## **Supplemental information**

## Contextual cues from cancer cells govern

## cancer-associated fibroblast heterogeneity

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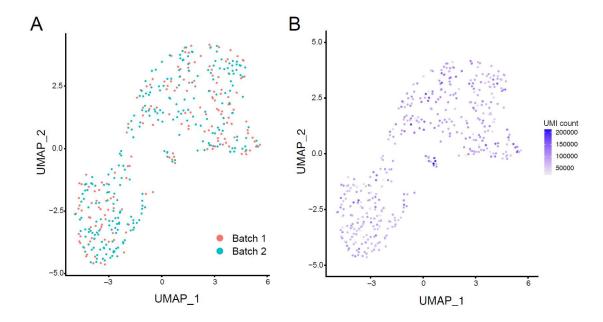


Figure S1. Single-cell RNA sequencing quality controls. Related to Figure 1. (A, B) PCA plots depict batch #1 and #2 (A) and Unique Marker Identifier (UMI) numbers in each cell (B).



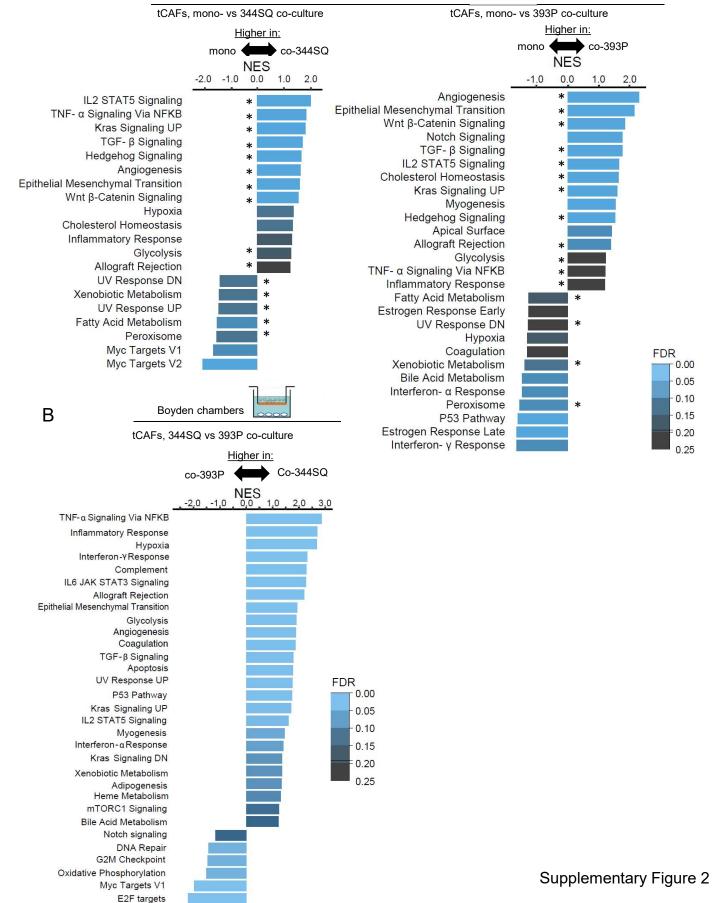
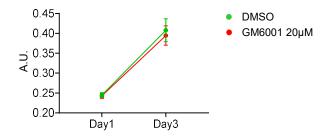


Figure S2. LUAD cells at either end of the EMT spectrum shape tCAF heterogeneity. Related to Figure 2. (A) GSEA of upregulated genes in tCAFs that were mono-cultured (mono-) or co-cultured with 344SQ cells (co-344SQ) or 393P cells (co-393P) in multicellular aggregates. n= 3 biological replicates per condition. (B) GSEA of upregulated genes in tCAFs that were co-cultured with 344SQ cells (co-344SQ) or 393P cells (co-393P) in Boyden Chambers. NES represented by bar length. FDR values color-coded. n= 5 biological replicates per condition. Hallmarks that were shared between Boyden chambers and multicellular aggregates are indicated (A, asterisks).



Supplementary Figure 3

Figure S3. Relative densities of tCAFs treated for indicated time periods with 20µM GM6001 (red) or vehicle dimethylsulfoxide (blue) determined by WST-1 assay. Related to Figure 4. A.U.: Absorbance units. n=3 biological replicates per condition.

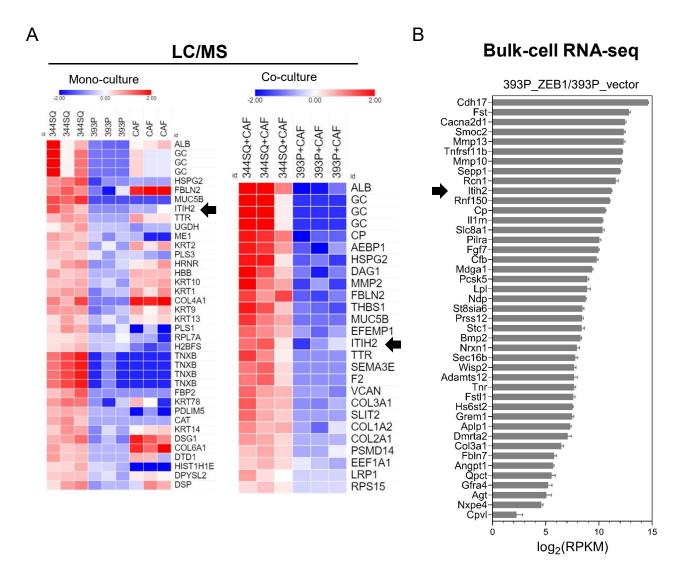


Figure S4. Identification of ZEB1-driven secreted factors. Related to Figure 6. (A) Heat map depiction of selected secreted factors identified by liquid chromatography-mass spectrometry analysis of conditioned medium samples from multicellular aggregates containing monocultured cells (left heat map) or co-cultured cells (right heat map). All proteins depicted had a P value < 0.05 (t-test). n=3 biological replicates per condition. (B) Relative levels of selected secreted factors identified by bulk-cell RNA sequencing (Tan et al., 2018). Values expressed as a ratio (393P\_ZEB1/393P\_vector). Log2FC: Log2 of fold change. n=3 biological replicates per condition