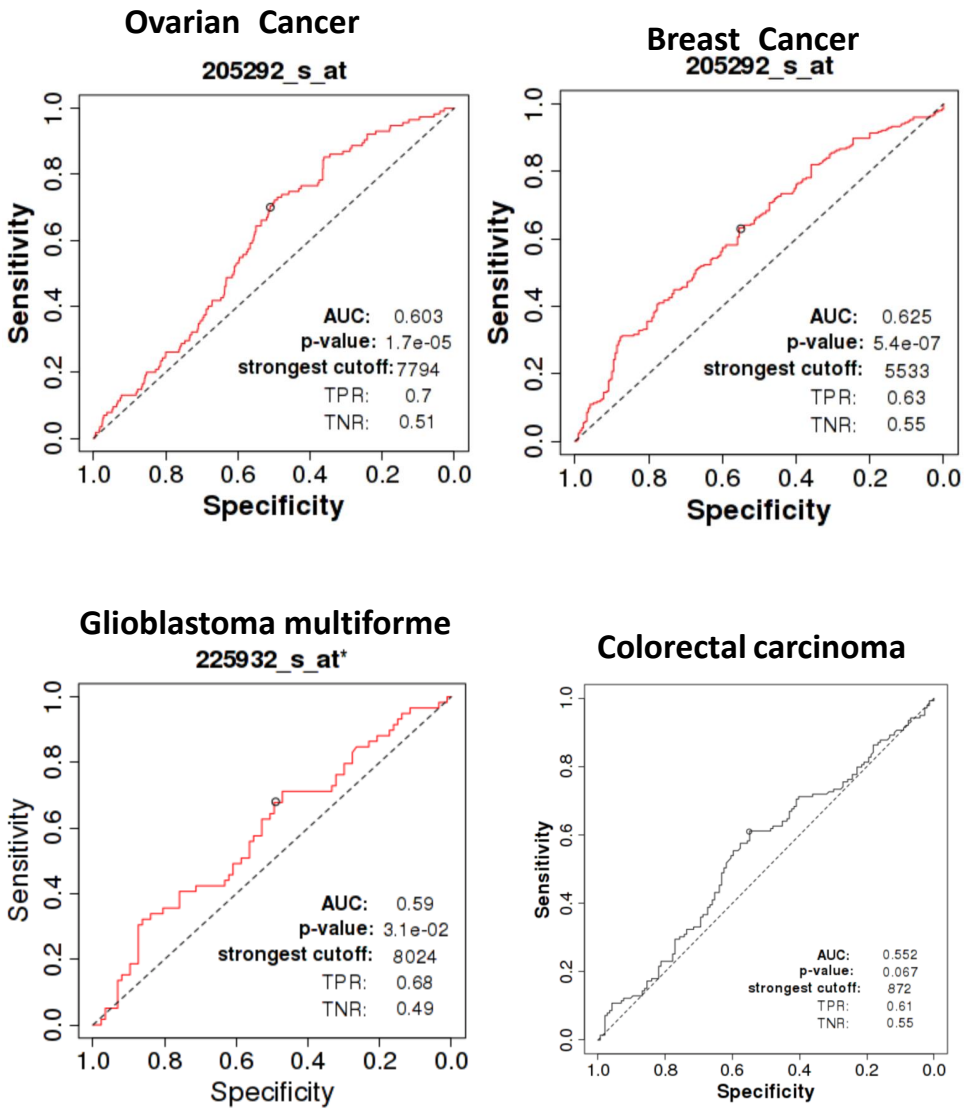

Figure S1 ROC curves were drawn via ROC plotter online ROC analysis (http://www.rocplot.org) to analyze the diagnostic efficacy of *HNRNPA2B1* gene expression in ovarian cancer, breast cancer, glioblastoma multiforme, and colorectal cancer.

