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Single cell transcriptome analysis defines heterogeneity of the adult murine pancreatic ductal tree

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ABSTRACT

Lineage tracing using genetically engineered mouse models is an essential tool for investigating cell-fate decisions of progenitor cells and biology of mature cell types, with relevance to physiology and disease progression. To study disease development, an inventory of an organ's cell types and understanding of physiologic function is paramount. Here, we performed single-cell RNA sequencing to examine heterogeneity of murine pancreatic duct cells, pancreatobiliary cells, and intrapancreatic bile duct cells. We isolated duct cells within the murine pancreas using a *Dolichos biflorus* agglutinin (DBA) lectin sorting strategy that labels all pancreatic duct cell types. Our data suggested the substructure of murine pancreatic duct cells is compartmentalized into three subpopulations. We describe an epithelial-mesenchymal transitory axis in our three pancreatic duct subpopulations and identify *SPP1* as a regulator of this fate decision as well as human duct cell de-differentiation. Our results further identify functional heterogeneity within pancreatic duct subpopulations by elucidating a role for Geminin in accumulation of DNA damage in the setting of chronic pancreatitis. Our findings implicate diverse functional roles for subpopulations of pancreatic duct cells in maintenance of duct cell identity and disease progression and establish a comprehensive road map of murine pancreatic duct cell, pancreatobiliary cell, and intrapancreatic bile duct cell homeostasis.

SIGNIFICANCE

Murine models are extensively used for pancreatic lineage tracing experiments and investigation of pancreatic disease progression. Here, we describe the transcriptome of murine pancreatic duct cells, intrapancreatic bile duct cells, and pancreatobiliary cells at single cell resolution. Our analysis defines novel heterogeneity within the pancreatic ductal tree and supports the paradigm that more than one population of pancreatic duct cells harbors progenitor capacity. We identify and validate unique functional properties of subpopulations of pancreatic duct cells including an epithelial-mesenchymal transcriptomic axis and roles in chronic pancreatic inflammation.

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INTRODUCTION

Pancreatic duct cells, while a minority of the composition of the pancreas, play an integral role in secretion and transport of digestive fluid containing proenzymes synthesized by acinar cells, electrolytes, mucins, and bicarbonate. They can serve as a cell of origin for pancreatic ductal adenocarcinoma (PDA) (1, 2) and have been implicated in the pathophysiology of multiple other diseases including cystic fibrosis (3) and pancreatitis (4).

Heterogeneity of a cell type becomes increasingly important in the context of disease and regeneration since different subpopulations can be the driving forces behind pathogenesis. The function of exocrine pancreatic cells is required for survival, yet these cells exhibit limited regenerative capabilities in response to injury. Chronic pancreatitis (CP) is a risk factor for pancreatic cancer. The underlying mechanisms for PDA progression in CP patients are incompletely understood and are likely multifactorial, including both genetic and environmental insults (5). Studies have shown that cytokines and reactive oxygen species generated during chronic inflammation can cause DNA damage. It has been hypothesized that an unlucky pancreatic cell might acquire DNA damage in the protooncogene *KRAS* or tumor suppressor genes *TP53* or *CDKN2A*, thereby accelerating malignant transformation (6, 7). Thus, it is imperative to understand the mechanisms by which DNA damage occurs in the setting of CP. Duct obstruction is one cause of CP, and the ability of ductal cells to acquire DNA damage in the setting of CP is incompletely understood.

In this report, we conducted single-cell RNA sequencing (scRNA-seq) on homeostatic murine pancreatic duct, intrapancreatic bile duct, and pancreatobiliary cells using a DBA$^+$ lectin sorting strategy, and present a high-resolution atlas of these murine duct cells. By extensively comparing our subpopulations to previously reported mouse and human pancreatic duct subpopulations (8-10), we both corroborate several previous findings and identify and validate novel duct cell heterogeneity with unique functional properties including roles for subpopulation markers in CP. Our findings suggest that multiple duct subpopulations retain progenitor capacity, which is influenced by expression of markers driving subpopulation identity.

RESULTS

scRNA-seq identifies multiple pancreas cell types with DBA lectin sorting

Previously reported subpopulations of murine pancreatic duct cells were identified by single cell analysis of pancreatic cells obtained using an islet isolation procedure; thus, exocrine duct cells were of low abundance (9). To circumvent this issue, we employed a DBA lectin sorting strategy that has been extensively used to isolate and characterize all murine pancreatic duct cell types (11, 12), to investigate murine duct heterogeneity. We isolated live DBA$^+$ cells from the pancreata of four adult female C57BL/6J littermates, and performed scRNA-seq on the pooled cells using the 10X Genomics platform (Figure 1A and S1A). After filtering out doublets and low-quality cells (defined by low transcript counts), our dataset contained 6813 cells. Clustering analysis identified 16 distinct cell populations with an average of 5345 transcripts per cell and 1908 genes per cell (Figure 1B and Dataset S1). Significantly differentially expressed genes (DEGs) when comparing a cluster to all other clusters are listed in Dataset S2. Annotation of these 16 clusters was accomplished by analysis of known markers (Figure 1B-D). Our dataset comprises 2 populations of ductal cells, a cluster of endothelial cells, one cluster of fibroblasts, and 12 immune cell clusters. As expected, murine endocrine and acinar cells are not present in our dataset because they are not DBA$^+$ cells. Gene and transcript counts for each cluster are shown in Figure S1B. We identified DBA$^+$Collagen I$^+$ fibroblasts and DBA$^+$CD45$^+$ immune cells by immufluorescence. CD31$^+$ endothelial cells are not DBA$^+$. Their presence in our dataset

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might be explained by the close juxtaposition of pancreatic duct cells with endothelial cells throughout the murine pancreas (Figure S1C).

Subpopulations of ductal cells are characterized by unique gene signatures and regulation of pathways

To get a better understanding of duct cell heterogeneity, we generated an Uniform Manifold Approximation and Projection (UMAP) plot using all duct cells (clusters 0 and 8), which revealed six distinct ductal clusters. Annotation of each duct cluster was accomplished using DEGs, Ingenuity Pathways Analysis (IPA) and upstream regulator analysis, and marker validation in murine and human pancreas (Figure 2A-D, Figure S1D-E, and Datasets S2-S4). Gene and transcript counts for each cluster are shown in Figure S1F and Dataset S1. We observed variable expression of known ductal markers within clusters. Notably, fewer murine duct cells express the transcription factor Hnf1b when compared to Sox9. This observation is in contrast to a previous report demonstrating a similar prevalence of adult murine Hnf1b$^+$ and Sox9$^+$ duct cells, which might be explained by different ductal cell isolation methods (Figure S1G) (13).

Cluster 0

Cluster 0 contains the most cells of all duct clusters in the dataset (Dataset S1). A gene that positively regulates Ras signaling *Mmd2*, the voltage-gated potassium channel protein encoded by *Kcne3*, as well as the ATP-binding cassette (ABC) transporter chloride channel protein encoded by *Cftr,* were significantly upregulated in cluster 0 when compared to all other ductal clusters (Figure 2C and Dataset S2). IPA showed upregulation of hepatic fibrosis signaling pathway in cluster 0 (Figure 2D and Dataset S3). IPA upstream regulator analysis predicted an activated state for the transcriptional regulator *Ctnnb1* in cluster 0. Predicted activation of D-glucose and growth factors Fgf2, Lep, and Hgf, suggest cluster 0 is a metabolically active duct cell subpopulation (Dataset S4). Notably, cluster 0 shows upregulation or activation of multiple genes whose alteration play important roles in the pathophysiology of pancreatic diseases such as *CFTR* for hereditary chronic pancreatitis (14) and *TGFB2* and *CTNNB1* for pancreatic cancer (15-17) (Dataset S2).

To validate gene expression patterns and determine the location of cluster 0 cells within the hierarchical pancreatic ductal tree (18), we next examined expression of select significantly DEGs. *Gmnn*, an inhibitor of DNA replication, was present in both clusters 0 and 2, so we decided to examine histologically, and were surprised to find rare protein expression of *Gmnn*, which was in contrast to the widespread RNA expression depicted by the feature plot (Figure S2A). After examining more than 1500 main pancreatic duct cells from 5 donors, we were unable to find a GEMININ positive cell, indicating very low or absent expression of *GMNN* in human main pancreatic ducts. *Spp1*, which encodes for Osteopontin, and *Wfdc3*, which are significantly DEGs in both clusters 0 and 2, show cytoplasmic expression in all mouse and human pancreatic duct types (Figure S2B-C and Table S1).

Cluster 1

Cells in cluster 1 have significantly upregulated expression of the exosome biogenesis gene *Rab27b* as well as *Ppp1r1b* that encodes for a molecule with kinase and phosphatase inhibition activity (Figure 2A-C and Dataset S2). IPA upstream regulator analysis predicted an activated state for the transcriptional regulator *Smarca4* and the two growth factors Tgfb1 and Gdf2 (Dataset S4). IPA results showed an enrichment in molecules regulating Calcium Transport I (Figure 2D and Dataset S3). Intracellular calcium signaling in pancreatic duct cells is an important regulator of homeostatic bicarbonate secretion (19). *PPP1R1B*, *SMARCA4*, and *TGFB1* have well described roles in the pathogenesis of pancreatic cancer (20-22). We

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observed expression of markers of cluster 1, *Anxa3* and *Pah*, which are also DEGs in cluster 4, to have cytoplasmic expression in all mouse and human pancreatic duct types (Figure S3A-B and Table S1). Co-staining of CFTR, a marker of cluster 0, and ANNEXIN A3 show both overlapping and non-overlapping patterns of expression in human intercalated ducts, validating the heterogeneity observed in our murine pancreatic duct dataset in human pancreatic duct cells (Figure S3C).

Cluster 2

Cluster 2 is characterized by low level or lack of expression of multiple ductal cell markers (*Cftr*, *Kcne3*, *Sparc*, *Mmd2, Krt7*) found in other clusters (Figure 2B-C and Figure S1G). IPA analysis showed significant overrepresentation of molecules from several pathways involved in Arginine metabolism in cluster 2 (Figure 2D and Dataset S3). Cluster 2 has the lowest average expression of total genes and transcripts (Figure S1F and Dataset 1). We therefore posit that cluster 2 represents a stable, fairly transcriptionally and metabolically inactive duct cell subpopulation when compared to other duct clusters.

