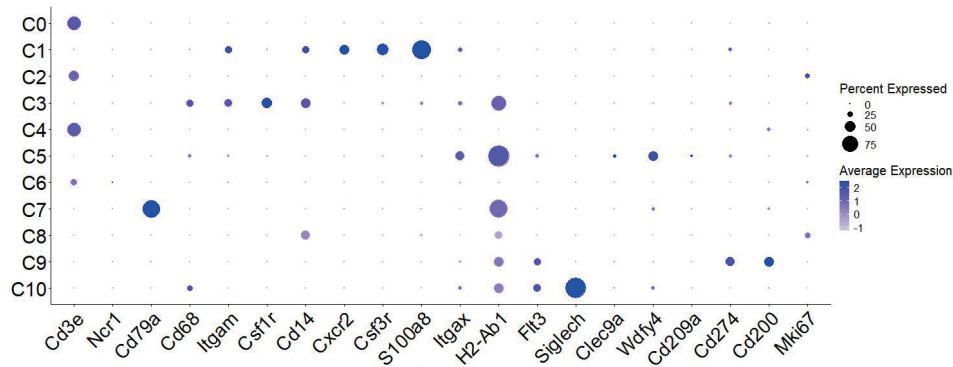
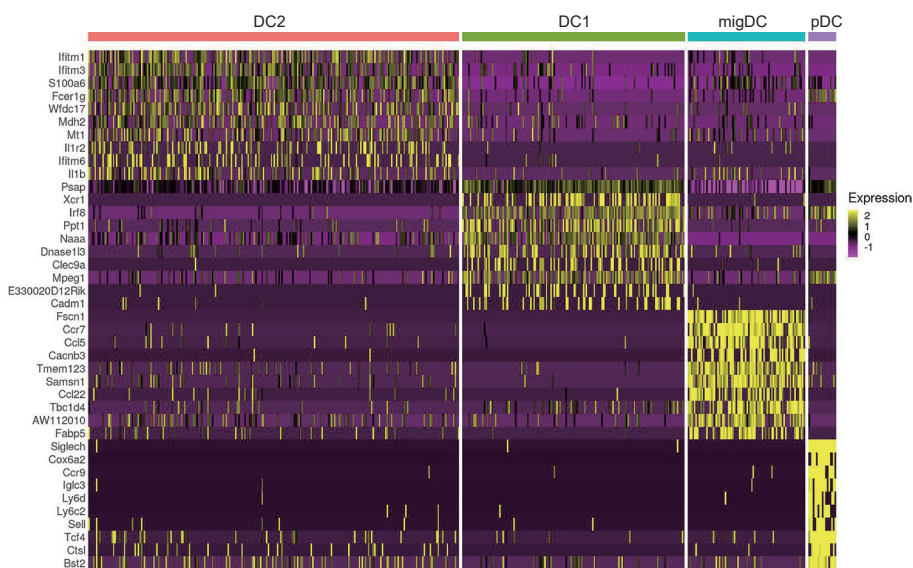


# Supplementary Figure S3

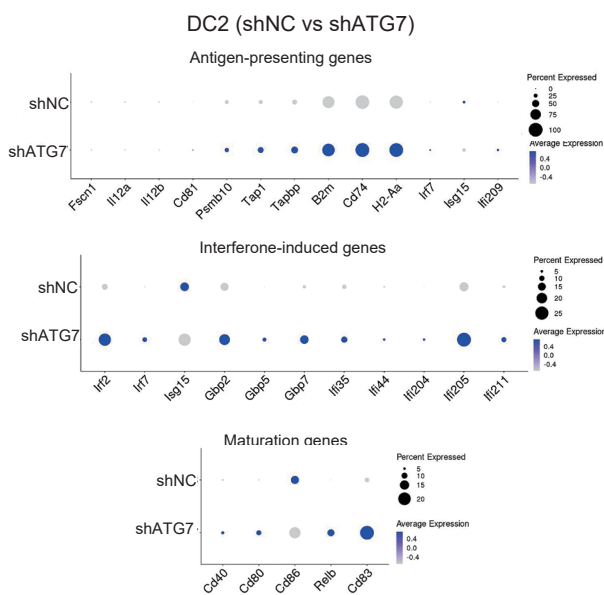
A



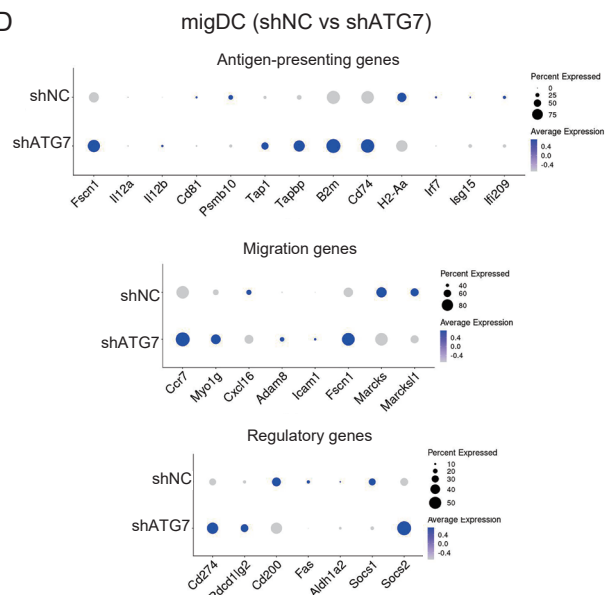
B



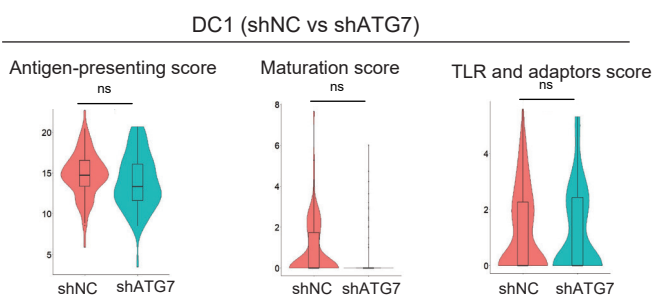
C



D



E



**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).