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## **Supplemental information**

### MicroRNA-378 contributes to osteoarthritis

#### by regulating chondrocyte autophagy and

#### bone marrow mesenchymal stem cell chondrogenesis

Lu Feng, Zhengmeng Yang, Yucong Li, Qi Pan, Xiaoting Zhang, Xiaomin Wu, Jessica Hiu Tung Lo, Haixing Wang, Shanshan Bai, Xuan Lu, Ming Wang, Sien Lin, Xiaohua Pan, and Gang Li



**Supplementary Figure 1. A.** The best, representative and worst results of Safranin O/fast green staining of OA mice cartilage. **B.** Semi-quantitative analysis of OA score. OA cartilage histopathology grade and stage were evaluated accordingly. OA score=grade X stage.

OA cartilage histopathology grade: Grade 0, cartilage surface intact; Grade 1, surface intact; Grade 2, surface discontinuity; Grade 3, vertical fissures; Grade 4, erosion; Grade 5, denudation; Grade 6, deformation. OA cartilage histopathology stage: Stage 0, No OA activity seen; Stage 1, <10%; Stage 2 10-25%; Stage 3, 25-50%; Stage, 4 > 50%.



Supplementary Figure 2. Negative control of IHC staining of Col X and Mmp13 positive chondrocytes without primary antibodies application in articular cartilage of WT and miR-378 TG mice at the age of 3-month-old and 12-month-old at low magnitude. Sections were counterstained with hematoxylin (Scale bar= $200 \,\mu$ m).



**Supplementary 3. A.** Micro-CT image reconstruction of subchondral bone in WT and miR-378 TG mice at the age of 12 months. **B-E.** The BMD (**B**), BV/TV (%) (**C**), Tb.Th (**D**) and Tb.Sp (**E**) were also evaluated (n=8, \*p<0.05).



**Supplementary Figure 4. A&B.** Safranin O&fast green staining (A) and OARSI scores (B) of knee joint cartilage collected from both Sham and OA groups at week 3 and week 6 post ACLT+DMM surgery (n=8, \*\*\*p<0.001).



Supplementary Figure 5. A&B. miR-378 expression level in cartilage of WT and miR-378 TG mice (A) and in chondrocyte of WT and miR-378 TG mice with/without IL-1 $\beta$  treatment were studied by using Real-time PCR (B). The relative miRNA expression was normalized to mmu-miR-103a-3p (n=4; \*\*p<0.01, \*\*\*p<0.001).



Supplementary Figure 6. A-G. Semi-quantitative analysis of all the Western blot bands in Figure 3F (A), 3G (B), 4G (C), 5C (D), 5I (E), 5J (F) and 6C (G) (n=3; \*p<0.05, \*\*p<0.01, \*\*\*p<0.001).



**Supplementary Figure 7. A&B.** Semi-quantitative analysis of cell fluorescence in Figure 3H (A) and 5K (B) (n=6; p<0.05, p<0.01, p<0.001).



**Supplementary Figure 8.** A&B. Semi-quantitative analysis of IHC staining in Figure 4A (A) and 6I (B) (n=6; \*p<0.05, \*\*p<0.01).



**Supplementary Figure 9.** Schematic diagram to show the miRNA target gene screening procedure. The TargetScan and ENCORI software were applied for *in silico* analysis of conserved 3'-UTR binding sites of miR-378 target genes respectively. The overlapped genes were listed.



Supplementary Figure 10. A. The anti-miR-378-3p mediated lentivirus infected in articular cartilage 4 weeks after OA induction. Scale bar: 100  $\mu$ m. B. The miR-378-3p expression level in cartilage of miR-378 TG mice upon receiving anti-NC and anti-miR-378-3p lentivirus injection was detected by Real-time PCR analysis. The relative miRNA expression was normalized to mmu-miR-103a-3p (n=4; \*\*p<0.01).



Supplementary Figure 11. IHC staining (A) and quantitative analysis of the percentage of iNos (B) and Cox2 (C) positive areas in articular cartilage from two group of mice at week 4 post ACLT+DMM surgery (n=8; \*p<0.05). Sections were counterstained with hematoxylin. Scale bars: 50  $\mu$ m.



**Supplementary Figure 12. A&B.** Chondrocytes were characterized by Toluidine blue O staining (**A**) and IHC staining using Col II antibody (**B**). Scale bar: A, 100 μm; B, 50 μm.



**Supplementary Figure 13.** Schematic diagram to show the regulation role of miR-378 on autophagy and chondrogenesis during OA progression.

# Supplementary Table 1. Primers used for vector construction and Real-time PCR assays

Primers for Real-time PCR				
miNos	NM_010927	F	CGAAACGCTTCACTTCCAA	51
		R	TGAGCCTATATTGCTGTGGCT	
mCox2	NM_011198	F	CAGACAACATAAACTGCGCCTT	71
		R	GATACACCTCTCCACCAATGACC	
mBeclin-1	NM_019584	F	TTTTCTGGACTGTGTGCAGC	171
		R	GCTTTTGTCCACTGCTCCTC	
mAcan	NM_001361500	F	CAACTATCCAGCCATCC	160
		R	AATAGCTCTGTAGTGGAACA	
mSox9	NM_011448	F	AGAAAGACCACCCCGATTACAAGT	209
		R	CGGCGGACCCTGAGATTG	
mCol2a1	NM_031163	F	AGAACAGCATCGCCTACCTG	161
		R	CTTGCCCCACTTACCAGTGT	
mCol10a1	NM_009925	F	CATCTCCCAGCACCAGAATC	152
		R	GTGTCTTGGGGGCTAGCAAGT	
mMmp13	NM_008607	F	GCCATTTCATGCTTCCTGAT	98
		R	CTCTGGTGTTTTGGGATGCT	
mSox6	NM_011445	F	TGCGACAGTTCTTCACTGTGG	195
		R	CGTCCATCTTCATACCATACG	
mAtg2a	NM_194348	F	CCAGCCTAGCAGCCAGTATC	331
		R	CAGCAGAGCCTCTTGAGCTT	
mYwhaz	NM_0011740	F	CAGTAGATGGAGAAAGATTTGC	92
		R	GGGACAATTAGGGAAGTAAGT	
hSOX6	NM_017508	F	TGAGGAGCTACCAACACTTGTCA	121
		R	TCGGAAGGAATATAGGGAACATAACT	
hATG2A	NM_015104	F	TGGCCATGGTCAAACTGTGT	65
		R	TGACCTAAGTAGTGGTGCAGCAA	
hYWHAZ	NM_003406	F	ACCGTTACTTGGCTGAGGTTGC	130
		R	CCCAGTCTGATAGGATGTGTTGG	

"m" stands for "mouse"; "h" stands for "human".