Cluster 3

Cluster 3 cells are located almost entirely within cluster 8 of the UMAP containing 16 DBA^+ clusters (Figure S1E). This, along with high expression of genes regulating cilia biogenesis (*Foxj1*, *Cfap44, Tuba1a*) led to the identification of cluster 3 as intrapancreatic bile duct cells (Figure 2A-C and Dataset S2). Expression of cilia biogenesis genes is more prominent in intrapancreatic bile duct cells when compared to pancreatic duct cells (Figure S3D, Dataset S2, and data not shown). IPA showed upregulation of p53 signaling, NRF2-mediated oxidative stress response, PI3K signaling in B lymphocytes, Senescence pathway among other pathways and inhibition of cell cycle: G1/S checkpoint regulation (Figure 2D and Dataset S3). IPA upstream regulator analysis predicted an activated state for transcriptional regulators *Foxa2*, *Tp53*, *Foxo3*, *Mtpn*, *Tp63*, *Smarca4*, *Nfe2l2*, *Myc*, *Tcf7l2*, *Atf4*, *Pax7*, *Smarcb1*, *Mitf*, *Sp1*, *Rel*, *Lhx1*, *Gli1*, and an inhibited state for transcriptional regulators *Mdm4*, *Gmnn*, and *Hdac1*. Five different microRNAs including mir-17 and mir-25 were all predicted to be in an inhibited state by IPA upstream regulator analysis when compared to all other duct clusters in the dataset (Dataset S4). These results highlight the differences between cellular pathways essential for homeostatic function of pancreatic duct cells and intrapancreatic bile duct cells.

Cluster 4

Cells in cluster 4 have significantly higher expression of *Tgfb3* and *Dclk1* when compared to all other ductal clusters (Figure 2C and Dataset S2). *Dclk1* labels tuft cells which are present in normal murine intrapancreatic bile ducts and pancreatobiliary ductal epithelium, but not in normal murine pancreatic ducts (23). *Dclk1* also marks rare normal murine pancreatic duct cells (24). Clustering analysis of $Dclk1^+$ cells in our dataset showed no subpopulations of $Dclk1^+$ ductal cells (data not shown). IPA showed 144 significantly differentially expressed pathways when comparing cluster 4 to all other ductal clusters (Figure 2D and Dataset S3). Yap, a transcriptional regulator essential for homeostasis of biliary duct cells (25), was predicted to be in an activated state by IPA upstream regulator analysis (Dataset S4). Cluster 4 also contained a small population (13 cells) of *Dmbt1* and *Ly6d*-expressing cells previously identified in extrahepatic biliary epithelium (25) (Figure S4A). These 13 cells appeared as a small population separate from other cells in cluster 4 in the UMAP (Figure 2A). Similar to the IF validation reported for extrahepatic biliary epithelial cells (BECs) (25), our IF validation of *Dmbt1* and *Ly6d*-expressing cells using Cxcl5, another marker of this subpopulation, shows a greater abundance of these cells than what would be expected given the number identified in the clustering analysis (13). It is possible that this cell type is sensitive to single cell dissociation. Cells in cluster 4 are juxtaposed to pancreatic duct cells (clusters 0, 1, and 2) in the UMAP,

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suggesting transcriptional commonalities with pancreatic duct cells. In addition, *Dmbt1* and *Ly6d*-expressing cells are present in cluster 4, suggesting a bile duct identity. Based on these shared features of bile and pancreas ducts, we postulate that cluster 4 contains pancreatobiliary duct cells.

Cluster 5

Replicating duct cells are characterized by high expression of *Mki67*, *Cenpf*, and *Cenpe* and comprise 1.65% of all duct cells in our dataset (Figure 2A-C, Figure S3D, and Dataset S2). The location of proliferating ductal epithelium is close to clusters containing intrapancreatic bile duct and pancreatobiliary cells. In addition, cluster 5 shares 6/25 DEGs with cluster 3. These data suggest that cluster 5 is comprised primarily of proliferating cluster 3 and 4 cells (Figure 2A, Figure S1E, and Dataset S2). IPA and upstream regulator analysis showed several of the same pathways and factors as those seen in clusters 3 and 4 (Datasets S3-S4). Consistent with previous reports (26, 27), pancreatic duct cells are fairly mitotically inactive.

Summarily, our high resolution single cell analysis has identified the substructure of murine pancreatic duct cells and characterized pancreatobiliary and intrapancreatic bile duct cells.

Comparison of clusters defines heterogeneity within duct subpopulations

We next sought to determine the relationships between duct clusters by examining their similarities and differences. Dendrogram analysis, Pearson's correlation, and DEGs revealed close relationships between clusters 0 and 2 as well as clusters 1 and 4 (Figure 3A-B and Dataset S2). Comparison of clusters 0 and 2 showed only 9 significant DEGs, suggesting a shared core gene expression program (Figure 3C-D). Overrepresentation of molecules regulating the cell cycle was observed in cluster 0 when compared to cluster 2 (Figure 3E). The DEGs upregulated in cluster 0 promote duct cell function (*Cftr*, *Tuba1a*, *Kcne3*), suggesting that cluster 0 comprises workhorse pancreatic duct cells (28).

When comparing pancreatobiliary cells of cluster 4 to pancreatic duct cells in cluster 1, one of the most striking differences is the enrichment in expression of genes regulating assembly of cell junctions including tight junctions, epithelial adherens junction signaling, regulation of actin-based motility by Rho, and actin cytoskeleton signaling. A strong network of stress fibers, comprised of actin filaments, myosin II, and other proteins, that function in bearing tension, supporting cellular structure, and force generation may be important for pancreatobiliary cell function and maintenance (Figure 3F-H and Datasets S3-S4) (29, 30). Cluster 4: *Dmbt1*$^{+}$*Ly6d*$^{+}$ cells are characterized by strong upregulation of pathways regulating Xenobiotic metabolism when compared to all other cluster 4 cells suggesting a prominent role for these cells in the bile acid and xenobiotic system (BAXS) (Figure 3I-K, and Datasets S3-S4) (31). Comparison of intrapancreatic bile duct cells and pancreatobiliary cells showed many unique features of these populations including upregulation of EIF2 signaling in pancreatobiliary cells and upregulation of coronavirus pathogenesis pathway in intrapancreatic bile duct cells (Figure S4B-D and Datasets S3-S4).

Pancreatobiliary cells express a gene signature enriched in several targets of the Hippo signaling pathway Yap

Two subpopulations of adult murine hepatic homeostatic BECs, A and B, have been previously described (25). To determine if these subpopulations are present in intrapancreatic bile duct (cluster 3) and pancreatobiliary cells (cluster 4), we aligned our dataset with an adult hepatic murine BEC scRNA-seq dataset comprised of 2,344 homeostatic BECs (25). Intrapancreatic bile duct and pancreatobiliary cells aligned well with hepatic BECs, with no apparent batch

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effect (Figure S5A). Intrapancreatic bile duct cells primarily cluster together with hepatic BECs expressing subpopulation B genes, and pancreatobiliary cells primarily cluster together with hepatic BECs expressing subpopulation A genes (Figure S5B-G and Dataset S1-S2). The subpopulation A expression signature contains many genes significantly enriched as Yap targets, a signature that has been previously proposed to reflect a dynamic BEC state as opposed to defining a unique cell type (25).

DBA$^+$ lectin murine pancreas sorting identifies previously missed ductal subpopulations

To determine the novelty of duct cell heterogeneity manifested using DBA$^+$ lectin sorting of murine pancreas, we next compared our DBA$^+$ murine pancreatic ductal clusters to previously reported subpopulations of mouse and human pancreas duct cells. Using inDrop and an islet isolation pancreas preparation, Baron *et al.* (2016) identified the substructure of mouse and human pancreatic duct cells (9). Two subpopulations of mouse pancreatic duct cells characterized by expression of *Muc1* and *Tff2* (subpopulation 1) and *Cftr* and *Plat* (subpopulation 2) were described. While *Cftr* expression is characteristic of our cluster 0 (Figure 2C), *Muc1*, *Tff2*, and *Plat* expression didn't typify any murine DBA$^+$ pancreatic duct subpopulation (Figure S6A). Two subpopulations were similarly described for human pancreas duct cells characterized by expression of 1) *TFF1*, *TFF2*, *MUC1, MUC20,* and *PLAT* and 2) *CFTR* and *CD44*. *Tff1* is not expressed in murine DBA$^+$ ductal cells (clusters 0-5). *Cd44* is significantly upregulated in pancreatobiliary cells, and *Muc20* as well as *Tff2* are significantly upregulated in 4:*Dmbt1*$^+$*Lyd6*$^+$ cells (Dataset S2 and Figure S6A-B). Dominic Grün *et al*. (2016) previously reported 4 subpopulations of human pancreatic duct cells characterized by expression of *CEACAM6*, *FTH1*, *KRT19*, and *SPP1* using an islet isolation pancreas preparation and the CEL-seq protocol (10). While *Spp1* is significantly upregulated in DBA$^+$ pancreas duct clusters 0 and 2, *Fth1* doesn't characterize any murine DBA$^+$ pancreas duct population, and *Krt19* is significantly upregulated in pancreatobiliary cells (Dataset S2, Figure S1G, and Figure S6C). *CEACAM6* has no mouse homolog. The differences in pancreatic ductal subpopulation identification may be due to single cell methodology (inDrop, CEL-seq, and 10X Genomics), pancreas preparation method (islet isolation vs DBA$^+$ lectin sorting), differences in ductal cell numbers analyzed, or potential differences between mouse and human duct cells.

