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Hic-5 Regulates Extracellular Matrix-associated Gene Expression and Cytokine Secretion in Cancer Associated Fibroblasts

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Abstract

The focal adhesion protein, Hic-5 plays a key role in promoting extracellular matrix deposition and remodeling by cancer associated fibroblasts within the tumor stroma to promote breast tumor cell invasion. However, whether stromal matrix gene expression is regulated by Hic-5 is still unknown. Utilizing a constitutive Hic-5 knockout, Mouse Mammary Tumor Virus-Polyoma Middle T-Antigen spontaneous breast tumor mouse model, bulk RNAseq analysis was performed on cancer associated fibroblasts isolated from Hic-5 knockout mammary tumors. Functional network analysis highlighted a key role for Hic-5 in extracellular matrix organization, with both structural matrix genes, as well as matrix remodeling genes being differentially expressed in relation to Hic-5 expression. The subcellular distribution of the MRTF-A transcription factor and expression of a subset of MRTF-A responsive genes was also impacted by Hic-5 expression. Additionally, cytokine array analysis of conditioned media from the Hic-5 and Hic-5 knockout cancer associated fibroblasts revealed that Hic-5 is important for the secretion of several key factors that are associated with matrix remodeling, angiogenesis and immune evasion. Together, these data provide further evidence of a central role for Hic-5 expression in cancer associated fibroblasts in regulating the composition and organization of the tumor stroma microenvironment to promote breast tumor progression.

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Keywords

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Introduction:

The tumor microenvironment (TME) is comprised of fibroblasts, endothelial cells, adipocytes, immune cells, as well as non-cellular components including an array of extracellular matrix (ECM) proteins, soluble cytokines and chemokines that cooperate to exert a major influence on carcinogenesis and cancer progression [1]. Cancer associated fibroblasts (CAFs) stimulated, in part, by tumor cell secreted factors, such as TGF- β , PDGF, and EGF have distinct characteristics as compared to normal fibroblasts [2] and exhibit crosstalk with both tumor cells and immune cells to promote tumor progression [3]. Additionally, CAFs themselves secrete growth factors such as HGF, FGF, PDGF and IGF to enhance tumor cell growth and survival [4, 5], as well as TGF- β and EGF that induce epithelial mesenchymal transition (EMT) in tumor cells [4, 6]. Furthermore, CAF-immune cell crosstalk is now understood to be a major source of immunosuppression in the TME [3, 7]. For example, CAF-derived TGF- β dampens the anti-tumor CD8 T cell response while promoting pro-tumorigenic Treg activity. CAFs can also influence M2 macrophage polarization by secreting cytokines such as IL-6 and CXCL12 [8–10], again leading to a suppressive environment [11]. Importantly, CAFs significantly contribute to the composition, organization and function of the stromal extracellular matrix (ECM), firstly through the secretion of structural matrix proteins, matrix crosslinking enzymes and matrix protease enzymes [12–14] and second through cell-ECM adhesion-regulated mechanical manipulation of the assembled matrix, as a result of their hypercontractile phenotype, to promote tumor invasion and migration [15]. Finally, CAFs secrete soluble cytokines to promote endothelial cell proliferation, tube formation, and the recruitment of endothelial progenitor cells, thus inducing angiogenesis to promote tumor growth [7, 16, 17].

Hic-5 (TGF β 111) is a focal adhesion scaffold protein that belongs to the paxillin family of LIM domain proteins [18–20]. The paxillin family of focal adhesion proteins play key roles in transducing integrin-mediated signals from the ECM to regulate cell behaviors, most notably cell migration [18, 21, 22]. Previous studies from our lab have shown that in a Mouse Mammary Tumor Virus-Polyoma Middle T-Antigen (MMTV-PyMT) breast tumor mouse model, Hic-5 plays a critical role in controlling tumor progression through CAF-dependent regulation of stromal matrix deposition and remodeling [23]. Mechanistically, Hic-5 was shown to be essential for RhoA-mediated CAF mechano-signaling to promote fibrillar adhesion formation, fibronectin fibrillogenesis and collagen fiber alignment [24], which is frequently associated with enhanced breast tumor cell invasion [25–27]. In addition, Hic-5 expression has been shown to promote the cytoplasmic-nuclear translocation of myocardin related transcription factor A (MRTF-A), to mechanically regulate myofibroblast differentiation in a TGF- β -dependent manner [28]. Hic-5 has also been shown to generate a tumor-promoting stroma by regulation of lysyl oxidase and collagen 1 in colorectal cancer [29]. Similar roles for Hic-5 have been reported in other

fibrosis-associated disorders including pancreatitis/pancreatic tumors [30], intestinal fibrosis [31] and hypertrophic scarring [32].

Herein, we have utilized Hic-5 knockout CAFs, isolated from the MMTV-PyMT breast tumor mouse model, to perform RNAseq and cytokine array analyses. We show that Hic-5 impacts the differential expression of key stromal ECM structural and regulatory genes. Our study also revealed that the production and secretion of pro-angiogenic factors and chemokines was impacted by Hic-5 expression, highlighting the role of Hic-5 in promoting a pro-tumor microenvironment in breast cancer.

