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DATABASE ANALYSIS

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Special AT-rich Sequence Binding-Protein 1 (SATB1) Correlates with Immune Infiltration in Breast, Head and Neck, and Prostate Cancer

Authors' Contribution:
Study Design A
Data Collection B
Statistical Analysis C
Data Interpretation D
Manuscript Preparation E
Literature Search F
Funds Collection G

ABCDEF 1 Hua Ge
BCDE 2 Yan Yan
CEF 1 Maozhao Yan
EF 1 Lingfei Guo
CF 1 Kun Mao

1 Department of Gastrointestinal Surgery, The Third Affiliated Hospital of Zunyi Medical University (The First People's Hospital of Zunyi), Zunyi, Guizhou, P.R. China
2 Quality Control Department, The Third Affiliated Hospital of Zunyi Medical University (The First People's Hospital of Zunyi), Zunyi, Guizhou, P.R. China

Corresponding Author: Hua Ge, e-mail: zyyyhuage@126.com
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Background: SATB1 is essential in gene regulation and associates with T cell development. Aberrant SATB1 expression has been reported in various neoplasms. However, correlations between SATB1 and tumor immune infiltration and prognosis in malignancies still remains unclear.

Material/Methods: We used Oncomine and the Tumor Immune Estimation Resource database to explore the expression of SATB1 in cancers. In addition, Kaplan-Meier plotter, PrognoScan, and Gene Expression Profiling Interactive Analysis were also used to assess the effects of SATB1 on clinical prognosis. Furthermore, correlations between cancer immune infiltration and SATB1 were analyzed via Tumor Immune Estimation Resource.

Results: The results demonstrated that SATB1 correlates with prognosis in different types of cancers, such as breast invasive carcinoma (BRAC), head and neck cancer (HNSC), and prostate adenocarcinoma (PRAD). Decreased expression of SATB1 was associated with poor overall and progression-free survival of BRAC patients with positive estrogen receptor (ER) as well as mutated TP53. In addition, B cells, CD8+ T cells, CD4+ T cells, macrophages, neutrophils, and dendritic cells infiltration in BRAC, HNSC, and PRAD were also correlated with SATB1 expression level. Moreover, we found strong correlations between SATB1 and various immune markers for BRAC, HNSC, and PRAD.

Conclusions: In BRAC, HNSC, and PRAD patients, SATB1 has potential to serve as a prognostic indicator for predicting tumor immune infiltration and prognosis.

MeSH Keywords: Breast Neoplasms • Head and Neck Neoplasms • Prognosis • Prostatic Neoplasms • Tumor Escape

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Background

Breast invasive carcinoma (BRCA), head and neck cancer (HNSC), and prostate adenocarcinoma (PRAD) are common malignancies in the world, and they remain a major public health problem [1]. The immune infiltrate mechanism is involved in the development of cancers, and immunotherapy has been proven to be a promising strategy in BRCA, HNSC, and PRAD [2–4]. In BRCA, human epidermal growth factor receptor 2 (HER2) is partially mediated by immune mechanisms and HER2 positive patients respond well to HER2 targeted therapy [5]. For HNSC patients with recurrence and metastases, anti-PD1 antibodies can improve the overall survival (OS) [6,7]. In addition, immuno-therapeutic medicine such as anti-PD1 and anti-CTLA4 show a partial response in PRAD patients [8]. Studies also have indicated that tumor infiltrating neutrophils (TINs) and tumor associated macrophages (TAMs) have effects on survival and therapeutic efficacy in cancer patients [9,10]. Therefore, exploring novel immune-related therapeutic targets is important for facilitating individualization and optimization of cancer patients in treatment.

The special AT-rich sequence binding-protein 1 (SATB1) is one kind of protein that binds to nuclear matrix. SATB1 participates in the mechanisms of chromatin remodeling and regulates gene expression [11]. SATB1 can activate or repress genes by interacting with the PDZ domain of chromatin modifying enzymes [12]. Abnormal expression of SATB1 has been reported in different neoplasms such as glioma, nasopharyngeal, breast, lung, pancreatic, liver, colorectal, kidney, bladder, prostate, ovarian, lymphoma, and so on [13]. SATB1 is essential in T cell maturation and is correlated with thymocyte development and T-helper 2 (Th2) cell activation [14]. A recent study suggested that SATB1 regulates PDCD1 expression during T cell activation and prevents T cell exhaustion, and that dysregulation of this pathway results in anti-tumor immune dysfunction [15]. These findings reveal that SATB1 plays vital roles in tumor infiltrating lymphocytes. However, the specific mechanism of SATB1 in the regulation of tumor immunity remains unclear.

In this study, Oncomine, PrognoScan, Kaplan-Meier plotter (K-M plot), and Gene Expression Profiling Interactive Analysis (GEPIA) were employed to estimate the correlation between the prognosis of cancer patients and SATB1. Additionally, we explored SATB1 expression in immune infiltrating cells in multiple tumors through the Tumor Immune Estimation Resource (TIMER) database. Our results provided insight on SATB1 in tumor-immune interactions in BRCA, HNSC, and PRAD.

Material and Methods

Oncomine analysis

We used Oncomine (*https://www.oncomine.org/*) and the TIMER site (*https://cistrome.shinyapps.io/timer/*) to assess the expression of SATB1 in different cancers [16,17]. The threshold was as follows: fold change=1.5, *P*-value=0.001.

PrognoScan Analysis

PrognoScan (*http://www.abren.net/PrognoScan/*) was employed to assess the correlation between SATB1 and survival in cancer patients [18]. Cox *P*-value <0.05 was considered to be statistically significant.

K-M plot analysis

The K-M plot (*http://kmplot.com/*) is a website which can evaluate the survival of breast, ovarian, lung, and gastric cancer patient samples [19]. Thus, we explored the effect of SATB1 on prognosis in breast, ovarian, lung, and gastric cancer patients via K-M plot.

GEPIA analysis

Among 33 different types of cancer, GEPIA (*http://gepia.cancer-pku.cn/*) was employed to generate survival curves for gene expression. We analyzed gene correlation for given sets of The Cancer Genome Atlas (TCGA) data, and Person's correlation coefficient was also calculated. The SATB1 gene symbol is displayed on the x-axis, and other interested genes are shown on the y-axis.

TIMER analysis

TIMER is a website tool based on TCGA, which includes 10 897 samples across 32 cancers to evaluate tumor immune infiltration [17]. We analyzed the association between SATB1 and immune infiltration cells, including B cells, CD4+ T cells, CD8+ T cells, macrophages, neutrophils, and dendritic cells (DCs). We looked at the expression level of SATB1 versus tumor purity [20]. Additionally, we also estimated the correlation between SATB1 and biomarkers of tumor infiltrating cells, including markers of CD8+ T cells, T cells (general), B cells, monocytes, TAMs, M1 and M2 macrophages, neutrophils, natural killer (NK) cells, DCs, T-helper 1 (Th1) and Th2 cells, follicular helper T (Tfh) cells, T-helper 17 (Th17) cells, regulatory T cells (Tregs), and exhausted T cells [21]. TIMER can generate scatter plots as well as Spearman's correlation and *P*-value. The SATB1 gene symbol is displayed on the x-axis, and correlated gene symbols are shown on the y-axis. The expression level of genes was adjusted to log2 RSEM. A flow chart of the study design is shown in Figure 1.

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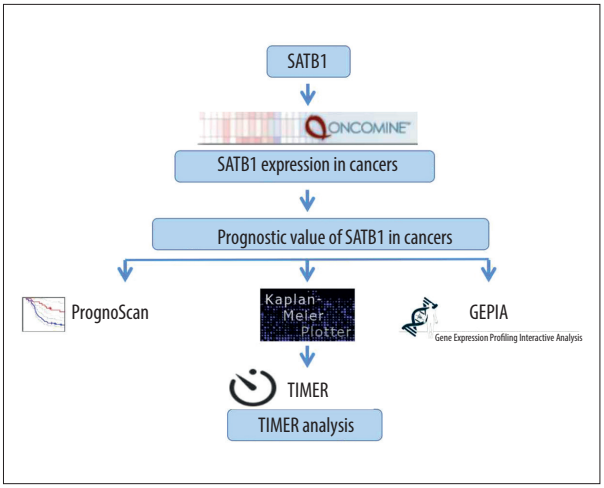

Figure 1. Flow chart of the study procedures.

Statistical analysis

Survival curves were produced via PrognoScan and K-M plot. The results of Oncomine are shown as *P*-value and fold change. K-M plot, PrognoScan, and GEPIA results are shown as hazard ratio (HR), *P*-value or Cox *P*-value. $P<0.05$ was considered to be statistically significant.

Results

SATB1 expression in various cancers

As revealed in Figure 2A, the results from the Oncomine database indicated that the expression of SATB1 was lower in brain, breast, colorectal, head and neck, lung, leukemia, lymphoma, liver, ovarian, melanoma, and sarcoma carcinomas, while SATB1 expression was increased in leukemia and myeloma tissues in some data sets.

To investigate the expression of SATB1 in malignancy, we used RNA-seq data from TCGA. As presented in Figure 2B, SATB1 expression was decreased in bladder urothelial carcinoma (BLCA), BRCA, cholangiocarcinoma (CHOL), colon adenocarcinoma (COAD), esophageal carcinoma (ESCA), HNSC, kidney renal clear cell carcinoma (KIRC), kidney renal papillary cell carcinoma (KIRP), liver hepatocellular carcinoma (LIHC), lung adenocarcinoma (LUAD), lung squamous cell carcinoma (LUSC), PRAD, rectum adenocarcinoma (READ), skin cutaneous melanoma (SKCM), stomach adenocarcinoma (STAD), and uterine corpus endometrial carcinoma (UCEC) tissues. However, SATB1 expression was increased in kidney chromophobe (KICH) tissues.

