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Supplemental Information

**miR-892b Inhibits Hypertrophy
by Targeting KLF10 in the Chondrogenesis
of Mesenchymal Stem Cells**

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SUPPLEMENTARY TABLES

Table S1. Primer List for Cloning of Gene Expression Plasmids

Plasmid name	Sequences (5' to 3')	Direction	Product	Restriction Enzyme site
pCDH-miR-892b-copGFP	GCTAGCTGGAGAGCAGTGGGATGAGCATT	Forward	miR-892b	NheI-EcoRI
	GAATTCATCTTGAGGATGCCTGAGGTCCA	Reverse		
pECFP-hKLF10	AGATCTATGCTCAACTTCGGTGCCTC	Forward	KLF10	BglIII-SalI
	GTCGACTCACTGTGTGGGAGCAGG	Reverse		
pLKO.1-shKLF10-C1	CCGGGAGTATGTATTCCCTGGAACAACCTCGAG TTGTTCCAGGAATACATACTCTTTTTG	Forward	KLF10 shRNA	AgeI-EcoRI
	AATTCAAAAAGAGTATGTATTCCCTGGAACAA CTCGAGTTGTTCCAGGAATACATACTC	Reverse		
pLKO.1-shKLF10-C2	CCGGGAACCCTCTCAAGTGTCAAATCTCGA GATTTGACACTTGAGAGGGTCTTTTTG	Forward	KLF10 shRNA	AgeI-EcoRI
	AATTCAAAAAGAACCCTCTCAAGTGTCAAA TCTCGAGATTTGACACTTGAGAGGGTTC	Reverse		
pMIR-KLF10-3'UTR-WT	CTAGTTTGGTCTCAGCGGGAGCCAGTGA	Forward	KLF10 3'- UTR	SpeI-HindIII
	AGCTTCACTGGCTCCCGCTGAGACCAAA	Reverse		
pMIR-KLF10-3'UTR-MUT	CTAGTTTGGTCTCAGCGGGAATTCATGA	Forward	KLF10 3'- UTR	SpeI-HindIII
	AGCTTCATGAATCCCGCTGAGACCAAA	Reverse		
pMIR-WNT6-3'UTR-WT	CTAGTTTAGACTGGAAAAAAGCCAGTCA	Forward	WNT6 3'- UTR	SpeI-HindIII
	AGCTTGACTGGCTTTTTTCCAGTCTAAA	Reverse		
pMIR-WNT6-3'UTR-MUT	CTAGTTTAGACTGGAAAAAATTCATCA	Forward	WNT6 3'- UTR	SpeI-HindIII
	AGCTTGATGAATTTTTTCCAGTCTAAA	Reverse		

