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Supplemental Information

Promotion Effects of miR-375 on the Osteogenic Differentiation of Human Adipose-Derived Mesenchymal Stem Cells

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Supplemental Figures:



Figure S1 (related to main figure 2). Transduction efficiency of lentivirus containing miR-375, anti-miR-375, or control vectors. (A) Micrographs of GFP-positive hASCs under ordinary and fluorescent light. Scale bars: 500 μ m. (B) Left: relative miR-375 expression in miR-375 and NC groups as determined by qRT-PCR. Right: relative miR-375 expression in anti-miR-375 and anti-NC groups as determined by qRT-PCR. U6 was used for normalization. Data are represented as mean \pm SD; *p < 0.05, **p < 0.01 (n = 3 independent experiments).



Figure S2 (related to main figure 2). miR-375 knockdown inhibits the osteogenic differentiation of hASCs. hASCs were transfected with lentivirus expressing anti-miR-375 or control vector (anti-NC), and cultured in proliferation medium (PM) or osteogenic medium (OM). (A) Alkaline phosphatase (ALP) staining on day 7, Alizarin Red S (ARS) staining on day 14, and von Kossa (VK) staining on day 21 after osteogenic induction. (B) ALP activity on day 7 and ARS mineralization assay on day 14 after osteogenic induction. (C) Relative mRNA levels of *RUNX2* and *ALP* measured by qRT-PCR on day 7 of osteogenic induction. Relative mRNA levels of *OSX* and *OCN* measured by qRT-PCR on day 14 of osteogenic induction. *GAPDH* was used for normalization. (D) Confocal microscopy of OCN with DAPI counterstaining on day 14 after osteogenic induction. Scale bars:

200 μ m. (E) Left: western blot of OCN protein level on day 14 after osteogenic induction. GAPDH was used as the internal control. Right: quantification of band intensities. Data are represented as mean ± SD; *p < 0.05, **p < 0.01 (n = 3 independent experiments).



Figure S3 (related to main figure 3). miR-375 overexpression promotes heterotopic bone formation in vivo. (A) Representative micro-CT images of bone formation in miR-375 and NC groups. (B) Quantitative analysis of bone volume/tissue volume (BV/TV) and bone surface/tissue volume (BS/TV) in miR-375 and NC groups. Data are represented as mean \pm SD; *p < 0.05, **p < 0.01 (n = 3 independent experiments).



Figure S4 (related to main figure 7). miR-375 suppresses *YAP1* via directly targeting its 3'UTR. (A) Binding site of miR-375 in the 3'UTR of *YAP1*-WT mRNA (mutated bases in the 3'UTR of *YAP1*-MT are underlined). (B) Luciferase activity of cells with miR-375 overexpression in the *YAP1*-WT or *YAP1*-MT groups. (C) Relative mRNA and protein levels of YAP1 in miR-375 and NC groups as determined by qRT-PCR and western blot. GAPDH was used for normalization and the internal control. (D) Relative mRNA levels of *YAP1* at various time points during the osteogenic differentiation of hASCs as determined by qRT-PCR. *GAPDH* was used for normalization. Data are represented as mean ± SD; *p < 0.05, **p < 0.01 (n = 3 independent experiments).



Figure S5 (related to main figure 7). Knockdown of *YAP1* enhanced the osteogenic differentiation of hASCs. (A) Alkaline phosphatase (ALP) staining on day 7 and Alizarin Red S (ARS) staining on day 14 after osteogenic induction. (B) ALP activity on day 7 and ARS mineralization assay on day 14 after osteogenic induction. (C) Relative mRNA levels of *RUNX2* and *OCN* as determined by qRT-PCR on day 14 of osteogenic induction. *GAPDH* was used for normalization. Data are represented as mean \pm SD; *p < 0.05, **p < 0.01 (n = 3 independent experiments).

