

GNPNATI is a Biomarker That Predicts a Poor Prognosis of Breast Cancer

Yuying Zhou^{1,*}, Wu Xue^{2,*}, Xinyu Meng^{2,*}, Adheesh Bhandari^{2,3,*}, Hanqian Zeng⁴, Rajan KC⁵, Suzita Hirachan⁶, Erjie Xia²

¹Department of Oncology and Hematology, Wenzhou Hospital of Integrated Traditional Chinese and Western Medicine, Wenzhou, Zhejiang, People's Republic of China; ²Department of Breast Surgery, The First Affiliated Hospital of Wenzhou Medical University, Wenzhou, Zhejiang, People's Republic of China; ³Department of Surgery, Breast and Thyroid Unit, Primera Hospital, Kathmandu, Nepal; ⁴Department of Surgical Oncology, Taizhou Hospital of Zhejiang Province Affiliated to Wenzhou Medical University, Linhai, Zhejiang Province, People's Republic of China; ⁵Central Department of Zoology, Tribhuvan University, Kirtipur, Kathmandu, Nepal; ⁶Department of General Surgery, Breast and Thyroid Unit, Tribhuvan University, Teaching Hospital, Kathmandu, Nepal

*These authors contributed equally to this work

Correspondence: Erjie Xia, Department of Breast Surgery, The First Affiliated Hospital of Wenzhou Medical University, Wenzhou, Zhejiang, People's Republic of China, Tel +86 577 5557 8527, Email erjiexia1@126.com; Yuying Zhou, Department of Oncology and Hematology, Wenzhou Hospital of Integrated Traditional Chinese and Western Medicine, Wenzhou, Zhejiang, People's Republic of China, Tel +86 15757194239, Email yuying_ne@163.com

Background: Breast cancer (BC) is increasingly becoming the primary reason for death in women, which sounded the alarm. Thus, finding a novel management target for BC is imminent.

Materials and Methods: The data on gene expression and clinicopathological characteristics were downloaded from The Cancer Genome Atlas (TCGA). The expression of *GNPNATI* in 40 paired breast cancer and adjacent tissues was measured by quantitative real-time polymerase chain reaction (qRT-PCR). Univariate and Multivariate logistic regression methodology was applied to analyze the prognostic factors for lymph node metastasis (LNM). Based on the status of breast cancer-related receptors, patients were distributed into six groups, and then the Kaplan-Meier survival analysis with a Log rank test was applied to investigate the involvement among the expression of *GNPNATI* and overall survival (OS).

Results: We found higher expression of *GNPNATI* was connected with poor survival in breast cancer by COX regulation analysis. GO, KEGG, and GSEA analysis prompted that *GNPNATI* was connected with the defense mechanism of cells, cell proliferation, and division. Immunization infiltration analysis showed that high *GNPNATI* was negatively connected with 16 immunization infiltration cell types and positively connected with four immunization infiltration cell types.

Conclusion: As a whole, our results indicated that *GNPNATI* might be a probable biomarker for diagnosis and prognosis in breast cancer.

Keywords: *GNPNATI*, biomarker, breast cancer, diagnosis, prognosis

Introduction

Breast cancer is one of the most common malignant cancers in the world. There has been an increase in the incidence of breast cancer. The 2020 global cancer statistics report showed that the number of breast cancer patients had surpassed lung cancer in women. New breast cancer cases accounted for 30% of women newly diagnosed with cancer in 2020.^{1,2} It was estimated that there would be 2.3 million new breast cancer cases around the world in 2021. At the same time, for the individual, the probability of individual breast cancer increases with age. If a woman could live to natural death, she would have a 12.9% chance of developing breast cancer.¹ In China, the number of new breast cancer cases also increased from 300,000 to 420,000 from 2015 to 2020.² With the continuous development of genome technology and the advancement of the human genome sequence project, our understanding of the development mechanism of breast cancer has also deepened.³ Based on previous studies, we could find that breast cancer was a heterogeneous disease, characterized by a variety of genomes, gene expression profiles, and molecular markers.^{4,5} According to the expression level of human epidermal growth factor receptor (HER2) and

hormone receptor (HR), breast cancer was divided into three main subtypes of breast cancer: luminal A, luminal B, and HER2+ and basal-like.⁶

In recent years, with the progress of diagnosis and treatment levels, more and more patients have been treated according to the subtypes and individual situations, which greatly prolongs the lifespan of breast cancer patients.⁷ The 5-year overall survival rate was more than 95% for patients in the early stages.⁸ But, the 5-year overall survival rate of advanced breast cancer patients was less than 40%. Therefore, early diagnosis and treatment of breast cancer are very important to improve the patient's survival rate and quality of life.

The glucosamine-phosphate N-acetyltransferase 1 (*GNPNAT1*), also known as *GNAI*, *GNPNAT*, and *GPNAT1*, is a key enzyme gene that promotes the biosynthesis of uridine diphosphate-N-acetylglucosamine and the metabolism of glucose. Feng et al found that *GNPNAT1* was upregulated in NSCLC, and patients with high *GNPNAT1* levels had a poor prognosis. (10.2147/CMAR.S367857) Liu et al found that *GNPNAT1* was upregulated in LUAD and *GNPNAT1* overexpression was correlated with DNA copy amplification, low DNA methylation, and downregulation of hsa-miR-30d-3p ($= -0.17, < 0.001$). *GNPNAT1* expression was linked to B cells, CD4T cells, and dendritic cells. (10.3389/fmolb.2021.605754) In one previous research, *GNPNAT1* was connected with resistance to prostate cancer castration therapy through the PI3K-AKT pathway.⁹ There was also a lot of research showing that *GNPNAT1* was related to the prognostic of lung adenocarcinoma, and the expression level of *GNPNAT1* was connected with the immune regulation of lung adenocarcinoma.^{10–16}

Here, based on The Cancer Genome Atlas (TCGA) dataset and our own dataset, we found that the expression level of *GNPNAT1* in tumors was significantly higher than in corresponding control tissues in breast cancer and higher expression of *GNPNAT1* was connected with poor survival in breast cancer by COX regulation analysis. In the meanwhile, *GNPNAT1* was connected with the defense mechanism of cells, cell proliferation, and division through GO, KEGG, and GSEA analysis. Immunization infiltration analysis showed that high *GNPNAT1* was negatively connected with 16 immunization infiltration cell types and positively connected with four immunization infiltration cell types. This study showed that *GNPNAT1* might be a probable biomarker for diagnosis and prognosis in breast cancer.

Materials and Methods

Ethics: Our experimental protocols have been granted by the Ethical Review Committee of the First Affiliated Hospital of Wenzhou Medical University (Approval No. 2012–57), and informed consent was obtained from each patient before their tissues were used.

Patients and Breast Tissue Samples Collection of Validated Set

Forty patients, who were diagnosed as primary breast cancer patients by two pathologists at least, were selected. All patients had complete baseline clinical data. With written informed consent, we collected the tumor tissues and non-neoplastic breast tissues of the 40 breast cancer patients in operation. After resection, samples were put in liquid nitrogen as quickly as possible. If the samples were not used for RNA extraction immediately, they would be stored in a -80°C refrigerator.

Cell Lines and Cell Culture

In this investigation, our proposed hypothesis was validated using a range of breast cancer cell lines, namely MDA-MB-231, MCF-7, MDA-MB-463, MDA-MB-468, BT-474, MDA-MB-453, T47D, along with a human mammary epithelial cell line, MCF-10A. All cell lines were procured from the Cell Bank of the Shanghai Chinese Academy of Sciences in Shanghai, China.

T47D, MCF-7, and MDA-MB-231 cell lines were cultured in DMEM medium (Gibco, Invitrogen, Carlsbad, CA, USA), supplemented with 10% Fetal Bovine Serum (Gibco) and 1% penicillin/streptomycin (Solarbio, Beijing, China). The incubation conditions included an atmosphere of 5% CO₂ at a temperature of 37°C. For BT-474 and MDA-MB-468 cell lines, RPMI 1640 medium (Gibco) was employed, enriched with 10% Fetal Bovine Serum and 1% penicillin/streptomycin. The cells were incubated under conditions of 5% CO₂ and 37°C. MCF-10A cells were cultured in DMEM-F12 medium (Gibco) supplemented with 10% Fetal Bovine Serum and 1% penicillin/streptomycin. The incubation conditions included an atmosphere of 5% CO₂ at 37°C.

