

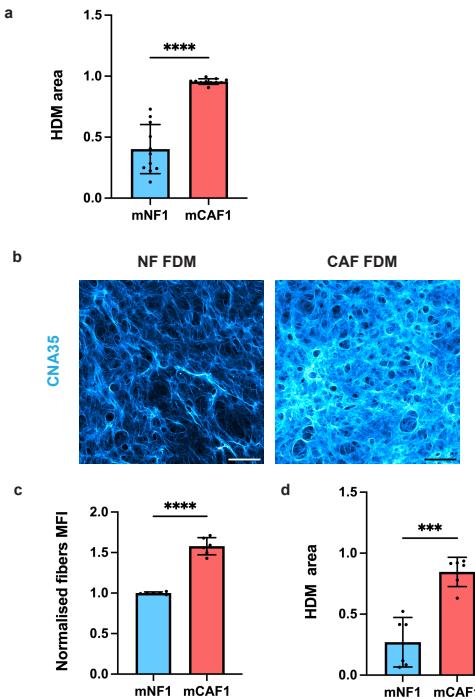
Supplementary Material

Fibroblast-derived matrix models desmoplastic properties and forms a prognostic signature in cancer progression

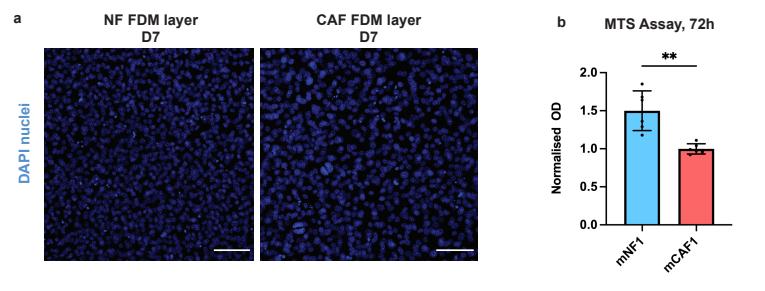
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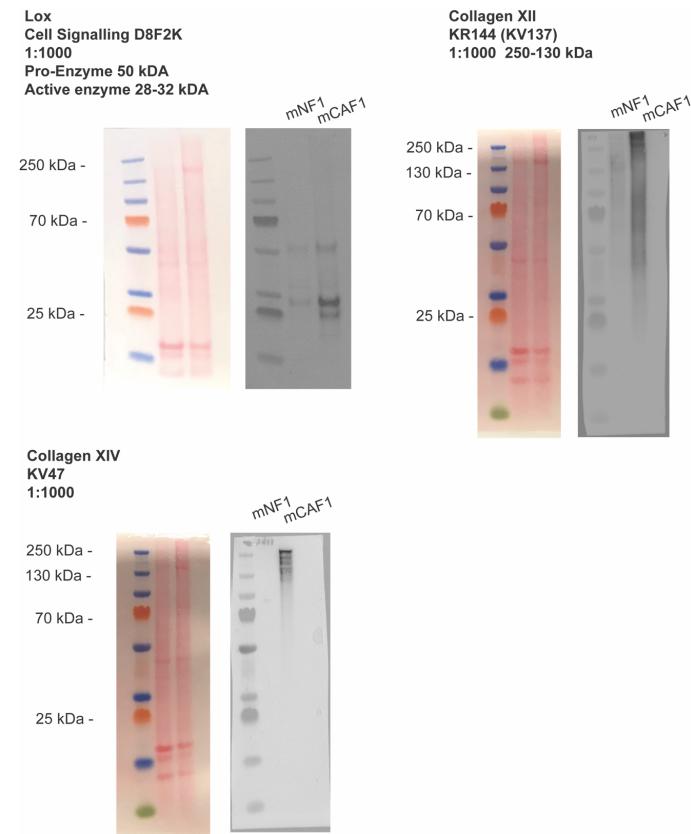
1 Supplementary Figures



