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Cross-species single-cell analysis of pancreatic ductal adenocarcinoma reveals antigen-presenting cancer-associated fibroblasts

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Abstract

Cancer-associated fibroblasts (CAFs) are major players in the progression and drug resistance of pancreatic ductal adenocarcinoma (PDAC). CAFs constitute a diverse cell population consisting of several recently described subtypes, although the extent of CAF heterogeneity has remained undefined. Here we employ single-cell RNA sequencing to thoroughly characterize the neoplastic and tumor microenvironment content of human and mouse PDAC tumors. We corroborate the presence of myofibroblastic CAFs (myCAFs) and inflammatory CAFs (iCAFs) and define their unique gene signatures *in vivo*. Moreover, we describe a new population of CAFs that express MHC class II and CD74, but do not express classical co-stimulatory molecules. We term this cell population “antigen-presenting CAFs” (apCAFs), and find that they activate CD4⁺ T cells in an antigen-specific fashion in a model system, confirming their putative immune-modulatory capacity. Our cross-species analysis paves the way for investigating distinct functions of CAF subtypes in PDAC immunity and progression.

Keywords

Single-cell analysis; pancreatic cancer; CAFs; MHC class II; heterogeneity

INTRODUCTION

Pancreatic ductal adenocarcinoma (PDAC) is a deadly disease that thus far has no effective treatment (1). PDAC is characterized by an abundance of non-malignant stromal cells that support the proliferation, survival and invasion of cancer cells (2). Among these stromal cells, cancer-associated fibroblasts (CAFs) play a major role in facilitating tumor growth (3). CAFs produce components of the extracellular matrix (ECM), which has been shown to provide survival and migration cues to cancer cells (4,5), and to physically interfere with drug delivery in PDAC mouse models (6-8). CAFs mediate collagen crosslinking in the extracellular space, thereby modulating tumor stiffness and facilitating cancer progression (9-11). CAFs also secrete multiple cytokines, chemokines and growth factors, which support cancer cells both directly and indirectly (3). While these CAF-derived factors serve as direct survival signals to cancer cells, they also alter the immune cell milieu by inhibiting the activity of immune-effector cells and recruiting immune-suppressive cells, allowing cancer cells to evade immune surveillance (12-18).

Given the evidence suggesting that CAFs play a tumor-supportive role, therapeutic strategies to deplete fibroblasts should be an effective strategy to target PDAC. However, the dogma that CAFs are solely tumor-promoting has been challenged in recent years by studies aiming to target stromal fibroblasts. For instance, while ablation of cells that express the myofibroblast marker alpha smooth muscle actin (α SMA) in a PDAC mouse model reduced desmoplasia, the resulting tumors were highly undifferentiated, intratumoral blood vessels were further diminished in number with hypoxic necrosis evident, and the animal survival was shortened (19). Additionally, chronic treatment with a Smoothed Inhibitor or neoplastic cell deletion of Sonic Hedgehog 1, a major mediator of desmoplasia, in a PDAC

mouse model, resulted in a similar phenotype (20,21). These studies suggest that some CAFs function to restrain tumor growth, rather than accelerate it. The use of a Hedgehog pathway reporter allele revealed that nearly all α SMA-expressing fibroblasts are hedgehog-responsive, linking myofibroblasts with the tumor-restraining Hedgehog pathway (20). Further supporting this notion, a clinical trial that combined chemotherapy with IPI-926, a small molecule inhibitor of the Hedgehog pathway, failed to show benefit and was aborted due to a shortened patient overall survival (22,23) (). This suggests that the Hedgehog-responsive fibroblasts attenuate tumor progression and the pathophysiology of PDAC *in vivo*.

One way to reconcile these contrasting observations is to abandon the original notion of CAFs as a uniform population of cells in favor of a new model, where the tumor microenvironment comprises a heterogeneous population of CAFs with different functions within PDAC tumors. In support of this idea, we previously demonstrated the coexistence of two distinct subtypes of CAFs in PDAC, CAFs expressing high levels of α SMA, which we therefore named “myofibroblastic CAFs” (myCAF), and CAFs expressing low levels of α SMA but high levels of cytokines and chemokines, which we named “inflammatory CAFs” (iCAF) (16). These two CAF subtypes were found in disparate locations relative to the cancer cells: whereas myCAF were primarily adjacent to cancer cells, iCAF were located in the desmoplastic areas of the tumor, farther away from the cancer cells (16). While our results demonstrate the existence of more than one CAF population in the PDAC microenvironment, the full complement of CAF populations remains unclear. To address this question, we sought to investigate the heterogeneity of CAFs in PDAC at single-cell resolution.

Here, we applied single-cell RNA sequencing to PDAC tumor tissue from six human patients, adjacent normal pancreas tissue from two of these patients, and PDAC tumors from four *Kras⁺/LSL-G12D*; *Trp53⁺/LSL-R172H*; *Pdx1-Cre* (KPC) mice. This method identified various subpopulations known to be present in PDAC tumors, including ductal epithelial cells, a variety of myeloid and lymphoid cells, as well as different subsets of fibroblasts. We further confirmed the existence of distinct myCAF and iCAF subpopulations and defined gene signatures that characterize these populations *in vivo*. Interestingly, we also identified a new CAF subtype that expresses MHC class II-related genes and induces T cell receptor (TCR) ligation in CD4⁺ T cells in an antigen-dependent manner. We therefore named these cells antigen-presenting CAFs (apCAF). We demonstrated that apCAF can convert into myofibroblasts upon suitable culture conditions, suggesting that pancreatic CAF subpopulations represent dynamic and interconvertible states.

RESULTS

Single-cell analysis uncovers the complexity of human PDAC

To comprehensively catalog the populations of cells that are present in human PDAC, we undertook a single-cell RNA-sequencing approach to transcriptionally characterize large number of cells from primary tumors. Six tumors from untreated PDAC patients and adjacent-normal pancreas tissues from two of these patients (Supplementary Table S1) were enzymatically digested to generate single-cell suspensions (Supplementary Table S2).

Fluorescence-activated cell sorting (FACS) was used to isolate viable cells via DAPI staining, and to enrich for fibroblasts by negative selection of non-fibroblast populations (Fig. 1A). Single cells from each sample were captured and sequenced using a droplet-based approach (24). To increase our analytic power, data from the viable cells fraction of all tumor and adjacent-normal samples were combined into a single set for a total of 21,200 cells (Supplementary Fig. S1A-D). Highly variable genes were identified from the combined dataset, and these were used to embed the dataset in two dimensions using t-Distributed Stochastic Neighbor Embedding (t-SNE). Density-based clustering (25) was used to identify 15 distinct clusters, with an average of 5,246 transcripts and 1,576 genes per cluster (Fig. 1B; Supplementary Fig. S1E and S1F; Supplementary Table S3). Signature genes within each cluster were cross referenced with known markers of cell populations from the literature to identify the different cell types that are represented by the clusters (Fig. 1C; Supplementary Table S4).

Within the viable cell fraction, the majority of cells in our analysis (89%) were classified as immune cells, including various cell types of the myeloid and lymphoid lineages (Fig. 1B; Supplementary Table S4). This bias towards immune cells in our cell suspension suggests that immune cells are readily detached from PDAC tissues. In contrast, fibroblasts comprised only 1.75% of the cells sorted, reflecting the challenge in releasing this population in a viable state from the tumor (Fig. 1B, cluster 7). We also detected the glandular components of the pancreas – acinar cells (Fig. 1B, cluster 6) and ductal cells, for which three distinct clusters were identified (Fig. 1B; Supplementary Table S3, clusters 2, 8 and 15). The profiles of cell clusters seen in each specimen were heterogeneous (Supplementary Fig. S1G and S1H), however, as a group, tumor and adjacent-normal tissues both contributed to all cell clusters (Supplementary Fig. S1I and S1J). Notably, the fibroblast cluster was derived mostly from tumor samples, in line with the rich fibrosis that is a hallmark of PDAC (Supplementary Fig. S1J, cluster 7).

Ductal cell subpopulations are present in human PDAC

Recently, several studies have defined distinct subtypes of PDAC tumors based on bulk transcriptome analyses (26-28). To better characterize the ductal cell populations in PDAC tumors, we isolated cells from the three ductal clusters and performed a separate clustering analysis to allow for subtle differences to be detected. We identified four distinct sub-clusters of ductal cells (Fig. 1D), three of which were derived from both tumor and adjacent-normal samples, while one (sub-cluster 2) was derived solely from one adjacent-normal sample (Fig. 1D and E; Supplementary Fig. S1K; Supplementary Table S5). We compared marker genes of the ductal cell sub-clusters to the classical and basal-like gene signatures previously described in PDAC (26). We found genes belonging to the classical gene signature (*TFF1*, *TFF2*, *LYZ*, *VSIG2* and *CEACAM6*) expressed specifically in sub-clusters 1 and 4 (Fig. 1F; Supplementary Table S6), whereas most basal-like genes were not detected in our ductal cells (data not shown). Sub-cluster 4 also had a unique signature that distinguished it from sub-cluster 1 (Fig. 1F; Supplementary Table S6). Sub-clusters 2 was derived solely from an adjacent-normal sample, expressing genes involved in lipid metabolism and processing (e.g. *APOA1*, *FABP1* and *ADIRF*). Sub-cluster 3 expressed among others, genes encoding many secreted proteins (e.g. *SPP1*, *CLU*, *MMP7*, *CTGF*,

COL18A1) and acinar proteins (e.g. *CTRB2*, *CFTR*) (Fig. 1F; Supplementary Table S6). Inter-patient heterogeneity was detected in the ductal sub-clusters, with almost all patients represented in sub-clusters 1 and 3, but only a minority in sub-clusters 2 and 4 (Supplementary Fig. S1K). Pathway analysis comparing the three tumor-derived clusters to sub-cluster 2 (adjacent-normal derived) found known PDAC driver pathways, such as the KRAS, p53 and hypoxia pathways, enriched in all three tumor-derived clusters, supporting their tumor origin (Fig. 1G). Inflammation-related pathways such as interferon gamma ($\text{IFN}\gamma$), TNF α , IL2/STAT5 and the complement pathway were also prominent in all the tumor-derived sub-clusters, likely reflecting the inflammatory nature of PDAC (Fig. 1G).

An immune-suppressive environment is predominant in human PDAC

In order to identify immune cell subpopulations within the myeloid and lymphoid lineages, we analyzed the two major immune cell clusters detected in human PDAC as two separate datasets, excluding all other cell types. Unsupervised dimensionality reduction and clustering were generated from all the cells belonging to cluster 3 (myeloid cells) or cluster 4 (T and natural killer (NK) cells), independently. We also separated adjacent normal-derived cells from tumor-derived cells to assess the nature of the immune cell populations in PDAC.

Analysis of the myeloid cluster revealed 6 distinct sub-clusters in tumor samples, and four sub-clusters in adjacent-normal samples (Fig. 2A; Supplementary Fig. S2A and S2B; Supplementary Table S7). More than 96% of the cells in this cluster were identified as monocytes and macrophages (sub-clusters 1, 2 and 4), while a minority of the cells (<4%) were identified as dendritic cells (DCs, sub-clusters 3, 5 and 6). Sub-cluster 4 was derived entirely from tumor samples (Fig. 2B; Supplementary Fig. S2B), and was annotated as alternatively-activated macrophages due to high expression of Osteopontin (*SPP1*), *LY6E* and the macrophage scavenger receptor *MARCO* (Fig. 2C; Supplementary Table S8). Both *MARCO* and *SPP1* have been associated with a non-inflammatory, immune-suppressive phenotype of macrophage activation (29-32). Expression of neutrophil markers (*S100A8*, *S100A9* and *GOS2*) was detected in the monocyte and macrophage sub-clusters, indicating further heterogeneity within these myeloid subpopulations (Fig. 2D). Two of the DC sub-clusters (sub-clusters 3 and 6) expressed *CD1A* and *CD207* and were therefore identified as “Langerhans-like” DCs (Fig. 2C; Supplementary Table S8). Sub-cluster 5 was identified as type 1 conventional DCs due to expression of *CLEC9A*, *BATF3* and *IRF8* (cDC1, Fig. 2C; Supplementary Table S8). cDCs were previously reported to cross-present antigens to CD8⁺ T cells, and their presence is correlated with response to checkpoint inhibitors in patients (33,34). However, the tumor microenvironment has been shown to educate cDCs towards a regulatory DC phenotype with immunosuppressive functions (35,36). Accordingly, the cDCs in our dataset strongly expressed indoleamine 2,3-dioxygenase 1 (*IDO1*) (Fig. 2C), which catalyzes tryptophan depletion and kynurenine production, both of which inhibit T cell proliferation and cytotoxicity (37).

