High SLC17A9 expression correlates with poor survival in gastric carcinoma

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Aim: To elucidate the clinicopathological significance and prognostic value of SLC17A9 expression in gastric carcinoma (GC). **Methods:** SLC17A9 mRNA level and its relationship with TP53 mutation was analyzed. SLC17A9 protein expression was examined by immunohistochemistry in 161 patients. **Results:** SLC17A9 mRNA and protein expression were higher in GC tissues than in adjacent normal tissues ($p < 0.01$). SLC17A9 mRNA expression was higher in GC tissues having mutated TP53 than in tissues with wild-type TP53 ($p < 0.001$). High SLC17A9 expression was also significantly associated with poor overall survival and recurrence-free survival and was also found to be an independent prognostic factor for long-term survival in GC patients. **Conclusion:** Our results show that SLC17A9 may serve as a potential prognostic biomarker in GC patients.

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Gastric carcinoma (GC) is one of the most common and lethal malignant cancers worldwide, especially in Eastern Asia [1,2]. GC imposes huge economic burdens on many families and countries [3]. Although advances in diagnosis and treatment have improved survival rates of patients with early GC [2], there is no effective treatment for patients with advanced GC, including targeted and immunotherapies [4]. Thus, a better understanding of the molecular mechanism of GC development may help us devise new therapeutic strategies and improve the prognosis of GC patients.

SLC17A9 is the fourth SLC17 gene type. It encodes a transmembrane protein involved in the transportation of small molecules [5]. As the first vesicular nucleotide transporter (VNUT), SLC17A9 participates in vesicular uptake, storage and secretion of nucleotides such as ATP and ADP [5–8]. SLC17A9 activity also plays an important role in maintaining lysosomal physiology and cell viability [9]. Recent studies indicate that overexpression of a short SLC17A9 transcript predicts poor survival in adult patients with T-cell acute lymphoblastic leukemia [10]. And SLC17A9 overexpression in colorectal cancer correlates with poor prognosis [11]. Although its specific role remains unclear, the above studies have suggested that SLC17A9 has a significant impact on cancer prognosis. But it is not clear whether high SLC17A9 expression correlates with poor survival in GC. Therefore, we conducted this study to quantify SLC17A9 expression in GC and normal tissues and then to assess its association with patients' prognoses.

First, the present study had evaluated the SLC17A9 mRNA level and its correlation with prognosis in GC using publicly available databases. Second, protein expression of SLC17A9 from our database had been analyzed using immunohistochemical (IHC) staining. Subsequently, correlations between SLC17A9 expression and clinicopathological parameters were analyzed, and the relationship between SLC17A9 and survival was determined. Furthermore, correlation between SLC17A9 mRNA expression and TP53 mutation was mined from publicly available databases, which might be a potential mechanism for SLC17A9 to promote GC formation.

Publicly available databases utilized by the present study are widely used by medical researchers from all over the world, whose results regarding SLC17A9 have been confirmed by this study. Therefore, the findings of this research have practical implications and update our knowledge of the roles of SLC17A9.

Materials & methods

Patient data

Data from 161 patients who received surgical treatment at the First Affiliated Hospital of Sun Yat-sen University (FAHSYSU) between 2004 and 2007 were chosen randomly and their follow-up data were retrospectively collected. Follow-ups were terminated by December 2017. None of the patients received chemotherapy or other treatments before sampling. Patients lost due to lack of compliance during follow-up or with incomplete data were excluded from this study. Clinicopathological characteristics of these patients included gender, age, tumor size, tumor location, Borrmann classification, differentiation, depth of invasion, lymph node metastasis, distant metastasis, clinical stage and carcinoembryonic antigen level. Patients were evaluated according to the recommendations made in the 8th edition of the American Joint Cancer Committee (AJCC) Tumor-Node-Metastasis (TNM) classifications. Another 61 patients who received surgical treatment in 2013 were chosen randomly for tissue microarrays.

Written informed consent was obtained from every patient. Ethical approval for clinical research was obtained from the Institutional Review Board of FAHSYSU.

Tissue microarrays

Paired adjacent normal and GC tissues of 61 patients were obtained from the Department of Pathology, FAHSYSU, and made into tissue microarrays (Servicebio, Wuhan, China) for IHC staining.

