Supplementary information

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 5.10⁵ 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 fibronectindependent 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. Suppl Fig. 1



SUPPLEMENTARY TABLE I

TARY 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 | | | | | | |

| | | | Bcan | Control | Bcan | | | GO | GO | GO |
|--------------|------------|---|-------|---------|-------|------------|-------------|---------------------------------|----------------------------------|-----------------------------------|
| Probeset | Gene Symbo | Description | FN | FN | PLL | Gene ID | Cytoband | BIOLOGICAL PROCESS | MOLECULAR FUNCTION | 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 of | 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 /// mitochondrie |
| 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, I | nucleotide binding /// GTPas | intracellular /// plasma membi |
| 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, I | 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 pro | 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, I | 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 developi | 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, I | 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 |
| | | | | I | I | | | | | |

SUPPLEMENTARY TABLE II

EFEMP1

ONCOMINE STUDIES

Gene Symbol:

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

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 microarravs | | 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 c |
| 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 (|
| | 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 0133 | normai brain vs oligodendrogiloma | 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 trichorhine |
| 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 le |
| | 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 le |
| | 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 le |
| 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 1195 | | 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 |
| 20 | 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 cvcl |
| 25 | HEAD/NECK | Toruner Head-Neck | 2004 | 4 | 16 | -0.304 | 0.766 | 201843 s at | Affymetrix U133 | | Association between gene expression |
| | 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 expression |
| 26 | LUNG | Beer Luna | 2002 | 10 | 86 | -7.141 | 9.80E-08 | U03877 at | Affvmetrix HuGeneFL | | Gene-expression profiles predict su |
| 27 | LUNG | Bhattachariee Lung | 2001 | 17 | 139 | -6.293 | 5.90E-08 | 32551 at | Affymetrix U95 | normal lung vs lung adenocarcinoma | Classification of human lung carcing |
| | LUNG | Bhattachariee Lung | 2001 | 17 | 21 | -5.649 | 3.30E-04 | 32551 at | Affvmetrix U95 | normal lung vs squamous cell carcinoma | Classification of human lung carcing |
| | 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 carcine |
| | LUNG | Bhattacharjee_Lung | 2001 | 17 | 20 | -7.977 | 7.70E-09 | 32551_at | Affymetrix U95 | normal lung vs carcinoid | Classification of human lung carcine |
| 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 internation |

