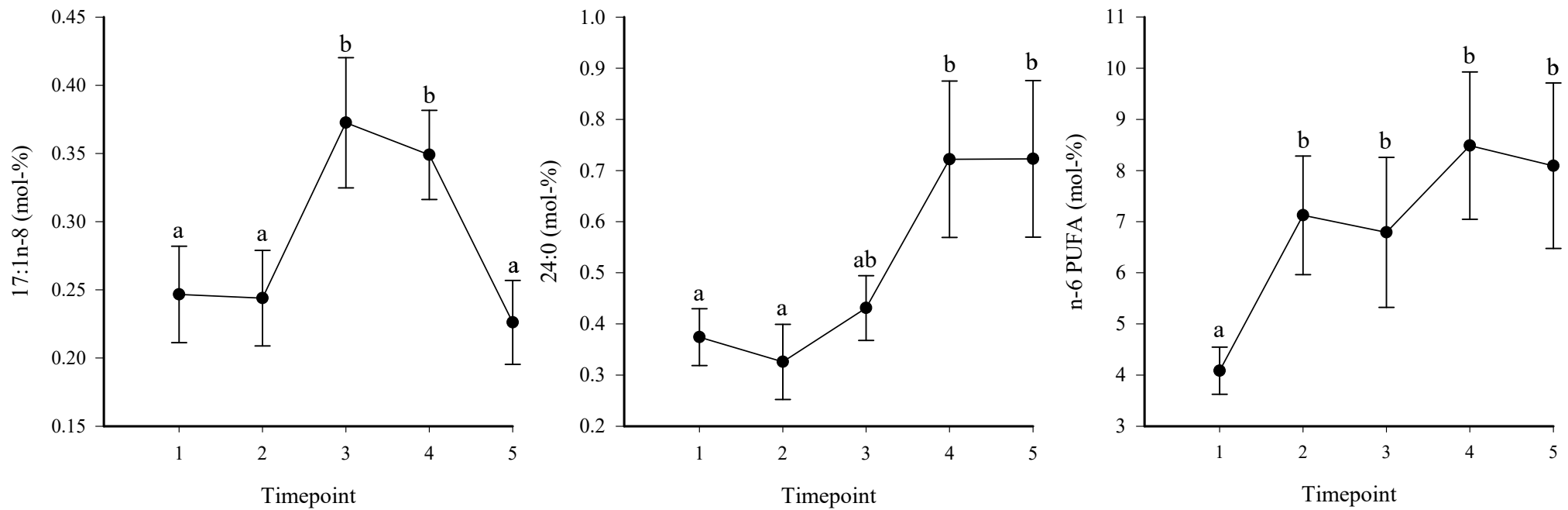


**Figure S1.** Expression profiling of the human hyaluronan synthase (*HAS*) gene family in fibroblast-like synoviocytes (mean + SE) at timepoint 1 = lag phase, timepoints 2–3 = proliferating cells, and timepoints 4–5 = high-density cells. Real-time quantitative PCR was used to determine the ratio of the mRNA expression of the three *HAS* genes relative to the control gene ribosomal protein lateral stalk subunit P0. Means with dissimilar letters indicate significant differences between the isoforms within a timepoint (Kruskal–Wallis ANOVA,  $p < 0.05$ ).



**Figure S2.** Temporal changes in the proportions of 17:1n-8, 24:0, and the sum of n-6 polyunsaturated fatty acids (PUFA) in fibroblast-like synoviocytes. Timepoint 1 = lag phase, timepoints 2–3 = proliferating cells, timepoints 4–5 = high-density cells. Dissimilar letters above means  $\pm$  SE indicate significant differences between timepoints (Kruskal–Wallis ANOVA,  $p < 0.05$ ).