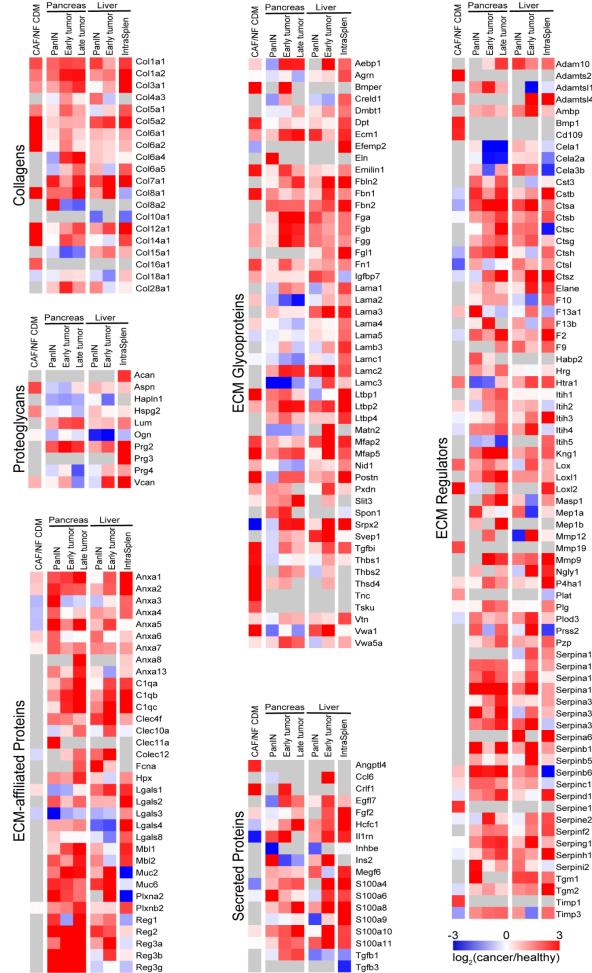
Supplementary Figure 1. **a.** mNF1 and mCAF1 FDMs density based on SHG maximum intensity projection. Quantified as high density matrix (HDM) area per field of view. n=3 repeats. **b.** Representative images of mNF1 and mCAF1 FDMs imaged after CNA35 probe staining (binding fibrillar collagens). **c.** mNF1 and mCAF1 FDMs ECM fibers mean fluorescent intensity (MFI). n=3 repeats. **d.** mNF1 and mCAF1 FDMs density based on CNA35 staining maximum intensity projection. Quantified as high density matrix (HDM) area per field of view. n=3 repeats. Unpaired t-test, *** – p-value < 0.001, **** – p-value < 0.0001. Scale bars 100 µm.



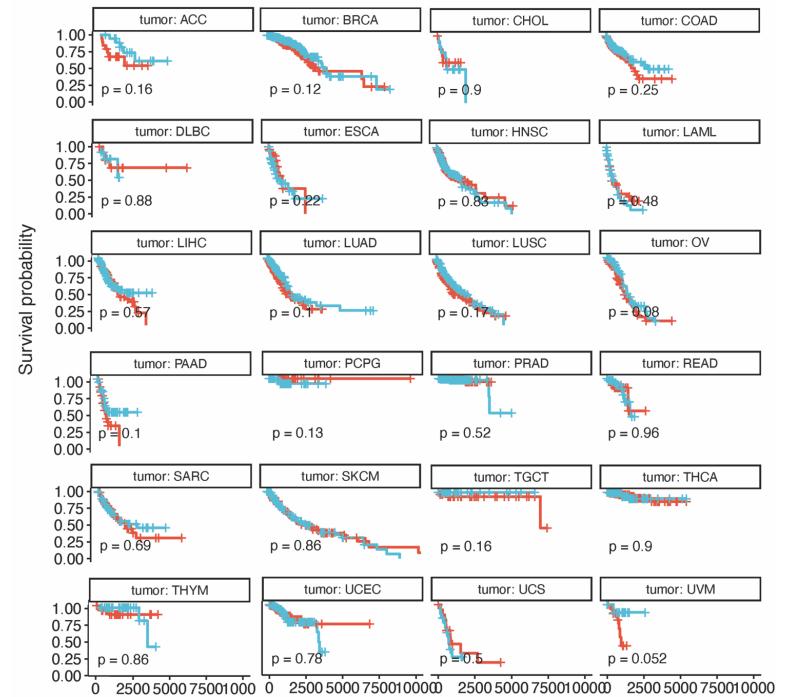
Supplementary Figure 2. mNF1 and mCAF1 confluence in FDM and difference in proliferation.
a. Representative image of mNF1 and mCAF1 cellular density at day 7 of FDMs deposition. Nuclei stained with DAPI. Scalebar 100 μ m. **b.** MTS proliferation assay at day 3 post seeding of mNF1 and mCAF1 in regular culture. n=2, 3 technical repeats per experiment. **– p-value < 0.01.



