OMTN, Volume 11

# **Supplemental Information**

## miR-208a-3p Suppresses Osteoblast

## **Differentiation and Inhibits Bone**

# Formation by Targeting ACVR1

Yasir Arfat, Muhammad Asim R. Basra, Muhammad Shahzad, Kashif Majeed, Nasir Mahmood, and Hina Munir

### **Supplementary Information**

#### **Supplementary Figure 1**



**Supplementary Figure 1**. Mechanical unloading increases bone resorption and inhibit bone mass *in vivo* (A-F). (A) Schematic diagram illustrating the experimental design (6-months-old, male mice n = 8). (B)

 $\mu$ CT of the distal femur. Trabecular bone parameters include bone volume/tissue volume ratio (BV/TV), trabecular separation (Tb. Sp) trabecular number (TB. N) and trabecular thickness (Tb. Th). (C) Representative images are showing three dimensional trabecular reconstructive architecture in distal femurs of baseline, control and HLU mice. (D)  $\mu$ CT measurements of bone mineral density (BMD) and bone mineral content (BMC). (E) Histomorphometric analysis of bone formation-related parameters (Ob.S/BS, MAR, BFR, and N.Ob/B.Pm) in baseline, control and HLU mice (F) qPCR analysis of bone formation-marker genes ALP, Col1a1 and OCN. All data were expressed as means ± SD. Significance is noted at these thresholds: \**P* < 0.05, \*\**P* < 0.01, \*\*\**P* < 0.001. One-way ANOVA with a *post-hoc* test was performed. Statistical differences between two groups were determined by Student's *t* test. n=8 mice in each group.

#### **Supplementary Figure 2A**



**Supplementary Figure 2B** 



### **Supplementary Figure 2C**



**Supplementary Figure 2D** 



**Supplementary Figure 2.** Summary of physical and biochemical analysis. Mice of each group were weighed daily for the first four days and then every two days. Every three days, cages were cleaned. Feeders and bottles were refilled with food and water every day. Weights were presented with  $\pm$ SD for each condition of housing. Each experimental group was compared to the others n = 6 mice per group. Differences were found to be statistically significant using *t* test. (A) represents body weight (B) calcium analysis in serum and urine (C) Soleus and Gastrocnemius muscle weight (D) Effect of unloading on femoral strength as assessed by three-

point; Area moment of Inertia; Bending energy absorption; Elastic modulus; Maximum force; Stiffness coefficient. All data were expressed as means  $\pm$  SD. Significance is noted at these thresholds: \**P* < 0.05, \*\**P* < 0.01, \*\*\**P* < 0.001. One-way ANOVA with a post-hoc test was performed. Statistical differences between two groups were determined by Student's t test. n=8 mice in each group.

#### **Supplementary Figure 3A**



**Figure 3**. miR-208a-3p targets ACVR1 to functionally inhibit osteoblast activity *in vitro*. (A) Relationship between miR-208a-3p and ACVR1 mRNA level (determined by real-time PCR) during osteoblast mineralization in MC3T3-E1 cells.

#### **Supplementary Figure 4A**



### **Supplementary Figure 4B**

Predicted consequential pairing of target region (top)		p) Seed	
	and miRNA (bottom)	match	Pcr
Position 1101-11053 of ACVR1 3'UTR	5'-CGGCCUAAGGACAGUCUAGACUG-	IIIIIIII 8mer	
mmu-miR-208	3' GCCGGAUGACGAGCAGAGAGCGC		

**Supplementary Figure 4.** Bioinformatics analysis predicted the relationship between miR-208a-3p and *ACVR1*. (A) Bioinformatics analysis by using miRNA target prediction software programs: TargetScan, miRanda, and miRWalk to screen for miR-208 targeting genes. (B) Bioinformatics analysis using TargetScan to predict relationship of miR-208 and its target gene MACF1and conserved site in UTR.

### **Supplementary Tables**

#### Supplementary Table 1. MiRNAs primer sequence

microRNAs	Primer sequence (5'to3')
mmu-miR-30	CUUUCAGUCGGAUGUUUGCAGC
mmu-miR-33-5p	GUGCAUUGUAGUUGCAUUGCA
mmu-miR-96-5p	UUUGGCACUAGCACAUUUUUGCU
mmu-miR-103a	AGCAGCAUUGUACAGGGCUAUCA
mmu-miR-130b-5p	ACUCUUUCCCUGUUGCACUACU
mmu-miR-137	ACGGGUAUUCUUGGGUGGAUAAU
mmu-miR-140-5p	CAGUGGUUUUACCCUAUGGUAG
mmu-miR-148a-3p	UCAGUGCACUACAGAACUUUGU
mmu-miR-154-3p	AAUCAUACACGGUUGACCUAUU
mmu-miR-183-5p	UAUGGCACUGGUAGAAUUCACU
mmu-miR-208a-3p	AUAAGACGAGCAAAAAGCUUGU
Mmu-miR-365-3p	UAAUGCCCCUAAAAAUCCUUAU
Mmu-miR-384-5p	UGUAAACAAUUCCUAGGCAAUGU
mmu-miR-542-3p	UGUGACAGAUUGAUAACUGAAA
U6-Forward	GTGCTCGCTTCGGCA GCA CATAT
U6-Reverse	AAAATATGGAA CGCTTCACGAA

Gene name	Primer sequence (5'to3')	
ACVR1-forward	GCAACCAAGAACGCCTCAATC	
ACVR1-Reverse	TTTCCCGACACACTCCAACAG	
GAPDH- Forward	TGCACCACCAACTGCTTAG	
GAPDH- Reverse	GGATGCAGGGATGATGTTC	
ALP - Forward	GTTGCCAAGCTGGGAAGAACAC	
ALP - Reverse	CCCACCCCGCTATTCCAAAC	
Col Ial-Forward	GAAGGCAACAGTCGATTCACC	
Col Ial - Reverse	GACTGTCTTGCCCCAAGTTCC	
Ocn–Forward	GAACAGACTCCGGCGCTA	
<i>Ocn</i> –Reverse	AGGGAGGATCAAGTCCCG	
<i>Runx2</i> –Forward	TGCACCTACCAGCCTCACCATAC	
<i>Runx2</i> – Reverse	GACAGCGACTTCATTCGACTTCC	
BMP2–Forward	CGAGACCTTCCAGATCACAGT	
<i>BMP2</i> – Reverse	GGGGAAGCAGCAACACTAGA	
Smad1- Forward	ACGCTGCTCATCCCACTAAT	
Smad1–Reverse	AGTTCCGCGTCATCCTGATA	
Smad5- Forward	AACCTGAGCCACAATGAACC	
Smad5– Reverse	GTGGCATATAGGCAGGAGGA	

Supplementary Table 2: mRNA primer sequence