The analysis of the T & NK cell cluster resulted in 5 distinct sub-clusters (Fig. 2E; Supplementary Fig. S2C; Supplementary Tables S9-S10). CD4⁺ T cells (sub-cluster 2) and regulatory T cells (Tregs) in particular (sub-clusters 3 and 5), were derived almost

exclusively from the tumor samples (Fig. 2F; Supplementary Fig. S2D). This is in line with the previously reported accumulation of immune-suppressive CD4⁺ T cells upon mutant *Kras* activation in a PDAC mouse model (38). Tregs expressed their typical gene signature, which included immune-inhibitory molecules like *CTLA4* and *TIGIT* (Fig. 2G; Supplementary Table S10). The role of Tregs in inhibiting immune responses in cancer has long been established (39,40), and mechanisms of Treg infiltration have been described in PDAC as well (41-43). Our data support the accumulation of Tregs during tumorigenesis. The CD8⁺ T cell population (sub-cluster 1) was characterized by low expression of activation markers for cytotoxicity such as Granzyme B (*GZMB*), Perforin (*PRFI*) and Interferon- γ (IFN γ , *IFNG*) (Fig. 2G). However, we could detect higher expression of *IFNG* in a subset of CD8 T cells that was exclusively derived from tumor samples, compared to lower expression in the subset of cells that was shared between tumor and adjacent-normal pancreas (Fig. 2H, upper sub-cluster 1). Concomitant with the expression of *IFNG*, these cells also expressed exhaustion markers such as *LAG3* and *EOMES*, suggesting that tumor-derived T cells had become exhausted after an initial activation phase. In contrast to CD8⁺ T cells, most of the NK cells (sub-cluster 4, marked by *NKG7* expression) remained activated and strongly expressed *GZMB*, *PRFI* and *IFNG* (Fig. 2G and H). Within the NK cell sub-cluster, we detected a group of T cells that share properties with NK cells, and are termed “NKT cells” (Fig. 2H, lower sub-cluster 4, asterisk). Cells in this subset expressed T cell-specific markers such as *CD3D* and *CD8A*, in contrast to NK cells which did not (Fig. 2H, upper sub-cluster 4). Altogether, our single-cell analysis of the immune cells present in PDAC tumors depicts a strong immune-suppressive microenvironment, consisting of several cell types known to mediate T cell inactivation in PDAC.

Distinct subtypes of cancer-associated fibroblasts are detected in human PDAC

With the goal of unraveling the full spectrum of CAF heterogeneity in PDAC, we next sought to use our single-cell analysis of human PDAC to corroborate our previous finding of myCAF and iCAF subpopulations in the PDAC microenvironment (16). To enrich for fibroblasts, antibodies directed against CD45, CD31 and EpCAM were used to deplete immune, endothelial and epithelial cells, respectively (Fig. 1A). Using this approach, we were able to isolate a fibroblast-enriched fraction from sample hT137 (hT137 FE). These cells were combined with the fibroblasts digitally extracted from the viable cell fraction of all other tumors, and all of these cells were analyzed together (Supplementary Table S11). A total of 962 fibroblasts were analyzed, which formed two distinct sub-clusters with unique gene signatures upon t-SNE analysis (Fig. 3A and B; Supplementary Table S12). Common fibroblast markers such as collagen type I alpha 1 chain (*COL1A1*), fibroblast activation protein alpha (*FAP*) and the mesenchymal cell marker vimentin (*VIM*) were expressed in both CAF subpopulations, confirming their fibroblast identity (Fig. 3C). Furthermore, we identified other common CAF markers that were expressed in both sub-clusters but have not been widely used as CAF markers, such as podoplanin (*PDPN*) and decorin (*DCN*) (Fig. 3C). *PDPN* has been shown to be expressed in a specific subtype of CAFs in colorectal cancer patients (44), and high *PDPN* expression in stromal fibroblasts was correlated with poorer prognosis in pancreatic cancer patients (45). *DCN* has been shown to be produced by fibroblasts in non-malignant diseases (46).

In accordance with our previous iCAF and myCAF characterization (16), sub-cluster 1 had enriched expression of Interleukin 6 (*IL6*), Interleukin 8 (*IL8*) and chemokines such as *CXCL1*, *CXCL2*, *CCL2*, and *CXCL12*, and was therefore identified as iCAFs (Fig. 3D, orange; Supplementary Table S13). Sub-cluster 2 was identified as myCAFs because it expressed high levels of α SMA (*ACTA2*) (Fig. 3E, green; Supplementary Table S13). The majority of the cells in both tumor-derived and adjacent-normal-derived samples were classified as myCAFs (Supplementary Fig. S2E and S2F; Supplementary Table S12). Although Platelet Derived Growth Factor Receptor Alpha (*PDGFRA*) is commonly used as a CAF marker in different settings, we found that it is predominantly expressed in iCAFs (Fig. 3D). Our analysis enabled the identification of new marker genes for each CAF subtype. Strong expression of complement factor D (*CFD*) and matrix proteins such as lamin A/C (*LMNA*) and dermatopontin (*DPT*) marked iCAFs (Fig. 3B and D; Supplementary Table S13). In contrast, myCAF markers included the contractile proteins transgelin (*TAGLN*), the myosin light chain 9 (*MYL9*), tropomyosins 1 and 2 (*TPM1*, *TPM2*), the ECM modulators matrix metalloproteinase 11 (*MMP11*) and periostin (*POSTN*), and the homeobox transcription factor *HOPX* (Fig. 3B and E; Supplementary Table S13). Notably, specific to iCAFs was expression of the hyaluronan synthases (*HAS1*, *HAS2*), the enzymes responsible for the synthesis of hyaluronan, a major component of the ECM identified as a significant barrier to treatment of PDAC (7,47) (Fig. 3D; Supplementary Table S13). In addition, iCAFs differentially expressed *AGTR1*, encoding angiotensin II receptor type 1 (AT1) (Fig. 3D), which is a subject for targeted inhibition in ongoing clinical trials in PDAC patients (48) (,). Using Gene Set Enrichment Analysis (GSEA), we identified pathways enriched among the differentially expressed genes in myCAFs and iCAFs. Smooth muscle contraction, focal adhesion, ECM organization and collagen formation were significantly upregulated in myCAFs (Supplementary Fig. S3A, Supplementary Table S14), while inflammatory pathways such as IFN γ response, TNF/NF- κ B, IL2/STAT5, IL6/JAK/STAT3, and the Complement pathway were upregulated in iCAFs (Supplementary Fig. S3B, Supplementary Table S14). These results are in concordance with pathways that we previously identified to be differentially expressed in bulk and single-cell RNA sequencing of mouse CAF subsets *in vitro* and *in vivo* (16,49).

We have recently determined that IL-1/JAK-STAT3 and TGF β /SMAD2/3 are two opposing pathways that induce either iCAF or myCAF formation, respectively (49). To confirm these pathways are active in our two CAF subpopulations, and to identify novel regulatory proteins that are differentially activated between human iCAFs and myCAFs, we applied the Virtual InfERENCE of Protein-activity by Enriched Regulon analysis (VIPER) algorithm (50). This algorithm uses the expression of the target genes regulated by a given protein (referred to as a regulon) as a reporter for that protein's activity. We first used the Algorithm for the Reconstruction of Accurate Cellular Networks (ARACNe) (51) to infer the regulons associated with transcription factors and signaling molecules in iCAFs and myCAFs. We then applied VIPER to identify the differentially activated regulators between the two CAF subtypes. In line with our recent observation on the determinants of iCAF and myCAF phenotypes (49), we found IL1R1 and STAT3 to be differentially activated in iCAFs, while TGF β 1 and SMAD2 were activated in myCAFs (Fig. 3F and G; Supplementary Tables S15-S16). Surprisingly, among the top differentially activated proteins in iCAFs compared to

myCAFs were the TGF β receptors TGFBR2 and TGFBR3 (Fig. 3H; Supplementary Table S15). The presence of active TGF β receptors in iCAFs, which do not show an activated TGF β program, may indicate a negative feedback loop arising from the absence of TGF β signaling in these cells. As expected, chemokine and cytokine networks (e.g. IL6, CCL2) were active in iCAFs, concomitant with activation of the NF- κ B pathway, which is known to regulate many inflammatory cytokines (Fig. 3F and G; Supplementary Tables S15-S16). Other transcription factors (EBF2, XBP1) and receptors (CD74, FCGRT) known to regulate immune response were among the top 10 most-active regulators in iCAFs, supporting the notion that the iCAF cluster contains immune-modulating cells (Fig. 3H and I). In addition, the hypoxia regulator HIF1 α and the redox regulators Nrf2 (NFE2L2) and superoxide dismutase 2 (SOD2) were active in iCAFs, suggesting a role for iCAFs in oxidative stress relief (Fig. 3F and G; Supplementary Tables S15-S16). Lastly, the angiotensin receptor AGTR1 is also active in the iCAF compartment (Supplementary Tables S16). In contrast, transcription factors known to promote a mesenchymal cell state (e.g. TWIST1, ZEB1, SNAI1 and SOX4) were active in myCAFs (Fig. 3F and G; Supplementary Table S15). These are known target genes of the TGF β pathway, consistent with our detection of TGF β activity in these cells. Additionally, non-canonical Wnt signaling molecules (WNT2, WNT5A), which are implicated in myocyte differentiation and fibrosis (52,53), were differentially active in myCAFs (Fig. 3F-I; Supplementary Tables S15-S16). Our protein activity analysis identifies new regulators of human CAFs and provides another level of divergence between the two CAF subpopulations. Altogether, our results lend further support to the existence of two functionally distinct CAF populations in human PDAC tumors.

Single-cell analysis of KPC tumors recapitulates human PDAC

While our results in human PDAC specimens confirmed the presence of iCAFs and myCAFs, this analysis was restricted to a relatively modest number of fibroblasts. To allow deeper CAF characterization, we extended our investigation to the KPC mouse model of PDAC (54). Pancreatic tumors from four KPC mice were dissociated into single cells. From each tumor we isolated two fractions of cells by FACS: (1) a viable cell population, and (2) a fibroblast-enriched population (Fig. 1A). Sorted cells were subjected to the same droplet-based protocol for single-cell capture and library preparation. The sequencing data from the viable cell populations isolated from the four KPC tumors were merged into one dataset containing a total of 11,260 viable cells, with a median of 5,989 unique transcripts and 1,916 unique genes per cell (Fig. 4A; Supplementary Fig. S4A-S4D; Supplementary Table S17). Clustering analysis of this dataset resulted in 12 clusters, with a median of 6,720 transcripts and 2,048 genes per cluster (Fig. 4A and B; Supplementary Fig. S4E-S4F; Supplementary Table S17). Cell type determination was performed using marker genes curated from the literature (Fig. 4A and B; Supplementary Table S18). Similar to human PDAC, KPC tumors contained a preponderance (~87%) of myeloid cells, consisting of mostly macrophages and neutrophils, with a small subset of DCs (Fig. 4A and B). However, mouse PDAC was distinct in its substantially lower fraction of B and T lymphocytes, in agreement with reports showing exclusion of T cells from pancreatic tumors in mouse models (17,55). The fraction of fibroblasts in the KPC tumors was similar to that of human PDAC samples (2% of all cells). With the exception of the “epithelial-to-mesenchymal transition (EMT)-like cells”

(cluster 12) that came from a single KPC tumor, all cell types were represented in all four KPC tumors (Supplementary Fig. S4G).

