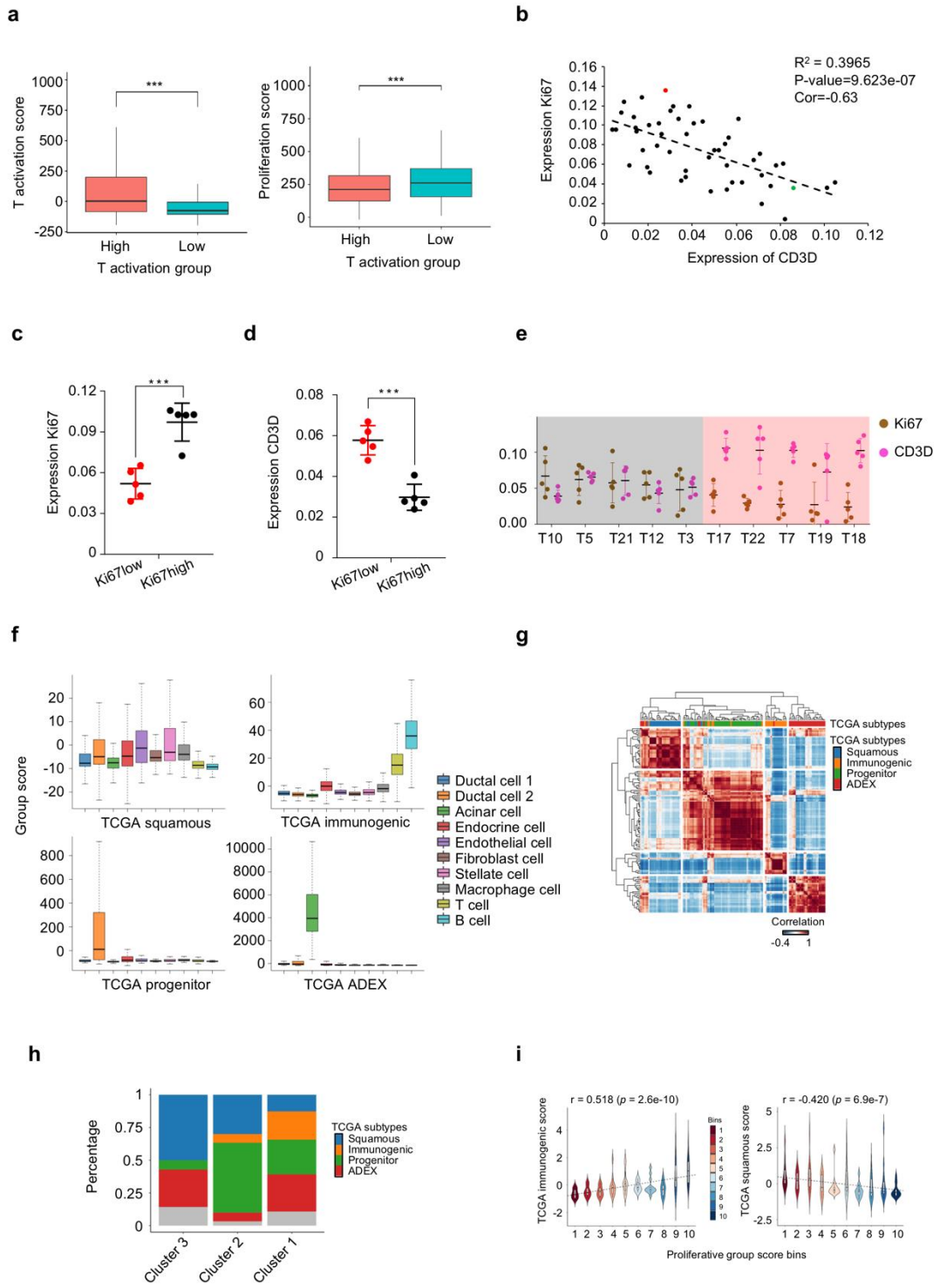**Figure S5. PDAC Subtypes Revised by analyzing expression profiles from thousands of tumor single cells, Related to Figure 5**

(**a**) Boxplot showing the T activation score and proliferative score of samples in two groups that divided by T activation score in PDAC single cell RNA-seq data. The *P* value was calculated using Wilcoxon rank sum and signed rank test.

(**b**) Correlations between the mean intensity of Ki67 in the area of tumor cells and the mean intensity of CD3D were shown (n=5 views/per patient x 10 patients=50 views). Red spot represented view of T22 and green spot represented view of T10 in (Figure 5f)

(**c-d**) Average Ki67 (c) or CD3D (d) expression of each patient (5 views/per patient) in these two groups were analyzed. "***" represented p < 0.001.

(**e**) Intensity of Ki67 and CD3D were shown among 10 PDAC patients. Patients were divided into Ki67-low (T10, T5, T21, T12, T3) and Ki67-high (T17, T22, T7, T19, T18) groups.

(**f**) Boxplot showing the signature scores for TCGA four subtypes in each cell type of PDAC.

(**g**) Heatmap depicting pairwise correlations between TCGA expression profiles ordered by their subtype annotations.

(**h**) Barplot showing relative TCGA subtype percentage for each PDAC group in Fig. 4d.

(**i**) Violin plots showing the signature scores of TCGA squamous and immunogenic subtype in ten bins that divided by increasing ranking of proliferative clustering score. Correlations of signature scores between proliferative cluster and TCGA subtype were measured using Spearman's rank correlation coefficient.