Six subpopulations of human pancreatic duct cells have been described using the 10X Genomics platform based on sorting for *BMPR1A*/*ALK3* (8). Using AddModuleScore in Seurat, we calculated a score comparing each of our murine duct clusters to the human ALK3$^+$ clusters (Figure S7A-F) (32). Murine pancreatic duct clusters 0-2 had the highest scores when compared to human ALK3$^+$ clusters 1 (*SPP1*$^+$ Stress/harboring progenitor-like cells) and 2 (*TFF1*$^+$ activated/migrating progenitor cells). Murine pancreatobiliary cells (cluster 4) scored the highest when compared to the human ALK3$^+$ cluster 3 (AKAP12$^+$ small ducts). The human ALK3$^+$ cluster 4 (*WSB1*$^+$ centroacinar cells) didn't distinguishably overlap with any DBA$^+$ mouse pancreas ductal clusters. DBA is expressed in murine centroacinar/terminal ducts as early as three weeks of age (33), thus these cells would be expected to be present in our dataset(11). Examination of centroacinar/terminal ductal cell markers *Hes1* (34), *Aldh1a1* (35), and *Aldh1b1* (36) showed broad expression enriched in either clusters 0 and 2 (*Hes1* and *Aldh1b1*) or clusters 1 and 4 (*Aldh1a1*), rather than a distinct subpopulation as is seen in the ALK3$^+$ human pancreatic duct dataset. *Aldh1a7* is negligibly expressed in murine duct clusters 0-5 (Figure S7G). Unlike in mouse DBA$^+$ pancreas ductal clusters, the human ALK3$^+$ dataset contains two ducto-acinar subpopulations characterized by expression of genes enriched in acinar cells. To assess the presence of ducto-acinar cells in adult murine pancreas, we performed immunolabeling for markers of the ALK3$^+$ human ducto-acinar clusters 5 (*CPA1*) and 6 (*AMY2A* and *AMY2B*). Although ducto-acinar cells, like centroacinar/terminal ductal cells, don't define a unique cluster in our DBA$^+$ murine duct subpopulations, we identified DBA$^+$Cpa1$^+$ and DBA$^+$α-

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amylase$^+$ ducto-acinar cells in adult murine pancreas (Figure S7H). Taken together, these data suggest murine centroacinar/terminal ductal and ducto-acinar cells are largely transcriptionally homogenous with other murine duct cell types.

RaceID3/StemID2 suggest murine DBA$^+$ duct cluster 0 and 2 cells are the most progenitor-like

Given the close relationships observed between DBA$^+$ duct clusters 0 and 2 as well as 1 and 4, we next assessed differentiation potential using RaceID3/StemID2 to predict cell types, lineage trajectories, and stemness (37). Unsupervised clustering with RaceID3 showed 17 clusters. RaceID3 clusters with 10 cells or less were removed from subsequent analyses, and Seurat duct clusters 3 and 5 are not included in this analysis (Figure 4A-B). RaceID3 clusters with the highest StemID2 score correlate to cells present in Seurat duct clusters 0 and 2 (Figure 4C and Figure S8A-B). The variable StemID2 scores observed for cells within Seurat duct clusters 0, 1, 2, and 4 suggest distinct stages of differentiation or maturation. Consistent with previous literature, the pancreatic ductal cell progenitor niche isn't restricted to a single cluster (8).

Pseudotime ordering identifies an epithelial-mesenchymal transition (EMT) axis in pancreatic duct cells

To further examine the lineage relationships among pancreas duct subpopulations, we ordered cells in pseudotime based on their transcriptional similarity (38). Monocle 3 analysis showed DBA$^+$ duct clusters 3 and 5 were disconnected from the main pseudotime trajectory, so we focused our analysis on DBA$^+$ duct clusters 0, 1, 2, and 4 (Figure S8C). Because RaceID3/StemID2 analysis showed Seurat clusters 0 and 2 have the highest StemID scores, we started the pseudotime ordering beginning with cluster 0 as Seurat clusters 0 and 2 are juxtaposed in the Monocle 3 clustering (Figure 4D-E and Figure S8D).

In Monocle 3 analysis, genes with similar patterns of expression that vary over time across the pseudotime trajectory are coalesced into modules (Figure 5A). We performed IPA and upstream regulator analysis, a pairwise comparison, comparing select clusters within a module to analyze the gene expression changes along the pseudotime trajectory (Figure 5B-D and Datasets S3-S5). Examination of pathways deregulated in modules 4 and 14 showed a shift in the molecules driving the Xenobiotic Metabolism CAR Signaling Pathway. The Xenobiotic nuclear receptor CAR is an important sensor of physiologic toxins and plays a role in their removal (39). This pathway is regulated by *Aldh1b1*, *Aldh1l1*, *Gstt2*/*Gstt2b*, *Hs6st2*, and *Ugt2b7* in clusters 0 and 2 and *Aldh1a1*, *Fmo3*, *Gstm1*, and *Sod3* in cluster 1, suggesting that these clusters might respond differently when exposed to toxins or play heterogenous roles in endogenous toxin elimination (Figure 5B-C).

Regulation of the Epithelial Mesenchymal Transition By Growth Factors Pathway was upregulated in cluster 1 when compared to cluster 0 in Module 34. Molecules altered in this pathway play variable roles in promoting the epithelial or mesenchymal state and include *Fgf12*, *Fgfr2*, *Fgfr3*, *Pdgfc*, and *Smad3* (Figure 5D). When comparing clusters 0 and 1, examination of EMT markers *Vim* and *Cdh1* showed a stronger probability of expression of *Cdh1* in cluster 1 and a stronger probability of expression of *Vim* in cluster 0 (Figure 5E). Using immunofluorescence (IF), we detected Vimentin$^+$ ductal cells in both mouse and human pancreas, validating this epithelial-mesenchymal transitional axis (Figure 5F).

***SPP1* is required for mature human pancreas duct cell identity**

Our analysis thus far has identified and validated multiple transcriptional programs expressed by murine pancreatic duct cells and predicted possible lineage relationships among them. To

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assess the function of select markers defining murine DBA$^+$ pancreas duct clusters, we next examined the consequences of their loss in the immortalized human duct cell line HPDE E6/E7. *Spp1*, a marker of clusters 0 and 2, has been shown by us and others to mark a pancreas duct cell type enriched in progenitor capacity (8, 40). *Gmnn*, a marker of cluster 0, acts to inhibit re-replication of DNA during DNA synthesis by inhibiting the prereplication complex (41, 42). *Anxa3*, a marker of clusters 1 and 4, inhibits phospholipase A2 and cleaves inositol 1,2-cyclic phosphate generating inositol 1-phosphate in a calcium dependent manner (43, 44). *PAH* and *WFDC3* were not expressed in HPDE E6/E7 cells (data not shown). We generated and validated *SPP1*, *GMNN*, and *ANXA3* knockout HPDE E6/E7 lines using CRISPR/Cas9 (Figure 6A-C). Strong, consistent phenotypes were observed among different knockout lines for each gene despite some lines not demonstrating full loss of the protein (HPDE E6/E7 *ANXA3* gRNA2 and HPDE E6/E7 *SPP1* gRNAs 1-4). Cellular morphology was similar to the scrambled (scr) gRNA control (45) for every knockout line except HPDE E6/E7 *SPP1* gRNAs 1-4, which displayed a dramatic change in cellular morphology. HPDE E6/E7 *SPP1* knockout cells showed prominent filipodia and significantly increased proliferation in both 2D and 3D assays. HPDE E6/E7 *ANXA3* and *GMNN* knockout lines also show significantly increased proliferative capacity in both 2D and 3D assays, a phenotype suggestive of increased progenitor function (Figure 6D-F, Figure S9A, and data not shown). The change in cellular morphology in HPDE E6/E7 *SPP1* knockout lines is accompanied by decreased duct function as measured by carbonic anhydrase activity (Figure 6G).

To assess the changes in HPDE E6/E7 *SPP1* knockout lines on a molecular scale, we performed bulk RNA-sequencing on all 4 HPDE E6/E7 *SPP1* knockout lines and the HPDE E6/E7 scr gRNA control. A significant increase in markers associated with epithelial-mesenchymal transition (EMT) (*VIM*, *ZEB1*, *TWIST1*, *MMP2*) was observed in HPDE E6/E7 *SPP1* knockout lines when compared to the control (Datasets S2-S4 and Figure 6H-I). Markers of mature duct cells (*HNF1B*, *SOX9*, *KRT19*) were significantly downregulated in HPDE E6/E7 *SPP1* knockout lines when compared to the control (Figure 6H, J-K and Dataset S2). Gene Set Enrichment Analysis (GSEA) showed positive enrichment of pathways that regulate embryogenesis (*HOX* genes and *NOTCH* signaling) and cell cycle regulation in HPDE E6/E7 *SPP1* knockout lines when compared to the HPDE E6/E7 scr gRNA control, supporting the notion that loss of SPP1 leads to a more immature, progenitor-like state (Figure S9B-E). Taken together, these results define unique functional properties for markers that characterize murine DBA$^+$ pancreas duct cells and suggest that *SPP1* is an essential regulator of human pancreatic duct cell maturation and function.

Geminin safeguards against accumulation of DNA damage in mouse ductal cells in the setting of chronic pancreatitis

One marker of the workhorse population of pancreatic duct cells *Gmnn* has previously been associated with chronic inflammatory diseases such as asthma (46). We therefore queried its role in pancreas inflammatory disease. *Gmnn* binds to Cdt1 and inhibits DNA replication during the S phase. Geminin is a crucial regulator of genomic stability; its inhibition in multiple cancer cell lines leads to DNA re-replication and aneuploidy (47, 48). To determine the requirement for *Gmnn* in normal homeostatic pancreatic ductal cells, we generated a conditional *Gmnn* floxed allele and crossed the mouse to the *Sox9–Cre*^{ERT2} (49) and *Hnf1b–Cre*^{ERT2} (50) lines (Figure S10). Adult mice, between the ages of 7-9 weeks, were injected with tamoxifen to ablate Geminin in mouse pancreatic duct cells. Tamoxifen injected *Sox9cre*$^{Tg/wt}$; *Geminin*$^{f/f}$, *Sox9cre*$^{Tg/wt}$; *Geminin*$^{f/wt}$, and *Hnf1b*$^{Tg/wt}$; *Geminin*$^{f/f}$ mice displayed no histological abnormalities as assessed by hematoxylin and eosin (H&E) staining and no significant alterations in DNA damage as assessed by ATR and γ-H2AX IF up to 6 months post tamoxifen injection (data not shown). We were unsurprised by these findings, given the low proliferation rate of murine

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pancreatic duct cells suggested by our single cell data. Thus, Geminin may only be required in the context of pathologies characterized by increased proliferation in the pancreas such as pancreatitis or PDA (51).

