

## Supporting Information

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Hyperplastic Human Macromass Cartilage for Joint Regeneration

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## **Supporting Information**

#### **Supplementary Experimental Procedures**

**CM ingredients verification.** All ingredients were added to DMEM/F12 as positive control. By removing one ingredient and keeping others constant, corresponding impacts on cell proliferation were identified (Table S4, Figure S2C, D). Primary chondrocytes were seeded in 96-well plate and cultured in candidate medium. The medium was refreshed at day 3. The effect was assessed by the area of cell clusters observed under the microscope (Olympus) at day 6.

**RNA extraction, reverse transcription, and quantitative real-time PCR.** Total RNA was isolated from samples using Trizol (Takara) and transcribed into cDNA using a ReverTra Ace® qPCR RT Master Mix (TOYOBO) according to the protocols. Quantitative real-time PCR was performed on the LightCycler®480 PCR System (Roche) using TB Green® Premix Ex Taq<sup>TM</sup> (Takara). The relative expression levels of each gene were analyzed using the  $2^{-\triangle Ct}$  method. The forward and reverse primers for each gene are shown in Table S5.

**Scanning electron microscopy.** According to previous reports, paraffin sections were deparaffinized and hydrated <sup>[1]</sup>. After sputter coated with gold particles, the samples were imaged with a scanning electron microscopy (SEM, Hitachi SU8010).

**Cell viability assessment of macro-cartilage.** Cell viability in macro-cartilage was assessed by Live/Dead staining and trypan blue staining.

For Live/Dead staining, macro-cartilage was incubated in 20 µм Calcein AM (Dojindo) and 20 µм Cellstain- PI (Dojindo) at 37°C for 30 min. After rinsed with

PBS, the stained macro-cartilage was visualized with a confocal microscope (Olympus, FV1000).

For trypan blue staining, macro-cartilage was digested into single cells and mixed with 0.4% trypan blue. The stained cells were quantified within 3 min through automated cell counter (Countstar).

#### Supplementary Figures



Figure S1. The polydactyly cartilage exhibits a hyaline cartilage-like phenotype.

(A) Representative images of polydactyly digital stained by Safranin- O
 (SO)/fast green. Scale bar: 200 μm.



# Figure S2. A screen-defined serum-free medium efficiently expands polydactyly chondrocyte *in vitro*. Related to Figure 1.

(A-C) Representative morphologies of primary polydactyly chondrocytes

cultured in different culture conditions. Scale bar: 200 µm. (**D**) Effect quantification of different additives (*n*=3, one-way ANOVA followed by Dunneett's multiple comparison test). All data were mean ± SEM. n.s  $p \ge 0.05$ , \*\*p < 0.01, \*\*\*\*p < 0.0001.





(A) Representative fluorescent images of proliferating cells (EdU) in CC and TC over time, DAPI labeled the nucleus. Scale bars: 100 µm. (B) Representative images of CC-chons and TC-chons stained with DAPI (nucleus) and Phalloidin (F-actin). Scale bars: 100 µm. (C) Representative images of immunofluorescent staining of COL1 in CC-chons and TC-chons. Scale bars: 100 µm. (D) Efficiency quantification of COL1 staining (n = 6, one-way ANOVA followed by Tukey's multiple comparison test). All data were mean ± SEM. n.s  $p \ge 0.05$ , \*\*p < 0.01, \*\*\*\*p < 0.0001.





(A) Cumulative fold expansion in CC and TC culture at day 6 and day 27 (*n*=3, unpaired two-tailed Student's t tests). (B) Representative images of Live (green)/Dead (red) staining in CC and TC tissues at day 6 and day 27. (C) The percentage of viable cells in CC and TC tissues at day 6 and day 27, characterized by trypan blue staining (*n*=3). (D) Representative images of immunofluorescent staining of PRG4 in CC and TC tissues (*n*=3, unpaired two-tailed Student's t tests). (E) Efficiency quantification of COL2A1, ACAN, PRG4 staining in CC and TC tissues. Scale bars: 100 µm. (F) Representative SEM images of CC and TC tissues. All data were mean ± SEM. n.s  $p \ge 0.05$ , \*\*p < 0.01, \*\*\*\*p < 0.0001.



Figure S5. Overall transcriptome analysis of macro-cartilage. Related to Fig 4.

(A) Principal-component analysis (PCA) plot of all samples. (B) Correlation coefficient matrix of all samples. (C) Principal-component analysis (PCA) plot of P0, CC-S2, TC-S2 and human articular cartilage at different developmental stage. (D) Volcano plot identifying genes that are differentially expressed between CC-S2 and P0.





(A) Venn diagram of the number of genes expressed in different stage of CC macro-cartilage (P0, CC-S1, CC-S2). (B) Volcano plots of differentially expressed genes between CC-S1 and P0. (C) Volcano plots of differentially expressed genes between CC-S2 and CC-S1. (D) GO enrichment analysis comparison between CC-S2 and CC-S1. (E) Heatmaps of genes drove early reprogramming.



Figure S7. Evaluation of articular cartilage repair at 6 weeks postoperatively. Related to Fig6.

(A) Overall repair of cartilage defects 6 weeks after implantation. (B) Representative images of repaired cartilage stained by SO/fast green. Scale bar: 200 µm. (C) ICRS-II scoring for histological assessment of regenerated cartilage (n = 3-6, one-way ANOVA followed by Tukey's multiple comparison test). All data were mean ± SEM. n.s  $p \ge 0.05$ , \*p < 0.05, \*p < 0.01, \*\*\*\*p < 0.001.



Figure S8. CC macro-cartilage elicits a relative weaker inflammatory response. Related to Fig6.