MDA-MB-453 and MDA-MB-463 cell lines were cultured in L-15 medium (Gibco) containing 10% Fetal Bovine Serum and 1% penicillin/streptomycin. The incubation was carried out at 37°C without the presence of CO₂.

MCF10A was cultured in DMEM-F12 medium (Gibco) at 37 °C under the atmosphere with 5% CO₂, which contains 10% fetal bovine serum (Gibco).

RNA Extraction, Reverse Transcription, and RT-qPCR

TRIzol (Thermo Fisher Scientific, Waltham, MA, USA) was used to isolate RNA from cells and 40 pairs of tissue. Then purity and concentration of RNA would be measured by spectrophotometric value and A260/A280 ratio. ReverTra Ace qPCR RT Kit (Toyobo, Osaka, Japan) was used to reverse transcription in an efficient ratio (1000ng RNA per 20μL system reacting). And an SYBR Premix Ex Taq II kit (RR820A, TaKaRa, Dalian, China) was used for Real-time reverse transcription-quantitative polymerase chain reaction (qRt-PCR) on an Applied Biosystems 7500 Real-Time PCR System. The mRNA expression compared with the GAPDH expression was calculated by the $2^{-\Delta\Delta C_t}$ equation. All procedures were performed according to standard instructions. All experiments were repeated at least three times. We bought all the primers from Sangon Biotech (Shanghai, China). The sequences of the primer are listed below: *GPNATI*: 5'-ATCCATTCTGTGCTAAGAGAG-3' (forward) and 5'-ATCCATTCTGTGCTAAGAGAG-3' (reverse). Each assay was performed in triplicate, and the steps were performed by standard description.

Characteristics Analysis

The normalized RNA-seq data and corresponding clinical information were obtained from The Cancer Genome Atlas (TCGA) genomic dataset (<https://cancergenome.nih.gov/>). The format of RNAseq was transformed from Fragments Per Kilobase per Million (FPKM) to transcripts per million reads (TPM) and the log₂ conversion. The clinicopathologic factors of the validated cohort were collected from The First Affiliated Hospital of Wenzhou Medical University (Wenzhou, Zhejiang, People's Republic of China). The *GPNATI* high expression set and the low expression set were distinguished by the median of whole TCGA breast cancer samples' *GPNATI* expression level. We analyzed the correlation between *GPNATI* expression and clinicopathologic factors by the based package of R software (3.6.3 Version).

Gene Expression Analysis

The different expression of *GPNATI* between normal and tumor tissues for diverse malignant tumors and different cancer subtypes in the TCGA dataset was output by the “Gene DE” module of Tumor Immune Estimation Resource, Version 2 (TIMER2, <http://timer.cistrome.org/>). The subtypes of breast cancer in the TCGA database which had not have enough normal tissues to make statistics analysis were supplemented with corresponding normal tissues of the Genotype-Tissue Expression (GTEx) database by the “Expression analysis -Box Plots” module of the Gene Expression Profiling Interactive Analysis, Version 2 (GEPIA2, <http://gepia.cancer-pku.cn/>). The visualization of *GPNATI* expression in different clinical subgroups was implemented by the ggplot2 package (3.3.3 Version) of R software (3.6.3 Version). GraphPad Prism software (7.0 Version) was used for analyzing the different expressions of the validated cohort.

ROC Curve and Survival Analysis

PROC package (1.17.0.1 Version) and ggplot2 package (3.3.3 Version) of R software (3.6.3 Version) were used to draw the ROC curve. We obtained survival maps and survival plots from GEPIA2. Statistical analysis of the association between *GPNATI* and survival was examined by the COX regression model using the survival package (3.2-10 Version) of R software (3.6.3 Version).

Nomogram and Prognostic Model

We constructed a nomogram to predict the probability that one breast cancer patient can live one year, three years, and five years based on multivariate Cox regression analysis. RMS package (6.2-0 Version) and survival package (3.2-10 Version) of R software (3.6.3 Version) were performed as tools that draw this nomogram. The c-index was the evaluation index that judged the nomogram's concordance.

Immune Infiltration Analysis

GSVA package (1.34.0 Version) of R software (3.6.3 Version) was used for immune infiltration analysis. The algorithm used was the ssGSEA (single-sample Gene Set Enrichment Analysis) method. Spearman correlation coefficients were used to evaluate the connection between *GNPNATI* expression and immune infiltration.

The Genetic Alteration Analysis

The alteration characteristics of *GNPNATI*, which contained mutation type, alteration frequency, and copy number alteration, were analyzed by cBioPortal (<https://www.cbioportal.org/>) web. In this part, the mutated sites of *GNPNATI* can be shown in the 3D protein structure model. The data of cBioPortal was from the TCGA database.

GNPNATI-Binding Proteins and *GNPNATI*-Correlated Genes Analysis

The STRING tool (<https://string-db.org/>) was used to download the list of the most significant 50 proteins that bind to *GNPNATI*, with support from experimental evidence. Additionally, the top 100 genes correlated with *GNPNATI* were obtained from GEPIA2. The visualization of these top 100 *GNPNATI*-correlated genes was generated using the Tumor Immune Estimation Resource 2 version (TIMER2, <http://timer.cistrome.org/>) in combination with the ggplot2 package (version 3.3.3) in R software (version 3.6.3). Furthermore, the ggplot2 package (version 3.3.3) in R software (version 3.6.3) was employed to create scatter plots for the top 5 *GNPNATI*-correlated genes, as well as a Venn diagram.

Functional Enrichment Analysis

Cluster Profiler package (version 3.14.3) along with org.Hs.eg.db package (version 3.10.0) within R software (version 3.6.3) were utilized for conducting Gene Ontology (GO) enrichment analysis as well as Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway analysis. The information for Gene Set Enrichment Analysis (GSEA) was sourced from MSigDB Collections (<https://www.gsea-msigdb.org/gsea/msigdb/index.jsp>), and the implementation of GSEA was carried out using the ggplot2 package (version 3.3.3) in R software (version 3.6.3). Protein-protein interaction (PPI) network analysis was performed using the STRING tool (<https://string-db.org/>).

Statistical Analysis

All experiments were conducted in triplicate. The distribution of data was assessed using the Shapiro–Wilk test. If the data followed a normal distribution, they were subjected to analysis using Student's *t*-test. Conversely, if the data did not adhere to a normal distribution, analysis was performed using either the Wilcoxon test or the Mann–Whitney test. Comparisons between two groups were assessed using the Student's *t*-test, while multiple group comparisons were analyzed using one-way ANOVA.

For examining the relationship between *GNPNATI* expression and clinicopathological features, a Chi-square test and logistic regression were employed. To evaluate the predictive value of *GNPNATI* expression for the prognosis of breast cancer patients, Cox regression analysis was employed.

All statistical analyses were conducted using SPSS 25.0 software, GraphPad Prism software (version 7.0), and R software (version 3.6.3). Statistical significance was considered at a threshold of $P < 0.05$. Data visualization was achieved using R software (version 3.6.3) and GraphPad Prism software (version 7.0).

Results

Baseline Characteristics of Patients

There were two cohorts (TCGA cohort and local verified cohort) in this study.

In the TCGA cohort, there were a total of 1083 breast cancer patients with the required clinical features downloaded from the TCGA database. The baseline characteristics of the *GNPNATI* high expression set and the low expression set in the TCGA cohort were shown in Table 1; a comparison of proportion between these sets was examined by the chi-square test. The baseline characteristics of our local verified cohort are listed in Table 2.

Table 1 Baseline Characteristics of the *GNPNAT1* High Expression Set and the Low Expression Set in the TCGA Cohort

Clinicopathologic Factors	High Expression	Low Expression	P value
Race			< 0.001***
Asian	23	37	
White	373	380	
Others	119	62	
Age (years)			0.411
<=60	293	308	
>60	248	234	
Histological type			< 0.001***
Infiltrating Ductal Carcinoma	356	416	
Infiltrating Lobular Carcinoma	128	77	
PR status			< 0.001***
Negative	208	134	
Indeterminate	1	3	
Positive	311	377	
ER status			< 0.001***
Negative	162	78	
Indeterminate	0	2	
Positive	359	434	
HER2 status			0.005**
Negative	294	264	
Indeterminate	5	7	
Positive	60	97	
Menopause status			0.074
Pre	99	130	
Peri	20	20	
Post	365	338	
T stage (AJCC7)			0.640
T1	137	140	
T2	318	311	
T3	72	67	
T4	14	21	
N stage (AJCC7)			0.013*
N0	283	231	
N1	168	190	
N2	47	69	
N3	37	39	
M stage (AJCC7)			1.000
M0	438	464	
M1	10	10	
Pathologic stage (AJCC7)			0.103
Stage I	98	83	
Stage II	323	296	
Stage III	106	136	
Stage IV	10	8	
Total	541	542	

Notes: *p-value < 0.05, **p-value < 0.01, ***p-value < 0.001.

