



An integrated bioinformatics analysis of the S100 in head and neck squamous cell carcinoma

Guo Bai^{1,2,3#}, Shijing Yue^{1,2,3#}, Yuanhe You^{2,3,4}, Jiong Zhao^{1,2,3}, Zhuowei Tian^{2,3,4}, Yanan Wang^{2,3,4}, Zhiyuan Zhang^{1,2,3,4}, Chi Yang^{1,2,3^}

¹Department of Oral Surgery, Shanghai Ninth People's Hospital, Shanghai Jiao Tong University School of Medicine, Shanghai, China; ²College of Stomatology, Shanghai Jiao Tong University, Shanghai, China; ³National Center for Stomatology, National Clinical Research Center for Oral Diseases, Shanghai Key Laboratory of Stomatology, Shanghai, China; ⁴Department of Oral and Maxillofacial-Head and Neck Oncology, Shanghai Ninth People's Hospital, Shanghai Jiao Tong University School of Medicine, Shanghai, China

Contributions: (I) Conception and design: C Yang, Z Zhang; (II) Administrative support: C Yang, Z Zhang; (III) Provision of study materials or patients: C Yang, Y Wang; (IV) Collection and assembly of data: G Bai, Y You, Z Tian; (V) Data analysis and interpretation: G Bai, S Yue, J Zhao; (VI) Manuscript writing: All authors; (VII) Final approval of manuscript: All authors.

[#]These authors contributed equally to this work.

Correspondence to: Chi Yang. Department of Oral Surgery, Shanghai Ninth People's Hospital, Shanghai Jiao Tong University School of Medicine, No. 639, Zhizaoju Road, Huangpu District, Shanghai 200011, China. Email: yangchi633@163.com; Zhiyuan Zhang. Department of Oral and Maxillofacial-Head and Neck Oncology, Shanghai Ninth People's Hospital, Shanghai Jiao Tong University School of Medicine, No. 639, Zhizaoju Road, Huangpu District, Shanghai 200011, China. Email: zhzy0502@163.com.

Background: This study aims to evaluate the expression profile and clinical value of the S100 family in head and neck squamous cell carcinoma (HNSCC).

Methods: The expression patterns, clinicopathological features, prognostic significance and underlying correlations of S100 family genes in HNSCC were determined by bioinformatics analysis with the application of several databases, including the The Cancer Genome Atlas (TCGA) and OncoPrint for differential expression gene (DEG) analysis, and a series of analysis tools, including Database for Annotation, Visualization and Integrated Discovery (DAVID), cBioPortal, Kaplan-Meier Plotter, Tumor Immune Estimation Resource (TIMER) and R software packages.

Results: The results from the study demonstrated that S100A4, S100A10, and S100A13 may act as prognostic markers through overall survival (OS), disease-free survival (DFS) and tumor infiltrating immune cell enrichment and a prognostic S100 family gene model comprising *S100A1–A4*, *S100A8*, *S100A10*, *S100A12*, and *S100A13* was identified. The messenger RNA (mRNA) expression of S100A1, S100A9, S100A14, and S100A7A was significantly different in HNSCC patients, together with a high mutation rate of the S100 family was found. Evaluation of clinicopathological value demonstrated the heterogeneity of S100 family functions. S100A1, S100A7, S100A8, S100A9, S100A13, S100A14, and S100A16 were observed to significantly correlate with multiple biological processes (BPs) of HNSCC, including initiation, lymph node metastasis, and lymphovascular invasion. In addition, the S100 family were significantly associated with epithelial-mesenchymal transition (EMT)-related genes.

Conclusions: This present study demonstrated that S100 family members are implicated in the initiation, progression, metastasis and survival of HNSCC.

Keywords: Head and neck squamous cell carcinoma (HNSCC); S100 family; bioinformatics analysis

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[^] ORCID: 0000-0001-9926-7431.

Introduction

Over 600,000 people worldwide are annually diagnosed with head and neck cancer (1,2). Head and neck squamous cell carcinoma (HNSCC) encompasses a group of biologically similar cancers arising from multiple anatomic subsites in the head and neck region, including the oral cavity, lip, larynx and hypopharynx (3). Despite recent advancements in treatment modalities for HNSCC, the long-term survival rates (40–50% survival for <5 years) have not been significantly improved over the past decade (4,5). Given the high mortality of HNSCC, it is vital to identify early diagnostic and prognostic biomarkers.

The S100 family consists of a group of low molecular weight (10,000 Da) proteins with two calcium-binding sites that have helix-loop-helix EF-hand type conformations (6). At least 25 closely related members have been identified in humans (7). Although S100 family members exhibit a high structural similarity, they are not functionally interchangeable and are implicated in many intracellular biological processes (BPs) such as proliferation, apoptosis, migration, differentiation and cell growth (6,8). In contrast to their intracellular functions, extracellular S100 proteins act in a cytokine-like manner by binding to cell surface receptors, such as the receptor for advanced glycation endproducts (RAGEs) and Toll-like receptors (TLRs) (9). Also, S100s have been revealed to promote tumor

progression by regulating tumor infiltrating immune cells and tumor immune response (10,11). Furthermore, previous studies have reported that S100 proteins are associated with the regulation of epithelial-mesenchymal transition (EMT), cancer stem cells (CSCs) and tumor heterogeneity in human carcinoma (12–15).

Due to the wide range of functions of S100 proteins, quantification and recognition of S100 family genes may contribute to the consideration of S100 proteins as biomarkers for the early diagnostic and prognosis, as well as targets for therapy. However, there is a lack of reports in analyzing S100 family members in HNSCC based on large cohort data, and the clinical value of these molecules in HNSCC remains to be ascertained. Therefore, the present study aimed to evaluate the expression profile and clinical value of the S100 family in HNSCC using a series of online databases. We present the following article in accordance with the STREGA reporting checklist (available at <https://tcr.amegroups.com/article/view/10.21037/tcr-22-1353/rc>).

Methods

The study was conducted in accordance with the Declaration of Helsinki (as revised in 2013).

Oncomine analysis

Oncomine is an online cancer gene expression microarray database that can be used to analyze S100 transcription levels in different cancers (<http://www.oncomine.org/resource/login.html>) (16). In this study, S100 messenger RNA (mRNA) expression in clinical cancer tissues with that in normal control tissues was compared. P value and fold change cutoffs were 0.05 and 2, respectively.

Differential expression gene analysis

Transcriptome RNA-sequencing (RNA-seq) data of HNSCC samples was obtained from the Cancer Genome Atlas (TCGA) database (<https://portal.gdc.cancer.gov/>) (17). Raw count data and relevant clinical information for the patients were also downloaded and extracted. The method of acquisition and application complied with the guidelines and policies. The differential expressions of S100 family proteins between the tumor tissues and normal tissues were analyzed using the Wilcoxon test and visualized by the R software (v4.0.3) and R package ggplot2 (v3.3.2). A P value

Highlight box

Key findings

- S100 family proteins are significantly associated with the development of HNSCC.

What is known and what is new?

- S100s could promote tumor progression by regulating tumor infiltrating immune cells and tumor immune response. They are associated with regulation of EMT, CSCs and tumor heterogeneity in human carcinomas.
- The mRNA expression of S100A1, S100A9, S100A14, and S100A7A was significantly different in HNSCC patients compared with other cancers. A prognostic S100 family gene model comprising S100A1–A4, S100A8, S100A10, S100A12, and S100A13 was identified in HNSCC. S100A4, S100A10, and S100A13 may act as prognostic markers.

What is the implication, and what should change now?

- A prognostic signature of the eight S100 genes could moderately predicted the prognosis of HNSCC patients. Further investigations are necessary to explore and verify the underlying molecular mechanisms.

of less than 0.05 was considered statistically significant.

Genes expression association

The dataset used comprised HNSCC mRNA-seq data from TCGA. A heat map of the correlation between S100 family genes and EMT-related genes of *SNAIL1* (18), *VIM* (19), *TWIST* (19), *CDH1* (20), *CDH2* (20) were performed by the Spearman correlation via R software package ggstatsplot (21), and is displayed by the R software package pheatmap (21). A P value of less than 0.05 was considered statistically significant.

Enrichment analysis of S100s family in HNSCC

The function enrichment analysis for gene ontology (GO) terms, including the BP, cellular component (CC), and molecular function (MF) categories were performed in the Database for Annotation, Visualization and Integrated Discovery (DAVID; version 6.8, <https://david.ncifcrf.gov/tools.jsp>) (22). The analysis threshold was determined by the false discovery rate (FDR) value, and FDR <0.05 for BP, FDR <0.17 for CC, and FDR <0.01 for MF indicate that the functional comment is significantly enriched.

Analysis of gene alteration frequency

cBioPortal (<https://www.cbioportal.org/>) is an open-access online resource for exploring and visualizing multidimensional cancer genomics dataset (23). HNSCC (TCGA, provisional) dataset was selected to analyze genetic alterations of S100 family genes in HNSCC. The genomic profiles included mutations, putative copy-number alterations, and mRNA expressions (RNA-seq V2 RSEM with z-scores =±2).

Kaplan-Meier plotter

The Kaplan-Meier plotter (<https://www.kmplot.com/>) is an online database comprises gene expression information and clinical outcome parameters of liver cancer, breast cancer, lung cancer and various cancer types (24). To analyze correlation of S100 family members with overall survival (OS) and disease-free survival (DFS) rates of HNSCC patients, samples were divided into two groups (low and high expression) based on median mRNA levels with a hazard ratio (HR) with 95% confidence intervals (CIs) and log-rank P values. Log-rank P values <0.05 were considered

as significant.

