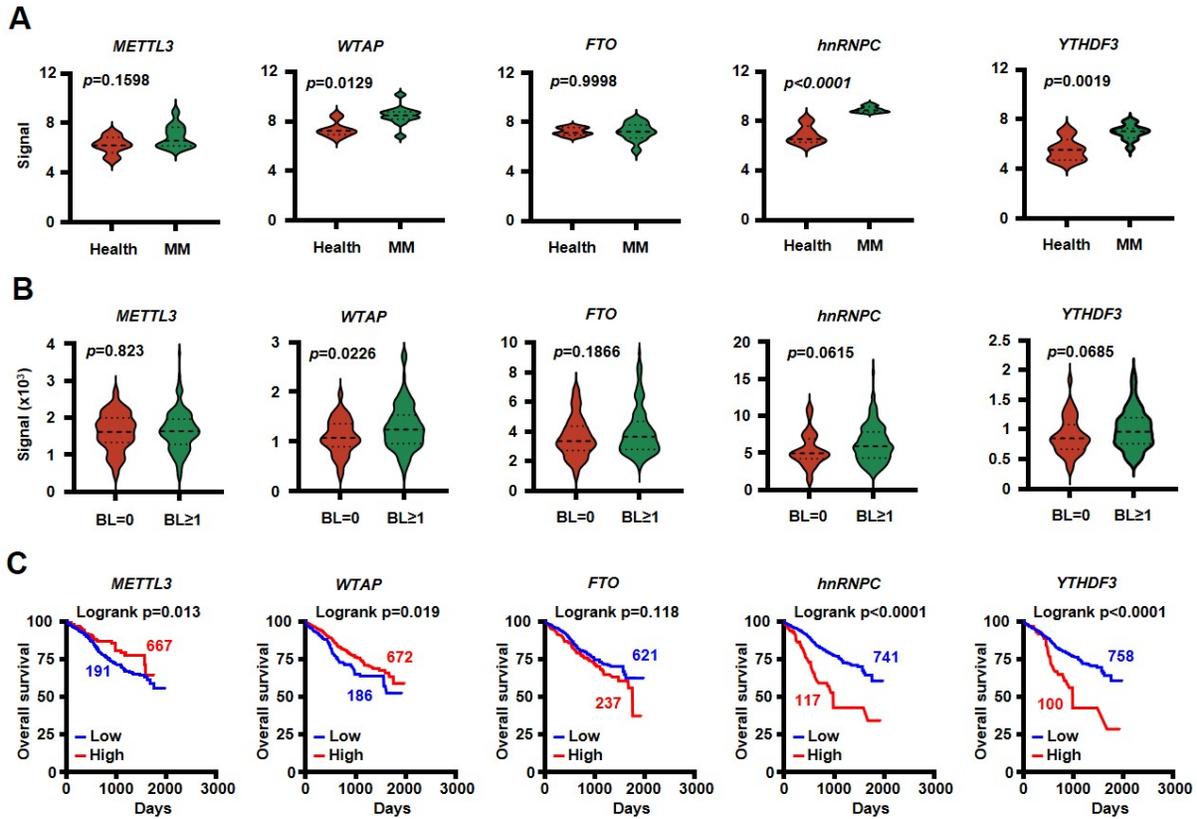


1 **Supplementary Figures**



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3 **Figure S1. m6A family genes mRNA levels in GSE6691 or GSE755 datasets and analysis of**
 4 **survival.**

5 (A) *METTL3*, *WTAP*, *FTO*, *hnRNPC* and *YTHDF3* mRNA levels in the plasma cells from
 6 myeloma patients (n = 12) compared to normal plasma cells from healthy donors (n = 5) (GEO:
 7 GSE6691). (B) *METTL3*, *WTAP*, *FTO*, *hnRNPC* and *YTHDF3* mRNA levels in malignant
 8 plasma cells of 37 myeloma patients without bone lesion (BL = 0) and 136 myeloma patients
 9 with bone lesion (BL ≥ 1) (GEO: GSE755). Data shown as averages ± SD. P values were
 10 determined by Student's *t* test. (C) Overall survivals in myeloma patients with high or low
 11 *METTL3*, *WTAP*, *FTO*, *hnRNPC* or *YTHDF3* expression.