Abbreviations: *GNPNAT1*, glucosamine-phosphate N-acetyltransferase 1; AJCC7, American Joint Committee on Cancer 7th edition.

Table 2 Baseline Characteristics of the *GNPNAT1* High Expression Set and the Low Expression Set in the Validated Cohort

Clinicopathologic Factors	High Expression	Low Expression
Age (years)		
<=60	11	15
>60	7	7
PR status		
Negative	18	18
Positive	0	4
ER status		
Negative	17	16
Positive	1	6
HER2 status		
Negative	16	11
Positive	2	11
Menopause status		
Pre	6	13
Post	12	9
T stage (AJCC7)		
T1	7	13
T2	10	7
T3	1	2
N stage (AJCC7)		
N0	13	13
N1	5	9
M stage (AJCC7)		
M0	18	22
Pathologic stage (AJCC7)		
Stage I	4	5
Stage II	11	15
Stage III	3	2
Total	18	22

Abbreviations: *GNPNAT1*, glucosamine-phosphate N-acetyltransferase 1; AJCC7, American Joint Committee on Cancer 7th edition.

GNPNAT1 is Overexpressed in Breast Cancer

In this study, we aimed to explore the carcinogenesis of human *GNPNAT1* in breast cancer. TIMER2 was applied to analyze the expression of *GNPNAT1* in breast cancer of TCGA. We found that the expression level of *GNPNAT1* in tumors was significantly higher than in corresponding control tissues in breast cancer ($P < 0.001$) (Figure 1A). However, the subtypes of breast cancer in TCGA did not have enough normal tissues to make a statistical analysis. To assess the expression distinction of *GNPNAT1* in different breast cancer subtypes, the normal tissues of the GTEx dataset were used as controls. We further confirmed that the expression of *GNPNAT1* in tumors was significantly upregulated in basal-like ($P < 0.05$), Her2+ ($P < 0.05$), Luminal A ($P < 0.05$), and Luminal B ($P < 0.05$) subtype (Figure 1B). To further evaluate the expression difference of *GNPNAT1* between the normal and tumor tissues of breast cancer, we detected the expression level of *GNPNAT1* in 40 pairs of tumor samples and nearby normal breast tissues via RT-qPCR. This result was consistent with the TCGA data, and a heat map was made to describe the difference in our verified cohort ($P < 0.0001$) (Figure 1C).

The Connection Between the Expression of *GNPNAT1* and Clinical Factors

To examine the part of *GNPNAT1* taking in breast cancer, we analyzed the association between the expression level of *GNPNAT1* and clinical factors. The whole patients were segmented into two sets (high expression group and low

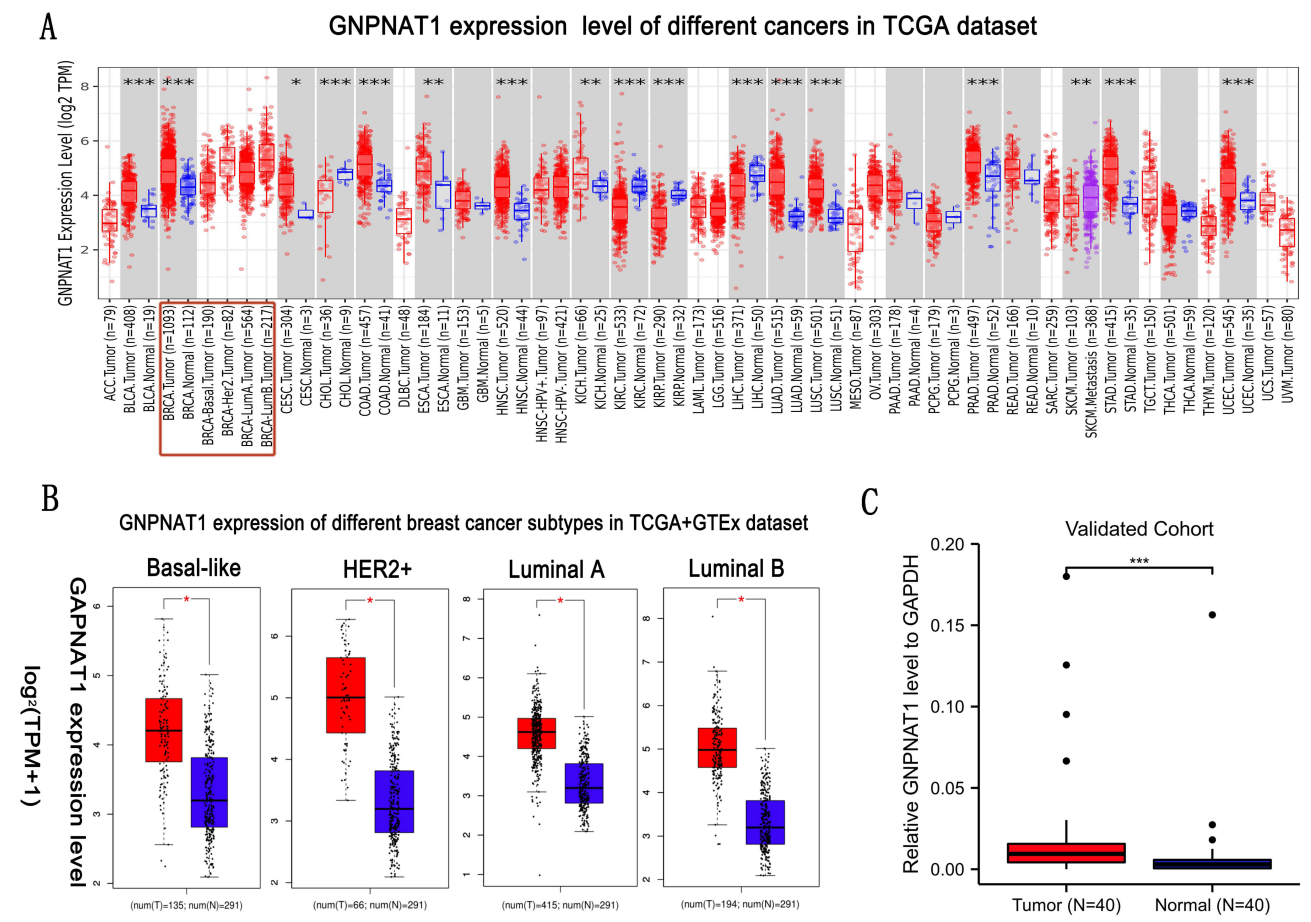


Figure 1 The expression level of *GNPAT1* in breast cancer. **(A)** The *GNPAT1* expression level of different cancers in the TCGA dataset. **(B)** *GNPAT1* expression of different breast cancer subtypes in TCGA+GTEX dataset. **(C)** *GNPAT1* expression in breast cancer invalidated cohort. * $P < 0.05$, ** $p < 0.01$, *** $p < 0.001$.

expression group), according to the median value. Then, we analyzed the connection between the expression of *GNPAT1* and clinical factors in the TCGA cohort by univariate logistic regression analysis and found that race ($P = 0.033$), Menopause status ($P = 0.032$), Histological type ($P < 0.001$), PR status ($P < 0.001$), ER status ($P < 0.001$), HER2 status ($P = 0.001$), N stage ($P = 0.003$), pathologic stage ($P = 0.025$) was different in the two sets in TCGA cohort (Table 3, Figure 2). There were also several other conclusions from the univariate logistic regression analysis in the TCGA cohort as follows: Asian breast cancer patients tended to express higher expression levels of *GNPAT1* than other races; Peri-menopausal and per-menopausal patients were likely to express higher expression levels of *GNPAT1* than pre-menopausal breast cancer patients; Infiltrating ductal histological type breast cancer patients were inclined to express higher expression level of *GNPAT1* than infiltrating ductal type; Breast cancer patients whose PR, ER and HER2 status were positively expressed a higher level of *GNPAT1* than negative; Similarly, Breast cancer patients with higher N or pathological stage also express higher expression level of *GNPAT1*.

The analysis of the expression difference of *GNPAT1* expression levels in different breast cell lines also verified that the expression of *GNPAT1* in breast cancer cell lines (MDA-MB-231, MCF-7, MDA-MB-463, MDA-MB-468, BT-474, MDA-MB-453, and T47D) was higher than normal breast cell line (MCF-10A) (Figure 3A).

