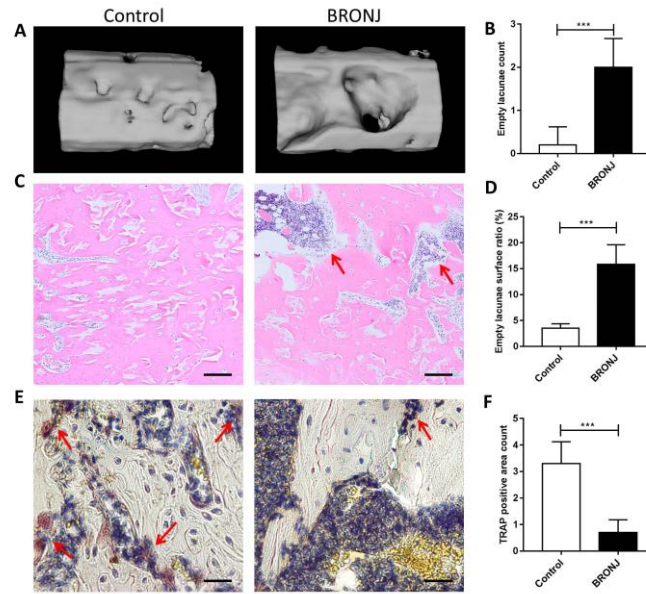
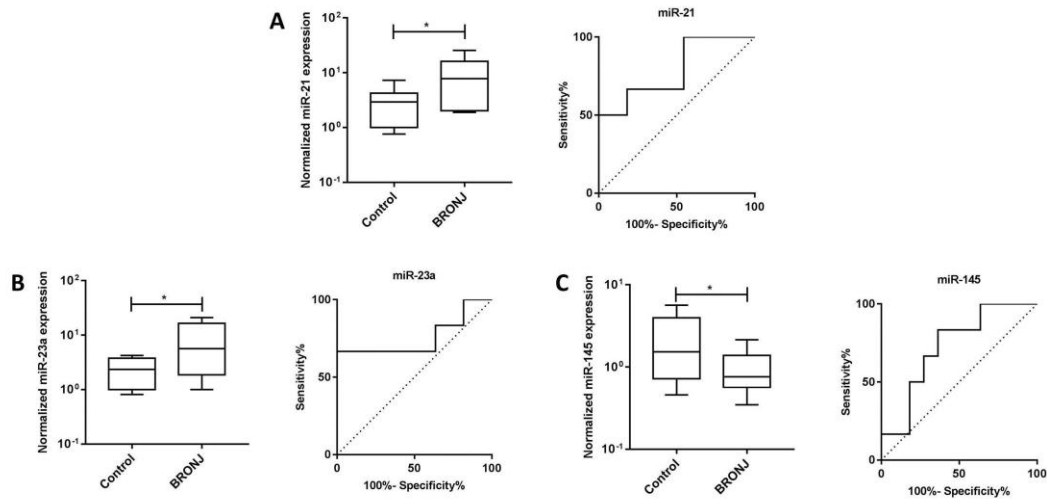


Supplementary data



**Figure S1.** The microCT scanning (A), empty lacunae count (B), HE staining (scale bar, 500  $\mu$ m) (C), empty lacunae surface ratio (D), TRAP staining (scale bar, 100  $\mu$ m) (E) and TRAP positive area count (F) of Control and BRONJ groups. Red arrows in (C) showed the bone lesion and inflammatory infiltration, red arrows in (E) showed TRAP positive area.



**Figure S2.** The normalized expressions and ROC curves of hsa-miR-21, hsa-miR-23a and hsa-miR-145 in the human sera of the control (n=11) and BRONJ (n=6) groups (\*p < 0.05).

Table S1. Clinical information of participants

	Control (n=11)	BRONJ (n=6)	<i>p</i> value
Age (years)	56.3 (49.0—68.0)	58.1 (47.0—66.0)	0.552
Gender(M/F)	0/11	0/6	\
Height (cm)	154.3 (148.0—165.0)	152.8 (146.0—163.0)	0.539
Weight (kg)	53.9 (43.0—67.0)	51.2 (47.0—65.0)	0.514

Table S2. Forward primer sequences

microRNA	Forward primer
Rno-miR-21	TAGCTTATCAGACTGATGTTGA
Rno-miR-23a	GGGGTTCCTGGGGATG
Rno-miR-28	CAGAAGGAGCTCACAGTCT
Rno-miR-124-1	CGTGTTACAGCGGACCTTGAT
Rno-miR-129-1	CTTTTTCGGTCTGGGCTTGC
Rno-miR-145	GTCCAGTTTTCCAGGAATC
Rno-miR-149	CTGGCTCCGTGTCTTC
Hsa-miR-21	TGTCGGGTAGCTTATCAGACTG
Hsa-miR-23a	TTCCTGGGGATGGGATT
Hsa-miR-145	ACCTTGCCTCACGGTCC