

Table S1 Survival analysis of KCTD12 expression in breast cancer patients (the PrognScan database)

Dataset	Probe ID	Endpoint	Number	COX P value	HR (95% CI)
GSE9195	212192_at	DMFS	77	0.016	0.26 (0.09–0.78)
GSE1456	212192_at	DSS	159	0.002	0.36 (0.19–0.69)
GSE9195	212192_at	RFS	77	0.036	0.37 (0.14–0.94)
GSE3494	212188_at	DSS	236	0.000	0.37 (0.24–0.56)
GSE2990	212188_at	RFS	62	0.005	0.41 (0.22–0.76)
GSE1456	212188_at	DSS	159	0.000	0.42 (0.28–0.64)
GSE2990	212188_at	DMFS	54	0.023	0.43 (0.21–0.89)
GSE3494	212192_at	DSS	236	0.000	0.44 (0.29–0.69)
GSE1456	212188_at	RFS	159	0.000	0.46 (0.31–0.67)
GSE11121	212192_at	DMFS	200	0.013	0.48 (0.26–0.85)
GSE1456	212192_at	RFS	159	0.010	0.48 (0.27–0.84)
GSE1456	212192_at	OS	159	0.012	0.48 (0.27–0.85)
GSE2990	212192_at	DMFS	54	0.021	0.50 (0.28–0.90)
GSE2990	212192_at	RFS	62	0.007	0.52 (0.32–0.84)
GSE4922	212188_at	DFS	249	0.000	0.52 (0.37–0.75)
GSE1456	212188_at	OS	159	0.001	0.53 (0.37–0.77)
GSE4922	212192_at	DFS	249	0.002	0.55 (0.38–0.80)
GSE6532	212188_at	RFS	87	0.044	0.58 (0.35–0.99)
GSE6532	212188_at	DMFS	87	0.044	0.58 (0.35–0.99)
GSE6532	212192_at	RFS	87	0.013	0.61 (0.41–0.90)
GSE6532	212192_at	DMFS	87	0.013	0.61 (0.41–0.90)
GSE2034	212188_at	DMFS	286	0.048	0.76 (0.58–1.00)

DMFS, distant metastasis-free survival; DSS, disease-specific survival; RFS, relapse-free survival; OS, overall survival; DFS, disease-free survival.

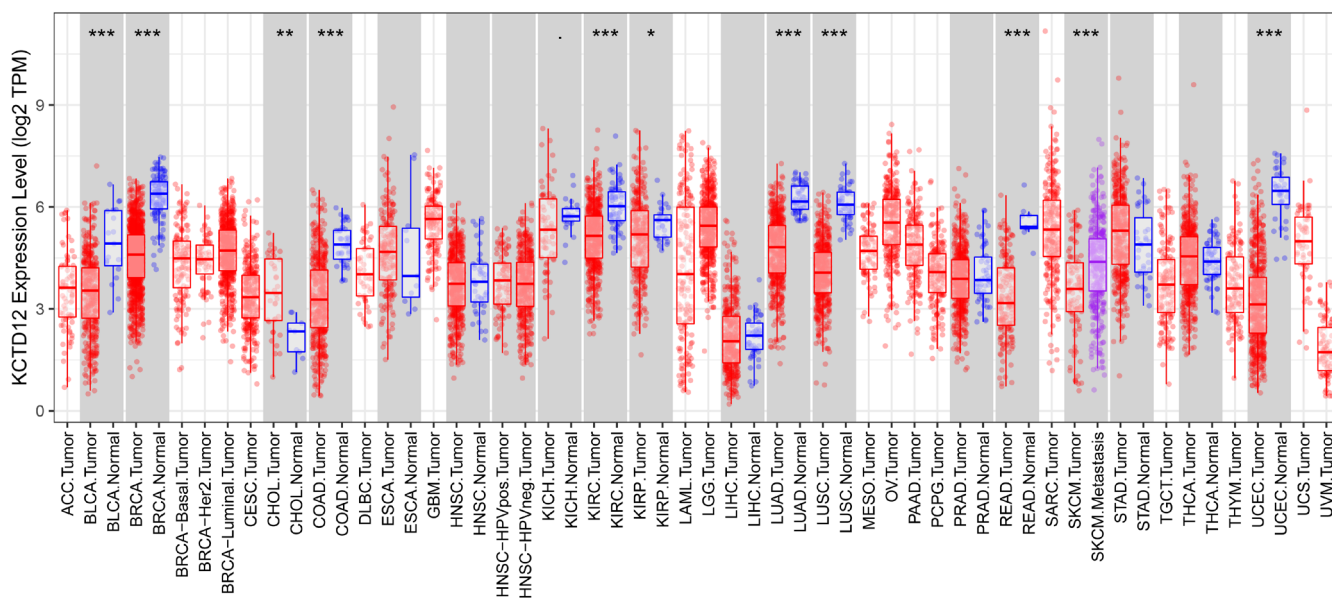


Figure S1 KCTD12 expression levels in different carcinomas. The expression levels of KCTD12 were compared between different types of carcinomas and matched normal samples. KCTD12, potassium channel tetramerization domain containing 12. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$.

