

**Table S1:** The detailed primers information of qRT-PCR, MSP, Sequenom MassARRAY quantitative methylation analysis and MeRIP-qRT-PCR

Gene	Primer	Sequence (5'-3')	Nt	Tm	Length of amplicon	GC%
<b>qRT-PCR</b>						
ZNF582-AS1	Forward	GTTCGTGTGTTTCGAGTCCCT	20	59.97	167	55.00
	Reverse	CGGAGTCAGAAGCTACCACC	20	59.83		60.00
MT-RNR1	Forward	CCTCACCACCTCTTGCTCAG	20	60.04	86	60.00
	Reverse	TTACGTGGGTACTTGCGCTT	20	59.97		50.00
MT-RNR2	Forward	GCAGCCGCTATTAAGGTTTCG	21	60.00	167	52.38
	Reverse	TATCATTTACGGGGGAAGGCG	21	59.93		52.38
RNA28SN5	Forward	GTGAGCCTTGAAGCCTAGGG	20	60.11	115	60.00
	Reverse	GGAACCCTTCTCCACTTCGG	20	60.04		60.00
U1 snRNA	Forward	GGGAGATACCATGATCACGAAGGT	24	61.78	118	50.00
	Reverse	CCACAAATTATGCAGTCGAGTTTCCC	26	62.75		46.15
GAPDH	Forward	GAAAGCCTGCCGGTGAATAA	20	60.32	113	55.00
	Reverse	GCATCACCCGGAGGAGAAAT	20	59.82		55.00
<b>MSP</b>						
ZNF582-AS1						
M Pair	MF	TAGTCGGAAGATGGCGTAGAC	21	59.05	95	52.38
	MR	GCCTAAAACTATATTTCCCGA	22	53.98		36.36
U Pair	UF	GTAGTTGGAAGATGGTGTAGATGT	24	58.02	96	41.67
	UR	ACCTAAAACTATATTTCCCAAAA	24	52.54		25.00
GAPDH	Forward	GAAAGCCTGCCGGTGAATAA	20	60.32	113	55.00
	Reverse	GCATCACCCGGAGGAGAAAT	20	59.82		55.00
<b>Sequenom MassARRAY</b>						
ZNF582-AS1	Forward	GGGTATTAGTTTTTGTGGATTTTAGA	27	59.26	394	30.00
	Reverse	AATAACACACCCAACACCACAA	22	60.05		41.00
<b>MeRIP-qRT-PCR</b>						
EEF1A1 Positive	Forward	CGGTCTCAGAACTGTTTGTTC	22	57.80	124	45.45
	Reverse	AAACCAAAGTGGTCCACAAA	20	55.88		40.00
EEF1A1 Negative	Forward	GGATGGAAAGTCACCCGTAAG	21	58.37	95	52.38
	Reverse	TTGTCAGTTGGACGAGTTGG	20	58.05		50.00
MT-RNR1	Forward	ACTGCTCGCCAGAACACTAC	20	60.04	113	55.00
	Reverse	GGTGAGGTTGATCGGGGTTT	20	59.69		55.00