IHC staining

Paraffin-embedded GC tissues of 161 patients were obtained from the Department of Pathology, FAHSYSU. IHC staining of these GC tissues, and tissue microarrays, were conducted as described previously [11]. An anti-SLC17A9 antibody (1:200; EMD Millipore, MA, USA) was used for IHC staining.

Evaluation of the IHC-stained slides was performed by two independent investigators who were blinded to the specimens. Results were scored by a semiquantitative method [12]. First, no staining or less than 10% of the tumor cells stained was considered negative (IHC 0). Second, in $\geq 10\%$ of tumor cells, IHC was scored using staining intensity as follows: 1 (weak), 2 (moderate) and 3 (strong). The last, scores of 0 and 1 were defined as low, and scores of 2 and 3 were defined as high SLC17A9 expression.

Bioinformatics analysis

RNASeq data for GC were downloaded from The Cancer Genome Atlas (TCGA) and Oncomine databases (<https://www.oncomine.org/>). The relationship between *SLC17A9* mRNA expression and *TP53* mutation was analyzed via LinkedOmics (<http://www.linkedomics.org/>). The prognostic value of the *SLC17A9* mRNA level was analyzed via the Kaplan–Meier plot (<http://www.kmplot.com/>).

Statistical analyses

SPSS version 17.0 (IBM, IL, USA) was used for data analyses. The relationship between SLC17A9 expression and features of tumor progression was analyzed using the χ^2 square test and Spearman correlation test. Kaplan–Meier survival curves were plotted, and the log-rank test was performed. Univariate and multivariate analyses were performed using the Cox proportional hazards model. The $p < 0.05$ was considered statistically significant.

Results

Higher SLC17A9 expression in GC tissues compared with normal gastric tissues

Data from TCGA were analyzed via UALCAN [13] (<http://ualcan.path.uab.edu/>). The results showed that the *SLC17A9* gene was upregulated in GC tissues compared with normal tissues (Figure 1A). *SLC17A9* mRNA levels in GC tissues ($n = 415$) were higher than those in normal tissues ($n = 34$; $p < 0.001$, Figure 1B). The *SLC17A9* mRNA level was also significantly upregulated with increasing tumor stage ($p < 0.001$, Figure 1C). Analogous results were seen in the Oncomine cohorts (Table 1). We further assessed SLC17A9 protein expression by tissue microarrays with paired adjacent normal and GC tissues of 61 patients. Protein expression of SLC17A9 was

Figure 1. Upregulation of *SLC17A9* in gastric carcinoma. (A) Analysis of TCGA data by a heat map. (B) *SLC17A9* mRNA expression in GC and normal tissues from TCGA database. (C) *SLC17A9* mRNA expression based on tumor stage from TCGA database. (D) Protein expression of *SLC17A9* was significantly higher in GC tissues compared with adjacent normal tissues.

*** $p < 0.001$.

GC: Gastric carcinoma; TCGA: The Cancer Genome Atlas.

significantly higher in GC tissues compared with adjacent normal tissues ($p < 0.001$, Figure 1D). Collectively, these data show that *SLC17A9* expression was upregulated in GC tissues.

Correlations between *SLC17A9* expression & clinicopathological parameters in GC

To explore the association between *SLC17A9* expression and clinicopathologic characteristics in GC, 161 paraffin-embedded GC tissues were examined for *SLC17A9* protein expression using IHC staining. *SLC17A9* was expressed heterogeneously in GC tissues. As shown in Figure 2, the *SLC17A9* proteins of most patients with GC were located in the cytoplasm and cytomembranes of tumor cells. According to *SLC17A9* protein expression in GC tissues as indicated by IHC scoring, there were 24 cases (14.9%) with an IHC score of 0, 52 (32.3%) with an IHC score of 1, 57 (35.4%) with an IHC score of 2 and 28 (17.4%) with an IHC score of 3.

The association between *SLC17A9* expression and clinicopathological variables was determined by the χ^2 square test and Spearman correlation test (Table 2). The constituent ratio between low and high *SLC17A9* expression groups was significantly different in tumor size ($p < 0.05$), depth of invasion ($p < 0.05$), lymph node metastasis

Table 1. Oncomine analysis of *SLC17A9* expression in gastric cancer.

