SUPPLEMENTARY TABLES AND FIGURES

Supplementary Table S1: Baseline Characteristics of the patients and Clinicopathological results in the series

Patients (n)	87
Age median (range)	73.0 yr (49–90)
Sex	M = 68 $F = 19$
Smoker status	No = 15 Currently smoker = 27 Ex smoker = 43 ND = 2
Stage	Papilloma = 1 Ta = 40 T1 = 36 T2 = 10
Grade	Low = 45 High = 37 PUNLMP = 4 ND = 1
Alterations in normal mucosa	Dysplasia = 6 Metaplasia = 1 Glandular cystitis = 1
Follow up, median (range)	864 d (34–1123)
Tumor size, median (range)	2 cm (0.5–7)
Number of implants, median (range)	1(1–10)
Specific death events	7*
Non-specific deaths	4**
Recurrence events	ND = 11 No recurrence = 43 Recurrence = 33
Time to recurrence, median (range)	186 d (96–433)
Stage of recurrence	Ta = 12 T1 = 12 T2 = 3 ND = 6
Grade of recurrence	Low = 12 High = 12 PUNLMP = 1 CIS = 2 ND = 6

(Continued)

Patients (n)	87
Previous tumor (non bladder)	16
	ND = 23 Yes = 15 (14 BCG; 1 mitomycin) No = 52

ND= Not determined

PUNLMP: Papillary urothelial neoplasia of low malignant potential

CIS: Carcinoma in situ

Supplementary Table S2: See Supplementary Table S2 file

Supplementary Table S3: See Supplementary Table S3 file

^{*} All deaths due to progression of invasive bladder cancer.

^{**} One patient died due to a lymphoma, another of sepsis secondary to mycosis fungoides, another due to progression of gastric tumor and another of chronic obstructive pulmonary disease decompensation

Supplementary Table S4: Significant overlap of genes following the same expression pattern of miR-200 with oncogenic pathways from MSigDB_Oncogenic_Signatures database

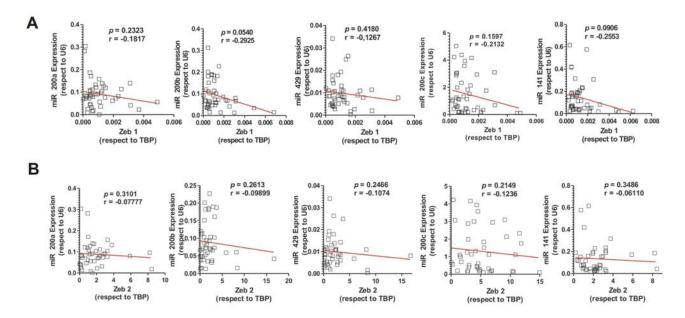
Term	Description	Overlap	<i>P</i> -value	Adjusted <i>P</i> -value
E2F1_UP.V1_DN	Genes down-regulated in mouse fibroblasts over-expressing E2F1	45/193	5.4151E-08	3.8332E-06
ATF2_S_UP.V1_DN	Genes down-regulated in myometrial cells over- expressing a shortened splice form of ATF2 [GeneI D = 1386] gene.	44/187	6.0844E-08	3.8332E-06
P53_DN.V1_DN	Genes down-regulated in NCI-60 panel of cell lines with mutated TP53 [GeneID = 7157].	44/192	1.1614E-07	5.4876E-06
BMI1_DN.V1_UP	Genes up-regulated in DAOY cells (medulloblastoma) upon knockdown of BMI1 [GeneID = 648] gene by RNAi.	37/147	1.6521E-07	6.2451E-06
BMI1_DN_MEL18_ DN.V1_UP	Genes up-regulated in DAOY cells (medulloblastoma) upon knockdown of BMI1 and PCGF2 [GeneID = 648] [GeneID = 7703] genes by RNAi.	36/145	3.2163E-07	1.0131E-05
KRAS.KIDNEY_ UP.V1_UP	Genes up-regulated in epithelial kidney cancer cell lines over-expressing an oncogenic form of KRAS [GeneID = 3845] gene.	35/145	8.2067E-07	2.201E-05
LEF1_UP.V1_UP	Genes up-regulated in DLD1 cells (colon carcinoma) over-expressing LEF1 [GeneID = 51176].	42/195	9.3165E-07	2.201E-05
ATF2_UP.V1_DN	Genes down-regulated in myometrial cells over- expressing ATF2 [GeneI D = 1386] gene.	40/187	1.9556E-06	4.1068E-05
MEL18_DN.V1_UP	Genes up-regulated in DAOY cells (medulloblastoma) upon knockdown of PCGF2 [GeneID = 7703] gene by RNAi.	33/141	2.986E-06	5.2722E-05
PTEN_DN.V1_UP	Genes up-regulated upon knockdown of PTEN [GeneID = 5728] by RNAi.	40/191	3.0685E-06	5.2722E-05
AKT_UP.V1_DN	Genes down-regulated in mouse prostate by transgenic expression of human AKT1 gene [Genel $D = 207$] vs controls.	39/187	4.4309E-06	6.4418E-05

