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The high-risk model associated with SYTL4 predicts poor prognosis and correlates with immune infiltration in AML

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ABSTRACT

Acute myeloid leukemia (AML) currently lacks a definitive cure. Studies have highlighted the involvement of SYTL4 expression levels in neoplasms, yet its specific roles in AML remain unexplored in the literature. Utilizing the TCGA and XENA databases, this study investigated SYTL4 expression levels in AML and identified associations between SYTL4 overexpression and clinicopathological features, prognosis, and immune infiltration in AML patients through genomic analysis. ROC analysis demonstrated the diagnostic value of SYTL4 overexpression in AML. Kaplan-Meier survival, Cox regression, and Lasso analyses were employed to explore SYTL4-coexpressed long non-coding RNAs linked to AML patient prognosis, alongside the construction of nomograms and risk models. SYTL4 expression was significantly elevated in AML and correlated with FAB classification, cytogenetic risk, IDH1 R140 mutation, and NPM1 mutation in cancer patients. SYTL4 overexpression signaled a poor prognosis, serving as a risk indicator for assessing adverse outcomes in AML patients. SYTL4 expression levels also correlated with AML immune cell levels and markers. COX regression analysis revealed that LINC01700, CPNE8-AS1, HOXA10-AS, LINC00899, and SYTL4 influenced adverse AML prognosis. Patients in the high-risk group for these factors experienced significantly poor outcomes, which were closely associated with aDC, CD8 T cells, and TH17 cells. In summary, SYTL4 overexpression is linked to poor prognosis and immune infiltration in AML, with the constructed risk model intended as a prognostic evaluation tool for AML patients.

1. Introduction

Acute myeloid leukemia (AML) is a hematopoietic malignancy associated with a poor prognosis [1]. Studies have confirmed that abnormal expression of genes, microRNAs and long non-coding RNAs occurs during the development of neoplasms, including AML [1–5]. For example, TBC1 domain family member 16 (TBC1D16) expression level has been linked to poor prognosis in AML patients. In AML cells, inhibition of TBC1D16 expression led to decreased cell proliferation and ERK phosphorylation level, and lowered sensitivity of U937 cells to cytarabine [1].

Studies have indicated that SYTL4 is notably higher significantly associated with tumorigenesis and development [6–8]. SYTL4 is significantly over-expressed in the corresponding cancer tissues compared to the normal tissues [8]. SYTL4 is the high expressed in triple-negative breast cancer (TNBC). TNBC patients of SYTL4 overexpression have a dismal prognosis, especially particularly following paclitaxel treatment in TNBC patients. Inhibition of SYTL4 expression can stabilize the microtubule network and slow microtubule growth. Up-regulation of SYTL4 expression can experience poor prognoses in paclitaxel-treated the TNBC patients [6]. At present, the roles and clinical values of SYTL4 in AML remain unexplored in the literature. Therefore, the roles of SYTL4 overexpression in AML progression are explored using the TCGA and XENA databases [9,10], and the nomogram and risk model related to SYTL4 are constructed to evaluate the prognosis of AML patients, which aims to assess as a novel predictive tool for AML patients.

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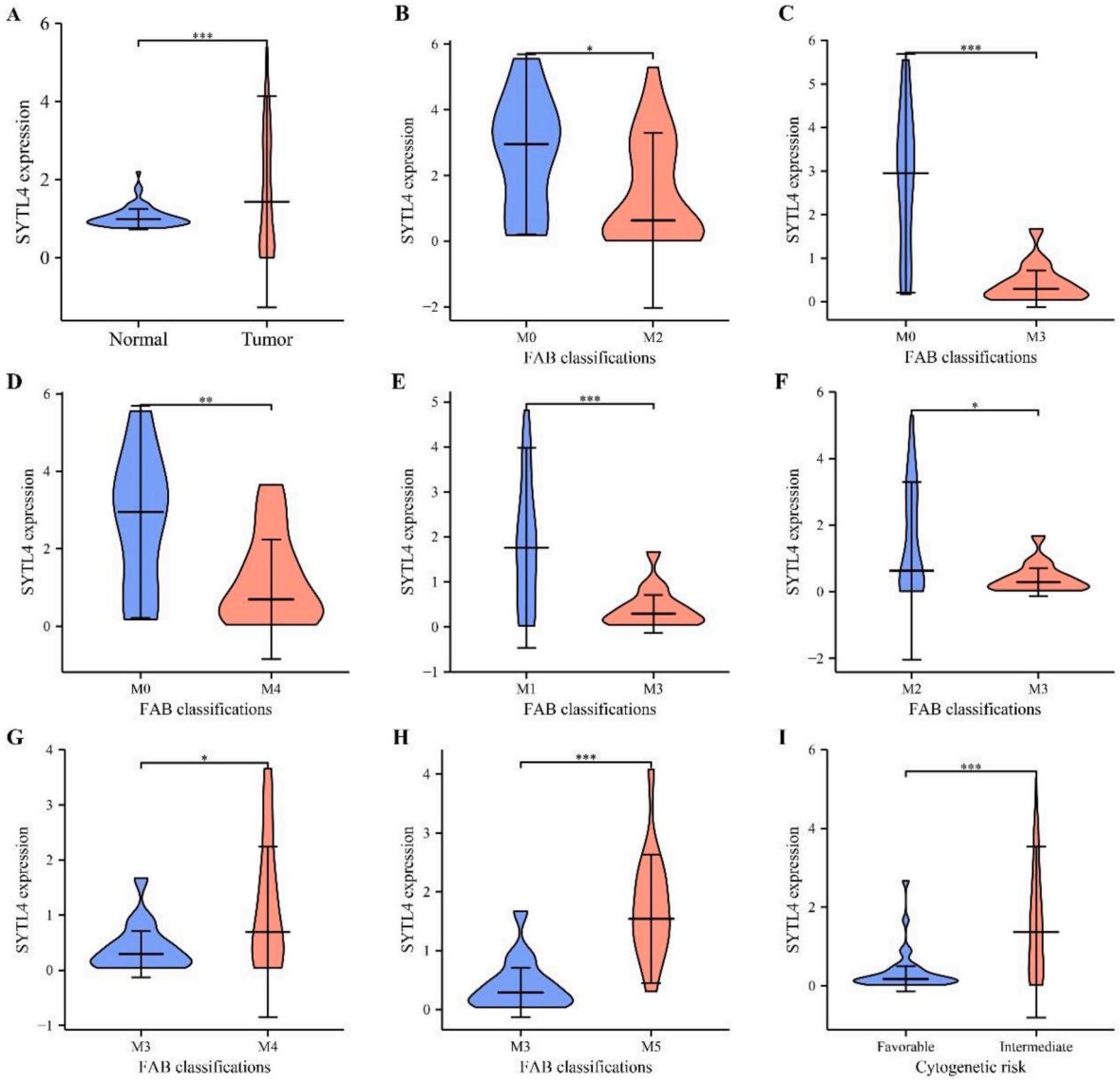

Fig. 1. SYTL4 was overexpressed in AML. (A) Normal vs AML; (B) M0 vs M2; (C) M0 vs M3; (D) M0 vs M4; (E) M1 vs M3; (F) M2 vs M3; (G) M3 vs M4; (H) M3 vs M5; (I) Favorable vs Intermediate.
Note: AML, acute myeloid leukemia.

2. Materials and methods

2.1. Identification of SYTL4 expression levels in AML

The gene expression TPM data for 70 normal samples were sourced from the GTEx database in XENA (https://xena.ucsc.edu/) database, while the TPM data for 173 AML samples were retrieved from the TCGA (https://portal.gdc.cancer.gov/) database [9,10]. Specifically, mRNA expression data for SYTL4 were extracted and merged from normal and cancer samples. The SYTL4 expression levels in normal and AML samples were compared using t-tests and visualized through violin plots.

