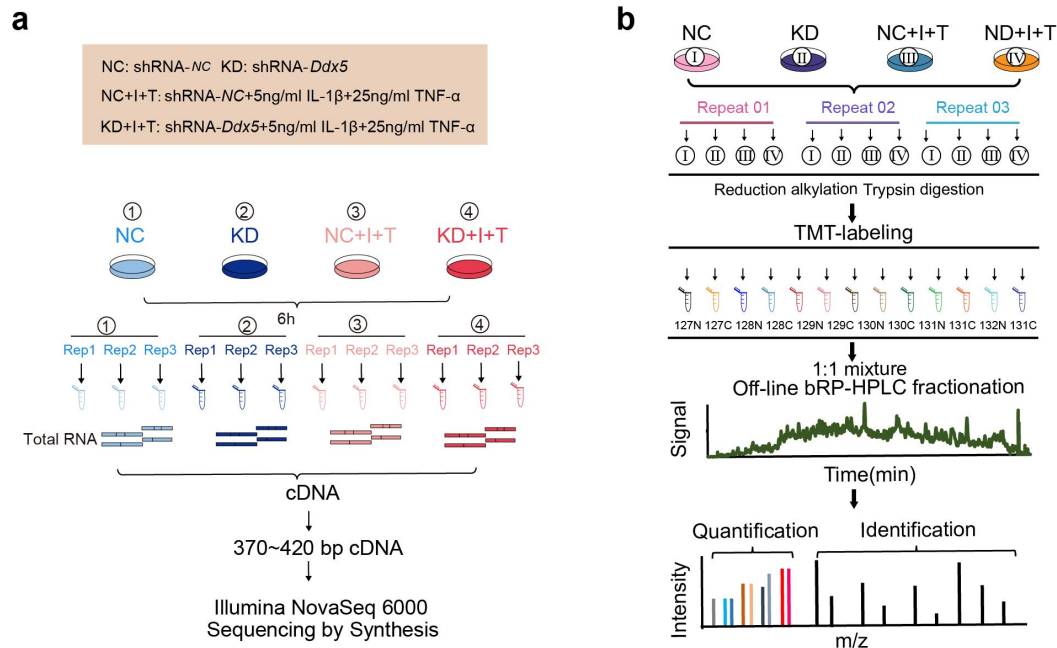


DDX5 inhibits hyaline cartilage fibrosis and degradation in osteoarthritis via alternative splicing and G-quadruplex unwinding

In the format provided by the
authors and unedited

1



2

3 **Supplementary Fig. 1. Technical diagrams of RNA-seq and proteomic**

4 **experiments. Related to Figure 3. (a)** The technical diagram of RNA-seq

5 experiment design in ATDC5 cells is shown without cytokine stimulation or

6 stimulated with IL-1 β combined with TNF- α for 6 h. **(b)** The experiment design in

7 ATDC5 cells with IL-1 β combined with TNF- α stimulation for 24 h is shown. For the

8 deep proteome profiling analysis, all the mass spectrometry data were searched

9 against UniProt mouse database (version 20180930) by Proteome Discoverer software

10 (2.5) with the SEQUEST HT search engine. Enzyme specificity was set to trypsin.

11 The 12-plex TMT label on lysine and peptide N-termini, carbamidomethylation of

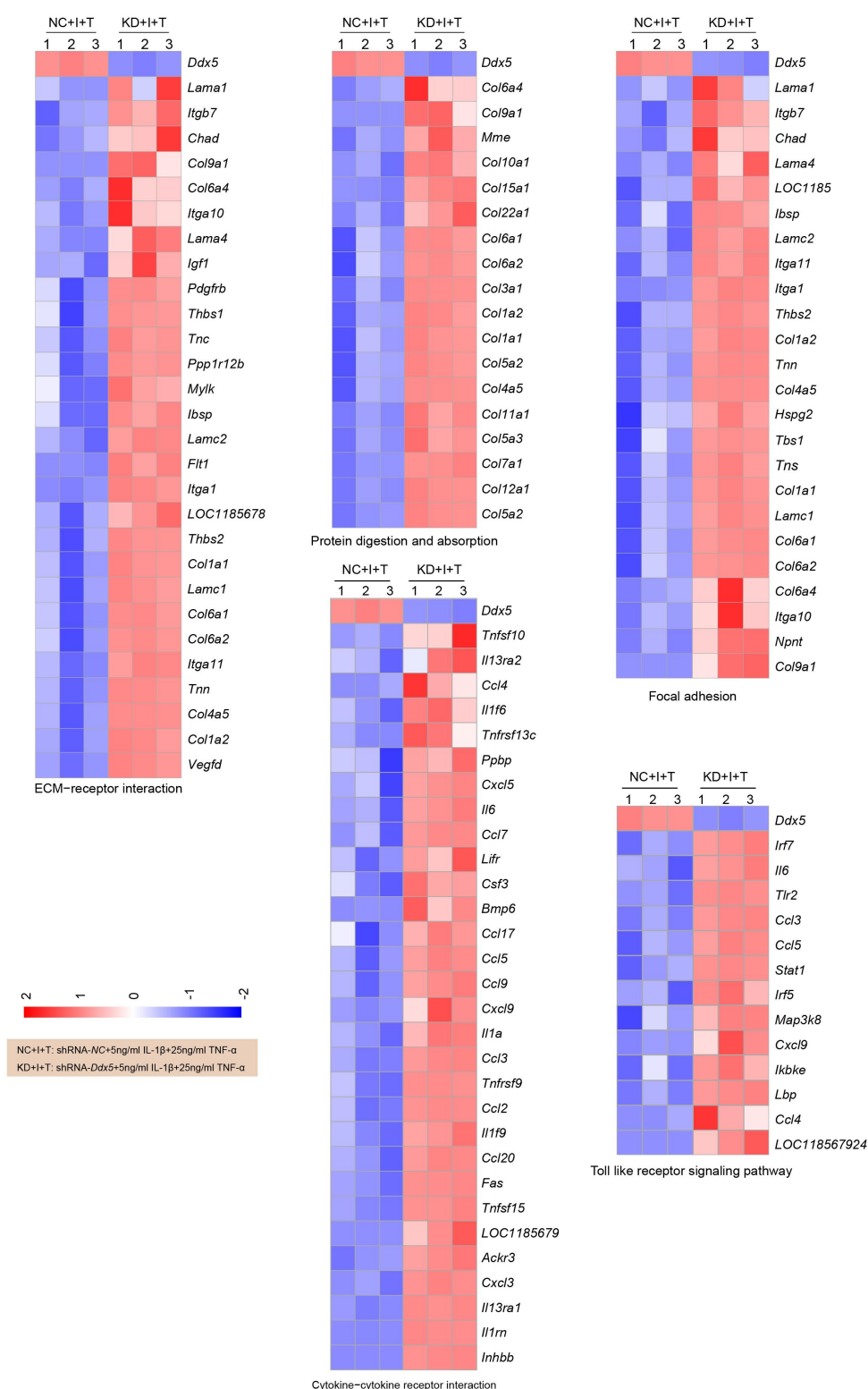
12 cysteine were set as fixed modifications. The acetylation of protein N-term and

13 oxidation of methionine were set as variable modifications. The maximum missed

14 cleavages were set at 2. The tolerances of MS and MS/MS were set at 20 ppm and

15 0.02 Da, respectively. The Percolator algorithm in PD was adopted to control peptide

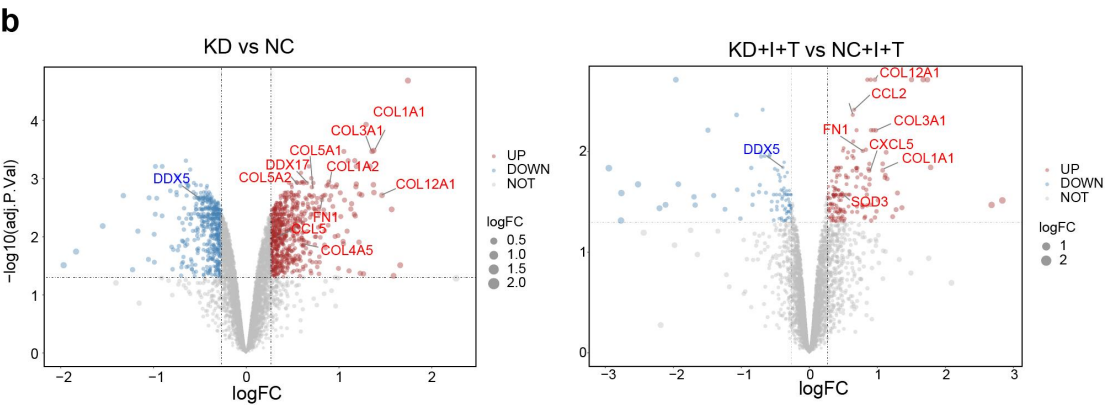
16 spectrum matches at a false discovery rate (FDR) and maximum delta Cn=0.05.