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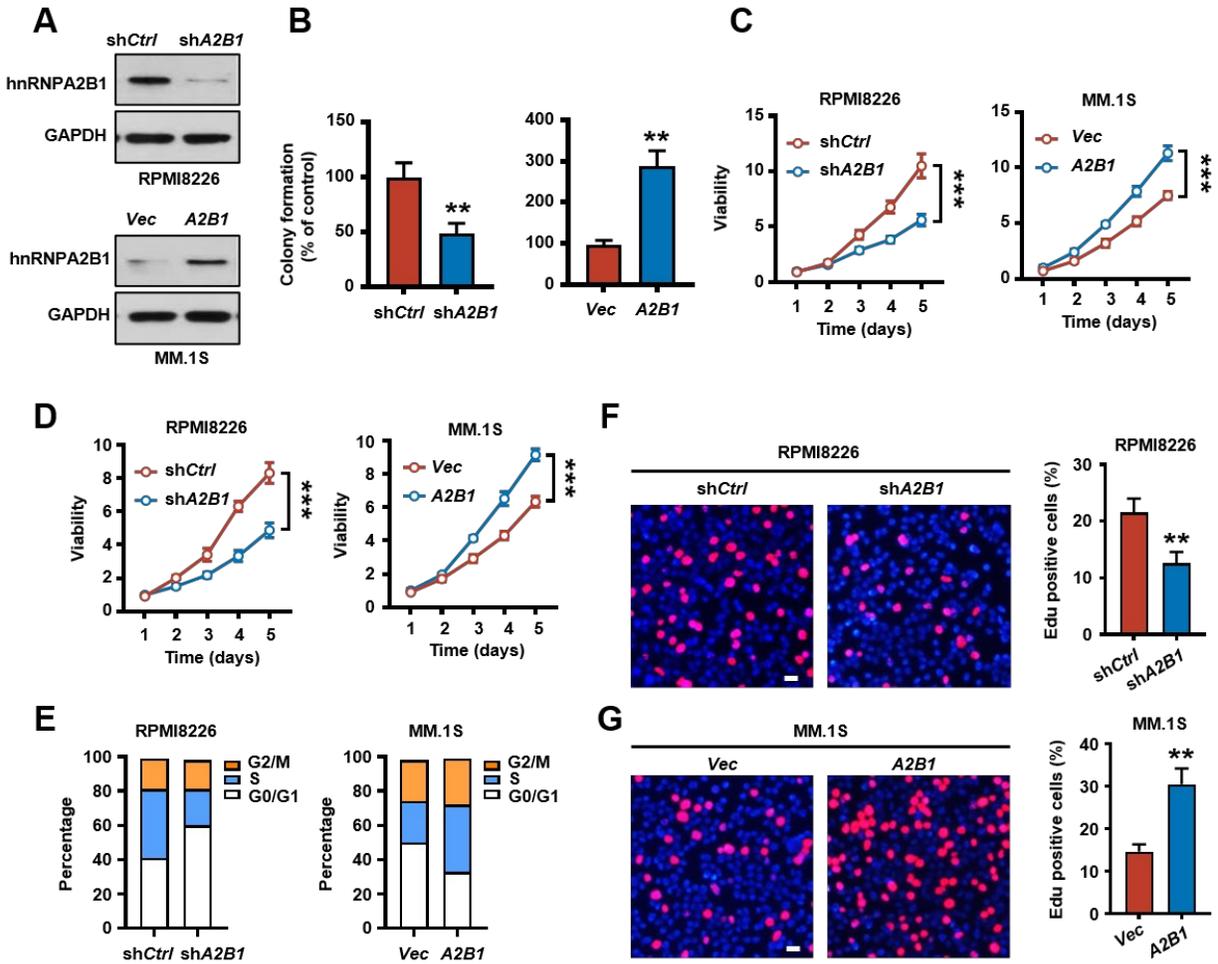
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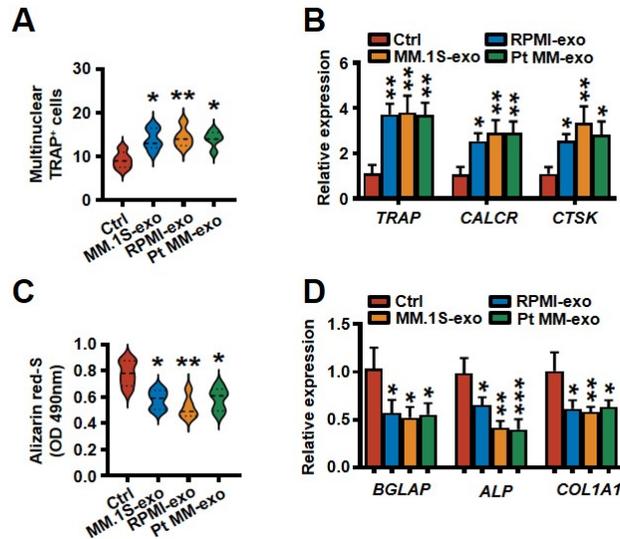
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19 **Figure S2. hnRNPA2B1 is associated with the growth of myeloma cells.**