Results and Discussion

Extracellular matrix-associated genes are differentially expressed in Hic-5 knockout CAFs

Previously, we reported a role for Hic-5 in cancer associated fibroblasts (CAFs) in promoting stromal matrix remodeling and breast tumor progression and invasion in a well-characterized PyMT tumor mouse model [33]. Hic-5 depletion in the Hic-5^{-/-}PyMT (Hic-5 KO) CAFs, within the tumor stroma resulted in diminished matrix deposition, reduced FAK signaling in the adjacent breast tumor cells and a decrease in the number of lung metastases and circulating tumor cells, while reduced tumor cell directional migration was observed *in vitro* in 3D extracellular matrices assembled by the Hic-5 KO CAFs [33]. To determine which genes may be regulated in association with Hic-5 expression in CAFs, Hic-5 Het and Hic-5 KO CAFs, isolated from 3 different mice, were subjected to bulk RNA sequencing analysis (RNAseq). Hic-5 Het cells were used as no significant difference was observed in tumor growth and latency between Hic-5 WT and Hic-5 Het mice in the original *in vivo* study [33]. A total of 48,408 genes were identified (Supp.1). Importantly, the isolated CAFs subjected to RNAseq expressed canonical fibroblast genes (VIM, ITGB1, PDGFRa, PDGFRb), but not endothelial (CD31), immune (CD45), or epithelial (EpCAM) genes (Fig. 1A and B) and western blotting confirmed expression of the CAF-specific marker alpha smooth muscle actin [34], as well as vimentin, while being negative for the epithelial marker, E-cadherin (Fig.1C). Using a filter of $p < 0.05$ and fold change of < -2.5 or > 2.5 , we identified a subset of 202 genes (Supp. 2) that were either positively or negatively regulated by Hic-5, as depicted in the Volcano plot (Fig 1A) and the heatmap depicting the unsupervised clustering of differentially expressed genes (Fig 1D).

KEGG pathway analysis was performed using Partek Flow software and a total of 21 pathways were identified with an enrichment score higher than three (Fig 1E). Notably, focal adhesions and the TGF- β signaling pathway were enriched by Hic-5 expression, consistent with its previously recognized functions in mechano-signaling and TGF- β signaling and regulation [24, 32, 35]. The other enriched pathways are sub-grouped into key pathways in cancer, immune activation associated, pathways in different cancer and cardiomuscular-associated pathways (Fig 1E). Gene ontology (GO) analysis revealed that extracellular matrix (ECM)-associated terms were highly enriched, including ECM genes, external encapsulating structure, extracellular region and ECM organization (Fig 1F).

Hic-5-regulated ECM genes are involved in various cancers

A closer examination of the ECM-associated genes that were differentially regulated by Hic-5 identified key structural matrix genes, as well as matrix remodeling genes (Fig 2A). Regulated matrix genes included the fibrillar collagen genes Col17a1, Col18a1, Col28a1, Col5a2 and Col9a3, proteoglycans/glycoproteins genes FMOD, MFAP5, SPARC, TNC, NID2 and OPTC, ECM anchoring genes PRELP, ABI3BP, NID2 and OPTC, ECM remodeling genes MMP9, MMP23, CELA1, ADAMTS5, CPZ and HPSE, and soluble proteins including cytokines and growth factors that are typically enriched in the tumor stroma, IGF1, CLEC3B, PTX3, SVEP1 and SFRP1 (Fig 2A). A list of the respective gene's full names is included in Table 1.

STRING analysis was next performed to identify experimentally-determined and computer-predicted protein-protein interactions amongst the Hic-5-regulated gene products. The network nodes represent a total of twenty-four ECM-associated genes, and each edge represents an interaction (Fig 2B). Col5a2 is central to the interactome of all five collagen isoforms (Fig 2B). It is a type V collagen that is associated with poor clinical outcome in multiple cancers including colorectal cancer [36], gastric cancer [37], bladder cancer [38] and prostate cancer [39]. SPARC, also known as osteonectin or BM-40, is another key ECM gene with multiple interactions with collagen Col5a2, Col9a3 and Col18a1, MMP9, proteoglycan FMOD, ECM anchoring protein NID2 and the chemokine IGF1. SPARC is a secreted glycoprotein that is important for collagen matrix assembly during mammalian development [40]. The capacity for SPARC to promote or inhibit cancer progression is context dependent. SPARC expression has been reported to have a positive correlation with bladder carcinoma [41], osteosarcoma [42], breast carcinoma [43], colorectal cancer [44], head and neck squamous cell carcinoma [45], lung squamous cell carcinoma [46], prostate carcinoma [47], gastric cancer [48] and melanoma [49]. Conversely, SPARC exhibited a tumor suppressor role in ovarian cancer by inhibiting metastasis [50].

Functional enrichment analysis using the STRING database identified over a hundred publications that were directly linked to the Hic-5-dependent ECM gene network (Supp. 3), identifying five functional categories into which the ECM genes were distributed, namely matrix assembly, fibrosis, TGF- β signaling, cancer and angiogenesis (Fig 2C). We determined that MMP9, Col18a1, FMOD, PTX3, ADAMTS5, IGF1 and TNC are associated with all five functionalities, whereas Col28a1, Col9a3, CPZ, CELA1, PRELP and OPTC were only associated with matrix assembly. The other genes were associated with at least two functions (Fig 2C). For the seven genes that were linked to most functionalities, their products are extracellular matrix proteins such as collagens and tenascin C (TNC), matrix proteases ADAMTS5, MMP9, the proteoglycan FMOD and soluble factors that regulate an immune response (PTX3) or cell growth (IGF1).