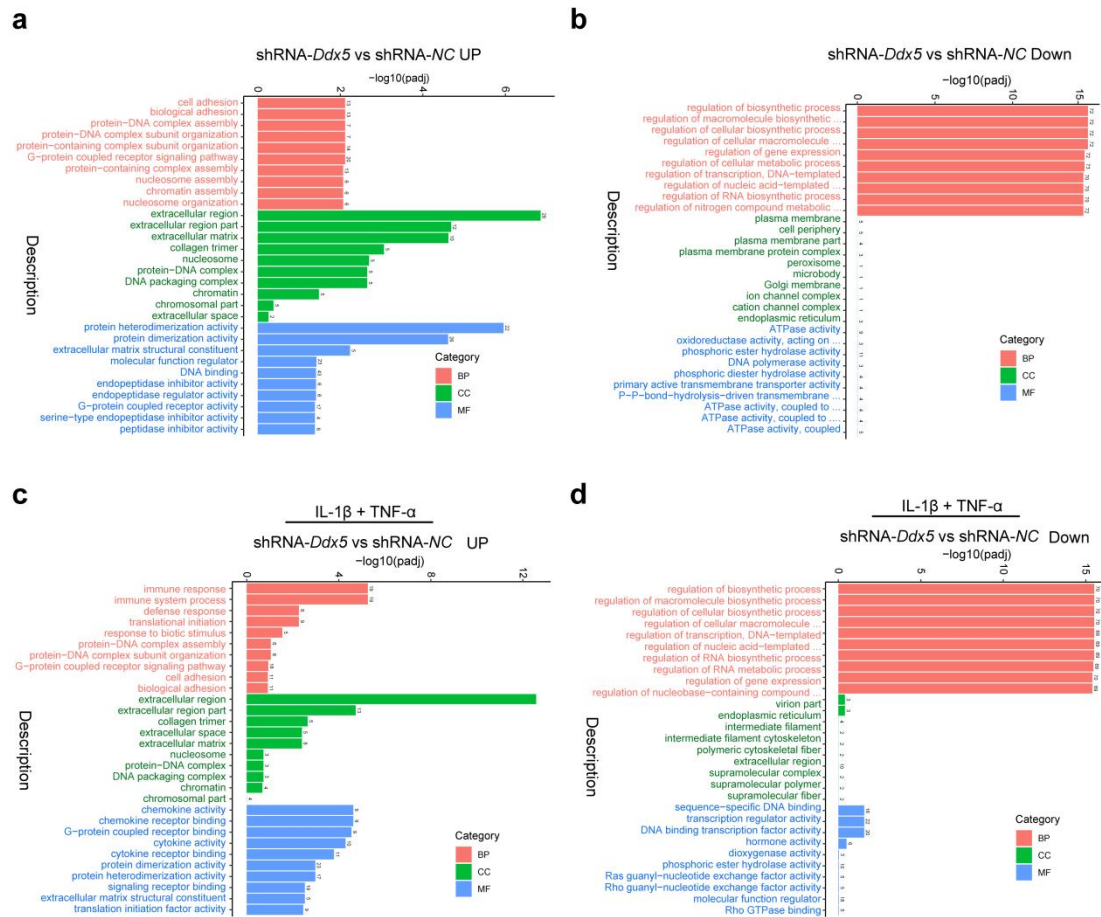
Supplementary Fig. 3. The knockdown of *Ddx5* results in the upregulation of genes related to inflammation and fibrosis in cytokine stimulation. Related to Figure 3. Heat map of gene expression (shRNA-*Ddx5* vs shRNA-NC) in the indicated pathway in ATDC5 cells (5 ng/ml IL-1 β combined with 25 ng/ml TNF- α , 6 h).

a

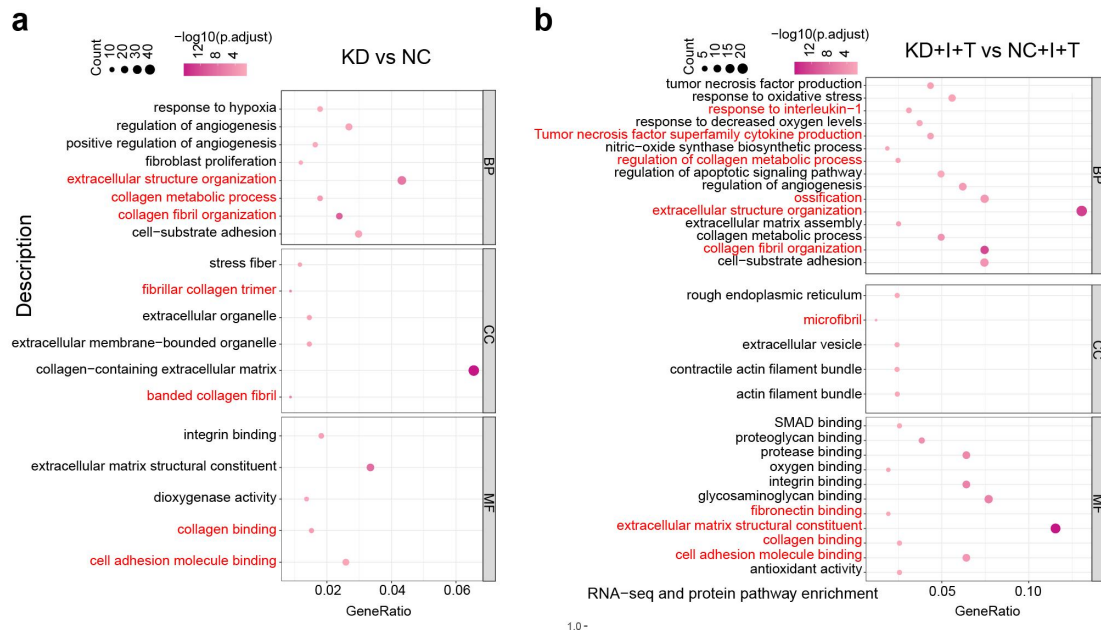
No.of identified proteins	No.of quantified proteins	KD vs NC	KD+I+T vs NC+I+T
7279	7184	715 (Up) 510 (Down)	387 (Up) 162 (Down)



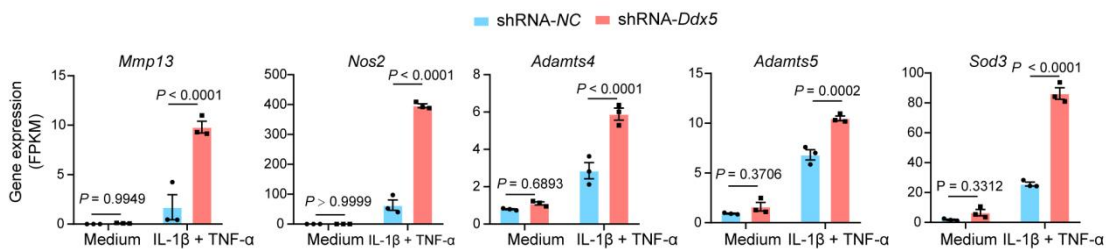
Supplementary Fig. 4. The knockdown of *Ddx5* results in the upregulation of proteins related to inflammation and fibrosis. Related to Figure 3. (a) The 12-plex TMT labeling-based quantitative proteomic analysis. The FDR of protein and peptide identification were all set to 1%. The proteins in treated group with 1.2 fold-change were filtered. The statistical analysis was used Student’s *t*-test and the *p*-value was cut-off at 0.05. **(b)** The volcano plot of the protein expression in ATDC5 cells without cytokine stimulation or stimulated with IL-1 β combined with TNF- α for 24 h.



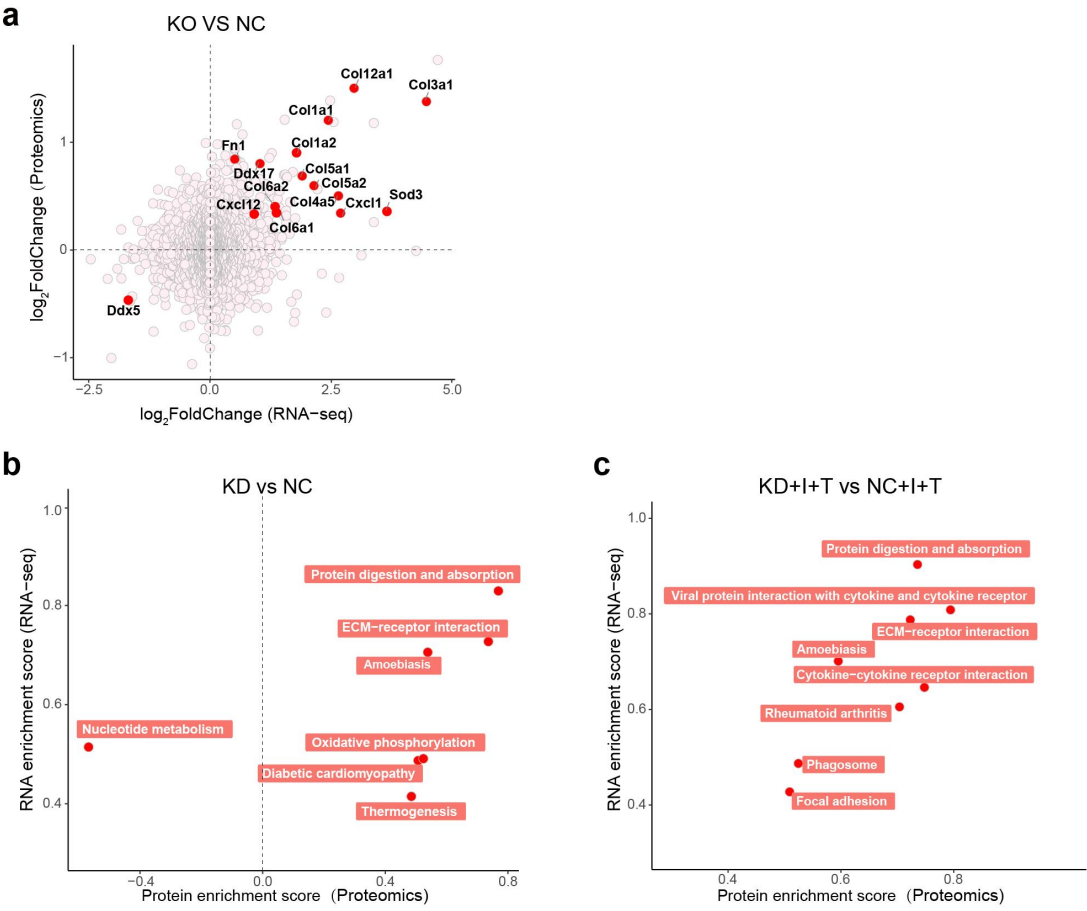
Supplementary Fig. 5. The GO analysis of upregulated and downregulated genes after *Ddx5* gene knockdown. Related to Figure 3. (a, b) GO enrichment analysis was performed on upregulated and downregulated genes (shRNA-*Ddx5* vs shRNA-NC) in ATDC5 cells without cytokine stimulation. (c, d) GO enrichment analysis was performed on upregulated and downregulated genes (shRNA-*Ddx5* vs shRNA-NC) in ATDC5 cells stimulated with combined with TNF- α stimulation for 6 h. The three main categories: biological process (BP), cellular component (CC), and molecular function (MF).