2.2. The relationship between SYTL4 expression and prognostic indicators in AML

The clinicopathological characteristics data of AML patients were sourced from the TCGA database. SYTL4 expression data were integrated with the clinical information of AML patients, excluding those with incomplete records. SYTL4 expression levels were analyzed within each subgroup based on FAB classification, cytogenetic risk, IDH1 R140, NPM1 mutations, and other parameters employing *t*-test. Patients were categorized by SYTL4 expression ranking and grouped into median, tertile, quartile, quintile, and based on the optimal P-value. Kaplan-Meier (K-M) survival analysis was conducted to ascertain the association between SYTL4 levels and the overall survival (OS) of AML patients [9,10].

2.3. Identification of the roles of SYTL4 overexpression as a prognostic marker in AML patients

The prognostic significance of SYTL4 expression levels in AML patients was assessed via ROC analysis, with the area under the curve (AUC) serving as the evaluation metric. Univariate and multivariate COX regression analyses investigated the impact of gender, age, WBC count, BM blasts, cytogenetic risk, PB blasts, FAB classification, FLT3 mutation, IDH1 R132 mutation, IDH1 R140 mutation, IDH1 R172 mutation, RAS mutation, NPM1 mutation, and SYTL4 expression on the OS of AML patients. Subsequently, a nomogram was developed based on the selection criteria of $P < 0.05$.

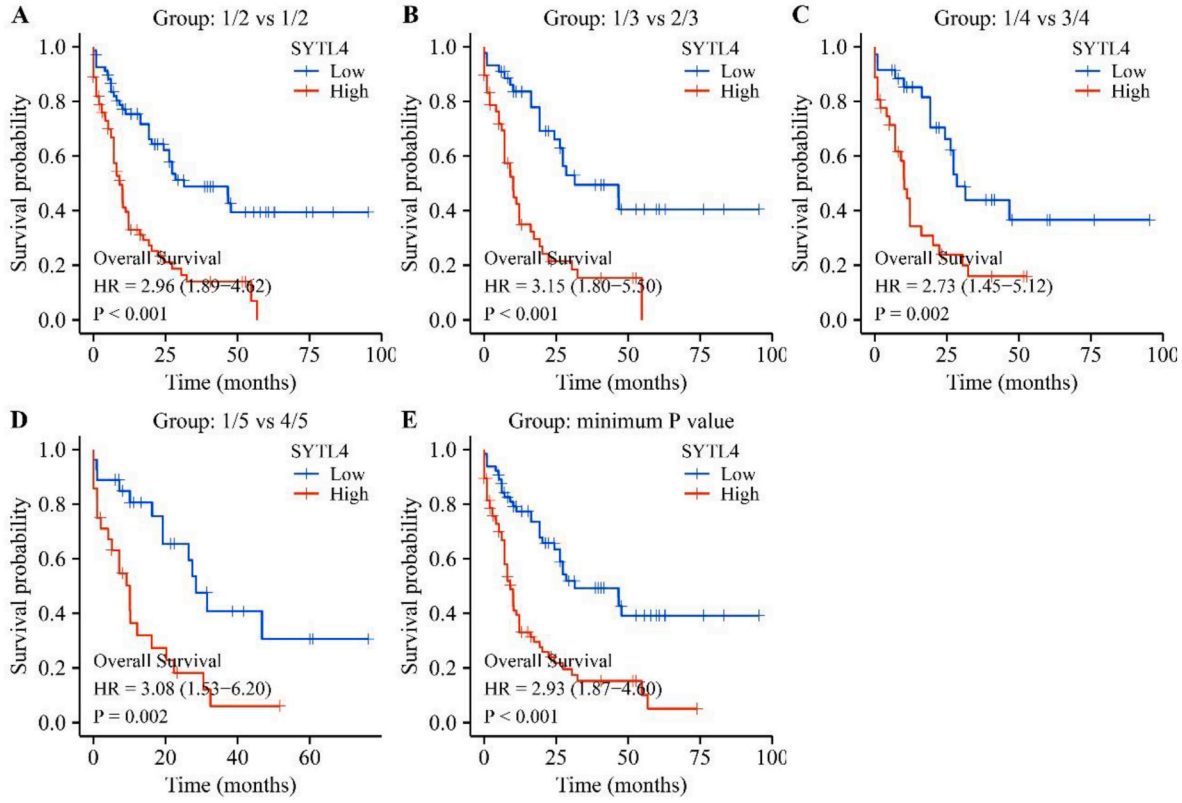

Fig. 2. SYTL4 overexpression was associated with the prognosis in AML patients. (A) Median value; (B) Tertile value; (C) quartile value; (D) Quintile value; (E) The best P value.
Note: AML, acute myeloid leukemia.

2.4. Identification of the relationship between SYTL4 expression and immune cell infiltration in AML

The immune cell levels in samples from AML patients in the TCGA database were computed through the single-sample gene set enrichment analysis (ssGSEA) method [9]. SYTL4 expression data were integrated with the data of immune cells and markers, and Pearson correlation analysis was employed to elucidate the associations between SYTL4 levels and immune cells as well as immune cell markers [9,11]. Moreover, the statistical significance of immune cells and markers was assessed within the high- and low-SYTL4 expression groups.

2.5. Construction of prognostic nomogram of SYTL4-related lncRNAs

Pearson correlation analysis was conducted to identify lncRNAs significantly correlated with SYTL4, with the screening criteria set at $P < 0.001$ and an absolute correlation coefficient of 0.5 for SYTL4-associated lncRNAs. K-M survival analysis was employed to investigate the associations between SYTL4-related lncRNAs (LINC01700, AC096677.1, CPNE8-AS1, LINC01694, AC135507.1AL590438.1, LINC01106, HOXA10-AS, AL023284.4, AC246787.2, AL354928.1, AC009237.14, FAM30A, AL1173273 AJ009632.2, AL590428.1, AC018552.3, ARHGAP22-IT1, CAVIN2-AS1, AC108058.1, ZMIZ1-AS1, HOXB-AS2, AC009237.15, LINC02805, A2M-AS1, AC026801.2, PCCA-DT, OR2A1-AS1, AC009121.4, LOXL1-AS1, AC099343.3, FER1L6-AS1, AC009163.7, SENCR, GATA2-AS1, AC133540.1, AC123912.4, LINC00853, AL133410.1, AP001122.1, TMSB15B- AS1, AC008760.1, AC129492.1, AC107223.1, LINC01012, AC011773.1, EXTL3-AS1, AC239809.3, AL135960.1, OXCT1-AS1, AL359094.1, LINC00899, AL008733.1, ADCY6-DT and AL121694.1) and OS in AML. Prognosis-related lncRNAs were considered significant at $P < 0.01$, leading to the development of a prognostic nomogram for lncRNAs in AML.

2.6. Construction of a risk model for SYTL4-related lncRNAs

The univariate COX regression analysis established the correlation between SYTL4-related lncRNAs (LINC01700, AC096677.1, CPNE8-AS1, LINC01694, AC135507.1, AL590438.1, LINC01106, HOXA10-AS, AL023284.4, AC246787.2, AL359094.1, and LINC00899) and SYTL4 levels and the OS of AML patients. A significance level of $P < 0.05$ was adopted as the threshold for LASSO regression analysis. Subsequently, a risk model for SYTL4-related lncRNAs was developed based on the key factors identified from LASSO analysis.

2.7. The relationship between risk model and immune cell infiltration in AML

K-M survival analysis determined the prognostic disparities between high- and low-risk groups, and Pearson correlation analysis was employed to investigate the link between the risk model and immune cell infiltration in AML.

2.8. Statistical analysis

The SYTL4 expression in AML was assessed via a *t*-test. K-M survival, ROC, and LASSO regression analysis were conducted to investigate prognostic factors in AML patients. Correlation analysis was applied to elucidate the association between SYTL4 expression and immune status in AML, with the significance criterion set at $P < 0.05$.