Fibromodulin (FMOD) is a proteoglycan that modulates collagen fibrillogenesis through interaction with the collagen cross-linking enzyme lysyl oxidase (LOX), therefore contributing to collagen fiber bundling and alignment of this major stromal ECM component. This aspect of fibrillar collagen remodeling is a key factor in promoting tumor invasion in human breast cancer patients [25, 27]. Importantly, Hic-5 KO CAFs are defective in assembling a highly ordered collagen/fibronectin matrix, in association with reduced

tumor cell signaling and invasion, both *in vivo* and *in vitro* [33]. The precise role of FMOD in cancer varies depending on cancer type and model system. For example, FMOD is up-regulated in chronic lymphocytic leukemia, mantle cell lymphoma, glioblastoma, prostate cancer and myxoma in human samples, whereas in a colon cancer mouse model and a small cell lung cancer cell line, FMOD was down regulated [51]. Secreted FMOD promotes cell migration by activating focal adhesion-associated integrin-FAK-Src-Rho GTPase signaling that results in remodeling of the actin cytoskeleton organization to promote cell migration [52]. FMOD is also involved in tumor angiogenesis through regulation of the expression of angiopoietin 2 (ANG2) and VEGF [53, 54], as recently demonstrated in gliomas [52]. Prolargin (PRELP) is structurally related to FMOD, and the STRING analysis indicates that both genes and protein of PRELP and FMOD can be co-expressed (Fig 2B). Accordingly, PRELP also serves as an ECM anchoring protein that connects the fibroblast cell surface to the ECM to enhance focal adhesion formation [55, 56].

CLEC3 is a calcium binding protein that localizes in the cytoplasm and extracellular matrix. Interestingly, although CLEC3 expression was reduced in Hic-5 KO CAFs, it does not have functional connections with the other differentially regulated genes in the STRING analysis (Fig 2B). Nevertheless, it is highly expressed in fibroblasts [57], and like Hic-5 is involved in the cellular response to TGF- β and is associated with tumor invasion, metastasis and extracellular proteolysis [58].

MMP23 is one of the less studied MMPs that and was downregulated in Hic-5 KO CAFs (Fig 2A). MMP23 was first documented as CA-MMP for its distinct cysteine array motif back in 1999 [59]. MMP-23 is involved in intracellular trafficking of potassium channels, and co-expression of MMP-23 and potassium channel KV1.3 is associated with colorectal cancers [60]. On the other hand, in human melanoma, MMP23 expression is correlated with recurrence in immune therapy patients and associated with worse outcome, as MMP-23 dampens T cell activity through cleavage of cytokine and chemokine regulatory proteins [61, 62].

The extracellular matrix proteases, MMP9 and ADAMTS5 have well-documented roles in the remodeling of the ECM and in promoting angiogenesis [63–67]. However, the role of MMP9 in pro-/anti-cancer progression is controversial. MMP9 is known to positively relate to cancer invasion, metastasis, and angiogenesis [63] and has been used as a predictor of poor clinical outcome in some cancers [68]. Meanwhile, high expression of MMP9, in contrast to MMP2, was found to be associated with a more favorable prognosis in cervical cancer [69]. MMP9 can also function as a potent regulator for the innate immune response and thus perform an anti-tumor role [70]. Therefore, MMP23 was downregulated in Hic-5 KO CAFs, while MMP9 was upregulated in this population, indicating that Hic-5 likely exerts a complex, bi-modal role in controlling ECM remodeling by this protease family in the tumor microenvironment.

Hic-5 regulates cytokine production in CAFs

In addition to their role in ECM deposition and remodeling within the tumor stroma, CAFs also secrete soluble factors and release membrane-bound microvesicles/exosomes, carrying miRNAs and proteins into the TME to influence tumor cell signaling, tumor angiogenesis,

as well as localized immune cell infiltration and activation [4, 71–73]. Hic-5 has previously been shown to regulate a TGF- β autocrine loop in myofibroblasts, suggesting that Hic-5 may also regulate growth factor/cytokine secretion in CAFs [32]. Since we also detected changes in the mRNA levels of several cytokines in the Hic-5 KO CAFs (Fig 2A), we performed a mouse cytokine array assay, using conditioned media from CAFs to identify secreted cytokines that were regulated by Hic-5 expression. A total of ten secreted cytokines were detected in two independent experiments (Fig 2D and E and Supp. 4).

Interestingly, neither Hic-5 Het and KO CAFs secrete detectable levels of most of the chemokine (C-X-C motif) ligands (CXCL), C-C motif chemokine ligands (CCL) or interleukins. However, the Hic-5 KO cells secreted reduced levels of the chemokine, CCL17 (Fig 2D and supp. 4). CCL17, also known as thymus and activation regulated chemokine (TARC), was the first identified T-cell chemoattractant CC chemokine, and is constitutively produced in the thymus [74]. In the TME, CCL17 secreted by cancer associated fibroblasts and neutrophils [75, 76] plays anti-tumor roles by recruiting immunosuppressive regulatory T cells [77, 78]. Thus, the impaired secretion of CCL17 by Hic-5 KO CAFs suggests a pro-tumor role for Hic-5 within the tumor stroma, by regulating the crosstalk between CAFs and immune cells.