| 32 | LUNG | Wachi_Lung | 2005 | 5 | 5 | -8.213 | 1.30E-04 | 201843_s_at | Affymetrix U133 | | Interactome-transcriptome analysis |
|----|--------------|---------------------------|------|-----|-----|---------|----------|---------------|----------------------|--|--|
| 33 | | Chen Liver | 2002 | 7 | 104 | -/ 31 | 8 80E-04 | IMAGE:1/02230 | IMAGE Consortium | banian liver disease ve banatecell, carcinema | Gene expression patterns in human |
| 55 | | Chen_Liver | 2002 | 76 | 104 | -1.083 | 0.002-04 | IMAGE:1492230 | IMAGE Consortium | non-tumor liver vs henatocell, carcinoma | Gene expression patterns in human |
| 34 | | Wurmbach Liver | 2002 | 10 | 35 | 2 /35 | 0.043 | 2018/3 s at | Affumetrix 11133 | non-tumor iver vs nepatoceii. carcinoma | Genome-wide molecular profiles of |
| 54 | LIVER | | 2007 | 10 | 55 | 2.400 | 0.02 | 201040_3_4 | Anymenix 0100 | | Schome wide molecular promes of t |
| 35 | MELANOMA | Hagg 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 | 0.002.00 | 201843 s at | Affymetrix U133 | | Metastatic potential of melanomas d |
| 00 | MELANOMA | Hoek Melanoma | 2006 | 3 | 24 | -0 441 | 0.674 | 201842 s at | Affymetrix 11133 | same study as #36_different probe | Metastatic potential of melanomas d |
| 37 | MELANOMA | Talantov Melanoma | 2005 | 25 | 45 | -10.13 | 2 60F-14 | 201842 s at | Affymetrix 11133 | | Novel genes associated with malign |
| 01 | | | 2000 | 20 | 10 | 10.10 | 2.002 11 | 201012_0_0 | 7 mymounx o roo | | Here genee accounted warmangn |
| 38 | OVARY | Hendrix Ovarian | 2006 | 4 | 41 | -13 33 | 1 80E-12 | 201842 s at | Affymetrix 11133 | ovary vs ovarian serous adenocarcinoma | Fibroblast growth factor 9 has onco |
| 00 | OVARY | Hendrix Ovarian | 2006 | 4 | 37 | -13 254 | 3 20E-12 | 201842 s at | Affymetrix 11133 | ovary vs ovarian endometroid adenocarcinoma | Fibroblast growth factor 9 has onco |
| | OVARY | Hendrix Ovarian | 2006 | 4 | 13 | -12 011 | 4 70F-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 40F-04 | 201842 s at | Affymetrix U133 | ovary vs ovarian clear cell adenocarcinoma | Fibroblast growth factor 9 has onco |
| 39 | OVARY | Lancaster Ovarian | 2000 | 3 | 31 | -1.35 | 0.301 | LI03877 at | Affymetrix HuGeneFl | ovary vo ovanan olcar och adonobaromorna | Gene expression patterns that chara |
| 40 | OVARY | | 2004 | 5 | 19 | -3.81 | 0.001 | 32551 at | Affymetrix U95 | | Selection of potential markers for en |
| 41 | OVARY | Welsh Ovarian | 2001 | 4 | 28 | -2 119 | 0.073 | U03877 at | Affymetrix HuGeneFl | | Analysis of gene expression profiles |
| | 0.17.11.1 | | 2001 | | 20 | 2 | 0.010 | eccert_at | | | |
| 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 11133 | | Gene expression profiling of microdi |
| 44 | PANCREAS | Ishikawa Pancreas | 2005 | 25 | 24 | -1.396 | 0.169 | 201842 s at | Affymetrix 11133 | | Experimental trial for diagnosis of pa |
| 45 | PANCREAS | Logsdon Pancreas | 2003 | 10 | 10 | 1 791 | 0.093 | LI03877 at | Affymetrix HuGeneFl | | Molecular profiling of pancreatic ade |
| 10 | 17 ANOTAL/10 | | 2000 | 10 | 10 | 1.701 | 0.000 | 000017_00 | | | indicidad proning of panoroado ado |
| 46 | PLEURA | Gordon Mesothelioma | 2005 | 5 | 40 | 3.385 | 0.015 | 201842 s at | Affymetrix U133 | mesothelioma | Identification of novel candidate onc |
| | | | 2000 | Ŭ | | 0.000 | 0.010 | 201012_0_4t | | | |
| 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 | 201843 s at | Affymetrix U133 | nmortalized 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 pros |
| | | | | | | | | _ | | | |
| 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 chromophobe 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 lo |
| 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 r |
| | | _ | | | | | | | - | | |
| 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 | ormal 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 |
| | | | | | | | | | | | |
| | | | | | | | | | | | |

<u>be classification by gene expression.</u> <u>Ider: a common carcinoma in situ gene expression signature exists disregarding histopathological classification.</u> <u>putcome in patients with invasive bladder cancer using oligonucleotide microarrays.</u>

extended gliomagenesis pathway maps and three novel MYC-interacting genes in human gliomas.
extended gliomagenesis pathway maps and three novel MYC-interacting genes in human gliomas.
extended gliomagenesis pathway maps and three novel MYC-interacting genes in human gliomas.
extended gliomagenesis pathway maps and three novel MYC-interacting genes in human gliomas.
extended gliomagenesis pathway maps and three novel MYC-interacting genes in human gliomas.
extended gliomagenesis pathway maps and three novel MYC-interacting genes in human gliomas.
extended gliomagenesis pathway maps and three novel MYC-interacting genes in human gliomas.
gental way maps and three novel MYC-interacting genes in human gliomas.
le analysis of neurofibromatosis 1-associated and sporadic pilocytic astrocytomas.
nolecularly and clinically distinct subtypes of glioblastoma multiforme.
-grade and low-grade gliomas.
cell factor induces angiogenesis within the brain.
cell factor induces angiogenesis within the brain.
cell factor induces angiogenesis within the brain.