Table S2. Primers and Probes List

Experiment	Gene or Probe	Sequences (5' to 3')	Direction	Accession No.	
Rq-PCR (Human)	<i>Col2a1</i>	AACCAGATTGAGAGCATCCG ACCTTCATGGCGTCCAAG	Forward Reverse	NM_033150	
	<i>Sox9</i>	ACTTGCAACAACGCCGAG CTGGTACTTGTAATCCGGGTG	Forward Reverse	NM_000346	
	<i>Col1a1</i>	CCCCTGGAAAGAATGGAGATG TCCAAACCACTGAAACCTCTG	Forward Reverse	NM_000088	
	<i>Col10a1</i>	ACGATACCAAAATGCCACAG GTACCTTGCTCTCCTTACTG	Forward Reverse	NM_000493	
	<i>Klf10</i>	AAAGTTCATCTGAAGGCC TCACAACCTTTCCAGCTACAG	Forward Reverse	NM_001032282	
	<i>Ihh</i>	ATGAAGGCAAGATCGCTCG GATAGCCAGCGAGTTCAGG	Forward Reverse	NM_002181	
	<i>Ptch1</i>	TCTTGGTGTGGTGTGGATG ATTGCTGATGGACGTGAGG	Forward Reverse	NM_000264	
	<i>Ptch2</i>	TGCTCTTTCTGGGACTGTTG AGCTTCTCCTTGGTGTAAATGC	Forward Reverse	NM_003738	
	<i>Smo</i>	ACAGCTACATCGCGCCCTTC AACAGCAGGGTAGCGATTTCGAG	Forward Reverse	NM_005631	
	<i>Gli-2</i>	AGCAGCAGCAACTGTCTGAGTGA GACCTTGCTGCGCTTGTGAA	Forward Reverse	NM_005270	
	<i>Wnt3a</i>	ATCAAGATTGGCATCCAGGAG CAATGGCGTGGACAAAGG	Forward Reverse	NM_033131	
	<i>Wnt7a</i>	GGGACTATGAACCGGAAAGC GGCCTGGGATCTTGTTACAG	Forward Reverse	NM_004625	
	<i>Wnt6</i>	GAGAGTGCCAGTTCAGTTC TGATGGCGAACACGAAGG	Forward Reverse	NM_006522	
	<i>Wnt9b</i>	AGTGCCAGTTTCAGTTCCG GGAAAGCTGTCTCTTGAAGC	Forward Reverse	NM_003396	
	<i>Ctnnb1</i>	GTTTCAAGTTCGTTGTTGCTGC GTTGTGAACATCCCGAGCTAG	Forward Reverse	NM_001098209	
	<i>Alpl</i>	GACAAGAAGCCCTTCACTGC AGACTGCGCCTGGTAGTTGT	Forward Reverse	NM_000478	
	<i>Gapdh</i>	ACATCGCTCAGACACCATG TGTAGTTGAGGTCAATGAAGGG	Forward Reverse	NM_002046	
	Northern blot	hsa-miR-892b	Bio-TCTACCCAGAAAGGAGCCAGTG	Anti-sense	MI0005538
	EMSA	IHPro-753-P1	AGGTTTGCGCCTGGCGGGGCACCCAGAGCC GGCTCTGGGGTGCCCGCCAGGCGCAAACCT	Top Bottom	
		IHpro-710-P2	AGGCGAGGCCAGGGCGGGGTGGGGCGCGTCC GGACGCGCCCCACCCCGCCCTGGCCTCGCCT	Top Bottom	
IHpro-689-P3		GGGGCGCGTCCAGGCGGGGAGGGCAAACCTCG CGAGTTTGCCCTCCCCGCTGGACGCGCCCC	Top Bottom		
ChIP	IHpro-345	TGGGTTGCGGTCTCCGTG	Forward		
		GGAAATGGAAGAGATCCGGGC	Reverse		
Genotyping	mKLF10-5-15	CCT TCCTGCCAACAACCTCTC	Forward		
	mKLF10-3-25	TCTGAGGAGTGACCCTTGCT	Reverse		
	Neo-5-1	TCGCCTTCTTGACGAGTTCT	Forward		

