

Supplementary material 1

Supplementary figures for: Pan-Cancer Multi-Omics Analysis Uncovers CHD4 Driving Tumor Progression via Epigenetic Regulation of Genomic Stability and the Immune Microenvironment

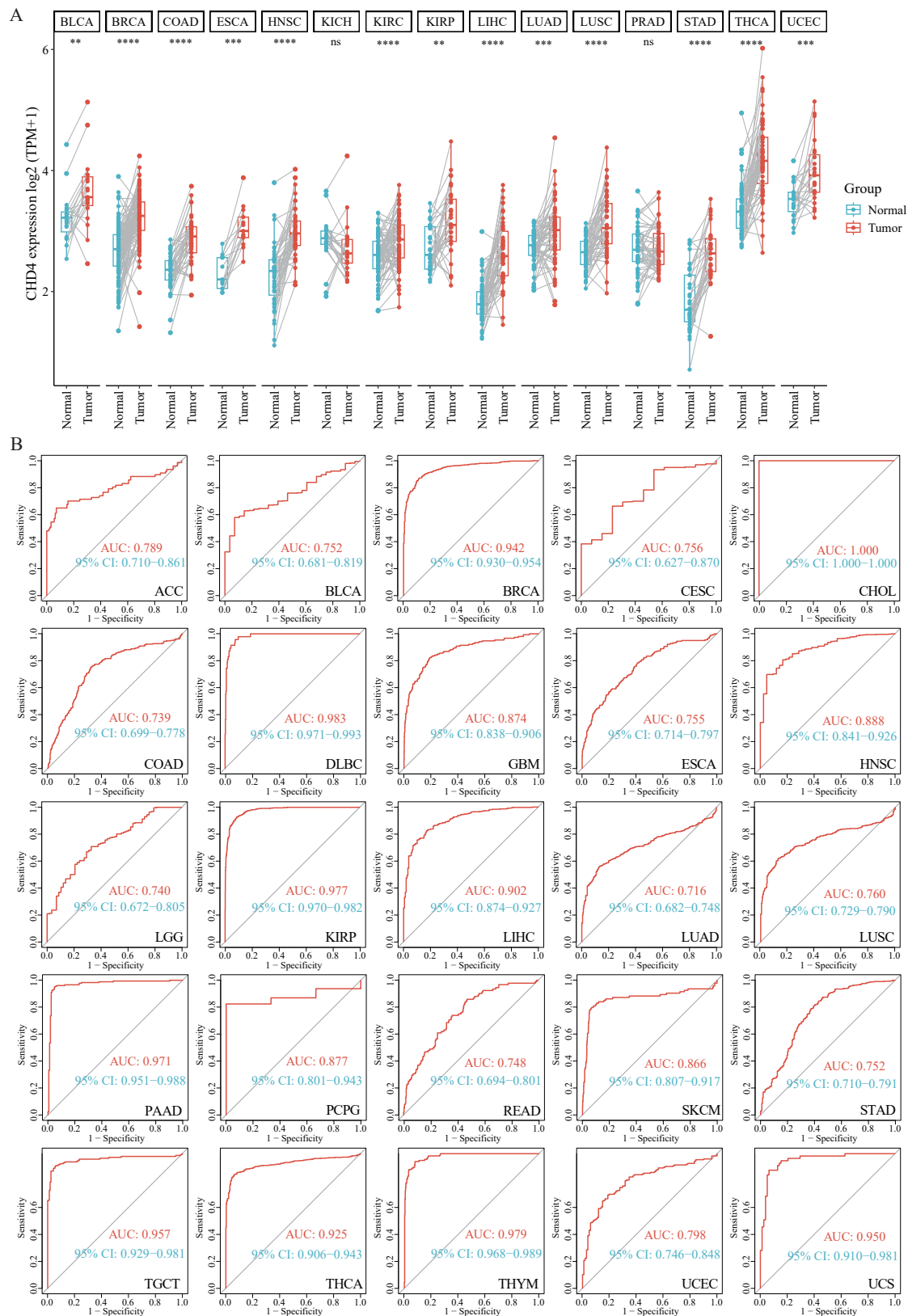


Figure S1: Pan-cancer assessment of CHD4's differential expression and diagnostic performance. **(A)** Differential CHD4 mRNA expression between tumor and adjacent normal tissues in TCGA cancers. **(B)** Pan-cancer diagnostic ROC curves. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$; ns: not significant