Establishment of prognostic S100s family gene model

Raw counts of RNA-seq data (level 3) and corresponding clinical information from 501 HNSCC patients were obtained from TCGA (<https://portal.gdc.cancer.gov/>). The least absolute shrinkage and selection operator (LASSO) regression algorithm for feature selection, using 10-fold cross-validation, the above analysis uses the R software package glmnet (v4.1-1).

Multifactor Cox regression was applied to analyze the 19 S100 proteins, and a risk model of 8 S100s family genes was ultimately established. The individualized risk score with coefficients was calculated to construct a prognostic signature separating the high-risk and low-risk groups. According to the median risk score, subgroups including low- and high-risk groups were established (25). For Kaplan-Meier curves, P values and HR with 95% CI were generated by log-rank tests and univariate Cox proportional hazards regression. timeROC (v0.4) analysis was performed to compare the predictive accuracy of each gene and risk score. All analytical methods above and R packages were performed using R software version 4.0.3 (The R Foundation for Statistical Computing, 2020). P<0.05 was considered as statistically significant.

Tumor-infiltrating immune cell scores based on the risk model

The correlation between signature risk score and the tumor-infiltrating immune cell (including B cells, CD4⁺ T cells, CD8⁺ T cells, macrophages, neutrophils, and dendritic cells) was performed using the Tumor Immune Estimation Resource (TIMER) database, a network resource that systematically evaluates the clinical effects of different immune cells in different types of cancer (<http://cistrome.dfci.harvard.edu/TIMER/>) (26). In the above analyses, P<0.05 was considered statistically significant.

Clinicopathological features evaluation

Genomic and clinical annotation data based on the TCGA primary HNSCC cohort were filtered for clinicopathological analysis. The ratio of neoplasm histologic grade (G1 + G2/G3 + G4), tumor size (T1 + T2/T3 + T4), nodal status (N0/N0+), perineural invasion (no/yes), pathological nodal extracapsular spread (no/yes),

lympho-vascular invasion (no/yes), the relationship between new tumor event (no/yes) after initial treatment and S100s expression (low/high) were evaluated.

Statistical analysis

Statistical analyses were carried out using SPSS Statistics 20.0 software (IBM SPSS, Chicago, IL, USA). The statistical differences between the experimental groups were analyzed by Student's *t*-test. The relationship between S100s expression and survival rates was analyzed using Kaplan-Meier curve. Clinicopathological features were evaluated by crosstab analyses and chi-squared tests were performed. Statistically, $P < 0.05$ and log-rank P values < 0.05 were considered statistically significant.

Results

Atlas of selected 19 S100 protein members in HNSCC

There are 21 S100 proteins, which are exclusively found in vertebrates, encoded in the human genome. The genes encoding 17 of 21 family members (S100A1–A14, S100A7A, S100A7L2 and S100A16) are located on chromosome 1q21, which is referred to as the epidermal differentiation complex (EDC) (27). The genes of the remaining 4 family members, namely, *S100B*, *S100G*, *S100P*, and *S100Z* are dispersed throughout the genome on chromosomes 21, X, 4, and 5, respectively. *S100G* and *S100A7L2* were excluded from this study because their detailed data were not sufficient for a comprehensive analysis. The full names and biological functions of the 19 included family members (S100A1–A14, S100A7A, S100A16, S100P, S100B, and S100Z) are summarized in [Table S1](#).

Transcriptional expression of the S100 protein family in HNSCC patients

First, the transcription expression changes of individual S100 proteins in HNSCC compared to normal tissues were analyzed using the Oncomine database ([Figure 1A](#)). S100A2, S100A3, S100A7, S100A7A, and S100A10 were mainly upregulated in HNSCC, while S100A1, S100A4, S100A6, S100A8, S100A9, S100A10, S100A12, S100A14, and S100P were downregulated in HNSCC. Furthermore, the mRNA expression level of S100 proteins between HNSCC and normal tissues was compared. As shown in [Figure 1B](#), the expression of S100A8, S100A9, and S100A14

was significantly lower in HNSCC tissues compared to normal control tissues, while the expression of S100A2, S100A3, S100A7A, and S100A10 was higher in HNSCC tissues compared to normal control tissues ($P < 0.01$), which was in accordance with S100 expression changes. The genetic alteration of S100 family members in HNSCC was then analyzed ([Figure S1A,S1B](#)). As shown in [Figure S1A](#), high mutation rates of the S100 family were observed in HNSCC patients (22.54%). Among all types of mutations, mRNA upregulation was the most common alteration (14.75%). The prognostic roles of gene alterations in patients with HNSCC were also analyzed, however, no significant correlations were observed between the presence of alterations and OS/DFS ($P = 0.135$ and $P = 0.781$, respectively, [Figure S1C](#)). In addition, correlations among S100 family members in HNSCC were verified ([Figure S2](#)). The expression of S100A7, S100A7A, S100A8, and S100A9 was positively correlated with each other. The expression of S100A16 was positively related with S100A14 and S100A2. Moreover, the expression of S100A4, S100A5, and S100A13 was negatively related to the expression of S100A7, S100A7A, S100A8, and S100A9.

Predicted functions of S100 proteins in HNSCC

According to the GO enrichment analysis, the cell components (CCs) of the S100 family were mainly enriched in the nucleus, extracellular exosome and cytoplasm ([Figure 2A](#)). RAGE receptor binding, protein binding and calcium ion binding were the three main enriched MFs of S100 proteins in HNSCC ([Figure 2B](#)). The enriched BPs of S100 proteins included the innate immune response, defense response to bacteria and fungi, positive regulation of the inflammatory response and positive regulation of I- κ B kinase/nuclear factor- κ B (NF- κ B) signaling ([Figure 2C](#)).

Association between S100 mRNA expression and HNSCC prognosis

Kaplan-Meier plotter curves and log-rank test analyses were performed to explore the effect of S100 mRNA expression on the survival of HNSCC patients. Higher expression of S100A10 and S100A13 indicated significantly poorer OS ($P < 0.05$). In contrast, lower expression of S100A4 was associated with significantly poorer OS ($P < 0.05$) ([Figure 3](#)). The average of the values high and low S100s mRNA expression was shown in [Table S2](#). In addition, only higher expression of S100A13 indicated significantly worse DFS for HNSCC patients ($P < 0.001$) ([Figure 4](#)).

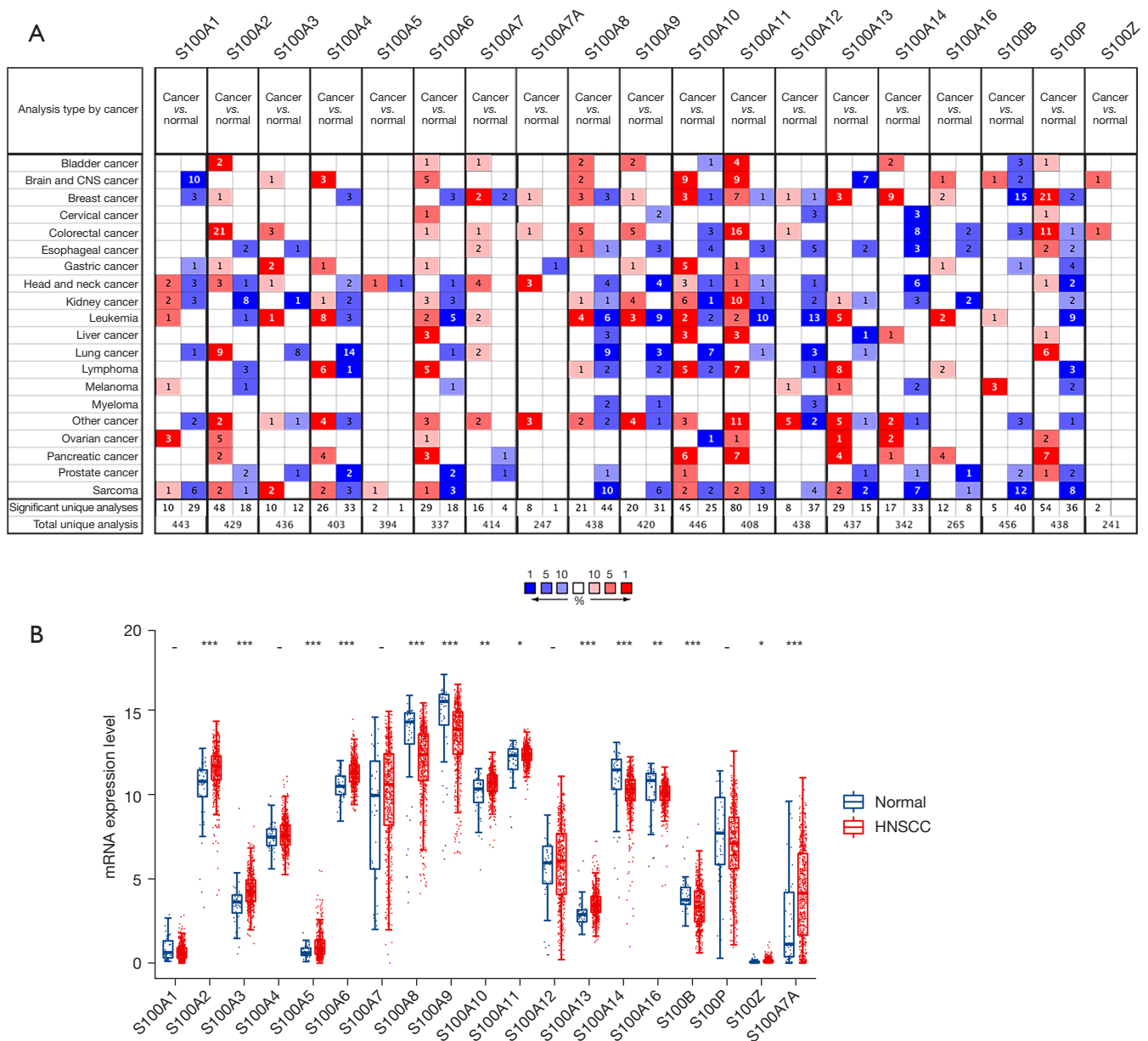


Figure 1 Transcription expression of S100 proteins in various cancers and HNSCC. (A) Number of datasets with statistical significance for S100s mRNA expression in different types of cancers: red, upregulated; blue, downregulated. (B) mRNA expression distribution of S100 proteins in HNSCC tumor tissues and normal tissues. *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$; -, not significant; CNS, central nervous system; mRNA, messenger RNA; HNSCC, head and neck squamous cell carcinoma.

