Supplementary Figure S3 CO-C1 C2 Percent Expressed C3 . 0 • 25 • 50 • 75 C4 C5 Average Expression C6 C7 C8 C9 C10 В DC1 migDC pDC Expression С D migDC (shNC vs shATG7) DC2 (shNC vs shATG7) Antigen-presenting genes Antigen-presenting genes shNC shNC shATG7 shATG7 Interferone-induced genes Migration genes shNC shNC shATG7 shATG7 Regulatory genes Maturation genes shNC shNC shATG7 shATG7 Ε DC1 (shNC vs shATG7) Maturation score Antigen-presenting score TLR and adaptors score shATG7 shNC shNC shATG7 shNC shATG7

Supplementary Fig. S3. scRNA-seq analysis of orthotopic syngeneic KPC1 shNC and shATG7 tumors

- (A) Dot plots showing the expression levels of well-known markers in the immune populations shown in Fig. 2C.
- **(B)** Heatmap of the top 10 differentially expressed genes (DEGs) in each of the DC clusters identified in Fig. 2D.
- (C, D) The expression levels of gene sets related to DC function were analyzed in DC2 (C) and migDC (D). The gene sets are listed in the dot-plots.
- (E) The expression levels of gene sets related to DC function were analyzed in the DC1.

Boxplots show a centerline, median; box limits, upper and lower quartiles; whiskers that extent up to $1.5 \times$ the interquartile range beyond the upper and lower quartiles (E). ns, not significant; analyzed using the Wilcoxon rank-sum test (E).