3. Results

3.1. The expression of SYTL4 in AML

The SYTL4 expression was notably higher in AML compared to

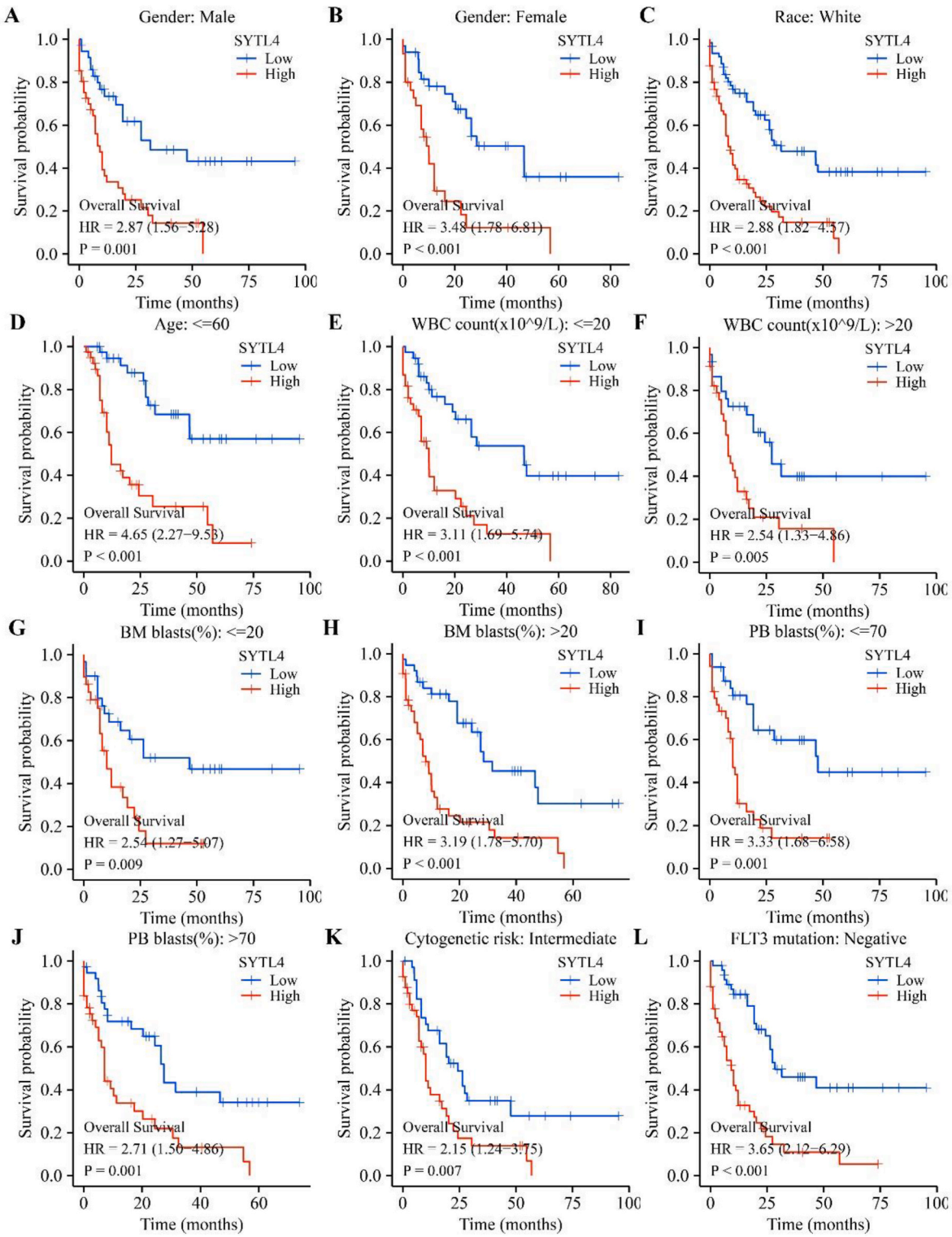

Fig. 3. SYTL4 overexpression in patients with was associated with dismal prognosis in AML patients based on the subgroup analysis. (A) Male; (B) Female; (C) Caucasian; (D) Age (≤ 60); (E) White blood cell count (≤ 20 × 10^9/L); (F) White blood cell count (>20 × 10^9/L); (G) BM blast (≤ 20 %); (H) BM blast (>20 %); (I) PM blast (≤ 70 %); (J) PM blast (>70 %); (K) Cytogenetic risk (intermediate); (L) FLT3 mutation (Negative).
Note: AML, acute myeloid leukemia.

normal samples (Fig. 1A). Upon categorizing based on the FAB classification, it was observed that SYTL4 expression levels were significantly reduced in M2, M3, and M4 patient samples in contrast to M0 samples (Fig. 1B–D). Furthermore, a significant decrease of SYTL4 expression levels was noted in M3 patient samples compared to M1 or M2 samples, while M4 and M5 patient samples exhibited lower levels compared to M3 patient samples (Fig. 1E–H). When considering cytogenetic risk grouping, SYTL4 expression levels were markedly higher in intermediate-risk patient samples compared to favorable-risk samples (Fig. 1I). Additionally, SYTL4 exhibited increased expression in poor-risk patient samples as opposed to favorable-risk samples (Fig. S1A). The SYTL4 expression was also elevated in poor-risk patient samples

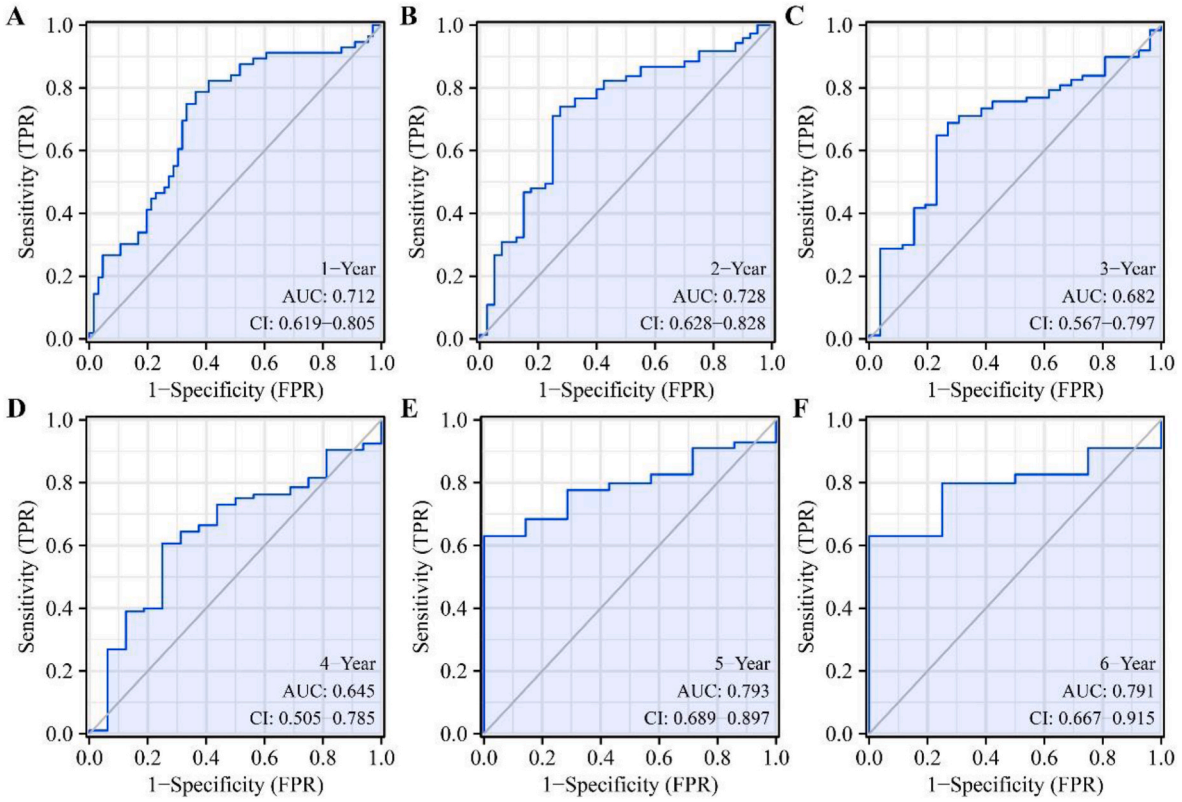

Fig. 4. The prognostic values of SYTL4 expression at 1–6 year OS in AML.
Note: AML, acute myeloid leukemia; OS, overall survival.

compared to intermediate-risk samples (Fig. S1B). Notably, elevated SYTL4 expression levels were observed in deceased patients with a negative IDH1 R140 mutation, positive NPM1 mutation, and under the OS condition (Figs. S1C–E).