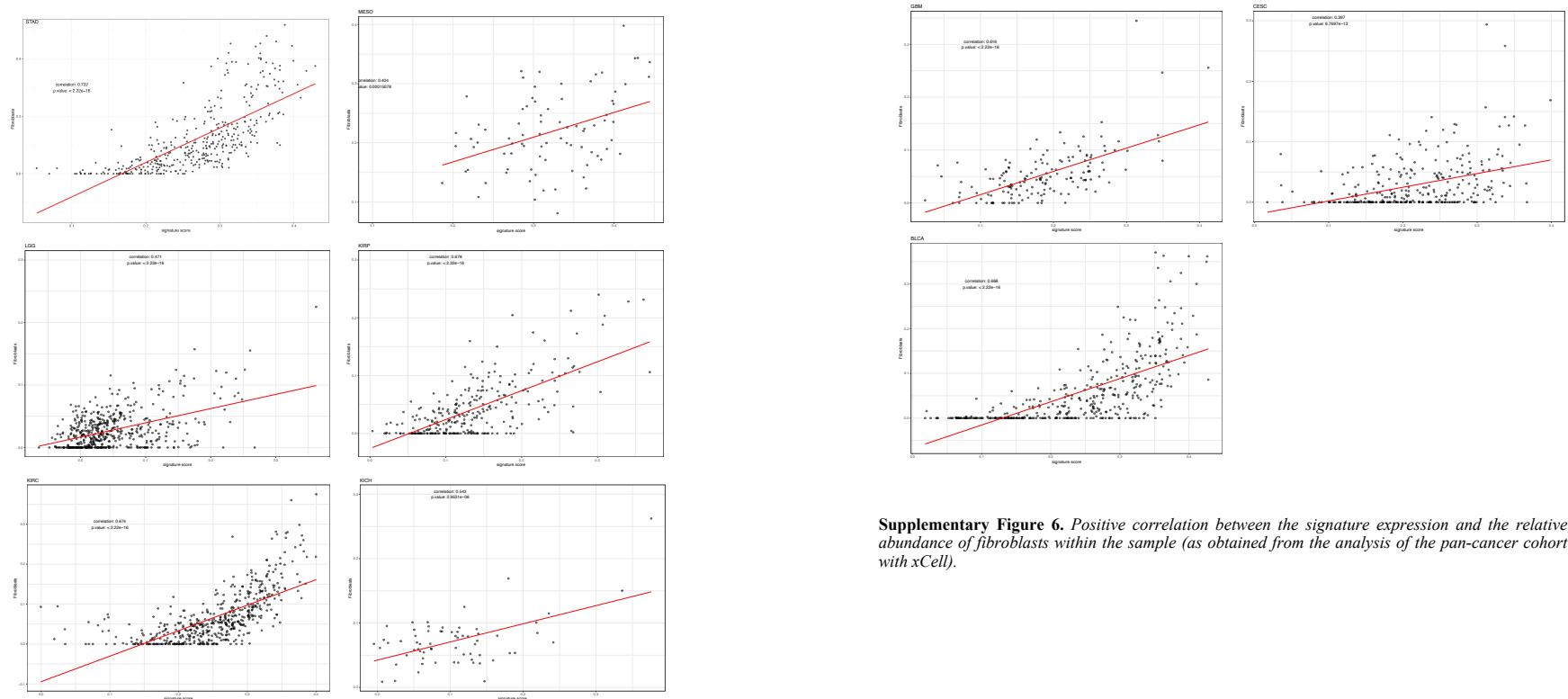
Supplementary Figure 3. Full membrane scans of the Western blots presented in Figure 2. with Ponceau dye staining to the left of the scans.