Supplementary Table S5: Significant overlap of genes following the opposite expression pattern of miR-200 with oncogenic pathways from MSigDB_Oncogenic_Signatures database

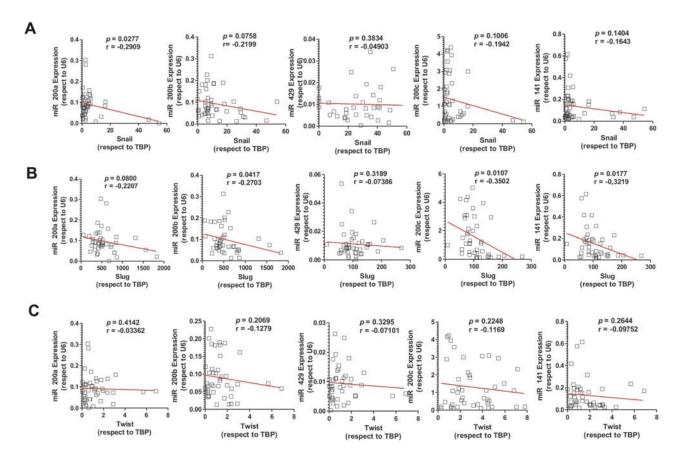
Term	Description	Overlap	<i>P</i> -value	Adjusted <i>P</i> -value
IL15_UP.V1_UP	Genes up-regulated in Sez-4 cells (T lymphocyte) that were first starved of IL2 [GeneID = 3558] and then stimulated with IL15 [GeneID = 3600].	27/192	0.00492204	0.4552887
PRC2_EDD_UP.V1_UP	Genes up-regulated in TIG3 cells (fibroblasts) upon knockdown of EED [GeneID = 8726] gene.	28/193	0.00287295	0.4552887
E2F3_UP.V1_DN	Genes down-regulated in primary epithelial breast cancer cell culture over-expressing E2F3 [GeneID = 1871] gene.	25/183	0.0091101	0.48997298
MYC_UP.V1_UP	Genes up-regulated in primary epithelial breast cancer cell culture over-expressing MYC [GeneID = 4609] gene.	25/186	0.0108324	0.48997298
P53_DN.V1_UP	Genes up-regulated in NCI-60 panel of cell lines with mutated TP53 [GeneID = 7157].	25/194	0.01673918	0.51612458
BCAT_BILD_ET_AL_ UP	Genes up-regulated in primary epithelial breast cancer cell culture over-expressing activated CTNNB1 [GeneID = 1499] gene.	8/49	0.05321878	0.99996626
PRC1_BMI_UP.V1_UP	Genes up-regulated in TIG3 cells (fibroblasts) upon knockdown of BMI1 [GeneID = 648] gene.	22/190	0.05862928	0.99996626
E2F1_UP.V1_UP	Genes up-regulated in mouse fibroblasts over-expressing E2F1 [GeneID = 1869] gene.	19/189	0.1817207	0.99996626