© AME Publishing Company.
https://dx.doi.org/10.21037/tcr-2024-2616

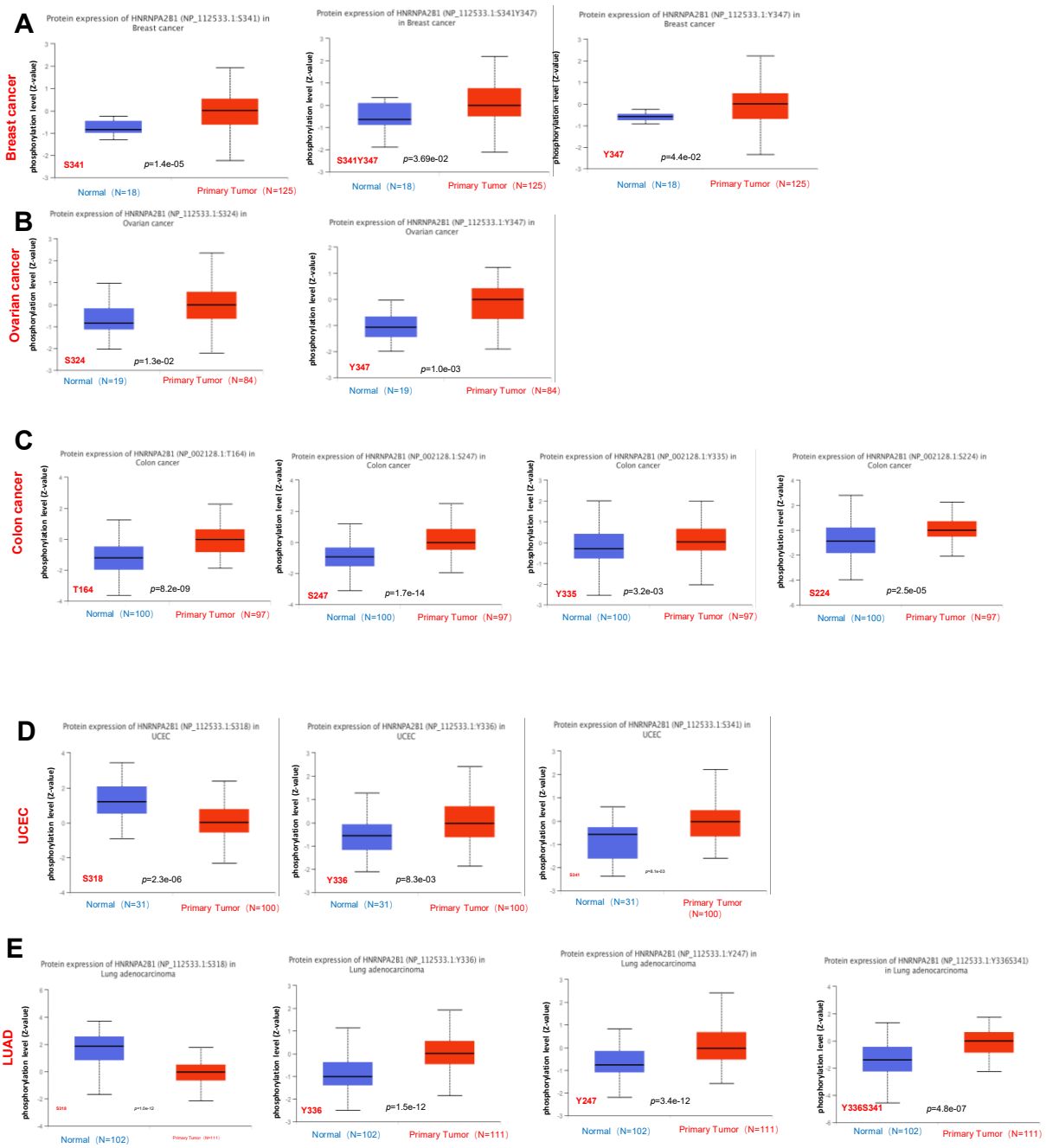

Figure S2 Differences in the phosphorylation levels of HNRNPA2B1 in normal tissues and primary tumor tissues. Analysis of HNRNPA2B1 protein phosphorylation in different tumors Based on the CPTAC dataset, we analyzed HNRNPA2B1 phosphorylation-related proteins (NP_112533.1_S212, S236, S259, S341, etc.; NP_002128.1_S90, S137, T164, etc.) in normal