A

Cancer(OS)	Total(N)	HR(95%CI)		p value
ESAD	81	1.962(1.040-3.700)		0.0374
GBM	84	1.76(1.025-3.021)		0.0404
LGG	530	1.578(1.114-2.235)		0.0102
HNSC	503	1.512(1.143-1.999)		0.0037
KICH	64	5.483(1.138-26.417)		0.0339
KIRC	541	0.658(0.459-0.943)		0.0228
KIRP	290	1.967(1.061-3.648)		0.0317
LIHC	373	1.88(1.328-2.661)		4e-04
LUAD	530	1.663(1.218-2.270)		0.0014
OSCC	329	1.809(1.301-2.517)		4e-04

B

Cancer(DSS)	Total(N)	HR(95%CI)		p value
ESAD	80	2.184(1.047-4.555)		0.0373
GBM	79	1.988(1.118-3.536)		0.0193
LGG	522	1.661(1.155-2.389)		0.0062
HNSC	478	1.44(1.006-2.061)		0.0465
KICH	64	9.56(1.150-79.466)		0.0367
KIRC	530	0.677(0.459-0.999)		0.0493
KIRP	286	3.607(1.715-7.586)		7e-04
LIHC	365	1.842(1.179-2.877)		0.0072
LUAD	495	1.613(1.116-2.333)		0.011
OSCC	312	1.637(1.063-2.520)		0.0253

C

Cancer(PFI)	Total(N)	HR(95%CI)		p value
ESAD	81	1.658(0.907-3.032)		0.1005