Supplementary Table S6: Primers used for qPCR

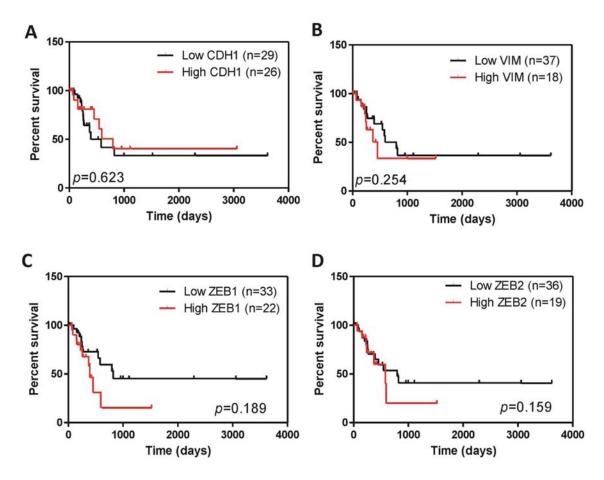
EZH2-for CGGTGTCAAAGGCCAATAAA EZH2-rev CGGTGCAAAGGCCAATAAA EZH2-rev CCGGTCCACTCCACATCTC VIM-RISpe AAGATTGCAGGGTGTTTTCG VIM-for GACCAGCTAACCAACGACAAA VIM-rev GAAGCATCCTCCTGCAAT CDH1-RISpe TGCTTAACCCCTCACATTAGG CDH1-Rispe GGTGTCATGGAAGGTGCT CDH1-rev GATGGCGGCATTGTAGGT ZEB 1-RISpe GTGTAACTGCACAGGACAA ZEB 1-for TTTTCCTGAGGACGTGTTCC ZEB 2-RISpe TTCTTCTCTGAGG TTCTTCTCTGGGGGTACTT ZEB 2-for AGGACATCTCCTCGCAT SNAIL 1-RISpe GGCAAAAGCACAAA SNAIL 1-rev GGCAAAAGCATCTGCACAGGAGAC SNAIL 1-rev GCCAGGAAGTCCCCTTGAAGG SNAIL 1-rev TTCCGGAGGACCTGAA SNAIL 1-rev TTCCGAGGACTCTAACTCAGAG SNAIL 1-rev TTCCGAGGACCTCAGACAGGACAC SUGGCAAAAGCATCTGGAGTTC SUUG-RISpe GTTGGTCAGGAGAGCAC SUGGCAGAAGCATCTGAGTCCCCTTG SUUG-RISpe GTTGGCAGAAAAGCATCTGAGTC SUUG-RISpe GTTGGCAGAAAAGCATCTGAGACC SUUG-RISpe GTTGGTCAGCACAGGAAAAATGCC SUUG-RISPE GTTGGACCACACATACCT SUUG-RISPE GTTGGACCACACATTACCT SUUG-RISPE ATTCCAGAAAACACTTTGCATCAGA TWIST-RISPE CACGCCCAGATAGAC TWIST-RISPE CACGCCCAGATAGAC TWIST-RISPE CACGCCCAGATAGAC TWIST-RISPE TTCCAGAAAACACTTTTGCATG MILL-RISPE TTCCAGAAAACACTTTTGCATG MILL-RISPE TTCCAGAAAAACACTTTTGCATG MILL-RISPE TTCCAGAAAAACACTTTTGCATG MILL-RISPE TTCCAGAAAAACACTTTTTTTTTAAA TWIST-FOT GGCCCAGAAACACTTTTC TWIST-RISPE TTCCAGAAAAACACTTTTTTTTTCAAGAAAAACACTTTTTTTT	Name	Sequence
EZH2-rev CCGCTCCACTCCACATTCTC VIM-RTspe AAGATTGCAGGGTGTTTTCG VIM-for GACCAGCTAACCAACGACAAA VIM-rev GAAGCATCCTCCTCGCAAT CDH1-RTspec TGCTTAACCCCTCACCTTGAAGG CDH1-for GGTCGTCATGGAAGGTGCT CDH1-rev GATGGCGGCTATTGCACGGTGT CDH1-rev GATGGCGGCATTGTAGGT ZEB 1-RTspec GTGTAACTGCACAGGGAGCA ZEB 1-for TTTTTCCTGAGGCACCTGAA ZEB 1-for TTTTTCCTGAGGCACCTGAA ZEB 1-rev TGAAAATGCACTGGTTCC ZEB 2-RTspec TTCTTCTCTGTGGCGGTACTT ZEB 2-for AGGAGCTGTCTCGCCTTG ZEB 2-rev GGCAAAAGCATCTGGAGTTC SNAIL 1-RTspec GGCAGAGTCCCAGATGAG SNAIL 1-rev ATCTCCGGAGGTGGGATG SLUG-RTspec GTTGGTCAGCACAGGAAAATGCC SLUG-for TTCGGACCCACACATTACCT SLUG-rev TTGGAGCACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	EZH2-RTspec	CCTGTCGACATGTTTTGGTC