We examined proliferation in human pancreas duct cells in CP patients (N=5 patients) and found a significant increase in Geminin expression when compared to normal human pancreatic duct cells (N=10 donors) (Figure 7A-B). Pancreatic duct ligation (PDL), an experimental technique that recapitulates features of human gallstone pancreatitis, results in an increase in proliferation of rat pancreatic duct cells (52, 53). To investigate the role of Geminin in mouse pancreatic duct cells in the setting of CP, we performed PDL on *Sox9cre*$^{Tg/wt}$; *Geminin*$^{f/f}$, *Sox9cre*$^{Tg/wt}$; *Geminin*$^{f/wt}$, *Hnf1b*$^{Tg/wt}$; *Geminin*$^{f/f}$ and littermate control mice (Figure 7C). As in the human setting, we also observed upregulation of Geminin in ductal epithelium in the control PDL mouse group (Figure 7D). Previously reported features of the PDL model were evident in our transgenic mice including replacement of parenchymal cells with adipose tissue, inflammation, and fibrosis (54, 55) (Figure S11A-B). Significant attenuation of Geminin expression was observed in *Sox9cre*$^{Tg/wt}$; *Geminin*$^{f/f}$, *Sox9cre*$^{Tg/wt}$; *Geminin*$^{f/wt}$, and *Hnf1b*$^{Tg/wt}$; *Geminin*$^{f/f}$ mouse pancreatic duct cells when compared to controls (Figure 7D and Figure S12A). Homozygous *Gmnn* loss in Sox9^{+} pancreatic ductal cells promoted an acute increase in proliferation, as assessed by BrdU incorporation, at Day 7 which became insignificant at Day 30 (Figures S12B-E). No changes were observed in apoptosis for any model or time point when compared to controls as assessed by cleaved caspase-3 IF (data not shown). Examination of DNA damage by γ-H2AX IF showed significantly increased γ-H2AX foci in *Sox9cre*$^{Tg/wt}$; *Geminin*$^{f/f}$ mice at Day 7, an observation that was sustained at Day 30 (Figure 7E-H). Assessment of DNA damage in *Sox9cre*$^{Tg/wt}$; *Geminin*$^{f/f}$, *Sox9cre*$^{Tg/wt}$; *Geminin*$^{f/wt}$, and *Hnf1b*$^{Tg/wt}$; *Geminin*$^{f/f}$ mice by ATR IF showed no significant changes (data not shown). The lack of phenotypes observed in the *Hnf1b*$^{Tg/wt}$; *Geminin*$^{f/f}$ model may be due to differences in recombination induced by the *Sox9–Cre*^{ERT2} and *Hnf1b–Cre*^{ERT2} lines, since fewer cells of the pancreatic ductal epithelium express Hnf1b (Figure S1G and Figure 7C). Taken together, these data suggest Geminin is an important regulator of genomic stability in pancreatic ductal cells in the setting of CP.

DISCUSSION

We present a single cell transcriptional blueprint of murine pancreatic duct cells, intrapancreatic bile duct cells, and pancreatobiliary cells. Notably, our single cell analysis showed that endothelial cells, fibroblasts, and immune cells are also obtained using the DBA^{+} lectin sorting strategy(12), and suggests that a subsequent ductal purification step is required to obtain pure pancreatic duct cells using this protocol. A static transcriptional picture in time has highlighted a very dynamic view of pancreas duct cell heterogeneity. Our study provokes reinterpretation of several previously published lineage tracing reports using ductal-specific Cre mouse lines, and will help plan future lineage tracing studies.

Cluster 0 workhorse pancreatic duct cells comprise the largest pancreatic duct subpopulation identified. Although clusters 0 and 2 share many markers, we found compelling differences in metabolic states as manifested in part by an overall lower gene and transcript count for cluster 2. IPA suggested that subpopulations of pancreatic duct cells may use different predominant mechanisms for bicarbonate secretion such as Cftr (56) for cluster 0 and calcium signaling for cluster 1 (57). One notable difference between clusters 0 and 2 vs 1 is the molecules which regulate the Xenobiotic Metabolism CAR signaling pathway. We observed expression of several genes, whose alteration contributes to PDA progression including *Tgfb2* and *Ctnnb1* in cluster 0 and *Ppp1r1b, Smarca4,* and *Tgfb1* in cluster 1. IPA upstream regulator analysis of Monocle 3 Module 14 predicted significant inhibition of *Kras* in cluster 1 when compared to cluster 0. Additionally, IPA upstream regulator analysis comparing cluster 2 vs 0 in

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Module 19 predicted activation of Myc and Mycn in cluster 2. These genes play central roles in homeostasis of pancreatic duct cells, and it's possible that distinct ductal cell subpopulations which are actively expressing these pathways may have different predispositions to PDA with mutations in these genes, heterogeneity which may also contribute to development of different subtypes of PDA.

We identified an EMT axis in pancreatic duct cells using Monocle 3 and validated this observation in mouse and human duct cells. *Spp1* is one gatekeeper of this epithelial to mesenchymal transitory duct phenotype as manifested by loss of ductal markers, reduced duct function, and upregulation of EMT genes in HPDE E6/E7 *SPP1* knockout cells when compared to controls. Clusters 0 and 2, characterized by strong expression of *Spp1*, show the highest StemID2 scores. *SPP1* knockout HPDE E6/E7 cells display prominent filipodia and the highest proliferative capacity of all markers examined when compared to controls. Taken together, these phenotypes along with upregulation of pathways regulating mammalian development (Notch signaling and Hox genes) manifested by GSEA suggest SPP1 loss promotes human duct cell de-differentiation.

In human pancreas duct cells, the subpopulation characterized by *SPP1* expression is described as "stress/harboring progenitor-like cells" (8). We observed significant deregulation of 14 cancer-related IPA pathways for which pathway directionality was known in HPDE E6/E7 *SPP1* knockout lines vs HPDE E6/E7 scr gRNA controls. 13/14 of these cancer-related pathways, including Pancreatic Adenocarcinoma Signaling, were in a direction suggestive that *SPP1* loss protects against tumor progression in human pancreatic duct cells. These findings are in agreement with published studies suggesting that *SPP1* loss ameliorates aggressiveness of pancreatic cancer cells (58, 59) and colon cancer cells (60, 61).

The requirement for Geminin in prevention of DNA re-replication initiation has been postulated to be when cells are stressed to divide quickly (62). We were unable to detect DNA damage with Geminin loss in homeostatic pancreatic duct cells, which may be due to the low proliferation rate of pancreatic duct cells and/or the presence of compensatory mechanisms with redundant function, such as ubiquitin-dependent degradation of Cdt1 at the time of replication licensing (63-66). Compensatory mechanisms are not sufficient to rescue the effects of Geminin loss in pancreatic duct cells in the context of CP, the result of which is accumulation of sustained DNA damage evident by γ-H2AX, but not ATR labeling. It has been previously reported that ATR is activated in Geminin-depleted colon cancer cell lines (67). Activation of the ATR-Chk1 pathway isn't a major player in pancreatic duct cells in the setting of CP (68), suggesting different mechanisms participate in sensing Geminin depletion-induced DNA damage in different experimental systems and tissues.

MATERIALS AND METHODS

Preparation of pancreatic duct cells for single cell analysis

Pancreata from four 9 week old female C57BL/6J littermates (Jackson Labs, Stock 000664) were dissected, digested into single cells, and the DBA^+ fraction obtained as previously described (12). Subsequently, live DBA^+ cells were isolated for scRNA-seq by excluding propidium iodide (Thermo Fisher Scientific, P3566) positive single cells during FACS. scRNA-seq was performed by the Institute for Human Genetics Genomics Core Facility at University of California San Francisco (UCSF) using the 10X Genomics platform. Briefly, live, single, DBA^+ pancreatic cells were loaded onto the microfluidic chip to generate single cell GEMs (Gel Bead-In EMulsions). Following cell lysis and unique barcode labeling, the cDNA library of 18,624 live pancreatic cells was generated using the Chromium Single Cell 3 GEM, Library & Gel Bead Kit v2 (10X Genomics). The cDNA library was sequenced on one lane using an Illumina HiSeq 4000.

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Single cell RNA-seq data processing

scRNA-seq data was generated on the 10X platform (10X Genomics, Pleasanton, CA) according to Single Cell 3' protocol (v2 Chemistry) recommended by the manufacturer (69). The Cell Ranger software pipeline (version 2.1.1) was used to demultiplex cellular barcodes, map reads to the genome and transcriptome using the STAR aligner, and produce a matrix of gene counts versus cells. Doublets were filtered by excluding cells having RNA counts > 30000 and mitochondrial genes percentage > 10% in addition to using Scrublet (70). The R package Seurat (71) was used to process the unique molecular identifier (UMI) count matrix and to perform data normalization (gene expression measurements for each cell were normalized by total expression, and log-transformed), dimensionality reduction, clustering, ductal cell isolation, and differential expression analysis. We identified three clusters enriched in genes from 2 different cell types including: 1) acinar and T cell, 2) acinar cell and macrophage and 3) acinar cell and duct cell. Because our dataset doesn't contain a population of acinar cells (they aren't DBA^+), doublet detector algorithms won't remove acinar cell doublets from our dataset. Based on this reasoning, we removed these clusters containing a high threshold level of expression of acinar cell genes.

Generation of *Geminin* conditional floxed allele

The general strategy to achieve Cre recombinase-mediated conditional gene ablation was to flank exons 3 and 4 of *Mus musculus Gmnn* by *loxP* sites (Figure S10A). The arms of homology for the targeting construct were amplified from BAC clone RP23-92G13 by PCR with high fidelity Taq polymerase. One primer contained a *loxP* site and a single SphI site which was used to verify the presence of the *loxP* site associated with it. Finally, the selectable cassette *CMV-hygro-TK* was incorporated into the targeting vector. The selectable marker itself was flanked by two additional *loxP* sites generating a targeting vector containing three *loxP* sites. Such a strategy allows the generation of ES cells with both a knockout allele and a conditional knockout allele after Cre mediated removal of the selection cassette *in vitro*. The targeting vector was sequenced to guarantee sequence fidelity of exons 3-4 and the proper unidirectional orientation of the three *loxP* sites. The complete left arm of homology was about 3200bp in length and the right arm of homology was 2100bp in length.

V6.5 ES cells were electroporated (25µF, 400V) with the three *loxP* sites-containing targeting construct, and hygromycin selection was performed to identify correctly targeted ES cells. Successfully targeted ES cells (*3loxP*) were identified with Southern blot (Figure S10B). These *3loxP* ES cells were then electroporated with a Cre-expressing plasmid and counter-selected with ganciclovir. ES cells that contained either one *loxP* or two *loxP* sites, respectively, were identified by Southern blot (Figure S10C). An ES cell clone was chosen that carried the conditional knockout allele (two *loxP* sites flanking exons 3 and 4) and was used for blastocyst injections to generate chimeric founder mice. $Gmnn^{f/f}$ mice displayed normal litter sizes. For routine genotyping of $Gmnn^{f/f}$ mice, the primers GCCTCGAACTCAGAAATCCA (primer A) and AACACAAAATTTGGCCTGCT (primer B) were used. To identify the deleted allele by PCR, primer C (TAGCCCGGACTACACAGAGG) can be used with primer A.

