

1 **Cancer Associated Fibroblasts Mediate Cancer Progression and Remodel the**
2 **Tumouroid Stroma**

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17 *Keywords: Cancer Associated Fibroblasts, 3D Cancer Models, Cancer Invasion,*
18 *Vasculogenesis and Angiogenesis*

1 I declare that the manuscript in its submitted form has been read and approved by all
2 authors and is not being considered for publication elsewhere. The authors also
3 declare no conflicts of interest.

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1 **Abstract**

2 Background: Cancer associated fibroblasts (CAFs) are highly differentiated and
3 heterogenous cancer stromal cells that promote tumour growth, angiogenesis and
4 matrix remodelling.

5 Methods: We utilised an adapted version of a previously developed 3D in vitro model
6 of colorectal cancer, composed of a cancer mass and surrounding stromal
7 compartment. We compared cancer invasion with an acellular stromal surround, a
8 'healthy' or normal cellular stroma and a cancerous stroma. For the cancerous
9 stroma we incorporated six patient-derived CAF samples to study their differential
10 effects on cancer growth, vascular network formation, and remodelling.

11 Results: CAFs enhanced the distance and surface area of the invasive cancer mass
12 whilst inhibiting vascular-like network formation. These processes correlated with the
13 upregulation of hepatocyte growth factor (HGF), metalloproteinase inhibitor 1 (TIMP1)
14 and fibulin 5 (FBLN5). Vascular remodelling of previously formed endothelial
15 structures occurred through the disruption of complex networks and was associated
16 with the up-regulation of vascular endothelial growth factor (VEGFA) and down-
17 regulation in vascular endothelial cadherin (VE-Cadherin).

18 Conclusion: These results support, within a biomimetic 3D, in vitro framework, the
19 direct role of CAFs in promoting cancer invasion and that CAFs are also key
20 components in driving vasculogenesis and angiogenesis.

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1 **Summary Box**

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3 What is already known on this subject?

- 4 • Colorectal cancer is one of the most common types of cancers for males and
- 5 females with poor five year survival outcomes
- 6 • 3D models of cancer have been used more extensively to recapitulate cancer
- 7 growth and the cancer stroma
- 8 • Whilst 3D models of cancer recreate the spatial distribution of cells to one
- 9 another, measuring invasion and how the stroma changes poses a difficult
- 10 challenge within these models
- 11 • Cancer associated fibroblasts are known to aid cancer invasion and promote
- 12 vasculature towards it whilst molecular pathways are poorly understood

13 What are the new findings?

- 14 • A novel compartmentalised 3D cancer model was used to study how a
- 15 cancerous stroma might impact cancer growth
- 16 • Cancer associated fibroblasts increase cancer invasion and are capable of
- 17 affecting vasculogenesis and angiogenesis
- 18 • Molecular pathways involved within these process relate to the breakdown of
- 19 the matrix and remodelling of vasculature

20 How might it impact on clinical practice in the foreseeable future?

- 21 • The model can be used to model the patient-specific tumour stroma and will
- 22 pose as a drug testing platform for personalised medicine

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1 **Introduction**

2 **Cancer associated fibroblasts and tumour growth.** The permissive role of the
3 tumour microenvironment in contributing to the process of tumour progression is
4 increasingly recognised¹. Within this complex and dynamic stromal response, cancer
5 associated fibroblasts (CAFs) are of particular interest². CAFs are highly
6 differentiated and activated fibroblasts that comprise a range of subtypes and
7 phenotypes³. In the healthy colon tissue, resting fibroblasts line the lamina propria
8 adjacent to the epithelium and precryptal fibroblasts contour the walls of the crypts
9 contributing to tissue integrity⁴. Some subtypes of CAFs are derived from these local
10 fibroblast populations that appear to reside in the margins of the tumour. Other
11 subtypes may migrate from distant sites such as the bone marrow (BM) whilst other
12 are speculated to have derived from other cell types that differentiate into CAFs.
13 CAFs are also believed to be (differentiated) cancer cells through the
14 endothelial/epithelial-mesenchymal transition (EMT)^{3,4}. Furthermore, mesenchymal
15 stem cells (MSCs) have been thought to be able to differentiate into CAFs and
16 consequently give rise to other stromal cells such as endothelial cells (ECs)². CAFs
17 promote tumour growth⁵ by the overexpression of growth factors, cytokines,
18 chemokines and matrix-remodelling enzymes whilst increasing stiffness of the
19 tumour⁶. This stiffening in itself can drive tumour growth. Recent work has
20 highlighted the role of stiff tumour tissue on cellular communication network factor 1
21 (CCN1) regulation in endothelial cells, which enhances melanoma cell-endothelium
22 interaction to promote metastasis through the vasculature⁷. The reactive stroma is in
23 an inflammatory state and under constant stress such as oxygen and nutrient
24 deprivation. CAFs induce the tumour macrophage polarization towards the M2
25 phenotype, also known as tumour activated macrophages (TAM)³, major

1 orchestrators of cancer-related inflammation⁸. This process is driven mainly by
2 interleukin-6 (IL-6), which is highly expressed by CAFs⁹. The key signature of CAFs
3 is the overexpression of alpha smooth muscle actin (α SMA), a contractile stress fibre
4 also expressed by myofibroblasts during wound healing¹⁰.

5

6 A number of “CAF markers” are used to differentiate between normal fibroblasts
7 (NFs) and CAFs. They include fibroblast-specific protein-1 (FSP-1/S100A4),
8 fibroblast-activating protein (FAP), platelet-derived growth factor receptor (PDGFR)
9 and prolyl 4-hydroxylase subunit alpha-1 (P4HA1), however, CAFs are a highly
10 heterogenous population with various activation states present, which makes them
11 difficult to be characterised^{3,6}. Initially, CAFs repress tumour growth due to gap
12 junction formation amongst activated fibroblasts, but consequently they pave the way
13 for extracellular matrix (ECM) remodelling and stiffening¹¹. The ECM is remodelled
14 physiologically and chemically during cancer progression due to factors expressed
15 and released by the cancer cells and CAFs. This includes proteases breaking down
16 the ECM through increased covalent cross-linking of collagen fibrils, a process
17 mediated by lysyl oxidase (LOX)^{12,2}. This in turn increases interstitial fluid pressure
18 within the tissue, which activates CAFs to upregulate transforming growth factor beta
19 (TGF- β -1)³ and matrix metalloproteinases (MMPs) thus promoting and guiding cancer
20 cell tissue invasion¹³. Stiffness plays a major role in cancer progression and
21 mechanotransduction of the matrix is required for the generation and maintenance of
22 CAFs^{14,15}. CAFs produce and secrete a number of soluble factors which stimulate
23 neighbouring stromal cells to secrete further tumour growth supporting soluble
24 factors¹⁶. This cancer-stroma cross-talk recruits immune cells and local vasculature
25 due to CAFs increasingly excreting vascular endothelial growth factor (VEGF)⁹.