Diagnostic Value of the Expression of *GNPAT1* in Breast Cancer

In this study, to evaluate the diagnostic value of *GNPAT1* expression in breast cancer, a ROC curve analysis was conducted. As shown in Figure 3B, the Area Under the Curve (AUC) of *GNPAT1* was 0.756, which indicated a high diagnostic value in distinguishing tumor and normal.

Table 3 The Correlation Between *GNPNAT1* Expression and Clinicopathologic Factors in the TCGA Cohort

Characteristics	Total (N)	OR (95% CI)	P value
Race (Others vs Asian)	994	0.558 (0.323–0.948)	0.033*
Age (>60 vs <=60)	1083	0.898 (0.706–1.141)	0.377
Menopause status (Post vs Pre & Peri)	972	0.735 (0.553–0.974)	0.032*
Histological type (Lobular vs Ductal)	977	0.515 (0.374–0.705)	<0.001***
PR status (Positive vs Negative)	1030	1.882 (1.447–2.454)	<0.001***
ER status (Positive vs Negative)	1033	2.511 (1.858–3.416)	<0.001***
HER2 status (Positive vs Negative)	715	1.800 (1.257–2.596)	0.001**
T stage (T3&4 vs T1&2)	1080	1.032 (0.746–1.429)	0.848
N stage (N1&2&3 vs N0)	1064	1.449 (1.138–1.846)	0.003**
M stage (M1 vs M0)	922	0.944 (0.384–2.322)	0.899
Pathologic stage (III&IV vs I&II)	1060	1.379 (1.042–1.829)	0.025*

Notes: *p-value< 0.05, **p-value<0.01, ***p-value<0.001. The stages were graded according to AJCC7.
Abbreviations: *GNPNAT1*, glucosamine-phosphate N-acetyltransferase 1; AJCC7, American Joint Committee on Cancer 7th edition.

The Connection Between the Expression of *GNPNAT1* and Survival

To analyze the connection between *GNPNAT1* and survival, a Kaplan-Meier analysis was made. Univariate Cox regression analysis for overall survival indicated that higher expression of *GNPNAT1* was connected with poor overall survival (P=0.006, hazard ratio [HR]=1.57, 95% CI=1.137–2.168) (Table 4). We found that higher *GNPNAT1* expression, T stage, N stage, M stage, pathologic stage, age, and menopause status were correlated with overall survival (Table 4). The univariate COX regression analysis for disease-free survival also demonstrated a similar result that higher expression

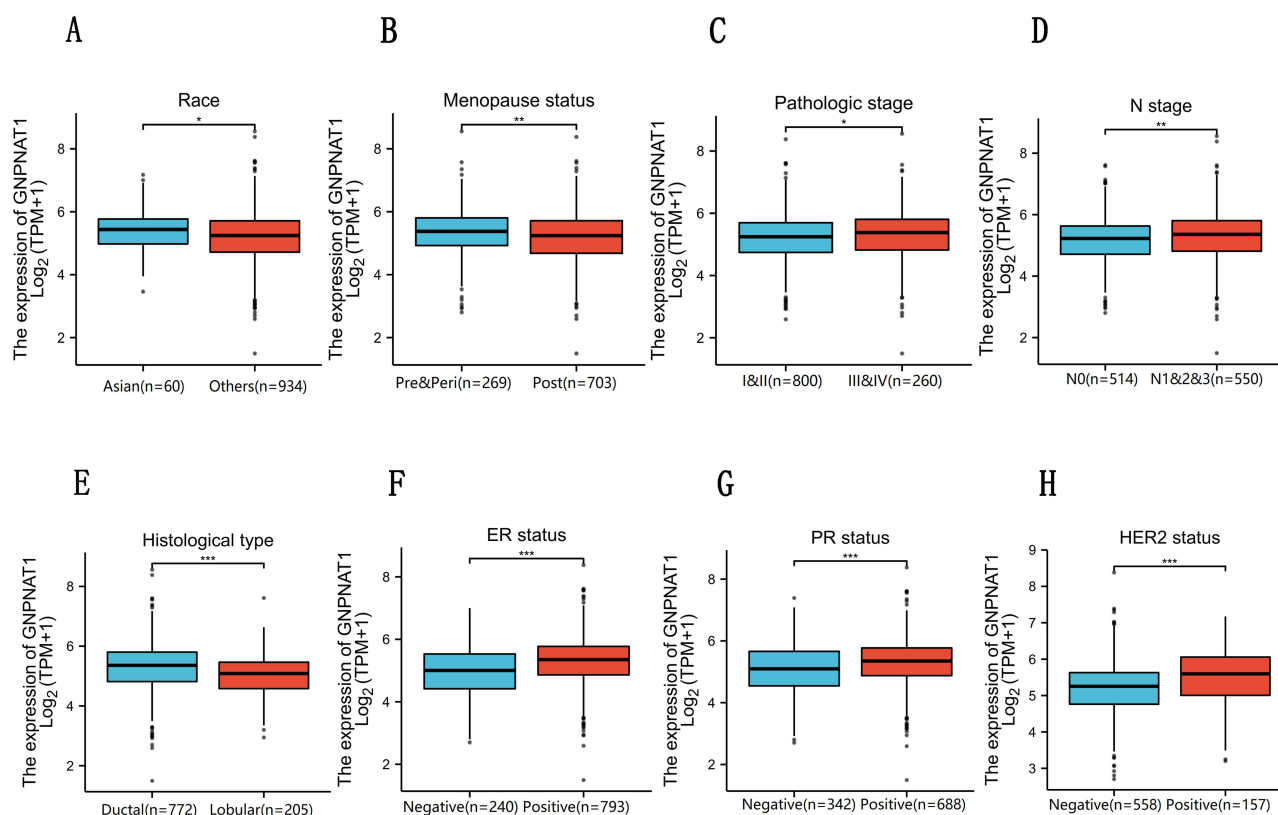


Figure 2 (A–H) *GNPNAT1* expression level in Race, Menopause status, Pathological stage, N stage, Histological type, ER status, PR status, and HER2 status based on different clinical features. *P<0.05, **p<0.01, ***p<0.001.

