Supplementary Figure S7

A  SCLC (U Cologne_2015); Patient tumors

- **CXCL1**
  - Expression level (RPKM)
  - DHX9\textsuperscript{high}: Red dots
  - DHX9\textsuperscript{low}: Blue dots
  - p = 0.02

- **CCL2**
  - Expression level (RPKM)
  - DHX9\textsuperscript{high}: Red dots
  - DHX9\textsuperscript{low}: Blue dots
  - p = 0.09

- **ISG15**
  - Expression level (RPKM)
  - DHX9\textsuperscript{high}: Red dots
  - DHX9\textsuperscript{low}: Blue dots
  - p = 0.07

- **RELB**
  - Expression level (RPKM)
  - DHX9\textsuperscript{high}: Red dots
  - DHX9\textsuperscript{low}: Blue dots
  - p = 0.07

B  Pan-cancer (TCGA); Patient tumors

- **Inflammatory response**
  - NES = 2.18
  - p value < 0.01

- **Interferon alpha response**
  - NES = 1.74
  - p value = 0.04

C  Patient tumors

- **Snyder_2014**
  - Estimated immune score
  - DHX9\textsuperscript{high}: Red dots
  - DHX9\textsuperscript{low}: Blue dots
  - p = 0.04

- **Van Allen_2015**
  - Estimated immune score
  - DHX9\textsuperscript{high}: Red dots
  - DHX9\textsuperscript{low}: Blue dots
  - p = 0.24

- **Hugo_2016**
  - Estimated immune score
  - DHX9\textsuperscript{high}: Red dots
  - DHX9\textsuperscript{low}: Blue dots
  - p = 0.45
Supplementary Figure S7.

A, Expression of immune-related genes in DHX9^{low} SCLC and DHX9^{high} SCLC patient tumors. Data were downloaded from cBioPortal. B, GSEA analysis with H (hallmark) gene sets, based on RNA-seq results of pan-cancer tumors (N = 100 DHX9^{low} versus N = 100 DHX9^{high}). C, Estimated immune score of tumor microenvironment in DHX9^{low} and DHX9^{high} melanoma patient tumors. Datasets were downloaded from cBioPortal.

Data represent mean ± SEM. ns, not significant; *p < 0.05, **p < 0.01, ***p < 0.001, ****p < 0.0001 by Mann-Whitney test (A).