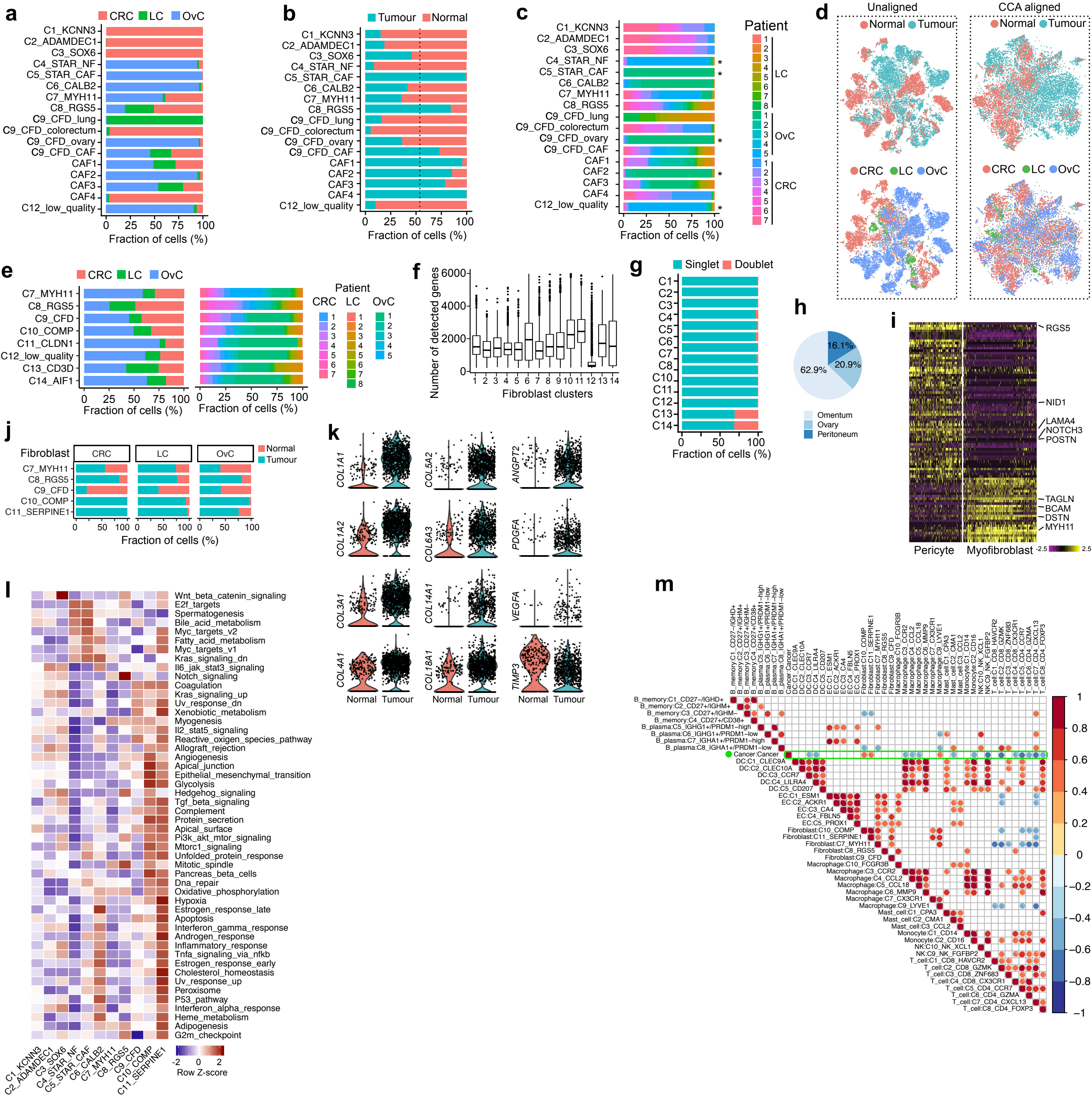
a
CRC LC OvC
C1_KCNN3
C2_ADAMDEC1
C3_SOX6
C4_STAR_NF
C5_STAR_CAF
C6_CALB2
C7_MYH11
C8_RGS5
C9_CFD_lung
C9_CFD_colorectum
C9_CFD_ovary
C9_CFD_CAF
CAF1
CAF2
CAF3
CAF4
C12_low_quality
0 25 50 75 100
Fraction of cells (%)
b
Tumour Normal
c
Patient
LC
OvC
CRC
*
d
Unaligned
CCA aligned
Normal Tumour
CRC LC OvC
e
C7_MYH11
C8_RGS5
C9_CFD
C10_COMP
C11_CLDN1
C12_low_quality
C13_CD3D
C14_AIF1
f
Number of detected genes
0 2000 4000 6000
1 2 3 4 5 6 7 8 9 10 11 12 13 14
Fibroblast clusters
g
Singlet Doublet
C1 C2 C3 C4 C5 C6 C7 C8 C10 C11 C12 C13 C14
0 50 100
h
16.1%
20.9%
62.9%
Omentum
Ovary
Peritoneum
i
RGS5
NID1
LAMA4
NOTCH3
POSTN
TAGLN
BCAM
DSTN
MYH11
Pericyte
Myofibroblast
-2.5 2.5
j
Fibroblast
CRC LC OvC
Normal
Tumour
C7_MYH11
C8_RGS5
C9_CFD
C10_COMP
C11_SERPINE1
0 50 100
Fraction of cells (%)
k
COL1A1 COL5A2 ANGPT2
COL1A2 COL6A3 PDGFA
COL3A1 COL14A1 VEGFA
COL4A1 COL18A1 TIMP3
Normal Tumour
l
Wnt_beta_catenin_signaling
E2f_targets
Spermatogenesis
Bile_acid_metabolism
Myc_targets_v2
Fatty_acid_metabolism
Myc_targets_v1
Kras_signaling_dn
Il6_jak_stat3_signaling
Notch_signaling
Coagulation
Kras_signaling_up
Uv_response_dn
Xenobiotic_metabolism
Myogenesis
Il2_stat5_signaling
Reactive_oxigen_species_pathway
Allograft_rejection
Angiogenesis
Apical_junction
Epithelial_mesenchymal_transition
Glycolysis
Hedgehog_signaling
Tgf_beta_signaling
Complement
Protein_secretion
Apical_surface
Pi3k_akt_mtor_signaling
Mtorc1_signaling
Unfolded_protein_response
Mitotic_spindle
Pancreas_beta_cells
Dna_repair
Oxidative_phosphorylation
Hypoxia
Estrogen_response_late
Apoptosis
Interferon_gamma_response
Androgen_response
Inflammatory_response
Tnfa_signaling_via_nfkb
Estrogen_response_early
Cholesterol_homeostasis
Uv_response_up
Peroxisome
P53_pathway
Interferon_alpha_response
Heme_metabolism
Adipogenesis
G2m_checkpoint
C1_KCNN3
C2_ADAMDEC1
C3_SOX6
C4_STAR_NF
C5_STAR_CAF
C6_CALB2
C7_MYH11
C8_RGS5
C9_CFD
C10_COMP
C11_SERPINE1
-2 0 2
Row Z-score
m
B_memory:C1_CD27−/IGHD+
B_memory:C2_CD27+/IGHM+
B_memory:C3_CD27+/IGHM−
B_memory:C4_CD27+/CD38+
B_plasma:C5_IGHG1+/PRDM1−high
B_plasma:C6_IGHG1+/PRDM1−low
B_plasma:C7_IGHA1+/PRDM1−high
B_plasma:C8_IGHA1+/PRDM1−low
Cancer:Cancer
DC:C1_CLEC9A
DC:C2_CLEC10A
DC:C3_CCR7
DC:C4_LILRA4
DC:C5_CD207
EC:C1_ESM1
EC:C2_ACKR1
EC:C3_CA4
EC:C4_FBLN5
EC:C5_PROX1
Fibroblast:C10_COMP
Fibroblast:C11_SERPINE1
Fibroblast:C7_MYH11
Fibroblast:C8_RGS5
Fibroblast:C9_CFD
Macrophage:C10_FCGR3B
Macrophage:C3_CCR2
Macrophage:C4_CCL2
Macrophage:C5_CCL18
Macrophage:C6_MMP9
Macrophage:C7_CX3CR1
Macrophage:C9_LYVE1
Mast_cell:C1_CPA3
Mast_cell:C2_CMA1
Mast_cell:C3_CCL2
Monocyte:C1_CD14
Monocyte:C2_CD16
NK:C10_NK_XCL1
NK:C9_NK_FGFBP2
T_cell:C1_CD8_HAVCR2
T_cell:C2_CD8_GZMK
T_cell:C3_CD8_ZNF683
T_cell:C4_CD8_CX3CR1
T_cell:C5_CD4_CCR7
T_cell:C6_CD4_GZMA
T_cell:C7_CD4_CXCL13
T_cell:C8_CD4_FOXP3
1 0.8 0.6 0.4 0.2 0 −0.2 −0.4 −0.6 −0.8 −1