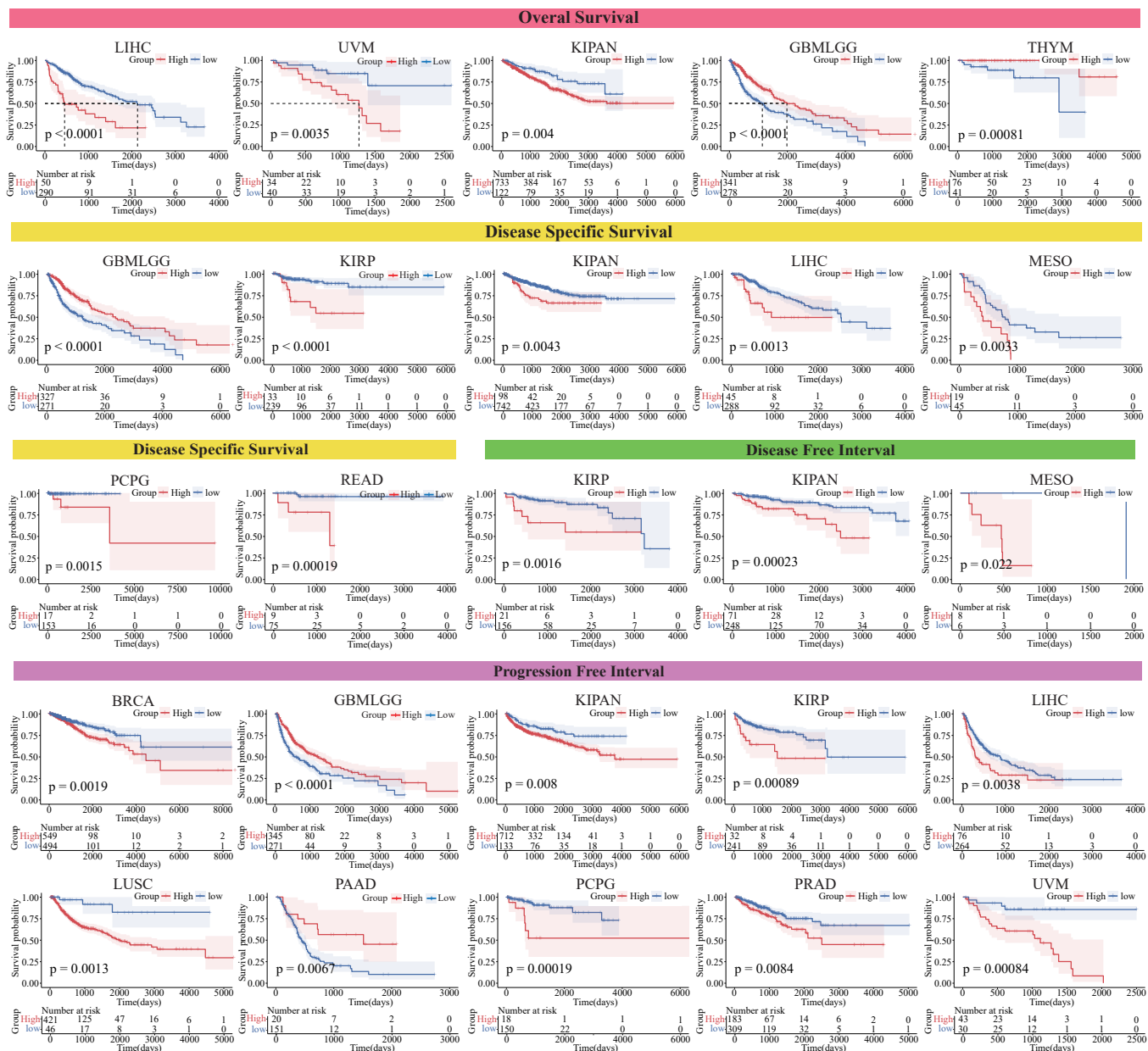


Figure S2: Prognostic value of CHD4 expression in pan-cancer analysis. Kaplan-Meier curves showing associations between CHD4 expression levels and overall survival (OS), disease-specific survival (DSS), disease-free interval (DFI), and progression-free interval (PFI) in indicated cancer types.

