

**Supplementary Table S1. List of primers used for ChIP assays.**

Gene	Primer
<i>TXNIP</i> Primer #1	Forward : 5'-TTCCTTTTCCTCCAGAAGCA-3'
	Reverse : 5'-TTCTACCTGCAAAGTTGGGG-3'
<i>TXNIP</i> Primer #2	Forward : 5'-CCTCCTATTTCCGTTCCACA-3'
	Reverse : 5'-TACTTTCAGGTTTGGGGCTG-3'
<i>TXNIP</i> Primer #3	Forward : 5'-CCTCAGAGACGGTGGTGTTT-3'
	Reverse : 5'-GGTGTGGACGTTTCTGGTCT-3'

Supplementary Table S2. Target CpG sites and sequences of primers used for pyrosequencing.

Gene	Primer		Size (bp)
<i>TXNIP</i>	Forward	5'-GAGAATAGAAGAGAGGGTATAAGTT-3'	98
	Biotinylated-reverse	5'-TTCTCCTTCCCCTTCCAATCCCTTAA-3'	
	Sequencing primer	5'-GTTGGGGGTGGGTGA-3'	

Supplementary Table S3. Primer sequences for methylated *TXNIP* and unmethylated *TXNIP* for methylation-specific polymerase chain reaction (MSP) analysis.

Gene	Primer
Methylated <i>TXNIP</i>	Forward : 5'-TGAAATACGTTTTTTTTATTTTCGT-3'
	Reverse : 5'-TATAAAACCGATATCTTCTCCTTCCCGT-3'
Unmethylated <i>TXNIP</i>	Forward : 5'-GATGAAATATGTTTTTTTTATTTTGT-3'
	Reverse : 5'-ATAAAACCAATATCTTCTCCTTCCCATT-3'

Supplementary Table S4. List of primary antibodies used in this study.

Antibody	Company	Catalog No.	Dilution	Applications	Source
UHRF1	Santa Cruz	sc-166898	1:1000; 1:200	WB; ICC	Mouse Mouse
	Epigentek	A-2714-100		ChIP	Rabbit
TXNIP	Thermo Fisher	PA5-29884	1:1000; 1:200	WB; ICC	Rabbit Rabbit
	Cell signaling	D5F3E	1:1000	WB	Rabbit
HPV16E6/18E6	Santa Cruz	sc-460	1:1000	WB	Mouse
HPV 16E7	Santa Cruz	sc-6981	1:1000	WB	Mouse
DNMT1	Abcam	Ab13537	1:1000	WB	Mouse
Trx1	Abcam	Ab26320	1:1000	WB	Rabbit
PARP	Cell signaling	46D11	1:1000	WB	Mouse
p27	Cell signaling	2552	1:1000	WB	Rabbit
USP7	Novus Biologicals	NB100-513	1:1000	WB	Rabbit
Lamin A/C	Santa Cruz	sc-6214	1:1000	WB	Goat
α -tubulin	Sigma	A5441	1:5000	WB	Rabbit
β -actin	Sigma	A2228	1:5000	WB	Mouse

WB; western blot, ICC; immunocytochemistry, ChIP; chromatin immunoprecipitation.

Supplementary Table S5. List of genes whose expression is up-regulated >2-fold in UHRF1-knockdown cells compared to control cells.