Pentraxin-3 (PTX3), which showed a large fold change reduction in the RNAseq analysis, was also reduced in the Hic-5 KO CAF conditioned media, as compared to the Hic-5 Het samples (Fig 2E). PTX3 is well-known for its role in innate immunity and inflammation [79]. It is also involved in endothelial cell dysfunction through various mechanisms. For example, PTX3 binds to fibroblast growth factor-2 (FGF2), thereby inhibiting FGF2 binding to endothelial cell receptors. This PTX3/FGF2 interaction is capable of suppressing angiogenesis in nude mice [80]. Conversely, PTX3 was shown to promote angiogenesis after stroke in a PTX3 knockout mouse model [81, 82].

MMP2 is another important matrix-targeting protease that is frequently implicated in remodeling of the tumor microenvironment to promote tumor cell invasion [83]. Our RNAseq analysis revealed that MMP2 was downregulated in Hic-5 KO CAFs, but did not reach statistical significance (p value 0.07, Fold change -2.53). Interestingly, MMP2 is also implicated in angiogenesis. Direct interaction of MMP2 with $\alpha v\beta 3$ integrin in blood vessels promotes endothelial cell proliferation and survival, as well as cell invasion by remodeling the surrounding matrix [84]. MMP2 is also involved in VEGF-mediated angiogenesis in lung cancer, as MMP2 RNA interference disrupted VEGF-dependent endothelial tube formation [85]. In contrast, the level of IGFBP-6, which is involved in cell growth and cell survival, was secreted at similar levels by both the Hic-5 Het and the KO CAFs (Fig 2E).

The decreased levels of secreted Pentraxin-3, MMP2 and VEGF from the Hic-5 KO CAFs, combined with the down-regulation of ECM genes like FMOD, further suggest an important role for Hic-5 promoting tumor angiogenesis through CAF-endothelial cell crosstalk (Fig 2E). [86].

Hic-5 modulates MRTF-A activity to indirectly regulate gene expression

Although there is no current evidence that Hic-5 functions as a transcription factor, it has been shown that Hic-5 acts as a co-regulator in nuclear receptor (glucocorticoid and androgen receptor) and transcription factor (SPI1, SMADs) mediated gene expression [87–90]. Additionally, Hic-5 can exert gene expression regulation through activation of other transcription factors, such as MRTF-A, by increasing the cell-ECM mechanosignaling and associated remodeling of the actin cytoskeleton, to promote MRTF-A nuclear translocation [28]. Therefore, we sought to examine whether Hic-5 may be regulating some of the cytoskeletal remodeling genes through modulating MRTF-A activity in the CAFs [91]. Indeed, when the cells were seeded overnight on a fibronectin-coated substrate, Hic-5 KO CAFs displayed increased cytoplasmic and decreased nuclear MRTF-A localization compared to Hic-5 Het CAFs (Fig 3A and B), suggesting impaired activity of MRTF-A in the absence of Hic-5 expression. Furthermore, the RNAseq data demonstrated that a subset of MRTF-A response genes were downregulated in the Hic-5 KO CAFs (Fig 3C), suggesting that Hic-5 can indirectly regulate CAF gene expression through mechano-signaling from focal adhesions.

In summary, we have performed RNAseq and cytokine array analysis on PyMT breast tumor-derived Hic-5 Het and KO CAFs. We have identified a cadre of ECM-associated genes and cytokines that are regulated by Hic-5 expression and play significant tumor-promoting roles in the stroma of the TME, including the deposition and remodeling of the ECM and the stimulation of tumor angiogenesis. These gene-regulatory functions of Hic-5, including its regulation of MRTF-A transcription factor localization, likely complement its previously reported role in focal adhesion mechanobiology to promote stromal ECM remodeling and breast tumor cell invasion [21, 24, 33], and in other fibrotic disorders such as pancreatitis/pancreatic cancer [30] and hypertrophic scarring [28, 29, 32, 92].

Material and Methods:

CAF isolation and culture

Cancer associated fibroblasts (CAFs) were isolated from Hic-5 Het and Hic-5 KO MMTV-PyMT tumor bearing mice, as previously described [33]. Briefly, tumors were minced and digested in digestion media (2mg/mL collagenase, 2mg/mL trypsin in 50:50 DMEM:F12, 5% FBS, 5µg/mL Insulin and 10 I.U. penicillin/10 µg/mL streptomycin) for 50 minutes at 37°C. Differential centrifugation was performed to separate the single CAFs from tumor organoids. CAFs were cultured and expanded in vitro using PyMT media (50:50 DMEM:F12 with 10% FBS, 2 mM L-glutamine and 10 I.U. penicillin/10 µg/mL streptomycin), 5% CO₂ and 37°C.

High throughput RNA-sequencing and gene-set analysis

Whole transcriptome profiling was performed on biological triplicates on Hic-5 Het and Hic-5 KO CAFs at the SUNY Molecular Analysis Core (SUNYMAC) facility at Upstate Medical University. RNA was isolated using Trizol reagent from confluent plates of ex vivo expanded cells. RNA quality and quantity were assessed using the RNA 6000 Nano Kit on the Agilent Bioanalyzer 2100. Sequencing libraries were prepared with the TruSeq Stranded