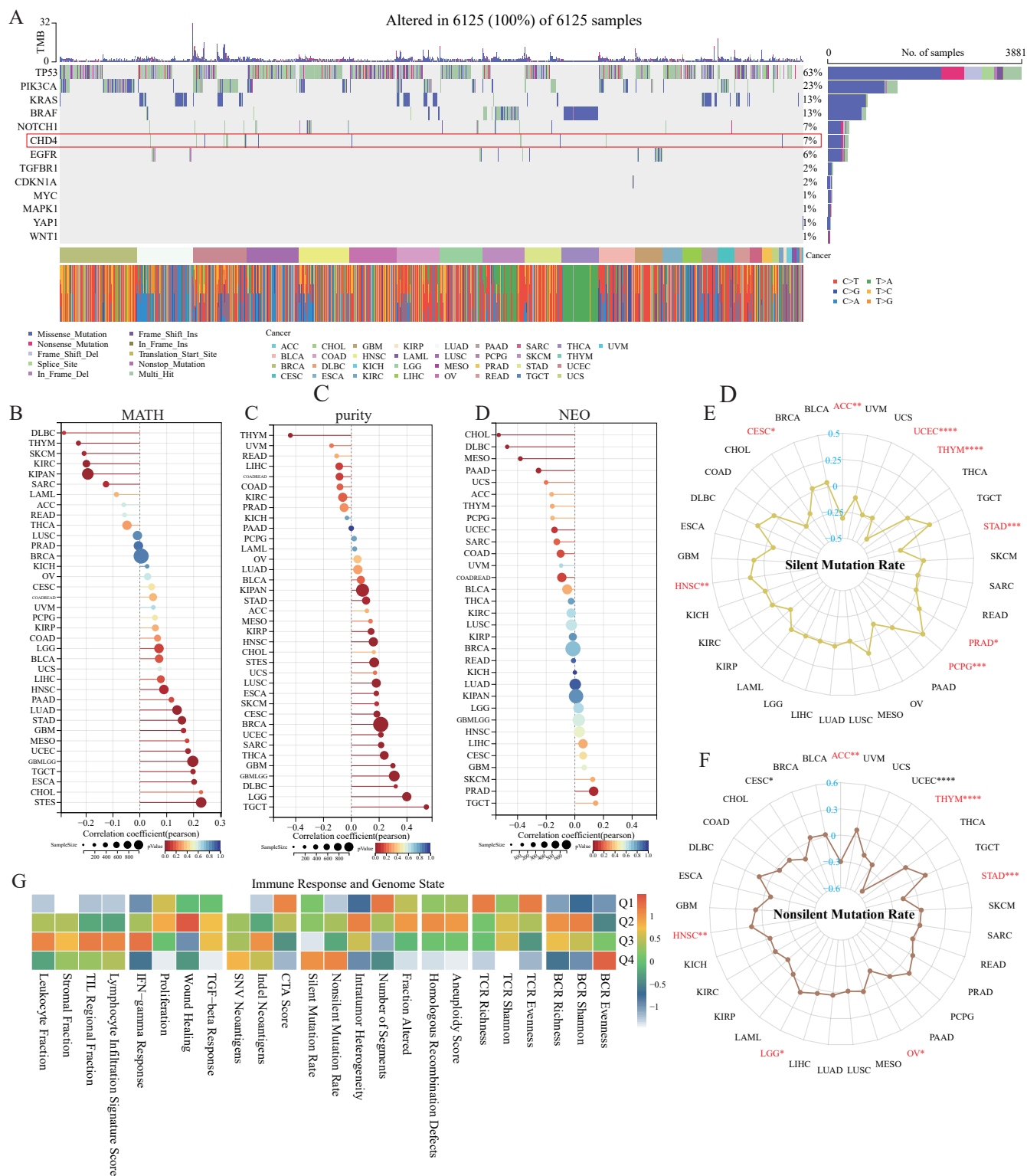


Figure S3: The genomic landscape and immunogenomic associations of CHD4 across cancers. **(A)** Waterfall diagram of CHD4 mutation in pan-cancer. **(B-D)** Lollipop plots of Spearman correlation between CHD4 expression and **(B)** mutant-allele tumor heterogeneity (MATH), **(C)** tumor purity, and **(D)** neoantigen load (NEO). **(E,F)** Radar charts showing Spearman correlation between CHD4 expression and **(E)** silent and **(F)** nonsilent mutation rates. The colored curve indicates the correlation coefficient; the blue value indicates the range. **(G)** Heatmap of average immune response and genomic characteristics stratified by CHD4 expression in pan-cancer.

