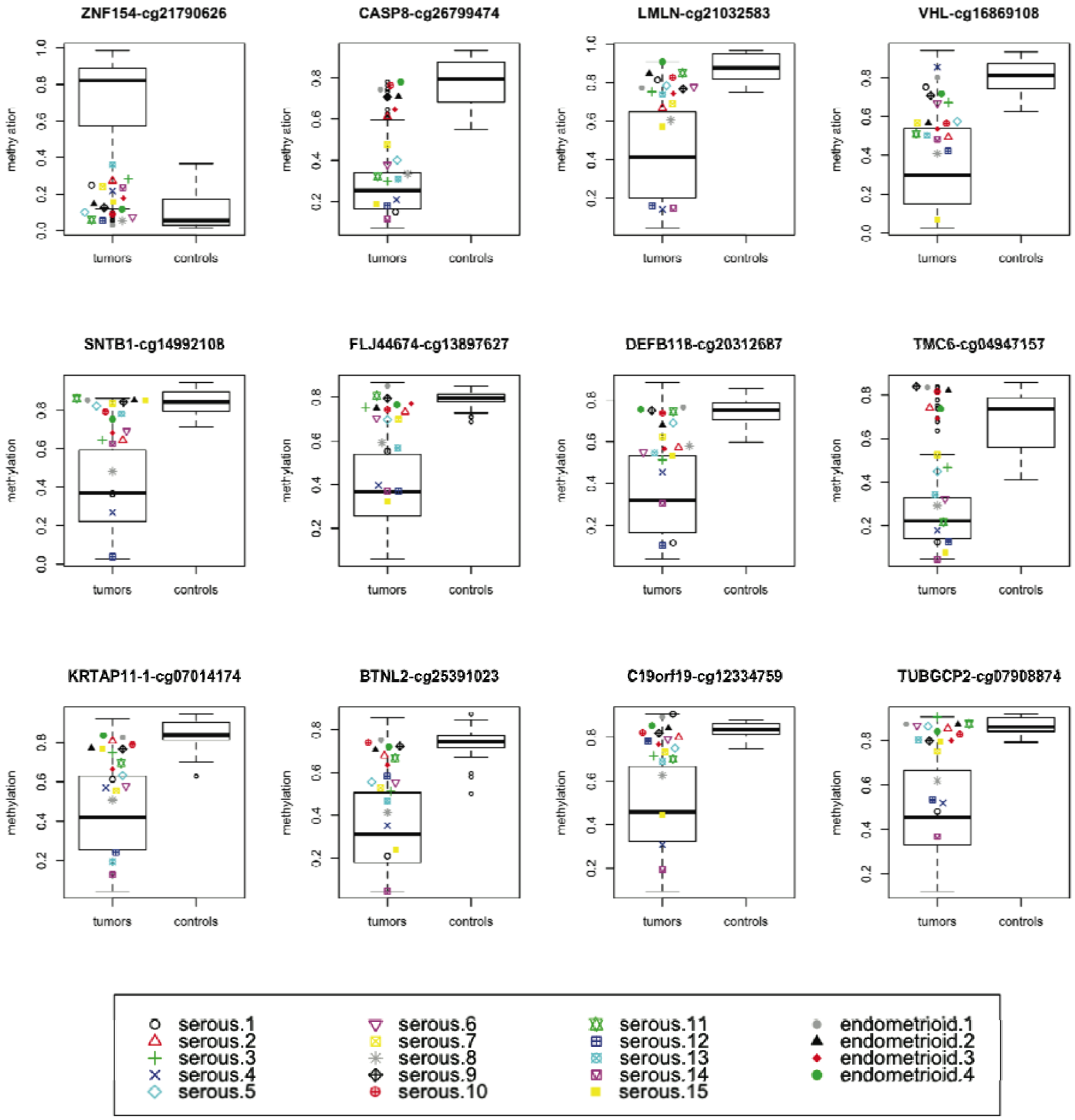

Figure S1. Methylation levels at selected loci for ovarian and endometrial cancer samples with relatively low levels of methylation at cg2179**0626-*ZNF154*.** The sample labeled as 'endometrioid.1' is the only one that corresponds to an endometrial cancer sample; all the rest correspond to ovarian tumors (either from the serous or the endometrioid histopathological subtypes). The vertical axes show level of methylation (beta values). Points correspond to individual samples, and they are superimposed over boxplots computed over the tumor and control subsets of the full sample collection.

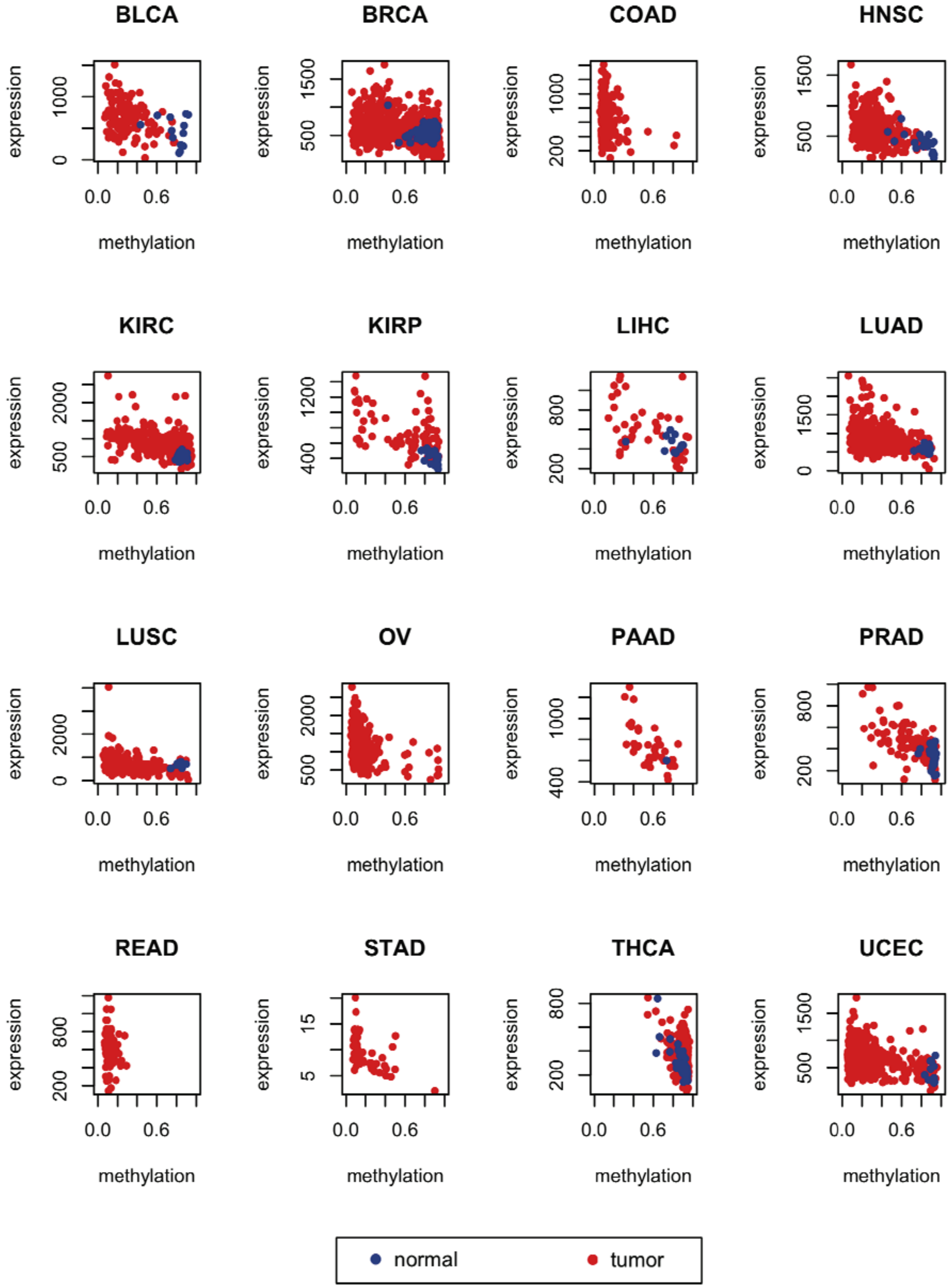

Figure S2. Expression of *CASP8* vs. methylation at probe cg2679**9474** in different cancer types from TCGA. RNA-Seq data was used for the STAD type and RNA-Seq V2 was used for all the other types (see "Materials and Methods" for details). Combined methylation and expression data was not available for any normal controls of the COAD, OV, READ and STAD types. Values of Spearman correlation, together with their associated levels of significance, are provided in Table 4.