Analysis of fibroblasts in KPC tumors reveals a novel CAF subtype with antigen presentation features

To discern fibroblast heterogeneity, we next analyzed the fibroblast-enriched fraction isolated from each of the KPC tumors. We combined the sequencing data from the fibroblast-enriched populations isolated from the four KPC tumors into one dataset consisting of 8,443 cells and analyzed them together. The fibroblast-enriched analysis resulted in 10 cell clusters, containing mostly EpCAM-negative ductal cells and fibroblasts (Fig. 4C; Supplementary Fig. S4H; Supplementary Table S19). Fibroblasts comprised half of the cells detected, and segregated into two main clusters. An additional small cluster of fibroblasts was identified as lipofibroblasts, a lineage of lipid-droplet containing fibroblasts, co-expressing lipid metabolism genes such as fatty acid binding protein 4 (*Fabp4*), and carbonic anhydrase 3 (*Car3*) (Fig. 4C, cluster 7) (Supplementary Table S20) (56). To further characterize the fibroblast populations, we separately analyzed the cells from the two main fibroblast clusters (clusters 5 and 6, Fig. 4C), and plotted these cells on a t-SNE plot (Fig. 4D). The 4,012 fibroblasts formed three sub-clusters, each with distinct gene signatures (Fig. 4D-E; Supplementary Fig. S4I; Supplementary Table S21). Sub-cluster 1 and sub-cluster 3 expressed marker genes that were very similar to the human iCAF and myCAF signatures, respectively (Fig. 4E; Supplementary Table S22). The iCAF sub-cluster (sub-cluster 1) was rich in the lectin *Clec3b*, as well as in chemokines and other inflammatory mediators such as *Il6*, *Cxcl1* and *Ly6c1* (Fig. 4E and F; Supplementary Table S22). Like human iCAFs, mouse iCAFs expressed higher level of the hyaluronan synthase *Has1* and specific collagens (e.g. *Col14a1*), suggesting that iCAFs have specific functions in ECM deposition (Fig. 4F). The myCAF sub-cluster (sub-cluster 3) showed high expression of the smooth muscle genes *Acta2* and *Tagln*, as well as *Igfbp3*, *Thy1*, *Col12a1* and *Thbs2* (Fig. 4E and F; Supplementary Table S22). A cross-species comparison between marker genes of the different subtypes demonstrated concordance between human iCAFs and mouse iCAFs, as well as between human myCAFs and mouse myCAFs (Supplementary Fig. S4J and S4K). Sub-cluster 2 was distinct from both iCAFs and myCAFs and expressed genes belonging to the Major Histocompatibility Complex (MHC) class II family, which are usually restricted to antigen presenting cells (APCs) of the immune system (Fig. 4E and G; Supplementary Table S22). Examples of these genes are histocompatibility 2, class II antigen A, alpha (*H2-Aa*) and beta 1 (*H2-Ab1*), encoding the alpha and beta chains of MHC class II in C57BL/6 mice, and *Cd74*, encoding the invariant chain. We therefore named these cells “antigen presenting CAFs” (apCAFs). In addition to MHC class II-related genes, apCAFs expressed other unique markers such as Serum Amyloid A3 (*Saa3*), that was implicated as a pro-tumorigenic factor in pancreatic CAFs (57) and Secretory Leukocyte Peptidase Inhibitor (*Sipi*), which was previously identified as a pro-inflammatory gene in dysplastic skin fibroblasts (Fig. 4E and G) (14). apCAFs also expressed pan-fibroblast markers such as *Col1a1*, *Col1a2*, *Dcn* and *Pdgn* at comparable levels to iCAFs and myCAFs, confirming that they are genuine fibroblasts (Fig. 4G). GSEA comparing all three CAF subtypes demonstrated upregulation of inflammatory pathways in mouse iCAFs (e.g. JAK/STAT signaling, cytokine interactions with their receptors and coagulation) (Supplementary Fig.

S5A, Supplementary Table S23). The pathways specifically upregulated in mouse myCAFs were EMT, myogenesis, ECM receptor interaction and focal adhesion (Supplementary Fig. S5B, Supplementary Table S23). The pathways up-regulated in iCAFs and myCAFs were similar to those found up-regulated in human iCAFs and myCAFs, respectively, by GSEA analysis, and to what we have previously showed *in vitro* and *in vivo* (16,49). Many pathways were uniquely upregulated in the newly defined apCAF subtype, including antigen presentation and processing, fatty acid metabolism, MYC targets and MTORC1 signaling (Supplementary Fig. S5C, Supplementary Table S23).

To detect master regulators that are active in these three murine CAF subpopulations, we performed protein activity analysis using the ARACNe and VIPER algorithms. Included amongst the most highly activated proteins in apCAFs were the MHCII-related genes *H2-Ab1* and *Cd74* (Fig. 4H, Supplementary Table S24). In addition, other regulators of immune activity were found up-regulated in apCAFs. For example, *Bcam* (CD239) and *F11r* (CD321), members of the immunoglobulin superfamily, and interferon regulatory factor 5 (*Irf5*) - an Interferon-regulating protein, were all differentially active in apCAFs (Fig. 4H). Compared to iCAFs and myCAFs, apCAFs also showed higher activity for *Stat1*, which is known to mediate MHCII expression in response to IFN γ (Supplementary Table S24). This suggests that apCAFs are regulated by IFN γ signaling *in vivo*. In addition, *Nfe2l2* and most prominently *Nfe2l3* (*Nrf2* and *Nrf3*, respectively) are specifically activated in apCAFs, indicating an antioxidant response in apCAFs (Fig. 4H, Supplementary Table S24). Mouse iCAFs show activity of *IL6* and *Ly6C1*, as expected, among other inflammatory proteins (Fig. 4H, Supplementary Table S24). Mouse myCAFs show high activity of *Heyl*, *Smad2*, *Snai1* and *Twist2*, as well as myCAF characteristic proteins such as *Pdgfr β* and several myosins (Fig. 4H, Supplementary Table S24). We also identified *Cd34* and *Fap* as proteins that are differentially active in iCAFs and myCAFs, respectively (Fig. 4H, Supplementary Table S24).

MHC class II is expressed in mouse CAFs

Having identified the surface protein PDPN as a pan-CAF marker by single-cell RNA sequencing, we used immunohistochemistry (IHC) to validate PDPN expression in all CAFs in autochthonous PanIN and PDAC lesions in KPC mice, and in PDAC tumors generated from orthotopically transplanted KPC-derived organoids (Supplementary Fig. S6A) (58). To further validate the inclusivity and specificity of PDPN as a CAF marker, we used the PDPN antibody to isolate CAFs from single-cell suspensions of KPC tumors using FACS. Antibodies against CD45, CD31, EpCAM and E-Cadherin were used to eliminate other cell types, prior to sorting PDPN-positive cells (Supplementary Fig. S6B). RNA was isolated and gene expression was measured by qPCR in PDPN-positive cells compared to unsorted tumor cells. Pan-CAF markers (*Col1a1*, *Col4a1*) as well as a subset of myCAF and iCAF markers were enriched in the PDPN-positive population (Supplementary Fig. S6C and S6D). MHC class II genes (*H2-Ab1*, *Cd74*) were also detected in PDPN-positive cells, but these were expressed in substantially lower levels compared to the unsorted cells, which contained immune cells (Supplementary Fig. S6E). Other apCAF markers (e.g. *Slpi*, *Saa3*) were expressed at slightly higher levels in PDPN-positive cells (Supplementary Fig. S6E). Thus, the PDPN-positive population broadly represents CAFs in KPC tumors.

To validate the expression of MHC class II genes in CAFs, we used RNA *in situ* hybridization (ISH) to simultaneously detect *H2-Ab1* and *Colla1* transcripts in KPC tumor sections. In addition to many single positive cells, representing either APCs (*H2-Ab1*-positive) or other CAFs (*Colla1*-positive), we also detected cells that expressed both transcripts, consistent with the presence of apCAF in murine PDAC (Fig. 5A). Additionally, sequential IHC of CD74 and PDPN demonstrated a fraction of stromal cells expressing both markers, providing further confirmation for the presence of apCAF in KPC tumors (Fig. 5B).

Isolation of three CAF subtypes by flow cytometry

To isolate and characterize apCAF and other CAF subpopulations, we examined our single-cell data and identified surface proteins that were uniquely expressed in each CAF subpopulation. In addition to MHC class II (MHCII), which was unique to apCAF, we identified Ly6C as an iCAF-specific surface marker (see Fig. 4E; Supplementary Table S22). Following the exclusion of immune and epithelial cells, we gated on PDPN-positive cells. Using Ly6C and MHCII antibodies, PDPN-positive cells segregated into three populations: (1) Ly6C-positive, (2) MHCII-positive, and (3) MHCII/Ly6C-double negative, presumably corresponding to iCAF, apCAF and myCAF, respectively (Fig. 5C). Flow cytometry analysis of twenty KPC tumors showed an average of 44.4% iCAF, 45.3% myCAF, and 10.3% apCAF within the PDPN-positive population (Fig. 5D). To validate this strategy for CAF sorting, cells were accordingly isolated by FACS, RNA was prepared, and qPCR analysis was performed. All three CAF subpopulations showed high expression of the pan-fibroblast markers *Colla1*, *Col4a1*, *Dcn* and *Pdpn*, compared to CD45-positive cells that were sorted concurrently (Supplementary Fig. S6F). MHCII-positive CAFs were unique in their high expression of *Cd74* and *H2-Ab1*, as well as the apCAF markers *Sipi* and *Saa3* (Fig. 5E). Ly6C-positive cells showed high relative expression of the iCAF markers *Il6*, *Cxcl12* and *Pi16* (Fig. 5F). Finally, cells that were negative for both MHCII and Ly6C, showed significantly higher relative expression of the myCAF markers *Acta2* and *Tgfb1*, suggesting an enrichment of myCAF in this population (Fig. 5G).

Although apCAF were identified as a subtype of fibroblasts in KPC tumors, they differed from myCAF and iCAF in expression of genes that are also found in the ductal cancer cell clusters, such as Mesothelin (*Msln*), Clusterin (*Clu*) and Keratin 19 (*Krt19*) (Fig. 4E; Supplementary Table S22), raising the possibility that apCAF arise from cancer cells that have undergone EMT. To test this, we isolated the different CAF subtypes by FACS, prepared DNA from the cells and performed PCR genotyping. While EpCAM-positive cancer cells sorted from the tumors harbored both the mutant and wild-type alleles of *Kras*^{G12D} and the mutant allele of *p53*^{R172H}, none of the CAF subpopulations harbored mutant *Kras* or *Trp53* alleles, confirming their mesenchymal origin (Supplementary Fig. S6G).

apCAF are detectable in human PDAC

Following the identification of apCAF in mouse PDAC tumors, we looked for evidence of these cells in our human single-cell data. We detected subsets of human CAFs expressing modest levels of the human leukocyte antigen (HLA) genes that encode MHC class II chains

(*HLA-DRA*, *HLA-DPA1* and *HLA-DQA1*) (Fig. 6A). These subsets also expressed *CD74*, which encodes the invariant chain, and *SLPI*, which is one of the prominent apCAF markers in mouse PDAC tumors (Fig. 6A). We found that 20.9% of the human CAFs co-expressed *HLA-DRA* and *CD74*, implying a capacity to generate a functional MHC class II structure in some CAFs (Fig. 6B and C). These cells were predominantly admixed with the iCAF population (Fig. 6A and B), and did not form a separate cluster. Accordingly, the VIPER regulator analysis that we performed on human CAFs showed that master regulators belonging to the antigen presentation machinery such as *CD74* and *XBP1* - a transcription factor involved in the ER stress response that is known to regulate MHC class II genes (59,60), were differentially active in iCAFs (Fig. 3H and I), supporting the presence of apCAF traits in human PDAC. To confirm the existence of apCAFs in human PDAC, we co-stained human PDAC sections for the fibroblast marker *COL1A1* and the invariant chain *CD74* by RNA ISH, and identified cells that expressed both transcripts (Supplementary Fig. S7A). IHC staining of human PDAC sections for the fibroblast marker *PDGFR β* and the MHC class II molecules *HLA-DR/DP/DQ* further demonstrated the presence of apCAFs in human PDAC (Supplementary Fig. S7B). Lastly, we performed imaging mass cytometry (IMC), combining multiple antibodies, and detected several examples of cells that co-expressed Collagen I, *CD74* and *HLA-DR*, but were devoid of *CD45* or epithelial markers, corroborating their apCAF identity (Fig. 6D).

apCAFs show dynamic features

We previously demonstrated that *in vitro*, myCAFs and iCAFs represent reversible cell states: iCAFs that are maintained in Matrigel with PDAC organoid-conditioned medium will convert to myfibroblasts if cultured in two-dimensional monolayer (2D) (16). We therefore sought to test whether apCAFs also have this inherent plasticity and can change into a different cell state given the appropriate culture conditions. To that end, we sorted apCAFs by FACS from KPC tumors and cultured them in 2D. We compared gene expression between freshly isolated apCAFs and 2D-cultured apCAFs, and whereas CAFs in both conditions expressed comparable levels of the pan-CAF marker *Pdpn* (Supplementary Fig. S8A), tumor-derived apCAFs lost their MHCII expression, along with other apCAF markers, following 2D culture (Fig. 7A, Supplementary Fig. S8B). Rather, sorted apCAFs cultured in 2D upregulated myCAF markers, similar to myCAFs isolated from KPC tumors and cultured in 2D (Fig. 7A, Supplementary Fig. S8B). Our results suggest that apCAFs are a dynamic fibroblast population and that they may require environmental cues to be maintained as a subpopulation.

apCAFs can present antigens to T cells

The presence of MHC class II molecules on apCAFs suggests that this CAF subtype interacts with $CD4^+$ T cells. To test this, we orthotopically transplanted KPC tumor organoids into the pancreas of MHCII-EGFP knock-in mice (Fig. 7B) (61), and allowed PDAC tumors to form. We confirmed that pancreatic tumors that develop in the orthotopic model contain the three CAF subtypes, similarly to the KPC model (Supplementary Fig. S8C). Next, we sorted by FACS the MHCII-expressing, GFP-positive CAFs as well as GFP-positive professional APCs from the transplanted tumors (Supplementary Fig. S8D). The presence of the GFP reporter allowed us to isolate MHCII-expressing cells without using an

MHCII antibody, thus ensuring the MHCII molecules remained intact. To test whether our sorted CAFs were capable of antigen presentation, we used the Ovalbumin-specific TCR transgenic OTII mouse model (62), in which T cells are activated when presented with an OTII-specific Ovalbumin peptide (OVA 323-339) by an APC. We incubated the sorted CAFs and professional APCs with the OVA peptide, and the OVA-loaded APCs and CAFs were co-cultured with OTII-derived CD4⁺ T cells for 17 hours (Fig. 7B). Professional APCs from the MHCII-EGFP orthotopic model induced early activation markers of TCR ligation (CD25 and CD69) in co-cultured T cells, in an OVA-specific manner (Fig. 7C and D). Whereas myCAFs and iCAFs did not induce a measurable T cell activation when loaded with OVA, apCAFs isolated from the same orthotopic tumors demonstrated the capacity to induce CD25 and CD69 in co-cultured T cells in an OVA-specific manner (Fig. 7C and D).