(A) Representative images of repaired cartilage stained by hematoxylin-eosin (HE). Scale bar: 100  $\mu$ m. (B) ICRS-II scoring for histological assessment of regenerated cartilage (*n*=3, unpaired two-tailed Student's t tests). All data were mean ± SEM. n.s *p* ≥ 0.05.

## Supplementary Tables

Number	Age	Sex	Experiment
1	11M26D	Female	
2	9M24D	Female	
3	1Y3M	Male	
4	1Y	Male	
5	1Y	Female	Establishment of culture
6	2Y	Female	conditions
7	1Y7M	Female	
8	1Y1M	Male	
9	5M3D	Male	
10	6M24D	Male	
11	11M	Male	Characterization of
12	7M	Female	CC-chons in 2D culture
13	1Y3M	Male	
14	4M10D	Male	
15	1Y11M	Male	
16	7M22D	Male	In vitro characterization of
17	3M10D	Female	macro-cartilage
18	5M12D	Female	
19	7M26D	Male	
20	13M	Female	
21	11M20D	Female	
22	4M8D	Male	Bulk RNA sequencing of of
23	11M	Female	macro-cartilage
24	6M17D	Female	
25	1Y1M	Female	

## Table S1. Donor information of human chondrocytes.

26	7M8D	Female	
27	1M9D	Male	
28	3M5D	Female	
29	3M1D	Female	
30	6M20D	Male	
31	2M	Female	Implantation of maara
32	5M21D	Male	
33	7M7D	Female	cartilage in rat joints
34	2Y10D	Female	
35	1Y	Female	
36	1Y	Female	

#### Table S2. Candidate supplement in combinatory screening.

Name	Description	Source	Catalog Number	Concentration
B27	B-27™ Supplement	Gibco	17504044	1×
	(50×), serum free			
bFGF	Fibroblast Growth	PenroTech	100-18B	30 ng·mL⁻¹
	Factor-basic			
TGFβ3	Transforming Growth	DoproToph	100-36E	10 ng·mL⁻¹
	Factor-β3	reprotecti		

## Table S3. Candidate additives in optimization screening.

Name	Description	Source	Catalog Number	Concentration
NEAA	MEM Non-Essential	Cibco	11140050	1 ×
	Amino Acids Solution	Gibco		

	(100×)			
L-Glu	L-Glutamine (200mм)	Gibco	25030081	2 тм
<b>SD</b>	Sodium Pyruvate	Ciboo	44000070	
56	(100тм)			I MM
Vc	Ascorbic Acid	Sigma	A92902	50 µg·mL⁻¹
PDGF-	Platelet-Derived Growth	DoproTooh	11 1 / D	20 ng ml -1
BB	Factor-BB	reprotecti	11-14D	20 ng·mL
DEX	dexamethasone	Sigma	D4902	10 <sup>-8</sup> м
Heparin	Heparin sodium	Selleck	S1346	2 µg·mL⁻¹
COL6	Collagen 6	Abcam	ab7538	2.5 µg·mL⁻¹

#### Table S4. Candidate components in verification experiment.

Name	Description	Source	Catalog Number	Concentration
	B-27™ Supplement	Ciboo	17504044	1×
D27	(50×), serum free	Gibco		
hEGE	Fibroblast Growth	PoproToch	100-18B	30 ng∙mL <sup>-1</sup>
DFGF	Factor-basic	reprotecti		
TGEB3	Transforming Growth	PenroTech	100-36E	10 ng.ml <sup>-1</sup>
төгрэ	Factor-β3	reprotecti	100-302	
	MEM Non-Essential			
NEAA	Amino Acids Solution	Gibco	11140050	1×
	(100×)			
L-Glu	L-Glutamine (200mм)	Gibco	25030081	2 mм
SP	Sodium Pyruvate	Cibco	11360070	1 mm
	(100mм)	Gibco		

Vc	Ascorbic Acid	Sigma	A92902	50 µg·mL⁻¹
PDGF-	Platelet-Derived Growth	DoproToch	11 1 <i>1</i> P	20 ng.ml -1
BB	Factor-BB	reprotecti	11-14D	20 ng mL
DEX	dexamethasone	Sigma	D4902	10 <sup>-8</sup> м
Heparin	Heparin sodium	Selleck	S1346	2 µg·mL⁻¹
COL6	Collagen 6	Abcam	ab7538	2.5 µg∙mL <sup>-1</sup>

## Table S5. Primer sequences for real-time quantitative PCR analysis.

Gene	Forward (5'-3')	Reverse (5'-3')
COL2A1	GTCTGTGACACTGGGACTGT	TCTCCGAAGGGGATCTCAGG
ACAN	CTGCAGACCAGGAGGTATGTGA	GTTGGGGCGCCAGTTCTCAAAT
SOX9	GGCGGAGGAAGTCGGTGAAGAA	GCTCATGCCGGAGGAGGAGTGT
FGF2	AGAAGAGCGACCCTCACATCA	CGGTTAGCACACACTCCTTTG
MMP13	ATGCAGTCTTTCTTCGGCTTAG	ATGCCATCGTGAAGTCTGGT
COL1A1	CGATGGATTCCAGTTCGAGTAT	CATCGACAGTGACGCTGTAGG
ADAMTS5	ATCACCCAATGCCAAGG	AGCAGAGTAGGAGACAAC
MATN3	TCTCCCGGATAATCGACACTC	CAAGGGTGTGATTCGACCCA
GAPDH	TGACGCTGGGGCTGGCATTG	GGCTGGTGGTCCAGGGGTCT

#### Reference

[1] G. N. Hall, W. L. Tam, K. S. Andrikopoulos, L. Casas-Fraile, G. A. Voyiatzis, L. Geris, F. P. Luyten and I. Papantoniou, *Biomaterials* **2021**, *273*, 120820.