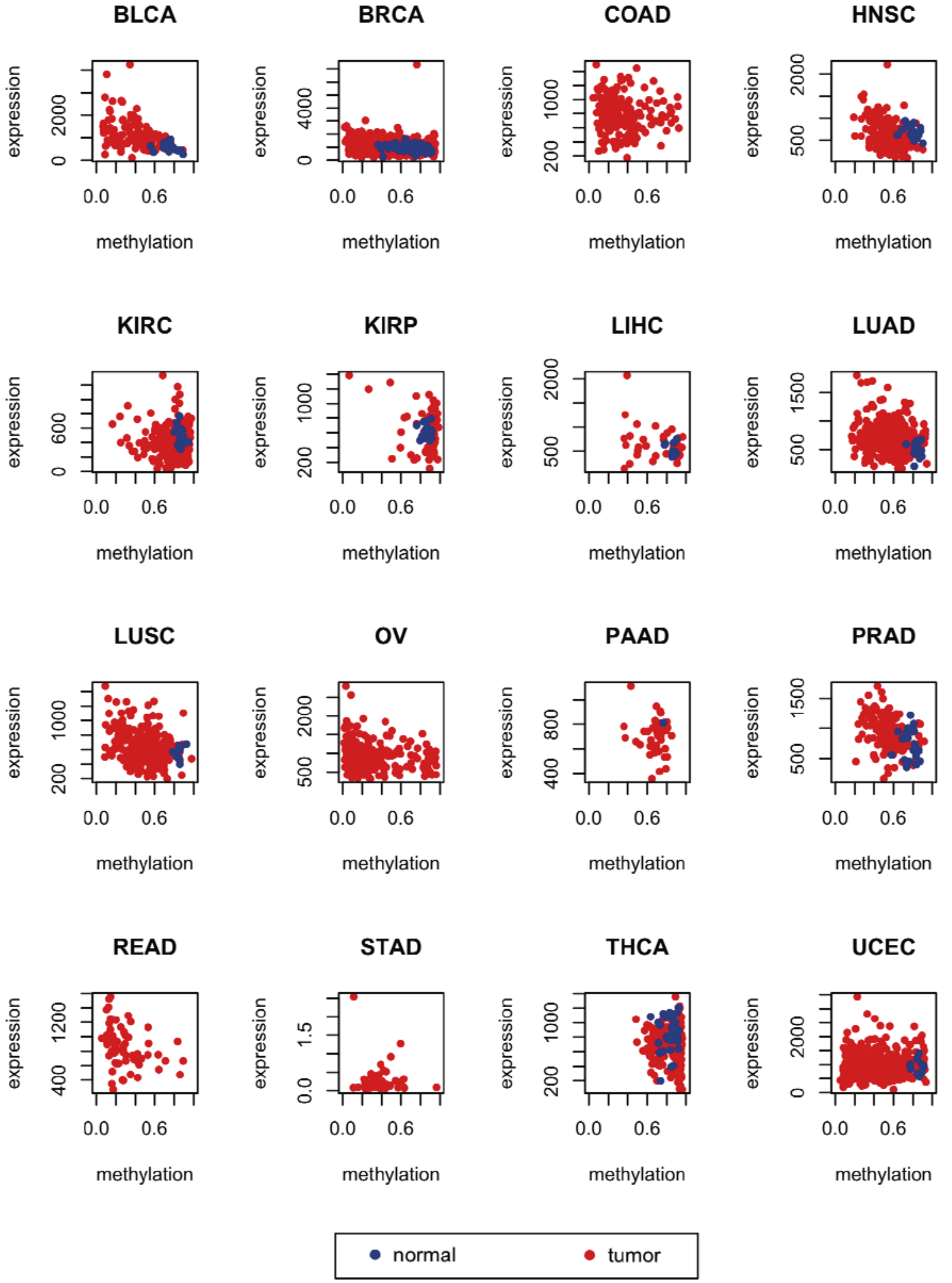

Figure S3. Expression of *VHL* vs. methylation at probe cg1686**9108** in different cancer types from TCGA. RNA-Seq data was used for the STAD type and RNA-Seq V2 was used for all the other types (see "Materials and Methods" for details). Combined methylation and expression data was not available for any normal controls of the COAD, OV, READ and STAD types. Values of Spearman correlation, together with their associated levels of significance, are provided in Table 4.

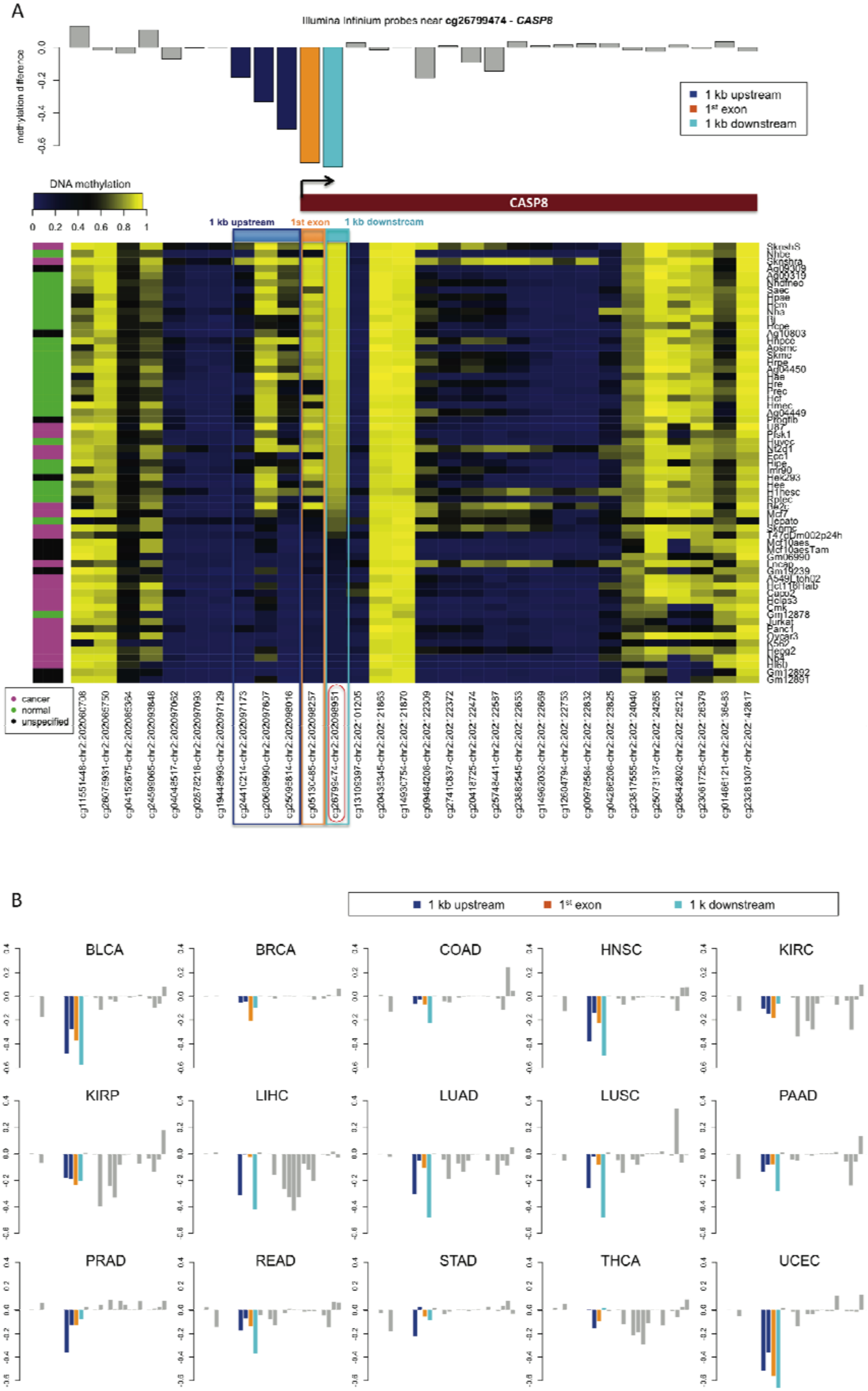
A
Illumina Infinium probes near cg26799474 - CASP8
methylation difference
0.0
-0.2
-0.4
-0.6
1 kb upstream
1st exon
1 kb downstream
DNA methylation
0 0.2 0.4 0.6 0.8 1
CASP8
1 kb upstream
1st exon
1 kb downstream
cancer
normal
unspecified
B
1 kb upstream
1st exon
1 k downstream
BLCA
BRCA
COAD
HNSC
KIRC
KIRP
LIHC
LUAD
LUSC
PAAD
PRAD
READ
STAD
THCA
UCEC
0.4
0.2
0.0
-0.2
-0.4
-0.6