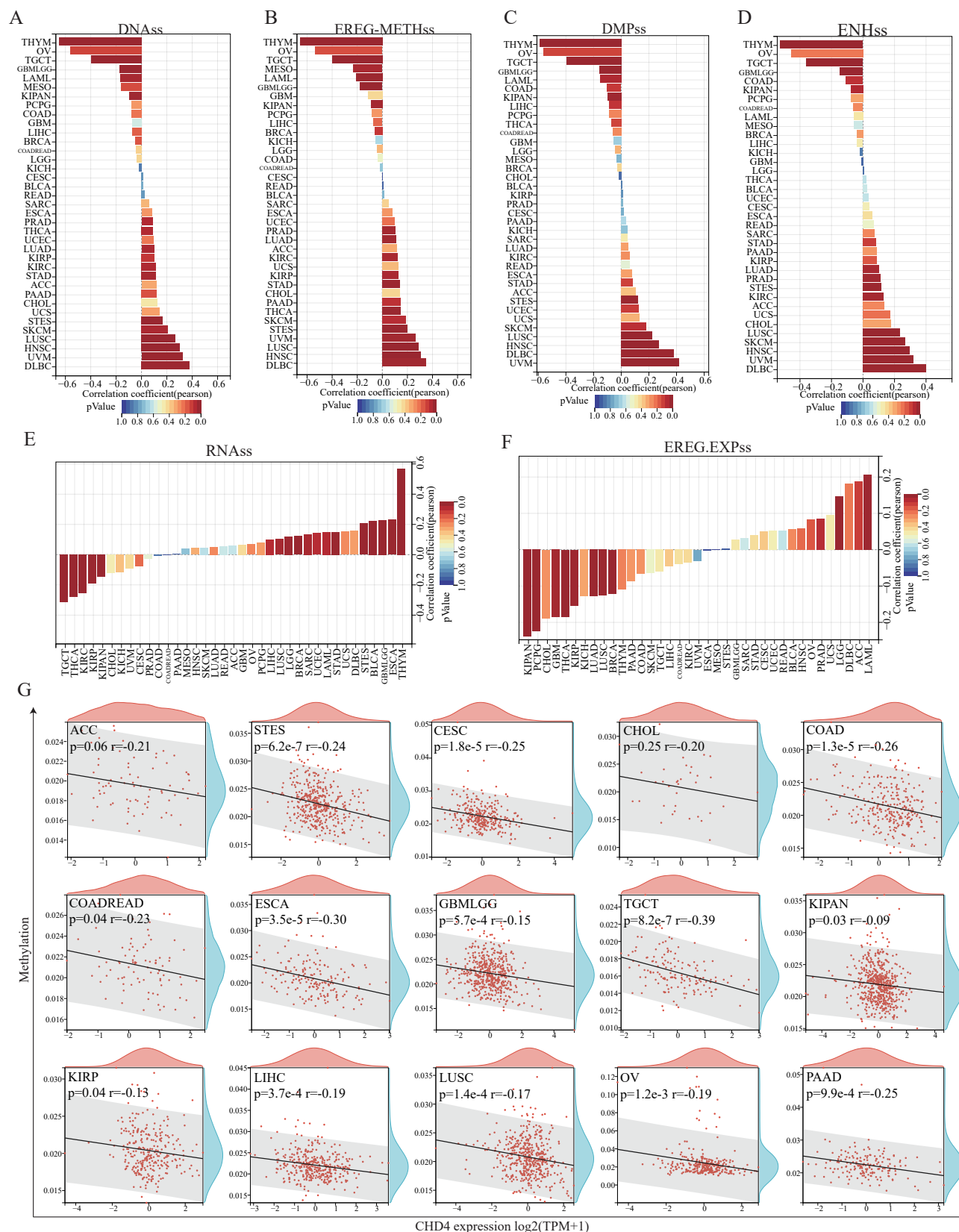
