Supplementary Figure S8





KPC2 shATG7



Supplementary Fig. S8. scRNA-seq analysis and immunofluorescence images revealed that CD8⁺ T cells in KPC-shATG7 tumors express high LAG3 levels

(A) Heatmap of the top 10 differentially expressed genes (DEGs) in each of the CD8⁺ T cell clusters identified in Fig. 5A.

(B) CD8⁺ T cells were divided into cells derived from shNC tumors (left) and those derived from shATG7 tumors (right).

(C) The proportions of the three $CD8^+$ T cell clusters in the two tumor groups.

(**D**, **E**) The dot plots showed the gene sets used for the comparison of the two groups of tumors: "Effector signature score" and "Proliferation score" in Prolif.CD8⁺ T cells (D), and "Exhaustion signature scores" in Prog.Exh.CD8⁺ T cells and Term.Exh.CD8⁺ T cells (E).

(F, G) Immunofluorescence analysis of orthotopic syngeneic KPC1 shNC/shATG7 tumors (Fig. 2A) and KPC2 shNC/shATG7 tumors (Supplementary Fig. S4B), showing cytotoxic CD8⁺ T cells (expressing CD8a [red] and granzyme B [green] or perforin [green]). Representative images are shown. The graphs show the proportions of granzyme B⁺ CD8a⁺ cells/DAPI⁺ cells (%) and perforin⁺ CD8a⁺ cells/DAPI⁺ cells (%), and granzyme B⁺ CD8a⁺ cells/CD8a⁺ cells (%) and perforin⁺ CD8a⁺ cells/CD8a⁺ cells (%).

(H) Representative immunofluorescence images of orthotopic syngeneic KPC2 shNC and shATG7 tumors (Fig. S4B); CD8a (red) and LAG3 (green). Quantification of LAG3⁺ CD8a⁺ cells/DAPI⁺ cells (%) and LAG3⁺ CD8a⁺ cells/CD8a⁺ cells (%) is shown.

Scale bars, 100 μ m (F-H). Bars, median; Error bars, mean \pm SD; *p < 0.05, **p < 0.01, ***p < 0.001; ns, not significant; analyzed using the Student's t-test.