Table S3. Antibody List

Name	Experiments	Type	Manufacturer (Cat No.)	Dilution Ratio	React. Buffer/ Ag. retrieval
<i>COL2A1</i>	Western blotting	Ms Monoclonal	EMD Millipore (MAB8887)	1/1,000	PBS-T
<i>SOX9</i>	Western blotting	Rb Polyclonal	Abcam (ab59265)	1/1,000	PBS-T
<i>COL1A1</i>	Western blotting	Ms Monoclonal	Abcam (ab90395)	1/500	PBS-T
<i>COL10A1</i>	Western blotting	Rb Polyclonal	Abcam (ab58632)	1/500	TBS-T
<i>ALP</i>	Western blotting	Ms Monoclonal	Abcam (ab54778)	1/1,000	PBS-T
<i>KLF10</i>	Western blotting	Rb Polyclonal	Abcam (ab73537)	1/1,000	PBS-T
	IHC			1/100	Citrate Bfr. /20 min at 95°C
<i>IHH</i>	Western blotting	Rb Monoclonal	Abcam (ab52919)	1/2,000	PBS-T
	IHC			1/200	0.2% Triton X-100 /20 min at RT
<i>PTCH1</i>	Western blotting	Rb Polyclonal	Abcam (ab53715)	1/1,000	PBS-T
<i>PTCH2</i>	Western blotting	Rb Polyclonal	Thermo Scientific (PA1-46223)	1/1,000	PBS-T
<i>SMO</i>	Western blotting	Rb Polyclonal	Abcam (ab38686)	1/1,000	PBS-T
<i>GLI-2</i>	Western blotting	Rb Polyclonal	Abcam (ab26056)	1/1,000	PBS-T
<i>WNT3A</i>	Western blotting	Rb Polyclonal	Abcam (ab28472)	1/1,000	PBS-T
<i>WNT6</i>	Western blotting	Rb Polyclonal	Biovision (3570-100)	1/500	PBS-T
<i>WNT7A</i>	Western blotting	Rb Polyclonal	Abcam (ab100792)	1/500	PBS-T
<i>WNT9B</i>	Western blotting	Rb Polyclonal	Abcam (ab69287)	1/500	PBS-T
<i>β-catenin</i>	Western blotting	Ms Monoclonal	Santa Cruz (sc-59737)	1/1,000	PBS-T
<i>GAPDH</i>	Western blotting	Ms Monoclonal	Santa Cruz (sc-47724)	1/1,000	TBS-T
<i>KLF10</i>	ChIP	Rb Polyclonal	GeneTex (GTX108661)	1/500	50 mM HEPES, 140mM NaCl, 1mM EDTA
<i>Osteocalcin</i>	IHC	Ms Monoclonal	Abcam (ab13418)	1/80	Pepsin Enzymatic /20 min at RT

SUPPLEMENTARY FIGURES

Figure S1

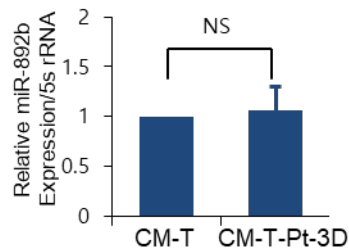


Figure S1. Expression of miR-892b induced by PTHrP at the early stage of chondrogenic differentiation.

PTHrP was treated only for the first 3 days of chondrogenic culture. The expression of miR-892b was analyzed after 3 weeks of differentiation, and compared with the group not treated with PTHrP. The data are shown as the mean \pm SD, NS = not significant ($P = 0.56$), 2-tailed Student's t-test, $n = 3$ donors.

Figure S2

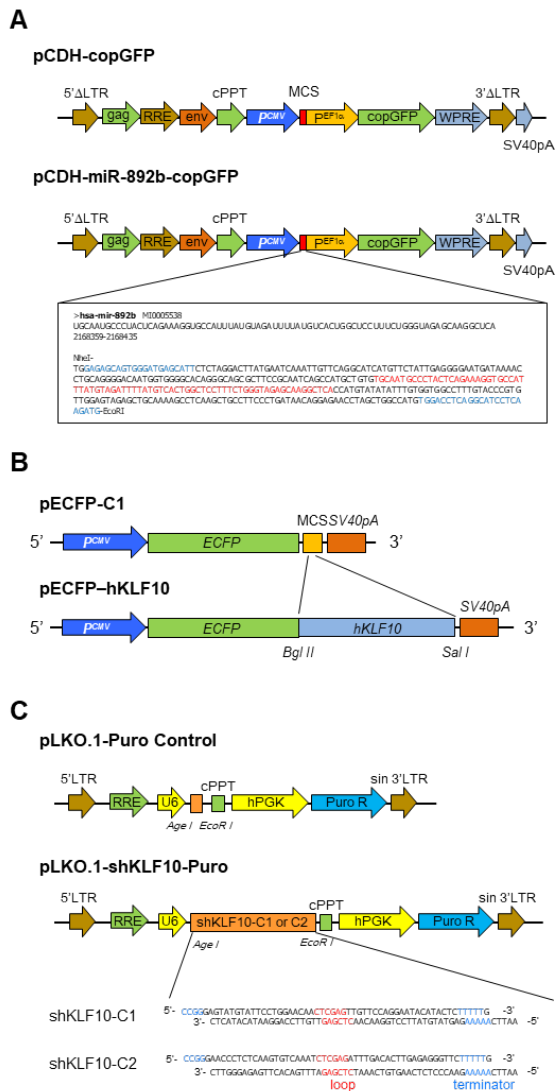


Figure S2. Construction of gene expression plasmids.