Professional APCs express costimulatory molecules on their cell surface, which provide the second signal necessary to induce CD4⁺ T cell clonal proliferation following TCR ligation (63). Therefore, we examined whether, in addition to MHC class II molecules, apCAFs also expressed genes encoding the costimulatory molecules CD80, CD86 and CD40. However, all CAF subtypes expressed low levels of the costimulatory genes compared to CD45-positive cells, with no differential expression for apCAFs over the other CAF subtypes (Fig. 7E). This suggests that apCAFs in PDAC play a different role compared to professional APCs *in vivo*.

DISCUSSION

In this study, we have used a droplet-based single-cell transcriptomics strategy to profile pancreatic tumors from human patients and KPC mice. We also employed a negative depletion strategy upstream of transcriptome profiling to enrich for fibroblasts, enabling a more comprehensive analysis of heterogeneity within this population. Consistent with previous publications (64,65), we identified numerous similarities between human PDAC and the tumors derived from the KPC mouse model, such as the predominance of macrophages over dendritic cells. Yet this cross-species comparison also identified differences between human PDAC and the mouse model that should be considered, such as differences in lymphocyte infiltration.

Previous studies have used single-cell transcriptomics to detail the composition of the normal human pancreas, focusing mostly on the endocrine lineages within the pancreatic islets, and the changes that occur during inflammation and aging (66-72). One of these studies focused on stellate cells, the resident fibroblasts of the pancreas, and identified two types of stellate cell activation in the normal pancreas, a standard activation and an immune activation, resembling the myCAF and iCAF classification (67). This suggests that physiological conditions other than cancer may contribute to a heterogeneous fibroblast activation in the pancreas. By detailing the subpopulations of cells present in adjacent-normal and PDAC tissues, our work complements these studies and provides new information about the cell types associated with pancreatic malignancy.

A recent study performed single-cell RNA sequencing analysis of four human intraductal papillary mucinous neoplasms (IPMNs) of different grades and of two human PDAC

samples, describing epithelial and stromal cell changes associated with carcinogenesis of the pancreas (73). While this study provides detailed description of the epithelial cells in pre-neoplastic and neoplastic conditions, the small number of stromal cells that was analyzed did not allow for a comprehensive delineation of the immune and fibroblast populations. Notably, the authors describe an abundance of myeloid cells with an immune-suppressive nature present in PDAC. Our study furthers this observation by highlighting several subpopulations of immune cells that were not detected in the previous study, such as NK cells, NKT cells, Tregs and alternatively-activated macrophages. Supporting our observation of iCAF and myCAF subpopulations, the authors of the previous study were able to identify these subpopulations in the two tested PDAC samples, albeit in different proportions than we detected. This discrepancy could be attributed to lower number of cells analyzed, to differences in digestion methods or to heterogeneity between the human tumors analyzed. Another recent preprint reported CAF subtypes in a different mouse model of PDAC, and showed similar populations of inflammatory CAFs and myofibroblastic CAFs (74). This study also detected expression of MHCII-related genes, however these were detected within the myofibroblastic CAF population, likely reflecting limited cell numbers in this study. Our work expands upon this study to show that the MHCII-expressing CAFs are a transcriptionally and functionally distinct subtype, which can be found in both mouse and human PDAC.

CAF heterogeneity has been reported in other tumor types as well. Two transcriptionally distinct CAF subtypes with differing α SMA expression were reported in colorectal cancer patients, supporting our findings in PDAC (44). A distinct CAF subtype was shown to maintain the cancer stem cell niche and was correlated with chemoresistance and poor prognosis in breast and lung cancer patients (75). Another subtype of breast cancer CAFs was shown to attract and induce Tregs (76). Moreover, a comparison between the fibroblasts of non-malignant lung tissue and lung tumor tissue showed variability in the expression of collagens and transcription factors between fibroblast subtypes (77), similarly to our observation. These examples demonstrate that functional heterogeneity among CAFs is a general feature of cancer, rather than a phenomenon specific to PDAC.

Our fibroblast analysis comprehensively evaluated the transcriptomes of the iCAF and myCAF subpopulations, which we had previously characterized (16), and provided novel marker genes for these cells (Fig. 7F). The VIPER master regulator analysis further implies that iCAFs and myCAFs take on diverse functions *in vivo*. Our study identifies the type 1 receptor for angiotensin II (AGTR1) as a marker for the iCAF population. This receptor is a leading target in active clinical investigations for patients with PDAC (,). An inhibitor of this receptor, Losartan, was shown to reduce intratumoral solid stress, leading to increased vascular perfusion and improved drug delivery (48,78). A major source of solid stress in PDAC tumors is hyaluronan (7), and the enzymes responsible for hyaluronan production are uniquely and specifically expressed in iCAFs (*HAS1* and *HAS2* in the human data, *Has1* and *Has2* in the mouse data). Our data suggest that the iCAF population, which is predicted to mediate solid stress in the tumor, would be targeted by Losartan. Therefore, in addition to the inflammatory signals we previously characterized as potential mediators of immune suppression, iCAF targeting may also be responsible for the efficacy of Losartan in treating PDAC.

Our work also uncovered a novel CAF subpopulation, apCAFs, which expresses MHC class II molecules and has the capacity to present a model antigen to CD4⁺ T cells *ex vivo* (Fig. 7F). However, apCAFs lack the costimulatory molecules needed to induce T cell proliferation. Therefore, we hypothesize that the MHC class II expressed by apCAFs acts as a decoy receptor to deactivate CD4⁺ T cells by inducing either anergy or differentiation into Tregs. In this case, apCAFs are expected to decrease the CD8⁺ to Treg ratio and curtail anti-tumor immunity. apCAFs thus might contribute to immune suppression in the PDAC microenvironment. Stromal cells of the lymph node have been shown to induce apoptosis of CD4⁺ T cells and reduce their efficiency to re-stimulate, in a mechanism involving peptide-MHCII complexes acquired from DCs (79). In another report, lymph node stromal cells induced CD4⁺ T cell population contraction, in an H2-Ab1-dependent manner (80). These examples support the premise that stromal cells have the capacity to act as non-professional APCs, in a manner that inhibits optimal T cell response.

We have previously reported on the ability of the iCAF and myCAF populations to interconvert (16). Similarly, apCAFs can differentiate into myCAFs upon culture, demonstrating that apCAFs are also a dynamic cell state. CAF plasticity can potentially be exploited to therapeutically promote the conversion of pro-tumorigenic CAFs into anti-tumorigenic ones, and to modulate CAF activity in the tumor (49). Further investigation is required in order to determine the intratumoral signals that induce apCAF formation and activation, and to define the role(s) that each CAF subtype plays in the PDAC microenvironment and tumor immunity.

METHODS

Human samples and mouse models.

Human PDAC resection specimens were obtained from the Sidney Kimmel Comprehensive Cancer Center at Johns Hopkins University and from Memorial Sloan Kettering Cancer Center. All tissue donations and experiments were reviewed and approved by the Institutional Review Board of Cold Spring Harbor Laboratory and the clinical institutions involved. Written informed consent was obtained prior to acquisition of tissue from all patients. The studies were conducted in accordance with ethical guidelines (Declaration of Helsinki). Samples were confirmed to be tumor or adjacent-normal based on pathologist assessment. KPC (*Kras⁺/LSL-G12D*; *Trp53⁺/LSL-R172H*; *Pdx1-Cre*) mice were previously described (54). MHCII-EGFP mice (MGI ID: 2387946, Symbol: H2-Ab1^{tm1Hpl}) (61) were obtained from the lab of Hidde Ploegh at Boston Children's hospital. Orthotopic transplantation of KPC-derived organoids into MHCII-EGFP mice was performed as previously described (58). B6.Cg-Tg(*TcraTcrb*)425Cbn/J (OTII) mice were purchased from Jackson laboratory (stock # 004194) (62). All animal procedures and studies were conducted in accordance with the Institutional Animal Care and Use Committee (IACUC) at Cold Spring Harbor Laboratory.

Sample preparation, staining and sorting for single cell RNA sequencing.

Tumor specimens from human patients and from KPC mice were minced and enzymatically digested in 10% FBS/DMEM supplemented with Collagenase D (Sigma #11088882001, 2.5

mg/ml), Liberase DL (Sigma #5466202001, 0.5 mg/ml) and DNase I (Sigma, D5025, 0.2 mg/ml) for 45 minutes at 37°C with agitation. Adjacent-normal specimens from human patients were minced and digested in Human Normal Organoid media (58) supplemented with Collagenase XI (Sigma C7657, 5 mg/ml), Y-27632 (STEMCELL Technologies, 10.5 µM) and DNase I (Sigma #D5025, 10 µg/ml) for 3 cycles of 8 minutes at 37°C with agitation. After each cycle, tissue pieces were let to settle down by gravity and supernatant was collected and quenched by excess advanced DMEM/F12 (#12634-010) supplemented with 1X GlutaMAX (Gibco #35050-061), 10 mM HEPES (Gibco #15630-080) and 1% of Penicillin/Streptomycin. Fresh digestion media was applied to the remaining tissue for the next digestion cycle, and cells collected from the each cycle were merged into one sample. Cell digestion of both tumor and adjacent normal samples were strained through 100 µm cell strainer and quenched with 2% FBS/PBS. The solution was spun down and cells were resuspended in ACK lysis buffer to eliminate red blood cells. After a 3 minutes incubation on ice, the ACK was quenched with 2% FBS/PBS. Cells were spun down, resuspended in PBS supplemented with 0.5% BSA and 2 mM EDTA and blocked with human FcR binding inhibitor (for human tissue, eBioscience #14-9161-73, 1:5) or with anti-mouse CD16/CD32 Fc Block (for mouse tissue, Biolegend, Clone 2.4G2, 1:50) for 15 minutes at 4°C. Staining of human tissue was performed with the following antibodies: CD45-AF647 (Biolegend, Clone H130, 1:20), CD31-AF647 (Biolegend, Clone WM59, 1:20) and EpCAM-AF647 (Biolegend, Clone 9C4, 1:20), for 30 minutes at 4°C. Staining of mouse tissue was performed with the following antibodies: CD45-AF647 (Biolegend, Clone 30-F11, 1:20), CD31-AF647 (Biolegend, Clone 390, 1:20) and EpCAM-AF647 (Biolegend, Clone G8.8, 1:20) for 30 minutes at 4°C. Prior to sorting, DAPI was added to cell suspension (Sigma #D8417, 1 µg/ml). Cells were sorted using BD FACSAria Fusion instrument and collected in 20% FBS/PBS. Following exclusion of debris, 50,000-100,000 DAPI-negative cells were collected from each sample (for 'viable cell' fraction). When enough cells were available, sorting for DAPI-, CD45-, CD31- and EpCAM-negative cells was performed (for 'fibroblast-enriched' fraction).

Single cell capture, library preparation and RNA sequencing.

Sorted cells were washed and resuspended in PBS containing 0.04% BSA. Cells were counted on Countess II automated cell counter (ThermoFisher), and up to 12,000 cells were loaded per lane on 10X Chromium microfluidic chips. Single cell capture, barcoding and library preparation were performed using the 10X Chromium™ version 2 chemistry, and according to the manufacturer's protocol (#CG00052). cDNA and libraries were checked for quality on Agilent 4200 TapeStation and quantified by KAPA qPCR before sequencing on a single lane of a HiSeq4000 (Illumina) to an average depth of 50,000 reads per cell.