linical outcome in breast cancer. our stroma promote breast cancer metastasis. ophalangeal syndrome in humans is overexpressed in breast cancer. sal-like human breast cancer. sal-like human breast cancer. lobular and ductal invasive breast carcinomas by laser microdissection and microarray analysis. lobular and ductal invasive breast carcinomas by laser microdissection and microarray analysis. lobular and ductal invasive breast carcinomas by laser microdissection and microarray analysis.

nset colorectal cancer that integrates diverse signaling pathways: implication for tumorigenesis. nset colorectal cancer that integrates diverse signaling pathways: implication for tumorigenesis. pilles of colorectal adenoma, adenocarcinoma, and normal tissue examined by oligonucleotide arrays.

tromal genes expressed in common between Barrett's esophagus and adenocarcinoma. gastric cancer by oligonucleotide microarrays. to adenocarcinoma is associated with the suppression of the transcriptional programs of epidermal differentiation. to adenocarcinoma is associated with the suppression of the transcriptional programs of epidermal differentiation.

ith tumorigenesis and metastatic potential of hypopharyngeal cancer by microarray analysis. signature associated with recurrent disease in squamous cell carcinoma of the head and neck. signature associated with recurrent disease in squamous cell carcinoma of the head and neck. le deregulation in human papillomavirus-positive and human papillomavirus-negative head/neck and cervical cancers. on profile and tumor invasion in oral squamous cell carcinoma.

irvival of patients with lung adenocarcinoma.

pmas by mRNA expression profiling reveals distinct adenocarcinoma subclasses.
 pmas by mRNA expression profiling reveals distinct adenocarcinoma subclasses.
 pmas by mRNA expression profiling reveals distinct adenocarcinoma subclasses.
 pmas by mRNA expression profiling reveals distinct adenocarcinoma subclasses.
 pmas by mRNA expression profiling reveals distinct adenocarcinoma subclasses.
 pmas by mRNA expression profiling reveals distinct adenocarcinoma subclasses.
 pmas by mRNA expression profiling reveals distinct adenocarcinoma subclasses.
 pmocarcinoma of the lung.
 nocarcinoma of the lung.
 nocarcinoma of the lung.
 inomas of smokers and nonsmokers.
 ssion between human pulmonary adenocarcinoma and a carcinogen-induced murine model.
 yal control for Q-RT-PCR from microarray data using a block bootstrap re-sampling scheme.

reveals the high centrality of genes differentially expressed in lung cancer tissues.

<u>
 liver cancers.</u>
 <u>
 liver cancers.</u>
 <u>
 HCV-induced dysplasia and hepatocellular carcinoma.</u>

melanoma progression. Jefined by specific gene expression profiles with no BRAF signature. Jefined by specific gene expression profiles with no BRAF signature. ant melanoma but not benign melanocytic lesions.

genic activity and is a downstream target of Wnt signaling in ovarian endometrioid adenocarcinomas. genic activity and is a downstream target of Wnt signaling in ovarian endometrioid adenocarcinomas. genic activity and is a downstream target of Wnt signaling in ovarian endometrioid adenocarcinomas. genic activity and is a downstream target of Wnt signaling in ovarian endometrioid adenocarcinomas. genic activity and is a downstream target of Wnt signaling in ovarian endometrioid adenocarcinomas. acterize advanced stage serous ovarian cancers. pithelial ovarian cancer with gene expression arrays and recursive descent partition analysis. s in normal and neoplastic ovarian tissue samples identifies candidate molecular markers of epithelial ovarian cancer.

sected pancreatic intraepithelial neoplastic lesions. lissected pancreatic ductal carcinomas using high-density DNA microarrays. ancreatic ductal carcinoma based on gene expression profiles of pancreatic ductal cells. enocarcinoma and chronic pancreatitis identifies multiple genes differentially regulated in pancreatic cancer.

pogenes and tumor suppressors in malignant pleural mesothelioma using large-scale transcriptional profiling.