Total RNA Library Prep Kit RiboZero Gold (Illumina: San Diego, CA), using 1 μ g of total RNA as input. Library size was assessed with the DNA 1000 Kit on the Agilent Bioanalyzer 2100, and libraries were quantified with the Qubit dsDNA HS Assay Kit (Invitrogen: Waltham, MA USA). Libraries were pooled and sequenced on the NextSeq 500 instrument (Illumina: San Diego, CA), with a single end 1 \times 75bp read using a High Output 150 cycle reagent kit. Fastq files were trimmed to remove adapter sequences using Cutadapt version 1.2.1 and were aligned using Bowtie2 version 2.2.5 to database Ensemble Transcripts release 86. Quantify to annotation modeling was performed via Partek E/M. Data was normalized by reads per kilobase per million (RPKM). Differential gene expression analyses were performed in Partek Flow using GSA task. The raw RNAseq data have been submitted to the NCBI GEO and the accession number is: GSE211898)

Mouse cytokine array analysis

Cytokine arrays were performed in duplicate according to the manufacturer's instructions (Mouse XL Cytokine Array Kit, Catalog # ARY028, R&D Systems: Minneapolis, MN USA). Briefly, confluent CAF cultures were grown in complete PyMT media. Once confluent, the media was changed to serum free PyMT media and incubated for 24 hours. The conditioned media was collected, filtered and incubated on the membranes overnight at 4°C with rocking, according to the manufacturer's recommendations. The membranes were incubated with the detection antibody cocktail for 1 hour at RT and Streptavidin-HRP for 30 minutes at RT with extensive washing in between. The Hic-5 Het and KO membranes were then developed using the Chemi-reagent mix and imaged simultaneously on a Bio Rad Chemiluminescent Imager. Mean pixel density was calculated from each spot and the fold change was calculated by dividing the densities from the average of the control densities (Hic-5 Het).

Immunofluorescence microscopy and western blotting

CAFs on FN-coated glass coverslips were fixed with 4% PFA in PBS for 15 min, permeabilized with 1% Triton X-100 in PBS for 15 min and blocked with 3% bovine serum albumin (BSA) for 1 h at room temperature (RT). Coverslips were then stained with MRTF-A (1:100; sc-390324, SANTA CRUZ Biotechnology) primary antibody diluted in 3% BSA for 2 hours at 37°C, followed by incubation in DyLight 550-conjugated goat anti-Mouse secondary antibody (1:400, 84540; Thermo Fisher) for 1 hours at RT. The coverslips were washed in PBS + 0.1% Triton X-100, and mounted. CAFs were imaged using a Zeiss Axioskop2 plus microscope fitted with a Q imaging EXi Blue CCD camera using a Plan-Apochromat 40X/0.75 NA objective. Antibodies used for western blotting were alpha smooth muscle actin (1:1000; A2547 Sigma Aldrich), Hic-5 (1:800; 611165. BD Biosciences), vimentin (1:1000; 5741s Cell Signaling), E-cadherin (1:1000; 3195 Cell Signaling) and GAPDH (1:1000; 60004-1-Ig Proteintech).

Statistical Analysis

All data were analyzed using a two-sided t-test using Microsoft excel or GraphPad Prism. Statistical significance is indicated by *P<0.05, **P<0.01, ***P<0.005. The data are mean \pm s.e.m. or SD as denoted in the figure legend.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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List of Abbreviations:

CAFs	Cancer Associated Fibroblasts
CLEC3	C-type lectin domain family 3
CCL17	C-C Motif Chemokine Ligand 17
CD31	Cluster of Differentiation 31
CD45	Cluster of Differentiation 45
CXCL	Chemokine (C-X-C) Motif Ligand
ECM	Extracellular Matrix
EGF	Epithelial Growth Factor
EMT	Epithelial Mesenchymal Transition
EpCAM	Epithelial Cell Adhesion Molecule
FGF	Fibroblast Growth Factor
FMOD	Fibromodulin
GO	Gene Ontology
Hic-5	Hydrogen Peroxide Inducible Clone 5
HGF	Hepatocyte Growth Factor
IGF	Insulin Growth Factor
IL6	Interleukin 6
ITGB1	Integrin Beta 1
LOX	Lysyl Oxidase
MMTV-PyMT	Mouse Mammary Tumor Virus-Polyoma Middle T-Antigen
MMP2	Matrix Metalloproteinase 2
MMP23	Matrix Metalloproteinase 23

MMP9	Matrix Metallopeptidase 9
MRTF-A	Myocardin Related Transcription Factor A
PDGF	Platelet Derived Growth Factor
PDGFRa	Platelet Derived Growth Factor Receptor Alpha
PDGFRb	Platelet Derived Growth Factor Receptor Beta
PRELP	Prolargin
PTX3	Pentraxin 3
RPKM	Reads per kilobase per million
SPARC	Secreted Protein Acidic and Cysteine Rich
TARC	Thymus and Activation Regulated Chemokine
TGF-β	Transforming Growth Factor Beta
TGFB1i1	Transforming Growth Factor Beta 1 Induced Transcript 1
TME	Tumor Microenvironment
TPM	Transcripts per million
TNC	Tenascin C
VEGF	Vascular Endothelial Growth Factor
VIM	Vimentin