Single cell data processing, quality control, and analysis.

The Cell Ranger pipeline (v1.3, 10X Genomics) was used to convert Illumina base call files to FASTQ files, align FASTQs to the hg19 reference (v1.2.0, 10X Genomics) for human samples and mm10 reference (v1.2.0, 10X Genomics) for mouse samples, and produce a digital gene-cell counts matrix. Samples were combined using the Cell Ranger aggregate function which subsamples digital counts matrices such that the number of confidently mapped transcriptomic reads are equal among all samples and creates a unified digital

counts matrix. Gene-cell matrices were filtered to remove cells with fewer than 500 transcripts and genes with fewer than 2 counts in 2 cells. The gene-cell matrices were then normalized such that the number of UMIs in each cell is equal to the median UMI count across the dataset and log transformed. Expression at 1000 highly variable genes in each dataset, selected as the genes with the highest dispersion, was used to reduce the dimensionality of the datasets to 3 dimensions using Barnes Hut approximate t-Distributed Stochastic Neighbor Embedding (BH t-SNE) (81) and cells were clustered using density-based spatial clustering of applications with noise (DBSCAN) (82) in t-SNE space (25). Cells that were not assigned cluster labels by DCSCAN were discarded from further analysis. Cluster marker genes were identified using one-vs-rest binary classification metrics. Briefly, for a given cluster, log mean expression of each gene was computed and compared to the log mean expression of that gene in cells outside the cluster. Genes with a log-fold difference in mean expression greater than 2 were used to construct receiver operator characteristic curves (ROC) and the area under the ROC (AUROC) was used to rank putative marker genes. These marker genes were used to assign cellular identities to clusters. Certain cell populations were subclustered by repeating the procedure described above. Interactive analysis was done using the CellView RShiny web application (83). The mouse RNA sequencing data are available at Gene Expression Omnibus (GEO) under the accession number GSE129455. The human RNA sequencing data have been submitted to dbGaP and the accession number is available upon request.

Key resources for single-cell analysis

1. 10X CellRanger software: version 1.3.0, md5sum: f399da7266d8d61036bd29851dcf8244, <https://support.10xgenomics.com/single-cell-gene-expression/software/downloads/1.3/>
2. 10X hg19 reference genome: version 1.2.0, md5sum: 74608d0a6fdd8c10e2918339a30c3c49, <https://support.10xgenomics.com/single-cell-gene-expression/software/downloads/1.3/>
3. 10X mm10 reference genome: version 1.2.0, md5sum: 6c8701a83c7b66ca123a6b4f149bec26, <https://support.10xgenomics.com/single-cell-gene-expression/software/downloads/1.3/>

Context-specific regulatory model and master regulator analysis of human and mouse CAFs.

Human and a mouse context-specific regulatory networks were reverse engineered by ARACNe (84) from human and mouse single cell gene expression profiles, respectively. ARACNe was run with 200 bootstrap iterations using 1824 transcription factors (genes annotated in gene ontology molecular function database, as GO:0003700, “transcription factor activity”, or as GO:0003677, “DNA binding”, and GO:0030528, “transcription regulator activity”, or as GO:00034677 and GO: 0045449, “regulation of transcription”) and 3477 signaling pathway related genes (annotated in GO biological process database as GO: 0007165 “signal transduction” and in GO cellular component database as GO:0005622, “intracellular”, or GO:0005886, “plasma membrane”). The human CAFs network has been generated from iCAFs and myCAFs cells previously identified based on gene expression

markers (iCAF signature: IL6, PDGFRA, CFD, PLA2G2A, HAS1, CXCL2, CCL2, CLU, EMP1, LMNA; myCAF signature genes: TAGLN, ACTA2, MMP11, PDGFRB, HOPX, POSTN). The mouse CAFs network has been generated from iCAFs, myCAFs and apCAFs previously identified based on gene expression markers (Supplementary Table S22). The regulatory models for human and mouse CAFs were generated from the ARACNe networks using the VIPER package (50). The most representative cells of each CAF subtype were identified in each cluster using the silhouette analysis (silhouette widths > 0.36 for human and silhouette widths > 0.3 for mouse), and used for the master regulator analysis. The master regulator analysis was performed by comparing each CAF subtype against the others using the msviper algorithm of the VIPER package.

In situ hybridization and immunohistochemistry.

Tissues were fixed in 10% normal buffered formalin for 16-24 hours. Tissues were embedded in paraffin and 5 μ m sections were cut and mounted on slides. Slides were rehydrated through histoclear and ethanol series, and antigen retrieval was performed in 10 mM citrate buffer, in a pressure cooker for 6 minutes. Tissues were blocked in 2.5% Normal Horse Serum blocking solution (Vector Laboratories #S-2012) and subjected to staining with the following antibodies: Podoplanin-Biotin (Biolegend, clone 8.1.1, 1:200) and CD74 (Biolegend, clone In1/CD74 1:200) for mouse sections, and HLA-DR,DP,DQ (Thermo Fisher Scientific, clone CR3/43, 1:50) and PDGFR β (Abcam #ab32570 1:400) for human sections. Horseradish Peroxidase (HRP)-Streptavidin (Vector Laboratories #SA-5704), ImmPRESS Alkaline Phosphatase anti-Rat IgG polymer (Vector Laboratories #MP-5444), ImmPRESS Alkaline Phosphatase anti-Mouse IgG polymer (Vector Laboratories #MP-5402) and ImmPRESS HRP anti-Rabbit IgG polymer (Vector Laboratories #MP-7401) were used as secondary antibodies. ImmPACT DAB peroxidase substrate (Vector Laboratories #SK-4105) and Vector Blue Alkaline Phosphatase substrate (Vector Laboratories #SK-5300) were used as substrates. Hematoxylin (Vector Laboratories #H-3404) and Nuclear Fast Red (Vector Laboratories #H-3403) were used as counterstains. In situ hybridization was performed using the RNAscope 2.5 HD duplex assay (ACD) according to the manufacturer's instructions. RNAscope probes that were used: Mm-H2-Ab1 (#414731) and Mm-Col1a1-C2 (#319371-C2) for mouse sections, and Hs-CD74 (#477521) and Hs-COL1A1-C2 (#401891-C2) for human sections.

Multiplexed imaging by imaging mass cytometry (IMC).

Formalin-fixed paraffin-embedded human PDAC tissues were cut into 5 μ m sections and mounted on slides. Slides were incubated for 15 minutes at 55°C in a dry oven, deparaffinized in fresh Histoclear, and rehydrated through a series of graded alcohols. Antigen retrieval was performed in a decloaking chamber (BioSB TintoRetriever) for 15 minutes at 95°C in Tris-EDTA, pH 9.2. After blocking in buffer containing 3% BSA, slides were incubated overnight at 4°C with a cocktail of metal-conjugated IMC-validated primary antibodies: CD45-89Y (clone HI30), α SMA-141Pr (clone 1A4), CD74-155Gd (clone LN2), HLA-DR-159Tb (clone LN3), EpCAM-158Gd (clone 9C4), E-Cadherin-158Gd (clone 4A2) and Collagen I-169Tm (polyclonal). The following day, slides were washed twice in DPBS and counterstained with iridium intercalator (0.25 μ M) for 5 minutes at room temperature, to visualize the DNA. After a final wash in ddH₂O, the slides were air dried for 20 minutes.

The slides were then loaded on the Fluidigm Hyperion imaging mass cytometer. Regions of interest were selected using the acquisition software and ablated by the Hyperion. The resulting images were exported as 16-bit .tiff files using the Fluidigm MCDViewer software and analyzed using the open source Histocat++ toolbox (85).

Flow cytometry and sorting of KPC CAFs.

KPC mouse tumors were digested and single cell suspensions were prepared as describe above for human tumors. Cells were resuspended in 2% FBS/PBS and blocked with anti-mouse CD16/CD32 Fc Block for 15 minutes at 4°C (Biolegend, clone 2.4G2, 1:50). The following antibodies were used in the different flow experiments (all from Biolegend at 1:200): CD45 (Clone 30-F11), CD31 (Clone 390), EpCAM (Clone G8.8), E-Cadherin (Clone DECMA-1), Podoplanin (Clone 8.1.1), CD140a (PDGFR α , Clone APA5), Ly6C (Clone HK1.4) and I-A/I-E (MHC class II, Clone M5/114.15.2). Staining with antibodies was performed for 30 minutes at 4°C. Prior to flow cytometry, DAPI was added to cell suspension (Sigma #D8417, 1 μ g/ml). 250,000 events were acquired from each sample on the BD LSR Fortessa. Cell sorting was done on the FACS Aria II (CSHL), using the same antibodies as indicated for flow. Sorted cells were collected into 10% FBS/DMEM at 4°C.

RNA preparation and qPCR.

Sorted cells were spun down and pellets were resuspended in Trizol. RNA was prepared by combining the standard Trizol/Chloroform extraction method with the PureLink RNA mini kit (Thermo Fisher Scientific #12183018A). cDNA was prepared using the TaqMan reverse transcription reagents (Thermo Fisher Scientific #N8080234), and qPCR was performed with TaqMan Universal Master Mix II without UNG (Thermo Fisher Scientific #4440047) on a QuantStudio 6 Flex Real-Time PCR system (Thermo Fisher Scientific). TaqMan probes that were used for qPCR: Cd74 (Mm00658576_m1), H2-Ab1 (Mm00439216_m1), Slpi (Mm00441530_g1), Saa3 (Mm00441203_m1), Il6 (Mm00446190_m1), Cxcl12 (Mm00445553_m1), Pi16 (Mm00470084_m1), Acta2 (Mm01546133_m1), Tgfb1 (Mm01178820_m1), Cd40 (Mm00441891_m1), Cd80 (Mm00711660_m1), Cd86 (Mm00444540_m1), Pdpn (Mm01348912_g1), Tagln (Mm00441661_g1), Myl9 (Mm01251442_m1), Col1a1 (Mm00801666_g1), Col4a1 (Mm01210125_m1), Dcn (Mm00514535_m1).

Gene Set Enrichment Analysis (GSEA).

Gene set enrichment analysis with GSEA (86) was performed between sub-clusters of human and mouse fibroblasts. The rank is based on differentially expressed genes between the sub-clusters, as computed with edgeR (87) for mouse samples and monocle (88) for human samples. The database used by GSEA is Molecular Signatures Database v6.1. Genes that were expressed in less than 10% of the cells in a given mouse sub-cluster or in less than 25% in a given human sub-cluster were filtered out of the analysis.

Genotyping of sorted CAFs.

DNA from sorted cells was prepared using QIAamp DNA micro kit (Qiagen #56304). PCR was performed using standard protocols with the following primers for Kras locus: forward

primer: 5'-GGGTAGGTGTTGGGATAGCTG-3', reverse primer: 5'-TCCGAATTCAGTGACTACAGATGTACAGAG-3'; and the following primers for p53 locus: forward primer: 5'-AGCCTGCCTAGCTTCCTCAGG-3', reverse primer: 5'-CTTGGAGACATAGCCACACTG-3'. PCR products were evaluated on ethidium bromide gel.

OTII CD4⁺ T cell enrichment and early activation assay.

Different CAF subtypes and CD45-positive APCs were isolated by FACS from tumors transplanted in MHCII-EGFP host mice. apCAFs and APCs were sorted by their GFP fluorescence. Between 13,000-25,000 sorted cells were incubated with 25 µg/ml OVA peptide 323-339 or without a peptide, in 10% FBS/DMEM for 3 hours in U-bottom 96-well plates, in a standard 37°C 5% CO₂ humid incubator. Lymphocytes were isolated from the spleen of OTII mice and were enriched for CD4⁺ T cells by negative selection using MojoSort mouse CD4 T cell isolation kit (Biolegend #480006). APC/CAF plates were washed twice, 50,000 CD4⁺ T cells were co-plated in 10% FBS/DMEM in each well, and plates were placed back in the incubator for 17 hours. Cells were then washed in 2% FBS/PBS, blocked in CD16/CD32 Fc Block (Biolegend, clone 2.4G2, 1:50) and stained with the following antibodies (all from Biolegend at 1:200): CD4 (Clone RM4-5), CD25 (Clone PC61) and CD69 (Clone H1.2F3) for 30 minutes at 4°C. DAPI (Sigma #D8417, 1 µg/ml) was added to cell suspension prior to reading on the cytometer.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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Statement of significance

Appreciating the full spectrum of fibroblast heterogeneity in pancreatic ductal adenocarcinoma is crucial to developing therapies that specifically target tumor-promoting CAFs. This work identifies MHC class II-expressing CAFs with a capacity to present antigens to CD4⁺ T cells, and potentially to modulate the immune response in pancreatic tumors.

