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Figure S1. (A) Chondrocyte-laden GelMA-HAMA hydrogel reinforced with multiphasic mPCL scaffold at day 1 of cell culture. (B) Top view SEM image of an mPCL scaffold. (C) Cross-sectional SEM image of mPCL scaffold showing distinct pore size zones. (D) mPCL scaffold stiffness is depth-dependent, with compressive modulus increasing as pore size decreases. (E) mPCL fibres were $12.66 \pm 0.55 \mu m$ in diameter. (F) Hydrogel heights of cell-free GelMA-HAMA hydrogels with or without mPCL fibre reinforcement (n = 4). (G) Hydrogel heights of GelMA-HAMA-mPCL hydrogels encapsulated with human articular chondrocytes at day 1 and day 28 of cell culture (n = 6). Groups that do not share a common Roman numeral are statistically different (p < 0.05).



Figure S2. Representative live/dead images of human articular chondrocytes in GelMA–HAMA-mPCL hydrogel constructs at the hydrogel surface. Images are taken from a single layer of a full-thickness z-stack image. Hydrogel constructs were fabricated with either bovine-derived (B) or porcine-derived (P) GelMA, crosslinked with IC2959 and 365 nm light (IC) or LAP and 405 nm light (LAP). Living cells appear green, dead cells appear red. Scale bars: 100 µm.



No PCL reinforcement

Figure S3. ECM accumulation in non-reinforced GelMA-HAMA hydrogel constructs after 28 days of cell culture. (**A-C**) Representative confocal images of human articular chondrocytes encapsulated in bovine-derived (B) or porcine-derived (P) GelMA, crosslinked with IC2959 and 365 nm light (IC) or LAP and 405 nm light (LAP). Immunoreactive regions for (**A**) collagen type II, (**B**) collagen type I and (**C**) aggrecan appear green. Cell nuclei are counterstained with DAPI (blue). (**D**) Integrated intensities for collagen II, collagen I and aggrecan. Asterisks indicate statistical difference between groups (*p < 0.05, ***p < 0.001) (AU: arbitrary units). n = 3 (3 donors, 1 construct per donor).

Gene	GenBank Number	Forward (5'-3')	Reverse (3'-5')	Product size (base pair)
RPL13A	NM_012423	CATAGGAAGCTGGGAGCAAG	GCCCTCCAATCAGTCTTCTG	157
TBP	NM_003194.4	GAGCCAAGAGTGAAGAACAGTC	CATCACAGCTCCCCACCATATT	123
MMP2	NM_004530.4	CCGTCGCCCATCATCAA	AGATATTGCACTGCCAACTCT	71
MMP13	NM_002427.3	ACTTCACGATGGCATTGCTG	CATAATTTGGCCCAGGAGGA	122
ACAN	NM_001135	GCCTGCGCTCCAATGACT	TAATGGAACACGATGCCTTTCA	106
COL1A2	NM_000089.3	GGCCCTCAAGGTTTCCAAGG	CACCCTGTGGTCCAACAACTC	166
COL2A1	NM_001844	GGCAATAGCAGGTTCACGTACA	CGATAACAGTCTTGCCCCACTT	79
COL10A1	NM_000493	ACCCAACACCAAGACACAGTTCT	TCTTACTGCTATACCTTTACTCTTTATGG	64
PRG4	NM_005807	GAGTACCCAATCAAGGCATTATCA	TCCATCTACTGGCTTACCATTGC	80

 Table S1. Forward (F) and reverse (R) primer sequences used for RT-PCR.