*Microarray studies:*

U87-MG cells were stably transduced with a control plasmid or with a plasmid carrying the complete coding sequence of the CNS-specific ECM proteoglycan brevican (Genbank #BC010571). Transduced cells were cultured for two weeks and checked for expression of full-length and processed fragments of brevican before further testing (21). Control and brevican-expressing cells were gently resuspended and dissociated in DPBS, transferred to fresh culture medium and plated on poly-L-lysine- or fibronectin-coated 60-mm culture dishes at a total density of 5.10^5 cells/dish. After three hours, non-adhered cells were washed and the remaining cells were quickly frozen on ethanol/dry ice and further processed in Trizol (Invitrogen) to prepare total RNA. Details of cell transduction, cell adhesion experiments and further analysis of protein expression in those cells have been previously described (21). Increased cell adhesion was observed to correlate directly with increased cell motility on the same substrate (21).

Quality of the extracted RNA was verified by capillary electrophoresis (Bioanalyzer 2100, Agilent). RNA samples were processed for hybridization to U133(+) 2.0 genechips (Affimetrix), that cover the complete human genome. Microarrays were performed in duplicate for each experimental condition (cell type X substrate). RNA hybridization, image scanning and data analysis were performed at the Functional Genomics Core Facility of Nationwide Children's Hospital (Columbus, Ohio).

Supplementary Fig. 1: Fibulin-3 is upregulated by combined effect of brevican and fibronectin. A) Experimental design followed to identify altered mRNA expression in response to neural (brevican) and mesenchymal (fibronectin) ECM components. Colored boxes (4 conditions in duplicate) represent potential microarray results for probesets upregulated in substrate-dependent

(row 1), brevican-dependent (row 2) or brevican/substrate-dependent (row 3) manners. Using this assay, fibulin-3 was the only ECM-related transcript overexpressed in a brevican- and fibronectin-dependent manner (Suppl. Table I). B) Validation of fibulin-3 expression in U87-MG cells processed as indicated above, using qRT-PCR. Results indicate relative expression (Delta-Delta Ct) of fibulin-3 mRNA over baseline values (control cells on PLL substrate = 1). GAPDH was used as normalizing reference. *PLL*, poly-L-lysine; *FN*, fibronectin.
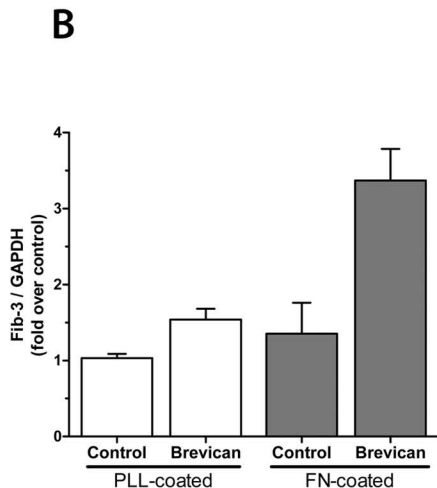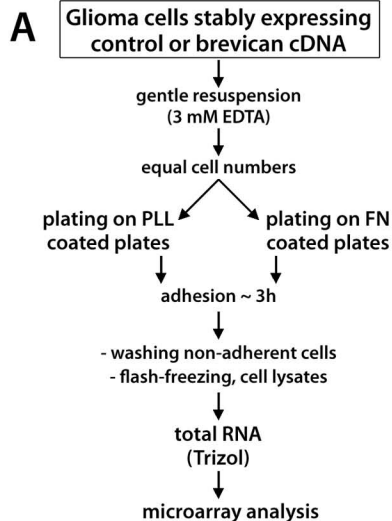
GENES UPREGULATED BY BREVICAN AND FIBRONECTIN IN GLIOMA CELLS

Bcan= brevican
FN= fibronectin
PLL= poly-L-Lysine

The table indicates transcripts that were upregulated in a brevican- and fibronectin-dependent manner

Mean values for each condition (brevican vs control cells, plated on FN or PLL) were normalized to the baseline values of control cells plated on PLL

Probesets were included in the table below when they matched the following conditions (see Suppl Fig. 1A)		
	Bcan(FN) / Control(FN) >2.00	
AND	Bcan(PLL) / Control (PLL) >0.75 and <1.25	
AND	Control(FN) / Control(PLL) >0.75 and <1.25	