The clinicopathological value of the S100 protein family based on the TCGA HNSCC cohort is summarized in *Table 1*. S100A2, S100A7, S100A9, S100A12, S100A14, S100A16, and S100A7A were identified as significant for the evaluation of neoplasm histologic grade and nodal invasion. For evaluation of new tumor events after initial treatment,

S100A13 was identified as significant.

An eight-gene prognostic signature of S100s in HNSCC

To further identify the S100 proteins that are significantly correlated with the prognosis of HNSCC patients, LASSO

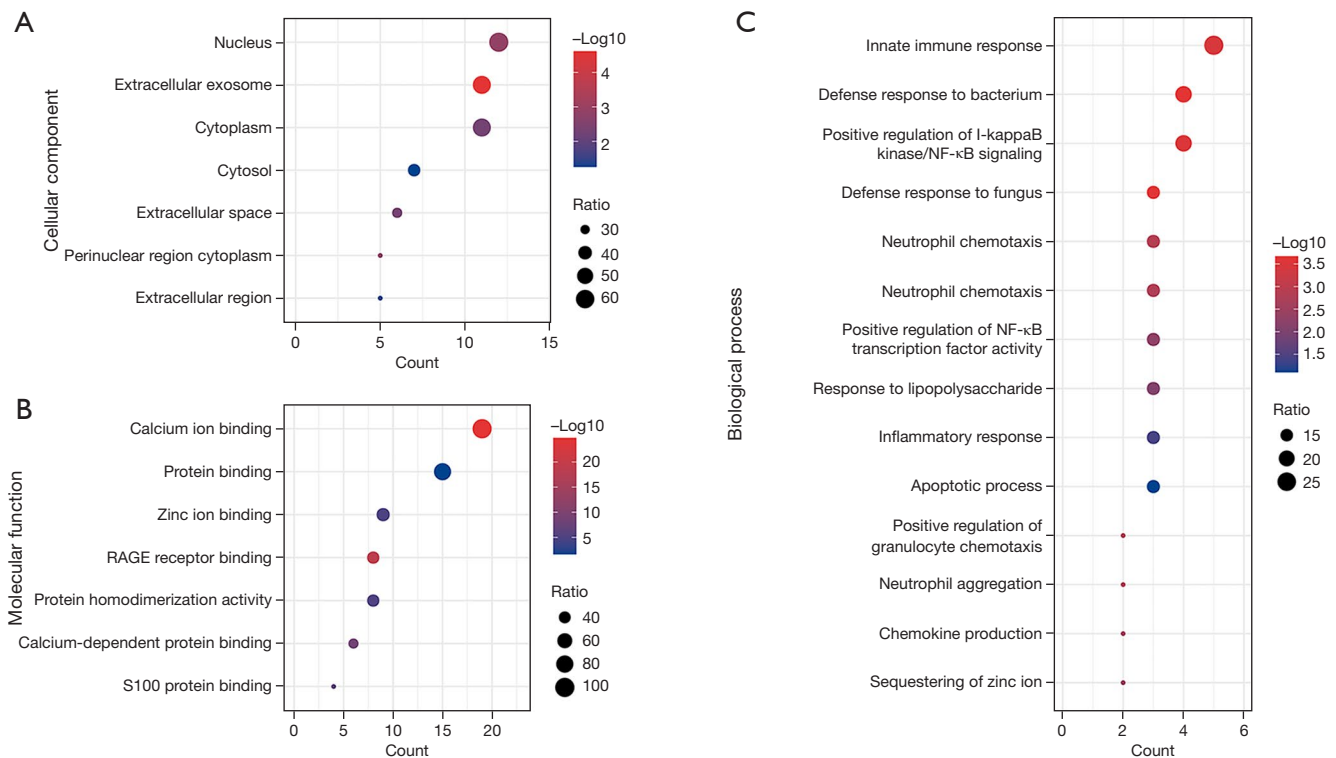


Figure 2 GO enrichment analysis of S100s in HNSCC. (A,B) The top most 7 enriched enrichment pathways in CCs and MFs, respectively. (C) The top most 14 enriched GO enrichment pathways in BPs. RAGE, receptor for advanced glycation endoprodukt; NF- κ B, nuclear factor- κ B; GO, gene ontology; HNSCC, head and neck squamous cell carcinoma; CC, cellular component; MF, molecular function; BP, biological process.

regression with tenfold cross-validation was performed. Under the optimal lambda value ($\lambda_{\min} = 0.0148$), 8 genes that were significantly associated with OS were identified among the 19 S100 genes (Figure 5A, 5B). Thereafter, the eight gene-based risk score was calculated based on their Cox coefficients as follows: risk score = $-0.1053 \times$ (expression level of *S100A1*) + $-0.1339 \times$ (expression level of *S100A2*) + $-0.1516 \times$ (expression level of *S100A3*) + $-0.2457 \times$ (expression level of *S100A4*) + $-0.0263 \times$ (expression level of *S100A8*) + $0.4372 \times$ (expression level of *S100A10*) + $-0.0121 \times$ (expression level of *S100A12*) + $0.1782 \times$ (expression level of *S100A13*). Based on the risk scores, the patients were divided into the high-risk group (n=251) and low-risk group (n=252) (Figure 5C). Figure 5D shows the survival status of all patients in the training group and Figure 5E presents the heatmap of the eight prognostic genes. The Kaplan-Meier survival curves showed that the high-risk group had worse OS than the low-risk group (Figure 5F). Moreover, the eight-gene prognostic signature showed moderate prediction ability in a time-dependent receiver operating

characteristic (ROC) analysis (Figure 5G) for 1-, 3-, and 5-year OS.

Negative correlation of S100 family members with tumor-infiltrating immune cells in HNSCC patients

The association of the mRNA expression status of the eight-gene prognostic signature with tumor-infiltrating immune cells was identified by TIMER in HNSCC patients. As illustrated in Figure 6, a negative correlation was found between S100 expression and all six types of immune cells (B cells, CD4⁺ T cells, CD8⁺ T cells, macrophages, neutrophils, and dendritic cells), thereby revealing prognostic value between S100 family mRNA expression and immune cell infiltration in HNSCC patients.

Correlation between S100 family proteins and EMT- and CSC-related genes, PD-1 and PDL1 genes

