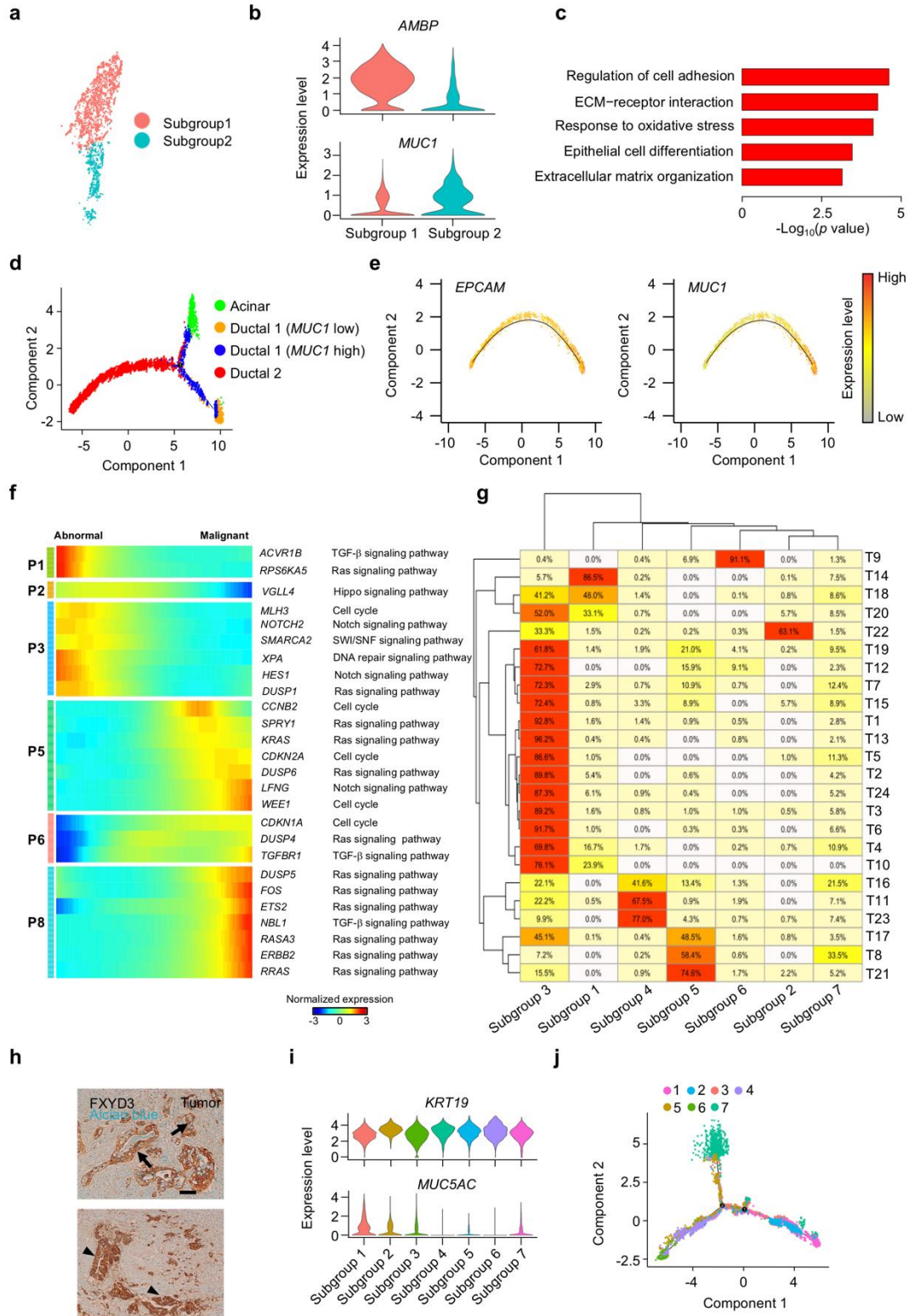


# Supplementary information, Figure S3



**Figure S3. Construction of Malignant Ductal Cell Progression Trajectory by Pseudo-time Analysis, Related to Figure 3**

(a) t-SNE representation of 2 subgroups generated from sub-clustering type 1 ductal cells in PDAC.

(b) Violin plots showing the expression level of representative markers for normal (*AMBP*) and neoplastic (*MUC1*) ductal cells in two subgroups.

(c) The representative functions enriched in subgroup 2.

(d) Pseudo-time of acinar, type 1 and 2 ductal cells in all PDAC samples inferred by Monocle2. Each point corresponds to a single cell. Sample information are shown.

(e) Expression of representative genes are mapped to the single-cell trajectory plot. Color key from grey to red indicates relative expression levels from low to high.

(f) Heatmap showing expression of representative known PDAC-associated genes across single cells. Corresponding pathways for each gene were also shown. Color key from blue to red indicates relative expression levels from low to high.

(g) Heatmap showing the percentage of each malignant cell subcluster in PDAC patients.

(h) IHC images of representative PDAC tissues from one patient stained for type 2 ductal cell marker (FXYD3) and PanIN staining (Alcian blue), which showed regions in or not in PanIN state. Scale bar, 100  $\mu$ m. Long arrow: Alcian blue/FXYD3 positive; Arrow head: FXYD3 positive.

(i) The violin plots showing the expression level of representative markers *KRT19* and *MUC5AC* for PanINs.

(j) Pseudo-time of 7 subgroups in type 2 ductal cells inferred by Monocle2. Each point corresponds to a single cell. Clusters information was shown.