Probeset	Gene Symbol	Description	Bcan FN	Control FN	Bcan PLL	Gene ID	Cytoband	GO BIOLOGICAL PROCESS	GO MOLECULAR FUNCTION	GO CELLULAR COMPONENT
240994_at	BRE	brain and reproductive organ-expressed (TNFRSF1A modulator)	5.710	1.004	1.560	9577	2p23.2	carbohydrate metabolic pro	peroxisome targeting seque	nuclear ubiquitin ligase comp
1553874_a_at	ZSCAN10	zinc finger and SCAN domain containing 10 (previous ZNF206)	5.389	2.126	1.076	84891	16p13.3	transcription /// regulation o	nucleic acid binding /// DNA	intracellular /// nucleus
1561616_a_at	DNAH6	dynein, axonemal, heavy polypeptide 6	4.136	1.313	1.069	1768 // 20	2p11.2	microtubule-based moveme	nucleotide binding /// motor	microtubule /// dynein comple
240262_at	CTNNA1	catenin (cadherin-associated protein), alpha 1, 102kDa	3.809	1.164	0.979	1495	5q31	cell adhesion /// cell adhesio	structural molecule activity /	cytoplasm /// cytoskeleton /
228440_at	PET112L	pet112-like (yeast)	3.493	1.459	0.942	5188	4q27-28	translation /// translation	translation factor activity, nu	mitochondrion /// mitochondri
36554_at	ASMTL	acetylserotonin O-methyltransferase-like	3.454	1.128	0.791	8623	Xp22.3; Yp1	melatonin biosynthetic proc	O-methyltransferase activity	---
237194_at	TSPAN5	tetraspanin-5 (transmembrane 4 superfamily member 9)	3.423	1.618	1.111	10098	4q23			membrane /// integral to mem
221892_at	H6PD	hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)	3.175	1.511	1.012	9563	1p36	carbohydrate metabolic pro	catalytic activity /// glucose-6	endoplasmic reticulum /// end
216797_at	----	Homo sapiens cDNA: FLJ23194 fis, clone REC00490	3.103	1.438	1.235	---	---	---	---	---
1569206_at	TCP11L2	t-complex 11 (mouse) like 2 (hypothetical protein MGC40368)	3.052	1.144	1.007	255394	12q23.3	---	---	---
232770_at	TUSC3	tumor suppressor candidate 3	2.954	1.044	1.389	7991	8p22	protein amino acid N-linked	dolichyl-diphosphooligosacc	endoplasmic reticulum /// end
1556122_at	RAB11B	RAB11B, member RAS oncogene family	2.893	1.257	0.981	9230	19p13.2	regulation of transcription, D	nucleotide binding /// GTPas	intracellular /// plasma membr
228486_at	SLC44A1	CDw92: solute carrier family 44, member 1	2.890	1.227	0.998	23446	9q31.2	transport /// choline transpo	choline transmembrane tran	membrane /// integral to mem
1553959_a_at	B3GALT6	UDP-gal:betagal beta 1,3-galactosyltransferase polypeptide 6	2.829	1.206	0.885	126792	1p36.33	glycosaminoglycan biosynth	galactosyltransferase activit	Golgi apparatus /// Golgi med
225453_x_at	CCDC124	coiled-coil domain containing 124 (hypothetical protein BC013949)	2.786	1.077	1.083	115098	19p13.11	---	---	---
239899_at	RNF145	ring finger protein 145 (hypothetical protein FLJ31951)	2.599	0.984	1.012	153830	5q33.3	---	protein binding /// zinc ion bi	membrane /// integral to mem
63305_at	PKNOX2	PBX/knotted 1 homeobox 2	2.582	1.326	0.977	63876	chr 11	regulation of transcription, D	DNA binding /// DNA binding	nucleus /// cytoplasm /// actin
1566785_x_at	NSF	N-ethylmaleimide-sensitive factor	2.531	1.094	1.023	728806	17q21.31-q2	---	nucleotide binding /// ATP bi	---
201842_s_at	**EFEMP1**	**EGF-containing fibulin-like extracellular matrix protein 1**	**2.479**	**0.982**	**0.900**	**2202**	**2p16**	visual perception	calcium ion binding /// protei	extracellular region /// protein
221133_s_at	CLDN18	claudin 18	2.376	0.876	1.243	51208	3q22.3	calcium-independent cell-ce	structural molecule activity /	plasma membrane /// tight jur
56256_at	SIDT2	SID1 transmembrane family, member 2	2.346	0.877	1.007	51092	11q23.3	---	---	membrane /// integral to mem
244391_at	TSEN2	tRNA splicing endonuclease 2 homolog (S. cerevisiae)	2.219	0.987	1.085	80746	3p25.1	tRNA splicing /// mRNA proc	tRNA-intron endonuclease a	tRNA-intron endonuclease co
204944_at	PTPRG	protein tyrosine phosphatase, receptor type, G	2.161	1.081	0.957	5793	3p21-p14	protein amino acid dephosp	carbonate dehydratase activ	integral to plasma membrane
1568365_at	KIFAP3	kinesin-associated protein 3	2.104	0.993	0.918	22920	1q24.2	protein complex assembly /	binding /// protein binding ///	endoplasmic reticulum /// kine
1558943_x_at	ZNF765	zinc finger protein 765 (hypothetical protein BC001610)	2.092	0.967	1.093	91661	19q13.41	regulation of transcription, D	nucleic acid binding /// zinc i	intracellular
209964_s_at	ATXN7	ataxin 7	2.090	0.862	1.154	6314	3p21.1-p12	transcription /// regulation of	protein binding /// zinc ion bi	intracellular /// nucleus /// nuc
201151_s_at	MBNL1	muscleblind-like (Drosophila)	2.083	0.999	0.888	4154	3q25	in utero embryonic developr	nucleic acid binding /// RNA	nucleus /// nucleus /// cytopla
222171_s_at	PKNOX2	PBX/knotted 1 homeobox 2	2.073	0.704	1.392	63876	chr 11	regulation of transcription, D	DNA binding /// DNA binding	nucleus /// cytoplasm /// actin
229366_at	CRBN	cereblon	2.009	0.992	0.975	51185	3p26.3	ATP-dependent proteolysis	ATP-dependent peptidase a	cytoplasm /// membrane
221477_s_at	SOD2	superoxide dismutase 2, mitochondrial	2.005	0.906	1.047	79099	6q25.3	response to superoxide /// r	superoxide dismutase activi	mitochondrion /// mitochondri