EMT is a vital bioprocess for the invasion and metastasis

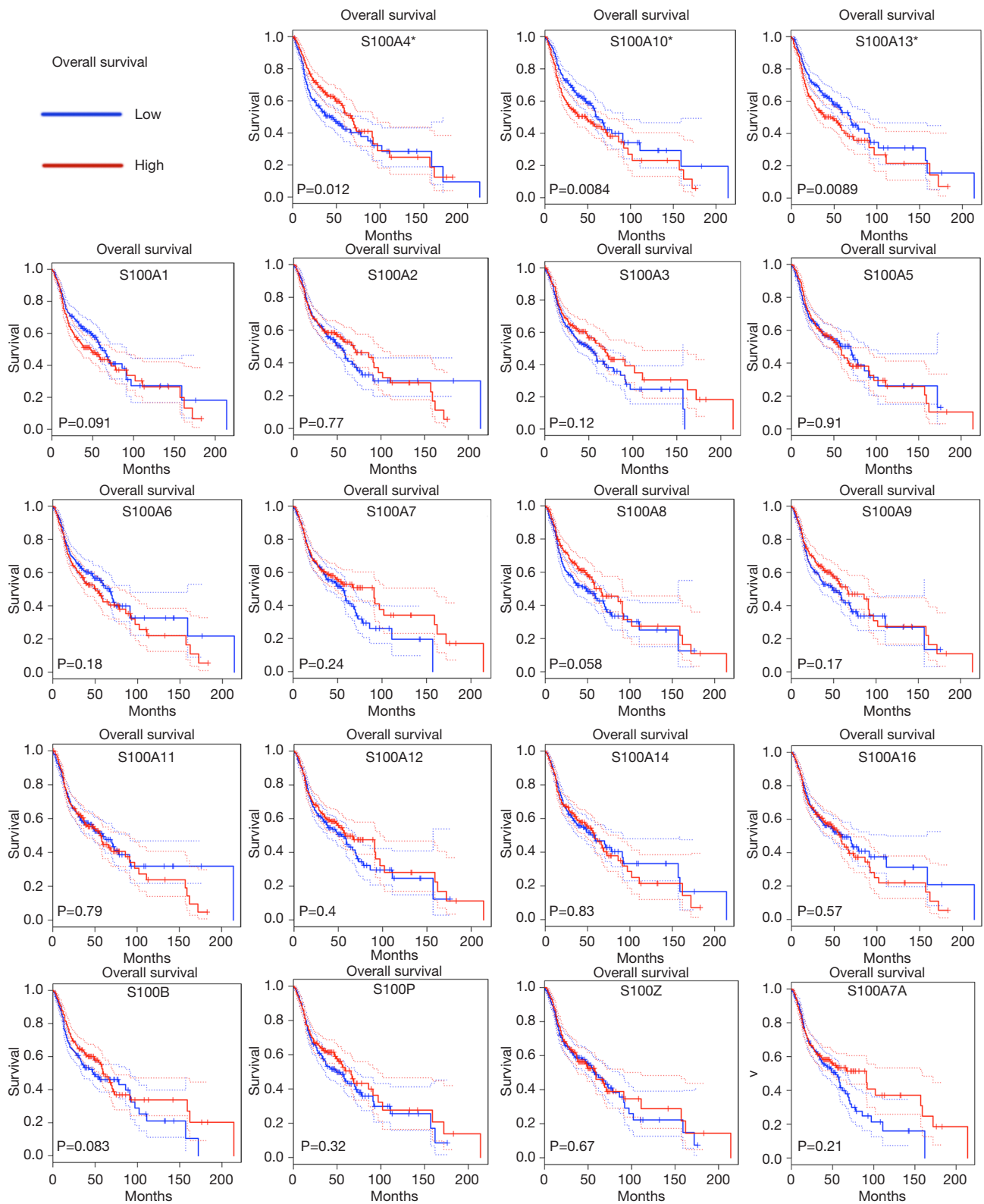


Figure 3 Prognostic value of S100s for the OS of HNSCC patients. The expression of S100A4, S100A10, and S100A13 were significantly associated with OS. *, $P < 0.05$. OS, overall survival; HNSCC, head and neck squamous cell carcinoma.

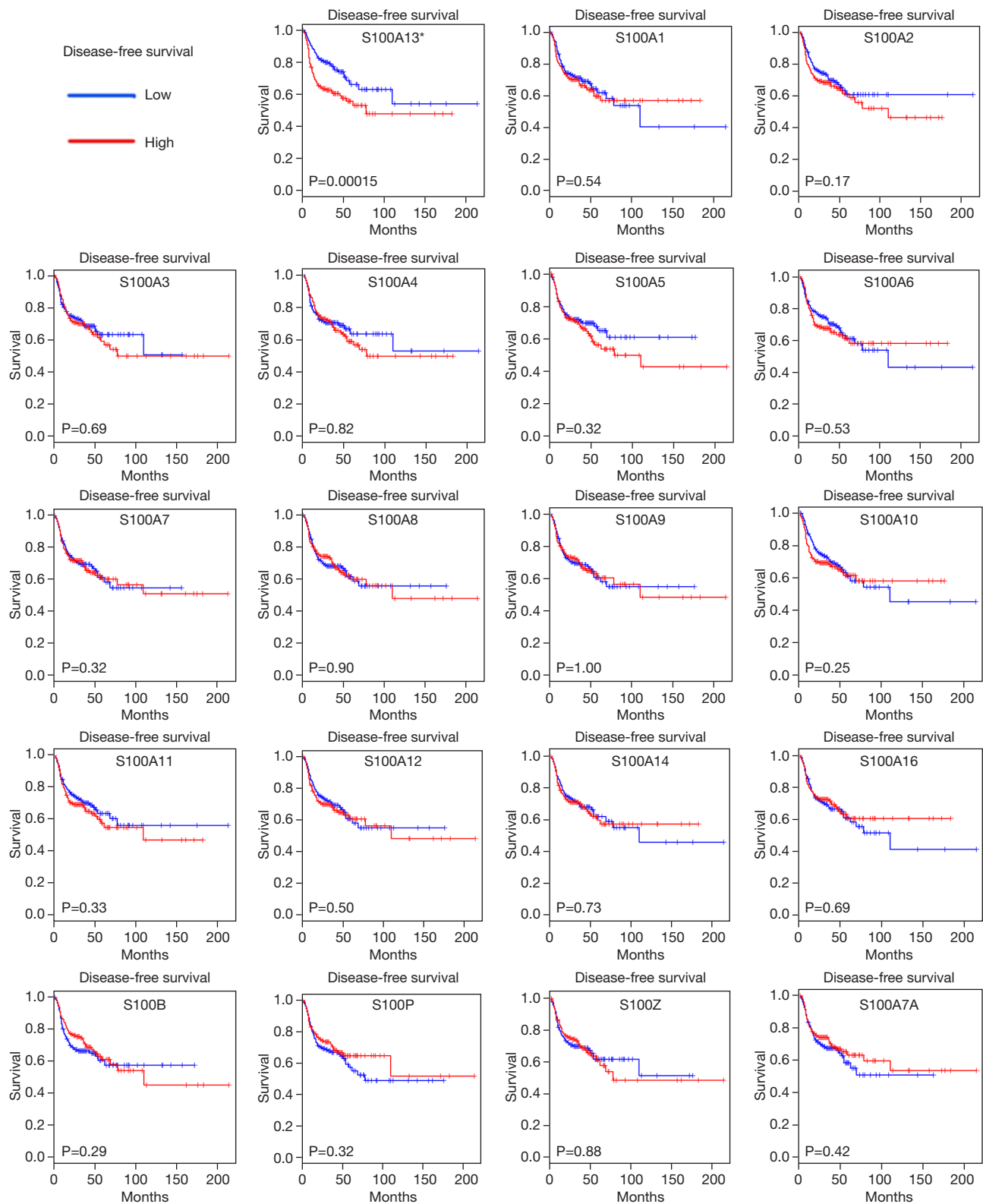


Figure 4 Prognostic value of S100s for the DFS of HNSCC patients. The expression of S100A13 was significantly associated with DFS. *, $P < 0.001$. DFS, disease-free survival; HNSCC, head and neck squamous cell carcinoma.

Table 1 Clinicopathological evaluation for the reported CSC biomarkers based on TCGA primary HNSCC cohort

S100 protein family	Neoplasm histologic grade (G1 + G2/G3 + G4), P value	Tumor size (T1 + T2/T3 + T4), P value	Nodal status (N0/N0+), P value	Perineural invasion (no/yes), P value	Pathological nodal extracapsular spread (no/yes), P value	Lympho-vascular invasion (no/yes), P value	New tumor event after initial treatment (no/yes), P value
S100A1	0.676	0.040 ^a	0.395	0.006 ^a	0.053	0.018 ^a	0.758
S100A2	<0.001 ^{ab}	0.117	0.017 ^a	0.419	0.061	0.020 ^{ab}	0.303
S100A3	0.168	0.128	0.167	0.270	0.308	0.264	0.570
S100A4	0.364	0.093	0.410	0.436	0.869	0.838	0.972
S100A5	0.171	0.267	0.436	0.336	0.896	0.282	0.733
S100A6	0.199	0.284	0.341	0.628	0.963	0.332	0.506
S100A7	<0.001 ^{ab}	0.540	0.013 ^a	0.244	0.013 ^{ab}	<0.001 ^{ab}	0.843
S100A8	<0.001 ^{ab}	0.147	0.662	0.905	0.254	<0.001 ^{ab}	0.808
S100A9	<0.001 ^{ab}	0.208	0.001 ^{ab}	0.289	0.070	<0.001 ^{ab}	0.401
S100A10	0.066	0.066	0.110	0.089	0.422	0.901	0.198
S100A11	0.001 ^{ab}	0.938	0.632	0.478	0.779	0.747	0.168
S100A12	<0.001 ^{ab}	0.093	0.001 ^{ab}	0.709	0.001 ^{ab}	<0.001 ^{ab}	0.982
S100A13	0.285	0.910	0.058	0.135	0.020	0.149	0.013 ^a
S100A14	<0.001 ^{ab}	0.157	0.461	0.289	0.004 ^{ab}	0.026 ^{ab}	0.207
S100A16	<0.001 ^{ab}	0.378	0.011 ^{ab}	0.234	0.009 ^{ab}	0.01 ^{ab}	0.093
S100B	0.047 ^a	<0.001 ^{ab}	0.613	0.401	0.477	0.582	0.874
S100P	0.116	0.999	0.126	0.532	0.105	0.464	0.544
S100Z	0.304	0.118	0.532	0.950	0.943	0.695	0.544
S100A7A	<0.001 ^{ab}	0.569	0.001 ^{ab}	0.860	0.001 ^{ab}	<0.001 ^{ab}	0.295

*, P<0.05; ^a, positive correlation with significance; ^b, negative correlation with significance. CSC, cancer stem cell; TCGA, The Cancer Genome Atlas; HNSCC, head and neck squamous cell carcinoma.

of HNSCC. Information on the underlying correlation between S100 family proteins and EMT-related genes is rare. The heatmaps shown in [Figure S3](#) elaborate the expression patterns of EMT-related genes (*SNAIL*, *VIM*, *TWIST1*, *CDH2*, and *CDH1*). Most of the S100 family members showed a significantly negative correlation with EMT-related genes, such as S100A8, S100A9, and S100A14. The same as in correlation with CSC-related genes ([Figure S4](#)). Programmed death 1 (PD-1; CD279) exerts an important role in immune homeostasis (28) and the expression of programmed death ligand 1 (PD-L1) has been identified in HNSCC (29). The relative mRNA expression levels of both S100s and PD-1, PD-L1 in HNSCC were analyzed ([Figure S5A,S5B](#)). [Table 2](#) shows the expression relationship between S100s members and related genes, and

P<0.05 was considered as significant correlation. Only PD-L1 showed significantly associated with OS rate in HNSCC patient (P=0.04937), as is shown in [Figure S5C](#).