LGG	530	1.335(1.008-1.769)		0.0439
KICH	64	2.839(0.613-13.148)		0.1821
KIRC	539	0.69(0.500-0.952)		0.0238
KIRP	289	2.625(1.543-4.467)		4e-04
LIHC	373	1.393(1.025-1.893)		0.0343
LUAD	530	1.435(1.100-1.873)		0.0078
STAD	372	1.378(0.894-2.124)		0.1462
THYM	119	3.655(1.539-8.684)		0.0033

**Supplementary Figure 1. Survival prognosis analysis of cancers.** (**A**) Illustrated is a forest plot delineating the association between the HSPA4 gene and Overall Survival (OS) in the TCGA dataset. (**B**) Illustrated is a forest plot delineating the association between the HSPA4 gene and Disease-Specific Survival (DSS) in the TCGA database. (**C**) Illustrated is a forest plot delineating the association between the HSPA4 gene and Progression-Free Interval (PFI) in the TCGA database.
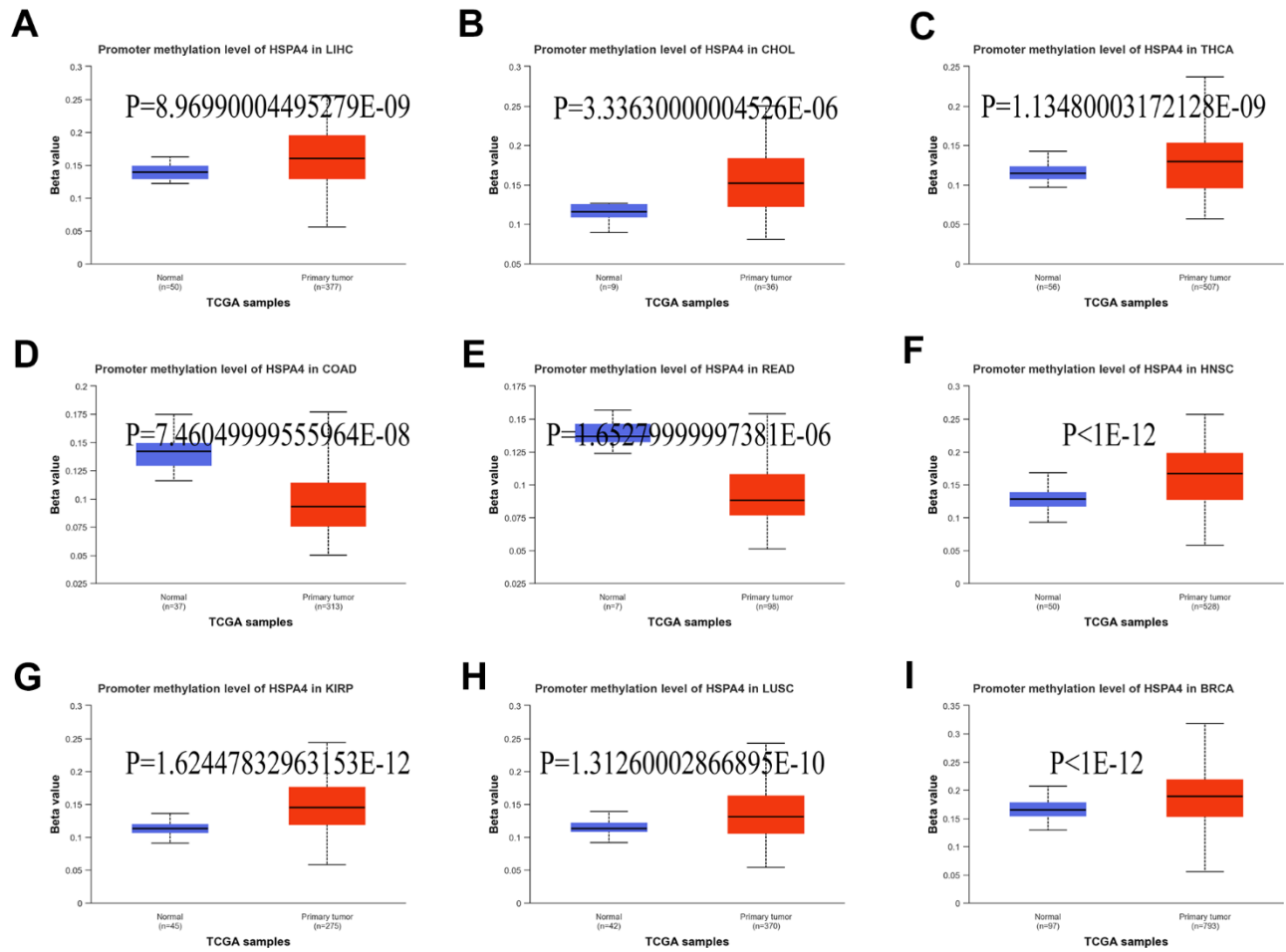
