Expanded View Figures

Figure EV1. PSCs play a role in mesenchymal-like PDAC cell migration in 3D organotypic co-cultures.

A An axial slice of the entire tumor containing pancreatic head and duodenum (left panel) was embedded in paraffin, and sections were cut and histochemically stained for PSR (right panel). Scale bar represents 1 cm.

B Gene expression of collagens in online available datasets of epithelial-like (blue) and mesenchymal-like (red) PDAC cell lines. Scale (0–10) represents log2 transformation.

C Schematic representation of organotypic mono and co-culture of PDAC cells and pancreatic stellate cells (PS-1). H&E staining was performed on organotypic cultures of indicated PDAC cell lines. Scale bar represents 100 μm.

D Organotypic mono- and co-cultures were stained for CK19 with IHC. Scale bar represents 100 μm.

E Organotypic PANC-1 mono- and co-cultures were stained for EpCAM with IHC. Scale bar represents 100 μm.

F Organotypic PS-1 monocultures were stained for α-SMA, CK19, and EpCAM with IHC. Scale bar represents 100 μm.

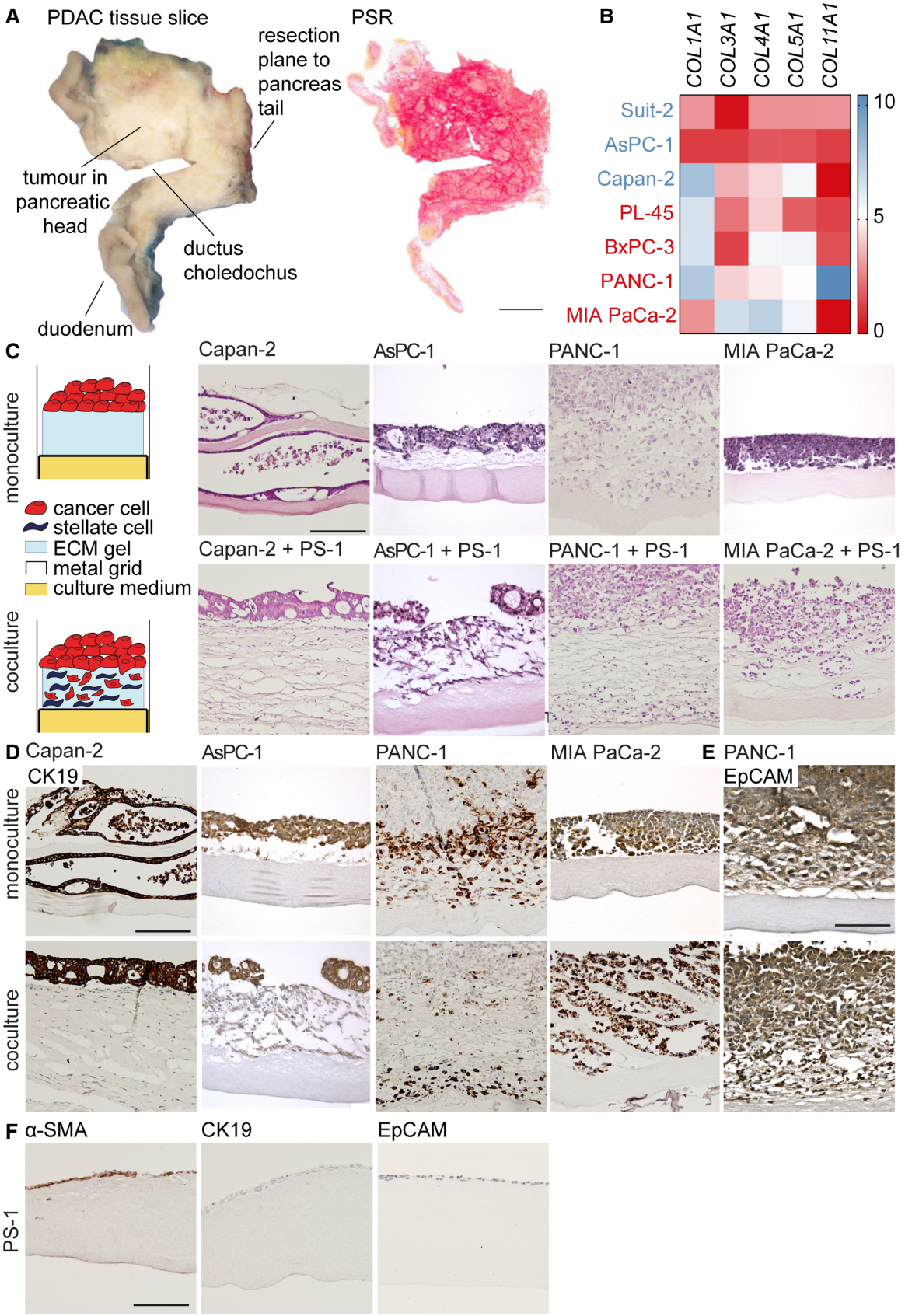

Figure EV1.

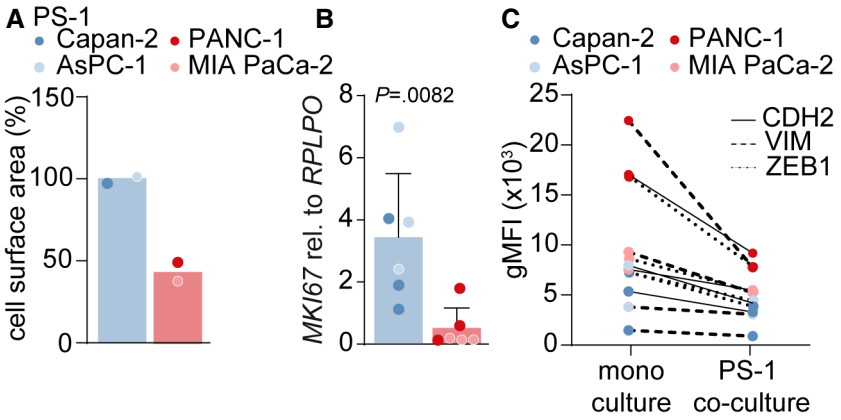

Figure EV2. PSCs reduce mesenchymal markers in PDAC cells.

A Quantification of cell surface area of PS-1 cells after treatment with CM from control (CM of PS-1 cells), epithelial (blue), or mesenchymal (red) cell lines, using ImageJ. Cell surface area was normalized to average epithelial CM value. For each cell line, area was measured once.

B Gene expression level of proliferation-marker *MKi67* in PS-1 cells after treatment indicated in panel A using qPCR. Data were normalized against control CM. Student's *t*-test. $n = 6$ per group, 3 biological replicates for each cell line.

C Mesenchymal markers CDH2, VIM, and ZEB1 were measured in PDAC cells that were mono- or co-cultured with mCherry-expressing PS-1 cells with flow cytometry. Representative graph of $n = 2$.

Data information: (B and C, A and B), data are represented as mean ± SD, Student's *t*-test.