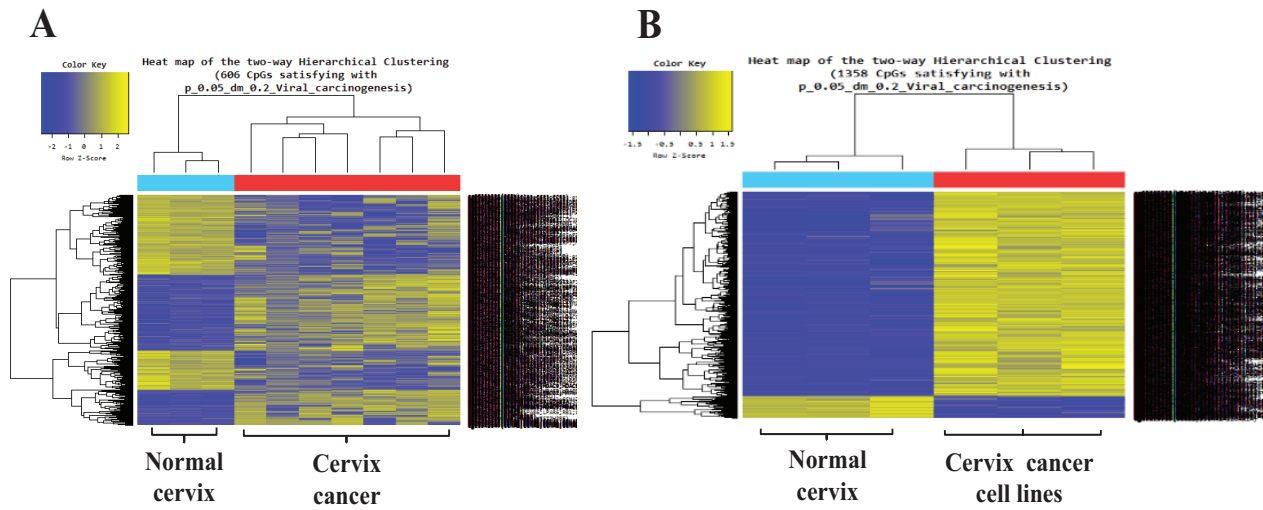
Gene symbol	UHRF1/CTL	Genbank accession No.	Gene Name
C8orf22	6.940	NM_001007176	Chromosome 8 open reading frame 22
QPRT	5.244	NM_014298	Quinolate phosphoribosyl transferase
H19	4.900	NR_002196	H19, imprinted maternally expressed transcript (non-protein coding)
TXNIP	3.890	NM_001313972	Thioredoxin-interacting protein
HPD	3.256	NM_001171993	4-hydroxyphenylpyruvate dioxygenase
MMP12	3.081	NM_002426	Matrix metalloproteinase 12
SVEP1	2.859	NM_153366	Sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1
MYL9	2.667	NM_006097	Myosin light chain 9
HOXA5	2.662	NM_019102	Homeobox A5
TCEB3C	2.607	NM_145653	Transcription elongation factor B polypeptide 3C (elongin A3)
CKMT1B	2.518	NM_020990	Creatine kinase, mitochondrial 1B
STAG3L2	2.437	NR_040584	Stromal antigen 3-like 2 (pseudogene)
PIIP5K1	2.403	uc001zsm.2	Diphosphoinositol pentakisphosphate kinase 1
IGHV2-70	2.325	OTTHUMT00000324215	Immunoglobulin heavy variable 2-70
C4BPA	2.276	NM_000715	Complement component 4 binding protein, alpha
YY1AP1	2.230	NM_001198899	YY1 associated protein 1
KAT8	2.227	XM_011545969	K(lysine) acetyltransferase 8
OLFML2A	2.224	NM_001282715	Olfactomedin like 2A
FITM2	2.212	NM_001080472	Fat storage-inducing transmembrane protein 2
SAP25	2.176	NM_001168682	Sin3A associated protein 25 kDa
ATP5G1	2.158	NM_001002027	ATP synthase, H ⁺ transporting, mitochondrial Fo complex subunit C1 (subunit 9)
P2RY6	2.110	NM_001277204	Pyrimidinergic receptor P2Y, G-protein coupled, 6
MICAL2	2.106	NM_001282663	Microtubule associated monooxygenase, calponin and LIM domain containing 2
GALT	2.097	NM_000155	Galactose-1-phosphate uridylyltransferase
PEG10	2.087	NM_001040152	Paternally expressed 10
CDH10	2.059	NM_006727	Cadherin 10, type 2 (T2-cadherin)
ITPK1	2.037	NM_001142593	Inositol-tetrakisphosphate 1-kinase
PALMD	2.010	NM_017734	Palmdelphin

Supplementary Table S6. List of hypermethylated genes in cervical cancer compared to the normal cervix.