1 Overexpression of IL-6 by CRC cells and CAFs drives cytokinetic angiogenesis and
2 further upregulates VEGF secretion through prostaglandin-E2 (PGE-2)
3 mediation¹⁷. The recruited vascular networks promote cancer escape from the
4 primary tumour and metastases. Colon CAFs specifically secrete growth factors, like
5 hepatocyte growth factor (HGF), which activates mitogen-activated protein kinase
6 (MAPK) and phosphatidylinositol 3-kinase (PI3K)/AKT pathways responsible for
7 cell survival and invasion of the cancer⁴.

8

9 **CAFs in 3D cancer models.** The use of CAFs in *in vitro* 2D and 3D cancer models
10 has been very limited in CRC and using patient-derived samples. CAFs cultured in
11 collagen have increased contractility compared to NFs¹². Previous approaches have
12 used spheroid formation, basic 2D invasion assays and microfluidic devices¹⁸ in
13 order to replicate the tumour stroma. These approaches are limited in their 3D
14 representation of the tumour stroma by lacking vital components, such as
15 vasculature and a clearly defined tumour-stroma margin through the
16 compartmentalisation of cancer mass and stroma. By replicating the tumour-stroma
17 margin it is possible to study the interplay of different cell populations during cancer
18 progression.

19 Our approach to engineering a 3D *in vitro* colorectal cancer model incorporates
20 patient-derived CAFs in the stromal compartment and allows us to study the patient-
21 specific effect on vasculature formation during cancer growth and progression. This
22 novel approach of modelling cancer-CAF interplay allows us to directly demonstrate
23 the cellular cross-talk between the cancer and stromal cells within a stable and stiff
24 ECM.

25

1 We hypothesised that invasion of cancer cells into the stromal compartment is
2 enhanced in the presence of CAFs as compared to normal human dermal fibroblasts
3 (HDFs), our control used for this project. We also studied how the presence of CAFs,
4 and the release of growth factors and cytokines, altered the formation of vascular
5 networks and remodelled pre-existing vascular networks.

6

7 **Materials and Methods**

8 **CAF isolation and propagation.** Primary human colorectal cancer associated
9 fibroblasts were isolated from tumour tissues acquired from surgeries at the Royal
10 Free Hospital. Patients provided informed consent for tissue donation for research,
11 ethics code: 11/WA/0077. Fresh samples were provided by the pathology team,
12 ensuring diagnostic margins were not compromised. Tissue was disaggregated
13 using a tumour dissociation kit (Miltenyi Biotec, Bergisch Gladbach, Germany) and
14 grown in Fibroblast Growth Medium 2 (Promocell, Heidelberg, Germany). For the
15 first 72 hours (h) cells were left undisturbed, following that, media changes were
16 done every 48 h in order to isolate the fibroblast cell population. The tissue samples
17 were called T7, T10 and T11 for the first round of successful samples and T6, T9
18 and T13 for the second lot of successful samples cultured. Patient-derived CAF
19 samples were then tested for positive vimentin expression and negative CK20
20 expression, to exclude colorectal epithelial cell contamination, and CD31, to
21 eliminate endothelial cell contamination. Metabolic activity of the first three CAF
22 samples was tested of different cell densities using PrestoBlue™ Cell Viability
23 Reagent (Thermo Fisher Scientific, Loughborough, UK). CAFs α SMA and metabolic
24 activity was assessed (*supplementary Figure 1*). A range of other general fibroblast
25 and more specific CAF gene markers were also investigated.

1 **Cell culture.** Human colorectal adenocarcinoma cell lines HT29 and HCT116 (both
2 European Collection of Cell Cultures through Sigma-Aldrich, Dorset, UK) were grown
3 in Dulbecco's Modified Eagle Medium (DMEM) at 1 000 mg/L glucose (Sigma-
4 Aldrich, Dorset, UK). Human adult-donor dermal fibroblasts (HDF) (Promocell,
5 Heidelberg, Germany) were grown in 4 500 mg/L glucose DMEM (Sigma-Aldrich,
6 Dorset, UK). Human umbilical vein endothelial cells (HUVEC) were grown in
7 Endothelial Cell Growth Medium (both Promocell, Heidelberg, Germany). After
8 isolation, CAF cells were cultured using Fibroblast Growth Medium 2 (Promocell,
9 Heidelberg, Germany). All media were supplemented with 10% Foetal Calf Serum
10 (FCS) (First Link, Birmingham, UK) as well as 100 units/mL penicillin and 100 µg/mL
11 streptomycin (Gibco™ through Thermo Fisher Scientific, Loughborough, UK). All cell
12 types were cultured at 5% carbon dioxide (CO₂) atmospheric pressure and at 37°C
13 temperature and routinely passaged in 2D monolayers. HDF and HUVECs were
14 used at passage ≤5.

15

16 **Complex 3D models of cancer (tumouroids).** All tumouroids were fabricated using
17 monomeric Type I rat-tail collagen (First Link, Birmingham, UK) and the [RAFT™](#)
18 [protocol](#) pages 8-9 (Lonza, Slough, UK) as previously described¹⁹. 10X MEM
19 (Sigma-Aldrich, Dorset, UK Sigma-Aldrich, Dorset, UK) was mixed with collagen and
20 neutralising agent (N.A.) (17% 10 M NaOH (Sigma-Aldrich, Dorset, UK) in 1 M
21 HEPES buffer Gibco™ through Thermo Fisher Scientific, Loughborough, UK)) and
22 mixed with cell suspension resulting in 80% collagen, 10% 10X MEM, 6% N.A. and
23 4% cells. For the artificial cancer masses (ACMs) 5x10⁴ cells/ACM of either less-
24 invasive HT29 or highly-invasive HCT116 cells were used and 240 µL of the
25 collagen mix was added to a 96-well plate (Corning® Costar® through Sigma-

1 Aldrich, Dorset, UK). The gel mix was polymerised at 37°C for 15 minutes (min),
2 followed by plastic-compression using the 96-well RAFT™ absorbers (Lonza,
3 Slough, UK). In order to produce ‘tumouroids’²⁰, the ACMs were nested into a
4 stroma. For the stroma, collagen solution as described above was prepared, and
5 ACMs were directly embedded into a 24-well plate (Corning® Costar® through
6 Sigma-Aldrich, Dorset, UK) containing 1.3 mL of the non-cross-linked collagen mix.
7 Extracellular matrix components were added to this stroma. In this case mouse
8 laminin²¹ 50 µg/mL (Corning® through Sigma-Aldrich, Dorset, UK) for an acellular
9 stroma additionally to 2.5x10⁴ HDFs/ CAF samples and 10⁵ HUVECs for a healthy or
10 cancerous stroma respectively (please refer to *Figure 1A* for more detail). The
11 tumouroids were polymerised at 37°C for 15 min and plastic-compressed using the
12 24-well RAFT™ absorbers (Lonza, Slough, UK). Tumouroids were cultured for up to
13 21 days at 5% CO₂ atmospheric pressure and 37°C with 50% media changes every
14 48 h. The media used was a 1:1 mix of the different types used for the cell types
15 within the tumouroids.