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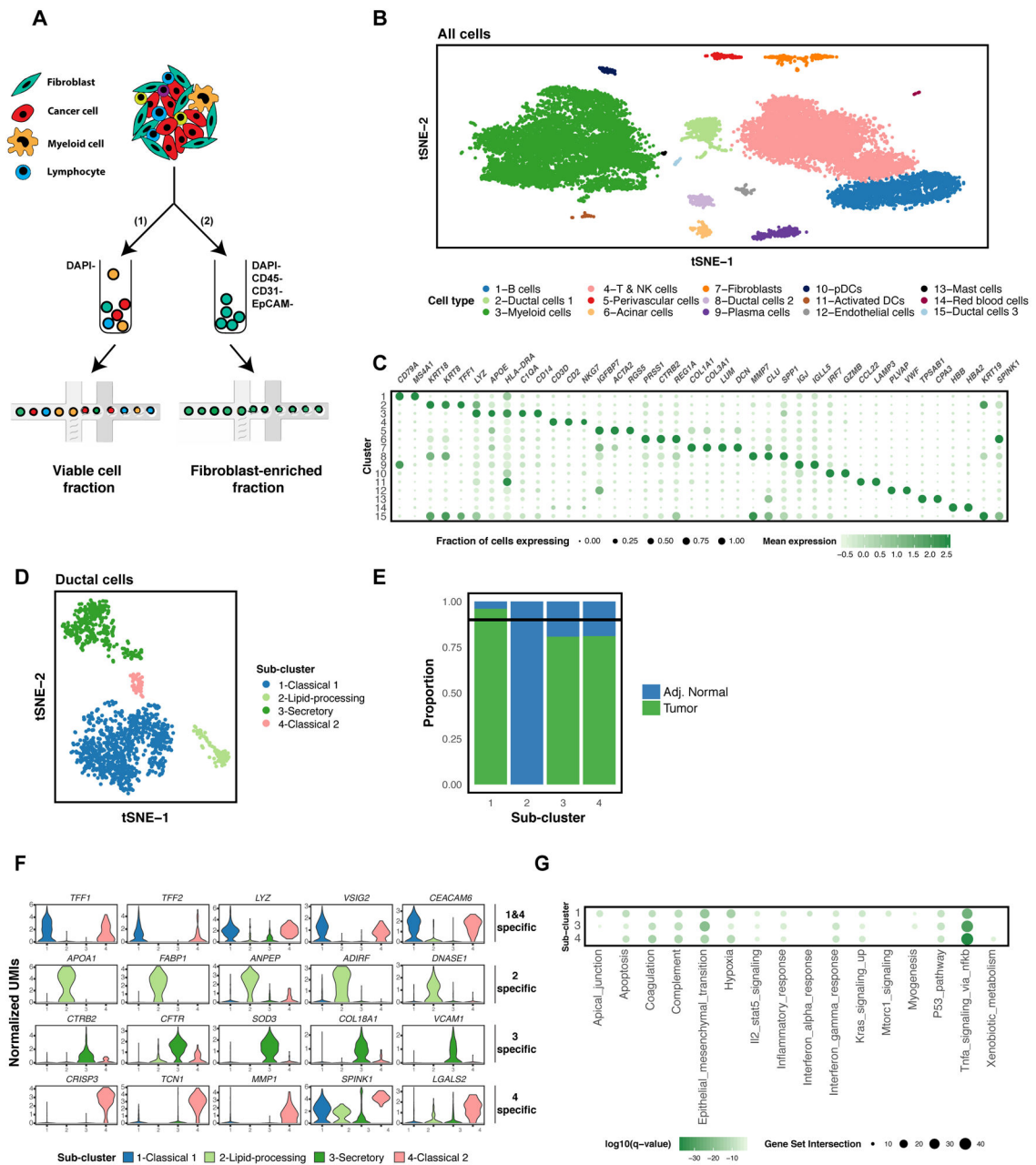


Figure 1. Single cell analysis uncovers ductal cell subpopulations in human PDAC.

A. Graphical scheme describing the workflow. Human and murine pancreatic tumors were dissociated into single cells. Two fractions of cells were collected by FACS from each sample: (1) all viable cell fraction (DAPI⁻) (2) fibroblast-enriched fraction (DAPI⁻, CD45⁻, CD31⁻, EpCAM⁻). The sorted cells from each fraction were subjected to single cell capture, barcoding and reverse transcription using the 10X Genomics platform. **B.** Unsupervised clustering of viable cells from 6 human PDAC resections and 2 adjacent-normal pancreata, represented as a t-Distributed Stochastic Neighbor Embedding (t-SNE) plot. Different cell type clusters are color-coded. **C.** Bubble plot showing selected cell type-specific markers across all clusters. Size of dots represents the fraction of cells expressing a particular marker

and intensity of color indicates level of mean expression. Legends are shown below. **D.** Re-clustering of the ductal cell types in the dataset (clusters 2, 8 and 15 from **B**), represented as a t-SNE plot. **E.** Proportion of cells from adjacent-normal pancreata and tumor resections present in each ductal cell sub-cluster. The horizontal black line represents the input contribution of adjacent-normal or tumor tissues into the dataset. **F.** Violin plot showing normalized expression of marker genes for the different ductal cell sub-clusters. **G.** Hallmark pathways enriched in the 3 tumor-derived ductal cell sub-clusters (sub-clusters 1, 3 and 4) relative to the adjacent-normal-derived ductal cell sub-cluster (sub-cluster 2). Size of dots represents intersection of upregulated genes (>2 logFC) with hallmark pathway gene sets and intensity of color indicates $\log_{10}(q\text{-value})$. Legends are shown below.

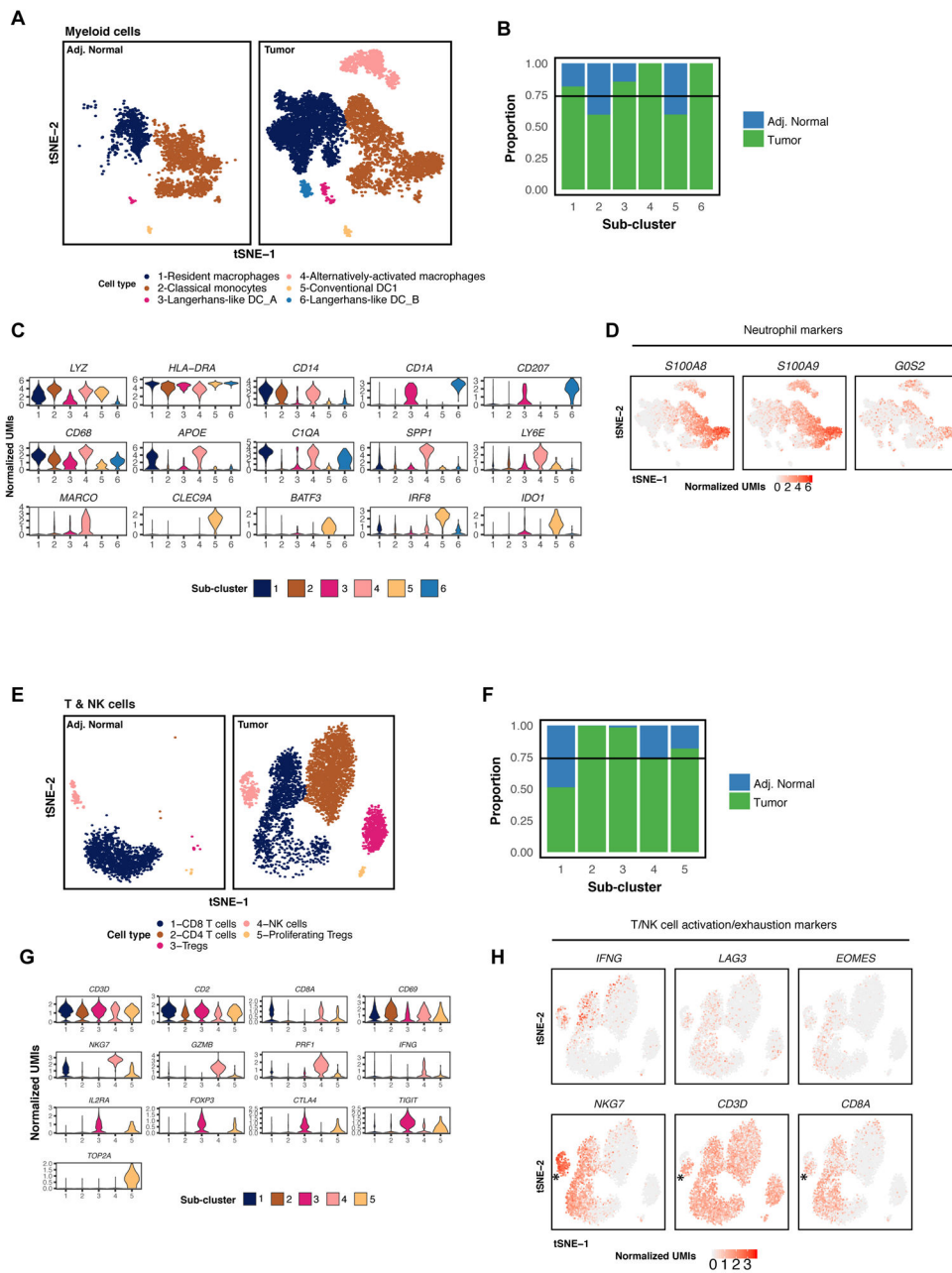


Figure 2. Immune-suppressive environment is dominating human PDAC.

A. Re-clustering of the myeloid cells in the human dataset (cluster 3 from Fig. 1B) represented as a t-SNE plot. **B.** Proportion of cells from adjacent-normal pancreata and tumor resections present in each myeloid cell sub-cluster. The horizontal black line represents the input contribution of adjacent-normal or tumor tissues into the dataset. **C.** Violin plots of selected genes, showing normalized expression in the different sub-clusters. **D.** t-SNE plots showing expression of selected neutrophil marker genes in the myeloid sub-clusters. Legend shows a color gradient of normalized expression. **E.** Re-clustering of the T & NK cells in the human dataset (cluster 4 from Fig. 1B) represented as a t-SNE plot. **F.** Proportion of cells from adjacent-normal pancreata and tumor resections present in each

lymphoid cell sub-cluster. The horizontal black line represents the input contribution of adjacent-normal or tumor tissues into the dataset. **G.** Violin plots of selected genes, showing normalized expression in the different sub-clusters. **H.** t-SNE plots showing expression of selected T/NK cell activation and exhaustion marker genes in the lymphoid sub-clusters. Legend shows a color gradient of normalized expression. Asterisk marks NKT cells within the NK cell cluster.