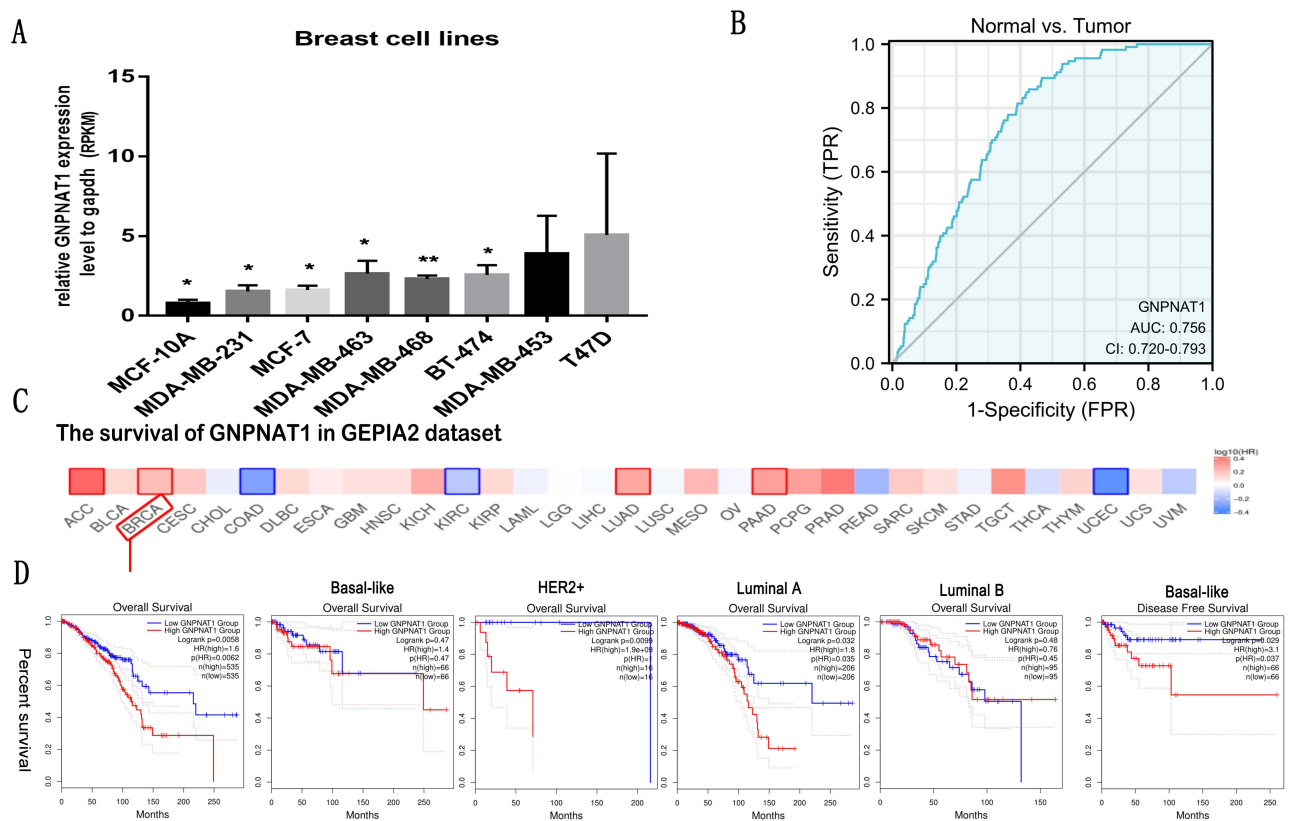


Figure 3 Diagnostic value of the expression of *GNPNAT1* and the correlation between *SND1* gene expression and the survival prognosis of cancers in TCGA. **(A)** The expression level of *GNPNAT1* in different breast cell lines. **(B)** ROC curve for differentiating normal people and breast cancer patients. **(C and D)** The survival map **(C)** and survival curves **(D)** of *GNPNAT1* in breast cancer from the GEPIA2 dataset. * $P < 0.05$, ** $p < 0.01$.

of *GNPNAT1* was connected with poor overall survival ($P = 0.042$, hazard ratio [HR] = 1.564, 95% CI = 1.016–2.408) (Table 5). Then, to verify overexpression of *GNPNAT1* was an independent risk factor for the overall survival of breast cancer patients, a multivariate analysis was made. Because the number of people whose M stage was M1 was too small to perform as an impact factor for multivariate COX regression analysis, we removed the M stage from multivariate COX

Table 4 Univariate COX Regression Analysis for Overall Survival in the TCGA Cohort

Characteristics	Total (N)	HR (95% CI)	P value
T stage (T3&4 vs T1&2)	1079	1.608 (1.110–2.329)	0.012*
N stage (N1&2and3 vs N0)	1063	2.239 (1.567–3.199)	<0.001***
M stage (M1 vs M0)	922	4.254 (2.468–7.334)	<0.001***
Pathologic stage (III&IV vs I&II)	1059	2.391 (1.703–3.355)	<0.001***
Race (Others vs Asian)	993	1.362 (0.432–4.289)	0.598
Age (>60 vs ≤60)	1082	2.020 (1.465–2.784)	<0.001***
Histological type (Lobular vs Ductal)	977	0.827 (0.526–1.299)	0.410
PR status (Positive vs Negative)	1029	0.732 (0.523–1.024)	0.068
ER status (Positive vs Negative)	1032	0.712 (0.495–1.023)	0.066
HER2 status (Positive vs Negative)	715	1.593 (0.973–2.609)	0.064
Menopause status (Post vs Pre & Peri)	971	2.348 (1.428–3.860)	<0.001***
<i>GNPNAT1</i> (High vs Low)	1082	1.570 (1.137–2.168)	0.006**

Notes: * p -value < 0.05, ** p -value < 0.01, *** p -value < 0.001. The stages were graded according to AJCC7.

Abbreviations: *GNPNAT1*, glucosamine-phosphate N-acetyltransferase 1; AJCC7, American Joint Committee on Cancer 7th edition.

Table 5 Univariate COX Regression Analysis for Disease Free Survival in the TCGA Cohort

Characteristics	Total (N)	HR (95% CI)	P value
T stage (T3&4 vs T1&2)	1059	1.902 (1.174–3.081)	0.009**
N stage (N1&2and3 vs N0)	1044	3.797 (2.222–6.489)	<0.001***
M stage (M1 vs M0)	903	7.454 (3.988–13.931)	<0.001***
Pathologic stage (III&IV vs I&II)	1041	3.519 (2.274–5.444)	<0.001***
Race (Others vs Asian)	974	0.804 (0.252–2.560)	0.712
Age (>60 vs ≤60)	1062	1.445 (0.941–2.219)	0.093
Histological type (Lobular vs Ductal)	958	0.471 (0.226–0.982)	0.045*
PR status (Positive vs Negative)	1010	0.519 (0.334–0.807)	0.004**
ER status (Positive vs Negative)	1013	0.559 (0.351–0.891)	0.015*
HER2 status (Positive vs Negative)	704	1.477 (0.740–2.948)	0.269
Menopause status (Post vs Pre & Peri)	961	1.560 (0.871–2.794)	0.135
<i>GNPNAT1</i> (High vs Low)	1062	1.564 (1.016–2.408)	0.042*

Notes: *p-value< 0.05, **p-value<0.01, ***p-value<0.001. The stages were graded according to AJCC7.

Abbreviations: *GNPNAT1*, glucosamine-phosphate N-acetyltransferase 1; AJCC7, American Joint Committee on Cancer 7th edition.

regression analysis. The results of multivariate analysis for overall survival showed that high *GNPNAT1* expression was an independent risk factor for overall survival of breast cancer patients (P=0.046, hazard ratio [HR]=1.422, 95% CI=1.006–2.010) (Table 6). The survival curves of *GNPNAT1* in the GEPIA2 dataset also demonstrated the same result (Figure 3C and D). Subgroup analysis according to different subtypes also showed similar consequences, that HER2+ (P=0.0099) and Luminal A (P=0.032) subtypes of breast cancer patients' overall survival time was connected with *GNPNAT1* expression level. Although the basal-like subtype was not significantly associated with overall survival, it was an independent risk factor for disease-free survival of breast cancer patients (P=0.029). Therefore, we constructed a nomogram to predict the 1-year, three-year, and five-year survival probability of breast cancer patients (C-index=0.663, 95% CI=0.633–0.693) (Figure 4).

Correlations Between the Expression of *GNPNAT1* Expression and Immune Infiltration

As shown in Table 7 and Figure 5, in different immune cell types, TFH, Tem, aDC, NK D56bright cells, Treg, T cells, Neutrophils, Th1 cells, iDC, NK CD56dim cells, B cells, DC, NK cells, Cytotoxic cells, CD8 T cells, and pDC were negatively connected with the expression level of *GNPNAT1*. Eosinophils, TCM, T helper cells, and Th2 cells were prominently positively connected with the expression level of *GNPNAT1*.

The analysis of the correlation between *GNPNAT1* and some famous immune checkpoints is shown in Figure S1.

Table 6 Multivariate COX Regression Analysis for Overall Survival in the TCGA Cohort

Characteristics	Total (N)	HR (95% CI)	P value
T stage (T3&4 vs T1&2)	1079	1.000 (0.609–1.643)	0.999
N stage (N1&2and3 vs N0)	1063	1.562 (1.015–2.403)	0.043*
Pathologic stage (III&IV vs I&II)	1059	1.760 (1.057–2.930)	0.030*
<i>GNPNAT1</i> (High vs Low)	1082	1.422 (1.006–2.010)	0.046*

Notes: *p-value< 0.05. The stages were graded according to AJCC7.

Abbreviations: *GNPNAT1*, glucosamine-phosphate N-acetyltransferase 1; AJCC7, American Joint Committee on Cancer 7th edition.

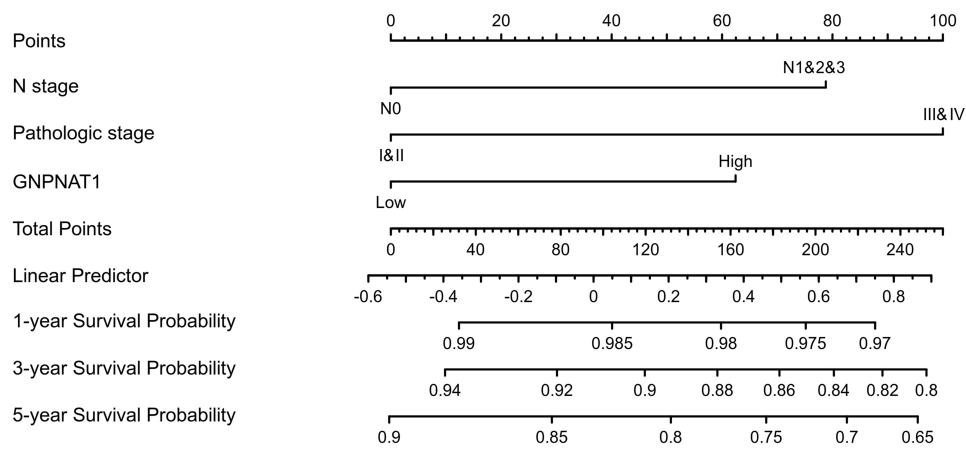


Figure 4 A nomogram for predicting the 1-year, 3-year, and five-year survival probability of breast cancer patients.