Cohort	Sample (n)	t-test	Fold change	p-value	Ref.
Cui <i>et al.</i>	Gastric cancer (80) vs normal (80)	2.003	1.204	0.023*	[14]
Deng <i>et al.</i>	Diffuse gastric adenocarcinoma (36) vs normal (98)	4.275	1.041	0.000***	[15]
	Gastric adenocarcinoma (63) vs normal (98)	4.574	1.072	0.000***	
	Gastric cancer (42) vs normal (98)	5.049	1.072	0.000***	
	Gastric intestinal type adenocarcinoma (38) vs normal (98)	5.879	1.109	0.000***	
	Gastric mixed adenocarcinoma (11) vs normal (98)	2.990	1.127	0.007**	
TCGA	Diffuse gastric adenocarcinoma (45) vs normal (94)	4.885	1.096	0.000***	
	Gastric adenocarcinoma (173) vs normal (94)	10.689	1.186	0.000***	
	Gastric intestinal type adenocarcinoma (41) vs normal (41)	6.560	1.261	0.000***	
	Gastric tubular adenocarcinoma (31) vs normal (94)	6.601	1.256	0.000***	
	Mucinous gastric adenocarcinoma (12) vs normal (94)	4.003	1.189	0.001**	
Wang <i>et al.</i>	Gastric cancer (12) vs normal (17)	1.765	1.439	0.047*	[16]

*p < 0.05; **p < 0.01; ***p < 0.001.
TCGA: The Cancer Genome Atlas.

($p < 0.01$) and AJCC stage ($p < 0.01$). *SLC17A9* expression in GC tissues was significantly correlated with tumor size ($p < 0.05$), lymph node metastasis ($p < 0.01$) and AJCC cTNM stage ($p < 0.01$).

SLC17A9 overexpression was associated with poor survival in GC

To determine the prognostic value of *SLC17A9* expression in GC, we first analyzed the data via the Kaplan–Meier plot [17]. Patients with a high *SLC17A9* mRNA level had worse overall survival (OS) (Figure 3A) and recurrence-free survival (RFS) (Figure 3B). Second, the prognostic role of *SLC17A9* protein expression was assessed by a Kaplan–Meier method. The follow-up period of the included patients ranged between 2 months and 156 months and the mean survival time of them was 63.5 ± 4.6 months. The mean survival of patients with low expression of *SLC17A9* was 82.8 ± 7.0 months while it was 45.5 ± 5.2 months for those patients with high *SLC17A9* expression. The 5-year OS rate of all patients was 37.1, and 52.1% in the *SLC17A9* low and 23.5% in the high *SLC17A9* expression group. These data indicated that patients with high *SLC17A9* expression had worse OS (Figure 3C) and RFS (Figure 3D) (both $p < 0.001$). Moreover, we determined the prognostic value of *SLC17A9* expression in early (cTNM I and II) and advanced (cTNM III and IV) GC. The results showed that patients with high *SLC17A9* expression had worse OS (Figure 3E) and RFS (Figure 3F) (both $p < 0.01$) in early-stage GC. Low *SLC17A9* expression was not associated with better OS ($p = 0.074$, Figure 3G) but was associated with better RFS ($p < 0.05$, Figure 3H) in advanced GC.

SLC17A9 expression was an independent prognostic factor for GC patient

The effects of *SLC17A9* expression and other clinicopathological variables on GC patients' prognoses were evaluated by univariate and multivariate analysis. The detailed results of the univariate analysis were demonstrated in Tables 3 and 4. The multivariate Cox regression analysis demonstrated *SLC17A9* expression as an independent predictor of OS ($p < 0.05$; Table 3) and RFS ($p < 0.01$; Table 4) in GC patients. In summary, we proved that *SLC17A9* expression could serve as a molecular marker to independently predict GC patients' prognoses.

The relationship between *SLC17A9* mRNA expression & *TP53* mutation in GC

LinkedOmics data [18] showed that *SLC17A9* mRNA expression was significantly associated with many gene mutations. As shown in Figure 4A, the expression of *SLC17A9* mRNA correlated positively with mutated *TP53*. *SLC17A9* mRNA levels in GC tissues with mutated *TP53* were higher than those with wild-type *TP53* ($p < 0.001$, Figure 4B). These results were from publicly available databases which were real world databases and were widely used in medical research. So, these results had practical implications.

Discussion

Our study demonstrates that high *SLC17A9* expression is significantly associated with poor prognosis and its expression may serve as a biomarker for the prognosis of patients with GC. First, we assessed the *SLC17A9* mRNA level from data in the TCGA and Oncomine database. The results indicated that the *SLC17A9* mRNA level was

Table 2. Correlations between SLC17A9 expression and clinicopathologic parameters of 161 gastric carcinoma patients.