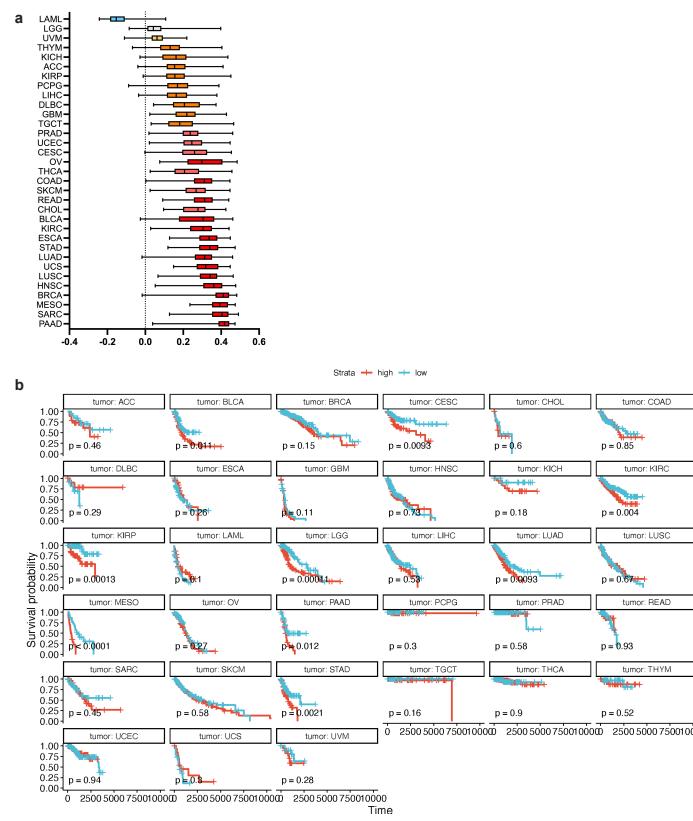
Supplementary Figure 4. Heatmap of all matrisome changes in PDAC dataset. Grey values represent non-detected proteins.



Supplementary Figure 5. Kaplan-Meir plots for full signature (non-significant p-values). For abbreviations see Supplementary Fig.4 legend.