Figure S4. Methylation near probe cg2679**9474** (highlighted in red), which is located near the promoter of gene *CASP8*. (**A**) Methylation levels in ENCODE cell lines. The heat map shows beta values for each pair of probe (columns) and cell line (rows). Rows are ordered according to decreasing values of methylation at cg2679**9474**, from top to bottom. The color side bar on the left shows cancer (magenta), normal (green) and unspecified (black) cell line annotations as provided by ENCODE. Probes located within 1 kb upstream from the TSS (blue), at the 1st exon (orange) and 1 kb downstream from the TSS (cyan) are highlighted. The bar plot above the heat map shows the difference in median methylation in cancer cell lines minus median methylation in normal cell lines for each individual probe. (**B**) Difference in median methylation in tumors vs. controls in different cancer types from TCGA. The color notation and the probe locations are the same as in the top panel. Positive values correspond to hypermethylation in tumors. Bars corresponding to probes that were masked as 'not available' (NA) in level 3 data from TCGA are shown as empty horizontal gaps.

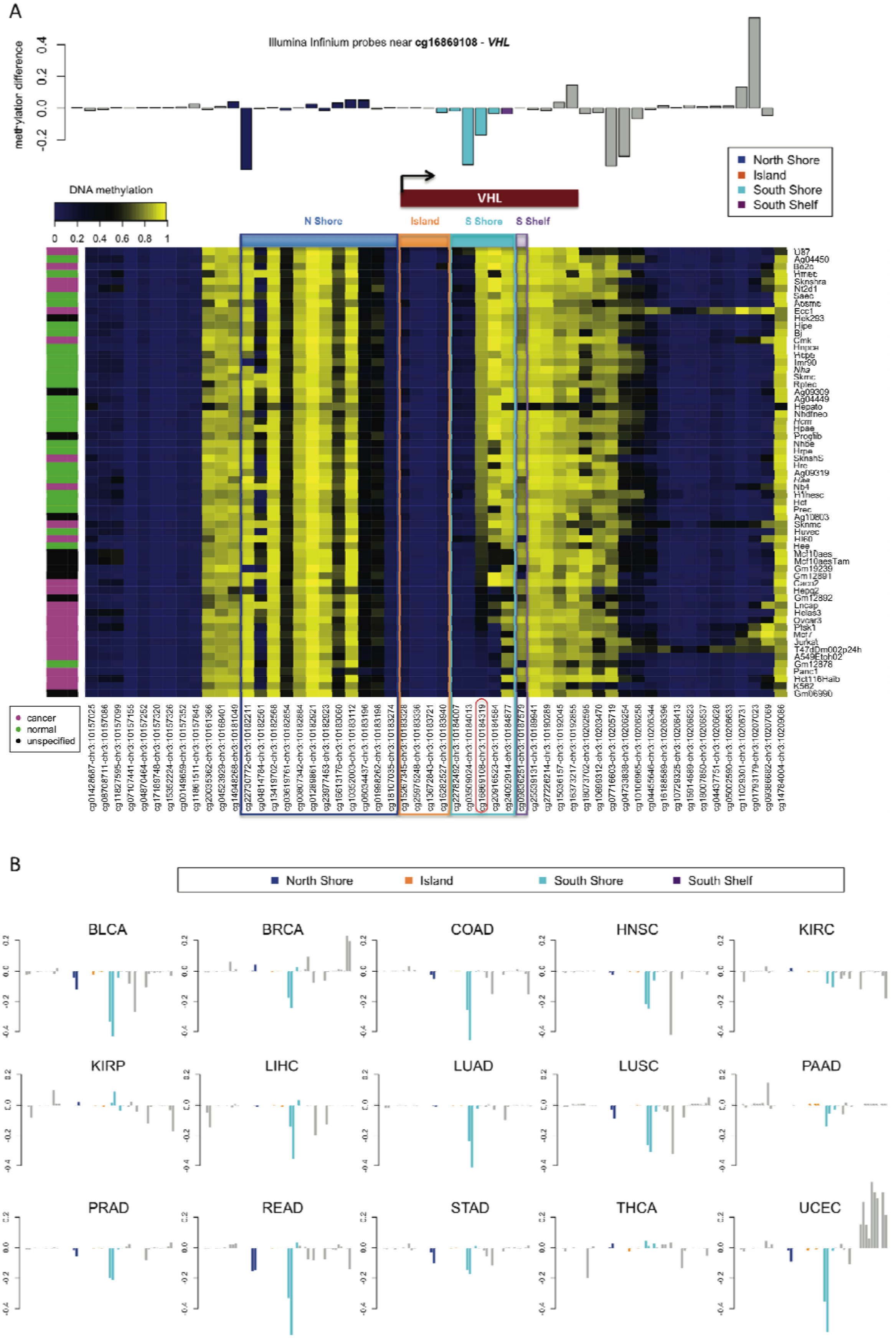
A
Illumina Infinium probes near cg16869108 - VHL
methylation difference
0.4
0.2
0.0
-0.2
North Shore
Island
South Shore
South Shelf
VHL
DNA methylation
0
0.2
0.4
0.6
0.8
1
N Shore
Island
S Shore
S Shelf
cancer
normal
unspecified
B
North Shore
Island
South Shore
South Shelf
BLCA
BRCA
COAD
HNSC
KIRC
KIRP
LIHC
LUAD
LUSC
PAAD
PRAD
READ
STAD
THCA
UCEC
0.2
0.0
-0.2
-0.4

Figure S5. Methylation near probe cg1686**9108** (highlighted in red), which is located in the south shore of a CpG island near the promoter of gene *VHL*. (**A**) Methylation levels in ENCODE cell lines. The heat map shows beta values for each pair of probe (columns) and cell line (rows). Rows are ordered according to decreasing values of methylation at cg1686**9108**, from top to bottom. The color side bar on the left shows cancer (magenta), normal (green) and unspecified (black) cell line annotations as provided by ENCODE. Probes located within the north shore (blue), island (orange), south shore (cyan) and south shelf (purple) of the CpG island are highlighted. The bar plot above the heat map shows the difference in median methylation in cancer cell lines minus median methylation in normal cell lines for each individual probe. (**B**) Difference in median methylation in tumors vs. controls in different cancer types from TCGA. The color notation and the probe locations are the same as in the top panel. Positive values correspond to hypermethylation in tumors. Bars corresponding to probes that were masked as 'not available' (NA) in level 3 data from TCGA are shown as empty horizontal gaps.