20 (A) Western blot shows expression of hnRNPA2B1 in RPMI8226 cells transfected with non-
 21 targeted shRNA (shCtrl) or *hnRNPA2B1* shRNA (shA2B1). MM.1S transfected with
 22 *hnRNPA2B1* cDNA (A2B1) or control vector (Vec). GAPDH served as western blot analysis
 23 loading control. (B) Summarized data for relative colony formation (colonies formed in shCtrl or
 24 Vec cells set to 100%). *P* values were determined by Student's *t* test. (C) Proliferation of
 25 RPMI8226 cells (shCtrl or shA2B1) or MM.1S cells (Vec or A2B1) in culture for 4 days, as
 26 determined by CellTiter-Glo Luminescent Cell Viability Assay. (D) CCK-8 assay showed the
 27 proliferation of RPMI8226 cells (shCtrl or shA2B1) or MM.1S cells (Vec or A2B1) in culture for
 28 4 days. (E) Cell cycle analysis was performed with flow cytometry in RPMI8226 cells (shCtrl or
 29 shA2B1) or MM.1S cells (Vec or A2B1). *P* values were determined using one-way ANOVA. (F,
 30 G) Representative images and the percentage of EdU-positive cells of RPMI8226 cells (shCtrl or
 31 shA2B1) or MM.1S cells (Vec or A2B1), as determined by EdU staining assay. Scale bar, 10 μ m.

32 *P* values were determined by Student's *t* test. Data are averages \pm SD. Each experiment was
33 repeated three times. ***P* < 0.01; ****P* < 0.001.

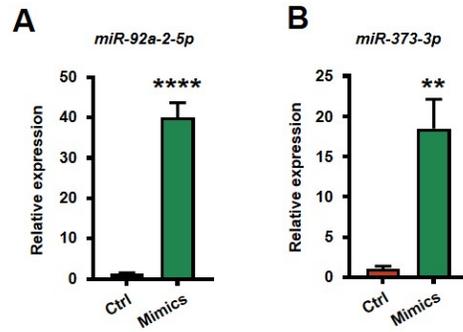
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63 **Figure S3. Myeloma cells exosomes enhance osteoclast differentiation and inhibit osteoblast**
 64 **differentiation *in vitro*.**

65 Precursors of osteoclasts were cultured in osteoclast medium treated with exosomes (20 $\mu\text{g/ml}$)
 66 isolated from MM.1S culture medium (MM.1S-exo), RPMI8226 culture medium (RPMI-exo) or
 67 patient myeloma cells culture medium (Pt MM-exo). Shown are the numbers of multinuclear (\geq
 68 3) TRAP⁺ cells (A) and relative expression of the *TRAP*, *CALCR*, and *CTSK* genes (B). MSCs
 69 were cultured in osteoblast medium treated with MM.1S-exo, RPMI-exo or Pt MM-exo (20
 70 $\mu\text{g/ml}$). Shown are the summarized data of Alizarin red S staining (C) and the relative expression
 71 of *BGLAP*, *ALP*, and *COL1A1* genes (D). Addition of PBS served as a control. Data are averages
 72 \pm SD. Each experiment was repeated three times. * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$. All P
 73 values were determined using one-way ANOVA.

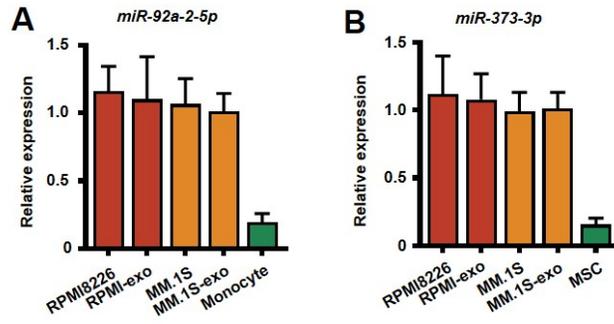
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81 **Figure S4. miR-92a-2-5p and miR-373-3p expression levels in monocytes or MSC**
 82 **transfected with miRNA mimics.**

83 Quantitative real-time PCR analysis shows the relative expression of *miR-92a-2-5p* (A) or *miR-*
 84 *373-3p* (B) in precursors of osteoclasts or MSCs transfected with *miR-92a-2-5p* or *miR-373-3p*
 85 mimics. Data are averages \pm SD. Each experiment was repeated three times. ** $P < 0.01$; **** P
 86 < 0.0001 . P values were determined by Student's t test.