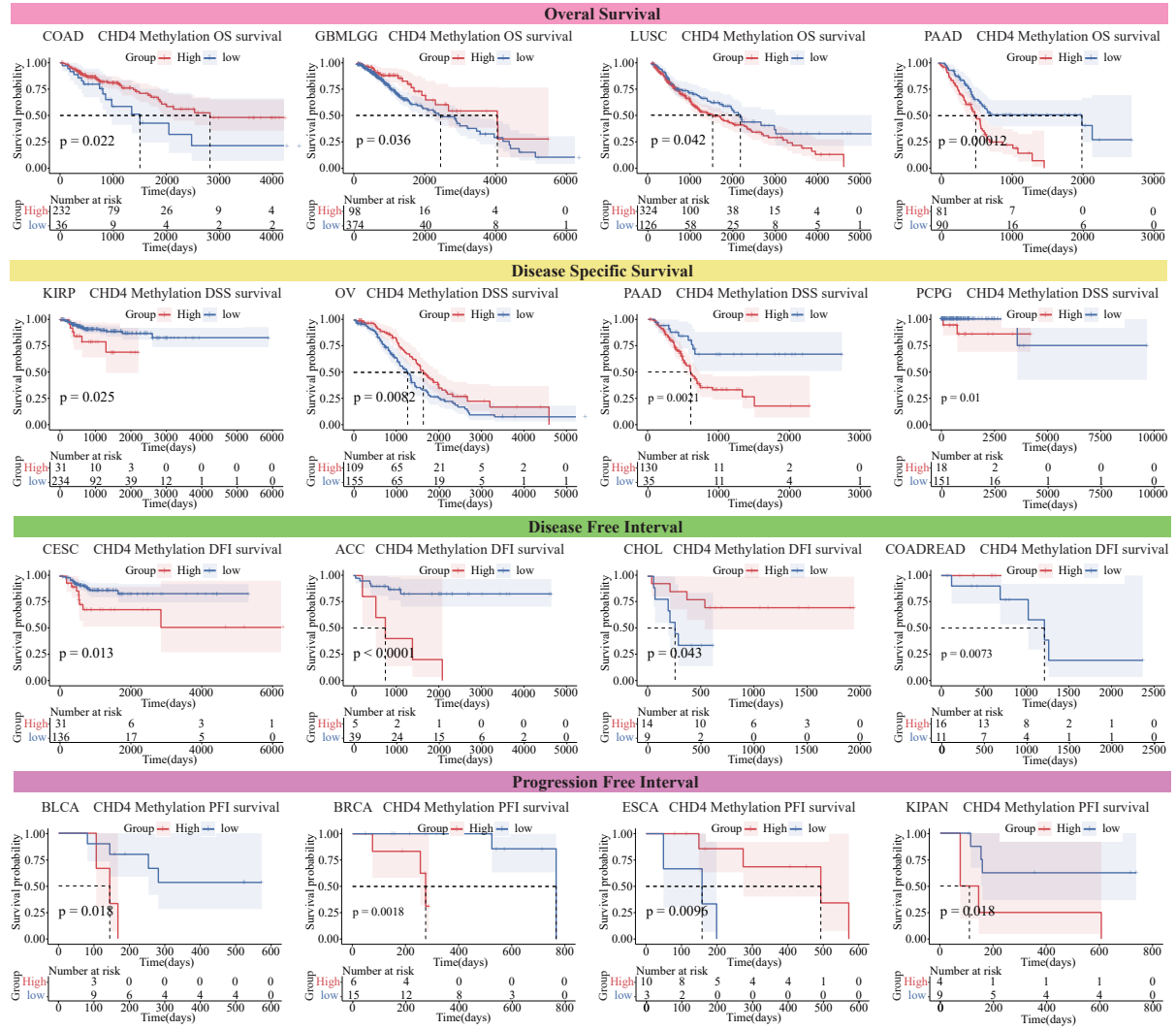