SUPPLEMENTARY TABLE II
ONCOMINE STUDIES

Expression of Fibulin-3 (*EFEMP-1*) mRNA (by microarray analysis) in solid tumors

t= (average signal in tumor - average signal in control) / standard deviation (control vs. tumor)

Gene Symbol: EFEMP1

t<0 and p<0.05 --> EFEMP1 significantly decreased in tumor tissue
t>0 and p< 0.05 --> EFEMP1 significantly increased in tumor tissue

Study	TISSUE	STUDY IDENTIFICATION	YEAR	# CONTROL SAMPLES	# TUMOR SAMPLES	t test value	p value	REPORTER	PLATFORM	OBSERVATIONS	LINK TO ORIGINAL STUDY
1	BLADDER	Blaveri_Bladder_2	2005	3	81	-2.268	0.144	AA875933	Stanford microarrays		Bladder cancer outcome and subtyp
2	BLADDER	Dyrskjot_Bladder_3	2004	14	40	-1.537	0.133	201842_s_at	Affymetrix U133		Gene expression in the urinary blad
3	BLADDER	Sanchez-Carbayo_Bladder_2	2006	48	109	-10.229	9.00E-19	201843_s_at	Affymetrix U133		Defining molecular profiles of poor o
4	BRAIN	Bredel_Brain_2	2005	4	31	6.424	3.20E-07	IMAGE:1492230	IMAGE Consortium	normal brain vs glioblastoma	Functional network analysis reveals
	BRAIN	Bredel_Brain_2	2005	4	8	3.757	0.004	IMAGE:1492230	IMAGE Consortium	normal brain vs oligodendroglioma	Functional network analysis reveals
	BRAIN	Bredel_Brain_2	2005	4	5	2.64	0.056	IMAGE:1492230	IMAGE Consortium	normal brain vs astrocytic tumor	Functional network analysis reveals
5	BRAIN	Bredel_Brain_3	2005	4	6	2.318	0.065	IMAGE:1492230	IMAGE Consortium	normal brain vs anapl. oligo.	Functional network analysis reveals
6	BRAIN	French_Brain	2005	6	27	1.426	0.186	228421_s_at	Affymetrix U133	normal brain vs anapl. oligo. and astro.	Gene expression profiles associated
7	BRAIN	Gutmann_Brain	2002	3	8	0.495	0.648	32551_at	Affymetrix U95	normal white matter vs pilocytic astro	Comparative gene expression profile
8	BRAIN	Liang_Brain	2005	3	30	6.878	6.70E-04	AA875933	Stanford microarrays	normal brain vs astrocytoma	Gene expression profiling reveals m
9	BRAIN	Rickman_Brain	2001	6	45	0.84	0.43	U03877_at	Affymetrix HuGeneFL	normal brain vs astrocytoma	Distinctive molecular profiles of high
10	BRAIN	Shai_Brain	2003	7	25	3.526	0.002	32551_at	Affymetrix U95	normal brain vs glioblastoma	Gene expression profiling identifies
11	BRAIN	Sun_Brain	2006	23	77	8.238	5.30E-12	201842_s_at	Affymetrix U133	normal brain vs glioblastoma	Neuronal and glioma-derived stem c
	BRAIN	Sun_Brain	2006	23	50	-0.919	0.361	201841_s_at	Affymetrix U133	normal brain vs oligodendroglioma	Neuronal and glioma-derived stem c
	BRAIN	Sun_Brain	2006	23	26	5.162	7.10E-06	201842_s_at	Affymetrix U133	normal brain vs astrocytoma	Neuronal and glioma-derived stem c
	BRAIN	Sun_Brain	2006	23	50	2.537	0.013	201842_s_at	Affymetrix U133	normal brain vs oligodendroglioma	Neuronal and glioma-derived stem c
12	BREAST	Finak_Breast	2008	6	53	12.336	6.90E-09	A_23_P501007	Agilent HG 44k	Outlier data, under revision at Oncomine	Stromal gene expression predicts cl
13	BREAST	Karnoub_Breast	2007	15	7	-4.317	4.10E-04	201843_s_at	Affymetrix U133		Mesenchymal stem cells within tumo
14	BREAST	Radvanyi_Breast	2005	9	47	-1.07	0.311	AA301867	Stanford microarrays		The gene associated with trichorhino
15	BREAST	Richardson_Breast_2	2006	7	40	0.657	0.515	228421_s_at	Affymetrix U133		X chromosomal abnormalities in bas
	BREAST	Richardson_Breast_2	2006	7	40	-7.825	8.10E-10	201843_s_at	Affymetrix U133	same study as #15, different probe	X chromosomal abnormalities in bas
16	BREAST	Turashvili_Breast	2007	5	5	0.65	0.535	228421_s_at	Affymetrix U133	breast ductal tissue vs invasive ductal carcinoma	Novel markers for differentiation of l