Prognostic value of SATB1 in cancers

The effect of SATB1 expression on survival was assessed through PrognoScan; the results are presented in Table 1. In particularly, the expression of SATB1 significantly affected prognosis in 7 types of cancers, including breast cancer (Figure 3A–3E),

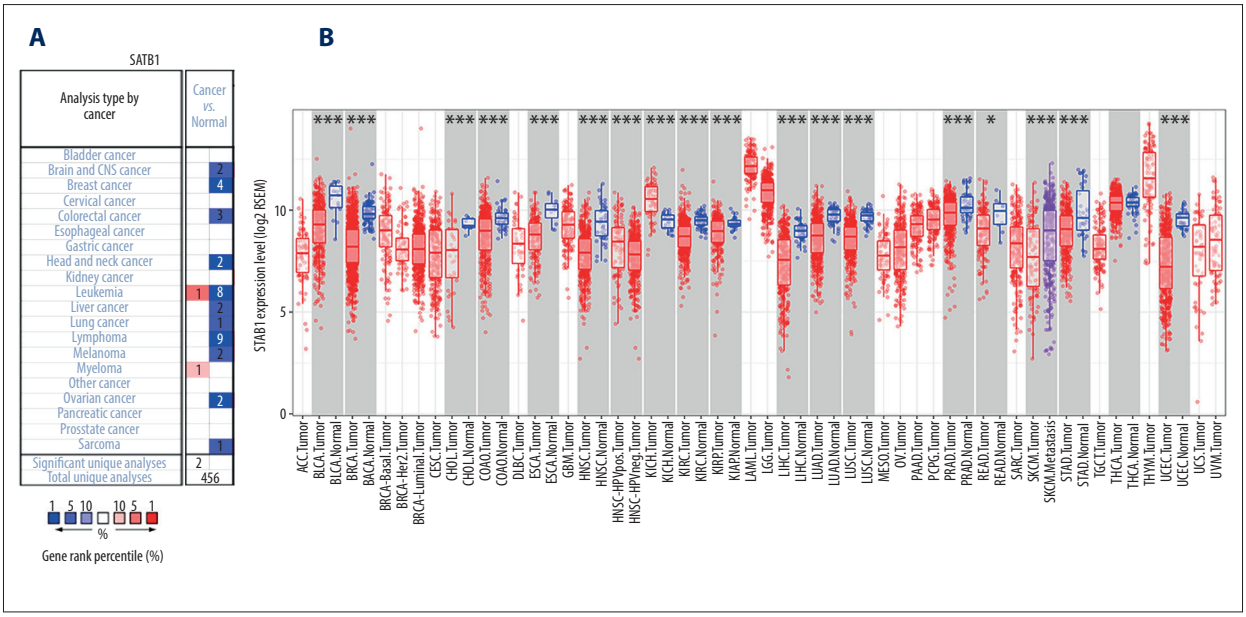

Figure 2. The expression of SATB1 in human cancers. (**A**) High or low SATB1 expression in data sets of different cancers in Oncomine database. (**B**) SATB1 expression levels in different tumor types from Tumor Immune Estimation Resource database (* $P<0.05$; ** $P<0.01$; *** $P<0.001$).

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Table 1. Relation between SATB1 expression and patient prognosis in different cancer using PrognosScan database.

Cancer type	Dataset	Endpoint	Array type	N	Cox *P*-value	HR [95% CI]
Bladde cancer	GSE5287	Overall survival	HG-U133A	30	0.057	0.55 [0.30–1.02]
	GSE13507	Overall survival	Human-6 v2	165	0.151	0.77 [0.54–1.10]
	GSE13507	Disease specific survival	Human-6 v2	165	0.018	0.53 [0.32–0.90]
Blood cancer	GSE12417-GPL96	Overall survival	HG-U133A	163	0.299	1.20 [0.85–1.68]
	GSE12417-GPL570	Overall survival	HG-U133_Plus_2	79	0.709	0.90 [0.51–1.57]
	GSE5122	Overall survival	HG-U133A	58	0.763	0.93 [0.56–1.53]
	GSE8970	Overall survival	HG-U133A	34	0.788	0.93 [0.55–1.57]
	GSE4475	Overall survival	HG-U133A	158	0.924	0.98 [0.71–1.36]
	E-TABM-346	Event free survival	HG-U133A	53	0.388	0.81 [0.50–1.31]
	E-TABM-346	Overall survival	HG-U133A	53	0.238	0.75 [0.46–1.21]
	GSE16131-GPL96	Overall survival	HG-U133A	180	0.116	0.76 [0.54–1.07]
	GSE2658	Disease specific survival	HG-U133_Plus_2	559	0.384	0.92 [0.76–1.11]
Brain cancer	GSE4271-GPL96	Overall survival	HG-U133A	77	0.004	0.60 [0.43–0.85]
	GSE7696	Overall survival	HG-U133_Plus_2	70	0.759	0.95 [0.70–1.30]
	MGH-glioma	Overall survival	HG-U95A	50	0.038	0.70 [0.50–0.98]
	GSE4412-GPL96	Overall survival	HG-U133A	74	0.101	0.69 [0.44–1.08]
	GSE16581	Overall survival	HG-U133_Plus_2	67	0.342	1.86 [0.52–6.66]
Breast cancer	GSE19615	Distant metastasis free survival	HG-U133_Plus_2	115	0.311	0.62 [0.25–1.56]
	GSE3143	Overall survival	HG-U95A	158	0.405	1.19 [0.79–1.78]
	GSE7849	Disease free survival	HG-U95A	76	0.857	1.05 [0.59–1.88]
	GSE12276	Relapse free survival	HG-U133_Plus_2	204	0.604	0.95 [0.80–1.14]
	GSE6532-GPL570	Distant metastasis free survival	HG-U133_Plus_2	87	0.463	0.86 [0.58–1.28]
	GSE6532-GPL570	Relapse free survival	HG-U133_Plus_2	87	0.463	0.86 [0.58–1.28]
	GSE9195	Distant metastasis free survival	HG-U133_Plus_2	77	0.178	1.57 [0.82–3.01]
	GSE9195	Relapse free survival	HG-U133_Plus_2	77	0.463	1.24 [0.69–2.23]
	GSE12093	Distant metastasis free survival	HG-U133A	136	0.599	0.86 [0.50–1.49]
	GSE11121	Distant metastasis free survival	HG-U133A	200	0.910	0.97 [0.58–1.63]
	GSE1378	Relapse free survival	Arcturus 22k	60	0.829	0.96 [0.66–1.39]
	GSE1379	Relapse free survival	Arcturus 22k	60	0.080	1.80 [0.93–3.46]
	GSE9893	Overall survival	MLRG Human 21K V12.0	155	0.001	0.72 [0.59–0.88]
	GSE2034	Distant metastasis free survival	HG-U133A	286	0.768	1.05 [0.77–1.43]
	GSE1456-GPL96	Relapse free survival	HG-U133A	159	0.326	0.77 [0.45–1.30]

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Table 1 continued. Relation between SATB1 expression and patient prognosis in different cancer using PrognosScan database.

Cancer type	Dataset	Endpoint	Array type	N	Cox *P*-value	HR [95% CI]
Breast cancer (continued)	GSE1456-GPL96	Disease specific survival	HG-U133A	159	0.219	0.68 [0.37–1.26]
	GSE1456-GPL96	Overall survival	HG-U133A	159	0.107	0.65 [0.39–1.10]
	GSE7378	Disease free survival	U133AAofAv2	54	0.366	0.71 [0.34–1.50]
	E-TABM-158	Relapse free survival	HG-U133A	117	0.597	0.91 [0.65–1.28]
	E-TABM-158	Disease specific survival	HG-U133A	117	0.702	0.93 [0.63–1.37]
	E-TABM-158	Distant metastasis free survival	HG-U133A	117	0.448	0.85 [0.57–1.28]
	E-TABM-158	Overall survival	HG-U133A	117	0.597	0.91 [0.65–1.28]
	GSE3494-GPL96	Disease specific survival	HG-U133A	236	<0.001	0.35 [0.20–0.62]
	GSE4922-GPL96	Disease free survival	HG-U133A	249	0.013	0.57 [0.36–0.89]
	GSE2990	Relapse free survival	HG-U133A	62	0.198	0.72 [0.44–1.18]
	GSE2990	Distant metastasis free survival	HG-U133A	125	0.037	0.53 [0.30–0.96]
	GSE2990	Relapse free survival	HG-U133A	125	0.004	0.52 [0.33–0.81]
	GSE2990	Distant metastasis free survival	HG-U133A	54	0.339	0.75 [0.41–1.36]
	GSE7390	Distant metastasis free survival	HG-U133A	198	0.749	1.04 [0.80–1.36]
	GSE7390	Overall survival	HG-U133A	198	0.886	0.98 [0.74–1.29]
	GSE7390	Relapse free survival	HG-U133A	198	0.781	1.03 [0.83–1.28]
Colorectal cancer	GSE12945	Disease free survival	HG-U133A	51	0.189	2.91 [0.59–14.36]
	GSE12945	Overall survival	HG-U133A	62	0.914	0.95 [0.39–2.32]
	GSE17536	Disease specific survival	HG-U133_Plus_2	177	0.739	1.07 [0.71–1.61]
	GSE17536	Overall survival	HG-U133_Plus_2	177	0.277	1.22 [0.85–1.73]
	GSE17536	Disease free survival	HG-U133_Plus_2	145	0.775	1.07 [0.66–1.74]
	GSE14333	Disease free survival	HG-U133_Plus_2	226	0.679	1.07 [0.77–1.50]
	GSE17537	Overall survival	HG-U133_Plus_2	55	0.821	1.07 [0.58–2.00]
	GSE17537	Disease free survival	HG-U133_Plus_2	55	0.532	1.24 [0.64–2.40]
	GSE17537	Disease specific survival	HG-U133_Plus_2	49	0.304	1.54 [0.68–3.51]
Lung cancer	jacob-00182-CANDF	Overall survival	HG-U133A	82	0.503	0.79 [0.40–1.56]
	HARVARD-LC	Overall survival	HG-U95A	84	0.551	1.15 [0.73–1.81]
	jacob-00182-HLM	Overall survival	HG-U133A	79	0.784	0.94 [0.58–1.50]
	MICHIGAN-LC	Overall survival	HuGeneFL	86	0.141	0.51 [0.21–1.25]
	jacob-00182-MSK	Overall survival	HG-U133A	104	0.013	0.48 [0.26–0.85]
	GSE13213	Overall survival	G4112F	117	0.025	0.70 [0.51–0.96]
	GSE31210	Overall survival	HG-U133_Plus_2	204	0.259	0.69 [0.37–1.31]

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Table 1 continued. Relation between SATB1 expression and patient prognosis in different cancer using PrognosScan database.