Discussion

Dysregulated S100 expression is a common feature in several human cancers, and each cancer exhibits a distinctive S100 protein profile. Emerging evidence indicates that the biology of most S100 proteins is complex and multifactorial, and these proteins actively contribute to tumorigenesis, cancer progression and metastasis (6,8). Great progress has been made since the past few years, but systematic analysis of the clinical value of S100 proteins in HNSCC is still inadequate. Here, the roles of 19 S100 protein families

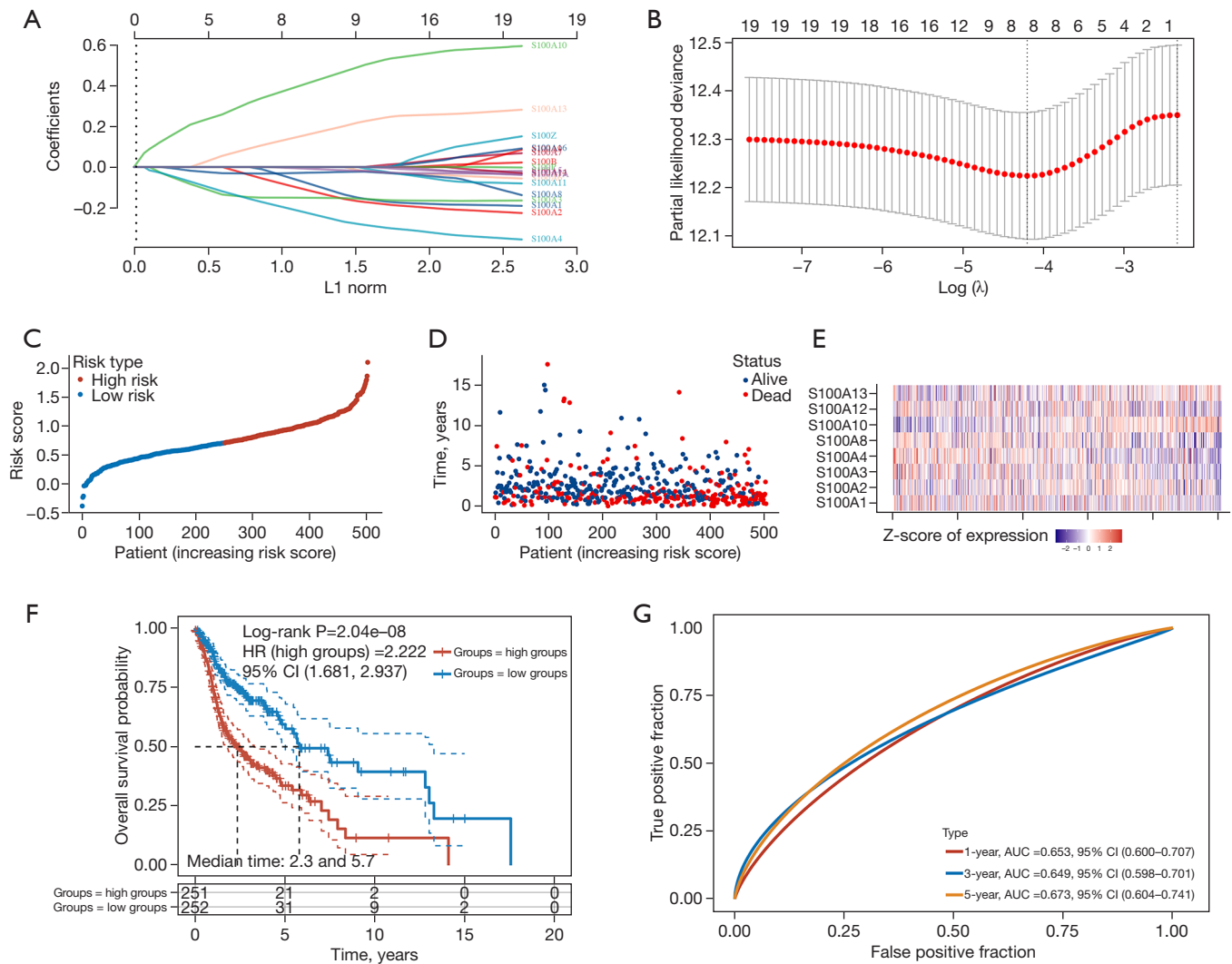


Figure 5 Identification of 8 significantly prognostic S100 genes and prognostic analysis of eight-gene signature. (A) The LASSO coefficient profile of 19 S100 family protein-coding genes. (B) LASSO regression with tenfold cross-validation obtained 8 prognostic genes using minimum lambda value. (C) The dotted curve of risk score and patients were divided into low- and high-risk group. (D) Survival status of the patients. More dead patients corresponding to the higher risk score. (E) Heatmap of the expression profiles of the eight prognostic genes in low- and high-risk group. (F) Kaplan-Meier survival analysis of the eight-gene signature. (G) Time-dependent ROC analysis of the eight-gene signature. HR, hazard ratio; CI, confidence interval; AUC, area under the curve; LASSO, least absolute shrinkage and selection operator; ROC, receiver operating characteristic.

were comprehensively evaluated through bioinformatics analysis based on over 500 primary HNSCC cases from the TCGA cancer database. Differential expression gene (DEG) analysis showed differences in the expression of S100 family members in HNSCC, indicating that S100 proteins play different but important roles in HNSCC development. The functional enrichment analysis results suggested that

S100 proteins might play an important role in the immune response during HNSCC via protein binding and NF- κ B related signaling pathways.

The clinicopathological features of HNSCC patients suggested that S100 proteins may regulate the occurrence and progression processes through different mechanisms, warranting further attention to demonstrate the underlying

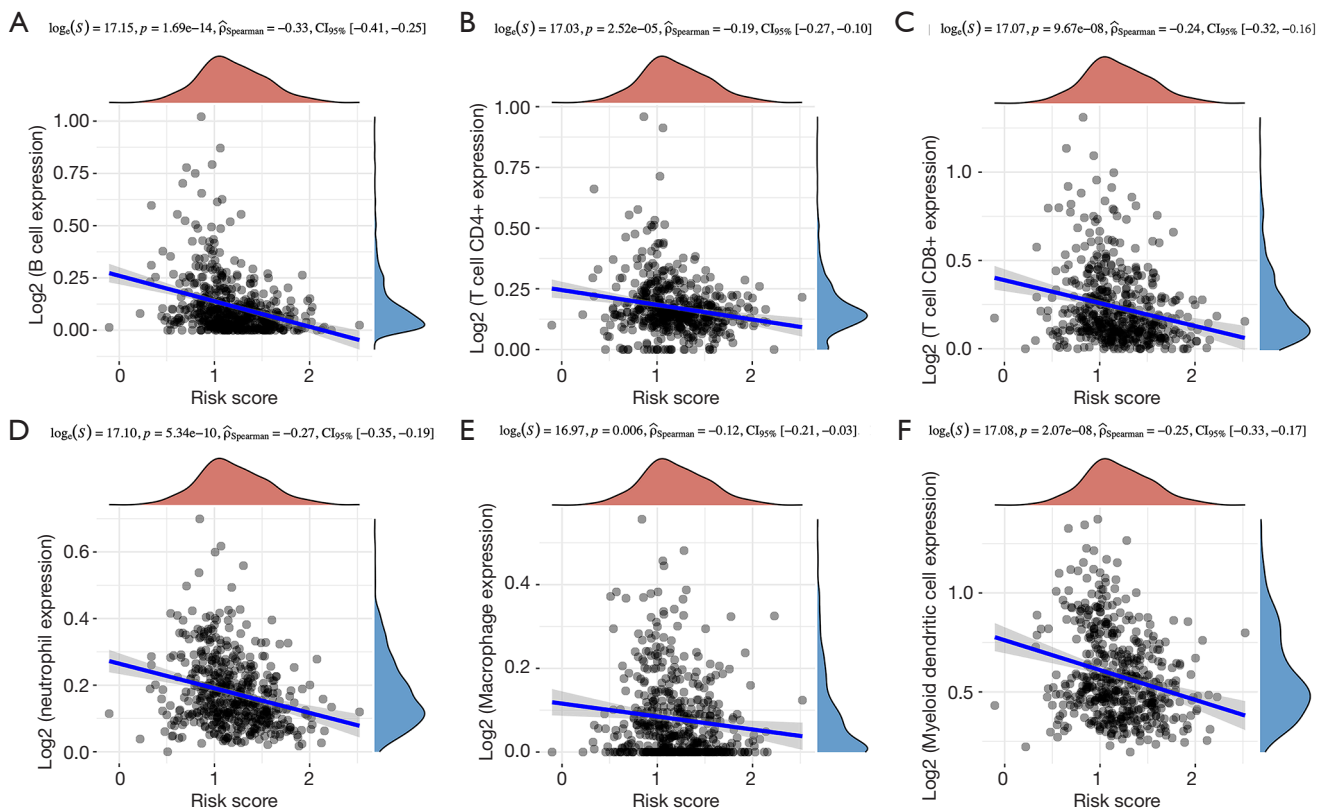


Figure 6 Negative relationships between the eight-gene prognostic signature and infiltration abundances of six types of immune cells. (A) B cells. (B) CD4 T cells. (C) CD8 T cells. (D) Neutrophils. (E) Macrophages. (F) Dendritic cells. CI, confidence interval.

heterogeneity. Eight S100 genes, namely, *S100A1–A4*, *S100A8*, *S100A10*, *S100A12*, and *S100A13* were identified for their significant association with HNSCC patient prognosis. The combined effect of these S100s were calculated. As an eight-gene prognostic signature, S100 proteins had a positive correlation with HNSCC patient survival with moderate prediction capability. Additionally, the S100 family-based signature manifested was closely related to the immune microenvironment, showing a negative relationship with different types of tumor-infiltrating immune cells.