**Table S1.** Fatty acid composition of the media, cells, and ultracentrifuged fraction (mean  $\pm$  SE).

Fatty acid	Control medium	Conditioned medium	Fibroblast-like synoviocytes	Extracellular vesicles	<i>p</i>
14:0	4.718 $\pm$ 0.168 <sup>a</sup>	4.678 $\pm$ 0.094 <sup>a</sup>	5.258 $\pm$ 0.166 <sup>b</sup>	5.618 $\pm$ 0.103 <sup>b</sup>	<0.0005
14:1n-5	0.399 $\pm$ 0.040 <sup>b</sup>	0.293 $\pm$ 0.017 <sup>a</sup>	0.434 $\pm$ 0.028 <sup>b</sup>	0.444 $\pm$ 0.024 <sup>b</sup>	<0.0005
15:0 <i>i</i>	0.262 $\pm$ 0.023 <sup>bc</sup>	0.220 $\pm$ 0.013 <sup>b</sup>	0.291 $\pm$ 0.018 <sup>c</sup>	0.153 $\pm$ 0.010 <sup>a</sup>	<0.0005
15:0 <i>ai</i>	0.378 $\pm$ 0.034 <sup>a</sup>	0.364 $\pm$ 0.018 <sup>a</sup>	0.563 $\pm$ 0.033 <sup>b</sup>	0.428 $\pm$ 0.023 <sup>a</sup>	<0.0005
15:0	0.288 $\pm$ 0.031 <sup>b</sup>	0.268 $\pm$ 0.013 <sup>b</sup>	0.284 $\pm$ 0.018 <sup>b</sup>	0.205 $\pm$ 0.014 <sup>a</sup>	<0.0005
DMA 16:0	0.651 $\pm$ 0.071 <sup>a</sup>	0.662 $\pm$ 0.055 <sup>a</sup>	1.190 $\pm$ 0.072 <sup>b</sup>	0.779 $\pm$ 0.055 <sup>a</sup>	<0.0005
16:0	30.563 $\pm$ 0.618 <sup>b</sup>	29.849 $\pm$ 0.466 <sup>b</sup>	25.963 $\pm$ 0.446 <sup>a</sup>	30.758 $\pm$ 0.298 <sup>b</sup>	<0.0005
16:1n-9	0.311 $\pm$ 0.035 <sup>a</sup>	0.466 $\pm$ 0.031 <sup>b</sup>	0.612 $\pm$ 0.033 <sup>c</sup>	0.353 $\pm$ 0.022 <sup>a</sup>	<0.0005
16:1n-7	1.309 $\pm$ 0.059	1.392 $\pm$ 0.046	1.479 $\pm$ 0.046	1.413 $\pm$ 0.043	0.125
16:1n-5	0.248 $\pm$ 0.032 <sup>a</sup>	0.349 $\pm$ 0.026 <sup>ab</sup>	0.501 $\pm$ 0.035 <sup>c</sup>	0.388 $\pm$ 0.032 <sup>b</sup>	0.001
17:0 <i>i</i>	1.065 $\pm$ 0.060 <sup>a</sup>	1.005 $\pm$ 0.057 <sup>a</sup>	1.306 $\pm$ 0.065 <sup>b</sup>	1.096 $\pm$ 0.042 <sup>a</sup>	0.004
17:0 <i>ai</i>	0.360 $\pm$ 0.048	0.281 $\pm$ 0.014	0.321 $\pm$ 0.017	0.307 $\pm$ 0.016	0.201
17:0	0.923 $\pm$ 0.025 <sup>c</sup>	0.850 $\pm$ 0.022 <sup>bc</sup>	0.817 $\pm$ 0.032 <sup>b</sup>	0.735 $\pm$ 0.020 <sup>a</sup>	<0.0005