Supplementary Figure 2. Methylation levels of HSPA4 promoter in cancers. The UALCAN tool was employed to analyze the methylation values of HSPA4 in both normal and primary tumor tissues, including: (**A**) LIHC, (**B**) CHOL, (**C**) THCA, (**D**) COAD, (**E**) READ, (**F**) HNSC, (**G**) KIRP, (**H**) LUSC and (**I**) BRCA.
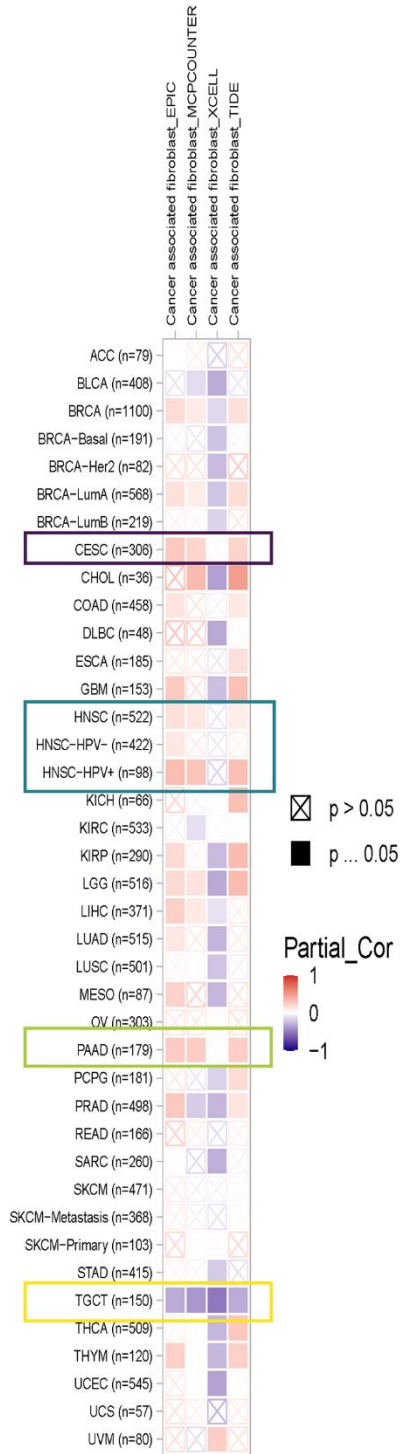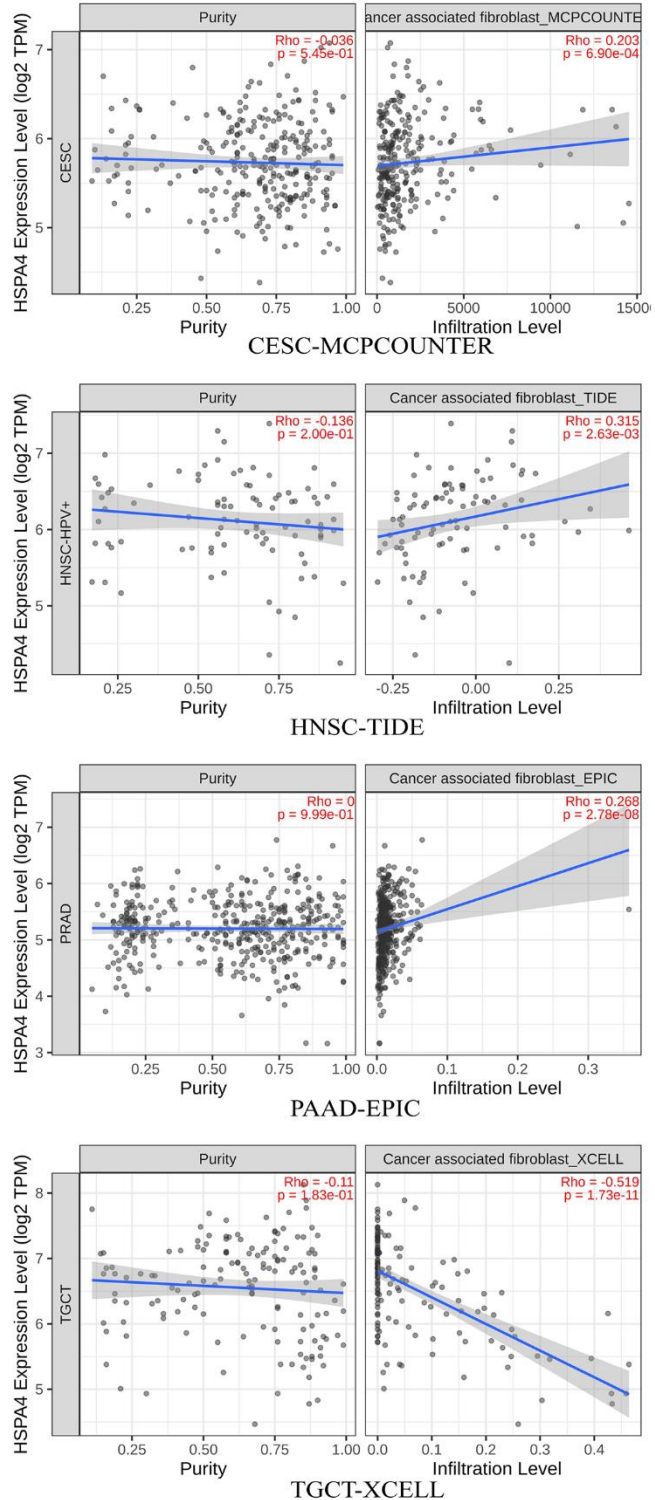
Supplementary Figure 3. Immune infiltration analysis. In a comprehensive analysis of cancers across TCGA, various algorithms were employed to investigate the potential correlation between SND1 gene expression levels and the infiltration levels of cancer-associated fibroblasts. (**A**) Pan-cancer heatmap generated using four distinct algorithms. (**B**) Scatter plot produced using one of the specified algorithms, illustrating the respective correlation.
