OMTN, Volume 26

## **Supplemental information**

## ac4C acetylation of RUNX2 catalyzed by NAT10

#### spurs osteogenesis of BMSCs and

### prevents ovariectomy-induced bone loss

W. Yang, H.Y. Li, Y.F. Wu, R.J. Mi, W.Z. Liu, X. Shen, Y.X. Lu, Y.H. Jiang, M.J. Ma, and H.Y. Shen

#### Supplementary data

	Normal control	Postmenopausal osteoporosis Patients	
Number	6	6	
Age (years)	56.38±6.98	65.45±6.82	
Sex	Female	Female	
Hight (cm)	156.35±7.49	154.94±5.64	
Weight (kg)	56.85±7.68	58.16±5.37	
BMI (kg/m <sup>2</sup> )	23.79±2.74	22.62±3.53	
Age of menarche			
(years)	14.25±2.04	13.16±1.18	
Age of menopause			
(years)	50.35±3.57	52.43±2.82	
Lumbar spine BMD			
(g/cm <sup>2</sup> )	1.53±0.24	0.56±0.31*	
Lumbar spine T score	0.35±1.07	-2.63±1.16*	
Total hip BMD			
(g/cm <sup>2</sup> )	1.15±0.24	0.61±0.17*	
Total hip <i>T</i> score	0.37±1.12	-1.83±0.58*	

### Table S1: Characteristics of the study subjects.

Data are shown as the mean  $\pm$  SD, n=6 in each group. P values for all variables are the result of independent t tests between the control and osteoporosis groups. \*p < 0.05, \*\*p < 0.01. BMI: body mass index; BMD: bone mineral density.

Species	NCBI	Gene	Forward Primer	Reverse Primer
	Gene ID	Name		
Human	2597	GAPDH	AAGGTGAAGGTCGGAGTCAA	AATGAAGGGGTCATTGATGG
Human	55226	NAT10	ATTCACACCGTAAGCAGCGA	CAGGTCATTCGGGGGTCTGTC
Mouse	98956	NAT10	CACAAACATTCGCTACTGCTACT	AACGCTTCAAAATCCTGGAGG
Human	860	RUNX2	AAAGACAAGCACAAGTAAATC	CATAATTGAACCCTCTATCCA
Human	4088	SMAD3	ATAGGTGCTTTGGGCGTATG	CTCTTGCCCTTTTCAACTGTCC
Human	3371	TNC	CAAAGATGTCCCAGTGACTGTC	CGCATTGTCCTAAGTTGTTGC
Human	1277	COL1A1	GCCTCAAGGTATTGCTGGAC	ACCTTGTTTGCCAGGTTCAC
Human	121340	Osterix	CCTCTGCGGGACTCAACAAC	AGCCCATTAGTGCTTGTAAAGG

# Supplementary Table 2: Primers of the analyzed genes

# Supplementary Table 3: The siRNA sequences of the analyzed genes.

Gene Name	Sense (5'-3')	Antisense (5'-3')
NAT10	GGGCCAGGCUGAACUAGUUTT	AACUAGUUCAGCCUGGCCCTT
siRNA1		
NAT10	GCAUUUGGGUACUCCAAUATT	UAUUGGAGUACCCAAAUGCTT
siRNA2		
Negative	UUCUCCGAACGUGUCACGUTT	ACGUGACACGUUCGGAGAATT
control		



Figure S1. Remodelin inhibits the osteogenic differentiation of BMSCs in vitro.

(A) Dot blot analysis demonstrated that the ac4C level of total RNA decreased in BMSCs treated with 20  $\mu$ M Remodelin, n=6. (B) Densitometry quantitation of (A), n=6. (C) Remodelin decreased calcium nodule formation (upper panels) and ALP staining (lower panels) (scale bar=250  $\mu$ m), n=6. (D) ARS staining was quantified as the absorbance at 562 nm, n=6. (E) ALP activity was determined as units per gram of protein per 15 min, n=6. (F) Remodelin decreased protein levels of the markers of osteoblast differentiation, RUNX2 and Osterix during osteogenic induction, n=6. (G) Quantification of band intensities, n=6. All data are presented as the means ± SDs. \**p* < 0.05, \*\**p* < 0.01 (n = 3 independent experiments).



Figure S2. NAT10 does not regulate the decay rate of Osterix during osteogenic differentiation. (A) The decay rate of mRNA and qPCR analysis of RUNX2 at the indicated times after overexpressing NAT10 and treating with Remodelin, n=6. (B) RUNX2 expression was quantified by qPCR after overexpressing NAT10 and treating with Remodelin, n=6. (C) qPCR analysis of Osterix at the indicated times after silencing NAT10, n=6. (D) Osterix expression was quantified by qPCR after silencing NAT10, n=6. (D) Osterix expression was quantified by a quantified by qPCR after silencing NAT10, n=6. (D) Osterix expression was quantified by a quantified by qPCR after silencing NAT10, n=6. (D) Osterix expression was quantified by qPCR after silencing NAT10, n=6. (D) Osterix expression was quantified by qPCR after silencing NAT10, n=6. (D) Osterix expression was quantified by qPCR after silencing NAT10, n=6. (D) Osterix expression was quantified by qPCR after silencing NAT10, n=6. (D) Osterix expression was quantified by qPCR after silencing NAT10, n=6. (D) Osterix expression was quantified by qPCR after silencing NAT10, n=6. (D) Osterix expression was quantified by qPCR after silencing NAT10, n=6. (D) Osterix expression was quantified by qPCR after silencing NAT10, n=6. (D) Osterix expression was quantified by qPCR after silencing NAT10, n=6. (D) Osterix expression was quantified by qPCR after silencing NAT10, n=6. (D) Osterix expression was quantified by qPCR after silencing NAT10, n=6. (D) Osterix expression was quantified by qPCR after silencing NAT10, n=6. (D) Osterix expression was quantified by qPCR after silencing NAT10, n=6. (D) Osterix expression was quantified by qPCR after silencing NAT10, n=6. (D) Osterix expression was quantified by qPCR after silencing NAT10, n=6. (D) Osterix expression was quantified by qPCR after silencing NAT10, n=6. (D) Osterix expression was quantified by qPCR after silencing NAT10, n=6. (D) Osterix expression was quantified by qPCR after silencing NAT10, n=6. (D) Osterix expression was quantified by

Data S1. The ac4C Peak locations of differentially acetylated genes.

Data S2. Gene ontology (GO) enrichment analysis of the differentially acetylated genes.