16

17 **CAF treatment.** To study the effect of CAFs on established endothelial networks,
18 CAFs were added to a mature tumouroid containing HDFs and HUVECs in the
19 stroma. A 1.0 mL suspension containing 2.5x10⁴ CAF cells was added to the media
20 mix at day 21 of established tumouroids. CAFs and tumouroids were subsequently
21 left to propagate in co-culture for 7 days with continuing 48 h 50% media changes.
22 This is additionally demonstrated in the *Figure 1B* below. Investigative
23 measurements were taken at day 21+1, day 21+3 and day 21+7 post CAF addition.
24 *ACTA2* levels were assessed after CAF additional as an internal control (full blots in
25 *supplementary Figure 2*).

1 **Immunofluorescence.** Tumouroids were formalin fixed using 10% neutrally buffered
2 formalin (Genta Medical, York, UK) for 30 min and then washed and stored in
3 phosphate buffered saline (PBS) (Gibco™ through Thermo Fisher Scientific,
4 Loughborough, UK). The tumouroids were permeabilised and blocked for 1 h at
5 room temperature using a solution of 0.2% Triton X 100 and 1% bovine serum
6 albumin (BSA) (both Sigma-Aldrich, Dorset, UK) in PBS. Primary antibody incubation
7 was performed overnight at 4°C followed by three 5 min wash steps with PBS.
8 Secondary antibody incubation was carried out the next day with a 2.5 h incubation
9 at room temperature followed by three 15 min wash steps with PBS. Antibodies were
10 diluted in the same Triton X 100 and BSA solution and suppliers and source were:
11 primary 1:200 anti-CK20 rabbit D9Z1Z (New England Biolabs, Herts, UK), anti-CD31
12 mouse JC70/A (Abcam, Cambridge, UK) anti-Vimentin mouse V9 (Santa Cruz,
13 Texas, US) and secondary 1:1000 anti-mouse Alexa Fluor® 488 IgG H&L ab150113
14 and anti-rabbit DyLight® 594 ab96885 (both Abcam, Cambridge, UK). All tumouroids
15 were counterstained with DAPI, using NucBlue™ (Invitrogen™ through Thermo
16 Fisher, Loughborough, UK).

17

18 **Measurement of invasion, endothelial networks and analysis.** All tumouroids
19 were imaged using the Zeiss AxioObserver with ApoTome.2 and Zeiss ZEN software
20 (Zeiss, Oberkochen, Germany). In order to measure the invasion from the original
21 ACM into the stromal compartment and the number of endothelial structures, 4
22 images were taken at a 10x magnification evenly spaced out in alignment with a
23 clock face at 12, 3, 6 and 9 o'clock on the same focal plane. This method has
24 previously been described¹⁹. The number of endothelial structures was quantified in
25 the same manner with images taken in the same positions but further into the

1 stromal compartment. All samples were assessed for average distance and surface
2 area of invasion and average number of endothelial structures in the stromal
3 compartment. The images obtained were then analysed in Fiji ImageJ software²².

4

5 **RNA extraction, cDNA Synthesis and real-time PCR.** RNA was extracted using
6 the phase separation TRI Reagent® and chloroform method²³ (both Sigma-Aldrich,
7 Dorset, UK). Total RNA obtained was quantified and assessed for integrity using the
8 NanoDrop™. Transcription into cDNA was conducted using the High-Capacity cDNA
9 Reverse Transcription Kit (Applied Biosystems™ through Fisher Scientific,
10 Loughborough, UK) on the T100™ Thermal Cycler (Bio-Rad, Watford, UK). Primers
11 were designed according to the MIQE with an annealing temperature (Ta) of 60°C,
12 sequences and efficiencies are listed in *Table 1* below, and were purchased through
13 Eurofins Genomics (Ebersberg, Germany). Gene target amplification was conducted
14 using iTaq™ Universal SYBR® Green Supermix on the CFX96™ Touch System
15 (both Bio-Rad, Watford, UK) in 10 µL reactions with 20 ng sample cDNA and primer
16 concentration of 0.2 µM. Relative gene expression was calculated using the ΔCt and
17 $2^{-\Delta\Delta\text{Ct}}$ method²⁴ normalising to reference gene *hypoxanthine-guanine*
18 *phosphoribosyltransferase (HPRT1)* with primers for this gene taken from
19 literature²⁵. Primer design parameters can be found in the supplementary section.

20

21 **ELISA.** Media aliquots from cultured tumouroids were taken at every 48 h media
22 change, kept in -80°C and analysed for vascular endothelia cadherin (VE-Cadherin)
23 active protein expression using the R&D Systems (Abingdon, UK) Human VE-
24 Cadherin Quantikine ELISA Kit according to the manufacturer's instructions. Results
25 were read on the Tecan Microplate Reader (Männedorf, Switzerland).

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Protein extraction and western blotting. CAF cell monolayers were lysed for protein with RIPA buffer containing protease inhibitor cocktail at 1:100 dilution (both Sigma-Aldrich, Dorset, UK). Protein content was established using the Pierce™ BCA Protein Assay Kit (Thermo Fisher Scientific, Loughborough, UK). Working solutions were made up to 0.5 µg/µL with RIPA and 2x Concentrate Laemmli Sample Buffer (Sigma-Aldrich, Dorset, UK). 10 µg protein was loaded onto 10% Mini-PROTEAN® TGX™ Precast 10-well protein gels and run at 200 Volts (V) for 45 min using the Mini-PROTEAN Tetra Cell and PowerPac™ 300 in tris-glycine SDS running buffer (all Bio-Rad, Watford, UK). Protein ladder SeeBlue™ Plus 2 Pre-stained Protein Standard (Invitrogen™ through Thermo Fisher Scientific, Loughborough, UK) was used. Dry transfer was conducted using Trans-Blot® Mini Nitrocellulose Transfer Packs and the Trans-Blot® Turbo™ Transfer System (Bio-Rad, Watford, UK). Membranes were blocked for 1 h with 5% milk (Sigma-Aldrich, Dorset, UK) (in tris-buffered saline and 1% Tween 20 (TBST), both Bio-Rad, Watford, UK)), incubated with 1° antibodies for α-SMA 1A4 and loading control β-tubulin N-20 in 5% milk overnight at 4°C at dilutions 1:1000 and 1:200 respectively followed by five quick and three 5 min washes with TBST. 2° antibodies IgG-HRP anti-goat sc-2953 and anti-mouse sc-2314 at 1:1000 dilutions were incubated for 1 h in 3% milk (all antibodies through Santa Cruz Biotechnology, Dallas, US), followed by three 15 min washes and developed using Pierce™ ECL Western Blotting Substrate (Thermo Fisher Scientific, Loughborough, UK). Blots were imaged using the ChemiDoc™ XRS imaging system and Image Lab™ software (Bio-Rad, Watford, UK).