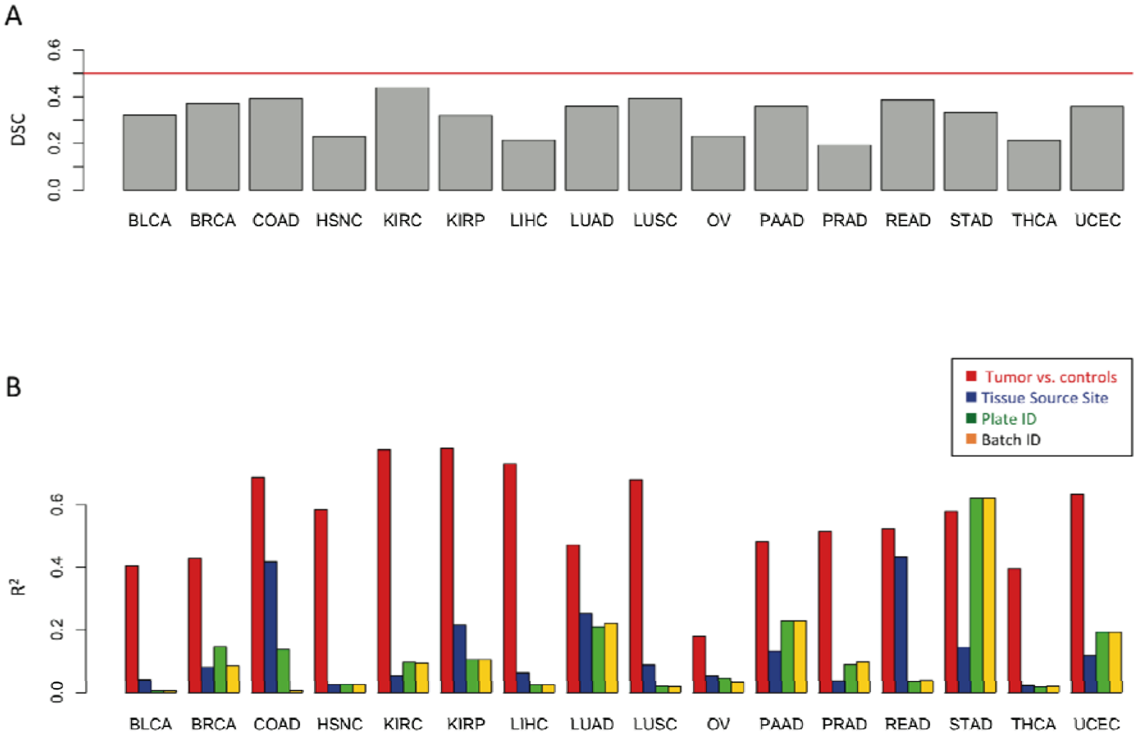

Figure S6. Analysis of batch effects on methylation data from TCGA. (a) DSC metric computed for each individual cancer type. (b) Percentage of variability of several labels explained by top five principal components (R^2) for each individual cancer type.

Table S1: ENCODE cell-lines used in methylation analysis.

cell	Description	Lineage	Tissue	Karyo
A549	epithelial cell line derived from a lung carcinoma tissue	endoderm	epithelium	cancer
AG04449	fetal buttock/thigh fibroblast	--	skin	normal
AG04450	fetal lung fibroblast	endoderm	lung	normal
AG09309	adult toe fibroblast	--	skin	--
AG09319	gum tissue fibroblasts	--	gingival	normal
AG10803	abdominal skin fibroblasts	--	skin	--
AoSMC	aortic smooth muscle cells	mesoderm	blood vessel	normal
BE2_C	neuroblastoma	ectoderm	brain	cancer
BJ	skin fibroblast	--	skin	normal
Caco-2	colorectal adenocarcinoma	endoderm	colon	cancer
CMK	acute megakaryocytic leukemia cells	mesoderm	blood	cancer
ECC-1	epithelial cell line derived from an endometrium adenocarcinoma	endoderm	luminal epithelium	cancer
GM06990	B-lymphocyte, lymphoblastoid	mesoderm	blood	--
GM12878	B-lymphocyte, lymphoblastoid	mesoderm	blood	normal
GM12891	B-lymphocyte, lymphoblastoid	mesoderm	blood	--
GM12892	B-lymphocyte, lymphoblastoid	mesoderm	blood	--
GM19239	B-lymphocyte, lymphoblastoid	mesoderm	blood	--
H1-hESC	embryonic stem cells	inner cell mass	embryonic stem cell	normal
HAEpiC	amniotic epithelial cells	--	epithelium	normal
HCF	cardiac fibroblasts	mesoderm	heart	normal
HCM	cardiac myocytes	mesoderm	heart	normal
HCPEpiC	choroid plexus epithelial cells	ectoderm	epithelium	normal
HCT-116	colorectal carcinoma	endoderm	colon	cancer
HEEpiC	esophageal epithelial cells	endoderm	epithelium	normal
HEK293	embryonic kidney	mesoderm	kidney	--
HeLa-S3	cervical carcinoma	ectoderm	cervix	cancer
Hepatocytes	primary hepatocytes	endoderm	liver	normal
HepG2	hepatocellular carcinoma	endoderm	liver	cancer
HIPEpiC	iris pigment epithelial cells	ectoderm	epithelium	normal
HL-60	promyelocytic leukemia cells	mesoderm	blood	cancer
HMEC	mammary epithelial cells	ectoderm	breast	normal
HNPCEpiC	non-pigment ciliary epithelial cells	--	epithelium	normal
HPAEpiC	pulmonary alveolar epithelial cells	--	epithelium	normal
HRE	renal epithelial cells	mesoderm	epithelium	normal
HRPEpiC	retinal pigment epithelial cells	ectoderm	epithelium	normal
HUVEC	umbilical vein endothelial cells	mesoderm	blood vessel	normal
IMR90	fetal lung fibroblasts	endoderm	lung	normal
Jurkat	T lymphoblastoid derived from an acute T cell leukemia	mesoderm	blood	cancer

K562	leukemia	mesoderm	blood	cancer
LNCaP	prostate adenocarcinoma	endoderm	prostate	cancer
MCF10A-Er-Src	mammary gland, non-tumorigenic epithelial	ectoderm	breast	--
MCF10A-Es-Tam	mammary gland, non-tumorigenic epithelial	ectoderm	breast	--
MCF-7	mammary gland, adenocarcinoma	ectoderm	breast	cancer
NB4	acute promyelocytic leukemia cell line	mesoderm	blood	cancer
NH-A	astrocytes	ectoderm	brain	normal
NHBE	bronchial epithelial cells	endoderm	epithelium	normal
NHDF-neo	neonatal dermal fibroblasts	mesoderm	skin	normal
NT2-D1	malignant pluripotent embryonal carcinoma	inner cell mass	testis	cancer
ovcar-3	ovarian adenocarcinoma	mesoderm	ovary	cancer
PANC-1	pancreatic carcinoma	endoderm	pancreas	cancer
PFSK-1	neuroectodermal cell line derived from a cerebral brain tumor	ectoderm	brain	cancer
PrEC	prostate epithelial cell line	epithelial	prostate	normal
ProgFib	fibroblasts, Hutchinson-Gilford progeria syndrome	--	skin	--
RPTEC	renal proximal tubule epithelial cells	--	epithelium	normal
SAEC	small airway epithelial cells	endoderm	epithelium	normal
SkMC	Skeletal Striated Muscle Cells	missing	muscle	normal
SK-N-MC	neuroepithelioma cell line derived from a metastatic supra-orbital human brain tumor	ectoderm	brain	cancer
SK-N-SH_RA	neuroblastoma	ectoderm	brain	cancer
SK-N-SH_S	human neuroblastoma	ectoderm	brain	cancer
T-47D	epithelial cell line derived from a mammary ductal carcinoma.	--	breast	cancer
U87	glioblastoma, astrocytoma	ectoderm	brain	cancer

Table S2: DNaseI hypersensitivity data for *ZNF154*, *CASP8* and *VHL*.