's in prostate cancer. te tissues: insights into gene expression patterns of prostate development during puberty.) prostate carcinoma during hormonal therapy identifies and rogen-responsive genes and mechanisms of therapy resistance. nalysis of prostate cancer reveals distinct transcriptional programs associated with metastatic disease. a transforming oncogene in human prostate cancer cells. prostatic hyperplasia: molecular dissection by gene expression profiling. te cancers. overexpression in prostate cancer. primary cultures from human prostate tumors: a molecular approach to predict clinical behavior of prostate cancer. cal prostate cancer behavior. ling of prostate cancer progression. ter protein 185 identified by expression profiling is associated with prostate cancer progression. er protein 185 identified by expression profiling is associated with prostate cancer progression. analysis of prostate cancer reveals signatures of metastatic progression. and surrogate molecular markers for dasatinib in prostate cancer: rationale for patient selection and efficacy monitoring. es candidate markers and pharmacological targets in prostate cancer. state cancer predicting tumor aggression and preceding development of malignancy.

ifferentially expressed genes in renal cell carcinoma by expression profiling on a global human 31,500-element cDNA array. Ifferentially expressed genes in renal cell carcinoma by expression profiling on a global human 31,500-element cDNA array. Ifferentially expressed genes in renal cell carcinoma by expression profiling on a global human 31,500-element cDNA array. Ifferentially expressed genes in renal cell carcinoma by expression profiling on a global human 31,500-element cDNA array. Ifferentially expressed genes in renal cell carcinoma by expression profiling on a global human 31,500-element cDNA array. Ifferentially expressed by complementary DNA microarray. If enal cell carcinoma gene expression identified by parametric analysis of microarray data. If enal cell carcinoma gene expression identified by parametric analysis of microarray data.

tifies genes with altered expression in salivary adenoid cystic carcinoma.

, including those in a 200-kb gene cluster at 12p13.31, is associated with in vivo differentiation of human male germ cell tumors.

d carcinoma reveals highly consistent profiles.

stinction between primary and metastatic squamous cell carcinomas in the lung.

titutive and hormonally regulated genes during endometrial neoplastic transformation. le deregulation in human papillomavirus-positive and human papillomavirus-negative head/neck and cervical cancers. ncer: molecular classification and prediction of radiotherapy response by DNA microarray.

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:



| | | Mean expression | Geometric mean | St. Dev. | Fold over | | | | Mean expression | Geometric mean | St. Dev. | Fold over | | | | Mean expression |
|-----------|-------------|-----------------|----------------|----------|-----------|---------|-----------|-------------|-----------------|----------------|----------|-----------|---------|-----------|-------------|-----------------|
| | reporter | intensity | (Log2) | (Log 2) | control | p value | | reporter | intensity | (Log2) | (Log 2) | control | p value | | reporter | intensity |
| FIBULIN-1 | 201787_at | 190.151 | 7.432 | 1.696 | 0.936 | 0.7885 | FIBULIN-2 | 203886_s_at | 32.200 | 5.360 | 1.604 | 0.666 | 0.1173 | FIBULIN-3 | 201842_s_at | 6387.342 |
| ASTRO | 202994_s_at | 142.518 | 7.079 | 1.507 | 0.893 | 0.5958 | ASTRO | | | | | | | ASTRO | 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 | 201787_at | 215.568 | 7.242 | 1.856 | 0.820 | 0.4295 | FIBULIN-2 | 203886_s_at | 27.704 | 5.278 | 1.656 | 0.629 | 0.0469 | FIBULIN-3 | 201842_s_at | 7211.082 |
| GBM | 202994_s_at | 121.095 | 6.623 | 1.808 | 0.651 | 0.0765 | GBM | | | | | | | GBM | 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 | 201787_at | 59.956 | 5.921 | 1.695 | 0.328 | 0.0003 | FIBULIN-2 | 203886_s_at | 31.801 | 4.911 | 1.509 | 0.488 | 0.0268 | FIBULIN-3 | 201842_s_at | 5297.654 |
| MIXED | 202994_s_at | 76.460 | 6.022 | 1.376 | 0.429 | 0.0004 | MIXED | | | | | | | MIXED | 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 | 201787_at | 81.008 | 6.133 | 1.609 | 0.380 | 0.0001 | FIBULIN-2 | 203886_s_at | 22.896 | 4.670 | 1.062 | 0.413 | <0.0001 | FIBULIN-3 | 201842_s_at | 2565.457 |
| OLIGO | 202994_s_at | 56.415 | 5.941 | 1.102 | 0.406 | <0.0001 | OLIGO | | | | | | | OLIGO | 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 | 201787_at | 270.289 | 7.528 | 1.176 | | | FIBULIN-2 | 203886_s_at | 120.630 | 5.946 | 1.649 | | | FIBULIN-3 | 201842_s_at | 2268.283 |
| CONTROL | 202994_s_at | 211.569 | 7.242 | 0.872 | | | CONTROL | | | | | | | CONTROL | 201843_s_at | 757.735 |
| | 202995_s_at | 554.702 | 8.639 | 0.562 | 1 | | | | | | | | | | 228421_s_at | 24.101 |
| | 207834_at | 185.257 | 6.892 | 0.707 | | | | | | | | | | | | |
| | 207835_at | 382.475 | 7.975 | 0.516 | | | | | | | | 1 | | | | |
| | Unif 2192 | 233.896 | 7.315 | 1.173 | 1 | | | Unif 2199 | 105.556 | 5.730 | 1.662 | l | | | Unif 2202 | 766.428 |