Characteristics	n	SLC17A9 Expression		χ^2	p-value	ρ^{***}	p-value
		Low (n = 76)	High (n = 85)				
Age		57.75 $\pm$ 12.17	57.89 $\pm$ 11.86				
<60 years	85 (52.8%)	43 (26.7%)	42 (26.1%)	0.827	0.363	0.072	0.366
$\geq$ 60 years	76 (47.2%)	33 (20.5%)	43 (26.7%)				
Gender							
Males	105 (65.2%)	49 (30.4%)	56 (34.8%)	0.035	0.851	-0.015	0.853
Females	56 (34.8%)	27 (16.8%)	29 (18.0%)				
Tumor location							
Proximal	35 (21.7%)	17 (10.6%)	18 (11.2%)	2.118	0.548	0.071	0.368
Middle	31 (19.3%)	18 (11.2%)	13 (8.1%)				
Distal	58 (36.0%)	25 (15.5%)	33 (20.5%)				
More than 2	37 (23.0%)	16 (9.9%)	21 (13.0%)				
Tumor size							
<5 cm	74 (46.0%)	43 (26.7%)	31 (19.3%)	6.532	0.011*	0.201	0.01*
$\geq$ 5 cm	87 (54.0%)	33 (20.5%)	54 (33.5%)				
Histologic type							
Other adenocarcinoma	137 (85.1%)	66 (41.0%)	71 (44.1%)	1.777	0.620	0.043	0.590
Signet ring	10 (8.1%)	4 (3.1%)	6 (5.0%)				
Mucinous	13 (6.2%)	5 (2.5%)	8 (3.7%)				
Undifferentiated	1(0.6%)	1(0.6%)	0 (0)				
Bornmann classification							
I	8 (5.0%)	3 (1.9%)	5 (3.1%)	7.541	0.057	0.064	0.421
II	32 (19.9%)	21 (13.0%)	11 (6.8%)				
III	102 (63.4%)	41 (25.5%)	61 (37.9%)				
IV	19 (11.8%)	11 (6.8%)	8 (5.0%)				
Differentiation							
Well	4 (2.5%)	3 (1.9%)	1 (0.6%)	1.502	0.472	0.067	0.397
Moderate	36 (22.4%)	18 (11.2%)	18 (11.2%)				
Poor	121 (75.2%)	55 (34.2%)	66 (41.0%)				
Depth of invasion							
T1	15 (9.3%)	8 (5.0%)	7 (4.3%)	11.032	0.012*	0.153	0.053
T2	15 (9.3%)	13 (8.1%)	2 (1.2%)				
T3	88 (54.7%)	37 (23.0%)	51 (31.7%)				
T4	43 (26.7%)	18 (11.2%)	25 (15.5%)				
Lymph node metastasis							
N0	50 (31.1%)	33 (20.5%)	17 (10.6%)	12.617	0.006**	0.225	0.004**
N1	51 (31.7%)	22 (13.7%)	29 (18.0%)				
N2	24 (14.9%)	6 (3.7%)	18 (11.2%)				
N3	36 (22.4%)	15 (9.3%)	21 (13.0%)				
Distant metastases							
M0	129 (80.1%)	65 (40.4%)	64 (39.8%)	2.638	0.104	0.128	0.106
M1	32 (19.9%)	11 (6.8%)	21 (13.0%)				
AJCC cTNM							
I+II	53 (32.9%)	35 (21.7%)	18 (11.2%)	12.244	0.001**	0.264	0.001**
III+IV	108 (67.1%)	41 (25.5%)	67 (41.6%)				
CEA level (μg/l)							
<5	142 (88.2%)	69 (42.9%)	73 (45.3%)	0.928	0.335	0.076	0.338
$\geq$ 5	19 (11.8%)	7 (4.3%)	12 (7.5%)				

*p < 0.05; **p < 0.01; ***p < Spearman's rank correlation coefficient.
CEA: Carcinoembryonic antigen; GC: Gastric carcinoma.