tumor tissues and primary tumors by UALCAN expression levels among developing tissues. Supplementary expression levels between normal and primary tumor tissues at selected sites: breast cancer (A), ovarian cancer (B), colon cancer (C), UCEC (D) and LUAD (E).

© AME Publishing Company.
https://dx.doi.org/10.21037/tcr-2024-2616

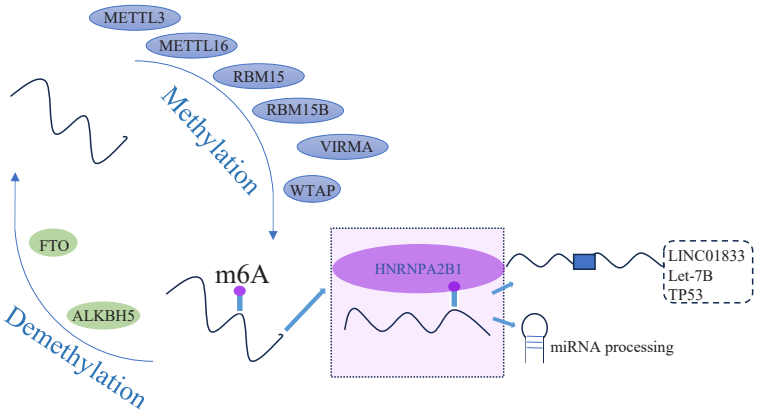

Figure S3 This diagram illustrates the dynamic process of DNA methylation regulation.