17:1n-8	0.339 $\pm$ 0.042 <sup>b</sup>	0.309 $\pm$ 0.019 <sup>b</sup>	0.289 $\pm$ 0.018 <sup>ab</sup>	0.240 $\pm$ 0.015 <sup>a</sup>	0.025
DMA 18:0	0.558 $\pm$ 0.058 <sup>a</sup>	0.521 $\pm$ 0.035 <sup>a</sup>	1.009 $\pm$ 0.057 <sup>b</sup>	0.612 $\pm$ 0.030 <sup>a</sup>	<0.0005
18:0	19.297 $\pm$ 0.615 <sup>ab</sup>	20.478 $\pm$ 0.326 <sup>b</sup>	18.605 $\pm$ 0.233 <sup>a</sup>	19.886 $\pm$ 0.144 <sup>b</sup>	<0.0005
18:1n-9	24.562 $\pm$ 0.252 <sup>bc</sup>	23.703 $\pm$ 0.289 <sup>b</sup>	22.264 $\pm$ 0.400 <sup>a</sup>	24.640 $\pm$ 0.223 <sup>c</sup>	<0.0005
18:1n-7	3.578 $\pm$ 0.203 <sup>b</sup>	3.443 $\pm$ 0.111 <sup>b</sup>	3.539 $\pm$ 0.076 <sup>b</sup>	2.850 $\pm$ 0.069 <sup>a</sup>	<0.0005
18:1n-5	1.428 $\pm$ 0.152 <sup>ab</sup>	1.433 $\pm$ 0.071 <sup>a</sup>	1.740 $\pm$ 0.082 <sup>b</sup>	1.718 $\pm$ 0.076 <sup>b</sup>	0.009
18:2n-6	1.875 $\pm$ 0.069 <sup>c</sup>	1.693 $\pm$ 0.040 <sup>b</sup>	1.623 $\pm$ 0.032 <sup>ab</sup>	1.578 $\pm$ 0.026 <sup>a</sup>	0.001
18:3n-6	0.358 $\pm$ 0.043 <sup>ab</sup>	0.416 $\pm$ 0.049 <sup>a</sup>	0.556 $\pm$ 0.036 <sup>c</sup>	0.604 $\pm$ 0.079 <sup>bc</sup>	0.002
18:3n-3	0.675 $\pm$ 0.056 <sup>a</sup>	0.711 $\pm$ 0.053 <sup>a</sup>	0.989 $\pm$ 0.054 <sup>b</sup>	1.063 $\pm$ 0.060 <sup>b</sup>	<0.0005
20:0	0.374 $\pm$ 0.045	0.448 $\pm$ 0.029	0.474 $\pm$ 0.029	0.385 $\pm$ 0.017	0.178
20:1n-9	0.196 $\pm$ 0.017	0.235 $\pm$ 0.021	0.270 $\pm$ 0.018	0.219 $\pm$ 0.012	0.100
20:3n-6	0.675 $\pm$ 0.117 <sup>ab</sup>	0.742 $\pm$ 0.070 <sup>b</sup>	1.184 $\pm$ 0.072 <sup>c</sup>	0.453 $\pm$ 0.033 <sup>a</sup>	<0.0005
20:4n-6	0.872 $\pm$ 0.200 <sup>b</sup>	1.086 $\pm$ 0.107 <sup>b</sup>	3.294 $\pm$ 0.543 <sup>c</sup>	0.355 $\pm$ 0.023 <sup>a</sup>	<0.0005
20:5n-3	0.394 $\pm$ 0.064 <sup>b</sup>	0.396 $\pm$ 0.050 <sup>b</sup>	0.435 $\pm$ 0.040 <sup>b</sup>	0.227 $\pm$ 0.023 <sup>a</sup>	0.001
22:0	0.762 $\pm$ 0.075	0.713 $\pm$ 0.041	0.781 $\pm$ 0.049	0.802 $\pm$ 0.038	0.767