Figure 2. Immunohistochemical analysis of SLC17A9 protein expression in gastric carcinoma and adjacent normal tissues. IHC staining of (A) the SLC17A9 protein in GC tissues and (B) adjacent normal tissues. GC: Gastric carcinoma; IHC: Immunohistochemistry.

significantly higher in GC than in normal tissues. Interestingly, the expression of *SLC17A9* mRNA correlated positively with *TP53* mutation. Second, we explored whether the expression of *SLC17A9* mRNA was related to a poor prognosis. The results from the Kaplan–Meier plot showed that patients with high *SLC17A9* mRNA expression had worse OS and RFS. Third, tissue microarrays for 61 patients showed that SLC17A9 protein expression was significantly higher in GC than in adjacent normal tissues. Furthermore, we performed IHC staining and analyzed the relationship between SLC17A9 expression and prognosis in 161 GC patients. The results were the same as that of the bioinformatics analysis. Finally, the multivariate Cox regression analysis demonstrated SLC17A9 expression as an independent prognostic factor of both OS and RFS in GC patients.

SLC17A9 is the fourth *SLC17* gene [5]. These genes are expressed widely in various organs such as the brain, and adrenal and thyroid glands [8]. The SLC17A9 protein is a VNUT that participates in transporting nucleotides [8]. As a VNUT, the SLC17A9 protein plays an important role in transporting ATP in airway neutrophils as well as

Figure 3. Gastric carcinoma patients overexpressing SLC17A9 have a poor prognosis. Kaplan–Meier plotter (A) OS and (B) RFS curves for GC patients with low and high SLC17A9 mRNA levels. GC patients with high SLC17A9 expression have worse (C) OS and (D) RFS than those with low SLC17A9 expression. Patients with high SLC17A9 expression have worse (E) OS and (F) RFS in early GC (cTNM I and II). (G) There is no significant difference in OS between the high and low SLC17A9 expression groups. (H) Patients with high SLC17A9 expression have worse RFS in advanced GC (cTNM III).
 cTNM: clinical tumor-node-metastasis; GC: Gastric carcinoma; HR: Hazard ratio; OS: Overall survival; RFS: Recurrence-free survival.

Figure 4. Relationship between *SLC17A9* mRNA expression and *TP53* mutation. (A) Volcano plot of the relationship between *SLC17A9* mRNA expression and multiple gene mutations. (B) *SLC17A9* mRNA expression in wild-type and mutant *TP53* GC.

*** $p < 0.001$.

GC: Gastric carcinoma.

Table 3. Cox proportional-hazard regression analysis for overall survival.

Characteristic	Univariate analysis				Multivariate analysis			
	p-value	HR	95.0% CI for Exp (B)		p-value	HR	95.0% CI for Exp (B)	
			Lower	Upper			Lower	Upper
Gender	0.022*	1.544	1.064	2.241				
Age	0.268	0.816	0.570	1.169				
Tumor location	0.730	1.032	0.865	1.230				
Tumor size	0.000***	2.088	1.442	3.025				
Histologic type	0.658	1.043	0.865	1.258				
Bornmann classification	0.006**	1.465	1.117	1.922	0.023*	1.453	1.052	2.008
Differentiation	0.011*	1.682	1.125	2.516				
Depth of invasion	0.000***	1.750	1.378	2.222				
Lymph node metastasis	0.000***	1.498	1.280	1.753				
Distant metastases	0.000***	3.763	2.466	5.742				
AJCC cTNM	0.000***	2.086	1.675	2.599				
CEA	0.028*	1.786	1.066	2.993				
SLC17A9 expression	0.000***	2.163	1.490	3.141	0.021*	1.622	1.077	2.444

*p < 0.05; **p < 0.01; ***p < 0.001.

AJCC: American Joint Cancer Committee; CEA: Carcinoembryonic antigen; cTNM: clinical tumor-node-metastasis; GC: Gastric carcinoma; HR: Hazard ratio.

Table 4. Cox proportional-hazard regression analysis for recurrence free survival.

Characteristic	Univariate analysis				Multivariate analysis			
	p-value	HR	95.0% CI for Exp (B)		p-value	HR	95.0% CI for Exp (B)	
			Lower	Upper			Lower	Upper
Gender	0.126	1.461	0.899	2.375				
Age	0.974	0.992	0.627	1.571				
Tumor location	0.639	0.948	0.759	1.184				
Tumor size	0.019*	1.740	1.097	2.760				
Histologic type	0.585	1.068	0.844	1.351				
Bornmann classification	0.003**	1.716	1.207	2.440	0.005**	1.847	1.208	2.822
Differentiation	0.053	1.606	0.993	2.595				
Depth of invasion	0.006**	1.483	1.118	1.968				
Lymph node metastasis	0.057	1.241	0.993	1.551				
AJCC cTNM	0.001**	1.737	1.251	2.412				
CEA	0.328	1.476	0.676	3.220				
SLC17A9 expression	0.000***	2.618	1.622	4.227	0.001**	2.348	1.393	3.958

*p < 0.05; **p < 0.01; ***p < 0.001.