Cancer type	Dataset	Endpoint	Array type	N	Cox *P*-value	HR [95% CI]
Lung cancer (continued)	GSE31210	Relapse free survival	HG-U133_Plus_2	204	<0.001	0.42 [0.27–0.66]
	jacob-00182-UM	Overall survival	HG-U133A	178	0.189	0.75 [0.49–1.15]
	GSE3141	Overall survival	HG-U133_Plus_2	111	0.775	1.07 [0.68–1.68]
	GSE14814	Overall survival	HG-U133A	90	0.080	0.55 [0.29–1.07]
	GSE14814	Disease specific survival	HG-U133A	90	0.029	0.43 [0.20–0.92]
	GSE8894	Relapse free survival	HG-U133_Plus_2	138	0.857	1.02 [0.83–1.25]
	GSE4573	Overall survival	HG-U133A	129	0.575	1.22 [0.62–2.40]
	GSE17710	Relapse free survival	Agilent-UNC-custom-4X44K	56	0.545	0.85 [0.50–1.44]
	GSE17710	Relapse free survival	Agilent-UNC-custom-4X44K	56	0.332	0.79 [0.49–1.27]
	GSE17710	Overall survival	Agilent-UNC-custom-4X44K	56	0.283	0.74 [0.43–1.28]
	GSE17710	Overall survival	Agilent-UNC-custom-4X44K	56	0.133	0.68 [0.41–1.12]
Ovarian cancer	GSE9891	Overall survival	HG-U133_Plus_2	278	0.485	0.94 [0.80–1.11]
	DUKE-OC	Overall survival	HG-U133A	133	0.199	0.91 [0.79–1.05]
	GSE8841	Overall survival	G4100A	81	0.203	1.82 [0.72–4.56]
	GSE26712	Overall survival	HG-U133_Plus_2	185	0.269	1.16 [0.89–1.50]
	GSE26712	Disease free survival	HG-U133_Plus_2	185	0.248	1.15 [0.91–1.46]
	GSE17260	Progression free survival	G4112A	110	0.237	0.89 [0.73–1.08]
	GSE17260	Overall survival	G4112A	110	0.342	0.88 [0.69–1.14]
	GSE14764	Overall survival	HG-U133A	80	0.706	1.07 [0.75–1.53]
Prostate cancer	GSE16560	Overall survival	6K DASL	281	<0.001	0.66 [0.54–0.81]
Renal cell carcinoma	E-DKFZ-1	Overall survival	A-RZPD-20	59	0.525	1.68 [0.34–8.29]
Skin cancer	GSE19234	Overall survival	HG-U133_Plus_2	38	0.021	0.50 [0.28–0.90]
Soft tissue cancer	GSE30929	Distant recurrence free survival	HG-U133A	140	0.348	1.28 [0.76–2.16]
Esophagus cancer	GSE11595	Overall survival	CRUKDMF_22K_v1.0.0	34	0.408	2.56 [0.28–23.76]
Eye cancer	GSE22138	Distant metastasis free survival	HG-U133_Plus_2	63	<0.001	0.67 [0.54–0.84]
Head and neck cancer	GSE2837	Relapse free survival	U133_X3P	28	0.18	0.81 [0.59–1.10]

HR – hazard ratio; CI – confidence interval.

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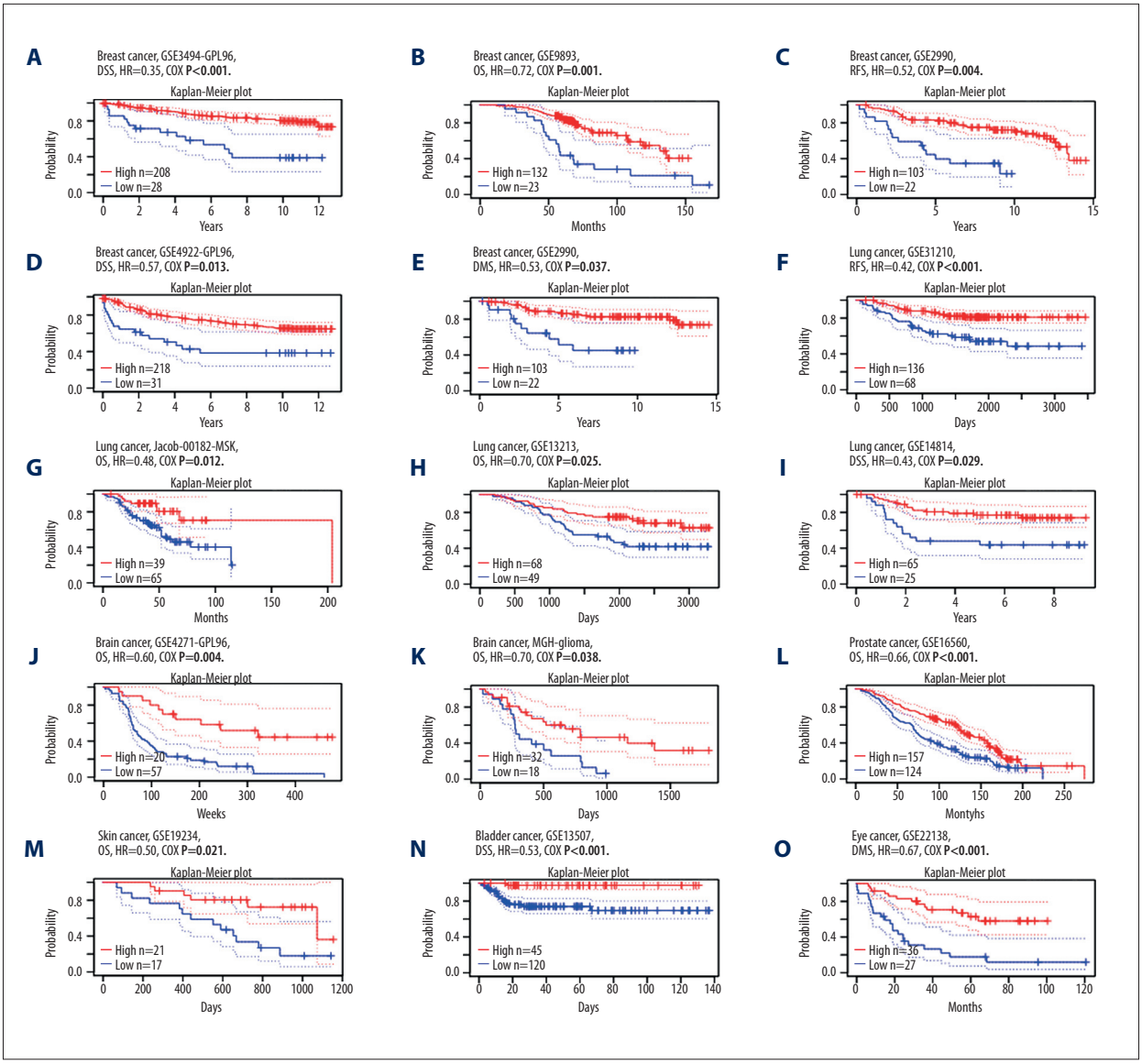

Figure 3. Kaplan-Meier survival curves comparing the increased and decreased expression of SATB1 in different types of cancer in PrognoScan. (**A–E**) Survival curves of DSS, OS, RFS, DFS, and DMFS in breast cancer cohorts [GSE3494-GPL96 (n=236), GSE9893 (n=155), GSE2990 (n=125), and GSE4922 (n=249)]. (**F–I**) Survival curves of RFS, OS, and DSS in lung cancer cohorts [GSE31210 (n=204), Jacob-00182-MSK (n=104), GSE13213 (n=117), and GSE14814 (n=90)]. (**J, K**) Survival curves of OS in brain cancer cohorts [GSE4271-GPL96 (n=77), MGH-glioma (n=50)]. (**L**) Survival curves of OS in prostate cancer cohorts [GSE16560 (n=281)]. (**M**) Survival curves of OS in skin cancer cohorts [GSE19234 (n=38)]. (**N**) Survival curves of DSS in bladder cancer cohorts [GSE13507 (n=165)]. (**O**) Survival curves of DSS in eye cancer cohorts [GSE22138 (n=63)]. DSS – disease-specific survival; OS – overall survival; RFS – relapse-free survival; DFS – disease-free survival; DMFS – distant metastasis free survival.

lung cancer (Figures 3F–3I), brain cancer (Figure 3J, 3K), prostate cancer (Figure 3L), skin cancer (Figure 3M), bladder cancer (Figure 3N), and eye cancer (Figure 3O). In addition, one cohort (GSE2990) [22] which included 125 samples of BRCA, demonstrated that decreased expression of SATB1 was associated with worse prognosis (relapse-free survival [RFS] HR: 0.52, 95% confidence interval [CI]: 0.33–0.81, Cox *P*: 0.004; distant metastasis free survival [DMFS] HR: 0.53, 95% CI: 0.30–0.96, Cox *P*=0.037).

We also used K-M plot to explore the prognostic effects of SATB1 based on Affymetrix microarrays. As shown in Figure 4A and 4B, a lower level of SATB1 was correlate with worse prognosis in BRCA patients (OS HR: 0.72, 95% CI: 0.58–0.89, *P*: 0.0027; RFS HR: 0.77, 95% CI: 0.66–0.90, *P*: 0.0012). In addition, a low level of SATB1 was correlated with poor OS in LUAD (HR: 0.57, 95% CI: 0.49–0.68) (Figure 4C). However, SATB1 had less influence

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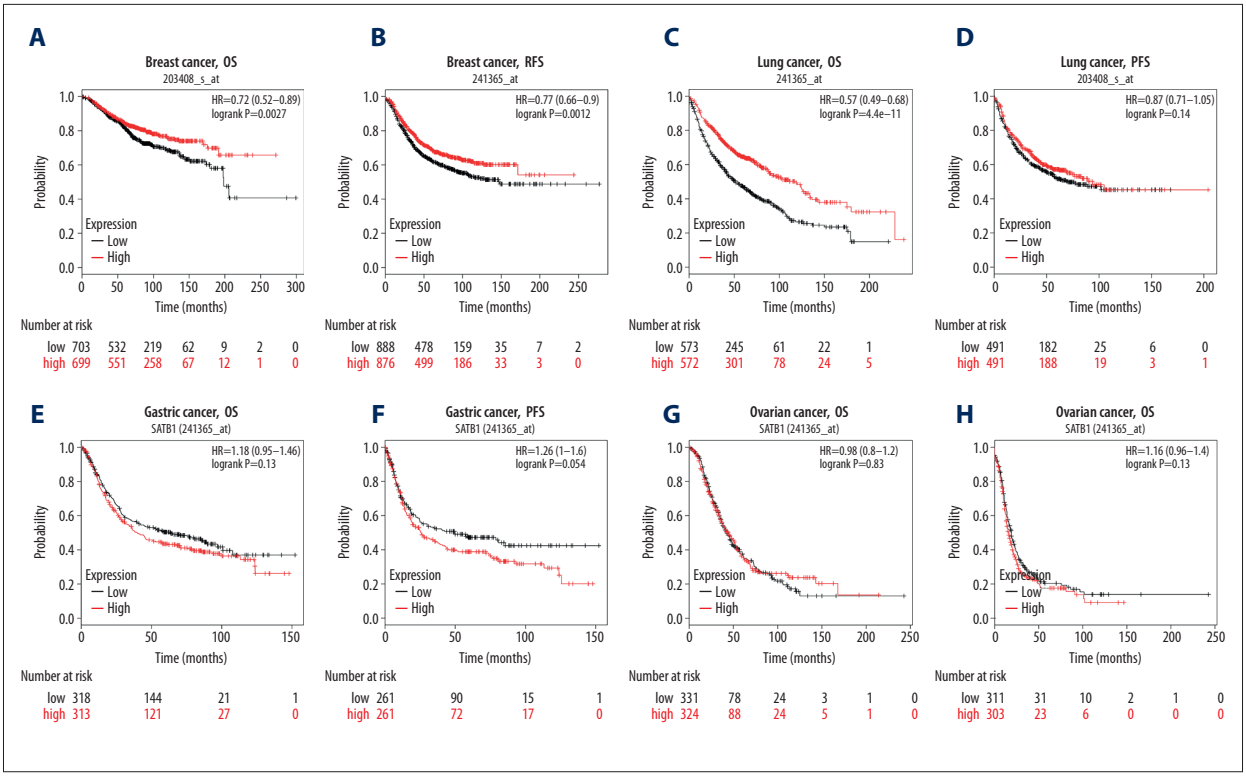

Figure 4. Kaplan-Meier survival curves comparing the expression of SATB1 in different types of cancer in Kaplan-Meier plotter database. (**A, B**) OS and RFS of breast cancer (n=1402, n=977). (**C, D**) OS and PFS of lung cancer (n=1145, n=982). (**E, F**) OS and PFS of gastric cancer (n 631, n=522). (**G, H**) OS and PFS of ovarian cancer (n=655, n=1435). OS – overall survival; RFS – relapse-free survival; PFS – progression-free survival.

on progression-free survival (PFS) (Figure 4D) in LUAD, and OS and PFS in gastric cancer and ovarian cancer (Figure 4E–4H).