Genetic Alteration of *GNPNAT1*

As shown in **Figures 6A and D**, the most common mutation of breast cancer was amplification, while the most frequent mutations in whole tumors were amplification and mRNA high. This conclusion was confirmed by the previous results

Table 7 Connection Between the Expression Level of *GNPNAT1* and the Immune Infiltration in the Tumor Microenvironment

Immune Cell	Spearman Correlation	P value
aDC	-0.091	0.003**
B cells	-0.147	<0.001***
CD8 T cells	-0.243	<0.001***
Cytotoxic cells	-0.241	<0.001***
DC	-0.185	<0.001***
Eosinophils	0.149	<0.001***
iDC	-0.128	<0.001***
Macrophages	-0.038	0.208
Mast cells	0.022	0.471
Neutrophils	-0.124	<0.001***
NK CD56bright cells	-0.109	<0.001***
NK CD56dim cells	-0.143	<0.001***
NK cells	-0.187	<0.001***
pDC	-0.417	<0.001***
T cells	-0.122	<0.001***
T helper cells	0.305	<0.001***
TCM	0.270	<0.001***
Tem	-0.090	0.003**
TFH	-0.064	0.034*
Tgd	0.014	0.644
Th1 cells	-0.127	<0.001***
Th17 cells	-0.002	0.939
Th2 cells	0.353	<0.001***
TReg	-0.119	<0.001***

Notes: *p-value< 0.05, **p-value<0.01, ***p-value<0.001.

Abbreviations: aDC, activated dendritic cell; DC, dendritic cell; iDC, immature dendritic cell; Macrophages; Mast cells; pDC, Plasmacytoid dendritic cell; TCM, T central memory; Tem, T effector memory; Tfh, T follicular helper; Tgd, T gamma delta; Treg, T regulatory cell.

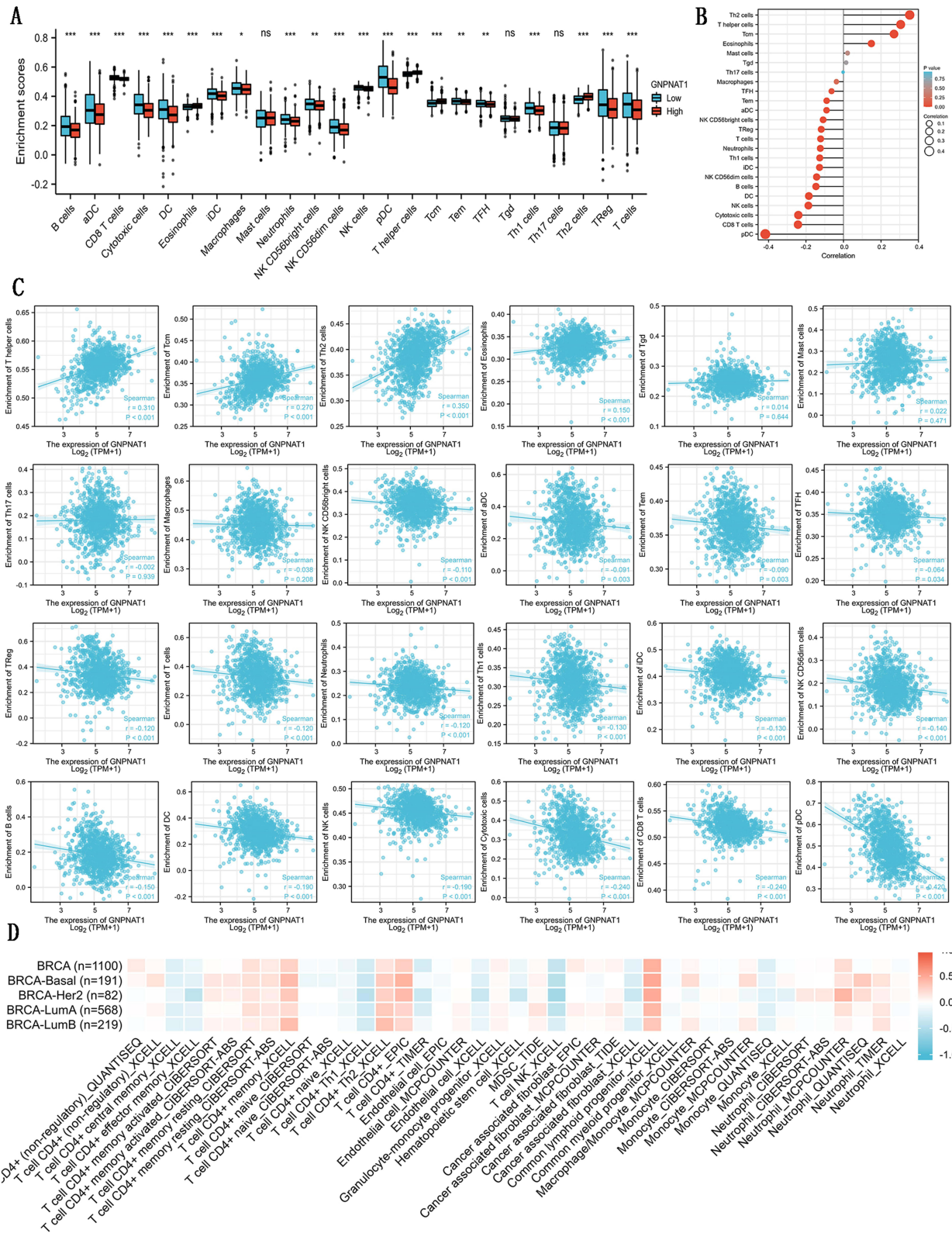


Figure 5 Correlations between the expression of *GNPNAT1* expression and immune infiltration. **(A)** The bar graph is about the immune infiltration level of different immune infiltration cells. **(B)** The lollipop figure is about the immune infiltration level of different immune infiltration cells. **(C)** The scatter diagrams about the immune infiltration level of different immune infiltration cells. **(D)** The heatmap about the correlation between different immune infiltration cells and breast cancer. * $P < 0.05$, ** $p < 0.01$, *** $p < 0.001$.

Table 8 The Basic Information of IHC Slice

Tissue Type	ID	Age	Gender
Normal	2773	23	Female
Tumor	2565	51	Female

catabolic, monosaccharide catabolic process (Figure 10A). The immunohistochemistry (IHC) from the Human Protein Atlas database also verified that *GNPNATI* protein was over-expressive in breast tumors (Figure 10B).

GNPNATI-Related Signaling Pathways Obtained by GSEA

To identify the mainly *GNPNATI*-related signaling pathways that are activated in breast cancer, a GSEA analysis was done (Figure 11). And we found several significant *GNPNATI*-related signaling pathways. In this study, we drew the top four pathways, including REACTOME MITOTIC TELOPHASE CYTOKINESIS, WP OMEGA9 FA SYNTHESIS, REACTOME COHESIN LOADING CHROMATIN, and REACTOME ESTABLISHMENT OF SISTER CHROMATID COHESION.

