

Figure S1: *VIM* expression and methylation in normal urothelium, bladder cancer and bladder cancer metastasis. (A) *VIM* immunohistochemistry results for normal urothelium (NU), non-muscle-invasive bladder cancer (NMIBC), muscle-invasive bladder cancer (MIBC) and metastasis (Met) tissues regarding the calculated immunoscore. (B) Methylation levels for NU, NMIBC, MIBC and Metastasis tissue samples by qMSP. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$ and **** $p < 0.0001$.

Figure S2: Cadherins genes expression in bladder cancer tissues. Transcript levels of (A) *CDH1*, (B) *CDH2* and (C) *CDH3* in non-muscle-invasive bladder cancer (NMIBC) tissues and muscle-invasive bladder cancer (MIBC) tissues by RT-qPCR. (D) Graphical representation of transformed log data comparison of *VIM*, *CDH1*, *CDH2* and *CDH3* transcript levels in bladder cancer tissue samples. Transcript levels were obtained by RT-qPCR.

Figure S3: CHIP-qPCR for histone PTMs across *VIM* promoter, in SVHUC1 immortalized urothelial cell line. CHIP-qPCR results for H3K27Ac, H3K36me2, H3K9me3 and H3K27me3 across *VIM* promoter region. *VIM* A represents a region ~325bp before TSS, and *VIM* B a region ~600bp before TSS. Results are normalized with the input of total sonicated chromatin.

Figure S1

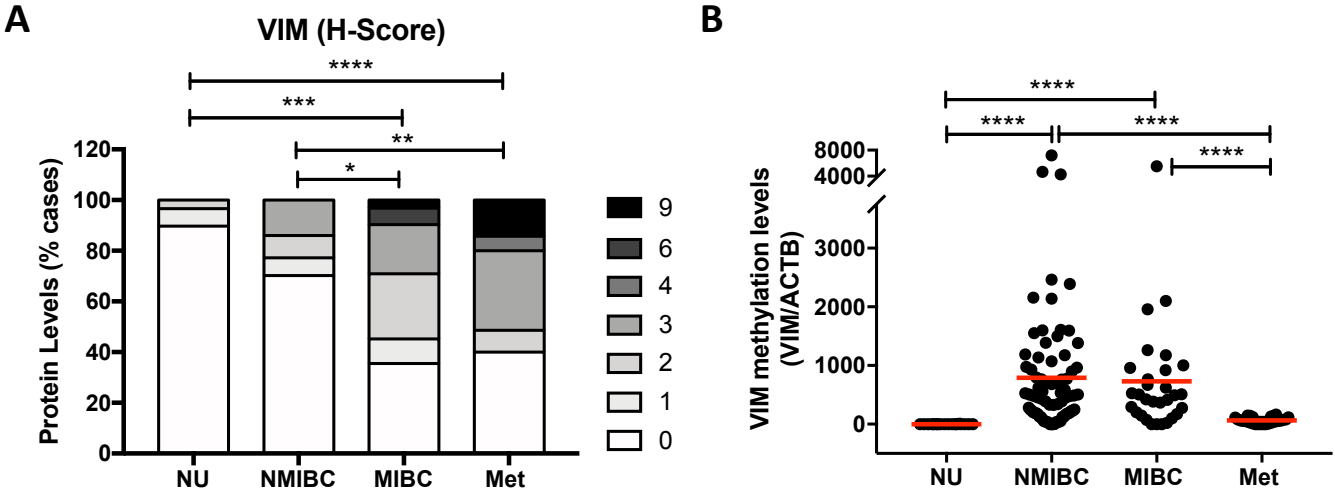
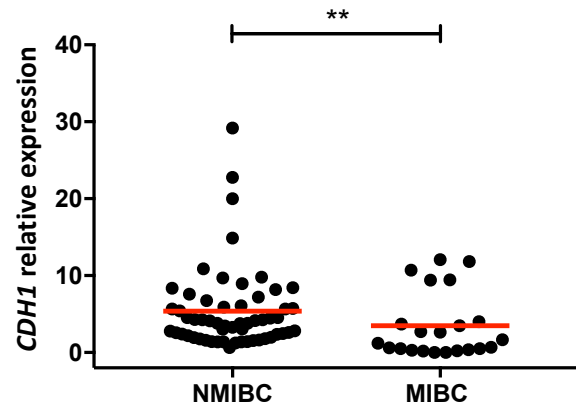
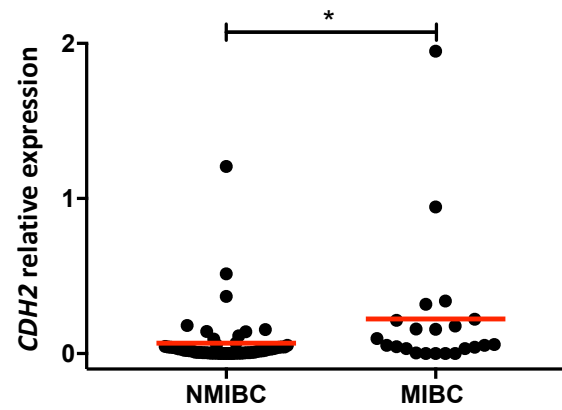