The expression profile and functions of S100 family proteins are quite different in HNSCC from that in other tumors. S100A7 has been found in various epithelial malignancies, including HNSCCs, and is associated with cancer initiation and poor prognosis. Inflammatory cytokines regulate S100A7 expression in cancers (30), implicating their roles in the tumor microenvironment. The S100A7 gene, together with NF- κ B transcription factors, plays an important role in inducing cell growth

by stimulating proliferation genes (31). As an oncogene, S100A7 is the major contributing factor in the occurrence of oral cancer and promotes local tumor progression by activating the mitogen-activated protein kinase (MAPK) signaling pathway via the Ras-related protein 2A (RAB2A) pathway (12). In addition, S100A7 promotes angiogenesis by regulating matrix metalloproteinase (MMP)13 and vascular endothelial growth factor (VEGF) (32). However, in the present study, S100A7 transcript expression in HNSCC showed no significant difference compared to normal tissue. Thus, *S100A7* was not included in the prognostic signature. S100A8 and S100A9 are often co-expressed and form a heterodimeric complex named as calprotectin. S100A8/A9 proteins are important constituents of the tumor microenvironment that critically contribute to the progression of tumors (33). Moreover, S100A8/A9 proteins work as inflammatory chemoattractant to recruit inflammatory cells to damaged tissues, thereby contributing to tumorigenesis and cancer metastasis (34). However, the results in the present study showed that S100A8/A9 were

Table 2 Correlation of S100 family members with PD-1 and PD-L1 of HNSCC patients

S100 family	PDCD1, P value	CD274, P value
S100A1	0.079	0.219
S100A2	<0.001 ^{ab}	0.792
S100A3	0.861	0.598
S100A4	<0.001 ^{aa}	0.725
S100A5	0.114	0.002 ^{ab}
S100A6	0.035 ^{ab}	0.094
S100A7	0.014 ^{ab}	0.187
S100A8	0.860	0.064
S100A9	0.429	0.017 ^{aa}
S100A10	<0.001 ^{ab}	0.253
S100A11	0.014 ^{ab}	0.792
S100A12	0.054	0.930
S100A13	0.219	0.018 ^{ab}
S100A14	0.009 ^{ab}	0.014 ^{ab}
S100A16	0.011 ^{ab}	0.077
S100B	<0.001 ^{aa}	0.002 ^{aa}
S100P	0.565	0.334
S100Z	<0.001 ^{aa}	0.002 ^{aa}
S100A7A	0.114	0.860

^{*}, P<0.05; ^a, positive correlation with significance; ^b, negative correlation with significance. PD-1, programmed death 1; PD-L1, programmed death ligand 1; HNSCC, head and neck squamous cell carcinoma.

downregulated in HNSCC with a negative correlation with the expression of EMT genes, supporting the notion that S100A8/A9 play multifaceted tumor-suppressive roles in HNSCC (14). Decreased expression of S100A8 and S100A9 has been reported to be associated with poor prognosis in oral carcinoma (35). At low concentrations, S100A8/A9 promotes tumor cell growth by activating the MAPK and NF- κ B signaling pathways, depending on RAGE ligation (36). Silencing endogenous S100A8 and S100A9 expression in TR146 cells increases MMP2 activity, thereby promoting cell invasion and migration (37). Cytoplasmic calprotectin also functions to control the cell cycle DNA damage checkpoint at G₂/M and block proliferation (38). S100A14 expression is associated with cancer differentiation, lymph node status and metastasis (39). High expression

of S100A14 acts as a mediator of EMT and regulates the proliferation, migration and invasion of human cervical and breast cancer cells (40,41). In contrast, S100A14 suppresses nasopharyngeal carcinoma (NPC) metastasis by inhibiting the NF- κ B signaling pathway and reversing EMT. Lower S100A14 expression is significantly correlated with shorter patient OS and distant metastasis-free survival in NPC patients (42), same in oral squamous cell carcinoma (OSCC) (43-45). Nevertheless, the analysis in the present study also supported that the expression of S100A14 is decreased in HNSCC and that low expression of this protein is associated with pathological nodal extracapsular spread and lymphovascular invasion.

S100A4, S100A10, and S100A13 are associated with the OS of HNSCC, and S100A13 is correlated with DFS, according to our analysis. S100A4, also known as metastasin, plays an important role in the invasion and metastasis of human malignant tumors and is considered an EMT marker for being a direct target of β -catenin/T-cell factor (TCF) (46-49). S100A10 upregulation has been reported in a number of cancers and is generally associated with a poor prognosis (50,51). S100A13 plays a key role in tumor growth and metastasis. High expression of S100A13 has been reported to be involved in tumor growth, metastasis and poor OS in thyroid tumors, melanoma and early-stage non-small cell carcinoma (52-54). However, the results in the present study indicated that HNSCC patients with high expression of S100A13 have a better prognosis. At the same time, S100A13 was found to be significantly associated with new tumor events after initial treatment, indicating that S100A13 is a potential biomarker for HNSCC recurrence. The other S100 proteins also showed clinical and pathological significance in HNSCC. Overexpression of S100A1 enhances the cancer cell proliferation, migration and lymph node metastasis in cervical cancer (28), breast cancer (29), and hepatocellular carcinoma (31). In contrast, the expression level of S100A1 in HNSCC tissues did not show any significantly change compared with that in normal tissues. S100A2 expression is downregulated in many cancers, and loss of S100A2 expression is associated with poor prognosis (31). Hence, S100A2 may be a tumor-suppressing protein that potentiates p53 by binding to the p53 transactivation domain, presumably contributing to restoring p53 function in cell arrest and apoptosis (55-59). However, S100A2 is upregulated in some cancers and acts as a tumor promotor (35). High S100A16 expression has been found to be significantly associated with poor prognosis in lung cancer (60) and prostate cancer (61). On the contrary,

S100A16 has been shown to be downregulated in HNSCC and to be associated with malignant phenotypes in OSCC. High S100B expression predicts a good OS in patients with ER-negative breast cancer and good distant metastasis-free survival in patients with breast cancer (62). The results in the present study confirmed that S100B is related to lymph node metastasis and has a significant effect on tumor size.

Conclusions

The results herein indicated that high mutation rate of the S100 family was observed in HNSCC. The mRNA expression of S100A1, S100A9, S100A14, and S100A7A was significantly different in HNSCC patients. In addition, the S100 family was significantly associated with EMT-related genes. For clinical value evaluation, multiple functions of the S100 family were demonstrated. For example, S100A1, S100A7, S100A8, S100A9, S100A13, S100A14, and S100A16 were observed to significantly correlate with initiation, lymph node metastasis, and lymphovascular invasion of HNSCC. In the present study, S100A4, S100A10, and S100A13 may act as prognostic markers. A prognostic signature of eight S100 genes, including *S100A1–A4*, *S100A8*, *S100A10*, *S100A12*, and *S100A13*, moderately predicted the prognosis of HNSCC patients. Considering the heterogeneity of S100 family members, further investigations are necessary to explore and verify the underlying molecular mechanisms.

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Footnote

Reporting Checklist: The authors have completed the STREGA reporting checklist. Available at <https://tcr.amegroups.com/article/view/10.21037/tcr-22-1353/rc>

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uniform disclosure form (available at <https://tcr.amegroups.com/article/view/10.21037/tcr-22-1353/coif>). The authors have no conflicts of interest to declare.

Ethical Statement: The authors are accountable for all aspects of the work in ensuring that questions related to the accuracy or integrity of any part of the work are appropriately investigated and resolved. The study was conducted in accordance with the Declaration of Helsinki (as revised in 2013).

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Table S1 Full names and biological functions of 19 S100 family members

S100 protein family	Description	Encoded gene	Functions
S100A1	S100 calcium binding protein A1	<i>S100A1</i>	Inhibit microtubule assembly; inhibit protein kinase C-mediated phosphorylation
S100A2	S100 calcium binding protein A2	<i>S100A2</i>	Tumor suppressor
S100A3	S100 calcium binding protein A3	<i>S100A3</i>	High affinity for Zinc; highly expressed in human hair cuticle
S100A4	S100 calcium binding protein A4	<i>S100A4</i>	Motility; invasion; tumor metastasis
S100A5	S100 calcium binding protein A5	<i>S100A5</i>	Higher affinity of Ca^{2+}
S100A6	S100 calcium binding protein A6	<i>S100A6</i>	Stimulate Ca^{2+} dependent insulin release; stimulate prolactin secretion; exocytosis; implicated in melanoma
S100A7	S100 calcium binding protein A7	<i>S100A7</i>	Overexpressed in hyperproliferative skin diseases; antibacterial activity; immunomodulatory activity
S100A8	S100 calcium binding protein A8	<i>S100A8</i>	Antifungal and antibacterial activity; inhibit casein kinase
S100A9	S100 calcium binding protein A9	<i>S100A9</i>	Inhibit casein kinase; associated with the disease cystic fibrosis; antifungal and antibacterial activity
S100A10	S100 calcium binding protein A10	<i>S100A10</i>	exocytosis and endocytosis
S100A11	S100 calcium binding protein A11	<i>S100A11</i>	Motility; invasion; tubulin polymerization; tumor metastasis
S100A12	S100 calcium binding protein A12	<i>S100A12</i>	Signal transduction; modulate various neutrophil activities; antibacterial activity
S100A13	S100 calcium binding protein A13	<i>S100A13</i>	Signal transduction
S100A14	S100 calcium binding protein A14	<i>S100A14</i>	Tumor suppressor; lower in cancerous tissue
S100A16	S100 calcium binding protein A16	<i>S100A16</i>	Promote differentiation of adipocytes
S100B	S100 calcium binding protein B	<i>S100B</i>	Neurite extension; proliferation of melanoma cells, stimulate Ca^{2+} fluxes, inhibit PKC-mediated phosphorylation; inhibit microtubule assembly
S100P	S100 calcium binding protein P	<i>S100P</i>	Associated with prostate cancer
S100Z	S100 calcium binding protein Z	<i>S100Z</i>	Higher affinity of Ca^{2+}
S100A7A	S100 calcium binding protein A7A	<i>S100A7A</i>	Involved in epidermal differentiation and inflammation