Discussion

As one of the most common malignant tumors in the world, the incidence of breast cancer is gradually increasing and has become the highest incidence of female cancers.^{1,2} Breast cancer is a highly heterogeneous disease, exhibiting a variety

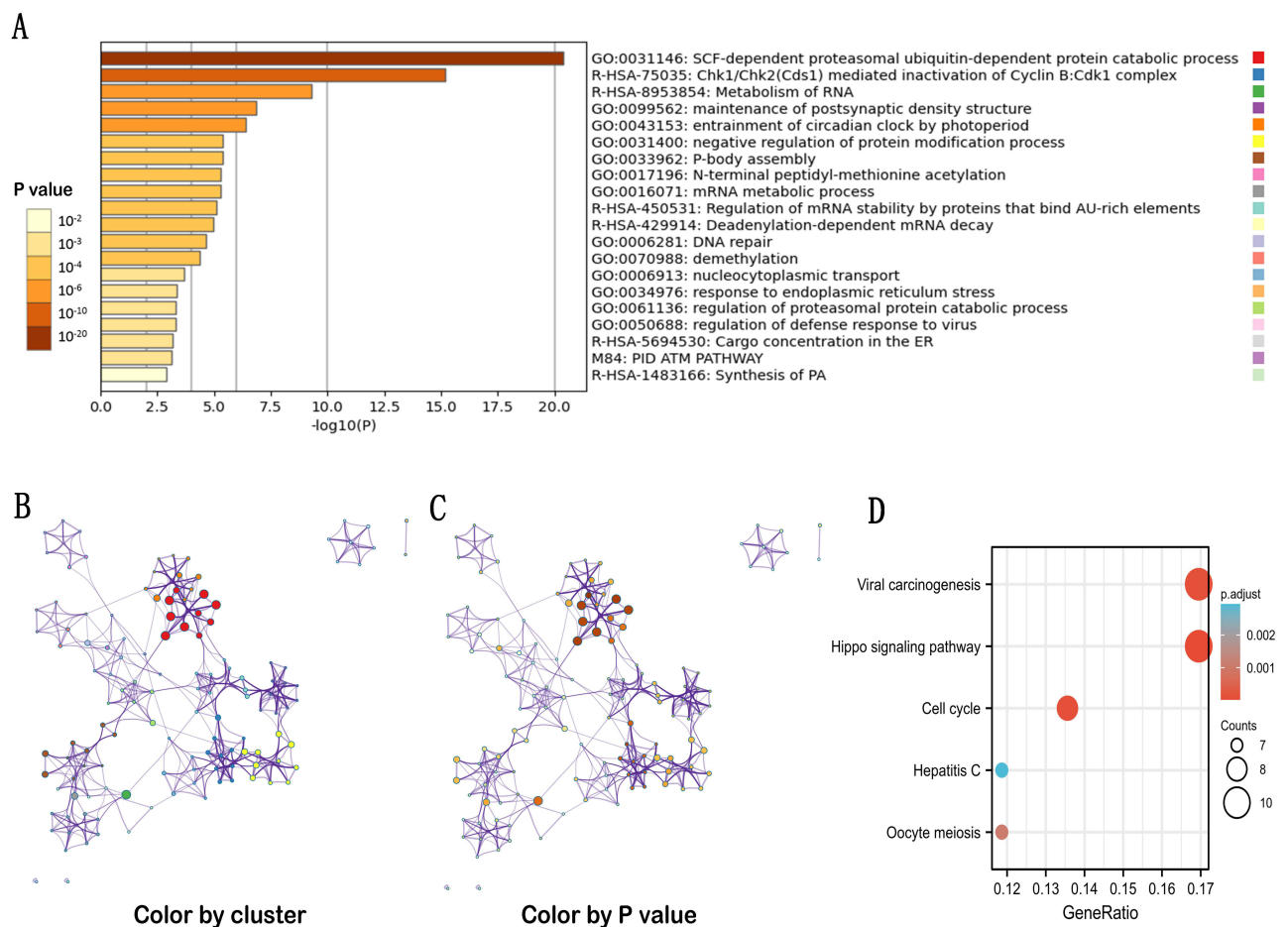


Figure 9 GO and KEGG enrichment analyses of *GNPNATI*. (A) GO enrichment analyses of *GNPNATI*. (B) GO enrichment interactive network colored by cluster-ID (C) and P-value. (D) KEGG enrichment analyses of *GNPNATI*.

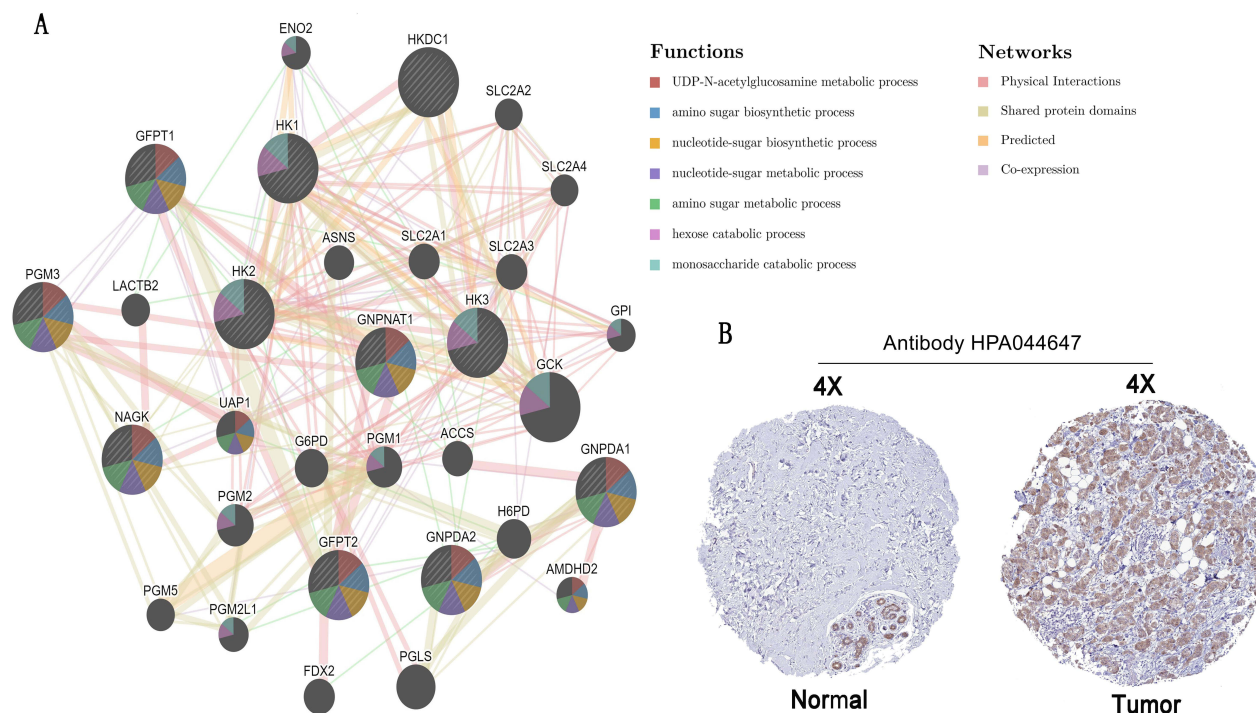


Figure 10 Protein–protein interaction network and IHC slices of *GNPNAT1*. **(A)** Protein–protein interaction network of *GNPNAT1*. **(B)** IHC slices of *GNPNAT1*.

of different changes in the genome, gene expression profiles, and molecular markers.^{4,5} The 5-year overall survival rate of early-stage breast cancer patients was more than 95%, while it was less than 40% in advanced breast cancer patients. Therefore, looking for new effective targets is very necessary for the early diagnosis and treatment of breast cancer.

GNPNAT1 plays a key role in the process of uridine diphosphate-N-acetylglucosamine biosynthesis and glucose metabolism. There were several types of research showing that *GNPNAT1* was connected with the prognostic of prostate cancer and lung adenocarcinoma.^{9–16} In prostate cancer, *GNPNAT1* was expressed higher in castration-resistant prostate cancer.⁹ In lung adenocarcinoma, previous studies indicated the expression level of *GNPNAT1* was not only associated with the survival rate of lung adenocarcinoma but also connected to immune infiltration, including immune cells, chemokines, and immune modulators.^{10–16} However, *GNPNAT1* had never been explored in breast cancer. These reports reminded us that *GNPNAT1* might be a potential oncogene, so we assumed that *GNPNAT1* might be a potential prognosis biomarker of breast cancer and might be associated with the survival rate. In this study, our guess was verified, and our results provide important first-hand information on the prognostic and therapeutic value of *GNPNAT1* in breast cancer.

In this study, we found that *GNPNAT1* was overexpressed in breast cancer, and it was confirmed by our own locally verified cohort. In the next clinical correlation analysis, we found higher expressions of *GNPNAT1* were connected with poor survival. A nomogram was constructed to predict the 1-year, three-year, and five-year survival probability of breast cancer patients.