VIM-RTspe AAGATTGCAGGGTGTTTTCG VIM-for GACCAGCTAACCAACGACAAA VIM-rev GAAGCATCTCCTCTGCAAT CDH1-RTspee TGCTTAACCCCTCACCTTGAAGG CDH1-for GGTCTGTCATGGAAGGTGCT CDH1-rev GATGGCGGCATTGTAGGT ZEB 1-RTspee GTGTAACTGCACAGGAGCA ZEB 1-for TTTTTCCTGAGGCACCTGAA ZEB 1-rev TGAAAATGCATCTGCTTCC ZEB 2-RTspee TTCTTCTCTGTGGCGTACTT ZEB 2-for AGGAGCTGTCTCGCTTG ZEB 2-rev GGCAAAAGCATCTGGATTC SNAIL 1-RTspee GGCAAAAGCATCTGGAGTC SNAIL 1-rev ATCCCGGAGGTGGAGC SNAIL 1-rev ATCCCGGAGGTGGAGC SNAIL 1-rev TTCGGACCCACACATTACCC SLUG-for TTCGGACCCACACATTACCT SLUG-rev TTCGACCACACATTTCCT TTCGACCCACACTTTTCCACTG TWIST-RTspee CACGCCCTGTTTCTTTGAA TWIST-for GGGCCGAGAACCTTTGGCATG SMI 1-RTspee ATGGTCAGCACAGATG SMI 1-RTSpee CACGCCCTGTTTCTTTGAA TWIST-rev TTCCAAGAAAATCTTTGGCATA SMI 1-RTSpee ATGGTTGTGCATCAATGAA SMI 1-RTSpee CACGCCTGTTTCTTTGAA TWIST-rev TTCCAAGAAAATCTTTGGCATA SMI 1-RTSpee ATGGTTGTGGCATCAATGAA SMI 1-RTSPEE ATGGTTTTTGCACTG TTCCCGTTGTTTCCATGAA SMI 1-RTSPEE ATGGTTTTAAAATCTACATA AGTGAAGAACAGTCCAGACTG	EZH2-for	CGGTGTCAAACGCCAATAAA
VIM-for GACCAGCTAACCAACGACAAA VIM -rev GAAGCATCTCCTCTGCAAT CDH1-RTspee TGCTTAACCCCTCACCTTGAAGG CDH1-for GGTCGTCATGGAAGGTGCT CDH1-rev GATGGCGGCATTGTAGGT ZEB 1-RTspee GTGTAACTGCACAGGAGACA ZEB 1-for TTTTCCTGAGGCACCTGAA ZEB 1-rev TGAAAATGCATCTGGTTTCC ZEB 2-RTspee TTCTTCTCGTGGCGTACTT ZEB 2-For AGGACACTTGAGT ZEB 2-rev GGCAAAAGCATCTGGATTC SNAIL 1-RTspee GGACAGAGACCCTGAA SNAIL 1-for GCTGCAGAGGAGCA SNAIL 1-rev ATCTCCGGAGGTGGATG SLUG-RTspee GTTGGTCAGAGAGACCCCTGAA SNAIL 1-rev TTCGGAGCACCAGAGAGACCCCCGAGACCCCCCCCCCCC	EZH2-rev	CCGCTCCACTCCACATTCTC
VIM -rev GAAGCATCTCCTCGCAAT CDH1-RTspee TGCTTAACCCCTCACCTTGAAGG CDH1-for GGTCTGTCATGGAAGGTGCT CDH1-rev GATGGCGCATTGTAGGT ZEB 1-RTspee GTGTAACTGCACAGGGAGCA ZEB 1-for TTTTTCCTGAGGCACCTGAA ZEB 1-rev TGAAAATGCATCTGTTCC ZEB 2-RTspee TTCTTCTCGTGGCGGTACTT ZEB 2-rev GGCAAAAGCATCTGGATTC SNAIL 1-RTspee GGACAGGACCCTGAA SNAIL 1-for GCTGCAGGAGCCCCTGA SNAIL 1-rev ATCCCGAGGACTCTAATCCAGA SNAIL 1-rev ATCCCGAGGACTCTAATCCAGA SUG-RTspee GTTGGTCAGCAGTAGCC SLUG-rev TTCGGACCCACACATTACCCT SLUG-rev TTGGAGCACACTTTCCCCTTG SLUG-rev