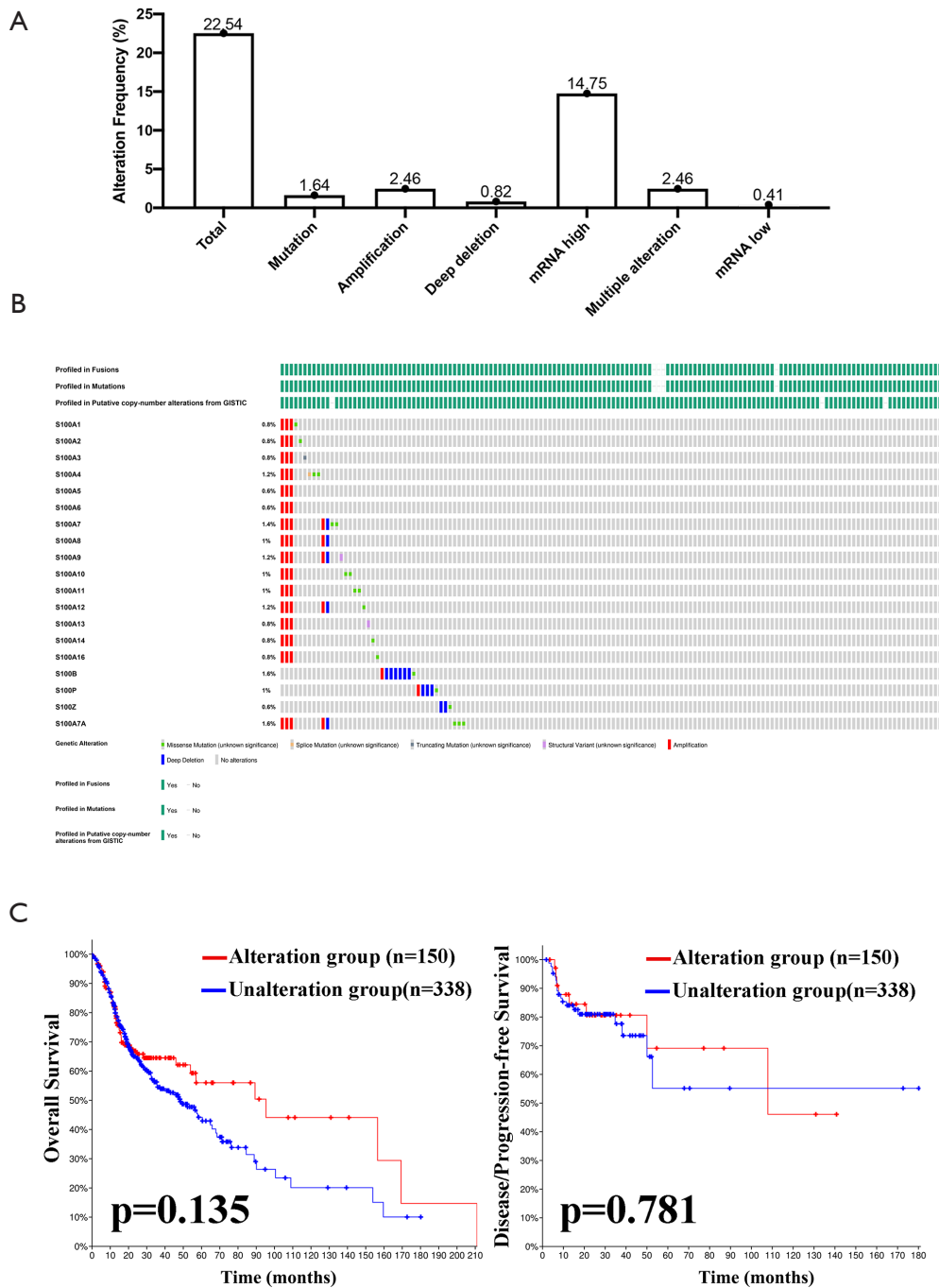


Figure S1 S100s gene mutation analysis in HNSCC. (A,B) S100 genes expression and mutations in 488 HNSCC patients were analyzed using cBioPortal. (C) Correlation between S100s gene mutation and survival in HNSCC patients. mRNA, messenger RNA; GISTIC, genomic identification of significant targets in cancer; HNSCC, head and neck squamous cell carcinoma.

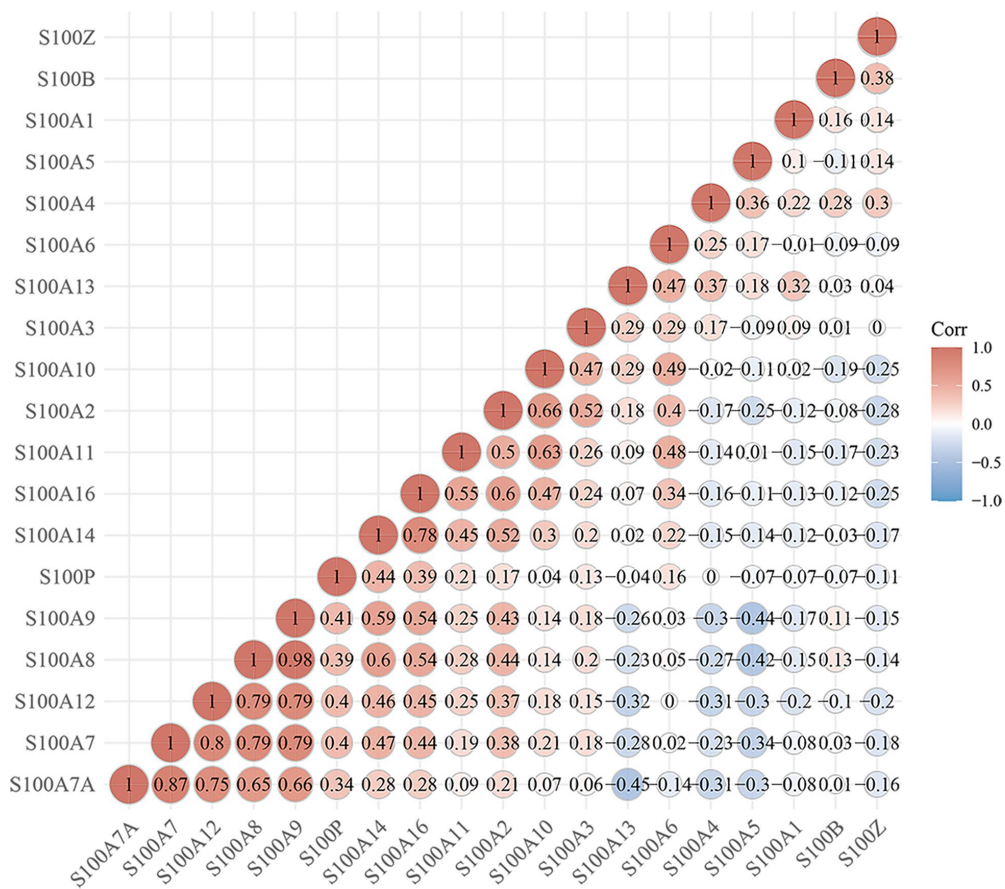


Figure S2 The associations among S100s in HNSCC were analyzed using the cBioPortal database. Darker colors indicate a stronger correlation. Corr, correlation; HNSCC, head and neck squamous cell carcinoma.

Table S2 The average values of high and low mRNA expression level for S100 family members in HNSCC patients

S100 protein family	mRNA expression level	Number of HNSCC patients	Average value	P value
S100A1	High	252	1.038	0.291
S100A1	Low	252	0.313	
S100A2	High	252	12.443	3.105
S100A2	Low	252	10.527	
S100A3	High	252	5.111	1.482
S100A3	Low	252	3.526	
S100A4	High	252	8.349	0.384
S100A4	Low	252	6.949	
S100A5	High	252	1.639	<0.001
S100A5	Low	252	0.527	
S100A6	High	252	11.898	3.247
S100A6	Low	252	10.635	
S100A7	High	252	12.479	0.108
S100A7	Low	252	7.537	
S100A7A	High	252	6.500	<0.001
S100A7A	Low	252	1.759	
S100A8	High	252	13.600	2.930
S100A8	Low	252	10.182	
S100A9	High	252	14.943	5.557
S100A9	Low	252	11.844	
S100A10	High	252	11.219	<0.01
S100A10	Low	252	10.019	
S100A11	High	252	12.768	0.053
S100A11	Low	252	11.927	
S100A12	High	252	7.799	0.235
S100A12	Low	252	3.938	
S100A13	High	252	4.164	3.514
S100A13	Low	252	2.888	
S100A14	High	252	10.978	6.704
S100A14	Low	252	9.182	
S100A16	High	252	10.550	<0.01
S100A16	Low	252	9.468	
S100B	High	252	4.364	<0.001
S100B	Low	252	2.355	
S100P	High	252	8.820	0.141
S100P	Low	252	5.169	
S100Z	High	252	0.229	<0.05
S100Z	Low	252	0.035	

mRNA, messenger RNA; HNSCC, head and neck squamous cell carcinoma.