© AME Publishing Company.
https://dx.doi.org/10.21037/tcr-2024-2616

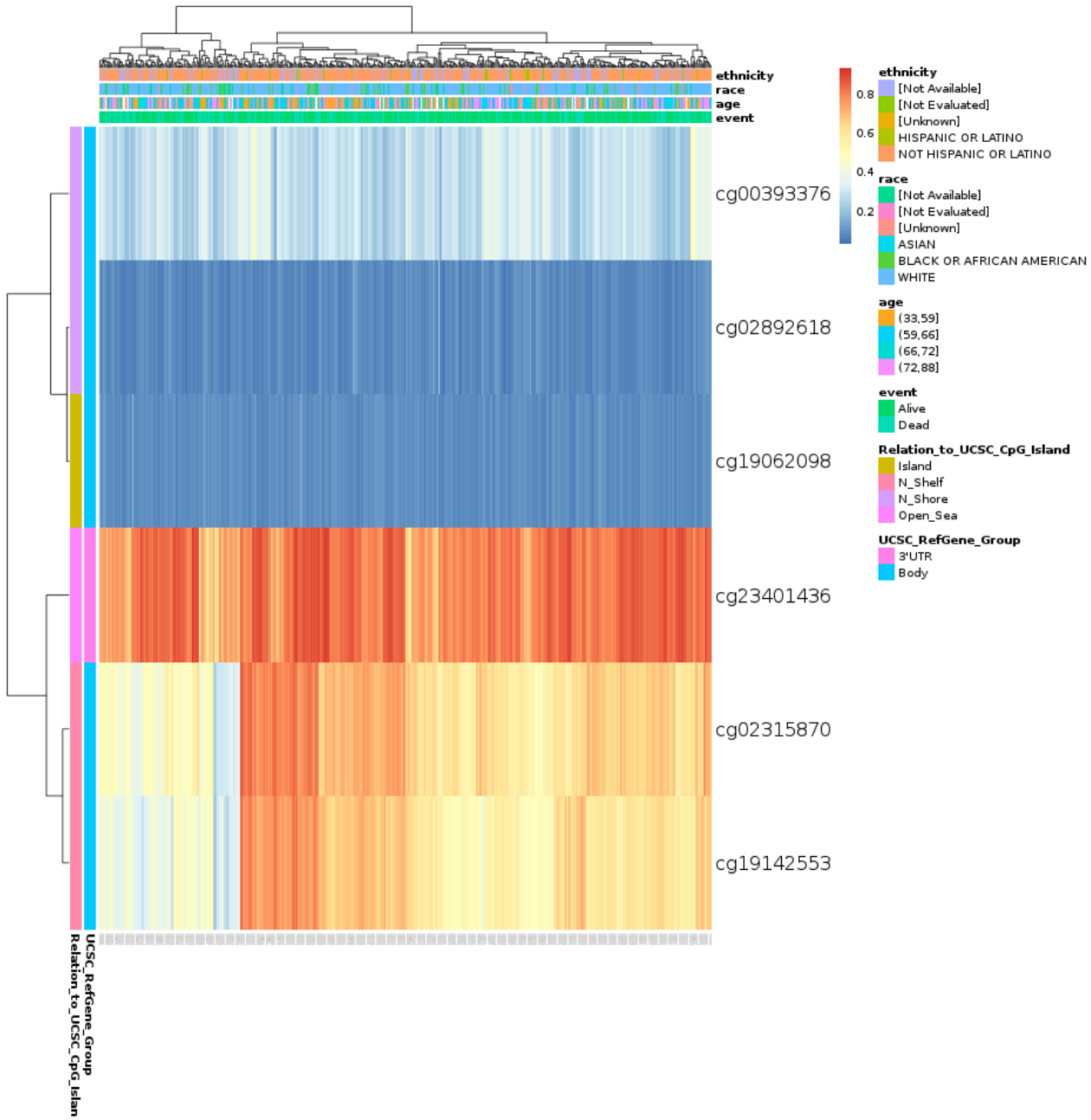

Figure S4 Different methylated regions associated with HNRNPA2B1. Different methylated regions associated with HNRNPA2B1 were presented via a heatmap via MethSurv (https://biit.cs.ut.ee/methsurv/).