	BREAST	Turashvili_Breast	2007	5	5	-2.215	0.0065	201843_s_at	Affymetrix U133	breast lobular tissue vs inv. lobular carcinoma	Novel markers for differentiation of l
	BREAST	Turashvili_Breast	2007	5	5	-0.946	0.384	201843_s_at	Affymetrix U133	same study as #16, different probe	Novel markers for differentiation of l
17	COLON	Hong_Colon	2007	10	12	4.039	7.20E-04	201842_s_at	Affymetrix U133		A susceptibility gene set for early on
	COLON	Hong_Colon	2007	10	12	-0.931	0.363	228421_s_at	Affymetrix U133	same study as #17, different probe	A susceptibility gene set for early on
18	COLON	Notterman_Colon	2001	18	18	-2.004	0.06	U03877	Affymetrix HuGeneFL		Transcriptional gene expression pro
19	DIGESTIVE	Hao_Esophagus	2006	15	5	3.496	0.016	IMAGE:1492230	IMAGE Consortium	esophagus	Gene expression profiling reveals st
20	DIGESTIVE	Hippo_Gastric	2002	8	22	-1.705	0.103	U03877_at	Affymetrix HuGeneFL	gastric	Global gene expression analysis of
21	DIGESTIVE	Kimchi_Esophagus	2005	8	8	0.514	0.616	201843_s_at	Affymetrix U133	esophagus	Progression of Barretts metaplasia t
	DIGESTIVE	Kimchi_Esophagus	2005	8	8	-0.22	0.831	201842_s_at	Affymetrix U133	esophagus, same as #21, different probe	Progression of Barretts metaplasia t
22	HEAD/NECK	Cromer_Head-Neck	2004	4	34	-3.529	0.002	32551_at	Affymetrix U95		Identification of genes associated wi
23	HEAD/NECK	Ginos_Head-Neck	2004	13	41	0.788	0.435	201843_s_at	Affymetrix U133		Identification of a gene expression s
	HEAD/NECK	Ginos_Head-Neck	2004	13	41	-0.177	0.86	201842_s_at	Affymetrix U133	same study as #23, different probe	Identification of a gene expression s
24	HEAD/NECK	Pyeon_Multi-cancer	2007	14	42	2.17	0.037	228421_s_at	Affymetrix U133		Fundamental differences in cell cycl
25	HEAD/NECK	Toruner_Head-Neck	2004	4	16	-0.304	0.766	201843_s_at	Affymetrix U133		Association between gene expressio
	HEAD/NECK	Toruner_Head-Neck	2004	4	16	0.258	0.799	201842_s_at	Affymetrix U133	same study as #25, different probe	Association between gene expressio
26	LUNG	Beer_Lung	2002	10	86	-7.141	9.80E-08	U03877_at	Affymetrix HuGeneFL		Gene-expression profiles predict su
27	LUNG	Bhattacharjee_Lung	2001	17	139	-6.293	5.90E-08	32551_at	Affymetrix U95	normal lung vs lung adenocarcinoma	Classification of human lung carcino
	LUNG	Bhattacharjee_Lung	2001	17	21	-5.649	3.30E-04	32551_at	Affymetrix U95	normal lung vs squamous cell carcinoma	Classification of human lung carcino
	LUNG	Bhattacharjee_Lung	2001	17	6	-2.291	0.067	32551_at	Affymetrix U95	normal lung vs small cell lung cancer	Classification of human lung carcino
	LUNG	Bhattacharjee_Lung	2001	17	20	-7.977	7.70E-09	32551_at	Affymetrix U95	normal lung vs carcinoid	Classification of human lung carcino
28	LUNG	Garber_Lung	2001	6	40	-5.384	2.30E-05	IMAGE:1492230	IMAGE Consortium	normal lung vs lung adenocarcinoma	Diversity of gene expression in ader
	LUNG	Garber_Lung	2001	6	13	-5.414	6.10E-05	IMAGE:1492230	IMAGE Consortium	normal lung vs squamous cell carcinoma	Diversity of gene expression in ader
	LUNG	Garber_Lung	2001	6	4	-5.398	0.006	IMAGE:1492230	IMAGE Consortium	normal lung vs small cell lung cancer	Diversity of gene expression in ader
	LUNG	Garber_Lung	2001	6	4	-0.274	0.801	IMAGE:1492230	IMAGE Consortium	normal lung vs large cell lung cancer	Diversity of gene expression in ader
29	LUNG	Powell_Lung	2003	11	11	-5.145	1.40E-04	U03877_at	Affymetrix HuGeneFL		Gene expression in lung adenocarci
30	LUNG	Stearman_Lung	2005	19	20	-7.5	3.30E-08	32551_at	Affymetrix U95		Analysis of orthologous gene expres
31	LUNG	Su_Lung	2007	31	31	-5.839	5.20E-07	201843_s_at	Affymetrix U133		Selection of DDX5 as a novel interna

