

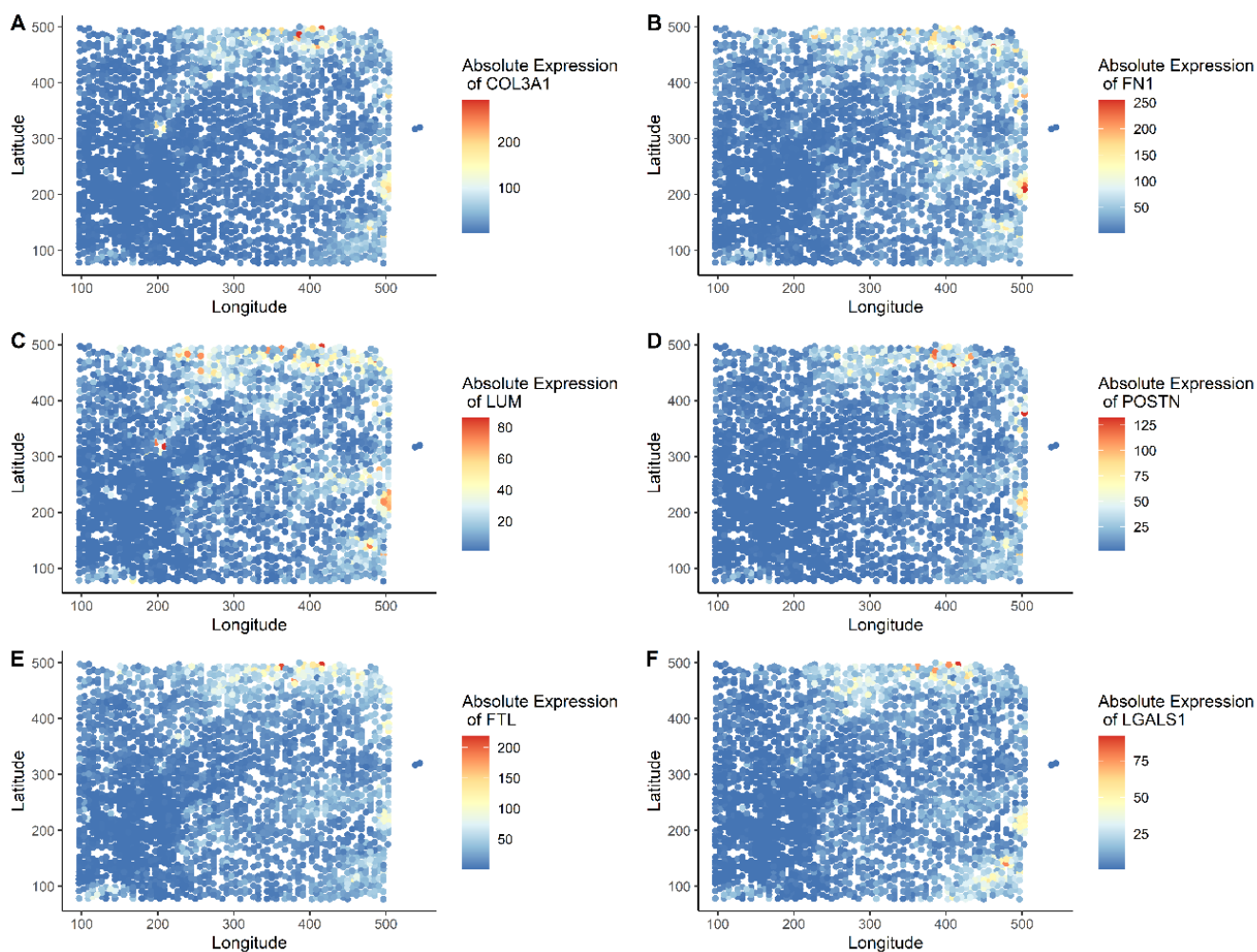
## Supplementary Materials

**Supplementary Table S1:** Validation of the differentially expressed genes identified by GATHER using pathway over-representation analysis based on Database for Annotation, Visualization and Integrated Discovery (DAVID – <https://david.ncifcrf.gov/>).

<i>CAF Marker</i>	Top 20 differentially expressed genes	The most significant over-represented KEGG pathway	P-value
<i>COL11A1</i>	High CAF vs. Medium CAF	Protein digestion and absorption	<0.001
	Medium CAF vs. Low CAF	ECM-receptor interaction	<0.001
<i>S100A4</i>	High CAF vs. Medium CAF	ECM-receptor interaction	<0.001
	Medium CAF vs. Low CAF	Protein digestion and absorption	<0.001
<i>CXCL12</i>	High CAF vs. Medium CAF	Protein digestion and absorption	<0.001
	Medium CAF vs. Low CAF	Focal adhesion	<0.001
<i>C3</i>	High CAF vs. Medium CAF	Lysosome	<0.001
	Medium CAF vs. Low CAF	Protein digestion and absorption	<0.001
<i>FBLN1</i>	High CAF vs. Medium CAF	PI3K-Akt signaling	<0.001
	Medium CAF vs. Low CAF	Focal adhesion	<0.001

**Supplementary Table S2:** Top 10 most significant differentially expressed genes in the dataset of the present study identified using two common RNA-seq data analysis methods such as edgeR and DESeq2.

<b>Methods</b>	<b>edgeR</b>	<b>DESeq2</b>
<b>G1</b>	<i>TMSB10</i>	<i>COL3A1</i>
<b>G2</b>	<i>COL3A1</i>	<i>FTL</i>
<b>G3</b>	<i>FN1</i>	<i>SPARC</i>
<b>G4</b>	<i>SPARC</i>	<i>TMSB10</i>
<b>G5</b>	<i>FTL</i>	<i>POSTN</i>
<b>G6</b>	<i>POSTN</i>	<i>FN1</i>
<b>G7</b>	<i>ACTB</i>	<i>LUM</i>
<b>G8</b>	<i>TMSB4X</i>	<i>VIM</i>
<b>G9</b>	<i>B2M</i>	<i>LGALS1</i>
<b>G10</b>	<i>LUM</i>	<i>B2M</i>



**Supplementary Figure S1:** The spatial distribution of six selected genes from the supplementary table T2 are shown. Longitude and latitude show the spatial coordinates of cells in the input tumor sample, and colors show the absolute expression of each of the selected genes over the tissue space. Red/blue color indicates high/low expression of the gene in a given cell.