TTGGAGCACACATTACCT SLUG-rev TTGGAGCACACATTACCT WIST-RTspee CACCCCCTGTTTCTTTGAA TWIST-RTspee ATGGTCAGAACATCTTTTTGCACTG TWIST-RTspee ATGGTCAGAACATTTTTTGCACTG TWIST-RTspee ATGGTTGTGCATCATTACATA BMI 1-RTspee ATGGTTGTGCATCAATGAAA BMI 1-RTspee ATGGTTGTGCATCAATGAAAAATCTTTTGGCATTA BMI 1-RTspee ATGGTTGTGGCATCAATGAAAAATCTTTTGGCATTACATGAACATGAACATTACCT BMI 1-rev TTCCCAGAAAAATCTTTTGGCATTACATTACATTACATT	VIM-RTspe	AAGATTGCAGGGTGTTTTCG
CDH1-RTspee TGCTTAACCCCTCACCTTGAAGG CDH1-for GGTCTGTCATGGAAGGTGCT CDH1-rev GATGGCGCATTGTAGGT ZEB 1-RTspec GTGTAACTGCACAGGGAGCA ZEB 1-for TTTTCCTGAGGCACCTGAA ZEB 1-rev TGAAAATGCATCTGGTGTTCC ZEB 2-RTspec TTCTTCTGTGGCGGTACTT ZEB 2-rov GGCAAAAGCATCTGGAGTTC SNAIL 1-RTspec GGACAGGAGCC SNAIL 1-RTspec GGACAGGAGCC SNAIL 1-rev ATCCCGAGGAGTCC SNAIL 1-rev ATCCCGAGGAGTCC SUG-RTspec GTTGGTCAGCAGAGACCC SUG-RTspec GTTGGTCAGCACAGAGACCC SUG-RTspec GTTGGTCAGCACAGAGAAAATGCC SUG-RTspec GTTGGTCAGCACAGAGAAAATGCC SUG-Frev TTGGACCCACACATTACCT SUG-Tev TTGGAGCAGAGACCTGAATG TWIST-RTspec CACGCCTGTTTCTTTGAA TWIST-for GGGCCGGAGACCTAGATG TWIST-rev TTCCAAGAAAATCTTTTGCATG TWIST-rev TTCCAAGAAAATCTTTTGCATA BMI 1-RTspec ATGGTTGTGGCATCAATG BMI 1-RTspec TTCCAGAGATGGCCCTTG BMI 1-rev TTCCCTTGTTCGATGCATTC TBP-RTspec GTGTTAAAATCTACATA BMI 1-rev TTCCTGTTGTTCGATTC TBP-RTspec GTGTTTAAAATCTACATA TBP-For AGTGAAGAACAGTCCAGACTG	VIM-for	GACCAGCTAACCAACGACAAA
CDH1-for GGTCTGTCATGGAAGGTGCT CDH1-rev GATGGCGGCATTGTAGGT ZEB 1-RTspee GTGTAACTGCACAGGGAGCA ZEB 1-for TTTTTCCTGAGGCACCTGAA ZEB 1-rev TGAAAATGCATCTGGTGTTCC ZEB 2-RTspec TTCTTCTGTGGCGGTACTT ZEB 2-for AGGACATGTCGCCTTG ZEB 2-rev GGCAAAAGCATCTGGAGTTC SNAIL 1-RTspee GGACAGAGTCCCAGATGAGC SNAIL 1-for GCTGCAGGAGTCCCAGATGAGC SNAIL 1-rev ATCCCGGAGGTGGGAGT SLUG-RTspec GTTGGCAGAGAGAGACCC SLUG-for TTCGGACCCACACATTACCT SLUG-rev TTGGACCCACACATTACCT SLUG-rev TTGGACCCACACATTTCGAG TWIST-RTspee CACGCCCTGTTTCTTGAA TWIST-for GGGCCGGAGACCTAGATG TWIST-rev TTTCCAAGAAAATCTTTGGCATA BMI 1-RTspee ATGGTTGTGCATGAAAATCTTTGGCATA BMI 1-RTspee ATGGTTGTGCATGAAAAATCTTTGGCATA BMI 1-RTspee ATGGTTGTGCATGAAAAATCTTTGGCATA BMI 1-rev TTCCAAGAAAATCTTTCGCATTG BMI 1-rev TTCCGTTGTTCAATGCATTC TBP-RTspec GTGTTTAAAATCTACATA TBP-For AGTGAAGAACAGTCCAGACTG	VIM -rev	GAAGCATCTCCTCCTGCAAT
