

Figure S1. Morphological analysis of unseeded matrices and of fibroblasts grown on tested matrices for 10 or 30 days. Scanning Electron Microscopy (SEM) images at high magnification are shown. a-c Strattice; d-f Permacol; g-i Biodesign; l-n Prolene. Bars: 100 μ m.

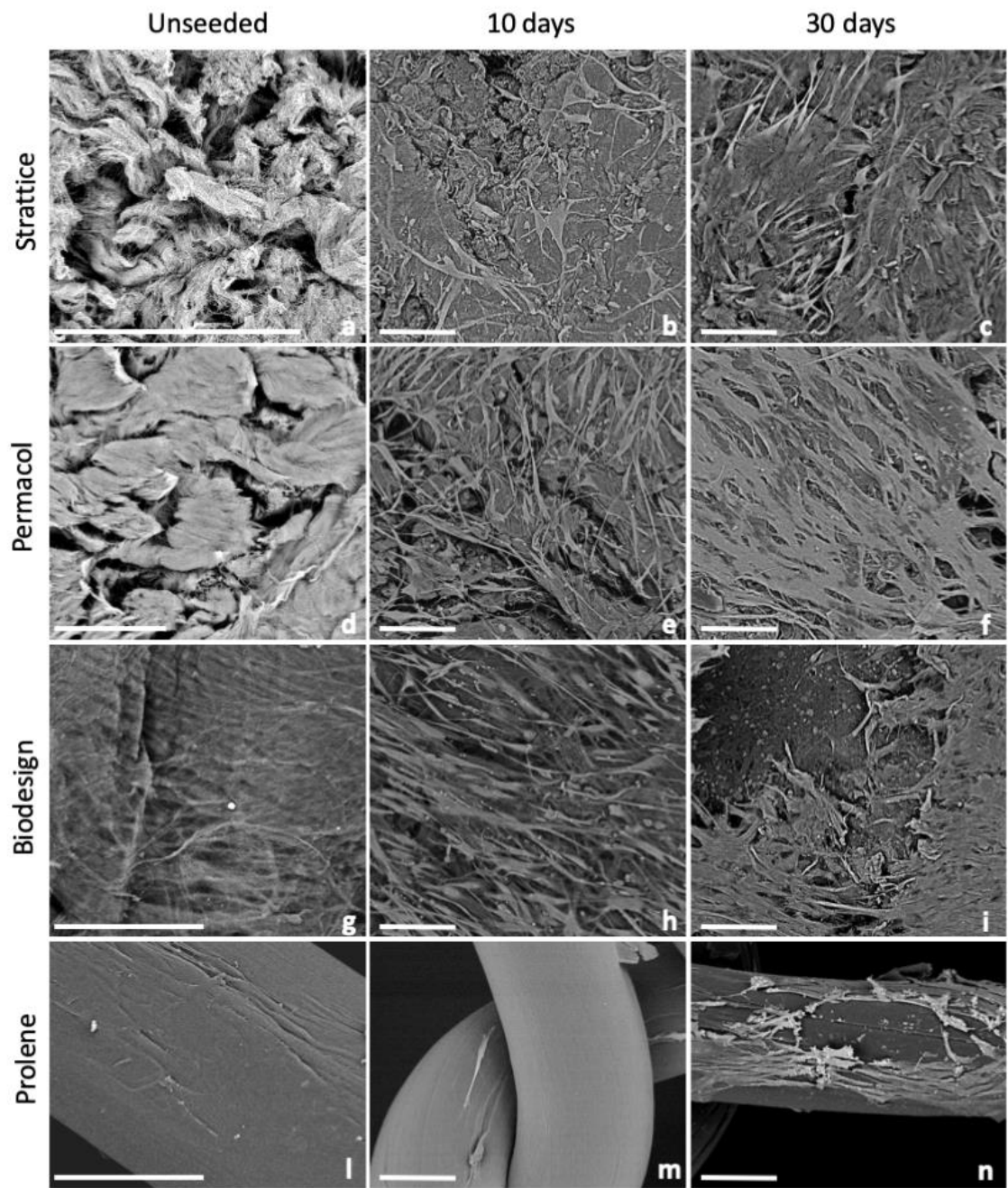


Table S1. Average Cq and standard error for each metalloproteinase under investigation and for the reference genes used in this work

The indicated values are the average of all technical (3 for each experiment) and biological replicates ($n=4$) performed for qPCR analyses for each condition in which fibroblasts were grown $\pm$ Standard Error. Control is represented by fibroblasts grown on plastics as described in Materials and Methods.