DNaseI hypersensitivity data for ZNF154 Cluster position: chr19:58,219,906-58,220,755

cellType	treatment	lab	karyotype	inCluster	signal
8988T	None	Duke	cancer	0	0
A549	None	AWG	cancer	0	0
Adult_CD4_Th0	None	UW	normal	1	34
AG04449	None	UW	normal	1	24
AG04450	None	UW	normal	1	27
AG09309	None	UW	NA	1	28
AG09319	None	UW	normal	1	37
AG10803	None	UW	NA	1	21
AoAF	None	UW	normal	1	34
AoSMC	serum_free_media	Duke	normal	1	27
BE2_C	None	UW	cancer	0	0
BJ	None	UW	normal	1	16
Caco-2	None	UW	cancer	1	15.5
CD20+	None	UW	normal	1	92
CD34+_Mobilized	None	UW	NA	1	157
Chorion	None	Duke	NA	1	17
CLL	None	Duke	cancer	1	59.5
CMK	None	UW	cancer	0	0
Fibrobl	None	Duke	normal	1	46
FibroP	None	Duke	normal	1	32
Gliobla	None	Duke	cancer	0	0
GM06990	None	UW	NA	0	0
GM12864	None	UW	NA	1	15.5
GM12865	None	UW	NA	1	50
GM12878	None	AWG	normal	1	23.5
GM12891	None	Duke	NA	1	55
GM12892	None	Duke	NA	1	25
GM18507	None	Duke	NA	1	13
GM19238	None	Duke	NA	1	34
GM19239	None	Duke	NA	1	21
GM19240	None	Duke	NA	1	25
H1-hESC	None	AWG	normal	1	45
H7-hESC	None	UW	NA	1	97
H9ES	None	Duke	NA	1	31.67
HA-h	None	UW	normal	1	44.5
HA-sp	None	UW	normal	1	15
HAc	None	UW	normal	1	76
HAEpiC	None	UW	normal	1	30
HBMEC	None	UW	normal	1	57

HCF	None	UW	normal	1	50.5
HCFaa	None	UW	normal	1	22
HCM	None	UW	normal	1	65
HConF	None	UW	NA	1	60
HCPEpiC	None	UW	normal	1	52
HCT-116	None	UW	cancer	0	0
HEEpiC	None	UW	normal	1	15
HeLa-S3	IFNa4h	Duke	cancer	0	0
HeLa-S3	None	AWG	cancer	0	0
Hepatocytes	None	Duke	normal	0	0
HepG2	None	AWG	cancer	0	0
HFF	None	UW	normal	1	66
HFF-Myc	None	UW	normal	1	27
HGF	None	UW	normal	1	21
HIPEpiC	None	UW	normal	1	49
HL-60	None	UW	cancer	0	0
HMEC	None	AWG	normal	1	39
HMF	None	UW	NA	1	28
HMVEC-dAd	None	UW	normal	0	0
HMVEC-dBl-Ad	None	UW	normal	1	35
HMVEC-dBl-Neo	None	UW	normal	1	32
HMVEC-dLy-Ad	None	UW	normal	0	0
HMVEC-dLy-Neo	None	UW	normal	1	19
HMVEC-dNeo	None	UW	normal	0	0
HMVEC-LBl	None	UW	normal	1	16
HMVEC-LLy	None	UW	normal	0	0
HNPCEpiC	None	UW	normal	1	42
HPAEC	None	UW	normal	1	12
HPAF	None	UW	normal	1	135
HPDE6-E6E7	None	Duke	normal	1	25.5
HPdLF	None	UW	normal	1	27
HPF	None	UW	normal	1	101
HRCEpiC	None	UW	normal	1	12
HRE	None	UW	normal	1	33
HRGEC	None	UW	normal	1	24
HRPEpiC	None	UW	normal	1	39.5
HSMM	None	AWG	normal	1	25
HSMMtube	None	AWG	normal	1	17.5
HSMM_emb	None	Duke	NA	1	12
HTR8svn	None	Duke	normal	1	23
Huh-7	None	Duke	cancer	0	0
Huh-7.5	None	Duke	cancer	0	0
HUVEC	None	AWG	normal	1	15
HVMF	None	UW	normal	1	18

iPS	None	Duke	NA	1	73
Ishikawa	4OHTAM_100nM_30m	Duke	NA	0	0
Ishikawa	Estradiol_100nM_1hr	Duke	NA	0	0
Jurkat	None	UW	cancer	0	0
K562	None	AWG	cancer	1	12
LNCaP	androgen	Duke	cancer	1	10
LNCaP	None	AWG	cancer	1	10
MCF-7	Hypoxia_LacAcid	Duke	cancer	0	0
MCF-7	None	AWG	cancer	0	0
Medullo	None	Duke	cancer	1	13
Melano	None	Duke	normal	1	56.5
Monocytes-CD14+_RO01746	None	UW	normal	0	0
Myometr	None	Duke	normal	0	0
NB4	None	UW	cancer	0	0
NH-A	None	UW	normal	1	49
NHDF-Ad	None	UW	normal	1	36.5
NHDF-neo	None	UW	normal	1	25
NHEK	None	AWG	normal	1	20
NHLF	None	UW	normal	1	63
NT2-D1	None	UW	cancer	1	69
Osteobl	None	Duke	normal	1	35
PANC-1	None	UW	cancer	0	0
PanIsletD	None	Duke	NA	1	30.5
PanIslets	None	Duke	normal	1	39.5
pHTE	None	Duke	NA	1	24
PrEC	None	UW	normal	0	0
ProgFib	None	Duke	NA	1	30
RPTEC	None	UW	normal	1	15
RWPE1	None	Duke	normal	0	0
SAEC	None	UW	normal	1	15
SK-N-MC	None	UW	cancer	0	0
SK-N-SH_RA	None	UW	cancer	0	0
SKMC	None	UW	normal	1	18
Stellate	None	Duke	normal	1	67
T-47D	None	Duke	cancer	0	0
Th1	None	AWG	NA	1	22.5
Th2	None	UW	NA	1	27
Urothelia	None	Duke	normal	1	22.5
Urothelia	UT189	Duke	normal	1	22.5
WERI-Rb-1	None	UW	cancer	0	0
WI-38	4OHTAM_20nM_72hr	UW	normal	1	17
WI-38	None	UW	normal	1	17

