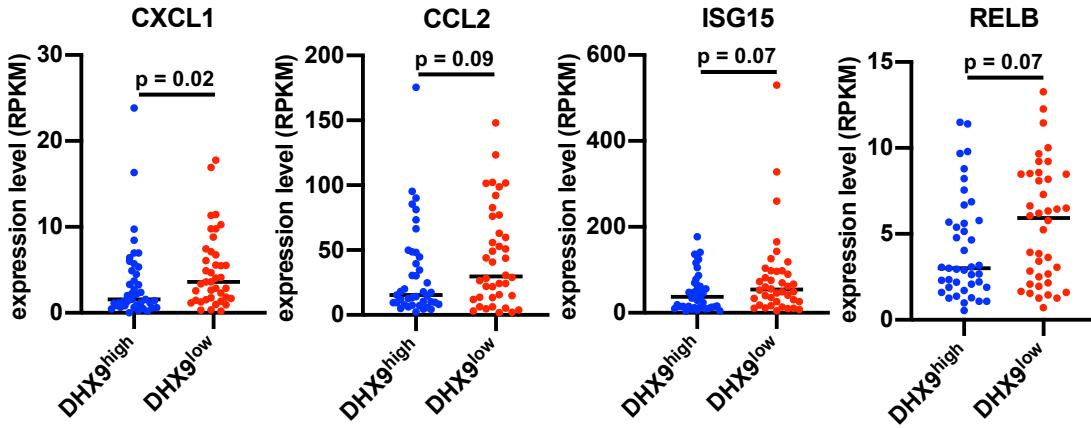
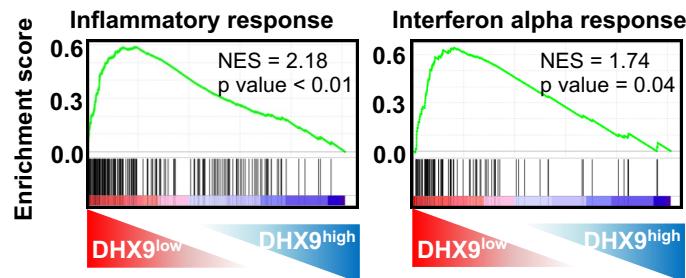


## Supplementary Figure S7

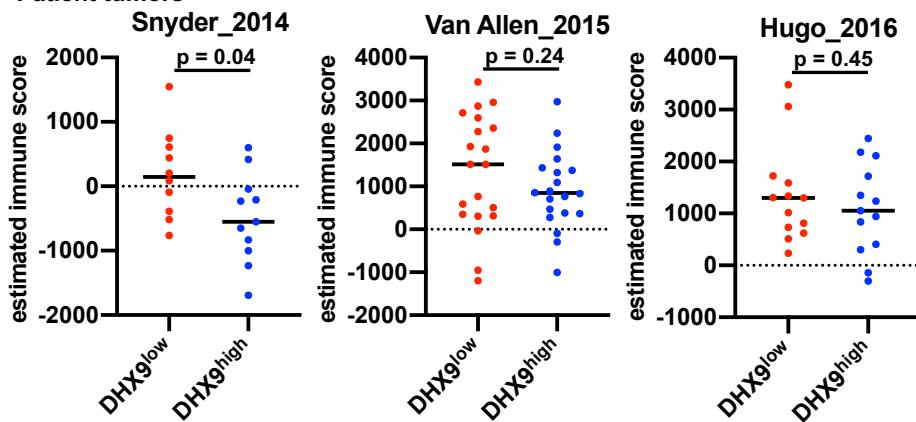
### A SCLC (U Cologne\_2015); Patient tumors



### B Pan-cancer (TCGA); Patient tumors



### C Patient tumors



**Supplementary Figure S7.**

**A**, Expression of immune-related genes in DHX9<sup>low</sup> SCLC and DHX9<sup>high</sup> 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<sup>low</sup> versus N = 100 DHX9<sup>high</sup>). **C**, Estimated immune score of tumor microenvironment in DHX9<sup>low</sup> and DHX9<sup>high</sup> melanoma patient tumors. Datasets were downloaded from cBioPortal.

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