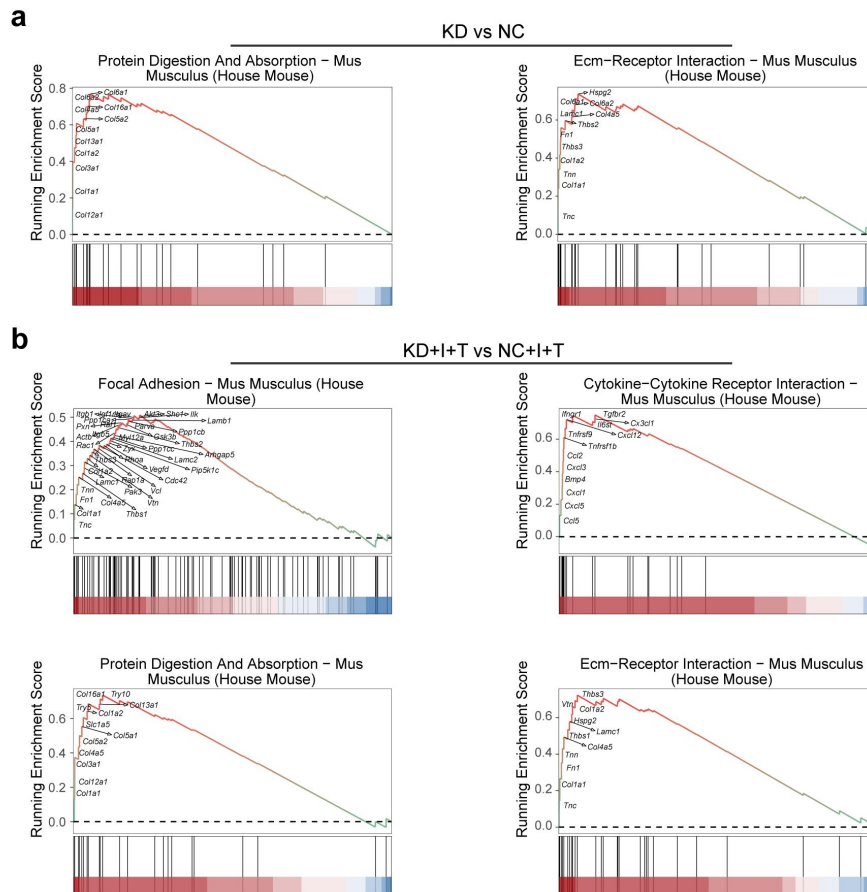
Supplementary Fig. 6. The proteomic analysis of *Ddx5* knockdown with cytokine stimulation in ATDC5 cells. Related to Figure 3. (a) GO enrichment analysis was performed on upregulated proteins (shRNA-*Ddx5* vs shRNA-NC) in ATDC5 cells without cytokine stimulation. **(b)** GO enrichment analysis was performed on upregulated proteins (shRNA-*Ddx5* vs shRNA-NC) in ATDC5 cells in ATDC5 cells with IL-1 β combined with TNF- α stimulation for 24 h.



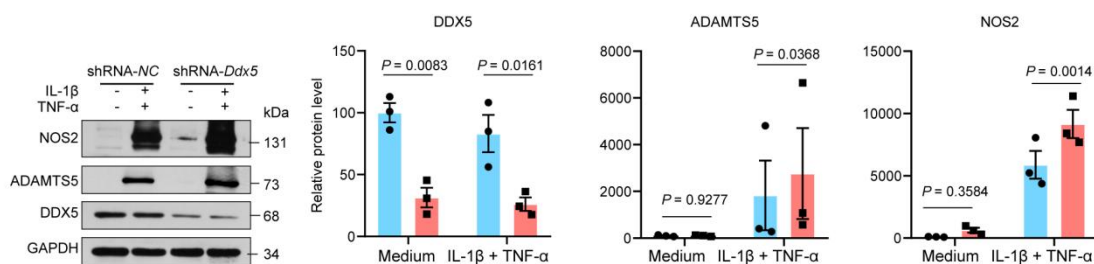
Supplementary Fig. 7. The knockdown of *Ddx5* results in upregulation genes related to cartilage degradation. Related to Figure 3. The expression of cartilage degradation-related genes *Mmp13*, *Nos2*, *Adamts* (4, 5), and *Sod3* in shRNA-NC and shRNA-*Ddx5* ATDC5 cells stimulated with 5 ng/ml IL-1 β combined with 25 ng/ml TNF- α or not for 6 h (n = 3 biologically independent experiments). All data are presented as the mean $\pm$ SEM. Two-way ANOVA with Sidak's multiple comparisons test was conducted.



58 **Supplementary Fig. 8. The common genes and pathways are enriched in both**
59 **RNA-seq data and proteomic data pathway analysis. Related to Figure 3. The**
60 **Bi-omics joint pathway analysis was conducted in ATDC5 cells without cytokine**
61 **stimulation or stimulated with IL-1 β combined with TNF- α .**

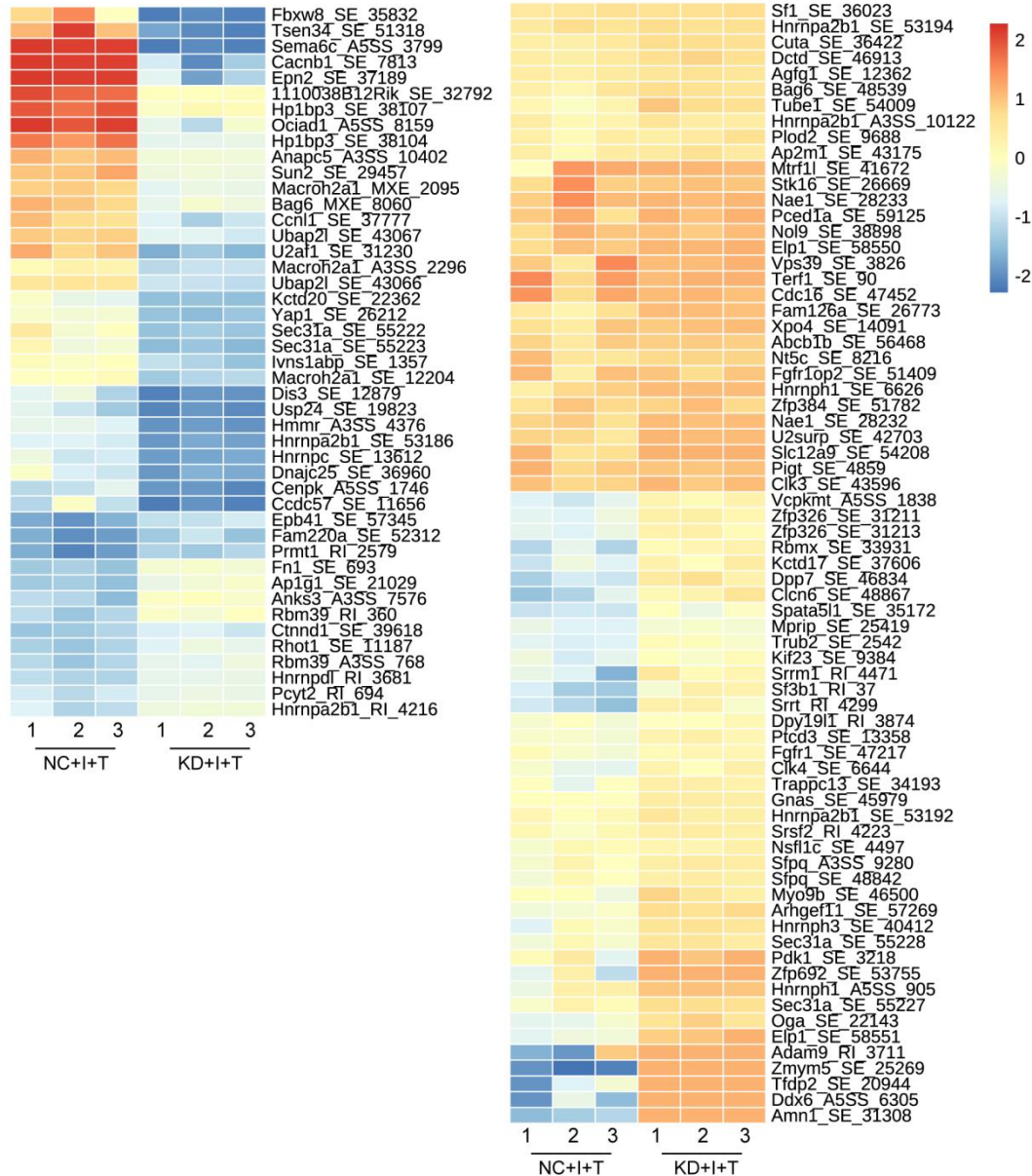


Supplementary Fig. 9. The GSEA analysis from proteomics data. Related to Figure 3. ATDC5 cells were stimulated with IL-1 β combined with TNF- α for 24 h or without cytokine stimulation.