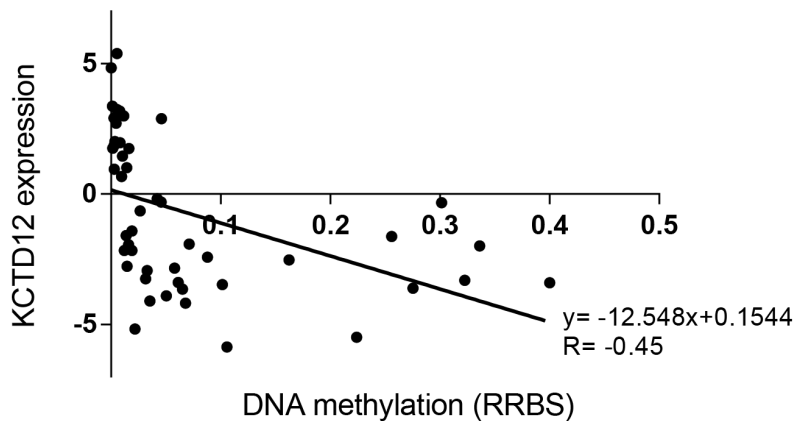


Figure S2 KCTD12 expression levels were negatively associated with methylation levels. Correlation analysis between KCTD12 expression levels and methylation levels in 50 BC cell lines. KCTD12, potassium channel tetramerization domain containing 12; BC, breast cancer.

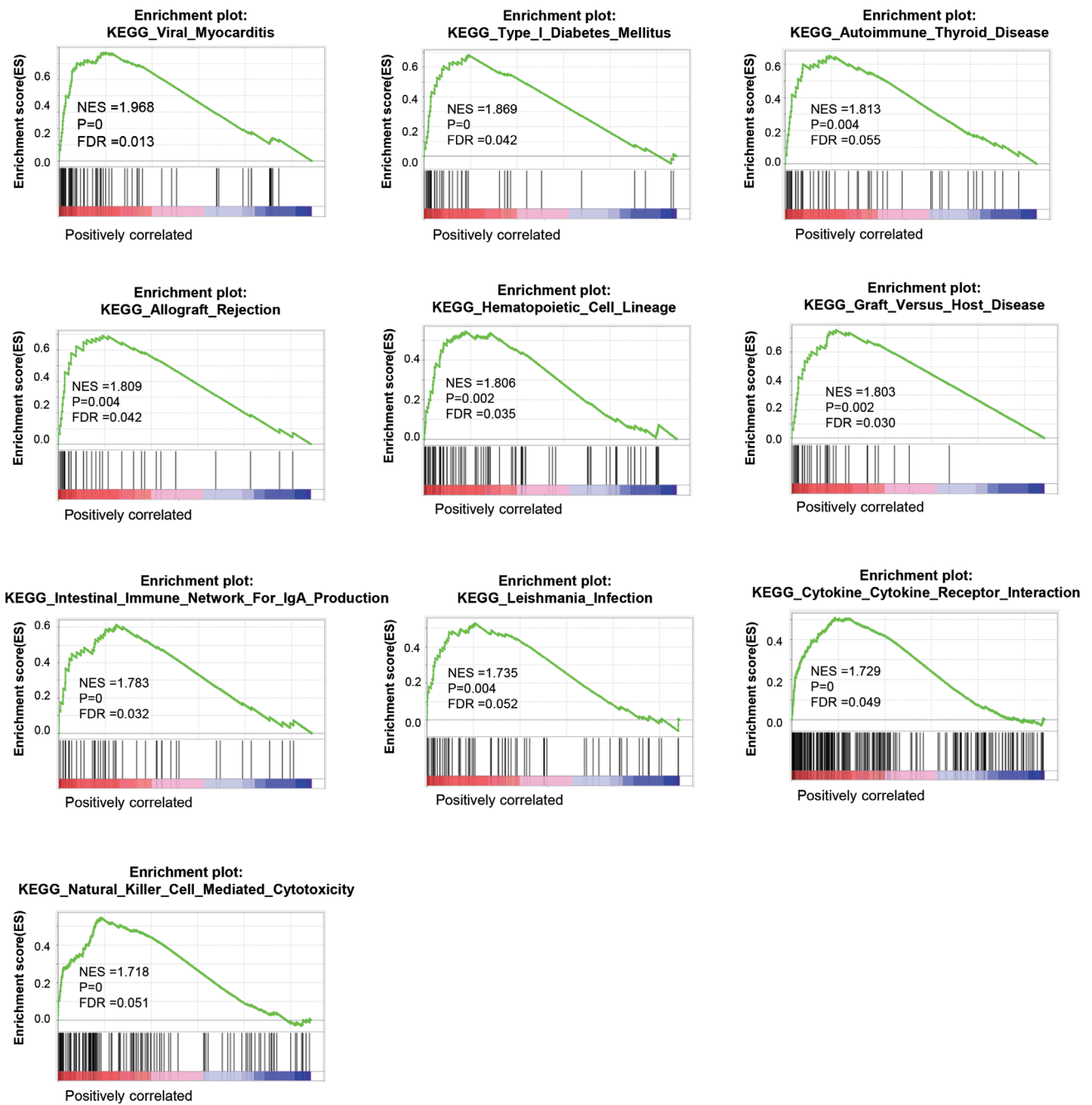


Figure S3 GSEA indicated that KCTD12 participated in the immune response of BC cell lines. GSEA was used on RNA-Seq data of 51 BC cell lines grouped by KCTD12 expression levels, and the top 10 ranked pathways of the high KCTD12 expression group are shown. KCTD12, potassium channel tetramerization domain containing 12; GSEA, gene set enrichment analysis.