Southern blot

For Southern blotting of genomic DNA, samples were digested with SphI or Bsu36I restriction enzymes for at least 4hrs and separated on an 0.8% agarose gel. The DNA was transferred to a Hybond-XL membrane (GE-Healthcare) in a custom transfer setup. Before assembly, the agarose gel was treated for 15min in depurination solution (21.5ml 37% HCl in 1L H_2O), briefly rinsed in H_2O and then soaked in denaturing solution (20g NaOH pellets, 87.6g NaCl in 1L H_2O) for 30min. After transfer, the DNA was crosslinked to the membrane with UV light. The PCR amplified external Southern blot probes were labeled with ^{32}P using the Prime-It II Random

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Primer Labeling kit from Stratagene. After hybridization of the probe and washing of the membrane, Kodak MS film was exposed to it and then developed.

Mice

The transgenic mouse strain *Sox9–Cre*^{ERT2} was obtained from Jackson Labs (Stock 018829), and *Hnf1b–Cre*^{ERT2} has been previously described (50). Mice were maintained on a mixed genetic background. To induce Cre recombination, mice were injected with 6.7mg tamoxifen (Actavis, NDC 0591-2473-30) via oral gavage three different days over the course of a week at 7-9 weeks of age. Pancreatic duct ligations were performed as previously described (72). BrdU (Sigma, B9285-1G) injections were performed 24 hours and 4 hours prior to dissection. Mice were genotyped by PCR or Transnetyx. All animal studies were approved by the Institutional Animal Care and Use Committee at UCSF.

Histology/immunostaining

Tissues were fixed in Z-Fix (Anatech Ltd., 174), processed according to a standard protocol, and embedded in Paraplast Plus embedding agent for histology, with DMSO (VWR 15159-464). For immunostaining, paraffin sections were deparaffinized, rehydrated, and antigen retrieval was performed, for all antibodies except BrdU, with Antigen Retrieval Citra (Biogenex, HK086-9K) using a heat-mediated microwave method. For immunostaining of BrdU, antigen retrieval was performed as previously described (73). For IHC, endogenous peroxidase activity was blocked by incubation with 3% hydrogen peroxide (Fisher Scientific, H325-100) following antigen retrieval. Primary antibodies were incubated overnight at 4°C. Secondary antibodies were used at 1:500 and incubated at room temperature for 1 hour (IHC) or 2 hours (IF). For IF, slides were mounted in ProLong Diamond Antifade Mountant with DAPI (ThermoFisher, P36962). For IHC, Vectastain Elite ABC kit (Vector Laboratories, PK-6100) and DAB Peroxidase (HRP) Substrate kit (Vector Laboratories, SK-4100) were used. Primary antibodies used in this study are listed in Table S2. Secondary antibodies used in this study were obtained from Life Technologies and Jackson Immunoresearch.

Immunostaining of cluster markers as well as the types of ducts within the ductal hierarchy tree were reviewed and classified by a board-certified pathologist. For expression analysis of selected markers in murine and human tissues, images shown are representative of at least 3 different donors or 9 week-old C57BL/6J mice. For quantification of BrdU, cleaved caspase 3, Geminin, Ki67, H2AX, and ATR, at least 60 cells from 3 different ducts were analyzed. Normal human tissue used in this study was obtained from research consented human cadaver donors through UCSF's Islet Production Core. Human pancreatic tissue specimens from five surgical resections from patients without pancreaticobiliary carcinoma or high grade pancreatic intraepithelial neoplasia were obtained. The pancreatic histologic section demonstrated chronic pancreatitis with loss of acinar parenchyma resulting in atrophic lobules along with variable fibrosis and chronic inflammation (most had no to sparse lymphocytic inflammation).

Immunocytochemistry

Cells were grown on coverslips in 6 well plates and fixed at RT for 15 minutes with 4% paraformaldehyde. Cells were permeabilized with permeabilization solution (0.1% w/v Saponin, 5% w/v BSA in PBS-/-). The primary antibody was incubated in permeabilization solution at 4°C overnight. After washing off unbound primary antibody with PBS-/-, the secondary antibody was incubated in permeabilization solution for 1 hour at RT. After washing off unbound secondary antibody with PBS-/-, cells were mounted using ProLong Diamond Antifade Mountant with DAPI (ThermoFisher, P36962).

RNA-seq

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RNA was isolated using the RNeasy Mini Kit (Qiagen, 74106) as per manufacturer's instructions. To obtain N=3 for the HPDE E6/E7 scr gRNA control, RNA was isolated on 3 different days of subsequent passages. A stranded mRNA library prep was prepared using PolyA capture and paired-end sequencing was performed by Novogene. 40 million reads were sequenced for each sample. Quality of raw FASTQ sequences was assessed using FASTQC. To process RNA-Seq libraries, adaptor sequences were trimmed using Cutadapt version 1.14 (requiring a length greater than 10 nt after trimming) and quality-filtered by requiring all bases to have a minimum score of 20 (-m 20 -q 20). Only reads that passed the quality or length threshold on both strands were considered for mapping. Reads were aligned to the human genome GRCh38 (hg38) with the STAR Aligner (version 020201). Ensembl reference annotation version 89 was used to define gene models for mapping quantification. Uniquely mapped reads for each gene model were produced using STAR parameter "--quantMode GeneCounts." Differential expression analysis was performed in R using DESeq2 (v.1.16.0) with the default parameters, including the Cook's distance treatment to remove outliers. The RNA-seq and scRNA-seq datasets were deposited to GEO (GEO accession #GSE159343).

Cell culture assays

HPDE E6/E7 cells (74) were cultured in DMEM (Life Technologies 11995073), 10% FBS (Corning, 35011CV), 1X Penicillin : Streptomycin solution (Corning, 30-002-CI). For CellTiter-Glo Luminescent Cell Viability Assays (Promega, G7570), 1500 cells were seeded in quadruplicate per cell line in a 96 well plate in 150uL media, and luminescence was measured 5 days after plating cells. Values depicted for all cell culture experiments represent the average of at least 3 independent experiments.

For 3D proliferation assays, 1000 cells were seeded in triplicate per cell line in a drop of growth-factor reduced Matrigel (Corning, 356231) diluted 1:1 with complete HPDE media. After 4 days, images were taken of each well. For quantification, at least 40 individual spheroids per well were manually circled and the area determined using ROI tools from ImageJ (version 2.0.0). The average area of each well was normalized to the average from triplicate wells of the HPDE E6/E7 scr gRNA.

For carbonic anhydrase activity assays, cell lysates were prepared using standard protocols and cell lysis buffer (Cell Signaling Technologies, 9803S) containing 100 mM PMSF, 1X cOmplete Protease Inhibitor Cocktail (Roche, 11697498001), and 1X PhosSTOP (Sigma Aldrich, 4906845001). Carbonic anhydrase activity was measured using the Carbonic Anhydrase Activity Assay Kit (Biovision, K472-100). For normalization, equal amounts of protein (10ug) per sample were used in the assay. Protein concentration was determined using the Pierce BCA Protein Assay Kit (Thermo Fisher Scientific, 23225).

Generation of stable knockout HPDE E6/E7 cell lines

For generation of stable knockouts, gRNAs were cloned into eSPCas-LentiCRISPR v2 (Genscript). gRNA sequences are included in Table S3. Each gRNA-containing plasmid was incorporated into lentivirus. HPDE E6/E7 cells were transduced with these lentiviruses, and cells expressing the gRNA-containing plasmid were selected for with puromycin. All cell culture experiments were performed using bulk transduced HPDE E6/E7 cells.

Western blotting

Cell lysates were prepared using standard protocols and RIPA buffer (Thermo Fisher Scientific, 89901) containing 100 mM PMSF, 1X cOmplete Protease Inhibitor Cocktail (Roche, 11697498001), and 1X PhosSTOP (Sigma Aldrich, 4906845001). PVDF membranes were incubated with primary antibodies overnight at 4°C. After RT incubation with the appropriate

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HRP-conjugated secondary antibody for 1 hour, membranes were developed using SuperSignal West Pico PLUS Chemiluminescent Substrate (Thermo Scientific, 34580).

Bioinformatics and statistical analysis

We used $p \leq 0.05$ as a cutoff for DEG inclusion for IPA and IPA upstream regulator analysis. Due to low cell number and high similarity, some comparisons did not yield an acceptable number of statistically significant DEGs (≤25), and we used a relaxed $p \leq 0.1$ as a cutoff for these in order to identify more targets. GSEA was performed on the identified DEGs with the GSEA software (version 3.0) in the pre-ranked mode, with the Reactome pathway dataset (version 7.2). Data are presented as mean ± SEM and were analyzed in GraphPad Prism or Microsoft Office Excel. Statistical significance was assumed at a *P* value of ≤ 0.05. *P* values were calculated with the unpaired *t*-test. For interpretation of statistical results from unpaired *t*-test, * = *P* value ≤ 0.05, ** = *P* value ≤ 0.01, *** = *P* value ≤ 0.001, and **** = *P* value ≤ 0.0001. For all statistical analyses, outliers were identified and excluded using the Grubbs' outlier test (alpha = 0.05) or ROUT (Q=10%).