DNaseI hypersensitivity data for CASP8 Cluster position: chr2:202,098,006-202,098,2

cellType	treatment	lab	karyotype	inCluster	signal
8988T	None	Duke	cancer	1	31
A549	None	AWG	cancer	1	54
Adult_CD4_Th0	None	UW	normal	1	103
AG04449	None	UW	normal	0	0
AG04450	None	UW	normal	0	0
AG09309	None	UW	NA	0	0
AG09319	None	UW	normal	0	0
AG10803	None	UW	NA	0	0
AoAF	None	UW	normal	1	13
AoSMC	serum_free_media	Duke	normal	0	0
BE2_C	None	UW	cancer	1	12
BJ	None	UW	normal	0	0
Caco-2	None	UW	cancer	1	91
CD20+	None	UW	normal	1	88
CD34+_Mobilized	None	UW	NA	1	359
Chorion	None	Duke	NA	1	25
CLL	None	Duke	cancer	1	38
CMK	None	UW	cancer	1	208
Fibrobl	None	Duke	normal	0	0
FibroP	None	Duke	normal	1	13
Gliobla	None	Duke	cancer	1	44
GM06990	None	UW	NA	1	120
GM12864	None	UW	NA	1	241
GM12865	None	UW	NA	1	460
GM12878	None	AWG	normal	1	52
GM12891	None	Duke	NA	1	31
GM12892	None	Duke	NA	1	53
GM18507	None	Duke	NA	1	44
GM19238	None	Duke	NA	1	59
GM19239	None	Duke	NA	1	47
GM19240	None	Duke	NA	1	86
H1-hESC	None	AWG	normal	1	10
H7-hESC	None	UW	NA	1	102
H9ES	None	Duke	NA	1	14
HA-h	None	UW	normal	0	0
HA-sp	None	UW	normal	0	0
HAc	None	UW	normal	0	0
HAEpiC	None	UW	normal	1	55
HBMEC	None	UW	normal	0	0
HCF	None	UW	normal	1	12

HCFaa	None	UW	normal	1	14
HCM	None	UW	normal	1	22
HConF	None	UW	NA	0	0
HCPEpiC	None	UW	normal	1	27
HCT-116	None	UW	cancer	1	160
HEEpiC	None	UW	normal	1	50
HeLa-S3	IFNa4h	Duke	cancer	1	13
HeLa-S3	None	AWG	cancer	1	13
Hepatocytes	None	Duke	normal	1	9
HepG2	None	AWG	cancer	1	114
HFF	None	UW	normal	0	0
HFF-Myc	None	UW	normal	0	0
HGF	None	UW	normal	0	0
HIPEpiC	None	UW	normal	1	21
HL-60	None	UW	cancer	1	318
HMEC	None	AWG	normal	1	25
HMF	None	UW	NA	1	22
HMVEC-dAd	None	UW	normal	0	0
HMVEC-dBl-Ad	None	UW	normal	1	80
HMVEC-dBl-Neo	None	UW	normal	1	21
HMVEC-dLy-Ad	None	UW	normal	1	18
HMVEC-dLy-Neo	None	UW	normal	0	0
HMVEC-dNeo	None	UW	normal	0	0
HMVEC-LBl	None	UW	normal	1	58
HMVEC-LLy	None	UW	normal	1	22
HNPCEpiC	None	UW	normal	0	0
HPAEC	None	UW	normal	1	21
HPAF	None	UW	normal	1	25
HPDE6-E6E7	None	Duke	normal	1	54
HPdLF	None	UW	normal	1	12
HPF	None	UW	normal	0	0
HRCEpiC	None	UW	normal	1	117
HRE	None	UW	normal	1	36
HRGEC	None	UW	normal	0	0
HRPEpiC	None	UW	normal	0	0
HSMM	None	AWG	normal	0	0
HSMMtube	None	AWG	normal	0	0
HSMM_emb	None	Duke	NA	0	0
HTR8svn	None	Duke	normal	1	19
Huh-7	None	Duke	cancer	1	44
Huh-7.5	None	Duke	cancer	1	28
HUVEC	None	AWG	normal	0	0
HVMF	None	UW	normal	1	44
iPS	None	Duke	NA	1	10

Ishikawa	4OHTAM_100nM_30m	Duke	NA	1	34
Ishikawa	Estradiol_100nM_1hr	Duke	NA	1	34
Jurkat	None	UW	cancer	1	1252
K562	None	AWG	cancer	1	43
LNCaP	androgen	Duke	cancer	1	45
LNCaP	None	AWG	cancer	1	45
MCF-7	Hypoxia_LacAcid	Duke	cancer	1	76
MCF-7	None	AWG	cancer	1	76
Medullo	None	Duke	cancer	0	0
Melano	None	Duke	normal	0	0
Monocytes-CD14+_RO01746	None	UW	normal	1	368
Myometr	None	Duke	normal	0	0
NB4	None	UW	cancer	1	363
NH-A	None	UW	normal	0	0
NHDF-Ad	None	UW	normal	1	19
NHDF-neo	None	UW	normal	0	0
NHEK	None	AWG	normal	1	39
NHLF	None	UW	normal	0	0
NT2-D1	None	UW	cancer	1	17
Osteobl	None	Duke	normal	0	0
PANC-1	None	UW	cancer	1	96
PanIsletD	None	Duke	NA	0	0
PanIslets	None	Duke	normal	1	11
pHTE	None	Duke	NA	1	32
PrEC	None	UW	normal	1	81
ProgFib	None	Duke	NA	0	0
RPTEC	None	UW	normal	1	100
RWPE1	None	Duke	normal	1	25
SAEC	None	UW	normal	1	44
SK-N-MC	None	UW	cancer	1	29
SK-N-SH_RA	None	UW	cancer	0	0
SKMC	None	UW	normal	0	0
Stellate	None	Duke	normal	0	0
T-47D	None	Duke	cancer	1	20
Th1	None	AWG	NA	1	87
Th2	None	UW	NA	1	92
Urothelia	None	Duke	normal	1	73
Urothelia	UT189	Duke	normal	1	73
WERI-Rb-1	None	UW	cancer	0	0
WI-38	4OHTAM_20nM_72hr	UW	normal	0	0
WI-38	None	UW	normal	0	0

DNaseI hypersensitivity data for VHL Cluster position: chr3:10,184,306-10,185,010

cellType	treatment	lab	karyotype	inCluster	signal
8988T	None	Duke	cancer	1	25
A549	None	AWG	cancer	1	17
Adult_CD4_Th0	None	UW	normal	1	20
AG04449	None	UW	normal	0	0
AG04450	None	UW	normal	0	0
AG09309	None	UW	NA	0	0
AG09319	None	UW	normal	0	0
AG10803	None	UW	NA	0	0
AoAF	None	UW	normal	0	0
AoSMC	serum_free_media	Duke	normal	0	0
BE2_C	None	UW	cancer	0	0
BJ	None	UW	normal	0	0
Caco-2	None	UW	cancer	0	0
CD20+	None	UW	normal	0	0
CD34+_Mobilized	None	UW	NA	1	15
Chorion	None	Duke	NA	1	12
CLL	None	Duke	cancer	1	8
CMK	None	UW	cancer	1	11
Fibrobl	None	Duke	normal	1	24
FibroP	None	Duke	normal	0	0
Gliobla	None	Duke	cancer	0	0
GM06990	None	UW	NA	1	14
GM12864	None	UW	NA	1	16
GM12865	None	UW	NA	1	34
GM12878	None	AWG	normal	1	20
GM12891	None	Duke	NA	0	0
GM12892	None	Duke	NA	1	14
GM18507	None	Duke	NA	1	25
GM19238	None	Duke	NA	1	28
GM19239	None	Duke	NA	1	10
GM19240	None	Duke	NA	1	13
H1-hESC	None	AWG	normal	1	14.5
H7-hESC	None	UW	NA	1	16
H9ES	None	Duke	NA	1	12
HA-h	None	UW	normal	0	0
HA-sp	None	UW	normal	0	0
HAc	None	UW	normal	0	0
HAEpiC	None	UW	normal	0	0
HBMEC	None	UW	normal	0	0
HCF	None	UW	normal	0	0
HCFaa	None	UW	normal	0	0