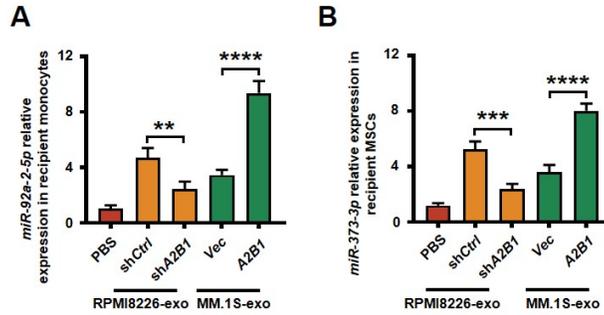
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105 **Figure S5. miR-92a-2-5p and miR-373-3p expression levels in myeloma cells, exosomes,**
 106 **monocytes and MSCs.**

107 Quantitative real-time PCR analysis shows the relative expression of *miR-92a-2-5p* (A) or *miR-*
 108 *373-3p* (B) in myeloma cells (RPMI8226, MM.1S), myeloma cells exosomes (RPMI-exo,
 109 MM.1S-exo), monocytes or MSCs. Data are averages \pm SD. Each experiment was repeated three
 110 times.

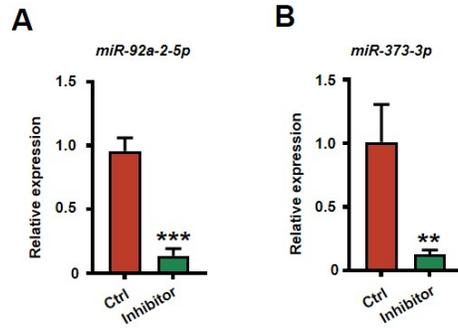
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130 **Figure S6. miR-92a-2-5p and miR-373-3p are packaged into exosomes and transported to**
 131 **recipient monocytes or MSCs.**

132 Quantitative real-time PCR analysis shows the relative expression of *miR-92a-2-5p* (A) or *miR-*
 133 *373-3p* (B) in recipient cells treated with exosomes isolated from RPMI8226 (shCtrl, shA2B1)
 134 and MM.1S (Vec, A2B1). Data are averages \pm SD. Each experiment was repeated three times.
 135 ** $P < 0.01$; *** $P < 0.001$; **** $P < 0.0001$. All P values were determined using one-way
 136 ANOVA.

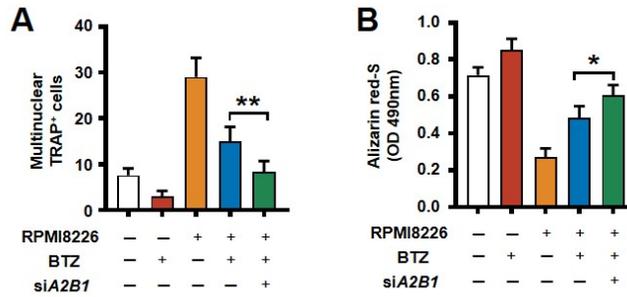
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154 **Figure S7. miR-92a-2-5p and miR-373-3p expression levels in monocytes or MSCs**
 155 **transfected with miRNA inhibitors.**