After GO and KEGG enrichment analysis, we identified several main terms, including viral carcinogenesis, Hippo signaling pathway, cell cycle, and oocyte meiosis. In GSEA analysis, the top four pathways of *GNPNAT1* were Reactome mitotic telophase cytokinesis, wp omega-9 fa synthesis, Reactome cohesin loading chromatin, and Reactome establishment of sister chromatid cohesion. These prompted us that *GNPNAT1* was connected with the defense mechanism of cells, cell proliferation, and division.¹⁷ These four pathways were all enriched in the group of high expression. REACTOME_MITOTIC_TELOPHASE_CYTOKINESIS is a pathway of cytokinesis whose activation would promote cell proliferation. It meant that the overexpression of *GNPNAT1* might promote cell division. The channel of WP OMEGA9 FA SYNTHESIS could control the synthesis of omega-9. Although the function of omega-9 is still unknown in breast cancer. But there were, several reports showed that the tumor cells might acquire energy through fatty acid metabolic pathways rather than glucose metabolic pathways.^{18,19} So, the channel of WP OMEGA9 FA SYNTHESIS might connect with the occurrence of breast tumors. As to REACTOME COHESIN LOADING CHROMATIN and

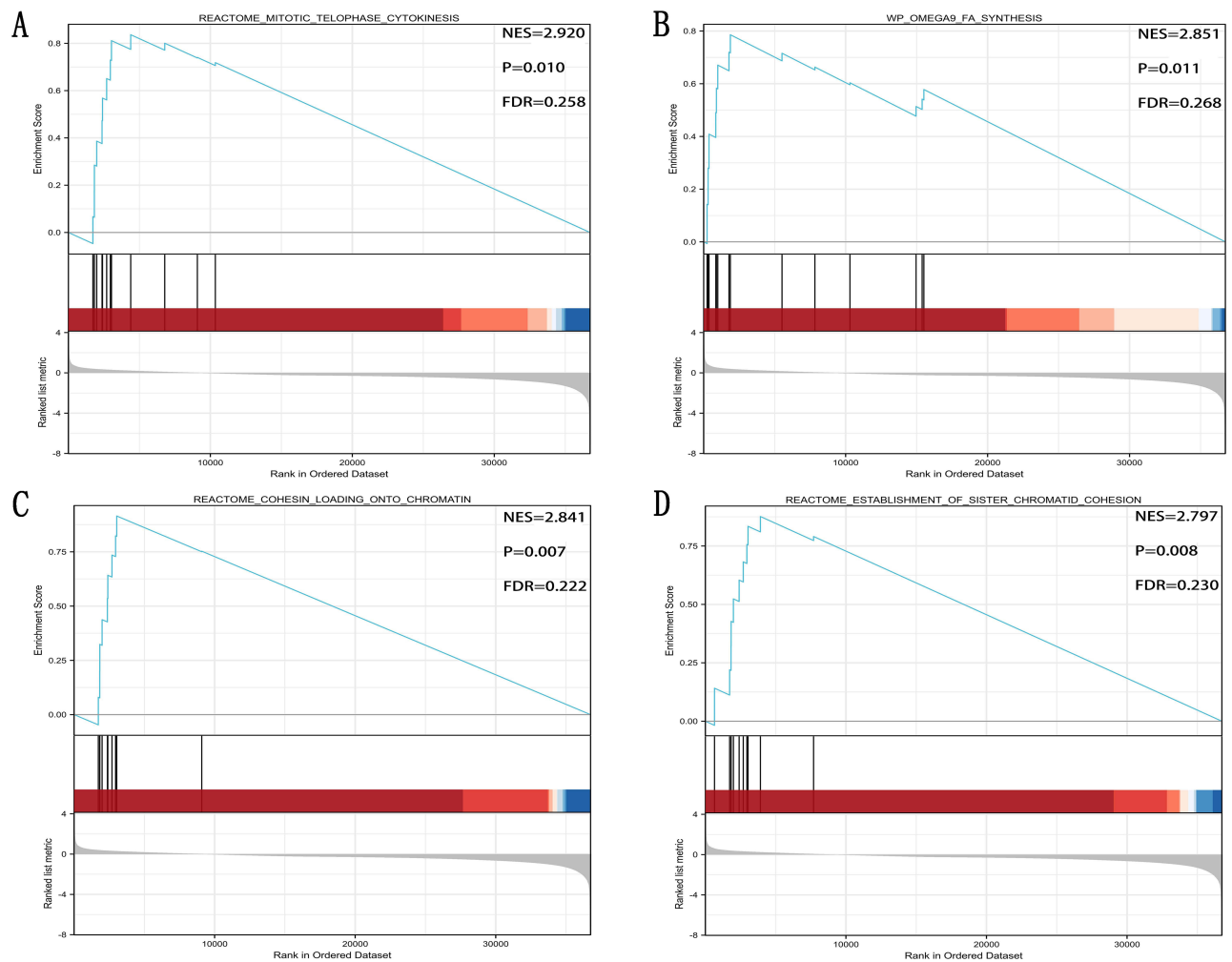


Figure 11 (A) Reactome mitotic telophase cytokinesis, (B) WP OMEGA9 FA synthesis, (C) Reactome cohesion loading chromatin, and (D) Reactome establishment of sister chromatid cohesion were the top four signaling pathways of *GNPNAT1*-related.

REACTOME ESTABLISHMENT OF SISTER CHROMATID COHESION, the acceleration of chromatin also would promote the proliferation of breast cancer. These four pathways of GSEA analysis further verified our hypothesis that *GNPNAT1* was a cancer-promoting gene. Cancer-promoting genes usually promote cell proliferation and division. Therefore, it was further confirmed that *GNPNAT1* might be a potential oncogene.

Immunization therapy is an important, newly developing emerging therapeutic method for breast cancer. The understanding of immunization infiltration is vital for the development of immunization therapy in breast cancer.^{20,21} The higher infiltration levels of B cells and T cells often predict a better prognosis of survival in breast cancer.²² NK cells can kill the target cells to play their immune role by activating caspase-independent pyroptosis.²³ *GNPNAT1* might serve as a diagnostic and prognostic biomarker and a novel target for intervention in BRCA patients in the future.²⁴ In this study, we found that the expression level of *GNPNAT1* was connected with the level of immunization infiltration. TFH, Tem, aDC, NK D56bright cells, Treg, T cells, Neutrophils, Th1 cells, iDC, NK CD56dim cells, B cells, DC, NK cells, Cytotoxic cells, CD8 T cells, and pDC, were negatively connected with the expression level of *GNPNAT1*. Eosinophils, TCM, T helper cells, and Th2 cells were prominently positively connected with the expression level of *GNPNAT1*. In the total 24 subtypes of immunization infiltration cells, high *GNPNAT1* was negatively connected with 16 immunization infiltration cell types and positively connected with 4 immunization infiltration cell types. We could conclude that the expression level was connected with immunization infiltration, and high expression of *GNPNAT1* predicted poor survival in breast cancer.

This study explored the connection between *GNPNATI* and breast cancer and could guide future fundamental experiments. However, there were several disadvantages to this study. Firstly, the main data were downloaded from a public database, so we could not confirm the authenticity and accuracy of the information. Secondly, the number of patients in the local verified cohort was too small; more cases are required to provide more strict results. Lastly, the mechanism of how *GNPNATI* promotes the occurrence and development of breast cancer needed further experiences *in vivo* and *in vitro* to verify. To further investigate the potential mechanism of *GNPNATI*'s action in breast cancer, we plan to do future fundamental experiments before long.

Conclusion

As a whole, our results indicated that *GNPNATI* was up-regulation in primary breast cancer tumors and higher expression of *GNPNATI* was connected with poor survival in breast cancer. Immunization infiltration analysis showed that high *GNPNATI* was negatively connected with 16 immunization infiltration cell types and positively connected with four immunization infiltration cell types. This study showed that *GNPNATI* might be a probable biomarker for diagnosis and prognosis in breast cancer and provide guidance for future fundamental experiments.

Data Sharing Statement

The datasets used and/or analyzed during the current study are available from the corresponding author Yuying Zhou upon reasonable request.

Ethics Approval and Consent to Participate

This study was approved by the Human Research Ethics Committee of the First Affiliated Hospital of Wenzhou Medical University, Wenzhou, China, and complied with the tenets of the Declaration of Helsinki. The ethical approval code is No. 2012-57. Each patient provided written informed consent before being enrolled in the study.

Consent for Publication

The patients issued Written informed consent for the publication of this research and accompanying images. A copy of the written consent is ready for review by the Editor in Chief of this journal.

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Author Contributions

All authors made a significant contribution to the work reported, whether that is in the conception, study design, execution, acquisition of data, analysis, and interpretation, or all these areas; took part in drafting, revising, or critically reviewing the article; giving final approval of the version to be published; agreeing on the journal to which the article has been submitted; and agree to be accountable for all aspects of the work.

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