HCM	None	UW	normal	0	0
HConF	None	UW	NA	1	15
HCPEpiC	None	UW	normal	0	0
HCT-116	None	UW	cancer	1	12
HEEpiC	None	UW	normal	0	0
HeLa-S3	IFNa4h	Duke	cancer	1	19
HeLa-S3	None	AWG	cancer	1	19
Hepatocytes	None	Duke	normal	1	15
HepG2	None	AWG	cancer	1	12
HFF	None	UW	normal	0	0
HFF-Myc	None	UW	normal	1	12
HGF	None	UW	normal	0	0
HIPEpiC	None	UW	normal	0	0
HL-60	None	UW	cancer	1	36
HMEC	None	AWG	normal	1	29
HMF	None	UW	NA	0	0
HMVEC-dAd	None	UW	normal	1	18
HMVEC-dBl-Ad	None	UW	normal	1	25
HMVEC-dBl-Neo	None	UW	normal	1	34
HMVEC-dLy-Ad	None	UW	normal	0	0
HMVEC-dLy-Neo	None	UW	normal	1	21
HMVEC-dNeo	None	UW	normal	1	13
HMVEC-LBl	None	UW	normal	0	0
HMVEC-LLy	None	UW	normal	1	27
HNPCEpiC	None	UW	normal	0	0
HPAEC	None	UW	normal	0	0
HPAF	None	UW	normal	0	0
HPDE6-E6E7	None	Duke	normal	0	0
HPdLF	None	UW	normal	0	0
HPF	None	UW	normal	0	0
HRCEpiC	None	UW	normal	1	14
HRE	None	UW	normal	1	8
HRGEC	None	UW	normal	0	0
HRPEpiC	None	UW	normal	0	0
HSMM	None	AWG	normal	1	16
HSMMtube	None	AWG	normal	1	14
HSMM_emb	None	Duke	NA	0	0
HTR8svn	None	Duke	normal	0	0
Huh-7	None	Duke	cancer	1	24.5
Huh-7.5	None	Duke	cancer	1	26
HUVEC	None	AWG	normal	0	0
HVMF	None	UW	normal	0	0
iPS	None	Duke	NA	1	12
Ishikawa	4OHTAM_100nM_30m	Duke	NA	0	0

Ishikawa	Estradiol_100nM_1hr	Duke	NA	0	0
Jurkat	None	UW	cancer	1	138
K562	None	AWG	cancer	1	12.5
LNCaP	androgen	Duke	cancer	1	17
LNCaP	None	AWG	cancer	1	17
MCF-7	Hypoxia_LacAcid	Duke	cancer	1	21
MCF-7	None	AWG	cancer	1	21
Medullo	None	Duke	cancer	1	23
Melano	None	Duke	normal	0	0
Monocytes-CD14+_RO01746	None	UW	normal	0	0
Myometr	None	Duke	normal	0	0
NB4	None	UW	cancer	1	16
NH-A	None	UW	normal	0	0
NHDF-Ad	None	UW	normal	0	0
NHDF-neo	None	UW	normal	0	0
NHEK	None	AWG	normal	1	12
NHLF	None	UW	normal	0	0
NT2-D1	None	UW	cancer	1	9
Osteobl	None	Duke	normal	1	9
PANC-1	None	UW	cancer	1	14
PanIsletD	None	Duke	NA	0	0
PanIslets	None	Duke	normal	1	15
pHTE	None	Duke	NA	1	9
PrEC	None	UW	normal	0	0
ProgFib	None	Duke	NA	1	12
RPTEC	None	UW	normal	0	0
RWPE1	None	Duke	normal	1	13
SAEC	None	UW	normal	0	0
SK-N-MC	None	UW	cancer	0	0
SK-N-SH_RA	None	UW	cancer	0	0
SKMC	None	UW	normal	0	0
Stellate	None	Duke	normal	1	9
T-47D	None	Duke	cancer	1	21
Th1	None	AWG	NA	1	45
Th2	None	UW	NA	1	12
Urothelia	None	Duke	normal	1	17
Urothelia	UT189	Duke	normal	1	17
WERI-Rb-1	None	UW	cancer	0	0
WI-38	4OHTAM_20nM_72hr	UW	normal	0	0
WI-38	None	UW	normal	0	0

Table S3: Differentially methylated probes in ovarian serous tumors.

TargetID	SYMBOL	MAPINFO	MedianControls	MedianSerous
cg21790626	*ZNF154*	chr19:58220494	0.03657751	0.8245316
cg08668790	*ZNF154*	chr19:58220662	0.04798249	0.7528151
cg10660256	*BHMT*	chr5:78407683	0.15657446	0.7689793
cg12111714	*ATP8A2*	chr13:26043472	0.21386432	0.7116522
cg19466563	*SPARCL1*	chr4:88450506	0.12725486	0.6153551
cg22980079	*C4orf8*	chr4:2627118	0.34951692	0.8067046
cg07922606	*HIST1H3E*	chr6:26225389	0.58709923	0.9540737
cg17706173	*C16orf30*	chr16:1582581	0.40096894	0.7639955
cg12880658	*CDO1*	chr5:115152386	0.01372329	0.3650002
cg03032025	*CPEB4*	chr5:173316748	0.21587957	0.55323
cg22462235	*LEFTY2*	chr1:226129481	0.3335976	0.6666326
cg13705284	*ACOX2*	chr3:58523313	0.25526749	0.5747562
cg20661303	*LEFTY2*	chr1:226129561	0.37006685	0.6650081
cg26799474	*CASP8*	chr2:202098951	0.86851666	0.2382682
cg20916523	*VHL*	chr3:10184584	0.84900791	0.2446743
cg27235662	*CLDN16*	chr3:190105986	0.9039005	0.3055797
cg21032583	*LMLN*	chr3:197685803	0.94806456	0.3927536
cg15422147	*SERPINB5*	chr18:61144339	0.78610117	0.2329661
cg03602500	*FLJ00060*	chr19:55047721	0.9080196	0.3649664
cg16869108	*VHL*	chr3:10184319	0.84705703	0.31596
cg06051311	*TRIM15*	chr6:30131001	0.76508194	0.2426632
cg18884741	*RABGEF1*	chr7:66204797	0.93986055	0.425796
cg14992108	*SNTB1*	chr8:121825470	0.88336541	0.3708138
cg19306866	*KRTAP6-2*	chr21:31970997	0.95074958	0.4402792
cg23968383	*ZNF572*	chr8:125984927	0.84402408	0.3348998
cg14062083	*KRTAP13-4*	chr21:31802829	0.88498456	0.3926638
cg01888566	*MEST*	chr7:130126513	0.6443697	0.15322
cg02490034	*MEST*	chr7:130125836	0.64065417	0.1555951
cg22190114	*NALP8*	chr19:56459234	0.95209142	0.4803644
cg17738194	*GK2*	chr4:80329388	0.77789038	0.3106485
cg07080946	*LUC7L*	chr16:280046	0.88832313	0.4258908
cg05244766	*GSTP1*	chr11:67350499	0.92939642	0.4673026
cg03552103	*SEPT10*	chr2:110373002	0.645785	0.1871901
cg07665060	*C19orf33*	chr19:38794598	0.61372166	0.1572842
cg11804789	*CST7*	chr20:24929716	0.70464385	0.2490312
cg24831427	*COQ3*	chr6:99842353	0.8327268	0.3857416
cg09971811	*CST7*	chr20:24930099	0.94576574	0.5014663
cg00344709	*ANKRD21*	chr21:14982225	0.84754433	0.4035949
cg13897627	*FLJ44674*	chr16:49378497	0.80328256	0.3666835
cg09682183	*UNC93A*	chr6:167705253	0.65820518	0.2216787
cg08947964	*CX62*	chr6:90603803	0.89996261	0.4653748

