***eLife’s* transparent reporting form**

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**Sample-size estimation**

* You should state whether an appropriate sample size was computed when the study was being designed
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* If no explicit power analysis was used, you should describe how you decided what sample (replicate) size (number) to use

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Details on sample sizes and statistical analyses are described in the figure legends.

**Replicates**

* You should report how often each experiment was performed
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* High-throughput sequence data should be uploaded before submission, with a private link for reviewers provided (these are available from both GEO and ArrayExpress)

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**Statistical reporting**

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* Report exact p-values wherever possible alongside the summary statistics and 95% confidence intervals. These should be reported for all key questions and not only when the p-value is less than 0.05.

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(For large datasets, or papers with a very large number of statistical tests, you may upload a single table file with tests, Ns, etc., with reference to sections in the manuscript.)

**Group allocation**

* Indicate how samples were allocated into experimental groups (in the case of clinical studies, please specify allocation to treatment method); if randomization was used, please also state if restricted randomization was applied
* Indicate if masking was used during group allocation, data collection and/or data analysis

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For analysis of IL1A expression in pancreatic cancer patient samples, samples were designated as TP63high or TP63low based on Z score expression values >0.35 or <0, respectively, as previously described in Somerville et al, *Cell Reports* (2018).

**Additional data files (“source data”)**

* We encourage you to upload relevant additional data files, such as numerical data that are represented as a graph in a figure, or as a summary table
* Where provided, these should be in the most useful format, and they can be uploaded as “Source data” files linked to a main figure or table
* Include model definition files including the full list of parameters used
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Supplemental File 1 contains the genes corresponding to the Group 1 and Group 2 PSC clusters and the ranked gene list used for GSEA. Supplemental File 2 contains the iCAF and myCAF gene signatures. Supplemental File 3 contains genes significantly upregulated in the human and mouse compartments of SUIT2-TP63 versus SUIT2-empty tumors and ranked gene lists used for GSEA. Supplemental File 4 contains genes significantly downregulated in each sorted fraction of TP63-negative versus TP63-positive KLM1 tumors and gene lists used for GSEA.

The RNA-seq and ChIP-seq data in this study is available in the Gene Expression Omnibus database https://www.ncbi.nlm.nih.gov/geo/ with accession number GSE140484 and reviewer token clapkyskrlqpjkj