

Supplementary Materials for

Pan-Cancer Analysis Reveals HDAC1 as a Key Regulator of Immune Infiltration and T Cell Exhaustion

Running title: A novel biomarker and therapeutic target for cancer immunotherapy

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Figure S1 to S3

and

Table S1

Figure S1

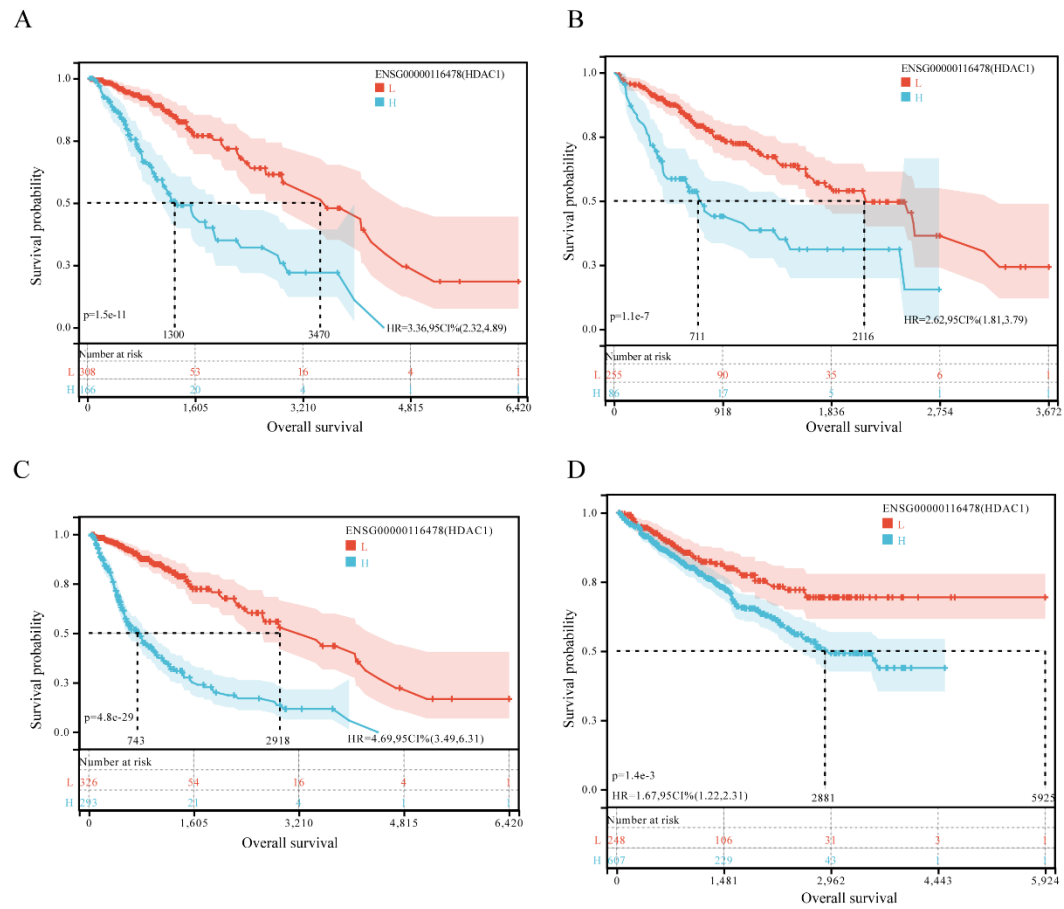


Figure S1. Kaplan-Meier survival analyses of HDAC1 expression across cancer types.

Kaplan-Meier overall survival curves comparing high (red) versus low (blue) HDAC1 expression groups in (A) LGG, (B) LIHC, (C) GBM, and (D) KIPAN. P-values were determined by log-rank test. HR, hazard ratio with 95% confidence interval.

Figure S2

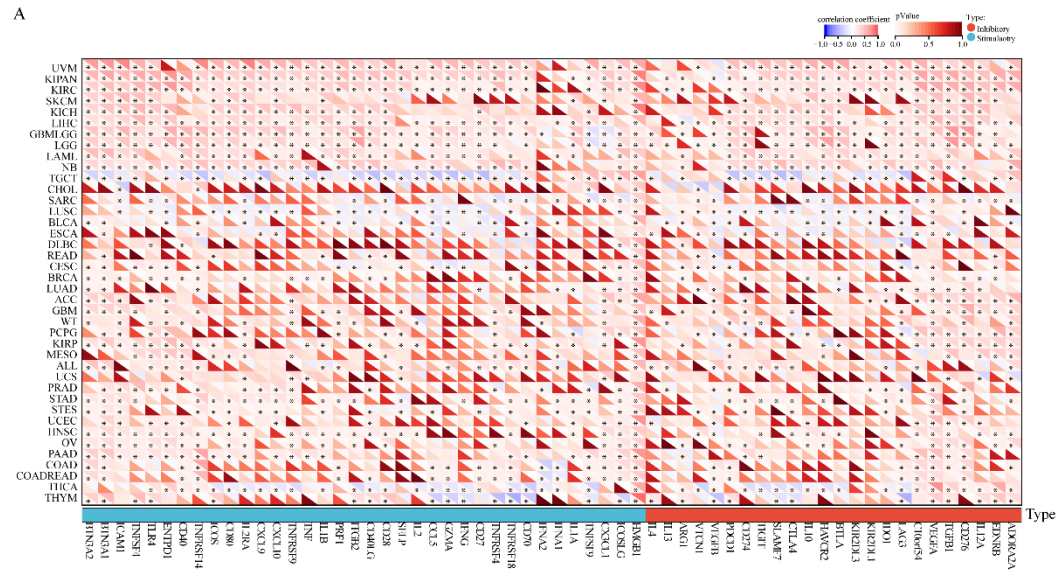


Figure S2. Correlation between HDAC1 expression and immune checkpoint genes in pan-cancer analysis.

(A) Pearson correlation matrix illustrating the relationship between HDAC1 mRNA expression and the expression of key immune checkpoint genes (e.g., PD-1/PDCD1, CTLA4, LAG3, TIM-3/HAVCR2) across the TCGA pan-cancer cohort. Each cell displays the Pearson correlation coefficient (r) and the corresponding P-value. Asterisks indicate the level of statistical significance. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$, **** $P < 0.0001$.

Figure S3



Figure S3. Uncropped original gel images corresponding to Figure 1D.

The full-length, uncropped gel images for the Western blot analysis shown in Figure 1D are presented. The images correspond to the detection of HDAC1 and the loading control (GAPDH). Sample order is consistent with that shown in the main figure. No additional image processing was performed except for uniform adjustment of brightness and contrast applied to the entire image.

Supplementary Table 1. Primers for qRT-PCR (Fig. 1).

	Forward	Reverse
mHDAC1	TGAAGCCTCACCGAATCCG CAT	TGGTCATCTCCTCAGCATTGG C
mHDAC2	GTTTTGTCAGCTCTCCACGG GT	CTTGGCATGATGTAGTCCTCCA G
mHDAC3	AACCTCATCGCCTGGCATTG AC	GTAGTCCTCAGAATGGAAGCG G
mGAPDH	AGGTCGGTGTGAACGGATT TG	TGTAGACCATGTAGTTGAGGT CA

Table S1 clarification: All primer sequences are provided in 5'-3' orientation. 'm' denotes mouse-specific primers.