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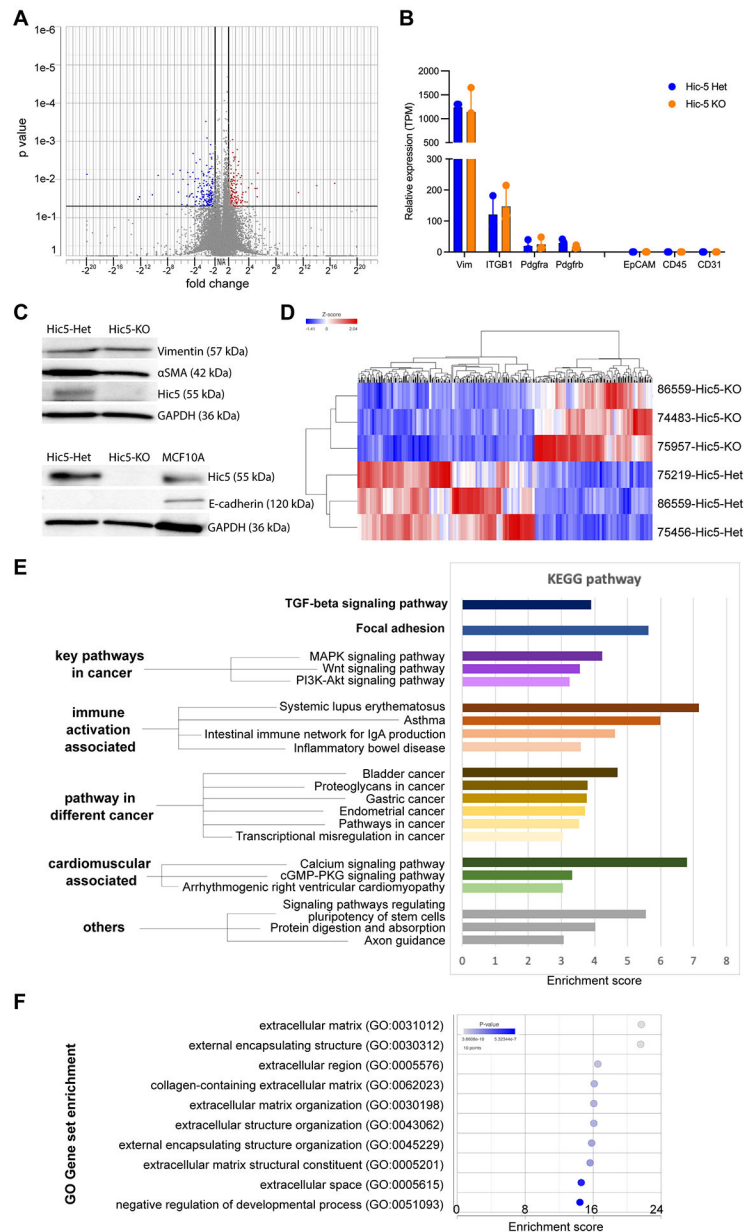


Figure 1. RNA-seq analysis shows differentially expressed extracellular matrix (ECM)-associated genes in Hic-5 Het versus KO CAFs. (A) Volcano plot of the up-regulated (64) and down-regulated (138) genes in the Hic-5 KO CAFs (p -value ≤ 0.05 , fold change < -2.5 or > 2.5). (B) Expression levels (TPM) of fibroblast, epithelial and endothelial genes from the RNAseq of Hic-5 Het and Hic-5 KO CAFs. (C) Western blot of Hic-5 Het, Hic-5 KO CAFs and MCF10A epithelial cells. (D) Heat map of significantly changed genes in Hic-5 Het and KO CAFs. N=3 CAF isolates from mice per genotype. (E) Pathway enrichment analysis shows enrichment of key pathways identified by KEGG. (F) Gene set enrichment analysis shows enrichment of extracellular matrix-associated genes regulated by Hic-5 expression.