1 **Statistical analyses.** All statistical analysis was conducted using GraphPad Prism 7
2 software. Data was tested for normality with the Shapiro-Wilk test ($n \geq 3$) or the
3 D'Agostino test ($n \geq 8$) and the appropriate test for statistical significance was applied
4 depending on data parameters (t-test, Mann-Whitney, One-way ANOVA with
5 Dunnet's Post Hoc or Kruskal-Wallis with Dunn's multiple comparisons test). The
6 tests used for each graph are outlined within the figure legends individually.
7 Significance was at p-values < 0.05 . All data points are represented as mean with
8 standard error mean (SEM) in graphs and values stated in text as mean with
9 standard deviation (STDEV). In general, $n=3$ with 3-4 technical replicates, details
10 described within the figure legends for each individual data set. F-values, t-values
11 and degrees of freedom (DOF) are stated within the figure legends for each set of
12 statistical tests. Two-tailed tests for significance were used when appropriate.

13

14 **Results**

15 **Extraction, propagation and characterisation of patient-derived CAF samples.**

16 Six patient-derived CAF samples ($n=6$) were established from tumour samples,
17 expanded on 2D tissue culture plastic (passage ≤ 3) and included in the tumouroid
18 model. The samples were of variable location and origin (*Figure 2A*), but all samples
19 were from the lower bowel, colon or rectum with 5 being of adenocarcinoma and 1
20 being of neuroendocrine type. Samples were obtained from varying levels of tumour
21 margin infiltration and vascular invasion. All samples were successfully cultured in
22 2D monolayers and tested for a number of fibroblast markers at the gene level
23 (*Figure 2B-G*). The data showed that all six samples were positive for *ACTA2*,
24 *S100A4*, *PDGFRA*, *FAP*, *IL-6* and *P4HA1*. This confirms that the cells are activated
25 fibroblasts, especially based on the high expression of *S100A4*, *PDGFRA* and *IL-6* in

1 all samples^{26,27&28}. Gene expression levels were compared between the samples
2 and HDFs and also between the different tumour fibroblast populations, which
3 showed varying levels of expression. Secondly, the western blots showed that the α -
4 SMA protein was expressed in all samples (*Figure 2H*), this is a measure previously
5 used to distinguish samples as CAFs²⁹. Thirdly, vimentin staining was done in CAF
6 tumouroids grown to confluency and the morphology was compared to normal HDFs
7 within tumouroids (*Figure 2 I&J*). It was observed that the CAF samples overall
8 appeared to have a much less organised internal structure.

9
10 **A healthy stroma does not upregulate cancer invasion significantly.** There is an
11 evident cross-talk between the cancer cells and surrounding stroma. Within the model,
12 two different CRC cell lines were used; the less invasive HT29 cells and the highly
13 invasive HCT116 cells.

14 The effect of adding cells to the stromal compartment was measured comparing
15 tumouroids with an acellular stroma to ones containing normal fibroblasts and a
16 primitive vascular network within the stroma (*Table 2*). Firstly, the number of invasive
17 bodies increased in the presence of a cellular stroma (*Figure 3A*), significantly in the
18 HT29 tumouroids ($p=0.0123$). However, the average distance of invasion decreased
19 significantly (*Figure 3B*) in the HT29 tumouroids ($p=0.0006$). The surface area of
20 invasion also decreased significantly (*Figure 3C*) in the presence of a cellular stroma
21 ($p<0.0001$) for both the HT29 and HCT116 tumouroids. In the tumouroids, , invasive
22 bodies can be observed in the stroma (*Figure 3D&E*) and extensive primitive
23 endothelial networks are formed (*Figure 3F*) whilst the fibroblast population reach
24 visible confluency by 21 days of growth in 3D.

1 When analysing the gene expression associated with the different invasion patterns,
2 a number of genes were significantly altered when going from an acellular to a cellular
3 stroma including *MMP2* for HT29 and HCT116 tumouroids ($p=0.001$ and $p=0.0098$
4 respectively), *TIMP1* ($p<0.0001$ and 0.0099 respectively) and *THBS1* ($p=0.0039$ and
5 $p=0.0007$ respectively) (*Figure 3G, H&I*). Overall, the number of invasive bodies
6 increased when incorporating a cellular stroma, the distance and surface area invaded
7 decreased (*Figure 3J*).

8 Additionally, *HIF-1a* was upregulated (*Figure 3K*) in the presence of a cellular stroma
9 compared to an acellular stroma in HT29 tumouroids ($p<0.0001$), indicating that there
10 was more hypoxia occurring. Interestingly, *MACC1* was downregulated in the
11 presence of a cellular stroma within the HT29 and HCT116 tumouroids ($p=0.0041$ and
12 0.0024 respectively) (*Figure 3L*).

13

14 **A cancerous stroma significantly upregulates cancer invasion.** CAFs were
15 incorporated into the cancer stroma within the 3D tumouroid model in order to
16 investigate the effect of a cancerous stroma on cancer growth. The CAF-derived
17 stroma caused an increase in the distance and surface area of invasion compared to
18 HDF-derived stroma (*Figure 4A,B,C&D and Table 3*). For the less-invasive HT29³⁰
19 tumouroids, samples T6, T10, T11 and T13 caused a significant upregulation in
20 distance of invasion ($p<0.0001$, 0.0014 , <0.0001 and <0.0001 respectively). In the
21 highly-invasive HCT116 tumouroids, CAFs statistically increased the average
22 distance of invasion (μm) in the presence of sample T13 ($p=0.0489$). The average
23 surface area invaded for HT29 tumouroids was significantly greater in the presence
24 of samples T6, T11 and T13 ($p<0.0001$ for all three). For HCT116 tumouroids, the