(A) After genomic DNA PCR, an intron fragment containing pre-miR-892b gene was cloned into NheI-EcoRI sites of pCDH-copGFP lentiviral plasmid. The blue letters represent PCR priming sites, and the red letters represent a sequence correspond to pri-miR-892b. (B) Human KLF10 gene amplified from cDNA of hMSCs was cloned into BglII-SalI sites of pECFP-C1 nonviral plasmid. The hKLF10 gene is fused to ECFP gene, enhanced cyan fluorescent protein. (C) pLKO.1 lentiviral plasmid was used to construct a lentiviral plasmid expressing KLF10 shRNAs. KLF10 shRNAs were designed by BLOCK-iTTM RNAi Designer (Thermo Scientific). The top and bottom single strands correspond to hKLF10 shRNAs was annealed, respectively, and then ligated to AgeI-EcoRI sites of pLKO.1 lentiviral plasmids.

Figure S3

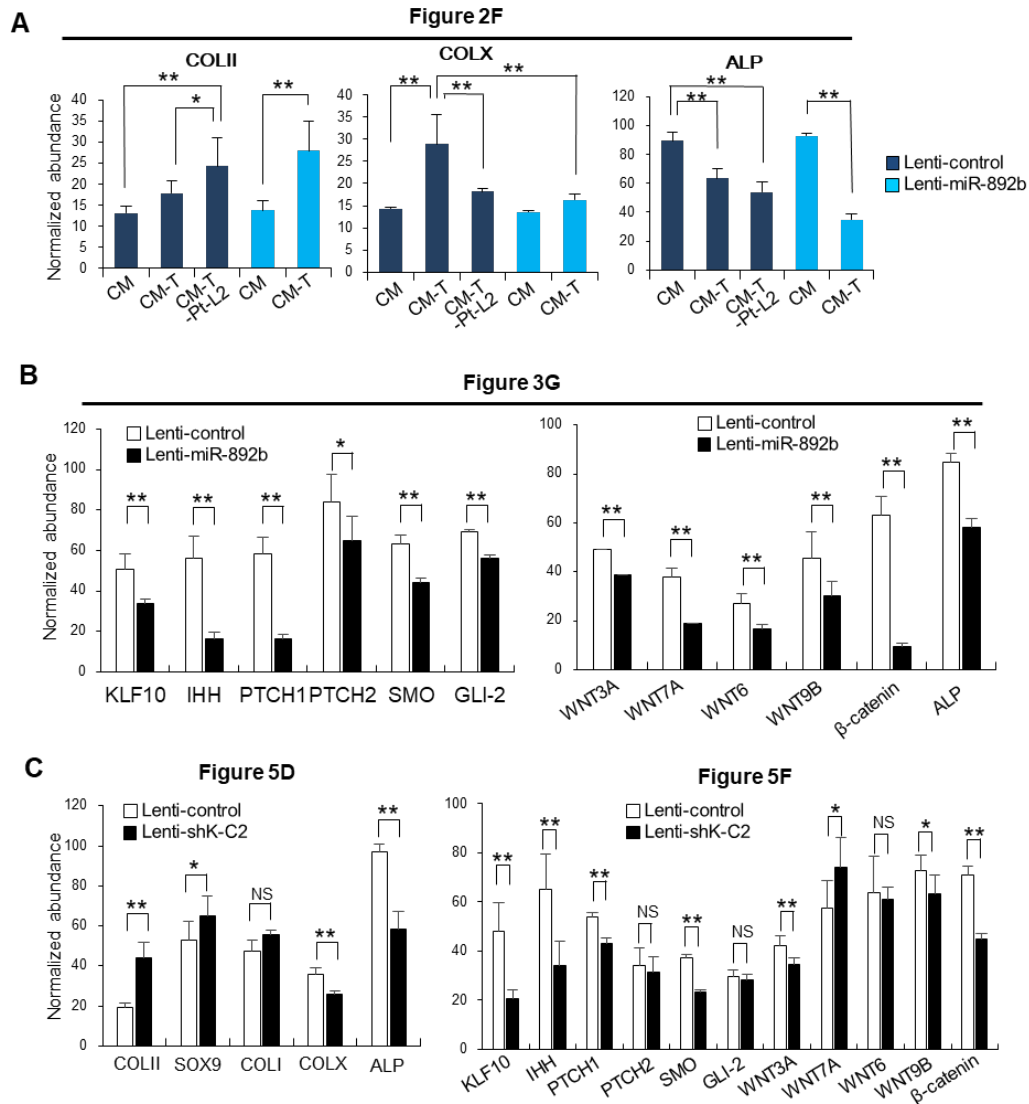


Figure S3. Statistical quantification of western blot image (by ImageJ).

The Western band was quantified using the ImageJ program, normalized to GAPDH band and statistically processed. (A) Statistical quantification of Figure 2F. The data are shown as the mean \pm SD, * $p < 0.05$, ** $p < 0.01$, one-way ANOVA followed by the Tukey test. (B) Statistical quantification of Figure 3G. The data are shown as the mean \pm SD, * $p < 0.05$, ** $p < 0.01$ by paired, 2-tailed Student's t-test. (C) Statistical quantification of Figure 5D and 5F. The data are shown as the mean \pm SD, * $p < 0.05$, ** $p < 0.01$, NS = not significant, by paired, 2-tailed Student's t-test.

Figure S4