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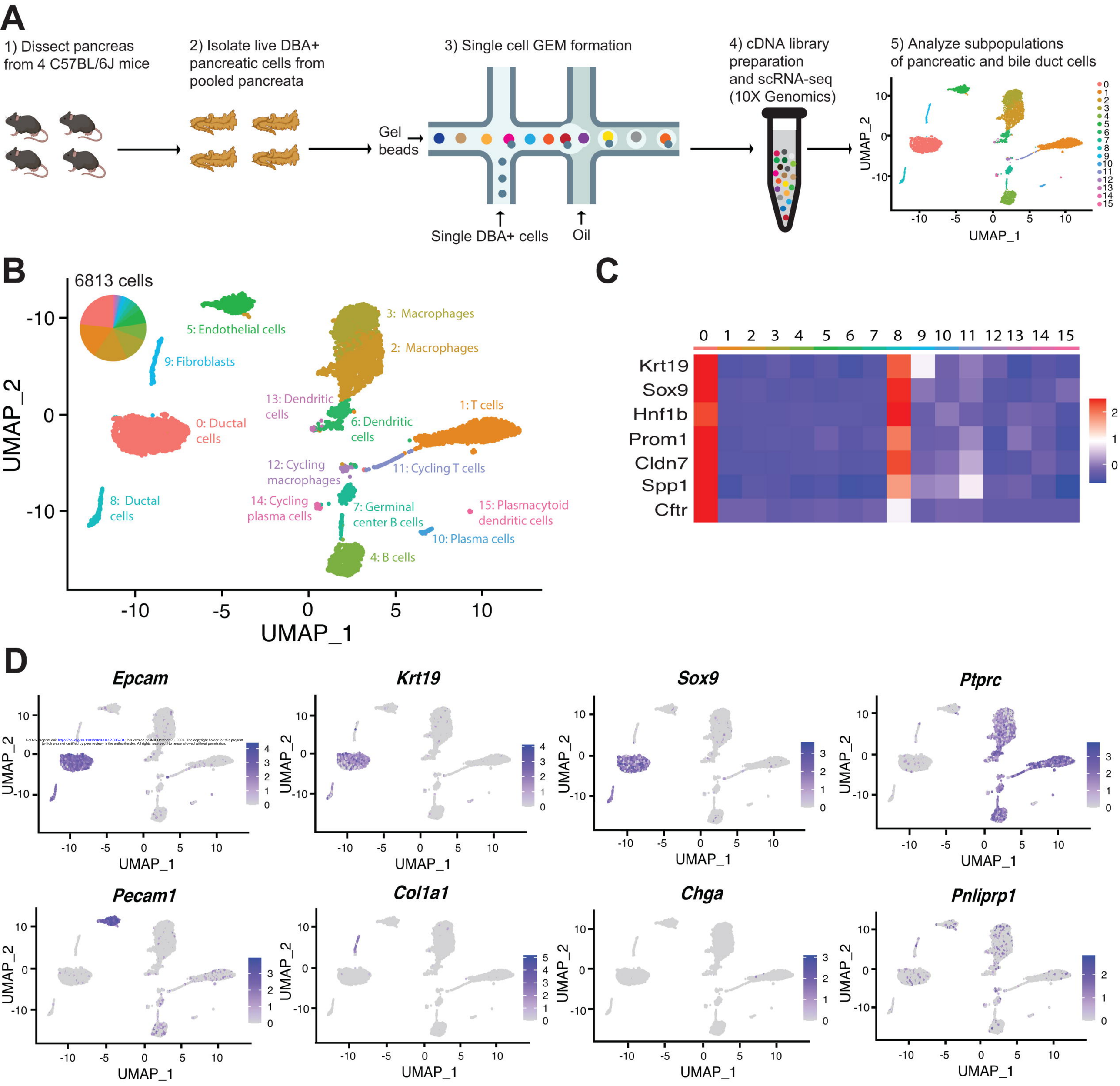

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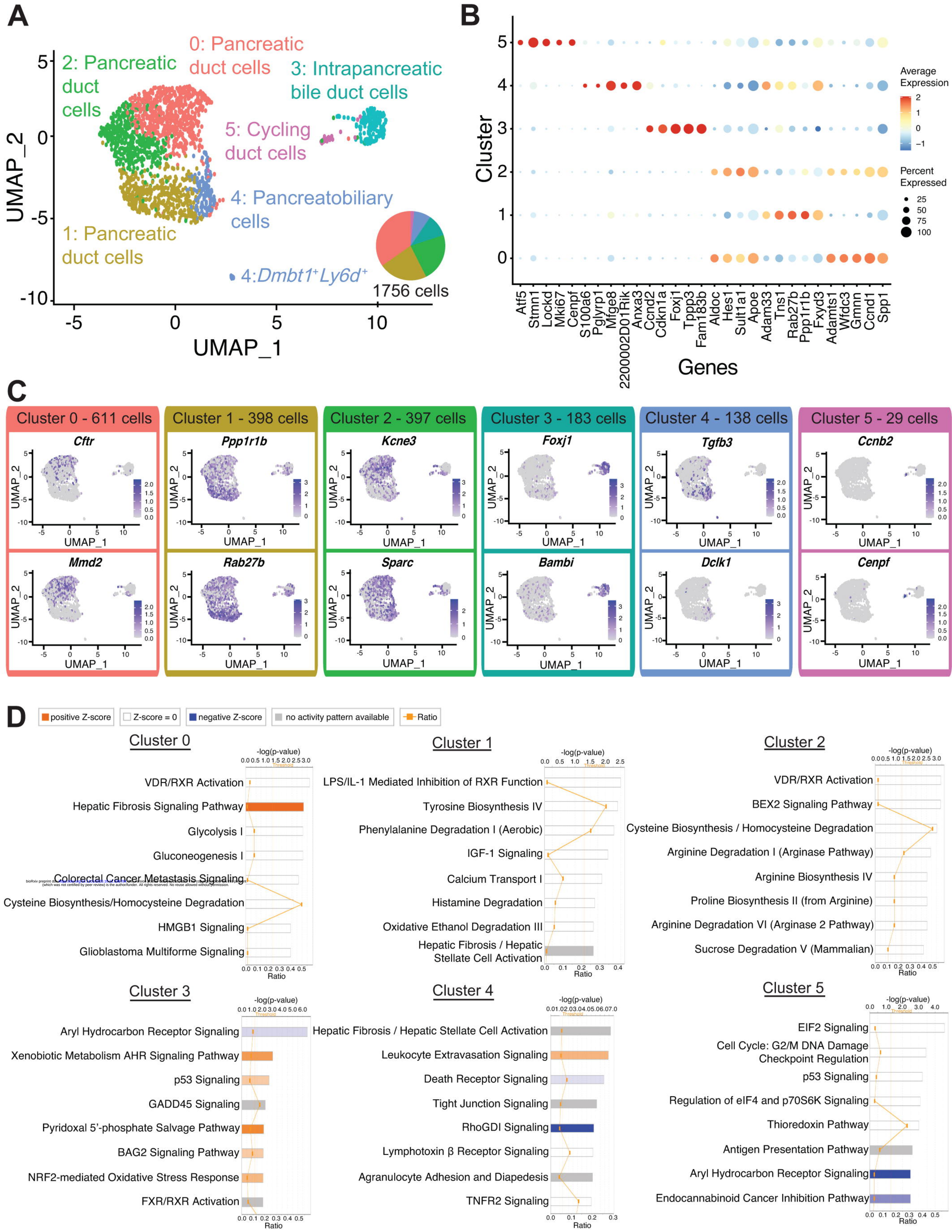

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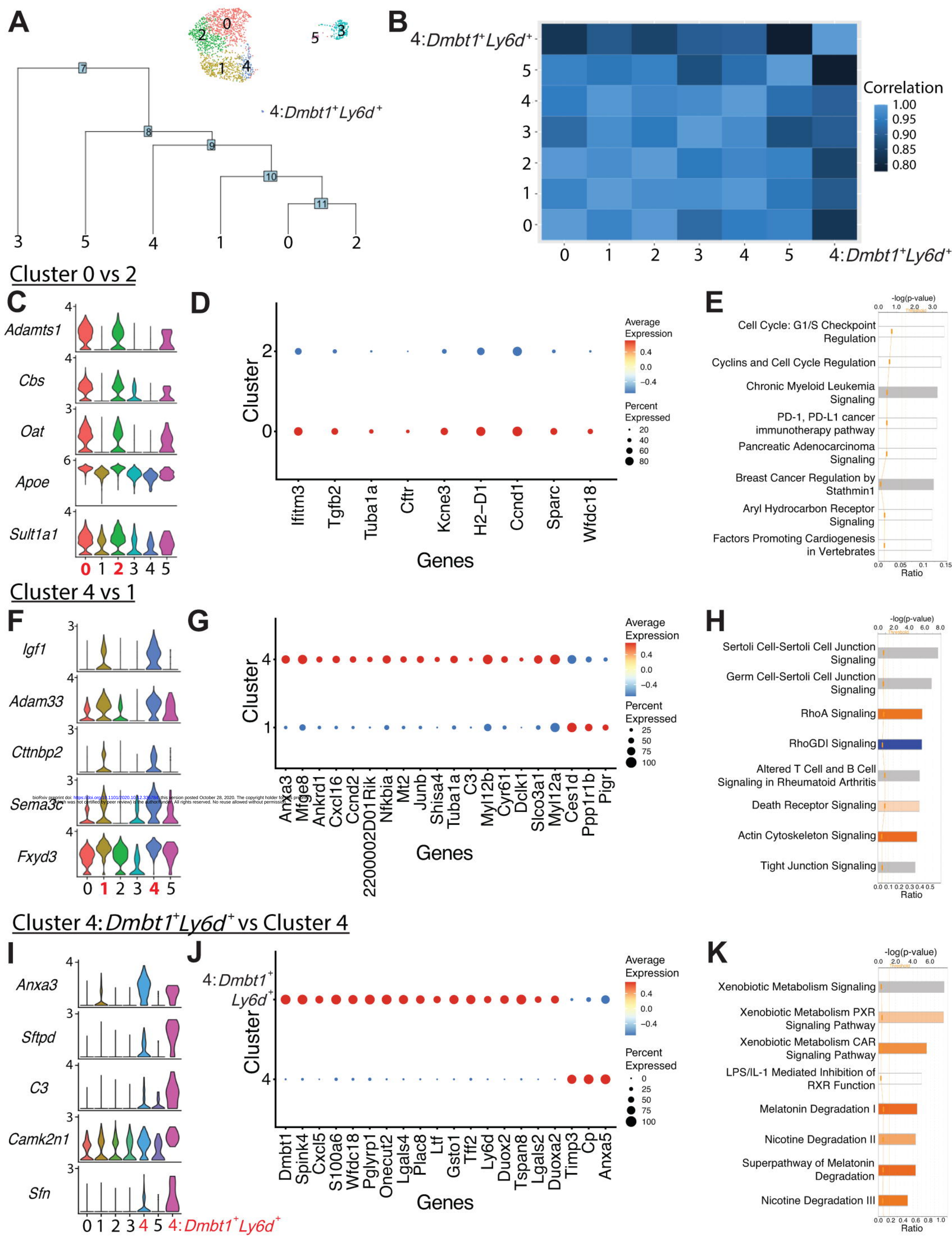