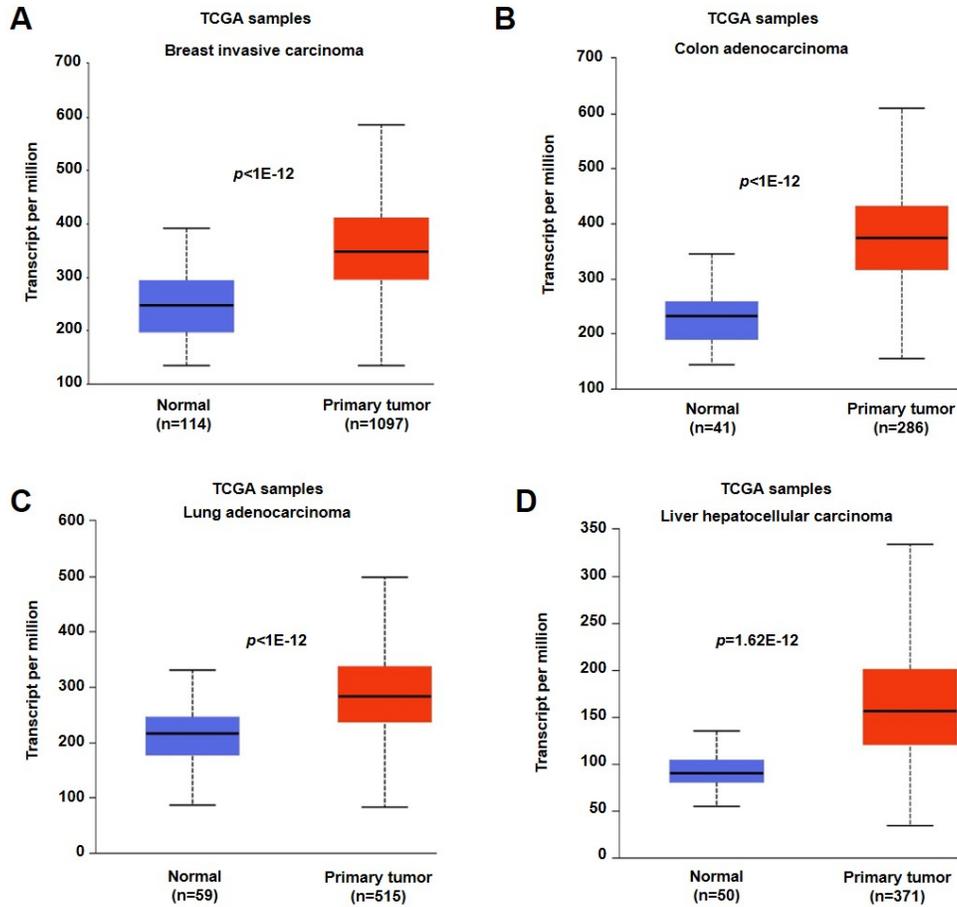
156 Quantitative real-time PCR analysis shows the relative expression of *miR-92a-2-5p* (A) or *miR-*
 157 *373-3p* (B) in precursors of osteoclasts or MSCs transfected with *miR-92a-2-5p* or *miR-373-3p*
 158 inhibitors. Data are averages \pm SD. Each experiment was repeated three times. ** $P < 0.01$; *** P
 159 < 0.001 . P values were determined by Student's t test.

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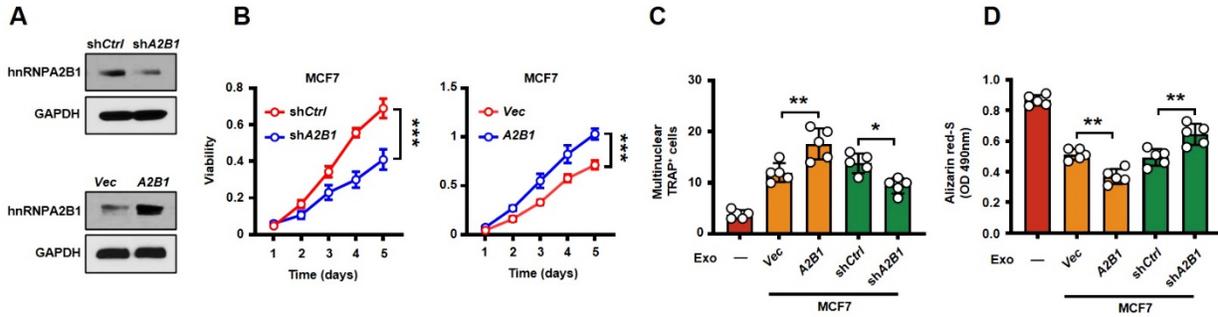
179 **Figure S8. Knockdown of hnRNPA2B1 promotes bortezomib efficiency in controlling**
 180 **myeloma-associated osteoclastogenesis activation and osteoblastogenesis inhibition.**
 181 Precursors of osteoclasts or MSCs were co-cultured with RPMI8226 cells transfected with or
 182 without siRNA against *hnRNPA2B1* (siA2B1) in the presence of bortezomib (10 nM) or not.
 183 Shown are the numbers of multinuclear (≥ 3) TRAP⁺ cells (**A**) and summarized data of Alizarin
 184 red S staining (**B**). Data are averages \pm SD. Each experiment was repeated three times. * $P <$
 185 0.05; ** $P <$ 0.01. All P values were determined using one-way ANOVA.