AJCC: American Joint Cancer Committee; CEA: Carcinoembryonic antigen; GC: Gastric carcinoma; HR: Hazard ratio.

epithelial, astrocyte, adrenal chromaffin and pancreatic cells [6–8,19,20]. Cao *et al.* [9] have shown that SLC17A9 functions as a lysosomal ATP transporter and maintains cell viability.

These studies indicate that the SLC17A9 protein plays an important physiological role in many cells. Conversely, abnormal expression of SLC17A9 can lead to disease. For example, functional abnormalities of the SLC17A9 protein are related to disseminated superficial actinic porokeratosis [21]. An aberrantly overexpressed short mRNA transcript of the *SLC17A9* gene is present in most cases of T-cell acute lymphoblastic leukemia, predicting a poor prognosis in adults [10]. Some studies revealed that SLC17A9-deficient cells exhibited lysosome dysfunction and underwent cell death [9]. Furthermore, SLC17A9 knockdown can decrease cell migration in human lung cancer cells [22]. A recent study indicated that SLC17A9 overexpression in colorectal cancer correlated with poor prognosis [11]. It was proven that high SLC17A9 expression heralded poor prognoses of GC patients which deepened our understanding of the initiation and progression of GC.

We also found that high expression of SLC17A9 in GC tissues was related to a greater tumor size, depth of invasion, lymph node metastasis and AJCC cTNM stage. However, the impact of SLC17A9 on GC, and

its mechanisms, was not examined, which is a limitation of this study. The SLC17A9 protein functions as an ATP transporter and regulates cell viability [11]. Because ATP is involved in various tumor cell metabolic processes, especially glycolysis [23] that is critical for sustaining cancer cell proliferation and aggressiveness [24,25], we extrapolate that upregulating SLC17A9 expression promotes the proliferation and invasion abilities of GC cells by enhancing glycolysis.

The SLC17A9 protein is associated with cell migration, and SLC17A9 knockdown decreases cell migration in human lung cancer cells [22]. The VNUT is responsible for vesicular ATP release and neutrophil migration [20]. Also, microglial migration is mediated by ATP release from lysosomes [26]. Based on these findings, we infer that SLC17A9 overexpression may increase the metastatic ability of GC cells. The above studies indicated that SLC17A9 played an important role in the storage, transportation and release of ATP. Moreover, as a post-translational modification, ubiquitination is an ATP-dependent process sequentially mediated by three enzymes [27,28] and supports aberrant oncogenic signaling for survival and metastasis [29]. According to these studies, SLC17A9 may affect tumor cell survival by modulating ubiquitination. Importantly, we discovered that *SLC17A9* mRNA expression correlated positively with *TP53* mutation in GC. *TP53* is a tumor suppressor gene and its mutation plays an important role in the development and progression of many cancers, including GC [30]. And P53 degradation is regulated via the ubiquitin–proteasome system [27]. Therefore, it is worth for further research to explore the mechanism of SLC17A9 in GC and its relationship with *TP53* mutations.

Conclusion

Taken together, our results show that high SLC17A9 expression indicates a poor prognosis in GC patients. Thus, SLC17A9 might serve as an independent prognostic factor for GC patients.

Summary points

- SLC17A9 was overexpressed in gastric carcinoma (GC) tissues compared with adjacent normal tissues.
- High SLC17A9 expression indicates poor overall survival and recurrence-free survival in GC patients.
- SLC17A9 expression is an independent predictor of overall survival and recurrence-free survival in GC patients.
- High SLC17A9 expression may be a valuable independent biomarker to predict poor prognosis for GC patients.
- *SLC17A9* mRNA expression correlates positively with *TP53* mutation.

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Financial & competing interests disclosure

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Ethical conduct of research

Ethical approval was obtained by the First Affiliated Hospital, Sun Yat-sen University and the authors have followed the principles outlined in the Declaration of Helsinki for all human or animal experimental investigations. In addition, for investigations involving human subjects, informed consent has been obtained from the participants involved.

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