#	Tissue	Study	Year					Probe	Platform	Comparison	Title
32	LUNG	Wachi_Lung	2005	5	5	-8.213	1.30E-04	201843_s_at	Affymetrix U133		Interactome-transcriptome analysis
33	LIVER	Chen_Liver	2002	7	104	-4.31	8.80E-04	IMAGE:1492230	IMAGE Consortium	benign liver disease vs hepatocell. carcinoma	Gene expression patterns in human
	LIVER	Chen_Liver	2002	76	104	-1.983	0.049	IMAGE:1492230	IMAGE Consortium	non-tumor liver vs hepatocell. carcinoma	Gene expression patterns in human
34	LIVER	Wurmbach_Liver	2007	10	35	2.435	0.02	201843_s_at	Affymetrix U133		Genome-wide molecular profiles of l
35	MELANOMA	Haqq_Melanoma	2005	10	22	-5.834	9.80E-06	AA875933	Stanford microarrays		The gene expression signatures of r
36	MELANOMA	Hoek_Melanoma	2006	3	18	1.624	0.121	201843_s_at	Affymetrix U133		Metastatic potential of melanomas c
	MELANOMA	Hoek_Melanoma	2006	3	24	-0.441	0.674	201842_s_at	Affymetrix U133	same study as #36, different probe	Metastatic potential of melanomas c
37	MELANOMA	Talantov_Melanoma	2005	25	45	-10.13	2.60E-14	201842_s_at	Affymetrix U133		Novel genes associated with malign
38	OVARY	Hendrix_Ovarian	2006	4	41	-13.33	1.80E-12	201842_s_at	Affymetrix U133	ovary vs ovarian serous adenocarcinoma	Fibroblast growth factor 9 has onco
	OVARY	Hendrix_Ovarian	2006	4	37	-13.254	3.20E-12	201842_s_at	Affymetrix U133	ovary vs ovarian endometroid adenocarcinoma	Fibroblast growth factor 9 has onco
	OVARY	Hendrix_Ovarian	2006	4	13	-12.011	4.70E-09	201842_s_at	Affymetrix U133	ovary vs ovarian mucinous adenocarcinoma	Fibroblast growth factor 9 has onco
	OVARY	Hendrix_Ovarian	2006	4	8	-5.43	4.40E-04	201842_s_at	Affymetrix U133	ovary vs ovarian clear cell adenocarcinoma	Fibroblast growth factor 9 has onco
39	OVARY	Lancaster_Ovarian	2004	3	31	-1.35	0.301	U03877_at	Affymetrix HuGeneFL		Gene expression patterns that chara
40	OVARY	Lu_Ovarian	2004	5	19	-3.81	0.015	32551_at	Affymetrix U95		Selection of potential markers for ep
41	OVARY	Welsh_Ovarian	2001	4	28	-2.119	0.073	U03877_at	Affymetrix HuGeneFL		Analysis of gene expression profiles
42	PANCREAS	Buchholz_Pancreas	2005	6	8	-0.669	0.517	NM_004105	Operon OligoSet 2.0		Transcriptome analysis of microdiss
43	PANCREAS	Grutzmann_Pancreas	2003	11	14	-1.764	0.094	201843_s_at	Affymetrix U133		Gene expression profiling of microdi
44	PANCREAS	Ishikawa_Pancreas	2005	25	24	-1.396	0.169	201843_s_at	Affymetrix U133		Experimental trial for diagnosis of pa
45	PANCREAS	Logsdon_Pancreas	2003	10	10	1.791	0.093	U03877_at	Affymetrix HuGeneFL		Molecular profiling of pancreatic ade
46	PLEURA	Gordon_Mesothelioma	2005	5	40	3.385	0.015	201842_s_at	Affymetrix U133	mesothelioma	Identification of novel candidate onc
47	PROSTATE	Dhanasekaran_Prostate	2001	22	59	-3.138	0.004	IMAGE:1492230	IMAGE Consortium		Delineation of prognostic biomarkers
48	PROSTATE	Dhanasekaran_Prostate_2	2004	12	25	-4.553	2.30E-04	IMAGE:1492230	IMAGE Consortium		Molecular profiling of human prostat
49	PROSTATE	Holzbeierlein_Prostate	2003	4	23	-1.795	0.155	32551_at	Affymetrix U95		Gene expression analysis of human
50	PROSTATE	LaTulippe_Prostate	2002	3	23	-2.242	0.107	32551_at	Affymetrix U95		Comprehensive gene expression an
51	PROSTATE	Liu_Prostate	2006	13	44	-5.497	2.90E-05	201842_s_at	Affymetrix U133		Sex-determining region Y box 4 is a
52	PROSTATE	Luo_Prostate	2001	9	16	-2.463	0.023	IMAGE:1492230	IMAGE Consortium		Human prostate cancer and benign