Supplemental Tables

Upregulation		Downregulation	
Gene Name	Fold Change	Gene Name	Fold Change
MMP1	8.0583	DEPTOR	0.3794
MMP3	5.8323	ERG1	0.399
COL10AQ	3.633	MGARP	0.404
PARRES2	2.6751	CTSC	0.4061
ADRA2A	2.5316	MEST	0.4194
CXCL5	2.391	FRZB	0.4449
COL10A1	2.2842	INMT	0.4455
AKRICI	2.2155	SERPINB2	0.4468
CD163	2.1417	FHL1	0.4661
G0S2	2.0636	HSPB7	0.4697
		FAM43A	0.4709
		EFHD1	0.473
		KPTAP1-5	0.4809
		ELN	0.4836

Table S1. Gene expression in the osteogenic differentiation of hASCs transfected with miR-375 by microarray analysis (p < 0.001).

Table 1 shows the fold changes of gene expression: ≥ 2 indicates upregulation and ≤ 0.5 indicates downregulation. *DEPTOR* decreased most among the downregulated genes with miR-375 overexpression in hASCs.

Table S2. Sequences of RNA and DNA oligonucleotides.

Name	Sense Strand/Sense Primer (5'-3')	Antisense Strand/Antisense Primer (5'-3')		
siRNA				
DEPTOR1	GUCAUCAUCUCAAGACCUATT	UAGGUCUUGAGAUGAUGACTT		
DEPTOR2	GUCUGUCAGUUUGUCGUCUTT	AGACGACAAACUGACAGACTT		
<i>YAP1-</i> 1	GGUGAUACUAUCAACCAAATT	UUUGGUUGAUAGUAUCACCTT		
YAP1-2	GACGACCAAUAGCUCAGAUTT	AUCUGAGCUAUUGGUCGUCTT		
NC	UUCUCCGAACGUGUCACGUTT	ACGUGACACGUUCGGAGAATT		
Primers for a	IRT-PCR			
miR-375 RT primer GCTGTCAACGATACGCTACCTAACGGCATGACAGTGTCAGCCTA				
miR-375	GTGCAGGGTCCGAGGT	AGCCGTTTGTTCGTTCGGCT		
U6	CTCGCTTCGGCAGCACA	AACGCTTCACGAATTTGCGT		
RUNX2	CCGCCTCAGTGATTTAGGGC	GGGTCTGTAATCTGACTCTGTCC		
ALP	ATGGGATGGGTGTCTCCACA	CCACGAAGGGGAACTTGTC		
OSX	CCTCTGCGGGACTCAACAAC	TAAAGGGGCTGGATAAGCAT		
OCN	CACTCCTCGCCCTATTGGC	CCCTCCTGCTTGGACACAAAG		
DEPTOR	TTTGTGGTGCGAGGAAGTAA	CATTGCTTTGTGTCATTCTGG		
YAPI	ACCCTCGTTTTGCCATGAAC	TTGTTTCAACCGCAGTCTCTC		
GAPDH	GAAGGTGAAGGTCGGAGTC	GAAGATGGTGATGGGATTTC		
Primers for ChIP-qPCR				
Ch-1	CCAGTAGCACTACATTTGGGTTAA	CTGTGGCAGCCATGACATTC		
Ch-2	CGTGGGCAACATAGCAAGAC	GCACCTCAGCCTCCAAAGTAA		
Ch-3	GGTGCCGTACTTCCGCCAATT	CTCCTCCAACTCTTCTTCTTCCTCTTC		
Ch-4	GTGGTGCCACTTCCTACCGA	CCCTGCCATCCTTCCCTCT		
Ch-5	GGTCGAGGTCACCACTGGATT	AGGGAGGAGCCGAGAAGCA		

Abbreviation: *DEPTOR*, dep-domain containing mTOR-interacting protein; *YAP1*, Yes-associated protein 1. *RUNX2*, runt-related transcription factor 2; *ALP*, alkaline phosphatase; *OSX*, osterix; *OCN*, osteocalcin.