3.2. SYTL4 overexpression was correlated with poor prognosis in AML patients

SYTL4 overexpression was linked to poor prognosis in AML patients across various subgroups (Fig. 2). Subgroup analysis revealed that within different demographic and clinical categories such as gender, ethnicity, age (≤60), white blood cell count (≤20 × 10^9/L), white blood cell count (>20 × 10^9/L), BM blast (≤20 %), BM blast (>20 %), PB blast (≤70 %), PB blast (>70 %), intermediate cytogenetic risk, negative FLT3 mutation, negative IDH1 R132 mutation, negative IDH1 R140 mutation, negative IDH1 R172 mutation, negative RAS mutation, and negative NPM1 mutation, patients with SYTL4 overexpression exhibited an unfavorable prognosis in AML (Fig. 3 and S2).

3.3. SYTL4 served as a prognostic risk marker for assessing poor outcomes in AML patients

The ROC analysis indicated that SYTL4 expression levels played a role in predicting the prognosis of AML patients, as illustrated in Fig. 4. Specifically, the AUC values for SYTL4 expression levels in AML patients with 1-, 2-, 3-, 4-, 5-, and 6-year OS were 0.712, 0.728, 0.682, 0.645, 0.793, and 0.791, respectively. Univariate and multivariate COX regression analyses revealed that age and SYTL4 overexpression were independent risk factors for poor prognosis in AML patients, as shown in Table 1. Furthermore, a prognostic nomogram related to SYTL4 was developed to assess the prognosis of AML patients (Fig. 5).

3.4. SYTL4 expression was associated with immune cell infiltration levels in AML

In AML, SYTL4 expression levels exhibited significant correlations with various immune cell types, including CD8 T cells, T helper cells, NK CD56dim cells, TFH cells, cytotoxic cells, Th1 cells, NK cells, aDCs, NK CD56bright cells, B cells, dendritic cells (DCs), immature DCs (iDCs), Tcm cells, mast cells, and Th2 cells (Fig. 6 and S3). Fig. 7 depicted the expression levels of immune cell types in the high- and low-SYTL4 expression groups. Moreover, correlation analysis revealed associations between SYTL4 expression levels and immune cell markers such as LAG3, KIR2DL3, KIR2DL4, KIR3DL2, KIR2DL1, KIR3DL1, GZMB, KIR2DS4, TBX21, FOXP3, CTLA4, STAT4, GATA3, CD68, STAT5A, CD8A, CD3E, KIR3DL3, PDCD1, NRP1, IFNG, and CCR8 (Table 2 and Fig. 8).

3.5. SYTL4-related prognostic nomogram

Based on our study criteria, SYTL4-associated lncRNAs comprised LINC01700, AC096677.1, CPNE8-AS1, LINC01694, AC135507.1, AL590438.1, LINC01106, HOXA10-AS, AL023284.4, AC246787.2, AL359094.1, and LINC00899 (Fig. S4). K-M survival analysis demonstrated a significant correlation between the expression levels of LINC01700, AC096677.1, CPNE8-AS1, LINC01694, AC135507.1, AL590438.1, LINC01106, HOXA10-AS, AL023284.4, AC246787.2, AL359094.1 and LINC00899and OS in AML patients (Fig. 9), with the development of a nomogram to evaluate OS in AML patients based on K-M survival results (Fig. 10).

3.6. SYTL4 related risk model was associated with immune cell infiltration in AML

Univariate COX regression analysis revealed that SYTL4-associated

Table 1
The prognostic factors on AML patients.

Characteristics	Total (N)	HR (95 % CI)	P	HR (95 % CI)	P
Gender	140				
Female	63	Reference			
Male	77	1.030 (0.674–1.572)	0.892		
Age	140				
≤60	79	Reference			
>60	61	3.333 (2.164–5.134)	<0.001	2.583 (1.633–4.084)	<0.001
WBC count (x10^9/L)	139				
≤20	75	Reference			
>20	64	1.161 (0.760–1.772)	0.490		
BM blasts (%)	140				
≤20	59	Reference			
>20	81	1.165 (0.758–1.790)	0.486		
Cytogenetic risk	138				
Favorable	31	Reference			
Intermediate	76	2.957 (1.498–5.836)	0.002	1.790 (0.855–3.748)	0.123
Poor	31	4.157 (1.944–8.893)	<0.001	1.700 (0.706–4.094)	0.237
PB blasts (%)	140				
≤70	66	Reference			
>70	74	1.230 (0.806–1.878)	0.338		
FAB classifications	139				
M0	14	Reference			
M1-7	125	1.033 (0.517–2.062)	0.927		
FLT3 mutation	136				
Negative	97	Reference			
Positive	39	1.271 (0.801–2.016)	0.309		
IDH1 R132 mutation	138				
Negative	126	Reference			
Positive	12	0.588 (0.238–1.452)	0.249		
IDH1 R140 mutation	138				
Negative	127	Reference			
Positive	11	1.131 (0.565–2.264)	0.727		
IDH1 R172 mutation	138				
Negative	136	Reference			
Positive	2	0.610 (0.085–4.385)	0.623		
RAS mutation	139				
Negative	131	Reference			
Positive	8	0.643 (0.235–1.760)	0.390		
NPM1 mutation	139				
Negative	106	Reference			
Positive	33	1.137 (0.706–1.832)	0.596		
SYTL4	140				
Low expression	68	Reference			
High expression	72	2.958 (1.893–4.623)	<0.001	1.958 (1.165–3.289)	0.011

Note: AML, acute myeloid leukemia.

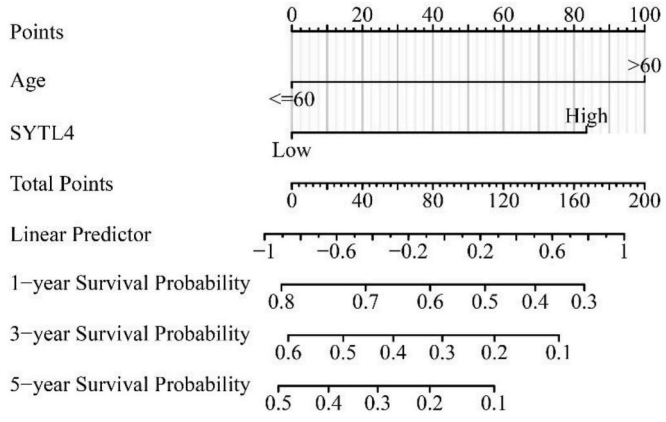

Fig. 5. SYTL4-related prognostic nomogram in AML.
Note: AML, acute myeloid leukemia.

LINC01700, AC096677.1, CPNE8-AS1, LINC01694, AC135507.1, AL590438.1, LINC01106, HOXA10-AS, AL023284.4, AC246787.2, AL359094.1, and LINC00899 were influential factors associated with poor prognosis in cancer patients (Table 3). LASSO regression analysis confirmed that LINC01700, CPNE8-AS1, HOXA10-AS, LINC00899, and SYTL4 were independent risk factors for a poor prognosis in AML patients. Utilizing a risk signature composed of LINC01700, CPNE8-AS1, HOXA10-AS, LINC00899, and SYTL4, high-risk patients demonstrated significantly unfavorable outcomes (Fig. 11). Moreover, the risk model exhibited significant correlations with aDCs, CD8 T cells, TH17 cells, and other factors (Fig. 12).