53	PROSTATE	Luo_Prostate_2	2002	15	15	-1.968	0.06	32551_at	Affymetrix U95		Gene expression analysis of prostat
54	PROSTATE	Magee_Prostate	2001	4	8	-0.807	0.447	U03877_at	Affymetrix HuGeneFL		Expression profiling reveals hepsin
55	PROSTATE	Nanni_Prostate	2006	3	22	0.683	0.557	201842_s_at	Affymetrix U133		Epithelial-restricted gene profile of p
56	PROSTATE	Singh_Prostate	2002	50	52	-2.711	0.008	32551_at	Affymetrix U95		Gene expression correlates of clinic
57	PROSTATE	Tomlins_Prostate	2006	22	30	-0.476	0.637	IMAGE:1492230	IMAGE Consortium		Integrative molecular concept mode
58	PROSTATE	Vanaja_Prostate	2003	8	27	0.979	0.347	228421_s_at	Affymetrix U133		Transcriptional silencing of zinc fing
	PROSTATE	Vanaja_Prostate	2003	8	27	-3.767	0.001	201842_s_at	Affymetrix U133	same study as #58, different probe	Transcriptional silencing of zinc fing
59	PROSTATE	Varambally_Prostate	2005	6	7	-3.005	0.025	201842_s_at	Affymetrix U133		Integrative genomic and proteomic a
60	PROSTATE	Wang_CellLine	2007	8	8	-4.913	0.001	201842_s_at	Affymetrix U133	immortalized prostate epithelium vs prostate carcinom	Identification of candidate predictive
61	PROSTATE	Welsh_Prostate	2001	9	25	-4.04	8.30E-04	32551_at	Affymetrix U95		Analysis of gene expression identifie
62	PROSTATE	Yu_Prostate	2004	23	64	-4.067	2.10E-04	32551_at	Affymetrix U95		Gene expression alterations in prost
63	RENAL	Boer_Renal	2001	162	160	-1.291	0.199	IMAGE:162112	IMAGE Consortium	kidney vs clear renal cell carcinoma	Identification and classification of dif
	RENAL	Boer_Renal	2001	162	160	0.502	0.616	IMAGE:162112	IMAGE Consortium	kidney vs clear renal cell carcinoma	Identification and classification of dif
	RENAL	Boer_Renal	2001	162	16	-0.322	0.755	IMAGE:162112	IMAGE Consortium	kidney vs chromphobe renal cell carcinoma	Identification and classification of dif
	RENAL	Boer_Renal	2001	162	16	0.176	0.871	IMAGE:162112	IMAGE Consortium	kidney vschromophobe renal cell carcinoma	Identification and classification of dif
64	RENAL	Gumz_Renal	2007	10	10	-0.774	0.452	201843_s_at	Affymetrix U133		Secreted frizzled-related protein 1 lc
65	RENAL	Higgins_Renal	2003	3	26	0.382	0.728	IMAGE:1492230	IMAGE Consortium		Gene expression patterns in renal c
66	RENAL	Lenburg_Renal	2003	9	9	0.73	0.477	228421_s_at	Affymetrix U133		Previously unidentified changes in re
	RENAL	Lenburg_Renal	2003	9	9	-0.729	0.483	201842_s_at	Affymetrix U133	same study as #66, different probe	Previously unidentified changes in re
67	SALIV. GLAND	FriersonHF_Salivary-gland	2002	6	16	-2.228	0.041	32551_at	Affymetrix U95		Large scale molecular analysis iden
68	SEMINOMA	Korkola_Seminoma	2006	6	91	17.763	8.10E-31	201842_s_at	Affymetrix U133		Down-regulation of stem cell genes,
69	THYROID	Huang_Thyroid	2001	8	8	-2.491	0.028	32551_at	Affymetrix U95		Gene expression in papillary thyroid
70	TONGUE	Talbot_Lung	2005	26	31	-1.939	0.058	32551_at	Affymetrix U95		Gene expression profiling allows dis
71	UTERUS	Mutter_Endometrium	2001	4	10	-1.316	0.275	U03877_at	Affymetrix HuGeneFL	normal endometrium vs endometrioid adenocarcinom	Global expression changes of const
72	UTERUS	Pyeon_Multi-cancer	2007	8	20	-2.008	0.056	201843_s_at	Affymetrix U133	normal cervix vs cervical cancer	Fundamental differences in cell cycl
73	UTERUS	Wong_Endometrium	2003	8	25	2.546	0.031	AA875933	Stanford microarrays	normal cervix vs cervical carcinoma	Expression genomics of cervical car