Figure S4: CHD4 correlates with cancer stemness and promoter methylation in pan-cancer analysis. **(A-F)** Bar charts of Spearman correlation coefficients between CHD4 expression and six cancer stemness indices: **(A)** DNAss, **(B)** EREG-METHss, **(C)** DMPss, **(D)** ENHss, **(E)** RNAss, and **(F)** EREG-EXPss. **(G)** The scatter plot shows the correlations between CHD4 expression and promoter methylation in pan-cancer.

A



B

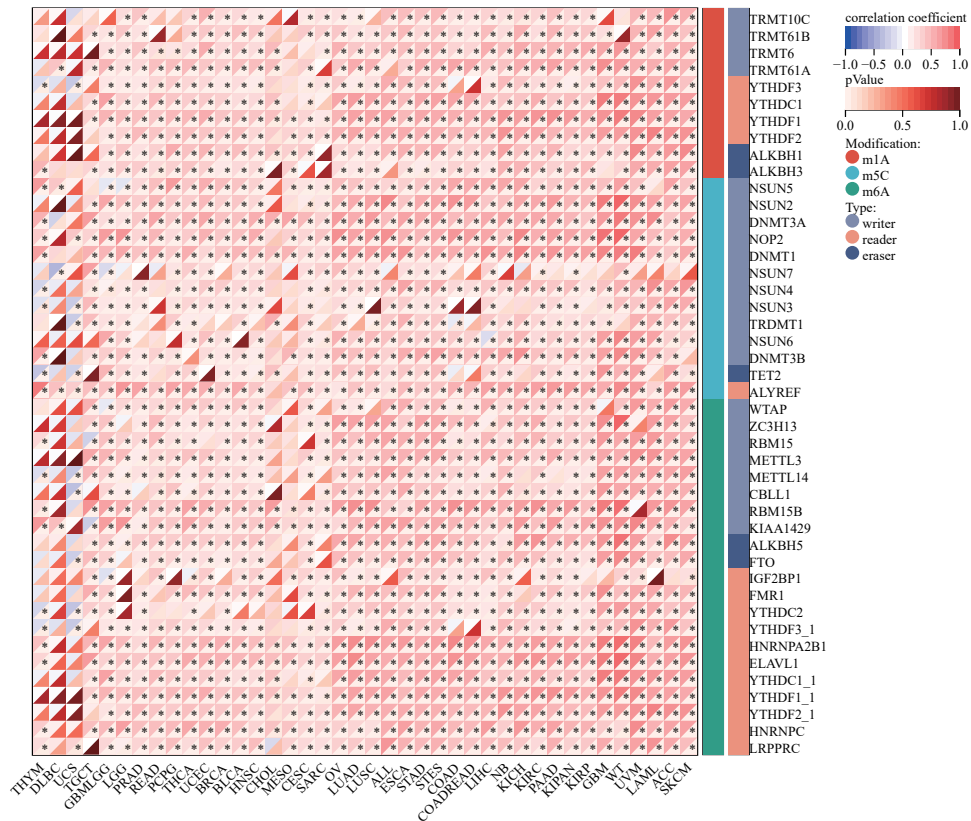


Figure S5: Prognostic and epitranscriptomic associations of CHD4 methylation. (A) Kaplan-Meier curves for overall survival (OS), disease-specific survival (DSS), disease-free interval (DFI), and progression-free interval (PFI) in patients stratified by CHD4 promoter methylation levels. **(B)** Heatmap of correlations between CHD4 expression and RNA modification regulator genes across pan-cancer.