© AME Publishing Company.
https://dx.doi.org/10.21037/tcr-2024-2616

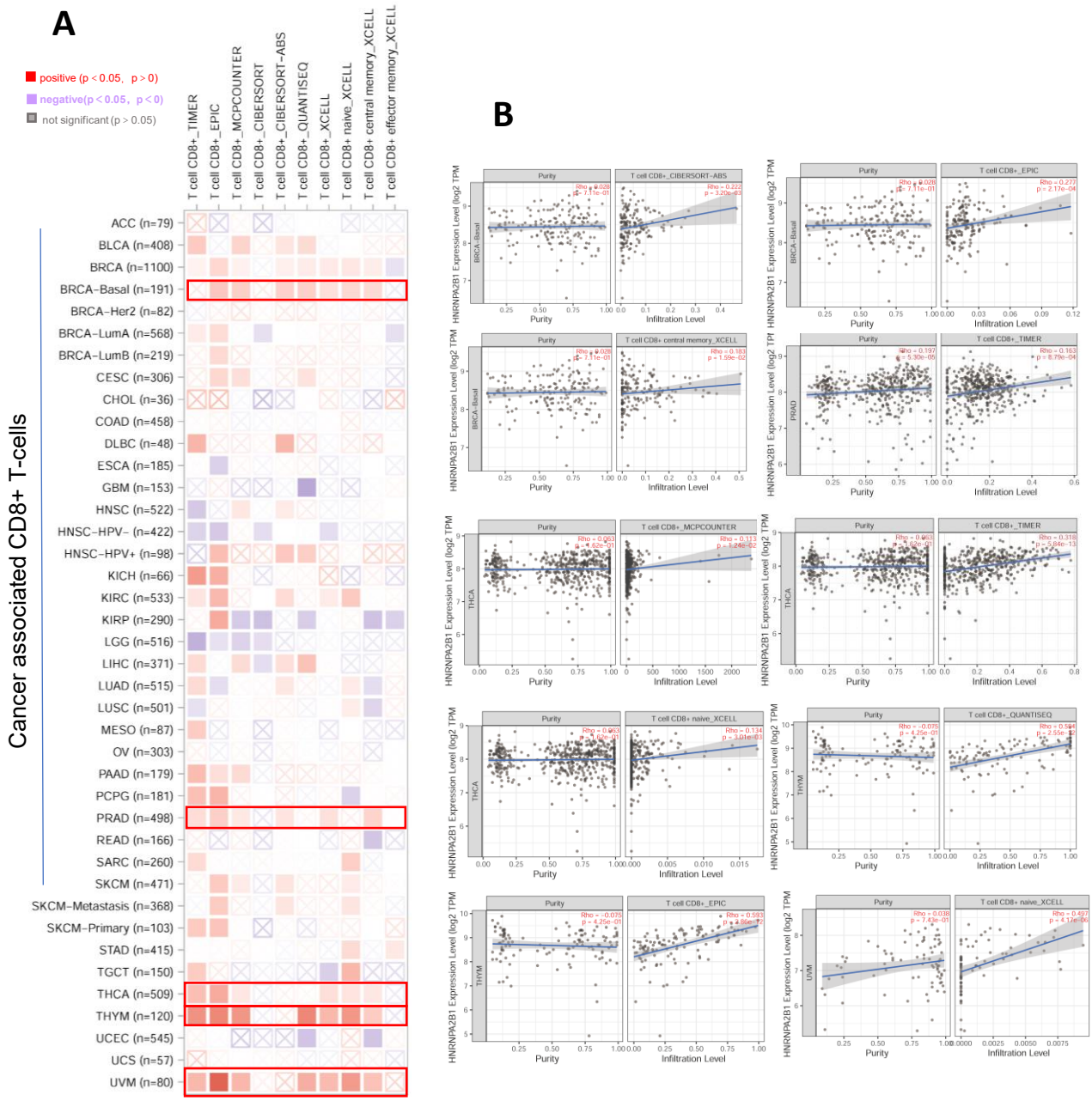

Figure S5 To explore the potential relationship between the infiltration level of CD8⁺ T cells and HNRNPA2B1 expression in different cancer types in the TCGA cohort. Different algorithms were used to explore potential correlations between the expression levels of the *HNRNPA2B1* gene and the infiltration levels of cancer-associated fibroblasts in all types of cancers in TCGA (A,B). TCGA, The Cancer Genome Atlas.