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ZEB 1-RTspec ZEB 1-for TTTTTCCTGAGGCACCTGAA ZEB 1-rev TGAAAATGCATCTGGTGTTCC ZEB 2-RTspec TTCTTCTCGTGGCGGTACTT ZEB 2-for AGGAGCTGTCTCGCCTTG ZEB 2-rev GGCAAAAGCATCTGGAGTTC SNAIL 1-RTspec GGCAGAAGCATCCAGATGAGC SNAIL 1-for GCTGCAGGACTCTAATCCAGA SNAIL 1-rev ATCTCCGGAGGTGGAGTG SLUG-RTspec GTTGGTCAGCACAGAGAAAATGCC SLUG-for TTCGGACCCACACATTACCT SLUG-rev TTGGAGCAGATTTTTGCACTG TWIST-RTspec CACGCCCTGTTTCTTTGAA TWIST-for GGGCCGAGAACCTTAGATC TWIST-rev ATGTCAAGAAAATCTTTGGCATA BMI 1-RTspec ATGGTTGTGCACTAGATG BMI 1-RTspec ATGGTTGTGCACTAGATG TTTCCAAGAAAATCTTTGGCATA BMI 1-rev TTCCAAGAATGCCCTTG BMI 1-rev TTCCTGTTGTTCGATGCATTC TBP-RTspec GTGTTTAAAATCTACATA TBP-for AGTGAAGAACAGTCCAGACTG	CDH1-for	GGTCTGTCATGGAAGGTGCT
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ZEB 2-RTspec ZEB 2-for AGGAGCTGTCTCGCCTTG ZEB 2-rev GGCAAAAGCATCTGGAGTTC SNAIL 1-RTspec GGACAGAGTCCCAGATGAGC SNAIL 1-for GCTGCAGGAGTCCCAGATGAGC SNAIL 1-rev ATCTCCGGAGGTGGGATG SLUG-RTspec GTTGGTCAGCACAGGAGAAAATGCC SLUG-for TTCGGACCCACACATTACCT SLUG-rev TTGGAGCAGTTTTTGCACTG TWIST-RTspec CACGCCCTGTTTCTTTGAA TWIST-for GGGCCGGAGACCTAATCCT TTTCCAAGAAAATCTTTGGCATA BMI 1-RTspec ATGGTTGTGGCATCAATG AA BMI 1-for GCTTCAAGATGGCCGTTTC BMI 1-rev TTCTCGTTGTTCGATGCATTTC TBP-RTspec GTGTTTAAAATCTACATA TBP-for AGTGAAGAACAGTCCAGACTG	ZEB 1-for	TTTTTCCTGAGGCACCTGAA
ZEB 2-for AGGAGCTGTCTCGCCTTG ZEB 2-rev GGCAAAAGCATCTGGAGTTC SNAIL 1-RTspec GGACAGAGTCCCAGATGAGC SNAIL 1-for GCTGCAGGAGTCCCAGATGAGC SNAIL 1-rev ATCTCCGGAGTGGGATG SLUG-RTspec GTTGGTCAGCACAGAGAGAAAATGCC SLUG-for TCGGACCCACACTTACCT SLUG-rev TTGGAGCAGTTTTTGCACTG TWIST-RTspec CACGCCTGTTTCTTTGAA TWIST-for GGGCCGAGACCTAGATG TWIST-rev TTTCCAAGAAAATCTTTGGCATA BMI 1-RTspec ATGGTTGTGGCATCAATG AA BMI 1-for GCTTCAAGATGGCCGCTTG BMI 1-rev TCCGTTGTTCGATGCATTC TBP-RTspec GTGTTTAAAATCTACATA TBP-for AGTGAAGAACAGTCCAGACTG	ZEB 1-rev	TGAAAATGCATCTGGTGTTCC