The effect of SATB1 on survival in different cancers was assessed using the GEPIA database. Decreased expression of SATB1 was associated with worse OS and disease-free survival (DFS) in KIRC, LGG, SKCM, and uveal melanoma (UVM); and DFS in PRAD and OS in SARC (sarcoma). Additionally, a high level of SATB1 was associated with worse DFS in STAD (P<0.05) (Table 2). These results suggested that SATB1 has the potential to predict prognosis in multiple types of cancers.

Low level of SATB1 impacts the prognosis of BRCA patients with positive estrogen receptor (ER) and mutated TP53

To comprehensive understand the potential mechanisms of SATB1 expression in BRCA, we used the K-M plot to explore the association between SATB1 and clinical characteristics of BRCA patients. As shown in Table 3, a low level of SATB1 was associated with poor OS and PFS in BRCA patients with positive estrogen receptor (ER) and mutated TP53. Meanwhile, a low level of SATB1 was also associated with PFS in patients with HER2 negative and luminal B of intrinsic subtype, and OS in patients with grade 2 and basal-like 2 of Pietenpol subtype (P<0.05).

SATB1 was associated with tumor immune infiltration in BRCA, HNSC, and PRAD

We used the TIMER database to investigate the associations of SATB1 and tumor immune infiltration in 33 types of cancer. As shown Figures 5–8, the results indicate that SATB1 was significantly correlated with tumor purity and B cell infiltration in 16 and 14 types of cancer, respectively. Additionally, SATB1 expression was associated with infiltration of CD8+ T cells, CD4+ T cells, macrophages, neutrophils, and DCs in 11, 19, 25, 16, and 18 types of cancer, respectively.

We further explored the specific cancer type in which SATB1 correlated with tumor immune infiltration. Accordingly, we found that SATB1 was negative related to tumor purity (r=–0.291, P=6.71e-21) and positive correlated with infiltration of B cells (r=0.116, P=2.83e-04), CD8+ T cells (r=0.251, P=1.89e-15), CD4+ T cells (r=0.218, P=7.86e-12), macrophages (r=0.151, P=1.95e-06), neutrophils (r=0.232, P=4.32e-13), and DCs (r=0.189, P=4.01e-09) in BRCA (Figure 5A). In addition, SATB1 was negative correlated with tumor purity (r=–0.103,

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Table 2. Correlation of SATB1 expression with prognostic values in diverse types of cancer in GEPIA.

Cancer type	Overall survival		Disease free survival	
	HR	*P*	HR	*P*
ACC	0.93	0.85	1.3	0.47
BLCA	0.78	0.098	1.0	0.87
BRCA	0.95	0.75	0.99	0.98
CESC	1.1	0.82	1.2	0.48
CHOL	0.61	0.33	0.45	0.091
COAD	1.0	1	1.1	0.73
DLBC	1.4	0.64	1.5	0.54
ESCA	0.81	0.37	1.2	0.48
GBM	1.3	0.13	0.81	0.32
HNSC	0.82	0.15	0.73	0.061
KICH	2.8	0.19	1.3	0.7
KIRC	0.58	0.00065	0.57	0.0026
KIRP	0.95	0.87	0.7	0.23
LAML	1.2	0.44	1	1
LGG	0.49	0.00011	0.64	0.0049
LIHC	0.91	0.58	0.94	0.66
LUAD	0.78	0.095	1.1	0.6
LUSC	0.84	0.22	0.81	0.25
MESO	0.95	0.8	0.77	0.34
OV	1.1	0.27	1.2	0.19
PAAD	0.76	0.18	1.2	0.44
PCPG	1.8	0.52	0.39	0.09
PRAD	1.8	0.36	0.56	0.0075
READ	0.77	0.58	2.1	0.14
SARC	1.6	0.023	1.4	0.092
SKCM	0.54	5.8e-06	0.72	0.0076
STAD	0.91	0.56	1.5	0.039
TGCT	0.43	0.46	0.65	0.24
THCA	0.58	0.28	1.2	0.48
THYM	0.28	0.096	0.58	0.24
UCEC	1	0.98	0.9	0.74
UCS	0.52	0.062	0.52	0.076
UVM	0.13	0.00016	0.31	0.021

GEPIA – Gene Expression Profiling Interactive Analysis; HR – hazard ratio; CI – confidence interval; ACC – adenoid cystic carcinoma; BLCA – bladder urothelial carcinoma; BRCA – breast invasive carcinoma; CESC – cervical squamous cell carcinoma; CHOL – cholangiocarcinoma; COAD – colon adenocarcinoma; DLBC – diffuse large B-cell lymphoma; ESCA – esophageal carcinoma; GBM – glioblastoma; HNSC – head and neck cancer; KICH – kidney chromophobe; KIRC – kidney renal clear cell carcinoma; KIRP – kidney renal papillary cell carcinoma; LAML – lymphoblastic acute myeloid leukemia; LGG – low-grade gliomas; LIHC – liver hepatocellular carcinoma; LUAD – lung adenocarcinoma; LUSC – lung squamous cell carcinoma; MESO – mesothelioma; OV – ovarian; PAAD – pancreatic adenocarcinoma; PCPG – paraganglioma; PRAD – prostate adenocarcinoma; READ – rectum adenocarcinoma; SARC – sarcoma; SKCM – skin cutaneous melanoma; STAD – stomach adenocarcinoma; TGCT – testicular germ cell tumors; THCA – thyroid carcinoma; THYM – thymoma; UCEC – uterine corpus endometrial carcinoma; UCS – uterine carcinosarcoma; UVM – uveal melanoma.

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Table 3. Correlation of SATB1 mRNA expression and prognosis in breast cancer with different clinicopathological characters by Kaplan-Meier plotter.

Clinicopathological characteristics	Overall survival (n=1402)				Progression-free survival (n=3955)			
	N	HR		*P*-value	N	HR		*P*-value
ER status								
Positive	548	0.56	(0.39–0.81)	0.0015	2061	0.8	(0.68–0.94)	0.0062
Negative	251	0.81	(0.51–1.80)	0.36	801	0.90	(0.72–1.13)	0.38
PR status								
Positive	83	0.38	(0.10–1.54)	0.16	589	0.92	(0.65–1.30)	0.62
Negative	89	0.69	(0.27–1.77)	0.43	549	0.89	(0.66–1.19)	0.42
HER2 status								
Positive	129	0.86	(0.43–1.73)	0.68	252	0.17	(0.76–1.81)	0.47
Negative	130	0.85	(0.36–2.01)	0.71	800	0.70	(0.54–0.91)	0.0078
Intrinsic subtype								
Basal	241	0.70	(0.43–1.14)	0.15	618	0.81	(0.63–1.04)	0.092
Luminal A	611	0.79	(0.55–1.12)	0.19	1933	0.93	(0.78–1.10)	0.39
Luminal B	433	0.71	(0.49–1.03)	0.071	1149	0.82	(0.68–0.99)	0.043
Lymph node status								
Positive	313	0.85	(0.58–1.25)	0.4	3951	0.83	(0.68–1.01)	0.064
Negative	594	0.83	(0.57–1.20)	0.31	2020	0.93	(0.79–1.10)	0.41
Grade								
1	161	0.57	(0.23–1.40)	0.21	345	0.96	(0.57–1.61)	0.87
2	387	0.65	(0.42–1.00)	0.047	901	0.88	(0.69–1.12)	0.29
3	503	0.80	(0.58–1.12)	0.19	903	0.88	(0.71–1.09)	0.25
TP53 status								
Mutated	111	0.41	(0.18–0.92)	0.025	188	0.52	(0.32–0.84)	0.0071
Wild type	187	0.70	(0.36–1.34)	0.28	273	0.98	(0.65–1.50)	0.94
Pietenpol subtype								
Basal-like 1	58	0.55	(0.18–1.70)	0.29	171	1.08	(0.67–1.74)	0.74
Basal-like 2	38	4.20	(0.89–19.86)	0.049	76	0.56	(0.27–1.15)	0.11
Immunomodulatory	100	0.82	(0.32–2.07)	0.67	203	0.65	(0.36–1.19)	0.16
Mesenchymal	73	0.81	(0.37–1.77)	0.59	177	0.78	(0.51–1.20)	0.26
Luminal androgen receptor	83	0.80	(0.41–1.56)	0.51	203	1.13	(0.76–1.70)	0.54

HR – hazard ratio; ER – estrogen receptor; PR – progesterone receptor; HER2 – human epidermal growth factor receptor 2.