| Geometric mean | St. Dev. | Fold over | | | | Mean expression | Geometric mean | St. Dev. | Fold over | | | | Mean expression | Geometric mean | St. Dev. | Fold over | |
|----------------|----------|-----------|----------|------------|-------------|-----------------|----------------|----------|-----------|----------|------------|-------------|-----------------|----------------|----------|-----------|---------|
| (Log2) | (Log 2) | control | p value | [| reporter | intensity | (Log2) | (Log 2) | control | p value | | reporter | intensity | (Log2) | (Log 2) | control | p value |
| 12.298 | 1.216 | 3.422 | < 0.0001 | FIBULIN-4 | 206580_s_at | 927.369 | 9.820 | 0.851 | 1.243 | 0.0600 | FIBULIN-5 | 203088_at | 393.713 | 8.249 | 1.618 | 0.827 | 0.3931 |
| 10.687 | 1.240 | 3.145 | < 0.0001 | ASTRO | 209356_x_at | 721.572 | 9.441 | 0.917 | 1.260 | 0.0658 | ASTRO | | | | | | |
| 4.160 | 1.184 | | 0.8342 | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | |
| 10.759 | 1.226 | 3.369 | <0.0001 | | Unif 30008 | 590.654 | 9.256 | 0.910 | 1.285 | 0.0454 | | Unif. 10516 | 222.558 | 7.509 | 1.890 | 0.820 | 0.4597 |
| | | | | | | | | | | | | | | | | | |
| 12.089 | 2.007 | 2.961 | 0.0001 | FIBULIN-4 | 206580_s_at | 1765.670 | 10.967 | 0.855 | 2.753 | < 0.0001 | FIBULIN-5 | 203088_at | 672.318 | 8.793 | 1.757 | 1.205 | 0.4248 |
| 10.296 | 2.109 | 2.398 | 0.0019 | GBM | 209356_x_at | 1429.208 | 10.618 | 0.920 | 2.849 | <0.0001 | GBM | | | | | | |
| 4.554 | 1.327 | | 0.0848 | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | |
| 10 999 | 2 070 | 3 979 | 0.0014 | | Unif 30008 | 1851 738 | 10 432 | 0.913 | 2 902 | < 0.0001 | | Unif. 10516 | 719 082 | 8 237 | 2 027 | 1.358 | 0 2605 |
| 10.000 | 2.070 | 0.010 | 0.0011 | L | 0 | 10011100 | 101102 | 0.010 | 2.002 | | I | 0 | 1101002 | 0.201 | 2.027 | 1.000 | 0.2000 |
| 11 599 | 1 592 | 2 108 | 0.0013 | FIBUI IN-4 | 206580 s at | 770.016 | 9 251 | 1 013 | 0.838 | 0 2057 | FIBUL IN-5 | 203088 at | 360 821 | 7 881 | 1 814 | 0.640 | 0.0920 |
| 9.973 | 1.681 | 1.917 | 0.0073 | MIXED | 209356 x at | 502.096 | 8.790 | 1.148 | 0.803 | 0.1689 | MIXED | 200000_u | 0001021 | 1.001 | | 0.010 | 0.0020 |
| 3.750 | 1.228 | | 0.2257 | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | |