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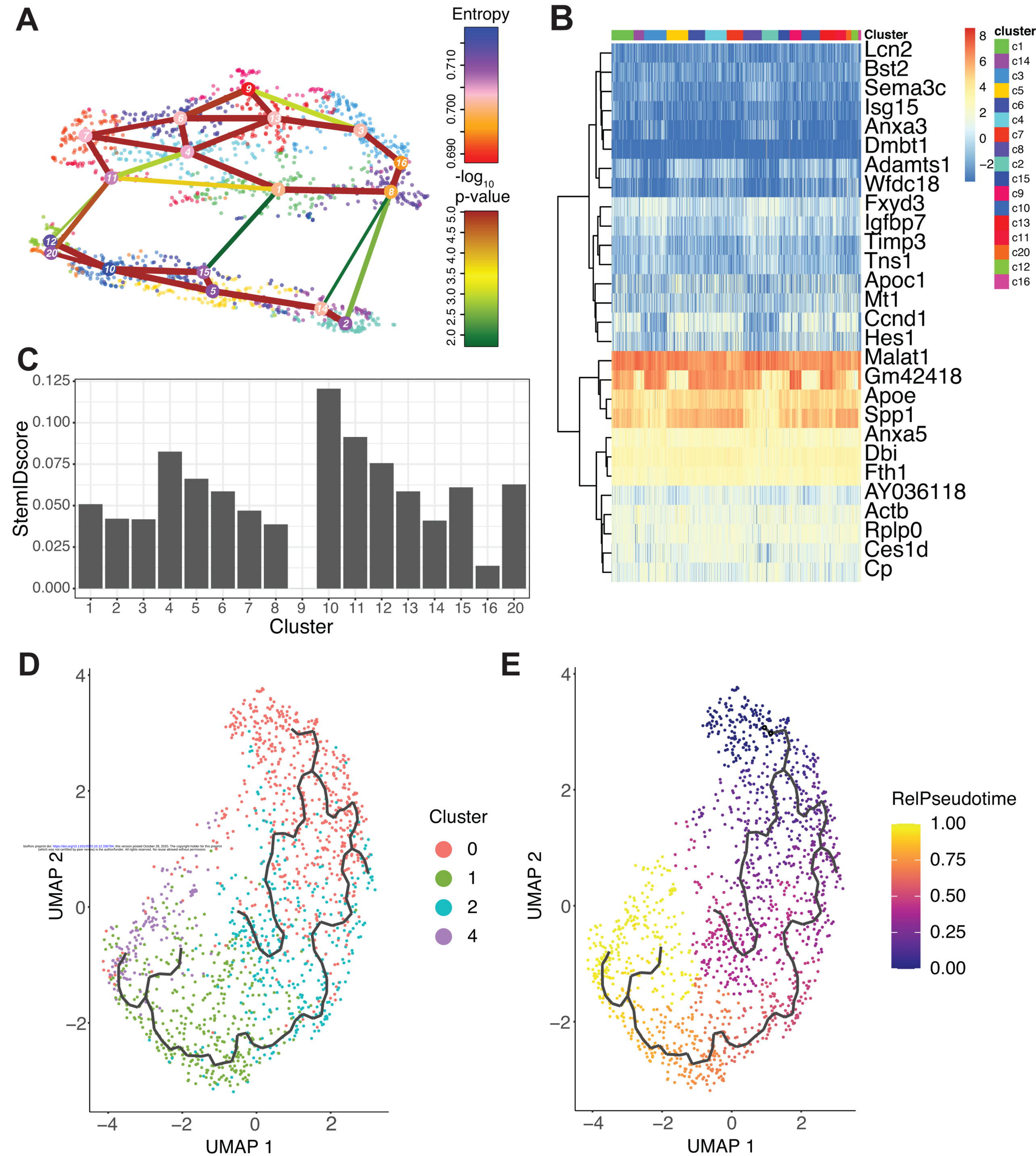

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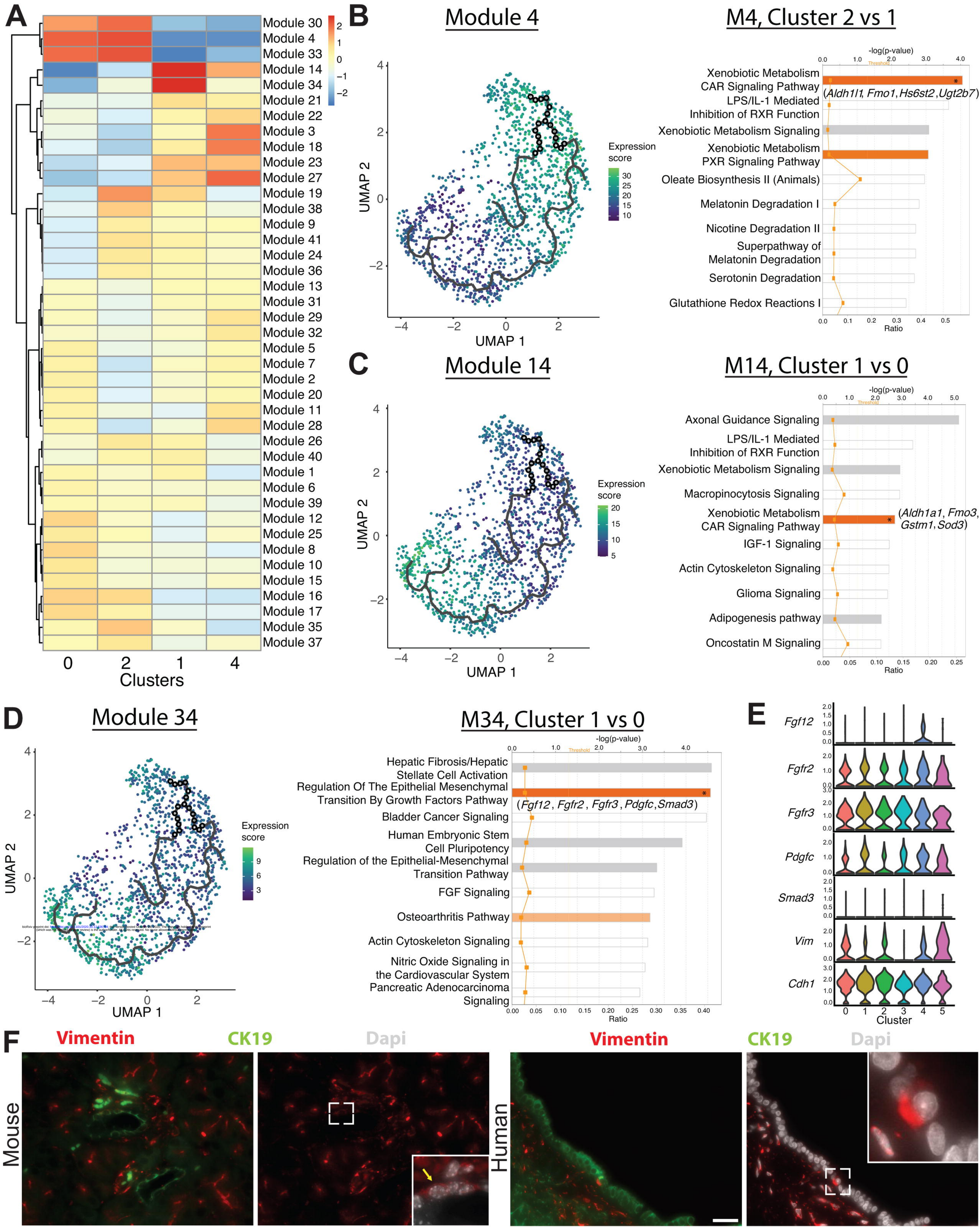
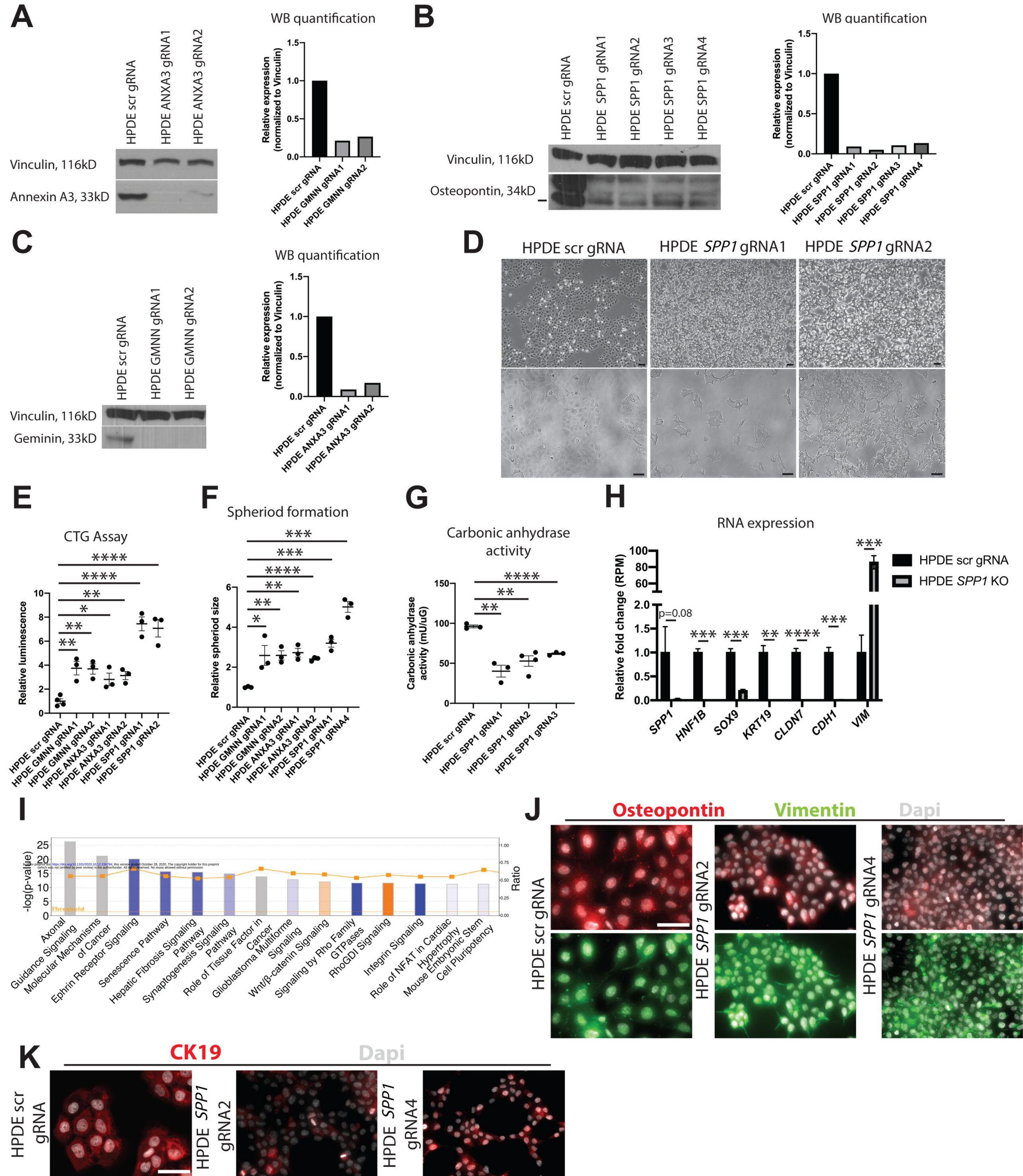