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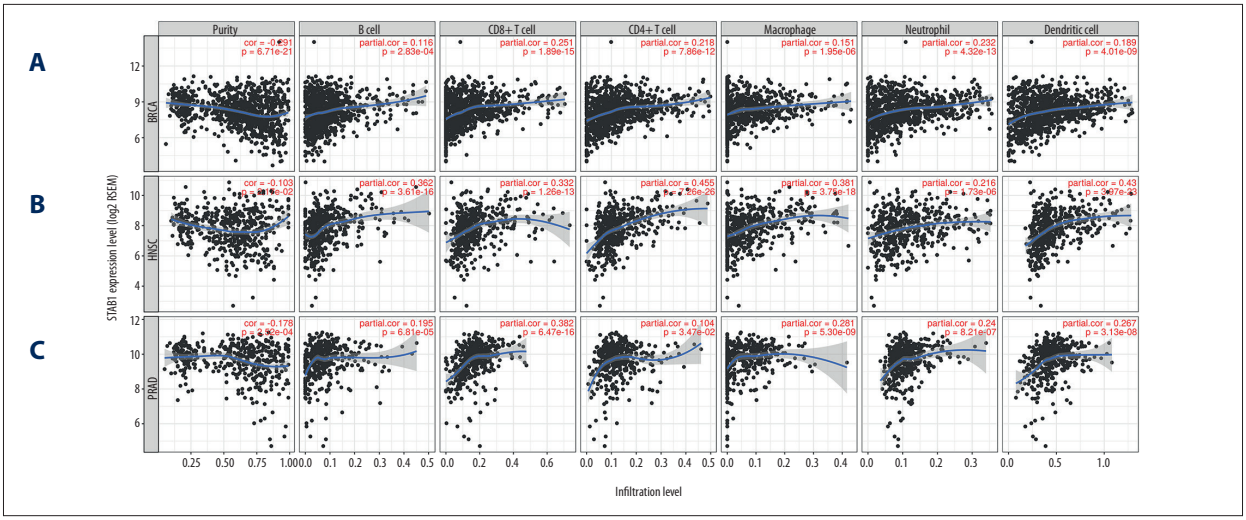
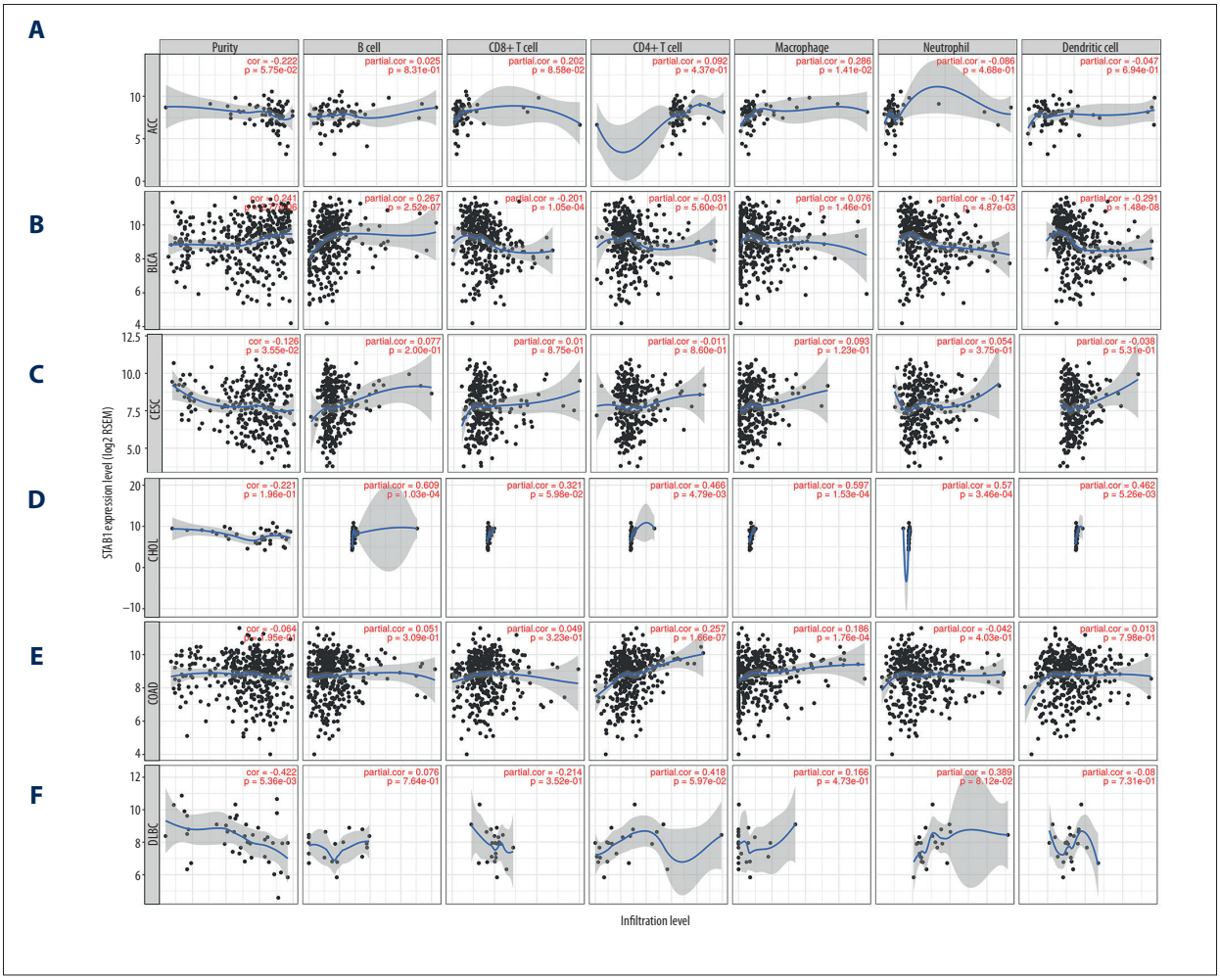


Figure 5. SATB1 expression is negatively correlated with tumor purity and positively correlated with infiltration levels of B cells, CD8+ T cells, CD4+ T cells, macrophages, neutrophils, and dendritic cells in BRCA, HNSC, and PRAD. (**A**) Correlation of SATB1 expression with immune infiltration level in BRAC (n=1093). (**B**) Correlation of SATB1 expression with immune infiltration level in HNSC (n=520). (**C**) Correlation of SATB1 expression with immune infiltration level in PRAD (n=497). BRCA – breast invasive carcinoma; HNSC – head and neck cancer; PRAD – prostate adenocarcinoma.



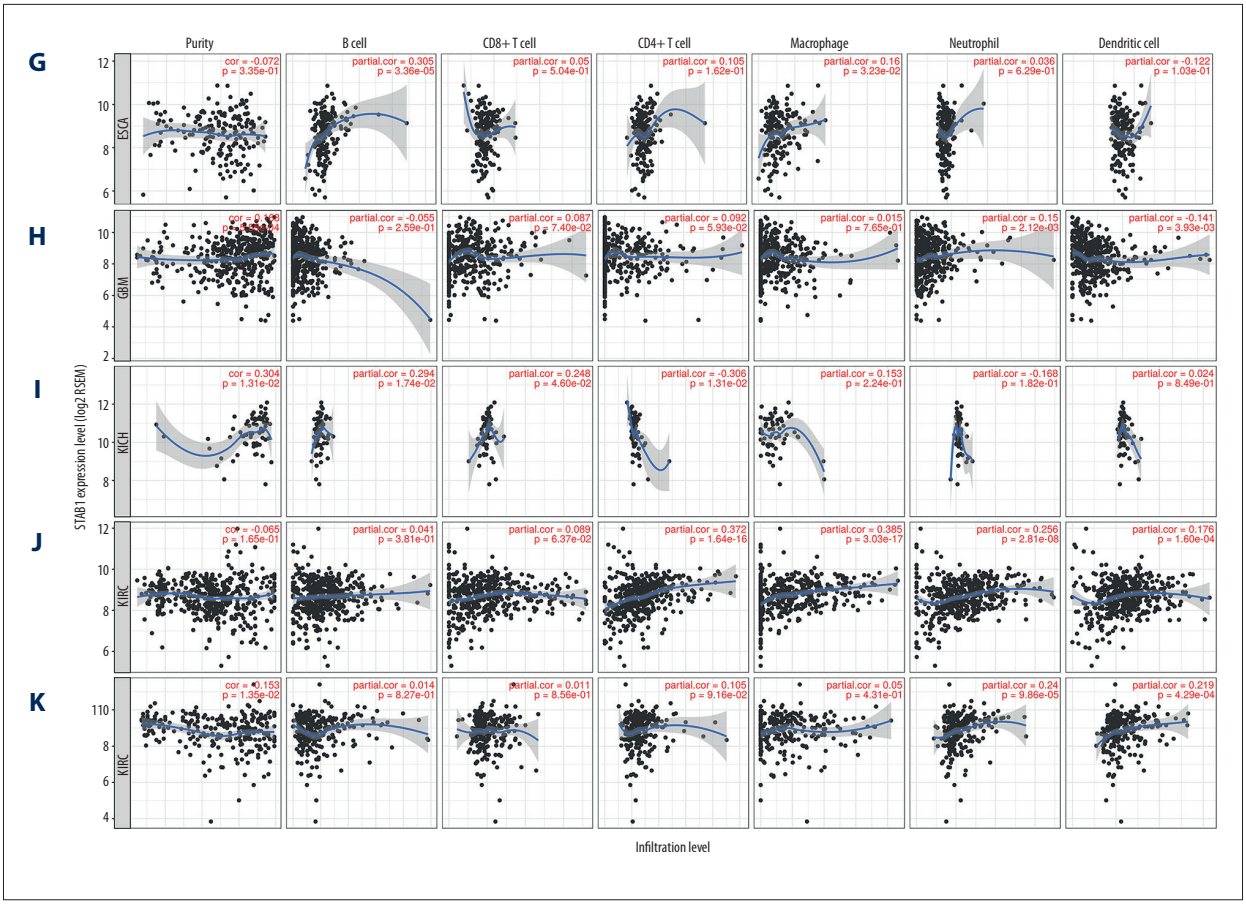


Figure 6. Association of SATB1 expression with immune infiltration levels in (**A**) ACC. (**B**) BLCA. (**C**) CESC. (**D**) CHOL. (**E**) COAD. (**F**) DLBC. (**G**) ESCA. (**H**) GBM. (**I**) KICH. (**J**) KIRC. (**K**) KIRP. ACC – adenoid cystic carcinoma; BLCA – bladder urothelial carcinoma; CESC – cervical squamous cell carcinoma; CHOL – cholangiocarcinoma; COAD – colon adenocarcinoma; DLBC – diffuse large B-cell lymphoma; ESCA – esophageal carcinoma; GBM – glioblastoma; KICH – kidney chromophobe; KIRC – kidney renal clear cell carcinoma; KIRP – kidney renal papillary cell carcinoma.

P=2.17e-02) and positive correlated with infiltration of B cells (r=0.362, *P*=3.61e-16), CD8+ T cells (r=0.332, *P*=1.26e-13), CD4+ T cells (r=0.455, *P*=7.26e-27), macrophages (r=0.381, *P*=3.75e-18), neutrophils (r=0.216, *P*=1.73e-06), and DCs (r=0.430, *P*=3.97e-23) in HNSC (Figure 5B). Furthermore, SATB1 expression was negative correlated with tumor purity (r=-0.178, *P*=2.52e-04) and positive correlated with infiltration of B cells (r=0.195, *P*=6.81e-05), CD8+ T cells (r=0.382, *P*=6.47e-16), CD4+ T cells (r=0.104, *P*=3.47e-02), macrophages (r=0.281, *P*=5.30e-09), neutrophils (r=0.240, *P*=8.21e-07), and DCs (r=0.267, *P*=3.13e-08) in PRAD (Figure 5C). Our findings indicate that SATB1 is essential in immune cells infiltration in BRAC, HNSC, and PRAD.