| 9.999 | 1.570 | 1.989 | 0.0028 | [| Unif 30008 | 442.202 | 8.628 | 1.144 | 0.831 | 0.2470 | | Unif. 10516 | 169.448 | 6.803 | 2.246 | 0.503 | 0.0467 |
| | | | | _ | | | | | | | | | | | | | |
| 11.297 | 1.343 | 1.710 | 0.0039 | FIBULIN-4 | 206580_s_at | 535.224 | 9.346 | 0.336 | 0.895 | 0.3356 | FIBULIN-5 | 203088_at | 180.143 | 7.221 | 1.695 | 0.405 | 0.0002 |
| 9.849 | 1.328 | 1.760 | 0.0024 | OLIGO | 209356_x_at | 380.565 | 8.850 | 1.033 | 0.837 | 0.2028 | OLIGO | | | | | | |
| 3.810 | 0.947 | | 0.1588 | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | |
| 0.872 | 1 260 | 1 822 | 0.0008 | ŀ | Unif 30008 | 345 679 | 8 670 | 1.032 | 0.861 | 0.2830 | | Unif 10516 | 68 720 | 6 23/ | 1 878 | 0 339 | 0.0001 |
| 0.012 | 1.200 | 1.022 | 010000 | L | 00000 | 0-10.010 | 0.010 | 1.002 | 0.001 | 0.2000 | | | 00.720 | 0.204 | 1.070 | 0.000 | 0.0001 |
| 10 523 | 0.432 | I | | FIBUI IN-4 | 206580 s at | 1077 461 | 9 506 | 0 264 | 1 | | FIBULIN-5 | 203088 at | 599 091 | 8 524 | 0.713 | | |
| 9.034 | 0.512 | | | CONTROL | 209356 x at | 779.325 | 9.108 | 0.327 | | | CONTROL | 200000_at | 000.001 | 0.024 | 0.710 | | |
| 4.107 | 0.830 | | | 2001 | u | 110.020 | 0.100 | 0.02. | | | 50OL | | | | | | |
| | | 1 | | | | | | | | | | | | | | | |
| | | J | | | | | | | | | | | | | | | |
| 9.007 | 0.501 |] | | | Unif 30008 | 665.242 | 8.895 | 0.341 |] | | | 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 | aRT-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 2 forward | E' TOACOTOCTOCTOCTOCT | humon | | independent control for Eibulin 2 overcession in human aposimone |
| Fibulin-3 reverse | 5-IGAGGICCITCIGCIGGI | human | | independent control for Fibulin-3 expression in numan specimens |
| | 3-00200212001010001100 | numan | | |
| 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 2 forward | | humon | | used to detect onice variants of human fibulin 2 with and without |
| Fibulin-3 forward | | human | | the pop-coding exon 2 |
| | 3-0777000001110770711010 | numan | | |
| MMP2 forward | 5'-CCATCGAGACCATGCGGAAG | human / rat / mouse | aRT-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 | |
| | | | | |
| ADAMIS4 forward | 5'-GTAGATICGTGGAGACACTG | rat | | |
| ADAWI 54 reverse | 5-ACCAAGTIGACAGGGTITCG | Ial | YR I-PCR | |
| ADAMTS5 forward | 5'-AGCTAGGTGATGACCATGAG | rat | aRT-PCR | |
| ADAMTS5 reverse | 5'-GGAGAACATATGGTCCCAAC | rat | aRT-PCR | |
| | | | | |