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SNAIL 1-for GCTGCAGGACTCTAATCCAGA SNAIL 1-rev ATCTCCGGAGGTGGGATG SLUG-RTspec GTTGGTCAGCACAGGAGAAAATGCC SLUG-for TCGGACCCACACATTACCT SLUG-rev TTGGAGCAGTTTTTGCACTG TWIST-RTspec CACGCCTGTTTCTTTGAA TWIST-for GGGCCGGAGACCTAGATG TWIST-rev TTTCCAAGAAAATCTTTGGCATA BMI 1-RTspec ATGGTTGTGGCATCAATG AA BMI 1-for GCTTCAAGATGGCCGCTTG BMI 1-rev TCCGTTGTTCGATCC TBP-RTspec GTGTTTAAAATCTACATA TBP-for AGTGAAGAACAGTCCAGACTG	ZEB 2-rev	GGCAAAAGCATCTGGAGTTC
SNAIL 1-rev ATCTCCGGAGGTGGGATG SLUG-RTspec GTTGGTCAGCACAGGAGAAAATGCC SLUG-for TTCGGACCCACACATTACCT SLUG-rev TTGGAGCAGTTTTTGCACTG TWIST-RTspec CACGCCCTGTTTCTTTGAA TWIST-for GGGCCGGAGACCTAGATG TWIST-rev TTTCCAAGAAAATCTTTGGCATA BMI 1-RTspec ATGGTTGTGGCATCAATG AA BMI 1-for GCTTCAAGATGGCCGCTTG BMI 1-rev TTCTCGTTGTTCGATGCATTC TBP-RTspec GTGTTTAAAATCTACATA TBP-for AGTGAAGACAGTCCAGACTG	SNAIL 1-RTspec	GGACAGAGTCCCAGATGAGC
SLUG-RTspec GTTGGTCAGCACAGGAGAAAATGCC SLUG-for TTCGGACCCACACATTACCT SLUG-rev TTGGAGCAGTTTTTGCACTG TWIST-RTspec CACGCCCTGTTTCTTTGAA TWIST-for GGGCCGGAGACCTAGATG TWIST-rev TTTCCAAGAAAATCTTTGGCATA BMI 1-RTspec ATGGTTGTGGCATCAATG AA BMI 1-for GCTTCAAGATGGCCGCTTG BMI 1-rev TTCTCGTTGTTCGATGCATTC TBP-RTspec GTGTTTAAAATCTACATA TBP-for AGTGAAGACAGTCCAGACTG	SNAIL 1-for	GCTGCAGGACTCTAATCCAGA
SLUG-for TTCGGACCCACACATTACCT SLUG-rev TTGGAGCAGTTTTTGCACTG TWIST-RTspec CACGCCCTGTTTCTTTGAA TWIST-for GGGCCGGAGACCTAGATG TWIST-rev TTTCCAAGAAAATCTTTGGCATA BMI 1-RTspec ATGGTTGTGGCATCAATG AA BMI 1-for GCTTCAAGATGGCCGCTTG BMI 1-rev TTCTCGTTGTTCGATGCATTC TBP-RTspec GTGTTTAAAATCTACATA TBP-for AGTGAAGAACAGTCCAGACTG	SNAIL 1-rev	ATCTCCGGAGGTGGGATG
SLUG-rev TTGGAGCAGTTTTTGCACTG TWIST-RTspec CACGCCCTGTTTCTTTGAA TWIST-for GGGCCGGAGACCTAGATG TWIST-rev TTTCCAAGAAAATCTTTGGCATA BMI 1-RTspec ATGGTTGTGGCATCAATG AA BMI 1-for GCTTCAAGATGGCCGCTTG BMI 1-rev TTCTCGTTGTTCGATGCATTC TBP-RTspec GTGTTTAAAATCTACATA TBP-for AGTGAAGAACAGTCCAGACTG	SLUG-RTspec	GTTGGTCAGCACAGGAGAAAATGCC