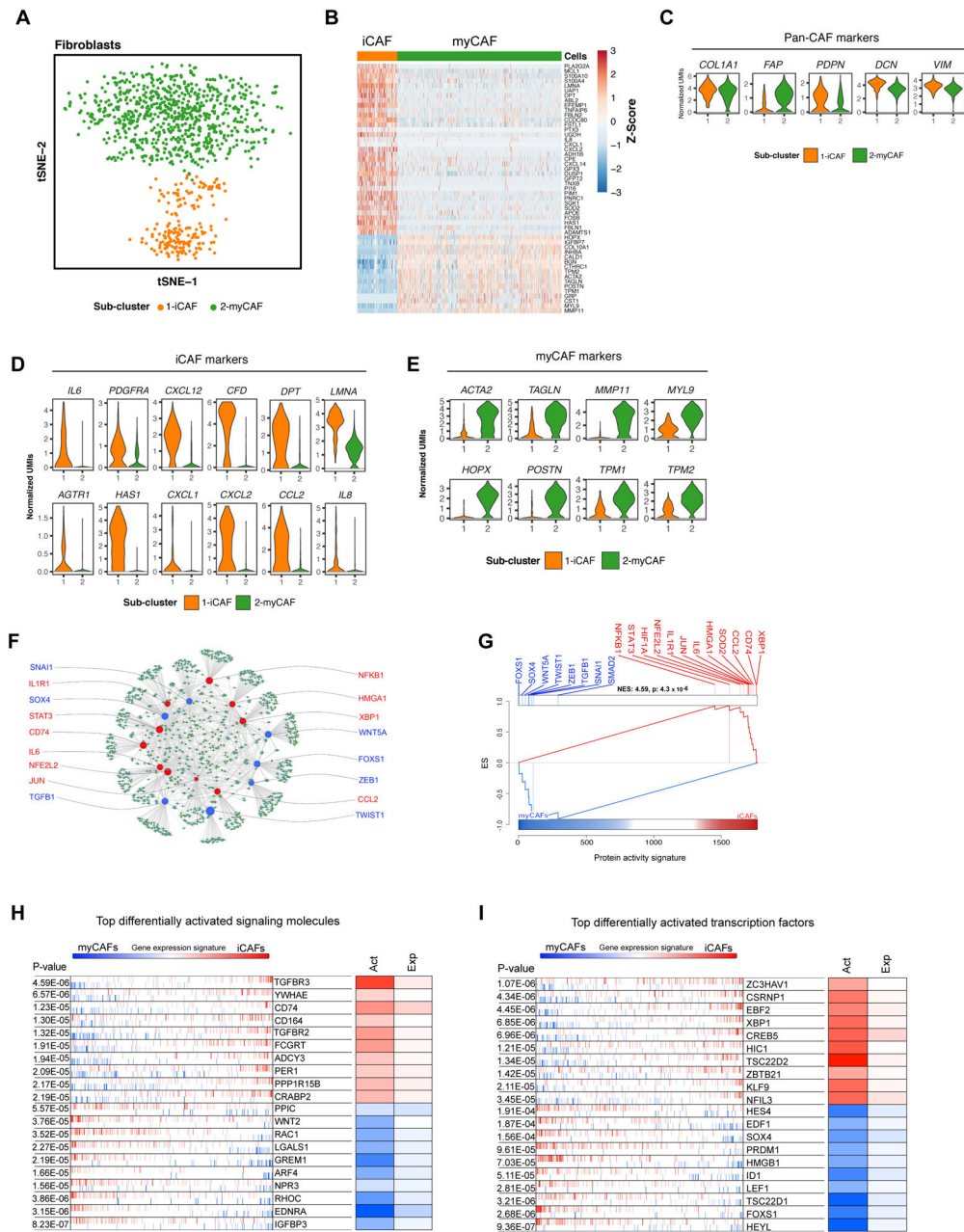


Figure 3. Distinct subtypes of cancer-associated fibroblasts are detected in human PDAC.

A. Re-clustering of cancer-associated fibroblasts in the human dataset (cluster 7 from Fig. 1B) represented as a t-SNE plot. **B.** Heatmap showing scaled normalized expression of discriminative marker genes between the two sub-clusters, with cells as columns and genes as rows. Color scheme represents Z-score distribution from -3 (blue) to 3 (dark orange). **C-E.** Violin plot of selected pan-CAF markers (**C**), iCAF markers (**D**) and myCAF markers (**E**) showing normalized expression in each of the sub-clusters. **F.** Network representation of selected differentially activated proteins between human iCAFs and myCAFs, as analyzed by VIPER. Proteins activated in iCAFs are shown in red; proteins activated in myCAFs are shown in blue. **G.** GSEA plot showing the enrichment score (ES) for a selected set of

differentially activated proteins in iCAFs (shown in red) and myCAFs (shown in blue). **H-I.** VIPER plot showing the enrichment for the top 20 differentially activated signaling molecules (**H**) or transcription factors (**I**) between iCAFs and myCAFs. The top bar represents the ranked gene expression signature between myCAFs and iCAFs. Regulatory target genes in each signaling molecule regulon or transcription factor regulon are represented by vertical lines projected along the gene expression signature. Each vertical line represents the position of a regulatory target gene in the ranked signature between myCAFs and iCAFs. The colors of the lines indicate if the regulatory targets are positively- (red) or negatively- (blue) regulated by their corresponding signaling molecule or transcription factor, according to the ARACNe/VIPER inferred regulatory model. The two-columns heatmap on the right shows the inferred differential activity (Act) and the differential gene expression (Exp) of each regulon. The column on the left shows the p-values associated with the enrichment of each regulon.

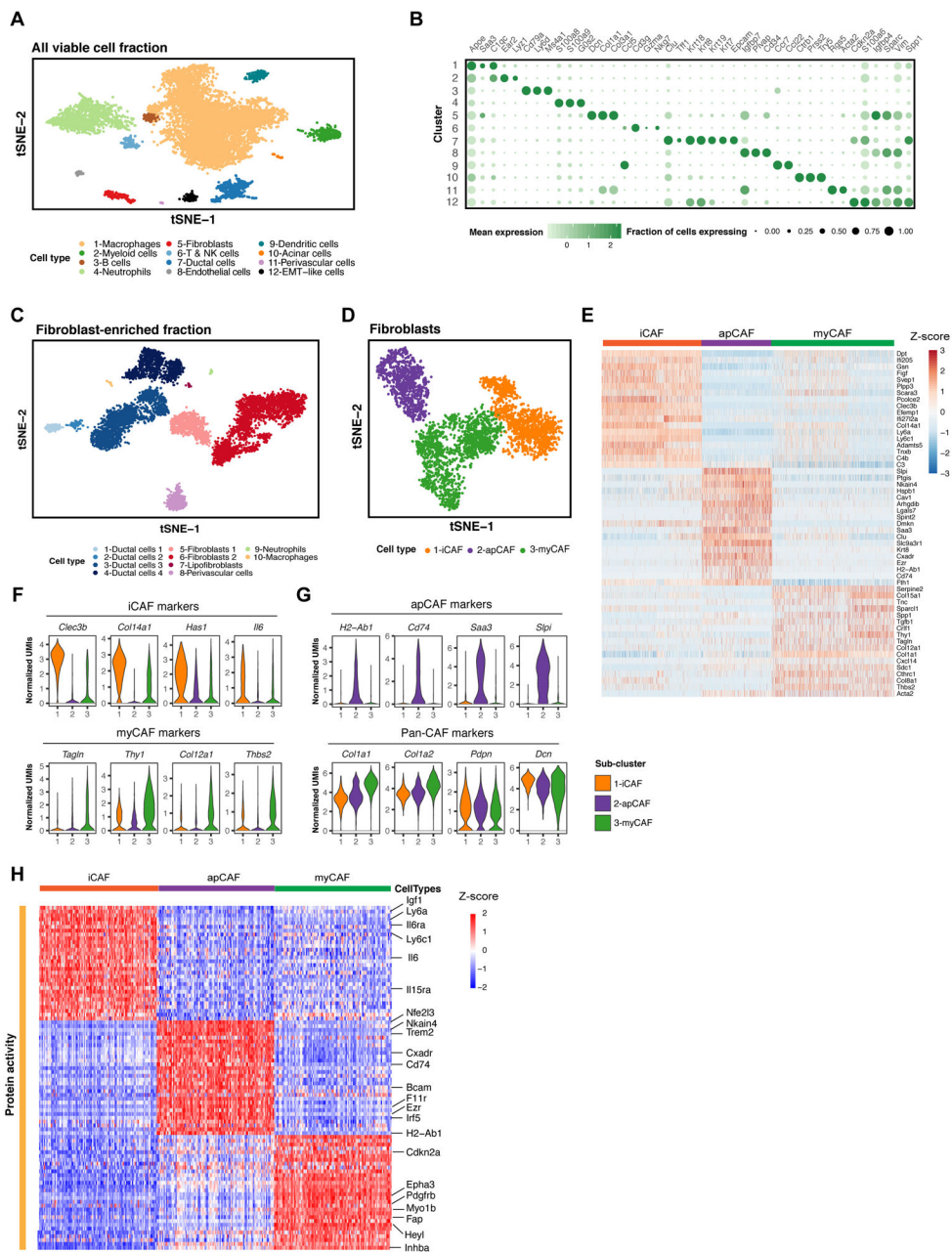


Figure 4. Single cell analysis of KPC tumors recapitulates human PDAC and reveals a novel CAF subtype.

A. Unsupervised clustering of all viable cells from four KPC mouse PDAC tumors, represented as a t-SNE plot. Different cell type clusters are color-coded. **B.** Bubble plot showing selected cell type-specific markers across all clusters. Size of dots represents fraction of cells expressing a particular marker, and intensity of color indicates level of mean expression. Legends are shown below. **C.** Unsupervised clustering of the fibroblast-enriched fraction from PDAC tumors of four KPC mice, represented as a t-SNE plot. Different cell type clusters are color-coded. **D.** Unsupervised re-clustering of the fibroblasts (clusters 5 and 6 from **C**) in the four KPC tumors, represented as a t-SNE plot. Different fibroblast sub-

clusters are color-coded. **E.** Heatmap showing scaled normalized expression of discriminative marker genes between the three fibroblast sub-clusters, with cells as columns and genes as rows. Color scheme represents Z-score distribution from -3 (blue) to 3 (dark orange). **F.** Violin plots of selected iCAF and myCAF markers, showing normalized expression in each of the sub-clusters. **G.** Violin plots of selected apCAF and pan-CAF markers, showing normalized expression in each of the sub-clusters. **H.** Heat map showing the top differentially activated proteins (red) in each CAF subtype, as predicted by VIPER analysis. Color scheme represents Z-score distribution from -2 (blue) to 2 (red).

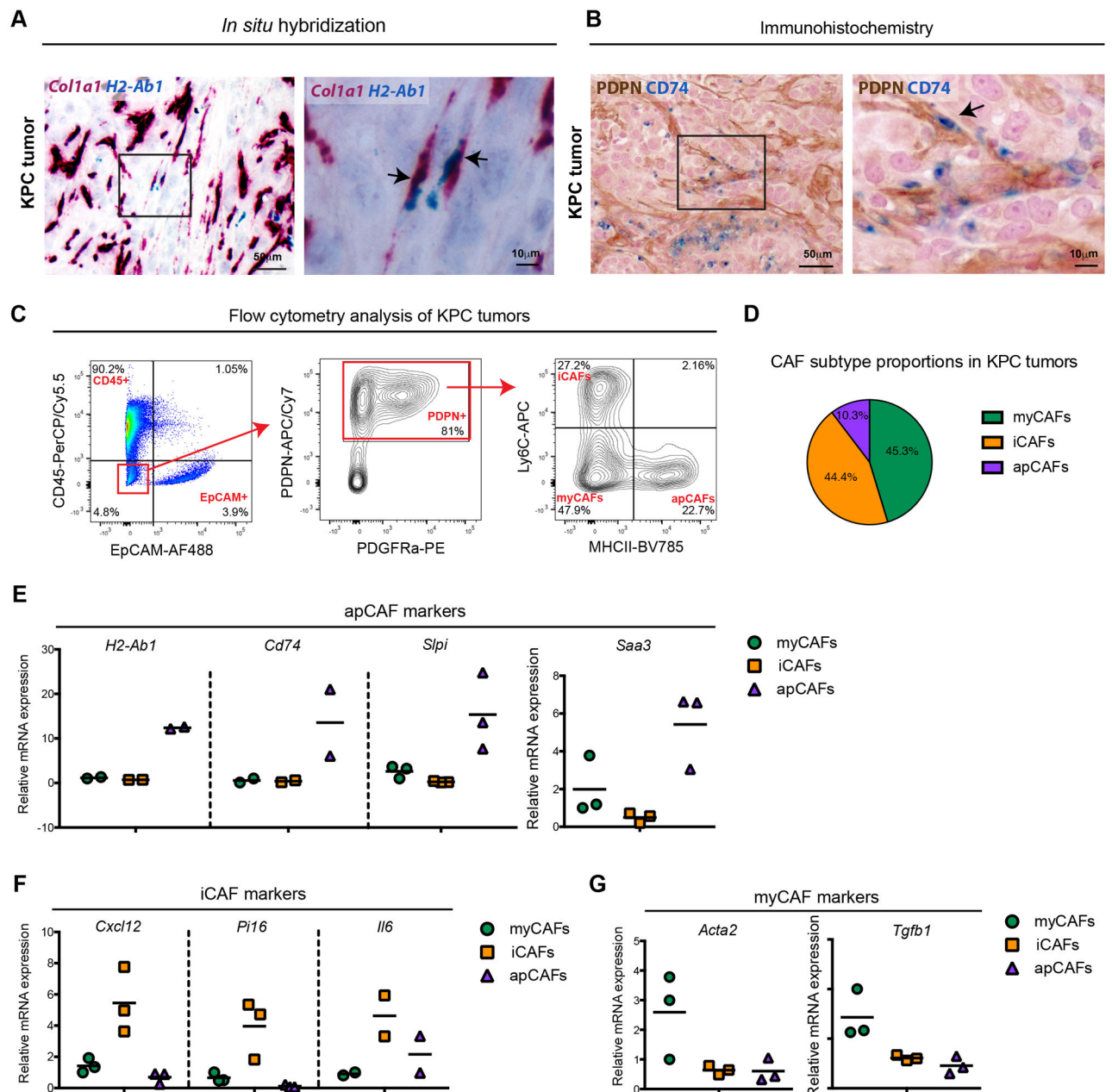


Figure 5. MHC class II expression characterizes a third CAF subpopulation in KPC tumors.
A. Duplex *in situ* hybridization of *Col1a1* and *H2-Ab1* in KPC tumor sections. The black square on the left panel is magnified in the right panel. Arrows indicate apCAFs. **B.** Sequential immunohistochemistry (IHC) of PDPN and CD74 in KPC tumor sections. The black square on the left panel is magnified in the right panel. Arrow indicates an apCAF. **C.** A representative flow cytometry analysis of cell suspension from a KPC tumor. Forward- and side-scatter were used to eliminate debris, and DAPI staining was used to eliminate dead cells. CD45 was used as an immune cell marker, EpCAM as an epithelial cell marker and PDPN and PDGFR α as fibroblast markers. Cells that were negative for both CD45 and EpCAM (red square on left panel), and positive for PDPN (red rectangle on middle panel)