cg14333454	*SFN*	chr1:27189298	0.70433774	0.27504
cg20312687	*DEFB118*	chr20:29956585	0.76502889	0.3360534
cg26530341	*TNFRSF10A*	chr8:23083353	0.89875736	0.4844262
cg21747271	*AIP*	chr11:67250052	0.52118809	0.1073659
cg25612480	*UBE2V2*	chr8:48920460	0.80129709	0.3893233
cg01883966	*STK19*	chr6:31938886	0.90706566	0.4984077
cg24459209	*PRG3*	chr11:57148215	0.85987747	0.4535433
cg12188860	*TOP1MT*	chr8:144416485	0.6801079	0.274037
cg25033144	*FLJ00060*	chr19:55048290	0.91409583	0.5092839
cg15746620	*EMR3*	chr19:14785849	0.55911787	0.1548895
cg03544379	*OR7C2*	chr19:15052824	0.7623347	0.3613651
cg01430430	*FLJ37078*	chr7:75914313	0.93338488	0.5354742
cg04947157	*TMC6*	chr17:76128481	0.58527724	0.1874531
cg07014174	*KRTAP11-1*	chr21:32253760	0.9007181	0.5042468
cg12867448	*ODF2*	chr9:131217480	0.87322244	0.4768746
cg11695358	*MAPK15*	chr8:144797963	0.85846335	0.46299
cg24423088	*KRTAP8-1*	chr21:32185365	0.98257501	0.5897868
cg09828634	*KRTAP19-2*	chr21:31859610	0.9153445	0.5230397
cg25890048	*OR5I1*	chr11:55703443	0.88126531	0.4906895
cg12348970	*SLC24A2*	chr9:19786543	0.96060129	0.5700768
cg16592658	*EBI3*	chr19:4229887	0.65013652	0.2607271
cg19226099	*MC3R*	chr20:54824085	0.71587515	0.3267257
cg21624282	*LOC122258*	chr13:113030783	0.90336076	0.5157704
cg26482939	*GNA15*	chr19:3136710	0.65954876	0.27778
cg10516359	*SLC35C1*	chr11:45827763	0.98327649	0.6045739
cg25391023	*BTNL2*	chr6:32374754	0.76031257	0.3817664
cg13038560	*FLJ22555*	chr2:200819113	0.95839098	0.5829611
cg18119407	*CFLAR*	chr2:201980504	0.77127	0.3963556
cg01136458	*CSMD1*	chr8:4853275	0.6526123	0.2780243
cg01390445	*LIPH*	chr3:185271312	0.94620603	0.5726364
cg12334759	*C19orf19*	chr19:475154	0.83249034	0.463692
cg12970081	*GPR32*	chr19:51273924	0.83567477	0.46962
cg03294491	*SMAD2*	chr18:45458243	0.60902801	0.2444005
cg07908874	*TUBGCP2*	chr10:135123006	0.89604818	0.5317799

Table S4: Differentially methylated probes in endometrioid ovarian and endometrioid endometrial tumors.

TargetID	SYMBOL	MAPINFO	MedianControls	MedianEndo
cg21790626	*ZNF154*	chr19:58220494	0.1510489	0.7978823
cg13164537	*CD226*	chr18:67624071	0.2324949	0.77222
cg12535715	*HTRA4*	chr8:38831693	0.326677	0.8065622
cg26391080	*SH2D4B*	chr10:82297397	0.2446444	0.7164751
cg04268405	*CHST3*	chr10:73723221	0.3038281	0.7697753
cg18003231	*SLC25A18*	chr22:18043745	0.338008	0.8015152
cg07221454	*MS4A10*	chr11:60552841	0.3696114	0.8319
cg27138018	*HAPLN2*	chr1:156589303	0.7018688	0.14438
cg20837735	*SERPINB5*	chr18:61144177	0.7766621	0.24563
cg04947157	*TMC6*	chr17:76128481	0.7826197	0.26564
cg16812893	*KRTAP15-1*	chr21:31813075	0.8299733	0.3148037
cg19863740	*PARVG*	chr22:44576869	0.8461855	0.3367151
cg24625388	*NEBL*	chr10:21463858	0.7409687	0.23289
cg15779716	*CDCP1*	chr3:45188208	0.7839137	0.2809805
cg16431978	*KRTAP13-3*	chr21:31797932	0.7818451	0.2855307
cg07908874	*TUBGCP2*	chr10:135123006	0.8462345	0.3531863
cg15503752	*ST6GALNAC1*	chr17:74639731	0.7422057	0.2551071
cg16869108	*VHL*	chr3:10184319	0.7775884	0.2921941
cg18484189	*NALP10*	chr11:7984973	0.7187174	0.2335832
cg09577651	*SIRPB1*	chr20:1600705	0.6798352	0.1949
cg00744433	*CXADR*	chr21:18884067	0.7040575	0.2209252
cg13699808	*PRKCBP1*	chr20:45985339	0.6632204	0.1804767
cg26799474	*CASP8*	chr2:202098951	0.7425413	0.2681976
cg05093686	*MAB21L1*	chr13:36050788	0.6973728	0.2235912
cg04958389	*PRSS2*	chr7:142178834	0.7819808	0.3094698
cg13015534	*ST6GALNAC1*	chr17:74639793	0.6793536	0.2117928
cg20312687	*DEFB118*	chr20:29956585	0.7488325	0.2844683
cg15928132	*CCKAR*	chr4:26492378	0.7338183	0.2702046
cg01119135	*C1orf116*	chr1:207205525	0.7210817	0.25862
cg23213217	*DEGS1*	chr1:224370155	0.6574602	0.1954208
cg06353345	*OR51B4*	chr11:5322976	0.7230261	0.2615176
cg13944141	*PRSS2*	chr7:142178732	0.7540907	0.29778
cg07705908	*SPDEF*	chr6:34523925	0.7049554	0.2499029
cg11204562	*C10orf81*	chr10:115511153	0.7813558	0.3263988
cg08970694	*HBE1*	chr11:5290746	0.760081	0.3058824
cg14992108	*SNTB1*	chr8:121825470	0.8063309	0.3536
cg07014174	*KRTAP11-1*	chr21:32253760	0.8254418	0.37355
cg18462653	*DEFB119*	chr20:29978176	0.6617294	0.2128086
cg25391023	*BTNL2*	chr6:32374754	0.7314647	0.2874903
cg21032583	*LMLN*	chr3:197685803	0.8614061	0.4180812

cg03973663	*LYN*	chr8:56791576	0.6723252	0.2311828
cg23092086	*CES7*	chr16:55909573	0.8311277	0.3922399
cg05656364	*VAMP8*	chr2:85804732	0.5811541	0.1435274
cg25336198	*INS*	chr11:2182618	0.7679843	0.3323422
cg07785936	*GPR39*	chr2:133174635	0.7735475	0.3384631
cg18414381	*EHF*	chr11:34642885	0.6534631	0.2197619
cg14826683	*SPRR2D*	chr1:153013830	0.7859129	0.3552492
cg15979932	*CUEDC1*	chr17:55980107	0.6582447	0.2276992
cg24816455	*SEMA3B*	chr3:50310766	0.5566738	0.1273792
cg06640279	*FAIM3*	chr1:207095153	0.6885841	0.2607817
cg02537838	*C20orf151*	chr20:61002595	0.7638559	0.3391269
cg14153740	*TRY1*	chr7:141957702	0.8020787	0.3783582
cg21414251	*OR12D2*	chr6:29364554	0.6287672	0.206
cg00480115	*FXYD3*	chr19:35606877	0.7187619	0.2969786
cg13897627	*FLJ44674*	chr16:49378497	0.7881786	0.3706771
cg11300809	*SGPP2*	chr2:223288637	0.7173604	0.3001219
cg10503138	*CNTN4*	chr3:2142391	0.824102	0.4089383
cg20856834	*OR12D3*	chr6:29342522	0.6801739	0.2690438
cg27496506	*TGM5*	chr15:43559170	0.6940689	0.2859037
cg12334759	*C19orf19*	chr19:475154	0.8420037	0.43519