22:1n-11	0.061 $\pm$ 0.011 <sup>bc</sup>	0.045 $\pm$ 0.005 <sup>ab</sup>	0.068 $\pm$ 0.005 <sup>c</sup>	0.031 $\pm$ 0.003 <sup>a</sup>	<0.0005
22:1n-9	0.151 $\pm$ 0.033 <sup>ab</sup>	0.125 $\pm$ 0.016 <sup>a</sup>	0.194 $\pm$ 0.018 <sup>b</sup>	0.098 $\pm$ 0.007 <sup>a</sup>	<0.0005
22:1n-7	0.042 $\pm$ 0.010 <sup>a</sup>	0.046 $\pm$ 0.007 <sup>a</sup>	0.053 $\pm$ 0.004 <sup>b</sup>	0.031 $\pm$ 0.003 <sup>a</sup>	0.001
22:4n-6	0.258 $\pm$ 0.079 <sup>ab</sup>	0.395 $\pm$ 0.076 <sup>b</sup>	0.323 $\pm$ 0.049 <sup>b</sup>	0.151 $\pm$ 0.023 <sup>a</sup>	<0.0005
22:5n-3	0.992 $\pm$ 0.239 <sup>a</sup>	1.156 $\pm$ 0.119 <sup>a</sup>	1.583 $\pm$ 0.114 <sup>b</sup>	0.901 $\pm$ 0.059 <sup>a</sup>	<0.0005
22:6n-3	0.611 $\pm$ 0.186 <sup>b</sup>	0.795 $\pm$ 0.117 <sup>b</sup>	1.055 $\pm$ 0.093 <sup>c</sup>	0.268 $\pm$ 0.017 <sup>a</sup>	<0.0005
24:0	0.325 $\pm$ 0.040 <sup>bc</sup>	0.357 $\pm$ 0.027 <sup>b</sup>	0.518 $\pm$ 0.054 <sup>c</sup>	0.172 $\pm$ 0.019 <sup>a</sup>	<0.0005
24:1n-9	0.141 $\pm$ 0.051 <sup>bc</sup>	0.079 $\pm$ 0.014 <sup>b</sup>	0.137 $\pm$ 0.016 <sup>c</sup>	0.037 $\pm$ 0.003 <sup>a</sup>	<0.0005
SFA	59.314 $\pm$ 1.028 <sup>b</sup>	59.510 $\pm$ 0.657 <sup>b</sup>	55.183 $\pm$ 0.499 <sup>a</sup>	60.547 $\pm$ 0.265 <sup>b</sup>	<0.0005
MUFA	32.767 $\pm$ 0.536	31.918 $\pm$ 0.278	31.578 $\pm$ 0.393	32.463 $\pm$ 0.159	0.219
PUFA	6.710 $\pm$ 0.823 <sup>ab</sup>	7.390 $\pm$ 0.546 <sup>b</sup>	11.041 $\pm$ 0.749 <sup>c</sup>	5.600 $\pm$ 0.204 <sup>a</sup>	<0.0005
n-6 PUFA	4.037 $\pm$ 0.417 <sup>ab</sup>	4.332 $\pm$ 0.279 <sup>b</sup>	6.981 $\pm$ 0.609 <sup>c</sup>	3.140 $\pm$ 0.113 <sup>a</sup>	<0.0005
n-3 PUFA	2.672 $\pm$ 0.442 <sup>a</sup>	3.058 $\pm$ 0.284 <sup>a</sup>	4.061 $\pm$ 0.219 <sup>b</sup>	2.460 $\pm$ 0.127 <sup>a</sup>	<0.0005
n-3/n-6 PUFA	0.647 $\pm$ 0.056 <sup>ab</sup>	0.670 $\pm$ 0.030 <sup>a</sup>	0.663 $\pm$ 0.038 <sup>a</sup>	0.799 $\pm$ 0.043 <sup>b</sup>	0.021

