

Epigenetic suppression of the T-box subfamily 2 (*TBX2*) in human non-small cell lung cancer

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SUPPLEMENTARY TABLES

Table S1: Members of the *TBX2* subfamily are hyper-methylated in NSCLC cell lines.

Genes	<i>TBX4</i>		<i>TBX5</i>	
	UM (%)	M (%)	UM (%)	M (%)
H1299	0	100	0.37	99.63
H1693	0	100	48.09	51.91
H1792	0.31	99.69	31.64	68.36
H23	0.04	99.96	0	100
H3255	0.21	99.79	99.95	0.05
H460	0.04	99.96	0.75	99.25
H1650	0.33	99.67	0.14	99.86
HCC827	0	100	26.42	73.58
NAC	98.73	1.27	98.8	1.2

UM, unmethylated fraction; M, methylated fraction; NAC, normal alveolar cells

Table S2: Primer sequences for *TBX2*, *TBX3*, *TBX4*, *TBX5* and *GAPDH* PCR analysis.

Gene	Sequence (5'-3')	Reference
<i>TBX2</i>	F-AGTGGATGGCTAAGCCTG	(Z. Zhang & Guo, 2014)
	R- ACGGGTTGTTGTCGATC	
<i>TBX3</i>	F-GAGGCTAAAGA ACTTTGGGATCA	Primer bank
	R- CATTTCGGGGTTCGGCCTTA	
<i>TBX4</i>	F- CACTACCAGCACGAGAAC	(Horie et al., 2017)
	R- CCAGATAGGATCGCTTGC	
<i>TBX5</i>	F- AAGTAAAGAATATCCCGTGGTC	(R. Ma et al., 2017)
	R- AGACTCGCTGCTGAAAGG	
<i>GAPDH</i>	F- GTCAGTGGTGGACCTGACCT	(Pasini et al., 2007)
	R- TCGCTGTTGAAGTCAGAGGA	

References

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