Correlation between SATB1 and immune marker sets

We investigated the associations between SATB1 and immune markers of diverse immune cells in BRCA, HNSC, and PRAD through the TIMER database. After adjustments for tumor purity, our findings revealed that SATB1 was significantly related to most immune markers of different immune cells and diverse T cells in BRAC, HNSC, and PRAD (Figure 9A–9C, Table 4).

As shown in Table 4, we discovered that the expression levels of gene markers of CD8+ T cell, T cells (general), B cells, and neutrophils had significant correlations with SATB1 both in BRAC and HNSC. In addition, the expression levels of gene markers of M1 macrophages and Th2 cells had significant correlations with SATB1 both in HNSC and PRAD. We also confirmed

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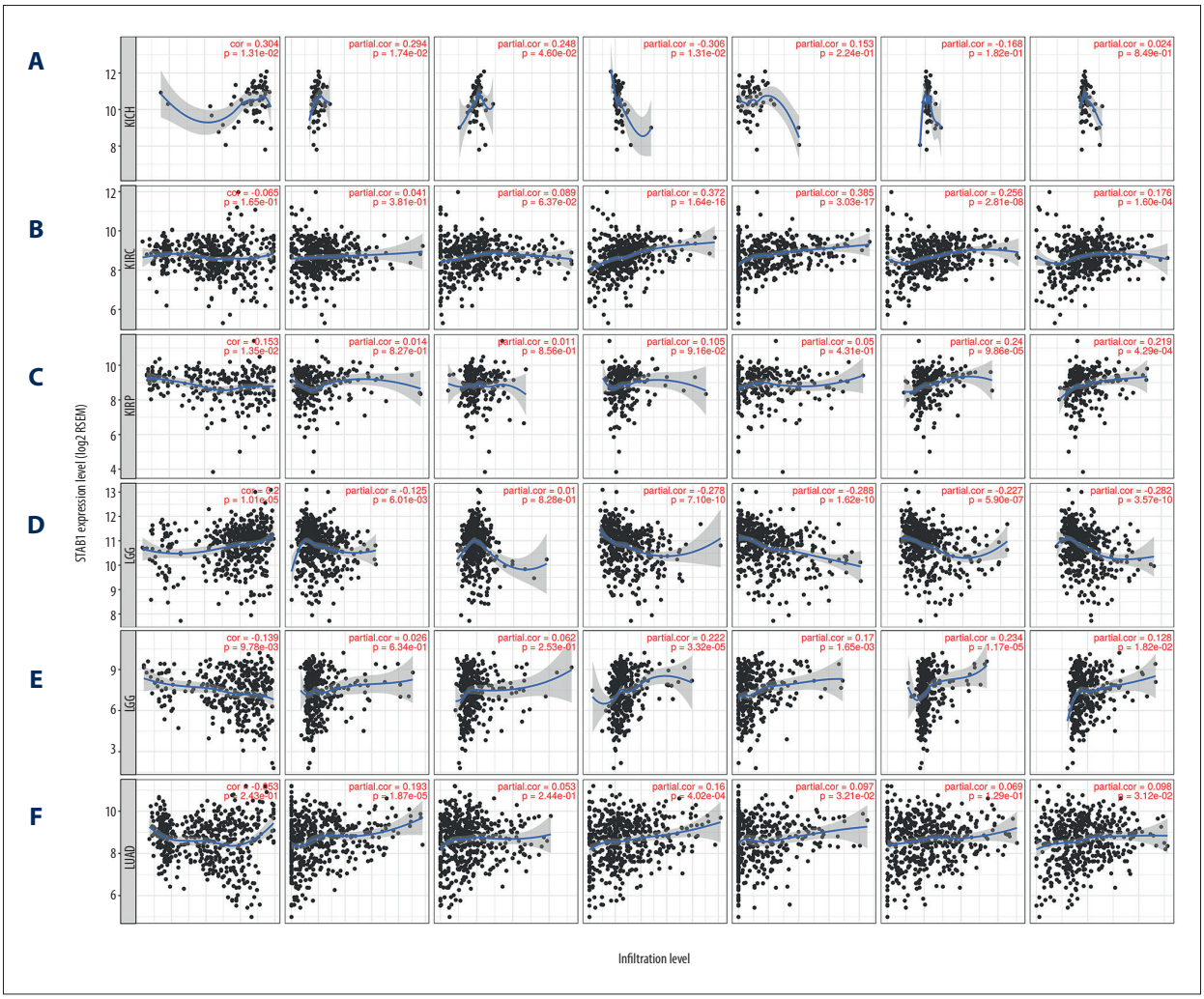
that the expression of gene markers of monocytes, TAMs, M2 macrophages, DCs, Th2 cells, Tfh cells, and Tregs significantly correlated with SATB1 in HNSC. These findings indicated that SATB1 is critical to immune escape in BRCA, HNSC, and PRAD microenvironments.

Discussion

The recognition that immune cells can identify and destroy cancer cells has promoted a tremendous shift in the perception of cancers, and immunotherapies have been shown to have curative effects in tumors which were resistant to regular therapy [23]. SATB1 can reprogram gene expression profiles and cause rapid phenotype changes. Increasingly, studies have demonstrated that SATB1 is essential in deterioration of tumors [13]. In our research, we found that aberrant SATB1 expression was related to prognosis in diverse cancers. Lower SATB1 expression correlated with poor survival in BRCA patients with positive ER and mutated TP53. Additionally, our results indicated that in BRAC, HNSC, and PRAD, the infiltration levels of immune cell and different immune gene markers were related to SATB1 expression. Therefore, our study provides a theoretical basis for understanding the function of SATB1 in tumor progression and its application as a tumor biomarker.

In this study, datasets in Oncomine and TIMER were used to explore the expression of SATB1 and its prognostic value in human cancers. We found SATB1 was differentially expressed between cancer and normal tissues in various malignancies. Oncomine analysis revealed that the expression of SATB1 was reduced in brain, breast, colorectal, head and neck, leukemia, liver, lung, lymphoma, melanoma, ovarian, and sarcoma carcinomas, while SATB1 expression was increased in leukemia and myeloma tissues. However, our findings from TCGA data indicated that SATB1 expression was decreased in BLCA, BRCA, CHOL, COAD, ESCA, HNSC, KIRC, KIRP, LIHC, LUAD, LUSC, PRAD, READ, SKCM, STAD, and UCEC; while SATB1 expression was increased in KICH. The differences of SATB1 expression among different types of cancer in diverse databases might be due to



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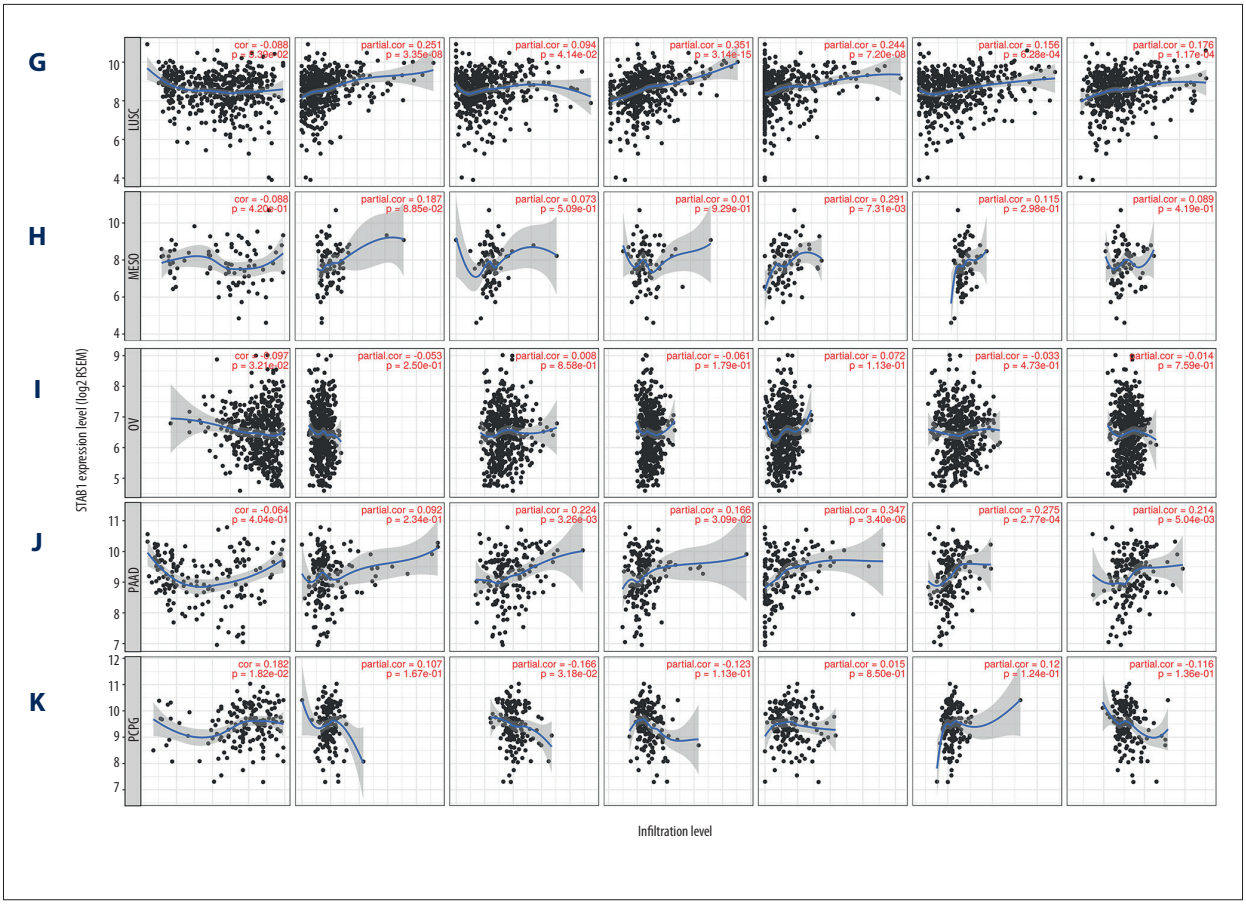

Figure 7. Association of SATB1 expression with immune infiltration levels in (**A**) LGG. (**B**) LIHC. (**C**) LUAD. (**D**) LUSC. (**E**) MESO. (**F**) OV. (**G**) PAAD. (**H**) PCPG. (**I**) READ. (**J**) SARC. (**K**) SKCM. LGG – low-grade gliomas; LIHC – liver hepatocellular carcinoma; LUAD – lung adenocarcinoma; LUSC – lung squamous cell carcinoma; MESO – mesothelioma; OV – ovarian; PAAD – pancreatic adenocarcinoma; PCPG – paraganglioma; READ – rectum adenocarcinoma; SARC – sarcoma; SKCM – skin cutaneous melanoma.

the diversity of biological functions of SATB1 as well as data collection approaches. However, we found consistent correlations between SATB1 and prognosis in breast, colorectal, head and neck, liver, lung, gastric, and sarcoma carcinomas. GEPIA analysis based on TCGA data indicated that lower SATB1 expression was related to a worse prognosis for certain cancer types, such as KIRC, LGG, SKCM, PRAD, SARC, and UVM, while elevated SATB1 expression correlated with a better prognosis in STAD. In addition, K-M plot and PrognoScan analysis indicated decreased SATB1 expression was related to short survival in breast, lung, brain, gastric, ovarian, prostate, skin, bladder, and eye cancer patients. Moreover, depletion of SATB1 led to poor OS and PFS in BRAC patients with positive ER and mutated TP53. Thus, these results demonstrated that SATB1 could be used as a prognostic indicator in multiple types of neoplasms.