4. Discussion

Studies have confirmed the association of SYTL4 with cancer progression [6–8,12]. Specifically, SYTL4 is found to be overexpressed in cancer tissues compared to normal tissues based on microarray analysis [8], and this overexpression correlates with poor prognosis in triple-negative breast cancer (TNBC) patients. Additionally, downregulation of SYTL4 expression has shown to delay cancer progression [6]. Furthermore, our findings indicate a significant elevation of SYTL4 levels in AML, which is associated with reduced OS. The expression levels of SYTL4 play a crucial role in assessing the prognosis of AML patients, with the AUC values for SYTL4 expression across 1–6 years of OS being 0.712, 0.728, 0.682, 0.645, 0.793, and 0.791, respectively. Notably, SYTL4 overexpression serves as an independent risk factor for poor outcomes in AML, suggesting its potential as a biomarker for dismal prognosis in AML patients.

An abnormal immune microenvironment is linked to cancer

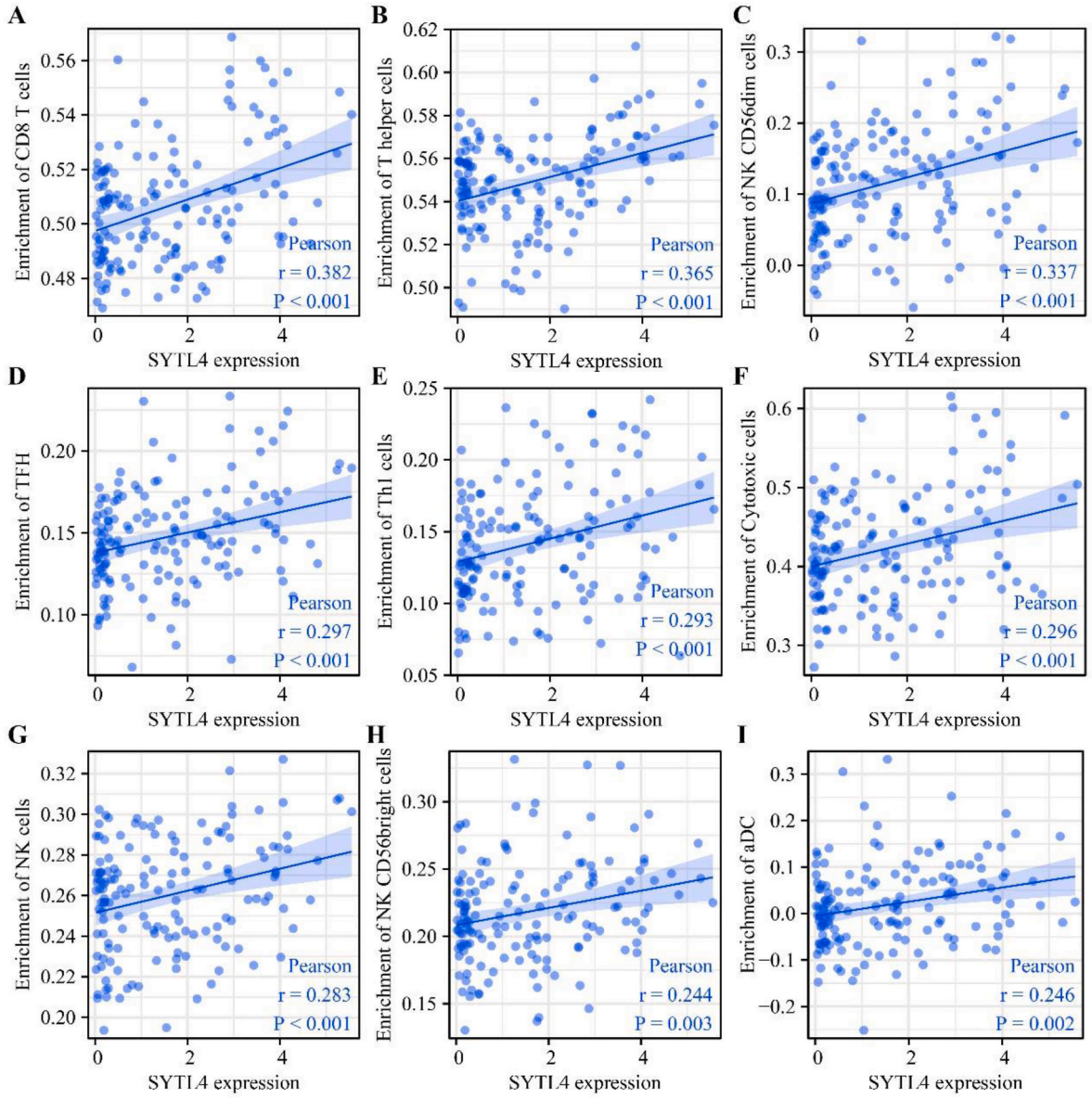

Fig. 6. SYTL4 expression was correlated with the levels of immune cell infiltration in AML. (A) CD8 T cells; (B) T helper cells; (C) NK CD56dim cells; (D) TFH; (E) Th1 cells; (F) Cytotoxic cells; (G) NK cells; (H) NK CD56bright cells; (I) aDC.
Note: AML, acute myeloid leukemia.

progression, and immunotherapy has the potential to enhance the survival of cancer patients [13–16]. The expression level of SYTL4 is notably correlated with various immune cell types, including CD8 T cells, T helper cells, NK CD56dim cells, TFH cells, cytotoxic cells, Th1 cells, NK cells, aDCs, NK CD56bright cells, B cells, DCs, iDCs, Tcm cells, mast cells, and Th2 cells. Moreover, it is significantly associated with immune cell markers, such as LAG3, KIR2DL3, KIR2DL4, KIR3DL2, KIR2DL1, KIR3DL1, GZMB, KIR2DS4, TBX21, FOXP3, CTLA4, STAT4, GATA3, CD68, STAT5A, CD8A, CD3E, KIR3DL3, PDCD1, NRP1, IFNG, and CCR8. Specifically, T cells, and immune cell markers PDCD1 and PD-L1 have been implicated in AML progression [17–19]. It is important to note that individual genes may have close associations with specific cell types. This study is preliminary, and further experimental studies will be conducted for validation. This preliminary research highlights the potential role of SYTL4 in AML progression through its interactions with immune microenvironment.

The risk model and nomogram show promise as new tools for evaluating the prognosis of cancer patients [20–23]. For instance, Li et al., demonstrated the effective use of an m6A/m5C/m1A regulated gene prognostic nomogram and risk model in predicting the prognosis of hepatocellular carcinoma patients [22]. Within our study, the expression levels of LINC01700, CPNE8-AS1, HOXA10-AS, LINC00899, and SYTL4 are significantly associated with OS in patients with AML, serving as independent risk factors for poor prognosis in this context. The risk model, based on these lncRNA expressions, identifies cancer patients at high risk who exhibit notably unfavorable prognoses. Furthermore, this risk model is significantly correlated with immune cells such as aDCs, CD8 T cells, and TH17 cells. Future work is needed to validate these findings and understand better the mechanisms and roles of SYTL4 in AML, along with its relationship to the immune system. In summary, SYTL4 is overexpressed and linked to poor prognosis, immune cell activity, and cellular markers in AML. The constructed risk model, featuring LINC01700, CPNE8-AS1, HOXA10-AS, LINC00899, and SYTL4, represents an effective tool for prognostic evaluation in AML patients.