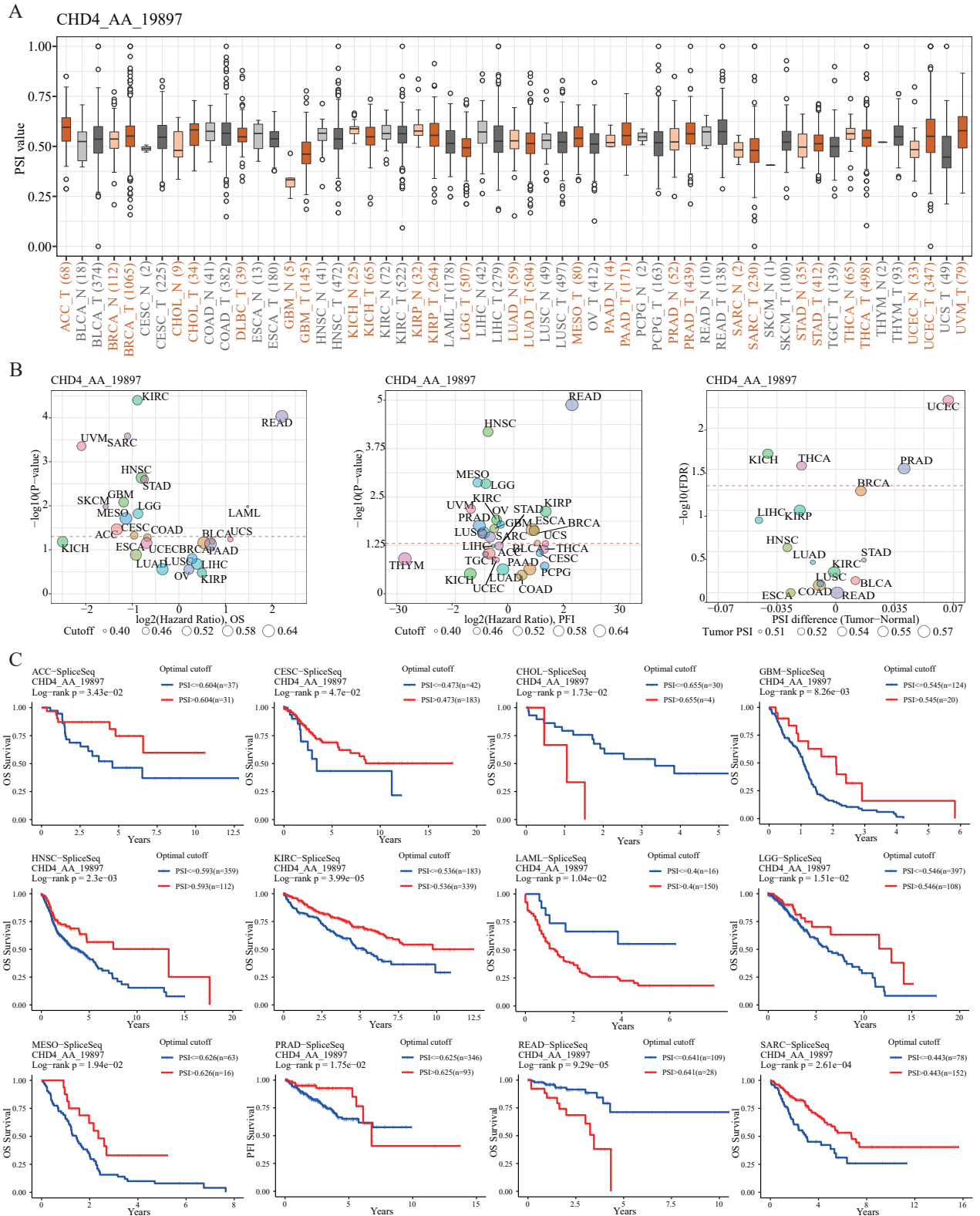


Figure S6: Prognostic significance of CHD4 alternative splicing. **(A)** Percent spliced in (PSI) values of the alternative splicing event CHD4_AA_19897 across pan-cancer, adjacent, and normal tissues. **(B)** TDiffrences in PSI values between tumor-adjacent tissue comparisons and their association with OS and PFI. The red dashed line indicates FDR = 0.05. Point size corresponds to tumor PSI values. **(C)** Kaplan-Meier curves from OncoSplicing showing the prognostic significance of CHD4_AA_19897.