IHH-836 bp promoter sequence within pGL4-836 vector

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-1203
AGATCTTTGGCTGCCCTCTTTAACATGGTCAGTCGGGGTTCTCTGGTAT
TCTGTTGACGTCACCAATTTTAGCTACCCCTTCTCTGCATATTGACCTATC
CCTTTGCAACTTCATATTGTCACTTTCAACAGTGTTCCTCAACTTAAAC
CCCTATTTGACTCTTCAAAGGGCTAGACTCCCCATCCCCAGTTTGACA
CCGACAGGCAGGCTGTGGGATGTGCACCAGGTTGATACAGAACCAGCT
CCACCAAGCTGAAGGGCGCTCGCCCGGGCCAGGGTGGGGCACCAGGT
TATGAGTGGCTCCTGCCTTTTGGGTTTGGCTTCCCCGCAGGGGACACCG
TAGGGGCTGTGGCTCCGGCCACTGCCCCCGCCCTCGCGTCCGGCC

ChIP Forward
GCGCCGTTGGGTGGCGGTCTCCGTGGGGTGGCAGCTCCTGTCCGGGAGG
TTTGGCCCTGGCGGGCACCACAGAGCCGGAAGAGCCGGTAGGGCGAGG
-753GGATGGG-747 pGL4-836-M1
CCAGGGGGGGTGGGGCGCGTCCAGGGGGGAGGGCAAACCTCGGGCAGC
-710GGATGGG-703 pGL4-836-M2
-689GGATGGG-683 pGL4-836-M3
GCAGGGGGCGCAGAGGGCAGCGGGCGGGCGGACGCGGGCGGAGGCGCG
AGCGGGACGAGGGCTGGCTAGTGCCGGGGCCGCCGCCGAGGGGGAGG
AGGCTGTGCTGCCCTTGTGTCAGGTTGCTGTGAGCGCACAGGAGGCA
GGGACATGGGTAGGGTGGGTCTGCGCGGGGCCCCGAGCCCGGATCTCTT
CCATTTCCCTCTCACTCGGCCCGGGCTGCGCCGACAGCGGCAGCAGC
ChIP Reverse
TCCCGCTCCGCCCGAGCCGCTGACCGCCGGGCCGGGTTGCTAACCGCG
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- 367

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Figure S4. Point mutation of GC-rich regions within Indian hedgehog proximal promoter.

Nucleotide sequence represent an 836-bp fragment containing three predicted SP1/KLF10 binding sites. The GGCGGGG binding sites were substituted to GGATGGG by gene synthesis. The mutated 836-bp fragments were respectively synthesized and subcloned to pGL4 vector.