UFA/SFA	0.671 ± 0.031 <sup>a</sup>	0.669 ± 0.018 <sup>a</sup>	0.778 ± 0.016 <sup>b</sup>	0.630 ± 0.006 <sup>a</sup>	<0.0005
DMA	1.209 ± 0.097 <sup>a</sup>	1.182 ± 0.082 <sup>a</sup>	2.198 ± 0.102 <sup>b</sup>	1.391 ± 0.079 <sup>a</sup>	<0.0005
DBI	0.568 ± 0.037 <sup>ab</sup>	0.594 ± 0.023 <sup>b</sup>	0.739 ± 0.028 <sup>c</sup>	0.513 ± 0.007 <sup>a</sup>	<0.0005
TACL	17.068 ± 0.037 <sup>bc</sup>	17.112 ± 0.018 <sup>c</sup>	17.059 ± 0.032 <sup>b</sup>	16.938 ± 0.011 <sup>a</sup>	<0.0005

*i* = iso, *ai* = anteiso, DMA = dimethyl acetal, *i.e.*, plasmalogen alkenyl chain derivative, SFA = saturated fatty acid, MUFA = monounsaturated fatty acid, PUFA = polyunsaturated fatty acid, UFA = unsaturated fatty acid (MUFA + PUFA), DBI = double bond index, TACL = total average chain length

Dissimilar superscript letters indicate significant differences between sample types within a row (Kruskal–Wallis ANOVA,  $p < 0.05$ )

**Table S2.** Primer sequences of the studied genes.

Gene		Sequence (5'–3')	Length
<i>RPLP0</i>	FOR	5' AGATGCAGCAGATCCGCAT 3'	319 bp
	REV	5' GTGGTGATACCTAAAGCCTG 3'	
<i>HAS1</i>	FOR	5' CAAGATTCTTCAGTCTGGAC 3'	124 bp
	REV	5' TAAGAACGAGGAGAAAGCAG 3'	
<i>HAS2</i>	FOR	5' CAGAATCCAAACAGACAGTTC 3'	187 bp
	REV	5' TAAGGTGTTGTGTGTGACTG 3'	
<i>HAS3</i>	FOR	5' CTTAAGGGTTGCTTGCTTGC 3'	194 bp
	REV	5' GTTCGTGGGAGATGAAGGAA 3'	
<i>CD44</i>	FOR	5' CATCTACCCAGCAACCCTA 3'	153 bp
	REV	5' CTGTCTGTCCTGTCGGTGAT 3'	
<i>IL-1<math>\beta</math></i>	FOR	5' TGGAGCAACAAGTGGTGT 3'	157 bp
	REV	5' TTGGGATCTACACTCTCCAGC 3'	
<i>IL-6</i>	FOR	5' TGCAATAACCACCCCTGACC 3'	163 bp
	REV	5' GTGCCCATGCTACATTTGCC 3'	
<i>TNF-<math>\alpha</math></i>	FOR	5' CCCAGGGACCTCTCTAATCA 3'	80 bp
	REV	5' GCTACAGGCTTGTCACCTCGG 3'	
<i>COX-2</i>	FOR	5' ATCTACGGTTTGCTGTGGGG 3'	156 bp
	REV	5' GCCTGCTTGCTGGAACAAC 3'	
<i>PPAR-<math>\alpha</math></i>	FOR	5' GCTGTCACCACAGTAGCTTG 3'	197 bp
	REV	5' TTCCAGAACTATCCTCGCCG 3'	
<i>PPAR-<math>\gamma</math></i>	FOR	5' TTCTCAAACGAGAGTCAGCCT 3'	126 bp
	REV	5' CAAAGGAGTGGGAGTGGTCT 3'	

*RPLP0* = ribosomal protein lateral stalk subunit P0, *HAS1–3* = hyaluronan synthase 1–3, *CD44* = cluster of differentiation 44, *IL-1 $\beta$ /6* = interleukin-1 $\beta$ /6, *TNF- $\alpha$*  = tumor necrosis factor  $\alpha$ , *COX-2* = cyclooxygenase 2, *PPAR- $\alpha$ / $\gamma$*  = peroxisome proliferator-activated receptor  $\alpha$ / $\gamma$