1 average surface area invaded by the cancer was significantly upregulated in the
2 presence of samples T6, T11 and T13 also ($p < 0.0001$ for all three).
3 This is shown in the images taken by day 21 of tumouroids (*Figure 4E&F*), which
4 demonstrate the increase in size of the invasive bodies in the presence of CAFs.
5 When comparing the effect of different cancerous stromal populations in the form of
6 CAF samples, T11 (neuroendocrine origin) appeared to consistently cause a
7 significant upregulation within HT-29 and HCT 116 tumouroids whilst T7 on average
8 showed the least effect (adenocarcinoma origin). A panel of 30 genes involved in
9 invasiveness and angiogenesis were investigated to compare the healthy and
10 cancerous stroma. Genes that were significantly upregulated in CAF-tumouroids
11 were *HGF*, *ACTA2* and *TIMP1* (*Figure 4G,H&I* respectively, non-significant genes in
12 *supplementary Figure 3*). In the HT29 tumouroids, *HGF* was upregulated significantly
13 in the presence of T9 ($p = 0.0105$) and within the HCT116 tumouroids, *HGF* was
14 significantly upregulated in the presence of samples T7 ($p = 0.0001$), T10 ($p = 0.0071$)
15 and T11 ($p = 0.0255$). There was a tendency for increased *ACTA2* in CAF-containing
16 HT29 tumouroids, but it was not statistically significant whilst for the HCT116
17 tumouroids, *ACTA2* was upregulated significantly in the presence of samples T7
18 ($p = 0.0015$) and T10 ($p = 0.0457$). Finally, *TIMP1* was highly overexpressed in the
19 presence of CAF samples. In the HT29 tumouroids, the presence of samples T6
20 ($p = 0.0010$), T9 ($p = 0.0001$), T10 ($p = 0.0026$) and T13 ($p = 0.0001$) significantly
21 increased *TIMP1* expression and in the HCT116 tumouroids, *TIMP1* expression was
22 significantly increased in the presence of samples T6 ($p = 0.0264$), T9 ($p = 0.0329$),
23 T10 ($p = 0.0001$) and T13 ($p = 0.0087$).

24

1 **The presence of CAFs within the tumouroid stroma inhibits vascular network**
2 **formation.** CAF containing tumouroids demonstrated an inhibition of
3 vasculogenesis; the *de novo* formation of endothelial networks³¹. This was seen as a
4 decrease in the number of elongated endothelial structures formed within the CAF
5 stroma by day 21 of tumouroid culture (*Table 4*). In the HT29 tumouroids (*Figure*
6 *5A*), the number of endothelial structures was reduced significantly in the presence
7 of samples T6, T7, T11 (all $p < 0.0001$) and T13 ($p = 0.0008$) compared to endothelial
8 structures in HDF containing tumouroids. In the HCT116 tumouroids (*Figure 5B*), the
9 presence of CAFs significantly decreased the average number of endothelial
10 structures for samples T6, T9 (both $p < 0.0001$), T10 ($p = 0.0479$), T11 ($p = 0.0215$)
11 and T13 ($p < 0.0001$) compared to HDF containing tumouroids.

12
13 Whilst in the HDF containing stroma, endothelial structures formed throughout the
14 entire stromal compartment of the tumouroids (*Figure 5C&D*), in the CAF containing
15 stroma the formation of complex endothelial structures was only observed around
16 invasive bodies from the cancer mass (*Figure 5E&F*). The protein levels of VE-
17 Cadherin, a protein involved in endothelial cell end-to-end fusion³², showed a
18 temporal decrease in VE-cadherin levels over the 21 day culture period. The amount
19 of produced VE-Cadherin (ng/mL) significantly decreased in the HT29 tumouroids
20 with sample T13 ($p = 0.0148$) from 22.07 ± 2.144 at day 2 to 12 ± 1 by day 21 (*Figure*
21 *5G*). Within the HCT116 tumouroids, the VE-Cadherin production significantly
22 decreased in the presence of T6 ($p = 0.0413$) going from 25.04 ± 2.649 at day 2 to
23 13.86 ± 1.415 by day 21 (*Figure 5H*). The gene expression levels of *FBLN5*, a gene
24 which inhibits endothelial cell proliferation³³, angiogenesis³⁴ and especially
25 sprouting³⁵, were measured in CAF- and HDF-tumouroids at day 21 (*Figure 5I*). In

1 the HT29 tumouroids samples T9, T10 (both $p=0.0001$) and T13 ($p=0.0007$) caused
2 a significant upregulation in the relative gene expression while in the HCT116
3 tumouroids, samples T7 ($p=0.0063$) and T9 ($p=0.0014$) significantly upregulated
4 *FBLN5* compared to the HDF-tumouroids.

5

6 **The disruption of pre-formed vascular networks by CAFs.** In order to investigate
7 the effect of CAFs on a developed, mature endothelial network (angiogenesis), CAF
8 samples were added on top of tumouroids at day 21 and propagated for 7 days.
9 Endothelial cells start off as single cells within the stroma on day 1 (*Figure 6A*) and
10 form complex, branched networks by day 21 (*Figure 6B*) in the presence of HDFs
11 within a tumouroid. After CAF addition, a disruption of the endothelial networks was
12 observed (*Figure 6C*). The disruption of vascular networks was assessed by
13 quantifying the number and complexity of endothelial structures. The number of
14 endothelial structures on day 21+7 decreased in the presence of all three CAF
15 samples for both the HT29 tumouroids and HCT116 tumouroids (*Figure 6D&E*). For
16 the HT29 tumouroids, samples T6, T9 and T13 significantly decreased the number of
17 endothelial structures after 7 days ($p=0.0155$, 0.0003 and <0.0001). Within the
18 HCT116 tumouroids, samples T6, T9 and T13 also caused a significant decrease in
19 the average number of endothelial structures after 7 days ($p=<0.0001$, <0.0001 and
20 0.0029). The vascular disruption was further confirmed by a significant decrease in
21 *CDH5* gene levels, coding for VE-Cadherin. Relative *CDH5* levels decreased
22 significantly ($p<0.0001$ for all) in both HT29 and HCT116 tumouroids at day 21+1,
23 day 21+3 and day 21+7 (*Figure 6F&G*). Furthermore, *FBLN5* gene expression
24 increased significantly after CAF addition (*Figure 6H&I*). In HT29 tumouroids
25 containing samples T6 and T9 on day 21+7 ($p=0.0001$ and 0.0395). Within the

1 HCT116 tumouroids, *FLBN5* was upregulated significantly for T13 at day 21+1
2 ($p=0.0001$), T9 and T13 for day 21+3 ($p=0.0261$ and 0.0024) and T6 and T13 for day
3 21+7 ($p=0.0300$ and 0.0001). Finally, *VEGFA* gene levels were analysed after CAF
4 addition (*Figure 6J&K*) and a general increase was measured. Within the HT29
5 tumouroids sample T9 caused a significant upregulation at day 21+1 ($p=0.02304$)
6 and samples T6 and T9 at day 21+7 ($p=0.0233$ and 0.0072). For the HCT116
7 tumouroids sample T13 caused a significant upregulation at day 21+1 ($p=0.0372$),
8 samples T6, T9 and T13 at day 21+3 ($p=0.0008$, 0.0071 and 0.0019) and sample
9 T13 for day 21+7 ($p=0.0282$).