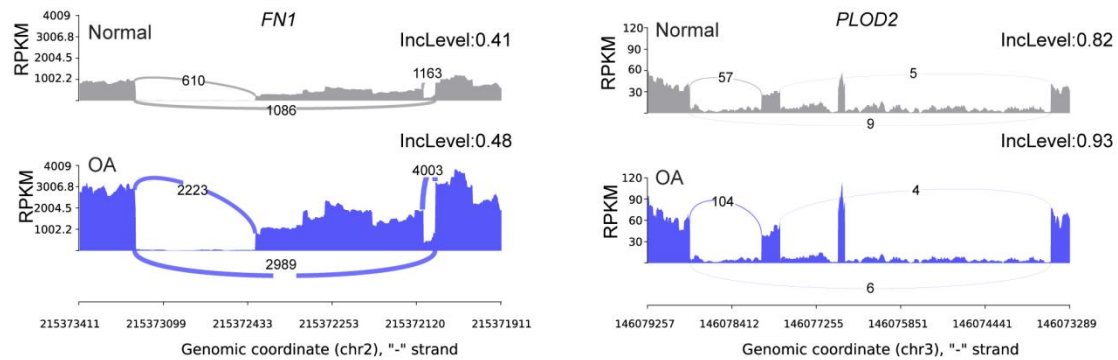
Supplementary Fig. 10. The knockdown of *Ddx5* results in upregulation proteins related to cartilage degradation. Related to Figure 4. Western bolt analysis of cartilage degradation-related proteins NOS2 and ADAMTS5 in shRNA-NC and shRNA-*Ddx5* ATDC5 cells stimulated with 5 ng/ml IL-1 β combined with 25 ng/ml TNF- α or not for 24 h. The density of NOS2 and ADAMTS5 was measured by Image

J software (n = 3 biologically independent experiments). All data are presented as the mean $\pm$ SEM. Two-way ANOVA with Sidak's multiple comparisons test was conducted.

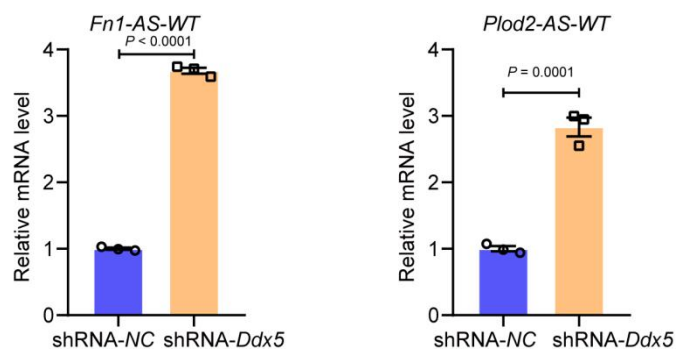


Supplementary Fig. 11. The most significant differential alternative splicing events between shRNA-NC and shRNA-Ddx5 ATDC5 cells. Related to Figure 5.

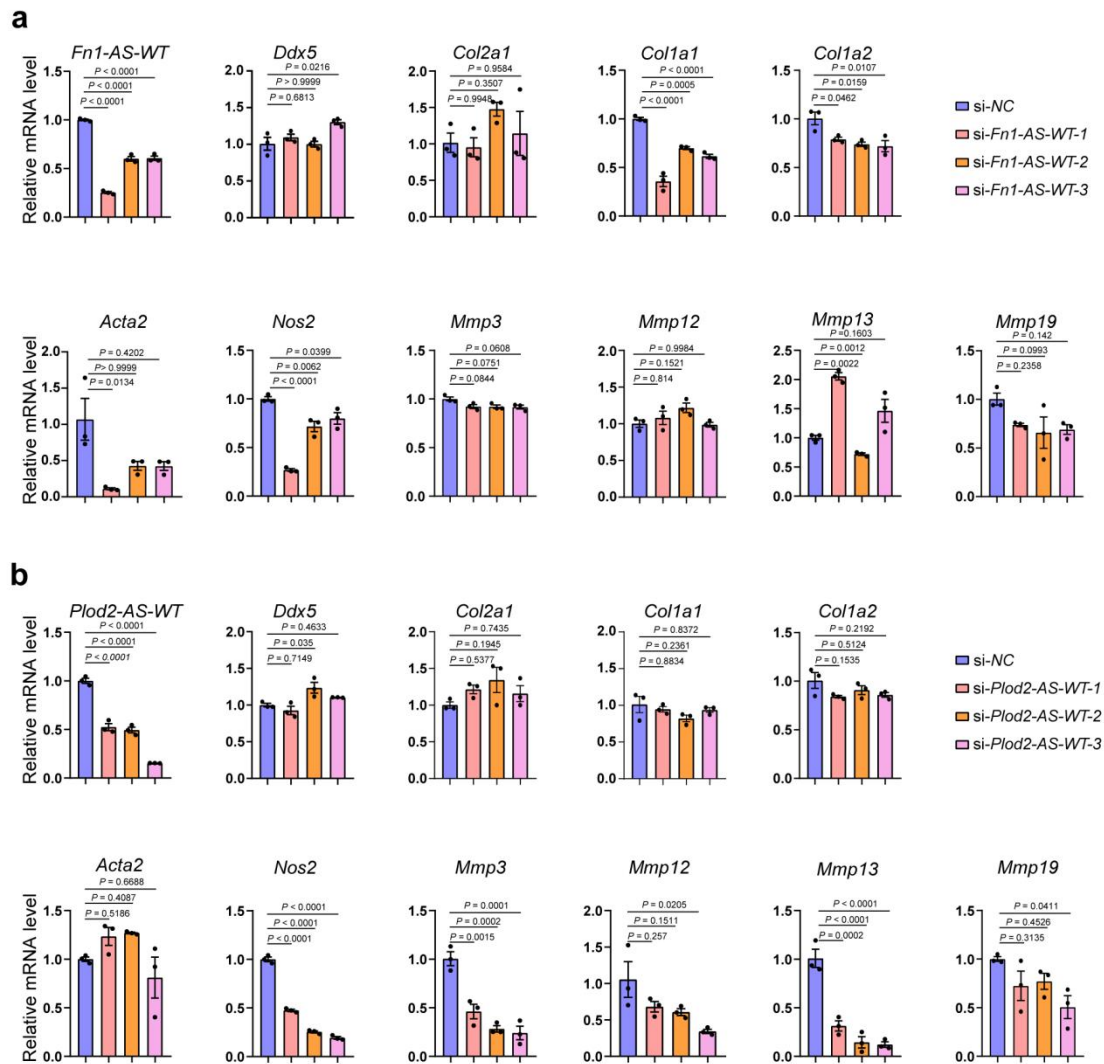
The shRNA-NC and shRNA-Ddx5 ATDC5 cells stimulated with IL-1 β combined with TNF- α for 6 h. Numbers of alternative splicing events in each category upon Ddx5 deletion are indicated. The screening cut off delta PSI > 20% and FDR < 1×10^{-8} .



