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Biomimetic tissue models reveal the role of hyaluronan in melanoma proliferation and invasion

Jiranuwat Sapudom^{1,2,3,§}, Khiet-Tam Nguyen^{3,§}, Steve Martin¹, Tom Wippold³, Stephanie Möller⁴, Mathias Schnabelrauch⁴, Ulf Anderegg³, Tilo Pompe^{1,*}

¹ Institute of Biochemistry, Faculty of Life Sciences, Universität Leipzig, 04103 Leipzig, Germany

² Division of Engineering, New York University Abu Dhabi, Abu Dhabi, UAE

³ Department of Dermatology, Venerology and Allergology, Universitätsklinikum Leipzig, 04103 Leipzig, Germany

⁴ INNOVENT e. V., Biomaterials Department, Prüssingstraße 27B, 07745 Jena, Germany

[§] equally contributed to this work

* Corresponding author

To whom Correspondence should be addressed:

Prof. Dr. Tilo Pompe

Postal address:	Leipzig University		
	Institute of Biochemistry		
	Johannisallee 21-23		
	04103 Leipzig		
	Germany		
Telephone/Fax:	+49 341 97 36931/9		
Email:	tilo.pompe@uni-leipzig.de		

Supplementary Table 1: Primer list

Gene	Gene Accession number	Start	Forward	End	Start	Reverse	End
Rpl-p0	NM_007475	512	GGACCCGAGAAGACCTCCTT	531	596	GCACATCACTCAGAATTTCAATGG	573
Has1	NM_008215	1107	CTATGCTACCAAGTATACCTCG	1128	1214	TCTCGGAAGTAAGATTTGGAC	1194
Has2	NM_008216.3	696	TGTACGGTGCCTTTTTAGCC	715	873	TTCACAGATTGCAAACATTTCC	852
Has3	NM_008217	1250	CAAGTCTTACTTTCGGGAATGG	1271	1449	TAGCCTTGATAATGCCCACC	1430
Ki67	NM_001081117.2	9709	GATGCAAAAACTCTGAAGGAGG	9730	9875	GGAGGTGAAAACCACACTGG	9856
Hyal1	NM_008317.5	1162	CCAAGGAATCATGCCAGG	1179	1339	GAGAAACTGGCAGGGTTGAG	1320
Hyal2	NM_010489.2	1180	ATAGTCAACGTGTCCTGGGC	1199	1318	TATGGCCAGGCACTAGGC	1301



Mouse gender

Figure S1: Weight of Ctrl and Has2-KD mice. The standard starting age for the 4OHT treatment was 8 weeks after birth and treatment lasted for 12 days. Weight of 4OHT-treated mice with ages between 7 and 35 weeks is shown. Both genders showed no weight specific effect due to *Has2*-KD. Different starting age of treatment did not result in any differences in body weight. Each dot represents an individual mouse.



Figure S2: Incomplete deletion of *Has2***-Exon2.** PCR amplification with flanking primers around *Has2*-Exon2 revealed successful but incomplete deletion in both full thickness skin samples and explanted fibroblasts. White arrows indicate undeleted alleles at 2440 bp in samples, where Credependent excision clearly occurred (257 bp product). L=ladder, H=water.



Figure S3: No compensation by Has isoenzymes. Full thickness skin samples were analyzed for all *Has* genes expression in RT-qPCR. Results were given as n(HasX) parts per million n(Rpl-p0). Compared to *Has2* gene expression, *Has1* and *Has3* expression were ~100-fold lower. While *Has2* expression was decreased by knockout induction, *Has1* and *Has3* expression kept their level. No compensatory upregulation was observed in these matched samples.

CTRL





Has2 KD

Figure S4: Overview of Ki67 expression in experimental tumors. Cryosections from tumors were stained with anti-Ki67 antibody (white) and DAPI (blue) as described in the methods section. Quantitation of the fluorescence signal was performed with Image J, see Figure 2. (scale bar: 500 μm).



Figure S5: Efficiency of decellularization method. (A) FbECMs were stained with HAPB and DAPI, and visualized using fluorescence microscopy. (Scale bars:100 μ m) (B) Quantification of mean (±SD) fluorescence signal intensity of HABP and DAPI using ImageJ (n = 3). Difference in HABP signal intensity could be observed in *Ctrl* and *Has2-KD* FbECM. Cells were fully removed as shown by absence of DAPI signal in (A).



Figure S6: Representative fluorescence images of EdU assay. GFP-tagged melanoma cells stained with EdU and DAPI. For the analysis, GFP signal were used to distinguish fibroblasts and melanoma cells in the coculture system. EdU positive cells were analyzed throughout the matrix thickness by counting cells using homebuilt MATLAB script.



Figure S7: Hyaluronidase-1 and -2 gene expression in skin and tumor. Full thickness skin and tumor mass samples were analyzed for *Hyal1* and -2 gene expression with RT-qPCR. Results were first calculated as n(HyalX) parts per million n(Rpl-p0) and then normalized to mean skin *Ctrl* values. Knockdown of *Has2* showed no effects on *Hyal1* or *Hyal2* expression, neither in skin nor in tumor sample. Tumor tissue gene expressions per cell were at ~30% compared to skin samples, but readily detectable.