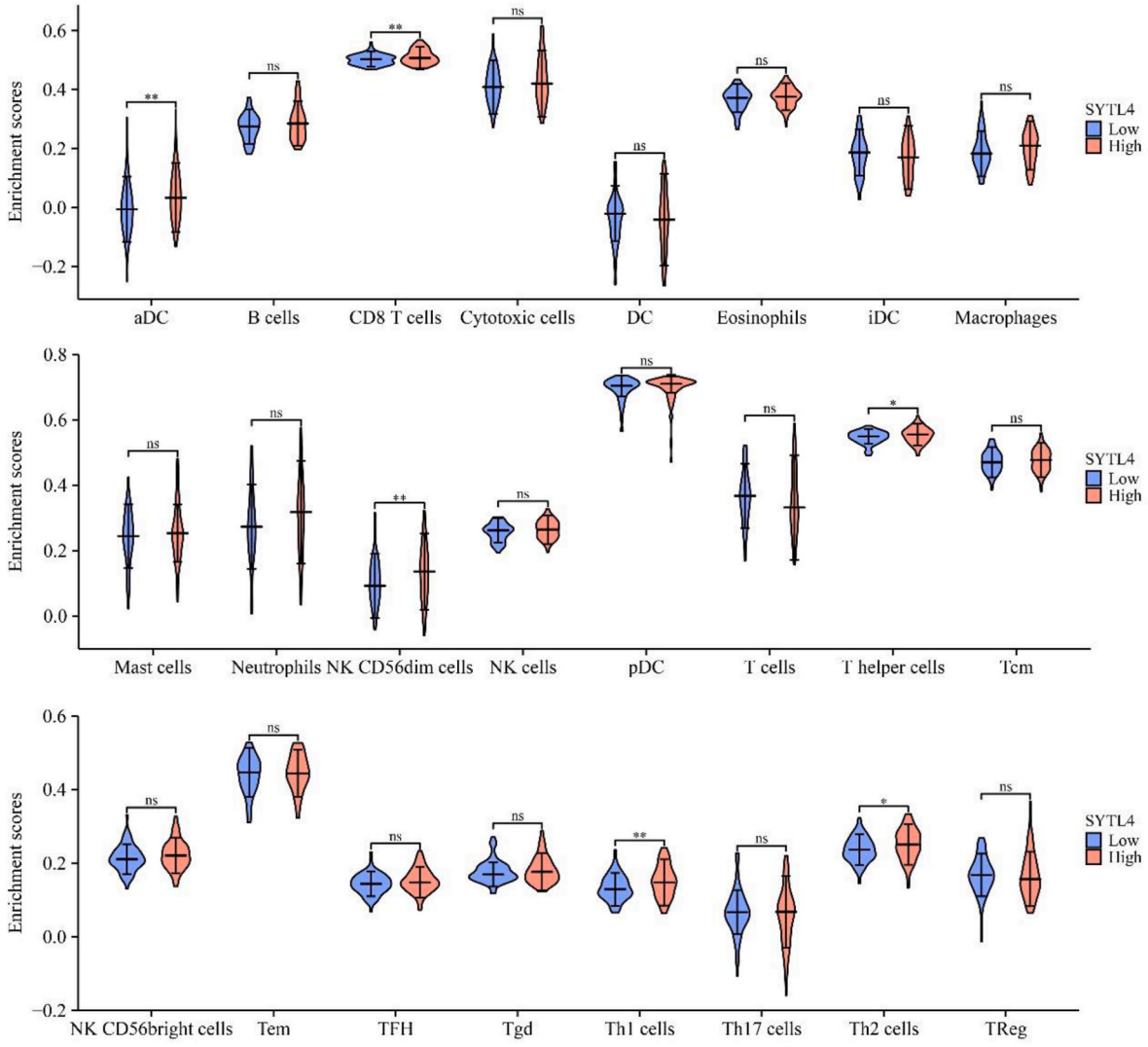

Fig. 7. The expression levels of immune cells in high- and low- SYTL4 expression groups in AML.
Note: AML, acute myeloid leukemia.

Table 2
SYTL4 expression correlated with the levels of immune cell markers in AML.

Markers	Correlation coefficient	P	Markers	Correlation coefficient	P	Markers	Correlation coefficient	P
LAG3	0.431	<0.001	IFNG	0.165	0.043	HLA-DQB1	−0.076	0.354
KIR2DL3	0.424	<0.001	CCR8	0.165	0.043	NOS2	0.075	0.359
KIR2DL4	0.413	<0.001	STAT5B	0.157	0.054	BCL6	−0.069	0.397
KIR3DL2	0.413	<0.001	STAT6	0.156	0.056	CD163	0.068	0.409
KIR2DL1	0.410	<0.001	PTGS2	0.152	0.063	CD2	0.060	0.462
KIR3DL1	0.400	<0.001	STAT3	0.149	0.069	IRF5	−0.059	0.470
GZMB	0.362	<0.001	CSF1R	−0.146	0.074	IL13	−0.058	0.478
KIR2DS4	0.313	<0.001	CD86	−0.139	0.089	MS4A4A	−0.053	0.521
TBX21	0.313	<0.001	CD8B	0.135	0.098	HLA-DPB1	0.053	0.519
FOXP3	0.291	<0.001	STAT1	0.129	0.114	VSIG4	−0.048	0.558
CTLA4	0.284	<0.001	CD1C	−0.125	0.126	IL17A	−0.046	0.577
STAT4	0.275	<0.001	CCR7	0.125	0.126	HLA-DPA1	0.045	0.585
GATA3	0.275	<0.001	ITGAX	0.120	0.143	IL10	0.039	0.636
CD68	−0.217	0.008	CD19	0.108	0.188	HLA-DQB3	0.039	0.634
STAT5A	0.216	0.008	HAVCR2	−0.107	0.193	ITGAM	0.039	0.630
CD8A	0.195	0.016	CD79A	0.104	0.205	CD3D	0.023	0.778
CD3E	0.189	0.020	IL21	0.103	0.207	HLA-DRA	0.014	0.860
KIR3DL3	0.186	0.022	TNF	−0.097	0.235	HLA-DQB2	−0.006	0.938
PDCD1	0.183	0.025	CCL2	0.095	0.245	CEACAM8	0.004	0.958
NRP1	−0.181	0.026						

Note: AML, acute myeloid leukemia.

