

Figure S1 (A,B) Heatmaps showing the top 60 upregulated (A) and downregulated (B) DEATGs in CRC. The rows and column represent the DEATGs and tissue samples, respectively. The color scale indicates the expression level of the DEATGs. Red and turquoise represent up- and down-regulation, respectively. (C) *WDR45* expression across various cancers in the TIMER database. (D) The alteration frequency of *WDR45* in pan-cancer. (E) The relationship between the type of CNAs and the mRNA expression of *WDR45*. (F) The relationship between the mutation type and the mRNA expression of *WDR45*. *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$.

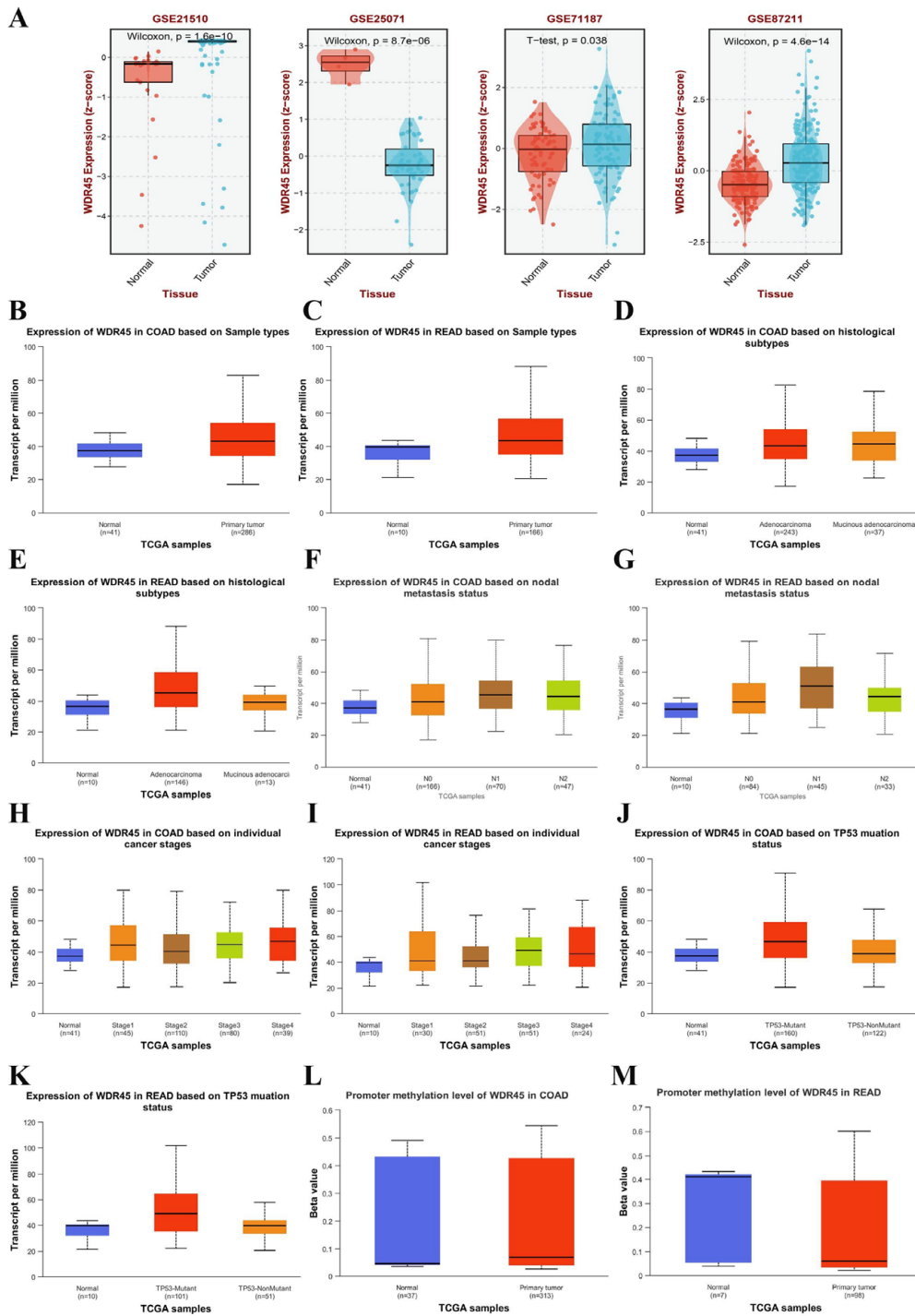


Figure S2 Expression profile of *WDR45* in tumor and normal tissues, and subgroup analyses of CRC patients. (A) Differential *WDR45* expression in CRC tumor and normal tissues across GEO datasets. (B,C) Differential *WDR45* expression in COAD or READ tumor tissues compared to normal tissues from TCGA database. (D) - (I) *WDR45* expression in CRC patient subgroups stratified by (D,E) histological subtype, (F,G) nodal metastasis status, and stage (H,I). (J,K) Differential *WDR45* expression by *TP53* mutation status in COAD and READ. (L,M) Differential promoter methylation of *WDR45* in tumor tissues and normal tissues of COAD and READ, respectively. *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$.