SUPPLEMENTARY TABLE III (A)
REMBRANDT DATA

Expression of Fibulin mRNA by microarray analysis, mean expression values

shaded cells: lower quality grade for transcript assignment to the reporter (reporter with annotation grade E or R) ==> vetted probesets

Unif: Unified gene expression. Results from the individual probesets were processed into splice-form based probesets, to show a gene-based view of the expression data
(additional information regarding unified gene view in http://caintegrator-info.nci.nih.gov/rembrandt)

Significant differences against controls:

up, p<0.05
up, p<0.001
down, p<0.05
down, p<0.001

	reporter	Mean expression intensity	Geometric mean (Log2)	St. Dev. (Log 2)	Fold over control	p value		reporter	Mean expression intensity	Geometric mean (Log2)	St. Dev. (Log 2)	Fold over control	p value		reporter	Mean expression intensity
FIBULIN-1 ASTRO	201787_at	190.151	7.432	1.696	0.936	0.7885	**FIBULIN-2 ASTRO**	203886_s_at	32.200	5.360	1.604	0.666	0.1173	**FIBULIN-3 ASTRO**	201842_s_at	6387.342
	202994_s_at	142.518	7.079	1.507	0.893	0.5958										201843_s_at	1910.852
	202995_s_at	401.986	8.635	0.982	0.997	0.9991										228421_s_at	17.304
	207834_at	101.476	6.594	0.724	0.814	0.0740											
	207835_at	231.040	7.737	0.638	0.848	0.0881											
	Unif 2192	163.697	7.249	1.691	0.955	0.8516		**Unif 2199**	27.963	5.174	1.605	0.680	0.1381		**Unif 2202**	1907.175
FIBULIN-1 GBM	201787_at	215.568	7.242	1.856	0.820	0.4295	**FIBULIN-2 GBM**	203886_s_at	27.704	5.278	1.656	0.629	0.0469	**FIBULIN-3 GBM**	201842_s_at	7211.082
	202994_s_at	121.095	6.623	1.808	0.651	0.0765										201843_s_at	2108.498
	202995_s_at	365.822	8.318	1.346	0.801	0.2144										228421_s_at	19.698
	207834_at	119.098	6.633	0.877	0.836	0.1369											
	207835_at	235.568	7.619	0.637	0.781	0.0051											
	Unif 2192	283.714	7.057	1.857	0.836	0.4757		**Unif 2199**	37.091	5.091	1.659	0.642	0.0578		**Unif 2202**	3164.583
FIBULIN-1 MIXED	201787_at	59.956	5.921	1.695	0.328	0.0003	**FIBULIN-2 MIXED**	203886_s_at	31.801	4.911	1.509	0.488	0.0268	**FIBULIN-3 MIXED**	201842_s_at	5297.654
	202994_s_at	76.460	6.022	1.376	0.429	0.0004										201843_s_at	1964.659
	202995_s_at	342.893	8.027	0.942	0.654	0.0063										228421_s_at	15.996
	207834_at	177.027	6.893	0.803	1.001	0.9949											
	207835_at	351.159	7.832	0.382	0.906	0.6244											
	Unif 2192	53.378	5.765	1.687	0.342	0.0004		**Unif 2199**	28.495	4.748	1.508	0.506	0.0358		**Unif 2202**	1888.352
FIBULIN-1 OLIGO	201787_at	81.008	6.133	1.609	0.380	0.0001	**FIBULIN-2 OLIGO**	203886_s_at	22.896	4.670	1.062	0.413	<0.0001	**FIBULIN-3 OLIGO**	201842_s_at	2565.457
	202994_s_at	56.415	5.941	1.102	0.406	<0.0001										201843_s_at	985.697
	202995_s_at	239.022	7.879	0.613	0.591	<0.0001										228421_s_at	12.799
	207834_at	120.259	6.801	0.750	0.939	0.5931											
	207835_at	212.895	7.717	0.520	0.836	0.0333											
	Unif 2192	72.821	5.964	1.602	0.392	0.0001		**Unif 2199**	20.574	4.496	1.055	0.425	0.0001		**Unif 2202**	1005.107
FIBULIN-1 CONTROL	201787_at	270.289	7.528	1.176			**FIBULIN-2 CONTROL**	203886_s_at	120.630	5.946	1.649			**FIBULIN-3 CONTROL**	201842_s_at	2268.283
	202994_s_at	211.569	7.242	0.872												201843_s_at	757.735
	202995_s_at	554.702	8.639	0.562												228421_s_at	24.101
	207834_at	185.257	6.892	0.707													
	207835_at	382.475	7.975	0.516													
	Unif 2192	233.896	7.315	1.173				**Unif 2199**	105.556	5.730	1.662				**Unif 2202**	766.428