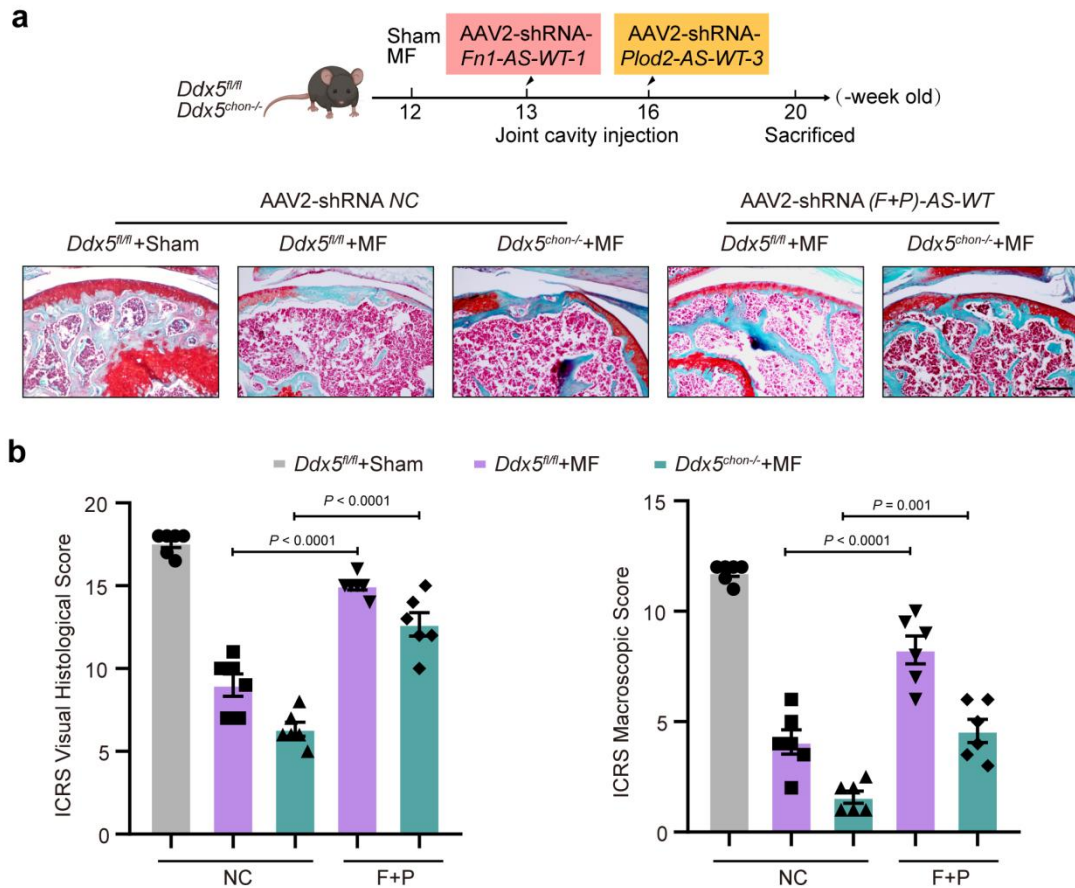
Supplementary Fig. 12. The *FN1* and *PLOD2* pre-mRNAs produce SE-type splicing by rMATS analysis of clinical OA cartilage samples. Related to Figure 5. The replicate multivariate analysis of transcript splicing (rMATS) software was used to analyze the splicing differences of the skipped exon (SE) in *FN1* and *PLOD2* genes between 10 human OA cartilage tissues and 10 normal controls (GSE114007).



Supplementary Fig. 13. The mRNA levels of *Fn1-AS-WT* and *Plod2-AS-WT* in ATDC5 cells. Related to Figure 5. The ATDC5 cells (shRNA-NC and shRNA-Ddx5) were stimulated with IL-1 β combine with TNF- α for 6 h (n = 3 repetition). All data are presented as the mean $\pm$ SEM. Student's *t*-test (unpaired) was conducted.

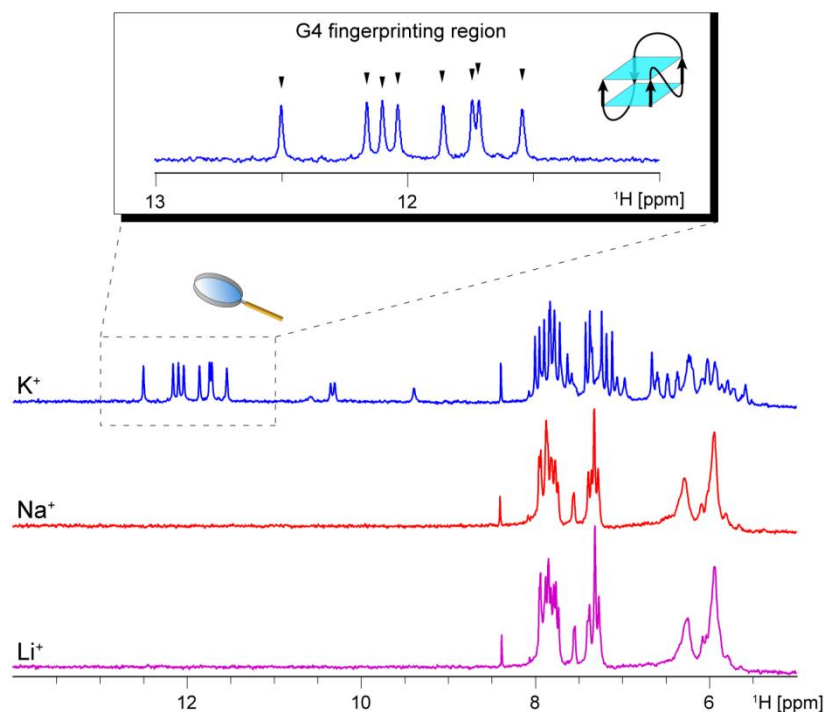


Supplementary Fig. 14. The knockdown of *Fn1-AS-WT* significantly decreases fibrosis by inhibiting *Col1a* (1, 2) and *Acta2* expression, while the knockdown of *Plod2-AS-WT* markedly reduces ECM degradation by inhibiting *Nos2* and *Mmps* (3, 12, 13, 19) expression. Related to Figure 6. The knockdown efficiency of siRNA and illustrated genes expression were analyzed by qPCR in primary mouse chondrocytes transfected with siRNA-*Fn1-AS-WT*-1/2/3- (a) or siRNA-*Plod2-AS-WT*-1/2/3 (b) for 24 h (n = 3 repetition). All data are shown as the mean $\pm$ SEM. a-*Acta2*, Kruskal-Wallis with Dunn's multiple comparisons test. One-way ANOVA with Tukey's multiple comparisons test was conducted in others.

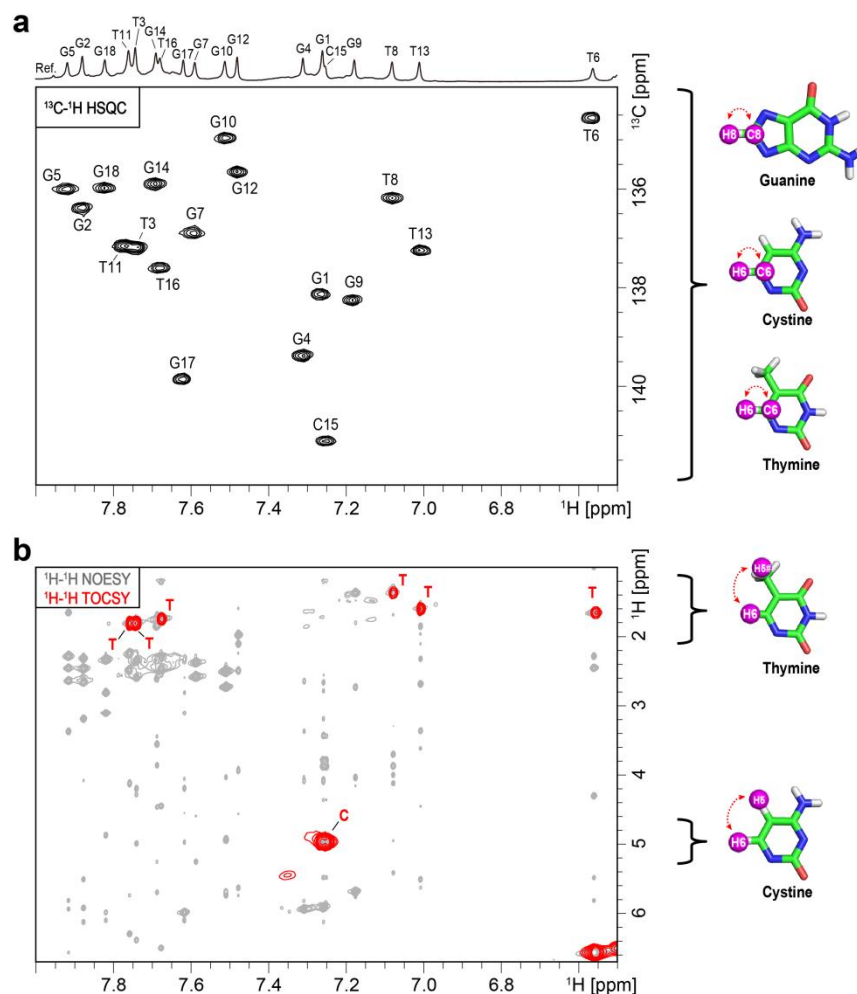


Supplementary Fig. 15. The knockdown of *Fn1-AS-WT* and *Plod2-AS-WT* variants reverses the aggravating phenotype of microfracture (MF) surgery induced by DDX5 deficiency. Related to Figure 6. (a) Representative SO&FG staining image from sham and MF mice intra-articular injected with AAV2-NC or AAV2-shRNA-(*Fn1*+*Plod2*)-AS-WT. (b) The sham and defect cartilage 8 weeks after MF surgery were shown. The ICRS Visual Histological Score and International Cartilage Repair Society (ICRS) macroscopic score of regenerated tissues analysis was analyzed (n = 6 mice/group). Scale bars, 100 μ m. All data are the mean $\pm$ SEM. One-way ANOVA with Tukey's multiple comparisons test was conducted.