	<i>MMP1</i>		<i>MMP2</i>		<i>MMP9</i>		<i>MMP13</i>		<i>B2M+GAPDH</i>	
	10 days	30 days	10 days	30 days	10 days	30 days	10 days	30 days	10 days	30 days
Control	22,81 $\pm$ 0,60		20,29 $\pm$ 0,17		37,72 $\pm$ 0,63		34,72 $\pm$ 0,72		17,79 $\pm$ 0,34	
Strattice	16,69 $\pm$ 0,05	19,33 $\pm$ 0,49	18,49 $\pm$ 0,12	20,71 $\pm$ 0,19	N.A.	31,17 $\pm$ 0,82	N.A.	31,59 $\pm$ 0,24	16,16 $\pm$ 0,01	18,66 $\pm$ 0,34
Permacol	18,10 $\pm$ 0,28	21,19 $\pm$ 0,38	22,88 $\pm$ 0,14	21,31 $\pm$ 0,15	31,73 $\pm$ 0,67	30,55 $\pm$ 0,48	33,60 $\pm$ 0,09	30,63 $\pm$ 0,31	18,48 $\pm$ 0,16	18,65 $\pm$ 0,34
Biodesign	20,92 $\pm$ 1,13	22,19 $\pm$ 0,28	24,83 $\pm$ 1,15	22,92 $\pm$ 0,24	36,47 $\pm$ 1,77	30,96 $\pm$ 0,64	36,03 $\pm$ 0,48	33,98 $\pm$ 0,80	20,00 $\pm$ 0,85	19,47 $\pm$ 0,45

Table S2. Sequences of primers used for gene expression analysis in this study.

Gene	Ref_Seq		Sequence (5' → 3')	Product length (bp)
<i>MMP1</i>	NM_001145938.1; NM_002421.3	F	AAGGTCTCTGAGGGTCAAGCA	59
		R	TCCCGATGATCTCCCCTGAC	
<i>MMP2</i>	NM_001127891.2; NM_001302508.1; NM_001302509.1; NM_001302510.1; NM_004530.5	F	GCCAAGTGGTCCGTGTGAA	86
		R	GCTGTTGTACTCCTTGCCATTG	
<i>MMP9</i>	NM_004994.2	F	TTCTGCCCCGACCAAGGATA	89
		R	TCCGGCACTGAGGAATGATCT	
<i>TIMP1</i>	NM_003254.2	F	GCAATTCCGACCTCGTCATCA	134
		R	GTCAGCGGCATCCCCTAAG	
<i>TIMP2</i>	NM_003255.4	F	GCTGCGAGTGCAAGATCAC	108
		R	GGTGCCCGTTGATGTTCTTC	
<i>MMP13</i>	NM_002427.3	F	GGAATTAAGGAGCATGGCGAC	76
		R	GCCCAGGAGGAAAAGCATGA	
<i>COL1A1</i>	NM_000088.3	F	CAAGACGAAGACATCCCACCAA	128
		R	ACGTCATCGCACAAACACCTT	
<i>COL1A2</i>	NM_000089.3	F	TGAAGATGGTCACCCTGGAAAA	65
		R	CACCCTGTGGTCCAACAAC	
<i>COL3A1</i>	NM_000090.3	F	TCGAGGCAGTGATGGTCAAC	90
		R	GGTCCAACCTTACCCTTAGCA	
<i>CTGF</i>	NM_001901.2	F	TGCACCGCCAAAGATGGT	148
		R	GCAGACGAACGTCCATGCT	
<i>IL6</i>	NM_000600.4; NM_001318095.1	F	TAGTGAGGAACAAGCCAGAGC	104
		R	TTGGGTCAGGGGTGGTTATTG	
<i>ACTA2</i>	NM_001141945.1; NM_001613.2	F	GGCAAGTGATCACCATCGGA	100
		R	GTGGTTTCATGGATGCCAGC	
<i>GAPDH</i>	NM_001289746.1; NM_001289745.1; NM_002046.5	F	GAAGGTGAAGGTCGGAGTC	226
		R	GAAGATGGTGATGGGATTTC	
<i>B2M</i>	NM_004048.2	F	AGGCTATCCAGCGTACTCCA	102
		R	ATGGATGAAACCCAGACACA	