Figure S2

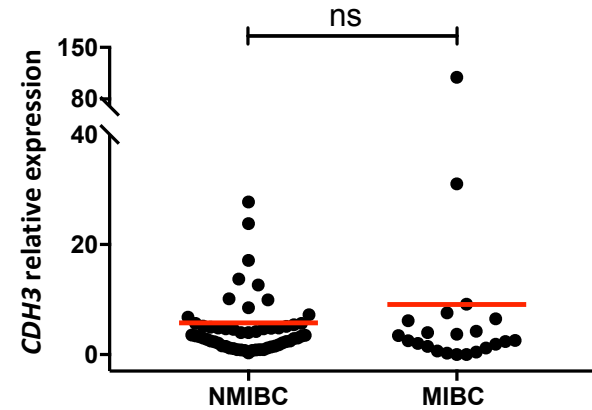
A



B



C



D

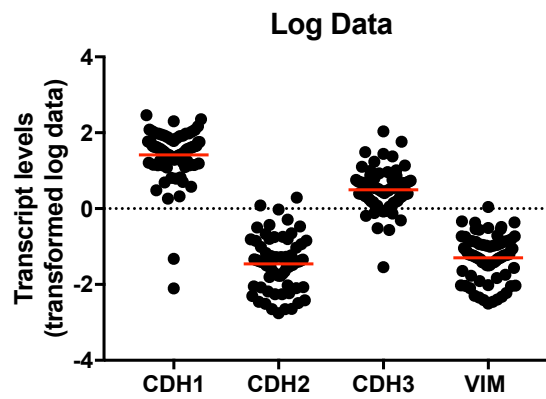


Figure S3

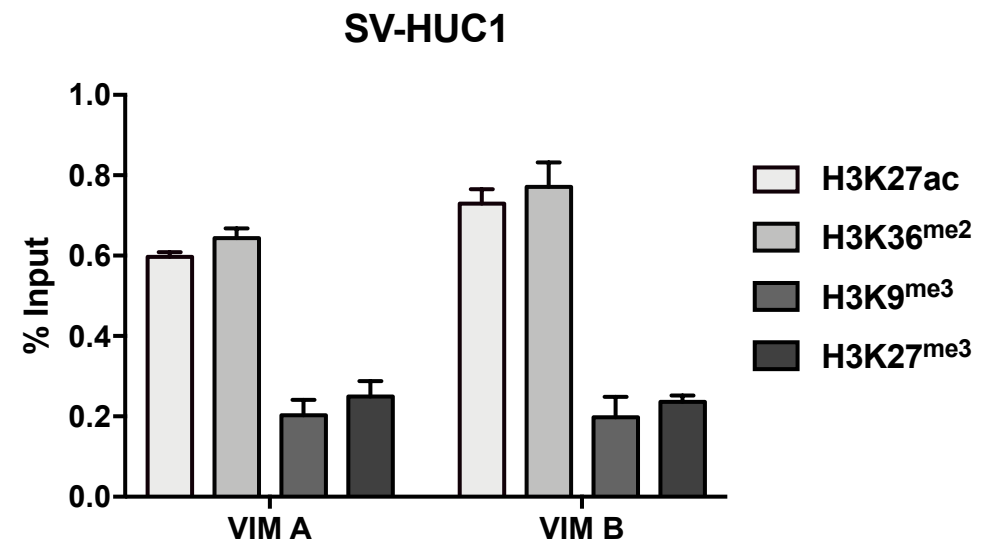


Table S1: Spearman correlation between *CDH1*, *CDH2*, *CDH3* and *VIM* transcript levels in Bladder cancer tissues. (Grey results are non-significant)

Spearman r	<i>CDH1</i>	<i>CDH2</i>	<i>CDH3</i>	<i>VIM</i>
<i>CDH1</i>		-0.224	0.212	-0.367
<i>CDH2</i>	-0.224		0.149	0.386
<i>CDH3</i>	0.212	0.149		-0.108
<i>VIM</i>	-0.367	0.386	-0.108	

Table S2: Primer sequences used in qMSP and RT-qPCR for studied genes.

Target Gene		Sequence (5' - 3')	T _{Annealing} °C
Quantitative Methylation Specific PCR			
ACTB	Forward Primer	TGGTGATGGAGGAGGTTTAGTAAGT	60
	Reverse Primer	AACCAATAAAACCTACTCCTCCCTTAA	
	Probe	FAM - ACCACCACCCAACACACAATAACAAACACA - MGB	
VIM	Forward Primer	TTCGGGAGTTAGTTCGCGTT	60
	Reverse Primer	ACCGCCGAACATCCTACGA	
	Probe	FAM - TCGTCGTTTAGGTTATCGT - MGB	
Real-Time Quantitative PCR			
CDH1	Forward Primer	CTTTGACGCCGAGAGCTACA	64
	Reverse Primer	AAATCACTCTGCCCAGGACG	
CDH2	Forward Primer	TGTATGTTTTCTTTTCAGTGAATCTT	60
	Reverse Primer	TGGAAAGCTTCTCACGGCAT	
CDH3	Forward Primer	ACGAAGACACAAGAGAGATTGG	60
	Reverse Primer	CGATGATGGAGATGTTTCATGG	
HPRT1	Forward Primer	TGACACTGGCAAAACAATGCAGACTT	60
	Reverse Primer	TTCGTGGGGTCCTTTTCACCAGCAA	

Table S3: References of antibodies used in ChIP assays for studied histones and histones posttranslational modifications.

Histone/ Histone PTM	Antibody Reference
H3	ab1791 (Abcam)
AcH3	06-599 (Millipore)
H3K4me3	ab8580 (Abcam)
H3K9Ac	17-658 (Millipore)
H3K9me3	07-442 (Millipore)
H3K27me3	07-499 (Millipore)
H3K27Ac	ab4729 (Abcam)
H3K36me2	ab9049 (Abcam)
H4	ab70701 (Abcam)
H4K20me3	ab9053 (Abcam)