## **Supplementary Tables**

Characteristics	
Age, (year)	
Mean ± SD	17.2 ± 5.6
Range	9-26
Sex	
Male	6 (46.1)
Female	7 (53.9)
Ethnicity	
Han	9 (69.2)
Minority	4 (30.8)
Smoking status	
Νο	12 (92.3)
Yes	1 (7.7)
Drinking status	
Νο	11 (84.6)
Yes	2 (15.4)
Tumour location	
Femur, n (%)	6 (46.1)
Tibia, n (%)	3 (23.1)
Humeral bone, n (%)	4 (30.8)
Enneking stage	
I, n (%)	4 (30.8)
II, n (%)	9 (69.2)
Tumour size	
≤5 cm, n (%)	4 (30.8)
>5 cm, n (%)	9 (69.2)
Pathological subtype	
Osteoblastic type	7 (53.8)
Chondroblastic type	3 (23.1)
Fibroblastic type	2 (15.4)
Telangiectatic type	1 (7.7)

**Table 2.** Primers and DNA sequences used in this study

Primer name	Primer Sequence (5'-3')
GAPDH-hF	TGACAACTTTGGTATCGTGGAAGG
GAPDH-hR	AGGCAGGGATGATGTTCTGGAGAG
circ_32279-hF	TTGCAGTGTATGTTGTCGGGTA
circ_32279-hR	TGAGTCACAAGCAACATCTGA
circ_24831-hF	CCAGCCTGTCTACATCAA
circ_24831-hR	TAAATCCGTGCTTCTCC
circ_2137-hF	TAGACTAATAAGTGACAGGGTT
circ_2137-hR	TGTTGGAAGTGGAGGGT
circ_6798-hF	CAGGGACGGCTTGATGG
circ_6798-hR	GCGAAGACAAAGTCGAGGG
circ_20403-hF	CTTTACCCAGAAATACCCAC
circ_20403-hR	TTTCCTGGATAGACCTGTTG

**Table 3.** The ten circRNAs with the largest difference in expression (upregulation, downregulation)

circ_name	location	geneName	logFC	logCPM	F	P value	FDR
circ_32279	chr7:32672154-32678977:-	DPY19L1P1	-8.8794	7.865574	32.37816	1.28E-08	5.88E-05
circ_24831	chr6:149208121-149285699:+	UST	-8.64624	6.850988	20.56511	5.78E-06	0.010905
circ_21841	chr12:50824277-50835426:+	LARP4	-8.45639	6.593937	16.61752	4.58E-05	0.029042
circ_21890	chr12:66603235-66611015:+	IRAK3	-8.42778	6.744892	18.7573	1.49E-05	0.015392
circ_22692	chr17:48814320-48819092:+	LUC7L3	-8.23093	6.407996	14.53618	0.000138	0.059889
circ_8523	chr14:71880664-71996087:+	SIPA1L1	8.451599	6.765993	18.73325	1.51E-05	0.015392
circ_2138	chr13:64576517-64608670:-	AK057471	8.512857	6.795144	19.34833	1.09E-05	0.012547
circ_2137	chr13:64564228-64608670:-	AK057471	8.579295	6.934739	20.5156	5.93E-06	0.010905
circ_6798	chr16:29917108-29917448:+	ASPHD1	9.122766	8.217934	40.84021	1.67E-10	1.54E-06
circ_20403	chr2:106774513-106782539:-	UXS1	10.33314	8.42944	48.26512	3.79E-12	6.96E-08

miRNA	Frequency
hsa-miR-4691-5p	24
hsa-miR-4731-5p	23
hsa-miR-3692-5p	22
hsa-miR-6764-5p	22
hsa-miR-8089	22
hsa-miR-6851-5p	21
hsa-miR-4685-5p	20
hsa-miR-762	20
hsa-miR-3064-5p	19
hsa-miR-5193	19

Table 4. The miRNA frequency

Table 5. The circRNA information in the network diagram

circ_name	location	Host_geneName	isoformName	Regulate
circ_2137	chr13:64564228-64608670:-	AK057471	uc001vii.1	UP
circ_23401	chr18:6263945-6312055:-	L3MBTL4	ENST00000400105	DOWN
circ_2138	chr13:64576517-64608670:-	AK057471	uc001vii.1	UP
circ_20486	chr2:122260742-122287901:-	CLASP1	uc010yyy.2	UP
circ_2868	chr12:70193988-70195501:+	RAB3IP	ENST00000247833	DOWN
circ_8917	chr19:2213537-2214595:+	DOT1L	ENST00000398665	UP
circ_18566	chr4:183245098-183268082:+	TENM3	ENST00000513201	UP
circ_32537	chr1:17668437-17668897:+	PADI4	uc009vpc.2	DOWN
circ_24851	chr6:154520801-154535410:-	IPCEF1	NM_001130699	DOWN
circ_16365	chr6:145148746-145157074:+	UTRN	NM_007124	DOWN
circ_3517	chr11:6962801-6977013:+	ZNF215	uc001mez.1	DOWN
circ_10351	chr7:23381682-23391205:-	IGF2BP3	NM_006547	UP
circ_15993	chr6:47251673-47254331:-	TNFRSF21	NM_014452	UP
circ_5670	chr17:34881058-34884033:-	MYO19	ENST00000431794	UP
circ_23338	chr19:8619360-8619627:-	MYO1F	NM_012335	DOWN
circ_15000	chr9:88233897-88248289:-	AGTPBP1	uc004aod.4	DOWN