Fig. S3

Fig. S3. Characterization of fibroblasts

a-c Fraction of cells in the unaligned fibroblast clusters colour-coded per cancer type (**a**), sample origin (**b**), or patient (**c**). **d** t-SNE plots showing unaligned and CCA aligned clusters colour-coded by sample origin (upper panels) and cancer type (low panels). **e** Fraction of cells in CCA-aligned fibroblast subclusters colour-coded per cancer type (left) or patient (right). **f** Number of detected genes for fibroblast clusters, combining both tissue-specific and shared subclusters. **g** Fraction of singlet and doublet cells detected for fibroblast clusters. **h** Fraction of mesothelium-derived cells from different tissues. **i** Heatmap of differentially expressed genes between pericytes and myofibroblasts. **j** Fraction of cells derived from normal (red) or tumour tissue (green) for shared fibroblast subclusters in each cancer type. **k** Violin plot showing differentially expressed genes from normal and tumour tissues. **l** Differences in cancer-hallmark pathway activities scored per cell by AUCell for fibroblast clusters. **m** Heatmap showing positive (red) and negative (blue) correlations between the prevalence of the different cell phenotypes in each patient. Only significant correlations ($p < 0.05$), as assessed by Pearson correlation, are shown. Positive correlations between cancer cells and CAFs (C10, C11) were detected.