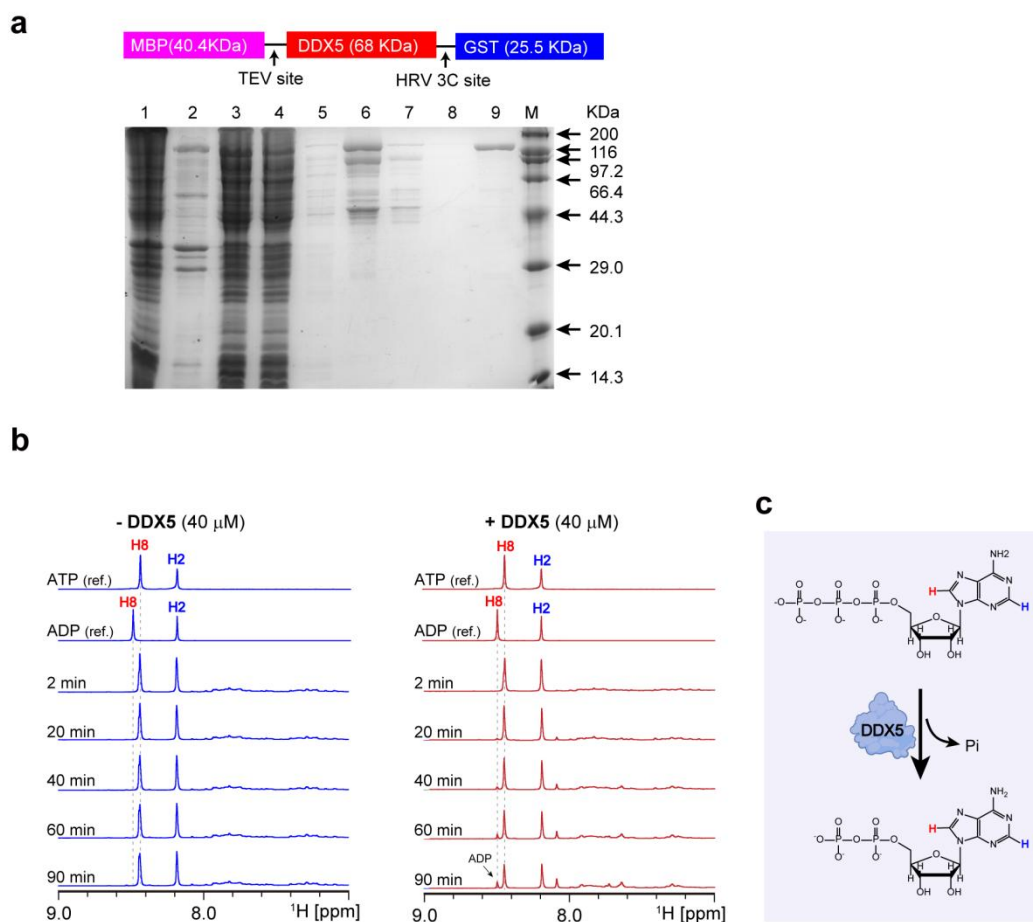
All data are presented as the mean $\pm$ SEM. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$ by one-way ANOVA.



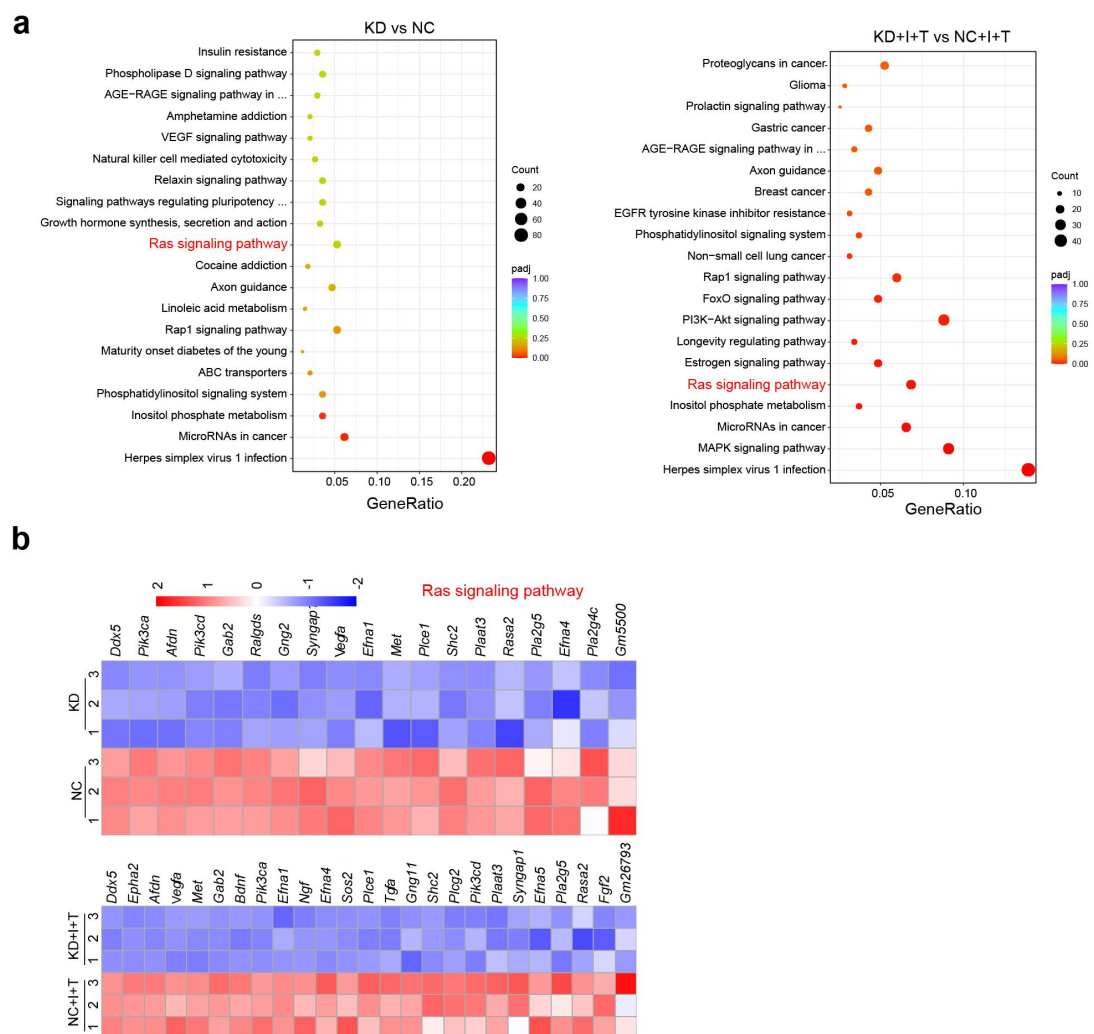
Supplementary Fig. 16. One-dimensional NMR spectra of position-689 in Li⁺ (magenta), Na⁺ (red), or K⁺ (blue) solutions, respectively. Related to Figure 7. The G4 fingerprinting region (11~13 ppm) of position-689 in K⁺ is magnified in the inset. Experimental conditions: 0.2 mM position-689, 20 mM Tris-HCl (pH 6.8), 100 mM LiCl/NaCl/KCl, 310 K.



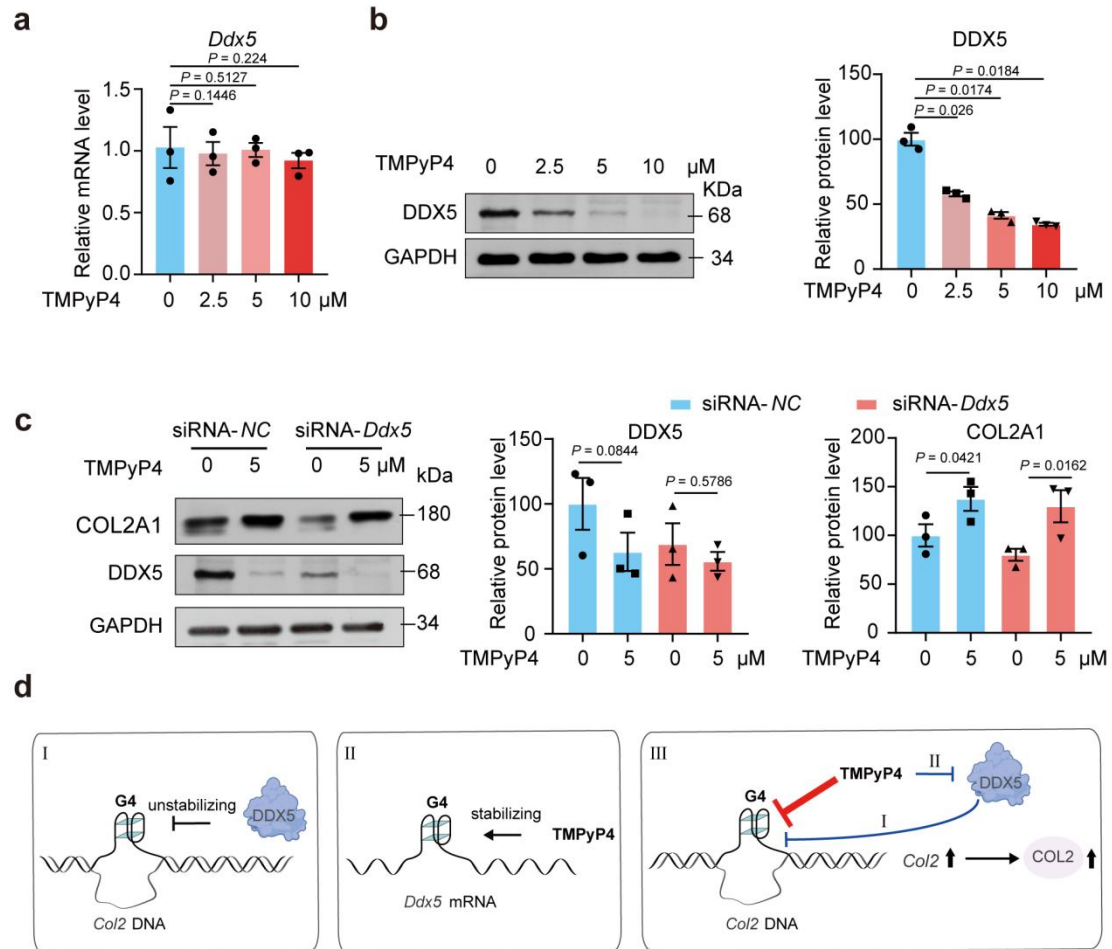
Supplementary Fig. 17. Aromatic-proton assignments of position-689 using two-dimensional through-bond NMR experiments. Related to Figure 7. The two protons correlated through bonds are labelled with magenta beads in the bases and shown on the right. **(a)** The expanded base H8/H6 proton region of the ¹H-¹³C HSQC spectrum. One-dimensional projections of aromatic base protons are shown on the top. **(b)** H6 proton of thymine and cytosine assignments using the two-dimensional spectra ¹H-¹H NOESY (coloured gray) and ¹H-¹H TOCSY (coloured red). Cross-peaks H6-CH₃ (thymine) and H6-H5 (cytosine) are labelled on the spectrum. Experimental conditions: 4 mM position-689, 20 mM K-Pi buffer (pH 6.8), 100 mM KCl and 298 K.