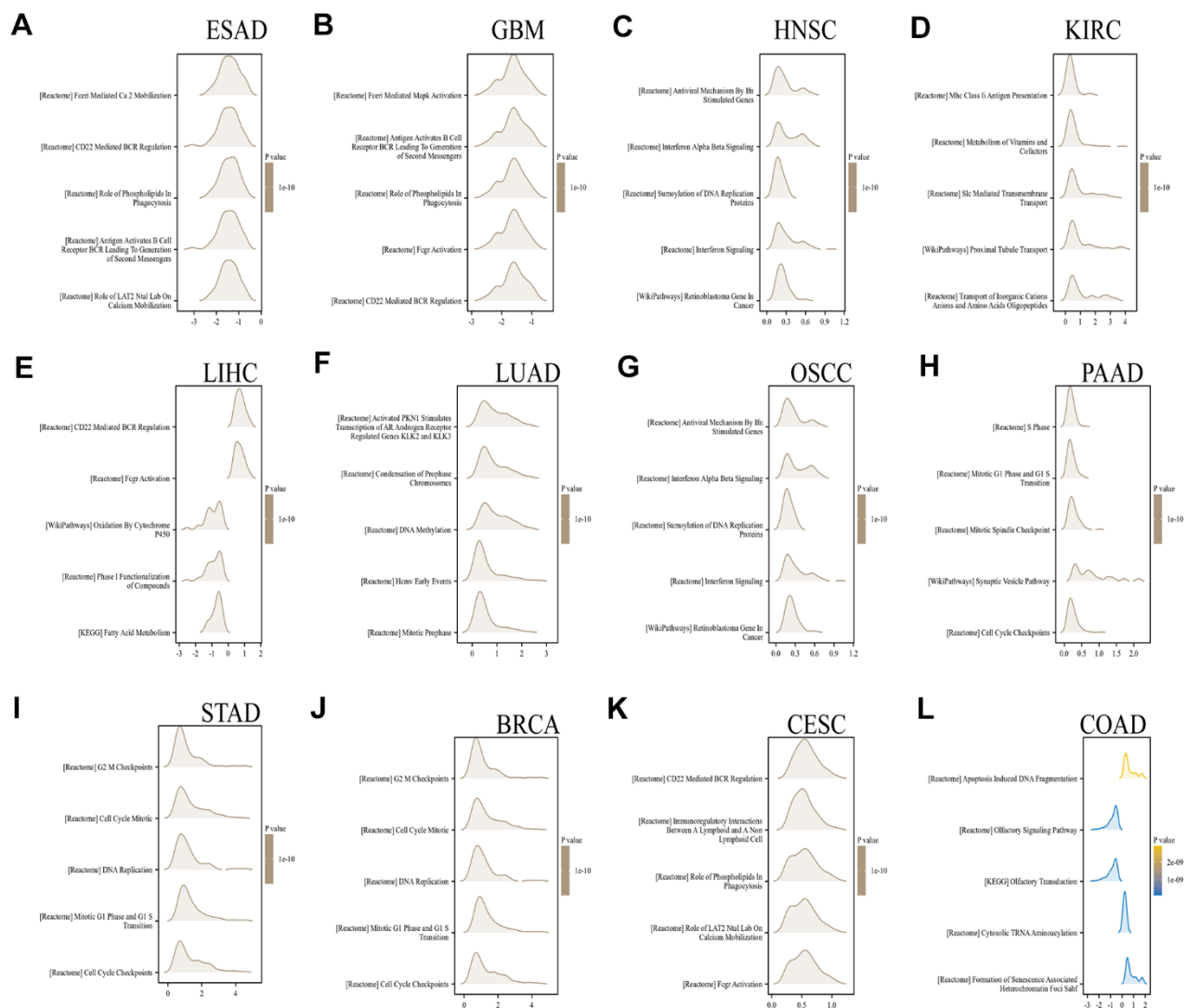
Supplementary Figure 4. GSEA enrichment analysis. GSEA for HSPA4 expression was conducted in (**A**) ESAD, (**B**) GBM, (**C**) HNSC, (**D**) KIRC, (**E**) LIHC, (**F**) LUAD, (**G**) OSCC, (**H**) PAAD, (**I**) STAD, (**J**) BRCA, (**K**) CESC, and (**L**) COAD. The y-axis represents a gene set, while the x-axis depicts the logFC distribution of core molecules within each gene set.