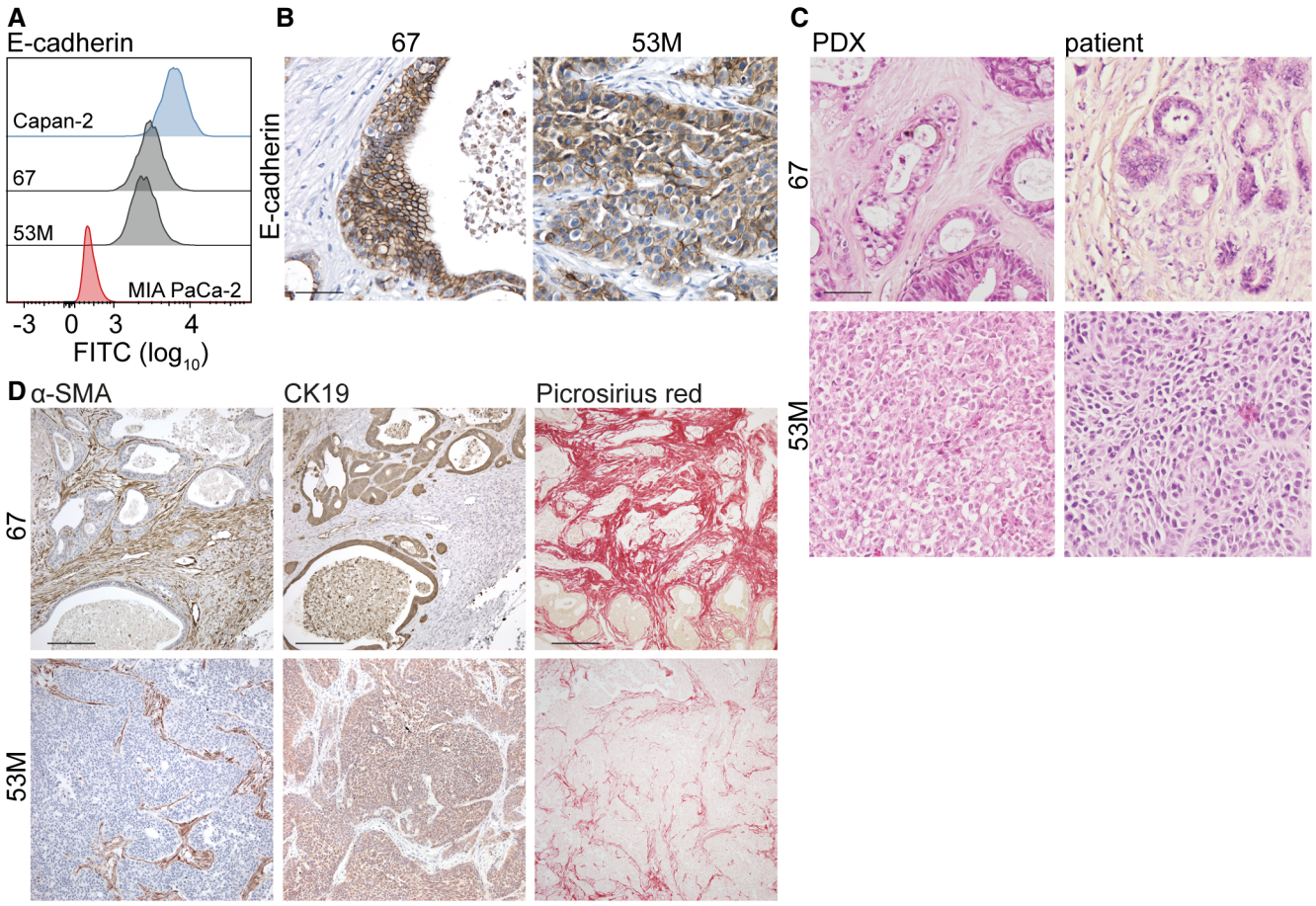

Figure EV3. Grading of established primary human PDAC cultures.

A Protein expression of E-cadherin in indicated cell lines was assessed with flow cytometry.

B E-cadherin was stained in established PDX tumors of 67 and 53M with IHC. Scale bar represents 50 μm.

C H&E histochemical staining was performed in established PDX tumors and matching primary PDAC tissue of patient 67 and 53M. Scale bar represents 50 μm.

D α-SMA, CK19, and PSR were stained in established PDX tumors of 67 and 53M with (immuno)histochemistry. Scale bar represents 200 μm for α-SMA and CK19 and 500 μm for PSR images.