Supplementary Fig. 18. NMR traces that partial DDX5 is used to catalyze the formation of ADP from ATP. Related to Figure 8. (a) DDX5 protein purification. The numbers 1-9 on the gel represent the following: 1. Bacteria liquid after ultrasonic lysis; 2. Precipitate after centrifugation; 3, Supernatant after centrifugation; 4. GST puncture liquid; 5. GST rinse liquid; 6. GST elution liquid; 7. MBP puncture liquid; 8. MBP rinse liquid; 9. MBP elution liquid; M represents protein marker (broad). **(b)** The aromatic region of one-dimensional NMR spectra are shown. Experimental conditions: 0.2 mM position-689, 0 μ M or 40 μ M DDX5, 20 mM Tris-HCl (pH 8.0), 10 mM KCl, 2.5 mM MgCl_2 , 2 mM DTT, and 310 K. The peaks of H8 and H2 protons are coloured red and blue, respectively. **(c)** A schematic illustration of DDX5 catalyzing the formation of ADP from ATP.

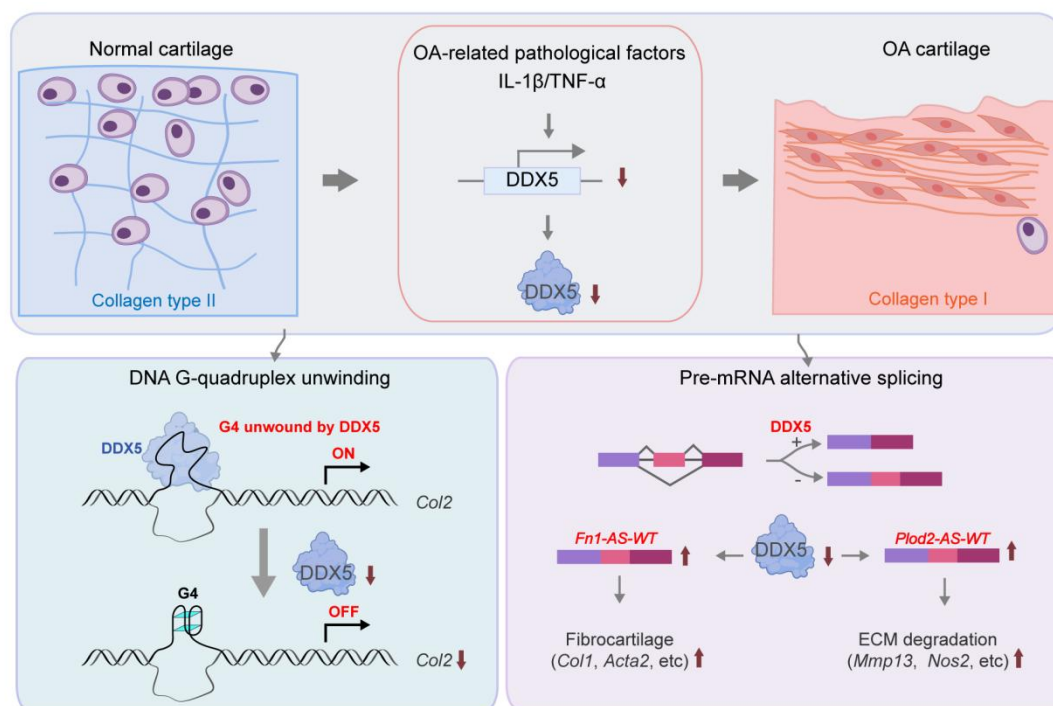


Supplementary Fig. 19. The KEGG analysis of downregulated genes after *Ddx5* knockdown. Related to Figure 3 and Discussion. (a) Downregulated gene-enriched KEGG pathway analysis (shRNA-*Ddx5* vs shRNA-NC) in ATDC5 cells without cytokine stimulation or stimulated with IL-1 β combined with TNF- α for 6 h. (b) Heat map of gene expression (shRNA-*Ddx5* vs shRNA-NC) in Ras signaling pathway in ATDC5 cells without cytokine stimulation or stimulated with IL-1 β combined with TNF- α for 6 h.



Supplementary Fig. 20. The effect of TmPyP4 on COL2 in primary mouse chondrocytes. Related to Discussion. (a) QPCR analysis of *Ddx5* in primary mouse chondrocytes was conducted with indicated doses of TMPyP4 for 12 h (n = 3 repetition). **(b)** Western bolt analysis of DDX5 in primary mouse chondrocytes was conducted with indicated doses of TMPyP4 for 24 h (n = 3 biologically independent experiments). Image J software for the density measurements. **(c)** Western bolt analysis of COL2A1 and DDX5 in primary mouse chondrocytes (siRNA-NC vs siRNA-*Ddx5*) was conducted with indicated doses of TMPyP4 for 24 h (n = 3 repetition). Image J software for the density measurements. **(d)** A schematic illustration for TMPyP4 regulation of *Col2*G4-DNA and *Ddx5*G4-mRNA. The *Col2*G4-DNA is unstabilized by DDX5 (I). The *Ddx5*G4-mRNA is stabilized by TMPyP4 (hypothesis) (II). The impact of the downregulated DDX5 on *Col2*G4 was

completely blocked by TMPyP4 as it continuously and directly unwound *Col2*G4 (III). All data are presented as the mean $\pm$ SEM. One-way ANOVA with Tukey's multiple comparisons test (a,b), and two-way ANOVA with Sidak's multiple comparisons test were conducted (c).



Supplementary Fig. 21. A mechanistic model is proposed to explain how DDX5-mediated alternative splicing and G4 unwinding to inhibit hyaline cartilage fibrosis and degradation in OA. The expression of DDX5 is significantly downregulated in response to OA-related pathological factors. The decrease of DDX5 exacerbates hyaline cartilage fibrosis in two ways. On the one hand, the reduction of DDX5 results in an increased G4 in the *Col2* promoter region, leading to a decrease in expression level of COL2. This decrease indicates a loss of the hyaline cartilage phenotype (left). On the other hand, the loss of DDX5 leads to a decrease in the splicing of Fn1 and Plod2 pre-mRNAs. Consequently, the upregulated *Fn1-AS-WT* and *Plod2-AS-WT* isoforms promote fibrotic cartilage phenotype and ECM degradation, respectively (right). Therefore, inducing the upregulation of DDX5 in chondrocytes can protect the integrity of articular cartilage and prevent cartilage fibrosis and degeneration.

Supplementary Table 1. ¹H NMR detection of the putative quadruplex sequences in the *Col2* promoter.

Position	Length	Sequence (5'→3')	G-Score	¹ H NMR Spectra ^b
689	18	GGTGGTGTGGTGTGC TGG	16	
736	26	GGGAGTGTCTGGTCA GGTCCATAGAGG	16	
1000	22	GGGCTAAGGTGGGG GGGTGGGG	36	
1040	23	GGCTGGAGGTCCAG GGATAGGGG	21	
1199	30	GGCCAGCGGTGCTC TATCCAGGCTAAGGG	20	
1461	20	GGATGGGGGATGGG TTAGGG	21	
1504	20	GGTGGGAGCTCACGG GCAGG	16	
1541	15	GGAAGGCAGGTCTGG	20	
1796	20	GGTTAGAGGGGGCAG TGTGG	16	
1827	15	GGGGGCGACCGGAGG	17	
1873	26	GGGCACATTGGGGGC GGGAAGCTGGG	39	
1908	17	GGCGACTGGCCTTGG	16	
1949	20	GGGCGGGCTCCGGG GGCGGG	39	
1979	25	GGTTACAGCCCCGC GGGGGGCTAGG	11	

^a Experimental conditions: 0.2 mM position-689, 20 mM K-Pi buffer (pH 6.8), 100 mM KCl, and 298 K.

^b The region of imino protons (10 ~ 14 ppm) are shown.