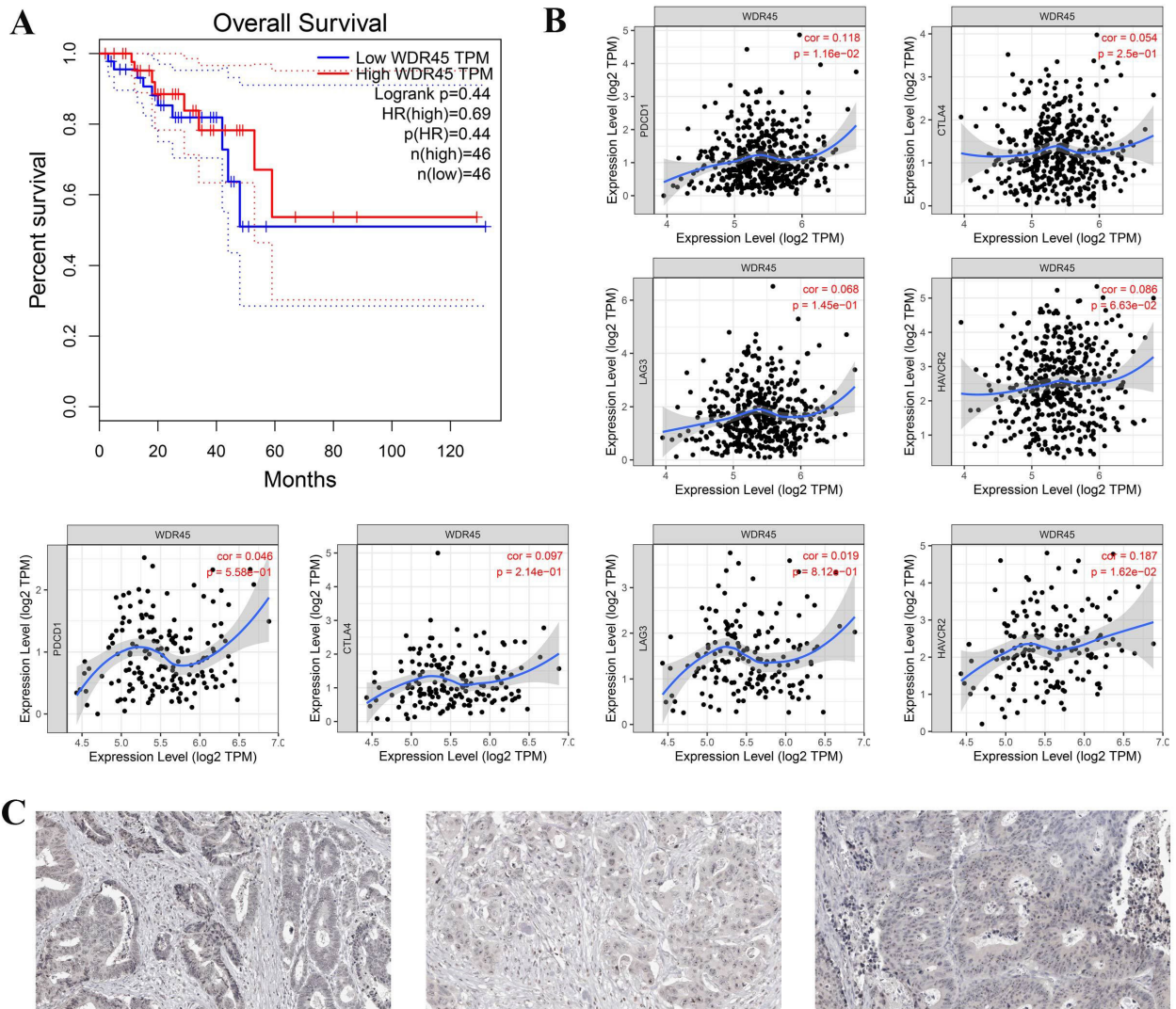


Figure S3 (A) The OS of READ patients with high and low expression *WDR45* based on TCGA data. (B) The relationship between *WDR45* expression and the immune checkpoint genes (*PDCD1*, *CTLA4*, *LAG3*, and *HAVCR2*) in COAD (upper) and READ (lower), analyzed by the TIMER database. (C) Representative IHC images of *WDR45* staining from the HPA database (<https://www.proteinatlas.org/ENSG00000196998-WDR45/cancer/colorectal+cancer#img;200x>).