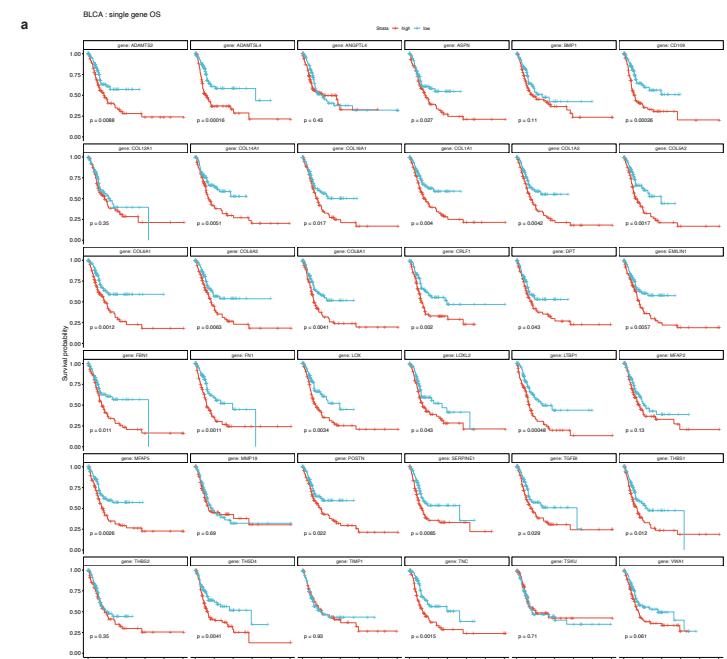


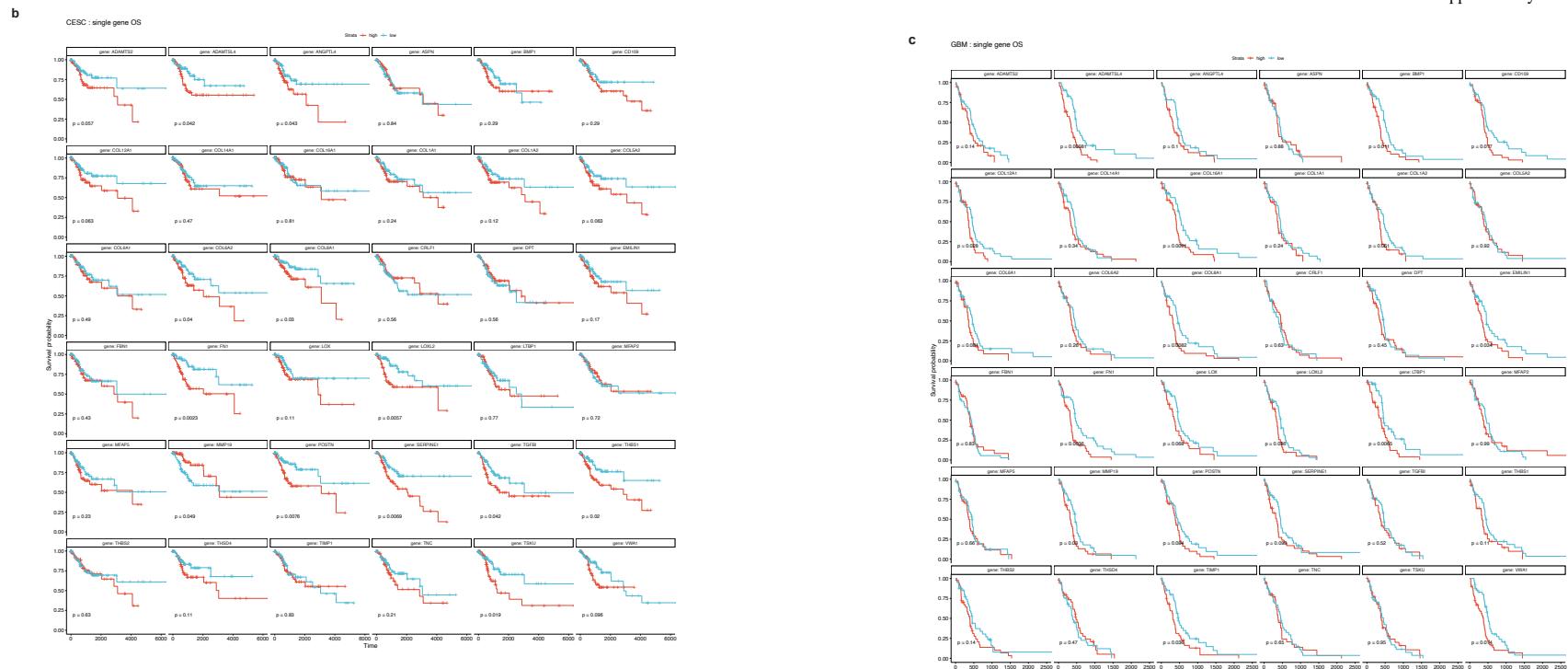
Supplementary Figure 6. Positive correlation between the signature expression and the relative abundance of fibroblasts within the sample (as obtained from the analysis of the pan-cancer cohort with xCell).