Another important finding in our research was that a low level of SATB1 was associated with different levels of immune infiltration in neoplasms, especially in BRAC, HNSC, and PRAD. Our results revealed that the SATB1 expression level had significant positive correlation with infiltration levels of B cells, CD4+ T cells, CD8+ T cells, macrophages, neutrophils, and DCs in BRAC, HNSC, and PRAD. M1 and M2 macrophage markers, such as NOS2, PTGS2, IRF5, CD163, VSIG4, and MS4A4A, showed weak to strong correlations with SATB1 expression, which indicated the regulating function of SATB1 in TAM polarization. Decreased SATB1 expression also was positively associated with the Treg and T cell exhaustion markers, such as FOXP3, CCR8, STAT5B, TGF β, and PD-1 in BRAC, HNSC and PRAD. In addition, significant correlations between SATB1 and the regulation markers of T helper cells, such as Th1, Th2, Tfh, and Th17, were found in BRAC, HNSC, and PRAD. These results suggest that SATB1 is correlated with tumor immune infiltration and plays a vital role in regulation and enrollment of tumor immune infiltrating cells in BRAC, HNSC, and PRAD.

Diverse mechanisms involved in the carcinogenesis, immune infiltration, and prognosis of SATB1 have been investigated.

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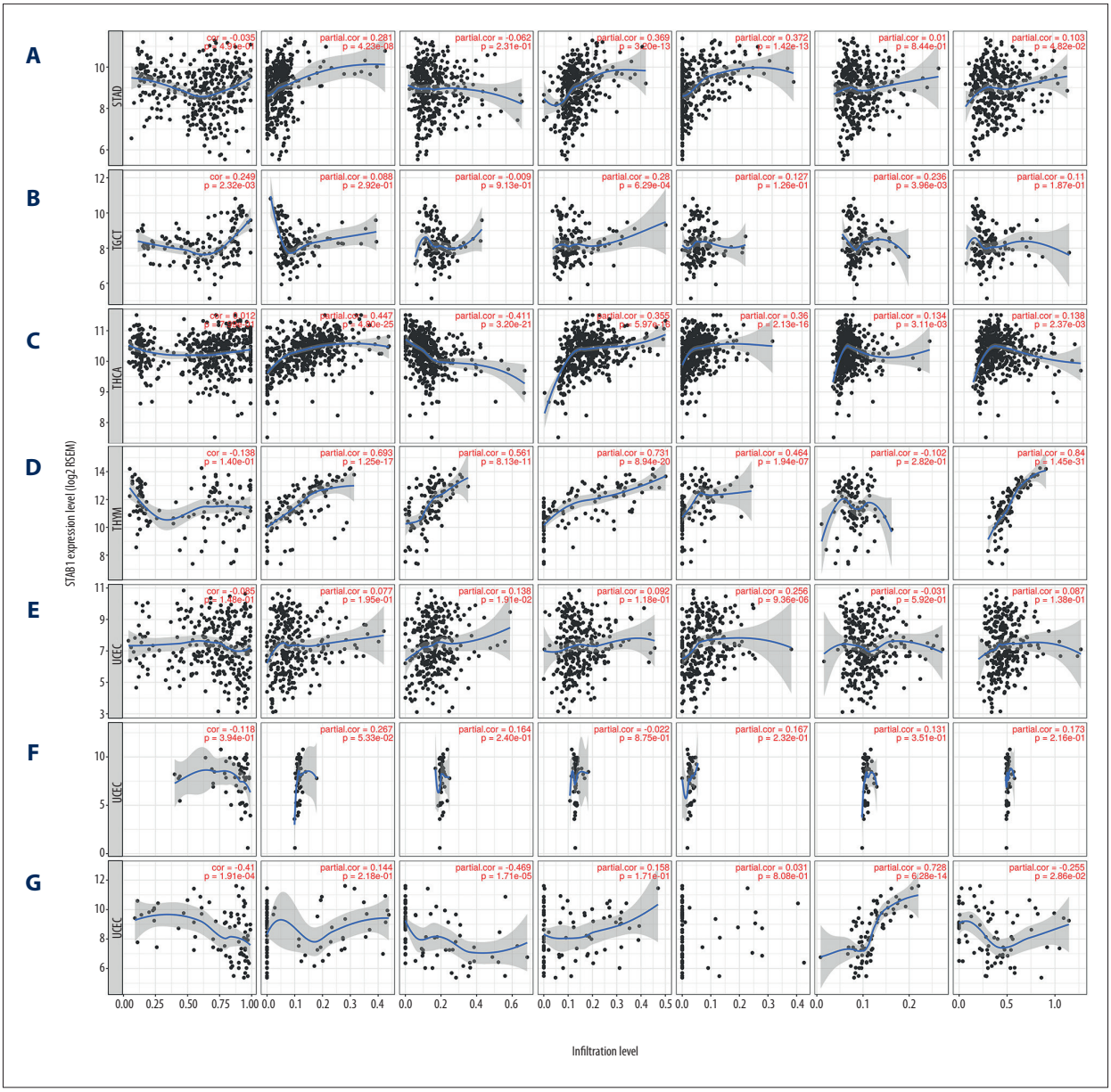

Figure 8. Association of SATB1 expression with immune infiltration levels in (**A**) STAD. (**B**) TGCT. (**C**) THCA. (**D**) THYM. (**E**) UCEC. (**F**) UCS. (**G**) UVM. STAD – stomach adenocarcinoma; TGCT – testicular germ cell tumors; THCA – thyroid carcinoma; THYM – thymoma; UCEC – uterine corpus endometrial carcinoma; UCS – uterine carcinosarcoma. UVM – uveal melanoma.

SATB1 has been shown to be aberrantly expressed in different types of cancers [24]. Generally, SATB1 expression has been positively related to tumor size, lymph node metastasis, tumor evolution, and prognosis in most cancer types [25–27]. A recent study reported that SATB1 regulates PDCD1 expression during T cell activation and prevents T cell exhaustion [15]. Tesone et al. reported that dynamic variations in SATB1 expression were required for the generation and immuno-stimulatory activity of conventional DCs; however, overexpressed SATB1 in differentiated DCs could convert them into pro-inflammatory or tolerogenic cells and prompt malignant transformation [28]. In an *in vivo* experiment, SATB1 knockdown in DCs could reverse the inflammation and carcinogenic activity, and enhance protective immune responses [28,29]. SATB1 also participates in the pathogenesis of cutaneous T-cell lymphoma, and depletion of SATB1 upregulates IL-5 and IL-9 [30]. Moreover, downregulation of SATB1 is involved in the suppressive effects of Tregs, which play a critical role in peripheral tolerance [31].

In this study, there were several limitations. First, the cutoff value varied in the different online databases, which may introduce potential heterogeneity. Second, the number of samples

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Table 4. Correlation analysis between SATB1 and relate genes and markers of immune cells in TIMER.

Description	Gene marker	BRCA				HNSC				PRAD			
		None		Purity		None		Purity		None		Purity	
		Cor	P	Cor	P	Cor	P	Cor	P	Cor	P	Cor	P
CD8+ T cell	CD8A	0.231	***	0.114	***	0.276	***	0.248	***	0.127	**	0.047	0.339
	CD8B	0.222	***	0.117	***	0.300	***	0.267	***	0.012	0.781	–0.039	0.430
T cell (general)	CD3D	0.212	***	0.081	*	0.199	***	0.160	***	0.035	0.437	–0.132	**
	CD3E	0.241	***	0.108	***	0.344	***	0.327	***	0.046	0.311	–0.042	0.387
	CD2	0.225	***	0.096	**	0.311	***	0.287	***	0.051	0.255	–0.041	0.402
B cell	CD19	0.193	***	0.078	*	0.330	***	0.312	***	–0.003	0.942	–0.178	***
	CD79A	0.234	***	0.108	***	0.386	***	0.375	***	0.017	0.713	–0.046	0.352
Monocyte	CD86	0.165	***	0.058	0.067	0.242	***	0.221	***	0.030	0.499	–0.069	0.161
	CD115 (CSF1R)	0.225	***	0.108	***	0.381	***	0.376	***	0.161	***	0.068	0.167
TAM	CCL2	0.206	***	0.115	***	0.343	***	0.323	***	0.062	0.168	0.000	0.997
	CD68	0.090	**	–0.114	0.660	0.126	**	0.114	*	0.064	0.154	0.146	**
	IL10	0.169	***	0.063	*	0.266	***	0.253	***	0.123	**	0.080	0.102
M1 Macrophage	INOS (NOS2)	0.182	***	0.162	***	0.372	***	0.377	***	0.175	***	0.115	*
	IRF5	–0.002	0.938	–0.073	*	0.104	*	0.100	*	0.153	***	–0.124	*
	COX2 (PTGS2)	0.384	***	0.311	***	0.018	0.689	0.019	0.671	0.308	***	0.240	***
M2 Macrophage	CD163	0.156	***	0.068	*	0.284	***	0.277	***	0.095	*	0.019	0.704
	VSIG4	0.132	***	0.041	0.198	0.269	***	0.261	***	0.004	0.373	0.047	0.337
	MS4A4A	0.186	***	0.070	*	0.282	***	0.268	***	–0.004	0.369	–0.127	**
Neutrophils	CD66b (CEACAM8)	0.076	*	0.101	**	0.112	*	0.105	*	0.027	0.541	0.023	0.636
	CD11b (ITGAM)	0.155	***	0.065	*	0.445	***	0.428	***	0.212	***	0.127	**
	CCR7	0.370	***	0.231	***	0.493	***	0.464	***	0.649	***	0.566	***
Natural killer cell	KIR2DL1	0.384	***	0.315	***	0.248	***	0.242	***	–0.033	0.463	–0.083	0.092
	KIR2DL3	0.117	***	0.058	0.068	0.210	***	0.191	***	–0.044	0.324	–0.017	0.733
	KIR2DL4	0.133	***	0.061	0.056	0.115	**	0.119	**	0.084	0.061	0.084	0.087
	KIR3DL1	0.168	***	0.100	**	0.218	***	0.209	***	0.062	0.166	0.035	0.478
	KIR3DL2	0.181	***	0.098	**	0.302	***	0.287	***	0.148	***	0.134	**
	KIR3DL3	0.101	***	0.065	*	0.088	*	0.070	0.123	0.045	0.315	0.053	0.282
	KIR2DS4	0.149	***	0.086	**	0.115	**	0.101	*	0.024	0.586	–0.042	0.387
Dendritic cell	HLA-DPB1	0.176	***	0.027	0.396	0.274	***	0.252	***	0.116	**	–0.217	***
	HLA-DQB1	0.142	***	0.039	0.217	0.193	***	0.166	***	0.033	0.466	–0.106	*
	HLA-DRA	0.199	***	0.072	*	0.296	***	0.276	***	0.053	0.235	–0.047	0.342
	HLA-DPA1	0.191	***	0.056	0.076	0.313	***	0.291	***	0.042	0.344	–0.061	0.215

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Table 4 continued. Correlation analysis between SATB1 and relate genes and markers of immune cells in TIMER.