10

11 **Discussion**

12 Our findings can be summarised as follows. First, a normal healthy stroma does not
13 upregulate cancer growth significantly in a 3D model with a defined cancer mass and
14 defines stromal compartments. Secondly, the presence of a cancerous CAF stroma
15 increased the distance and surface area of invasion of colorectal cancer (CRC) into
16 the stromal compartment whilst, at the same time, inhibiting vasculogenesis. These
17 processes were associated with the up-regulation of hepatocyte growth factor (*HGF*),
18 metalloproteinase inhibitor 1 (*TIMP1*) and fibulin 5 (*FBLN5*). Next, the re-modelling
19 appeared to occur through the process of disruption of complex endothelial networks
20 and was associated with up-regulation of vascular endothelial growth factor (*VEGFA*)
21 and a down-regulation in vascular endothelial cadherin (VE-Cadherin). These results
22 support, within a biomimetic, 3D, *in vitro* framework, the direct role of CAFs in
23 promoting cancer invasion and driving both vasculogenesis and angiogenesis.

24

1 The aspect that was increased in the presence of a healthy stroma was the increase
2 in invasive bodies, modelling the highly invasive cancers “dispersal” into a high
3 number of small clusters to invade the tissue. This is often due to the loss of
4 structure proteins such as cadherins and cytokeratins³⁶.

5 The second major finding of this novel work is the differential invasion rate and
6 pattern of less-invasive HT29 and highly-invasive HCT116 cancer cells in 3D
7 tumouroids in the presence of CAFs, causing an increase in the distance (up to 3-
8 fold) and surface area of invasion (up to 10-fold) over a 21-day period. CAFs pro-
9 invasive properties and their ability to enable cancer cells to metastasise has been
10 demonstrated previously^{37,38}. Logsdon et al.³⁹ described the importance of CAFs in a
11 3D pancreatic cancer model using Matrigel®-coated invasion chambers and soft-
12 agar colony formation and although this model showed an increased in proliferation
13 and metastasis during *in vivo* validation, the 3D model was not compartmentalised
14 and did not allow for a measurement of invasion *in vitro*. The majority of 3D cancer
15 models lack appropriate tensile force and stiffness associated with tumour tissue, as
16 they commonly use soft hydrogels, which have too high a water content⁴⁰. Our
17 biomimetic 3D *in vitro* cancer model (tumouroid) has a collagen density of up to 40x
18 higher compared to standard hydrogels and therefore mimics the *in vivo* stiff tumour
19 environment more closely²⁰; an important aspect especially for CAFs⁴¹.

20 The third of our observations can be interpreted in the following manner; CAFs play
21 a key role in vascular network formation and remodelling. Whilst it is understood that
22 CAFs play a major role in angiogenesis and recruiting vasculature towards the
23 cancer²⁷, in this study we also demonstrated that CAFs play a major role in
24 vasculogenesis and the disruption of vascular network formation. This aspect has
25 not been studied with the same rigour. Some studies have introduced CAFs at the

1 same time point as HUVECs and observed end-to-end fusion of the HUVEC cells
2 into endothelial structures⁴². Whilst this could be an observation of vasculogenesis,
3 our model, with tissue specific parameters including biomimetic matrix density,
4 shows no *de novo* formation of vascular networks in 3D in the presence of CAFs. At
5 25 000 CAFs per 24-well tumouroids, we observed 100% confluency of these cells in
6 3D by day 7, whilst HUVECs in our “normal” HDF containing cultures would not start
7 forming complex endothelial structures until at least day 14. Our data indicates that
8 CAFs start expressing factors that block complex vascular network formation, whilst
9 retaining ‘simple’ vascular/endothelial structures. One of the factors, that was
10 significantly increased, was *VEGFA*. Although *VEGFA* is the major player in
11 angiogenesis and involved in recruiting mature blood vessels towards the cancer, its
12 role in vasculogenesis is not as well understood. The major cross-talk between
13 cancer cells and endothelial cells in our set up was growth factor driven, which was
14 ascertained through an additional 3D set up. This set up demonstrated the
15 chemoattractant driven movement and recruitment of endothelial structures to the
16 cancer mass through an acellular ring placed between the cancer mass and stromal
17 compartment¹⁹. Interestingly, a study looking at cardiac mouse development found a
18 correlation between the disruption of vasculogenesis and elevated *VEFGA* levels⁴³.
19 This aspect could be observed within our work as the cancer cells and CAFs co-
20 evolve during tumour progression. This was further studied by Brown et al. when
21 looking at how the prevention of vasculogenesis but not angiogenesis prevented the
22 recurrence of glioblastoma in mice⁴⁴. Cancer cells are known for their high turnover
23 and over-production of angiogenic growth factors⁴⁵. This is in an attempt to recruit
24 host vasculature from surrounding tissues. The unregulated and upregulated
25 production and release of angiogenic growth factors by solid tumours results in the

1 formation of abhorrent and leaky vasculature surrounding tumours⁴⁶. We have
2 measured increased levels of VEGFA in our tumouroid cultures which are resulting
3 in disrupted vasculogenesis and angiogenic remodelling to form non-complex
4 networks. Vasculogenesis in cancer and especially in relation to the presence of
5 CAFs is not a major focus of research as angiogenesis and remodelling of cancer is
6 the biomimetic environment in which cancer arises. However, by gaining insights into
7 how cancer angiogenic signalling can influence vasculogenesis may help further our
8 understanding of tissue necrosis and vascular remodelling in cancer.

9
10 In our third observation we further showed that CAFs have the ability to disrupt pre-
11 formed *in vitro* vascular network (“CAF treatment”). By day 7, post CAF addition, the
12 endothelial networks that had previously formed were disrupted and an overall
13 decrease in the number of endothelial structures was observed. Furthermore, we
14 found a decrease of *CDH5* levels within the tumouroids. The role *CDH5* and the
15 corresponding protein VE-Cadherin is becoming more pertinent in the study of
16 angiogenesis as it has been specifically implicated in the local production of
17 junctions within complex endothelial networks³². The literature on CAF interaction
18 with VE-Cadherin is limited, although the role of CAFs as major sources of VEGFA
19 production is established and understood to be mediated through HIF-1 α /GPER
20 signaling⁴⁷. This particular gene (*VEGFA*) was increased after we added CAFs to our
21 cultures and in fact this will have played an important role in the disruption (or
22 angiogenesis) observed, however it would be crucial to study further how stromal
23 cells cause this angiogenesis as the normalisation of these remodelled vascular
24 networks has been a target for many antiangiogenic drugs⁴⁸.