were gated on for Ly6C and MHCII expression. The top left quarter shows iCAFs (Ly6C⁺, MHCII⁻), the bottom right quarter shows apCAFs (Ly6C⁻, MHCII⁺) and the bottom left quarter shows myCAFs (Ly6C⁻, MHCII⁻). **D.** Proportions of CAF subtypes from the PDPN-positive population in KPC tumors, as measured by flow cytometry analysis (n=20, % ±SEM: iCAFs 44.4±3.9, apCAFs 10.3±1.25, myCAFs 45.3±4.1). **E-G.** qPCR analysis of apCAF marker genes (**E**), iCAF marker genes (**F**) and myCAF marker genes (**G**) in the three CAF subtypes sorted from KPC tumors (n = 2 biological replicates). Black horizontal line represents mean value of data points. All transcripts were normalized to *Hprt*.

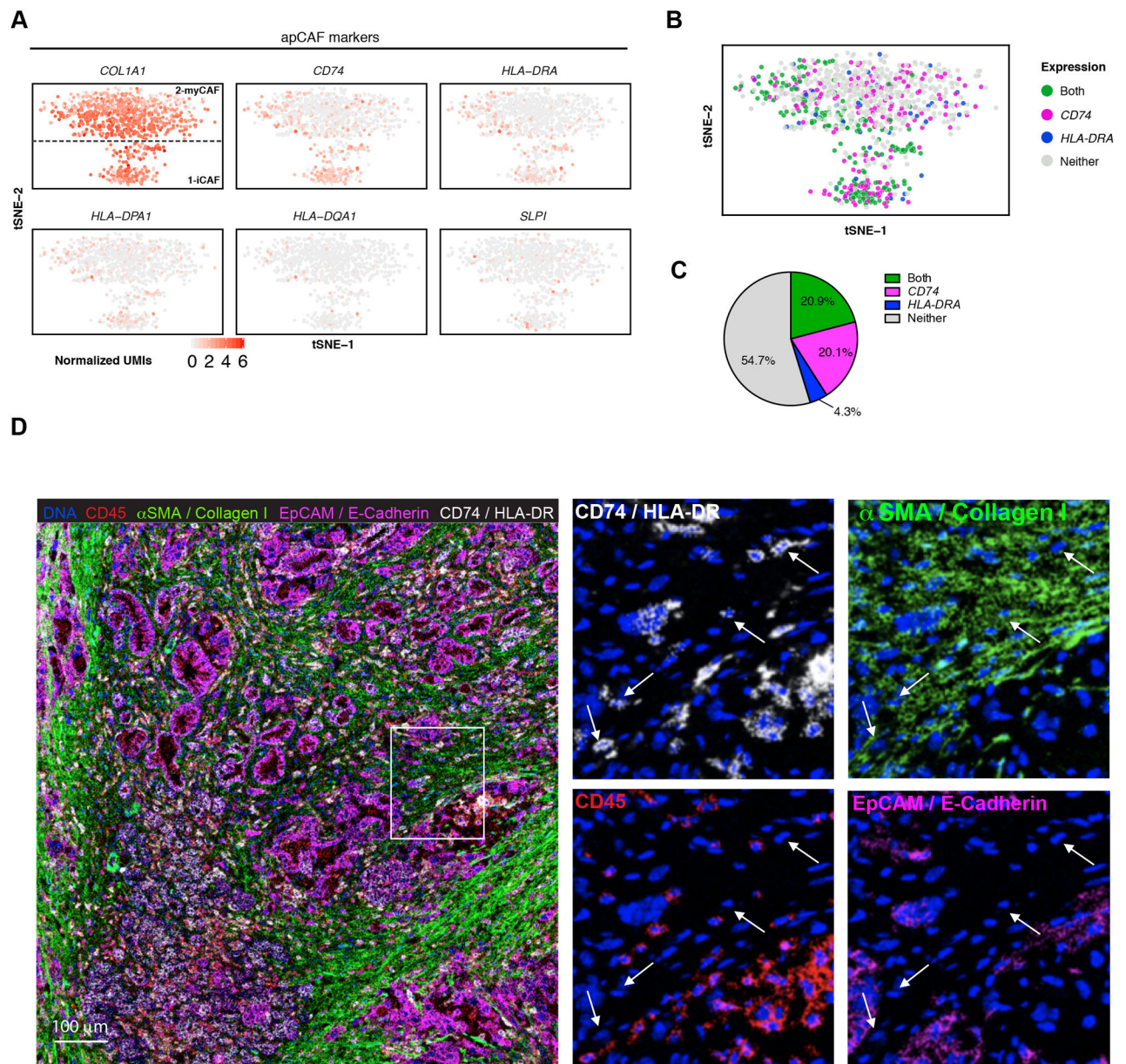


Figure 6. apCAFs are detectable in human PDAC.

A. Expression levels of *COL1A1* and selected apCAF marker genes in the human CAF dataset, represented as t-SNE plots. Legend shows a color gradient of normalized expression. Dotted line in the *COL1A1* t-SNE plot separates the iCAF and myCAF sub-clusters according to Fig. 3A. **B.** t-SNE plot showing binary expression scheme of *HLA-DRA* and *CD74* in human CAFs. Colors represent cells expressing *HLA-DRA* only (blue), *CD74* only (pink), both genes (green) or neither (gray). **C.** Quantification of the t-SNE plot shown in B. **D.** A representative image from an imaging mass cytometry (IMC) staining of human PDAC sections, using metal-conjugated antibodies. Tumor sections from 4 different patients were stained. The left panel shows a zoomed-out image. The small panels on the right show a magnification of the depicted area within the section (white rectangle), where

each panel is stained for a specific marker(s), as indicated. Errors are pointing to examples of apCAFs.

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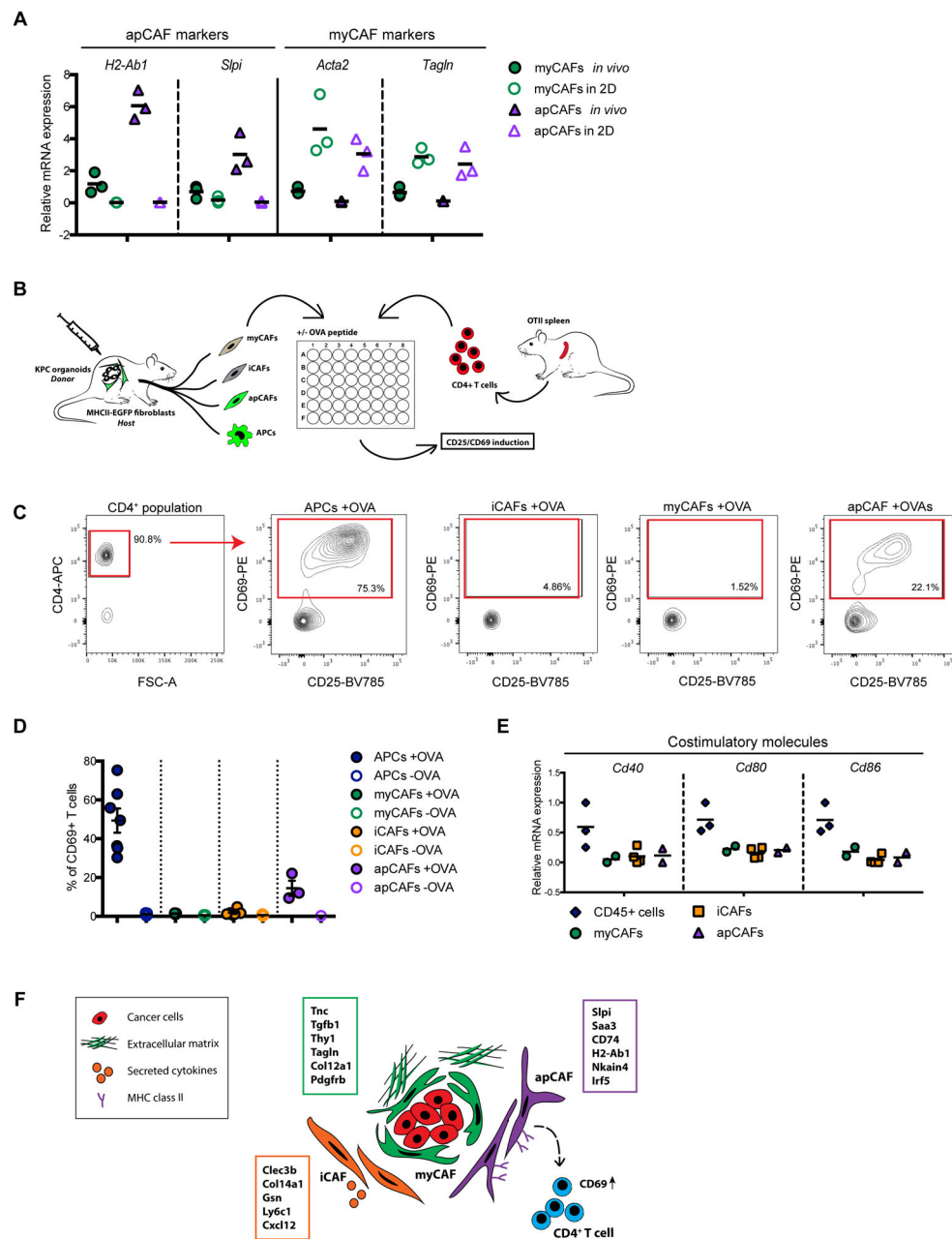


Figure 7. apCAFs can present antigens to T cells.

A. qPCR analysis of apCAF and myCAF marker genes in apCAFs sorted from KPC tumors (apCAFs *in vivo*) compared to the same population following culture in two-dimensional monolayer (apCAFs in 2D). myCAFs sorted from the same KPC tumors (myCAFs *in vivo*) and myCAFs grown in 2D (myCAFs in 2D) were used as positive controls for myCAF genes (n=3 biological replicates). Black horizontal line represents mean value of data points. All transcripts were normalized to *Hprt*. **B.** An illustration of the T cell activation assay: the three CAF subtypes and professional APCs were isolated from orthotopic tumors that were transplanted in MHCII-EGFP host mice (left side). Sorted cells were incubated with or without OVA peptide, and then co-cultured with CD4⁺ T cells that were isolated from OVA-

specific OTII mice (right side). After 17 hours of co-culture, T cells were analyzed by flow cytometry for early activation markers. **C.** An example of T cell early activation assay. CD4⁺ T cells that were co-cultured with OVA-loaded APCs or different CAF subtypes for 17 h, were washed and stained for T cell markers, and read on a flow cytometer. Debris and dead cells were excluded by forward- and side-scatter and by DAPI staining (not shown). Viable cells were stained for CD4, CD25 and CD69. A representative example of CD4 gating is shown on the most left panel. Each of the other panels shows the CD69⁺ population upon co-culture of T cells with different cell types, following an incubation with OVA. **D.** Quantification of three independent experiments of T cell early activation. Values \pm SEM are shown (n=7 for APCs and myCAFs, n=6 for iCAFs, n=3 for apCAFs). **E.** qPCR analysis of costimulatory molecules in the three CAF subtypes sorted from KPC tumors, compared to CD45⁺ cells sorted from the same tumors (n = 2 biological replicates). Black horizontal line represents mean value of data points. All transcripts were normalized to *Hprt*. **F.** Illustrated summary of CAF subpopulations and their functions in PDAC. Subpopulations and their unique features are highlighted by different colors: myCAFs in green, iCAFs in orange and apCAFs in purple. Selected markers of each subpopulation are listed in the corresponding boxes.