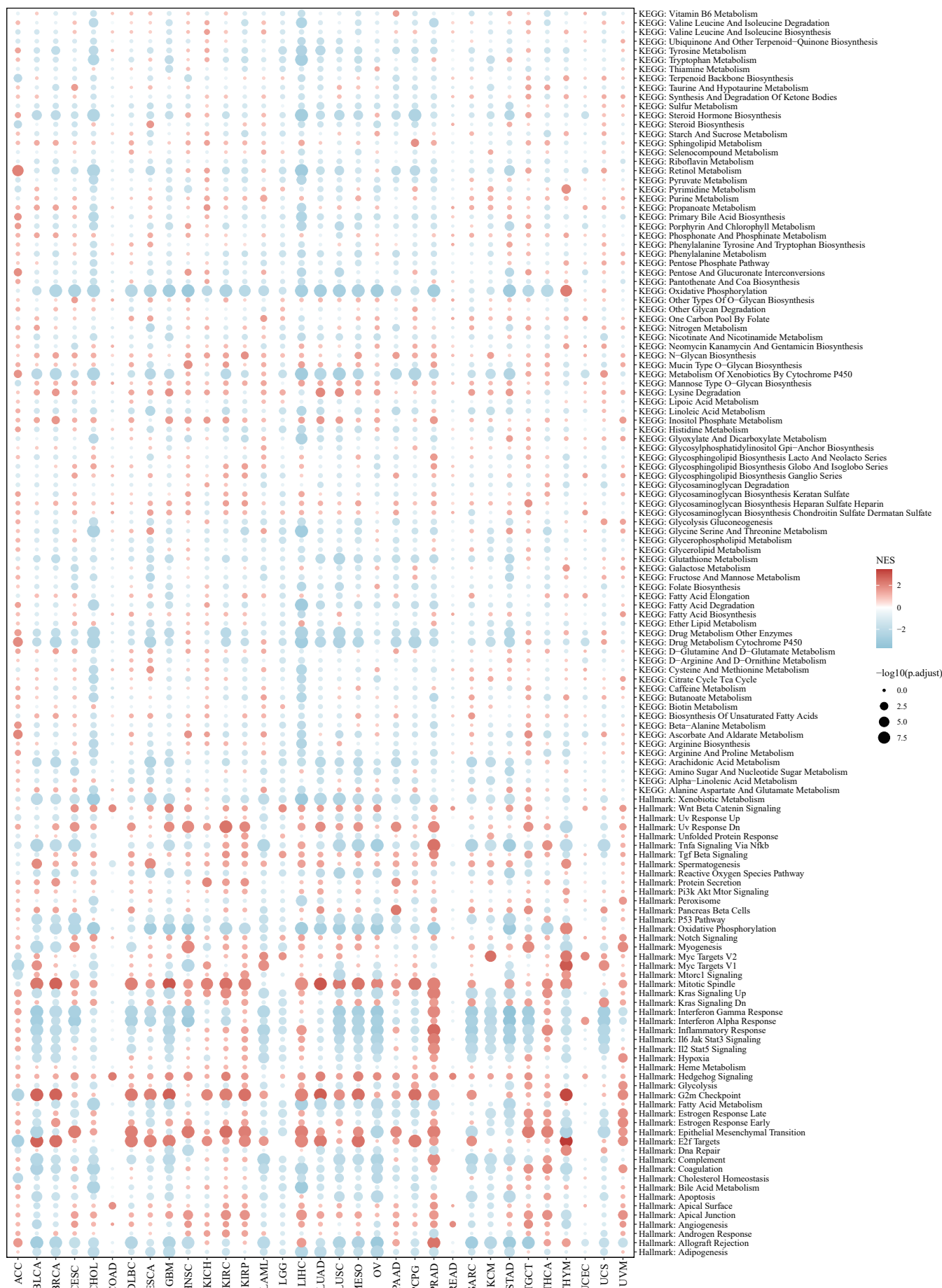


Figure S7: Gene Set Enrichment Analysis (GSEA) of CHD4-associated phenotypes. Bubble plot of GSEA results for Hallmark and KEGG pathways. Genes were ranked by $\log_2$ fold-change ($\log_2$ FC) comparing the top and bottom 30% of samples based on CHD4 expression. Point size corresponds to the normalized enrichment score (NES); color represents the FDR.

B