Supplementary Table 2. Clinical and demographic characteristics of the study population

Patient ID	OA1	OA2	OA3	OA4	OA5	OA6
Age(years)	61	84	77	68	73	82
Gender	Female	Female	Male	Female	Female	Female
Weight (Kg)	66	50	70	89	75	65
TKA	Left	Right	Left	Right	Right	Right
CRP (mg/dL)	3	2.3	1.5	28.8	7.8	9.5
ESR (mm/h)	10	14	10	16	38	20
WBC (109/L)	8.9	4.6	6	6.8	5.7	7.4
Lymphocyte (109/L)	3.4	1.4	2.1	1.9	1.1	3.4
Monocyte (109/L)	0.6	0.3	0.4	0.5	0.6	0.6
Blood glucose (mmol/L)	4.06	4.76	5.37	5.13	4.82	5.03
ALT (U/L)	26.2	17.6	11.7	12.8	15.8	12.7
AST (U/L)	23.8	24.4	15.7	17.6	24.5	14.6
Total Protein (g/L)	61.6	67.3	67.2	67.8	42.4	69.4
Serum albutnin (g/L)	38.7	40.9	39.2	39.8	30.2	39.4
BUN (mmol/L)	6	4.9	6.7	3.6	6.3	6.4
Cre (μmol/L)	48	56	73	45	55	64
TT (s)	18.8	17.5	17.2	17.1	16.8	16.6
APTT (s)	24.1	27.4	27.1	28	25.7	23.4
INR	0.91	0.89	0.92	0.94	0.95	0.94

Supplementary Table 3. Primer sequences used in qRT-PCR.

Gene	Primer
Mouse <i>Fnl-AS-WT</i>	Forward primer: GCCTGGAGTACAACGTCAGT Reverse primer: GGAAGAGTTTAGCGGGGTCC
Mouse <i>Plod2-AS-WT</i>	Forward primer: ACTCCCCTACTCCGGAACA Reverse primer: GCAGTTGATATCAGCCGTCCA
Mouse <i>Mmp12</i>	Forward primer: CTGCTCCCATGAATGACAGTG Reverse primer: AGTTGCTTCTAGCCCAAAGAAC
Mouse <i>Mmp13</i>	Forward primer: CTTCTTCTTGTTGAGCTGGACTC Reverse primer: CTGTGGAGGTCAGTGTAGACT
Mouse <i>Mmp3</i>	Forward primer: TTGACTCAAGGGTGGATGCTGTCT Reverse primer: GCACATGCTGAACAAAGCACTTCC
Mouse <i>Acta2</i>	Forward primer: GTCCCAGACATCAGGGAGTAA Reverse primer: TCGGATACTTCAGCGTCAGGA
Mouse <i>Col2a1</i>	Forward primer: CAGGATGCCCCGAAAATTAGGG Reverse primer: ACCACGATCACCTCTGGGT
Human <i>GAPDH</i>	Forward primer: CGTCTTCACCACCATGGAGA Reverse primer: CGGCCATCACGCCACAGTTT
Mouse <i>Gapdh</i>	Forward primer: AGGTCGGTGTGAACGGATTTG Reverse primer: TGTAGACCATGTAGTTGAGGTCA

Human <i>DDX5</i>	Forward primer: GCCATGTCGGGTTATTTCG Reverse primer: GGTTCCTCAAACCTTCTTTCCAGA
Mouse <i>Ddx5</i>	Forward primer: TGTGATTGCAAGGCAGAACTTT Reverse primer: TGGCCAGCCCTGAGCTT
Mouse <i>Colla1</i>	Forward primer: TAAGGGTCCCCAATGGTGAGA Reverse primer: GGGTCCCTCGACTCCTACAT
Mouse <i>Colla2</i>	Forward primer: GTAACCTTCGTGCCTAGCAACA Reverse primer: CCTTTGTCAGAATACTGAGCAGC
Mouse <i>Col2a1</i> -promoter 515-759	Forward primer: CCCACCCTAGACTGGTTGAA Reverse primer: TCTATGGACCTGACCGACAC
Mouse <i>Col2a1</i> -promoter 1470-1590	Forward primer: ATGGGTTAGGGAGGCTGT Reverse primer: CGTTGTCCAGAATCCTAAA
Mouse <i>Nos2</i>	Forward primer: GGAGTGACGGCAAACATGACT Reverse primer: TCGATGCACAACTGGGTGAAC
Mouse <i>Mmp19</i>	Forward primer: GCTGACATTGCGCTCTCTTTC Reverse primer: CACTCCTTGATAGGTCCCCTC

Supplementary Table 4. Antibody information in this study.

Antibody	Brand	Apply
Rabbit anti-MMP13	1:100, Proteinch, 18165-1-AP	IHC
Rabbit anti-COL2A1	1:400; Rockland, 600-401-104S	IHC
Mouse anti-COL1A1	1:100; Santa Cruz Biotechnology, sc-293182	IHC
Rabbit anti-ADAMTS4	1:100, ABclonal, A2525	IHC
Mouse anti-NOS2	1:100; Santa Cruz Biotechnology, sc-7271	IHC
Rabbit anti-DDX5	Cell Signaling Technology, 9877s	IF (1:100) RIP (1:100) WB (1:1000)
Mouse anti-DNA G4	1:100, sigma, MABE1126	IF
Anti-EGFP	1:100, invitrogen, CAB4211	IF
Rabbit anti-COL1A1	1:1000, Abcam, ab34710	WB
Mouse anti-DDX5	1:100, Santa Cruz Biotechnology, sc-365164	ChIP

Rabbit anti-MMP3	1:500, abcam, ab52915	WB
Mouse anti-GAPDH	1:1000, Abmart, M20028	WB
Rabbit anti-Actin	1:1000, Abmart, T40001M	WB
Rabbit anti-COL2A1	1:1000, Abcam, ab34712	WB
Rabbit anti-ADAMTS5	1:1000, Abcam, ab41037	WB

Supplementary Table 5. Primer sequences used in PCR.

Gene	Primer	Apply
Ddx5 Floxed:532 bp, WT:453 bp	P1: AATCTGGTCAGATGTTTGGGCTG P2: CTGAGTTACAGCATGAAGAAGCCAC	Genotyping
AggreCAN -cre ^{ERT} Wt: 299 bp Mut : 200 bp	19388: GTT ATA TTC CGG AGC CCA CA 19387: AAA AGC GAC AAG AAG ACA CCA 19388: AAAAGCGACAAGAAGACACCA oIMR8619: CTCCAGACTGCCTTGGGA AAA	Genotyping
Mouse <i>Fnl</i>	Forward primer: GTTACCCTTCCACACCCCAA Reverse primer: ATGGCGTAATGGGAAACCGT	RIP-PCR
Mouse <i>Plod2</i>	Forward primer: GAGAGGCGGTGATGGAATGAA Reverse primer: ACTCGGTAAACAAGATGACCAGA	RIP-PCR
Mouse <i>Ddx5</i>	Forward primer: TGTGATTGCAAGGCAGAACTTT Reverse primer: TGGCCAGCCCTGAGCTT	PCR
Mouse <i>Gapdh</i>	Forward primer: AGGTCGGTGTGAACGGATTG Reverse primer: TGTAAGACCATGTAGTTGAGGTCA	PCR
Mouse <i>Fnl-AS-SE25</i> 596/323	Forward primer: GAGAGGAGCACTACCCCA Reverse primer: GAGTAGCGCACCAAGAGGTT	PCR
Mouse <i>Plod2-AS-SE</i> 14 404/341	Forward primer: GGAGCACTGAGTCCTGATGG Reverse primer: TTTTCCTTCCAATCCACGGG	PCR

Supplementary Table 6. shRNA information

Gene	Sequence (5'→ 3')	
Mouse <i>Ddx5</i>	5'-CCGGCCTGGAAGACTGATTGACTTTCTCGAGA AAGTCAATCAGTCTTCCAGGTTTTTTG-3'	shRNA
Mouse <i>Fn1-AS-WT-1</i>	5'-CCGGGGGTACCGAATCACAGTAGTTCTCGAG AACTACTGTGATTCCGTACCCTTTTTTG-3'	shRNA
Mouse <i>Plod2-AS-WT-3</i>	5'-CCGGCCCAAAGGGTGTGTTTATGTACTCGAGT ACATAAACACACCCTTGGGTTTTTTG-3'	shRNA

Supplementary Table 7. siRNA information

Gene	Sequence (5'→ 3')	
Mouse <i>Fn1-AS-WT-1</i>	Sense: GGGUACCGAAUCACAGUAGUUTT Antisense: AACUACUGUGAUUCGGUACCCTT	siRNA
Mouse <i>Fn1-AS-WT-2</i>	Sense: GCGUUAUCACUCUCAUUAATT Antisense: UUA AUGAGAGUGAU AACGCTT	siRNA
Mouse <i>Fn1-AS-WT-3</i>	Sense: CAGUGUUUACACUGUCAAAATT Antisense: UUUGACAGUGUAAACACUGTT	siRNA
Mouse <i>Plod2-AS-WT-1</i>	Sense: CAAUGCUAGAGAU AUGACCUUTT Antisense: AAGGUCAUAUCUCUAGCAUUGTT	siRNA
Mouse <i>Plod2-AS-WT-2</i>	Sense: CCUACUCCGGAAACA UUCAATT Antisense: UUGGAAUGUUUCCGGAGUAGGTT	siRNA
Mouse <i>Plod2-AS-WT-3</i>	Sense: CCCAAAGGGUGUGUUUAUGUATT Antisense: TACAUA AACACACCCUUGGG	siRNA
Mouse <i>Ddx5</i>	Sense: CCUGGAAGACUGAUUGACUUUTT Antisense: AAAGUCAAU CAGUCUCCAGGTT	siRNA