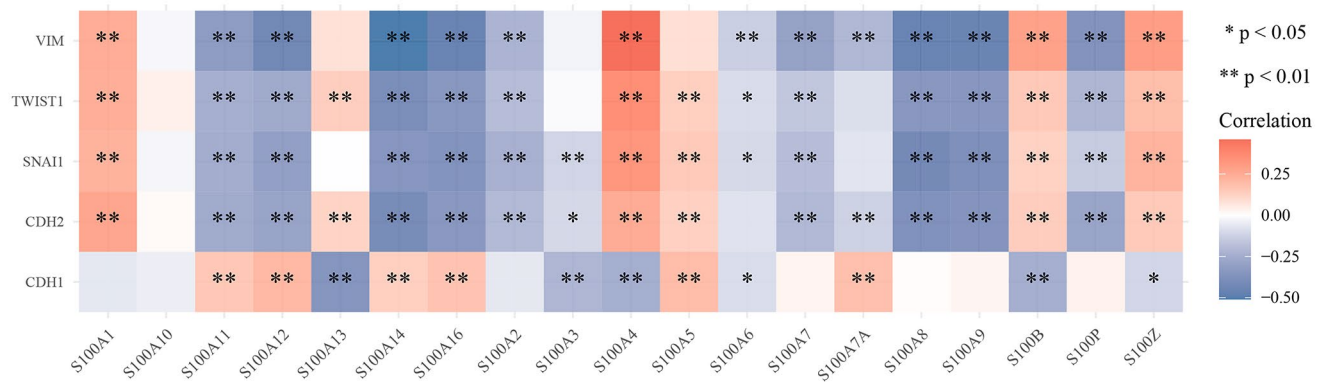


Figure S3 Heatmap of the correlations among five EMT genes and S100 genes in HNSCC. EMT, epithelial-mesenchymal transition; HNSCC, head and neck squamous cell carcinoma.

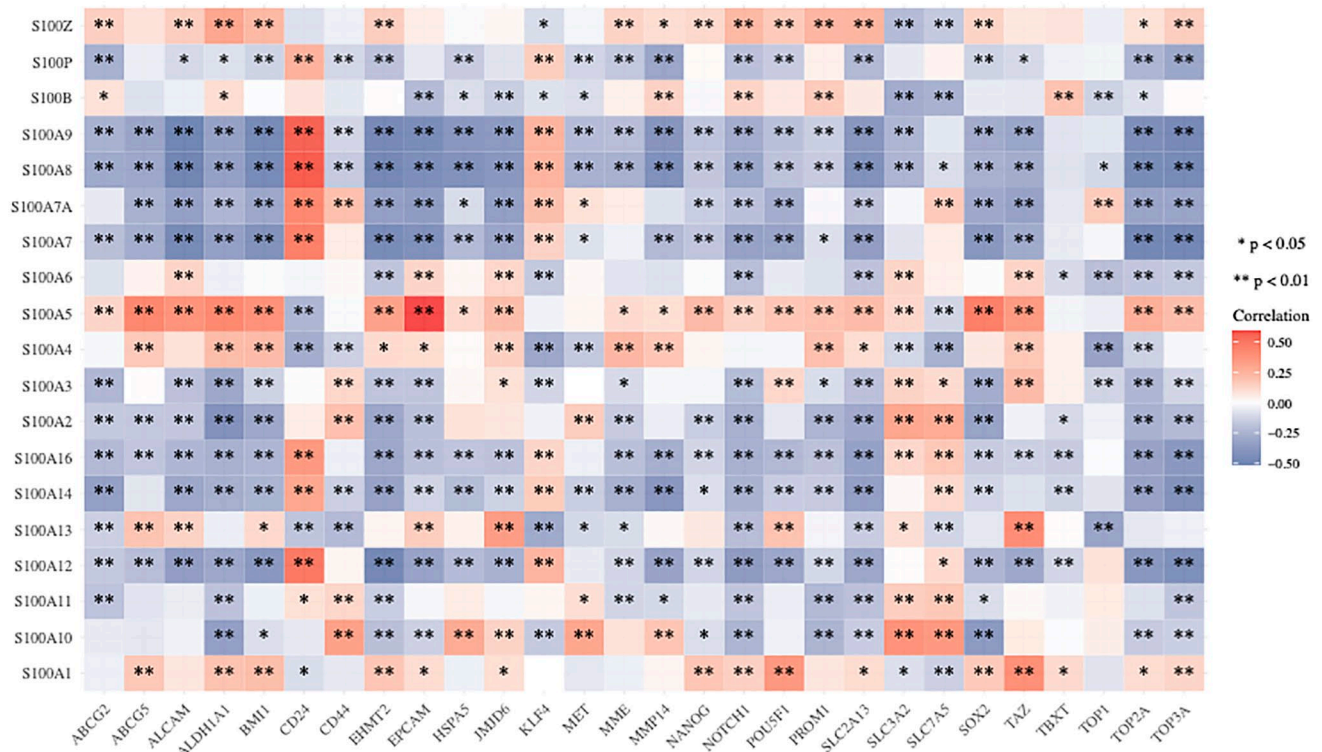


Figure S4 Heatmap of the correlations among CSC-related genes and S100 genes in HNSCC. CSC, cancer stem cell; HNSCC, head and neck squamous cell carcinoma.

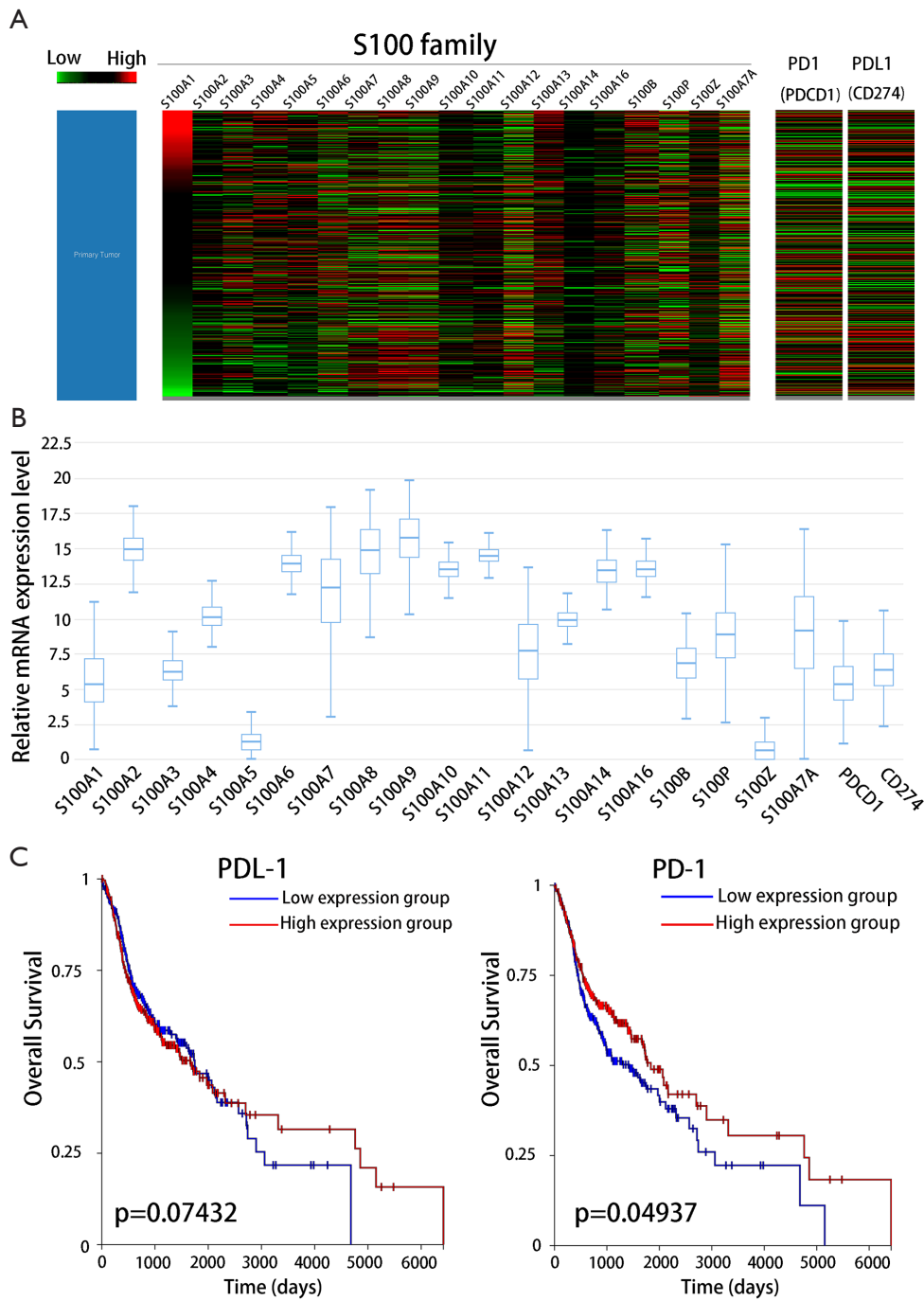


Figure S5 Roles of gene PD-1, PD-L1 in HNSCC. (A) Heatmap of the expression of gene PD-1, PD-L1 and S100 genes in HNSCC. (B) Transcriptional expression of gene PD-1, PD-L1 and S100 genes in HNSCC. (C) Correlation between PD-1, PD-L1 expression and OS in HNSCC patients. PD-1, programmed death 1; PD-L1, programmed death ligand 1; HNSCC, head and neck squamous cell carcinoma; OS, overall survival.