© AME Publishing Company.
https://dx.doi.org/10.21037/tcr-2024-2616

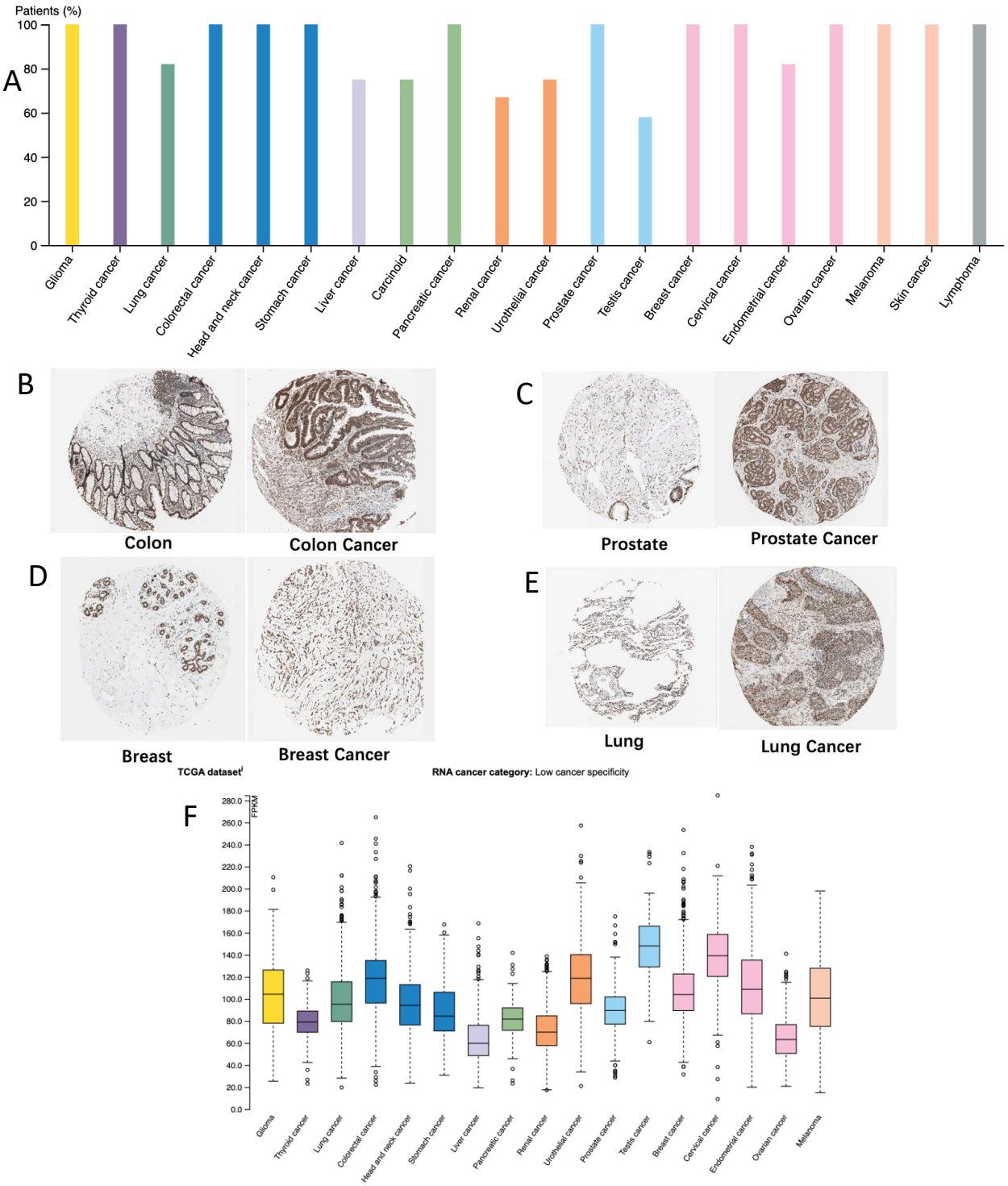

Figure S6 Expression level of the *HNRNPA2B1* gene in different tumors and pathological stages. Expression and distribution of the HNRNPA2B1 protein across cancers (A). On the basis of the HPA dataset, we analyzed HNRNPA2B1 protein expression levels, and immunohistochemistry (IHC) validation confirmed its elevation colorectal cancer (B), prostate cancer (C), breast cancer (D), lung cancer (E), and primary tissues. Expression and distribution of HNRNPA2B1 mRNA across cancers (F).