Description	Gene marker	BRCA				HNSC				PRAD			
		None		Purity		None		Purity		None		Purity	
		Cor	P	Cor	P	Cor	P	Cor	P	Cor	P	Cor	P
Dendritic cell (cintinued)	BDCA-1(CD1C)	0.275	***	0.161	***	0.389	***	0.372	***	0.201	***	0.104	*
	BDCA-4(NRP1)	0.309	***	0.235	***	0.314	***	0.316	***	0.034	0.449	0.028	0.566
	CD11c (ITGAX)	0.184	***	0.074	*	0.336	***	0.330	***	–0.024	0.599	–0.065	0.187
Th1	T-bet (TBX21)	0.230	***	0.109	***	0.267	***	0.237	***	–0.009	0.849	–0.064	0.190
	STAT4	0.320	***	0.207	***	0.267	***	0.246	***	0.093	*	0.021	0.674
	STAT1	0.089	**	0.039	0.222	0.019	0.670	0.000	0.998	0.281	***	0.240	***
	IFN-γ (IFNG)	0.172	***	0.080	*	0.069	0.118	0.028	0.540	0.031	0.489	0.003	0.948
	TNF-α (TNF)	0.147	***	0.111	***	–0.034	0.444	–0.040	0.372	0.070	0.119	–0.028	0.570
Th2	GATA3	–0.308	***	–0.251	***	0.202	***	0.182	***	0.196	***	0.115	*
	STAT6	0.022	0.468	–0.023	0.478	0.100	**	0.105	*	0.327	***	0.311	***
	STAT5A	0.219	***	0.141	***	0.215	***	0.189	***	0.072	0.108	–0.004	0.929
	IL13	0.085	**	0.041	0.196	0.165	***	0.147	**	0.053	0.238	–0.030	0.542
Tfh	BCL6	0.081	0.069	0.053	0.096	0.341	***	0.356	***	0.131	**	0.137	**
	IL21	0.150	***	0.083	**	0.335	***	0.300	***	0.015	0.731	0.017	0.732
Th17	STAT3	0.182	***	0.162	***	0.320	***	0.321	***	0.448	***	0.412	***
	IL17A	0.117	***	0.078	*	0.151	***	0.131	**	0.148	***	0.033	0.504
Treg	FOXP3	0.187	***	0.094	**	0.504	***	0.506	***	0.159	***	0.145	**
	CCR8	0.195	***	0.124	***	0.565	***	0.563	***	0.323	***	0.294	***
	STAT5B	0.247	***	0.207	***	0.449	***	0.437	***	0.433	***	0.434	***
	TGFβ (TGFB1)	0.097	**	–0.018	0.568	–0.201	***	–0.200	***	–0.085	0.058	–0.119	*
T cell exhaustion	PD-1 (PDCD1)	0.164	***	0.041	0.194	0.236	***	0.212	***	0.054	0.232	0.100	*
	CTLA4	0.211	***	0.114	***	0.224	***	0.196	***	–0.008	0.856	–0.046	0.352
	LAG3	0.062	*	–0.004	0.900	0.008	0.067	0.005	0.272	–0.152	***	–0.180	***
	TIM-3 (HAVCR2)	0.123	***	0.014	0.651	0.297	***	0.280	***	–0.007	0.120	–0.152	**
	GZMB	0.188	***	0.009	**	0.063	0.152	0.026	0.564	–0.021	0.644	–0.093	0.057

TIMER – Tumor Immune Estimation Resource; BRCA – breast invasive carcinoma; HNSC – head and neck squamous cell carcinoma; PRAD – prostate adenocarcinoma; TAM – tumor-associated macrophages; Th – T helper cell; Tfh – follicular helper T cell; Treg – regulatory T cell; Cor – R value of Spearman's correlation; None – correlation without adjustment. Purity – correlation adjusted by purity. * $P<0.01$; ** $P<0.001$; *** $P<0.0001$.

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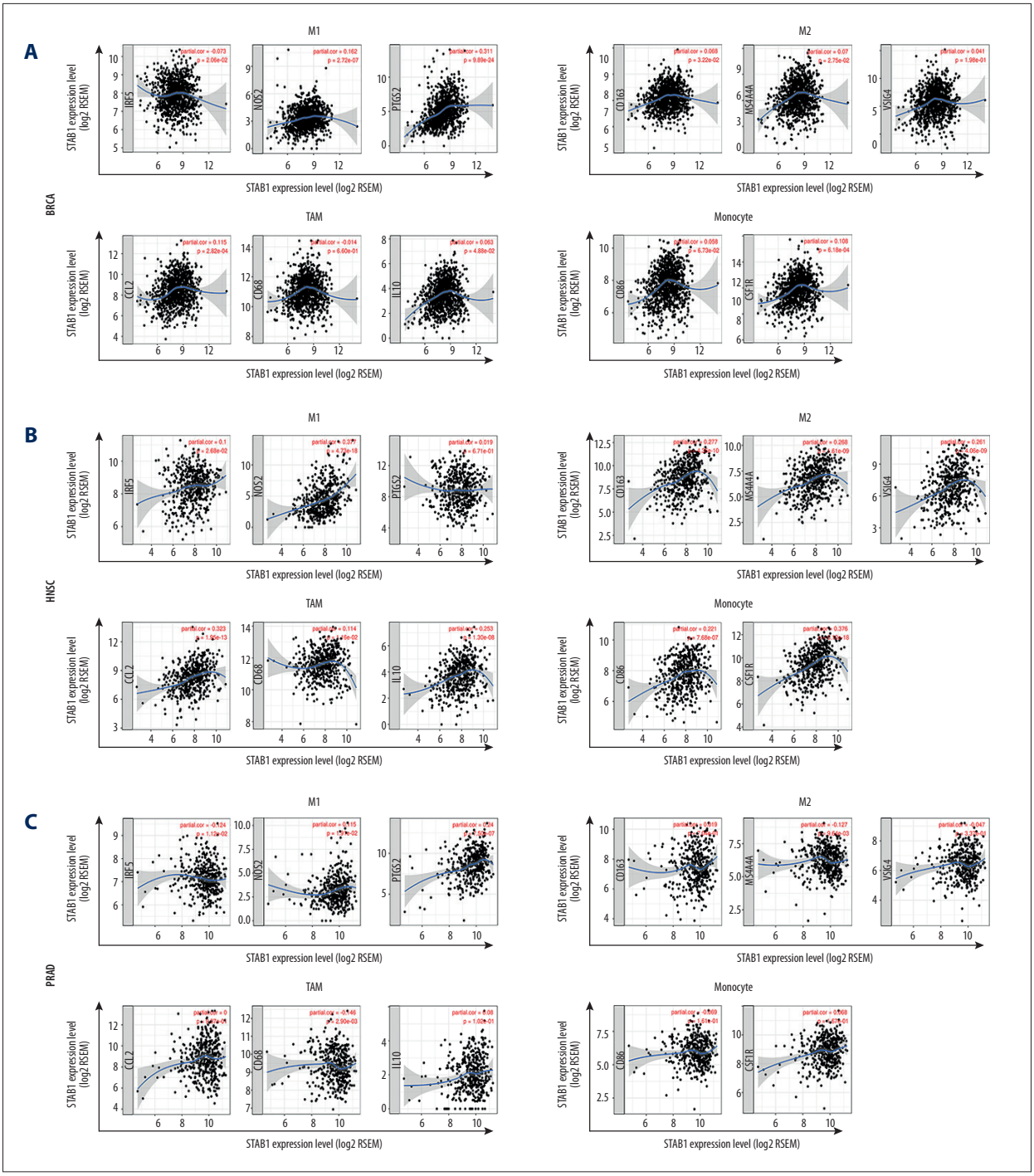

Figure 9. SATB1 expression correlated with macrophage polarization in BRAC, HNSC, and PRAD. Markers include CD86 and CSF1R of monocytes; CCL2, CD68, and IL10 of TAMs; NOS2, IRF5, and PTGS2 of M1 macrophages; and CD163, VSIG4, and MS4A4A of M2 macrophages. (**A**) Scatterplots of correlations between SATB1 expression and gene markers of M1 macrophages, M2 macrophages, TAMs, and monocytes in BRAC (n=1093). (**B**) Scatterplots of correlations between SATB1 expression and gene markers of M1 macrophages, M2 macrophages, TAMs, and monocytes in HNSC (n=520). (**C**) Scatterplots of correlations between SATB1 expression and gene markers of M1 macrophages, M2 macrophages, TAMs, and monocytes in PRAD (n=497). BRCA – breast invasive carcinoma; HNSC – head and neck cancer; PRAD – prostate adenocarcinoma; TAMs – tumor associated macrophages.

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in the different databases was still limited. Thus, in the future, more studies with a large number of samples are needed to provide more reliable evidence to validate the impact of SATB1 on tumor immune infiltration.

Conclusions

In summary, a low level of SATB1 expression was associated with poor survival rates and enhanced the immune infiltration level of B cells, CD8+ T cells, CD4+ T cells, macrophages, neutrophils, and DCs in various types of cancer, especially in BRAC, HNSC, and PRAD. Decreased SATB1 expression was also associated with the regulation of TAM, Treg, and T cell exhaustion in BRAC, HNSC, and PRAD. Thus, SATB1 possibly plays a vital role in enrollment and regulation of tumor immune infiltration in BRAC, HNSC, and PRAD.

Conflicts of interest

None.

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