TWIST-RTspec CACGCCTGTTTCTTTGAA TWIST-for GGGCCGGAGACCTAGATG TWIST-rev TTTCCAAGAAAATCTTTGGCATA BMI 1-RTspec ATGGTTGTGGCATCAATG AA BMI 1-for GCTTCAAGATGGCCGCTTG BMI 1-rev TTCTCGTTGTTCGATGCATTC TBP-RTspec GTGTTTAAAATCTACATA TBP-for AGTGAAGAACAGTCCAGACTG	SLUG-for	TTCGGACCCACACATTACCT
TWIST-for GGGCCGGAGACCTAGATG TWIST-rev TTTCCAAGAAAATCTTTGGCATA BMI 1-RTspec ATGGTTGTGGCATCAATG AA BMI 1-for GCTTCAAGATGGCCGCTTG BMI 1-rev TTCTCGTTGTTCGATGCATTTC TBP-RTspec GTGTTTAAAATCTACATA TBP-for AGTGAAGAACAGTCCAGACTG	SLUG-rev	TTGGAGCAGTTTTTGCACTG
TWIST-rev TTTCCAAGAAAATCTTTGGCATA BMI 1-RTspec ATGGTTGTGGCATCAATG AA BMI 1-for GCTTCAAGATGGCCGCTTG BMI 1-rev TTCTCGTTGTTCGATGCATTC TBP-RTspec GTGTTTAAAATCTACATA TBP-for AGTGAAGAACAGTCCAGACTG	TWIST-RTspec	CACGCCTGTTTCTTTGAA
BMI 1-RTspec ATGGTTGTGGCATCAATG AA BMI 1-for GCTTCAAGATGGCCGCTTG BMI 1-rev TTCTCGTTGTTCGATGCATTTC TBP-RTspec GTGTTTAAAATCTACATA TBP-for AGTGAAGAACAGTCCAGACTG	TWIST-for	GGGCCGGAGACCTAGATG
BMI 1-for GCTTCAAGATGGCCGCTTG BMI 1-rev TTCTCGTTGTTCGATGCATTTC TBP-RTspec GTGTTTAAAATCTACATA TBP-for AGTGAAGAACAGTCCAGACTG	TWIST-rev	TTTCCAAGAAATCTTTGGCATA
BMI 1-rev TTCTCGTTGTTCGATGCATTTC TBP-RTspec GTGTTTAAAATCTACATA TBP-for AGTGAAGAACAGTCCAGACTG	BMI 1-RTspec	ATGGTTGTGGCATCAATG AA
TBP-RTspec GTGTTTAAAATCTACATA TBP-for AGTGAAGAACAGTCCAGACTG	BMI 1-for	GCTTCAAGATGGCCGCTTG
TBP-for AGTGAAGAACAGTCCAGACTG	BMI 1-rev	TTCTCGTTGTTCGATGCATTTC
	TBP-RTspec	GTGTTTAAAATCTACATA
TBP-rev CCAGGAAATAACTCTGGCTCAT	TBP-for	AGTGAAGAACAGTCCAGACTG
	TBP-rev	CCAGGAAATAACTCTGGCTCAT



Supplementary Figure S1: Absence of significant correlation between the expression of miR-200 family members and ZEB1 A. and ZEB2 B. in NMIBC samples.



Supplementary Figure S2: Absence of significant correlation between the expression of miR-200 family members and *SNAIL* A. *SLUG* B. and *TWIST* C. in NMIBC samples.



Supplementary Figure S3: Kaplan Meyer distribution corresponding to the overall survival patients included in the TCGA database according the expression of E cadherin A. Vimentin B. ZEB1 C. and ZEB2 D. Patients were discriminated by the median values of expression from RNA seq data. p Values were obtained by the log rank test.