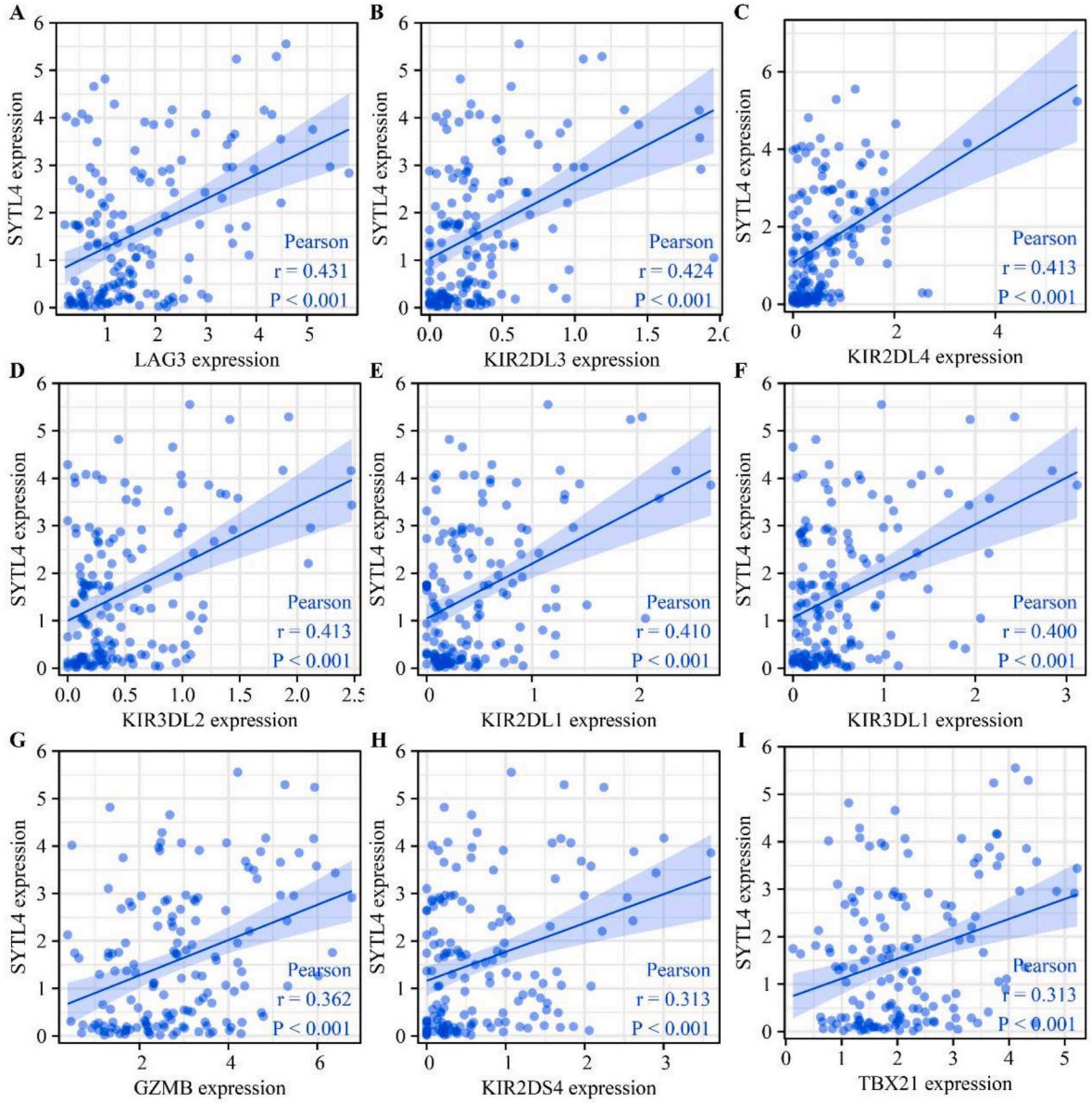

Fig. 8. SYTL4 expression correlated with the levels of immune cell markers in AML. (A) LAG3; (B) KIR2DL3; (C) KIR2DL4; (D) KIR3DL2; (E) KIR2DL1; (F) KIR3DL1; (G) GZMB; (H) KIR2DS4; (I) TBX21.
Note: AML, acute myeloid leukemia.

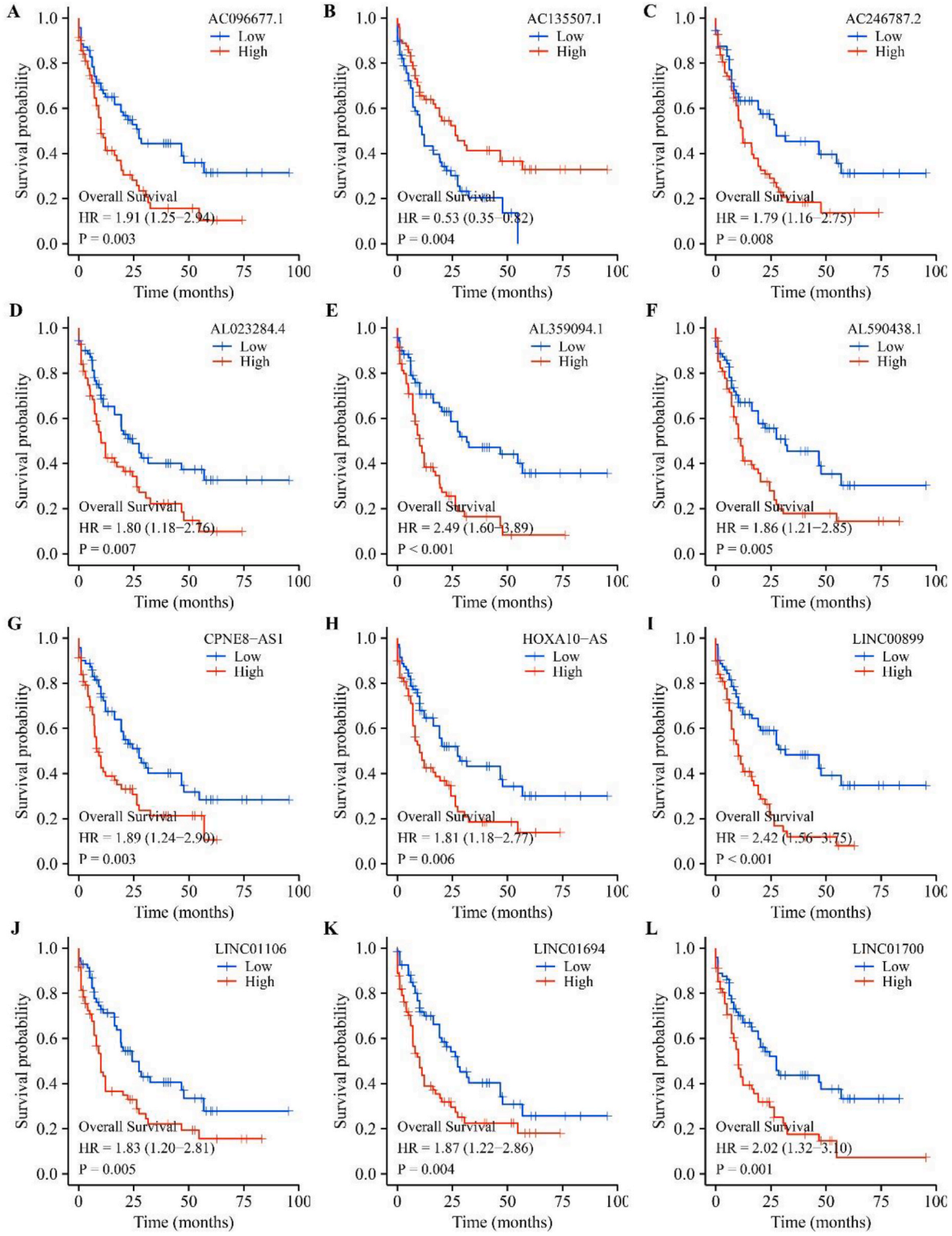

Fig. 9. The prognostic values of SYTL4 associated lncRNAs. (A) AC096677.1; (B) AC135507.1; (C) AC246787.2; (D) AL023284.4; (E) AL359094.1; (F) AL359094.1; (G) CPNE8-AS1; (H) HOXA10-AS; (I) LINC00899; (J) LINC01106; (K) LINC01694; (L) LINC01700.

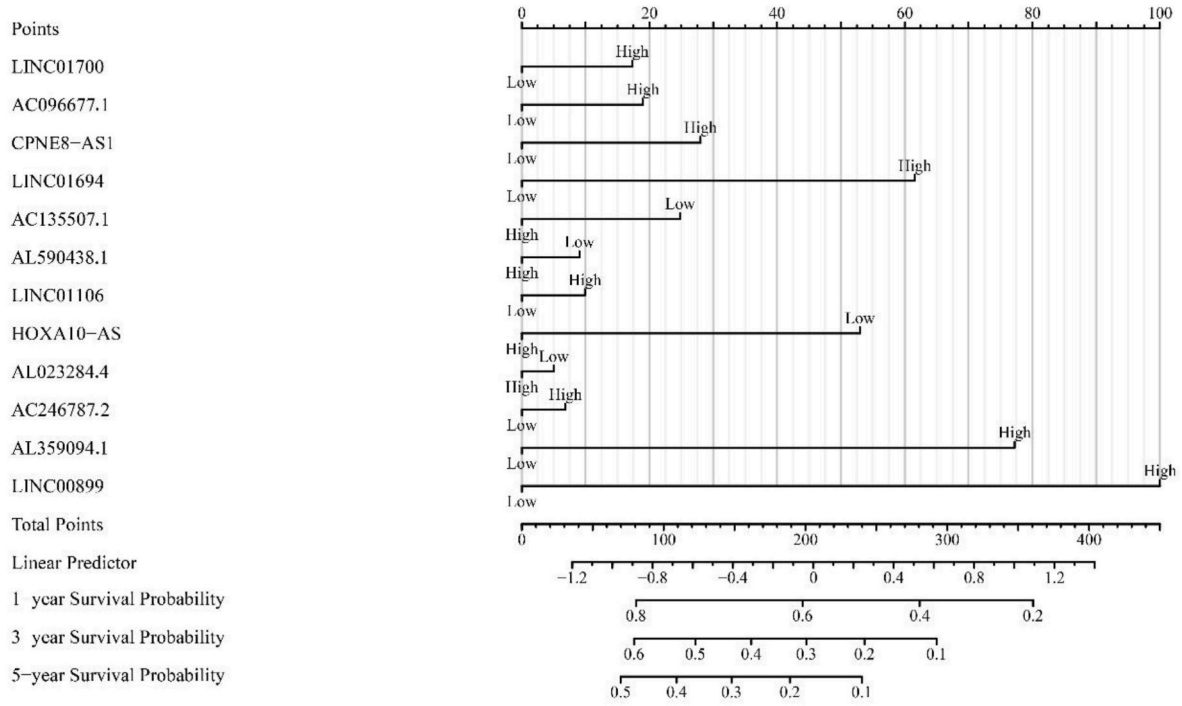

Fig. 10. The prognostic nomogram of SYTL4 associated lncRNAs.