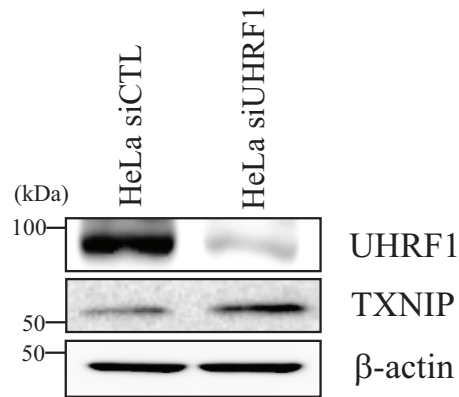
Gene symbol (CpG site)	Normal mean	Cervical cancer mean	Cervical cancer/normal comment	<i>P</i>-value
TXNIP (cg02988288)	0.128856033	0.47053453	Hyper	0.03927
TXNIP (cg26974062)	0.101393729	0.40645409	Hyper	0.01365
OLFML2A (cg01959390)	0.451834841	0.715879114	Hyper	0.00231
CDH10 (cg05683049)	0.073922453	0.60901039	Hyper	2.84E-05
CDH10 (cg14730815)	0.057685136	0.424309716	Hyper	2.52E-05
CDH10 (cg16714427)	0.067071094	0.578899292	Hyper	1.18E-05
CDH10 (cg17030055)	0.068899135	0.514865785	Hyper	1.85E-05
CDH10 (cg24432832)	0.091680265	0.613762834	Hyper	1.67E-05
CDH10 (cg26161643)	0.122283396	0.346583224	Hyper	0.00021
ITPK1 (cg00964698)	0.601194183	0.839136187	Hyper	0.02075
ITPK1 (cg08355895)	0.472789828	0.696375481	Hyper	0.01608
ITPK1 (cg09698854)	0.532038048	0.917787806	Hyper	5.04E-05
ITPK1 (cg23294361)	0.690010414	0.910117394	Hyper	0.00918

Supplementary Table S7. List of hypermethylated genes in cervical cancer cell lines compared to the normal cervix.

Gene symbol (CpG site)	Normal mean	Cervical cancer cell lines mean	Cervical cancer cell lines/normal comment	<i>P</i>-value
TXNIP (cg02988288)	0.128856033	0.967574057	Hyper	0.000142
TXNIP (cg26974062)	0.101393729	0.927913017	Hyper	0.001192
OLFML2A (cg01959390)	0.451834841	0.905100234	Hyper	0.009319
CDH10 (cg05683049)	0.073922453	0.608168651	Hyper	0.004418
CDH10 (cg14730815)	0.057685136	0.526541296	Hyper	0.005615
CDH10 (cg16714427)	0.067071094	0.594741504	Hyper	0.003561
CDH10 (cg17030055)	0.068899135	0.600413608	Hyper	0.000567
CDH10 (cg24432832)	0.091680265	0.645299537	Hyper	0.008217
CDH10 (cg26161643)	0.122283396	0.43557779	Hyper	0.000668
ITPK1 (cg00964698)	0.601194183	0.902120379	Hyper	0.009953
ITPK1 (cg08355895)	0.472789828	0.759944566	Hyper	0.016981
ITPK1 (cg09698854)	0.532038048	0.960753321	Hyper	0.000381
ITPK1 (cg23294361)	0.690010414	0.957237752	Hyper	0.010874



Supplementary Fig. S1. Heatmap of CpG methylation regions detected by Infinium MethylationEPIC microarrays in cervical cancer tissue and cell lines. (A) Hierarchical clustering of methylation states in cervical cancer tissue ($n = 7$) and normal cervix tissue ($n = 3$). (B) Hierarchical clustering of methylation states in cervical cancer cells (Caski, SiHa, and HeLa) and normal tissues ($n = 3$). DNA methylation values are represented using a colour scale from blue (low DNA methylation) to yellow (high DNA methylation).



Supplementary Fig. S2. TXNIP expression is increased and UHRF1 is decreased in siRNA-mediated UHRF1-knockdown cells. Expression levels of UHRF1 and TXNIP were measured by western blot analysis in siUHRF1 and siCTL cells. HeLa cells were transfected with small interfering (si) RNA targeting UHRF1 (siUHRF1; sc-76805) and control siRNA (siCTL; sc-37007) using lipofectamine RNAiMAX (Invitrogen) reagent. β -Actin was used as a control to ensure equivalent loading.