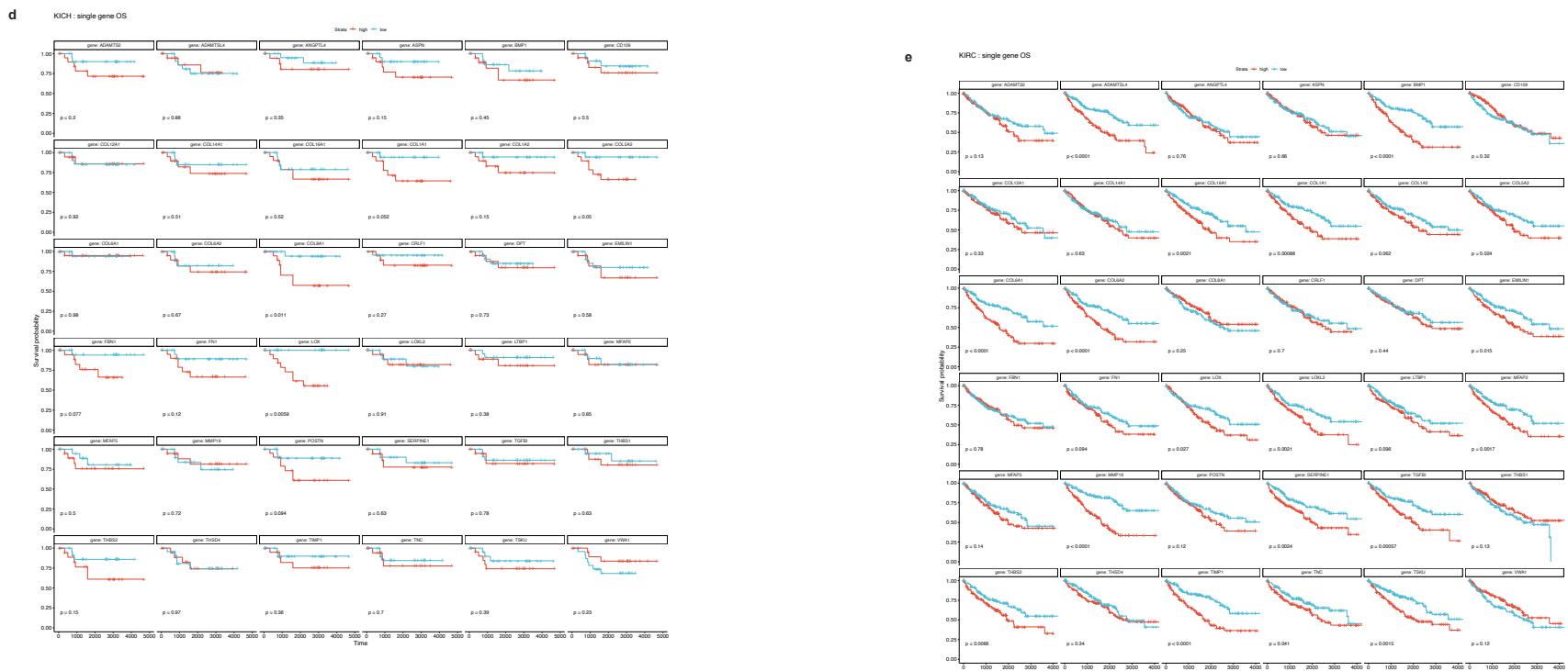


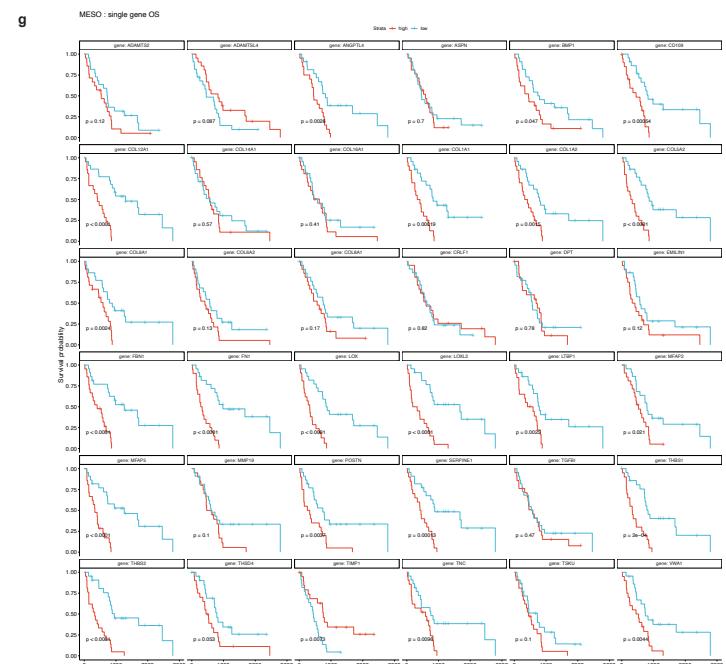
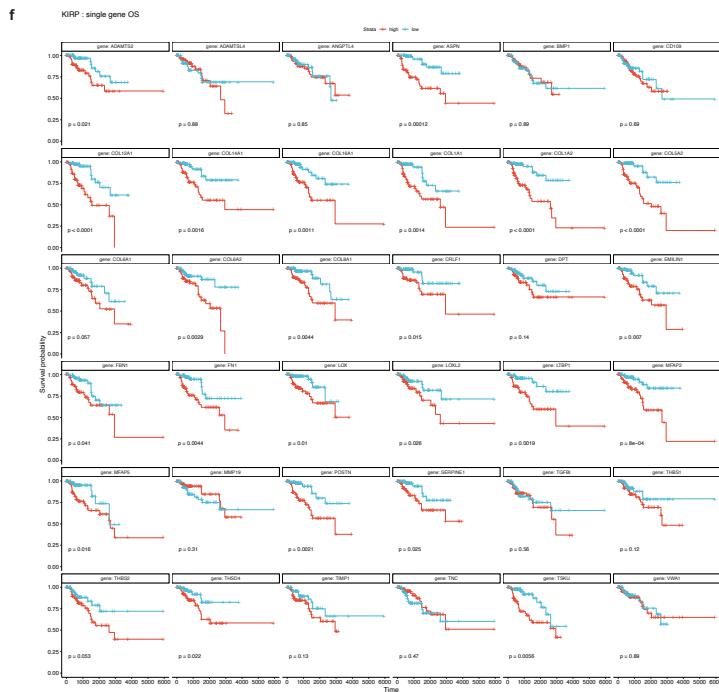
Supplementary Figure 7. Short CAF FDM signature is enriched in multiple cancer types in human and is prognostic of cancer patients' survival. **a.** Difference in the signature expression score (box plots summarize median with min and max). **b.** Kaplan-Meier plots of all analysed cancer types. Abbreviations: LAML-Acute Myeloid Leukemia; ACC-Adrenocortical carcinoma; BLCA-Bladder Urothelial Carcinoma; LGG-Brain Lower Grade Glioma; BRCA- Breast invasive carcinoma; CESC-Cervical squamous cell carcinoma and endocervical adenocarcinoma; CHOL-Cholangiocarcinoma; COAD-Colon adenocarcinoma; ESCA-Esophageal carcinoma; GBM- Glioblastoma multiforme; HNSC-Head and Neck squamous cell carcinoma; KICH- Kidney Chromophobe; KIRC-Kidney renal

