Table SI. Primer and oligonucleotide sequences.

Sequence type	**Sense (5'-3')**	**Antisense (5'-3')**
Primers		
KIAA1429	TCAGACTGTGAGGGTTGT	CAGGGTGAGCACTTGTTA
ZFPM2-AS1	TGCCTTCCTTCCCTTAT	GACGCTCAGTCGTTACATC
GAPDH	GCACCGTCAAGGCTGAGAAC	GGATCTCGCTCCTGGAAGATG
Oligonucleotides		
shNC	GATTCTGGATTAGTGCGTCTAGCTT	AAGCTAGACGCACTAATCCAGAATC
shKIAA1429-1	CGCTGAGCAAAGTTCTCATAT	ATATGAGAACTTTGCTCAGCG
shKIAA1429-2	CCCAACGATGGCACGAATTAC	GTAATTCGTGCCATCGTTGGG
siNC	CAUGUACGUGUUUAGGGUCGAC AUU	AAUGUCGACCCUAAACACGUACAUG
siZFPM2-AS1	GCAGAGTTGCACAGAAGAA	TTGGGCAATTAATTAAGCCA
oeKIAA1429	TAAGCTTGGTACCGAGCTCGATGGCGGTGGACTCG GCGA	CCCTCTAGACTCGAGCGGCCTTATCGTGTAAAGGA GCGTACATGACGACCT

ZFPM2-AS1, friend of GATA family member 2-antisense 1; shNC, negative control shRNA; shKIAA1429, shRNA targeting KIAA1429; siNC, negative control siRNA; siZFPM2-AS1, siRNA targeting ZFPM2-AS1; oeKIAA1429, KIAA1429 overexpression; shRNA, short hairpin RNA; siRNA, small interfering RNA.

Table SII. Top 20 genes positively correlated with KIAA1429 in The Cancer Genome Atlas-TARGET-osteosarcoma dataset.

Rank	Gene name	Correlation coefficient	Adjusted_P-value	Gene type
1	DPY19L4	0.78	$1.36x10^{-14}$	Protein coding
2	NBN	0.72	$3.45x10^{-10}$	Protein coding
3	CPNE3	0.7	$4.32x10^{-9}$	Protein coding
4	SNX16	0.68	$2.23x10^{-8}$	Protein coding
5	UBR5	0.66	$1.64x10^{-7}$	Protein coding
6	TRIQK	0.66	$2.67x10^{-7}$	Protein coding
7	TGS1	0.65	$8.60x10^{-7}$	Protein coding
8	VPS13B	0.64	$1.26x10^{-6}$	Protein coding
9	ARMC1	0.64	$1.28x10^{-6}$	Protein coding
10	YTHDF3	0.64	$1.32x10^{-6}$	Protein coding
11	RMDN1	0.64	$1.69x10^{-6}$	Protein coding
12	STK3	0.63	$2.24x10^{-6}$	Protein coding
13	NUDCD1	0.63	$2.38x10^{-6}$	Protein coding
14	ZC2HC1A	0.63	$4.50x10^{-6}$	Protein coding
15	RAD54B	0.62	$5.87x10^{-6}$	Protein coding
16	RBM12B	0.62	$7.49x10^{-6}$	Protein coding
17	ZFPM2-AS1	0.62	$8.95x10^{-6}$	Long non-coding
18	ANKRD46	0.62	$1.28x10^{-5}$	Protein coding
19	PDP1	0.61	$1.73x10^{-5}$	Protein coding
20	ZFAND1	0.61	$2.54x10^{-5}$	Protein coding