25

1 Our results need to be understood in the context of the following methodological
2 limitations. We report the interactions at the interface of a cancer mass and patient-
3 derived cancer associated fibroblasts in a 3D vascularized colorectal cancer model.
4 A total of six patient-derived CAF samples were successfully isolated and cultured
5 from colorectal cancer tissue samples. Primary CAF characterisation is a topic of
6 debate in literature. Some groups have done extensive characterisation on the gene
7 and protein level of 'CAF specific' markers^{49,50,27}. In this study, we successfully
8 demonstrated that our CAF samples expressed widely recognised markers for CAF
9 identification. CAF populations have often been classified based on their location
10 within the tumour margin⁵¹. For comparison purposes, we used human dermal
11 fibroblasts (HDFs) as our control or "healthy" stromal cells, which are not an
12 immortalised cell line and could also start to differentiate into CAFs while in co-
13 cultured with cancer cells within the tumouroids. It could be argued that most primary
14 fibroblast samples will adapt a cancerous phenotype due to being cultured on plastic
15 or in co-culture with cancer cells⁵². For future work it would be ideal to use paired
16 CAF and NF samples from the same patient as part of a larger comparison study.
17 Patient-derived NFs would serve as a better control and further our investigations
18 into what signalling is caused by CAFs. Additionally, following on from this work
19 potential of identifying what drives CAFs and their cancer promoting properties could
20 be pin pointed. One pathway would be to generate knockout CAFs with a deletion of
21 *HGF*, *TIMP1* and *FBLN5*; genes we found to be upregulated in the tumouroids and
22 possibly responsible for increased invasion and vascular remodelling. For example,
23 the inhibition of the HGF/c-Met signalling pathway is a compelling therapy to interfere
24 with tumour growth and angiogenesis⁵³. Along the lines of gene expression analysis,
25 a major limitation within this study is the use of the whole, multicellular tumouroid,

1 which does not allow for the analysis of single-cell signalling. This calls for the data
2 presented in this work to be called “observational” and highlights correlations, not
3 causations. Specific protagonists to VE-Cadherin such as could be used to
4 potentially normalise the “leaky vasculature” caused by VEGFA upregulation, which
5 are independent of one another.

6

7 **Additional Information Section**

8 **Authors’ contributions.** J.P. planned the work and carried out experiments and
9 subsequent analyses. T.M. conducted preceding optimisation and advised on the
10 interpretation of the data. K.S. and A.N. received the tissue samples, processed and
11 cultivated them in the first instance. M.E. M.L. and U.C. delivered design and
12 guidance for the project. All authors read, provided edits and approved the
13 manuscript.

14

15 **Ethical approval and consent to participate.** Primary human colorectal cancer
16 associated fibroblasts were obtained in accordance with the Declaration of Helsinki.
17 Samples were isolated from tumour tissues acquired from surgeries at the Royal
18 Free Hospital. Patients provided informed consent for tissue donation for research
19 under ethics reference 11/WA/0077 obtained through the North Wales Research
20 Ethics Committee (Central and East) through TAPb biobank.

21

22 **Consent to publish.** All authors give their consent to publish this manuscript.

23

24 **Data availability.** The data that supports the findings of this study are available from
25 the corresponding author (U.C.) on reasonable request.

1

2 **Competing interests.** The authors declare that there are no conflicts of interest.

3

4 **Funding.** Judith Pape receives a stipend and EU fee funding from the EPSRC as
5 part of the doctoral training program (DTP). Mark Emberton receives research
6 support from the United Kingdom's National Institute of Health Research (NIHR)
7 UCLH/UCL Biomedical Research Centre and became an NIHR Senior Investigator in
8 2015. This work was funded by the NIHR Invention for Innovation (i4i) programme.
9 Views expressed are those of the authors and not necessarily those of the NHS, the
10 NIHR or the Department of Health.

11

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1 Figure 1: Experimental set ups. (A) Birdseye view of the three main tumouroid set ups
2 used with respective cellular populations in the ACM and stroma. For all set ups, an
3 ACM was nested into a stromal compartment. Both consisted of 10% monomeric
4 collagen type 1 that had undergone plastic compression with the RAFT™ protocol.
5 The stroma was either acellular containing only laminin, healthy, containing HDFs and
6 HUVECs or cancerous containing one of six patient specific CAF samples. Schematic
7 was created using Servier Medical Art according to a Creative Commons Attribution
8 3.0 Unported License guidelines 3.0 (<https://creativecommons.org/licenses/by/3.0/>).
9 Adjustments and colour changes were made to the original cartoons. (B) The “CAF
10 Treatment” set-up. Tumouroids with a normal HDF containing stroma were left to
11 mature for 21 days. During this time endothelial networks developed. After this time,
12 one of three patient-specific CAF samples were applied to the mature tumouroids.

7 Figure 2: Patient specific CAF tissue sample characterisation. (A) Origin of samples
8 including the location of the original cancer mass, tumour type and any additional
9 notes. (B) 2D cell samples were analysed for fibroblast markers ACTA2 (alpha
10 smooth muscle actin), (C) S100A4 (fibroblast specific protein-1), (D) PDGFRA
11 (platelet derived growth factor receptor a), (E) FAP (fibroblast-activating protein), (F)
12 IL-6 (interleukin-6) and (G) P4HA1 (prolyl-4 hydroxylase). Value shown is normalised
13 to HPRT1 mRNA levels (mean ± SEM) with n=3 and 3 technical repeats. One-way
14 ANOVA with Dunnet’s Post Hoc for ACTA2, S100A4, FAP, PDGFRA and IL-6 and
15 Kruskal-Wallis with Dunn’s Multiple comparisons test p-values for P4HA1, with values
16 0.05=*, 0.005=**, 0.0005=*** and 0.00005=**** with DOF for first five genes all=20
17 and f-value for ACTA2=92.1, S100A4=136.7, FAP=31.83, PDGFRA=16.2 and IL-
18 6=13.76. (H) Western blot of α-SMA protein expression within 2D monolayers of cells
19 with LC=loading control beta-tubulin. (I) and (J) Visualisation of vimentin expression
20 of HDF and CAFs respectively when cultured in 3D with scale bar=100 µm for both
21 images and green=vimentin and blue=DAPI.

