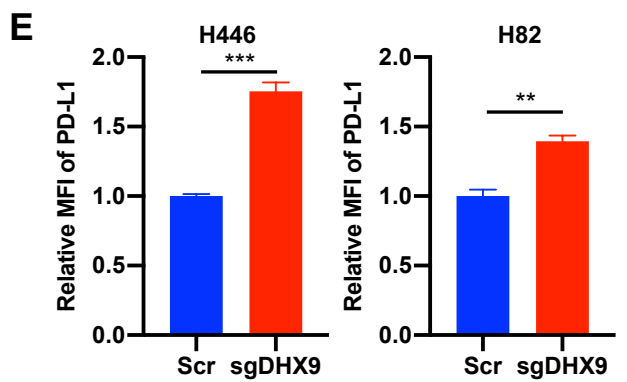
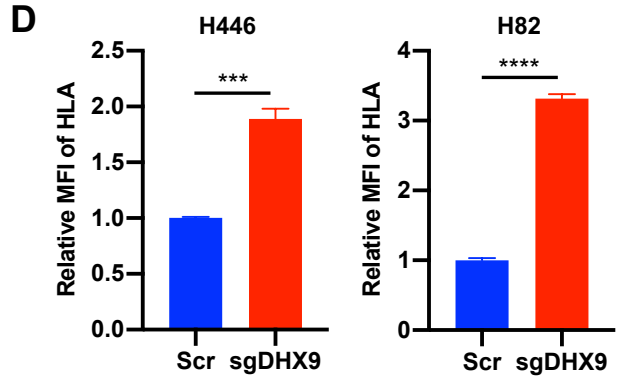
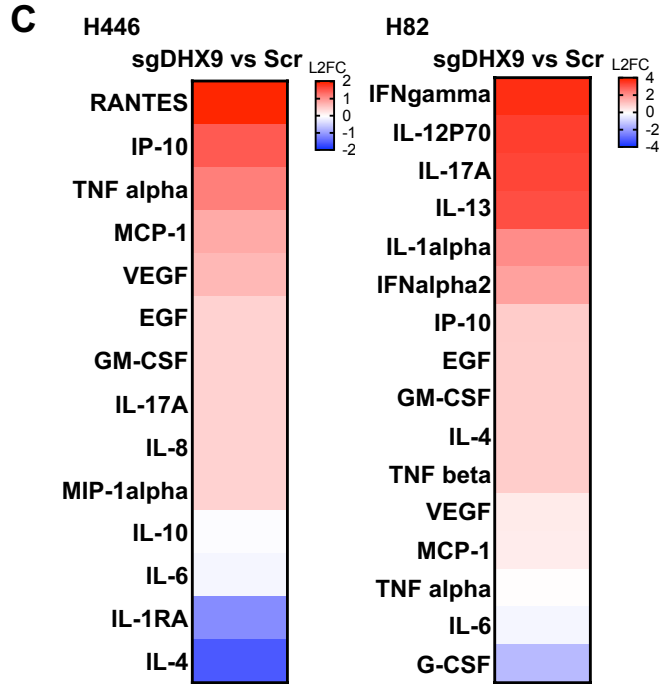
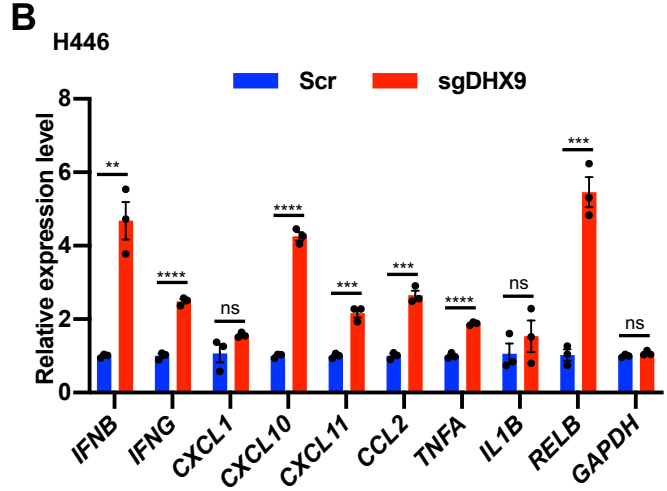
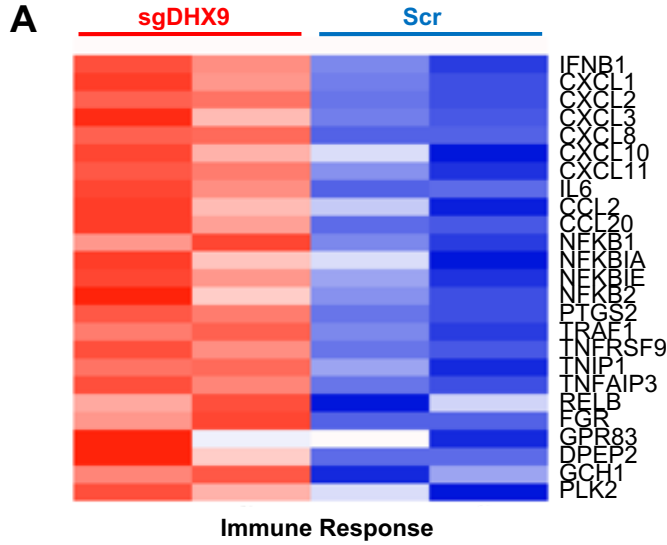


# Supplementary Figure S2



**Supplementary Figure S2.**

**A**, Heat map of RNA-seq results comparing Scramble and sgDHX9 H196 cells. **B**, qRT-PCR analysis of the immune-related genes comparing Scramble and sgDHX9 of H446 and H82 cells (n = 3). 36B4 gene was used as a reference. **C**, Log2 fold change (FC) of cytokine/chemokine differences of sgDHX9 compared to Scramble, of H446 and H82 cells. The cytokine/chemokine levels were quantified with Proteome Profiler Human Cytokine Array Kit. **D and E**, Flow cytometry analysis of HLA-A.B.C (D) or PD-L1 (E) expression on the cell surface of H446 and H82 cells (Scramble and sgDHX9). Data are representative of three independent experiments (left). Mean fluorescence intensity (MFI) was quantified by FlowJo (right) (n = 3).

Data represent mean  $\pm$  SEM. ns, not significant; \*p < 0.05, \*\*p < 0.01, \*\*\*p < 0.001, \*\*\*\*p < 0.0001 by unpaired Student's t test (B, D and E).