FIBULIN-4

reporter	Mean expression intensity	Geometric mean (Log2)	St. Dev. (Log 2)	Fold over control	p value
		12.298	1.216	3.422	<0.0001
ASTRO 206580_s_at	927.369	9.820	0.851	1.243	0.0600
ASTRO 209356_x_at	721.572	9.441	0.917	1.260	0.0658
		10.687	1.240	3.145	<0.0001
		4.160	1.184		0.8342
Unif 30008	590.654	9.256	0.910	1.285	0.0454
		10.759	1.226	3.369	<0.0001
		12.089	2.007	2.961	0.0001
GBM 206580_s_at	1765.670	10.967	0.855	2.753	<0.0001
GBM 209356_x_at	1429.208	10.618	0.920	2.849	<0.0001
		10.296	2.109	2.398	0.0019
		4.554	1.327		0.0848
Unif 30008	1851.738	10.432	0.913	2.902	< 0.0001
		10.999	2.070	3.979	0.0014
		11.599	1.592	2.108	0.0013
MIXED 206580_s_at	770.016	9.251	1.013	0.838	0.2057
MIXED 209356_x_at	502.096	8.790	1.148	0.803	0.1689
		9.973	1.681	1.917	0.0073
		3.750	1.228		0.2257
Unif 30008	442.202	8.628	1.144	0.831	0.2470
		9.999	1.570	1.989	0.0028
		11.297	1.343	1.710	0.0039
OLIGO 206580_s_at	535.224	9.346	0.336	0.895	0.3356
OLIGO 209356_x_at	380.565	8.850	1.033	0.837	0.2028
		9.849	1.328	1.760	0.0024
		3.810	0.947		0.1588
Unif 30008	345.679	8.679	1.032	0.861	0.2839
		9.872	1.269	1.822	0.0008
		10.523	0.432		
CONTROL 206580_s_at	1077.461	9.506	0.264		
CONTROL 209356_x_at	779.325	9.108	0.327		
		9.034	0.512		
		4.107	0.830		
Unif 30008	665.242	8.895	0.341		
		9.007	0.501		

FIBULIN-5

reporter	Mean expression intensity	Geometric mean (Log2)	St. Dev. (Log 2)	Fold over control	p value
ASTRO 203088_at	393.713	8.249	1.618	0.827	0.3931
Unif. 10516	222.558	7.509	1.890	0.820	0.4597
GBM 203088_at	672.318	8.793	1.757	1.205	0.4248
Unif. 10516	719.082	8.237	2.027	1.358	0.2605
MIXED 203088_at	360.821	7.881	1.814	0.640	0.0920
Unif. 10516	169.448	6.803	2.246	0.503	0.0467
OLIGO 203088_at	180.143	7.221	1.695	0.405	0.0002
Unif. 10516	68.720	6.234	1.878	0.339	0.0001
CONTROL 203088_at	599.091	8.524	0.713		
Unif. 10516	404.648	7.795	1.120		

SUPPLEMENTARY TABLE IV

TARGET SEQUENCES USED FOR RNA INTERFERENCE

	Target sequence
human Fibulin-3 siRNA1	5'-CACAACGTGTGCCAAGACATA
human Fibulin-3 siRNA2	5'-CACGCAATGCACTGACGGATA
rat Fibulin-3 siRNA1	5'-AGGCAACAACGATTTATGCAA
rat Fibulin-3 siRNA2	5'-ATGCGTTTGCCCGGTCTCAAA

PRIMERS USED FOR RT-PCR

Primer ID	Sequence	Species specificity	Use	Comments
GAPDH forward	5'-AGTCCATGCCATCACTGCCAC	human / rat / mouse	qRT-PCR	
GAPDH reverse	5'-ATGACCTTGCCCACAGCCTTG	human / rat / mouse	qRT-PCR	
Fibulin-3 forward	5'-TCAGACATCTTCCAGATACAG	human / rat / mouse	qRT-PCR	
Fibulin-3 reverse	5'-CCCACTATTATTGTCAATCTTAA	human / rat / mouse	qRT-PCR	
Fibulin-3 forward	5'-TGAGGTCCTTCTGCTGGTT	human	qRT-PCR	independent control for Fibulin-3 expression in human specimens
Fibulin-3 reverse	5'-GGAGGATACCTCTGCCTTCC	human	qRT-PCR	
Fibulin-3 forward	ACATGCCACTGTCTTCCTGG	rat	qRT-PCR	independent control for Fibulin-3 expression in rat tissues or cell lines
Fibulin-3 reverse	GTTTGCTGCCAGCTGAAACC	rat	qRT-PCR	
Fibulin-3 forward	5'-TCAGACATCTTCCAGATACAG	human / rat / mouse	RT-PCR	multi-species specific primers for semiquantitative RT-PCR
Fibulin-3 reverse	5'-CCCACTATTATTGTCAATCTTAA	human / rat / mouse	RT-PCR	
Fibulin-3 forward	5'-TCGCCAGATCAGACCCACG	human	RT-PCR	used to detect spice variants of human fibulin-3 with and without the non-coding exon 2
Fibulin-3 reverse	5'-GAAAAGGGCTTTCAACATTGTG	human	RT-PCR	
MMP2 forward	5'-CCATCGAGACCATGCGGAAG	human / rat / mouse	qRT-PCR	
MMP2 reverse	5'-CCTGTATGTGATCTGGTTCTTG	human / rat / mouse	qRT-PCR	
MMP9 forward	5'-TCATCCAGTTTGGTGTCGCG	human / rat / mouse	qRT-PCR	
MMP9 reverse	5'-GACCACAACTCGTCGTCGTC	human / rat / mouse	qRT-PCR	
ADAMTS4 forward	5'-GTAGATTCGTGGAGACACTG	rat	qRT-PCR	
ADAMTS4 reverse	5'-ACCAAGTTGACAGGGTTTCG	rat	qRT-PCR	
ADAMTS5 forward	5'-AGCTAGGTGATGACCATGAG	rat	qRT-PCR	
ADAMTS5 reverse	5'-GGAGAACATATGGTCCCAAC	rat	qRT-PCR	