© AME Publishing Company.
https://dx.doi.org/10.21037/tcr-2024-2616

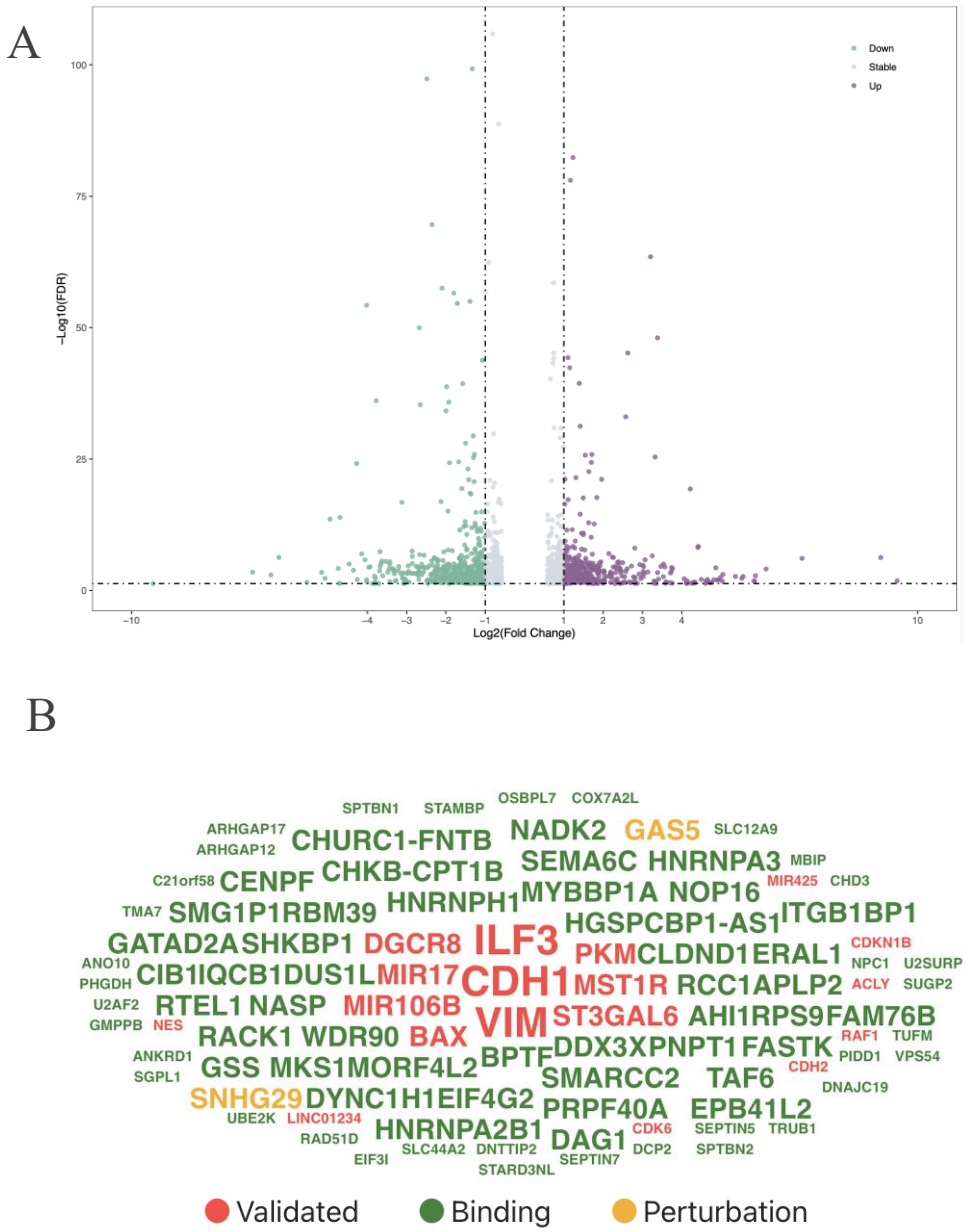

Figure S7 Volcano plots of DEGs from GSE52834 and GSE70061 (A); word cloud of the top 100 target genes of HNRNPA2B1 (B).