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204 **Figure S9. Expression of hnRNPA2B1 is elevated in some types of solid tumors.**
 205 Analysis of TCGA data assessing the *hnRNPA2B1* mRNA gene expression of in breast cancer
 206 cells (A), colon cancer cells (B), lung cancer cells (C) and liver cancer cells (D) compared with
 207 normal cells. Data are represented as mean \pm SD. *P* values were determined by Student's *t* test.

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Figure S10. Breast cancer cells *hnRNPA2B1* promote tumor cell growth, enhance osteoclastogenesis or inhibit osteoblastogenesis via exosomes.

(A) Western blot shows expression of *hnRNPA2B1* in MCF7 cells transfected with non-targeted shRNA (*shCtrl*) or *hnRNPA2B1* shRNA (*shA2B1*). MCF7 transfected with *hnRNPA2B1* cDNA (*A2B1*) or control vector (*Vec*). GAPDH served as loading control. (B) Proliferation of MCF7 (*Vec* and *A2B1*) or MCF7 (*shCtrl* and *shA2B1*) cells in culture for 4 days. Precursors of osteoclasts or MSCs were cultured in osteoclast medium or osteoblast medium treated with exosomes (20 $\mu\text{g/ml}$) isolated from MCF7 (*Vec* and *A2B1*) or MCF7 (*shCtrl* and *shA2B1*) cells culture medium. Shown are numbers of multinuclear (≥ 3) TRAP⁺ cells (C) and summarized data of Alizarin red S staining (D). Addition of PBS served as control. Data are averages \pm SD. Each experiment was repeated three times. * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$. All P values were determined using one-way ANOVA.

244 **Supplementary tables**245 **Table 1. Primers used in real time reverse transcription PCR analysis**

Gene	Forward	Reverse
<i>GAPDH</i>	CTGGGCTACTGAGCACC	AAGTGGTCGTTGAGGGCAATG
<i>hnRNP2B1</i>	ATTGATGGGAGAGTAGTTGAGCC	AATTCCGCCAACAAACAGCTT
<i>TRAP</i>	AGATCCTGGGTGCAGACTTC	AAGGGAGCGGTCAGAGAATA
<i>CALCR</i>	GGGAATCCAGTTTGTCGTCT	ACAAAGAAGCCCTGGAAATG
<i>CTSK</i>	CCATATGTGGGACAGGAAGA	CCTCTTCAGGGCTTTCTCAT
<i>BGLAP</i>	ACTGTGACGAGTTGGCTGAC	AAGAGGAAAGAAGGGTGCCT
<i>ALP</i>	TCCCAGTTGAGGAGGAGAAC	CCCAGGAAGATGATGAGGTT
<i>COL1A1</i>	TGTCAGCTTTGTGGACCTC	GGTGATTGGTGGGATGTCTT
<i>RUNX2</i>	TCAACGATCTGAGATTTGTGGG	GGGGAGGATTTGTGAAGACGG
<i>NFATc1</i>	CACCGCATCACAGGGAAGAC	GCACAGTCAATGACGGCTC

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256 **Table 2. Luciferase assay primers.**

Name	Forward	Reverse
<i>pGL2-IRF8</i>	CATCTCGAGCCAGGTCTTC CGGATGTTTCCAG	CAGAAGCTTCACCGACA TCTCGGCAGGGC
<i>pGL2-IRF8-Mut</i>	GATGGATGCAGGACGCA GACGGCCGTTAACGCCCA AGCGACGCACTTAGAC	GTCTAAGTGCCTCGCTT GGGCGTTAACGGCCGTCTG CGTCCTGCATCCATC
<i>pGL2-RUNX2</i>	CATCTCGAGAGCTTGAAG CACACCACTGTCCA	CAGAAGCTTTGGTTGGAG TGAGGGTGGAGGG
<i>pGL2-RUNX2-Mut</i>	AAATGTGTAACCAGACAC TGGCTTTTTTAAGGTAGG CTGAAACAAACACACATA TTTTACACTTAC	GTAAGTGTAATAATATGTGTGT TTGTTTCAGCCTACCTTAAAA AAGCCAGTGTCTGGTTAC ACATTT

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