

Table SI. Association of METTL3 expression with clinicopathological features of osteosarcoma.

Feature	N (n=60)	High METTL3 expression (n=30)	Low METTL3 expression (n=30)	P-value
Age, years				0.795
<18	34	18	16	
≥18	26	12	14	
Sex				0.604
Male	33	15	18	
Female	27	15	12	
Tumor size, cm				0.037
<5	27	9	18	
≥5	33	21	12	
Distant metastasis				0.020
Absent	17	4	13	
Present	43	26	17	

A total of 60 tumor tissue samples from patients with osteosarcoma was analyzed. Expression of METTL3 was assayed by reverse transcription-quantitative PCR and median expression level (1.026) was used as the cutoff. Data were analyzed by χ^2 or Fisher's exact test. $P < 0.05$. METTL3, methyltransferase-like 3.

Table SII. shRNA sequences.

Name		Sequence
METTL3	Sense	5'- CCGGAGCTACAGATCCTGAGTTAGACTCGAGTCTAACTCAG GATCTGTAGCTTTTTTG-3'
	Antisense	5'- AATTCAAAAAGCTACAGATCCTGAGTTAGACTCGAGTCTA ACTCAGGATCTGTAGCT-3'
NC	Sense	5'- CCGGCAACAAGATGAAGAGCACCAACTCGAGTTGGTGCTC TTCATCTTGTTGTTTTTG-3'
	Antisense	5'- AATTCAAAAACAACAAGATGAAGAGCACCAACTCGAGTTG GTGCTCTTCATCTTGTTG-3'
APEX1	Sense	5'- CCGGGATTAAGAAGAAAGGATTACTCGAGTAATCCTTTCTT CTTAATCTTTTTG-3'
	Antisense	5'- AATTCAAAAAGATTAAGAAGAAAGGATTACTCGAGTAATCC TTTCTTCTTAATC-3'

METTL3, methyltransferase-like 3; NC, negative control; APEX1, apurinic/apyrimidinic endodeoxyribonuclease 1.