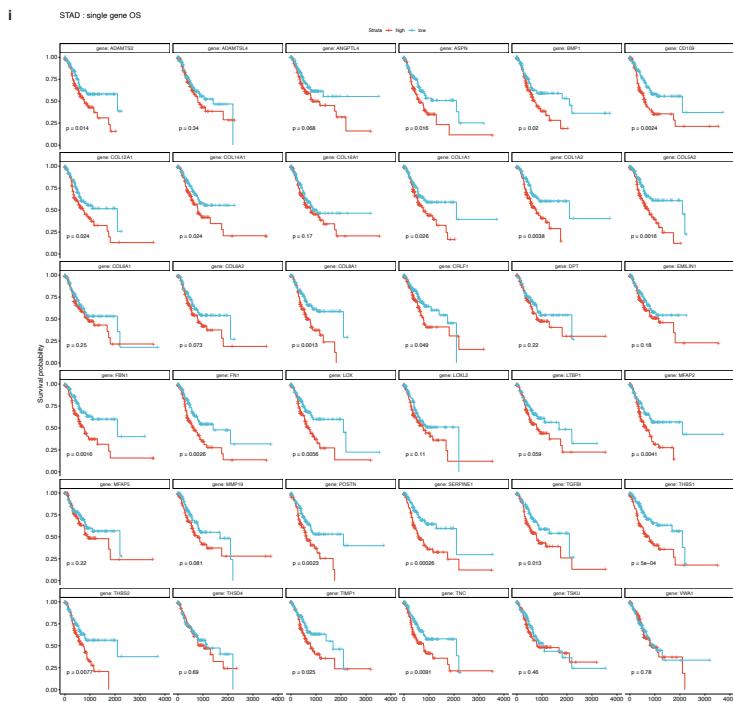
clear cell carcinoma; KIRP-Kidney renal papillary cell carcinoma; LIHC- Liver hepatocellular carcinoma; LUAD-Lung adenocarcinoma; LUSC-Lung squamous cell carcinoma; DLBC- Lymphoid Neoplasm Diffuse Large B-cell Lymphoma; MESO-Mesothelioma; OV-Ovarian serous cystadenocarcinoma; PAAD-Pancreatic adenocarcinoma; PCPG- Pheochromocytoma and Paraganglioma; PRAD-Prostate adenocarcinoma; READ- Rectum adenocarcinoma; SARC- Sarcoma; SKCM- Skin Cutaneous Melanoma; STAD- Stomach adenocarcinoma; TGCT- Testicular Germ Cell Tumors; THYM- Thymoma; THCA- Thyroid carcinoma; UCS- Uterine Carcinosarcoma; UCEC- Uterine Corpus Endometrial Carcinoma; UVM- Uveal Melanoma.