16 Figure 3: Average invasion into an acellular or healthy cellular stroma per sample. (A)
17 Number of invasive bodies, (B) distance of invasion and (C) average surface area of
18 invasion at day 21 of HT29 or HCT116 tumouroids (mean ± SEM). All n=3 with 4
19 technical repeats and showing Mann-Whitney p-values, with values 0.05=*, 0.005=**,
20 0.0005=*** and 0.00005=****. (D) Representative image of an invasive body, (E)
21 invasion into acellular stroma and (F) cellular stroma within HT29 tumouroids with
22 scale bar=50 µm, 500 µm and 100 µm respectively and with red=CK20, green=CD31
23 and blue=DAPI. Comparative gene expression between acellular and cellular stroma
24 in tumouroids at day 21 of growth for (G) MMP2 (matrix metalloproteinase 2), (H)
25 TIMP-1 (metalloproteinase inhibitor 1), (I) THBS1 (thrombospondin 1), (J) HIF-1α
(hypoxia inducible factor 1-alpha) and (K) MACC1 (metastasis associated in colon
cancer-1). Value shown is normalised to HPRT1 mRNA levels (mean ± SEM) with n=3
and 3 technical repeats showing Unpaired t-test p-values, with values 0.05=*,
0.005=**, 0.0005=*** and 0.00005=****.

1 Figure 4: Invasion into stromal compartment and gene upregulation. (A) HT29
 2 distance of invasion and (B) HCT116 distance of invasion into the stroma within
 3 tumouroid models at D21 and surface area of invasion within (C) HT29 and (D) HCT116
 4 tumourids at D21. Tumouroids contained either HDF cells or one of six patient-specific
 5 CAF tissue samples within the stromal compartment of the constructs. All mean \pm
 6 SEM with $n=3$ with 4 technical repeats and showing Kruskal-Wallis with Dunn's
 7 multiple comparison's test p -values, with values $0.05=*$, $0.005=**$, $0.0005=***$ and
 8 $0.00005=****$. (E) Representation of average invasive bodies at day 21 in a 'normal'
 9 HDF containing tumouroid in comparison to a (F) CAF containing tumouroid. Scale
 10 bar= $100\ \mu\text{m}$ for top and $500\ \mu\text{m}$ for bottom image, with red=CK20 and blue=DAPI.
 11 (G) ACTA2 (α -smooth muscle actin), (H) HGF (hepatocyte growth factor and (I)
 12 TIMP1 (metallopeptidase inhibitor 1) gene expression in tumouroids at day 21 of
 13 growth, comparing HDF containing stroma and CAF containing stroma. Value shown
 14 is normalised to HPRT1 mRNA levels (mean \pm SEM) with $n=3$ and 3 technical repeats.
 15 Ordinary one-way ANOVA Dunnett's multiple comparisons test with p -values $0.05=*$,
 16 $0.005=**$, $0.0005=***$ and $0.00005=****$ with $\text{DOF}=20$ for all and f -value for ACTA2 for
 HT29=4.213 and HCT116=12.31, f -value for HGF=3.836 for HT29 group and 16.3 for
 HCT116 group, and finally for TIMP1 f -value for HT29=37.21 and HCT116=11.25.

10 Figure 5: Endothelial structures formed within the cancerous CAF stroma. Number of
 11 endothelial structures formed within (A) HT29 and (B) HCT116 tumouroid stromal
 12 compartments at day 21 (mean \pm SEM) containing either HDF or one of six patient-
 13 specific CAF tissue samples. All $n=3$ with 4 technical repeats and showing Kruskal-
 14 Wallis with Dunn's multiple comparison's test p -values, with values $0.05=*$, $0.005=**$,
 15 $0.0005=***$ and $0.00005=****$. (C) Example images of normal endothelial structure
 16 formation within a HDF containing stroma HCT116 tumouroid at day 21 at the cancer-
 stromal edge and with a (D) budded invasive body within a HT29 tumouroid. Scale
 bar= $100\ \mu\text{m}$ for left and $50\ \mu\text{m}$ for right image and red=CK20, green=CD31 and
 blue=DAPI. (E) Images showing the decreased formation of complex endothelial
 structures within a CAF containing stroma at day 21 near the cancer-stroma edge, (F)
 as well as around a budding invasive body, the only occurrence of endothelial
 structures within these conditions. Scale bar= $50\ \mu\text{m}$ and red=CK20, green=CD31 and
 blue=DAPI. Active VE-Cadherin protein released into the media of one of six CAF
 containing (G) HT29 or (H) HCT116 tumouroids over 21 days (mean \pm SEM). Paired
 t -test comparisons test between day and day 21 with p -values $0.05=*$, $0.005=**$,
 $0.0005=***$ and $0.00005=****$ with $\text{DOF}=2$ for both and t -value for HT29=8.115 and
 HCT116=4.766. (I) FBLN5 (fibulin-5) expression at day 21 within the HDF or one of
 six CAF containing HT29 or HCT116 tumouroids (mean \pm SEM). Value shown is
 normalised to HPRT1 mRNA levels (mean \pm SEM) with $n=3$ and 3 technical repeats.
 Ordinary one-way ANOVA Dunnett's multiple comparisons test with p -values $0.05=*$,
 $0.005=**$, $0.0005=***$ and $0.00005=****$.

Figure 6: Disruption of mature endothelial network caused by the addition of CAFs.
 (A) Example of single cell endothelial cells at day 1 of tumouroid growth, (B) example
 of matured networks at day 21 in an HDF containing stroma and finally (C) example
 of disrupted networks at day 21+7 (21 days normal HDF stroma growth plus 7 days
 post CAF addition). Scale bar= $100\ \mu\text{m}$ and green=CD31 and blue=DAPI. Number of
 endothelial structures formed within (D) HT29 and (E) HCT116 tumouroid stromal
 compartments at day 21+7 (mean \pm SEM) containing either HDF or one of six patient-
 specific CAF tissue samples. All $n=3$ with 4 technical repeats and showing Kruskal-
 Wallis with Dunn's multiple comparison's test p -values, with values $0.05=*$, $0.005=**$,
 $0.0005=***$ and $0.00005=****$. CDH5 (VE-Cadherin) gene expression in (F) HT29 and
 (G) HCT116 tumouroids, FBLN5 (fibulin-5) expression in (H) HT29 and (I) HCT116
 tumouroids and VEGFA (vascular endothelial growth factor) expression in (J) HT29
 and (K) HCT116 tumouroids after CAF addition at days 1, 3 and 7 (mean \pm SEM).
 Value shown is normalised to HPRT1 mRNA levels (mean \pm SEM) with $n=3$ and 3
 technical repeats. Ordinary one-way ANOVA Dunnett's multiple comparisons test with
 p -values $0.05=*$, $0.005=**$, $0.0005=***$ and $0.00005=****$.