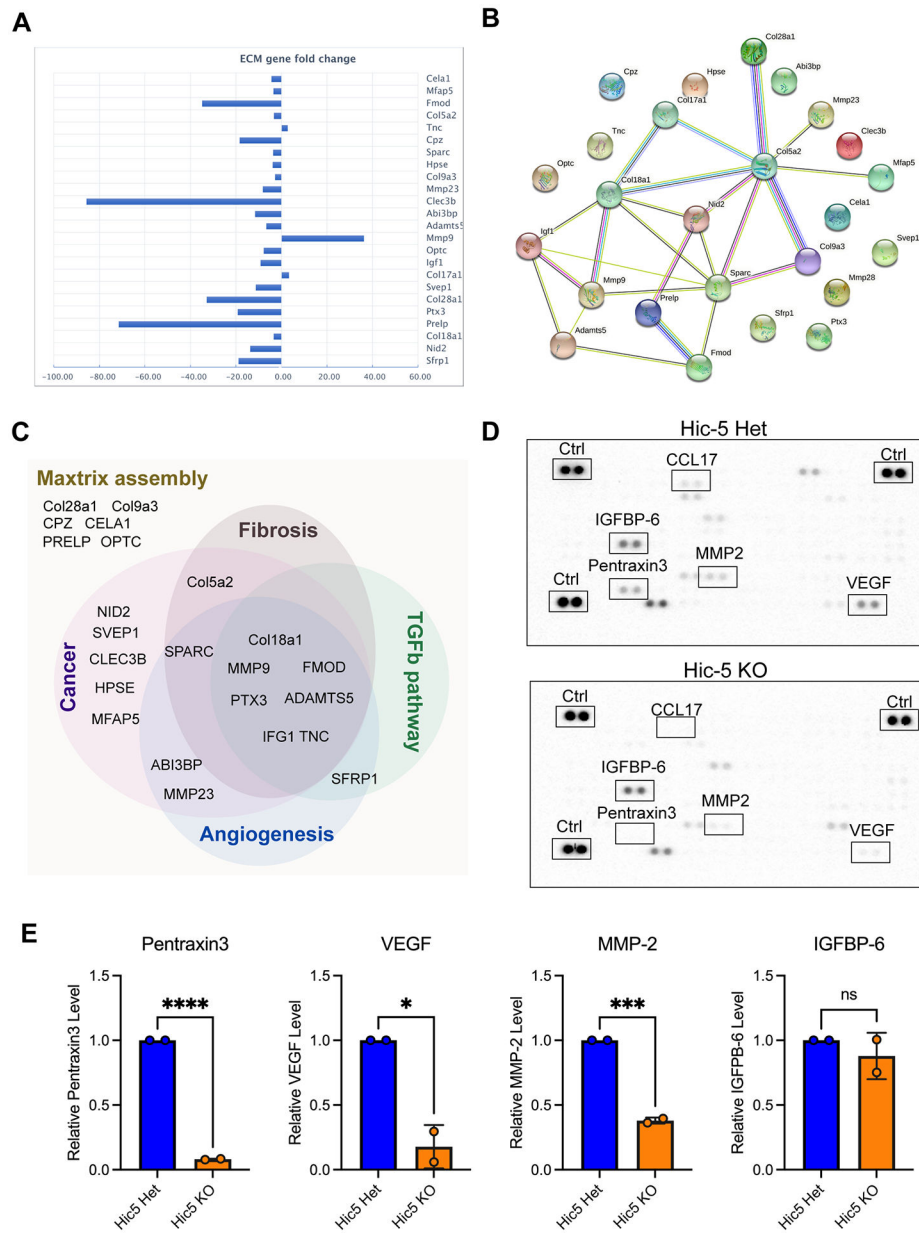


Figure 2. Hic-5-regulated ECM genes are associated with cancer, fibrosis, TGF- β signaling and angiogenesis. (A) Relative expression, as determined by RNAseq analysis, of the 24 genes of the ECM signature, in Hic-5 KO versus Hic-5 Het CAFs. (B) Bioinformatics analysis by STRING to reveal functional interactions between the differentially expressed ECM genes. Cyan: interactions from curated database; purple: experimentally determined interactions; green: gene neighborhood; red: gene fusion; blue: gene co-occurrence; yellow: textmining; black: co-expression; light blue: protein homology. (C) Venn diagram highlighting the ECM genes interrelationship with key cancer associated pathways. (D) Representative cytokine array analysis from condition media of cultured Hic-5 Het and KO CAFs. (E) Quantification of angiogenesis-associated cytokine production from the cytokine array. Each dot represents

the average of duplicate values from two independent experiments $n=2$. A t-test was performed. Data are mean \pm SD, * $p<0.05$, *** $p<0.005$, and **** $p<0.001$

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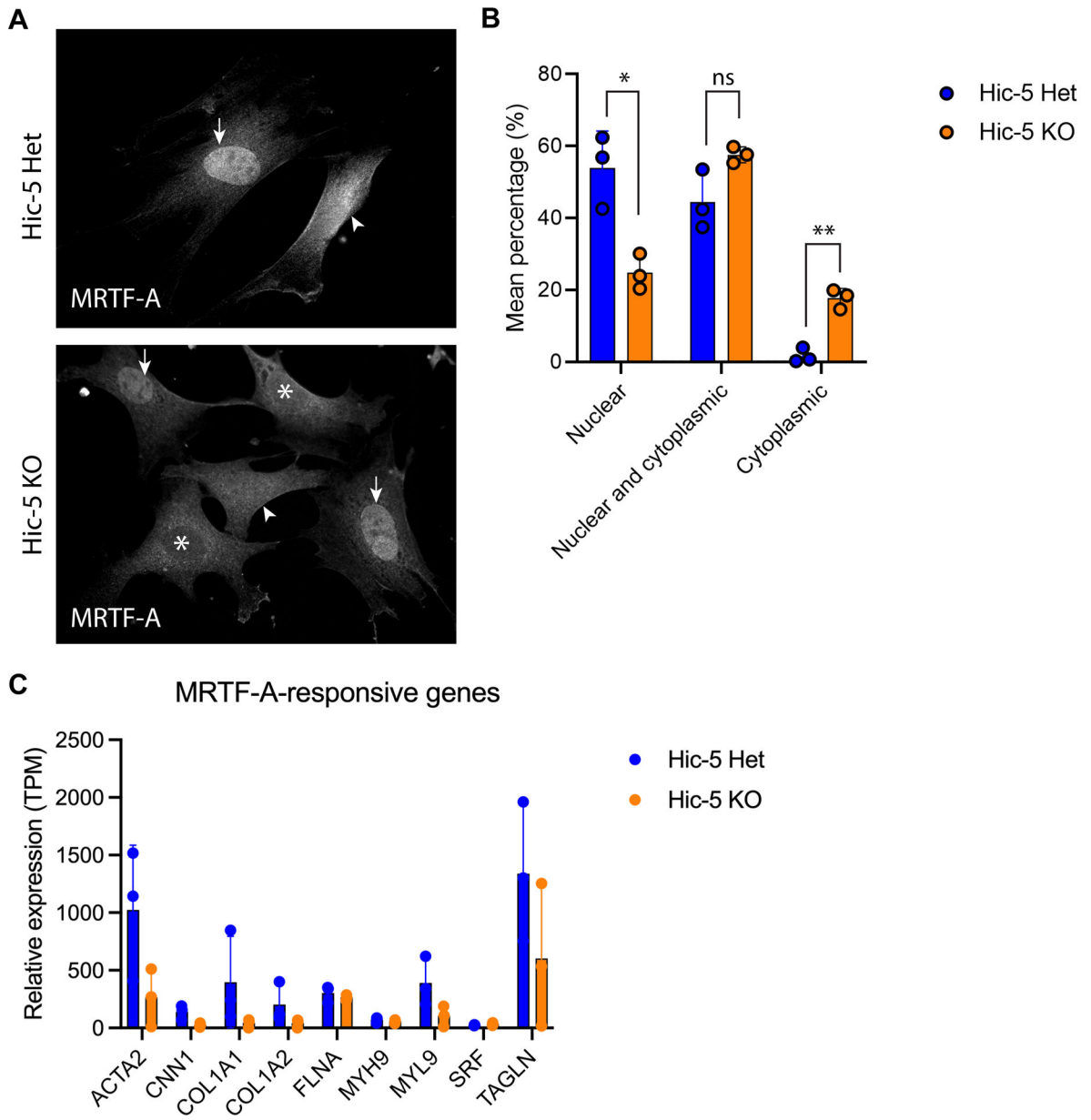