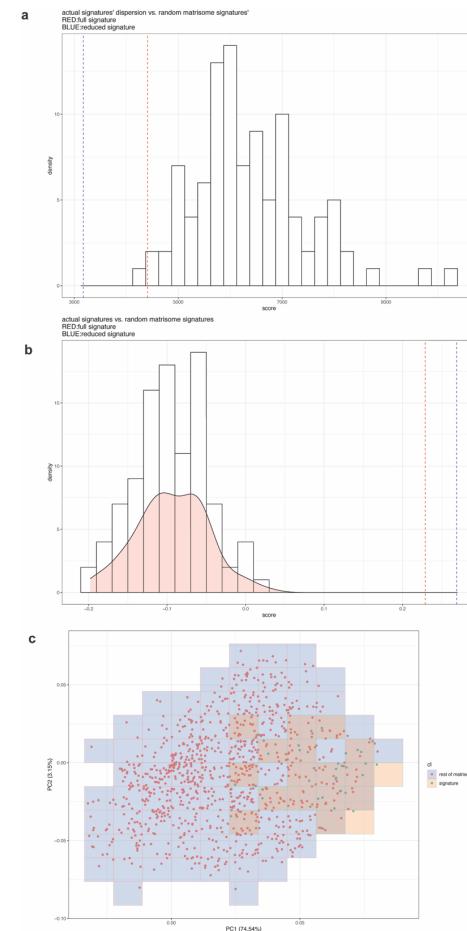






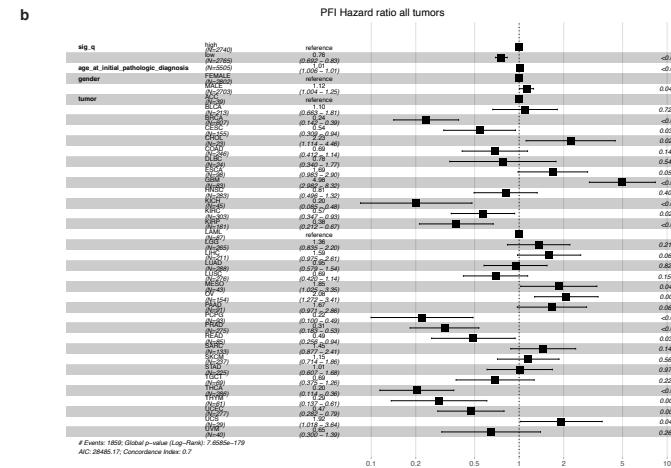
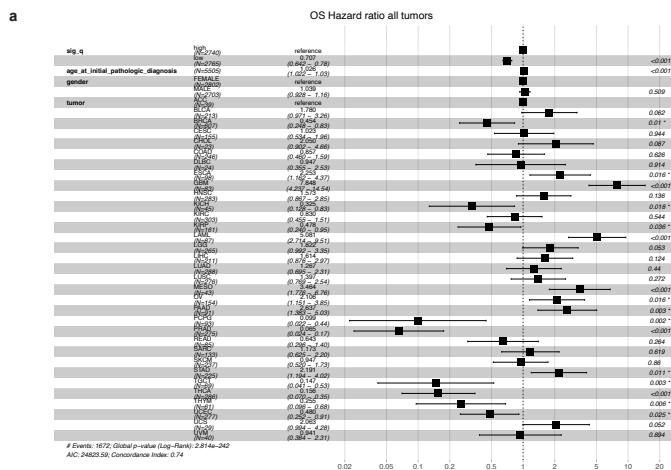


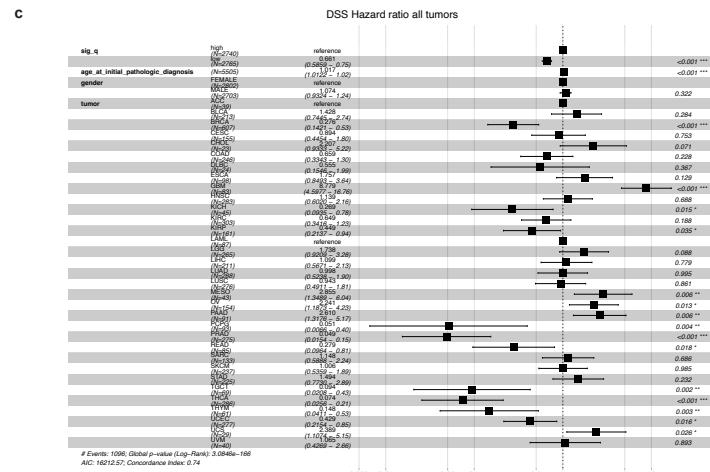
Supplementary Figure 8. Overall survival based on the high (red) or low (blue) expression of each single gene in the 'long' gene signature, for every cancer type shown in Figure 4. Indicated on each graph are the p-values. **a**- BLCA; **b**- CESC; **c**- GBM; **d**- KICH; **e**- KIRC; **f**- KIRP; **g**- MESO; **h**- LGG; **i**- STAD cancers.



Supplementary Figure 9. Signature performance comparing to the rest of matrisome. Comparison of **a**) dispersion and **b**) expression of the short/reduced signature (blue line) and long/full signature (red line) versus 100 random matrisome sets of comparable size. **c**) PCA plot with binned probability hex

superimposed that shows a separation of gene expression between the genes that make the signature and those that do not based on pan-cancer expression profiles.





Supplementary Figure 10. Cox Proportional Hazard (CoxPH) analysis for **a**) OS (overall survival), **b)** PFI (progression-free survival) and **c)** DSS (disease-specific survival) evaluating signature scores together with age, sex, and tumor type.

Supplementary Tables Legends

Table 1. Compiled proteomics datasets of NF and CAF FDMS and PDAC. (1st Tab – NFCAF data matched to PDAC data post-matrisome filtering with the long signature highlighted; 2nd-8th Tabs – Single comparisons data healthy vs cancer including all robustly detected proteins).