A
Module 30
Module 4
Module 33
Module 14
Module 34
Module 21
Module 22
Module 3
Module 18
Module 23
Module 27
Module 19
Module 38
Module 9
Module 41
Module 24
Module 36
Module 13
Module 31
Module 29
Module 32
Module 5
Module 7
Module 2
Module 20
Module 11
Module 28
Module 26
Module 40
Module 1
Module 6
Module 39
Module 12
Module 25
Module 8
Module 10
Module 15
Module 16
Module 17
Module 35
Module 37
0 2 1 4
Clusters
B
Module 4
UMAP 2
UMAP 1
Expression score
M4, Cluster 2 vs 1
-log(p-value)
Xenobiotic Metabolism CAR Signaling Pathway
(Aldh1l1, Fmo1, Hs6st2, Ugt2b7)
LPS/IL-1 Mediated Inhibition of RXR Function
Xenobiotic Metabolism Signaling
Xenobiotic Metabolism PXR Signaling Pathway
Oleate Biosynthesis II (Animals)
Melatonin Degradation I
Nicotine Degradation II
Superpathway of Melatonin Degradation
Serotonin Degradation
Glutathione Redox Reactions I
Ratio
C
Module 14
UMAP 2
UMAP 1
Expression score
M14, Cluster 1 vs 0
-log(p-value)
Axonal Guidance Signaling
LPS/IL-1 Mediated Inhibition of RXR Function
Xenobiotic Metabolism Signaling
Macropinocytosis Signaling
Xenobiotic Metabolism CAR Signaling Pathway
(Aldh1a1, Fmo3, Gstm1, Sod3)
IGF-1 Signaling
Actin Cytoskeleton Signaling
Glioma Signaling
Adipogenesis pathway
Oncostatin M Signaling
Ratio
D
Module 34
UMAP 2
UMAP 1
Expression score
M34, Cluster 1 vs 0
-log(p-value)
Hepatic Fibrosis/Hepatic Stellate Cell Activation
Regulation Of The Epithelial Mesenchymal Transition By Growth Factors Pathway
(Fgf12, Fgfr2, Fgfr3, Pdgfc, Smad3)
Bladder Cancer Signaling
Human Embryonic Stem Cell Pluripotency
Regulation of the Epithelial-Mesenchymal Transition Pathway
FGF Signaling
Osteoarthritis Pathway
Actin Cytoskeleton Signaling
Nitric Oxide Signaling in the Cardiovascular System
Pancreatic Adenocarcinoma Signaling
Ratio
E
Fgf12
Fgfr2
Fgfr3
Pdgfc
Smad3
Vim
Cdh1
Cluster
F
Vimentin
CK19
Dapi
Mouse
Human



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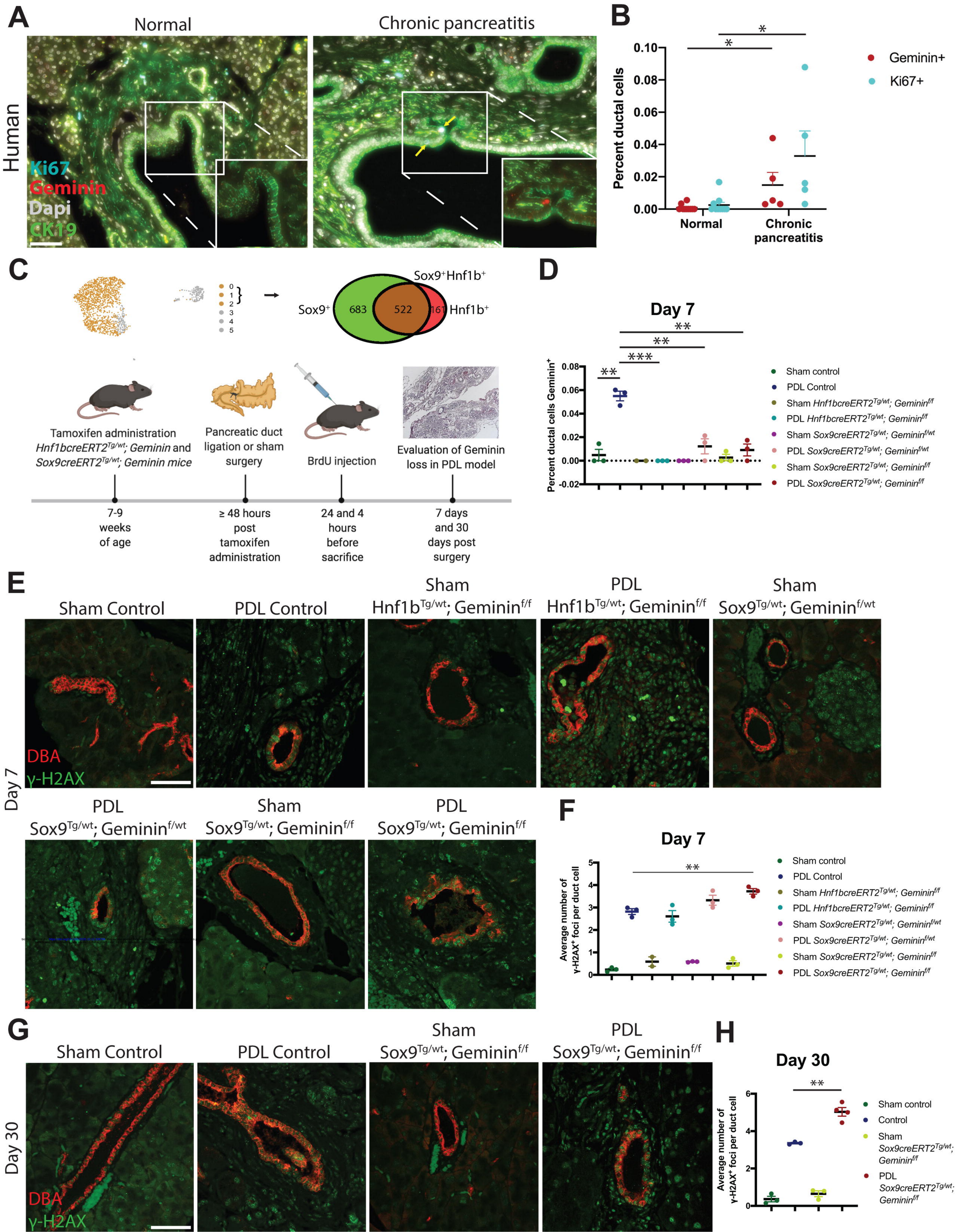
A
Normal
Chronic pancreatitis
Human
Ki67
Geminin
Dapi
CK19
B
Percent ductal cells
0.10
0.08
0.06
0.04
0.02
0.00
Normal
Chronic pancreatitis
Geminin+
Ki67+
C
0
1
2
3
4
5
Sox9+Hnf1b+
Sox9+
683
522
161
Hnf1b+
Tamoxifen administration
Hnf1bcreERT2Tg/wt; Geminin and
Sox9creERT2Tg/wt; Geminin mice
Pancreatic duct ligation or sham surgery
BrdU injection
Evaluation of Geminin loss in PDL model
7-9 weeks of age
≥ 48 hours post tamoxifen administration
24 and 4 hours before sacrifice
7 days and 30 days post surgery
D
Day 7
Percent ductal cells Geminin+
0.08
0.06
0.04
0.02
0.00
-0.02
Sham control
PDL Control
Sham Hnf1bcreERT2Tg/wt; Geminin f/f
PDL Hnf1bcreERT2Tg/wt; Geminin f/f
Sham Sox9creERT2Tg/wt; Geminin f/wt
PDL Sox9creERT2Tg/wt; Geminin f/wt
Sham Sox9creERT2Tg/wt; Geminin f/f
PDL Sox9creERT2Tg/wt; Geminin f/f
E
Sham Control
PDL Control
Sham Hnf1bTg/wt; Geminin f/f
PDL Hnf1bTg/wt; Geminin f/f
Sham Sox9Tg/wt; Geminin f/wt
Day 7
DBA
γ-H2AX
PDL Sox9Tg/wt; Geminin f/wt
Sham Sox9Tg/wt; Geminin f/f
PDL Sox9Tg/wt; Geminin f/f
F
Day 7
Average number of γ-H2AX+ foci per duct cell
Sham control
PDL Control
Sham Hnf1bcreERT2Tg/wt; Geminin f/f
PDL Hnf1bcreERT2Tg/wt; Geminin f/f
Sham Sox9creERT2Tg/wt; Geminin f/wt
PDL Sox9creERT2Tg/wt; Geminin f/wt
Sham Sox9creERT2Tg/wt; Geminin f/f
PDL Sox9creERT2Tg/wt; Geminin f/f
G
Sham Control
PDL Control
Sham Sox9Tg/wt; Geminin f/f
PDL Sox9Tg/wt; Geminin f/f
Day 30
DBA
γ-H2AX
H
Day 30
Average number of γ-H2AX+ foci per duct cell
Sham control
Control
Sham Sox9creERT2Tg/wt; Geminin f/f
PDL Sox9creERT2Tg/wt; Geminin f/f