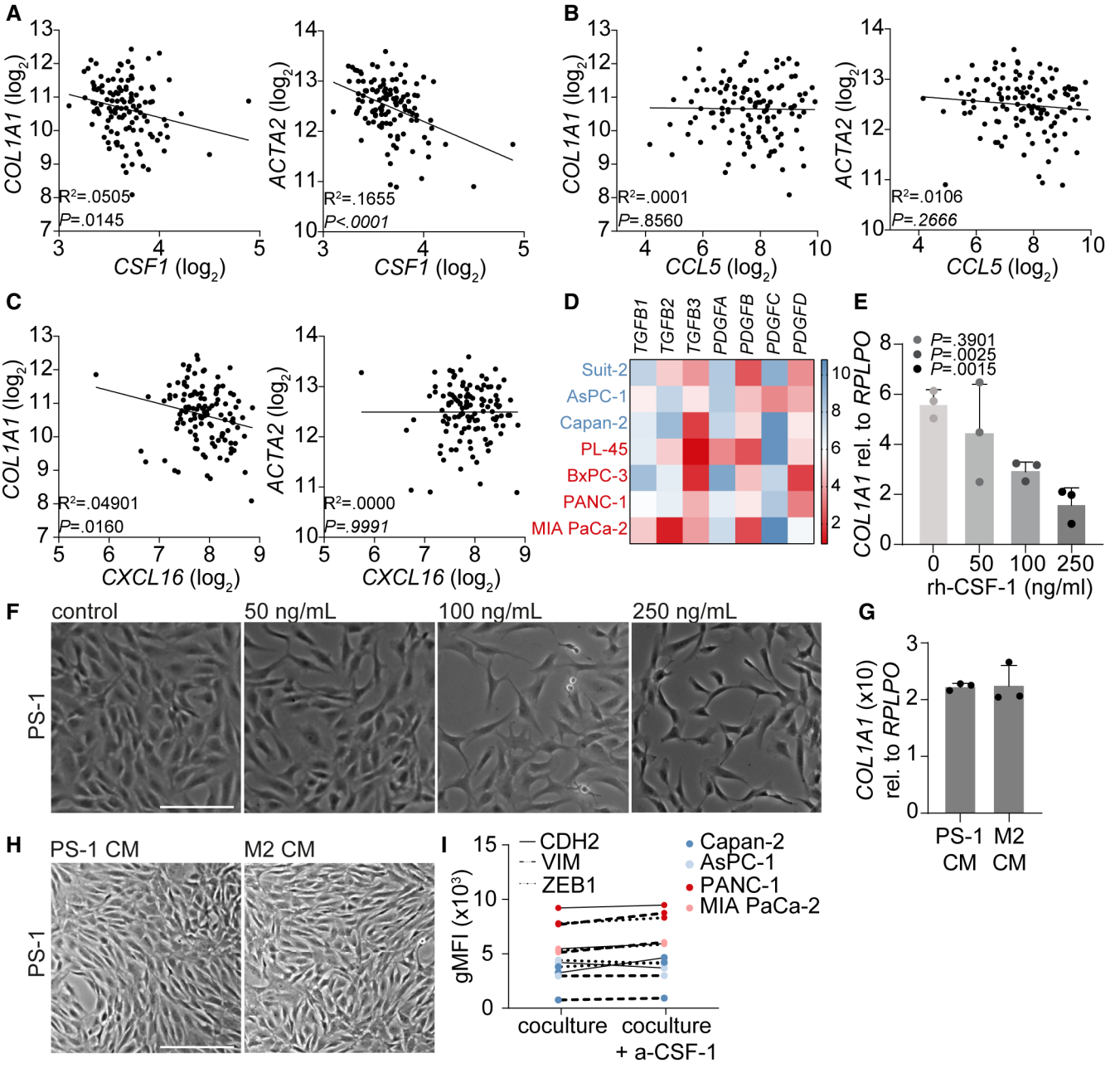

Figure EV4. *CSF1* expression correlates with *COL1A1* and *ACTA2* in tumors.

A–C Correlation between *CSF1* (A), *CCL5* (B), and *CXCL16* (C) gene expression and *COL1A1* or *ACTA2* gene expression in online available PDAC patient datasets. R^2 and *P*-value were analyzed with linear regression.

D Expression of stromal activation markers *TGFB1-3* and *PDGFA-D* in online available datasets of epithelial-like (blue) and mesenchymal-like (red) PDAC cell lines. Scale (2–10) represents $\log_2$ transformation.

E Relative gene expression of *COL1A1* in PS-1 cells exposed to indicated concentrations of recombinant human CSF-1 using qPCR. n = 3 biological replicates per group.

F Brightfield images of PS-1 cells after treatment indicated in panel E. Scale bar represents 100 μm.

G Relative gene expression of *COL1A1* in PS-1 cells after 72-h treatment with control CM (PS-1 CM) or M2 macrophages CM using qPCR. n = 3 biological replicates per group.

H Brightfield images of PS-1 cells after 72-h treatment with control CM (PS-1 CM) or M2 macrophages CM. Scale bar represents 100 μm.

I Mesenchymal markers CDH2, VIM, and ZEB1 were measured in PDAC cells that were co-cultured with mCherry-expressing PS-1 cells with or without CSF1R inhibition using flow cytometry. Representative graph of n = 2.

Data information: (E and G), data are represented as mean ± SD, Student's *t*-test.