© AME Publishing Company.
https://dx.doi.org/10.21037/tcr-2024-2616

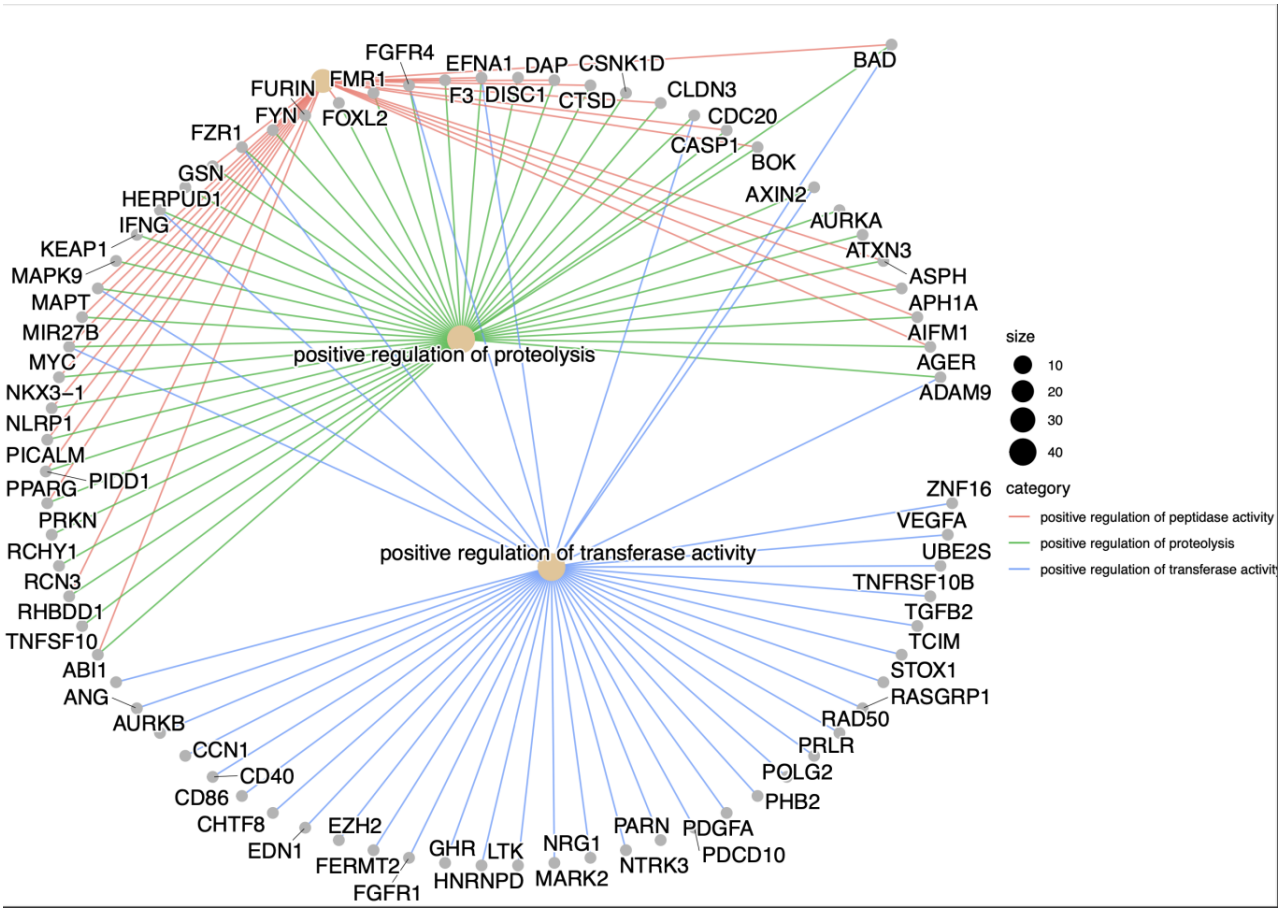

Figure S8 Network diagram illustrating the associations between enriched functional sets and pathway sets.

© AME Publishing Company.
https://dx.doi.org/10.21037/tcr-2024-2616