Table 3
The prognostic lncRNAs and SYTL4 on AML patients.

LncRNAs	Total (N)	HR (95 % CI)	P
LINC01700	140		
Low	72	Reference	
High	68	2.020 (1.316–3.103)	0.001
AC096677 1	140		
Low	70	Reference	
High	70	1.915 (1.247–2.941)	0.003
CPNE8-AS1	140		
Low	71	Reference	
High	69	1.895 (1.238–2.900)	0.003
LINC01694	140		
Low	68	Reference	
High	72	1.868 (1.218–2.864)	0.004
AC135507 1	140		
Low	68	Reference	
High	72	0.532 (0.346–0.819)	0.004
AL590438 1	140		
Low	71	Reference	
High	69	1.857 (1.208–2.853)	0.005
LINC01106	140		
Low	69	Reference	
High	71	1.834 (1.197–2.810)	0.005
HOXA10-AS	140		
Low	71	Reference	
High	69	1.810 (1.183–2.771)	0.006
AL023284 4	140		
Low	71	Reference	
High	69	1.801 (1.175–2.760)	0.007
AC246787 2	140		
Low	72	Reference	
High	68	1.789 (1.164–2.751)	0.008
AL359094 1	140		
Low	70	Reference	
High	70	2.491 (1.596–3.887)	<0.001
LINC00899	140		
Low	71	Reference	
High	69	2.421 (1.565–3.745)	<0.001
SYTL4	140		
Low	68	Reference	
High	72	2.958 (1.893–4.623)	<0.001

Note: AML, acute myeloid leukemia.

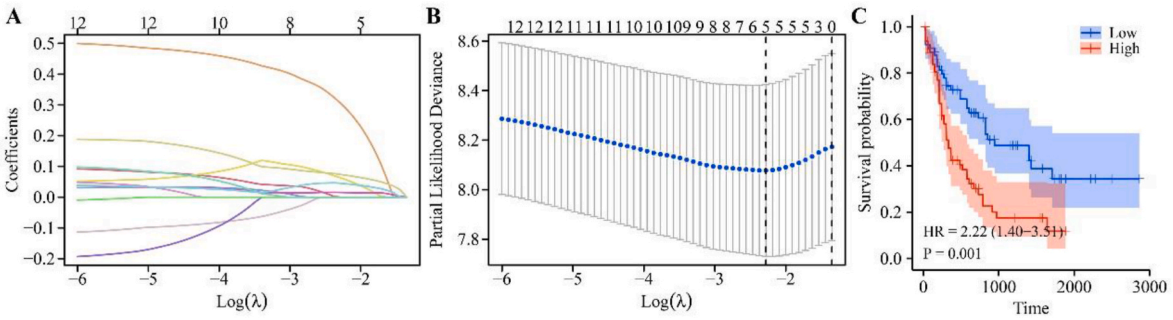

Fig. 11. SYTL4 associated risk model correlated with the prognosis in AML.
Note: AML, acute myeloid leukemia.

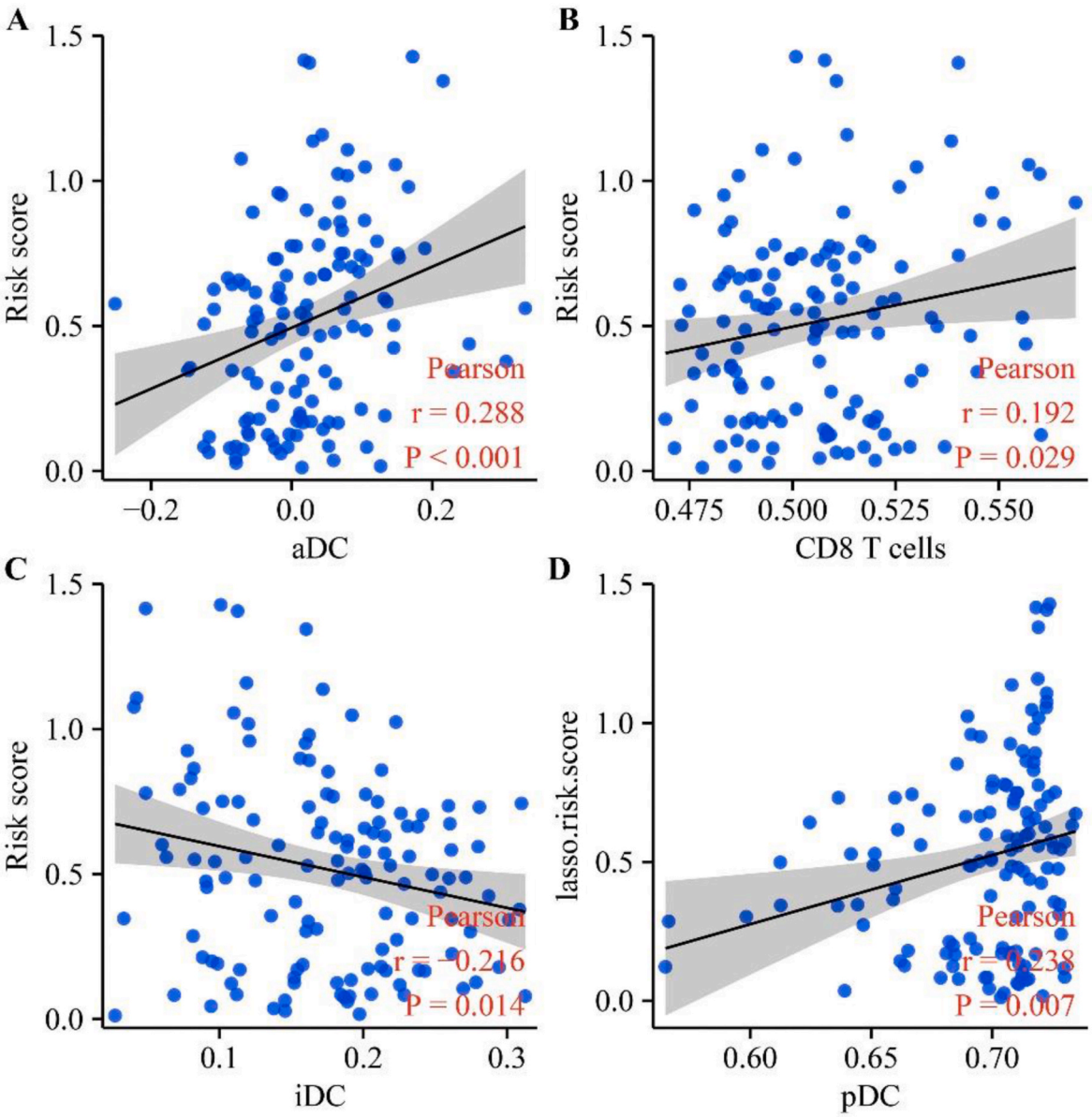

Fig. 12. SYTL4 associated risk model significantly correlated with immune cell levels. (A) aDC; (B) CD8 T cells; (C) iDC; (D) pDC.

Author contributions

Bo-Hui Peng and Qiang Guo conceptualized the research topic and supervised its implementation. Dan Li and Ke Shi authored the manuscript, which was subsequently revised by Qiang Guo. Ke Shi and Dan Li analyzed and visualized the study data. All authors consented to the publication of the final manuscript.

Ethics statement

Not applicable.

Data availability

The data can be directly obtained from the TCGA and XENA databases, or study-specific data can be requested from the corresponding authors.

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Declaration of competing interest

No.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.bbrep.2024.101859.

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