Figure 3. Hic-5 expression regulates MRTF-A subcellular distribution. (A) Representative MRTF-A localization in Hic-5 Het and Hic-5 KO CAFs. Nuclear MRTF-A localization (arrows), nuclear and cytoplasmic MRTF-A (arrowheads), cytoplasmic MRTF-A (asterisk). (B) Quantification of the percentage of cells exhibiting the three MRTF-A localization phenotypes. N=3. Data presented as mean \pm s.e.m. * $p < 0.05$ ** $p < 0.01$ (C) Expression levels (TPM) of MRTF-A-responsive genes from the RNAseq of Hic-5 Het and Hic-5 KO CAFs.

Table 1.

Differential Extracellular Matrix genes

Gene Name	Description	Cancer / Disease	References
Abi3bp	ABI Family Member 3 Binding Protein	thyroid tumorigenesis; Kashin-Beck disease	[93, 94]
Adams5	ADAM Metallopeptidase With Thrombospondin Type 1 Motif 5	glioblastoma; NSCLC; breast cancer	[95–97]
Cela1	Chymotrypsin Like Elastase 1	pancreatic cancer	[98]
Clec3b	C-Type Lectin Domain Family 3 Member B	lung adenocarcinoma; clear cell renal cell carcinoma	[99, 100]
Col17a1	Collagen Type XVII Alpha 1 Chain	SCC; melanoma; breast cancer; cervical cancer; pancreatic carcinoma, thyroid cancer; colorectal cancer; lung cancer; salivary gland cancer	reviewed in [101]
Col18a1	Collagen Type XVIII Alpha 1 Chain	Knobloch Syndrome; breast cancer	[102, 103]
Col28a1	Collagen Type XXVIII Alpha 1 Chain	colon cancer; bipolar disorder	[104]
Col5a2	Collagen Type V Alpha 2 Chain	gastric cancer; prostate cancer; bladder cancer; colorectal cancer	[39, 105, 106]
Col9a3	Collagen Type IX Alpha 3 Chain	Stickler syndrome; retinal detachment;	[107, 108]
Cpz	Metalloprotease Z	Neuroblastoma	[109]
Fmod	Keratan Sulfate Proteoglycan Fibromodulin	Chronic lymphocytic leukemia; glioblastoma; prostate cancer; colon cancer	reviewed in [110]
Hpse	Heparanase	atherosclerosis; fibrosis; breast cancer	reviewed in [111]
Igf1	Insulin Like Growth Factor 1	breast cancer; lung cancer; prostate cancer; colorectal cancer	reviewed in [112]
Mfap5	Microfibril Associated Protein 5	colon cancer; ovarian cancer; pancreatic cancer	[113, 114]
Mmp23	Matrix Metallopeptidase 23	melanoma	[61]
Mmp9	Matrix Metallopeptidase 9	breast cancer; cervical cancer	reviewed in [63, 115]
Nid2	Nidogen 2	colon cancer; oral squamous cell carcinoma; gastric cancer; lung cancer	[116–119]
Optc	Oculoglycan	high myopia; open-angle glaucoma	[120, 121]
Prep1	Proline And Arginine Rich End Leucine Rich Repeat Protein	rheumatoid arthritis; chronic leukemia	[56, 122]
Ptx3	Pentraxin 3	sepsis; prostate cancer; endometrial cancer; nonalcoholic fatty liver disease	[123–126]
Sfrp1	Secreted Frizzled Related Protein 1	acute myeloid leukemia; gastrointestinal stromal tumor	[127, 128]
Sparc	Secreted Protein Acidic And Cysteine Rich	bladder carcinoma; osteosarcoma; breast carcinoma; colorectal cancer; HNSCC; LSCC; gastric cancer; melanoma	[40–43, 45–50]
Svep1	Sushi, Von Willebrand Factor Type A, EGF And Pentraxin Domain Containing 1	atherosclerosis; Congenital Glaucoma	[129, 130]
Tnc	Tenascin C	brain tumors; breast cancer; gynecologic cancer; prostate cancer; lung cancer; gastrointestinal cancer	reviewed in [131]