Supplemental information and figure captions

1. RNA and cDNA yield in samples processed for RT-PCR analysis.

We assayed our RNA yields/sample over the course of 16 days. They were: Day 1: 740-980ng; Day 3: 720-1100ng; Day 5: 820-940ng; Day 7: 920-1020ng; Day 8: 570-2920ng, and Day 16: 2020-5760ng. As we generally used 7ng of RNA for each RT-PCR reaction, our cDNA yield could allow us to perform 81-822 RT-PCR reactions per RNA preparation.

2. Reference factors in statistical analysis.

In RT-PCR analyses, when we compared the gene expression in chondrocytes in different scaffolds at a specific time point, and under a specific condition (control, IL-1β or TNFα), one-way ANOVA was used, and the factor was the scaffolding material. In RT-PCR analysis, when we compared gene expression in chondrocytes grown in different scaffolds over different cytokine treatments, we used two-way ANOVA, and the factors were the scaffolding material and treatment. In cytokine release analysis, we used two-way ANOVA as we compared the

release kinetics among the materials over time in each treatment (IL-1β or TNFα). Thus the factors for this statistical analysis were the scaffolding material and time. In water uptake analysis, we used one-way ANOVA to compare their water uptake ability in three different materials, and the factor was the scaffolding material. In toluidine blue quantification and H&E analyses, we used one-way ANOVA to compare three different materials under one specific treatment (either in control, or IL-1β or TNFα treatment). Thus the factor in this case was the scaffolding material.

Supplemental figure captions:

S1. Cartilage marker Sox9 expression in isolated chondrocytes. Sox9 expression in freshly isolated chondrocytes was analyzed by immunocytochemistry analysis. Bright field (BF) image (left), fluorescence image (middle), and merged image (right) are shown. Scale bar: 100μm. All cells were positive for Sox9 staining.

S2. Statistical analysis on cytokine release kinetics of the scaffolds, showing detailed statistical comparisons. Linear graphs in cytokine release kinetics of different materials in Figure 8 were formatted into bar graphs to show detailed statistical comparisons. **(A)** Percent release of IL-1β from scaffolds at each time point. **(B)** Cumulative release analysis of IL-1β from the scaffolds. **(C)** Percent release of TNFα from scaffolds at each time point. **(D)** Cumulative release analysis of TNFα from scaffolds. Data present mean ± SD. Statistical analysis of the data was determined by two-way ANOVA. *p<0.05.

S table1. Sequences of gene-specific primers used in the RT-PCR analysis. Forward (FWD) and reverse (REV) primer sequences and accession numbers for all the PCR primers are listed.